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dst^2

Development of structurally detailed statistically testable models of marine populations

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Consolidated Progress Report: 1 January 2001 to 31 December 2001

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Co-ordinator:

Dr. G. Stefánsson
Marine Research Institute
PO Box 1390
Skúlagata 4
Reykjavík
Iceland

Phone: +354 552 0240
Fax: +354 562 3790
email: gunnar@hafro.is

Participants:

1	Co-ordinator:	Marine Research Institute, Reykjavík, Iceland	MRI
2	Contractor:	Institute of Marine Research, Bergen, Norway	IMR
3	Contractor:	Danish Institute for Fisheries Research, Charlottenlund, Denmark	DIFRES
4	Contractor:	Science Institute, University of Iceland	SCUI
5	Contractor:	University of Bergen, Norway	UiB
6	Contractor:	Fisheries Research Services, Aberdeen, UK	FRS
7	Contractor:	The Centre for Environment, Fisheries and Aquaculture Science, Lowestoft, UK	CEFAS
8	Contractor:	Institut Francais de Recherche pour l'Exploitation de la Mer, Nantes, France	IFREMER

Project summary

Report structure

This second dst^2 progress report is structured in exactly the same manner as the first report, i.e. separated into this summary, a short description of the status of each workpackage and a collection of documents describing in more detail progress on individual components of each workpackage. The summary is intended to provide an overview, with an emphasis on the status of each deliverable, milestone etc.

It is quite noticable in this second report, that there have been staffing problems at the MRI and FRS, leading to delays in a few deliverables. As seen in this summary, however, this is not a large fraction of the total and some other deliverables are ahead of schedule. In addition it should be noted that the staffing issues were solved at the MRI mid-year 2001 and at FRS in January 2002. Thus it is envisaged that these delays, though somewhat inconvenient, will not affect the project as a whole.

The workpackages are in 5 groups:

Number	WP group	Workpackages
1	Data warehouse	1.1-1.7
2	Structural models/programming	2.1-2.4
3	Estimation and inference w/programming	3.1-3.2
4	Estimation of parameters outside program	4.1-4.3
5	Case studies	5.1-5.3

Following these short summary subsections, the following sections summarise the current state of work for each workpackage. Within each workpackage status description, “time to completion of workpackage” refers to the current estimate of total time left to completing the package, i.e. from 1. January, 2002. Each workpackage also contains an estimate of the amount of time initially intended for the workpackage along with the current estimate of time allotted to it, to date. Further, each workpackage lists the status of all deliverables in some detail.

Several annexes are included with this report. These annexes describe completed, current or planned work relating to the workpackages in somewhat more detail than the relatively short report body.

The numbering convention in this report is taken from the first report, including slight changes in numbering of deliverables and WPs from the original Technical Annex.

Status of project as a whole

Data bases (WP 1)

The data for implementing the models will be set up in the form of a data warehouse. All important aspects of development of the data warehouse are proceeding as planned. Thus, initial data descriptions are available; XML and CORBA approaches have been tested; initial data sets are available on schedule and the main components of the data warehouse are now defined.

As last year, items behind schedule in this group of tasks are the validation of the MRI data base and CORBA testing. This is in both cases due to lack of manpower and will simply proceed at a slower pace than originally envisioned. As described in workpackage group 1, this has no effect on other parts of the project. Since DIFRES has been able to design and implement components of the data warehouse without reference to CORBA, this delay has not impeded the project as a whole either. On the positive side, new staff members have been added to the

MRI group and work has proceeded at a considerably faster pace, starting mid-year 2001.

Models (WP 2 and 3)

Only few model components are due at this time, but for the most part these are ahead of schedule. For instance, models for growth increments and proposals for process error implementations are now being tested using novel methods.

Earlier lagging items such as the formal definition of the model in state-space form have now been completed for the single-species case.

Computer program (WP 2 and 3)

The model is being implemented as a computer program, Gadget, combining mathematical models of the biology with statistical estimation techniques. As intended, the beta stage of Gadget was distributed to members as version 1.0.00 in June, 2001, whereas the current version is 1.0.03. This version includes parallel computing and a considerably updated growth model.

Programming is thus still largely on or ahead of schedule.

As noted in the first project report, it is envisaged that more issues need to be addressed in the program than anticipated in the Technical Annex. Of these, special programs have been specially developed for investigating sensitivity of solutions to perturbation in the parameter space, etc.

Status of objectives

The 4 primary objectives driving the current project were described in the technical annex and are summarised here for clarity.

Objective 1 of the project is to collect relevant data and to provide objective means of analysing these. The intention is to assemble relevant data in a highly-disaggregated form in a database format which is designed to hold many different classes of data but which can provide summarised data extractions in a format amenable to the analytic routines.

Work towards this objective was the main effort during the first year of the project and has proceeded during the second year. Fulfilling the objective includes database programming and design as well as organising data.

Objective 2 is to validate present estimates of the stock sizes, exploitation histories and the associated uncertainties for a number of case studies, using statistically appropriate models that include detailed descriptions of growth, migration and predation.

As noted in the first project report, although most of the project is aimed towards this objective in the longer term, work directly on this will not commence until much later in the project. Any evaluation on how this objective is being met must wait until the third year of the project or so.

Current work in this context focuses on the development of statistical models. In particular, this involves development of appropriate likelihoods and methods for comparing them.

Objective 3 is to evaluate whether, when and how increased complexity in models enhances the ability to provide management advice in: (a) Advising on effects of closed area restrictions (b) Advising on the state of the stocks and annual catch forecasts (c) Advising on small-scale fishery effects such as local depletion of forage species.

This objective will only become the focus of work in the last two years of the project. In the meantime, however, several approaches to evaluating appropriate model complexity have been and will be investigated. It is fairly well known that effects of some model components can be quite confounded and thus the corresponding parameters poorly determined. Current work at MRI focuses on identifying such confounding and investigating precisely what the effects of the various parameters is on all model components as well as on all likelihood components. This is a prerequisite for evaluating the adequacy and estimability of complex models, since it has been found that chasing too many parameters can and will lead to spurious estimates when the data inadequately determines the model as a whole. This is obvious in simple models but the effects can be quite surprising in models of the form considered here.

Objective 4 is to evaluate and validate some current perceptions of limit reference points for safe exploitation of key resources, using models which take spatial concerns and multispecies interactions into account. Current stock management advice is based on comparison of population parameters with biological reference points that are all evaluated on an aggregate-model, single-species basis. The objective will be met when a comparison of the consequences of stock management based on simple-model advice and management based on detailed-model advice has been drawn for at least one case study.

Although work on this objective was not due to start until 2002, Annex D.8 describes work now completed (and initial work was also reported upon in the report for 2000). It is seen that the work has already resulted in some suggestions on how to proceed with multispecies reference points.

Status of deliverables

A deliverable indicates completion of a specific piece of code, evaluation of methods, completion of data sets or test runs etc. Details on the completion of deliverables is indicated within each workpackage, a summary is provided in the following table.

Due year	Due now	Completed	In normal progress	Lagging	Total
2000-2001	24	16		8	24
2002-2003	0	4	27		31
Total	24	20	27	8	55
%	44	36	49	15	

It is seen that 15% of the deliverables are somewhat behind schedule. The extent of this varies from a few months delay to complete rescheduling, as detailed elsewhere. However, it is also seen that 85% of all deliverables are in normal progress or completed.

Further summary tables describing the state of deliverables according to their due date and completion status is given in Annex A

Status of milestones

Milestones refer to completion of major tasks within the project. The milestones for dst^2 are:

M1: Table definitions. Complete definitions are available for all tables to be seen in the final data warehouse. This is a prerequisite for programming the data warehouse.

These definitions are now complete for all the fundamental data to be put into the data warehouse. This includes all current data sets used in fish stock assessments, along with biological samples which refer to regular single-species research.

Not included in this first round are the data on stomach contents and from acoustic surveys. Handling of these is postponed until later in the project.

M2: Data entry for the case studies completed. This is a prerequisite for loading the data warehouse.

For all case studies a minimum of a prototype data set is currently available, enabling development and testing for all case studies. Naturally, some debugging of tools and further data validation will continue into the third year of the project. It is envisaged that initial loading of the data warehouse(s) will take place in 2002.

M3: Prototype structural elements and inference tools defined and programmed. This is a prerequisite for being able to test some of the detailed models.

This milestone, due at the end of 2002 will most likely be reached on time. Thus, maximum likelihood estimation can be undertaken on parallel computer architectures in order to make the largest models feasible. Prototypes of most biological component models are available but a few modules need more developement from the present rather rough stage.

It is envisaged that the model will continue to be developed interactively as the case studies proceed, but the prototype is almost complete.

M4: Prototypes implemented for the case studies and developed further.

Due, end of 2002, several prototypes are complete and are being developed further. Others are in their earlier stages but are developing.

The remaining milestones are to be reached later in the project.

M5: Appropriate parameterization for case-study models chosen by statistical hypothesis-testing. In particular this implies that model fitting procedures are available.

This milestone is due at the end of 2003. Prototype model fitting procedures are available but likelihood functions need to be further developed in accordance with results from goodness-of-fit tests which indicate traditional probability distributions for fisheries data to be seriously invalidated.

M6: Evaluation of implications of new models compared with simpler models completed.

This milestone is due at the end of 2003. Initial tests indicate that this will require the full length of time indicated, since this is a very complex issue indeed. Basically, this refers to comparing models where the likelihood function is a composite of many individual components, which is a non-trivial statistical problem. To add to the confusion, issues such as how to weight individual components are still unsolved. Approaches to this are being developed (see Annex to the first report and Annex D.2)

The time table for the project as a whole, including milestones, is given in Fig. 1. It is seen that milestones, M1 and M2, were due in 2000-2001 and both are considered complete, though the data entered being in prototype form and certainly requiring further editing.

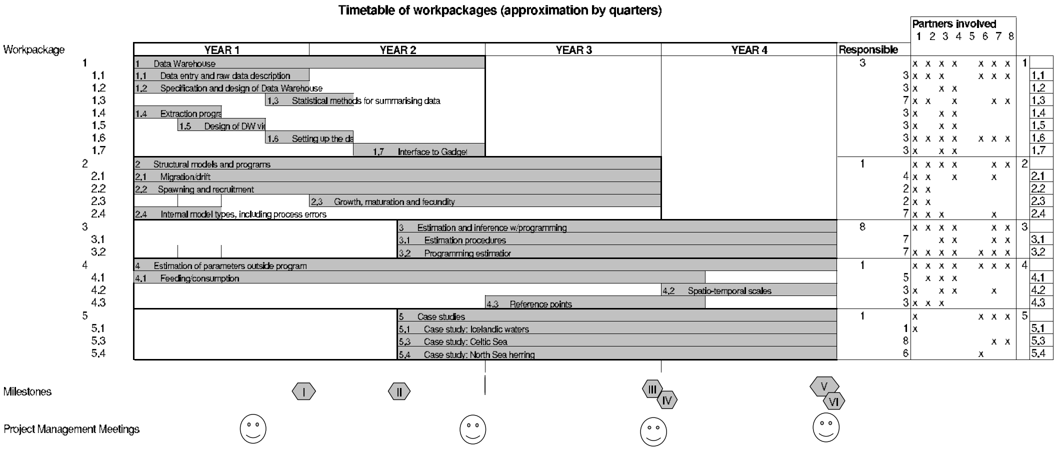


Figure 1: Time table

Contents

1 Workpackage group: Data warehouse

1.1 Workpackage: Data entry and raw data description

Start date or starting event: February 2000

N^o of the partner responsible: 3

N^{o}s of other partners involved: 1,2,6,7,8

Table 1: Person-months by partner on within workpackage

Partner	1	2	3	4	5	6	7	8
2000	24	1	0	0	.	12.6	0	0.0
2001	35	0	0.7		.	0.0	2	0.5
Total to date	59	1	0.7	?		12.6	2	0.5
Total planned	120	2	6	3	.	14.0	3	0.5

Time to completion of workpackage (current estimate): 24

Objectives

To enter, correct and document raw data in the institutional data bases in order to have the foundations required for compiling the data warehouse.

To create the basis for the data warehouse

Description of work conducted to date

As noted in the first dst^2, the main point and most important part of this workpackage is to “get the raw data in order” so as to enable its inclusion in the various data warehouses. This workpackage is largely complete except for MRI which has undertaken a greater task under this item in terms of revision of the institutional data base.

MRI (1):
Work is ongoing towards Deliverable D1.1.1 with established testing procedures developed, as reported earlier, A description of the existing database is available at the MRI website, http://www.hafro.is (in Icelandic).

IMR (2):
Norwegian herring catch and survey data for 1991 - 1998 have been assembled, and were sent to Aberdeen for inclusion in the DW in early February 2001. (D1.1.2)

DIFRES (3):
An important main point in 2001 was to test the exchange format and the data warehouse upload program with real data from the raw databases. Test data for the North Sea herring database was extracted from the raw database into the exchange format and used for the testing. The tests showed that data can be extracted successfully from the raw database into the exchange formats, and then uploaded to the data warehouse using the Internet based upload program.

Data from the Danish raw database was extracted and send to the North Sea herring database. The data were exchanged in the DST2 exchange format.

FRS (6):

The composition of the North Sea Herring Data Base has been agreed and the data acquired as described in the first dst^2 report.

CEFAS (7):
As-yet unpublished stomach contents data were collected from stations throughout the Celtic Sea during the annual spring groundfish surveys of 1991-1994. Extensive data are available for mackerel (1979, 1986) and qualitative data are available for most demersal species. 3314 records (for cod, haddock, hake, whiting, megrim, monkfish, plaice and sole) have been computerised, and efforts to enter data for pelagic species (mackerel, blue whiting and horse mackerel) will continue throughout 2002.

IFREMER (8):
In addition to basic French data for the Celtic Sea collated and reported earlier, original stomach sampling data for the Celtic sea has finally been located. The data, collected between 1977 and 1985, has been published in summarised form (du Buit 1982, 1992, 1995ab, Du Buit & Merlinat 1987) but unfortunately only raw data records exist on paper. Further funds will be found in 2002 in order to computerise the raw stomach data.

du Buit, M.-H. (1982) Essai d'évaluation de la prédation de quelques téléostéens en Mer Celtique. J. Cons. int. Explor. Mer, 40: 37-46.
du Buit, M.-H. (1992) Alimentation de la Cardine,Lepidorhombus whiffiagonis en Mer Celtique. Cah. Biol. Mar. 33: 501-514.
du Buit, M.-H. (1995a) Food and feeding of cod (Gadus morhua L.) in the Celtic Sea. Fisheries Research 22: 227-241.
du Buit, M.-H. (1995b) Diet of hake (Merluccius merluccius.) in the Celtic Sea. Fisheries Research 28: 381-394.
du Buit, M.-H. & Merlinat, F. (1987) Alimentation du merlan Merlangius merlangus L. en Mer Celtique. Rev. Trav. Inst. Pêches marit. 49: 5-12.

Deliverables

The outcome of this work will be corrected databases containing the raw data which form the bases for the data summaries used in the data warehouses.

D1.1.1: Corrected, documented data base for Icelandic waters. Q5

D1.1.2: Corrected, documented data base for North Sea herring. Q5

D1.1.4: Corrected, documented prototype data base for the Celtic Sea. Q5

Milestones and expected results

This is work towards milestone M2.

1.2 Workpackage: Specification and design of Data Warehouse

Start date or starting event: February, 2000

N^o of the partner responsible: 3

N^{o}s of other partners involved: 1, 4

Time to completion of workpackage (current estimate): 0

Summary: This work package is considered complete. Thus, a DW has been specified and designed, though a CORBA solution has not been implemented yet. CORBA development will continue as a part of other WPs. No doubt there will be some revisions to the design during the remainder of the project, but these are expected to be minor.

Table 2: Person-months by partner within workpackage

Partner	1	2	3	4	5	6	7	8
2000	2	.	2	1.5	.	.	.	.
2001	3	.	8.8		.	.	.	.
Total to date	5	.	10.8		.	.	.	.
Total planned	5	.	11	12	.	.	.	.

Objectives

To design coordinated modules and structures of the DW along with programs for import and export.

Description of work conducted to date

DIFRES has had the lead on this workpackage with considerable input from all participating organisations, much of which was obtained during two plenary meetings in 2000, one in 2001 and through electronic communication.

An overall systems architecture has been agreed upon as reported in the first dst^2 report.

DIFRES (3):
The exchange format and the database design was presented and discussed at the annual DST2 meeting in June 2001. Some minor additions and changes of the DW design were suggested. The design of the common DW design and the exchange format was approved at the meeting, and will be evaluated again, when the system is set up for the Icelandic waters DW (Q8-9) . The extraction and aggregation of raw data from institutional databases are left to the institutions themselves.

Deliverables

D1.2.1: DW design. Q5 **Complete**

Milestones and expected results

This is work towards milestone M1.

1.3 Workpackage: Statistical methods for summarising data

Start date or starting event: October, 2000

N^o of the partner responsible: 7

N^{o}s of other partners involved: 1, 2, 4, 8

Table 3: Person-months by partner within workpackage

Partner	1	2	3	4	5	6	7	8
2000	2	0	.	0	.	.	0	0.5
2001	3	0	.	0	.	.	0	0.0
Total to date	5	0	.	0	.	.	0	0.5
Total planned	6	3	.	3	.	.	2	0.5

Time to completion of workpackage (current estimate): 0

Summary: This work package is considered complete. Partners involved have set up methods for summarising data from the original scale of individual measurements to DW summaries, usually through simple addition. It has, however, been shown (Annex D.1), that, though usable, the statistical basis for these may not be ideal, but proposals for revised techniques are not available yet due to the complexity involved.

Objectives

To define the computational methods to be used when computing the summary tables to be used in the data warehouses.

Description of work conducted to date

Work on this workpackage towards deliverable D1.3.1 started at MRI and IFREMER, as reported earlier.

MRI 1
Work in 2001 concentrated on statistical procedures for the analysis of length distributions (Annex D.1). This has indicated possible likelihood functions and also indicated that some short-cuts towards data summaries may be available. Formal likelihood function estimation of aggregated length distributions are, however too complex for inclusion in data extraction routines. The extraction phase is therefore left in the form of summation, allowing the possibility of later modifications to either the extraction phase (from the databases into the DW) or the subsequent aggregation for presentation from the DW.

CEFAS (7) and IFREMER (8)
In order that French and UK (England and Wales) landings data for the Celtic Sea could be combined, sumarised and circulated among dst2 partners, it was necessary (for legal reasons) to eliminate all data in which individual vessels could be identified. French and UK landings records were categoriesd by vessel size (3 categories) and gear (9 categories), and new ‘dst2’ identifiers were appended to each entry in the database. Summary tables containing the number of vessels or fishing ’sequences’ falling into each of these categories were then produced and compared (E.2).

Deliverables

D1.3.1: Algorithms and a set of SQL programs to be used for taking the raw data and converting the data into summaries useful for ecosystem modelling. Q7 **Complete**

Milestones and expected results

This is work towards milestone M2.

1.4 Workpackage: Extraction programs (prototypes)

Start date or starting event: February, 2000

N^o of the partner responsible: 3

N^{o}s of other partners involved: 1, 4

Summary: This work package is considered complete. Thus, prototype programs of some form are available to extract data from data bases and case studies have been able to convert these to Gadget input files. This WP was reported on in the first dst^2 report.

Time to completion of workpackage (current estimate): 0

Objectives

To define and write prototype programs to extract data from raw data bases into data warehouse tables and Gadget data files.

Deliverables

Table 4: Person-months by partner within workpackage

Partner	1	2	3	4	5	6	7	8
2000	5	.	1	3	.	.	.	
2001	0	.	0.5	?	.	.	.	
Total to date	5	.	1.5	1	.	.	.	
Total planned	5	.	8	3	.	.	.	

D1.4.1: Prototype data sets for Gadget and prototype data warehouse views. Q3 **Complete**

Milestones and expected results

This is work towards milestones M1, M4.

1.5 Workpackage: Design of DW views and structures

Start date or starting event: April, 2000

N^o of the partner responsible: 3

N^{o}s of other partners involved: 1,4

Summary: This work package is almost complete. The structures are complete but more views will be developed.

Table 5: Person-months by partner within workpackage

Partner	1	2	3	4	5	6	7	8
2000	1	.	2	0.5	.	.	.	.
2001	1	.	0.5		.	.	.	.
Total to date	2	.	2.5	?	.	.	.	.
Total planned	12	.	7	12.0	.	.	.	.

Time to completion of workpackage (current estimate): 6

Objectives

To design the data structures of the data warehouse.

To develop a modern data warehouse using CORBA technology.

To design an Internet based program that can report the content of the data warehouse in a predefined set of views.

Description of work conducted to date

All the main aspects of this workpackage are on schedule, notably the overall design of the data structures, which are complete. The work here has been led by DIFRES, building on input from other partners during meeting and electronic mail. As with other aspects relating to the data warehouse, work has focussed on the basic data needed to make a database which serves the fundamental Gadget runs. Thus, this phase has not included acoustic or stomach content data. Such further data sets will be developed at a later stage during the project, partially under other work packages.

MRI (1) and DIFRES (3): A design document for implementing CORBA technology in the Internet based DW user interface was presented in the report for year 2000. The basic design is still the same but by introducing an Internet Server to host the user interface program the final solution will be more flexible. Then the solution can also work without CORBA using HTTP instead. The design also uses XML when data are extracted from the data warehouses. The updated design is shown in Annex B.1

The CORBA technology has been delayed for several months due to manpower problems. These problems have now been solved and work on CORBA will commence in 2002.

A preliminary design of the data views was finished in 2000. The user interface has been tested and presented. The overall design of the user interface is presented in Annex B.2, and the design of the security set up for the data warehouses in Annex B.3

Deliverables

D1.5.1: Design of data warehouse views. Q4 **Complete** in the form of prototype views.

D1.5.2: Design of the database structures. Q4 **Complete**

Milestones and expected results

This is work towards milestones M1, M4.

Milestone M1 is complete when this workpackage is complete.

1.6 Workpackage: Setting up the data warehouse

Start date or starting event: End of 1.5

N^o of the partner responsible: 3

Table 6: Person-months by partner within workpackage

Partner	1	2	3	4	5	6	7	8
2000	8	1	6	2	.	1.9	0.0	0.3
2001	1	0	3.9		.		0.5	0.2
Total to date	9	1	9.9	?	.	?	0.5	0.5
Total planned	24	3	32	24	.	14	1	0.5

Time to completion of workpackage (current estimate): 3

Objectives

To provide the data description, links and formats required to implement the DW programs for all case studies in a unified manner.

To implement and test the security software, browser- and e-mail-based import software and SQL based data warehouse export software to Gadget at selected sites.

To implement and test CORBA technology at selected sites.

To evaluate and select a technology for the DW.

To implement the DW at all sites.

Description of work conducted to date

In light of understanding gained during this project, deliverable D1.6.4 has been replaced by a more appropriate deliverable, which is to utilise XML for metadata (descriptions of the content of the data warehouse) and test CORBA for connecting the data warehouses. This joint use of the two approaches will give a considerably more useful data warehouse than originally envisaged.

MRI (1) and DIFRES (3): The database and the Internet based user interface has been exported from DIFRES to MRI and installed there in order to implement the Icelandic Waters DW. In 2002 the updated system will be exported to the other data base institutions and installed there.

An HTTP based solution has been implemented and tested. This solution can work alone or be combined with CORBA as shown in Annex B.1

At DIFRES XML has been used in other project when data are uploaded and requested from the data warehouse. XML is most useful for exchanging data, since it put the data in a relational structure and makes it possible to validate the exchange structure and the data itself and easily upload the data (see Annex B.4).

In DST2 XML could be used to extract data from the data warehouse as shown in Annex B.1.However in the DST2 project we do not gain anything by using XML compared to using traditional technology.

In 2002 the data warehouses have to be installed at the 3 sites. A work plan for 2002 has been set up. This work plan includes the incorporation of CORBA and XML technology and the installation of the 3 data warehouse sites (Annex B.5)

At the MRI, the data base engine, PostgreSQL, to be tested as a basis for the data warehouse, is set up under Solaris, the prototype DW tables from DIFRES have been set up, database views have been defined and uploads into the DW have been tested. It is envisaged that a functional DW will be ready Q1, 2002.

As a common data storage format has been agreed upon, the goal of this sub work package has shifted towards the design of this common format and a format for exchanging data. The data storage format is described in Annexes in the report for 2000 as is the exchange format.

SCUI (4):
Subsequent to initial tests of CORBA in 2001, DW work at SCUI has been dormant in 2002 due to manpower problems. Subsequent work will be joint between SCUI and MRI, i.e. further testing of CORBA with PostgreSQL at MRI, organised by SCUI.

FRS (6):
Data concerning North Sea Herring for all tables, except Table 8, are ready to be loaded into a Warehouse. The related look-up tables are being prepared.

Celtic Sea: CEFAS (7) & IFREMER (8)
The French and English Celtic sea data have been prepared in the same formats. So far the data base is still in ACCESS, partly for convenience of the teams. This is progress towards D1.6.9.

Deliverables

D1.6.1: Each institute provides descriptions of the data storage format used for all data sets to be used as a basis for the DW. Q6 **Complete**

D1.6.2: Known techniques of DW implementation using XML are described in detail and tested. Q6 **Complete**

D1.6.3: CORBA technology described in detail and tested. Q6 **Revised schedule**

D1.6.4: The results of using CORBA and XML compared to select the appropriate technology. Q7 **Modified deliverable**, see above.

D1.6.5: Final choice of DW software set up, tested and distributed. Q8

D1.6.6: Data warehouse for Icelandic waters. Q9

D1.6.7: Data warehouse for North Sea herring. Q9

D1.6.9: Data warehouse for the Celtic Sea. This will include biological sampling data for the period 1984-1999 and tagging data. As such the data warehouse will be incomplete but will demonstrate the future potential for further incorporation of data, once available. Q9

Milestones and expected results

This is work towards milestones M4, M5, M6.

Milestone M4 is complete when this workpackage is complete.

1.7 Workpackage: Interface to Gadget

Start date or starting event: End of 1.6

N^o of the partner responsible: 3

N^{o}s of other partners involved: 1,4

Table 7: Person-months by partner within workpackage

Partner	1	2	3	4	5	6	7	8
2000	2	.	1	0	.	.	.	.
2001	2	.	0		.	.	.	.
Total to date	4	.	1	?	.	.	.	.
Total planned	18	.	10	12	.	.	.	.

Time to completion of workpackage (current estimate): 6

Summary: The emphasis is currently on redefining the Gadget input file structure so that Gadget configuration data are separate from biological measurements, and the biological data will be stored in column format. This will drastically simplify the effort needed to extract Gadget input data from the DW.

Objectives

To define and write procedures to extract data from data warehouses into the file formats which are used by the assessments and hypothesis testing modules.

Description of work conducted to date

At the DST2 meeting in June, 2001 it was decided to separate the data requested from the DW and the Gadget configuration data into 2-3 files.

A meeting of programmers was scheduled for Q9 to coordinate programming on Gadget, with special emphasis on Gadget file formats.

Deliverables

D1.7.1: Software to set up all data and parameter files for Gadget. Q9

Milestones and expected results

This is work towards milestones M5, M6.

M1 needs to be completed before this workpackage can be completed.

2 Workpackage group: Structural models

2.1 Workpackage: Migration/drift

Start date or starting event: February, 2000

N^o of the partner responsible: 4

N^{o}s of other partners involved: 1, 2, 7

Table 8: Person-months by partner within workpackage

Partner	1	2	3	4	5	6	7	8
2000	1	0	.	10	.	.	0.0	.
2001	6	3	.	18	.	.	0.5	.
Total to date	7	3	.	28	.	.	?	.
Total planned	8	12	.	45	.	.	6.0	.

Time to completion of workpackage (current estimate): 24

Objectives

To develop a migration model for use in Gadget.

To evaluate the data needs for estimating migration parameters.

To identify potential environmental variables that might lead to a better understanding of fish migration and larval drift.

Description of work conducted to date

A basic migration model was developed by the end of 2000.

MRI (1):
Recent work (2000) has involved allowing the proportions which migrate between areas to vary from year to year, yet in a time series fashion, so that too much variability in migration is penalised. This type of flexibility is an essential addition to the current framework since the migrations do vary but there is not enough data to estimate annual migration completely freely.

Current and immediate future work involves testing the estimability of these parameters, including estimation of the variance of the point estimates.

IMR (2):
The project work uses Mathematica as technical platform for compliance with the assessment models SeaStar (Norwegian spring spawning herring) and Bifrost (capelin).

The basic algorithms for migration and estimation have been constructed along with basic infrastructure software like avoidance of land. A baseline model for migration of capelin was set up and parameters connected to year-to-year migration of immature capelin were estimated in order to test the software. Available simulated data for temperature and current from the period 1997-1999 were transferred to Mathematica lists and the co-ordinates translated from an X-Y system to geographical position co-ordinates. A model for migration where the individual migration vector depends on temperature and current will be built and tested on migration of pre-spawning capelin in the above period in the course of 2002.

SCUI (4):
1. Project definitions, specification and mathematical formulation of model factors and forces have been developed further. This includes identifying, constructing hypotheses about and formulating how environmental features like temperature distributions, boundaries between

warm and cold water masses and oceanic currents, and "internal variables" such as state of maturity and energy reserves affect movements and spatial distribution.

2. The development of an initial discrete, individual based model is completed. The model is based on the hypothesis that the velocity of each fish is determined by two forces: a tendency to follow the movements of its neighbours and random changes in speed and direction. By an appropriate choice of probability density functions for these random changes, the fish can be made to move either as a coherent school towards a specified point or area (migrations mode), or to move in small schools in different direction (feeding mode). In addition, boundaries are defined, such as depth contours, certain isotherms, current boundaries, and the behaviour at such boundaries has been specified and programmed.

3. Further work on defining, formulating and programming a continuous model of density and velocity as a function of time, location (and "physiological state"). Definitions and mathematical formulation of the relevant forces influencing spatial distributions have been developed further. Mathematical descriptions of the collective motion of organisms and analysis of a density-velocity model.

CEFAS (7):
Tagging/recapture records (24885) for sole, plaice and cod have been entered into the Celtic Sea data base. Most cod were recaptured within same rectangle as where they were originally released (Annex E.3), thus providing limited scope for modelling migration patterns in the Celtic Sea. Data for sole and plaice are more extensive and offer greater scope for future modelling work (also see workpackage 5.3).

Preliminary analyses to determine the rates and extent of horizontal movement of cod, has been carried out by the CEFAS Behaviour Team for the Celtic, North and Irish Seas. Data has been disaggregated into juvenile and adult size-classes, and the output of this work will be a series of maps.

CEFAS's current North Sea cod electronic tagging programme, which runs until 2004, is yielding high-quality spatial data on rates and extents of horizontal movement. A wider tagging programme (CODYSSEY), which will involve tagging studies in the Barents Sea, Baltic Sea, North Sea and Icelandic/ Faroe plateau, is currently under consideration by the European Commission.

Deliverables

D2.1.1: Initial, simple migration model. Q4. **Complete**

D2.1.2: A proposed mathematical model formulation for use in Gadget, based on comprehensive theoretical analysis of the biolological and physical properties of the system, e.g. currents and temperature. Q12

D2.1.3: Evaluation of reduction in variances as a result of reducing uncertainty in different data sources, including tagging data, survey indices and hydrographic information, using simulation with Gadget. Q12

Milestones and expected results

This is work towards milestones M5, M6.

Parts of this task provide input to milestone M3, almost complete.

2.2 Workpackage: Spawning and recruitment

Start date or starting event: February, 2000

N^o of the partner responsible: 2

N^{o}s of other partners involved: 1

Table 9: Person-months by partner within workpackage

Partner	1	2	3	4	5	6	7	8
2000	1	32	.	.	.	.	.	.
2001	0	28	.	.	.	.	.	.
Total to date	1	60	.	.	.	.	.	.
Total planned	18	88	.	.	.	.	.	.

Time to completion of workpackage (current estimate): 24

Objectives

To formulate a description of the recruitment process in order to have a model of the full life-cycle of each species.

Description of work conducted to date

MRI (1):
Gadget includes a simple spawning module, developed at MRI, but not been tested yet. The next step in developing the biological modelling component of Gadget at the MRI will be to close the life cycle by allowing the spawning module to generate eggs which will drift (using the migration module) to nursery areas. As a first step towards obtaining realistic abundance values the mortality in each region will be estimated or set to give magnitudes corresponding to survey indices.

IMR (2):
Northeast Arctic Cod:
Egg and larval abundance estimates for Northeast Arctic cod estimated from the Russian ichthyoplankton surveys (1959-1993) were combined with available estimates of stock reproductive potential and abundance indices for the larval, pelagic juvenile and demersal juvenile stages to determine when the recruitment signal can first be detected (Mukhina et al. in review). The correlation between recruitment and relative egg abundance was stronger than the correlations between recruitment and proxies for stock reproductive potential (e.g., spawner biomass) suggesting that the transition from potential egg production to realized egg abundance is a critical stage. Correlations between recruitment and the relative abundance of larval and juvenile stages were frequently weak or non-significant. Measurement error in the stage abundance indices likely contributes to this weakness.

A novel model that can incorporate age diversity index from the spawning grounds and a temperature from the Kola section during August to December is developed to analyse stock-recruitment relationships. It is demonstrated that such a model accounts for 70% of the variation in the Northeast Arctic cod recruitment. This is a considerable improvement over the Ricker Model ($R^2 = 0.33$). This new model can be also used for prediction purposes based on climate forecasts.

A model of size preferences in cod cannibalism, based on data on cod stomach content and estimates of abundance of cod by size, has been developed for Northeast Arctic cod (Bogstad, 2001). The preferred predator length/prey length ratio for cod preying on cod was found to be 3.1, and the size preference was found to be asymmetric. This model can be used in Fleksibest/Gadget to describe cod cannibalism, together with other factors such as capelin abundance.

Relationships between amphipods, capelin and cod in the Barents Sea, which may be quite important for cod recruitment, have been analysed (Dalpadado et al., 2001). Work on analysing the stomach content of young cod (1-2 years) to investigate the relationship between observations on growth and stomach content for these age groups, has started.

An inverse relationship between the average fish length in a cohort at the 0-group stage and at age 2 has been found (Helle et al., 2002). Ottersen et al. (2002) found that the reason for this negative correlation probably is that cohorts with high mean length as 0-group also are abundant cohorts. Such abundant cohorts are distributed over a larger area so that large proportions of these cohorts are found in areas with low temperatures and bad growth conditions. This leads to low growth rates after bottom settling as 0-group, causing the mean length at age 2 to be low.

References: Bogstad, B. 2001. A model for size preferences in cannibalism in Northeast Arctic cod (Gadus morhua L.) WD 15, ICES Arctic Fisheries Working Group, Bergen 24 April- 3 May 2001.

Dalpadado, P., Borkner, N., Bogstad, B., and Mehl, S. 2001. Distribution of Themisto (Amphipoda) spp. in the Barents Sea and predator-prey interactions. ICES J. Mar. Science 58: 876-895.

Helle, K., Pennington, M., Bogstad, B. and Ottersen, G., 2002. Some environmental factors that influence the growth of Arcto-Norwegian cod from the early juvenile to the adult stage. Env. Biol. Fish. (accepted).

Mukhina, N.V., Marshall, C.T., and Yaragina. N.A. in review. Tracking the signal in year-class strength of Northeast Arctic cod through multiple survey estimates of egg, larval and juvenile abundance.

Ottersen, G., Helle, K. and Bogstad, B. 2002. Do abiotic mechanisms determine interannual variability in length-at-age of juvenile Arcto-Norwegian cod? Can. J. Fish. Aquat. Sci. 59: 57-65.

Further descriptions of IMR work on cod cannibalism are provided in Annex C.6 and a model of Norwegian spring spawning herring is described in Annex C.7.

Deliverables

D2.2.1: A module to describe the recruitment process. Q12

Milestones and expected results

This is work towards milestones M3, M5, M6 of which M3 the part towards M3 need to be comleted in 2002 (D2.2.1).

2.3 Workpackage: Growth, maturation and fecundity

Start date or starting event: February, 2001

N^o of the partner responsible: 2

N^{o}s of other partners involved: 1

Table 10: Person-months by partner within workpackage

Partner	1	2	3	4	5	6	7	8
2000	1	12	.	0	.	.	.	.
2001	11	8	.	2	.	.	.	.
Total to date	12	20	.	2	.	.	.	.
Total planned	12	30	.	28	.	.	.	.

Time to completion of workpackage (current estimate): 24

Objectives

To evaluate different models of growth and maturation including dispersion of length at age, and models for effective fecundity related to nutritional state as well as maternal effects on recruitment.

To model the relationship between growth and consumption taking into account body size and metabolic costs, in order to make predictions of growth in the short term.

Description of work conducted to date

MRI (1):
The growth models developed earlier and described in the dst^2 report for 2000 have been tested extensively, c.f. Annex C.5.

IMR (2):
Progress towards quantifying the reproductive potential of Northeast Arctic cod included: a) the development of a preliminary fecundity model which can be used to establish year-specific fecundity/length relationships; and b) the construction of historical age/length keys from Norwegian sources. Using these a preliminary time series for total egg production was reconstructed (1946-2000). Several discrepancies were noted between the total egg production time series and spawner biomass, the causes of which are being investigated further. However, the approaches used to model the growth parameters (maturity-, weight- and fecundity-at-length) show good agreement with the newly available time series for maturity- and weight-at-age (ICES 2001) as well as historical data on liver condition (Yaragina and Marshall 2000) and capelin stock biomass. The possible incorporation of this "process" information into stock assessment was explored by developing additional reference points that are explicit for reproductive potential and by examining how effective the current reference points for spawner biomass and fishing mortality are in conserving reproductive potential (Marshall et al. 2001).

Trawl samples and acoustic data collected by Norwegian research vessels during the first quarter of the year in the Barents Sea and in the Lofoten area have been used to determine the maturing fraction by 5 cm length groups of Northeast Arctic cod. A maturation model where the length dependence is described by a sigmoid function was used. Interannual variations in length at 50% of maturation of cod (L_{50}) are analysed. (L_{50}) is fairly stable (between 66 and 71 cm) during the period for which data are available, and does not show a particular time trend, suggesting that length dependence explains most of the variation in maturation. This model for maturation can be used when applying Gadget/Fleksibest to Northeast Arctic cod.

ICES 2001. Report of the Arctic Fisheries Working Group. ICES CM 2001/ACFM:19.

Marshall, C.T., Yaragina, N.A., and Thorsen, A. 2001. Evaluating the effectiveness of biological reference points in conserving reproductive potential. ICES CM 2001/V:17.

Yaragina, N.A., and Marshall, C.T. 2000. Trophic influences on interannual and seasonal variation in the liver condition index of Northeast Arctic cod (Gadus morhua). ICES J. Mar. Sci. 57: 42-55.

IMR (2) and IFREMER (8):
Partners 2 and 8 prepared a review of growth models for length-based population dynamics models including those currently used in Gadget and some potential models from the literature (C.3). The review includes a summary description of each model including the number of estimable parameters and the problems encountered when using different growth models within the current project. This is progress towards D2.3.1.

SCUI (4):
Initial work on formulating how migrations and movements may depend on the physiological or maturation status of the organisms.

Deliverables

D2.3.1: Mathematical models of the growth and maturation process. Q12

Milestones and expected results

This is work towards milestone M3, the prototype of D2.3.1 towards M3 is done.

2.4 Workpackage: Internal model types, including process errors

Start date or starting event: February, 2000

N^o of the partner responsible: 7

N^{o}s of other partners involved: 1,2,3,7

Table 11: Person-months by partner within workpackage

Partner	1	2	3	4	5	6	7	8
2000	6	1	2.1	.	.	.	0.0	0.5
2001	0	2	0.0	.	.	.	0.5	1.0
Total to date	6	3	2.1	.	.	.	0.5	1.5
Total planned	2	6	4.0	.	.	.	6	2.0

Time to completion of workpackage (current estimate): 0

Summary: This workpackage is almost complete. From a mathematical and programming point of view an approach has been developed where process error can easily be included in almost any model parameter. Considerable external work has been done on Bayesian approaches and new growth update functions have been implemented in Gadget. Some further enhancements will be developed, but this will be continued as part of other WPs.

Objectives

To define appropriate internal population models.

To incorporate process error through time series models within Gadget

Description of work conducted to date

MRI (1):
The main MRI work to the internal models has been in extensive model testing, with an emphasis on growth functions (Annex C.5).

IMR (2):
A mathematical description of Fleksibest, which is a single-species application of a Gadget-type model, has been published (Frøysa et al., 2002).

A description of various methods of implementing length growth in a length-structured population model will soon be submitted for publication (Bogstad, Trenkel and Frøysa, Annex C.3).

Frøysa, K. G., Bogstad, B., and Skagen, D. W. 2002. Fleksibest - an age-length structured fish stock assessment tool with application to Northeast Arctic cod (Gadus morhua L.). Fisheries Research 55: 87-101.

CEFAS (7):
Work continues on a joint (CEFAS & IFREMER) review paper concerning state-space models and the Kalman Filter. Examples will be formulated of how the Kalman filter can be used to

model biological processes (e.g. recruitment, fishing mortality, biomass, catch at age, catch at length, weight at age) and assess the state of fish stocks.

IFREMER (8):
The mathematical model formulation of a general population dynamics model in state space form including spatial and multi-species aspects has been presented at the annual project meeting in June 2001 and amended following the discussion at the meeting (Annex C.4). This completes deliverable D2.1.1.

Comparison of Bayes and maximum likelihood estimators in an age structured single species stock assessment model has been carried out in a simulation study. The results showed that Bayes estimator is a useful estimator, which is better than the maximum likelihood in the sense that it is less biased and has a much lesser variance, cf:

Nielsen, A and P. Lewy, (2002) *Comparison of the frequentist properties of Bayes and the maximum likelihood estimators in an age-structured fish stock assessment model*, Canadian Journal of Fisheries and Aquatic Sciences, **59**(1), 136–143.

This completes D2.4.3.

Deliverables

D2.4.1: Mathematical formulation of general populations dynamics models in state space form. Q3 **Complete**

D2.4.2: Corresponding program modules. Q4 **Complete**

D2.4.3: Prescription to incorporate relevant prior information into population dynamics models (model structure, parameter distributions, etc.). Q4 **Complete**

Milestones and expected results

This is work towards milestone M3 which has been reached in terms of requirements from this workpackage.

3 Workpackage group: Estimation and inference

3.1 Workpackage: Estimation procedures

Start date or starting event: July, 2001

N^o of the partner responsible: 7

N^{o}s of other partners involved: 3,4,7,8

Table 12: Person-months by partner within workpackage

Partner	1	2	3	4	5	6	7	8
2000	6	0	1.2	0	.	.	0	0
2001	17	2	3.7	2	.	.	0	3
Total to date	23	2	4.9	2	.	.	0	3
Total planned	24	12	4	16	.	.	7	8

Time to completion of workpackage (current estimate): 24

Summary This package is close to being on schedule. For example, though D3.1.1 is not complete in the form of a published paper, it is available in the form of a computer program.

Similarly, work towards D3.1.2 has resulted in a battery of tests, which have indicated that a complete revision of statistical assumptions needs to be undertaken for fisheries data.

Objectives

To identify the probability distributions, likelihood functions and prior distributions appropriate to mathematical descriptions of fish population dynamics.

To specify the range of circumstances under which different methods of parameter estimation may be used, together with guidance on the calculation of appropriate confidence statements.

To model and program simulation procedures describing the marine ecosystem, using a detailed, structured approach.

To define and test methods to verify goodness-of-fit measures for general likelihood functions in a highly nonlinear framework.

To list, evaluate and propose methods for statistical testing of hypotheses in Gadget.

Description of work conducted in to date

As seen in earlier reports, it is well known that probability distributions appropriate for fisheries data tend not to be of standard form, e.g. data tend not to be i.i.d., tend to be non-Gaussian and generally both overdispersed and spatially correlated. This is certainly true for Gadget input data as indicated by preliminary testing (Annex D.2).

Prior distributions on parameters have been postponed until such time that likelihood functions have been adequately defined for most data sets.

MRI (1):
Considerable effort has been put into the selection of likelihood functions and current work involves the development of appropriate likelihood functions for length distributions (where it is easy to see from the data that e.g. multinomial distributions are not at all appropriate, c.f. Annexes D.1 and D.2). The completion of this work needs to precede e.g. Bayes priors, methods for testing model complexity etc.

Initial work on comparing weights attached to likelihood components indicates a possibility of estimating these, even when the models used are not exactly correct. This work, set out in an Annex of the first dst^2 report and first conducted in 2001, will be continued in 2002, possibly extended to attempt to estimate influential observations or influential constraints in nonlinear models such as gadget.

The work towards the goodness-of-fit is sufficiently developed to be classified as complete (D3.1.2, cf D.2) and estimation techniques (D3.1.2) are well underway, given that the methods are available and tested but not fully documented.

IMR (2):
The Fleksibest source code have merged with the Gadget source code, enabling the Fleksibest model to be run with Gadget. A coordinator for further development of the Gadget code has been appointed.

DIFRES (3):
The work on developing a stochastic multispecies model has been continued along the lines described in last years report. Two main changes have taken place. The first is that the continuous approach has been replaced by a discrete. This is due to estimation problems with likelihood functions based on numerical integration. The second is that stomach content models - in contrast to deterministic multispecies models - have been changed from being age based to be length based. This decision is based on bootstrap estimates of the distribution of the stomach content observations. Analyses show that for given predator and prey species the observed weight proportions in the stomach in some cases have correlations close to one and

hence are close to be linearly dependent for a range of age groups. This applies for instance to weight proportions of the 2-, 3- and 4 group of sandeel in the stomach of 2 year old cod. In most cases these high correlations are caused by that externally given age/length keys are used to translate a length groups to age groups for both predator and prey. As changing the stomach content models to be length based seems to be the most reasonable solution to the problem this has been done in combination with age based catch models. Furthermore, semi-separable models for total fishing mortality have been introduced in combination with inclusion of survey data in the likelihood. The work, Lewy and Vinther (2002) is described in Annex D.3.

IFREMER (8):
Work on probability distributions for survey and commercial effort data has been carried out using the Celtic sea data. Several distributions (lognormal, Gamma and normal) have been fitted to the individual (survey) haul data and the impact of the choice of distribution on the assessment of the state of the community has been evaluated. The comparison was carried out using indicators for the impact of fishing such as diversity indices and the proportion of non-commercial species in the community (draft paper submitted to Canadian Journal of Fisheries and Aquatic Sciences, Annex D.4).

Commercial effort data was modelled in a generalised linear modelling framework in order to identify homogeneous fishing zones (see also workpackage 5.2). It was found that by transforming monthly effort data using a third root transformation, the stronlgy skewed data could be approximated by a normal distribution. The choice of transformation was based on an anlysis of mean-variance relationships. A number of exponential distributions were also tested but none allowed to remove strong patterns in the residuals of the GLM.

SCUI (4):
Initial work on parameterization of a migration model and identification of parameters which can be estimated from field and tagging data.

Deliverables

D3.1.1: Mathematical descriptions of estimation methods for model components. Q8

D3.1.2: Descriptions of goodness-of-fit tests for composite likelihoods. Q8 **Complete**

D3.1.3: Implementations and tests of different estimation procedures in different scenarios. Q12

D3.1.4: Algorithmic description of estimation methods and goodness- of-fit tests to facilitate programming both within and outside of Gadget. Q12

Milestones and expected results

This is work towards milestones M3, M5 and M6, with prototypes towards M3 reached earlier than half-way through the workpackage which was planned.

3.2 Workpackage: Programming estimation

Start date or starting event: July, 2001

N^o of the partner responsible: 7

N^{o}s of other partners involved: 1,2,3,4,6,7,8

Time to completion of workpackage (current estimate): 12

Summary Work on this workpackage has proceeded very rapidly. It is envisaged that this package will be completed a year ahead of schedule, thus enabling more work to be put into WP 1.* which are somewhat lagging.

Table 13: Person-months by partner within workpackage

Partner	1	2	3	4	5	6	7	8
2000	6	1	3.1	0	.	0	0	0.0
2001	26	2	3.5	0	.		0	1.0
Total to date	32	3	6.6	0	.	?	0	1.0
Total planned	36	12	4.0	16	.	4	6	3.5

Objectives

To program statistical (maximum likelihood) estimation of unknown parameters in these simulations.

To evaluate several different minimization algorithms and select algorithms for use with Gadget.

To obtain a general version of Bayesian analysis as an option in Gadget.

To incorporate processes formulated in Tasks 2 and 4 into the collection of modules.

To evaluate the possibilities of using parallel processing on a network of processors when estimating very many parameters in a complex multispecies spatially disaggregated model.

To evaluate the effects of incorporating automatic differentiation in the minimisation algorithms in Gadget and implement the possibility.

Description of work conducted to date

MRI (2):
A composite algorithm joining together global optimisation (simulated annealing), robust coordinate search (Hooke and Jeeves) and a final, accurate quasi-Newton algorithm (BFGS) running in parallel on a network of workstations is now functional and has been extensively tested. Each of these algorithms needed to be changed considerably from the single-processor version, in order to utilise multiple processors.

Parallel processing was implemented using PVM. In order to do this considerable features needed to be rewritten from scratch, including mechanisms for detecting machine failures, identifying slow machines and reallocating work, etc. Testing in 2001 focussed on evaluating the possible use of Condor as an allocator of CPU resources. It is expected that these tests will be completed in 2002.

The effects of parallel processing are being evaluated in order to estimate the improvements in run-times for models of different sizes on different-size networks. This is expected to be complete in 2002.

Prototype data sets have been made available (haddock example in the first report and 3-species example, too voluminous to print) for testing purposes (completing D3.2.5).

IMR (2):
Hooke and Jeeves optimization has been improved by including an extra argument giving initial search step length, independent of rho.
The simulated annealing algorithm has been tested on the Fleksibest application of Gadget in order to:

1. explore the robustness of SA.
2. find good values for important numerical parameters like the initial temperature T, the temperature reduction factor RT, the number of cycles NS and the number of iterations before temperature reduction, NT.
3. explore whether there exists a unique solution to the present problem and analyse the

solutions from runs with different initial temperature and seeds.

4. try to find rules of thumb for when to change from SA to Hooke and Jeeves (HJ).

As expected, simulated annealing was found to be robust, but slow. An almost unique solution seems to exist. More details can be found in Frøysa Annex D.5.

DIFRES (3):
The implementation of the stochastic multispecies model is in progress using AD Model Builder and C. The part dealing with catch and survey likelihood functions has been completed while the stomach content part is in preparation.

IFREMER (8):
The work carried out by IFREMER consists of the contribution to growth model formulations reported under WP 2.4.

Deliverables

D3.2.1: Program modules to carry out estimation for likelihood and Bayesian estimation. Q8 **Likelihood estimation complete, Bayesian postponed**

D3.2.2: A selected (composite) minimisation algorithm. Q12 **Complete**

D3.2.3: A program which can utilise parallel processing for improved performance. Q8 **Complete**

D3.2.4: An evaluation of the effect of parallelisation. Q12

D3.2.5: A set of standard fisheries examples that can be used to check that algorithms are correctly implemented and that results are consistent with those obtained using commercially available software. Q10 **Complete**

Milestones and expected results

This is work towards milestones M3 and M6, with deliverables for M3 finished earlier than scheduled.

4 Workpackage group: Estimation of parameters outside program

4.1 Workpackage: Feeding/consumption

Start date or starting event: February, 2000

N^o of the partner responsible: 5

N^{o}s of other partners involved: 2, 3, 4

Table 14: Person-months by partner within workpackage

Partner	1	2	3	4	5	6	7	8
2000	.	1	1.3	0	2	.	.	.
2001	.	1	12.1	0	26	.	.	.
Total to date	.	2	13.4	0	28	.	.	.
Total planned	.	3	8.0	4.0	58	.	.	.

Time to completion of workpackage (current estimate): 14)

Objectives

To develop a multi-species spatially explicit feeding/consumption model based on habitat and diet selection with an evolutionary fitness basis

To estimate sampling error of stomach contents data in the NS Stomach Sampling data base.

Description of work conducted to date

IMR (2):
IMR has provided some advice to UiB on how to use stomach content data to calculate the consumption of herring by cod in the Barents Sea.

DIFRES (3):
Bootstrapped data on the distribution of stomach content data from ICES Stomach Sampling Project 1991 for the North Sea have been analysed. The age based analyses showed that for given predator the observed relative stomach content for specific age groups of prey species in some cases have correlations close to one. To avoid such almost linearly dependent observations it was decided to change length based predation selectivity models, see Workpackage 3.

As the variance of the relative stomach content observations is needed in a stochastic multispecies model the variance structure was analysed. A main result is that the variance can be expressed by term dependent on the prey species and a term independent of the prey species, which depends on the expected value of the observations. The correlation structure needs to be further analysed. A paper on the subject is in preparation.

UiB (5):
The work conducted to date relates to deliverables D4.1.1, D4.1.2, and D4.1.3. The work related to D4.1.1 and WP 4.1.2 is to develop a multi-species spatially explicit feeding/consumption model. The biological model is individual-based and relies on habitat and diet selection with an evolutionary fitness basis. The spatial model uses input data from an ocean circulation model, and some work has been associated with developing computer code for linking the biological model with the physical model. The biological model relies on a bioenergetics growth model. There exists bioenergetics models suitable for cod and herring, but not for capelin. Some effort has therefore been invested into modifying a herring bioenergetics model to better suit capelin. This work is now finished and the manuscript is enclosed (Huse & Gjøsæter MS). Another important element in the predator-prey modelling using bottom-up approaches as here is the modelling of behaviour. In the individual-based model, behaviour is implemented using adapted random walk, a technique that uses a genetic algorithm to evolve threshold values for when to depart a habitat and where to go respectively. A paper describing the adapted random walk technique, with an application on the Barents Sea capelin, has recently been published (Huse, G. 2001. Modelling habitat choice in fish using adapted random walk. *Sarsia* 86:477-483). The results show that this technique compares favourably with similar sized neural network based models in modelling fish movements. Furthermore the adapted random walk concept functions intuitively and allows parameter values to be estimated both from observations and by using a genetic algorithm and life cycle simulation as in Huse (2001). A cod-capelin-herring model is being developed based on adapted random walk, but the results are too premature to warrant presentation in this report.

The aim of D4.1.3 is to provide estimates of cod's consumption of capelin and herring. A method for estimating cod's fish consumption has been developed. The method is tested for consumption of herring in the period 1992-1997, and the description and preliminary results of this work is enclosed (Johansen et al. MS). At this point there are some problems related to applying the method on stomach data before 1992, because the prey body length, which is crucial for consumption estimation, is measured in 5 cm intervals. This might be too imprecise since the method is based on calculating fresh weight (undigested weight) of prey. The effect of 5 cm length groups on the total estimates may however be studied with the data from 1992-1997, by reorganising the prey in 5 cm length groups.
The cod-capelin-herring model will eventually (towards Q12) be forced with temperature fields for the period 1992-1997. The predicted cod consumption of capelin and herring in the respecti-

ve years will be compared to the relative indices of cod's predation over the period. This work has been initiated, and will be intensified during spring as the individual based models and consumption estimates are finalised.

Annexes:

D.6 Huse G & Gjøsæter G. (MS). An evaluation of a bioenergetics model for capelin.

D.7 Johansen GO, Bogstad B, Mehl S & Ulltang Ø. (MS). Natural mortality of juvenile herring (*Clupea harengus* L.) in the Barents Sea due to predation by North-east Arctic cod (*Gadus morhua* L.).

Deliverables

D4.1.1: Age- and size-dependent growth and predation mortality for cod, capelin and juvenile herring in the Barents Sea. Q9

D4.1.2: Distribution of cod, capelin and juvenile herring in the Barents Sea. Q9

D4.1.3: Estimates of cod's consumption of capelin and herring related to prey density, stock overlap and physical factors. Q9

D4.1.4: Estimation of the distribution or the variance of the relative stomach contents. Q9

D4.1.5: Final vital statistics to Gadget: Q12

Milestones and expected results

This was initially foreseen as work towards milestones M3 and M5, though this may not end up being required for completion of M3.

4.2 Workpackage: Spatio-temporal scales

Start date or starting event: January, 2003

N^o of the partner responsible: 3

N^{o}s of other partners involved: 1, 3, 4, 7

Table 15: Person-months by partner within workpackage

Partner	1	2	3	4	5	6	7	8
2000	0	.	1.3	0	.	.	0.0	.
2001	0	.	0	0	.	.	0.0	.
Total to date	0	.	1.3	0	.	.	0.0	.
Total planned	6	.	10.0	6	.	.	10.8	.

Time to completion of workpackage (current estimate): 24

Objectives

To investigate the adequate spatial and temporal scales to be used in Gadget.

To explore the importance of spatial inhomogeneity for the assessments North Sea fish stocks.

To identify the extent of the spatial and temporal distribution of species within the Celtic Sea.

Description of work conducted to date

This workpackage is not due to start until 2003.

MRI (1):
Work has not started on this workpackage.

DIFRES (3):
The MSVPA and MSFOR algorithms have been used to explore the importance of spatial inhomogeneity for the assessments of North Sea fish stock. However, a full spatially disaggregated MSVPA is not technically possible, and a more simple approach was applied. Results for the traditional one-area MSVPA was combined with quarterly data on stock distribution data (IBTS data) by ICES Roundfish Area, spatial disaggregated catch (STCF database) and stomach contents data (task 4.1.) to estimate local food suitability coefficients and fishing mortalities (see the report for 2000 for details). These values can then be used in a multispecies catch projections (MSFOR) for evaluation the importance of spatial inhomogeneity.

For the North Sea 1991 is the only year for which all the type of data mentioned are available. The method described has been applied to the division of the North Sea in two are sub-areas, a northern and a southern part. The method seems to work properly and the estimated fishing mortalities by sub-area were reasonable, except for a few cases where the STCF catches were taken in a sub-area with no fish (according to the IBTS). No further analysis of local fishing mortality or food suitabilities have been done.

CEFAS (7):
Considered long-term temporal patterns of species abundance in survey data and commercial landings data. Drafted paper intended for publication in Journal of Applied Ecology: The effects of exploitation and environmental change on the trophic structure of the Celtic Sea fish community (cf the report for 2000)

Deliverables

D4.2.1: Effects of different levels of disaggregation in Gadget. Q14

D4.2.2: Quantification of the importance for fish stock assessment of spatial disaggregation. Q14

D4.2.3: Estimation of the distribution or the variance of the relative stomach contents. Q14

D4.2.4: Estimates of biological parameters required as inputs to WP 5.2. Q10

Milestones and expected results

This is a part of the work towards several milestones (M3-M6).

4.3 Workpackage: Reference points

Start date or starting event: January, 2002

N^o of the partner responsible: 3

N^{o}s of other partners involved: 1, 2

Time to completion of workpackage (current estimate): 15

Objectives

To develop multispecies biological reference points

To indicate how medium-term simulations can be conducted in Gadget

Table 16: Person-months by partner within workpackage

Partner	1	2	3	4	5	6	7	8
2000	0	0	5.0	.	.	.	.	.
2001	0	0	1.1	.	.	.	.	.
Total to date	0	0	6.1	.	.	.	.	.
Total planned	6	3	12.0	.	.	.	.	.

Description of work conducted to date

This workpackage is due to start in 2002.

DIFRES (3):

In multispecies fish communities, predation levels change dynamically in response to changes in the abundance of predator and prey species, as influenced by the fisheries that exploit them. In addition to community-level metrics, it remains necessary to track the abundance of each species relative to its biological reference point. In situa-tions with many interacting species exploited by multiple fishing fleets it can be com-plicated to illustrate how the effort of each fleet will affect the abundance of each spe-cies. We have adapted the AMOEBA approach to graph the reference levels of multiple interacting species exploited by multiple fleets. This method is illustrated with ten species and eight fishing fleets in the North Sea. We fit a relatively simple response-surface model to the predictions of a fully age structured multispecies model. The re-sponse-surface model links the AMOEBA for fishing effort to separate AMOEBAs for spawning stock biomass, fishing mortality, and yield. Ordination is used to give the shape of the AMOEBAs functional meaning by relating fish species to the fleets that catch them. The aim is to present the results of dynamic multispecies models in a format that can be readily understood by decision makers. Interactive versions of the AMOEBAs can be used to identify desirable combinations of effort levels and to test the compatibility of the set of single-species BPRs. The work is described in Annex D.8.

Deliverables

D4.3.1: Definition of multispecies reference points for North Sea fisheries and sustainable multi fleet fisheries. Q12

Milestones and expected results

Results from this task include multispecies reference points and proposals on how to conduct medium-term simulations from Gadget.

5 Workpackage group: Case studies

5.1 Workpackage: Case study: Icelandic waters

Start date or starting event: July, 2001

N^o of the partner responsible: 1

N^{o}s of other partners involved:

Time to completion of workpackage (current estimate): 24

Objectives

Table 17: Person-months by partner within workpackage

Partner	1	2	3	4	5	6	7	8
2000	1	.	.	.	.	.	.	.
2001	18	.	.	.	.	.	.	.
Total to date	19	.	.	.	.	.	.	.
Total planned	96	.	.	.	.	.	.	.

To implement prototype models for Icelandic waters, based on a common program base and the data warehouse for the region.

Description of work conducted to date

MRI (1):
Prototype datasets have been generated as a part of Workpackage group 1 and prototype model runs have been developed, including a prototype cod-capelin-shrimp model.

These initial model runs indicate several requirements for changes to the base Gadget model. In particular, it has been seen that the likelihood functions for length distributions need to be completely changed and common assumptions of (log-)normality are usually incorrect. Thus a proposal for generic improvements to the model is now available.

Work has also been undertaken to set up input files for marine mammals. Since the units for these species are totally different from most fish stocks, these definitions require considerable work but may provide explanation of some of the variability in mortality of fish stocks.

Inclusion of multispecies effects in population dynamics models inevitably affects management advice Annex E.1.

Deliverables

D5.1.1. Prototype data sets for the area around Iceland. Q6 **Complete**

D5.1.2. Prototype model run. Q7**Complete**

D5.1.3. Proposed generic model improvements (to be programmed in workpackage 3). Q9 **Complete**

D5.1.4. Prototype data warehouse with data for this case study based on definitions in workpackage 1. Q9

D5.1.5. Adopted model run on adopted data set: Proposed model explains data adequately. Q16

D5.1.6. Answers to case study questions: Hypothesis tests conducted with Gadget and have obtained directions on importance of complexity in models. Q16

Milestones and expected results

This workpackage is a part of the work towards milestones M4, M5 and M6.

5.2 Workpackage: Case study: Celtic Sea

Start date or starting event: July, 2001

N^o of the partner responsible: 8

N^{o}s of other partners involved: 7

Table 18: Person-months by partner within workpackage

Partner	1	2	3	4	5	6	7	8
2000	.	.	.	.	.	.	0	3.0
2001	.	.	.	.	.	.	5	2.7
Total to date	.	.	.	.	.	.	5	5.7
Total planned	.	.	.	.	.	.	11	15.0

Time to completion of workpackage (current estimate): 24

Objectives

To implement models for selected species in the Celtic Sea that incorporate both spatial and temporal information on the stocks.

To validate model system components and incorporate into a prototype system for the evaluation of closed areas.

To consider management parameters such as total biomass by area, spawning stock biomass (SSB) by area, and catch by metier by area.

Description of work conducted to date

CEFAS (7):
Gathered database of stomach contents data for Celtic Sea fish, and considered how species might be divided into functional groups for the purpose of modelling, on the basis of Bray-Curtis similarity coefficients and hierarchical agglomerative clustering.

Started constructing preliminary Ecopath food-web model of the Celtic Sea and assimilating groundfish survey data, diet data and fishery data. Also started gathering data on growth parameters and locating possible sources of benthos data. Plan to evaluate the effect of aggregating or disaggregating different model components, and/or isolating individual target species. Considered whether fishery target species are also ecologically important species.

Considered relationship between fish size and trophic level in Celtic Sea and North Sea fish annex in report for 2000.

Dates of interim meetings: Lowestoft (6-8 May 2001), Nantes (28-29 January 2002)

Combined Celtic Sea database (Annex E.2)

French and UK landings records were categoriesd by vessel size (3 categories) and gear (9 categories), and new ‘dst2’ identifiers were appended to each entry in the database. Summary tables containing the number of vessels or fishing ’sequences’ falling into each of these categories were then produced and compared (also see workpackage 1.3 and Annex E.2).

Number of individual records entered into database

CEFAS (7):
Stomach contents records (3314), otolith readings (64083), survey length records (85127), survey numbers & weights (11263), tagging/recapture records (24885), commercial catch records (2009460), market sampling length records (314343), length/maturity records (61311), depth records (500), bottom stress records (479), temperature records (3408), sediment records (284), vessel records (84380).

Analysis of French fishing activity (Annex E.4)

IFREMER (8):
The French commercial catch data was analysed and fishing metiers were identified based on catch profiles (catch in value). Six main metiers were defined (Annex E.4).

The French commercial effort data was further analysed in order to establish homogenous zones and seasons of fishing activity. For this the times spent fishing in a given statistical rectangle per month for the years 1991-1998 was modelled using generalised models and using month, rectangle and year as explanatory covariables. The estimated rectangle coefficients were then grouped using a Wald test as the distance statistics. The same method was applied to the month coefficients. This leads to the definition of 12 spatial zones and 5 seasons (Annex E.4).

Revised species list for Celtic Sea GADGET model (Annex E.5).

Established importance of different target and non-target species in terms of commercial catch, abundance in the community (survey data), monetary value, predation impact, prey for other consumers (see annexe celticEcopath.doc.). Examined dietary overlap and interaction between chosen species using a preliminary ECOPATH model. Revised list of up-to 14 species to be included in final GADGET model: cod, whiting, hake, haddock, Nephrops, blue whiting, mackerel, horse mackerel, sole, plaice, megrim (L. whiffiagonis & L. boscii), monkfish (L. piscatorius & L. budegassa).

Compared French & UK survey data (Annex E.6)

CEFAS (7) and IFREMER (8):
The consistency of the survey data, given that the surveys are carried in different seasons, use different gear and vessels, and that the duration of the available series differs (French 1991-2001, UK-autumn 1981-1988, UK-spring 1981-2001) was carried out by looking at single species abundance estimates and comparing community indicators. Although differences for individual species estimates were found, overall trends as well as community indicators provided similar signals. This analysis provides reassurement that the French and UK survey data series can be used together in fitting a Gadget model for the Celtic sea. The study results are summarised in Annex E.6.

Stomach contents database & modelling

Both UK and French stomach contents records are in the process of being computerised (from raw paper records/logbooks). These different data-sets provide complimentary but different information concerning the feeding behaviour of Celtic Sea fishes. The UK data (1991-1994), comprises detailed information on the capture location, the length of a given predator, the number of prey items in a given stomach, the state of digestion and where possible the length of individual prey items. The French data (1977-1985) is not geographically explicit but it does comprise of the length of the predator, the number and weight (in grams) of individual prey items. For hake, the French data also provides the length of individual prey fishes. In addition the UK data were primarily collected in the spring (and for years when survey data are available) whilst the French data were collected in the autumn.

The combined UK and French data will provide geographically and temporally explicit, information on the interactions between different species in the Celtic Sea GADGET model. It will provide detailed information concerning size-selectivity patterns and the statistical properties inherent in the data will be explored using the procedures developed by Stefánsson & Pálsson (1997), including presence-absence modelling.

Stefánsson, G. & Pálsson, Ó.K. (1997), Statistical evaluation and modelling of the stomach contents of Icelandic cod (Gadus morhua). Canadian Journal of Fisheries and Aquatic Science 54, 169-181.

Running GADGET (under the guidence of partner 1, MRI)

Initial attempts to operate GADGET within the UNIX emulator CYGWIN, highlighted many problems and conflicts. However construction of single-species, single-area GADGET models within Linux (version 7) has been more successful for cod (UK) and whiting (France). These preliminary models will be combined into a multi-species model at a meeting in Nantes during March 2002. All GADGET models constructed by partners 7 and 8 will use common 'time' and 'area' files, and data-files will span the period 1991-1998. It was agreed that blue whiting (*Micromesistius poutassou*) should be the next species modelled, since this interacts strongly with both cod and whiting. It is intended that the GADGET models constructed will initially be Single area - single species-single fleet models, building on the haddock example presented in the 2000-2001 dst2 report. Models will then be combined into multi species - single area and multi species - multi area models.

Tagging data (Annex E.3)

Tagging/recapture records (24885) for sole, plaice and cod were entered into the Celtic Sea data base. Most cod were recaptured within same rectangle as where they were originally released (Annex E.3), thus providing limited scope for modelling migration or drift. Data for sole and plaice are more extensive and offer greater scope for future modelling work (also see workpackage 2.1).

Deliverables

D5.2.1. Prototype data sets for the Celtic Sea. Q6 **Complete**

D5.2.2 Adopted model run for each species based upon agreement with existing historical data and knowledge of the fishery. Q16

D5.2.2 Comparison of externally estimated parameters with values obtained using the GADGET modelling approach. Any difference in the estimates obtained to be explored. Q12

D5.2.3 Comparative evaluation of simple model approach (single species) and complex model approach (multi-species). Q14

Milestones and expected results

This workpackage is a part of the work towards milestones M4, M5 and M6.

5.3 Workpackage: Case study: North Sea herring

Start date or starting event: Completion of North Sea Herring components of the Data Warehouse.

N^o of the partner responsible: 6

N^{o}s of other partners involved:

Table 19: Person-months by partner within workpackage

Partner	1	2	3	4	5	6	7	8
2000	.	.	.	.	.	0	.	.
2001	.	.	.	.	.		.	.
Total to date	.	.	.	.	.	?	.	.
Total planned	.	.	.	.	.	50	.	.

Time to completion of workpackage (current estimate): 24

Objectives

To implement prototype models for North Sea herring, based on a common program base and a data warehouse for the area and species in question, and to investigate the appropriateness of current short- and medium-term management approaches.

Description of work conducted to date

This workpackage was due to start mid-year 2001 when prototype runs are due to start.

FRS (6): Due to staff turn-over, work for this package has just started. A framework for validation and testing is being set up. No results are yet available.

Deliverables

D5.3.1. Prototype model run. Q7 **Delayed. To be conducted in 2002**.

D5.3.2. Proposed generic Improvements (to be programmed in WP 3). Q9

D5.3.3. Adopted model run on adopted data where the model explains data adequately. Q16

D5.3.4. Evaluations of key project objectives for case study:

D5.3.4.1.Validation of conventional estimates of stock size and exploitation rates using the 'gadget' modelling approach, and exploration of main points of difference. Q16

D5.3.4.2. Comparative evaluation of complex-model and simple-model approaches to estimating short-term catch forecasts and stock sizes. Q16

D5.3.4.3. Validation of existing management approaches for North Sea herring. Q16

Milestones and expected results

This workpackage is a part of the work towards milestones M4, M5 and M6.

A Deliverables

This section provides summaries of all deliverables, ordered according to their due status, indicating their completion status.

It must be noted that in several cases the definition of "complete" is subjective. The approach taken is to list a deliverable as "complete" if a product is available. In some cases the product is a required prototype, in other cases a final product was originally envisaged but it has been found that a prototype is sufficient at present and advancement on other workpackages can proceed as planned. In some cases (e.g. D1.1.1) a prototype is available but is not enough and in these cases the delay or revised schedule is duly noted.

More detail on each deliverable in relation to the corresponding workpackage is given in the body of the report.

A.1 Status of due deliverables

The following table lists the deliverables due by the end the second year, not earlier reported as complete, along with their due quarter and completion status.

WP		Deliverable	Quarter	Status
1.1	D1.1.1	Corrected, documented data base for Icelandic waters.	Q5	Currently ongoing at a revised (delayed) pace
1.1	D1.1.2	Corrected, documented data base for North Sea herring.	Q5	Ongoing. Database nearly complete. Data are being prepared for the Warehouse.
1.1	D1.1.4	Corrected, documented prototype data base for the Celtic Sea.	Q5	Complete
1.2	D1.2.1	DW design.	Q5	Complete (in the form of a prototype DW).
1.3	D1.3.1	Algorithms and a set of SQL programs to be used for taking the raw data and converting the data into summaries useful for ecosystem modelling.	Q7	Complete
1.5	D1.5.1	Design of data warehouse views.	Q4	Complete
1.6	D1.6.2	Known techniques of DW implementation using XML are described and tested	Q6	Complete
1.6	D1.6.3	CORBA technology described in detail and tested.	Q6	Simple tests finished by SCUI in 2000. Restarted in 2002
1.6	D1.6.4	The results of using CORBA and XML compared.	Q7	Starting in 2002 (revised schedule and deliverable).
1.6	D1.6.5	Final choice of DW software set up, tested and distributed.	Q8	First distribution has been sent from DIFRES to MRI.

2.1	D2.1.1	Initial, simple migration model.	Q4	Complete
2.4	D2.4.1	Mathematical formulation of general populations dynamics models in state space form.	Q3	Complete
2.4	D2.4.3	Prescription to incorporate relevant prior information into population dynamics models.	Q4	Complete
3.1	D3.1.1	Mathematical descriptions of estimation methods for model components.	Q8	Algorithms available. Documentation pending.
3.1	D3.1.2	Descriptions of goodness-of-fit tests for composite likelihoods.	Q8	Completed (Annex D.2)
3.2	D3.2.1	Program modules to carry out estimation for likelihood and Bayesian estimation.	Q8	Likelihood-based estimation complete. Bayesian part postponed.
3.2	D3.2.3	A program which can utilise parallel processing for improved performance.	Q8	Complete
5.1	D5.1.1	Prototype data sets for the area around Iceland.	Q6	Complete.
5.1	D5.1.2	Prototype model run (Iceland).	Q7	Complete
5.2	D5.2.1	Prototype data sets for the Celtic Sea area.	Q6	Complete
5.3	D5.3.1	Prototype model run for North Sea herring.	Q7	Delayed, revised pace.

There are a large number deliverables in this project, of which the above 20 are due at this time.

A.2 Earlier deliverables, now completed

The following table lists those deliverables which were due and completed before this year of reporting.

Deliverable	Quarter	Status		
1.4	D1.4.1	Prototype data sets for Gadget and prototype data warehouse views.	Q3	Complete
1.5	D1.5.2	Design of the database structures.	Q4	Complete
1.6	D1.6.1	Each institute provides descriptions of the data storage format used.	Q6	Complete.
2.4	D2.4.2	Corresponding general population dynamics program modules.	Q4	Complete

A.3 The next steps

The following table lists the remaining deliverables, due in 2002-3.

1.6	D1.6.6	Data warehouse for Icelandic waters.	Q9	Prototype in place
1.6	D1.6.7	Data warehouse for North Sea herring.	Q9	Ongoing
1.6	D1.6.9	Data warehouse for the Celtic Sea.	Q9	Ongoing
1.7	D1.7.1	Software to set up all data and parameter files for Gadget.	Q9	Ongoing, mainly through revisions to Gadget input file formats.
2.1	D2.1.2	A proposed mathematical (migration) model formulation for use in Gadget.	Q12	Ongoing at MRI, SCI, UiB.
2.1	D2.1.3	Evaluation of reduction in variances as a result of reducing uncertainty in data sources.	Q12	Started, MRI.
2.2	D2.2.1	A module to describe the recruitment process.	Q12	Ongoing, mainly at IMR. Closure of life cycle in Gadget ongoing at MRI.
2.3	D2.3.1	Mathematical models of the growth and maturation process.	Q12	Preliminary models available.
3.1	D3.1.3	Implementations and tests of different estimation procedures in different scenarios.	Q12	
3.1	D3.1.4	Algorithmic description of estimation methods and goodness-of-fit tests.	Q12	
3.2	D3.2.2	A selected (composite) minimisation algorithm.	Q12	Complete
3.2	D3.2.4	An evaluation of the effect of parallelisation.	Q12	
3.2	D3.2.5	A set of standard fisheries examples that can be used to check that algorithms are correctly implemented.	Q10	Complete

4.1	D4.1.1	Age- and size-dependent growth and predation mortality for cod, capelin and juvenile herring in the Barents Sea.	Q9	
4.1	D4.1.2	Maps of horizontal distribution of cod, capelin and juvenile herring in the Barents Sea.	Q9	
4.1	D4.1.3	Estimates of cod's consumption of capelin and herring related to prey density, stock overlap and physical factors.	Q9	
4.1	D4.1.4	Estimation of the distribution or the variance of the relative stomach contents.	Q9	
4.1	D4.1.5	Final vital (consumption) statistics to Gadget.	Q12	
4.2	D4.2.1	Effects of different levels of disaggration in Gadget.	Q14	
4.3	D4.3.1	Definition of multispecies reference points for North Sea fisheries.	Q12	

5.1	D5.1.3	Proposed generic model improvements (to be programmed in task 3).	Q9	Complete.
5.1	D5.1.4	Prototype data warehouse with data for this case study based on definitions in task 1.	Q9	
5.1	D5.1.5	Adopted model run on adopted data set.	Q16	
5.1	D5.1.6	Answers to case study questions.	Q16	
5.2	D5.2.2	Adopted model run for each species.	Q16	
5.2	D5.2.2	Comparison of externally estimated parameters with Gadget.	Q12	
5.2	D5.2.3	Comparative evaluation of simple model approach (single species) and complex model approach (multi-species).	Q14	
5.3	D5.3.2	North Sea herring. Proposed generic Improvements .	Q9	
5.3	D5.3.2	North Sea herring. Proposed generic Improvements (to be programmed in WP 3).	Q9	
5.3	D5.3.3	North Sea herring. Adopted model run on adopted data set.	Q16	
5.3	D5.3.4	North Sea herring. Evaluations of key project objectives for case study.	Q16	

B Datawarehouse

B.1 DST2 data warehouse solution

Figure 1 shows an Internet/CORBA solution for the data warehouse interface. The solution involves an Internet server with PHP interface and CORBA access to the databases. Only two of the 3 data warehouse sites are shown on the figure.

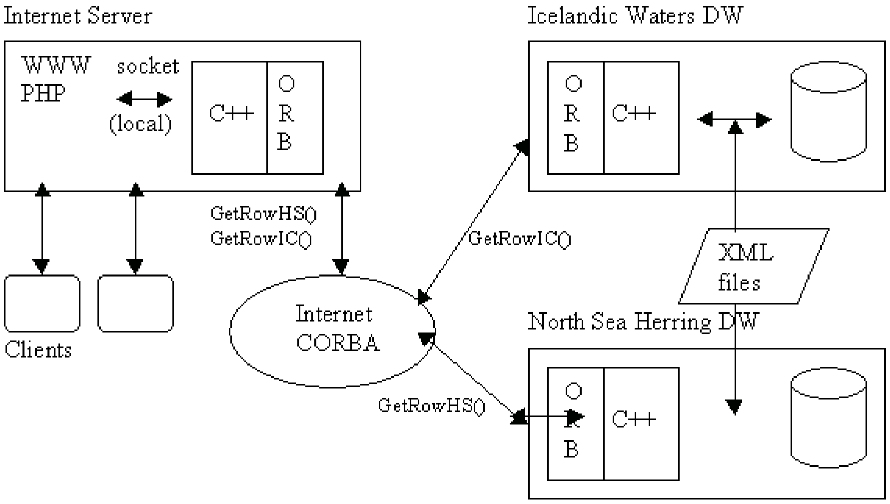


Figure 1. CORBA solution

Figure 1. CORBA solution

The user interface is programmed in PHP and runs on an Internet server. The database component is programmed in C++ (or java) so it works with the Object Request Broker. CORBA transparently sends the data request to the right database server. The data from the database is returned in XML format. Data can also be uploaded in XML format. If CORBA is to complicated to implement and alternative solution is to use HTTP between the Internet server and the database servers instead. This is a much simpler solution, but the databases will have to be explicitly accessed from the user interface.

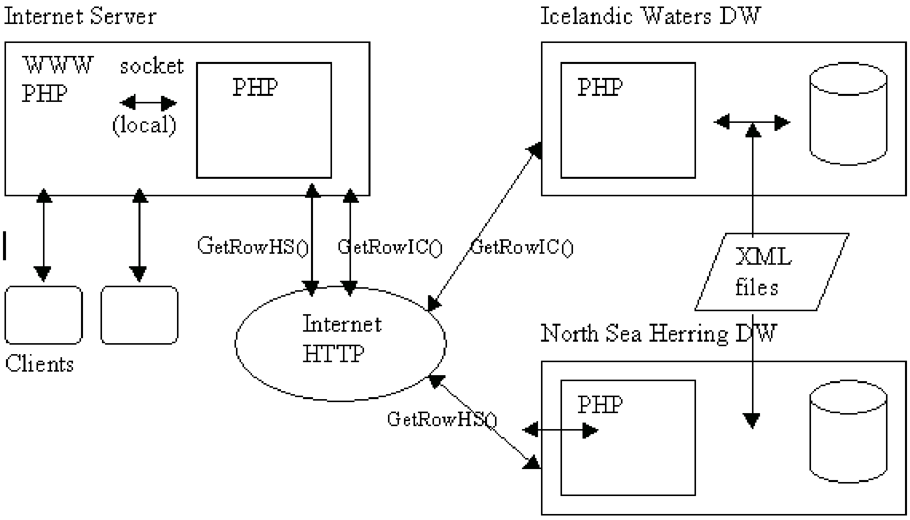
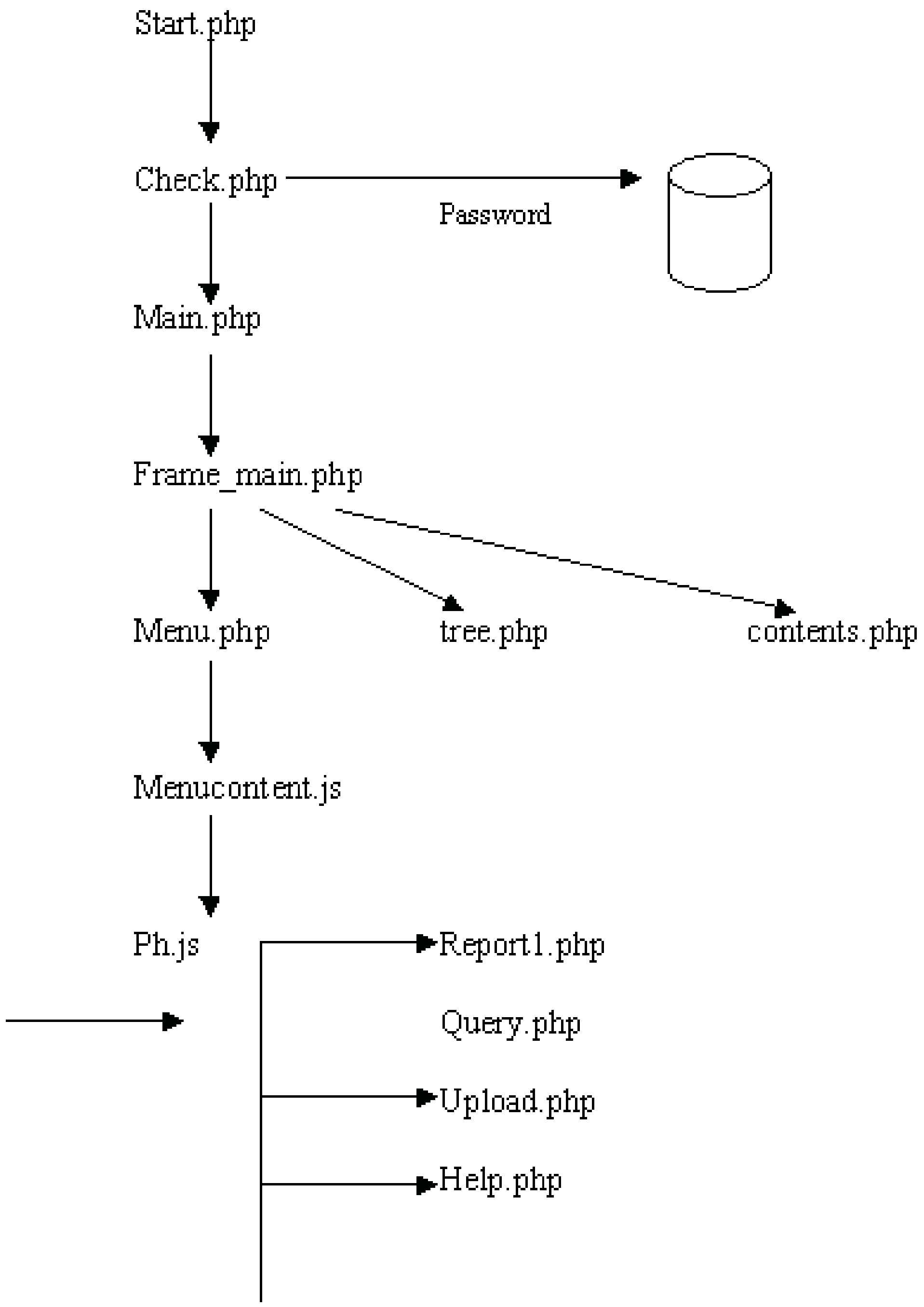


Figure 2. HTTP solution

B.2 The Web Interface program

The structure of the existing Web Interface prototype application is complicated and may be better structured in the final version. The main structure of the application is:



The user interface is installed as a website on an Apache server. The interface connects to the data warehouse, which is a PostgreSql database. When the client links to the website the start.php program is loaded. The program requests a username and a password, which are checked in the database. The username is associated with a database role; which determines what the user can do in the system. The possible roles are Dst2Reader, Dst2Writer and Dst2Admin.

The main program displays a frameset with three frames, the menu, the data tree and the contents. The menu is build by a javascript (menucontents.js). The menu points are managed by another javascript (Ph.js), which displays the right php file in the contents frame.

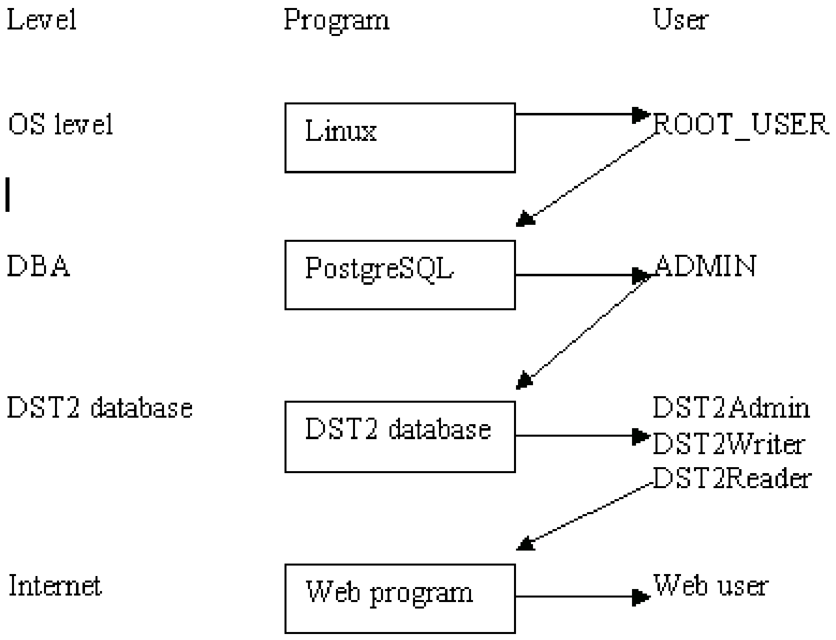
Dependent on the chosen menu item the program jumps to the page; which holds the wanted functionality. The following functionalities are built in the user Interface:

Report1:	Fixed data report system
Query:	Free SQL based data request from the data warehouse
Upload:	Upload of data to the data warehouse
Help.php:	Links to different documents

The user can also access the user administration page if the user has administrator role. New functionalities can easily be linked to the system.

B.3 Security system on the data warehouse server

The system operates with different users and passwords at different levels. At the Linux level there must be a ROOT_USER, which can install the PostgreSQL. At the PostgreSql level there is a database manager (DBA) called ADMIN, which can create the DST2 database. On the DST2 database level there are three user groups (database roles), DST2Admin with all rights, DST2Writer with write and read access and DST2Reader with read access only. The users on the Web interface are registered in the DST2 database with one of the three database roles. The security system is shown here:



B.4 XML and its use in the DST2 project

What is XML?

XML stands for Extensible Markup Language. Thus XML is a markup language like HTML. The extensible part makes it possible to define your own markup language in normal text formats and send data as a XML file to anyone else. The receiver can then use XML tools to easily retrieve the data from the XML file. XML is an easy way for different applications to talk to each other. If an application can understand XML then it can send or receive any kind of information to any other application that understands XML.

XML is a specification created by the World Wide Web Consortium (W3C), the same consortium behind HTML. It is free to use and well documented. The specification can be found at www.w3.org/XML.

XML and data exchange Like HTML, XML uses tags to define its elements and the tags can be nested. If the names of tables and data fields are used as tags, XML can depicts the structure of a whole relational database. Figure 1 shows a XML file with a few sample data and environment data from the DST2 database. There is a one to many relation between Sample and Environment. In this example 2 sample records with each 2 related environment records are shown. This example is very simple of course, in fact it is possible to send all the data from all the tables in the DST2 database, in a single XML file.

```
<?xml version="1.0" encoding="UTF-8"?>
<!-- edited with XML Spy v4.2 U (http://www.xmlspy.com)
by Peter Sandbeck (Danmarks Fiskeriundersogelser) -->
<DST2 xmlns:xsi="http://www.w3.org/2001/XMLSchema-instance"
xsi:noNamespaceSchemaLocation="dst2.xsd">
      <Sample>
            <Institute>DFU</Institute>
            <Year>1998</Year>
            <Quarter>2</Quarter>
            <Month>5</Month>
            <Region>3</Region>
            <Division>34</Division>
            <Subdivision/>
            <Gridcell/>
            <Areaaggregate>2</Areaaggregate>
            <Timeaggregate>2</Timeaggregate>
            <Vesselclass/>
            <VesselSubclass/>
            <Gearclass/>
            <GearSubclass/>
            <Environment>
                  <Week>20</Week>
                  <DepthStratum>5</DepthStratum>
                  <Temperature>10.5</Temperature>
                  <Salinity>29.3</Salinity>
                  <Zooplankton>5.5</Zooplankton>
            </Environment>
            <Environment>
                  <Week>20</Week>
                  <DepthStratum>15</DepthStratum>
                  <Temperature>9.2</Temperature>
                  <Salinity>30.5</Salinity>
                  <Zooplankton>150.5</Zooplankton>
            </Environment>
      </Sample>
<Sample>
            <Institute>DFU</Institute>
            <Year>1999</Year>
            <Quarter>2</Quarter>
            <Month>5</Month>
            <Region>3</Region>
            <Division>34</Division>
            <Subdivision/>
            <Gridcell/>
            <Areaaggregate>2</Areaaggregate>
            <Timeaggregate>2</Timeaggregate>
            <Vesselclass/>
            <VesselSubclass/>
            <Gearclass/>
            <GearSubclass/>
            <Environment>
                  <Week>20</Week>
                  <DepthStratum>5</DepthStratum>
                  <Temperature>9.5</Temperature>
```

```
                  <Salinity>28.3</Salinity>
                  <Zooplankton>12</Zooplankton>
            </Environment>
            <Environment>
                  <Week>20</Week>
                  <DepthStratum>15</DepthStratum>
                  <Temperature>8.6</Temperature>
                  <Salinity>30.0</Salinity>
                  <Zooplankton>200</Zooplankton>
            </Environment>
      </Sample>
</DST2>
```

Figure 1. XML file with Sample and Environment data (simplified)

XML schemas

In order to make the data exchange efficient the users must agree upon the structure of the XML file. Which data do we want to exchange, how are they structured and which data types are used for which data? A XML schema is such a file which describes the structure of a XML document. XML schemas have some advantages over other kinds of document type definitions (DTD). The XML schema itself is written in XML, so it can be used by applications as any other XML document. XML schemas can also include other XML schemas by defining them as namespaces. This makes it possible to use the same tags in different XML schemas. The XML parser know where to lookup the definition of a given tag by looking at the namespace for that tag. It is also possible to include data type definitions, maximum and minimum values for data elements, enumeration value sets and whether a given data element is optional or mandatory. This kind of information is defined as attributes to the XML elements. Figure 2 shows a XML schema corresponding to the XML file shown in figure 1. In figure 1 it is also shown, how the XML file is linked to the XML schema.

```
<?xml version="1.0" encoding="UTF-8"
?>
<xs:schema xmlns:xs="http://www.w3.org/2001/XMLSchema">

<xs:complexType name="DST2Type">
<xs:complexContent>
      <xs:restriction base="xs:anyType">
       <xs:sequence minOccurs="1" maxOccurs="unbounded">

<xs:element name="Sample" type="SampleType"/>
        </xs:sequence>
      </xs:restriction>
</xs:complexContent>
</xs:complexType>

<xs:complexType name="SampleType">
<xs:complexContent>
      <xs:restriction base="xs:anyType">
       <xs:sequence>
             <xs:element name = "Institute" type ="InstituteType"/>
            <xs:element name = "Year" type ="YearType"/>
            <xs:element name = "Quarter" type ="QuarterType"/>
            <xs:element name = "Month" type ="MonthType"/>
            <xs:element name = "Region" type ="RegionType"/>
```

```
            <xs:element name = "Division" type ="DivisionType"/>
            <xs:element name = "Subdivision" type ="SubdivisionType"/>
            <xs:element name = "Gridcell" type ="GridcellType"/>
            <xs:element name = "Areaaggregate" type="AreaaggregateType"/>
            <xs:element name = "Timeaggregate" type="TimeaggregateType"/>

            <xs:element name = "Vesselclass" type="VesselclassType"/>
            <xs:element name = "VesselSubclass" type="VesselSubclassType"/>
            <xs:element name = "Gearclass" type="GearclassType"/>
            <xs:element name = "GearSubclass" type="GearSubclassType"/>

<xs:sequence minOccurs="0" maxOccurs="unbounded">

            <xs:element name = "Environment" type="EnvironmentType"/>
       </xs:sequence>
       </xs:sequence>
</xs:restriction>
</xs:complexContent>
</xs:complexType>

<xs:complexType name="EnvironmentType">

<xs:complexContent>
      <xs:restriction base="xs:anyType">
       <xs:sequence>
             <xs:element name = "Week" type ="WeekType"/>
            <xs:element name = "DepthStratum" type ="DepthStratumType"/>

<xs:element name = "Temperature" type ="TemperatureType"/>

<xs:element name = "Salinity" type="SalinityType"/>

<xs:element name = "Zooplankton" type="ZooplanktonType"/>

       </xs:sequence>
</xs:restriction>
</xs:complexContent>
</xs:complexType>

<xs:simpleType name="InstituteType">
<xs:restriction base = "xs:string">
</xs:restriction>
</xs:simpleType>

<xs:simpleType name="YearType">
<xs:restriction base = "xs:float">
<xs:maxInclusive value="2100"/>
<xs:minInclusive value="1900"/>
</xs:restriction>
</xs:simpleType>

<xs:simpleType name="QuarterType">
<xs:restriction base = "xs:float">
<xs:maxInclusive value="4"/>
<xs:minInclusive value="1"/>
</xs:restriction>
```

```
</xs:simpleType>

<xs:simpleType name="MonthType">
<xs:restriction base = "xs:float">
<xs:maxInclusive value="12"/>
<xs:minInclusive value="1"/>
</xs:restriction>
</xs:simpleType>

<xs:simpleType name="RegionType">
<xs:restriction base = "xs:string">
</xs:restriction>
</xs:simpleType>

<xs:simpleType name="DivisionType">
<xs:restriction base = "xs:string">
</xs:restriction>
</xs:simpleType>

<xs:simpleType name="SubdivisionType">

<xs:restriction base = "xs:string">
</xs:restriction>
</xs:simpleType>

<xs:simpleType name="GridcellType">
<xs:restriction base = "xs:string">
</xs:restriction>
</xs:simpleType>

<xs:simpleType name="AreaaggregateType">

<xs:restriction base = "xs:string">
</xs:restriction>
</xs:simpleType>

<xs:simpleType name="TimeaggregateType">

<xs:restriction base = "xs:string">
</xs:restriction>
</xs:simpleType>

<xs:simpleType name="VesselclassType">

<xs:restriction base = "xs:string">
</xs:restriction>
</xs:simpleType>

<xs:simpleType name="VesselSubclassType">

<xs:restriction base = "xs:string">
</xs:restriction>
</xs:simpleType>

<xs:simpleType name="GearclassType">
<xs:restriction base = "xs:string">
```

```
</xs:restriction>
</xs:simpleType>

<xs:simpleType name="GearSubclassType">

<xs:restriction base = "xs:string">
</xs:restriction>
</xs:simpleType>

<xs:simpleType name="WeekType">
<xs:restriction base = "xs:float">
<xs:maxInclusive value="52"/>
<xs:minInclusive value="1"/>
</xs:restriction>
</xs:simpleType>

<xs:simpleType name="DepthStratumType">

<xs:restriction base = "xs:float">
<xs:maxInclusive value="10000"/>
<xs:minExclusive value="0"/>
</xs:restriction>
</xs:simpleType>

<xs:simpleType name="TemperatureType">

<xs:restriction base = "xs:float">
<xs:maxInclusive value="50"/>
<xs:minInclusive value="-5"/>
</xs:restriction>
</xs:simpleType>

<xs:simpleType name="SalinityType">
<xs:restriction base = "xs:float">
<xs:maxInclusive value="50"/>
<xs:minInclusive value="0"/>
</xs:restriction>
</xs:simpleType>

<xs:simpleType name="ZooplanktonType">

<xs:restriction base = "xs:float">
<xs:minExclusive value="0"/>
</xs:restriction>
</xs:simpleType>

<xs:element name="DST2" type="DST2Type"/>

</xs:schema>
```

Figure 2. XML schema for DST2 data (only Sample and Environment data)

XML file browsing and data validation

Since XML files are simple text files they can be read by normal text editors. Some special XML editors like XMLSpy are able to display the data in a more readable form. They can also check that the XML document is syntactically correct and applies to its defined XML schemas. The most advanced XML viewers are also able to examine the defined element restrictions and validate the data according to these. By using such a program the users can check the XML files before they are exchanged. The file checking also includes data validation according to the schema. The XML file in figure 1 has been evaluated with the XML schema in figure 2 with the program XMPSpy. The XML file is valid according to the XML schema.

Downloading and uploading of data in XML files

Most modern databases and programming languages include components to handle XML documents. This makes it possible to move data from a XML file to an object in a program without having to do much programming. The object in the program can then handle data, evaluate data and upload the data to a database. If the structure of the data in XML equals the structure in the database table, the uploading of data can also be done without much programming. The same applies for data downloading from a database to a program. XML can also be used to send data between two software components e.g. a database interface component and a user interface component. The data is streamed to an intermediate XML file by one component and the file is read by the other component. Since data is stored in XML, both the structure of the database table and the data itself is moved between the two software components.

XML and DST2

In the DST2 project it was decided not to use XML as the data exchange format for several reasons. The most important reason was that the users, which have to deliver data to the three database sites are not familiar with XML. It would be very difficult for them to extract data in a predefined XML structure. It is much easier to extract the data in a simple character separated format. The data exchange format should also be used to send data directly from one user to another. By using character separated text files it is easier to upload data directly into e.g. a spreadsheet program. Another reason is that the gadgets for the data models are not able to import data in XML format, but also requires character separated formats. However XML can be used to exchange data between the database and the user interface programs. This will be useful when a CORBA or HTTP interface is incorporated at the database sites for data querying. The data queried in the database can be streamed to a XML file, from which the interface program retrieves the queried data. Since the structure of the XML file reflects the queried data defined by SQL strings, it is not convenient to define XML schemas in this case.

B.5 Work plan for 2002

Task	**Date**	**Responsible**
Lookup data in DB	Jan. 15, 2001	MRI
DB extra fields in exchange Format and upload program	Jan., 15	DIFRES, (MRI)
Programmers meeting CORBA/HTTP?, XML?	January	All
Data in all databases	Mar, 1	All
Design document of CORBA and XML solution	Apr, 1	MRI/DIFRES
Design document of Web server	Apr, 1	DIFRES/MRI
Implementation of ORB And C++	Dec, 1	MRI
Implementation of Web Server	Dec, 1	DIFRES
Create output DW files = input for gadgets	Dec, 1	MRI/DIFRES
Finish of project	Dec, 15	ALL

C Biological modelling

C.1 A model of the formation of fish schools and migrations of fish

RH-28-2001

Simon Hubbard, Petro Babak,
Sven Th. Sigurdsson and Kjartan G. Magnússon

Division of Applied Mathematics and Computer Science
Science Institute, University of Iceland
Dunhaga 3
107 Reykjavík
Iceland

Abstract. We consider an individual based, discrete and stochastic model for the collective motion of fish. The fish are regarded as self-propelled interacting particles, such that the motion of individual fish is governed by two" forces": a tendency to imitate the motion of other fish in a local neighbourhood and an external vector field, such as a temperature gradient or food density gradient. In addition, there is a stochastic component, which can be defined in such a way that the entire group will tend to move in the direction towards a specified region, taken to be the spawning grounds. The model includes boundaries representing for example isotherms or depth contours where specific behaviour of individual fish can be defined. We then present simulations of a hypothetical fish stock migrating between feeding grounds and spawning grounds.

1. Introduction.

Some pelagic fish species, such as capelin (Mallotus villosus) and herring (Clubea harangus), undertake extensive feeding and spawning migrations, covering distances of several hundred miles (Vilhjámsson, 1994; Misund et al, 1998; Slotte and Fiksen, 2000). These movements may to some extent be governed by genetic factors, but the timing and route of the migrations are also influenced by a variety of other factors: environmental conditions such as boundaries between warm and cold water masses, certain isotherms which, as a rule, the fish do not cross, bottom topography, oceanic currents, density of food, and internal variables such as the physiological state and the state of maturity of each fish. In addition, the population density may influence the extent of feeding migrations. Field observations of the size, shape, density, speed and behaviour of herring schools have shown that there is considerable variability in these parameters, depending on whether the fish are searching for food, moving to or from the spawning grounds, searching for spawning sites, etc (Nøttested et al, 1996; Misund et al, 1998).

The capelin stock in the Central North Atlantic provides a good illustration of the migration phenomena (Vilhjalmsson, 1994). The movements of this fish stock are shown in Fig. 1. The stock migrates northward in early summer to feeding grounds in the Jan Mayen area and returns in late summer to the North and Northwest coast of Iceland. It gradually moves clockwise around the island and ends up at the spawning grounds off the Southwest coast in March-April. In some years a component of the stock migrates in a counter-clockwise direction to the spawning grounds. The size of this component is very variable. A number of features have been observed in connection with the migrations of this stock:

- Schools tend not to cross fronts between cold and warmer waters but to migrate along these boundaries. This applies also to certain isotherms, such as –1° C. This tendency not to cross but migrate along cold water fronts is also known in N. -Atlantic herring (Misund et al, 1998).
- Cruising speeds are highly variable and the schools may halt completely for a while.

- The geographical path is fairly constant, but may vary, particularly due to changing locations of cold water fronts and isotherms.
- The spawning stock enters the spawning grounds in a number of runs, possibly along different routes.
- Part of the stock may undertake feeding migrations; part may stay in more or less the same location.

Although the motivation behind this work is an attempt to simulate and predict the spawning and feeding migrations of North Atlantic capelin and North Atlantic herring, the model presented here is nevertheless generic in the sense that it describes general movements between feeding grounds and spawning grounds. The species and area specifics are the overall region containing the movements of the stock under consideration, the spawning area, the general feeding areas, boundaries such as isotherms and depth contours, and scalar fields for temperature and food density.

The purpose in developing a model to describe and predict migrations and spatio-temporal distributions is primarily to construct a tool whereby various assumptions and hypotheses about mechanisms and other factors, environmental and otherwise, which may influence the migrations and spatial distribution of fish may be tested. The model predictions will eventually be compared to various types of field data such as acoustic survey data, tagging data, data on the spatial distribution of catches, etc.

A number of different kinds of models have been developed to describe migrations. The simplest type is based on transition matrices (Tjelmeland and Bogstad, 1998). The overall region is divided into a number of sub-areas and a transition matrix $A(t)$ is defined whose elements $a(i,j,t)$ are simply the fraction of the fish in sub-area i which move to sub-area j between times t and $t+1$. This model is purely empirical in the sense that the values of the matrix elements are estimated from whatever data is available on spatio-temporal distributions or are simply the results of guesswork. Another approach which injects some biology into the model via behavioural evolutionary ecology is to predict the migratory pattern by optimising a fitness function, usually the total expected reproduction, by selecting the most profitable habitats through time (Fiksen, Giske and Slagstad, 1995). A third approach is to model the spatial distribution as a continuum by transport-diffusion equations or Navier-Stokes type equations (Okubo, 1986; Toner and Tu, 1995, 1998).

The model described here concentrates on individual fish in a school. It is discrete in time, individual based and stochastic. The motion of a fish has a deterministic and a stochastic component. The former is governed by two principal forces: firstly, an alignment force which makes an individual fish (or small school) attempt to imitate the motion of its neighbours, and secondly, a force which is determined by an external vector field, such as a temperature gradient or a food density gradient. The deterministic part of the motion of each fish is therefore determined by the inclination to follow the group and by a tendency to move towards a more favourable environment in terms of temperature and/or food density. In addition, the speed and direction of motion are influenced by random perturbations. The probability density function for this random variable is parameterised such that a tendency of the fish to move in specified directions can be varied. These directions are determined by so-called attracting regions, usually spawning areas, and the movements are therefore determined by non-local effects in addition to the local forces. This directional tendency is strong in the period prior to the spawning season, but weak or non-existent on the feeding grounds.

Boundaries are defined by specified isotherms, by cold water fronts and by specified depth contours. No-flux conditions hold at such boundaries in the sense that schools, which cross such boundaries are “pushed” back by the action of a gradient field e.g. a temperature field.

Vicsek et al (1995) present a simple model for the motion of self-driven interacting particles in a plane. This model will form a starting point for the work described in this paper and will therefore be briefly described here. All particles have the same fixed speed, but each particle is characterized by a direction of motion given by an angle θ. The dynamical equations for the position of the i-th particle are governed by the equation

$$\begin{pmatrix} x_i(t+\Delta t) \\ y_i(t+\Delta t) \end{pmatrix} = \begin{pmatrix} x_i(t) \\ y_i(t) \end{pmatrix} + v \begin{pmatrix} \cos\theta_i(t) \\ \sin\theta_i(t) \end{pmatrix} \Delta t \tag{1}$$

where v is the speed of the particles and $\theta_i(t)$ is the angle of the direction of motion of the i-th particle at time-step t. This angle is in the interval $(-\pi, \pi]$ and is updated at each time-step as follows

$$\theta_i(t+\Delta t) = \langle \theta_j(t) \rangle_{i,r} + \xi_i^t \tag{2}$$

where $\langle \theta \rangle_{i,r}$ denotes the average angle of motion of all particles inside a circle of radius r surrounding the given particle (including the particle itself) and the ξ's are independent random variables, uniformly distributed, i.e.

$$\xi \sim U\left[-\frac{\eta}{2}, \frac{\eta}{2}\right] \tag{3}$$

representing the noise in the motion. The assumption of uniformness means that all perturbation angles in the interval are equally likely. The average angle $\langle \theta \rangle_{i,r}$ is obtained by taking the direction angle of the average of individual direction vectors i.e.

$$\left(\langle \cos\theta_j \rangle_{i,r}, \langle \sin\theta_j \rangle_{i,r} \right) \tag{4}$$

where the average is taken over all particles within a distance r of particle i.

The updated direction angle of particle i is therefore the direction angle of the average of the unit direction vectors for all neighbouring particles plus a random perturbation. Equation (2) has some biological basis since there is experimental evidence showing that fish sense the motion of their neighbours - visually and by means of the lateral line -and change their motion on the basis of this information (Partridge, 1982).

Model (1)-(4) is of some interest since the spatial patterns exhibited have similarities to field observations of schooling fish. For high values of noise (i.e. large η) the particles tend to form groups moving coherently in random directions. This pattern has been observed in North Atlantic herring on feeding grounds with schools swimming around in various directions searching for prey (Misund et al, 1998). At low noise values (and high densities) the motion becomes ordered on a macroscopic scale and all the particles tend to move in the same spontaneously selected direction (Vicsek et al, 1995). This pattern corresponds to the motion of schools on migration. The motion can therefore change from a pattern where small schools move randomly in different directions – this type of motion will be called a feeding mode – to the coherent motion of all schools (as one large school) in the same direction, by decreasing the value of the noise. This type of motion will be called a migration mode. Periodic boundary conditions are imposed in the Vicsek model, meaning that the motion is on a torus and because of the symmetric probability distribution on ξ the direction taken by the whole school in the migration mode is arbitrary and random. This is not appropriate for a migration model and will need to be modified.

We will attempt to generalise Vicsek's model by introducing a number of other features, such as variable speeds, "directional" noise instead of uniform noise, boundaries and boundary conditions and force fields due to temperature and food density.

2. Model description

2.1 Dynamical equations

The model consists of a collection of particles (or fish) moving in a plane, within a prescribed domain. The particles are self-propelling, with particle i having speed v_i , and a direction of motion given by the angle θ_i. The general dynamical equations for the position of the i-th particle are

$$\begin{pmatrix} x_i(t+\Delta t) \\ y_i(t+\Delta t) \end{pmatrix} = \begin{pmatrix} x_i(t) \\ y_i(t) \end{pmatrix} + v_i(t) \begin{pmatrix} \cos\theta_i(t) \\ \sin\theta_i(t) \end{pmatrix} \Delta t \tag{5}$$

where the unit vector in the direction of the velocity vector is the normalized weighted average of two unit vectors. The first,

$$\underline{p}(t) = \begin{pmatrix} \cos\varphi_i(t) \\ \sin\varphi_i(t) \end{pmatrix}$$

represents the effects of the neighbouring particles on the direction of motion. The direction angle of this vector is calculated as in Vicsek's model, i.e. by

$$\varphi_i(t+\Delta t) = \langle \varphi_j(t) \rangle_{i,r} + \xi_i^t \tag{6}$$

where $\langle \varphi \rangle_{i,r}$ denotes the average angle of motion of all particles inside a circle of radius r centred on the i-th particle. The particles therefore try to align themselves with the average direction of motion of the particles in their local neighbourhood. The term ξ_i^t is a random perturbation of the direction angle.

The other unit vector is

$$\underline{q_i}(t) = \frac{\nabla T(x_i(t), y_i(t))}{\|\nabla T(x_i(t), y_i(t))\|}$$

i.e. in the direction of the gradient of a potential function *T(x,y)*, for example temperature or food density. This vector is set to zero if the gradient is zero.

The speed is calculated by

$$v_i(t+\Delta t) = \langle v_j(t) \rangle_{i,r} + \varsigma_i^t \tag{7}$$

where $\langle v \rangle_{i,r}$ denotes the average speed of all particles inside a circle of radius r centred on the i-th particle and ζ_i^t is a random perturbation. The particles therefore try to match the speed of their neighbours.

The weighted average of the two unit vectors is

$$\underline{w}_i(t) = \big((1-\alpha_i(t))\underline{p}_i(t) + \alpha_i(t)\underline{q}_i(t)\big), \qquad 0 < \alpha_i(t) < 1 \tag{8}$$

and the velocity is therefore

$$v_i(t)\begin{pmatrix} \cos\theta_i(t) \\ \sin\theta_i(t) \end{pmatrix} = v_i(t)\frac{\underline{w_i}(t)}{\|\underline{w_i}(t)\|} \tag{9}$$

which is thus the weighted average of two terms, the first one representing the tendency to follow the group and the second a tendency to react to local environmental conditions and move in the direction of increasing food density or lower/higher temperatures. The weights α will depend on time and can in theory be different for different particles. Furthermore, the weights may depend on the local environmental conditions, i.e. on $T(x,y)$ and/or $\nabla T(x,y)$.

Two remarks are appropriate at this point. Firstly, the time increment Δt is chosen in such a way that a fish aligns itself completely with the average direction of its neighbours in time Δt and also adjusts it speed completely in that time increment, see equations (6) and (7). Secondly, one way of quantifying the weights α is to let them depend on the time constants associated with the two factors determining the direction of motion. Let T$_1$ be a characteristic reaction time to changes in the average direction of motion of the particles in the neighbourhood of a specified particle and let T$_2$ be the characteristic reaction time to the environmental gradient. We have defined Δt to be the reaction time of a particle in aligning itself to the average direction of motion and can therefore put $T_1 = \Delta t$. Assuming that the characteristic reaction time to the environmental gradient is $T_2 = \beta\Delta t$, we can put

$$\alpha = \frac{\frac{1}{\beta\Delta t}}{\frac{1}{\Delta t} + \frac{1}{\beta\Delta t}} = \frac{1}{\beta+1} \qquad \text{and hence} \qquad 1-\alpha = \frac{\beta}{\beta+1}.$$

Thus, if β>1, i.e. the reaction time to the direction of the neighbours is less than the reaction time to the environmental gradient, then the unit vector in the former direction gets a higher weight.

We sometimes have occasion to use the term “force”. It is however not used in the standard physical sense, but in a rather loose way meaning a vector which influences the direction a particle will move in.

2.2 Formulation of noise

With uniform noise the eventual direction of motion in the migration model is undetermined. We therefore modify the probability distribution of the noise component and formulate a so-called “directional noise” where some directions are more likely than others. The probability density of ξ is given by

$$p_\xi(x) = \frac{2\gamma}{\eta^2}x + \frac{1}{\eta}, \qquad -\frac{\eta}{2} \le x \le \frac{\eta}{2} \tag{10}$$

where

$$\gamma = \kappa_\theta \frac{\theta_i^0(t) - \theta_i(t)}{\pi}, \qquad 0 \le \kappa_\theta \le 1 \tag{11}$$

see Figure 2, where the parameter $\theta_i(t)$ is the direction angle of the motion of the i-th particle. The angle, $\theta_i^0(t)$, is defined as follows. We specify an attracting point, which typically is in the spawning region. The parameter $\theta_i^0(t)$ is the direction angle from the present position of the particle to the attracting point, i.e. the direction angle of the vector $(x_0 - x_i(t), y_0 - y_i(t))$ where $(x_i(t), y_i(t))$ are the co-ordinates of the present position of the i-th particle and (x_0, y_0) are the co-ordinates of the attracting point. Thus, if the difference between the actual angle, $\theta_i(t)$, and the desired angle, $\theta_i^0(t)$, is positive, then it follows that the slope of the probability density function for the perturbation angle is positive. This means that positive perturbation angles are more likely than negative ones and hence the particle is more likely to move in the direction towards the attracting point than away from it, see Fig. 3. When a fish is ready to start on its spawning migration – e.g. when it has achieved a sufficient level of energy reserves – it experience a "pull" from the spawning grounds such that the random changes in direction are more likely to be towards the spawning grounds, than away. This "pull" can be simulated in the model by means of the directional noise described above.

Usually, κ_θ will be taken to be either zero or one, i.e. the directional noise is either switched on or off. The noise is uniform if $\kappa_\theta = 0$, but fully directional if $\kappa_\theta = 1$. Note that $-\pi < \theta_i^0 - \theta_i(t) \le \pi$ and thus $|\gamma| \le \kappa_\theta$. The expected value of ξ is

$$E[\xi] = \frac{\gamma\eta}{6}$$

and the variance

$$V[\xi] = \frac{\eta^2}{36}(3 - \gamma^2)$$

The variance with the directional nose "off"- i.e. $\kappa_\theta = 0$ - is $\frac{\eta^2}{12}$, but decreases as the directional noise is "switched on", i.e. $\frac{\eta^2}{18} \le V[\xi_{\kappa=1}] \le \frac{\eta^2}{12}$, depending on $\theta_i^0(t) - \theta_i(t)$.

We further note that the expected value implies that the expected characteristic reaction time to the "pull" is $\frac{6\pi}{\eta}\Delta t$.

The probability distribution of ζ, the random component of speed is given by

$$p_\varsigma(x) = \frac{2\lambda}{\mu^2}x + \frac{1}{\mu} \qquad -\frac{\mu}{2} \le x \le \frac{\mu}{2} \tag{12}$$

where

$$\lambda = \kappa_v \max\left\{\min\left\{v_0 - v_i(t), 1\right\}, -1\right\}, \quad 0 \le \kappa_v \le 1 \tag{13}$$

Here v_0 is a reference speed or an average cruising speed. Thus particles which are moving slower than the reference speed are more likely to speed up and particles moving faster are more likely to slow down. This reference speed may depend on environmental conditions and/or the physiological state of the fish. The above formulation of λ means that $|\lambda| \leq \kappa_v \leq 1$, which ensures that $p_\varsigma(x)$ is non-negative. As with the directional noise, κ_v is usually set to zero or one.

2.3. Environmental force fields

The motion may be influenced by an external gradient field $\nabla T(x,y)$ as discussed above. In the simulations described below, we consider two different gradient fields: one given by the food density and another given by the temperature. The $\nabla T(x,y)$ -term in equation (8) is a weighted average of these two gradient fields, where the weights may vary with location and time. We refer to the $\nabla T(x,y)$ direction as a "preferred direction" at *(x,y)*.

2.4. Boundaries and boundary conditions

The movements of the particles are restricted by boundaries, which in the context of migrating fish can be specific isotherms, boundaries between warm and cool water masses, specific depth contour lines, etc. These boundaries are in general, not crossed or only to a limited extent and boundary conditions are imposed to ensure this. The boundary conditions considered are of three types, two types represent the behaviour of particles encountering physical obstacles, and the third represents the boundary between two different states within the domain, which the particles can cross to a limited extent. The condition at a boundary are: 1) Tangential condition, where the direction of the motion becomes tangential to the boundary; 2) reflective condition, where the particle is reflected off the boundary and 3) repulsion condition, where the particle once it is on the wrong side of a boundary, experiences a force field pointing out of the region and is therefore "repulsed" back towards the boundary (Fig.4). For example, a fish may cross an isotherm before realising that the temperature conditions are unfavourable, and subsequently re-cross the boundary as directed by a temperature gradient field.

3. Simulations

The simulations described here show a hypothetical cycle of migrations between feeding and spawning grounds. Most of the main features discussed above are illustrated in this scenario (Fig. 5). The feeding grounds are at the top of each panel (north) and the spawning grounds at the bottom (south), just south of a barrier representing an island surrounded by a depth or temperature contour which the fish cannot cross. To the west there is another boundary representing a temperature isotherm, which the fish prefer not to cross. They are drawn to the spawning grounds by directional noise but to the feeding grounds by a gradient field for food density. The temperature field acts at the western boundary repulsing the fish, which happen to cross the boundary, back to the eastern side of this isotherm. The motion on the local scale is governed by the alignment force for direction and speed as described above, in addition to the environmental force field and the random perturbations which are uniformly distributed except on spawning migrations where the distribution is skewed giving rise to directional noise.

A surface for food density is defined, where the height of the surface increases towards the feeding grounds, giving rise to a gradient field pointing in that direction. This hypothetical surface is shown in Fig. 6. The prime feeding grounds are inside the dashed curve. Outside this curve the gradient field draws the fish towards the prime feeding grounds – i.e. α>0 in Equation (8). Once the fish find themselves on the prime feeding grounds, i.e. inside the dashed curve, their motion will no longer be affected by the gradient field – i.e. $\alpha = 0$. The rationale is that the food density on the prime feeding grounds is sufficiently high so that the fish do not need to search for areas of higher density. However, the density is not homogeneous on the prime feeding grounds and fish build up energy reserves at different rates depending on their location. When a critical energy level is reached those fish start to migrate to the spawning grounds. The timing of the onset of spawning migration is therefore different for fish in different locations.

Fig. 5 (a-f) shows "snapshots" taken from a simulation showing a cycle of spawning and feeding migrations. Each circle represents a group of particles, where a group is defined as a set of particles such that every particle within the group is less than a set distance from at least one other particle within the group. The circle is centred on the average position of the particles in the group and has an area proportional to the number of particles in a group. A line segment shows the average direction and speed of the group. The values of the various parameters are given in Table 1.

Parameter	Symbol	Value
Number of particles	n	250
Size of domain in x direction		1000
Size of domain in y direction		2000
Size of local neigbourhood		1.0
Relative weighting	a	0.003
Angle noise amplitude	h	0.075
Speed noise amplitude	m	0.05
Time step	?t	0.1
Reference velocity inside feeding and spawning areas	v(0)	0.5
Reference velocity outside feeding and spawning areas	v(0)	1.0

Table 1: Values of parameters in the simulations.

In Fig. 5a the fish are all within the feeding area denoted by the dashed closed curve. Should they happen to stray outside, the gradient field will quickly guide them back in, towards the area of higher food density. However, inside the curve there is no preferred direction ($\alpha = 0$); the only forces affecting the motion are the alignment force and random perturbations with a uniform distribution. The particles form small groups moving coherently, i.e. a typical “feeding mode” behaviour.

Each fish has an associated “energy” level, which increases only when the fish is inside the feeding area. As the energy of a fish reaches a threshold level the directional noise is switched on and the fish is drawn towards the spawning area, with the attracting point being the centre of the spawning area. This is shown in Fig. 5b. The directional noise is switched on at different times for different schools of fish, depending on when they reach the threshold level, which again depends on where they have been feeding.

The fish may encounter and react to a repulsive boundary (a dashed line) and an “island” (a solid ellipse). The repulsive boundary represents an isotherm with the fish preferring to stay on the eastern (warmer) side of this boundary. The fish may cross to the west side, but are repulsed back towards the boundary by a preferred direction determined a temperature gradient field. The “island” does not necessarily represent a coastal boundary but, for example, a depth or temperature contour. The boundary condition on this boundary is reflective. In spite of the reflective boundary conditions the fish nevertheless follow the boundary, as shown in Fig. 5c, due to the influence of the other fish since the “reflected” fish align themselves with the others. The majorirty of the fish are guided clockwise around the island due to the repulsive boundary to the west. The motion is not influenced by food density, and the temperature field only comes into play when the repulsive boundary is crossed. The directional noise is therefore the only factor responsible for the direction of motion outside the constraint of boundaries.

Once the particles have reached the spawning region (shown as a dashed ellipse, Fig. 5d), they experience uniform noise. Outside the spawning region they are guided by a directional noise back towards the spawning region. Again the fish form coherently moving small schools as shown in Fig.7a which is a “blow-up” of the spawning region in Fig. 5d. It may appear as if schools overlap or small schools are contained inside bigger schools, but this is not the case. The size of the each circle representing a school is not related to the physical dimensions of the school, only to the number of individuals in the school. Figure 8 illustrates this by giving two different representations of the motion of schools on the spawning grounds. The upper panel shows the circles but the lower panel shows the direction of motion of individual particles. This shows that the schools are distinct even though the respective circles overlap to some extent. Furthermore, it is clear that particles in each school all have more or less the same velocity and are therefore moving as a coherent whole.

At a fixed point in time on the cycle all the fish switch from a spawning mode to a feeding mode. The directional noise is no longer active, preferred directions are switched on and the migration towards the feeding grounds is governed by the gradient vector field for food density. As shown in Fig. 5e all the fish take the easterly route around the island because of the repulsive boundary and move in few relatively large schools. Schools may get temporarily caught in the corner between the island and the repulsive boundary, trying to take the westerly route but they escape eventually. Fig. 5f shows the fish having returned to the feeding area, with small schools moving coherently in different directions. Fig. 7b is a “blow-up” of the feeding area showing the distribution in the size and direction of schools.

Fig. 9 shows the complete trajectories of five individual fish, the upper panel illustrating the southward spawning migration and the lower panel, the northward feeding migration. The five spawning migration paths are fairly distinct – one fish even takes the westerly route around the island in spite of the repulsive boundary - and have an erratic appearance. The reason is that fish start the migration at different times and are guided towards the spawning grounds by the directional noise giving the paths a highly stochastic appearance. On the other hand, all fish start the feeding migration at the same time, encouraging alignment, and the direction of motion is to a large extent governed by a deterministic gradient field which is constant in time. All trajectories are rather similar as a consequence.

The results from a second simulation where the position of the repulsive boundary is further to the west is shown in Fig. 10. This boundary no longer crosses the island boundary and has therefore little or no influence on the migration. Only the main differences from the previous simulation are shown.

The fish start in a feeding mode in the feeding area moving in small schools as in the previous simulation. They then individually switch to the migration mode as the directional noise is “switched on”, moving towards the spawning region. Fish taking the westerly route around the island no longer encounter the repulsive boundary (Fig 8a), which formerly repelled them towards the easterly migration route. They therefore arrive at the spawning grounds along two different routes. Once in the spawning region the fish again form small groups, until they all start the northward feeding migration, again taking two migration routes around the island with the westerly component moving along the temperature boundary (Fig. 8b). Once the feeding region is reached the fish yet again form small coherently moving schools, and the simulation returns to the initial state.

4. Discussion

The model described here adds a variety of different features to the basic model presented by Viczek et al (1995). The latter model consists of self-propelled interacting particles moving at constant speed in a square with periodic boundary conditions with the direction of motion being governed by an alignment force plus a uniform random variable. The type of motion resulting depends on the magnitude of the variance of this random variable. Basically, the particles move in random directions in small groups (schools) for high values of noise, but all move in a coherent manner in the same direction if the noise is small. The modifications presented here are the following:

Variable speed has been introduced such that particles attempt to imitate the speed of their neighbours. A random perturbation in speed is added to the average. A reference speed is given such that the particles are more likely to speed up if they are moving slower than the reference speed and to slow down if moving faster. This reference speed may depend on environmental conditions, e.g. it may be low if the food density is high and vice versa and it may also depend on the ambient temperature. It could also be the most efficient cruising speed with respect to energy expenditure and may depend on the physiological condition of the fish and so on.

The possibility of letting the reference speed depend on environmental conditions has not been explored here. However, one characteristic of migrations is that cruising speeds are highly variable and the schools may even halt completely for a while (Vilhjálmsson, 1994). This may be accomplished in this model by letting the reference speed vary, e.g. with environmental conditions and/or the physiological condition of the fish.

Directional noise was introduced making some changes in direction more likely than others. This has the effect of influencing the motion such the schools move towards an attracting region, which is taken to be the spawning grounds. The directional noise is switched on and off depending on the location and the internal energy state of the fish. Thus, the fish start the spawning migrations from the feeding grounds when a critical energy threshold has been reached and the directional noise is switched on. Similarly, it is switched off when the spawning grounds are reached.

Boundaries and boundary conditions were introduced which can represent isotherms, boundaries between warm and cold water masses, depth contours, etc. Various types of boundary conditions ensure either that these boundaries are not crossed at all or if they are, then the fish are likely to move out again. Such boundaries will of course greatly influence the path the migrating schools take. The path may for example be clockwise around an island or both clockwise and counter-clockwise, depending on the location of a cold water front pushing the migration one way.

Environmental fields, representing gradient fields for temperature and food density were introduced. The motion may be driven completely by these forces. For example, a food density field directed towards the prime feeding grounds governs the feeding migration.

The migration as defined by the timing of the migration and the geographical path is governed by a kind of control system whereby the various forces are switched on and off. Thus, directional noise, which drives the spawning migrations, is switched on when a critical energy threshold is reached on the feeding grounds and off when the spawning grounds are reached. The influence of the food density gradient is switched on after spawning (it does not influence the spawning migration, since feeding is probably not important during this period) and the feeding migration is governed by the food density. Similarly, temperature sensitivity is switched on when the fish get into areas where the temperature is unfavourable and the temperature gradient repulses the fish out of these areas.

Although a great deal is known about what drives and governs the migrations of animals, this knowledge is by no means complete. Modelling the migration phenomena is therefore somewhat ambiguous since the empirical and biological basis for such modelling is frequently rather limited. For example, it is not well known what factors govern the migrations of capelin from feeding grounds in the far north to the spawning grounds south of Iceland i.e. what determines the start of the spawning migrations, how do the fish find their way to the spawning grounds, why do they spawn where they do and so on. These are the classic questions regarding animal migrations. It is likely that environmental conditions determine the timing and the precise route of the migration, as does the physiological state of the fish, but the basic migration pattern is possibly determined by genetic factors which draw the fish in the general direction towards the spawning grounds. This can be regarded as the action of a long range force which "pulls" the fish towards an attracting region. We have modelled this force as a directional noise, which has the effect of swinging the motion of the schools towards the spawning grounds.

Although modelling migrations is problematic due to the incomplete knowledge of the governing factors, a model can nevertheless be of great value since it allows different assumptions and hypotheses to be tested by comparing model predictions to field observations. This has not been done in this paper. What has been done is to formulate various mechanisms, which can make fish, and fish schools behave in a manner which is at least superficially similar to real situations.

The caplin migrations in the Central North Atlantic are to some extent a motivation for this modelling exercise, but the simulations presented here should not be taken literally as describing these migrations. For one thing, most of the capelin dies after spawning and there is therefore no feeding migration of a post-spawning stock. The northward migration can however, be considered to be the feeding migrations of the maturing class which will spawn in the following spring.

Some features have been left out in the simulations described in the paper. Repulsion and attraction forces between individual particles are an option in the model, but this feature was not included in the simulations described here. However, simulations have been carried out with these forces included. The results were not qualitatively different, but particle clusters are less dense as would be expected.

It should be noted that the model, which is described here, constitutes the initial steps towards constructing a model, which can satisfactorily describe migrations by using environmental data on temperature and food distribution and is parameterized in such a way that some of the parameters can be estimated using field observations. Some of the mechanisms are promising, e.g. alignment force, directional noise and repulsive boundary conditions, but there are many unresolved questions. For example, the connection between the different scales - i.e. the scale on which the interaction between particles take place (< 1 meter) and the scale of migration distances (tens of nautical miles) - needs to be investigated and a way found to combine them in an efficient and logical manner? The question whether the behaviour and the spatial patterns remain unchanged in a statistical sense when a region is blown up must also be addressed. This requires a statistical measure whereby the different spatial patterns and modes (feeding mode and migration mode) can be characterized. A related question is whether it is possible to think of a particle as a "super-individual" whereby a particle is regarded as a school of fish all behaving in an identical manner and moving as one individual.

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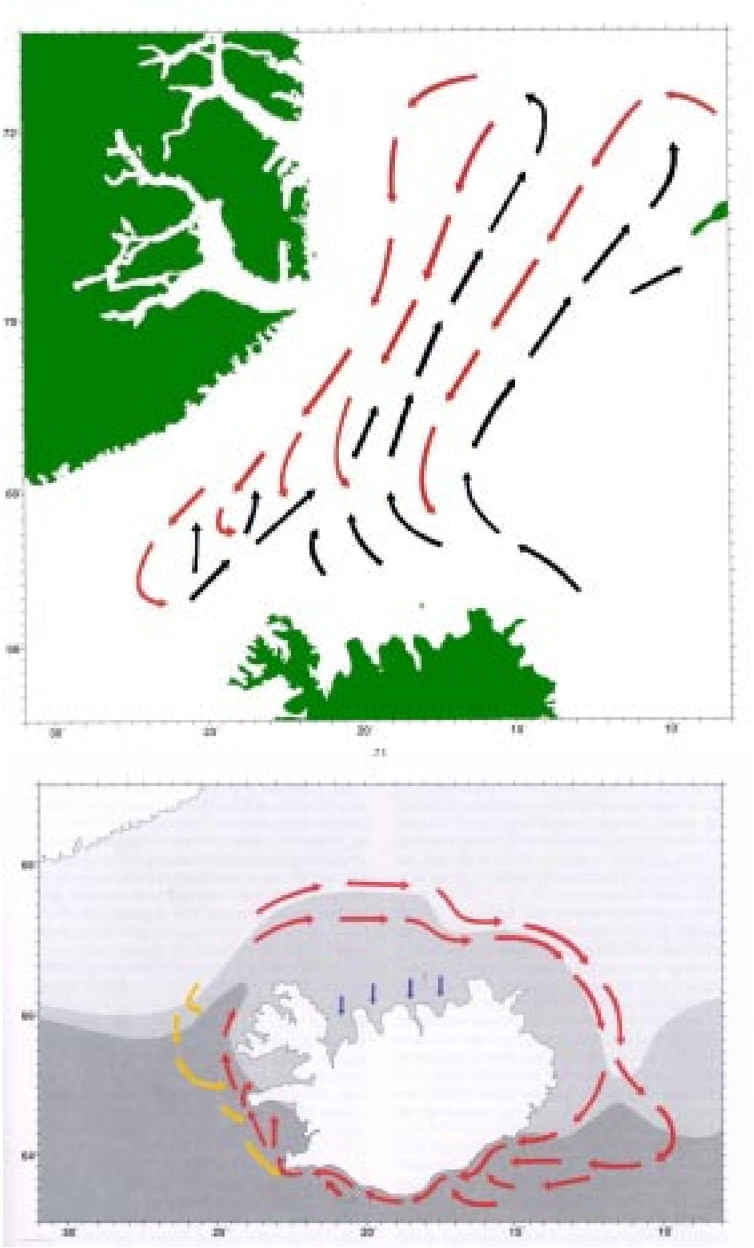

Figure 1: Feeding and spawning migrations of the Central North Atlantic stock of capelin. From Vilhjálmsson (1994).

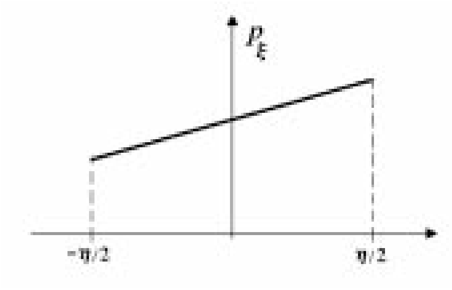

Figure 2: Probability density function of ξ, the random perturbation in direction angle.

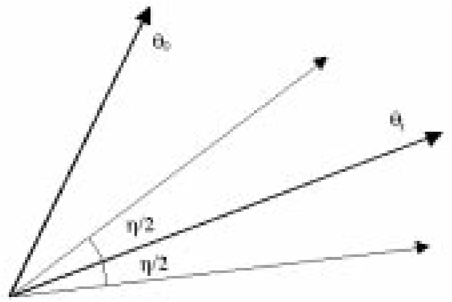

Figure 3: The desired direction, given by θ_0, the actual direction of motion of the particle, given by θ_i, and the range of possible perturbations. In the situation shown here the particle is more likely to turn to the left.

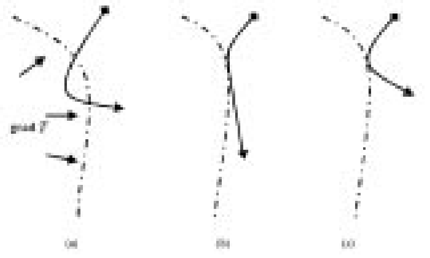

Figure 4: Illustration of the three different types of boundary conditions:(a) repulsive condition, (b) tangential condition and (c) reflective condition

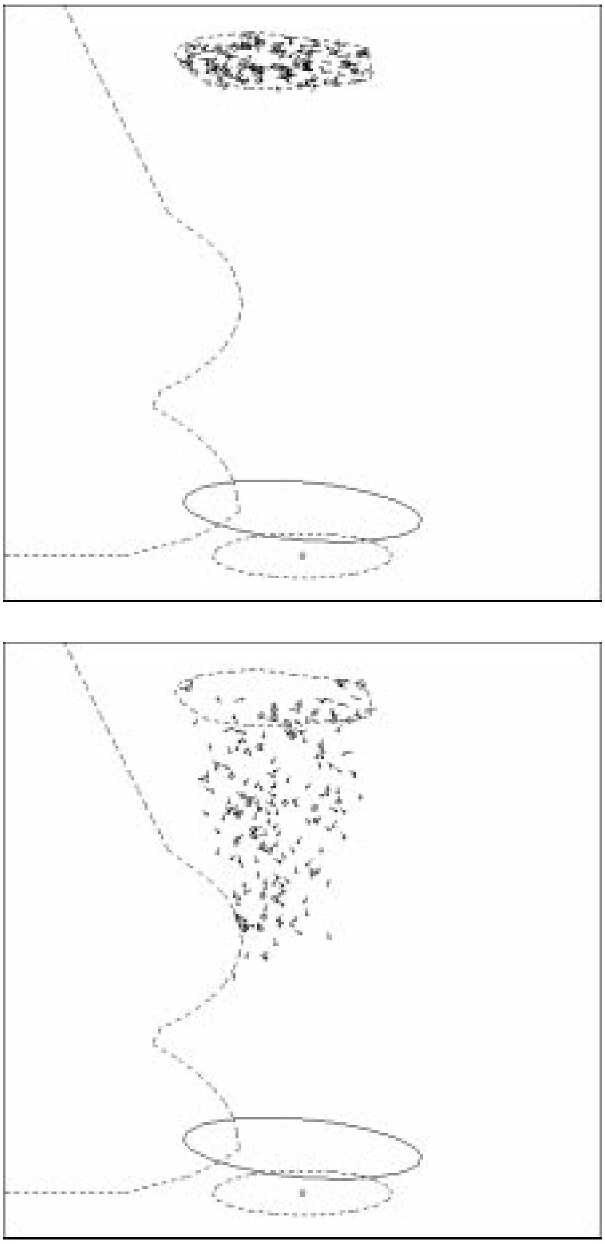

Figure 5: Simulation of one migration cycle between feeding and spawning grounds with an easterly temperature boundary. The panels show "snapshots" at different stages of the cycle. Panels (a) and (b).

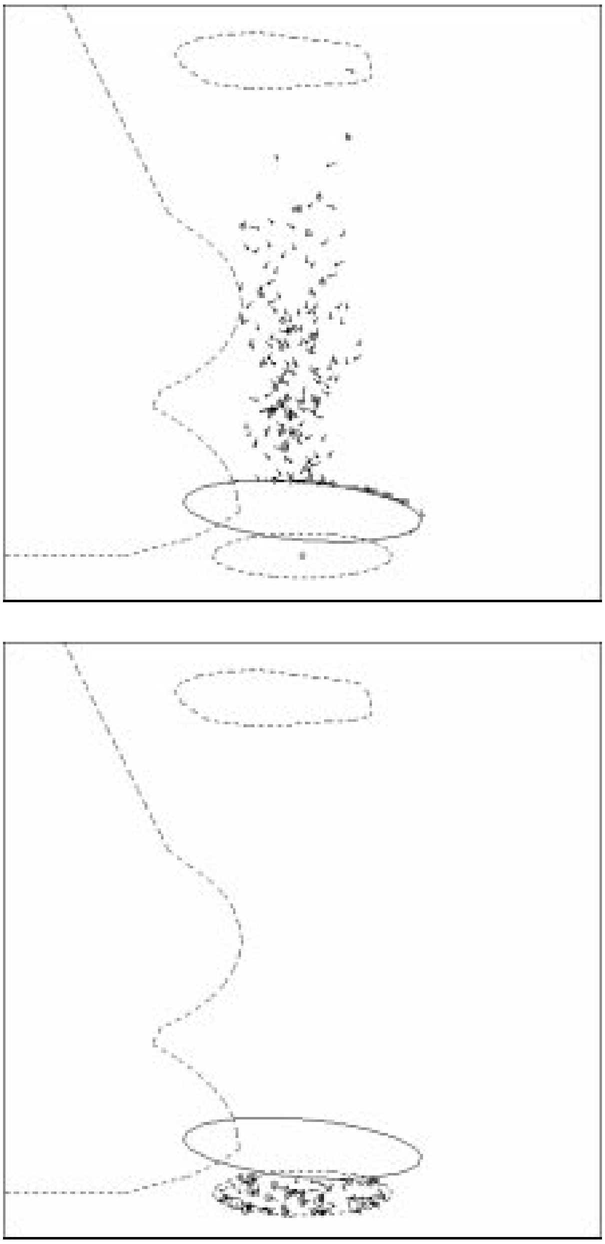

Figure 5: Simulation of one migration cycle between feeding and spawning grounds with an easterly temperature boundary. The panels show “snapshots” at different stages of the cycle. Panels (c) and (d).

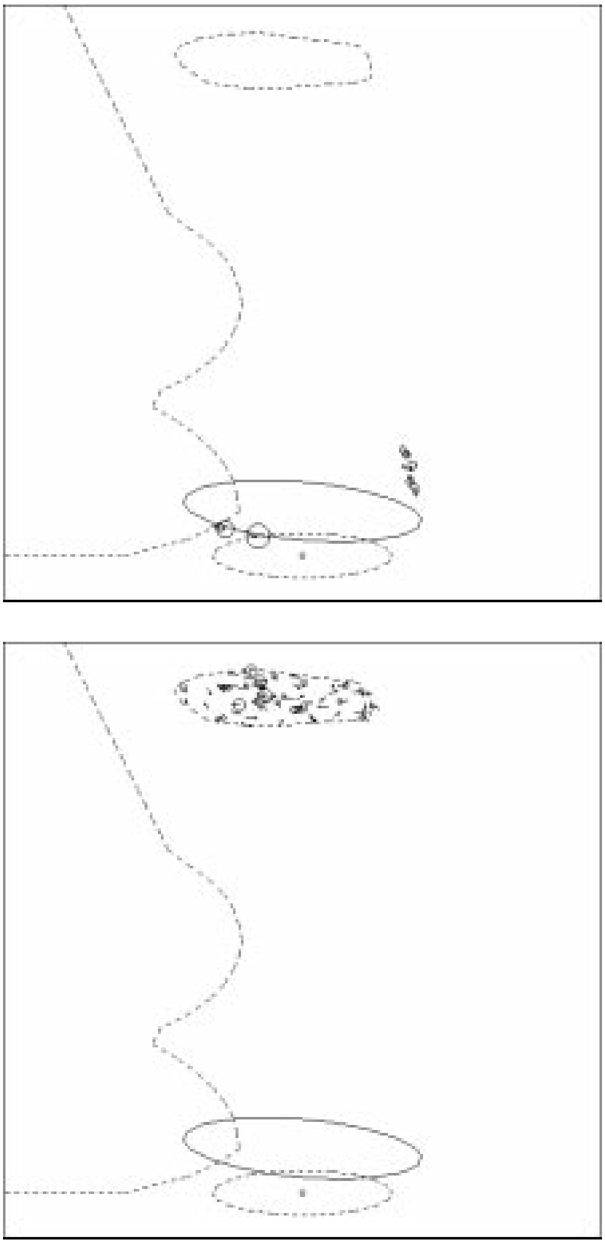

Figure 5: Simulation of one migration cycle between feeding and spawning grounds with an easterly temperature boundary. The panels show “snapshots” at different stages of the cycle. Panels (e) and (f).

Figure 6. A hypothetical food density surface with the associated gradient field. The dashed line is the boundary of the prime feeding grounds. The gradient does not play any part in the motion inside this boundary but the different density values affect how quickly the fish reaches a critical energy threshold allowing it to leave for the spawning grounds.

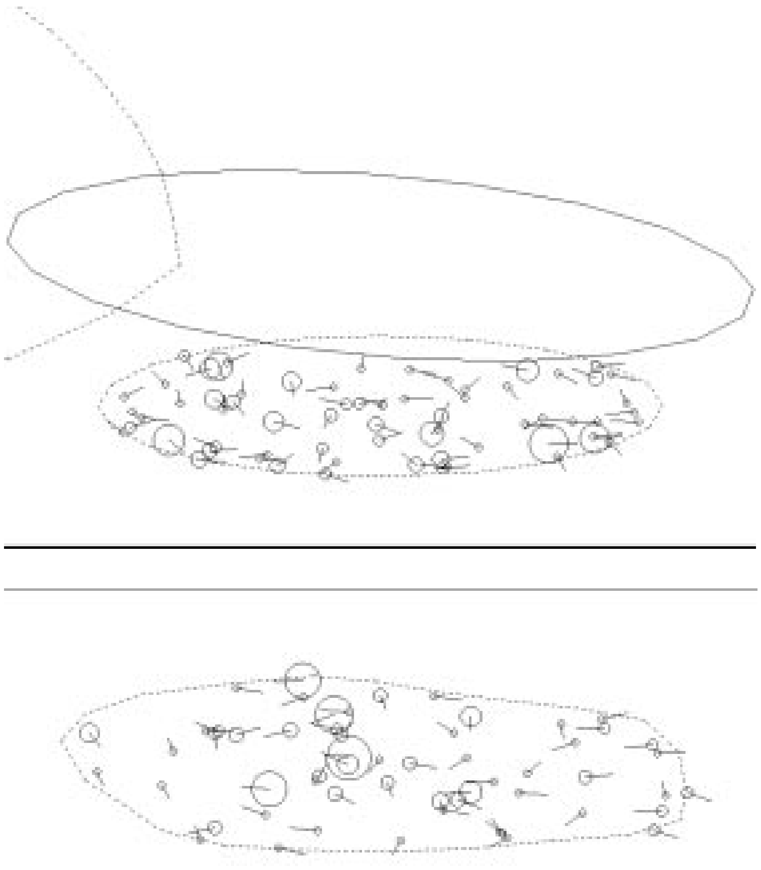

Figure 7. A close-up view of the distribution of schools on the spawning grounds (a, upper figure), and feeding grounds (b, lower figure). The area of each circle is proportional to the number of fish in the school and the line segment gives the direction of motion.

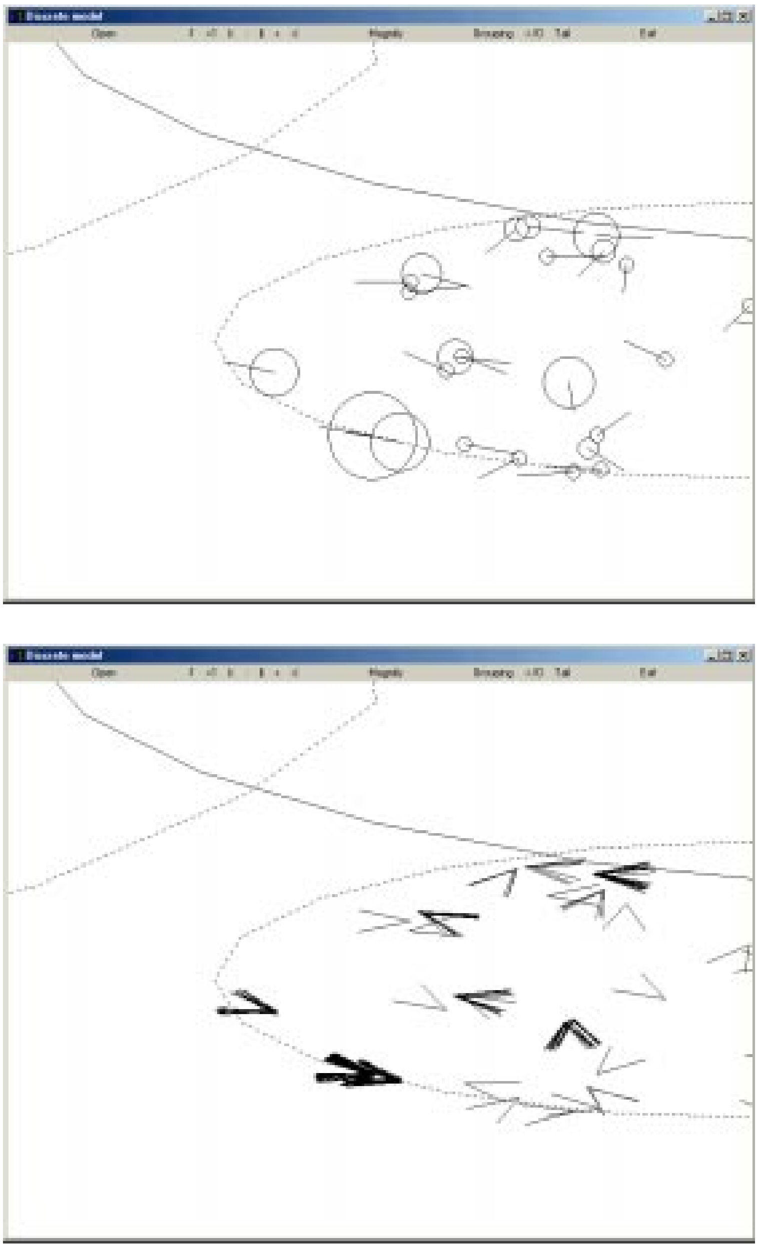

Figure 8. Direction of motion of schools and individual particles.

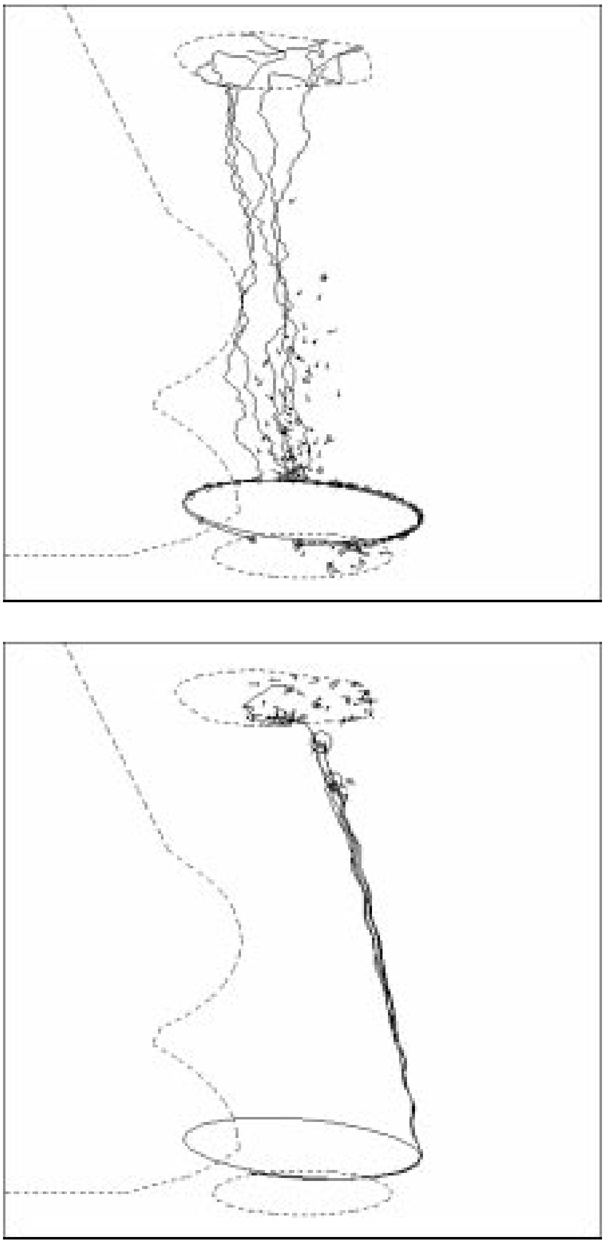

Figure 9. Five sample paths for five different particles. The upper panel shows the spawning migration and the lower panel the feeding migration.

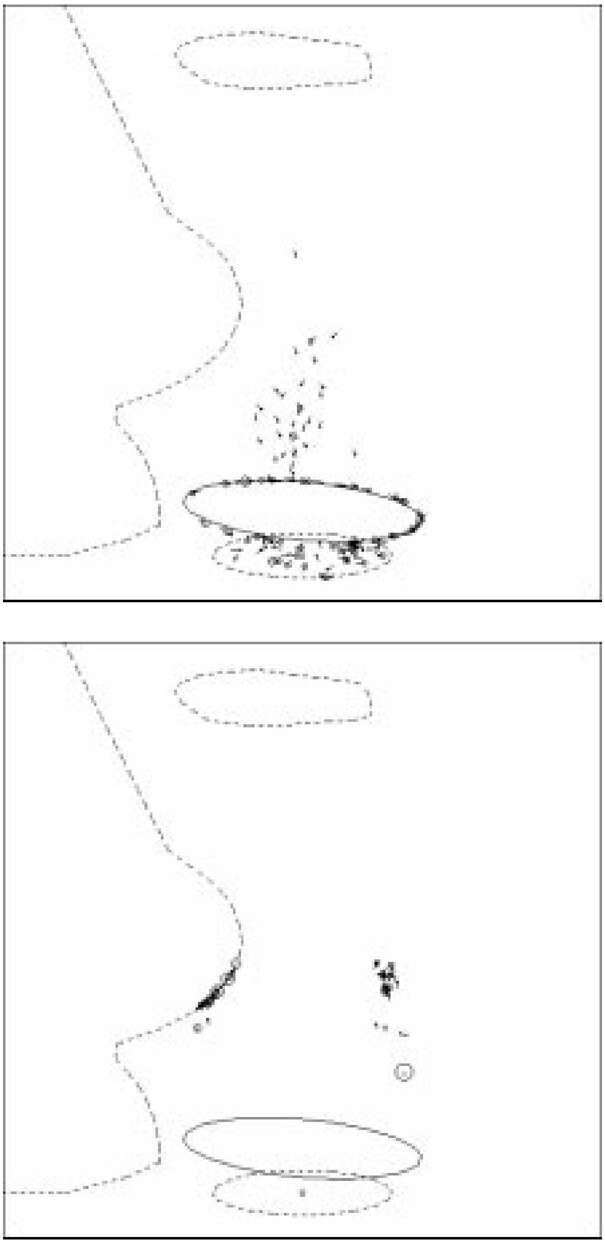

Figure 10. Two snapshots of the migration cycle with the temperature boundary in a more westerly location. Upper and lower panels show the spawning and feeding migations respectively.

C.2 Continous distributed model of fish migration

Sven Sigurdsson, Petro Babak, Simon Hubbard, Kjartan Magnusson
Science Institute, University of Iceland

The aim with the model proposed below is to:

- Aid in the assessment of what type of migration models might be included into a more general prediction model of changes in fish stock size (DST^2 ,2001)
- Test various assumptions on what external factors may influence fish migration.
- Provide a continous counterpart to discrete particle migration models that are being developed concurrently (Hubbard et al., 2001)
- Develop a distributed analogue to compartmental models like BORMICON where migration between compartments is simply described in terms of transition matrices, specifying what percentage of the total stock in one compartment will move to the neigbouring compartment because of migration and/or dispersion in a given timeinterval (BORMICON, 1997)

The model is a single species model that takes into account maturity distribution. We try to strike a balance between simplicity by only including clearly defined factors, and generality to enable testing of a variety of assumptions on fish migration.

The **values** that the model simulates are:

$\rho(t,x,y,m)$, the **density** of fishstock at time t, location (x,y), and maturity level m

$\boldsymbol{v}(t,x,y,m) = [u(t,x,y,m), v(t,x,y,m)]^T$, the **lateral velocity** of the fishstock at time t, location (x,y), and maturity level m, and

$\mu(t,x,y,m)$, the **the rate of change of maturity,** $\frac{dm}{dt}$ of the fishstock at time t, location (x,y), and maturity level m.

The **input** into the model, apart from initial values and boundary conditions around the region under consideration, are:

$\boldsymbol{p}(t,x,y,m)$, **preferred direction** whose role is to align the direction of movement of the fish to that of its neighbours, turn the fish towards preferred food and/or temperature conditions, and towards some preferred location or path during spawning migration.

v_p (t,x,y,m), **preferred speed** whose role is to control the speed of the fish and adjust it to the speed of its neighbours.

$\rho_p(t,x,y,m)$ **preferred density** whose role is to push the fish apart if the density becomes too high as well as possibly attract the fish to each other if the density becomes too low. This density may eg. depend on food density and hence on time and location.

$\boldsymbol{v}_c(t,x,y)$, **carrying velocity** by sea-currents that will presumably only play a significant role in the case of very young fish.

These input parameters could depend on the output of separate sea-current and transport models.

We refer to Hubbard et al. (2001) for a more detailed discussion on the motivation behind such a fish migration model and to Patridge, (1982), Giske et al. (1998) and Krause et al. (2000) for background information on spatial dynamics of fish but in order to illustrate the possible role of the input parameters introduced above consider the following scenarios that we would like to be able to simulate and are partly motivated by information on migration of capelin in the seas around Iceland (Vilhjálmsson, 1994):

a) During **feeding migration** the fish tends to remain at the same location while there is enough food supply but moves towards greater food supply when the **food concentration** (or possibly the ratio between food and fish concentration) drops below a given threshold value f_0. If the food is eg. plankton its concentration may have been obtained from a separate model of sea-currents and plankton transport. Here we may specify $v_p = 0$ and $\boldsymbol{p} = 0$ and set ρ_p to some specified value while the food concentration is $\geq f_0$ but let $\boldsymbol{p}$ be in the direction of the gradient of the food concentraion and set v_p to some specified speed when f_0 drops below this value, thus guiding the fish towards higher concentration. In order to introduce appropriate randomness into the movement of the fish we may introduce a random component into $\boldsymbol{p}$ and/or v_p.

b) During **spawning migration** the fish is heading for a given location of spawning but halts on its way at a given **temperature barrier** in the sea, and will not cross it until it has exceeded a given maturity threshold, m_0 The exact location of the temperature barrier may have been obtained from a separate model of sea-currents and temperature distribution. Here we may specify $\boldsymbol{p}$ in the whole region so that it points towards the spawning location and let the size of v_p correspond to some estimated cruising speed. Specified no-flow boundaries will take care of the fact that the fish has to go around possible obstacles on the way.

   We could then deal with the **temperature barrier** by:

   i) resetting v_p (t,x,y,m) to 0 for $m<m_0$ at $(x,y)-$ values in some strip upstream from the barrier so as to slow the fish down until its maturity level has reached m_0.
   ii) specifying $\boldsymbol{p}(t,x,y,m)$ for $m<m_0$ in such a way that it points upstream away from the barrier in the neighbourhood of it thus forcing the fish back away from the barrier until its maturity level has reached m_0.
   iii) introducing a no-flow internal boundary at the barrier for $m<m_0$ thus effectively stopping the fish from crossing it until its maturity level has reached m_0.

   Our aim in the mathematical model and the corresponding numerical model presented below is to be able to deal with such side-conditions in an effective manner. In particular, a numerical model based on a weak formulation of the mass continuity equation, and on an unstructured finite element triangulation of (x,y)-space, offers considerable flexibility in dealing with irregular no-flow boundary conditions, external as well as internal, while ensuring at the same time mass conservation.

Mathematical model

Mass balance:

$$\frac{\partial \rho}{\partial t} + \nabla \cdot (\rho \boldsymbol{v}) + \frac{\partial}{\partial m}(\rho \mu) = 0 \qquad (1)$$

Momentum balance:

$$\frac{\partial(\rho \boldsymbol{v})}{\partial t} + \nabla \cdot (\rho \boldsymbol{v} \otimes \boldsymbol{v}) + \frac{\partial}{\partial m}(\rho \mu \boldsymbol{v}) = \rho \begin{bmatrix} a & -b \\ b & a \end{bmatrix} \boldsymbol{v} + \rho c(\boldsymbol{v}_c - \boldsymbol{v}) + d\nabla \rho + \rho e \nabla^2 \boldsymbol{v} \qquad (2)$$

Here

$$a = \log\left(\left(\frac{v_p}{|\boldsymbol{v}|}\right)^{\frac{1}{\tau_a}}\right) \approx \frac{1}{\tau_a|\boldsymbol{v}|}(v_p - |\boldsymbol{v}|) \quad \text{if } v_p \approx |\boldsymbol{v}| \tag{3}$$

where v_p is the preferred speed and
τ_a is the time constant of adjustment to this speed.

$$b = \frac{1}{\tau_b}\sin^{-1}\left(\frac{up_y - vp_x}{|\boldsymbol{v}|}\right) \approx \frac{up_y - vp_x}{\tau_b|\boldsymbol{v}|} \quad \text{if } \boldsymbol{p} \approx \frac{1}{|\boldsymbol{v}|}\boldsymbol{v} \tag{4}$$

where $\boldsymbol{p} = [p_x \quad p_y]$ is the preferred direction and
τ_b is the time constant of adjustment to that direction
$\sin^{-1}\left(\frac{up_y - vp_x}{|\boldsymbol{v}|}\right)$ is the angle between $\boldsymbol{v}$ and $\boldsymbol{p}$

c is a drag coefficient reflecting the drag fource between the fish and the surrounding water.

$$d = d'(\rho - \rho_p) \tag{5}$$

for some constant coefficient d' where ρ_p is the preferred density.

e is a kinematic viscosity coefficient reflecting the randomness in the fish movement.

By expanding the left hand side of the momentum equation and substituting from the mass equation we obtain the follwing **velocity equation**:

$$\frac{D\boldsymbol{v}}{Dt} = \begin{bmatrix} a & -b \\ b & a \end{bmatrix}\boldsymbol{v} + c(\boldsymbol{v}_c - \boldsymbol{v}) - \frac{d}{\rho}\nabla\rho + e\nabla^2\boldsymbol{v} \tag{6}$$

where $\frac{D\boldsymbol{v}}{Dt} = \frac{\partial \boldsymbol{v}}{\partial t} + (\boldsymbol{v}\cdot\nabla)\boldsymbol{v} + \mu\frac{\partial \boldsymbol{v}}{\partial m}$ is the total derivative, including the maturity level.

In our simulations we apply this equation rather than the momentum equation but note that this implies that we may get non-zero velocity at a given time and location even if the concentration is zero at that location at the given time. When applying the model for simulations in this way we will thus have to introduce an auxiliary condition that brings the velocity to zero when the density drops below a specified tolerance value.

In some simulations we omit the dependence of ρ and $\boldsymbol{v}$ on the maturity level, m. This effectively corresponds to that we work with total concentration defined by:

$$\rho(t,x,y) := \int_0^1 \rho(t,x,y,m)dm \tag{7}$$

and the average velocity defined by

$$\boldsymbol{v}(t,x,y) := \frac{\int_0^1 \rho(t,x,y,m)\boldsymbol{v}(t,x,y,m)dm}{\rho(t,x,y)} \tag{8}$$

when $\rho \neq 0$, assuming that the maturity level is normalized to the interval [0,1].

Integrating through the mass balance equation (1) with respect to m from $m = 0$ to $m = 1$ we get that:

$$\frac{\partial \rho}{\partial t} + \nabla(\rho \boldsymbol{v}) = \rho\mu|_{m=0} - \rho\mu|_{m=1} = 0 \tag{9}$$

where ρ and $\boldsymbol{v}$ on the left-hand side now denote the total concentration and average velocity respectively. We can integrate through the velocity equation (6) in a similar manner, obtaining a corresponding equation for the average velocity, except that there will be a slight descrepancy because of the nonlinear terms that we shall simply disregard.

If

$$\frac{d\boldsymbol{v}}{dt} = \begin{bmatrix} a & -b \\ b & a \end{bmatrix} \boldsymbol{v} \tag{10}$$

with constant coefficients a and b we have that

$$\boldsymbol{v}(t + \Delta t) = e^{a\Delta t} \begin{bmatrix} \cos(b\Delta t) & -\sin(b\Delta t) \\ \sin(b\Delta t) & \cos(b\Delta t) \end{bmatrix} \boldsymbol{v}(t)$$

With our choice of a and b given above, setting $\tau_a = \tau_b = \Delta t$, and fixing the value of $\boldsymbol{v}$ to the velocity at the start of the time interval we get that

$$\boldsymbol{v}(t + \Delta t) = \left(\frac{v_p}{|\boldsymbol{v}(t)|}\right)^{\frac{\Delta t}{\tau_a}} \begin{bmatrix} \cos\left(\frac{\Delta t}{\tau_b}\theta\right) & -\sin\left(\frac{\Delta t}{\tau_b}\theta\right) \\ \sin\left(\frac{\Delta t}{\tau_b}\theta\right) & \cos\left(\frac{\Delta t}{\tau_b}\theta\right) \end{bmatrix} \boldsymbol{v}(t) = v_p \boldsymbol{p}(t) \tag{11}$$

where θ denotes the angle between the velocity $\boldsymbol{v}$ and the preferred direction $\boldsymbol{p}$ at time t.

Thus by introducing the appropriate randomness into the preferred speed and the preferred direction this part of the model may thus be viewed as the continous counterpart of the discrete model presented by Vicsek et al. (1995) and extended by Hubbard et al. (2001).

By viewing the velocity equation (10) as an equation describing the motion of a single particle we would in particular have a model that corresponds to this model of Vicsek except that it is continous, rather than discrete, in time.

In the model (1) and (6) which is continous both in space and time the randomness is essentially incorporated into the final diffusion term on the right hand side of (6).

The preferred direction $\boldsymbol{p}$ may in general be composed of different components each associated with its specific time constant. Typically we may have a component that is in the average direction of the surrounding fish in some specified neighbourhood Ω with radius ϵ. The angle of this direction, θ_{aver}, may be defined as

$$\theta_{aver} = \tan^{-1}\left(\frac{\iint\limits_{\Omega} \rho(t,\xi,\eta) sin\left(\theta(t,\xi,\eta)\right) d\xi d\eta}{\iint\limits_{\Omega} \rho(t,\xi,\eta) cos\left(\theta(t,\xi,\eta)\right) d\xi d\eta}\right) \tag{12}$$

where

$$\left[\ \cos\left(\theta(t,\xi,\eta)\right) \quad \sin(\theta(t,\xi,\eta))\ \right] = \frac{1}{|\boldsymbol{v}(t,\xi,\eta)|}\boldsymbol{v}(t,\xi,\eta) \tag{13}$$

and the angle according to equation (12) is modified appropriately when $\cos(\theta(t,\xi,\eta)) \leq 0$.

Secondly, we may have a component in the direction of the gradient of a temperature or a food density function. Denote the angle of this direction θ_{grad}. Finally we may have a component that is in the direction towards some spawning ground. Denote the angle of this direction θ_{spawn}. Denoting the corresponding time constants with τ_{align}, τ_{grad}, and τ_{spawn} we then set

$$\frac{1}{\tau_b} = \frac{1}{\tau_{align}} + \frac{1}{\tau_{grad}} + \frac{1}{\tau_{spawn}} \tag{14}$$

and

$$\begin{aligned}\theta_b \quad &= \quad \frac{1}{1+\frac{\tau_{align}}{\tau_{grad}}+\frac{\tau_{align}}{\tau_{spawn}}}\theta_{aver} \\ &\quad + \frac{1}{1+\frac{\tau_{grad}}{\tau_{align}}+\frac{\tau_{grad}}{\tau_{spawn}}}\theta_{grad} + \frac{1}{1+\frac{\tau_{spawn}}{\tau_{align}}+\frac{\tau_{spawn}}{\tau_{grad}}}\theta_{spawn}\end{aligned} \tag{15}$$

i.e. a linear combination of the three angles where the angle associated with the shortest timeconstant carries the largest weight, and such that

$$\frac{\theta_b}{\tau_b} = \frac{\theta_{aver}}{\tau_{align}} + \frac{\theta_{grad}}{\tau_{grad}} + \frac{\theta_{spawn}}{\tau_{spawn}} \tag{16}$$

Note, however that this is not equivalent to taking the same linear combination of the respective directions as is done in Hubbard et al.(2001), the difference being most pronounced when two of the directions are opposite each other. Furthermore in Hubbard et al. the effect of the spawning direction is included implicitly by introducing an appropriate assymetry into the random part of $\boldsymbol{p}$ rather then including it explicitly as is done above.

Also note that for the alignment to be effective the relationship between the radius of the neighbourhood Ω, ε, the preferred speed, v_p, and the time constant, τ_{align}, must be such that the fish does not escape from the neighbourhood before it senses it, i.e. one must have that

$$v_p\tau_{align}<\varepsilon \tag{17}$$

Czirok and Vicsek (2000) consider a continous model, without maturity, with the same mass continuity equation as above, and where the velocity equation may be expressed in the form:

$$\begin{aligned}\frac{D\boldsymbol{v}}{Dt} \quad &= \quad \frac{1}{\tau_a}\left(\frac{v_p}{|\boldsymbol{v}|}-1\right)\boldsymbol{v} + \frac{1}{\tau_b}\left(\frac{\iint\limits_{\Omega}\rho(t,\xi,\eta)\boldsymbol{v}(t,\xi,\eta)d\xi d\eta}{\iint\limits_{\Omega}\rho(t,\xi,\eta)d\xi d\eta} - \boldsymbol{v}\right) \\ &\approx \quad \frac{1}{\tau_a}\left(\frac{v_p}{|\boldsymbol{v}|}-1\right)v + \frac{1}{\tau_b}\left(\nabla^2\boldsymbol{v} + \frac{1}{\rho}\nabla\left(\rho\nabla\boldsymbol{v}\right)\right) \qquad \text{as}\,\varepsilon\to 0\end{aligned} \tag{18}$$

where ϵ denotes the radius of the neighbourhood Ω. Here we omit, for the sake of simplicity, a pressure term and a viscosity term analogous to the last two terms on the right hand side of equation (6). We note that the first term on the right hand side is the same as in equation (6) if $v_p \approx |\boldsymbol{v}|$ (cf. equation (7)). In order to compare the second term on the right hand side with the corresponding term in the velocity equation (6) consider the case when this is the only term present on the right hand side, $\boldsymbol{v}(t,x,y) = [u(t,x,y) \quad 0]^T$, the speed within the neighbourhood Ω of (x,y) is constant at time t, and we advance by timestep $\Delta t\ = \tau_b$.

According to (18) we then get that:

$$\boldsymbol{v}(t+\Delta t, x+\Delta t u(x,y,t), y) \approx \frac{\iint\limits_{\Omega} \rho(t,\xi,\eta)\boldsymbol{v}(t,\xi,\eta)d\xi d\eta}{\iint\limits_{\Omega} \rho(t,\xi,\eta)d\xi d\eta} \tag{19}$$

whereas according to equation (6)

$$\boldsymbol{v}(t+\Delta t, x+\Delta t u(x,y,t), y) \approx u(x,y,t)\,[\cos\theta_{aver} \quad \sin\theta_{aver}]^T$$

Here we have that:

$$\theta_{aver} = \tan^{-1}\left(\frac{\iint\limits_{\Omega} \rho(t,\xi,\eta)v(t,\xi,\eta)d\xi d\eta}{\iint\limits_{\Omega} \rho(t,\xi,\eta)u(t,\xi,\eta)d\xi d\eta}\right)$$

since the speed is uniform within the neighbourhood Ω, and hence

$$\boldsymbol{v}(t+\Delta t, x+\Delta t u(x,y,t), y) \approx \frac{u(t,x,y)}{|\iint\limits_{\Omega} \rho(t,\xi,\eta)\boldsymbol{v}(t,\xi,\eta)d\xi d\eta|} \iint\limits_{\Omega} \rho(t,\xi,\eta)\boldsymbol{v}(t,\xi,\eta)d\xi d\eta \tag{20}$$

Thus the direction of the velocity in both cases becomes the same but whereas the speed remains constant according to equation (6) it is reduced by a factor:

$$\frac{\left|\iint\limits_{\Omega} \rho(t,\xi,\eta)\boldsymbol{v}(t,\xi,\eta)d\xi d\eta\right|}{|\boldsymbol{v}(t,x,y)| \iint\limits_{\Omega} \rho(t,\xi,\eta)d\xi d\eta} \tag{21}$$

according to equation (18). It should however also be noted that this reduction in speed will to some extent be counteracted through the first term on the right-hand side of (18) whose effect is to keep the speed to the value v_p

The term $d\nabla\rho$ in equation (2) acts effectively as a pressure force while d>0. By specifying d as is done in equation (5) so that d<0 when ρ<ρ_p in order to maintain the preferred density ρ_p and encourage group formation we get sharp fronts in the density values at $\rho = \rho_p$, causing difficulties in numerical simulations. An alternative would be to set $d = 0$ when ρ<ρ_p so that the group formation will solely be result of the alignment effect (and the randomness) as is the case in the discrete model of Vicsek.

Finally not that in the case of larvae or very young fish where the carrying velocity is predominate the velocity equation may be reduced to setting

$$\boldsymbol{v} = \boldsymbol{v}_c - \frac{d}{c\rho}\nabla\rho \tag{22}$$

Substitituting into the mass balance equation it becomes:

$$\frac{\partial\rho}{\partial t} = \nabla\left(\frac{d}{c}\nabla\rho\right) + \nabla(\rho\boldsymbol{v}_c) \tag{23}$$

i.e. a transport type equation with a diffusion term and a convection term.

When we include in our model dependence on maturity we need in addition to equations (1) and (2), an equation for the **rate of change of maturity**. Typically such an equation may be of the form (cf. BORMICON, 1997):

$$\mu = \frac{m}{1-m}\left(\beta\frac{dl}{dt} + \gamma^*\right) \tag{24}$$

where l denotes the length of the fish and the time-derivative $\frac{dl}{dt}$ may depend on available energy in terms of eg. heat or food and thus on time and location.

The equation is based on the assumption that we have the following functional relationship between maturity, m, length l, and age, a

$$m = \frac{1}{1+e^{\alpha-\beta l(t)-\gamma a(t)}}$$

for some constants, α, β andγ (so that m lies in fact in the interval $[1/(e^{\alpha}+1), 1]$ rather than [0,1]) and $\gamma^* = \gamma\frac{da}{dt}$.

We further observe that if the maturity index is to reflect the relative amount of eggs produced, as might be appropriate when modelling the spawning migration of capelin, we may in addition to the maturity index wish to include an **energy index**, that may eg. reflect to relative weight of fish and will thus increase due to food consumptipn but decrease because of movement and egg production. Denoting such an energy index by E we might typically have equations of the following form:

$$\begin{aligned}\frac{dm}{dt} &= \alpha(1-m)E \\ \frac{dE}{dt} &= \beta E^{2/3} - \delta m - \gamma E - \lambda\frac{dm}{dt}\end{aligned} \tag{25}$$

where the coefficientα would depend on time, the coefficient β on availability of food and temperature, and the coefficients δ and γ on velocity. This additional index would complicate the model since density, ρ, and velocity, $\boldsymbol{v}$, would now depend on t, x, y, m, and E, but conceptually the new index, E, would enter into the mass and momentum equations in exactly the same way as the index m.

Finite element model

We present a spatial approximation of the continous model above, using a finite element Galerkin approach with triangular elements. This allows considerable flexibility in terms in treating irregular domains and boundaries. Furthermore the scheme presented below has the important property of ensuring mass conservation. The basic structure of the scheme is identical to that described in Sigurdsson (1992,1994) for the numerical simulation of shallow water flow. For the sake of simplicity we omit any dependence of ρ and $\boldsymbol{v}$ on maturity. The inclusion of maturity is computationally analogous to replacing a single layer shallow water flow model by a multilayer one.

Stability considerations lead us to consider a so-called staggered approximation where the velocity, $\boldsymbol{v}$, is approximated by constants within the triangular elements and the density, ρ, is approximated by a continous function, linear within elements, and thus specified by the approximate values at the corners of the elements.

The **approximation of the mass balance equation** will be based on the following weak reformulation:

$$\iint_D \left(\frac{\partial\rho}{\partial t} + \nabla(\rho\boldsymbol{v})\psi\right) dS = \oint_{\partial D} \rho\boldsymbol{v}\cdot\boldsymbol{n}\psi ds + \iint_D \left(\frac{\partial\rho}{\partial t}\psi - \rho\boldsymbol{v}\cdot\nabla\psi\right) dS = 0 \tag{26}$$

where D denotes the whole domain under consideration, $\boldsymbol{n}$ unit outward normal on the boundary,∂D, and ψ denotes an arbitrary piecewise differentiable test function on D. By allowing ψ take any value at the boundary ∂D and dropping the boundary integral term on the right hand side we enforce the "natural" boundary condition of no normal outflow along the boundary.

Within a triangular element ΔABC the corresponding approximation becomes:

$$\frac{|\Delta|}{12}\begin{bmatrix} 2 & 1 & 1 \\ 1 & 2 & 1 \\ 1 & 1 & 2 \end{bmatrix} \frac{d}{dt}\begin{bmatrix} \rho_A \\ \rho_B \\ \rho_C \end{bmatrix} + \frac{\bar{\rho}}{2}\begin{bmatrix} a_x & a_y \\ b_x & b_y \\ c_x & c_y \end{bmatrix}\begin{bmatrix} u \\ v \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \\ 0 \end{bmatrix} \tag{27}$$

where

$|\Delta|$ is the area of the triangular element
$\rho_i, \quad i = A, B, C$ are the approximate ρ - values at the corners of the element
$\bar{\rho} = \frac{\rho_A+\rho_B+\rho_C}{3}$ is the approximate ρ - value at the centre of the element
$\boldsymbol{a} = [a_x \; b_x]^T$ is an outward normal vector on the element side opposite cornerpoint A whose length is that of the element side, similarily for $\boldsymbol{b}$ and $\boldsymbol{c}$.
$\boldsymbol{v} = [u \; v]^T$ is the approximate $\boldsymbol{v}$-value at the centre of the element.

Note that if ψ denotes a linear test function over the element that takes the value 1 at the corner point A and the value 0 on the opposite side then $\nabla\psi = -\frac{1}{2|\Delta|}\boldsymbol{a}$.

Also note that we should have included a boundary integral term for the boundary of the element $\partial\Delta$. When assembling the element equations into a global equation these boundary terms, however, cancel out against each other at internal boundaries between elements, reflecting the fact that the mass that flows out through the side of one element is the same as the mass flowing into the neigbouring element. If the boundary of the element coincides with the boundary of the region the flow term also disappears by the enforced boundary condition of no normal flow through such an outer boundary. Thus we can in in fact ignore this boundary integral term.

The left hand side of the **approximate velocity equation** will be approximated by:

$$|\Delta|\frac{d}{dt}\left[\begin{array}{c} u \\ v \end{array}\right] + \frac{1}{2}\left((u_a+u)a_x + (v_a+v)a_y\right)\left\{\left[\begin{array}{c} u_a \\ v_a \end{array}\right] - \left[\begin{array}{c} u \\ v \end{array}\right]\right\}$$

where $\boldsymbol{v}_a = [u_a \; v_a]^T$ denotes the approximate velocity in the adjacent element that the outward normal $\boldsymbol{a}$ points into. Here we are assuming that this is an upstream element in the sense that $((u_a+u)a_x + (v_a+v)a_y)<0$ and the only such element and thus effectively using an upstream approximation to the convective term. If there are more/other upstream elements there will be a corresponding term for them.

The right hand side of the velocity equation will be approximated by:

$$\begin{array}{rcl} |\Delta|\left[\begin{array}{cc} a & -b \\ b & a \end{array}\right]\left[\begin{array}{c} u \\ v \end{array}\right] & + & |\Delta|\, c\left[\begin{array}{c} u_c - u \\ v_c - v \end{array}\right] + \frac{d}{2\bar{\rho}}\left[\begin{array}{ccc} a_x & a_y & a_z \\ b_x & b_y & b_z \end{array}\right]\left[\begin{array}{c} \rho_A \\ \rho_B \\ \rho_C \end{array}\right] \\ & + & \frac{e}{3}\left(\frac{\boldsymbol{a}\cdot\boldsymbol{a}}{|\Delta|+|\Delta_a|}(\boldsymbol{v}_a - \boldsymbol{v}) + \frac{\boldsymbol{b}\cdot\boldsymbol{b}}{|\Delta|+|\Delta_b|}(\boldsymbol{v}_b - \boldsymbol{v}) + \frac{\boldsymbol{c}\cdot\boldsymbol{c}}{|\Delta|+|\Delta_c|}(\boldsymbol{v}_c - \boldsymbol{v})\right) \end{array}$$

By redefining a as:

$$\begin{array}{rcl} a^* & = & a - c - \frac{e}{3\,|\Delta|}\left(\frac{\boldsymbol{a}\cdot\boldsymbol{a}}{|\Delta|+|\Delta_a|} + \frac{\boldsymbol{b}\cdot\boldsymbol{b}}{|\Delta|+|\Delta_b|} + \frac{\boldsymbol{c}\cdot\boldsymbol{c}}{|\Delta|+|\Delta_c|}\right) + \\ & & \frac{1}{2\,|\Delta|}\left((u_a+u)a_x + (v_a+v)a_y\right) \end{array}$$

and introducing the vector:

$$\begin{array}{rcl} \boldsymbol{r} & = & c\boldsymbol{v}_c + \frac{e}{3\,|\Delta|}\left(\frac{\boldsymbol{a}\cdot\boldsymbol{a}}{|\Delta|+|\Delta_a|}\boldsymbol{v}_a + \frac{\boldsymbol{b}\cdot\boldsymbol{b}}{|\Delta|+|\Delta_b|}\boldsymbol{v}_b + \frac{\boldsymbol{c}\cdot\boldsymbol{c}}{|\Delta|+|\Delta_c|}\boldsymbol{v}_c\right) \\ & & -\frac{1}{2\,|\Delta|}\left((u_a+u)a_x + (v_a+v)a_y\right)\boldsymbol{v}_a \end{array}$$

the approximation to the velocity equation may be expressed as:

$$\frac{d}{dt}\left[\begin{array}{c} u \\ v \end{array}\right] = \left[\begin{array}{cc} a^* & -b \\ b & a^* \end{array}\right]\left[\begin{array}{c} u \\ v \end{array}\right] + \frac{d}{2\bar{\rho}\,|\Delta|}\left[\begin{array}{ccc} a_x & a_y & a_z \\ b_x & b_y & b_z \end{array}\right]\left[\begin{array}{c} \rho_A \\ \rho_B \\ \rho_C \end{array}\right] + \boldsymbol{r} \qquad (28)$$

By assembling these element systems into a global system, the partial differential equations have now been transformed into a nonlinear system of ordinary differential equations, in the approximate values for $\boldsymbol{v}$ within each element and ρ at the nodal points between elements. We refer to Sigurdsson (1994) for a brief description of how such a system can be integrated efficiently with respect to time.

It is of particular interest to compare discrete and continous models with respect to alignment and group formation. The simplest approach to such a comparison is to introduce a regular triangulation where the area of each triangle is half the area of the neighbourhood Ω. A suitable approximation for θ_{aver} defined by equation (12) will then be:

$$\theta_{aver} = \tan^{-1}\left(\frac{(\rho_B+\rho_C)\frac{v+v_a}{|\boldsymbol{v}+\boldsymbol{v}_a|}+(\rho_C+\rho_A)\frac{v+v_b}{|\boldsymbol{v}+\boldsymbol{v}_b|}+(\rho_A+\rho_B)\frac{v+v_c}{|\boldsymbol{v}+\boldsymbol{v}_c|}}{(\rho_B+\rho_C)\frac{u+u_a}{|\boldsymbol{v}+\boldsymbol{v}_a|}+(\rho_C+\rho_A)\frac{u+u_b}{|\boldsymbol{v}+\boldsymbol{v}_b|}+(\rho_A+\rho_B)\frac{u+u_c}{|\boldsymbol{v}+\boldsymbol{v}_c|}}\right) \tag{29}$$

A simple quantitaive measure that could be used for comparison between results from a continous and a discrete model is ICS, index of cluster size (see eg. Cressie (1991) , p. 590). For a rectangular region, subdivided into m squares of uniform size, and including N particles in such a way that X_i particles fall within subsquare number i we define

$$ICS \;=\; \frac{S^2}{\bar{X}} - 1 \tag{30}$$

where

$$\bar{X} = \frac{1}{m}\sum_{i=1}^{m} X_i = \frac{N}{m} \quad \text{and} \quad S^2 \;=\; \frac{1}{m-1}\sum_{i=1}^{m}(X_i - \bar{X})^2 \tag{31}$$

$ICS \approx 0$ if the particles are randomly distributed, $ICS<0$ if they are uniformly distributed and $ICS>0$ if they form clusters. The same formula can be used when the number of subareas is doubled by splittings each square into two triangles.

Using this same triangularization in the finite element approximation of the continous model an ICS for a discrete model at a given time can be compared with the corresponding index for the continous model defining within each triangular element

$$X_i = |\Delta|\,\frac{\rho_A+\rho_B+\rho_C}{3} \quad \text{and} \quad N = \sum_{i=1}^{m} X_i \tag{32}$$

where N will remain constant by the fact that the mass is conserved in the finite element scheme as long as there is no netflow of mass out through the boundary.

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C.3 Implementation of growth variability in a length-structured population dynamics model

Bjarte Bogstad, IMR, Bergen, Norway

Verena Trenkel, IFREMER, Nantes, France

Kristin Guldbrandsen Frøysa, IMR, Bergen, Norway

C.3.1 Abstract

In length-structured population dynamics models with discrete length classes as used in fisheries, implementation of length growth is a crucial issue. In addition to a biological model for the average growth in length for individuals in a given length class, methods for moving individuals from one length group to another to comply with this average growth are needed.

Another important issue is to reflect the observed variance in the length distribution of the population properly. Several methods based on various statistical distributions (binomial, beta-binomial, gamma, log-normal) are presented and discussed, together with a method based on a lookup table. The variance of the length distribution for the smallest individuals and the ratio between growth rate and width of length groups are found to be key parameters. It is also an advantage that the resulting distribution is a continuous function of its parameters, which is the case for all methods except the lookup table. The lookup table is, however, more flexible. It is concluded that simulation studies are needed to identify the most appropriate method for a given population model and study population.

Introduction

In a population dynamics model, it may be useful to model the abundance by size groups instead of by age groups, or one may model the abundance by age *and* size. The size distribution may be represented either as the number of individuals in discrete size groups or by some statistical distribution function. We will here consider only the case where the size is represented by discrete length groups, and assume that the length of an individual never can decrease with time. In addition to a biological model for the average growth in length for individuals in a given length class, models for moving individuals from one length group to another to comply with this average growth are needed. Among the length-structured models where such an implementation of length growth has been needed are the multispecies-multiarea-multifleet simulation models BORMICON (Stefánsson and Pálsson 1997, 1998) and MULTSPEC (Bogstad et al. 1997), as well as the single-species model Fleksibest (Frøysa et al., 2002). All three have been developed for fisheries stock assessment purposes and both BORMICON and Fleksibest have now been implemented in a single C++ software package called Gadget (Anon., 2001); further reference to these models will be to Gadget. A formal discussion of methods for implementation of length growth in such models has not yet been presented in the literature.

We define

- l - fish length in cm (real number)
- l_r - discrete length, mid point in length group no. r.
- l_{min} - minimum fish length in model
- l_{max} - maximum fish length in model
- L - total number of length groups
- m - time step number

- Δt - length of time step - assumed to be constant
- N^m - state vector (length L) of numbers per length group at time m
- $N^m[r]$ - number of fish in length group r at time m
- n - maximum number of length groups a fish can grow in one time step
- $\delta l(l_r, m)$ - average length incrementngth during time step m for fish in length group r; may be affected by time-varying entities such as environmental conditions, prey abundance, stock size etc.

We assume all length groups to be of identical width

$$\Delta l = \frac{l_{max} - l_{min}}{L} \tag{1}$$

The mid point in length group r is given by

$$l_r = l_{min} + (r - \frac{1}{2})\Delta l, r = 1, L \tag{2}$$

In population models which are structured by length groups (they may additionally be structured by age group, sex, area etc.), the mean growth during a time step is calculated. This may be based on simple models such as the von Bertalanffy growth model (von Bertalanffy 1934, 1938), a power or linear growth function or formulated as a general growth model (Schnute 1981) with these functions as special cases. Growth could also be modelled as a function of population density (Walters and Post 1993).

The von Bertalanffy growth function can be written as:

$$\delta l(l_r, m) = (L_\infty - l_r)(1 - \exp(-k(m)\Delta t)) \tag{3}$$

The power growth function is:

$$\delta l(l_r, m) = k(m)\Delta t\, l_r^q \quad q \leq 0 \tag{4}$$

Linear growth is obtained for $q = 0$.

A key parameter when studying the modelling of length growth is the average length growth (measured in length group units) of individuals (fish) in length group r during time step m

$$\mu_r(m) = \frac{\delta l(l_r, m)}{\Delta l} \tag{5}$$

We define $p(i, r|\mu_r(m))$ as the transition probability of going from length group r to i during time step t_m.

As growth is a number-conserving process, the following condition needs to be satisfied:

$$\sum_{i=r}^{i=r+n} p(i, r|\mu_r(m)) = 1 \tag{6}$$

The number of fish growing from length group r to length group i during time step m is N_r^m, where

$$N_r^m[i] = N^{m-1}[r]p(i, r|\mu_r(m)) \tag{7}$$

In order to get the correct average growth, the following additional condition should be satisfied:

$$\sum_{i=r}^{i=r+n} (i-r)p(i,r|\mu_r(m)) = \mu_r(m) \tag{8}$$

Hence, in order to ensure the correct average length increase as given by (mugrowth), growth is implemented by distributing fish from a given length class over a range of length classes (including the current one) according to a probability distribution.

The number of fish in length group i after growth has taken place, is given by

$$N^m[i] = \sum_{r=i-n}^{i} N^m[r] = \sum_{r=i-n}^{i} N^{m-1}[r]p(i,r|\mu_r(m)) \tag{9}$$

Equation 9 gives the sum of the fishes from the $n+1$ length groups that grow into length group i (including those which remain in length group i).

For length groups close to the ends of the length range, some modifications to the equations above are needed to account for boundary conditions.

If additional processes other than growth take place during a given time step equations 7 and 9 have to be modified. An example formulation when processes such as mortality and maturation are included, is described in Frøysa et al. (2002).

The transition probabilities need to be chosen in a way which gives the length distribution the appropriate variance. It should be noted that the variance of the distribution of fish growing from length group r, N_r^m, can be computed based on $p(i,r|\mu_r(m))$. However, the variance of the new total length distribution after growth has taken place, N^m, is dependent on both the variance in the initial length distribution N^{m-1} and of $p(i,r|\mu_r(m))$. Thus, although the variance of $p(i,r|\mu_r(m))$ may be easy to compute analytically, it will be very difficult to find an analytical expression for the variance of the new total distribution N_1^m.

C.3.2 Methods for implementing growth variability

For implementing the growth distribution a parametric function is needed that has enough parameters to allow some minimal flexibility to track length distributions of an age group, yet with enough parsimony in parameters to allow for the estimability of the parameters involved.

It is especially important to represent the spread of length distribution properly in a model which is structured both by length and age. The reason for this is that in a model with age structure, the length distribution for each cohort is modeled and compared to data separately, while a model with only length structure only keeps track of the length distribution of the entire population. Thus a length-structured model will be less influenced than a length- and age-structured model by how the distribution of growth on length is implemented.

A first step would be to attempt to estimate individual transition probabilities, however this results in many parameters that have to be estimated. Another approach would be to estimate variance, skewness and kurtosis and go from these to transition probabilities, but there is no trivial transformation between the two.

Assuming the number of permissible length group increases to be fixed, a binomial distribution or a (truncated) Poisson distribution could be used. However, by fixing the value of mean growth, the single free parameter in in both distributions is determined, leaving no flexibility for adjusting the distributions. Alternatively, a flexible distribution such as the 4-parameter inverse lambda distribution might be used (Ramberg et al., 1979), but parameter estimation tends to be difficult.

In this paper we will describe in some details six methods of various degree of flexibility for implementing length growth distributions, i.e. methods of calculating $p(i,r|\mu_r(m))$:

1. Lookup table
2. Binomial distribution
3. Two-category binomial distribution
4. Beta-binomial distribution
5. Gamma distribution
6. Lognormal distribution

Methods 1 and 4 are presently implemented in Gadget, while method 3 was implemented in the MULTSPEC model. For simplicity, growth is considered time-independent in the following analysis, thus we set

$$\mu_r(m) = \mu_r \tag{10}$$

Lookup table

In the lookup table approach, transition probabilities $p(i,r|\mu_r)$ are calculated *a priori* for combinations of mean length growth values μ_r and length growth variances σ_r^2 (measured in length group units).

In order to ensure correct variances, the following equation needs to be satisfied:

$$\sum_{i=r}^{i=r+n} (i-r-\mu_r)^2 p(i,r|\mu_r) = \sigma_r^2 \tag{11}$$

Equations (growthcons), (growth2) and (growth3) are then solved simultanously for $p(i,r|\mu_r)$. Often all three equations can not be solved exactly. Then (growthcons) is solved exactly and much more weight put on approximating (growth2) than (growth3). In summary this means that priority is put on conservation of the number of fish, then to get the average growth (in length) correct and finally to get the dispersion correct. In other cases there might be more than one combination satisfying the equation exactly. In those cases the solution having the fewest numbers of extrema is chosen to get as smooth a solution as possible.

To avoid having to provide $r = 1, \dots L$ variances, the following mean-variance relationship is formulated $\sigma_r^2 = k_0 + k_1\mu_r$ where k_0 and k_1 are constants that are either fixed (user specified) or estimated. Typical values from Gadget runs for Northeast Arctic cod with 2.5cm wide length groups are $k_0 = -0.05$ and $k_1 = 0.6$.

The lookup table for $p(i,r|\mu_r)$ is then generated by solving the preceeding equations for values of μ_r (e.g. every 0.01) and σ_r (e.g. every 0.05) on a systemmatic grid. A 4-point interpolation is used if the calculated values of μ_r and σ_r lie between table values.

Binomial distribution

The probability for growth of $x = i - r$ length groups is defined by the binomial distribution for n the total admissable number of length groups.

$$p(i,r|\mu_r) = P[X = x = i - r] = \binom{n}{x} p_r^x (1-p_r)^{n-x} = \frac{\Gamma(n+1)}{\Gamma(x+1)\Gamma(n-x+1)} p_r^x (1-p_r)^{n-x} \tag{12}$$

For a given n, the probability p_r is different for each length group. Given mean growth μ_r, it is defined by $p_r = \mu_r/n$. The variance of the distribution of fish originally in length group r after growth has taken place, N_r (equation 7), is given by $\sigma_r^2 = np_r(1-p_r)$. Although this distribution can certainly be used, it is clear that no flexibility is allowed at all and in fact it would be quite unlikely for such a rigid distribution to satisfy the specified requirements of attaining the correct distribution of length.

Two-category binomial distribution

This method was used for the MULTSPEC model (Bogstad et al., 1997, S. Tjelmeland, IMR, Bergen, pers. comm.). The fish is simply distributed over two adjacent length groups in order to get the appropriate mean length growth. Let $c_r = int(\mu_r)$, $d_r = \mu_r - int(\mu_r)$ and $i = r + c_r$.

Then $p(i, r|\mu_r) = 1 - d_r$ and $p(i+1, r|\mu_r) = d_r$, while for other values of i, $p(i, r|\mu_r) = 0$.

This is equivalent to first shifting all fish in length class r c_r length classes upwards and then applying a binomial distribution with $n = 1$ and $p = d_r$ to calculate the transition probabilities. This distribution is even more restrictive than the general binomial distribution, but is very easy to implement.

Beta-binomial distribution

The beta-binomial distribution is an extension of the binomial distribution presented where binomial probabilities p_r are not fixed but come from Gamma distributions. This approach can be formulated so as to provide a single estimable parameter in addition to the mean growth in length group units, μ_r.

For a given binomial probability p_r, the beta distribution is defined for arbitrary real values of $\alpha_r > 0$ and $\beta_r > 0$ by

$$f(p_r) = \frac{\Gamma(\alpha_r + \beta_r)}{\Gamma(\alpha_r)\Gamma(\beta_r)} p_r^{\alpha_r - 1}(1-p_r)^{\beta_r - 1}, \quad 0 \le p_r \le 1 \tag{13}$$

It is well-known that the mean of this distribution is given by

$$E(p_r) = \frac{\alpha_r}{\alpha_r + \beta_r} \tag{14}$$

This approach results in the following marginal distribution of the length increments. Setting $x = i - r$:

$$\begin{aligned}
P[X=x] &= \int_{p_r=0}^{1} P[X=x|p_r] f(p_r) dp_r \\
&= \int_{p_r=0}^{1} \frac{n!}{x!(n-x)!} p_r^x (1-p_r)^{n-x} \frac{\Gamma(\alpha_r+\beta_r)}{\Gamma(\alpha_r)\Gamma(\beta_r)} p_r^{\alpha_r-1}(1-p_r)^{\beta_r-1} dp_r \\
&= \frac{\Gamma(n+1)\Gamma(\alpha_r+\beta_r)}{\Gamma(x+1)\Gamma(n-x+1)\Gamma(\alpha_r)\Gamma(\beta_r)} \int_{p_r=0}^{1} p_r^{x+\alpha_r-1}(1-p_r)^{n-x+\beta_r-1} dp_r \\
&= \frac{\Gamma(n+1)\Gamma(\alpha_r+\beta_r)}{\Gamma(x+1)\Gamma(n-x+1)\Gamma(\alpha_r)\Gamma(\beta_r)} \frac{\Gamma(x+\alpha_r)\Gamma(n-x+\beta_r)}{\Gamma(n+\alpha_r+\beta_r)} \\
&= \frac{\Gamma(n+1)}{\Gamma(n-x+1)\Gamma(x+1)} \frac{\Gamma(\alpha_r+\beta_r)}{\Gamma(n+\alpha_r+\beta_r)} \frac{\Gamma(n-x+\beta_r)}{\Gamma(\beta_r)} \frac{\Gamma(x+\alpha_r)}{\Gamma(\alpha_r)}
\end{aligned}$$

Since for any positive number, y, the relationship $\Gamma(y+1) = y\Gamma(y)$ holds, it also follows that for any integer $x \ge 1$ and $\alpha_r, \beta_r > 0$,

$$\frac{\Gamma(x+\alpha_r)}{\Gamma(\alpha_r)} = (x-1+\alpha_r)(x-2+\alpha_r)(x-3+\alpha_r)\cdot\ldots\cdot(\alpha_r+1)\alpha_r,$$

and

$$\frac{\Gamma(n-x+\beta_r)}{\Gamma(\beta_r)} = (n-x-1+\beta_r)(n-x-2+\beta_r)(n-x-3+\beta_r)\cdot\ldots\cdot(\beta_r+1)\beta_r,$$

and finally, for $n \geq 1$.

$$\frac{\Gamma(\alpha_r+\beta_r)}{\Gamma(n+\alpha_r+\beta_r)} = \frac{1}{(n-1+\alpha_r+\beta_r)(n-2+\alpha_r+\beta_r)(n-3+\alpha_r+\beta)\cdot\ldots\cdot(1+\alpha_r+\beta_r)(\alpha_r+\beta_r)}$$

Based on this, the transition probabilities can be rewritten as

$$\begin{aligned} p(i,r|\mu_r,\alpha_r,\beta_r) = P[X=x=i-r] &= \frac{\{n\cdot(n-1)\ldots\cdot(n-x+1)\}}{x!} \\ &\cdot \frac{(n-x-1+\beta_r)(n-x-2+\beta_r)\cdot\ldots\cdot(\beta+1)\beta_r}{(n-1+\alpha_r+\beta_r)(n-2+\alpha_r+\beta_r)\cdot\ldots\cdot(1+\alpha_r+\beta_r)(\alpha_r+\beta_r)} \\ &\cdot (x-1+\alpha_r)(x-2+\alpha_r)(x-\ 3+\alpha_r)\cdot\ldots\cdot(\alpha_r+1)\alpha_r \end{aligned}$$

The mean of the beta-binomial distribution is given by

$$\mu_r = nE[p_r] = \frac{n\alpha_r}{\alpha_r+\beta_r} \tag{15}$$

Thus, as μ_r is given and if we assume that β is the same for all length groups r, the above equation can be rearranged to obtain $\alpha_r = \frac{\beta\mu_r}{n-\mu_r}$.

The variance of the beta-binomial distribution is given by

$$\sigma_r^2 = np_r(1-p_r)(1+(n-1)\tau_r^2), \tag{16}$$

where $\tau_r^2 = \frac{\alpha_r\beta_r}{(\alpha_r+\beta_r)^2(\alpha_r+\beta_r+1)}$ is the variance of the beta distribution (Mc Cullagh and Nelder, 1989, p. 140). If we assume that β is the same for all length groups r, the variance can then be expressed in terms of μ_r and β as

$$\sigma_r^2 = \frac{n^2\mu_r(n-\mu_r)((\beta+1)n-\mu_r)+(n-1)(\mu_r)^2(n-\mu_r)^3}{n^3((\beta+1)n-\mu_r)} \tag{17}$$

where

$$\lim_{\beta\to\infty}\sigma_r^2 = \mu_r - \frac{\mu_r^2}{n} \tag{18}$$

gives a lower limit of the variance which can be represented by this formulation.

Transition probabilities $p(i,r|\mu_r,\beta,n)$ can now readily be generated from the beta-binomial distribution, given specified values of μ_r, β and n.

Gamma distribution

The gamma distribution can be used to describe the distribution of growth on length, similarly to the way the beta-binomial distribution is used. The only difference is that length is modelled as a continuous variable and not in terms of length classes. An example of this approach is given by Sullivan et al. (1990). Using our notation, their approach can be described as follows:

The gamma distribution expressed in terms of the parameters α_r and β is

$$g(x|\alpha_r, \beta) = \frac{x^{\alpha_r - 1} e^{-x/\beta}}{\beta^{\alpha_r} \Gamma(\alpha_r)} \tag{19}$$

where x represents $\delta l(l_r)$. The mean change in length is given by $\delta l(l_r) = \alpha_r \beta$ and the variance is given by $\sigma_r^2 = \alpha_r \beta^2 = \beta \delta l(l_r)$ which is proportional to the mean. The proportion of individuals growing from length class r to i, $p(i, r|\delta l(l_r))$, can be found by integrating over the length range $(l_i - \Delta l/2, l_i + \Delta l/2)$:

$$p(i, r|\delta l(l_r)) = \int_{l_i - \Delta l/2}^{l_i + \Delta l/2} g(x|\alpha_r, \beta) dx \tag{20}$$

The advantage of using a gamma distribution is that it allows zero growth (the distribution includes zero) but no negative growth. A maximum growth limit ($n\Delta l$) can be implemented by truncating the gamma distribution and rescaling the proportions obtained using equation 20. In this method, variance is modelled jointly for all length classes through the free parameter β. Thus only one parameter needs to be estimated. No further optimisation is necessary as equations 6 and 8 are always fulfilled.

Lognormal distribution

In age- and length-based models, the length distribution at age can be modelled directly as done by De Leo and Gatto (1995). They have built an age and length structured model for European eel (*Anguilla anguilla* L.) and handle body growth from one age (year) to the next and the distribution of length at age in the following way.

Mean length at age $L(a)$ is described by the usual von Bertalanffy growth function or any other growth function. Actual length at age in the population is then assumed to follow a lognormal distribution. Thus the length of any individual of age a is given by

$$l(a) = L(a)\gamma \tag{21}$$

$$\gamma \sim log\mathcal{N}(1/\sigma^2, 1/\sigma^2)) \tag{22}$$

This implies that the variance $V[l(a)] = L(a)^2\sigma^2$, thus the length distribution becomes wider with increasing age.

Writing the von Bertalanffy growth model in terms of annual length growth per age group, we obtain

$$l(a+1) = \gamma L_\infty (1 - e^{-k}) + e^{-k} l(a) \tag{23}$$

which is equivalent to

$$l(a+1) = \alpha\gamma + \beta l(a)$$

which shows more clearly the linear relationship.

We now determine the length class i (length l_i) into which individuals of length class r (having length l_r) and age a will grow in a given year

$$l_i(a+1) = \gamma_r L_\infty (1 - e^{-k}) + e^{-k} l_r(a) \tag{24}$$

where $\gamma_r = l_r(a)/L_\infty$ as by equation (eqgamma).

Note, that with this method length classes become wider as age progresses, i.e. the authors work with changing definitions of length classes. A way to recover the original definition of length classes would be to first calculate the new limits of each length class after growing and then fit the lognormal to obtain the probabilities of the midpoints (or more accurately the cumulative probabilities over the range) of the original length classes. Population numbers can then be redistributed into the original length classes proportional to those probabilities.

To summarise, the particular modelling assumptions used by De Leo and Gatto are that i) length at age follows a lognormal distribution with fixed shape parameter $1/\sigma$ which is either known or has to be estimated and ii) fast growing individuals will always be growing faster independent of age and vice versa for slow growing individuals as the lognormal distribution for describing variability in individual growth is assumed constant for all ages.

C.3.3 Discussion

How well the six growth models can represent the actual growth depends on the values of the average growth measured in length groups per time step, μ_r, and the initial variance of the length distribution measured with length groups as unit. Thus, the choice of length group width and time step is important.

Methods 1, 3 and 4 have been used in length-based models, but it has not been tested how well they reproduce observed length distributions when simulations are made for a period of several years. This is also dependent on whether the other length-dependent processes in the models are adequately modelled.

Methods 2 and 3 are quite restrictive, but very easy to implement.

Some tests have been made of method 4, using Gadget. Both for Icelandic and Northeast Arctic cod (*Gadus morhua* L.) we have approximately for the length distribution at a given age $\bar{l} = \sigma^2$, measured in cm, where $\bar{l}$ is the mean length at age and σ is the standard deviation of the mean length at age. The growth rate of both stocks is approximately 10cm/year. In runs for Icelandic cod, $\Delta t = 1month$ and $\Delta l = 1.0cm$ have been used, while for Northeast Arctic cod, $\Delta t = 3months$ and $\Delta l = 2.5cm$ have been used. Linear growth was assumed in both cases. This give values of $\delta l = 10/12cm$ in the Icelandic cod case and $\delta l = 10/4cm$ in the Northeast Arctic cod case. Using equation 5, this gives $\mu = 0.83$ and $\mu = 1.0$, respectively.

The initial variance σ^2 measured in length groups is, however, quite different in these two cases. Using a mean length of 50 cm as an example, for 1 cm length groups, σ^2 measured with length groups as a unit is of course the same as that measured in cm, i.e. $\sigma^2 = 50$. Using 2.5 cm length groups as measuring unit we have, $\sigma = \sqrt{50}(cm) = \sqrt{50}/2.5(lengthgroups) = \sqrt{8}$, i.e. $\sigma^2 = 8$.

Problems were encountered in model runs for Northeast Arctic cod ($\mu = 0.83$, $\sigma^2 = 8$), where β drifted towards infinity during estimation in runs with $n = 5$. These problems did not occur for Icelandic cod ($\mu = 1.0$, $\sigma^2 = 50$). The reason for this is probably that in the Northeast Arctic cod case, the beta-binomial distribution leads to a too high variance after some time steps. Decreasing n could possibly solve this problem.

Method 1 may give better fit (smaller value of objective function) than methods 2-6 because it is more flexible by allowing strange shapes of the distribution which can not be approximated by a continuous function. A major problem with method 1 is that relatively small changes in the parameters μ_r and σ_r^2 can sometimes lead to relatively large changes in the proportions, by jumping from one solution fulfilling (growth3) to another. This becomes a serious problem in optimizing algorithms using the gradient. Methods 2-6 do not have this problem.

The parameters β (methods 4 and 5) and k_0 and k_1 (method 1) are estimated so that the overall fit of the length distribution to the observations becomes as good as possible, it seems infeasible to estimate one value of these parameters for each length group. Future work includes a close scrutiny of how variations in these parameters affect the growth update and how this affects the final length distributions, conditional on all the other model components. If mortality is length-dependent, an analytical study of how a length distribution develops is quite complicated.

For comparison of the performance of all the six methods of implementing length growth, simulation studies for different population models and study populations are needed.

It should be noted that all these approaches are Markovian. In order to take into account systematic (e.g. genetic) differences in growth between individuals, other approaches are needed.

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C.4 Length-based population dynamics models in state space form

Verena Trenkel, IFREMER, Nantes, France
Carl O'Brien, CEFAS, Lowestoft, England
Bjarte Bogstad, IMR, Bergen, Norway

Not to be cited without prior reference to the authors

C.4.1 Introduction

In this document length-based population dynamics models in state space form are described. The models range from single species single area approaches to multispecies and multiareas formulations. They correspond to the model choices possible within the Bormicon modelling framework. The models are written in state space form in order to facilitate the application of alternative parameter estimation methods such as Bayesian and sequential estimation methods in addition to maximum likelihood estimation.

C.4.2 Basic population model

The single species population dynamics model in state space form proposed by Sullivan (1992) is taken as the basic model which is then extended step by step. The model is written in matrix notation with N_t the vector of population numbers at length (n length classes) at time/year t.

$$N_t = PS_{t-1}N_{t-1} + R_t + \omega_t \tag{1}$$

$$\omega_t \sim MVN(0, \Sigma^{\omega_t})$$

where P is the time independent lower diagonal transition matrix for body growth, S_{t-1} is the diagonal survival matrix which is time specific and R_t the recruitment vector. Note that Sullivan assumed a multinormal process error.

Extending the state vector to distinguish two population groups, for example immature and mature animals, and allowing any process error distribution, the model becomes

$$N_t = BPS_{t-1}N_{t-1} + R_t + \omega_t \tag{2}$$

$$\omega_t \sim iid$$

with B the maturation matrix. To clarify the model structure, this single species model with two population groups and the same n length classes per group is written in expanded form. The elements $N_{u,i,t}$ of the state vector describe numbers in population group u ($u = (1, 2)$) and length class i ($i = 1, \dots, n$) at time t.

$$\begin{pmatrix} N_{1,1,t} \\ \vdots \\ N_{1,n,t} \\ N_{2,1,t} \\ \vdots \\ N_{2,n,t} \end{pmatrix} = \begin{pmatrix} O & O \\ B^1 & O \end{pmatrix} \begin{pmatrix} P^1 & O \\ 0 & P^2 \end{pmatrix} \begin{pmatrix} S^1_{t-1} & 0 \\ 0 & S^2_{t-1} \end{pmatrix} \begin{pmatrix} N_{1,1,t-1} \\ \vdots \\ N_{1,n,t-1} \\ N_{2,1,t-1} \\ \vdots \\ N_{2,n,t-1} \end{pmatrix} \tag{3}$$

$$+ \begin{pmatrix} R_{1,1,t-1} \\ \vdots \\ R_{1,n,t-1} \\ 0 \\ \vdots \\ 0 \end{pmatrix} + \begin{pmatrix} \omega_{1,1,t} \\ \vdots \\ \omega_{1,n,t} \\ \omega_{2,1,t} \\ \vdots \\ \omega_{2,n,t} \end{pmatrix} \tag{4}$$

The maturation submatrix B^1 is a diagonal matrix of the form

$$B^1 = \begin{pmatrix} b_1 & \dots & 0 \\ \vdots & b_i & \vdots \\ 0 & \dots & b_n \end{pmatrix} \tag{5}$$

with b_i the probability that an immature individual of length i becomes mature between time $t-1$ and t. Both growth transition submatrices P^1 and P^2 are lower diagonal matrices

$$P^u = \begin{pmatrix} p_{u,1,1} & 0 & \dots & 0 \\ p_{u,1,2} & p_{u,2,2} & \dots & 0 \\ \vdots & & & \vdots \\ p_{u,1,n} & p_{u,2,n} & \dots & p_{u,n,n} \end{pmatrix}$$

where $p_{u,i,h}$ indicates the probability of growing from length class i into length class h for animals belonging to population group u (here immature or mature).

Survival submatrices for all population groups have the same diagonal form

$$S^u_{t-1} = \begin{pmatrix} s_{u,1}(t-1) & \dots & 0 \\ \vdots & s_{u,i}(t-1) & \vdots \\ 0 & \dots & s_{u,n}(t-1) \end{pmatrix}$$

with $s_{u,i}(t-1)$ the survival probability of length class i (population group u) between $t-1$ and t .

C.4.3 Population model extensions

Multiple areas
In order to extend the model to include multiple areas, say m areas, we need to expand the state vector to contain one population vector (with two subgroups) per area. In addition, a migration matrix M needs to be defined. Thus the population dynamics model becomes

$$N_t = MBPS_{t-1}N_{t-1} + R_t + \omega_t \tag{6}$$

where $N_t = [N_{1,1,1,t}, N_{1,1,2,t}, \dots, N_{1,1,n,t}, N_{1,2,1,t}, \dots, N_{1,2,n,t}, N_{2,1,1,t}, \dots, N_{2,1,n,t}, \dots, N_{m,2,n,t}]$ with $N_{j,u,i,t}$ the population size in area j, group u in length class i at time t.

The transition matrix between areas M is the identity matrix if there is no migration. Otherwise

$$M = \begin{pmatrix} A_{1,1} & O & A_{2,1} & O & \dots & A_{1,2} & O \\ O & D_{1,1} & O & D_{2,1} & \dots & O & D_{m,1} \\ \vdots & & & & & & \vdots \\ A_{1,m} & O & A_{2,m} & O & \dots & A_{m,m} & O \\ O & D_{1,m} & O & D_{2,m} & \dots & O & D_{m,m} \end{pmatrix}$$

where O are null matrices and all matrices $A_{j,k}$ refer to immature animals and $D_{j,k}$ to mature animals. Both type of matrices have the same structure. The elements $a_{j,k}$ (or $d_{j,k}$) denote the probability of migrating from area j to area k. In order to prevent animals from leaving the modelled areas the condition $\sum_{j=1}^{m} a_{j,k} = 1$ is imposed.

Multiarea matrices for other processes such as growth P and survival S are formed by putting the area specific matrices along the diagonal of the multi area matrix.

Multispecies and multiple areas

Assuming that area definitions are the same for all species, a multispecies formulation can be obtained by writting separate models for all species. Species interactions are expressed in the biological models of growth and survival (see below).

C.4.4 Observation models

A range of different observation types are available such as scientific survey observations, commercial catch data, port sampling data, log book information and stomach content data. For each type a different observation model is formulated. All data related to commercial fishing operations can be fleet specific.

For abundance indices $I^s_{j,t}$ (structured by length class) for area j and species s we write

$$I^s_{j,t} = q^s(t) N^s_{j,t} + \epsilon^I_t \tag{7}$$

${\epsilon^I}_t \sim iid$ for $\forall s$ or

$$I^s_{j,t} \sim \begin{cases} Gamma \\ logNormal \end{cases}$$

$q^s(t)$ corresponds to the catchability of species s by the survey gear. Note that the observation error distribution is the same for all species.

The model for total commercial catches (in tonnes) can be formulated as

$$C^s_{j,t} = \sum_{i=1}^{n} \frac{F(s,j,i,t) N(s,j,i,t) \alpha^\beta_i}{Z(s,j,i,t)} e^{-Z(s,j,i,t)} + \epsilon^C_t \tag{8}$$

$$\epsilon^C_t \sim iid$$

or

$$C^s_{j,t} \sim \begin{cases} Normal \\ Gamma \end{cases}$$

Here, a weight-length relationship of the form

$$W = \alpha l^\beta \tag{9}$$

is used when converting from numbers to biomass.

The observation model for length-frequency samples for commercial catches is similar but has a different error distribution

$$C^s_{j,i,t} \sim Multinomial \qquad i = 1, \dots n$$

where $F(s, j, i, t)$ is the fishing mortality of length class i of species s in area j at time t and $p_{s,j,i,t}$ the sampling proportion.

There are other types of observations such as stomach content data and tagging information for which appropriate observation models need to be formulated.

C.4.5 Biological processes

Although in the above general model formulations time steps are assumed to be of length one year, shorter and unequal time steps are also possible. In that case the above models apply to each time step with the difference that some process matrices might become identity matrices for certain time steps. Furthermore, recruitment might be seasonal in which case R_t is a vector of zeros for off-season periods.

In the following the functional forms for the individual process probabilities are described.

Migration

Migration between areas is assumed to affect immature and mature animals in different ways. Migration probabilities (denoted $a^s_{j,k}$ for immature animals of species s and $d^s_{j,k}$ for mature animals) are taken to be constant for a given species s and for a given season. Thus for immature animals migrating from area j to k

$$a^s_{j,k}(season) = a^s_{j,k} \qquad \forall j, k$$

$$X|a^s_{j,k} \sim multinomial(a^s_{j,1}, \dots a^s_{j,n}, Y)$$

$$\sum_{j=1}^{m} a^s_{j,k} = 1$$

Migration probabilities are then used in multinomial distributions to determine the number of individuals, X, that actually migrate.

Maturation

The transition matrix B describes maturation. Assuming that maturation probabilities are logistic functions of body length $l(i)$ only, we can write for area j and species s the maturation probabilities as

$$b^s_{j,i} = \frac{1}{1 + exp(-\alpha^{s,j}(l(i) - l^{s,j}_{50}))}$$

$$X|b^s_{j,i} \sim Bin(b^s_{j,i}, Y)$$

where $\alpha^{s,j}$ and $l^{s,j}_{50}$ are parameters and the latter indicates the length at which 50 percent of all individuals are mature. If there is no difference between areas, parameters are the same for all j. The number of animals,X, becoming mature for any given length class, area and species is assumed to be a binomial random variable with the above probabilities.

Body growth

Various functions describing mean growth exist. A common model for growth increments is based on the von Bertalanffy growth function

$$l_{t+1} = L_{\inf}(1 - e^{-k}) + e^{-k} l_t \tag{10}$$

where l_t is body length at time t and $L_{\inf}$ and k are parameters. In general, mean growth of length class i is noted $\Delta l(i)$ which means that the target length of length class i which had mean length $l(i)$ can be written as

$$l = (l(i) + \Delta l(i))\epsilon^{\Delta l}$$

In a multispecies model the growth rate should be made a function of prey abundance.

Assuming a Gamma distribution for l (and consequently for $\epsilon^{\Delta l}$), the probabilities of the growth matrix P are obtained by integrating the Gamma distribution over the limits of each target length class i'. For simplicity superscripts for species s and subscripts for areas j have been omitted.

$$p^s_{u,i,i'} = \int_{l_{i'_{low}} - l(i)}^{l_{i'_{up}} - l(i)} p(\Delta l^s | \alpha^s_i, \beta^s) d\Delta l \tag{11}$$

$$p(\Delta l^s | \alpha^s_i, \beta^s) = \frac{\Delta l^{\alpha^s_i - 1} e^{-\Delta l/\beta}}{\beta^{s(\alpha^s_i)} \Gamma(\alpha^s_i)} \tag{12}$$

where α^s_i (length class i) and β^s are parameters. As the mean of the distribution is fixed, $\alpha^s_i = \Delta l/\beta^s$ and β^s is the only free parameter. Taking these growth probabilities in a multinomial distribution, we obtain

$$X|p^s_{u,i,i'} \sim multinomial(b^s_{i,1}, \ldots b^s_{i,n}, Y)$$

Other approaches are possible. See Bogstad et al. (2002).

Survival

Two approaches to modeling mortality (and hence survival) are implemented in the Gadget code at present: The BORMICON approach (Stefánsson and Pálsson, 1998) and the Fleksibest approach (Frøysa et al., 2002). The Fleksibest approach has so far only been used for a single-species case where cannibalism is included.

The BORMICON approach:

The abundance $N(s,j,i,t+1)$ of fish of species s in area j belonging to length class i at time $t+1$ is calculated from the abundance at time t in the following way:

$$N(s,j,i,t+1) = (N(s,j,i,t) - \frac{\sum_v Cons(v,s,j,i,t) + \sum_f Catch(f,s,j,i,t)}{W(s,j,i,t)})e^{-M1(s,l(i))} \tag{13}$$

Thus, first the fish lost due to predation (Cons) and catch are subtracted, and then the (residual) natural mortality $M1(s,l(i))$ is applied.

Consumption $Cons$ (in biomass) is a function of abundance of all predator species v and the suitability $S_{s,v}(l(i),l(k))$ of prey species s (length class i) for predator v (length class k). It is calculated in the same way as in Bogstad et al. (1997): Let

$S_{s,v}(l(i),l(k))$ - the suitability of length group i of prey s as food for length group k of predator v

$N(s,j,i,t)$ - The number of individuals in length group i of prey s

$W(s,j,i,t)$ - The weight of individuals in length group i of prey s

$N(v,j,k,t)$ - The number of individuals in length group k of predator v

$W(v,j,k,t)$ - The weight of individuals in length group k of predator v

Define

$\Phi(v,s,j,i,k,t) = S_{s,v}(l(i),l(k))N(s,j,i,t)W(s,j,i,t)$

$\Psi(v,j,k,t) = \frac{\sum_{i,s}\Phi(v,s,j,i,k,t)}{\sum_{i,s}\Phi(v,s,j,i,k,t)+otherfood(v,j,t)}$

We then have

$$Cons(v,s,j,i,t) = N(v,j,k,t)H_v(W(v,j,k,t),T_j)\Psi(v,j,k,t)\frac{\Phi(v,s,j,i,k,t)}{\sum_{i,s}\Phi(v,s,j,i,k,t)} \tag{14}$$

where T_j is the temperature in area j and H_v is a predator-specific function denoting maximum consumption by a predator at a given temperature. The function Ψ is called feeding level.

The catch is modelled in a similar way: If $C_{f,j,t}$ is the total catch in biomass by fleet f in area j during time step t, the catch during that time step is given by

$$Catch(f,s,j,i,t) = C_{f,j,t}\frac{\Phi(f,s,j,i,t)}{\sum_f \Phi(f,s,j,i,t)} \tag{15}$$

here $\Phi(f,s,j,i,t)$ is used identically to $\Phi(v,s,j,i,k,t)$ for predation.

The difference between the BORMICON approach and the approach taken in Bogstad et al. (1997) is that in the latter paper fishing mortality was modelled by one value for each age group or for each sub-stock.

The Fleksibest approach:

Since this is a single-species approach, the species index is omitted. It has not been applied to a multi-area case yet, we have modified the equations in (Frøysa et al., 2002) to account for a multi-area extension and also by using predator length instead of predator age.

Survival probabilities $S_{j,i,t}$ for individuals of length i and living in area j are given by:

$S_{j,i,t} = e^{-Z(j,i,t)}$

The total mortality is given as

$$Z(j,l(i),t) = F(j,l(i),t) + M(j,l(i),t) \tag{16}$$

where $F(j,l(i),t)$ is the fishing mortality and $M(j,l(i),t)$ is the natural mortality.

Fishing mortality The total fishing mortality in area j, $F(j,l(i),t)$ is the sum over the partial fishing mortalities $F_f(j,l(i),t)$:

$$F(l(i),t) = \sum_{f=1}^{N_f} F_f(l(i),t) \tag{17}$$

The partial fishing mortality $F_f(j, l(i), t)$ is a product of a time- and area dependent fishing level and a selection curve, both fleet specific:

$$F_f(j, l(i), t) = \xi_f(j, t) S_f(l(i)) \tag{18}$$

$S_f(l(i))$ is the selectivity of fleet f.

Natural mortality The natural mortality $M(j, l(i), t)$ can be divided into predation mortality M2 and residual natural mortality M1, as in multispecies VPA (Helgason and Gislason, 1979; Pope, 1979).

The total natural mortality can then be written as

$$M(j, l(i), t) = M1(l(i)) + M2(j, l(i), t) \tag{19}$$

In the present implementation for NEA cod, the only predation mortality accounted for is cannibalism.

Cannibalism mortality Cannibalism is modelled as a function of prey length, the biomass of the fishes which are able to eat the prey and the biomass of alternative food (to account for prey switching). It is assumed that cannibalism only takes place on the immature part of the stock and that both immature and mature fishes are predators. The functional form is developed for North-East Arctic cod in particular, and the functions are based on data for this stock (Bogstad and Mehl, 1997; Bogstad et al., 1994, ICES, 2000).

To calculate the cannibalism predator potential $\Phi(j, i, t)$, we calculate the biomass of the immature and mature stock of length $\geq c\,l(i),\ c \geq 1$.

$$M2_{imm}(j, l(i), t) = \frac{\alpha(j, t) * f(l(i))}{\zeta(j, t)} * \Phi(j, i, t) \tag{20}$$

$$f(l(i)) = \exp(-\beta * l(i)^{\gamma}) \tag{21}$$

$$\zeta = \eta(j, t)^{\delta} \tag{22}$$

$$\Phi(j, i, t) = \Sigma_{u=imm}^{mat} \Sigma_{k=m}^{n} N(u, j, k, t) W(u, j, k, t) \tag{23}$$

$$l(m-1) < c\,l(i) < l(m) \tag{24}$$

$\eta(j, t)$ is the biomass of alternative food.

$\alpha(j, t)$, β, γ and δ must be positive numbers.

Residual natural mortality We have chosen a function describing the residual natural mortality which allows for higher natural mortality of small and large fish than of fish of intermediate lengths. This is similar to the assumption made by Tretyak (1984).

$$M1(l) = \begin{cases} \frac{a_1}{b_1 + l'} & l_{min} \leq l < l_1 \\ c & l_1 \leq l \leq l_2 \\ \frac{a_2}{b_2 + l'} & l_2 < l \leq l_{max} \end{cases} \tag{25}$$

$$l' = l * (M1(l_{max}) - M1(l_{min})) \tag{26}$$

Note that a_1, a_2, b_1, b_2 must be chosen so that $M1(l)$ is continuous at $l = l_1$ and $l = l_2$.

Recruitment

Recruitment can be modelled by a random variable $r^s_{j,t}$ indicating the number of recruits for species s in area j and a random variable l indicating the length distribution of these recruits. The smallest length considered for a given species is $l^s(i)$ whereas the largest is $l^s(n)$ as there are n length categories.

$$R^s_{j,t} = r^s_{j,t} l^s$$

$$r^s_{j,t} \sim uniform(l^s(1), l^s(n))$$

$$l^s \sim Gamma(\alpha^s_r, \beta^s_r)$$

The number of recruits $r^s j, t$ can be modelled by a stock-recruit relationship or taken as unknown parameter.

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C.5 Detailed examination of a GADGET model

The gadget program is a sophisticated and complex tool for building ecosystem models, which can themselves be highly complex. It is therefore important to periodically examine the model formulation and dynamics in some detail in order to identify possible problems and bugs within the system. Gadget produces summary results in the form of a likelihood statistic, broken down into separate components, and also outputs information of the modelled population. These numbers allow for the optimization of the model parameters, and give an indication of the dynamics of the model simulation, but do not capture all the details, and may not reveal underlying problems.

A detailed examination was made of the haddock example model in order to study the details of the simulation, and propose solutions to any problems found, either in the code or in the model formulation. Many of the issues described below apply to general model formulation, and have been tested on a three species model. Several of the tools developed to examine the model dynamics (e.g. automated sensitivity testing, plots of different aspects of the modelled population) will be made generally available to ensure that users are able to conduct such testing on their models with a minimum of difficulty.

There are two different, but related areas which can cause problems for a gadget model. There can be problems with the code or the model formulation which lead to unrealistic features of a modelled population, such as the ones described int eh ‘growth’ section, below. There can also be problems with the optimization routines, and their ability to converge to a realistic solution. This can occur even where a perfectly good target solution exists, but where model mis-specification distorts the population it can place added strain on the optimizers.

Optimization

The optimization routines attempt to find the parameter set which, for a given model formulation, produces the lowest likelihood score. However during the optimization an alternative local optima may be selected. In some circumstances, such as when the local optima has a likelihood score very close to the global optimum, this is not necessarily a problem. It is not entirely clear what exact weights should be assigned to each likelihood component, and therefore different optima with similar weights should all be viewed as possible solutions. Indeed the presence of different parameter values producing essentially the same modelled stock is a valid model result. However in some cases the local optima selected can be clearly unrealistic, and not represent an adaquate solution. Furthermore problems in the code or model formulation can lead to the creation of more unrealistic optima, producing more ’wrong’ solutions to attract the optimizers. Model mis-specification may also affect the likelihood surface in such as way as to prevent otherwise realistic solutions being arrived at.

This project therefore aimed to conduct thorough tests of the Hooke and Jeeves and Paramin optimization routines, using the haddock example as a case study. The Hooke and Jeeves was found to be able to reach a realistic optimimum from many, but not all, starting points. Restarting the optimization form the point arrived at at the end of the first optimization helped in some, but not all cases. A number of different changes were then made, both to the code and to the model formulation, in order to improve the ability of H&J to converge to a realistic solution. Howver such convergence cannot be guarenteed, and in many cases it can still fail. Paramin does not suffer from these problems, and has proved capable of converging from all the start points tested on the haddock model. It is however, unclear if this remains the case for all possible model formulations. In all cases it is recommended that any ’solution’ be tested by restarting the optimization from the ‘solution’ and checking that the same solution is arrived at.

Improvements

A number of changes have been made to the code and the model formulation to improve the reliability of the gadget optimization. Each of the changes improves gadget's ability to converge to an acceptable solution. However it needs to be recognized that this is still not perfect, and the optimisation routines can still fail. If this is suspected to be the case then repeat optimizations with different starting points may transcend this problem, or the paramin optimization program can be employed instead.

Combined SA and H&J:
A change was made to the gadget code allowing for the possibility of a short (and user definable) run of simmulated annealing prior to swithcing to Hooke and Jeeves, the ability to converge to a realistic optimum is increased. Simmulated annealing is able to rapidly move to the vicinity of sensible solutions, but is very slow at homing on the exact solution, whereas Hooke and Jeeves is fast, but not good at dealing with complex topography. Gadget models tend be characterized by a likelihood surface which is relatively smooth around a number of feasable solutions, and much more complex further away from these solutions. Thus the combination of Simmulated Annealing to move into the vicinity of a solution, and Hooke and Jeeves to identify the exact location is a useful and viable technique. This multiple optimization technique is further in the more powerful paramin optimization routines, but the approach adopted here represents a viable balance between power and computer time, and allows this balance to be adjusted according to the problem adressed, and the computing resources available.

Added an ability to attempt to escape being trapped by a bounds:
Many of the 'artifical' unrealistic local optima are caused by pre-set bounds. The bounds are implimented to prevent the program needing to search across an excessively large range of parameter values, and are implemented by imposing a rapidly increasing penalty weight on any parameter beyond these bounds. If the likelihood surface is descending when a bound is reached then this rapidly rising likelihood penalty allows for the possibility of generating local optima at these points. The new version of the code forces the optimizer to increase its step size (i.e. search further and further afield for a better point) if required, in order to attempt to escape an optima located at, or near, one of the bounds. There is an implicit assumption in this approach that any optima located on one of the bounds is not a correct solution. This is justified since the bounds should be set beyond any reasonable values, otherwise the final solution is determined by pre-set boundary values rather than by internal model dynamics.

Increased understocking penalties:
Much of the unpredictable behaviour of the optimising functions stems from attempting to compare situations where the fishing data contains fish, and the model has zero, or very few, fish in corresponding age and length categories. By increasing the understocking penalties dramatically this problem can be reduced, and the optimizers helped to seek realistic solutions. By increasing the penalty weights on understocking by two orders of magnitude the overall likelihood score of the optimized solution was lowered, indicating the benefits of avoiding unrealistic solutions.

Non-continuity of likelihood functions

Some of the likelihood functions have pre-specified values to deal with cases where a particular age-length cell has zero fish in the model, but a non-zero number in the corresponding data file. On investigation it was found that in some cases the change from normal comparisons to this pre-set value was discontinuous. This was fixedby adding a smooth function connecting the two regions. The weight applied to comparing zero modelled fish in a given cell to a data cell with fish present was also set to be higher than the weight arising from the modelled cell simply having a very small number of fish. This ensured that increasingly unrealistic models acquired increasingly high penalty weights, forcing the optimizers to move to more realistic solutions.

These modifications have resulted in a minor change in the likelihood score for the haddock example (inlcuded in the latest releases).

Model specification

The detailed structure of the modelled population was also investigated in detail in order to identify any mis-specification within the model.

Growth
The mean length growth for each age&legnth cell is calculated for each timestep. This calculated mean growth then has to be translated into actual growth within the model. However it was unclear if this translation was actually being done correctly. A number of seperate, but related, problems were discovered, which had meant that the calculated mean growth rate was different from that actually implemented.

A number of internal limits exist within the model (in addition to those specified in the bounds file). These exist for reasons of computational efficiency and were set wide enough that they should not effect the model results. However because the operation of the optimizers these internal limits had a major impact on the outcome of the model. Furthermore these problems are not immediately apparent at the level of the population as a whole, and may thus pass un-noticed during the diagnostics phase of model bulding.

Limits were set on the maximum number of categories that a fish was permitted to grow in a given time step, and on the maximum and minimum length at age of the stock. The limits were chosen so that only a very small number of fish could reasonably be expected to exceed them, and thus it was believed that there would be no adverse impact on the model results. Having these limits prevents the program having to waste time examining a large number of empty cells. However there is a problem.

Consider a parameter which would lead to high growth rates, and thus an excessively high number of large fish. This in turn would create a large number of age&length cells with significant numbers modelled fish, but zero fish in the corresponding data set. Each of these would attract a penalty weight, and the optimizer would reject this solution and seek a different one. Now consider the situation with a maximum size limit in place. Every fish computed to exceed this limit would be resized to be in largest allowed length category. This would give a penalty weight for that length category, since this cell would have an unrealistically high number of fish present. However this penalty is not as high a weight as the summed penalty for all the cells matching against zero data in the case without the maximum length limit in place. The model is attempting to fit a distribution with only a few free parameters (2 in the case of growth) to a complex data set. Any solution is therefore a comprimise, with a certain discrepancy between the model and the data. By artifically reducing the penalty for a large right-hand tail through imposing a 'wall' in the way described, a new set of solutions can be produced, which may result in a lower overall weight. There is thus the possibility to create local optima using the 'wall' imposed by the limit to build against, which would not exist if that limit was removed. These local optima can attract the optimizers. Worse, by 'reshaping' the distribution with this wall it may be that what should be the global optima is no longer a possible solution.

The resulting populations contain unrealistic ‘spikes’ in the length distributions, and furthermore because fish exceeding the limit are simply reduced in size, the actual mean growth rates implemented for the modelled fish aredifferent from those computed. However there is no way to identify that that the actual mean growth rates do not match the calculated ones, and the unrealistic length distributions are not immediately apparent. At the scale of the whole population the 'overprinting' effect from different year classes produces a smooth, and apparently reliable distribution, the problems only become apparent on examining the length distibutions for a single cohort.

A similar problem arises with the maximum number of length categories a fish is permitted to grow in a single timestep. At first sight it seems reasonable to impose such a limit, as fish do have physical limits on how fast they can grow, so this appears to be a case where computational efficiency can be gained with no loss of model accuracy. However such a limit, even one significantly higher than could be expected to occur in the real population creates a similar 'wall' which can create artifical local optima for the optimizers to converge to. In this case the calcluated mean growth needs to be converted into a growth distribution for each age&length cell. This is done by means of betabinomial distribution with the program typically optimising a single parameter, beta. Withoutthe an upper limit a low value of beta typically results in a long right hand tail, with some fish growing unrealistically large amounts. This would normally be selected against, and a higher value of beta employed. However with the upper limit employed those rapid growing fish are reassigned to the highest growht category permitted. The computation is carried out in a manner which ensures that the computed mean is still preserved, however this means that the shape of the distribution is altered in the process. The resulting distribution has two peaks, one at zero growth categories, one at the maximum, and a lesser number at the categories in between. This clearly unrealistic distribution was used to assign growth fish in certain age&length cells. However when the population is examined as whole the problem is not visible, the cumulative effects of many hundreds of such distributions is a smooth, and apparently reasonable, distribution.

It should be noted that in both these cases removal of the artifical bounds allowed new optima to be reached with lower (and therefore better) likelihhod scores. These optima simply did not exist with the restrictive bounds in place, due to the artificial distortion of the likelihood surface. In both cases the solution is the same - to remove the artificial constraints. This allows the possibility of the parameter values which will produce unrealistic modelled populations. However the optimizers compare key characteristics of the real and modelled populations (or at least of the real and modelled catches), and thus can select against such solutions. Thus this should not be a problem if the optimizers are sufficiently powerful. Rather than trying to impose constraints on the model to make it impossible to arrive at unrealistic solutions it is better to work on the model formulation and optimization routines in order to ensure that such solutions can be rapidly examined and abandoned.

Summary

After a detailed investigation of the model dynamics and optimization several problems were identified. Those which were caused by problems in the code were rectified. Those caused by problems in the model specification were fixed for the haddock example. Details of the potential pitfalls identified will need to be included in future documentation in order to ensure that they are not re-created in new models. The gadget optimizer has been improved, but still cannot be guaranteed to converge in 100% of cases. The paramin optimizer was found to be significantly more robust. Finally a number of diagnostic tools were developed during this procedure which will be included future releases ofgadget to enable users to assess any newly developed models.

C.6 A model for size preferences in cannibalism in Northeast Arctic cod (*Gadus morhua* L.)

Bjarte Bogstad, Institute of Marine Research, P.O.Box 1870 Nordnes, N-5817 Bergen, Norway

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Introduction

Cannibalism in Northeast Arctic cod (*Gadus morhua* L.), which is an important cause of mortality of young cod, is highly variable from year to year (Bogstad *et al.*, 1994; Bogstad and Mehl, 1997; ICES, 2001). In models for assessment of current stock size and for prediction of stock development for Northeast Arctic cod, cannibalism has been included (ICES, 2001; Frøysa et al., 2001). Cannibalism is there modelled as a function of predator abundance, prey length and capelin (*Mallotus villosus*) abundance. The model formulations for cannibalism have not been thoroughly discussed, however. In this paper we attempt to develop a model of size preferences in cod cannibalism, based on data on cod stomach content and estimates of abundance of cod by size. The model can be utilized by the new assessment tool for Northeast Arctic cod - Fleksibest (Frøysa *et al.*, 2001).

Material and methods

According to Bogstad *et al.* (1994), cod is able to prey on cod which is half its own length or shorter. The prey (cod) length distribution for given predator length is rather wide, and thus it is not obvious which prey (cod) length groups is preferred by a predator cod of a given length. This size preference is what we attempt to model here.

In order to describe the size preference of cod preying on cod, data on stomach content as well as data on abundance of cod are needed. Annual data on cod stomach content of Northeast Arctic cod are available from the period 1984-2000. They were extracted from the joint Norwegian-Russian stomach content data base (Mehl and Yaragina, 1992). The stomachs were analysed individually. Predator length was recorded to the nearest cm. In the period 1984-1992, the prey length was recorded in the following groups within the range relevant for cod as prey: 5.0-6.9 cm, 7.0-9.9 cm, 10.0-14.9 cm, 15.0-19.9 cm, 20.0-24.9 cm, 25.0-29.9 cm, 30.0-39.9 cm, 40.0-49.9 cm, 50.0-69.9 cm. From 1993 onwards, prey length was recorded to the nearest cm. In order to transform the data to 5cm prey length groups used in the analysis, the cod in the 30.0-39.9 cm and 40.0-49.9 cm length groups was assumed to be evenly distributed on the two 5 cm groups within those intervals. Cod in the 50.0-69.9 cm group was assumed to belong to the 50.0-54.9 cm group, as cod longer than 55 cm has not been found in cod stomachs.

Abundance at age estimates from the assessment made for Northeast Arctic cod for the period 1984-1999 (ICES, 2001) were averaged to give an estimate of the average age distribution. This age distribution was combined with length at age data (5 cm length groups) from the Norwegian bottom trawl survey in the Barents Sea in February (Jakobsen *et al.*, 1997) and the Lofoten acoustic survey (Korsbrekke, 1997) to give an average length distribution of the stock.

Cod prey < 10 cm were excluded from the analysis because cod of this length is mainly found pelagic, and our sampling of cod stomachs is mainly from bottom trawl hauls. Cod = 110 cm were excluded from the analysis because few stomach samples are available for cod of this length. Also, the abundance of cod of this size is very low. No cod was found in stomachs of cod < 20 cm, and these (predator) length groups were excluded from the analysis.

Modelled consumption

We assume that the consumption of cod by cod can be calculated as total consumption by cod multiplied by the proportion of cod in the diet of cod. Further, this has to be divided on cod (prey) length groups. The modelled consumption rate (kg/quarter) by one (predator) cod of length L of cod (prey) of length l, $C_{mod}(l,L)$, can then be formulated as:

$$C_{mod}(l,L) = C_{max}(L)P_{cod}(L)\frac{f(l,L)N(l)W(l)}{\sum\limits_{l} f(l,L)N(l)W(l)} \tag{1}$$

$N(l)$ is the number of cod of length l and $W(l)$ is the weight of cod of length l. C_{max} (L) describes the maximum consumption rate by cod of length L, $P_{cod}(L)$ is the proportion (in weight) of cod in the diet of cod of length L and $f(l,L)$ describes the preference of cod of length l by cod of length L. Below, we discuss how the various components in (1) should be formulated.

C_{max} (L) is assumed to depend on fish weight $W(L)$ in the same way as described by Jobling (1988), i.e.

$C_{\max}(L) = \alpha(W(L))^{0.802}$ A length-weight relationship for cod was estimated from all predators in the stomach content data base for which length (L-cm) and weight (W-kg) was recorded, giving

$$W(L) = 0.0000068L^{3.06}, R^2 = 0.99, p < 0.0001 \tag{2}$$

This gives

$$C_{\max}(L) = \alpha L^{2.45} \tag{3}$$

$P_{cod}(L)$ increases with increasing L (Bogstad *et al.* 1994). The proportion of cod in the stomach content (here assumed to be equivalent to the proportion in the diet) of cod for each 5 cm length group was calculated from the stomach content data base. Assuming $P_{cod}(L)$ to be a function of L, the following parameters were obtained by fitting data for the interval 20-110 cm:

$$P_{cod}(L) = 0.0145 + 5.1 \cdot 10^{-7}(L-20)^3 \tag{4}$$

The fit is shown in Fig. 1

In order to formulate $f(l,L)$, it seems reasonable to start by plotting predator length vs. prey length for cod preying on cod (Fig. 2).

Only stomachs where the length of the cod prey was recorded are included. The prey and predator sizes are represented by the midpoint of the recorded size interval. A linear regression line is included:

$$l_{prey} = 0.42 + 0.24L_{pred}, R^2 = 0.27, p < 0.0001, N = 3853 \tag{5}$$

Since the data show that prey length generally is less than about half the predator length (Fig. 2), a simple assumption describing the length preference would be (r_1 close to 2)

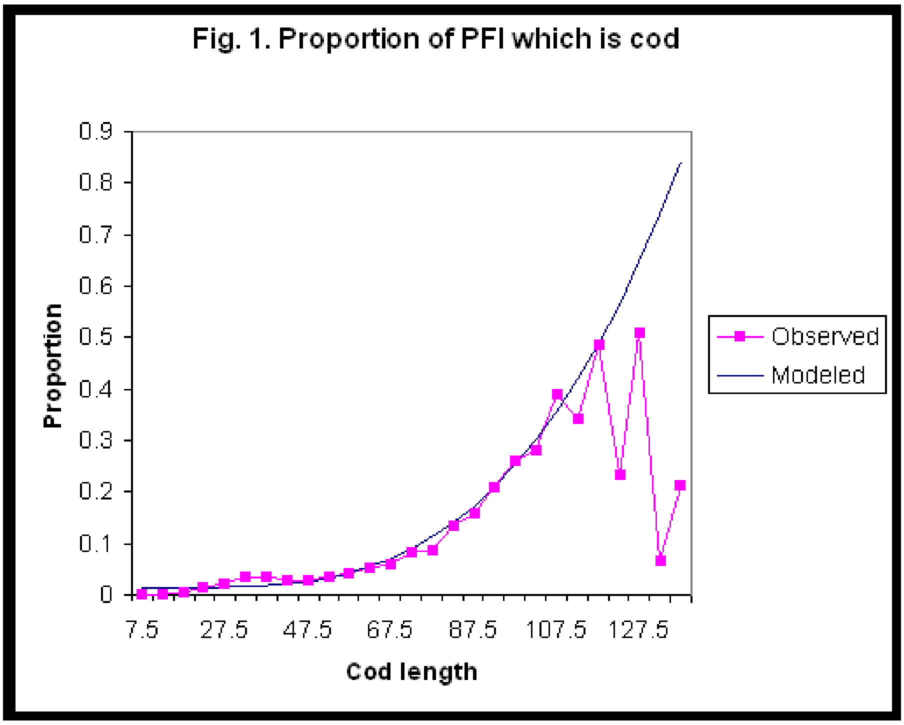

Figure 1: Observed and modelled proportion of cod in the cod, by predator length group

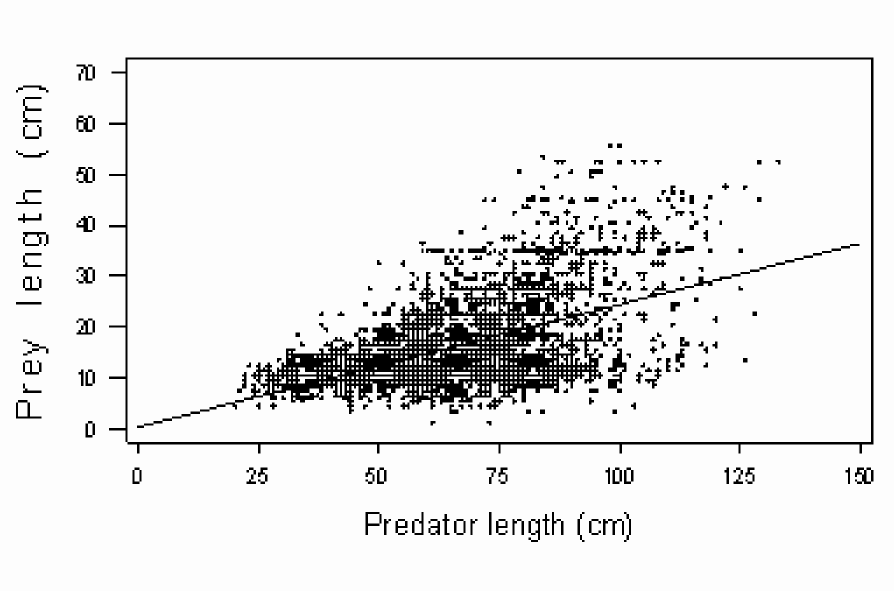

Figure 2: Prey size vs. predator size for cod preying on cod, for the period 1984-2000.

$$
\begin{aligned}
f(l,L) &= 1, L > r_1 l \\
f(l,L) &= 0, L < r_1 l
\end{aligned}
\tag{6}
$$

An alternative is an asymmetric bell-shaped function for *f(l,L)*:

$$f(l,L) = e^{-\frac{(\ln\frac{L}{l}-p_1)^2}{p_2}} \text{if} \ln\frac{L}{l} \leq p_1 \text{and} f(l,L) = e^{-\frac{(\ln\frac{L}{l}-p_1)^2}{p_3}} \text{if} \ln\frac{L}{l} > p_1 \tag{7}$$

This is one of the functions implemented in BORMICON (Stefánsson and Pálsson, 1997) to describe prey suitability. With p_2=p_3, it becomes symmetrical and equivalent to the size selection model suggested by Andersen and Ursin (1977). Andersen and Ursin used weights instead of lengths in their model, but if the exponent in the weight-length relationship for predator and prey is the same, the formulations are equivalent. The Andersen and Ursin size selection model has been used in the Multispecies Virtual Population Analysis (MSVPA) model (Gislason and Sparre, 1987), which has been applied e.g. to the North Sea and the Baltic.

It should be noted that the function $f(l,L)$ describes cannibalism on the population level, and thus incorporates both actual prey size preferences as well as geographical overlap between predator and prey. The smallest cod is distributed farther east and north than the larger cod (Ottersen *et al.*, 1998).

Calculation of length distribution in the stock

In the calculations of cod abundance by age made by the ICES Arctic Fisheries Working Group (ICES, 2001), cod cannibalism is accounted for. Using these data in the calculations in the present paper thus introduces circularity in the reasoning, but as we do not consider it possible to use survey abundance indices directly in the calculations, no better approach seems to be available at present.

The average proportion of the cod stock which has age a and maturity stage (immature/mature) s is given by

$$P_{vpa}(a,s) = \frac{1}{16}\sum_{y=1984}^{1999}\frac{N_{vpa}(y,a,s)}{N_{vpa}(y)} \tag{8}$$

where $N_{vpa}(y,a,s)$ is the abundance in year y of fish of age a and maturity stage s, as estimated by the VPA (ICES, 2001) and $N_{vpa}(y)$ is the total abundance of cod in year y. Abundance estimates for ages 3-13+ are taken directly from ICES (2001). They are extended down to ages 1 and 2 in the same way as done by ICES (2000) (M=0.2+cannibalism).

The length distribution from the winter survey, $N_{winter}(y,a,l)$ is applied for immature cod. The proportion of fish in a given length group for a given age is averaged over the time period:

$$P_{imm}(l|a) = \frac{1}{16}\sum_{y=1984}^{1999}\frac{N_{winter}(y,a,l)}{N_{winter}(y,a)} \tag{9}$$

where

$$N_{winter}(y,a) = \sum_{l} N_{winter}(y,a,l) \tag{10}$$

For the mature cod, the length distribution from the Lofoten survey, $N_{Lofoten}(y,a,l)$ (available for 1985-1999) is applied:

$$P_{mat}(l|a) = \frac{1}{15}\sum_{y=1985}^{1999}\frac{N_{Lofoten}(y,a,l)}{N_{Lofoten}(y,a)} \tag{11}$$

where

$$N_{Lofoten}(y,a) = \sum_{l} N_{Lofoten}(y,a,l) \tag{12}$$

The resulting average length distribution in the stock is then given by:

$$N(l) = \sum_{s=imm}^{mat}\sum_{a=a\min}^{a\max} P_{vpa}(a,s)P_s(l|a) \tag{13}$$

Observed consumption

The observed consumption is calculated based on the stomach content data and the evacuation rate model developed by dos Santos and Jobling (1995). Essentially the same methodology as in Bogstad and Mehl (1997) is used, but the calculations are made based on individual stomachs.

The average consumption rate of cod of length l by cod of length L (kg/year) is given by:

$$C_{obs}(l,L) = \frac{1}{NS(L)}\sum_{k=1}^{NS(L)} R_{cod,l,k} \tag{14}$$

where *NS(L)* is the number of cod stomach samples from length class L for the period 1984-2000. No weighting by catch rate in trawl hauls is applied.

The consumption rate (kg/quarter) by an individual cod of weight W of cod prey in length group l is calculated in the same way as Bogstad and Gjøsæter (2001) calculated the consumption of capelin (*Mallotus villosus*) by cod:

$$R_{cod,l,k} = \begin{cases} \frac{2.19 \ln 2 e^{\gamma T_k} W_k^{\delta} S_{cod,l,k}}{\alpha_{cod}(1.42 S_k)^{\beta}}, S_{cod,l,k} > 0 \\ 0, S_{cod,l,k} = 0 \end{cases} \tag{15}$$

where $S_{cod,l,k}$ is the stomach content (g) of cod of length l in cod no. k (in length group L), S_k is the total stomach content (g) of cod no. k , T_k is the ambient temperature (°C), W_k is body weight (g) and α_{cod} is a prey-specific half-life constant. The values of the constants are $\beta = 0.52$, $\delta = 0.26$, $\gamma = 0.13$ and α_{cod} (α for cod as prey) $= 84$. In this working document, a constant temperature of 5° C was used for all stations. The factor 2.19 is included to obtain the consumption in kg/quarter (Fleksibest unit for consumption) rather than in g/h.

The following quantity is then minimized:

$$\sum_{L=L\min}^{L\max} NS(L)\sum_{l=l\min}^{l\max}\left(C_{obs}(l,L) - C_{mod}(l,L)\right)^2 \tag{16}$$

5 cm length groups are used both for predators and preys, and the mid-point is used to represent the length groups: l_{min}=12.5 cm, l_{max}=52.5 cm, L_{max}=22.5 cm, L_{max}=107.5 cm.

Results

The fit is described in the table below, as well as in Figs. 3 and 4 (Linear and bell-shaped length preference, respectively)

Model	SSQ	%
F(l,L)=1 (L>r_ll)	7.25	100
Bell-shaped	2.04	28

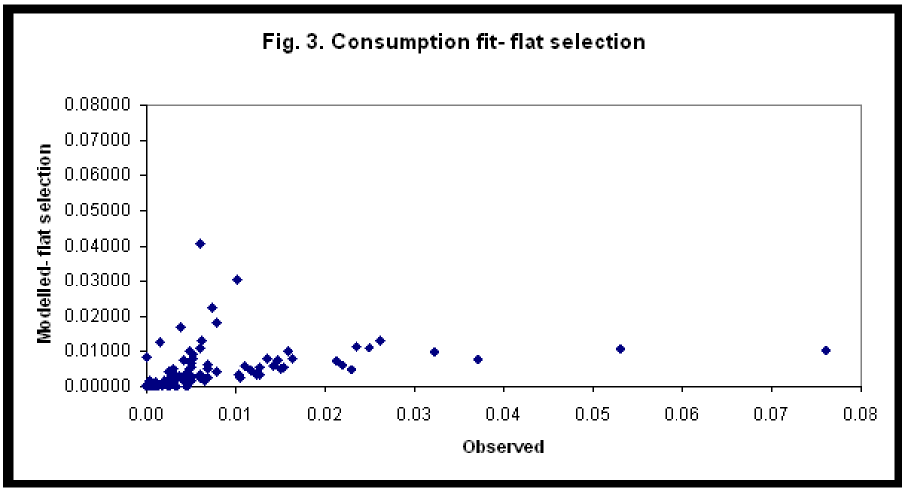

Figure 3: Observed and modelled consumption using f(l,L) described by equation (6).

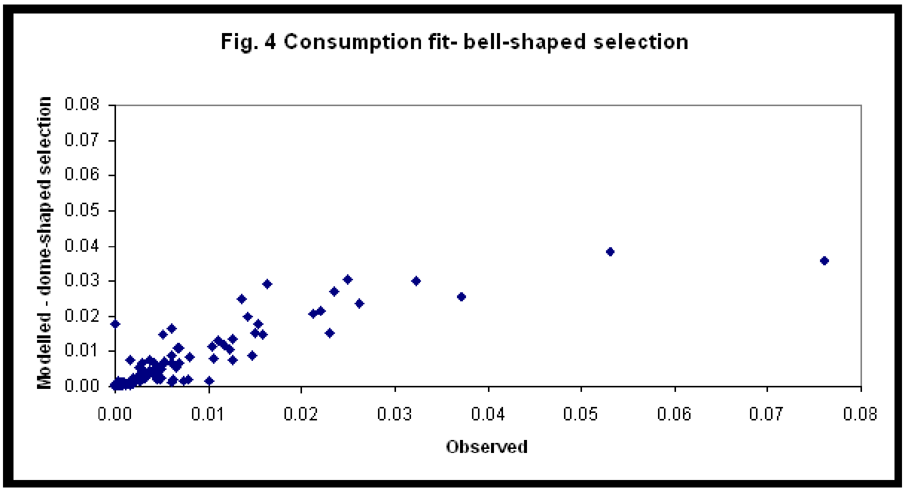

Figure 4: Observed and modelled consumption using f(l,L) described by equation (7).

When fitting the predation model (Eq. 1) to the data using Eq. (16), the following parameter estimates were obtained:

f(l,L) described by (6):

Parameter	Value
α	8.72E-06
r_1	1.8

f(l,L) described by (7):

α	1.66E-06
p_1	1.12
p_2	0.015
p_3	0.228

This indicates that the preferred predator length/prey length ratio is $e^{1.12} = 3.06$.

f(l,L) from (7) is shown in Fig. 5.

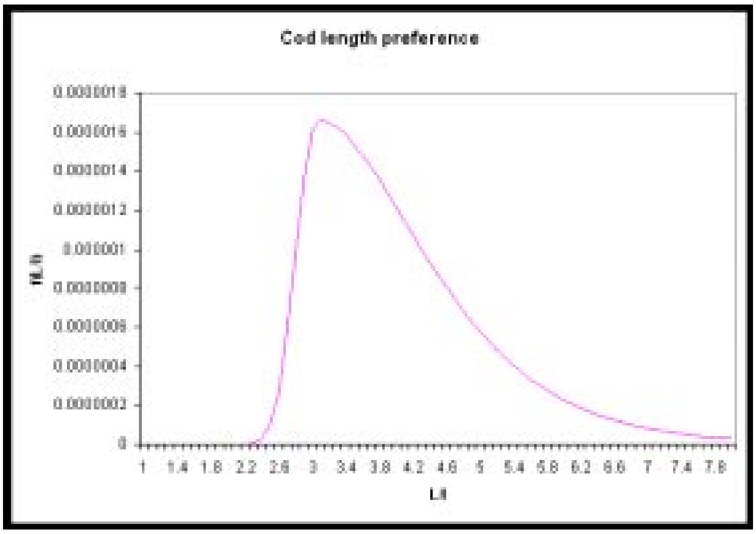

Figure 5: The function f(l,L) as estimated by the predation model (eq. 7).

A similar analysis (using weight instead of length in the suitability function) was carried out by the ICES Multispecies Assessment Group (ICES, 1996). Several prey, among those cod, were analysed. Generally, a wider spread of prey lengths was found for Northeast Arctic cod than for North Sea cod.

Discussion

A model for prey size selection in cod cannibalism has been established. An asymmetric bell-shaped curve gave a much better fit to the data than assuming that the cod prey equally on all cod smaller than given size (close to half its own size). For application in assessment and prediction of cannibalism mortality for the Northeast Arctic cod stock, the year-to year variation in cannibalism also need to be explained. One likely reason for the variation is fluctuations in the abundance of the capelin (*Mallotus villosus*) stock in the Barents Sea. A first approach to this could be to make the parameter α dependent on capelin abundance.

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C.7 Norwegian spring spawning herring model

A. Slotte (IMR)

One of the main aims of this subtask is to produce a model, which could predict spawning distribution of Norwegian spring spawning herring (NSS herring) and the coherent recruitment. The model is based on the assumption that both spawning distribution and recruitment is influenced by environmental factors, stock size and -structure (length composition, condition) as described in previous studies (Slotte 1999a, b; Slotte and Fiksen 2000). As a part of the present project, Slotte (2001) has reviewed all factors that influence choice of spawning grounds in in NSS herring, and Røttingen and Slotte (2001) have studied the development of the southernmost spawning fraction in detail. In addition, Osskarsson et al (in press) have studied the maturation, fecundity and atresia in relation to size, condition and distance of spawning migration in NSS herring. All these studies have added valuable information for the present modelling work, in understanding the spawning migration and recruitment of this stock.

In another study on NSS herring finished in 2001, different stock-environment recruitment models have been fitted to a time series of spawning stock-, spawning distribution-, recruitment- and temperature data extending back to 1907 (Fiksen and Slotte, in press). Here a new index has been developed based on the ambient temperature in the larval drift trajectories during the early larval life along the Norwegian coast. This index has been used an addition to the more traditional and indirect temperature index from the Barents Sea (the average annual temperature in the Kola transect). These indexes are highly correlated. The models show highly significant effects of both spawning stock and temperature. The inclusion of the temperature term in the stock-recruitment models removes the autocorrelation from the residuals, and improves their explanatory ability by 6 - 9%, the coastal and Barents Sea temperature index explains equally much. The interdependence between recruitment success and subsequent spawning stock biomass is explored, and the conclusion is that this is not likely to generate the stock-recruitment relationship. In fact this analysis suggests that the collapse of the Norwegian spring spawning herring stock in the period 1950-1970 was not caused by reduced recruitment, but by the drop in spawning stock biomass induced by the increased fisheries in this period. This modelling work forms a good basis for the actual modelling of present spawning migration and recruitment.

As part of an attempt to model the spawning distribution of NSS herring, a major work has been carried out to split the entire Norwegian coast and Shelf areas into squares of 25 km^2, which based on historic information are suitable for spawning if they are shallower than 230 m and contain substrates like rock, stones and gravel. The developed dataset of possible spawning sites is entirely based on data of bottom substrates collected in sea maps. It contains data on position (middle of the square), average depth, and an area from 1-25 km^2 with spawning substrates, which correspond very well with historic observations of spawning distribution. In the projected model only a limited number of herring will be allowed to spawn at each m^2, since the survival of eggs is density dependent. Herring will initiate spawning migration from wintering grounds of Vestfjorden, northern Norway. The historic temperature data along the coast from 1935 and upward demonstrate that larvae will drift through higher temperatures and hence survive better the farther south they hatch. Thus, each herring will have to allocate energy between migration and fecundity based on the information of temperature along the coast, their own migration potential (body length and weight), and the density of fish.

The final model of spawning distribution and coherent recruitment is still under development. The next thing planned is to run a test model with actual data on abundance by length and weight, and annual temperatures along the coast from the period 1990 (when the stock first started to winter in Vestfjorden) and onwards. The predicted distribution and coherent recruitment will be compared with observed distribution and recruitment to test and perhaps tune the model. This work and model is expected finished by August 2002.

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D Estimation and Inference

D.1 Analysis of Categorical Length Data from Groundfish Surveys

DRAFT

Birgir Hrafnkelsson
deCODE Genetics, Lynghals 1, 110 Reykjavik, Iceland,
birgirh@decode.is
and Gunnar Stefansson
Marine Research Institute, Skulagata 4, P. O. Box 1390, 121 Reykjavik, Iceland,
gunnar@hafro.is

Author's Footnote

Birgir Hrafnkelsson is Statistician, deCODE Genetics, Lynghals 1, 110 Reykjavik, Iceland (email:birgirh@decode.is). Gunnar Stefansson is Head of Modeling Division, Marine Research Institute and Associate Professor, Department of Mathematics, University of Iceland, Hjardarhagi 2-6, 107 Reykjavik, Iceland (email:gunnar@hi.is). This research was performed while the first author was employed at the Marine Research Institute and was partially supported by EU research grant QLK-CT1999-01609.

Summary

An extension of the multinomial model of counts is presented to account for over-dispersion and different correlation structure. Such models are needed in biological applications such as survey of heterogeneous populations.

Expensive annual surveys of cod populations are conducted world-wide by marine research organizations. Typically, on trawl haul is taken at a few dozen tow locations (stations) that are distributed in a stratified manner over the entire survey area. At each such station and for a given species, a sub-sample of fish is taken and these are length measured, resulting in a vector containing the frequency in each length category. One of the goals of such a survey is to estimate the length distribution of pre-specified species within a particular area.

Three models are developed for such length data, and subsequently compared, using cod as an example. The models are the standard multinomial model and two hierarchical models where within each station the numbers in the categories are assumed to follow a multinomial distribution with some corresponding sample size and a probability vector while the probability vectors at the stations are not equal but they come from a common distribution with a certain mean and a covariance. The distribution of the probability vectors in the two hierarchical models is the standard Dirichlet distribution and the logistically transformed multivariate Gaussian distribution, respectively.

The data analyzed exhibits variances that are larger than those of the standard multinomial model and correlations that are stronger than the correlations of the multinomial-Dirichlet distribution while the hierarchical model based on the multinomial distribution and the logistically transformed multivariate Gaussian distribution appeared to capture the complex covariance structure of the data. The parameters in the models are estimated using a Bayesian estimation procedure.

Keywords: Bayesian estimation; Dirichlet random variables; Hierarchical models; Markov chain Monte Carlo; Multinomial random variables

D.1.1 Introduction

A major focus of marine research programmes is on the development of fish populations. To facilitate such research, enormous efforts are undertaken to sample the fish populations in various ways.

This paper describes some of the fundamental data sets obtained in marine research and how they are commonly analysed. It is indicated in this section in what manner standard assumptions in these analyses are violated. The data section subsequently describes the data sets used and illustrates how serious the deviations from common assumptions are for particular data sets.

The two most fundamental data sets obtained from sampling of fish populations are the length measurements of individual fish and abundance indices (e.g. total catch per tow), each of which can be obtained from marine surveys or commercial fisheries. Other data sets can be highly important in individual situations but at least one of these two types is always a part of analyses of fish population dynamics.

The statistical aspects of direct measurements of abundance have been extensively documented (see e.g. Pennington, 1983; Stefansson, 1996) and will not be discussed further. Length measurements of individual fish are done on discrete scales (e.g. 1 cm or 1mm groupings) and are therefore commonly analysed as count data (though alternatives exists, e.g. when estimating growth). Although fundamental to stock assessment, the properties of these data have not been extensively studied and the data sets have generally been analysed using simple techniques. This paper demonstrates that assumptions underlying these techniques are seriously violated and methods are provided to alleviate these problems.

Within models of fish population dynamics it is common practise to either use lognormal errors or a multinomial distribution when investigating numbers which by their nature are counts or estimated counts. Examples include models for catches in numbers at age (e.g. Gudmundsson, 1994, Gavaris, 198x, ...), models for the frequency of fish in a given length group (e.g. MacDonald and Pitcher, 19xx and Methot, 19xx). Interestingly, the multinomial distribution is frequently referred to as a more plausible alternative to the assumption of lognormal errors (e.g. MacDonald and Pitcher, 19xx).

Taking a basis in multinomial models, the first violation of common assumptions is of an overdispersion type. From a biological viewpoint it must be recalled that fish do not behave as independent individuals, but (in the case of most species) they have some form of common behaviour, which leads to aggregations in feeding and spawning areas. It is therefore to be expected that the counts in a given length cell should behave in an overdispersed fashion, similarly to the total counts or abundance, as observed for those data. This may not simply result in a skewed distribution but can lead to a distribution with a heavy right tail and a spike at zero (e.g. Jacobson, 199?, Stefansson, 1996).

The overdispersion issue in the multinomial is well-studied and alternative model frameworks are known, such as using a beta-binomial or a general overdispersed multinomial (McGullagh and Nelder, 19xx).

A more subtle, but no less serious violation is due to correlation between the counts in the length cells. For adjacent cells this is not the slightly negative correlation due to the nature of multinomial counts but rather a high positive correlation between the counts. Since fish of similar size will tend to behave in a fashion more similar than fish of very different sizes, a positive correlation is to be expected. The biological reason for this can be food preference, where the size of the predator enforces restrictions on the preferred size of prey, leading to similarly sized fish tending to appear grouped in similar locations (which may vary temporally). On the other hand, for a piscivorous and cannibalistic species it is also reasonable to expect a highly negative correlation between the counts in very different length groups, both because evolution can plausibly lead to juveniles tending to be in nursery areas different from feeding areas of adult fish and also because a high mortality due to cannibalism would lead to reduced observed counts of small fish, even if the small fish had ventured in the area of adults. Thus biological concerns indicate that counts should have a correlation structure very different from that observed in a simple multinomial counting experiment.

Classical methods of analysis start with some summaries of the data sets, usually aggregating through simple summaries. Naturally, the actual uncertainty associated with these summaries may be very different from that estimated using the simple models. This becomes a major issue when combining different data sources, where it has been noticed that the choice of weighting factors given to different data sets in a log-likelihood function can give very different results (Stefansson, 1998). Recent models of fish population dynamics tend to be highly complex, combining several such data sets in a nonlinear model and therefore requiring some form of weighting attached to each data set (Stefansson and Palsson, 1998). For this reason there is considerable incentive to obtain a better description of the statistical properties of the various measurements, to be used for defining appropriate log-likelihood components with a weighting of unity.

D.1.2 The Data

The data set used for the present study is chosen to be typical of length sampling of fish in marine surveys. The data consist of measurements of cod from the main groundfish survey in Icelandic waters (Palsson et al, 1989). These survey is designed with cod as a target species, and thus cod are sampled and measured from each trawl haul or station where they occur. If manageable, the entire haul is measured, but for large hauls a sample is measured.

The survey encompasses the ocean shelf off Iceland, down to 500m depth, with an average of over 500 stations per year for 17 years. This includes a highly variable ecosystem, and hence a subset of 142 stations from March, 1999 is used. The selected stations in questions corresponds to a single important area for cod. The number of length measured cod at each station ranges from 7 to 418 with a median of 72. The original length measurements are recorded in 1 cm intervals (e.g. 9.5-10.5 cm). These are grouped into 5cm intervals for the present analysis, except for the first and last intervals which contain cod of length 4.5-10.5 cm and over 95.5 cm, respectively, giving a total of 19 categories for most of the ensuing analyses.

In the simplest binomial model the variance is difficult to disentangle from sample size and therefore the effect of overdispersion can best be illustrated by taking a fixed number (50) of fish (by random subsampling) at each of the 98 stations containing at least 50 length measurements. Under the assumption of iid samples, the counts obtained in a particular length group should follow a binomial distribution at each station. Having further fixed the total number sampled at each station, all the counts might be expected to come from the same binomial distribution. Fig. 1 provides a histogram of the number of fish of length less than 26.5 cm, along with the theoretical distribution, which is very close to Gaussian in this case. It is clear that the data are much more dispersed than a binomial model would dictate (a simple test being that the tails have almost zero probability but a fair number of observations fall into the tails). In accordance with this observation, a simple chi-square goodness-of-fit test for the hypothesis for the null hypothesis that the numbers come from the binomial distribution rejects the null hypothesis very strongly.

The conclusion is, therefore, that the counts do not correspond to counts from identical binomial distributions and some form of overdispersion is needed to explain the data.

Again by subsampling with a fixed sample size at a each station, it is possible to obtain vectors with the counts in each of the 19 categories. A natural first model for these counts would be a multinomial distribution but given the preceding paragraph, it should be at least modified to account for overdispersion. The multinomial model dictates a certain correlation structure, which is based on the slightly negative covariance, $-np_ip_j$, between any pair of cells. Again, this can easily be verified using the data, since a pair of length cells is sampled at each station and entire set of pairs can be used to compute a correlation. These correlations are plotted against the lag (distance between length categories) in Fig. 2, as one point for each correlation at each lag. Again, it is seen that this structure is very different from that obtained from a multinomial model (a simple test being the number of positive correlations at lag 1, where all the observed correlations are positive but the model predicts a negative expected correlation).

It should be noticed that there appears to be a pattern in Figure 2, that is, for the first three lags the correlations are mainly positive, while for lags between 4 and 10 the correlations are ranging from being weak and positive to being moderate and negative. For higher lags the correlations are mainly weak and negative. This is in perfect accordance with the biological issues raised earlier.

D.1.3 Three Categorical Models

In this section we view three categorical distribution models and illustrate how one would estimate the parameters in these models using Bayesian estimation methods based on Markov chain Monte Carlo (MCMC). We assume that the form of the data is such that each observation is a vector of categorical counts. The sum over each vector is not necessarily fixed, however, our analysis is conditioned on the sum over each vector.

The first model is the commonly known multinomial model with a fixed probability vector θ for each observation, (McCullagh and Nelder 1989, chap. 5). We will refer to this model as the standard multinomial model. The second model is the Dirichlet-multinomial model, Mosimann (1966). That model is a hierarchical model where each vector of observed categorical counts has a multinomial distribution with a particular probability vector, while the probability vectors have a standard Dirichlet distribution (Johnson and Kotz (1972), pp. 231-235). The papers by Lu, Gumberland, Mayer and Eckhardt (1999) and Vasko, Toivonen and Korhola (2000) discuss applications of the Dirichlet-multinomial model. Gange, Jacobson and Muñoz (1996) discuss extensions of the Dirichlet-multinomial model. The third model is like the second model except that the probability vectors do not have a standard Dirichlet distribution, but have the same distribution as logistically transformed multivariate Gaussian random variables. Aitchison (1985) discusses models of this type on the simplex. We will refer to the third model as the logit-Gaussian-multinomial model. This model has a more flexible covariance structure than the Dirichlet-multinomial model. For references on Bayesian hierarchical models see, Diggle, P. J., Tawn, J. A., and Moyeed, R. A. (1998), Waller, L. A., Carlin, B. P., Xia, H., and Gelfand (1997) Wikle, C. K., Berliner, L. M., and Cressie, N. (1998).

We are primerily interested in θ where in all three models

$$E(X_q) = m_q\theta, \qquad q = 1, ..., Q,$$

where X_q denotes the qth categorical count vector, m_q is the number of objects that are categorized and Q is the number of counts vectors. In the second and the third model the probability vector corresponding the qth observation, denoted by p_q, is thought of as a random variable where

$$E(p_q) = \theta, \qquad q = 1, ..., Q,$$

and p_q has a non-zero covariance matrix as well. In the first model we can think of the p_q's as being fixed where $p_q = \theta$ for all q's.

Let X_{qj} denote the count in the jth category of the qth observation and let p_{qj} be the corresponding probability, and then write $X_q = (X_{q1}, ..., X_{qJ})^{\mathrm{T}}$ and $p_q = (p_{q1}, ..., p_{qJ})^{\mathrm{T}}$. The sum of the elements of X_q is denoted by m_q, that is, $m_q = \sum_{j=1}^{J} X_{qj}$. Further, let $X = (X_1^{\mathrm{T}}, ..., X_Q^{\mathrm{T}})^{\mathrm{T}}$, $m = (m_1, ..., m_Q)^{\mathrm{T}}$ and $p = (p_1^{\mathrm{T}}, ..., p_Q^{\mathrm{T}})^{\mathrm{T}}$.

The Standard Multinomial Model
The standard multinomial model can be written as

$$X_q | m_q, \theta \sim Mult_J(m_q, \theta), \qquad q = 1, ..., Q,$$

where $\theta_j > 0$, $j = 1, ..., J$, and $\sum_{j=1}^{J} \theta_j = 1$. The mean and covariance of X_q given m_q are

$$E(X_q|m_q) = m_q\theta, \qquad Var(X_q|m_q) = m_q\Psi, \qquad q = 1, ..., Q,$$

where

$$\Psi = \Psi(\theta) = \text{diag}(\theta) - \theta\theta^{\mathrm{T}},$$

and diag(z) denotes a diagonal matrix with the vector z on the diagonal. The correlation between the numbers in any two categories is,

$$Corr(X_{qj}, X_{qi}) = -\sqrt{\frac{\theta_j\theta_i}{(1-\theta_j)(1-\theta_i)}}, \qquad i, j = 1, ..., J, \quad i \neq j, \quad q = 1, ..., Q. \qquad (1)$$

>From (1) we see that the correlation will be negative and weak if both θ_j and θ_i are small.

If we use a Dirichlet prior for θ with parameters β, so that apriori

$$\theta \sim Dir_J(\beta),$$

where $Dir_J(\beta)$ denotes a Dirichlet distribution on a $J-1$ dimensional simplex with parameter $\beta = (\beta_1, ..., \beta_J)^{\mathrm{T}}$, then the posterior distribution of θ given m and X is

$$\pi(\theta|m, X) \propto \left\{ \prod_{q=1}^{Q} f(X_q|m_q, \theta) \right\} \pi(\theta)$$

where $f(X_q|m_q, \theta)$ denotes the multinomial probability mass function with parameters m_q and θ, and $\pi(\theta)$ is the Dirichlet prior for θ with parameter β. It is straight forward to show that the above posterior is a Dirichlet distribution of the form

$$(\theta|m, X) \sim Dir_J(\beta + \sum_{q=1}^{Q} X_q).$$

It is relatively easy to sample from the Dirichlet distribution, so posterior samples of θ are easy to obtain.

The Dirichlet-Multinomial Model
The Dirichlet-multinomial model can be written as

$$X_q | m_q, p_q \sim Mult_J(m_q, p_q), \qquad p_q \sim Dir_J(\alpha). \qquad q = 1, ..., Q.$$

The p_q's follow a Dirichlet distribution and hence the mean and the covariance of the p_q's are

$$E(p_q) = \theta, \qquad Var(p_q) = \tau\Psi, \qquad q = 1, ..., Q,$$

where

$$\alpha_0 = \sum_{k=1}^{J} \alpha_k, \quad \theta = \alpha/\alpha_0, \quad \text{and} \quad \tau = (\alpha_0 + 1)^{-1}, \quad 0 < \tau < 1,$$

see Schervish (1995). The correlation between p_{qi} and p_{qj} is the same as the correlation between X_{qi} and X_{qj} in (1).

The marginal mean of X_q given m_q is

$$E(X_q) = m_q\theta, \qquad q = 1, ..., Q,$$

and the marginal variance is

$$Var(X_q) = m_q\Psi + \tau m_q(m_q - 1)\Psi = m_q\{1 + \tau(m_q - 1)\}\Psi, \qquad q = 1, ..., Q.$$

Here is it clear how τ controls the over-dispersion in the model. It is also evident that the correlation within the X_q's is the same as the correlation within the p_q's. The marginal mean and variance of a two stage hierarchical model can be found by using the formulas $E(X) = E(E(X|Y))$ and $Var(X) = E(Var(X|Y)) + Var(E(X|Y))$, see e.g. Casella and Berger (1990) p. 153.

We assume apriori that the elements of α are independent. We denote the prior distribution for α by $\pi(\alpha)$ and the prior distribution for α_j by $\pi(\alpha_j)$, $j = 1, ..., J$, and write

$$\pi(\alpha) = \prod_{j=1}^{J} \pi(\alpha_j).$$

We propose an exponential distribution with mean γ_j as a prior for α_j. The posterior distribution of α and p given m and X is

$$\pi(\alpha, p|m, X) \propto \left\{\prod_{q=1}^{Q} f(X_q|m_q, p_q)\pi(p_q|\alpha)\right\}\pi(\alpha).$$

In order to generate samples from the above posterior distribution, we iterate from the following distributions

$$\begin{aligned}
\pi(\alpha_j|m, X, \alpha_{-j}, p) &\propto \left\{\prod_{q=1}^{Q} f(X_q|m_q, p_q)\pi(p_q|\alpha)\right\}\pi(\alpha_j), \qquad j = 1, ..., J,\\
\pi(p_q|m, X, \alpha, p_{-q}) &\propto f(X_q|m_q, p_q)\pi(p_q|\alpha), \qquad q = 1, ..., Q,
\end{aligned}$$

where p_{-q} denotes a vector containing all the elements of p except for the elements of p_q. The components in the Gibbs sampler above are derived and specified in Appendix A. Once samples of α have been simulated, then samples of θ, τ and the covariance or the correlation within the p_q's can be obtained from the above formulas.

The Logit-Gaussian-Multinomial Model
The logit-Gaussian-multinomial model can be written as

$$X_q|m_q, p_q \sim Mult_J(m_q, p_q), \qquad p_{qj} = \frac{\exp(\eta_{qj})}{1 + \sum_{k=1}^{J-1}\exp(\eta_{qk})}, \qquad j = 1, ..., J-1,$$

$$p_{qJ} = \frac{1}{1 + \sum_{k=1}^{J-1}\exp(\eta_{qk})}, \qquad \eta_q \sim Gau(\mu, W^{-1}), \qquad q = 1, ..., Q,$$

where $\eta_q = (\eta_{q1}, ..., \eta_{q,J-1})^{\mathrm{T}}$. Let $\eta = (\eta_1, ..., \eta_Q)^{\mathrm{T}}$. We will refer to the distribution of the p_q's as the logit-Gaussian distribution. In this model the covariance matrix of the p_q's is denoted by Ω where

$$Var(p_q) = \Omega, \qquad q = 1, ..., Q$$

and as in the Dirichlet-multinomial model, let $E(p_q) = \theta$, $q = 1, ..., Q$. The marginal mean and covariance of X_q in terms of θ, Ψ and Ω are

$$E(X_q) = m_q\theta, \qquad Var(X_q) = m_q\Psi + m_q(m_q - 1)\Omega, \qquad q = 1, .., Q.$$

and are found in the same way as the corresponding formulas for the Dirichlet-multinomial model in Section 3.2.

Recall that the parameter space of θ is simply $\theta_j > 0$, $j = 1, ..., J$, and $\theta_1 + ... + \theta_J = 1$. Let H_* denote the upper $(J-1) \times (J-1)$ block of a $J \times J$ matrix H. Given a vector θ, the parameter space of Ω_* is such that the matrices Ω_* and $(\Psi_* - \Omega_*)$ have to be positive definite. This arises from the following facts. The matrix Ψ_* can be written as $(\text{diag}(\theta_*) - \theta_* \theta_*^{\mathrm{T}})$, where z_* denotes the vector z excluding its last element. Any matrix that has the same form as Ψ_* is a positive definite matrix provided that $\theta_j > 0$, $j = 1, ..., J-1$, (see, McCullagh and Nelder (1989), p. 168). Then

$$E\{\text{diag}(p_{1*}) - p_{1*} p_{1*}^{\mathrm{T}}\} = \Psi_* - \Omega_*$$

must also be a positive definite matrix. The jth diagonal element of Ω_* and $(\Psi_* - \Omega_*)$ can be written as $\tau_j \theta_j (1 - \theta_j)$ and $(1 - \tau_j)\theta_j(1 - \theta_j)$. For these diagonal elements to be greater than zero, we need $0 < \tau_j < 1$, which is what we expect marginally. But this constraint also puts bounds on the off-diagonal elements of Ω_* as well. The above bounds for Ω_* are true for any covariance matrix of p where p is on the simplex.

If we let $J = 3$ and write the matrix Ω_* as

$$\Omega_* = \begin{bmatrix} \tau_1\theta_1(1-\theta_1) & \rho\{\tau_1\theta_1(1-\theta_1)\tau_2\theta_2(1-\theta_2)\}^{1/2} \\ \rho\{\tau_1\theta_1(1-\theta_1)\tau_2\theta_2(1-\theta_2)\}^{1/2} & \tau_2\theta_2(1-\theta_2) \end{bmatrix}$$

then the matrix $(\Psi_* - \Omega_*)$ can be written as

$$\Psi_* - \Omega_* = \begin{bmatrix} (1-\tau_1)\theta_1(1-\theta_1) & -\theta_1\theta_2 - \rho\{\tau_1\theta_1(1-\theta_1)\tau_2\theta_2(1-\theta_2)\}^{1/2} \\ -\theta_1\theta_2 - \rho\{\tau_1\theta_1(1-\theta_1)\tau_2\theta_2(1-\theta_2)\}^{1/2} & (1-\tau_2)\theta_2(1-\theta_2) \end{bmatrix}.$$

Since $\Omega*$ and $(\Psi_* - \Omega_*)$ must be positive definite matrices then obvious bounds for τ_1, τ_2 and ρ are $0 < \tau_j < 1$, $j = 1, 2$, and $|\rho| < 1$. It can be shown that for some τ_1 and τ_2 within the above bounds, the upper bounds for ρ are

$$\min\left(1, (\tau_1\tau_2)^{-0.5}\left[\{(1-\tau_1)(1-\tau_2)\}^{0.5} - (\theta_1\theta_2)^{0.5}\{(1-\theta_1)(1-\theta_2)\}^{-0.5}\right]\right)$$

and the lower bounds for ρ are

$$\max\left(-1, -(\tau_1\tau_2)^{-0.5}\left[\{(1-\tau_1)(1-\tau_2)\}^{0.5} + (\theta_1\theta_2)^{0.5}\{(1-\theta_1)(1-\theta_2)\}^{-0.5}\right]\right).$$

If, for example, $\theta_1 = 0.8$, $\theta_2 = 0.1$, $\tau_1 = 0.4$ and $\tau_2 = 0.1$, then the bounds for ρ are $-1 < \rho < 0.3409$. The point $(\theta_1, \theta_2) = (0.8, 0.1)$ is close to one corner of the simplex and given these values for the variances there is not a possibility of a stronger positive correlation. If we let $\theta_1 = \theta_2 = 0.45$, $\tau_1 = \tau_2 = 0.999$ then the bounds for ρ are $-0.8200 < \rho < -0.8180$. Interestingly enough, if we look at a Dirichlet distribution on the two dimensional simplex and let $\theta_1 = \theta_2 = 0.45$, $\tau = 0.999$, then the resulting correlation is -0.8182 which falls within the bounds above.

Of course we can find bounds for τ_2 given some τ_1 and ρ. Basically, the elements in (τ_1, τ_2, ρ) can not take all the values in the region $0 < \tau_j < 1$, $j = 1, 2$, and $|\rho| < 1$, for $(\Psi_* - \Omega_*)$ to be positive definite. These bounds can by written as

$$-1 < \frac{-\theta_1\theta_2 - \rho\{\tau_1\theta_1(1-\theta_1)\tau_2\theta_2(1-\theta_2)\}^{1/2}}{\sqrt{(1-\tau_1)\theta_1(1-\theta_1)(1-\tau_2)\theta_2(1-\theta_2)}} < 1.$$

Knowing the bounds of Ω is an important part of understanding the covariance structure of X_q in the logit-Gaussian-multinomial model,

Denote the prior for μ and W by $\pi(\mu, W)$. We assume apriori that μ and W are indpendent, so that

$$\pi(\mu, W) = \pi(\mu)\pi(W),$$

where $\pi(\mu)$ and $\pi(W)$ denote the prior distributions of μ and W, respectively. The posterior distribution of μ, W and η given m and X is

$$\pi(\mu, W, \eta | m, X) \propto \left\{ \prod_{q=1}^{Q} f(X_q | m_q, p_q(\eta_q)) \pi(\eta_q | \mu, W) \right\} \pi(\mu) \pi(W)$$

where $\pi(\eta_q|\mu, W)$ is a Gaussian distribution with mean μ and covariance matrix W^{-1}.

For generation of samples from the above posterior distribution, we iterate from the following distributions

$$\begin{aligned} \pi(\mu | m, X, W, \eta) &\propto \left\{ \prod_{q=1}^{Q} \pi(\eta_q | \mu, W) \right\} \pi(\mu) \\ \pi(W | m, X, \mu, \eta) &\propto \left\{ \prod_{q=1}^{Q} \pi(\eta_q | \mu, W) \right\} \pi(W) \\ \pi(\eta_q | m, X, \mu, W, \eta_{-q}) &\propto f(X_q | m_q, p_q(\eta_q)) \pi(\eta_q | \mu, W), \quad q = 1, ..., Q, \quad j = 1, ..., J-1, \end{aligned}$$

where η_{-q} denotes a vector containing all the elements of η except for the elements of η_q. The components in the Gibbs sampler above are derived and specified in Appendix A.

The functional form of the transformations of μ and W to $\theta = \theta(\mu, W) = E(p_q)$ and $\Omega = \Omega(\mu, W) = Var(p_q)$ are very complicated, in fact they can be written as non-trivial integrals. To get posterior samples of θ and Ω we use a stochastic integration for each sampled pair of μ and W. That is, for the ith observation of μ and W in the MCMC sample, denoted by $(\mu^{(i)}, W^{(i)})$, we draw 100,000 times from a multivariate Gaussian distribution with mean $\mu^{(i)}$ and precision matrix $W^{(i)}$. Each of these 100,000 vectors are transformed with the logistic function and we get a corresponding p-vector. Then a sample mean and a sample covariance matrix based on these 100,000 p-vectors is computed. The sample mean is an approximation of

$$\theta^{(i)} = \theta(\mu^{(i)}, W^{(i)}) = E(p_q)^{(i)},$$

while the sample covariance matrix is an approximation of

$$\Omega^{(i)} = \Omega(\mu^{(i)}, W^{(i)}) = Var(p_q)^{(i)}.$$

D.1.4 ResultS

In this section we analyze categorical length data of cod that were collected for a certain area. We analyze the data using the three models discussed in Section 3. Figures 3, 4 and 5 show the length distribution when the estimation is based on the standard multinomial model, the Dirichlet-multinomial model and the logit-Gaussian-multinomial model, respectively. In the these three figures the point estimate shown is based on the posterior mean, and the error bars show the marginal 90% credible sets for each category. It is clear from these three figures that the point estimates that the three methods provide are quite different. For example, the point estimate of the 5th category is below 0.2 under the Dirichlet-multinomial model, Figure 4, but above 0.25 under the logit-Gaussian-multinomial model, Figure 5, and the two 90% credible sets do not overlap. The standard multinomial model has the tightest credible sets for all categories while the logit-Gaussian-multinomial model gives wider credible sets more often than the Dirichlet-multinomial model does.

Figures 6, 7 and 8 show the posterior correlation between the individual θ's versus lag in terms of categories for the standard multinomial model, the Dirichlet-multinomial model and the logit-Gaussian-multinomial model, respectively. Figure 8 shows both high positive and negative correlations while Figures 6 and 7 show weak negative and weak positive correlations. So the posterior distribution for θ is different under the three models in terms of correlation.

Figure 9 shows the estimated correlations between the elements of the probability vectors based on the posterior median, that is, $Corr(p_{qi}, p_{qj}) = \Omega_{ij}(\Omega_{jj}\Omega_{jj})^{-0.5}$, $i, j = 1, ..., J-1$, $q = 1, ..., Q$, when the Dirichlet-multinomial model is assumed while Figure 10 shows the same when the logit-Gaussian-multinomial model is assumed. In the Dirichlet-multinomial model the probability vectors follow a Dirichlet distribution while in the logit-Gaussian-multinomial model they follow a logit-Gaussian distribution. When Figures 9 and 10 are compared to Figure 2, it is obvious that there is a substantial positive and negative correlation suggested by the data that the Dirichlet distribution can not capture while the logit-Gaussian distribution appears to be flexible enough to capture the correlation. The correlations in Figure 10 are estimates of Ω only, while the correlations in Figure 2 are estimates of the correlations within X_q, where the variance of X_q is $Var(X_q) = m_q\Psi + m_q(m_q-1)\Omega$ for some q, so the diagonal element of the term $m_q\Psi$ will deflate the correlations. This could explain why the correlations in Figure 2 are somewhat closer to zero than the correlations in Figure 10.

Figure 11 shows the estimate of the overdispersion parameters τ_j, $j = 1, ..., J$, based on the posterior median, along with a marginal 90% credible set under the logit-Gaussian-multinomial model. In the case of the Dirichlet-multinomial model the overdispersion parameter is the same for all categories. The posterior median of τ is 0.0749 and its marginal 90% credible set is $(0.709, 0.0793)$. As can be seen in Figure 11, the overdispersion parameters are not equal and it would not be reasonable to assume they were equal. Again, this is an indicator of the Dirichlet distribution not being flexible enough for the data.

If we put all of the above facts of our analysis together then everything points to the fact that a flexible model like the logit-Gaussian-multinomial is needed to model the data. The standard multinomial model does not apply at all and the Dirichlet-multinomial model is not flexible enough for the data, particularly when it comes to modeling the correlation.

D.1.5 Discussion

In this paper we have presented a model that we refer to here as the logit-Gaussian multinomial model. This model appears to capture the covariance structure of data like the one we analyzed in Section 4, that is, categorical data that has larger variance and stronger correlation than data from the standard multinomial distribution would. Categorical data are common in fisheries science, in particular categorized length distributions, and age distributions. Investigation of categorical length and age data on other fish species indicate that a nontrival covariance structure is need to model the data.

By using a Bayesian estimation approach that is based on MCMC, we are able to obtain the posterior distribution of the vector parameter θ in the three models described in Section 3. By comparing the three posterior marginal distributions for θ, we see that the two models we jugde to be inadequate for the data, lead to an incorrect inference for θ. This maybe what one would expect but we feel this is an important fact and is a motivation for applying the logit-Gaussian multinomial model.

In the application in Section 4 each observed count vector is coming from a particular location. This potentially introduces a spatial correlation in the data. Investigating the spatial correlation is beyond the scope of this paper. Future research regarding the spatial behavior of these kind of data involves finding a model that takes into acount the correlation between categories at same site, and the spatial correlation, simultaneously.

Once estimates of the parameters have been found by using MCMC, one has posterior samples of θ. These samples can be used to construct an approximate log-likelihood component for θ as a part of a larger model. The vector θ could be parameterized in the larger model as $\theta = f(\psi)$ where f is some function and ψ are parameters. An approximate log-likelihood component could be a quadratic term of the form

$$l(\psi) = \{f(\psi) - E(\theta|X)\}^{\mathrm{T}}\{Var(\theta|X)\}^{-1}\{f(\psi) - E(\theta|X)\},$$

where $E(\theta|X)$ and $Var(\theta|X)$ are the posterior mean and covariance of θ. Another approach is to approximate a log-likelihood component for θ

$$l(\psi) = [h\{f(\psi)\} - E\{h(\theta)|X\}]^{\mathrm{T}}[Var\{h(\theta)|X\}]^{-1}[h\{f(\psi)\} - E\{h(\theta)|X\}],$$

where $h(x)$ is such that $h_j(x) = \log(x_j) - \log(1 - \sum_{k=1}^{J-1} x_k)$, $j = 1, ..., J-1$, and $E\{h(\theta)|X\}$ and $Var\{h(\theta)|X\}$ are the posterior mean and covariance of $h(\theta)$. This proposal of mixing Bayesian methods with likelihood method may not sound like the right thing to do, however, when working with large models and many different data sources with no simple or obvious way to handle the categorical data, an approach like this may be necessary.

Appendix: Gibbs Samplers

The Dirichlet-Multinomial Model

Step 1: The conditional distribution of α_j given m, X, p and α_{-j}, $j = 1, ..., J$, is

$$\pi(\alpha_j|m, X, p, \alpha_{-j}) \propto \left\{ \prod_{q=1}^{Q} f(X_q|m_q, p_q)\pi(p_q|\alpha) \right\} \pi(\alpha_j), \qquad j = 1, ..., J.$$

where

$$X_q|m_q, p_q \sim Mult_J(m_q, p_q), \qquad q = 1, ..., Q,$$

$$p_q|\alpha \sim Dir_J(\alpha), \qquad q = 1, ..., Q,$$

and the prior for α_j is an exponential distribution

$$\alpha_j \sim Exp(\gamma_j), \qquad j = 1, ..., J.$$

The conditional distribution of α_j does not have a known form, so to simulate from it a Metropolis-Hastings step is needed.

Step 2: The conditional distribution of p_q given m, X, p_{-q} and α, $q = 1, ..., Q$, is

$$\pi(p_q|m, X, p_{-q}, \alpha) \propto f(X_q|m_q, p_q)\pi(p_q|\alpha), \qquad q = 1, ..., Q.$$

The product of the two distributions is proportional to a Dirichlet distribution with parameter $(\alpha + X_q)$,

$$p_q \sim Dir_J(\alpha + X_q), \qquad q = 1, ..., Q.$$

The Logit-Gaussian-Multinomial Model *Step 1*: The conditional distribution of μ given m, X, W and η is

$$\pi(\mu|m, X, W, \eta) \propto \left\{ \prod_{q=1}^{Q} \pi(\eta_q|\mu, W) \right\} \pi(\mu)$$

where

$$\eta_q|\mu, W \sim Gau(\mu, W^{-1}), \qquad q = 1, ..., Q,$$

and the prior distribution for μ, $\pi(\mu)$, is a Gaussian distribution

$$\mu \sim Gau(\gamma_\mu, W_\mu^{-1}).$$

Then the resulting conditional distribution of μ is a Gaussian distribution

$$\mu|m, X, W, \eta \sim Gau(\{QW + W_\mu\}^{-1}\{W\sum_{q=1}^{Q}\eta_q + W_\mu\gamma_\mu\}, \{QW + W_\mu\}^{-1}).$$

Step 2: The conditional distribution of W given m, X, μ and η is

$$\pi(W|m, X, \mu, \eta) \propto \left\{\prod_{q=1}^{Q}\pi(\eta_q|\mu, W)\right\}\pi(W)$$

where we let the prior distribution for W be an improper Wishart distribution

$$\pi(W) \propto |W|^{-J/2}\exp\{-\mathrm{tr}(P_0W)/2\} \tag{2}$$

where $P_0 = \epsilon I_{J-1}$, I_{J-1} is a $(J-1)$ dimensional identity matrix, and $\epsilon = 0.01$. The resulting conditional distribution of W is a Wishart distribution,

$$W|m, X, \eta, \mu \sim Wis_{J-1}(\{\sum_{q=1}^{Q}(\eta_q - \mu)(\eta_q - \mu)^{\mathrm{T}} + P_0\}^{-1}, Q).$$

The above distribution is a proper Wishart distribution provided that $Q \geq (J-1)$.

Step 3: The conditional distribution of η_q given m, X, μ, W and η_{-q} is

$$\pi(\eta_q|m, X, \mu, \Sigma, \eta_{-q}) \propto f(X_q|m_q, p_q(\eta_q))\pi(\eta_q|\mu, \Sigma), \qquad q = 1, ..., Q.$$

To simulate from the conditional distribution of η_q a Metropolis-Hastings step is needed.

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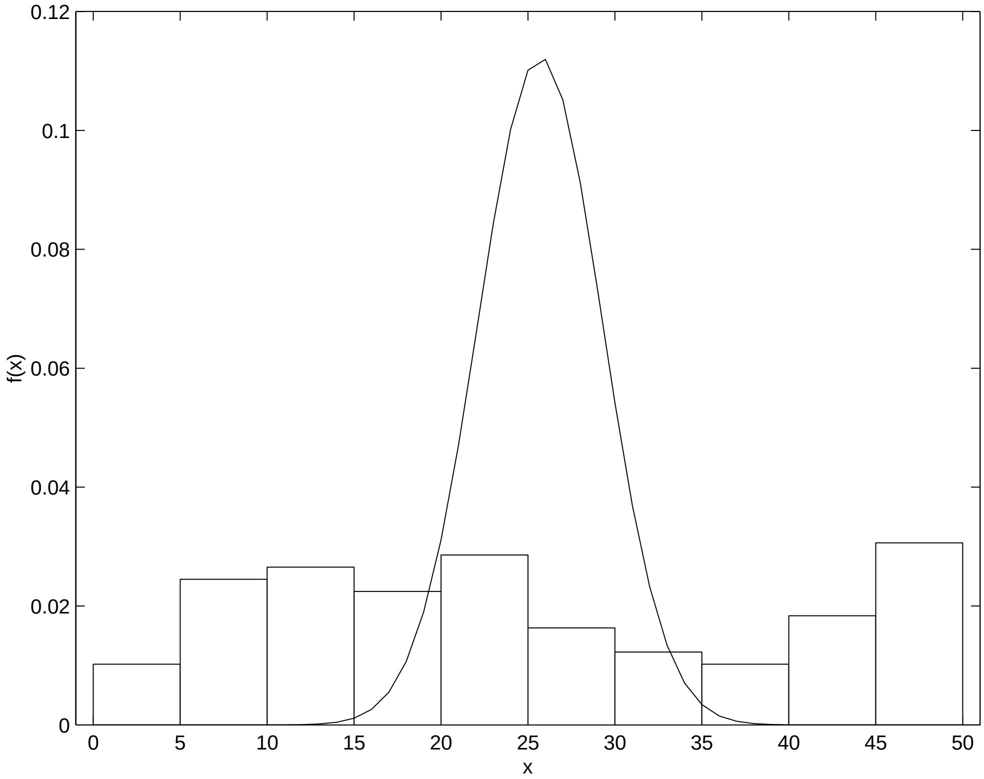

Figure 1: A histogram of the number of cod out of 50 that are less than 26.5 cm in length. The smooth curve is the probability mass function of a Binomial random variable with parameters $n = 50$ and $p = 0.514$. Based on data from 98 station at which 50 or more cod were length measured. Exactly 50 cod were randomly selected at each of these 98 station.

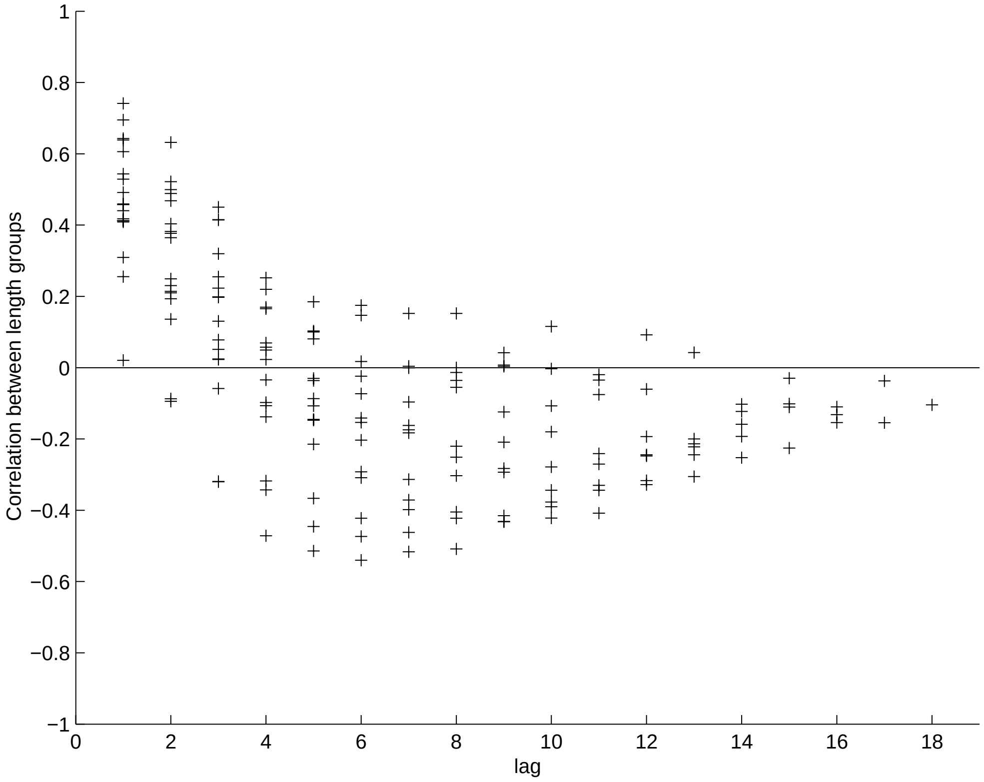

Figure 2: The correlation between the categorical counts. Based on data from 98 station at which 50 or more cod were length measured, then exactly 50 cod were randomly selected at each station to calculate the correlation.

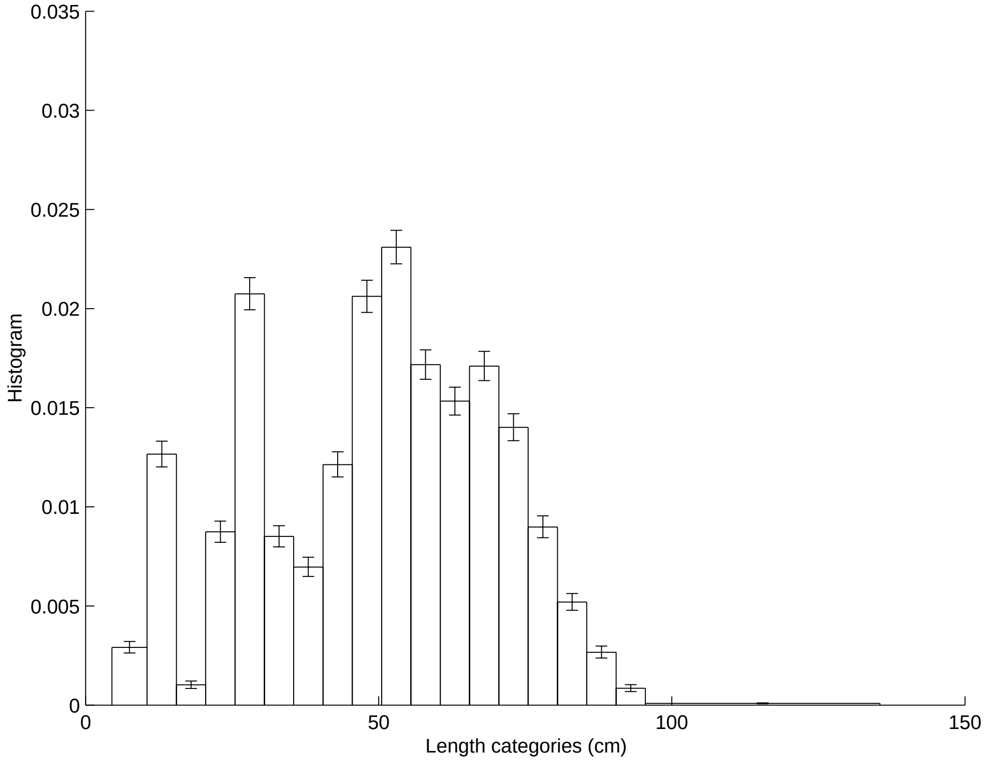

Figure 3: A histogram of the length distribution with a marginal 90% credible set for each length category when the standard multinomial model is assumed.

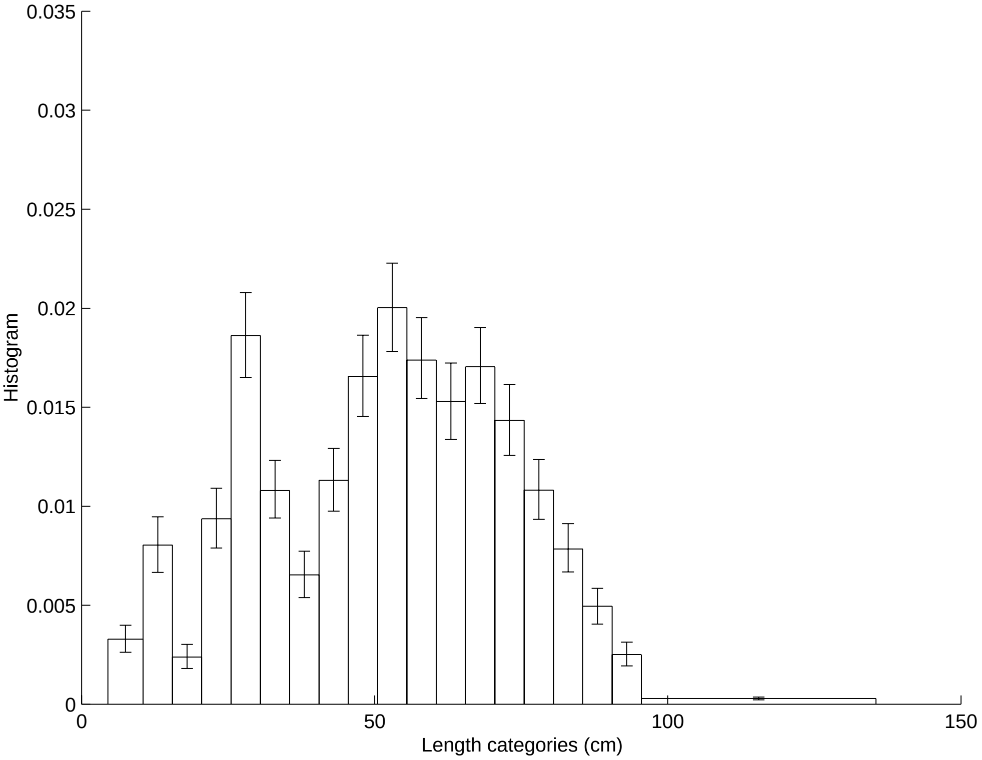

Figure 4: A histogram of the length distribution with a marginal 90% credible set for each length category when the Dirichlet-multinomial model is assumed.

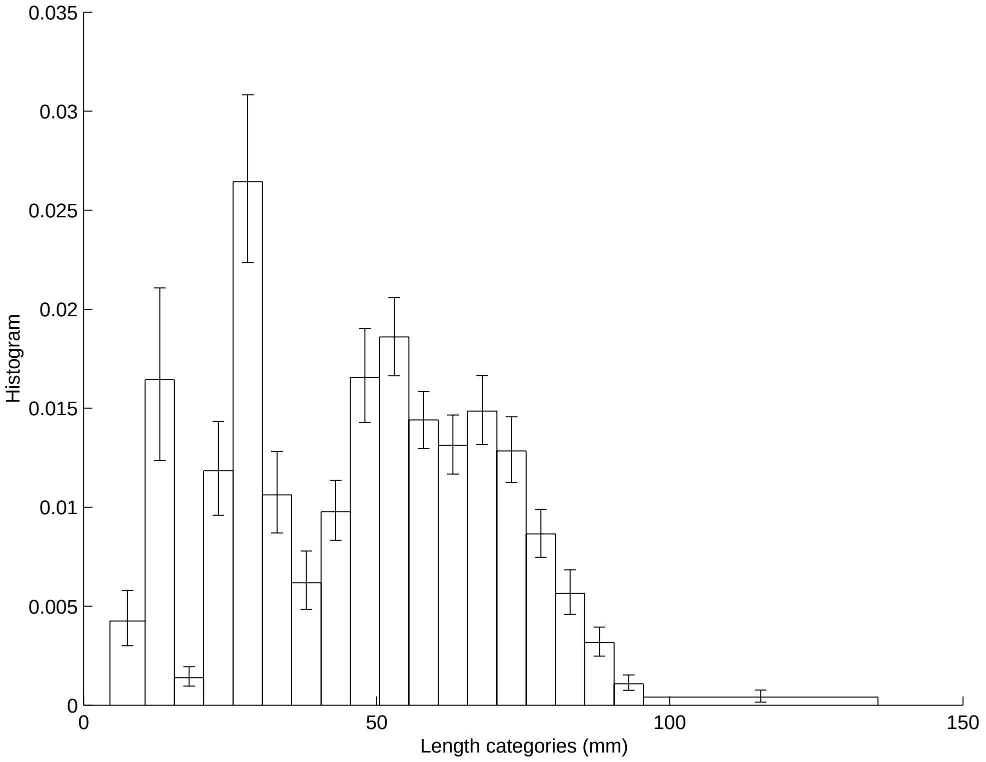

Figure 5: A histogram of the length distribution with a marginal 90% credible set for each length category when the logit-Gaussian-multinomial model is assumed.

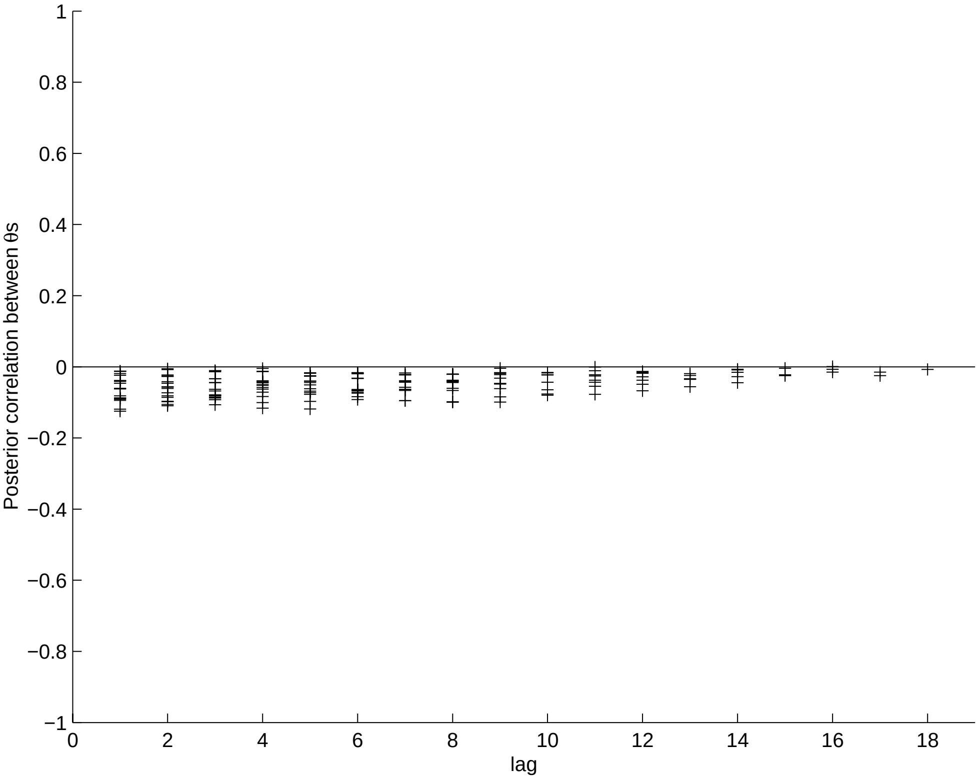

Figure 6: The posterior correlation between the proportions of each length category as a function of distance between categories when the standard multinomial model is assumed.

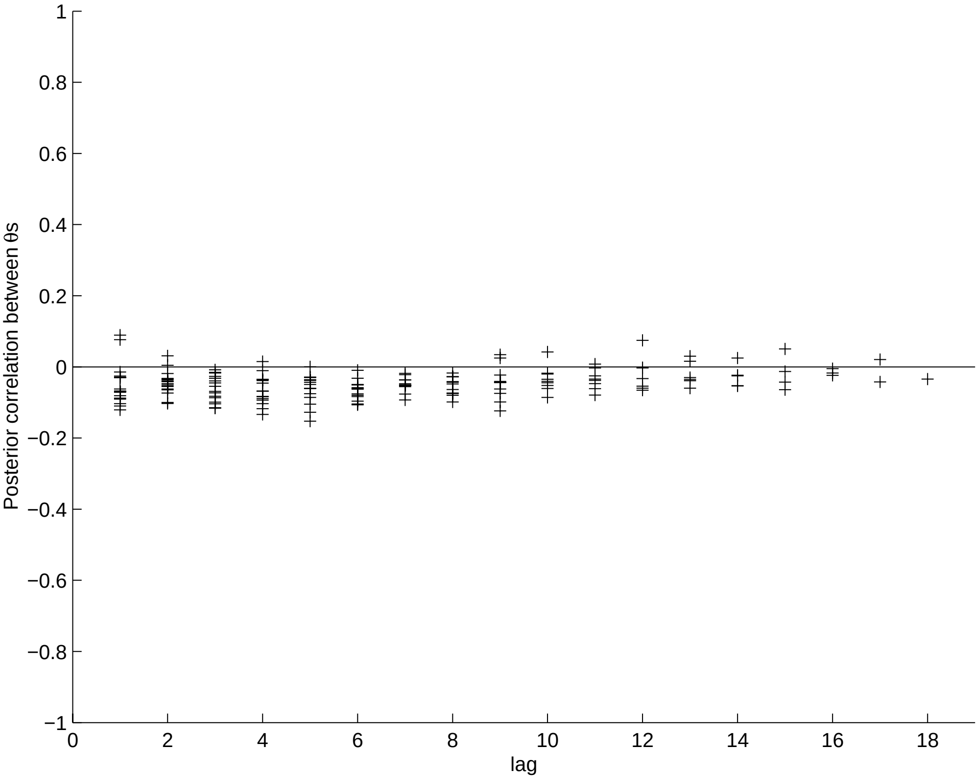

Figure 7: The posterior correlation between the proportions of the length categories, that is the θ's, as a function of distance between categories when the Dirichlet-multinomial model is assumed.

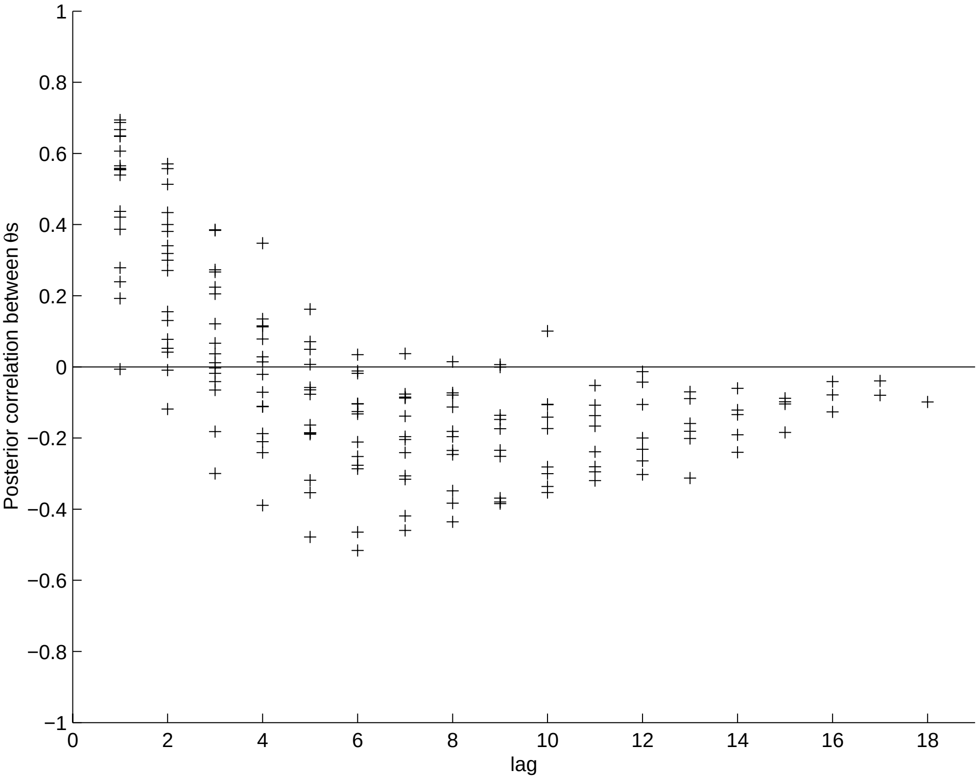

Figure 8: The posterior correlation between the proportions of the length categories, that is the θ's, as a function of distance between categories when the logit-Gaussian-multinomial model is assumed.

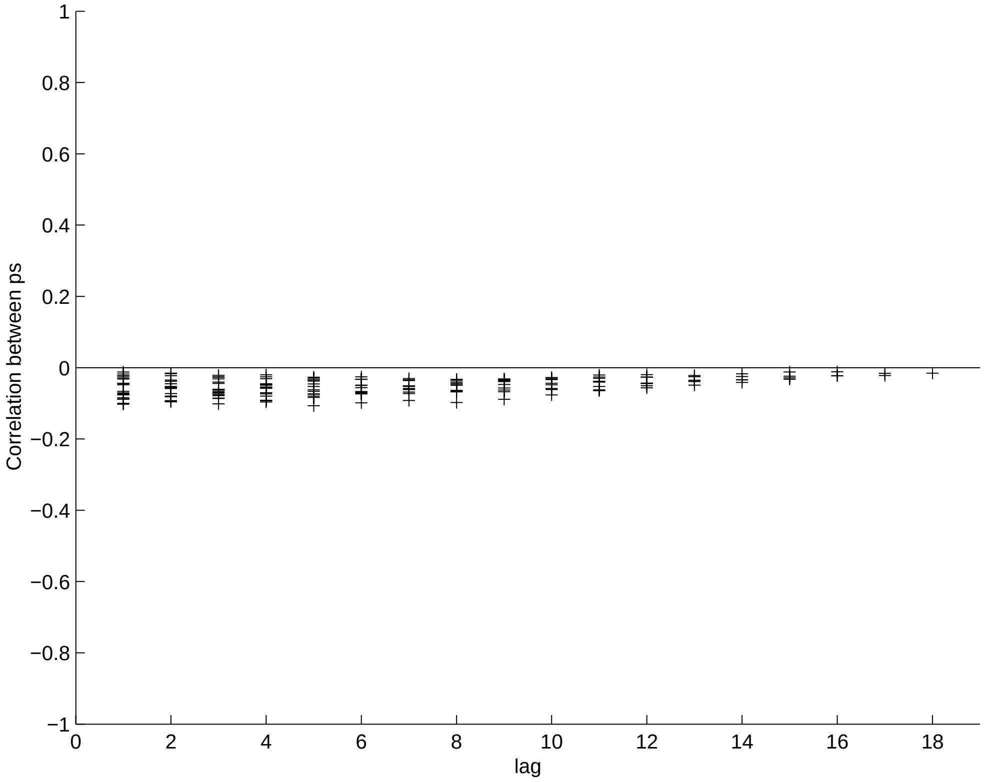

Figure 9: The correlation between the proportions of each length category within station, that is $Corr(p_{qi}, p_{qj})$, as a function of distance between categories when the Dirichlet-multinomial model is assumed.

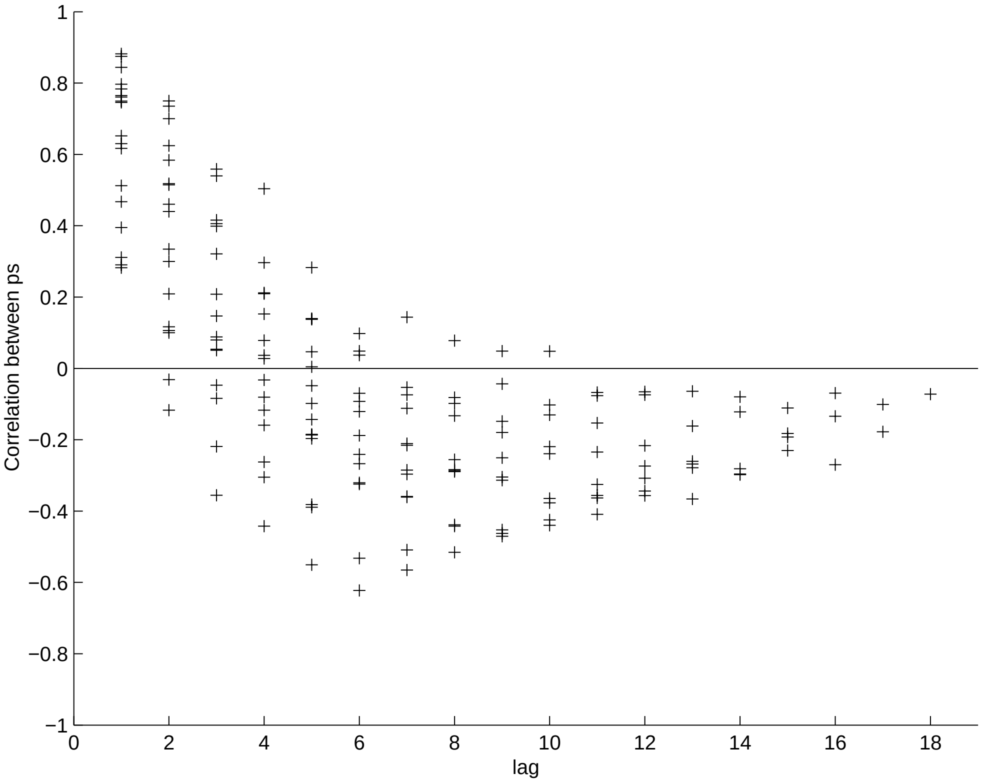

Figure 10: The correlation between the proportions of each length category within station, that is $Corr(p_{qi}, p_{qj})$, as a function of distance between categories when the logit-Gaussian-multinomial model is assumed.

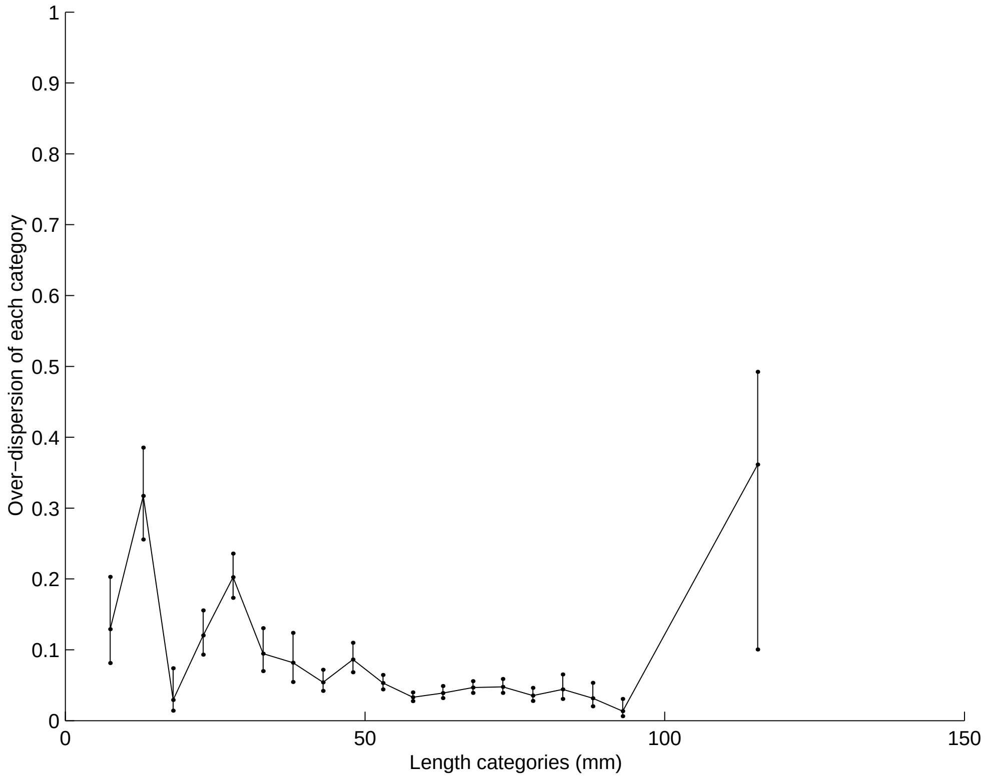

Figure 11: The over-dispersion parameter of each length category, τ_j, $j = 1, ..., J$, along with its marginal 90% credible set when the logit-Gaussian-multinomial model is assumed.

D.2 Goodness of fit tests for Gadget likelihood functions

Gunnar Stefansson
Marine Research Institute, Skulagata 4, P. O. Box 1390
121 Reykjavik, Iceland,
gunnar@hafro.is

Abstract Gadget is a program which can simulate the development of multiple fish stocks in several areas, while being harvested by an arbitrary number of fleets. The program can further estimate parameters by comparing diverse model outputs to several data sources which can be modelled using arbitrary likelihood functions.

The adequacy of the model as an explanation of the data can be evaluated using any number of goodness-of-fit tests. This paper describes some of these tests, new ones are developed and preliminary results are reported on the applications of these tests to real data.

Introduction

When several data sources are combined in an analysis one issue which emerges is the specification and verification of likelihood functions to be used for comparing the data to the model.

It must be noted that, when a specific test indicates that a specified distribution should be rejected, this may imply either a failure of the distributional assumption or a failure of the model providing parameters for the distribution. The rejection must therefore not be taken unilaterally to indicate a problem with the distribution, but rather an indication of a general problem. Subsequent analysis of the raw data and of the model behaviour is needed to specify exactly where the problem lies.

Multinomial distributions

The simplest method to evaluate whether data really come from a multinomial distribution is to compare the observed count in each cell to the predicted count based on the modelled proportions, computing

$$X^2 = \sum_{i=1}^{p} \frac{(O_i - E_i)^2}{E_i}$$

using obvious notation for observed counts, expected counts and the number of categories. If the model estimates of expected counts are correct and the data truly satisfy the multinomial assumption, then $X^2 \sim \chi^2_{p-1}$ and the hypothesis is usually rejected if X^2 is too large, i.e. if $X^2 > \chi^2_{p-1,1-\alpha/2}$.

In this connection it must be remembered that when using Gadget, usually a huge number of observations are available so that the expected counts (which are of course estimated) are normally considered fixed.

Combining several tests for multinomial distribution

Several different multinomial χ^2-tests can be combined fairly easily if the same number of categories is used for each test. Thus, if results from independent comparisons should all satisfy $X_i^2 \sim \chi^2_p$, $i = 1, \dots, n$ when the distributional assumptions are satisfied, then in addition to comparing each one to $\chi^2_{p,1-\alpha/2}$, the collection of test statistics can be verified to come from a χ^2_p-distribution.

The combination test can be done either using a new χ^2-test or be based on a Kolmogorov test.

In practise this has been implemented using those length distributions which cut across several length classes. Here the modelled and observed length distributions have been aggregated into a fixed number (e.g. 5) length groups, thus fixing the number of degrees of freedom.

Alternative tests for multinomial distribution

In addition to the usual χ^2-tests, several alternative tests exist to evaluate the goodness-of-fit of the multinomial assumption. Some of these have been used for typical fishery data sets.

First, when generalized linear models are used, the resulting fitted deviance for the multinomial distribution follows a χ^2-distribution. This has been evaluated using fairly extended models of the mean response and found to be an inadequate assumption for some tested cases (Stefansson and Palsson, 1997). This test could in principle be used in place of the test above based on X^2.

Second, it is possible to design special tests for whether individual pairs of cells follow the binomial distribution. For tested cases it is found that the observed variances from data sets are much greated than predicted from a binomial variance (Hrafnkelsson and Stefansson, 2002).

Thirdly, it can be evaluated whether the correlations between counts in pairs of length groups are slightly negative ($-np_ip_j$) as predicted from multinomial theory, and this assumption is similarly found to be totally invalidated for data sets tested (Hrafnkelsson and Stefansson, 2002).

These last two tests are of a different nature from the first and the tests based on X^2.

D.2.1 Gaussian distributions

If a Gaussian (and independence) assumption is used, the corresponding negative likelihood components are proportional to terms of the form

$$\sum_{i=1}^{n} (y_i - \mu_i)^2 ,$$

each of which has a distribution proportional to a χ^2_n distribution, if the means μ_i are known. In practice, the number of observations will be large and the subtraction of the degrees of freedom due to parameter estimation will not usually be an issue.

The nuisance parameter, σ^2 needs to be estimated, usually from the same data with

$$\hat{\sigma^2} = \frac{\sum_{i=1}^{n} (y_i - \hat{\mu}_i)^2}{n-q},$$

where q denotes the number of estimated parameters.

In the current setting, the number of estimated parameters in the Gadget setting is a highly dubious concept, since the parameters are estimated based on minimizing many more sums simultaneously. It is probably the most reasonable approach to assume $q = 0$, but some simulation testing is needed to evaluate this.

Normality of the standardised residuals (before squaring) is usually tested using Kolmogorov's D-statistic, but sometimes using χ^2, multinomial fashion, after appropriate grouping. Neither test is truly nonparametric (i.e. distribution-free) when the mean is estimated as here (cf Moore and Spruill, 1975) and in particular, χ^2 would be more applicable if a minimum χ^2-criterion is used for estimation, rather than maximum likelihood.

Combining several tests for the Gaussian distribution

Within Gadget a large number of likelihood components will typically be of the Gaussian type.

D.2.2 Tests of independence

Given that many data sets are indexed by time, it is natural to consider the autocorrelation in the various likelihood residual. Specific tests for Gadget output or generic likelihood components are not currently available but need to be developed as a part of future research.

These tests can not be easily integrated into the other χ^2-tests above and are therefore not considered further in this paper.

D.2.3 Evaluating combined likelihoods

One remaining question pertains to how it is possible to combine the various likelihood components into a single test statistic, ideally giving more power to identify conflicts between model and data. Thus, although it is certainly possible to apply a battery of tests to all components, it would be quite useful to have a single statistic which could be applied to the likelihood components as a whole, resulting in a single test for detecting unlikely values.

Naturally, this can be done if the likelihood functions are "structured" so that all components have the same degrees of freedom and are independent.

D.2.4 Results

In order to evaluate the adequacy of the usual statistical assumptions of (log-)normality and a multinomial distribution for various Gadget input data sets in a typical scenario, a sample scenario was taken and a battery of tests conducted.

The majority of tests for the multinomial distribution have rejected this as an assumption. Thus it is seen that there is not an immediate need to further develop such tests. Rather, the immediate need is to modify these assumptions, i.e. find distributional assumptions which apply in the fisheries setting. Although some work has been undertaken in this fashion (Hrafnkelsson and Stefansson, 2002), practical likelihood functions do not yet exist for fisheries length distributions.

Similarly, a very large number (about 45%) of tests for normality were rejected. It follows that the emphasis needs to be on modifying the assumption rather than further developing these tests.

D.2.5 Discussion

It is well-known that under fairly general assumptions, $-2lnL$, for each component group, does have an asymptotic χ^2_{n-q} distribution for large sample size n in each group, if the number q reflects the number of parameters estimated by this component group.

In the Gaussian case, this holds also for individual components with $n = 1$ and $q = 0$, which might be expected to apply approximately when there are many data points in total (across all components), relative to the number of parameters (including nuisance parametrs).

In general, for enough data, it is seen that the likelihood components can each be expected to follow a χ^2_{n-q}-type distribution, where n is the number of data items in each block and q is approximately 0. It is therefore an interesting future project to evaluate under what general conditions this can be extended down to the extreme case of $n = 1$.

It would be a particularly useful exercise to develop a single test statistic which could be used as a generic tool for testing the adequacy of the Gadget composite likelihood function. Such an indicator would immediately point a finger to further required analysis of individual deviations.

At present, however, the goodness-of-fit tests are seen to be sufficiently developed that they can reject most currently used likelihood functions used in fisheries. Further development therefore must await more appropriate distributional assumptions.

Acknowledgements

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D.3 Formulation Of A Stochastic Age/Length Structured Multispecies Model

Peter Lewy and Morten Vinther

Draft January 2002

Introduction

Development of a stochastic multi-species model

The model developed is supposed to include a historical part, "VPA", and a prediction part. The model assumes that the area considered is homogeneous with respect to growth and mortality. Migration within the area will not be considered.

Stock dynamics including fishing and predation mortality of commercially important stocks will be described using commercial and survey catch-at-age data and stomach contents data. The model will be based on ICES MSVPA (reference). However, the food preferences of the predators, the suitability parameters, will be modelled further to reduce the number of parameters, using the formulation of Andersen and Ursin or other formulations.

The model will be implemented as modules such that separate processes will be clearly separated and exchangeable. The following modules be included:

- Data input/database module
- Modules for predation and growth models.
- A module for definition of the likelihood function for the catch-at-age observations.
- A module for definition of the likelihood function for the stomach contents observations
- An output module enabling graphical and other presentations.

The prediction model may be fleet based and include technical interactions, i. e. that the catch composition by species and age for each fleet is accounted for by the model.

Notation
s denotes the species
$prey$ denotes the prey species
$pred$ denotes the predator species
a, b denotes the age
q denotes the season
y denotes the year
$C(s, a, y, q)$ denotes observed catch in numbers
$\hat{C}(s, a, y, q)$ denotes the expected catch in numbers
$\sigma(s, a)$ denotes the standard deviation of log catches
$CPUE(survey, s, a, y, q)$
$\sigma(survey, s, a)$ denotes the standard deviation of log CPUE
$N(s, a, y, q)$ denotes the stock numbers in the sea
$Z(s, a, y, q)$ denotes total mortality rate
$F(s, a, y, q)$ denotes fishing mortality rate
Y denotes the number of years available
$A(s)$ denotes the number of age groups
NOS denotes the number of seasons
RSs denotes the season where the fish is recruited to the fishery

$M1(s,a,y,q)$ denotes natural mortality excluding predation
$M2(prey,a,y,q)$ denotes predation mortality
$SUIT(prey,l_{prey},pred,l_{pred},q)$ denotes suitability for given prey/age and predator/age species
$\eta(pred)$ denotes the parameter expressing the log "mean" of the preferred prey size
$\sigma_{pref}(pred)$ denotes the "standard deviation" in the food preference function
$\rho(prey,pred)$ denotes vulnerability parameters
$STOM(prey,l_{prey},pred,l_{pred},y,q)$ denotes the observed average weight proportion of prey $(prey,l_{prey})$ to the total weight of the stomach contents of predator $(pred,l_{pred})$ by year and season.
$w(s,a,y,q)$ denotes the mean weight at age
$Food(pred,b,y,q)$ denotes the food intake

Modelling total catch-at-age observations

Catch-at-age is considered a stochastic variable subject to sampling and process variation. The probability model for these observations is a multiplicative model e.g. as defined by Lewy (200?):

Catch at age is assumed to be log normal distributed with log mean equal to log of the standard catch equation, i.e. $\ln(C(s,a,y,q)) \sim \text{Normal}(E(\ln(C(s,a,y,q)),\sigma^2_{catch}(s,a))$. The variances for the fully exploited fish may be assumed having the same variance. Thus, the likelihood function, L_C, associated with the catches is

$$L_C = \prod_{s,a,y,q} \frac{1}{\sigma_{catch}(s,a)\sqrt{2\pi}} \exp(-(\ln(C(s,a,y,q)) - E(\ln C(s,a,y,q))))^2/(2\sigma^2_{catch}(s,a))) \quad (1)$$

Where

$$E(\ln(C(s,a,y,q)) = \ln(\frac{F(s,a,y,q)}{Z(s,a,y,q)}(1-\exp(-Z(s,a,y,q))N(s,a,y,q)) \quad (2)$$

The negative log-likelihood for total catches then becomes:

$$l_C = -\ln(L_C) \propto -4Y\sum_{s,a} A(s)\ln(\sigma_{catch}(s,a)) \sum_{s,a,y,q} (\ln(C(s,a,y,q)) - E(\ln(C(s,a,y,q))))^2/(2\sigma^{(}_{catch}s,a))) \quad (3)$$

Modelling survey indices

$CPUE(survey,s,a,y)$ in analogy with the commercial catches the survey indices are assumed lognormal distributed with mean.

$$E(\ln(CPUE(survey,s,a,y)) = \ln(Q(survey,s,a,y,q)\bar{N}(s,a,y,q))$$

where Q indicates catchability of the survey and q is the quarter in which the survey takes place. Log variance, $\sigma(survey,s,a)$ for the fully exploited fish is assumed to the same. The log-likelihood is on the same form as equation (3).

Modelling fishing mortality

Total fishing mortality is for each species, $F(s,a,y,q)$ is modelled as a partly separable model (the species index, s, is left out for convenience):

$F(a,y,q) = F_1(a,y)F_2(y)F_3(a,y,q)$

This model assumes fishing mortality by age, year and quarter can be split up into age/year, year and age/year/quarter effects.

The range of year considered may be divided into a number of periods, T_{year} , such that

$F_1(a,y) = F_1(a, period)$ for each y in the $period$ = 1,2, ... ,T_{year}

Correspondingly

$F_3(a,y,q) = F_3(a, period, q)$

The age groups, for instance the fully exploited, may be combined as well:

$F_1(a, period) = F_1(a_{limit}, period)$ for $a \geq a_{limit}$ and $period = 1, 2, \ldots\ T_{year}$

$F_3(a, period, q) = F_3(a_{limit}, period, q)$ for $a \geq a_{limit}$ and $period = 1, 2, \ldots\ T_{year}$

The age interval from the first age up to a_{limit} may be further divided into several intervals.

In order to ensure unique parameters two ties have to be set. We have chosen to fix $F_2(y=1)$=1 and $F_3(a, period = T_{year}, q=4)$=1.

In general if we have Y years, A age groups we $4YA$ observations and $5a_{limit}T_{year}$- 2 parameters. If Y = 20, A=10, T_{year}=2 and a_{limit}=3 we have 800 observations and 28 parameters.

Survival of the stocks

The survival of the stock in the sea is described by the usual exponential decay equation.

$$N(s,a,y,q+1) = N(s,a,y,q)\exp(-Z(s,a,y,q)) \tag{4}$$

$$N(s,a,y+1,q=1) = N(s,a,y,q=\text{lastseason})\exp(-Z(s,a,y,q=\text{lastseason}) \tag{5}$$

Initial stock size, i.e. the stock in the first year and recruitment over years are considered as parameters in the model while the remaining are considered as functions of the parameters recursively determined by equations (4) and (5).

The stock parameters are $N(s, a \geq NOS - RS(s), y=1, q=1), N(s, a=0, y, q=RS(s))$ for all species, years and age groups $a \geq 1$, where NOS is the number of seasons and $RS(s)$ is the season where species s is recruited to the fishery.

In a multispecies model including fish predation total mortality, $Z(s,a,y,q)$ are divided into three components, predation mortality, other mortality and fishing.

$$Z(s,a,y,q) = M1(s,a,q) + M2(s,a,y,q) + F(s,a,y,q) \tag{6}$$

If M1 and M2 are assumed known the model described so far is a stochastic single species assessment model (e.g. Lewy ???) where each of the species can be treated independently of the interactions due to predation.

Stomach contents models

Modelling of predator food preference on the North Sea scale is based on relative stomach content observations calculated as weighted averages by Roundfish area weighted with the density of the predators. (reference til MV paper). These observations, the length based $STOM(prey, preylength, pred, predlength, y, q)$ and the corresponding age based observations are assumed to be stochastic variables subject to sampling and process variations. A probability distribution for these observations has to be specified to calculate the likelihood function.

In spite of that the catch models are age structured the stomach contents models considered will – in contrast to deterministic multispecies models - be length based. This decision is based on bootstrapping the stomach content observations (Vinther 2001), which show that for given predator and prey species the observed weight proportions in the stomach in some cases have correlations close to one and hence are close to be linearly dependent for a range of age groups. This applies for instance to weight proportions of the 2-, 3- and 4 group of sandeel in the stomach of 2 year old cod, $STOM(sandeel, a, cod, 2, y, q)$ for a=2,3,4. In most cases this is caused by that externally given age/length keys are used to translate a length groups to age groups for both predator and prey. As a consequence we have chosen to model food preference based on length.

For a given predator/length the observations, proportions of the prey species/length groups included, may further be correlated of two reasons: 1. The proportions are summing to one. 2. Specific prey items may occur in the stomachs in a systematic pattern due to the combined effect of the preference of the predator and the spatial overlap of prey species and the predator. Thus, for a given predator the observations of all prey species, $(STOM(prey, preylength, pred, predlength, y, q))_{prey,length}$, need to be described by a multivariate distribution which includes correlation between observations. Two possibilities are considered: A Dirichlet and a multivariate log normal distribution. A Dirichlet distribution has been rejected because the correlations between variables in distribution are negative. However, bootstrap estimates of the distribution of stomach contents observations of commercially important North Sea species (mave reference) indicates the observations in some cases are heavily positive correlated. In stead a multivariate log normal distribution has been utilised. Thus the expected value and the variance/covariance matrix of log $STOM$ has to modelled or specified.

The expected value of log $STOM$ is modelled using the theory developed by Andersen and Ursin (1977) and the modifications made by Gislason and Helgason (1985), which resulted in the deterministic Multispecies VPA, MSVPA.

—————————————————————————————
Længdebaseret formulering

The expected value of log observations is:

$$E(\ln(STOM(prey, l_{prey}, pred, l_{pred}, y, q))) =$$
$$\ln(\frac{\bar{N}(prey, l_{prey}, y, q)w(l_{prey}(y,q))(SUIT(l_{prey}(y,q), l_{pred}(y,q))}{\sum\limits_{prey, l_{prey}} \bar{N}(prey, l\_prey, y, q)w(l_{prey}(y,q))SUIT(l_{prey}(y,q), l_{pred}(y,q))})$$

where $SUIT(l_{prey}(y,q), l_{pred}(y,q))$ are parameters describing the combined effect of food availability and preference. As stock numbers are age based in the catch model stock numbers by length in the above equation need to be expressed by age. This is done using length/age keys which for each age group gives the proportion by length group: If β denotes the proportion of fish in length group l of a year old fish $(\sum\limits_{l} \beta(l, a, y, q) = 1)$ we have $N(l, y, q) = \sum\limits_{a} \beta(l, a, y, q)N(a, y, q)$

Using this formula we approximate $\bar{N}(l,y,q) \cong \sum_a \beta(l,a,y,q)\bar{N}(a,y,q)$, which holds exactly if $Z(l,a,y,q) = Z(l,y,q)$ for all age groups. This assumption seems to be reasonable. Insertion of the latter formula into the expected value of ln $STOM$

$$\begin{aligned} &E(\ln(STOM(prey,l_{prey},pred,y,q)) = \\ &\ln\left(\frac{w(l_{prey}(y,q))SUIT(l_{prey}(y,q),l_{pred}(y,q))\sum_a \beta(l_{prey},a,y,q)\bar{N}(prey,a,y,q)}{\sum_{prey,l_{prey}}\{w(l_{prey}(y,q))SUIT(l_{prey}(y,q),l_{pred}(y,q))\sum_a \beta(l_{prey},a,y,q)\bar{N}(prey,a,y,q)\}}\right) \end{aligned} \tag{7}$$

In the ICES MSVPA the suitability parameters are estimated directly (assuming that they are independent of the year). This is not convenient in a stochastic model because of the large number of parameters. Thus, suitability is modelled as suggested by Andersen and Ursin (1977):

$$\begin{aligned} &SUIT(l_{prey}(y,q),l_{pred}(y,q)) = \\ &\rho(prey,l_{prey},pred,l_{pred},q)\exp\left(-\frac{\ln\frac{(\ln \mathrm{l_pred}(y,q)}{\mathrm{l_prey}(y,q)} - \eta(pred))^2}{2\sigma^2_{pref}(pred)}\right) \end{aligned} \tag{8}$$

where ρ is a vulnerability parameter, where $\eta(pred)$ denote the relative size preference of the predator and $\sigma^2_{pref}(pred)$ the "variance" of size preference function. As the stomach content observations are length based suitability accordingly is expressed in terms of length and the relative size preference and the "variance" therefore refer to length.

The vulnerability parameter, ρ, which includes both a spatial overlap of predator and prey and the species food preference, may accordingly be divided into an overlap factor and food preference:

$$\rho(prey,l_{prey},pred,l_{pred},q) = overlap(prey,l_{prey}(y,q),pred,l_{pred}(l_{pred}(y,q))\rho(prey,pred)$$

The overlap factor may be quantified and estimated using data from IBTS surveys. In the latter model food suitability depends on the three independent factors: The spatial overlap, a specific species preference and a size preference.

As in Gislason and Helgason (1985) the age structured predation mortality is determined by

$$M2(prey,a,y,q) = \sum_{pred,b} \frac{\bar{N}(pred,b,y,q)Food(pred,b,y,q)SUIT(a_{prey}(y,q),b_{pred}(y,q))}{AVAIL(pred,b,y,q)} \tag{9}$$

where

$$\begin{aligned} AVAIL(pred,b,y,q) &= \\ &\sum_{prey,a} \bar{N}(prey,a,y,q)w((prey,a,y,q)SUIT(a_{prey}(y,q),b_{pred}(y,q)) \\ &+ OTHERFOOD(pred,b,y,q)SUIT(OF,pred,b,y,q) \end{aligned} \tag{10}$$

The age based suitability in equations (9)and (10) is estimated using the length based formulation, (8), by

$$\begin{aligned} &SUIT(a_{prey}(y,q), b_{pred}(y,q)) \\ &\qquad \rho(prey, l_{prey}, pred, l_{pred}, q) \exp\Big(- \frac{(\ln \frac{\bar{\mathrm{l}}_{\mathrm{pred}}(\mathrm{b}_{\mathrm{pred}}(\mathrm{y},\mathrm{q}))}{\mathrm{l}_{\mathrm{prey}}(\mathrm{a}_{\mathrm{prey}}(\mathrm{y},\mathrm{q}))} - \eta(pred))^2}{2\sigma^2_{pref}(pred)} \Big) \end{aligned}$$

where $\bar{l}_{pred}(b_{pred}(y,q))and\bar{l}_{prey}(a_{prey}(y,q))$

denote the mean length of the age groups. As the suitability parameters appear in the likelihood functions referring to both catch-at-age and stomach content observations the estimated parameters are affected of both sources of information.

Food intake may taken from the literature or may be modelled by:

$$Food(pred, b, y, q) = \alpha(pred, q) weight(pred, b, y, q)^{\beta(pred)} \tag{11}$$

As the size of other food is not known suitability for this prey is modelled by excluding the size dependent term:

$$\begin{aligned} SUIT(OTHERFOOD, pred, l, , q) &= \rho(OTHERFOOD, pred, l, q) \\ &= \rho_1(OTHERFOOD, pred, q) + \rho_2(OTHERFOOD, pred, q) l \end{aligned}$$

The model is based on the assumption that other food is less suitable for larger than smaller predators. Hence the slope, ρ_2, in the linear approximation should be less than zero.

The variance/covariance matrices of $(\ln STOM(prey, l_{prey}, pred, l_{pred}, y, q))_{prey,a}$, $D(pred, l_{pred}, y, q)$, used in the likelihood function are – apart for the variances – assumed to be known values. The values are the covariances are the values obtained from the bootstrapping procedure. The variances in the model are modelled as follows:

$$\begin{aligned} &VAR(\ln STOM(prey, l_{prey}, pred, l_{pred}, y, q)) = \qquad (12) \\ &\frac{\lambda(pred) E(\ln STOM(prey, l_{prey}, pred, l_{pred}, y, q))(1 - E(\ln STOM(prey, l_{prey}, pred, l_{pred}, y, q))}{n_{stomach}(y, q)} \end{aligned}$$

(12)

where $\lambda(pred)$ are parameters to be estimated and where $n_{stomach}(y,q)$ denotes the number of hauls in the samples. The variance structure is similar to the variance in the Dirichlet and the multinomial distributions. It supported by analyses of the bootstrapped stomach observations.

The likelihood function, L_{STOM}, for the relative stomach contents observations now can be expressed by the standard density function of the multivariate normal distribution:

$$\begin{aligned} L_{STOM} \cong &\prod_{pred, l_{pred}, y, q} |A(pred, l_{pred}, y, q)|^{1/2} \\ &\times \exp(-0.5 RES'(pred, l_{pred}, y, q) A(pred, l_{pred}, y, q) RES(pred, l_{pred}, y, q) \end{aligned} \tag{13}$$

where the positive definite matrix $A = D^{-1}$ and D is the variance/covariance matrix of the observations, $\ln STOM(pred, l_{pred}, y, q)_{pred, l_{pred}}$, where $RES^{'}$ denotes the transposed vector

$$RES(pred, l_{pred}, y, q) = \ln STOM(pred, l_{pred}, y, q) - E(\ln STOM(pred, l_{pred}, y, q)$$

where

$$\ln STOM(pred, l_{pred}, y, q) = \begin{pmatrix} \ln STOM(prey1, l^1_{prey_1}, pred, l_{pred}, y, q) \\ \cdot \\ \ln STOM(prey1, l^{n_1}_{prey_1}, pred, l_{pred}, y, q) \\ \cdot \\ \cdot \\ \ln STOM(prey\mathrm{m}, l^1_{prey_m}, pred, l_{pred}, y, q) \\ \cdot \\ \ln STOM(prey\mathrm{m}, l^n_{prey_m}m, pred, l_{pred}, y, q) \end{pmatrix}$$

$$E(\ln STOM(pred, l_{pred}, y, q)) = \begin{pmatrix} E(\ln STOM(prey1, l^1_{prey_1}, pred, l_{pred}, y, q)) \\ \cdot \\ \\ E(\ln STOM(prey1, l^{n_1}_{prey_1}, pred, l_{pred}, y, q)) \\ \cdot \\ \\ \cdot \\ \\ E(\ln STOM(prey\mathrm{m}, l^1_{prey_m}, pred, l_{pred}, y, q)) \\ \cdot \\ \\ E(\ln STOM(prey\mathrm{m}, l^{n_m}_{prey_m}, pred, l_{pred}, y, q)) \end{pmatrix}$$

and where n_i denotes the number of length groups of prey species i.

Stock-recruitment relationship

Stock-recruitment is modelled using a parameterised model. Assuming recruitment is lognormal distributed the parameters for species are estimated by multiplying the likelihood function with a penalty function derived from

$$R(s, y) = g(SSB(s, y), \alpha(s), \beta(s)) \exp(\sigma(s)\varepsilon(y))$$

where R denotes the recruits, s denotes the species, g the stock-recruitment relation chosen, αandβ S-R parameters, σ the standard deviation and ε a standardized normal distribution.

The total likelihood function, L, then becomes

$L = L_C * L_{STOM} * L_{S-R}$

The parameters in the model are:

$N(s, a \geq NOS - RS(s), y = 1, q = 1), N(s, a = 0, y, q = RS(s))$

$M1(s, a)$

$F_1(s, a), F_2(s, y), F_3(s, q)$

$\rho(prey, pred)$

$\eta(pred)$

$\sigma^2_{catch}(s)$

$\sigma^2_{pref}(pred)$

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D.4 Performance of indicators derived from abundance estimates for detecting the impact of fishing on a fish community

DRAFT
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Verena M. Trenkel and Marie-Joëlle Rochet
Laboratoire MAERHA, IFREMER, Rue de l'Ile d'Yeu, BP 21105, 44311 Nantes, France
Verena.Trenkel@ifremer.fr

Abstract

Population and community indicators for the impact of fishing are often estimated using abundance estimates instead of raw sampling observations. Methods are presented for testing null hypotheses of non-significant impacts and where possible, for calculating the statistical power. The indicators considered concern populations (intrinsic growth rate, total mortality, exploitation rate and a new indicator, the change in fishing mortality required to reverse population growth) and communities (k- and partial dominance curves, a biodiversity index, size spectrum and proportions of various population groups). The performance of these indicators is compared for the Celtic sea groundfish community based on achieved precision, statistical power and availability and estimation method of reference points. Among population indicators, mean length in the catch was most precisely estimated and the corresponding hypotheses tests had consistently large powers. Total mortality performed reasonably well. In contrast, both the intrinsic population growth rate and the exploitation rate gave unreliable results. All tested community indicators performed similarly well. Indicators for which the direction of change caused by fishing is predictable, such as the proportion of non-commercial species or piscivores in the community, are promising indicators at the community level.

Introduction

Assessing the impact of fishing on different components of the ecosystem is an important part of recent attempts to introduce ecosystem consideration into fisheries management (Anonymous 1999a; Hall 1999; ICES 2000). Various indicators have been proposed for measuring the direct and indirect impacts on fish and benthic communities (Die and Caddy 1997; FAO 1999; Rice 2000; Rochet and Trenkel in prep). In this paper we compare the performance of selected indicators applied to French groundfish survey data for the Celtic sea using three statistical criteria : estimation precision, achieved testing power (if available) and availability and estimation method of reference points. Until now, indicators have mainly been assessed based on theoretical considerations (Rice 2000; Rochet and Trenkel in prep), which is only part of the story.

The ecological theory underpinning certain indicators allows the determination of reference points expressing the null hypothesis of a stationary system. Measurable impacts of fishing are affirmed if the indicator value for a community of interest is above the reference point. For a number of indicators, no theory exists that would allow the definition of reference points or even the range of acceptable indicator values. Hence consistent changes over time that might indicate the impact of fishing are looked for. Given that most indicators vary under the influence of forces other than fishing, evidence for the presence of fishing impacts will be provided by simultaneous rejection of null hypotheses for several indicators.

For detecting significant impacts of fishing, direct comparison of indicator values with reference points is only possible in the uncommon case of fully censused communities. In general, communities have to be sampled. In order to obtain conclusions about the community, inference has to be drawn within a hypothesis testing framework where reference points or no change are taken as null hypotheses that are tested against alternative hypotheses representing the impact of fishing.

Most existing indicators are based on estimates or observations of population abundances generally obtained from research vessel surveys. If random samples from the community have been taken, the empirical sampling distribution of an indicator can be used directly for hypothesis testing. Furthermore, randomization tests rearranging the spatial or temporal origin of individual samples can be used for comparing years and areas (Clarke 1990) and for comparing patterns to null models, which assume similar structures (Veech 2000). An application of these methods to the groundfish community of the Northern North sea can be found in Greenstreet and Hall (1996).

In the case of stratified, adaptive or non-random sampling designs, the raw (haul) data do not form a representative sample of the studied community. Instead, abundance estimates by species have to be calculated giving appropriate weights to each sample. As a consequence, empirical sampling distributions of indicators are not available and simple randomization cannot be carried out.

For a selection of commonly used indicators we propose methods for obtaining indicator sampling distributions and carrying out hypotheses tests when the indicators have been estimated using abundance estimates. The selected indicators fall into two categories: indicators measuring the state and dynamics of individual populations, and indicators for the whole community structure and functioning (Tables 1 and 2). To the best of our knowledge, their sampling distributions derived from abundance estimates have not been studied so far.

We decompose the process of determining indicator sampling distributions into several tasks. First, data requirements are examined (Tables 1 and 2). Data sources for estimating indicators and their reference points are summarised in table 3. Most indicators dealt with in this study are based on annual abundance estimates by species, $N_i(t)$, or by length group and species, $N_{l,i}(t)$. Second, appropriate abundance estimators are chosen and their distributions are determined. Third, given the definition of indicators and the distribution of the input information, appropriate estimation methods are selected for indicators that represent model parameters, for example the intrinsic population growth rate r which is a parameter of a simple population dynamics model. If the estimation method makes parametric assumptions, such as normality for linear regression, the actual distribution of the input information is checked. Fourth, given the sampling distributions of abundance estimates and appropriate estimation methods, the resulting distribution of indicator estimates are studied. Hypotheses tests are carried out for indicators with reference points; linear time trends are tested for the other indicators. If possible, the statistical power of hypotheses tests is estimated.

Methods

Abundance estimation

Fish numbers per haul generally have strongly skewed distributions. The question of which estimator to use for obtaining abundance estimates in this case has attracted attention from several authors. Pennington (1983) states that estimators based on the lognormal distribution are more efficient than estimates based on sample means. However, Myers and Pepin (1990) based on a simulation study recommend using lognormal-based estimators only if the lognormal distribution assumption for non-zero observations is justified, as these estimators are sensitive to assumption violations. Hence, it is advisable to test the distribution of numbers per haul.

For the Celtic sea groundfish community, two examples of empirical distributions of observed numbers per haul are given in figure 1. Note the skewness and the long right-hand tails. Empirical distributions for all strata and years for which a reasonable number of hauls (n>15) was available were compared to Gamma, Normal and log-Normal (non-zero observations only) distributions (chi-square tests); none of the distributions could be rejected as being inappropriate for any of the tested species.

If the appropriateness of the lognormal distribution cannot be confirmed as in our example, we propose to follow the advice given by Myers and Pepin (1990) and use simple mean-based sample estimators. For the Celtic sea this involves for each species i (or length class) taking the mean per stratum (including hauls were the species was not observed), divide by the swept area, multiply by the stratum area and then sum over all strata. This gives abundance estimates $\hat{N}_i$. Variances $\hat{V}[\hat{N}_i]$ are estimated correspondingly.

Looking at the relationship between abundance estimates $\hat{N}_i$ and their variances $\hat{V}[\hat{N}_i]$ is a second way of trying to identify the distribution of abundance estimates. For this the slope of the linear regression of $\log(V[\hat{N}(t)])$ on $\log(\hat{N}(t))$ is estimated. For our example we found that $V[\hat{N}] \propto \hat{N}^2$ for most species by testing for slopes equal to two. Two observations can be made: 1) abundance estimates are heteroscedastic; 2) Gamma and lognormal distributions exhibit this particular mean-variance relationship. Hence either of them could be used to describe the distribution of estimated abundances. For certain estimation methods we do not need to know the full distribution. It is sufficient to stabilize variances, which can be achieved by log-transformations (Scheffé 1959). Normal error distributions are then appropriate for the log-transformed abundance estimates.

Abundance indices are relative measures of population numbers; a factor of proportionality stands between the two. This factor of proportionality differs between species and it is often referred to as catchability. If estimates of catchability are available, abundance indices can be corrected. In our case no catchability estimates were available and catchabilities of 1 were assumed for all species. The effect of this assumption is that indicators involving more than one species will represent the part of the community accessible to the survey gear rather than the real community.

Estimation, sampling distributions and hypotheses tests

Indicator estimation methods are summarised in table 1 (column 5) for population indicators and table 2 (column 3) for community indicators. In the following we briefly review all indicators, explain estimation methods that differ from standard use and comment on their reference points. All equations are provided in tables 1 and 2.

- Intrinsic population growth rate r

It is estimated using annual population abundance estimates. The population dynamics model underlying this indicator can be linearised by taking logarithms of both sides (eq. 1). As the log-transformation is also applied to abundance estimates, the transformation stabilizes variances and justifies the use of standard regression techniques for estimating r as the slope. However, in the transformed model, residuals are serially correlated as the independent variable form a time series. We take account of this by formulating a first order autoregressive model for residuals. Taking r=0 as the reference point assumes that without any noticeable impact of fishing the population would be stable although randomly varying between years.

- Total mortality rate Z

The estimation method is based on a simple population dynamics model for a given cohort. The age-based model is transformed into a length-based model using the von Bertalanffy growth function (eq. 2). In order to use estimated numbers at length for a given year instead of a cohort, it is assumed that recruitment has been constant in the past in addition to a constant total mortality rate, the later assumption implying constant fishing pressure. Some insight concerning the validity of these assumptions can be obtained by estimating Z using data from different years. If the assumption is appropriate, similar estimates should be obtained. Z could be estimated by linear regression of the linearized catch curve (log-transformation). The alternative is to avoid the normality assumption of linear regression and use a generalized linear model with log-link and quasi likelihood function. Estimating the reference point Z* requires an estimate of length at first capture L_c. To obtain reliable estimates, we used the first 5-cm length class accounting for at least 10% of total catch.

- Exploitation rate F/Z

Fishing mortality F is estimated from catch data (landings and discards) and estimated population abundances (eq. 3). Total mortality Z is estimated as above and assumed constant over the most recent years. For the Celtic sea, we have discards data only for 1997 and hence estimate fishing mortality for that year only. The reference point F/Z=0.5, which represents an upper limit, was proposed based on production considerations (Alverson and Pereyra 1969; see also discussion in Rochet and Trenkel submitted).

- Mean length in catch L_{bar}

It is estimated using numbers at length per species (eq. 4); its value should be above length at maturity L_{mat} in order to give at least half the individuals of a cohort a chance to reproduce.

- Change in fishing mortality required to reverse population growth rate ΔF

This indicator is derived from a simple two-stage Leslie type population dynamics model (eq. 5, Rochet and Trenkel in prep). It measures the change in fishing mortality required to reverse population growth, keeping all other model parameters constant. The uncertainty in the estimate of population growth is taken into account. The reference point has been derived empirically (Rochet and Trenkel in prep). It represents the average interannual variation (%CV) in fishing mortality observed in North and Celtic sea stocks.

- Biodiversity index Δ_1

This biodiversity index is defined as the probability that two individuals randomly chosen from the community will belong to different species (eq. 6; Hurlbert 1971). It is estimated using species abundance estimates.

- k-dominance and partial dominance curves

The k-dominance curve is the cumulative relative abundance of ranked species plotted against their log-rank (Clarke 1990, eq. 7). For the partial dominance curve the relative abundance of a given species is calculated only with respect to species of lower rank (Clarke 1990, eq. 8). While the shape of the k-dominance curve is dominated by the single most abundant species, the partial dominance curve allows the study of several of the more abundant species.

- Species composition

We carry out a non-parametric Kruskall-Wallis test to compare species distributions (abundances by species) between years. If a long time series was available, the method proposed by Solow (1994) for detecting trends using orthogonal combinations of original compositions could also be used.

- Proportion of non-commercial species

The relative importance of non-commercial species in community is expressed either in terms of abundance or biomass (eqs. 9 & 10). In this study, non-commercial species are all species with no market value. Under the impact of fishing, this proportion is expected to increase. The relationship of the proportion of non-commercial species with time is modelled by a logistic regression (GLM with binomial distribution and logit-link function) where time is the explanatory variable. A positive slope is taken to suggest significant impacts of fishing.

- Distribution of mean population length

Using mean length of all individual populations, the distribution of mean length in the community is obtained. Fishing is expected to shift the distribution to smaller lengths. It is not obvious how to define the size of a fish, as they change their size during their whole life. Rather than asymptotic size L_∞, which is generally poorly estimated for exploited fish populations due to truncated age distributions, mean length of fish in each population might be a better size index. Thus we use mean length of mature fish to reduce the undue influence of recruits on the estimate.

- Size-abundance relationship

The relationship between mean population length and population abundance is supposed to be linear with a negative slope. The reduction in abundance caused by fishing is expected to be higher for species with larger body size and hence the slope of the relationship should decrease under the impact of fishing (eq. 11; see review in Rochet and Trenkel in prep).

- Total biomass and total numbers

It is estimated as the sum of all species biomasses or abundances (eq. 12). The effect of fishing on these indicators is unknown, but any increasing or decreasing time trend could be a sign for changes occuring in the community. Hence, a time trend is tested for by means of robust linear regression (MM method, Franke et al. 1984) which avoids making normality assumptions.

- Proportion of piscivores

All species in the community are assigned to relevant trophic groups: planktivores, piscivores and benthivores on the basis of established knowledge from the literature. The proportion of piscivores (eq. 13) is expected to decrease under the impact of fishing as piscivores are most of the time the preferred targets of commercial fishing. As for the the proportion of non-commercial species, time trends are estimated using logistic regression.

- Average individual weight

The average weight of an individual in the community is estimated using total biomass and abundances (eq. 14). It is expected to decrease as the result of fishing as both bigger individuals and larger species are being removed.

- Size spectrum

A trigonometric model is used to describe the size spectrum (Rochet and Trenkel in prep) in contrast to the commonly used linear model in order to take account of the non-linear features of the spectrum (eq. 15). Model parameters are estimated using abundance estimates at length (5 cm length classes all species confounded) and a generalised linear model with log-link and Gamma error distribution (McCullagh & Nelder 1989). Log-transformed lengths, $\log(L_t)$, are centred to limit correlations between parameter estimates. Year-effects for all three model parameters are tested by comparing model fits with and without year-effects using log-likelihood ratio tests (McCullagh & Nelder 1989). The five centimeter length classes were used as a compromise between the desired precision of abundance estimates and the number of length classes available to fit the relationship.

For population indicators, sampling distributions and methods used for carrying out hypotheses tests are provided in columns 8 and 9 of table 1. Given the estimation procedures described above, normal distributions are justified for all indicators of this class.

For community indicators, methods used for obtaining sampling distributions, null hypotheses and alternative hypotheses are summarised in columns 4-7 of table 2. Note that no reference points are available for this class of indicators. Given the estimation procedure, normal distribution assumptions are justified for some indicators. For other indicators independent parametric bootstraps of species abundance (or biomass) estimates are used and confidence intervals for indicator estimates are obtained using the percentile method (Efron & Tibshirani 1986). Note that this assumes that species abundance estimates are independent which seems reasonable for trawl data. For the Celtic sea example, both lognormal and Gamma distributions seem appropriate. Hence, both are used in order to test the robustness of hypothesis tests to parametric assumptions underlying the implemented bootstrap. Confidence intervals for k-dominance curves and partial dominance curves are obtained by recalculating the curves for each bootstrap sample. For testing differences between years we use pointwise (rankwise) confidence intervals, because the comparison tests are for each rank and not for the overall curves. Instead of using parametric bootstraps of individual abundance estimates we could also have bootstrapped individual hauls (non parametric bootstrap) and recalculated abundance estimates and indices for each bootstrap sample. Unfortunately, not enough hauls were carried out in some strata for this to be an option for our survey data.

Power functions

The statistical power of a hypothesis test is the probability that the alternative hypothesis is accepted given it is correct. A clear description of the concept of power analysis can be found in Peterman (1990). Hence in order to calculate the power, it is necessary to know the parametric distribution of the indicator under the alternative hypothesis. Unfortunately we know the distribution of the alternative hypothesis only for the selected population indicators. As all population indicator estimates are assumed to follow normal distributions, the power function is only described for population growth rate r and total mortality Z. Throughout this study we will consider an achieved power of at least 0.8 to be satisfactory and use a significant level of $\alpha = 0.05$ ($\alpha = 0.025$for one-sided tests).

For the intrinsic population growth rate r, the two sided hypothesis test with H_0: $r = 0$ versus $\mathrm{H}_1 : r \neq 0$ gives the power function $\beta(r) = 2P_r(G{>}c - r/\sqrt{V[r]})$ where G is a standard normal random variable and $\beta(0) = \alpha$ if $P_r(G{>}c) = \alpha = 0.025$.

For the total mortality Z, the power function for the one-sided hypothesis test $\mathrm{H}_0 : Z \leq Z^*$ versus $\mathrm{H}_1 : Z{>}Z^*$ is $\beta(Z) = P_Z(G{>}c + (Z^* - Z)/\sqrt{V[Z]})$

where G is again a standard normal random variable and c is a constant such that $\beta(Z^*) = \alpha$ if $P_{Z^*}(G{>}c) = \alpha = 0.05$.

The variances used in the power functions are those estimated from the data. In order to estimate the increase in power obtainable by increasing the precision of the input information (coefficient of variation or variance of abundance estimates), the variance of indicator estimates has to be formulated as a function of the CV (or variance) of the input information. For r and Z, these functions are developed in Appendix 2. It is not obvious to us how to obtain these functions for the remaining population indicators.

Celtic sea ground fish community

The Celtic sea is a continental shelf sea situated in the triangle between France, Ireland and Great Britain. The area considered in this study extends from 48° to 51° North and from 6° to 11° West. It supports an international fishery and the main commercial species are assessed by ICES working groups. Total international landings have increased steadily since the 1950's from about 70 000t to around 300,000 t in the late 1990's (Pinnegar et al. in press).

Fisheries information

The French trawler fleet accounts for about one half of total international landings from this area (estimated from Stock Assessment Working Group Reports). Discards sampling surveys of the French trawler fleet operating in the Celtic sea are undertaken at irregular intervals; the most recent survey was carried out in 1997. In this survey, a multilevel sampling design stratified by métier was used (Rochet et al. submitted). Landings were sampled on return to port of the selected boats. French commercial landings information for 1997 was also used.

Survey information

In this study we use data from the French groundfish surveys (EVHOE) for the years 1997-2000. The survey series actually started in 1990, was interrupted from 1992 to 1996 and the survey area was extended in 1997. This change coincided with a change in survey vessel and sampling design. Whereas hauls were placed on a systematic grid for the old design, the new design has stratified random hauls (10 strata). In the year of the change of vessel, an intercalibration study was carried out (Pelletier 1998). Unfortunately, a number of indicators showed important differences between 1990/91 and the latter part of the series but it proved impossible to disentangle the effects due to changes in the survey protocol and changes caused by fishing or other causes. Hence we resolved to remove the first part of the series.

During each cruise, 56 to 69 30-minutes-tows (4 knots) were carried out with a GOV36/47 bottom trawl fitted with a 20 mm mesh codend liner. All fish were identified, weighted by species and individually measured. The survey trawl is particularly suited for demersal species but not very good at catching benthic species such as megrim, anglerfish or *Nephrops* (Borges et al. 1999).

Species selection

Abundance indices for many rare or badly sampled species were too unreliable to be used. As a consequence, indicators aiming at individual populations and some of the community indicators were not calculated for all species. To select a group of representative species from the studied community, we checked that the size spectrum and the k-dominance curves for selected species were not significantly different to those of the whole community. This way a list of 25 species was obtained (see Appendix 1). The selected species contributed 99 percent of the total estimated biomass and around 93 percent of total estimated numbers. The selected species assemblage contained 17 commercial and eight non-commercial species. They belonged to four trophic groups: demersal benthivores (10 species), demersal piscivores (nine species), pelagic planktivores (four species) and pelagic piscivores (two species). Trophic classifications were based on Whitehead et al. (1986) and Greenstreet (1996).

Results

Results of population indicator tests are summarized in table 4. Growth rate estimates for 19 populations indicated that there was no evidence to reject the null hypothesis of stable populations (r not significantly different from 0), whereas three populations were significantly increasing (dab, Norway pout and mackerel) and three were significantly decreasing (argentines and scaldfish). Note that two of the decreasing populations are non-commercial species. Standard linear regression techniques, which ignore the autocorrelation between residuals, provided different growth rate estimates for a number of populations though test results were identical (results not shown). The power of most tests was rather low. Figure 2 gives estimates and the power of tests for some representative species. Note the difference in scale for cod (*Gadus morhua*) for which the precision of estimated abundances indices should be multiplied by about 2 (CV divided by 2) in order to detect a growth rate of around 0.12 being significantly different from zero with a power of 0.8.

Total mortality estimates Z were obtained by assuming stable population length structures in any given year. The results confirmed that for 17 populations length structures were indeed stable as estimates were not significantly different between years (two sided 5% level tests; results not shown). Nevertheless, average (over all years) total mortality estimates were calculated for all species and one-sided tests (2.5% significance level) revealed that for six species total mortality was outside safe limits ($Z>Z^*$); the test could not be carried out for one species (*Capros aper*) due to the lack of the necessary information to calculate the reference value Z*. Thus for 18 species, no evidence was found to reject the hypothesis of acceptable levels of total mortalities given the high uncertainties inherent in mortality estimates and ignoring any uncertainty in the estimates of Z*. Figure 3 shows total mortality estimates for selected species using every year of the time series separately. Note that estimates are rather similar between years except for *Arnoglossus laterna* and perhaps *Gadus morhua*, where estimates varied between years indicating that the population length structure might not be stable. Using data for 1998, the statistical powers were calculated. They were around one for most species but there were notable exceptions with very low power. For *A. laterna,* the power for the test that total mortality was above the limit value Z* was low (0.34 using 1998 data). In order to increase tha test power to around 0.8, the variance of abundance estimates (by length class) would have to at least divided by 4 (75% reduction).

Looking at exploitation rates F/Z, six species had estimated values equal or significantly above the reference point of 0.5 (one sided 5% level); testing powers were satisfactory for only 9 species. Assuming catchabilities equal to 1 when estimating abundance indices certainly led us to underestimate certain population abundances. Thus we overestimated fishing mortality F and as a consequence obtained large exploitation rate estimates. That this should be so can be seen by comparing our estimates for F with those obtained by ICES stock assessment working groups (Anonymous 1999b&c, 2000). The resulting exploitation rates are generally much lower than ours although the opposite case occurred for whiting, mackerel, sole and horse mackerel (Table 4).

The test for the impact of fishing on population length structure is based on the comparison of mean length in the catch L_{bar} with length at maturity L_{mat}. This test was found to be less optimistic since only for nine populations no evidence was found that they were not in the safe range (L_{bar}>L_{mat}). However, the statistical power of these tests was quasi zero. For 15 populations L_{bar} was significantly lower than L_{mat} with statistical powers of one.

Large reductions (100%) in fishing mortality would be required to significantly invert the decreasing population trends of the three populations with r significantly smaller than zero. Thus the estimated necessary changes in F are much higher than the suggested 20% threshold. Similarly, for all other populations it is concluded that they were insensitive to fishing mortality as even stopping fishing would not significantly change the growth rate.

Test results for community indicators are provided in table 5. There was no significant linear trend in biodiversity as measured by Δ_1(Figure 4). Confidence intervals based on Gamma and lognormal parametric bootstraps were similar. Like biodiversity, neither k-dominance curves nor partial dominance curves changed their form significantly over time (Figure 5). Confidence intervals based on Gamma and lognormal parametric bootstraps were similar (results not shown). Despite their stable form, an inversion in the dominant species was observed. While blue whiting was the most abundant species in 1997, it was boarfish in 2000. Note that the shape of k-dominance curves was entirely determined by the four most abundant species. Compared to k-dominance curves, partial dominance curves suggested a more even community structure. A Kruskal-Wallis test confirmed that species compositions (in numbers) were similar for all years.

The distribution of mean population lengths (survey) fluctuated from year to year (Figure 6). However, no significant change was detected in the distribution when comparing 1997 with 2000. No significant linear relationship between mean size and population abundance index was found for any of the study years, hence changes in the relationship could not be tested for. However, scatter-plots were similar between years with most species remaining in the same position, indicating that whatever form the relationship has, it was rather stable over the study period (Figure 7).

The proportion in biomass of non-commercial species (no commercial value) in the community has remained rather stable over the study period whereas the proportion in numbers increased from [0.20, 0.38] in 1997 to [0.47, 0.70] in 2000; the ranges are 95 percent confidence intervals based on a parametric bootstrap (Gamma distribution). No time trend in either total biomass or total abundance of animals in the community was found although there was a slight insignificant decreasing trend of mean weight of individuals in the community. The proportion of piscivores expressed as biomass or as numbers did not show a significant time trend over the study period.

No significant differences between years were found for the shape of the annual size spectra, however the size spectra were shifted vertically. A model with separate intercepts for each year provided a significantly better fit compared to a model with a common intercept. No improvement in fit was found when including year-effects for both other parameters. As there was no linear time trend in estimated annual intercepts, we concluded that no directed change ocurred in the size structure of the community.

Case study discussion

Overall not much evidence was found for rejecting the general null hypothesis that no change had happened to the structure of the Celtic sea ground fish community during the study period. However, many ongoing changes might have remained undetected due to the shortness of the time series and to imprecise estimates, which resulted in low statistical power of some tests. On the other hand, as the Celtic sea has been increasingly exploited during the last 30 years, any important changes might have happened long before the period considered in this study.

When considering populations individually, we saw that fishing was an unimportant source of mortality for non-commercial species. However, due to the high uncertainty in some indicator estimates, statistical power varied largely. Uncertainty was also responsible for the failure as an indicator of the change in fishing mortality required to reverse a population trend.

We use the number of significant hypotheses tests for each species to identify apparently impacted species (Table 4, last column). The most impacted species were *Argentina silus, Limanda limanda* and *Scomber scombrus.* These species belong to different trophic groups; hence feeding type does not provide an explanation for the findings; this is confirmed by the stable proportion of piscivores. However, all three species are commercially exploited.

Community indicators should add another point of view to the diagnostic obtained from looking at single populations. However, few detectable changes were found in community structures. The only indicator pointing at changes was the proportion of non-commercial species which increased. The individual population analysis had already revealed this for *Trisopterus esmarkii.*

Generally speaking, our aim to obtain clear answers was hindered by large uncertainties in survey abundance estimates as well as biased abundance estimates resulting from a lack of catchability estimates. In particular, estimates of fishing mortality seemed to be too high in comparison with estimates obtained by VPA. Coefficients of variation for indicator estimates varied between 10 and 200 percent (Table 6). In comparison, abundance, biomass and discards estimates had CVs of 30-40 percent. For certain indicators, this large uncertainty prevented us from drawing firm conclusions. This was particularly true for the intrinsic growth rates, which were estimated with low precision. In order to prove intrinsic population growth rates of around 0.1 to be significantly different from zero, for most species the CV of abundance estimates would need to be halved from the achieved 30% to something around 15%. This would imply a large increase in the number of hauls per survey.

Despite the uncertainties, the emerging picture is that fishing impacted a number of populations of the Celtic sea groundfish community primarily because individuals of too small a size were killed. This might be caused by too small mesh sizes used by bottom trawlers. This conclusion is supported by the large amounts of small fish discarded by the French bottom trawlers (Rochet et al. submitted). The impacted species were almost exclusively commercial species. As a result the proportion of non-commercial species rose over the study period.

Discussion

Indicator performance

The performance of indicators was evaluated using three criteria: the achieved precision of the indicator estimate expressed as percentage coefficient of variation, the power of the hypotheses tests (when available) and the existence and justification of the reference point (Table 6). In terms of precision, mean length in the catch L_{bar} of individual species was most precise with an average CV of 0.02%. The intrinsic population growth rate r and the exploitation rate F/Z were least precise. They had CVs of around 100%. Most other indicators had CVs of around 20%.

In terms of testing power, L_{bar} came of first again with satisfactory power for 15 out of the tested 25 species. This test was only carried out for one year (1997), as it requires discard estimates, which were not available for all years. Testing powers were similar for the other population indicators, but testing powers could not be calculated for any of the community indicators.

Most reference points for population indicators are estimates with unknown precision. In the case of L_{bar} and Z theory exists to motivate the choice, although the actual value has to be estimated. We used published biological parameters with unknown precision for the estimation which precluded us from estimating the precision of reference points. However, were this information available, hypotheses tests could easily be adapted. The reference point for the exploitation rate is clearly the most arbitrary. Currently no reference points are available for any of the community indicators. Nevertheless, for some community indicators it is possible to ascertain the expected direction of change. Hence these indicators are preferable to those for which not even the direction of change is known.

In this study we tested the new indicator ΔF , which describes the change in fishing mortality required to reverse decreasing population growth. Significantly negative population growth was only found for three populations, as growth estimates were generally imprecise. Under these circumstances very large changes in fishing mortality would be necessary to reverse population growth. Unfortunately, the approximations used for carrying out the calculations are not applicable if very large changes in F are necessary. Hence, the results of this indicator have to be taken as an indication rather than at face value.

Having looked at indicators individually, we now turn to investigate the agreement between population indicators. Some of the indicators are theoretically linked and should therefore provide the same answers. As expected, test results for Z and L_{bar} showed the largest agreement: both tests were significant for seven species; six additional species had significant tests for L_{bar} only. Thus, for the case study Z did not provide any information that was not provided by L_{bar} . In addition, the latter was estimated with higher precision and had satisfactory testing power for most species. Unfortunately, the estimation of L_{bar} requires discards as well as landings information and is therefore probably not estimable for many populations. In three cases were null hypotheses simultaneously rejected for L_{bar} and *r,* indicating that there is also some agreement between these two indicators.

In conclusion, mean length in the catch was found to be a powerful population indicator. As catch data rely on generally expensive discards sampling, we suggest that the merits of alternative length-based indicators such as mean length in individual populations and possibly in the community and should be explored including the definition of appropriate reference points. For community indicators, only estimation precision and the existence of an expected direction of change could be compared. The biodiversity index Δ_1 and the parameters of the model describing the size spectrum were found to be estimated most precisely. Unfortunately, their expected direction of change is currently not available. In contrast, estimates of all indicators for which this is the case, e.g. average individual weight in the community, the proportion of piscivores and the proportions of non-commercial species, had coefficient of variations of 14-30%.

Input data

Two shortcomings concerning the Celtic sea data can be identified: unknown catchability factors and imprecise abundance estimates. Regarding catchability, indicators based on proportions are only affected by relative catchability, which we assumed to be equal for all species. In contrast, indicators based on absolute abundance indices additionally suffer from bias due to the relationship between indices and population numbers. We think that this was the main cause for our unreliable estimates of fishing mortality. Some confidence that community indicators (e.g. biomass, mean weight, Shannon index) are robust to the particular survey design and thus variations in catchability, comes from studies using data obtained with different survey gear (Wantiez 1996). However, this is not true for population indicators.

Imprecise abundance estimates are to a large extent due to the spatial distribution of animals which for many species is not uniform over the study area for various reasons, e.g. depth and substrate preferences. Hence the underlying population distributions are skewed and increasing the number of hauls would increase the precision of abundance estimates but probably only slowly. However, this points at another dimension that needs to be considered when studying indicators for the impact of fishing: the spatial scale. While the appropriate spatial scale might be the stock area for a single population, it is not obvious what it should be for a community.

Some evidence for the importance of the spatial scale is provided by the finding that species diversity is an exponential function of the size of offshore banks (Frank & Shakell 2001). On the other hand, it seems obvious that the more homogenous the underlying community is, the more precise indicator estimates are going to be. For the Celtic sea we could chose sampling strata as units for the assessment, with the problem however that the number of hauls per stratum varies from 2 to 23 depending on strata area (mean 8 hauls) thus causing the problem of variable precision.

Statistical issues

Two main statistical issues arise from this study: multiple testing and parametric assumptions made for obtaining indicator distributions. For population indicators, five hypothesis tests were carried out separately for each population. As population indicators are not using exactly the same information, we argue that testing levels for a given species do not need to be adjusted. However, tests with Bonferroni adjusted significance levels are obtained by using the results for the 1% level in table 4 (marked as **). The conclusions remain unchanged for the reasonably precise indicators L_{bar} and Z. Remains the question of adjusting the testing level concerning the same indicator across species. We would argue that it is reasonable to consider populations separately and hence not to adjust individual population tests for the same indicator. Indeed, adjustments seem only required if the individual population tests serve as evidence for the overall significance of an indicator.

For a number of community indicators we had to resort to parametric bootstraps of the abundance estimates. We found that the results for the Celtic sea groundfish community were rather insensitive to the chosen parametric distribution. Both Gamma and lognormal distributions for abundance estimates led to similar indicator estimates and identical conclusions for hypotheses tests. Thus the results presented seem to be robust to this assumption.

Conclusions

Based on the results presented we would recommend the use of L_{bar} , Z, $\bar{b}$ and the proportion of non-commercial species which can all be estimated with reasonable precision and for which we know what kind of effect fishing has. In addition, size spectra might have some potential provided theoretical developments or large empirical studies will allow to better predict the effects of fishing and the setting of reference points. From this study also follows that when a synthesis of indicator results is attempted, for example using multivariate methods such as canonical correlation analysis or principal component analysis, indicator results should be weighted appropriately, for example by the inverse of their precision. The choice of indicators to include in the first place should however be guided by their importance with respect to management goals.

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Table 1. Indicators for measuring the impact of fishing on population *i*. Null hypotheses represent no significant impact of fishing. CI = confidence interval.

Indicator	Description	Required information	Model	Estimation method	Null hypothesis H$_0$	H$_0$ Reference	Indicator distribution	Hypothesis test method
r$_i$	intrinsic population growth rate	$N_i(t)$	$N_i(t) = N_i(t-1)e^{r_i} = \lambda_i N_i(t-1)$(1)	$\log(\hat{N}_i(t)) = \alpha_i + r_i t + \varepsilon_{i,t}$ $\varepsilon_{i,t} = \beta_i \varepsilon_{i,t-1} + \omega_{i,t}$ $\omega_{i,t} \sim N(0, \sigma_i^2)$	$r_i = 0$		Normal	0 within 95 % CI of $\hat{r}_i$
Z_i	total mortality	$N_{l,i}(t)$, $t_{0_i}, k_i, L_{\infty_i}$	cohort $N_i(t) = N_i(0)e^{-Z_i t}$ $N_{l,i}(t) = \exp\Big(\ln(N_i(0) - Z_i\Big(t_{0_i} - \frac{1}{k_i}\ln\Big(1 - \frac{l_l}{L_{\infty_i}}\Big)\Big)\Big)$ (2)	GLM: log-link, quasi likelihood with $var \propto mean^{\beta_i}$	$Z_i < Z_i^* = \frac{(L_{\infty_i} - L_{mat_i})k_i}{L_{mat_i} - L_{c_i}}$	Die & Caddy (1997)	Normal	Z_i^* above 95 percentile point of $\hat{Z}_i$
F_i/Z_i	exploitation rate	$C_i(t)$, $N_i(t), Z_i$	$F_i(t) = C_i(t)/N_i(t)$ (3)	$\hat{F}_i(t) = \hat{C}_i(t)/\hat{N}_i(t)$ $\hat{V}[F_i(t)] = \hat{V}[C_i(t)]/\hat{N}_i(t)^2 + \hat{C}_i(t)^2\hat{V}[N_i(t)]/\hat{N}_i(t)^4$ (Kendall & Stuart 1977)	$F_i/Z_i < 0.5$	Alverson & Pereyra (1969)	Normal	0.5 above 95 percentile point of $\hat{F}_i/\hat{Z}_i$
L_{bar_i}	mean length in catch	$C_{l,i}$	$L_{bar_i} = \frac{1}{C_i}\sum_{l=1}^{L} C_{l,i} l_l$ (4)	$\hat{L}_{bar_i} = \frac{1}{\hat{C}_i}\sum_{l=1}^{L}\hat{C}_{l,i} l$ $\hat{V}[\hat{L}_{bar_i}] = \hat{L}_{bar_i}^2 \times \left(\frac{\sum_{l=1}^{L} l_l^2 \hat{V}[\hat{C}_{l,i}]}{\left(\sum_{l=1}^{L} l_l \hat{C}_{l,i}\right)^2} + \frac{\hat{V}[\hat{C}_i]}{\hat{C}_i^2}\right)$	$L_{bar_i} > L_{mat_i}$	Caddy & Mahon (1995)	Normal (central limit theorem)	L_{mat_i} below 5 percentile point of $\hat{L}_{bar_i}$
ΔF_i	Change in F to reverse population growth	F_i, Z_i, α_i, λ_i	$\Delta F_i = \exp(\Delta r / e_F - 1)$ $e_F = \frac{F_i}{\lambda_i}\frac{\lambda_i e^{-Z_i}}{\alpha_i e^{-Z_i} - \lambda_i(1+\alpha_i)}$ $\lambda_i = \exp(r_i)$ (5)	$\hat{e}_F = \frac{\hat{F}_i}{\hat{\lambda}_i}\frac{\hat{\lambda}_i e^{-\hat{Z}_i}}{\alpha_i e^{-\hat{Z}_i} - \hat{\lambda}_i(1+\alpha_i)}$ $\hat{\lambda}_i = \exp(\hat{r}_i + V[\hat{r}_i]/2)$ $\hat{\Delta} r = lowerCI(\hat{r}_i)$	$\Delta F_i\% > 20\%$	Rochet & Trenkel (in prep)	Unknown	$\hat{\Delta F}_i\% > 20\%$

$N_i(t)$ = total abundance of species *i*; k_i & L_{∞_i} = parameters of van Bertalanffy growth model; l = length class; $C_i(t)$ = total catch (discards + landings); $C_{l,i}$ = catch in length class *l*; F_i = fishing mortality; L_{mat_i} = length at maturity; L_{c_i} = length at first capture; α_i = age at maturity; l_l = length of length class *l*; L_i = number of length classes.

Table 2. Indicators and their data requirements for measuring the impact of fishing on a community consisting of S species (i=1, ... S). Null hypotheses represent no current impact of fishing or no change. CI= conf. interv.; LM: linear regression. $N_i(t)$ = abundance of species i; B = biomass; $\bar{L}_i$ = mean length of species i (mature animals); N_l = numbers in length class l; l_l = length of length class l; M = natural mortality; F = fishing mortality; r = intrinsic population growth rate; t = year.

Indicator	Info basis	Estimator	Distribution	Null	Alternative	Test method
Δ_1	$N_i(t)$	$\hat{\Delta}_1 = \frac{\hat{N}}{\hat{N}-1}[1-\sum_{i=1}^{S}(\frac{\hat{N}_i}{\hat{N}})^2]$ $V[\hat{\Delta}_1] \approx \sum_i^S V[\hat{N}_i](\frac{2\hat{N}_i}{\hat{N}^2} - \sum_i \frac{2\hat{N}_i^2}{\hat{N}^3})$ (6)	parametric bootstrap of abundance estimates	no change	increase or decrease	overlapping 95% CI
k-dominance curve	$N_i(t)$	$D_i = \sum_{i=1}^{i} \hat{N}_i/\hat{N} N_i > N_{i+1}$ (7)	parametric bootstrap of abundance estimates	no change	-	rank-wise comparison of CI
Partial dominance curve	$N_i(t)$	$D_k = \sum_{i=1}^{k} \hat{N}_i / \sum_{j=k}^{S} \hat{N}_j N_j < N_1$ (8)	parametric bootstrap of abundance estimates	no change	-	rank-wise comparison of CI
Species composition	$N_i(t)$			species distribution similar in all years	years are different	non-parametric Kruskal-Wallis test
Proportion of non-commercial species: biomass abundance	$B(t), B_n(t)$ $N(t), N_n(t)$ n=non-commercial	$\hat{B}_n(t)/\hat{B}(t)$ (9) $\hat{N}_n(t)/\hat{N}(t)$ (10)	parametric bootstrap of biomass/abundance estimates; GLM binomial distribution with logit-link	$rmlogit(N_n(t)/N(t)) = a + ct$ $c = 0$	increase in proportion of non-commercial species c > 0	empirical bootstrap distribution of time effect
Distribution of mean population length	$\bar{L}_i$	$\hat{\bar{L}}_i = \frac{1}{\hat{N}_i}\sum_{l=l_{mat}}^{L} l_l \hat{N}_{i,l}$		no change	shift to smaller sizes	non-parametric Kolmogorov-Smirnov test
Size – abundance relationship	$N_i(t), \bar{L}_i(t)$	$\log(\hat{N}) = a + b\log(\hat{\bar{L}})$ (11)	Gaussian assumptions	b =0 no trend	$b \neq 0$	F-test
Total biomass Total numbers	$B(t)$ $N(t)$	$\hat{B}(t) = \sum_i B_i(t)$ (12)	unknown	$B(t) = a + ct$ c=0, no trend	$c \neq 0$	Robust regression for time effect
Proportion of piscivores: biomass abundance	$B(t), B_p(t)$ $N(t), N_p(t)$ p=piscivores	$\hat{B}_p(t)/\hat{B}(t)$(13) $\hat{N}_p(t)/\hat{N}(t)$	parametric bootstrap; GLM bin+logit	$\text{logit}(N_p(t)/N(t)) = a + ct$ $c = 0$	decrease in proportion of piscivores c<0	empirical bootstrap distribution of time effect
Average individual Weight, Length (community)	$\bar{b}(t)$ $\bar{l}(t)$	$\bar{b}(t) = \hat{B}(t)/\hat{N}(t)$ (14)	Gaussian assumption	$\bar{b}(t) = a + st$ $s = 0$, no trend	$s \neq 0$	Linear regression $V[\hat{s}] = (t't)^{-1}\bar{V}[\hat{b}(t)]$
Size spectrum	$N_l(t)$	$N_l(t) = a_t \exp^{b_t(l_l-\bar{l})} \exp^{c\sin(l_l-\bar{l})}$ (15)	unknown	$a_t = a$ $b_t = b$ $c_t = c$ no year effect	$a_t \neq a$ $b_t \neq b$ $c_t nec$	model comparison by log-likelihood ratio tests

Table 3. Sources of information used for estimating population and community indicators and their reference points for the impact of fishing.

Information type	Description	Research vessel surveys	Landings & port sampling	Discards sampling
$N(t), N_l(t)$	Population abundance indices (total, by species, by length, by year …)	x		
$B(t)$	Biomass (total, by species, by year..)	x		
$\bar{b}(t)$	Average individual weight	x		
k, L_∞	Growth function parameters	x		
$C(t), C_l(t)$	Catch in numbers (total by species, by length)	x	x	
α	Age at maturity	x		
L_{mat}	length of maturity	x		
L_c	length at first capture		x	x

Table 4. Estimated indicators, hypothesis test results and testing power for Celtic sea groundfish populations. e_F: elasticities of λ to F; Δr: change in intrinsic population growth rate required to significantly invert the population trend. Hypotheses test results: * 5% level; ** 1% level; # test not possible due to lack of information for reference point.

Species	r	std(r)	power	Z	std(Z)	power (98)	F/Z	std(F/Z)	power	F/Z $	L_{bar}	std(l_{bar})	power	e_F	e_F $	Δr	$\Delta F\%$	#sign
Null hypothesis		r = 0			Z>Z*			F/Z<0.5				L_{bar}>L_{ma}					$\Delta F\%$ < 20%	
Argentina silus	-0.89*	0.13	1.0	1.74**	0.42	1	0.004	0.008	0		25.2**	5.4E-03	1	-0.0010		0.64	-100	3
A. sphyraena	-0.83*	0.1	1.0	2.5	0.22	1	0.001	4E-04	0		17.7	2.4E-03	0	-0.0001		0.64	-100	1
Arnoglossus imperialis	0.04	0.29	0.03	0.74	0.08	0.05	0.18	0.14	0.24		13.0	2.2E-03	0	-0.0235		-0.61		0
A. laterna	-0.3*	0.05	0.98	1.75	0.36	0.34	0.01	0.01	0		14.3	8.4E-03	0	-0.0006		0.20	-100	1
Aspitrigla cuculus	-0.06	0.12	0.03	0.75	0.17	1	0.39	0.27	0.89		19.8**	9.0E-04	1	-0.0765		-0.18		1
Callionymus lyra	0.15	0.09	0.09	0.02	0.06	1	0.11	0.09	0		22.4	5.5E-03	0	-0.0120		-0.32		0
Capros aper	0.3	0.11	0.49	3.01	0.29		0.01	0.01	0		10.2#	2.2E-04	NA	NA		-0.51		0
Eutrigla gurnardus	0.25	0.78	0.05	0.84	0.21	0.05	0.85*	1.02	0.98		22.1**	1.1E-03	1	-0.0532		-1.77		2
Gadus morhua	0.13	0.12	0.06	0.13	0.07	0.05	3.71**	3.30	1	0.83	47.6**	1.1E-02	1	-0.4481	-0.14	-0.37		2
Hippoglossoides platessoides	0.19	0.11	0.12	2.45**	0.22	1	0.02	0.03	0		17.1**	3.8E-03	1	-0.0009		-0.42		2
Lepidorhombus whiffigonis	-0.04	0.09	0.03	0.26	0.03	0.05	1.81	1.18	1	0.62	25.7**	2.2E-03	1	-0.2518	-0.09	-0.13		1
Limanda limanda	0.2**	0.01	1.0	1.99**	0.4	1	0.13	0.15	0.21		18.8**	3.6E-03	1	-0.0060		-0.19		3
Lophius budegassa	0.08	0.06	0.05	0.08	0.06	0.05	5.52*	12.97	0.98	0.67	33.1**	1.1E-02	1	-0.3113	-0.05	-0.21		2
L. piscatorius	0.04	0.18	0.03	0.12	0.05	0.05	3.88**	4.20	0.99	0.69	44.6	2.0E-02	0	-0.2487	-0.07	-0.40		1
Merluccius merluccius	-0.12	0.54	0.04	0.73	1.19	1	0.10	0.11	0.01	0.64	23.2**	4.3E-03	1	-0.0124	-0.10	-0.94		1
Merlangius merlangus	0.39	0.13	0.80	0.95	0.11	0.05	0.23	0.16	0.49	0.73	30.2	7.3E-04	0	-0.0223	-0.14	-0.64		0
Micromesistius poutassou	-0.06	0.21	0.03	1.22**	0.13	1	2E-04	1E-04	0	0.64	19.2**	2.6E-03	1	0.0000	-0.09	-0.35		2
Nephrops norvegicus	0.43	0.12	0.93	0..34	0.04	0.05	15.42**	21.80	0.99	0.69	28.3**	5.9E-04	1	-0.8343	-0.09	-0.66		2
Pleuronectes platessa	-0.49	0.68	0.18	0.09	0.06	0.05	3.43**	2.77	1	0.84	27.9**	5.8E-03	1	2.9811	-0.12	-0.84		2
Scomber scombrus	1.35*	0.25	1.0	0.65**	0.08	1	0.12	0.17	0.28	0.63	26.5**	2.6E-03	1	-0.0037	-0.09	-0.86		3
Scyliorhinus canicula	-0.06	0.37	0.03	0.33**	0.05	1	0.19	0.20	0.54		44.3**	1.1E-02	1	-0.0223		-0.66		2
Solea vulgaris	-0.11	0.75	0.03	0.01	0.06	1	0.38	0.81	0.93	0.85	30.3	1.4E-02	0	-0.0562	-0.12	-1.36		0
Trachurus trachurus	-0.16	0.42	0.04	0.85	0.12	0.05	0.01	0.01	0	0.67	23.5**	1.6E-03	1	-0.0013	-0.08	-0.65		1
Trisopterus esmarkii	0.42*	0.07	1.0	0.49	0.05	1	0.01	0.02	0		15.8	1.3E-03	0	-0.0009		-0.29		1
T. minutes	-0.12	0.2	0.04	3.97	0.26	1	0.004	0.005	0		17.1	7.8E-04	0	-0.0001		-0.28		0

Table 5. Hypothesis test results for community indicators for the Celtic Sea groundfish community. All tests are carried out with 5% significance levels.

Indicator	Test result	Sign
Biodiversity Δ_1	no change over time	N
K-dominance curve	no change in shape over time	N
Partial dominance curve	no change in shape over time	N
Species composition	no difference between years : p=0.77	N
Proportion of non-commercial species *	increase in numbers: p=0.002 no increase in biomass: p=0.13	Y N
Distribution of mean length in community	no difference between 1997 and 2000 (p=0.9995)	N
Size-abundance relationship	no linear relationships found; no test possible	na
Total biomass	no linear time trend : p=0.85	N
Total numbers	no linear time trend : p=0.93	N
Proportion of piscivores	no decrease in numbers: p=0.58 no decrease in biomass: p=0.17	N
Average individual weight in community	no linear trend:p=0.713	N
Shape of size spectrum	year effect for intercept: p=0.0295 no year effect for shape parameters: p= 0.828	N

* for names of non-commercial species see Appendix 1

Table 6. Performance and characteristics of indicators for the impact of fishing on the Celtic sea groundfish community and precision of input information. Indicators are ordered by decreasing precision. na= not available.

Performance criteria	Measure	Input information				Indicator estimates													
		$\hat{N}_i(t)$	$\hat{B}_i(t)$	$\hat{D}_i(t)$ *	$\hat{F}_i(t)$	L_{bar_i}	$\hat{\Delta}_1(t)$	size spectrum slope	$\hat{Z}_i(t)$	prop. piscivores biomass	$\hat{B}(t)$	$\hat{N}(t)$	prop. non-comm. abundance	prop. non-comm. biomass	prop. piscivores abundance	$\bar{b}(t)$	$\hat{r}_i$	$\hat{F}_i/\hat{Z}_i(t)$	$\Delta\hat{F}_i$
No. of estimates		100	100	25	100	25	4	4	100	4	4	4	4	4	4	4	100	100	
Precision (%CV)	median	28	28	40	80	0.02	9	1	12	14	16	18	19	21	22	26	93	110	na
	mean	34	33	46	92	0.02	9	10	20	14	15	18	18	22	22	26	204	119	na
Power of hypothesis test	# tests ≥ 0.8					15/25	na	na	7/25	na	na	na	na	na	na	na	7/25	9/25	na
Reference point	status					unknown precision	na	na	unknown precision	direction	na	na	direction	direction	direction	direction	theoretical basis	arbitrary	unknown precision
Type of indicator						pop. state	comm. state	comm. state	pop. state	comm. state	comm. state	comm. state	comm. state	comm. state	comm. state	comm. state	pop. state	fishing pressure	management response

*D= discards

APPENDIX 1

Selected species for an assessment of fishing on the Celtic sea groundfish community. Published information on their life history traits. Commercial species are underlined. PEPA = pelagic planktivore; PEPI= pelagic piscivore; DEBE= demersal benthivore; DEPI= demersal piscivore.

Sources: A=Albert (1991) ; B= Bergstad (1993); D=Dorel et al.; DT=Deniel and Tassel (1986); FT=Fontaine and Theret (1982); Fishbase=Froese and Pauly (1999); G=Gibson and Ezzi (1980);J=Jennings et al. (1999);T=Trouvery (1978); Q=Quéro (1984); R=http://www.ifremer.fr/maerha/life_history.html; V=Verdoit (1999); W=ICES Working Groups (Anonymous 1999, (Anonymous 1999c, 2000, 2001); We=Westhaus (1982). # Whitehead et al. 1986 and Greenstreet 1996.

#	Species	Name	$\alpha[y]$	Source	$\frac{A_{max}(y)}{M[y^{-1}]}$	Source	L$_{mat}$	Source	L	k	Source	trophic group#
1	*Argentina silus*	Greater argentine	4-9	B	30-35	B			42.7	0.21	We	PEPA
									48.87	0.16		
2	*Argentina sphyraena*	Argentine	1.8	F	7	F			28.4	0.41	F	PEPA
3	*Arnoglossus imperialis*	Imperial scaldfish	3	F	11	Q			20	0.26	F	DEBE
4	*Arnoglossus laterna*	Scaldfish	2-3	G	9	G	11	F	21.1	0.26	F	DEBE
5	*Aspitrigla cuculus*	Red gurnard	1.4-2	F	20	F	25	F	43.1	0.31	FT	DEBE
6	*Callionymus lyra*	Dragonet	2.5	J	6	F	17	F	23	0.51	F	DEBE
7	*Capros aper*	Boar fish							19	0.5	guess	DEBE
8	*Eutrigla gurnardus*	Grey gurnard	3.5	F	16	F	24	F	40.5	0.38	FT	DEPI
9	*Gadus morhua*	Cod					59	F	109.5	0.38		DEPI
10	*Hippoglossoides platessoides*	Long rough dab	2-3	Q	10	Q	15	F	40	0.28	F	DEBE
11	*Lepidorhombus whiffigonis*	Megrim	2.8	W	0.2	W	28	F	66	0.11	D,	DEPI
12	*Limanda limanda*	Dab	2.6	DT			29	F	41.8	0.54	DT	DEBE
									36.1	0.63		
13	*Lophius budegassa*	Black anglerfish	7	W	0.15	W			100	0.11	D	DEPI
14	*Lophius piscatorius*	Monkfish	6	W	0.15	W	35	F	150	0.088		DEPI
15	*Merlangius merlangus*	Whiting	2	W	0.2	W	28	F	66.2	0.175	D	DEPI
16	*Merluccius merluccius*	Hake	3.8	W	0.2	W	50	R	127.5	0.074	D	DEPI
17	*Micromesistius poutassou*	Blue whiting	3.2	W, Q, F	16-20	Q, F	22.5	R	39.9	0.15	D	PEPA
			3-5									
18	*Nephrops norvegicus*	Norway lobster		V, W	0.30.2	W	31	W	68.2	0.124	D	DEBE
			3.4						49.2	0.17		
19	*Pleuronectes platessa*	Plaice	3	W	0.12	W	30	R	49.8	0.165	D	DEBE
20	*Scomber scombrus*	Mackerel	2	W, Q, F	6-20	Q, F	30	F, R	36.2	0.49	D	PEPI
			3.5									
21	*Scyliorhinus canicula*	Small-spotted catshark	5	F	22	F	54	F	90.0	0.09- 0.13	R	DEPI
22	*Solea vulgaris*	Sole	3	W	0.1	W	29	R	33.6	0.378	D	DEBE
									42.5	0.278		
23	*Trachurus trachurus*	Horse mackerel	3.5	W, Q	15	Q	24	R	44.9	0.2	T	PEPI
			4.5									
24	*Trisopterus esmarkii*	Norway pout	2.3	J	3-8	Q, F	14	F	23	0.52	J	PEPA
25	*Trisopterus minutes*	Poor cod	1-4	F	5	Q	13	F	33.5	0.18- 0.48	A	DEPI

APPENDIX 2

In the standard linear model $Y = \alpha + \beta X$, the estimated slope β (estimated by least squares) follows the normal distribution $\beta \sim N((X'X)^{-1}X'Y, \sigma^2(X'X)^{-1})$. Given the model is correct, the residual variance is equal to the variance of independent observations and the following estimator applies $\hat{\sigma}^2 = V[\hat{y}]$. In the case of estimating linear time trends of a given indicator, given it can be assumed to be normally distributed, $\hat{\sigma}^2$ is estimated as the average of the annual variances.

The variance of intrinsic growth rate as a function of the coefficient of variation (CV) of abundance indices is estimated approximately based on standard regression theory as $\hat{V}[\hat{r}_i] = (t't)^{-1}\ln(CV[\hat{N}_i]^2 + 1)$ with t the centred time vector. This uses the standard result that for lognormal variables the variance of the log-transformed data is approximately given by $V[\ln(N)] \approx \ln(CV[N]^2 + 1)$. The power function of the hypothesis test for different CV estimates relative to the CV obtained with the actual data can then be calculated.

The variance of total mortality as a function of the variance of the input abundances estimates is obtained using the following approximation based on the log-transformed estimation model (eq 2 in table 1) $V[\hat{Z}_i] \approx (X_i'X_i)^{-1}\ln\left(\frac{1}{L}\sum_{l=1}^{L}\frac{\sqrt{V[\hat{N}_{i,l}]}}{N_{i,l}} + 1\right)$ where L is the number of length classes, X_i is a vector with elements $x_{i,l} = t_{0_i} - \frac{1}{k_i}\ln\left(1 - \frac{l_l}{L_{i,\infty}}\right)$ with l_l the length corresponding to the midpoint of length class l.

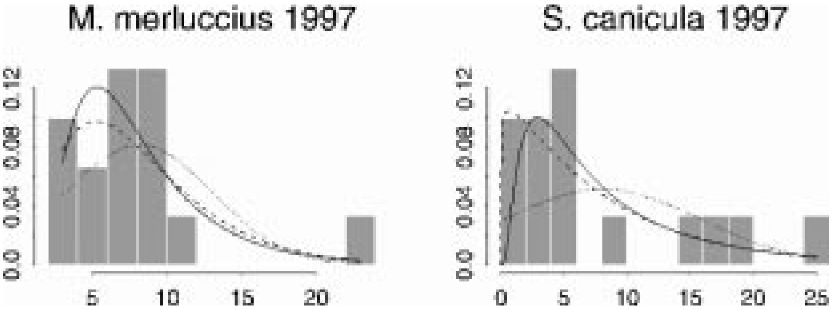


Figure 1: Example empirical distributions of numbers per haul from French Celtic sea groundfish survey. Fitted distributions : Normal (dots), Gamma (solid line), lognormal (broken line).

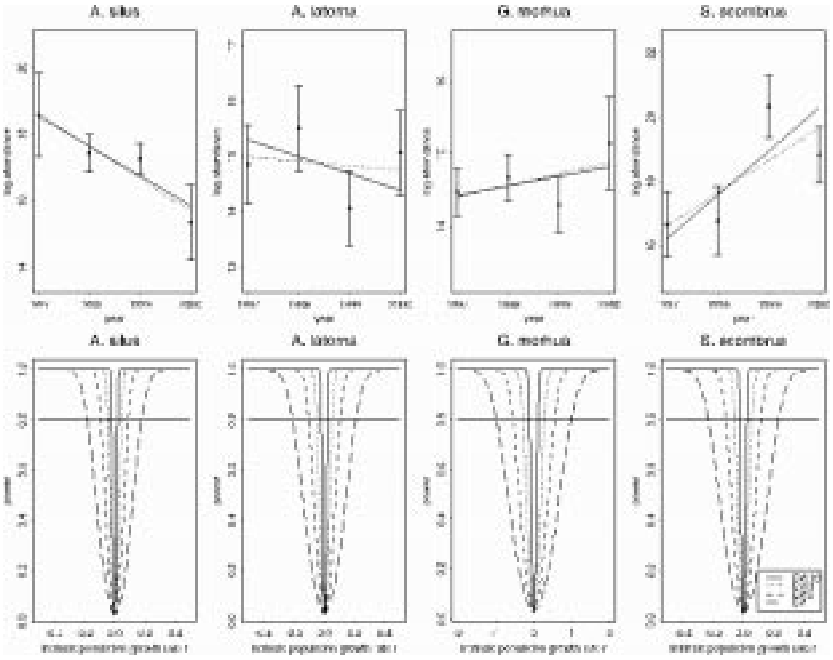


Figure 2: Abundance estimates and intrinsic population growth rate (top row; autoregressive model solid line, linar model broken line) and estimates of power of hypothesis test (bottom row) for H_0 : r=0, for selected species of Celtic sea groundfish community. Two model types have been fitted to explore the effects of autocorrelated errors.

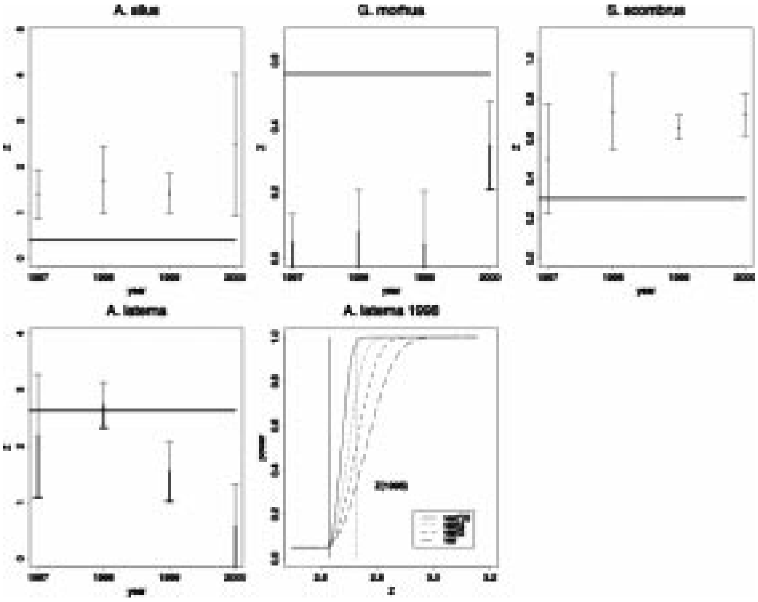


Figure 3: Annual total mortality rate estimates based on equilibrium assumption for selected species of Celtic sea groundfish community (test value Z^* horizontal lines). Example of statistical power of hypothesis test H_0 $Z<Z^*$ for *Arnoglossus laterna* and for different values of variance of input abundance estimates. The vertical dotted line indicates point estimate for total mortality using 1998 data.

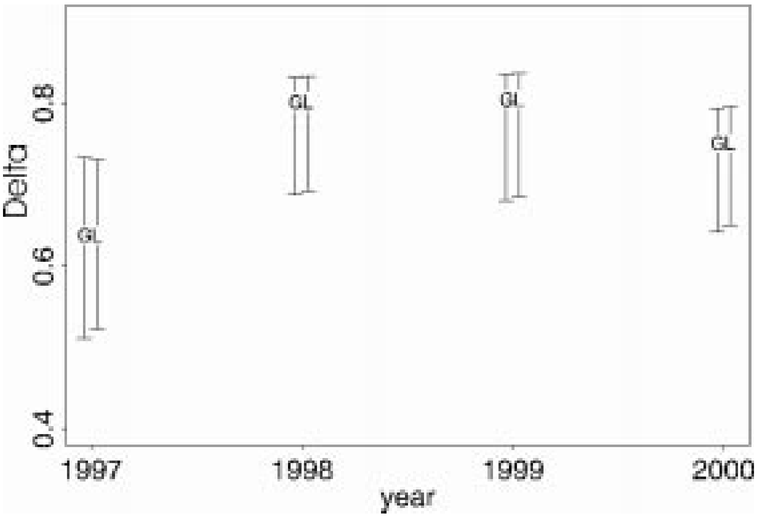
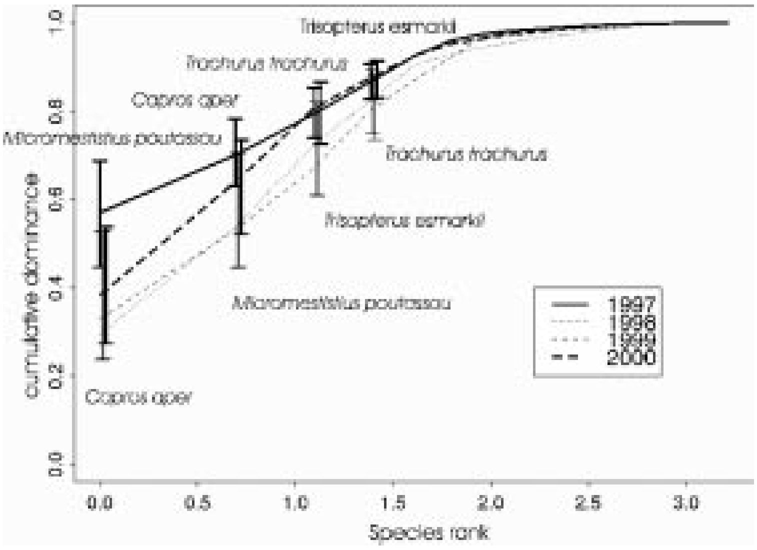


Figure 4: Diversity index Δ_1 (probability of interspecies encounters) with 95% confidence intervals for Celtic sea groundfish community (G=Gamma parametric bootstrap; L= Lognormal parametric bootstrap).

a)



b)

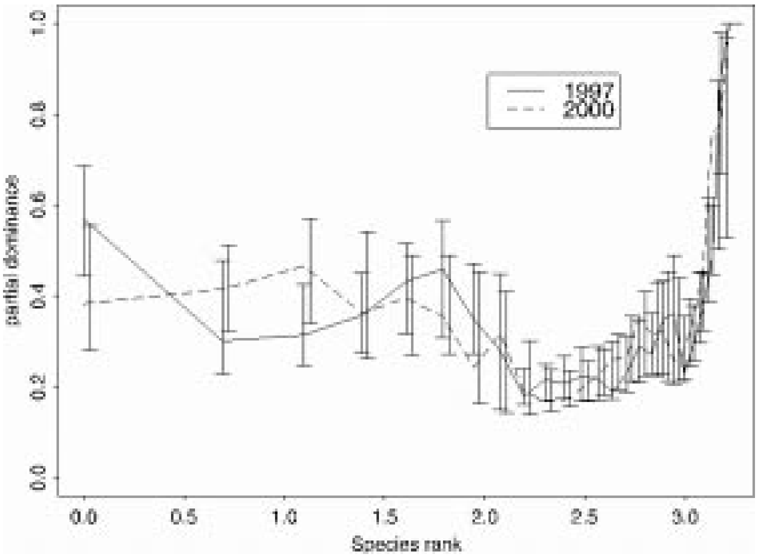


Figure 5: Annual k-dominance curves (a) and partial dominance curves (b) for Celtic sea groundfish community with pointwise 95% confidence intervals (Gamma parametric bootstrap). Dominant species are indicated for 1997 and 2000. Species rank is the logarithm of the rank.

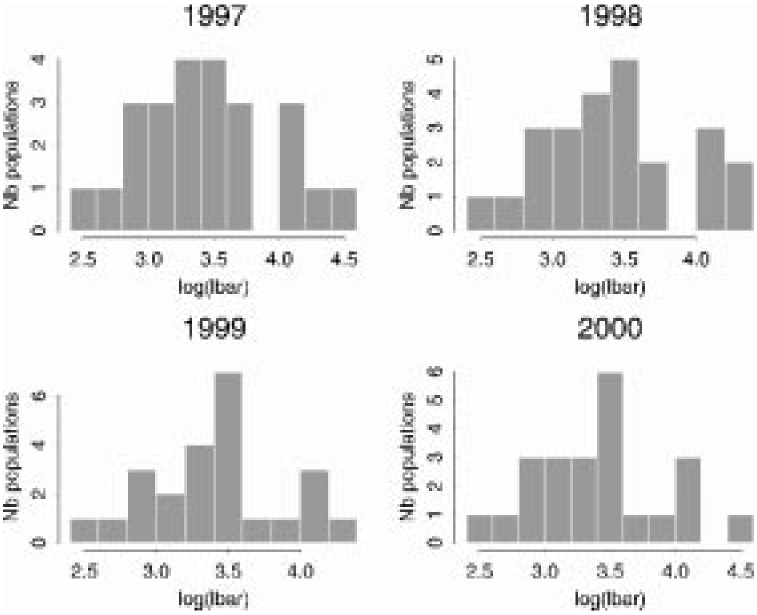


Figure 6: Distribution of mean population lengths (log-transformed) in Celtic sea groundfish community based on representative species selection.

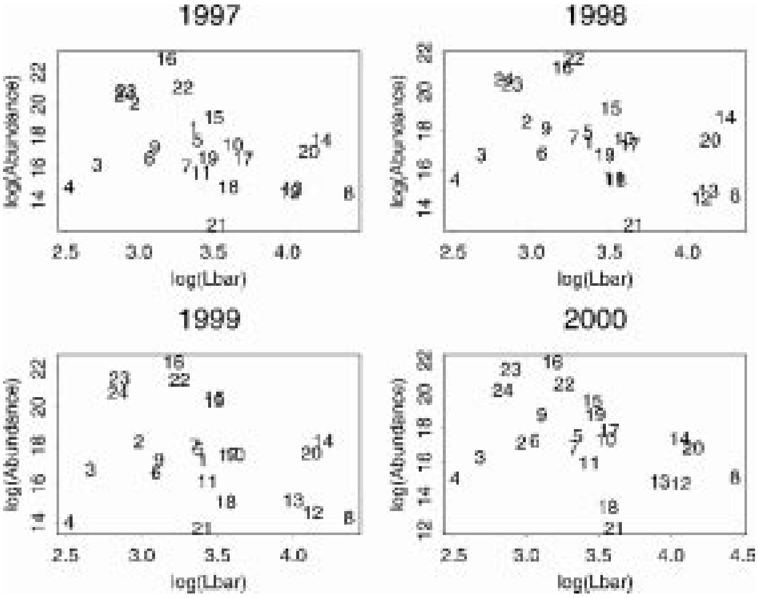


Figure 7: Annual size-abundance relationship on log-scale for Celtic sea groundfish community based on representative species selection; numbers refer to species (see list in Appendix 1).

D.5 Results and recommendations on test runs of Fleksibest with Simulated Annealing (SA)

By Kristin Guldbrandsen Frøysa, IMR, Bergen, Norway

Simulated Annealing is a direct numerical method. Unlike many other numerical methods, the method also allows “uphill” steps, i.e. the method is not always looking for a better solution. By doing so in a sensible way, SA may be able to escape from local optima. For more information, see Corana et.al. and W. L. Goffe. Notation is taken from Goffe. The notation is also consistent with the parameter names in the input file to Gadget/Fleksibest.

The input parameters to SA are:

MAXEVL	Maximum number of function evaluations
T	“Temperature”, a number indicating the probability of accepting an uphill step
RT	The temperature reduction factor, ratio between two different temperature levels.
NT	The number of iterations on a temperature level. Each iteration contains NS*N function evaluations.
N	The number of parameters to be estimated.
EPS	The error tolerance for termination. Note! Termination is based on the likelihood scores from several (i.e. NEPS) temperature levels.
NEPS	The number of temperature levels to be used when determining convergence.
NS	The number of cycles, i.e. how many times the parameters are estimated with the same VM-vector.
ISEED1	First seed for the random number generator.
ISEED2	Second seed for the random number generator.

Input/output parameter:
VM A N-dimensional vector giving the search interval around the present values of the parameters. VM is adjusted NT times at each temperature level. The finale elements in VM are supposed to give indications of how well estimated the individual parameters are.

The main issues

All runs were done with the same 112 parameters to be estimated, and the problem studied is supposed to be a typical case for assessment of NEA cod. The starting point was the parameter values from the official assessment of NEA cod at AFWG2001. Various runs were started to explore how SA works. The main indicator used was the likelihood score. The likelihood score of the AFWG2001 assessment was $1.72*10^7$.

The purposes of the tests were:

1. explore the robustness of SA.
2. find good values for important numerical parameters like the initial temperature T, the temperature reduction factor RT, the number of cycles NS and the number of iterations before temperature reduction, NT.
3. explore whether there exists a unique solution to the present problem and analyse the solutions from runs with different initial temperature and seeds.
4. try to find rules of thumb for when to change from SA to Hooke and Jeeves (HJ).

The results can be summed up as follows:

1. SA is very robust with respect to finding a good solution, even if the starting point is far away from the optimal solution. By a good solution we here mean a solution that has a likelihood score that is close to the lowest score found for the present model. A rather good solution may be found even with a low initial temperature, but to be sure to find a good solution, the initial temperature must be high and RT must also be relatively high. These parameter choices will normally give a very long run, which may take many hours.
2. If nothing is known about the goodness of the initial point (far or close to the optimal solution), the initial temperature should be set to a high value, e.g. a million. If the initial point is supposed to be a fairly close to the solution, an initial temperature between 1000 and 10000 should be chosen. If your initial guess is supposed to be very close to the optimum, you can try an initial temperature of 100, but you should also consider only to use Hooke and Jeeves, as SA is inefficient in such cases. NS and NT should at least be set to five, we think that NS=NT=10 is a good first suggestion. It may be more to gain by increasing NT than to increase NS. RT should be in the range 0.6-0.9, with RT=0.8 as a first try.
3. There seems to be an almost unique solution in this case. Most of the parameters differ less than 5 % between the different runs where the likelihood scores were approximately equal, but the parameters connected to the spread of the mean length growth seem to be unstable, and changed up to 50% from one run to another.
4. Simulated annealing is in general very slow in finding the optimal solution, but it is efficient in finding the area in the parameter space where the solution lies. One thing to try can thus be to run SA over a few temperature levels, and than try HJ. But we have examples of that HJ get trapped into local minima, even if the starting point is rather close to the solution in likelihood score. All solutions found by HJ should thus be tested by a SA run to see if local optima are found. One can also try to change from SA to HJ when SA has reached a reasonable convergence criteria, e.g. that 2 successive temperature levels does not improve the likelihood score by more than 500-1000. But this may be time consuming and inefficient, because SA may be run for hours with little improvement.

General comments to the use of Simulated Annealing:

Simulated annealing is in general a slow, but robust method if the initial temperature and the temperature reduction factor RT are sufficiently high. Thus SA will in principle always be able to find the global optimum or come very close to it, but to a high cost (e.g. a run with 200000 functions evaluations). A high initial temperature may be necessary to remove the possibility of being trapped in a local optimum. A too low initial temperature or a too fast temperature reduction may result in finding a local, not global optimum. To be sure to find the correct solution, the temperature must be set much higher than necessary in most cases, thus the run time will be much longer than needed to find the optimum in most cases. A way around this can be to reduce the initial temperature significantly, and also to consider to reduce the number of function evaluations at each temperature level (i.e. reduce NS and/or NT), and than do several runs with different seeds. By choosing different seeds, the parameter space is searched in completely different ways. We have examples of runs that have converged to a local optimum have converged to a solutions much closer to the global optimum merely by changing the seeds in SA.

By comparing the results from the different runs, one can check if some of the runs have been trapped in local optimum instead of converging to the global optimum. If most of the solutions are rather close to each other, one can use some of those as starting points for new runs with SA (with reduced initial temperature) or with Hooke and Jeeves to get a better solution. It also seems that SA has a tendency to slow down after some temperature levels, i.e. that it may be more to gain by running different runs with a more modest starting temperature and different seeds than running one very long run with high initial temperature and very slow reduction of the temperature. Another possibility is to switch to HJ after a few temperature levels.

Which runs were done?

To test the robustness, we did some runs with two modified optfiles.
Each parameter was changed at random by up to 50 %. We chose two optfiles which gave one order of magnitude higher likelihood score than the original optfile. Even with a very low initial temperature (T=100) and a maximum number of 60000 function evaluations, the best run has a likelihood score that is somewhat better than the likelihood score of the official AFWG2001 assessment. For some of the other runs the likelihood scores are slightly worse than the AFWG2001 result. The most interesting feature in all these runs are that the likelihood score is reduced by one order of magnitude at the first temperature level, and that far the most gain is at that level. Thus SA seems to be efficient to point out the right search area, even if one starts far away from the solution.
A lot of runs were performed with the same starting values (AFWG2001 result) to study the effect of the starting temperature and the temperature reduction factor RT. A maximum of 60000 function evaluations were set in all runs.

Table 1: The table lists the runs performed to study the influence of different initial temperatures and the speed of temperature reduction. All the runs had the same starting parameters.

	Temperature				
RT	40	75	100	1000	10000
0.6			x		
0.75			x		
0.8	x	x	x	x	x
0.85			x		

For all runs with T = 100 or T = 40, the likelihood score was between 1.66756 $*10^7$ and 1.66875$*10^7$, i.e. very similar results. With T= 1000 the score was 1.67253$*10^7$ and with T=10000 the score was 1.69253$*10^7$. For the highest initial temperatures (T=1000 and T=10000), the parameter space may be searched in an inefficient way, by spending too much time searching far away from the optimum. With a limited number of function evaluations, the highest initial temperatures gave the worst results. The parameter values from these runs were not analysed in any detail.

We also did SA runs with the best solution ever found as the starting point. Hardly any improvement was gained, in particular it was demonstrated that an initial temperature higher than 100 was waste of computer time. Thus it was confirmed that there is no use in a too high start temperature if the starting point is a good guess.
Test runs with HJ with starting points taken from good SA runs were performed. For the best solution from SA (which we think is very close to the global optimum), no improvement was found by using HJ. For some of the other initial points minor improvements were found. A HJ run was also performed with the parameters from AFWG2001. There was an improvement in the likelihood score, but the solution did not converge to the best present solution, indicating that a local optimum was found.

D.6 An evaluation of a bioenergetics model for capelin

Draft Manuscript

Geir Huse and Harald Gjøsæter

A bioenergetics model for capelin is presented. The model is established by modifying a herring bioenergetics model. The herring model predicts too low growth based on a time series of input data capelin stomach content and ambient temperature. Arguments about basic ecological differences between herring and capelin, such as differences in ambient temperature and maximum body size, are used to modify the consumption and respiration parts of the model. By increasing consumption at low temperatures, reducing growth dependence on body size, and decreasing the activity level, the model predictions on capelin growth from age 1 to 2 and 2 to 3 were improved substantially. The bioenergetics model developed is recommended for usage on capelin, but more experimental work is called for in order to improve our knowledge of capelin bioenergetics and energy flow in Arctic ecosystems.

Key words: capelin, bioenergetics, herring, growth, Barents Sea, model, consumption,

Geir Huse, Department of Fisheries and Marine Biology, University of Bergen, PO box 7800, N-5020 Bergen,Norway, tel: +47 55 58 44 39, fax: +47 55 58 44 50, email: geir.huse@ifm.uib.no, *Harald Gjøsæter, Institute of Marine Research, PO Box 1870, Nordnes, N-5817 Bergen, Norway, email:*harald@imr.no

Introduction

The Barents Sea capelin (*Mallotus villosus*) is a planktivorous forage species and plays a key role in transferring energy from zooplankton to the higher trophic levels, such as cod and marine mammals (Gjøsæter, 1998). Capelin growth is known to vary extensively between years due to changes in ambient temperature, prey availability and stock density (Gjøsæter and Loeng, 1987; Gjøsæter, 1999). Despite its important ecological role, there is little knowledge of the bioenergetic processes of capelin growth. Bioenergetics models define the mass balance relationship between the amount of food consumed by a fish and its growth (Brandt and Hartmann, 1993). Such models can be used either to estimate consumption of prey from observed growth trajectories, or growth from data on ambient temperature and feeding level (Hewett and Johnson, 1992). The Hewett and Johnson bioenergetics model (H&J, Hewett and Johnson, 1992) relies on a number of equations and parameter values, and since the estimation of these involves a great deal of experiments, the list of species for which parameter values exist, is rather short. It is therefore common to "borrow" bioenergetics expressions from other, related species for which bioenergetics expressions exist (Ney, 1993). The H&J model has been applied on several occasions for calculating the growth of the Barents Sea capelin in spatial models using parameter values for herring (Fiksen *et al.*, 1995; Huse and Giske, 1998). Although herring is a pelagic planktivorous species like the capelin, and adapted to the cold Arcto-Boreal waters, we do not know to which degree the bioenergetics of the two species can be treated as similar for modelling purposes. Since the bioenergetics model relies on a number of parameters and functions, there are many ways to modify the model to accommodate observations. Rather than doing a tuning of arbitrary parameters, it might be fruitful to look for ecologically relevant differences between herring and capelin that can be used to improve the bioenergetics model. There are at least two areas where the species differ; ambient temperature and maximum body size. Capelin tend to have a lower ambient temperature than herring, and can therefore be expected to have a more efficient growth pattern at lower temperatures. While herring can reach a size of 500 g at age 15, Barents Sea capelin rarely get above 30 g at age 5, and their weight at age differs substantially. These differences are likely to be reflected in the bioenergetics of the two species. Also there is great variation in model sensitivity to the different parameters, and especially the model is sensitive to the changes in feeding level and the exponential allometric relationships (Bartell *et al.*, 1986). The objectives of the current study are therefore to evaluate the herring bioenergetics model as a model for capelin growth by using input data taken from capelin surveys in the Barents Sea, and if necessary modify this model to improve its fit with observations of capelin growth. The best model will then be evaluated for its usefulness as a bioenergetics model for capelin.

Materials and methods

Observations of capelin feeding conditions

To test the bioenergetics model we used data on stomach fullness and ambient temperature collected by the Institute of Marine Research (IMR), Bergen. Stomach fullness is recorded by an examination of the visual appearance of the stomach using the scale listed in Table 1. It was assumed that an empty stomach corresponded to a feeding level (P-value in Hewett & Johnson (1992)) of 0, and a full stomach corresponded to a feeding level of 1 (maximum). Between these extremes the feeding level scale is linear. The average stomach fullness index observed for the capelin was used in the analysis. The temperature data that were used are depth integrated over the range 10-200 m. Temperature is recorded for most of the capelin samples, and together these data provide the input necessary to run the bioenergetics model. Only samples where more than 20 capelin stomachs were investigated were included in the current analysis.

Table 1: *The index used by IMR for recording stomach fullness, and the associated feeding level scale used in the bioenergetics model.*

Index	Description	Feeding level
1	Empty	0.00
2	Very little content	0.33
3	Some content	0.66
4	Full	1.00

The bioenergetics model

Bioenergetics models define the mass balance relationship between the amount of food consumed by a fish (C) and its growth (Brandt and Hartmann, 1993). The basic bioenergetics equation is (Hewett and Johnson, 1992):

$$C = R + S + F + U + G \tag{1}$$

where R is respiration, S is specific dynamic action, F is egestion, U excretion and G is growth (negative or positive). A set of functions and parameters are used to estimate each of the variables in Eq. 1. As mentioned above these functions and parameter values differ among species of fish, and it generally involves a great deal of experimental work to figure out the relationships for each variable in Eq. 1. We implemented the equations and parameter values for herring provided by Hewett and Johnson (1992) in a FORTRAN program to estimate capelin growth. The herring parameters are mostly provided by Rudstam (1988). The only external input needed to run this model is ambient temperature and feeding level. This model is extensively documented elsewhere (Hewett and Johnson, 1992), and we will only go into detail where needed.

Results

Field data

The feeding level of capelin was low during winter and relatively high during summer with a peak in July (Fig. 1). The number of samples is divided unevenly over the year, and reflects the survey activity. There is generally good coverage early in the year, and especially in September when there historically has been surveys targeted for capelin. The coverage is particularly poor during November and December, which correspond to the periods of lowest feeding activity in capelin (Fig. 1, Lund (1981)). The input data for bioenergetics model are shown in Fig. 2. The corresponding temperature data show that the highest ambient temperature actually occurs in April and the lowest in November (Fig. 2). Both these months are, however, poorly covered both with regard to capelin samples and temperature measurements (Fig. 1).

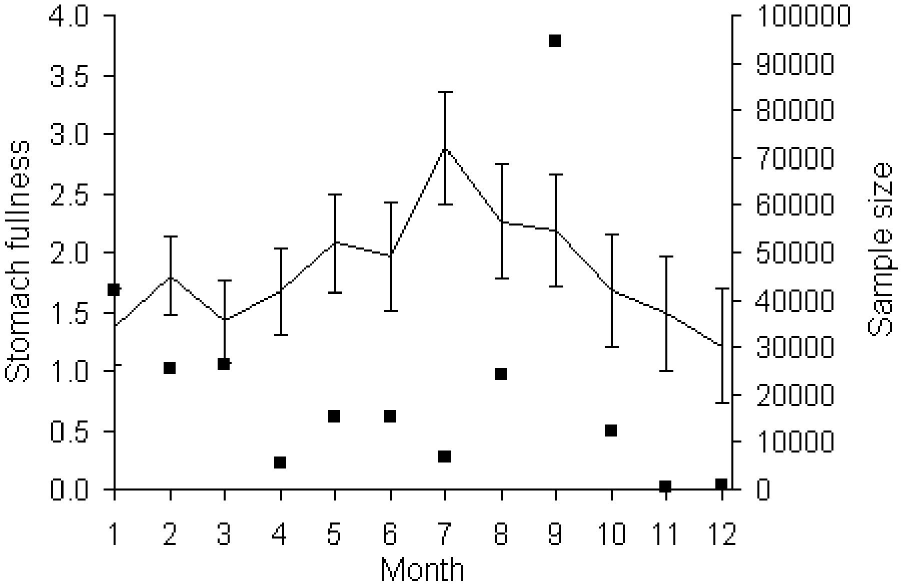


Figure 1: *Average monthly index of stomach fullness (± standard deviation) and number of capelin investigated over the time series 1979-1999 (full squares) based on data from IMR surveys.*

Simulations

We simulated the growth from age 1 to 2 and 2 to 3. The average weight of 1, 2 and 3 year old capelin in September over the time series 1979-1999 was 3.8, 11.1, and 19.1 g respectively. Two year old capelin above 14 cm in length in September tend to spawn the following spring after which they die (Gjøsæter, 1998). In order to simulate the actual growth from age 2 to 3 one has to disregard this maturing component. This was done by basing the average weight of 2 year olds on individuals below 14 cm in length when calculating growth from age 2 to 3. Based on these considerations the average estimate of two year olds not expected to mature the following spring was 8.1 g. Average values rather than values from a single year were used to get coverage over the entire year (Fig. 2).

The standard herring model

Initially we used the H&J model with parameter values for herring to provide growth patterns and size development from ages 1 to 2 and 2 to 3. The model results suggest that the model underestimates the potential for growth at low temperatures for which capelin is well adapted (Fig. 3a). This results in a negative capelin growth over the year, with substantial positive growth only during September (Fig. 3b). The "spike" in the graph around 0°C due to a change in the activity function at this temperature. The results are obviously sensitive to changes in temperature and feeding level. Since there are problems related to transferring the subjective stomach fullness to a feeding level, the growth estimates were given for feeding level increased

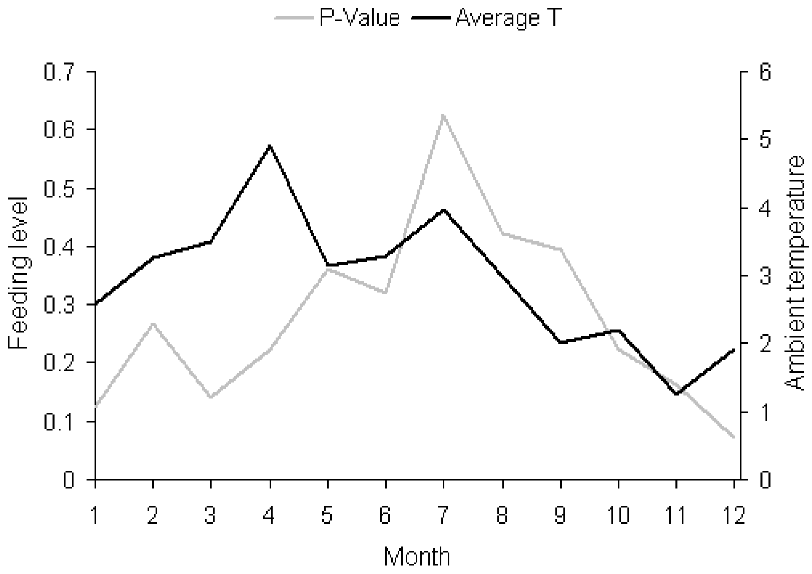


Figure 2: *Average feeding level and ambient temperature of capelin over the time series 1979-1998 used as input data in the bioenergetics model. See Table 1 for conversion between the index of stomach fullness and feeding level.*

and decreased by 25% (Fig. 3b).

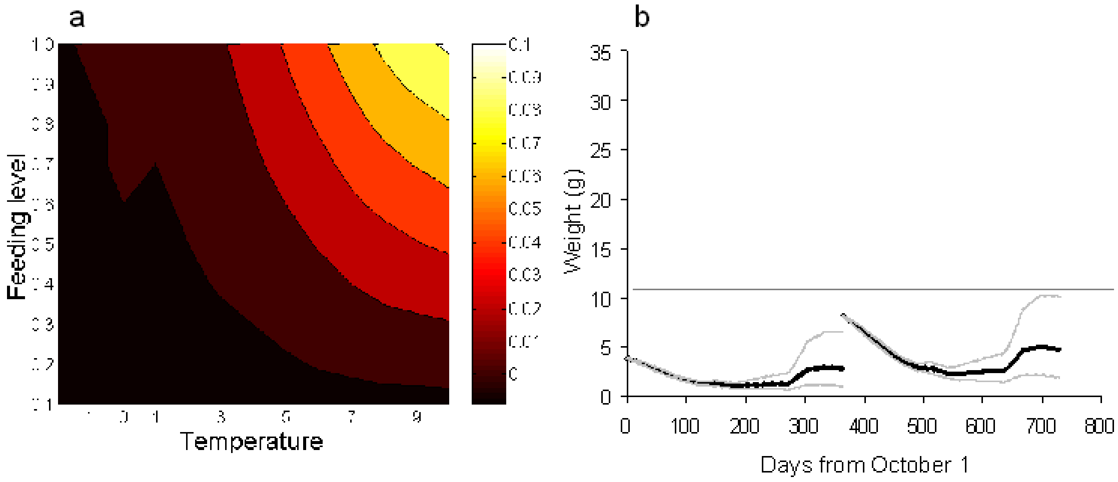


Figure 3: *Growth pattern as a function of feeding level and temperature (a) and simulated growth trajectory (b) from age 1 to 2 and 2 to 3 based on the bioenergetics model with parameter settings for herring. The thin grey lines indicate weight development with a consistently increased and decreased feeding level of 25% respectively. Horizontal lines indicate weight of 2 and 3 year old capelin respectively.*

Modifying consumption

While there is great variation between species in respiration and consumption, there is generally smaller differences in egestion, excretion and specific dynamic action (Bartell *et al.*, 1986). We therefore focussed on modifying relations associated with respiration and consumption. First we modified the bioenergetics model with regard to temperature dependence function in the consumption part of the model. Consumption is estimated as a function of a size specific maximum feeding level (C_{max}), the feeding level (FL), and a temperature dependence function ($F_C(t)$):

$$C = C_{max} \cdot FL \cdot F_C(t) \tag{2}$$

The temperature dependence function is the Thornton & Lessem algorithm (Thornton and Lessem, 1978), a rather complex function that involves several parameter values. We changed the parameter θ of this function, which is the lower temperature at which dependence is 0.1 (for herring) of the maximum rate from 1 to 0. The effect of this change on the temperature dependence function is essentially to increase consumption at lower temperatures (Fig. 4). The effect on growth pattern is seen in Fig. 5a, and as expected the change improves growth conditions for lower water temperatures.

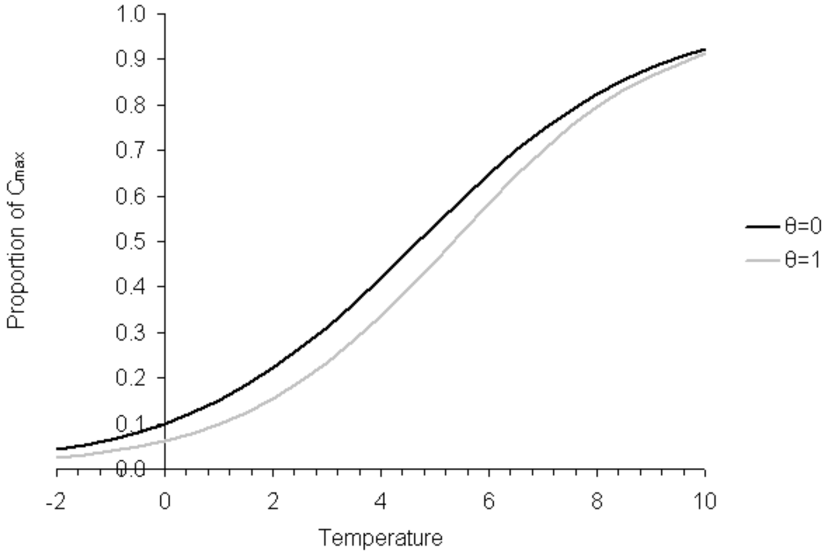


Figure 4: *The consumption dependence on water temperature for the herring model (θ=1) and the suggested capelin model (θ=0).*

Even though the modified temperature dependence function improves model performance, the predicted growth is still below the observed (Fig. 5b). Also the sensitivity to the feeding level or rather body weight, is very strong (high and low lines). This means that errors in the feeding level greatly affects the results. Since capelin is smaller at age than herring we tried to modify the allometric relationship associated with calculating the C_{max} (Eq. 2):

$$C_{max} = a_C \cdot W^{b_C} \tag{3}$$

where W is body weight of fish and a_C and b_C are constants. We reduced b_C from –0.256 to -0.330. This modification decreased the sensitivity to the body size of the fish, but also reduced the growth (Fig. 6).

Modifying respiration
To make growth predictions fit better with the observed weight at age, we modified the respiration part of Eq. 1. The basic equation used to estimate respiration (R) is:

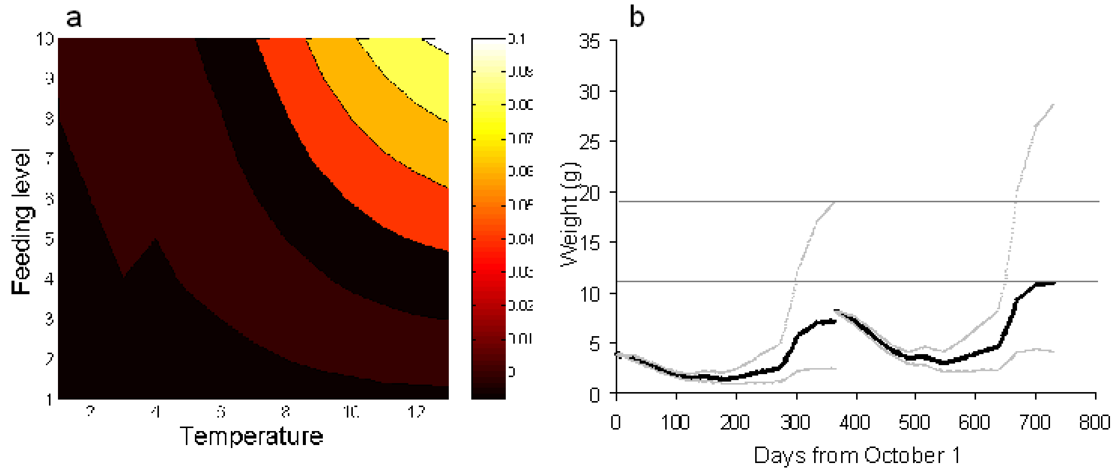


Figure 5: *Growth pattern as a function of feeding level and temperature (a) and simulated growth trajectory (b) from age 1 to 2 and 2 to 3 based on the bioenergetics model with è=0. The remaining model is similar to Hewett & Johnson (1992). The thin grey lines indicate weight development with a consistently increased and decreased feeding level of 25% respectively. Horizontal lines indicate weight of 2 and 3 year old capelin respectively.*

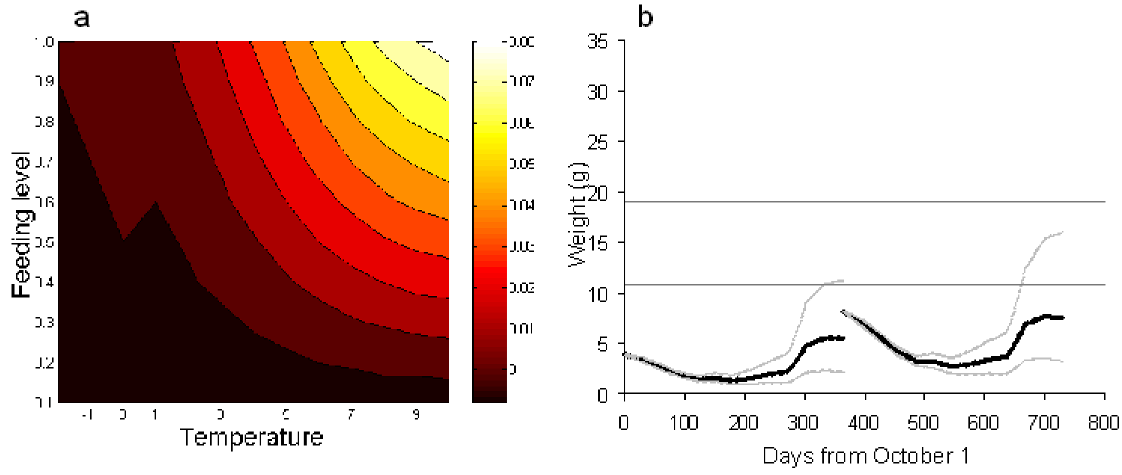


Figure 6: *Growth pattern as a function of feeding level and temperature (a) and simulated growth trajectory (b) from age 1 to 2 and 2 to 3 based on the bioenergetics model with è=0,* b_C *=-0.33. The remaining model is similar to Hewett & Johnson (1992). The thin grey lines indicate weight development with a consistently increased and decreased feeding level of 25% respectively. Horizontal lines indicate weight of 2 and 3 year old capelin respectively.*

$$R = a_R \cdot W^{b_R} \cdot F_R(t) \cdot A \tag{4}$$

where a_R and b_R are constants, $F_R(t)$ is a water temperature dependence function, and A is activity level. Despite the modification of the consumption relationship, the predicted growth is lower than the observed capelin growth. Next we therefore tried modifying the respiration part of the model. This was done by targeting the parameter T_0, which is the coefficient for swimming speed dependence of metabolism in the activity relation:

$$A = e^{(T_0 \cdot V)}$$

where V is swimming velocity in cm s^{-1}. By decreasing T_0, the respiration cost is decreased. When the original value of 0.03 was reduced to 0.012 the growth was increased to fit closely with the observed weight at age of two and three year olds (Fig. 7). The growth prediction is still rather sensitive to body weight (feeding level), but if the original b_C had been kept, the predicted growth for the 25% increased feeding level would be 70 g rather than 35 (Fig. 7).

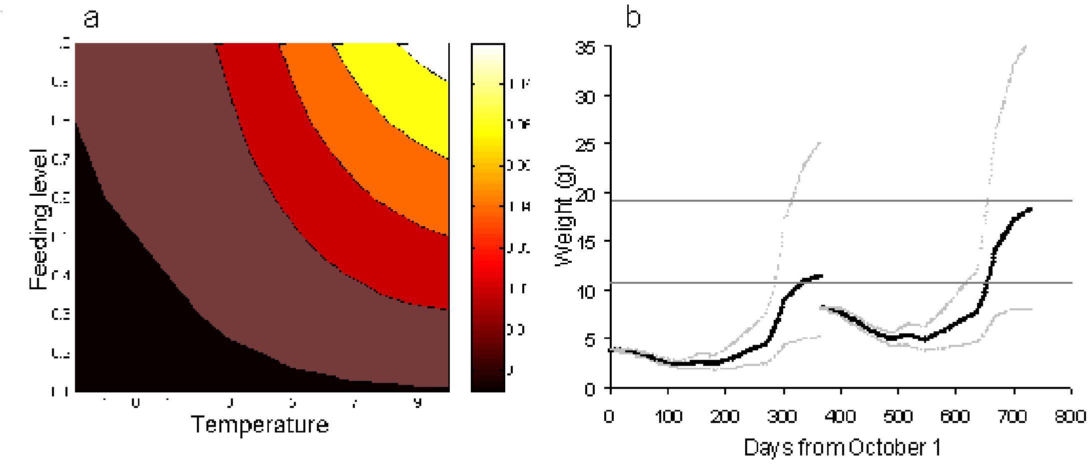


Figure 7: *Growth pattern as a function of feeding level and temperature (a) and simulated growth trajectory (b) from age 1 to 2 and 2 to 3 based on the bioenergetics model with è=0,* $b_C = -0.33$, *and* $T_0=0.012$. *The remaining model is similar to Hewett & Johnson (1992). The thin grey lines indicate weight development with a consistently increased and decreased feeding level of 25% respectively. Horizontal lines indicate weight of 2 and 3 year old capelin respectively.*

Temperature sensitivity
The model results are sensitive to errors in the temperature as well, even though it is even more sensitive to changes in the feeding level. Some sensitivity runs for age 2 to 3 showed that with a consistent increase and decrease of 25% respectively in ambient temperature, the growth prediction for the final model (Fig. 7) increased and decreased by 83% and 44% respectively. Similar numbers for 10% changes are 28% and 22%. This illustrates the dependence of the results of bioenergetics models on correct estimates of ambient temperature.

Discussion

Due to the prominent role of capelin in many ecosystems, it is important to have knowledge about its growth dynamics. Even though there have been performed extensive studies of capelin growth in relation to climatic factors and zooplankton abundance (Gjøsæter and Loeng, 1987; Hassel *et al.*, 1991; Skjoldal *et al.*, 1992; Gjøsæter, 1998), there has been little or no experimental work to improve the understanding of the bioenergetics of capelin growth. Such information is needed for existing models relating to the ecology of capelin (Fiksen *et al.*, 1995; Huse and Giske, 1998), and can potentially be used in management models.

The annual life cycle of the Barents Sea capelin is reflected in the observations of feeding level and ambient temperature (Fig. 2). During summer the capelin feed in frontal areas in the northern part of the Barents Sea, hence the lower ambient temperature during summer than winter. Lund (1981) found that the feeding level of capelin was at its highest during the fall. The present data suggest that the feeding activity peaked during summer, but there was still a high feeding activity during August to September. During the winter the feeding activity is rather low, but in spring the capelin feed on krill and may have a rather high feeding level (Lund, 1981).

Although the observed temperature and feeding level data are average values with a rather crude resolution in time and space, the results suggest that the herring model underestimates growth substantially for the low ambient temperatures at which capelin live. By a set of modifications, the model performance was improved to eventually provide a model of somewhat robustness. For this final model (Fig. 7) the predictions compared relatively well with observations of capelin growth, but the sensitivity of the bioenergetics model to the feeding level and temperature shows that the interpretation of the stomach fullness index into feeding level (Table 1) is a key issue in this respect. The reduced growth over the winter months seen in the growth simulations corresponds to changes in fat level of capelin (Vilhjálmsson, 1994). Since the lost fat is replaced by water there is not a similar change in the body weight of capelin.

Since capelin is a key species in sub-Arctic ecosystems in the Atlantic and Pacific, it is important to understand its growth dynamics. Bioenergetics models are nice tools for analysing the consequences of changing conditions on the growth of fish species. This contribution shows that by building on the bioenergetics relations established for herring, a model for capelin may be established. As of yet we recommend using the developed model for simulating capelin growth, since it is an improvement over existing models. Nevertheless care should be taken since the model is not based on experimental work on capelin. We hope that the current contribution can motivate more experimental work to improve our understanding of capelin growth and the energy flow in the Barents Sea and similar ecosystems.

Acknowledgements

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D.7 Natural mortality of juvenile herring (Clupea harengus L.) in the Barents Sea due to predation by North-east Arctic cod (Gadus morhua L.).

Geir Odd Johansen, Bjarte Bogstad, Sigbjørn Mehl, Øyvind Ulltang

Johansen, G.O.; Bogstad, B.; Mehl, S.; Ulltang, Ø. xxxx. Natural mortality of juvenile herring (*Clupea harengus* l.) in the Barents Sea due to predation by North-east Arctic cod (*Gadus morhua* l.). MANUSCRIPT.

Geir Odd Johansen: University of Bergen. Department of Fisheries and Marine Biology, PO Box 7800, N-5020 Bergen, Norway.
e-mail: geir.johansen@ifm.uib.no

Introduction

The natural mortality of juvenile herring in the Barents Sea is highly variable between years. Hamre (1994) puts forward a hypothesis on the relationship between herring, capelin (*Mallotus villosus* Müller 1776) and cod (*Gadus morhua* L.) in the Barents Sea. He points out that the herring is important for the interactions in the fish community of the Barents Sea, both as food for cod and as a predator on capelin larvae. He also points out that the interaction between cod and herring depends on the size of the capelin stock, as cod seems to prefer this species to herring. Year classes of Norwegian spring-spawning herring that are abundant at the 0-group stage can be strongly reduced during the first years of life (Barros and Toresen, 1998). Barros et al. (1998) found that more than 90% of this inter-cohort variation in mortality can be explained by the ratio between the abundances of capelin and juvenile cod. They suggested that when the capelin-cod ratio is low, the cod consume more juvenile herring than if the ratio is high, to compensate for the shortage of capelin. This is in accordance with Hamre's hypothesis.

In this paper these hypotheses about the predator-prey interaction between cod and herring in the Barents Sea will be tested for the first time with data on herring consumption by cod. Consumption of juvenile Norwegian spring–spawning herring by North-east Arctic cod will be estimated from the cod stomach data from the Barents Sea.

Materials and methods

Stomach content data from cod were taken from the joint IMR-PINRO stomach database at the Institute of Marine Research (IMR) in Bergen, Norway. This database includes stomachs sampled at both Norwegian and Russian regular demersal fish surveys in 1984-1997. Most of these surveys are not targeted for stomach sampling. Most of the cod were caught by bottom trawl, mainly in the first quarter of the year and in September/October. A detailed description of the general survey methodology can be found in Jakobsen et al. (1997) and Lepesevich & Shevelev (1997). Some of the data are from surveys of pelagic fish and shrimp. The sampling design has undergone modifications during the period of interest to this study. The maximum number of stomach samples per 5 cm group of cod has changed from two in 1992-95 to one after 1995 (Bogstad *et al.*, 1995; Jakobsen *et al.*, 1997). Details about the sampling procedures are given in Mehl (1989) and Mehl & Yaragina (1992).

In this study the analyses were restricted to the period 1992-97. In the period 1992-93 there was a gradual change in the methods for recording the prey size of herring, from 5 cm to 1 cm groups. The material sampled before 1992 was therefore considered to be too imprecise for this study.

The data were divided into five sample intervals of the year, motivated by the temporal distribution of hauls. The sample intervals were defined as: 1 Jan-31 Mar, 1 Apr-31 May, 1 Jun-9 Jul, 10 Jul-15 Oct, and 16 Oct-31 Dec. In the following they are referred to as interval 1-5, respectively. Note that the temporal and spatial distribution of hauls varied between years and intervals. A detailed description of the temporal structuring, and the temporal and spatial distribution of the hauls representing the raw data is given by Johansen (Johansen, 2002).

Consumption of herring by individual cod was estimated as number of herring consumed per time unit, referred to as predation rate. This limited the analysis to prey that was counted. The estimates were based on estimating the digestion times for the consumed herring, i.e. the time the prey has been digested in the stomach of the predator. Digestion times were estimated by using a gastric evacuation model (GEM), which describe the reduction in weight of a prey in a predator stomach due to digestion as a function of time (Bromley, 1994). A similar approach is described in Mergardt & Temming (1997) for estimating the diel pattern of food intake in whiting (*Merlangius merlangus* L.). Digestion times for herring were estimated by relating the weight of the partly digested prey (W_p) in the cod stomach to the weight of that prey when it was ingested (W_f). The weight of ingested prey was estimated from a length-weight regression based on survey data from the Institute of Marine Research (IMR) in Bergen. The residuals in a log-linear length-weight regression were found to be curvilinear (Pepin, 1995), and as a result a polynomial length-weight relationship were fitted:

$$Log(W_f) = \alpha + \beta Log(L) + \gamma Log(L)^2, \tag{1}$$

where W_f = weight of fresh prey and L = total body length of prey (cm). This limited the analysis to prey with measured lengths only. This resulted in 862 herring observations from 436 stomachs.

Gastric evacuation model (GEM)

The GEM used in this study is based on the general GEM:

$$\frac{dS}{dt} = -R \times S^B \tag{2}$$

(Jones, 1974), with variables S = the stomach content weight (g), R = standard evacuation rate, b = constant defining degree of curvilinearity. Integrating (2) gives:

$$S_t = \left[S_0^{(1-B)} - R(1-B)t \right]^{\frac{1}{1-B}} \tag{3}$$

for $B \neq 1$. In this model S_t = stomach content at time t (g), t = time after ingestion and S_0 = initial stomach content (g). R incorporates the effects of temperature, food type predator size and other factors (Jones, 1974).

Following Temming & Andersen (1994), (3) was expanded to a multivariable model describing the effects of temperature, predator size and meal size:

$$S_t = \left[M^{1-B} - R' e^{AT} W^C M^D (1-B)t\right]^{\frac{1}{1-B}} \tag{4}$$

with additional variables M = meal size (g) (substitute for S_0), T = temperature (°C), W = predator weight (g), and parameters A = temperature coefficient, C= predator weight coefficient, D = meal size coefficient and R' = food type constant. According to Temming & Andersen (1994), the effect of including the meal size correction on R' is negligible when fitting the GEM to experimental data. They recommend the use of a simpler model without this term:

$$S_t = \left[M^{1-B} - R' e^{AT} W^C (1-B)t\right]^{\frac{1}{1-B}} \tag{5}$$

Back-calculation of digestion times for individual cod.

To calculate digestion times of herring, equation (5) was rearranged to:

$$t = \frac{(S_t^{(1-B)} - M^{(1-B)})}{-R' e^{AT} W^C (1-B)} \tag{6}$$

where t is an estimate of digestion time. Substituting W_p for S_t and W_f (from (1)) for M enables the estimation of the digestion time of a herring of weight W_p and length L in the stomach. Parameters B = 0.43, R' = 0.02886, A = 0.137, and C = 0.047 are estimates from gastric evacuation experiments reported in Temming & Andersen (1994). Temperature was taken from a digital temperature atlas for the Barents Sea based on IMRs hydrographic measurements. The temperature was averaged for 50 m and below at each station, and then averaged in space for each area.

Consumption estimates

Predation rate for cod containing measurable herring of the given 2 cm group was estimated as the number of prey in the stomach with an estimated digestion time $\leq t_{max}$, divided by t_{max}. For each size group of herring, digestion time was obtained from (6) using the environmental temperature and setting cod weight equal to the median weight of cod that had measurable herring of the given size group in the stomach for data from 1992-97 (Table 1). t_{max} was defined as the lower limit of the time range within which all herring were measurable and was found by plotting the cumulative frequency of measurable herring as a function of digestion time grouped within 1-hour intervals. Assuming a stable feeding rate for cod, there is an expected linear relationship between these variables, until the digestion time reaches a level where herring starts to become immeasurable due to digestion. This breakpoint in the relationship defines t_{max}. The breakpoint was found by visual inspection of the plot and the residuals of a linear regression of the relationship (Figure 1). Assuming that the herring becomes immeasurable when a certain proportion of its weight is digested, and setting predator weight constant, rearranging (6) gives a log-linear relationship between herring body length ($TL_{herring}$) and t_{max}. Linear regression of this relationship at the reference temperature 4°C ($T4$) ($\ln(t_{\max}) = -1.3829 + 1.6442 \ln(TL_{herring})$, df = 8, $r^2 = 0.96$, $p < 0.0001$), was used to estimate t_{max} for different 2 cm size groups of herring (Table 1). t_{max} at other temperatures for the same size groups were estimated by the relationship

$$t_{\max,T} = \frac{\exp(A \cdot T4)}{\exp(A \cdot T)} \cdot t_{\max,T4}$$

.

Mean predation rate for cod containing measurable herring was estimated for each age group of herring, a and each length group of cod, L as:

$$\mu_{a,L} = \frac{1}{n_L} \sum_{j=1}^{n_L} \sum_{i=1}^{m_{a,j}} \left(\frac{y_{a,j,i}}{t_{\max}} \right), \tag{7}$$

where $y_{a,j,i}$ = number of herring of age a in herring observation i in cod stomach j with digestion time = t_{max}, $m_{a,j}$ = number of length measurable herring observations of age a in cod stomach j, n_L = number of cod stomachs in length group L containing length measurable herring. The mean predation rate is expressed as number of herring consumed per cod per hour.

Consumption was then calculated for each year, time interval, area, age group of herring and length group of cod as:

$$C_{y,q,s,a,L} = N_{y,q,s,L} \times P_{y,q,s,L} \times \mu_{y,q,s,a,L} \times h_q, \tag{8}$$

where $N_{y,q,s,L}$ = number of cod of length group L in year y, interval q and area s, $P_{y,q,s,L}$ = proportion of all cod stomachs from length group L sampled in year y, interval q and area s, containing measurable herring, $\grave{\imath}_{y,q,s,a,L}$ = the year, interval and area specific mean predation rate as defined in (7), and h_q = duration in hours of interval q. The areas used correspond to the strata systems used by IMR during standard bottom trawl surveys on demersal fish in the Barents Sea in winter and autumn (Figure 2). The winter system where used in intervals 1-2, and the autumn system in intervals 3-5. In the following the areas will be denoted *strata*.

Age of herring in the cod stomachs was estimated with length-at-age relationships for juvenile spring spawning herring in the Barents Sea, based on survey data on length at age from the Institute of Marine Research (IMR) in Bergen, Norway (Appendix I). The length-at-age relationships were based on 13 235 individual juvenile herring from an area north of 68°N and east of 19°E in the period 1992-97. Age was determined with scales or otoliths. Only data where the age zones were easy to count (defined as quality 1 and 2 in the database at IMR) were selected, to increase the precision of the length-at-age relationships. In intervals with missing data, the upper length limit of an age group was taken from the same year class in the next interval. Exceptions were 1-group in interval 1 in 1996 and 1997, and 2-group in interval 1 in 1997, where upper limits were taken from interval 3 in the respective age groups and years. This procedure relies on an assumption of limited growth of juvenile herring in the Barents Sea during the winter period, as observed by Orlova et al. (Orlova *et al.*, 1995). Note that for 1-group in interval 3 in 1995, the upper limit is the mean for all years in this interval. This was done because the upper limit of an age group could not be transferred backwards from interval 4 to 3 due to extensive growth in this period of the year.

Abundance of cod ($N_{y,q,s,L}$) was calculated by scaling the bottom trawl survey index to the VPA estimate of total abundance in the following way: The number at age A in the beginning of year y, $NV_{y,A}$ is available from the VPA (ICES, 2001). The stock abundance in time period q can then be calculated as $NV_{y,q,A} = NV_{y,A}e^{-(F_{y,A}+M_{y,A})t_q/12}$, where t_q is the number of months from the start of the year to the mid-point of time period q. F and M is the fishing mortality and natural mortality, respectively. Adjustments also need to be made for the proportion of the total stock that is outside the survey area: One should adjust for the proportion by age found in the Lofoten (ICES, 2001) and Svalbard areas for the winter survey (intervals 1 and 2). For the summer survey, one may assume that the entire stock is covered.

Assume that a survey estimate of abundance by stratum s and length L is available at time q in year y, $n_{,y,q,s,L}$. The total survey estimate (entire area) of age A fish is given by $n_{\ y,q,A}$. These abundance indices are calculated in the same way as described in Jakobsen et al. (1997). Age-length keys are calculated on main areas o consisting of several strata. Let $R_{y,q,o,A,L}$ be the proportion of fish in year y, interval q and main area o, which is of age A and length L.

The survey-to-VPA scaling factor by age is given by: $\alpha_{y,q,A} = \frac{NV_{y,q,A}}{n_{y,q,A}}$

One can then calculate abundance by length in each main area using the age-length key, and use this to calculate the abundance by length in each stratum:

The abundance by length in each main area is given by:

$$N_{y,q,o,L} = \sum_A n_{y,q,o,A}\alpha_{y,q,A}R_{y,q,o,A,L}$$

and the abundance by length in each strata by

$$N_{y,q,s,L} = \frac{n_{y,q,s,L}}{n_{y,q,o,L}} N_{y,q,o,L}$$

Note that swept-area estimates from autumn 1995 were used in autumn 1994, because of missing data.

The consumption estimates were summed over length groups of cod and strata to get total consumption of different age groups of herring in each interval.

Some extrapolation was needed to estimate the yearly consumption, due to variable temporal and spatial coverage in the temperature and stomach data. The temperature data were given on a quarterly basis, and data from quarters 1, 2, 3 and 4 were used to estimate temperature in intervals 1, 2, 4 and 5, respectively. For interval 3 temperature data for quarter 2 and 3 was combined. In quarter 4 in 1994-1997 some stratum means were missing, and were estimated as follows: The difference between average temperature in stratum s in year y and quarter Q ($\overline{T_{y,Q,s}}$) and the year and quarter specific mean temperature for the 0-200 m depth range from the Russian hydrographic section off the Kola peninsula ($\overline{K_{y,Q}}$) (Tereshchenko, 1996) were calculated for the period 1992-1997 as: $dif_{y,Q,s} = \overline{T_{y,Q,s}} - \overline{K_{y,Q}}$. A linear regression of these differences in quarters 3 and 4 ($\text{dif}_{y,4,s}$ = -0.0092 + 0.8566 ($\text{dif}_{y,3,s}$), df = 37, r^2 = 0.81, $p <$ 0.0001), combined with the mean Kola section temperature in quarter 4 was used to estimate the missing stratum means.

The stomach data were segregated on size groups of cod and age groups of herring. Results from Johansen (Johansen, 2002; 200x) were used to set the rules used when extrapolating. If a stratum contained < 5 trawl hauls with stomach samples, predation rates, averaged over the neighboring strata with = 5 hauls with stomach samples in the same interval, was extrapolated in space. The proportion of cod with measurable herring in their stomachs was calculated for the neighboring strata combined. If neighboring strata also lacked sufficient data, temporal extrapolation from other intervals was carried out, preferably from the same stratum. In intervals 1-2 this was done if the target stratum had < 2 neighboring strata with = 5 hauls with stomach samples, while in intervals 3-5 only 1 neighboring stratum with sufficient data was required. In interval 1 in 1995-1997 missing data in stratum 9 were completed with data from stratum 8, as this is the only neighboring stratum. If the stratum contained some hauls with herring, these data were included in the average. In cases of spatial extrapolation to strata where predation on herring by cod only takes place in parts of the stratum, or the intensity of predation is lower compared to the main areas (Johansen, 2002), the proportion of cod with measurable herring in their stomachs was corrected according to the approximate proportion of the cod population assumed to consume herring in that strata (Figure 2).

An overview of the scheme for temporal extrapolation of the predation rate is given in Table 2. In interval 1, 2 and 3, similar spatial distribution of herring in cod stomachs was assumed (Johansen, 2002). Note that the strata system used in interval 3 was different from intervals 1 and 2, because the distribution of cod in interval 3 is more similar to the distribution found during the autumn survey. In interval 4 and 5 similar spatial distribution of one year and older herring in cod stomachs was assumed (Johansen, 2002); Johansen 200x), except from stratum 11 (Figure 2). Herring is not found in cod stomachs in this stratum in interval 5 (Johansen, 2002). In interval 5, 0-group herring has a more southeastern distribution compared to interval 4 (R. Toresen IMR pers com.), and is not found in stomachs west of 36°E (Johansen 200x). For this age group the total average for all strata in interval 4 was applied to strata 17 and 130 in interval 5.

The consumption estimates were compared to estimates of herring stock sizes and mortalities derived from acoustic surveys of immature herring carried out in the Barents Sea in May/June each year (Toresen *et al.*, 1998). Cod's accumulated consumption of 1-group herring in intervals 3-5 in year y and of 2-group herring in intervals 1-2 in year y+1 (C_{1-2}) was compared to $N_{1,y} - N_{2,y+1}$, where $N_{1,y}$, $N_{2,y+1}$ are the estimated herring stock sizes of 1- and 2-group during the acoustic surveys. The total instantaneous mortality coefficients generated by cod on herring were estimated by $\ln(N_{1,y}/N_{2,y+1}) \times C_{1-2}/(N_{1,y} - N_{2,y+1})$. The analysis was limited to the 1991-1992 year classes of herring because the relative precision of the acoustic estimates of the following weak year classes was considered too low for such calculations.

Database operations, calculations and statistical analysis were done with SAS 8.1 for Windows (SAS Institute Inc., Cary, NC, USA).

Results

Estimates of consumption of juvenile herring by cod in the Barents Sea in the period 1992-1997 are given in Table 3.

Comparison between the consumption estimates and estimates of herring stock sizes and mortalities derived from acoustic surveys of immature herring will be included in the complete manuscript.

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Tables

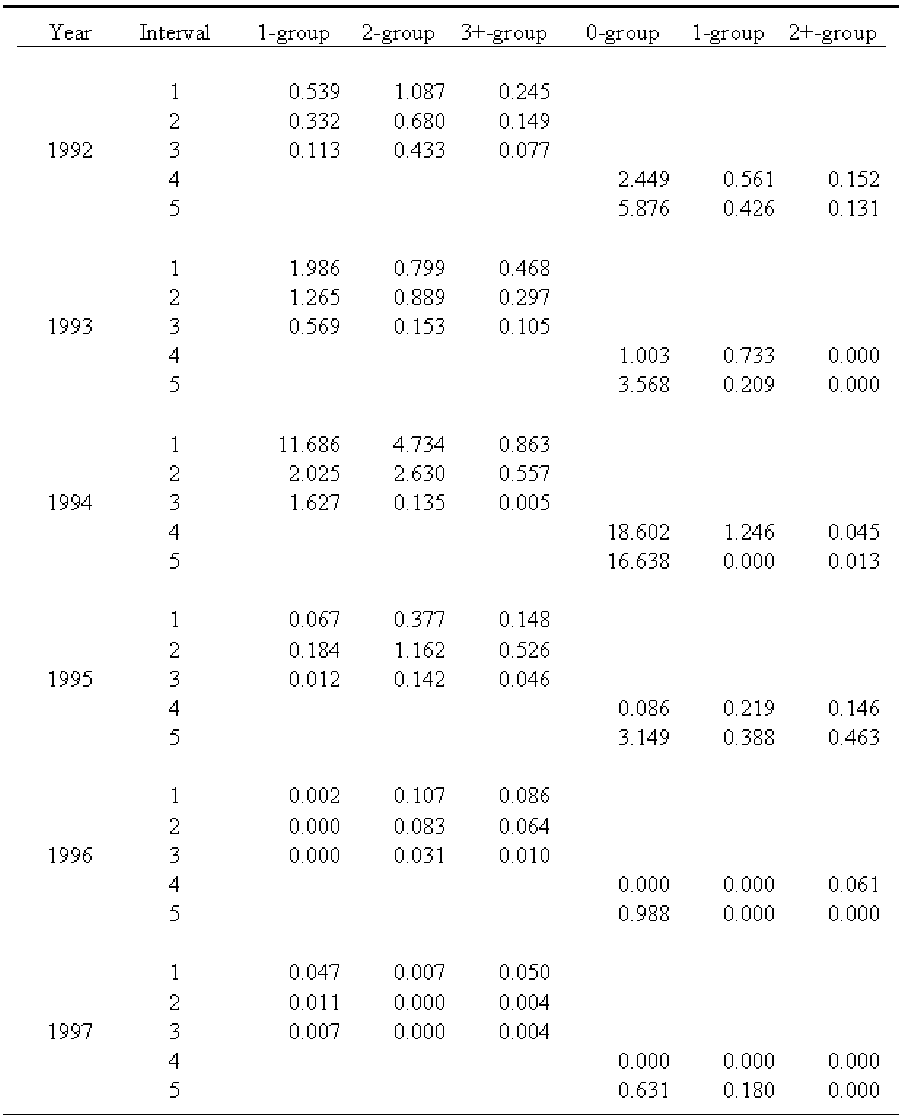
Table 1: Length of herring in 2 cm groups (TL herring) and median weight of the cod (W_{med} cod) used to find the hypothetical breakpoint in the relationship between the cumulative frequency of measurable herring as a function of digestion time grouped within 1-hour intervals. Data are from 1992-97. Maximum time range (t_{max}) in hours within which all the herring within the given 2 cm group were measurable at 4°C is estimated by: $\ln(t_{\max}) = -1.3829 + 1.6442 \ln(TL_{herring})$

TL herring (cm)	n	W_{med} cod (kg)	t_{max} (h)
< 8	42	0.98	6.151
8 - 10	53	0.93	9.298
10 - 12	41	1.11	12.932
12 - 14	57	1.38	17.020
14 - 16	86	1.71	21.535
16 - 18	116	1.88	26.456
18 - 20	91	2.90	31.764
20 - 22	52	3.72	37.446
22 - 24	30	3.55	43.488
> 24	39	3.73	49.878

Table 2: Scheme for temporal extrapolation of data.

Interval	Strata	Interval extrapolated from	Strata extrapolated from	Herringage
2	All	1	The same	All
3	14 (summer strata)	1	Average of 1, 4, 5 (winter strata)	All
3	15 (summer strata)	1	Average of 2, 4, 6 (winter strata)	All
3	16 (summer strata)	1	Average of 7, 8, 11, 12 (winter strata)	All
3	160 (summer strata)	1	Average of 7, 8 (winter strata)	All
3	17 (summer strata)	1	Average of 7, 8, 13 (winter strata)	All
5	All, except 11	4	The same	1+
5	17, 130	4	Average of all strata	0

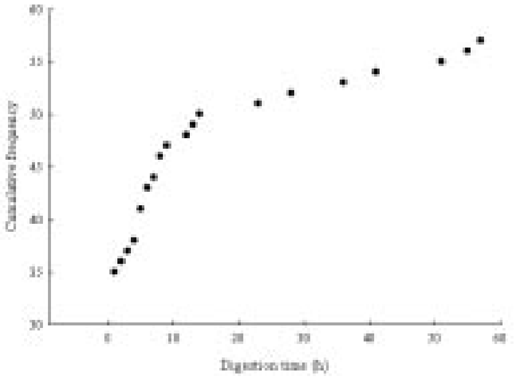
Table 3. Consumption of juvenile herring in the Barents Sea by Northeast Arctic cod in the period 1992-1997. The estimates are in billion individuals.



Year	Interval	1-group	2-group	3+-group	0-group	1-group	2+-group
1992	1	0.539	1.087	0.245			
	2	0.332	0.680	0.149			
	3	0.113	0.433	0.077			
	4				2.449	0.561	0.152
	5				5.876	0.426	0.131
1993	1	1.986	0.799	0.468			
	2	1.265	0.889	0.297			
	3	0.569	0.153	0.105			
	4				1.003	0.733	0.000
	5				3.568	0.209	0.000
1994	1	11.686	4.734	0.863			
	2	2.025	2.630	0.557			
	3	1.627	0.135	0.005			
	4				18.602	1.246	0.045
	5				16.638	0.000	0.013
1995	1	0.067	0.377	0.148			
	2	0.184	1.162	0.526			
	3	0.012	0.142	0.046			
	4				0.086	0.219	0.146
	5				3.149	0.388	0.463
1996	1	0.002	0.107	0.086			
	2	0.000	0.083	0.064			
	3	0.000	0.031	0.010			
	4				0.000	0.000	0.061
	5				0.988	0.000	0.000
1997	1	0.047	0.007	0.050			
	2	0.011	0.000	0.004			
	3	0.007	0.000	0.004			
	4				0.000	0.000	0.000
	5				0.631	0.180	0.000

Figure 1

a)



b)

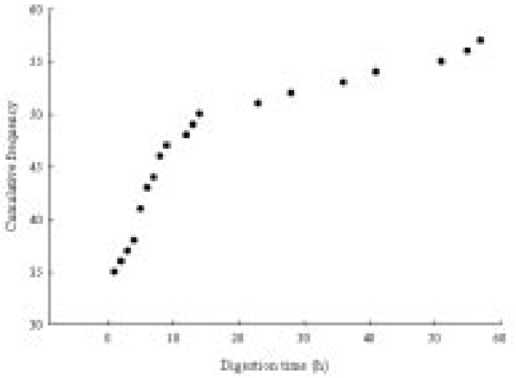


Figure 1. Example of the relationship between digestion time and cumulative frequency of observations within 1-hour groups (a), and the residuals from a simple linear regression of this relationship (b). Temperature was set to 4°C and the size group of herring was 12-14 cm. Arrows indicates how the breakpoints were found by visual inspection of the plots.

Figure 2

Figure 2. Stratification and extrapolation scheme for estimating consumption of herring in the Barents Sea in 1992-97. Crosshatching, right slanting and left slanting indicates extrapolation to 100%, 50 % or 25% of the cod population in that stratum, respectively. In cases where only a part of a stratum is hatched, the hatching indicates the spatial distribution of herring in cod stomachs in that stratum. a, b and c indicates sampling intervals 1-2, 3 and 4-5 respectively.

D.8 Using AMOEBAs to Integrate Multispecies, Multifleet Fisheries Advice

ICES CM 2001/Session T

Jeremy Collie, Henrik Gislason, and Morten Vinther

In multispecies fish communities, predation levels change dynamically in response to changes in the abundance of predator and prey species, as influenced by the fisheries that exploit them. Until community-level biological reference points (BRPs) can be identified, it remains necessary to track the abundance of each species relative to its BRP. In situations with many interacting species exploited by multiple fishing fleets it can be complicated to illustrate how the effort of each fleet will affect the abundance of each species. We have adapted the AMOEBA approach to graph the reference levels of multiple interacting species exploited by multiple fleets. This method is illustrated with ten species and eight fishing fleets in the North Sea. We fit a relatively simple response-surface model to the predictions of a fully age structured multispecies model. The response-surface model links the AMOEBA for fishing effort to a separate AMOEBAs for spawning stock biomass and other quantities of interest. Ordination is used to give the shape of the AMOEBAs functional meaning. The aim is to present the results of dynamic multispecies models in a format that can be readily understood by decision makers. Interactive versions of the AMOEBAs can be used to identify desirable combinations of effort levels and to test the compatibility of the set of single-species BPRs.

J. Collie: University of Rhode Island, Graduate School of Oceanography, Narragansett, RI 02882, USA [tel: +1 401 874 6859, fax: +1 401 874 6240, e-mail: jcollie@gso.uri.edu, H. Gislason, University of Copenhagen, c/o Danish Institute for Fisheries Research, Charlottenlund Castle, 2920 Charlottenlund, Denmark [tel: +45 3396 3361, fax: +45 3396 3333 e-mail: hg@dfu.min.dk, M. Vinther, Danish Institute for Fisheries Research, Charlottenlund Castle, 2920 Charlottenlund, Denmark [tel: +45 3396 3353, fax: +45 3396 3333, e-mail: mv@dfu.min.dk]

Introduction

There is widespread acceptance that an ecosystem perspective is needed to manage marine fisheries (NRC 1999,) but much less practical experience on how to do so. It is now recognized that ecosystems themselves cannot be managed; it is the human users of ecosystems that must be regulated (Bax 1999). In marine fisheries, two approaches have emerged for incorportating ecosystem considerations into management decisions (Murawski 2000). One is to identify indicators of ecosystem status, ecosystem health, and ecosystem services ( ). The metrics of community ecology, such as species diversity and indices and size spectra, can be borrowed (Rice 2000). Ecological quality objectives represent one attempt to make ecosystem indices operational (ref). However, for most ecosystem indices there is little theoretical understanding of how they respond to harvesting, or what a desirable reference level of the index should be (Larkin 1996). The concept of ecosystem health seems an intuitive analogy with the human body, but it breaks down on closer examination because there is no homeostasis in ecosystems (Link). We can recognize a sick or disturbed ecosystem when we see it, but as yet have no objective measure of ecosystem health.

An alternative approach is to incorporate additional ecosystem constraints into traditional management decisions. These constraints have been considered as additional levers to nudge the management process toward meeting ecosystem, or at least community-level objectives (Bax 1999). Another way to view these constraints is that they additional dimensions or objectives to be satisfied in fishery management plans. Examples of ecosystem constraints are limits on the take marine mammals in fisheries, catch limits on forage fish to preserve their predators, and area closures to protect structural epifauna. Progress can be expected with both approaches, but in the short-term it will be more pragmatic to incorporate ecosystem considerations as

additional constraints to existing fishery management plans (Murawski 2000).
Among the most important ecosystem considerations in marine fish communities are trophic interactions among the fish species. There is empirical evidence that the mortality rate of prey species depends on predator abundance and, conversely, that predator growth rates depend on prey abundance (Collie 2001). Competition among fish species is more difficult to demonstrate empirically, but its existence is implied by most energy budgets, which show that fish production is ultimately limited by production at lower trophic levels (ref?).
There is a strong parallel between the two approaches to incorporating ecosystem considerations and the types of multispecies models used for each approach. Models of the entire ecosystem (e.g. network models, dynamic ecosystem models) should lend themselves to the derivation of ecosystem metrics (Hollowed et al. 2000). On the other hand, community-level models of interacting species are more useful for adding ecosystem constraints to the single-species models that are widely used in fisheries management. A second dichotomy is whether the multispecies models is age structured or just tracks the total abundance or biomass of each species (Hollowed et al. 2000); age-structured models are most widely used in the management of temperate marine fish.
The European Common Fisheries Policy has multiple objectives (Halliday and Pinhorn 1996). In the short term these are a) to ensure the continuity of each stock as a commercially viable resource; b) to decrease the fishing effort in overexploited stocks in order to ensures yields that are stable from year to year; and c) to ensure the highest possible catch from stocks, consistent with a) and b) and taking into account the relationship among stocks. ICES provides biological advice to the EU on meeting these objectives. Precautionary biomass (B_{pa}) and fishing mortality (F_{pa}) levels have been established for each stock to meet objectives a) and b). Objective c) implies that fishery yields should be maximized, subject to the biological constraints and multispecies interactions.
When does multispecies advice matter in fisheries management? In the short term, the feeding requirements of predators must be considered when setting annual harvest quotas for forage fish species (e.g. capelin off Norway). In the medium term, biological reference points may need to be adjusted to account for variable predation rates on prey species and variable growth rates of predators (Collie and Gislason 2001). Long-term management strategies need to account for the implicit trade-offs in prey and predator yields (May et al. 1979). In boreal ecosystems with a small number of interacting species, it may be straightforward to condition the reference levels of a target species on the abundances of interacting species. In temperate ecosystems with a large number of fish species, the increased dimensionality necessitates different approaches.
Age-structured multispecies models (e.g. MSFOR) can be used to investigate the consequences of different fishing mortality rates while accounting for predator-prey interactions (Gislason). Such projections have not been routinely used in fisheries management, partly because of their intensive data and computing requirements, but mainly because the increased complexity of multispecies models is thought to hinder decision making (Brugge and Holden 1991). Pope (1989) proposed fitting a simpler response-surface model to the results of the more complicated multispecies model, and then using the response-surface model to investigate alternative levels of fishing effort. The ICES Multispecies Assessment Working Group used a multispecies Schaefer or Fox model fit to the projections of the MSFOR model (ICES 1992). This approach greatly simplifies the multispecies model, but leaves the problem of visualizing the results in as many dimensions as there are interacting species and fishing fleets. Joint levels of $F_{0.1}$ and F_{msy} for interacting fishing fleets can be calculated (Pope 1989) but such community-wide indices do not insure that reference levels for individual species will be met.

Pope (1997) emphasized that “waterver model of complex, multispecies, multifleet, multiarea fisheries is adapted, it will be of little use in the real world unless its results can be presented to the managers in as clear and unambiguous fashion as possible.” The results of multispecies models can be presented with decision tables or radar plots. AMOEBAs are extensions of radar plots that can be useful for visualizing multidimensional situations in which several constraints must be met simultaneously (Laane and Peters 1993). Pioneered in the Netherlands in the context of water quality objectives, AMOEBA is the Dutch acronym for “a general method of ecosystem description and assessment” (Ten Brink et al. 1991). The use of AMOEBAs has also been proposed for meeting ecological quality objectives in the North Sea (Scheveningen conference 1999).

In this paper we show how AMOEBAs can be used to visualize the results of multispecies models applied to the North Sea fish community. We extend the AMOEBA concept by giving the shape of the AMOEBA functional meaning and by making them change dynamically in response to changing effort levels. The ultimate objective of this work is to present the results of multispecies fishery models in a format that can readily understood and used by decision makers.

Methods

In this paper we analyzed the multispecies, multifleet fishery of the North Sea. Multispecies VPA and projections were made using the 4M program (Vinther et al., 2001). 4M (Multi-species, Multi-Fleet and Multi-Area Model) package is a newer and extended implementation of the MSVPA/MSFOR programs previously used by the ICES Multispecies Assessment Working Group.

The forecasts were based on an MSVPA run similar to the so-called ”key-run” made at the last Multispecies Assessment Working Group Meeting (ICES 1997). This MSVPA included data for ten VPA species (Table 1) for the period 1974-1995 such that 1996 became the first projection year. Recruitment in the projections was assumed to follow a Ricker stock-recruitment relation fitted to the MSVPA output. This was done for all VPA species except North Sea mackerel for which an arithmetic mean of the estimated recruits in 1986-1995 was used. Abundance of species without analytical assessment (“other predators”) was kept constant at the 1995 level in the projections.

Fishing mortalities (F) estimated for 1995 by the MSVPA were used as base line or status quo levels in the projections. These F values were partitioned to partial F by fleet according to catch numbers given by the STCF database (Anon., 1991; Lewy et al., 1992, which includes detailed catch information for 56 national fleets fishing in the North Sea in 1991. These 56 fleets were aggregated into eight new fleets defined by the gear used or target species; the “Other” fleet includes national fleets that didn’t fit the grouping. Average partial F over the age range used by ICES in the calculation of reference F values, are presented in Table 2. The exploitation pattern and the relative importance (of what ?) have changed considerably since 1991 and the projection results of management options must be interpreted with care.

Projections of yield and spawning stock biomass (SSB) were made for the *status quo F*, and with changes in F of plus/minus 10%, 25% and 50% for both all fleets combined, and by individual fleet. Each projection was run for 50 years to a (near) equilibrium state. The 4M model accounts for discarded catch but only the retained yield was modelled with the multispecies logistic model. Response-surface models were fit to the projections in which fishing effort for each fleet was increased by 10% in turn. The projections with fishing effort reduced by 25% were used to compare the predictions of the simple response-surface model with those of the age-structured 4M model.

The response-surface model is a multispecies production model of either the Schaefer or Fox form. Separate parameters were estimated to predict changes in spawning stock biomass (SSB) or yield in weight. The subscript s indicates the species (s=1, ... ,n) and g indicates the fleet (g=1,..,m). With the Schaefer model, the equilibrium SSB for species s is:

$$SSB_s = a_s - \sum_g b_{sg}\varepsilon_g$$

where ϵ_g is the fishing effort in fleet g scaled relative to the fishing effort in a reference year (1995). The parameters of the model $\{a,\, b\}$ are estimated from the partial derivatives

$$\frac{\partial SSB_s}{\partial \varepsilon_g} = -b_{sg}$$

For each species, *SSB* was predicted with the 4M model for the status quo effort level and a 10% increase in the effort of each fleet in turn. These calculations can be expressed in matrix notation as:

$$S = E \cdot B$$

where S is an $(m{+}1){\times}n$ matrix of *SSB* values, E is an $(m{+}1){\times}(m{+}1)$ matrix of ones with ϵ_g on the diagonal and B is the $(m{+}1){\times}n$ matrix of parameter estimates, with one column for each species. This system of equations was solved by inverting the effort change matrix, *E*.

Analagous equations can be written to predict the equilibrium yield of a given fleet, f:

$$Y_{sf} = \alpha_{sf}\varepsilon_f - \sum_g \beta_{sfg}\varepsilon_f\varepsilon_g$$

Dividing by ϵ_f, yield per unit effort, *YPUE* is:

$$YPUE_{sf} = \alpha_{sf} - \sum_g \beta_{sfg}\varepsilon_g$$

The parameters of this model α, β can be estimated by calculating a Jacobian matrix of:

$$\frac{\partial YPUE_{sf}}{\partial \varepsilon_g} = -\beta_{sfg}$$

where g indexes all the fleets. In matrix notation,

$$U = E \cdot P$$

where U is an $(m{+}1){\times}n$ matrix of *YPUE* values and E is the $(m{+}1){\times}(m{+}1)$ effort-change matrix. The $(m{+}1){\times}n$ matrix of parameter estimates, P can be estimated from the inverse of *E*, and once obtained it can be used to predict yield for different levels of fishing effort. A separate yield model was estimated for each fishing fleet. Fishing mortality rates corresponding to different combinations of fishing effort were calculated as:

$$F_s = \sum_g \varepsilon_g F_{sg}^{1995}$$

where the partial fishing mortalities in 1995 were taken from Table 2.

AMOEBA plots were used to display changes in SSB, yield and fishing mortality resulting from changes in fishing effort. Ordination of the status-quo table of yields by species and fleets was

used to calculate angles for the AMOEBAs. The PCA loadings gave the angles for the fishing fleets and the PCA scores gave the corresponding angles for the fish species. The AMOEBAs were then used to investigate the consequences of different combinations of fishing effort.
Effort levels corresponding to the multispecies maximum sustainable yield (msy) can be found by maximizing the yield of each fleet as defined in Eq. 4. Let

$$Y_f = \sum_s Y_{sf}$$

$$\alpha_f = \sum_s \alpha_{sf}$$

$$\beta_{fg} = \sum_s \beta_{sfg}$$

be the aggregate values for fleet f summed over species. Then aggregate yield can be expressed as

(10)

$$Y_f = \alpha_f \varepsilon_f - \sum_g \beta_{fg} \varepsilon_f \varepsilon_g$$

The partial derivative of yield with respect to effort in fleet f is:

$$\frac{\partial Y_f}{\partial \varepsilon_f} = \alpha_f - \sum_{g \neq f} \beta_{fg} \varepsilon_g - 2\beta_{ff} \varepsilon_f$$

The multispecies msy is obtained when these partial derivatives are set to zero for all fleets simultaneously (Pope 1989). Let B be the $m \times m$ matrix with -2β_{ff} on the main diagonal and -β_{fg} in the remainder. In vector notation, msy is obtained when

$$\underline{\alpha} = B \cdot E_{msy}$$

and the vector E_{msy} can be obtained from the inverse of B. Effort levels for maximum economic yield (E_{mey}) can be approximated by assuming that at status quo effort levels fishing costs equal the revenue or yield (Pope 1997). Then E_{msy} can be obtained from:

$$\underline{\alpha} - Y_{sq} = B \cdot E_{mey}$$

where Y_{sq} is the vector of status quo yields for each fleets. Further constraints on the effort levels may be required to ensure that the SSBs of all species are above the precautionary levels (B_{pa}) and that the fishing mortality rates are below F_{pa}. Bounded nonlinear optimization was used to identify a set of effort levels to maximize yield while ensuring SSB $\geq B_{pa}$ and $F \leq F_{pa}$ for all species.

Results

The predictions of SSB and yield with a 25% decrease in effort for all fleets agree very well with the projections from the 4M model (Fig. 1). In this validation, the multispecies production model was used to predict conditions other than the data that were used to estimate the model parameters. This close agreement indicates that the simpler response-surface model captures the main dynamics of the fishery and can be used to investigate different effort combinations, within a range around the status-quo levels.

The multispecies projections incorporate both technical and biological interactions (Table 3). Technical interactions occur because most fishing gears catch more than one species. Beam trawls catch sole and plaice and thus the SSB of both species would increase with a decrease in effort in the beam trawl fleet. Biological interactions occur because of predation among the modeled species. For example a decrease in seine effort would lead to an *increase* in the SSB of the predator cod and but would *decrease* herring SSB because of increased predation. These species interactions can be plotted in three dimensions for a single species and pairs of fleets. Haddock SSB would *increase* with decreased effort in the trawl fishery and *decrease* with decreased effort in the industrial fishery due to increased abundance of the predators cod, whiting, and saithe (Fig. 2).

Ordination was used to project the entire table of fleet-by-species interactions in two dimensions. The first two principal components accounted for 55% of the variance in the status-quo yield table. In the AMOEBA plots, the directions of the fleet vectors correspond to the directions of the species caught by that fishing gear (Fig. 3). It can easily be seen that sandeel is caught by the industrial fishery and that sole and place are caught with beam trawls. The orientation of these arrows makes it easier to see which species will be affected by changes in fishing effort of particular fishing fleets.

With status quo effort levels, plaice, whiting, and cod SSB would all be below their precautionary biomass (B_{pa}) levels, and plaice, sole, cod, saithe, and herring fishing mortality would exceed the precautionary (F_{pa}) levels (Fig. 3). The MSY effort levels were much higher than status quo for several of the fleets (Table 4), but yields in the industrial, seine, and saithe fleets would increase only slightly. At E_{msy}, SSB would be below B_{pa} for all species except sole, mackerel, Norway pout, and sandeel, and fishing mortality would exceed F_{pa} for all species except mackerel and Norway pout.

Effort levels for maximum economic yield (E_{mey}) were all less than the status quo except for the fixed gear (Table 4). Neither E_{msy} nor E_{mey} was well defined for fixed gear, as there was a tendency for these estimate to take extreme values [check the parameter estimates]. For the remaining fleets E_{mey} was less than one because fishing costs were assumed to exceed revenues at high effort levels. At E_{mey} cod SSB would be below B_{pa} and fishing mortality would exceed F_{pa} for plaice, cod, and herring (Fig. 4), but all the other biological constraints would be met. With bounded nonlinear optimization, a combinations of effort levels was identified that would satisfy all the biological constraints while maximizing yield (Table 4). This combination required substantial reduction in the industrial, pelagic, and trawl fleets in order to raise cod SSB above B_{pa} and to decrease fishing mortality on cod and herring (Fig. 5).

Discussion

We have shown how AMOEBAs can be constructed and used to display the main interactions in a multispecies, multifleet fishery on a single page. These plots sufficiently capture the orthogonal nature of the fishery objectives. The biological objectives require satisfying the B_{pa} and F_{pa} constraints for each species. Our results indicate that these constraints can be jointly met even when predator-prey interactions are included. For the prey species, the benefits of decreased fishing mortality appear to outweigh the increased predation mortality that occurs that occurs with increased predator abundance. At the optimal effort levels (Table 4) the SSB of all species would be higher than the status quo levels. This result differs from earlier MSFOR projections in which the result of increased mesh size was to decrease the yields of the prey species (Pope 1991). The earlier MSFOR projections did not include stock-recruitment relationships and thus decoupled recruitment from fishing mortality. In the 4M model, recruitment of the prey species increases with lower fishing mortality and higher SSB. However, the stock-recruitment relationships remain uncertain because they were fit to short time series of variable data. The incorporation of the stock-recruitment relationships also tends to cause oscillations in the projected abundances.

Economic objectives operate at the fleet level. We used the yield in weight of each fleet as a surrogate for economic performance. It would be preferable to express yield in monetary units to account for price differences among species. However, we lacked price data that were appropriately averaged over time, subfleets, and size of fish. Therefore, in our estimate of MEY we implicitly assumed that the value per weight of each fleet's catch would remain constant with different effort levels. Pope (1997) also found that attaining MEY would require reducing effort in the roundfish and industrial fleets, with the other fleets kept near their status quo levels.

Social objectives are usually expressed at a finer level of geographic detail (e.g. fishing ports) than the main fleets in our model. One approach would be to include an AMOEBA for social objectives (e.g. employment) an to assume that ports with similar gears would be similarly affected by effort changes (Pope 1997). However, if there are substantial national differences, even within the main gear groups, a two-tiered approach may be required. A coarser management model with aggregated fishing fleets would operate at the international level. The output from this model would then be made available to national groups to make second-stage models at further levels of disaggregation (Pope 1997).

In this study, we used a multispecies Scheafer model to describe the North Sea multispecies fishery. It was at first surprising that a simple production model could match the 4M model predictions so closely. However the multispecies Scheafer model was fit to the projections, and the simpler model appears to capture the main interactions. In this manner, simplified management advice can be given without further need for the more detailed biological model. The multispecies Schaefer model was very convenient for this application because the projections can be made almost instantly, which facilitates an interactive computer model. The model projections should be most reliable close to the status quo effort levels. The MSAWG cautioned against extrapolating beyond a range of one half or twice the status quo effort (ICES 1992).

The essential features of this display is that the AMOEBAs are linked with a multispecies model and that projections can be made simply by altering effort levels. Alternative model formulations could be used and/or extensions made to the present model. One approach would be to use the 4M model to make all the projections, without fitting the simpler Schaefer model. An alternative is to fit the multispecies production model directly to catch and abundance data without accounting for age structure (e.g. Collie and DeLong 1999). Detailed accounting of age structure may be unnecessary unless changes in mesh size are investigated or there is a large price differential with size of fish. In this study the biological interactions appeared to be secondary to the direct fishery effects on each species. However we may have down-played the biological interactions by ignoring variations in the predation mortality inflicted by the "other predators" in Table 1. Nor did we consider the potential bottom-up effects of the prey species on their predators.

The multispecies Schaefer model was fit to equilibrium conditions and therefore did not consider the time dynamics of moving from the status quo to the desired situation. These equilibrium solutions give useful targets relative to present conditions, but in practice it would be useful to have AMOEBAs for 1-5 year projection as well. It would also be useful to incorporate stochasicity, especially to account for uncertainty in the stock-recruitment relationships. If a stochastic multispecies model were used, the arrow heads in each AMOEBA could be replaced with error bars. The bio-economic objectives could also be extended, for example by including effort-cost relationships and price elasticity; such extensions would give a higher value to reducing fishing effort. Social objectives could also be represented with AMOEBAs but the challenge is that, to be included, they must be quantified (Pope 1997).

The combinations of effort levels in Table 4 were meant more for illustration than for prognostication. The partial fishing mortalities were based on 1991 values (Table 2); fishing patterns have almost certainly changed since then. Before making actual projections, the status quo effort levels would need to be updated from 1995 to present. Nevertheless, several general conclusions can be made regarding multispecies reference points. Joint levels of $F_{0.1}$ and F_{msy}

can be calculated with the methods of linear algebra, but they are of limited usefulness because of the tendency for extremely high or low values for some fleets. Reference levels based on MEY appear to be more useful because they prevent extreme effort levels and because of the explicit link to bioeconomics. A priority should be to incorporate more realistic cost functions.

Our results suggest that it is possible to satisfy the B_{pa} and F_{pa} levels of all species but that substantial reductions in fishing effort of some fleets would be necessary. Relative to the status quo, there would also be foregone yield, although this loss would at least be partially compensated by increased catch per unit effort. In reality, we should not rely on projections with effort levels less than one half the status quo. Fishing effort will be reduced in a step-wise fashion, with multispecies models refit at each step.

The AMOEBA plots are very useful for displaying the trade-offs among biological, economic, and social objectives. It is unlikely that any “optimal” effort combination will be chosen. More realistically, solutions will be sought that maximize the objectives while violating as few constraints as possible (Pope 1997). The advantage of the AMOEBA approach is that these trade-offs can be viewed explicitly. We have also developed an interactive version of the program in which the effort levels can be changed in the graphic interface. In summary, we have demonstrated a method for the clear and concise presentation of advice for a complex, multifleet fishery. Incorporation of biological interactions does require a multispecies model, but the presentation of advice is no more complex than that required for the technological interactions among fishing fleets.

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Table 1: Species included in multispecies assessment

	Age groups	Predator/Prey
VPA species		
Cod	0-11+	Yes/Yes
Haddock	0-11+	Yes/Yes
Whiting	0-10+	Yes/Yes
Saithe	0-15+	Yes/(Yes)
Mackerel (North Sea stock)	0-15+	Yes/(Yes)
Herring	0-9+	No/Yes
Norway pout	0-3+	No/Yes
Sandeel	0-6+	No/Yes
Plaice	0-15+	No/(Yes)
Sole	0-15+	No/(Yes)
Other predators (Abundance given as input)	Size or age groups	
Grey gurnards	0-3	Yes/No
Western stock mackerel	0-1	Yes/No
Raja radiata	0-3	Yes/No
Grey seals	1	Yes/No
Sea birds	1	Yes/No
Other species	1	Yes/No

* Prey (Yes) indicates very low predation mortality

Table 2: Average fishing mortality by fleet and species as used in the *status quo* projection. Also listed are the precautionary reference levels for fishing mortality (F_{pa}) and spawning stock biomass (B_{pa}) from ICES 2000. For herring and mackerel only, the status quo SSB levels were used as proxies for B_{pa} because these two stocks have components that are not resident in the North Sea.

	Species									
Fleet	Cod	Haddock	Whiting	Saithe	Plaice	Sole	Herring	Mackerel	Sandeel	Norway pout
Beam trawl	0.03	+	0.01	+	0.35	0.35	+	+	0	0
Fixed gear	0.10	+	+	+	0.02	0.02	+	+		
Industrial (small meshed trawl)	0.02	0.01	0.04	0.05	+	+	0.05	0.02	0.36	0.36
Pelagic (purse seine and trawl)	+	+	+	0	+	+	0.47	0.10	+	+
Saithe (trawl)	0.01	0.01	+	0.09	+		+	+		
Seine net	0.21	0.30	0.16	0.01	0.05	+	+	+	0	0
Trawl	0.28	0.35	0.27	0.16	0.05	0.03	0.11	0.01	+	+
Other gears	0.16	0.05	0.01	0.11	0.07	0.11	0.20	+	0.01	+
All fleets	0.81	0.73	0.49	0.42	0.55	0.51	0.83	0.12	0.36	0.36
Precautionary F level	0.65	0.70	0.65	0.40	0.30	0.40	0.25	0.17	0.59	0.84
Precautionary biomass level (kt)	150	140	315	200	300	35	311*	86*	600	150

* Status quo SSB used as a proxy for B_{pa}

* Constrained to prevent a negative estimate.

Table 3: Percent change in spawning stock biomass of each species resulting from a 25% decrease in fishing effort of each fleet in turn. Negative values result from increases in predator populations.

	Species									
Fleet	Cod	Haddock	Whiting	Saithe	Plaice	Sole	Herring	Mackerel	Sandeel	Norway pout
Beam trawl	2.89	-0.77	-0.14	0.05	19.80	25.41	-0.39	0.00	0.14	-0.03
Fixed gear	5.81	-0.62	-0.74	0.13	0.61	1.30	-0.10	0.00	0.22	0.40
Industrial (small meshed trawl)	4.47	-2.12	3.48	4.15	0.05	0.04	17.85	1.91	12.90	7.84
Pelagic (purse seine and trawl)	0.71	0.12	0.23	0.01	0.01	0.00	14.99	12.73	-0.37	-0.13
Saithe (trawl)	0.97	0.25	-0.10	6.45	0.08	0.01	-0.12	0.03	-0.02	0.21
Seine net	13.24	5.36	-0.20	1.34	2.46	0.06	-3.34	0.00	-0.21	-2.30
Trawl	20.93	3.57	0.23	12.03	3.02	1.86	-0.30	1.47	-0.02	-2.18
Other gears	13.82	0.01	-1.39	8.17	4.12	8.48	15.83	0.02	0.64	0.90

Table 4: Reference levels of fishing effort identified with the multispecies Schaefer model.

	Effort relative to status quo		
Fleet	E_{msy}	E_{mey}	E_{opt}
Beam trawl	0.98	0.53	0.55
Fixed gear	0.2*	2.08	0.73
Industrial (small meshed trawl)	1.77	0.51	0.22
Pelagic (purse seine and trawl)	0.81	0.82	0.21
Saithe (trawl)	3.02	0.96	0.54
Seine net	2.39	0.71	0.56
Trawl	1.42	0.86	0.24
Other gears	1.11	0.86	0.55

E Case Studies

E.1 Multi-Species and Ecosystem Models in a Management Context

Gunnar Stefansson

Abstract

The final decades of the twentieth century saw the emergence and first applications of multi-species models of marine ecosystems along with a general recognition of the potential importance of taking into account multi-species interactions when managing fisheries.

Multi-species effects can include biological and technical interactions. Technical interactions are frequently of concern, for example when discards of certain species are believed to be a consequence of the management system. Biological interactions may fundamentally change the perspective of how to utilise an ecosystem, since a fishery or a moratorium on a predator may completely change the survival of a prey and conversely, fishing on a prey may affect the growth of a predator.

Modern research on multi-species modelling is highly multidisciplinary in nature, drawing on expertise from fishery science, fish biology, ecology, hydrography, mathematics, statistics, economics, operations research and computer science. As the models become more detailed and complex, they are able to address more issues that are of concern to managers but at the same time it becomes ever more difficult to interpret results.

Fundamental issues are raised in the multi-species context, and particularly so when fishing is viewed in the light of the precautionary approach. Some multi-species research has indicated that heavier fishing with smaller mesh sizes may lead to more profits for the fishing industry, whereas most earlier single-species research has indicated that low fishing pressure, particularly on juveniles, would be beneficial for the resource and the fishery. Conclusions from other research have indicated that economic considerations such as maximum economic yield may not be applicable and have failed to lead to sustained utilization whereas the traditional view has been that long-term economic views will generally lead to sustainable use of the resources.

This paper seeks to resolve some of these apparent conflicts, drawing on the multidisciplinary nature of fishery science. It is seen that almost all points of view lead to the conclusion that fishing with low fishing pressure is not only sustainable but in accordance with the precautionary approach. Further, almost all multi-species concerns strengthen the need for reduced fishing pressure.

It is also argued that simple management measures such as quotas, effort control or areal closures alone may not suffice to maintain viable fisheries in multi-species ecosystems.

Introduction

This paper endeavours to describe recent developments in multi-species modelling approaches and how the results from those developments will or are likely to affect management decisions. To this end, the sections following the introduction describe common current single-species methods of assessment and prediction, together with a description of multi-species issues that must be taken into account. Multi-species effects tend to be classified into two different types: biological and technical interactions. The paper discusses the importance of each of these effects, modelling approaches and how these effects affect the possible utilization of the resources.

It turns out that quite a few important management questions can only be addressed through the use of complex models, which include several species, areas and fine temporal scales. Such questions include the effects of closed areas, multi-species effects of a moratorium on fishing for a predator, and so on. Finally, given the current state of many of the world's commercial fisheries and problems recently found in management advice given in many regions, it seems clear that tools are needed to evaluate the ecosystems in a more comprehensive manner than previously. This is particularly important in light of recent observations which imply that entire ecosystems have collapsed primarily (and quite commonly) due to overfishing (Jackson *et al.*, 2001).

Models that include several species and their interactions have existed for quite some time, starting with the Lotka-Volterra models and later the emergence of models that can incorporate very many species. The first true applications of multi-species models of marine ecosystems were, however, seen closer to the end of the twentieth century (e.g. ICES, 1991).

Since the multi-species models need to be spatially dis-aggregated, they must contain a migration component in addition to biological and technical interactions. These models are therefore much more complex internally than previous single-species models. The paper describes some of these issues, together with a related problem, that of using difficult and complex data sets to estimate unknown parameters of the models. When combined with prediction, the modelling approach requires a conglomerate of expertise from a variety of subject areas. This multidisciplinary nature of modern research on multi-species models is detailed in a separate section of this paper.

Some fundamental issues are raised in the multi-species context, and particularly so when fishing is viewed in the light of the precautionary approach. In fact some conclusions appear to be in conflict and there is a need to resolve these conflicts in order to pave the way for reasonable management. Some of these conflicts can be resolved by drawing on the multidisciplinary nature of fishery science. Generally speaking, fishing with low fishing pressure is sustainable, economical, and in accordance with the precautionary approach. Most multi-species considerations further strengthen the need for reduced fishing pressure.

Along with the application of the models comes a general recognition of the potential importance of taking into account multi-species interactions when managing fisheries. Thus, some of the first applications by advisory bodies immediately implied that fundamental understanding of the effects of fisheries could, at least in principle, be seriously affected by multi-species considerations.

One such fundamental issue in managing marine resources is the overall level of fishing mortality to be exerted on the fish stock(s). The decisions on overall levels of harvest need to be based on all aspects of knowledge, first biological, but no less economic and social. Decisions on sensible fishing pressures paves the way for what control systems can be implemented, since they must be designed to achieve predefined goals.

It will be seen that simple management measures such as quotas, effort control or areal closures alone will not in general suffice to maintain viable fisheries in multi-species ecosystems. Rather, combinations of these measures are needed to safeguard against the various issues raised in the multi-species context.

The single-species models of assessment and prediction

The most common single-species models include recruitment, growth, maturation and mortality due to fishing and natural causes. In their simplest forms (Beverton and Holt, 1957) these models commonly assume constant natural mortality, constant growth, a constant maturation pattern by age and a constant fishing pattern by age.

Analyses of the effects of fishing may use these assumptions in order to evaluate the likely development of a yearclass and its possible utilization. Even the simplest such analyses need to consider the effects of incorrect assumptions. These computations subsequently provide first indications of potential yield from the resource, but need some estimate of yearclass size as input.

In order to obtain such typical yearclass sizes, some assessment of the resource is needed. Classical methods include those which track individual yearclasses, from the initial VPA (Gulland, 1965) to more recent statistical methods that incorporate more appropriate statistical assumptions. Whatever the methods, the outcome will be some stock estimate, typically in terms of the historical number of fish by age and year, up through the last data year.

In order to evaluate the effects of management policies, the effects of these need to be modelled. Usually this is done by predicting the stock forward in time (i.e. from the assessment year), under the given harvest policy.

In order to undertake predictions, some stock-recruitment relationship also needs to be used. This can be estimated from data, assumed to be a constant or to be of some general form. It turns out that the stock-recruitment relationship is of crucial importance when estimating the sustainability of a harvest policy or probability of stock collapse.

The natural next steps involve the addition of factors such as cannibalism and density-dependent growth, if any of these are believed to be important.

These single-species techniques, still fairly simple, have been used extensively to estimate medium- and long-term consequences of management actions.

Alternative approaches to assessments and predictions have been developed. These include aggregate models that require less data but also provide less output. Such simpler models may be very useful and even prove better than the more dis-aggregate models in some circumstances (Butterworth *et al.*, 1990). It is clear, however, that overly simple models cannot answer any of the more complicated issues in multi-species research.

The above model classes range from very simple static biomass production models, through dynamic total biomass models, to age-dis-aggregated dynamic stock production models. Unknown parameters (e.g. recruitment) in the last model class are usually estimated using statistical methods of fitting models to data (but see below). Although given different names, such as HITTER-FITTER (see e.g. Punt and Butterworth, 1991) or ADAPT (Gavaris, 1990), resulting techniques are all of the general form of adapting an internal model to data.

All these single-species assessment models are of the form of an internal black-box, which simulates an ecosystem based on some parameters. Results from different parameter values are compared to data and the parameters are estimated by finding the best fit to the observed measurements.

In order to estimate the various unknown parameters of the models, statistical methods are used. During most of the last century this step was skimmed over by using simple assumptions (such as independent log-normal errors), though in rare cases these were augmented by using known statistical distributions believed to better describe the sampling process.Subsequent analyses indicate that these assumptions are far from correct and that the sources of variation in the measurements are sufficiently complex to warrant the development of completely new statistical distributions to describe the data sets. This was noted early on for abundance data (Pennington, 1983; Lo *et al.*, 1992, Stefansson, 1996), but for other biological data, such as length distributions, simpler assumptions have been used (McDonald and Pitcher, 1979), sometimes extended to multinomial distributions (Methot, 2000). Recent research has indicated that these various extensions still suffer from being highly inadequate descriptions of reality (Hrafnkelsson and Stefansson, 2001).

Although these statistical issues may seem esoteric, the results of incorrect statistical assumptions can, unfortunately, have devastating effects on overall conclusions. This is best seen by considering the best currently applied single-species assessment methods, which can not only provide stock estimates but can also estimate uncertainty (Patterson *et al.*, 2001). One way of describing the uncertainty is to provide intervals that describe probability. A statistical method will, for example, provide a biomass level below which it is highly unlikely that the true biomass can lie. In particular, such a 1% lower confidence bound is designed in such a fashion that the true biomass should only be below it in 1% of all assessments. The best illustration of the problem involved is that recent research has indicated that when the standard statistical assessment methods report a 1% lower bound on a biomass value, in reality the true probability of being below that value can easily be 30%, and the most commonly used assessment methods give a corresponding underestimate of uncertainty (Gavaris *et al.*, 2000; Patterson *et al.*, 2000; Restrepo *et al.*, 2000).

The result of the statistical issues above is that even if management has been aiming for a low fishing mortality, e.g. to be 99% certain of the stock staying above a depletion level, the actual probability may have been 30% of falling below that critical point (Gavaris *et al.*, 2000).

For predictions it is essential to take into account the high degree of uncertainty involved in predictions of the development of marine species. Most management bodies need to know not only immediate and future yields but also probability of stock collapse, inter-annual variation in yield, likely rebuilding time, etc. The fact that recent work in this area has indicated that previous estimates of uncertainty may have been severely underestimated and that new and sophisticated statistical methods are required raises serious issues of reliability of predictions in general.

In spite of their problems, single-species models have provided guidance on methods for rational utilization of fish stocks. In a nutshell, general results from these models are the following:

- A low fishing mortality will generally decrease the probability of stock collapse.
- Low-to-medium fishing mortalities will not usually lead to reduced harvests.
- High fishing mortalities may lead to reduced harvests.
- High fishing mortality may lead to stock collapse.
- Economic considerations tend to imply a need for even lower fishing mortality than implied by biological models alone.

These results may not be completely universal conclusions from all single species models, but very nearly so. These resulting points of view will be termed the single species *basic premises* as they have resulted in fundaments used in fisheries management worldwide.

This is not meant to imply that the single species models are correct or provide an adequate description of the ecosystem, but merely that the tenet of a low fishing mortality remains applicable as more complex situations are analysed.

Apparently, in many cases, the broad results of severe management actions have been predicted adequately using fairly simple models. Thus, for example, a number of stocks have shown reduced total mortality during reduced fishing pressure and have even regained earlier levels following such management action (e.g. herring, Jakobsson, 1980). This is not true in all cases however, as in some cases mortality does not appear to decrease following a stock collapse, even if fishing is reduced to a moratorium. For stocks which have not recovered under moratoria, reports are available on apparent increases in natural mortality (Sinclair, 2001). In other cases revised models have indicated that a change in natural mortality is not required in order to explain available data on stock collapse, but a better statistical model is needed (Myers and Cadigan, 1994).

Multi-species effects

Although there are several examples of fisheries which can be classified simply as cases of overfishing and the importance of reducing fishing intensity is clear, there are quite a number of instances where the questions raised are somewhat more complex than these. Simple examples of questions such as the predicted effects of a closed area or the effect of an increase in a predator stock on its prey involve a necessary deviation from the simple models. It is simply not enough, for many (if not most) purposes, to have simple eye-glasses. Rather, the analyses and interpretations must commonly take into account the fact that species do not live in isolation.

Biological interactions

In order to model multi-species effects, it is necessary first to develop a list of effects that may be important. This is the difficult step in modelling, as the mathematical and statistical models will follow naturally once a conceptual biological model has been developed.

Following the single-species models in the previous section, the next natural steps in model extensions involve the biological interactions between species. Typically, these interactions involve predation and the resulting primary effect of predation on the mortality of the prey (Helgason and Gislason, 1979). The second factor to be taken into account is the effect of the predation on the growth of the predator. Depending on the ecosystem and species combinations, one or both factors may be important (ICES, 1991, Stefansson *et al.*, 1998).

As for single-species models, approaches to the multi-species models vary from simple model extensions through holistic approaches where the main processes in the system are cast in a unified mathematical framework. Even in the holistic approach, however, there is considerable scope for choice, ranging from the very simple ECOPATH approach (Christenesen and Pauly, 1990), which starts as a simple equilibrium biomass flow model, through models such as MSVPA, which are dynamic and age dis-aggregated for all (or most) species.

These first models are useful in determining the main multi-species effects in the systems. In particular, ECOPATH is designed to indicate whether most important players in the system are included and MSVPA will similarly indicate the most important sources of predation mortality for each species.

Although in principle spatial factors may be important even when just considering one species, these factors become crucial when biological interactions are considered. The reason for this is of course the question of spatial overlap between the predator and prey species, which has been demonstrated in many ecosystems to be highly variable, resulting in widely varying predation mortality (e.g. Bogstad *et al.*, 1994; Bogstad and Tjelmeland, 1990). The decision to take spatial variation into account has several important consequences, the obvious one being the requirement for a more realistic and much more complex model For example, migration typically depends on the maturity stage of the fish, thus further implying that the model must take into account the difference in behaviour of mature and immature fish.

In variable ecosystems where some species are tightly coupled with a predator-prey relationship of considerable importance for both species, it therefore becomes important to incorporate fishing, predation mortality, maturation, migration and growth as dependent on consumption (Stefansson and Palsson, 1998).

These models inevitably include a large number of parameters, values of which can only be estimated using statistical techniques. Although in principle standard statistical methods can be used, fisheries data are very difficult to handle and highly specialized methods are required.

Although it will not be known in advance how complex the models need to be, it is clear that testing the effects of complexity can only be done using highly detailed models. A possible conclusion from such model tests may be that the increased complexity is not, but this cannot be known in advance. Recent work has indicated that highly complex models can indeed be evaluated and tested using advanced statistical techniques (Helu *et al.*, 2000).

Technical interactions

Technical interactions are frequently of concern, such as when discards of certain species are believed to be a consequence of the management system. Further, different components of a fleet may target different components of a stock, most notably some components of the fishery may target the spawning stock in a spawning area during spawning time whereas another part of the fishery may target smaller juvenile fish.

For this reason, when technical interactions are concerned, the need quickly arises to take into account fine temporal and spatial scales.

In terms of modelling, once multispecies interactions have been included, few issues or added complexity tend arise due to the inclusion of technical interactions. In contrast, if fleet behaviour is added as a model component, together with the fleet's response to economic issues, then a considerably different emphasis may develop (Olafsson *et al.*, 1991).

Model complexity

As mathematical models become more complex, there is increased potential for serious issues of confounding to appear. The net effects of such confounding can become quite serious. One of the simplest forms of such confounding appears in disputes over whether mortality is mainly due to fishing or natural causes.

These simple confounding issues and resulting debates can in many cases be easily resolved. In most fields of science it is standard practice to use designed experiments to verify what models are incorrect. Contrary to popular belief, large-scale experiments are also common in fisheries, although rarely designed explicitly to answer specific questions. Examples of such experiments include complete closures of fisheries due to stock collapses or wars, and implementations of strict management measures based on model predictions. Such experiments have repeatedly demonstrated that the basic premises of single-species fish population dynamics as mentioned earlier are fundamentally correct (Jakobsson and Stefansson, 1998), though there are noteworthy exceptions (Sinclair, 2001).

It is of course exceedingly useful to have such experimental results that verify model predictions. In more complicated models, the confounding between factors can unfortunately be of such a nature that it is impossible, using current methods, to verify true relationships.

Multi-species modelling approaches

Modern research on multi-species modelling is highly multidisciplinary in nature, drawing on expertise from fishery science, fish biology, ecology, hydrography, mathematics, statistics, economics, operations research and computer science. Naturally, the more extensive the inclusion of such factors, the more complex the models.

It must be noted, however, that some of the most important conclusions regarding fisheries and overfishing do not depend on complex models. In particular, some particularly simple techniques can be used to demonstrate serious overfishing. If the sole purpose of analysis is to find such effects, then there is often no need to go into excessively complex models.

In some cases, relatively simple extensions to single species models can be used to verify effects of individual multi-species interactions. Thus the effect of a predator or a prey species can sometimes be entered as a simple regression variable (Pope and Knights, 1982; Stefansson *et al.*, 1998).

When developing models of the highly complex type considered here, the first step needs to be to define the biological factors to be taken into account. Having done this, the next step involves defining the corresponding mathematical model of the processes involved, followed by implementing the models in a computer program using statistical estimation techniques.

The statistical aspects of the models become even more important in the multi-species models than in the single-species case. This is due to the increase in the number of data sets that must be used. In the single-species case, these will be only a few data sets, but even there the weight given to each data set may be quite important. In the multi-species case, a combination of either incorrect weights or inappropriate statistical assumptions may completely invalidate the output from the models (Stefansson, 1998).

Having obtained the basic framework, the most promising current direction appears to be to build models of increasing complexity by comparing them to data in a stepwise fashion (Helu *et al.*, 2000). This does, however, require appropriate statistical assumptions. Some of the current modelling work attempts to address all of these issues (Anon, 2001).

Economic considerations must be taken into account if it is of interest to compare different fishing strategies, since they may lead to a shift in catches from one species to another and thus the regimes can only be compared using costs and income rather than simple biological yield. When attempting to find optimal harvest strategies or only to compare different strategies, methods of operations research, including maximization of utility functions, or at least comparisons of utility, are commonly used (Danielsson *et al.*, 1997). These issues are important and may certainly affect results in individual situations, but are unlikely to change the principle of low fishing mortality and are outside the scope of the present paper.

The precautionary approach in the multi-species context

Traditional economic analysis would imply that fishing should be in such a manner as to ensure maximum long-term profits (or, more generally, maximum utility). Depending on what factors are taken into account, this has sometimes been simplified to maximizing total yield of a species in the long term, leading to maximum sustainable yield (MSY), corresponding fishing mortality (F_{MSY}) or other biological measures (e.g. $F_{0.1}$), which do not take economic considerations directly into account but aim for effort slightly lower than that giving maximum yield, as would happen if a cost function were used.

The fundaments of these approaches have come under considerable fire in recent years, particularly due to the (near-) collapse of many fish stocks (Mangel *et al.*, 1996). It is, however, clear that most of the major stock collapses have occurred due to a combination of several factors, one or more of which led to considerable overfishing. Thus, fishing from most currently collapsed stocks simply was not in accordance with MSY or any other similar criterion so these case studies tend not to affect the MSY principle *per se*.

This does not alleviate the problem, however. The fact remains that stocks collapse and do so even when official policy is to maintain moderate harvests from the stocks. The reasons are usually not a policy of overfishing or a policy of fishing over MSY (there are of course exceptions where management directly aims for high fishing mortality, but these will not be addressed here). Rather, the official policies tend to be of moderate fishing, but the problem becomes one of a failure to attain this goal. The question becomes how to revise policy in order to ensure that harvests are sustainable despite the considerable uncertainty involved both in the science and in the implementation. In particular, it would usually be quite adequate to maintain a policy of MSY as a target, if it could be ensured that this would rarely be exceeded.

In order to suggest remedies, it is of some importance to recognize a few causes rather than just the symptoms. Direct and documented causes of stock collapse or problems (serious and unexpected declines) include the following: incorrect advice on stock status; fishing well over advised levels; and lack of advice on danger levels and multi-species or environmental effects.

The precautionary approach, stated in its simplest form, implies that care needs to be taken to ensure that fishing is undertaken in a sustainable manner and that when uncertainty is present, this should be taken into account by reducing fishing mortality. In implementing the precautionary approach, reference points have been defined. Loosely, they are defined in order to set rules that satisfy the criterion that as long as fishing is within bounds defined by the reference points, fishing mortality will not exceed specified harvest rates.

Now, considering the present framework, these things become a bit more complicated. The easiest example involves a prey species that has been reduced to a very low level. Overfishing a predator species may then re-instate the prey to previous levels much faster than any other measure, but this would clearly violate the precautionary approach as regards the predator. At present there is no system in place to address issues such as this.

In the multi-species context, it is possible in principle that heavier fishing with smaller mesh sizes may lead to more profits for the fishing industry, whereas most single-species research has indicated that low fishing pressure, particularly on juveniles, would be beneficial for the resource and the fishery. Examples where quite different results are obtained from multispecies research include the North Sea (ICES, 1991). It is indeed easy to envisage how this can happen, simply through a reduction in the abundance of a predator leading to an increase in prey species.

The specific North Sea results were obtained from forward projections that included some multi-species interactions, notably predation mortality. On the other hand there is considerable information to the effect that heavy fishing on juveniles can dramatically increase the probability of stock collapse. It is not clear in any general sense, what the net or overall effect of e.g. heavy fishing on a predator would be in the long term. Clear results, however, include the effect of heavy fishing quickly drawing stocks to stock collapse and of no fishing, in which case species can survive for millions of years. It would seem, therefore, that very strong evidence indeed is required to conclude that high fishing mortality of juveniles is beneficial.

In examples where economic concerns have been included, at least one case study exists where it was predicted that the result of reducing fishing mortality on a predator would lead to more than 50% reduction in catches of a prey (Danielsson *et al.*, 1997). In that particular case, economic analyses indicated that it was nonetheless beneficial to the fishing industry to accept those reductions since the predicted total profits more than outweighed the negative aspects. Interestingly, in this case the prey species did indeed collapse subsequent to an increase in the predator biomass.

Management in the multi-species context

Initially, the inclusion of multi-species interactions, technical interactions, advanced mathematical and statistical models leads to considerable obfuscation. Thus, it is no longer uniformly clear whether mesh sizes should be increased or reduced, or whether fishing pressure needs to be reduced or increased to obtain sustainable fishing mortality.

Upon some reflection, however, it is clear that the emerging figure is not as muddy as might appear at first. It must be noted at the outset that decisions on utilization need to take note of the precautionary approach. This implies that any uncertainty needs to be interpreted in favour of reduced fishing pressure. Thus, the fact that some new issues and questions are raised has no effect at all on principles such as a need to maintain low fishing mortality. Until clearly understood, such issues and questions merely urge more caution than before. Only in the case when it has been shown clearly that the complex models are a demonstrably better description of the system and demonstrated how species should be utilised under the new system should they be used for management purposes. For example, multispecies models incorporating predation mortality by adults alone may indicate a need for increased fishing pressure but if the models do not include potential recruitment failure then their results can not be used to draw a conclusion of increasing fishing mortality.

In practice most multi-species and technical interaction models lead to conclusions that further emphasize the need for low fishing mortality.

- Results that indicate that fluctuations in a predator species may have adverse effects on survival of a prey imply that fishing effort on the prey must be reduced even further than previously thought.
- Results that indicate that the growth of a predator is positively influenced by the growth of a prey will imply that more care needs to be exercised in the prey harvest than before.
- Estimates of uncertainty will tend to be higher (and better) since more factors are included than before, leading to more aversion from high fishing mortality.

Multi-species results of a different nature include:

- In a 3-species system, reduced pressure on a top predator may adversely affect its immediate prey, an intermediate-level species. This species may have its own prey (or competitor), which will become successful due to the reduced predation (or competition) pressure. Examples of such systems appear to exist (Bogstad *et al.,* 1997).
- Effects of predation on stock-recruit relationships of prey appear to be very complex and the resulting effects on, for example, biological reference points are even more difficult to interpret, though initial results indicate that such reference points can be developed (Gislason, 1999).
- Some examples of multi-species results also exist where predicted effects of mesh changes contradict earlier single-species results (ICES, 1991). This is to be expected and in particular these may alleviate some of the unlikely optimistic biomass predictions which result from applying a suite of single-species models (with low and fixed natural mortality) and summing species-specific biomass values.

Finally, there are instances where a species may suffer very high or total mortality after spawning (Vilhjalmsson, 1994). In these cases, there is considerable incentive to fish up the stock before natural mortality occurs. In a few cases, a holistic approach has been taken, i.e. considerations of the effect of prey biomass on predator growth have been taken into account. In such situations, it has sometimes been found that the lack of catches of the prey species is offset by an increase in the growth of the predator, even to the extent of matching the loss. In the spatially explicit multi-species context, these factors crystallize even further, since it is clear that some of the dying prey will provide food for the predator. There is, therefore, even less incentive to fish hard on the prey. The full results of such analyses depend, however, on the economic importance of each of predator and prey. Such predator-prey price ratios may differ greatly from one ecosystem to another (e.g. the different price of anchovy compared to capelin).

It is seen that there may indeed be examples where the inclusion of multi-species effects implies that fishing pressure should be increased in order to obtain higher yields and even to obtain a more stable or sustainable fishery. As these finding appear to be exceptions, what remains, however, is the need to demonstrate this in individual situations. It is therefore not a valid argument to point to these exceptions and argue that this justifies increases fishing mortality. Such justification must be clearly demonstrated based on data and models for the given situation. The default methodology under the precautionary approach needs to be the prudent one of low fishing pressure since this appears to be the general situation and lack of knowledge of interactions simply qualifies as any other reduced knowledge and implies a need for low fishing mortality. This conclusion is even more important in the light of results that imply that simple control rules that ensure low fishing mortality will perform well even in situations of considerable variation in the true biological parameters of the populations (Walters and Parma, 1996).

A missing component in the models

Notably absent from most if not all current single- and multi-species biological and economic models is the concept of maximum potential effort. In a system with some form of limited entry this can be very different from the effort as intended by management. Basically, in a system with limited entry there is a possibility of an enormous dormant effort.

The inclusion of such a concept would immediately bring forward the following model components, which are currently not implemented in models of marine ecosystems:

(i) A large dormant effort results in a constant political pressure to increase realized effort. A model to take this into account should place a probability of a political decision to increase fishing mortality over a sustainable threshold, simply due to political pressure. This applies to all control systems.

(ii) At any given point in time, an increase in Total Allowable Catch (TAC) or effort allocation can always be realized, even if this is erroneous and leads to a major increase in fishing mortality. This applies not only to TAC and effort control systems but also to systems based on areal closures (for mobile species the effect of an areal closure may thus be negated by a large fleet fishing in adjacent areas).

(iii) An estimation error towards a low TAC (or effort) is unlikely to be realized as a low death rate symmetric to an overestimate. In addition to the political pressure, this is also a result of high grading, discarding of the species that will occur with other species that have not been underestimated, and an unknown slippage mortality due to excessive fishing activity on other species or size groups.

(iv) For a small fleet size, the effect of quota variation and discordance among species is negligible since the individual vessels will not be able to catch species that are not abundant. Basically this is due to the maximum possible excess effort in a small fleet. Thus there is a built-in guard against overfishing simply in the fleet size. With excessive dormant effort, however, vessels will find ways to fill all quotas, resulting in all overpredictions directly realized in mortality and excessive slippage in other species.

(v) An oversized fleet can subsidize the fishery of certain overfished species through the catch of a more abundant species. This can happen, for example, when the fishery for a depleted species cannot economically sustain individual fishing trips and a more abundant species justifies the trips and sailing time, but the catches of the depleted species can be taken at minimal additional costs during the trip. This only occurs as a consequence of the combination of multi-species issues and oversized fleet.

The potential effects of dormant capacity become particularly clear in light of multi-species (biological or technical) interactions and the concept is important enough to warrant inclusion in multi-species models and to be addressed by management systems.

Control systems in the multi-species context

Management systems typically depend on one or more of quotas, effort control, areal closures, or other technical measures, such as mesh size changes. Considerable scientific and empirical evidence has been provided for the performance of each of these systems. These control mechanisms can now be viewed in the light of knowledge gained from the development of the multi-species models. Some problems affect all of these system, most notably problems of discards or high grading and catchability variation.

High grading can be a general problem, particularly at high catch rates. Regardless of the control system chosen, it is economically viable for a vessel crew to decide to discard low-value fish for high-value catches under any limitation whatsoever. In particular, the limit put by the size of the hold in the vessel may be enough to warrant discards under high catch rates. It can be beneficial to the operations of a freezing trawler to discard an entire hold full of frozen fillets if they are of a low- value species, should the vessel find a spot with another species of high value. This can potentially occur under any control system (including free fishing).

Environmental changes can result in considerable changes in catchability which, when not taken into account, will lead to incorrect predictions (Stefansson and Eiriksson, 1998). These variations have an effect on the uncertainty of estimates of stock sizes and thus on appropriate effort, size of areal closure or TAC, thus affecting all control systems.

A few examples suffice to show that each of these systems, when implemented alone, suffers from deficiencies.

Failure of a well-designed quota system

Quota (or TAC) systems are based on deciding an annual TAC for each species. A well-designed quota system is one where the catches taken are in accordance with the quota set, which again is according to some system that aims to provide sustainable catches for the species involved. In principle, a quota system should not need to include other issues such as effort control or fleet size regulation, since the primary issue of fishing mortality is addressed directly by setting the TAC to achieve a pre-specified goal.

A quota system can thus in principle limit fishing mortality inflicted on a given species. Without any further limitations, however, a fleet can move its effort towards areas of high abundance of spawning fish or of high abundance of juveniles. Such an increased effort towards certain age groups can easily lead to very high fishing mortality on certain age groups. The following model is an example where an initial design of a quota system will fail badly through perturbations not covered by the quota system.

Suppose the quotas are intended to be set so that the TAC appropriate for each species is according to a sustainable fishing mortality. Several of the following problems have been recorded with such a set up, whereas others are plausible explanations for existing situations:

(i) Uncertainty in the estimate of the fishing mortality may give a considerable (e.g. 30%) overestimate of the desired quota of some species, resulting in increase in fishing mortality from the target. These effects tend to become hangover effects for several years, exacerbating the situation (Rivard and Foy, 1987). The true uncertainty in the population estimates has only recently been investigated systematically and found to be considerably larger than commonly estimated previously (Gavaris *et al.*, 2000).

(ii) Re-allocation of effort between areas can change the fishing pattern for a given species so that the juveniles or some other component gets twice the intended effort, leading to high probability of stock collapse (Rose, 1993). This problem can not be addressed in models unless spatial effects are modelled directly.

(iii) A species whose stock size has been overestimated can get a quota which is so high that it is virtually impossible to catch, leading to serious difficulties in a fleet which searches for this target species but catches only other species whose quota has already been taken. The net result can be a serious discard problem.

(iv) A species whose stock size has been underestimated may get discarded since it appears much more frequently in the catches than predicted. since it appears much more frequently in the catches than predicted.

(v) A species with very low tolerance to fishing can be overfished even when taken only (or mainly) as by-catch in a fishery for another species that is sustainably fished (Walker and Hislop, 1998). This is an important example of a multi-species effect not normally taken into account when a TAC system is designed.

(vi) The fishery for a prey species may well affect the growth of a predator in such a fashion that the total economic outcome of the combined fishery is worse than that of not fishing for the prey at all. This scenario has not been addressed in the precautionary approach, but seems to be plausible in the light of some case studies (e.g. Magnusson and Palsson, 1991; Danielsson *et al.*, 1997).

It is seen that, from a modelling and advisory point of view, there are problems involved in evaluating the effects of management actions in a TAC system, problems that are not addressed using the models in common use around the world. In order to evaluate these effects new and more detailed models are needed, taking into account spatial effects, multi-species effects and different statistical design. It is thus seen that from an implementational point of view that there are several issues which may not be addressed in any detail within a quota system. In particular, a quota system based on TAC allocations for individual species may not lead to a sustainable fishery for all species involved, even the target species, unless of course the TAC for each given species is set far below each target.

Failure of a well-designed effort-control system

An effort-control system is defined by some measures designed to limit the total effort that a fleet can exert. A well-designed system will attain the effort limitation intended and the intended effort level corresponds to some sustainable fishing mortality for certain target species under a given scenario.

The primary problem with this method is that the fleet is free to target its effort to any species, species group or species size class, within the system. The total effort reduction will typically be set to be adequate to harvest the system according to a sustainable fishing mortality under a specified harvest regime. In most fisheries this implies that the fleet has been fishing in several areas and on several species. The effort system should lead to sustainable use of the resource if there are no changes in how the fleet proportionally targets each part of the species complex.

This design completely missed the multi-species viewpoints and spatial variation in species or age composition.

The net effect of this omission can be arbitrarily devastating. In the simplest example, the fleet initially consists of two discrete components, each of which fish for its own target species. In the typical scenario, the effort controls are designed to bring fishing mortality down to just below a collapse fishing mortality level, but in the best of worlds the target may be about half of the collapse mortality. In either case, if the price of one species increases sufficiently, the two fleets will both go for that species, leading to stock collapse. Given the first collapse, the fleets will target the second species.

A price change is not even needed for this to happen. Natural variation in stock size will usually be sufficient for a change in fleet behaviour. Thus, if the size of one stock goes sufficiently down due to natural variation, the fleet will target another species.

Finally, in no known cases of effort limitations has any attempt been made to account for the increase in catchability inherent in most fleets.

Examples are available of long-term catchability increases of 4.7% per year (Stefansson, 1998). In an effort control system the incentive for increasing efficiency is much greater than under free fishing or a quota system and thus catchability increases could be considerably greater than this. In such a system, with limitations on the total number of fishing days, the number of days allowed per year would therefore likely need to be reduced by e.g. 10% per year every year simply to ensure that fishing mortality would not be guaranteed to increase steadily.

Interestingly, this even happens for the smallest vessel classes, sometimes termed artisanal vessels or owner-operated vessels, typically with 1-2 crew members. Thus, there are examples of owner-operated vessels with 4 computerized winches and GPS positioning equipment. No formal estimates of catchability exist in this case, but from total catch figures it is clear that it is possible to maintain considerable catches with such configurations.

In some countries, these vessel classes tend to receive different treatment from the rest of the fishing fleet. However, the catches have exactly the same effect on fishing mortality, regardless of the political status of the fishery and recent research even indicates that human interventions may have had considerable effects on marine populations for hundreds and even thousands of years (Jackson *et al.*, 2001), further driving home the importance of taking into account the artisanal fisheries.

It is seen that the usual single-area, single-species models of assessment do not take into account the likely variation due to species switching or spatial re-allocation within an effort-control system. Advice based on these models is therefore unlikely to capture much of the variation due to the system itself.

In addition to the advisory problem, a pure effort-limitation system does not in general guarantee conservation of fish stocks in any sense. It is, however, clear that reducing effort to zero will work. It follows that the only way in which effort limitations will work is if the limitations are such the fleet can not induce high fishing mortality even with complete re-targeting of total potential effort, **and** the effort is further reduced every year to account for possible efficiency increase.

Failure of a well-designed areal closure

Areal closures are designed to protect a certain collection of stock components. A well-defined areal closure succeeds in eliminating fishing from the area in question.

Areal closures are sometimes temporary closures of small areas. These clearly will have little effect in a general overfishing situation. Similarly, closures that are only temporary (e.g. short seasonal closures) cannot provide any guarantee against overfishing, which can take place in other areas at other times. For example, common closures of spawning grounds during spawning time provide little protection for spawning fish since the spawning stock can be reduced to arbitrarily small levels through fishing on immature fish or on mature fish outside the spawning season. The net effect of fishing 50% of a yearclass before it matures is exactly the same as fishing 50% of the yearclass on the spawning grounds as the yearclass is preparing to spawn for the first time.

Closures of major portions of the fishing grounds have, on the other hand, apparently been seen to considerably affect fishing mortality (Murawski *et al.,* 2000)and such measures have been found to positively affect the abundance in adjacent areas (Roberts *et al.*, 2001, McClanahan and Mangi, 2000).

Some existing closures of entire juvenile grounds are also likely to have an effect on the survival of juveniles (e.g. Vilhjalmsson, 1994) and thus on the survival of the stock (Myers and Mertz, 1998), but this does not seem to have been demonstrated through any evaluations of the effects of such closures. In fact, when interpreting evaluations of closures it must be noted that many positive reports assume isolated adult stock components, either in modelling assumptions (Nowlis and Roberts, 1998) or in case studies which refer explicitly to reef fisheries (e.g. Bohnsack, 1998).

In general, this may not hold, however. Suppose an areal closure is implemented in order to protect a given species. The simplest example where this will not suffice consists of a single species which has a migration pattern between certain areas, one of which is taken to be the closed area.

The crucial factors in determining the effect of a permanent areal closure will be the rate of emigration from the area and the fishing mortality outside the area. This is because, if no other restrictions are implemented, then there is no intrinsic upper bound on the fishing mortality that can be implemented outside the closed area. Thus, the only upper bound on mortality due to fishing is simply the emigration rate. If the closed area is increased, the emigration rate is reduced and in the limit the areal closure will provide full protection.

In some situations knowledge may be available about the migration rate and it may also be possible to estimate fishing mortality with reasonable reliability. In these cases, it is in principle possible to estimate the effects of the areal closure. It is clear that such computations are essential if areal closures are to be generally useful as management tools. This implies a need for models that incorporate migration explicitly and provide estimates not only of the effect of fishing in the open areas but also of the associated uncertainty.

In cases when such data are not available, it is very difficult to make any sensible statements as to the effect of areal closures except of a generalist type. In particular, it is clear that there are many scenarios where unlimited fishing activity outside a closed area may lead to stock collapse. This will certainly be possible under several known migration patterns. Examples include such diverse species as tuna and cod.

Thus it is seen that current single-area assessment models do little to predict the effects of an areal closure and, in the usual absence of scientific data on migration rates (including their uncertainty), it is not possible to provide advice on the net effect of these closures. Calling such areas sanctuaries does not in any way change the basic problem that the full effect of these on the population dynamics and sustainability is unknown and will in some cases be negligible.

It follows that the only situation when there is any sort of guarantee that an areal closure suffices to provide sustainability for a stock is when the area is so large that most of the stock is protected.

Failures of other technical measures

Other technical measures tend to be aimed at protecting certain age groups, length classes or maturity stages. Typically, these involve mesh size increases or other changes in fishing gear.

If the technical measures are not combined in any way with overall fishing mortality limitations, then fleet development can continue to increase total fishing mortality without any specified upper limit. Thus, in general, the technical measures cannot be expected to guarantee a sustainable fishery. Notably, the results that high juvenile mortality may be linked with high adult (fishing) mortality in a documented case study (Myers *et al.*, 1997) must be taken as a warning that hidden mortality can be considerable when total exerted effort is not limited. This hidden mortality may be due to slippage, discards or other (unknown) sources, but as long as it is linked to the total realised effort, the only way to reduce it is to reduce effort.

The multi-species effects of, for instance, mesh size changes are quite contradictory. Some available research indicates that mesh increases thought to be beneficial in a single-species scenario may not lead to catch increases in a multi-species scenario. These results have to date not taken into account spatial variation in species composition, which is in some cases known to completely change the outcome of the models.

The only instance when technical measures alone can be expected to provide a sustainable fishery is when they result in a complete termination of fishing on juvenile fish (Myers and Mertz, 1998). Even in this case, however, the mortality due to slipping through meshes is completely unknown and may be arbitrarily high unless some other measure is included to reduce total fishing mortality. Slipping mortality is not included in any standard assessment models.

It can therefore be seen that these technical measures are unlikely to be sufficient in general to provide a sustainable fishery. It can be further seen that the state of the art in population dynamics models is unable to provide adequate advice on the (multi-species) effects of these technical measures.

Combined control systems

It is seen that the usual control measures are not guaranteed to control fishing mortality and lead to sustainability. Some combinations are more likely than others to work, however.

- A combination of a TAC system with effort controls should reduce both the multi-species problem of re-allocation of effort between species (under effort-only control) and multi-species discard issue in the mis-specified TAC (in the TAC system).
- A combination of major closed areas for juveniles combined with a TAC system should reduce the (single-species) problems of fishing to unsustainable levels either due to re-allocation of effort to juveniles or overfishing in the open areas.
- A formal fleet reduction system in combination with any known control system will reduce all problems with every system. As with effort controls, however, a fleet reduction system is not enough on its own.
- An effort control system along with large areal closures is much more likely to provide sustainable utilization than either system alone, since the combination can both provide a refuge and ensure that total effort is limited outside the closed area.

Any of these combinations would have to be designed in such a manner as to aim for an adequate definition of each component. Naturally there would be no use in adding an effort system to anything else, unless the effort control was designed to truly control effort to sustainable levels.

The detailed implementation of such combined systems is outside the scope of the present paper. It is, however, clear that such combinations are quite possible, though they may become somewhat complex. For example, an effort control system can in principle easily be added onto a quota system with individually transferable quotas. Initially, this could be done by allocating each vessel its historical effort, subsequently allowing transfer of effort between vessels and reducing effort year-by-year sufficiently to guarantee more than compensation of efficiency increase. Naturally, effort of large vessels needs to count more than the effort of small vessels in such a system, but the precise numbers are largely irrelevant in order to see some of the benefits of the combination. The only important issue in this case is to reduce effort enough annually to guarantee a true reduction in potential fishing mortality.

As seen earlier, all of the systems are likely to fail in the case of dormant effort in the fleet. The usual exclusion of this effort from models leads directly to a bias in the predicted effects of all management action. Including multi-species and technical interactions in the prediction models may possibly alleviate the assessment problem somewhat but will not eliminate it completely. No current models are able to take into account the full potential effects of the overcapacity currently available in many of the world's fisheries.

Conclusions

The paper has indicated the directions which current multi-species models have taken, how they have been developed in attempts to answer some of the questions raised by management and take into account various important biological issues. In terms of the utilization of resources, it is seen that the basic premises of classical single-species analyses hold in most instances, namely that maintaining low fishing pressure remains a prudent policy, is in accordance with the precautionary approach, is likely to provide sustainable catches, and will result in good yields in the long term. However, concerns raised in modern statistical, spatial and multi-species models indicate that the maintenance of low fishing pressure is much more difficult than previously believed. This is due to a combination of many factors, from management issues in the multi-species context. through estimation problems due to biological and statistical issues raised in complex models of ecosystems. As a result, there is a much greater need to further reduce fishing mortality than ever considered previously.

It is seen that when these more complex models are developed, several practical issues arise in the interpretation of results, as well as in the development of the models. There are at present fundamental unsolved issues in the very model definitions (not to mention implementation in real situations or predicting the effects of management action). Simply put: Functioning holistic models are not yet available.

The most important result from developing these models, however, is the potential to view the system as a whole and the fisheries as a whole. As these models are developed it becomes obvious that species interactions, spatial patterns and technical interactions can have a devastating effect on predicted outcomes of traditional methods of fisheries management.

In particular, it follows from the analyses above that the use of any of the common regulatory systems alone may not suffice to maintain viable fisheries in multi-species ecosystems. In order to facilitate sustainable use of the resources, it is highly likely that a combination of most, if not all, systems is needed, including formal fleet reduction mechanisms. The models required to illustrate the problems are sufficiently simple that a formal model evaluation is superfluous. Unfortunately the reverse is not true since to illustrate that certain combined measures will actually work requires much more attention to detail.

Complex models are needed in order to evaluate the effects of complex regulatory measures. These models need extensive data, which in many cases is not available, such as data on consumption or migration rates. The lack of data is not an indication that the models are too complex, but rather that the effect of the management measures cannot be predicted. If management is to be in accordance with the precautionary approach and data are lacking, there is a need to implement control measures that will work in spite of the added uncertainty. Interestingly, the temptation by management not to take such conservative action often goes contrary to economically rational utilization, which would advocate (very) low fishing mortality.

In cases where data are available, the models can be used to evaluate the effects of control measures. In such cases it may be possible to reduce the size of a closed area or to demonstrate that a relaxation of the effort control will lead to greater catches without increasing the probability of overfishing.

The models can also be used to evaluate the need for extensive data. Thus, the increased prediction accuracy obtained through more surveys or increased tagging can only be evaluated using corresponding models. The use of the models is therefore not only to advise management on control measures but also to advise on the data needed in order to be able to predict the effects of the measures.

Finally, the basic tenets of single-species fish population dynamics probably need to be reworded somewhat in the light of developments worldwide. In particular, rather than fishing at any (or the maximum) level that appears to be sustainable, it appears from the considerations in this paper that an appropriate theme is:

Marine resources should be harvested using the minimum fleet size possible, at that minimum level of fishing mortality which does not demonstrably lead to a serious long-term loss of catch.

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E.2 Celtic Sea: Combining commercial vessel data

In order that French and UK (E & W) landings data for the Celtic Sea could be combined, sumarised and circulated among dst^2 partners, it was necessary (for legal reasons) to eliminate all data in which individual vessels could be identified. French and UK landings records were categoriesd by vessel size (3 categories) and gear (9 categories), and new 'dst^2' identifiers were appended to each entry in the database. Summary tables containing the number of vessels or fishing 'sequences' falling into each of these categories were then produced and compared.

Table 1. Number of UK (E & W) vessel records over the period 1991-1998, prosecuting fisheries in the Celtic Sea by gear type. Note that individual vessels may appear in more than one category over the course of the time-series.

	<12 m	12 - 24 m	>24
Mobile Gears	**584**	**765**	**237**
Beam trawls	75	107	88
Demersal trawls	573	720	167
Pelagic trawl & seine nets	32	180	17
Shellfish dredges	68	106	53
Mobile polyvalent	139	299	70
Passive Gears	**518**	**148**	**72**
Gears using hooks	156	35	45
Drift and fixed nets	450	132	45
Pots and traps	91	8	1
Passive polyvalent	157	26	18
Polyvalent (passive + mobile)	**256**	**99**	**20**

Table 2. Mean number of trip sequences (sequence = portion of trip spent in same statistical rectangle) per month by French vessels in the Celtic Sea. Note that individual vessels may appear in more than one category over the course of the time-series.

	<12 m	12 - 24 m	>24
Mobile Gears	**71**	**1079**	**360**
Beam trawls	2	10	2
Demersal trawls	63	1046	352
Pelagic trawl & seine nets	0	1	0
Shellfish dredges	0	0	0
Mobile polyvalent	6	23	6
Passive Gears	**111**	**87**	**24**
Gears using hooks	5	4	3
Drift and fixed nets	49	16	4
Pots and traps	0	0	0
Passive polyvalent	57	67	17
Polyvalent (passive + mobile)	**392**	**59**	**6**

E.3 Celtic Sea: Combining tag-recapture data

[CEFAS 2001]

Tag/recapture records (24885) for sole, plaice and cod were entered into the Celtic Sea data base. Most cod were recaptured within same rectangle as where they were originally released (Table 1), thus providing limited scope for modelling migration or drift. Data for sole and plaice (Tables 2 & 3) are more extensive and offer greater scope for future modelling work.

Table 1: Cod tag and recapture records from the Celtic Sea. Data arranged by ICES statistical rectangle.

	Release rectangle		
Recapture Rectangle	28E4	29E4	Grand Total
25E3	1		1
26E2		1	1
26E3		1	1
27E1	1		1
27E2		2	2
27E3	2	1	3
27E4		2	2
27E6		1	1
28E2	3	2	5
28E3	3	7	10
28E4	27	40	67
29E0	1		1
29E1		1	1
29E2		2	2
29E3	4	4	8
29E4	13	58	71
29E5	2	1	3
30E0	1		1
30E4	4	5	9
31E3	5		5
31E4		1	1
31E5	4	1	5
32E2	2	1	3
32E3	1		1
35E3		1	1
46E1	1		1
Grand Total	75	132	207

Table 2: Sole tag and recapture records from the Celtic Sea. Data arranged by ICES statistical rectangle.

	Release rectangle																	
Recapture Rectangle	26E8	27E9	28E6	29E5	29E6	29E7	30E7	30E8	30E9	30F0	30F1	32E5	32E6	34E5	35E5	35E6	36E6	Grand Total
24E3	1																	1
25E4	1																	1
25E5												1						1
26E4	2																	2
26E7	1	1																2
26E8	23	1																24
27E3	2											1	3					6
27E4								2				2						4
27E7	1	1						1										3
27E8	3	2																5
27E9	3	81																84
27F0		3																3
28E3		1						3		1		1	1					7
28E4	1	1						3		1		4	4					14
28E5	2	3						20		11	1	3						40
28E6	4	3				1		23	1	19								51
28E7	1							4		1								6
28E8	1	9						1				1						12
28E9	1	7						1										9
28F0		5																5
29E3												1	1					2
29E4	1							5				6	8					20
29E5	2	2						23		4								31
29E6	8	7				5		136		48								204
29E7	1					2		81		11								95
29E8	1	1						15		4								21
29E9	1							5		1								7
29F0								3		1								4
29F1								2		2								4
30D9								1										1
30E1												1						1
30E2												2						2
30E3													1					1
30E4		1				1		2		1		13	15				1	34
30E5												3	4					7
30E6	1							8		1	1							11
30E7						1	2	25		1								29
30E8								573		2								575
30E9								56	1	49	1	1				1		109
30F0		3						48	1	930	12	1						995
30F1								2		16	1							19
31E3												1	2					3
31E4										1		6	5					12
31E5												12	7			1	1	21
31E6												1						1
31F0								1										1
31F1	2							6		38	6							52

Table 2: Sole tag and recapture records from the Celtic Sea. Data arranged by ICES statistical rectangle (continued).

	Release rectangle																	
Recapture Rectangle	26E8	27E9	28E6	29E5	29E6	29E7	30E7	30E8	30E9	30F0	30F1	32E5	32E6	34E5	35E5	35E6	36E6	Grand Total
31F2		1								2	1	1						5
32E2												1	2					3
32E3												1					1	2
32E4												1	1					2
32E5												3	4					7
32E6													7					7
32F0										1								1
32F1										13	1						1	15
32F2		1								4		1						6
32F3		1						1		6								8
33E3												1						1
33E4												7	2					9
33F1								3		4	1							8
33F2										5								5
33F3								1		6								7
33F4										1	1							2
34E4													1					1
34E5													1					1
34F2		1						2		3	1							7
34F3										11								11
34F4										5								5
35E4													1					1
35E5															1			1
35E6																3		3
35F2										4								4
35F3								1			1							2
35F4								1		1								2
36E5															1	1	4	6
36E6								3								10	29	42
36F0										1								1
36F2										3								3
36F3										1								1
36F4								1										1
36F5										3								3
36F6										2								2
37E5																1		1
37E6																1	11	12
37F0								1		1								2
37F2										1								1
37F3												1						1
37F6										1								1
37F7								1										1
38E4								1										1
38E5																	1	1
38E8								1										1
38F0										2								2
39F2												1						1
Grand Total	64	136				10	2	1067	3	1224	28	79	70		2	18	49	2752

Table 3: Plaice tag and recapture records from the Celtic Sea. Data arranged by ICES statistical rectangle.

	Release Rectangle													
Recapture Rectangle	26E8	27E9	30E7	30E8	30E9	30F0	30F1	32E5	32E6	34E5	35E6	36E6	38E6	Grand Total
26E8	3													3
27E8	1													1
27E9		9												9
28E4					1			7			1			9
28E5								1						1
28E6	1			1	3	1		2			1			9
28E9		1				1								2
29E3								1	1					2
29E4					1			11	1		1			14
29E5				1	1	2		3						7
29E6		1		4	10	3	1	8				1		28
29E7	1	1		1		1								4
29E8					1			1			1			3
29E9					6									6
29F0					21	1								22
29F1					1	1								2
30E1											1	1		2
30E2								1						1
30E4								21	1		1			23
30E5								3						3
30E6				1	1									2
30E7			1											1
30E8				137	2									139
30E9	1			2	475	2		1						481
30F0					393	486	10							889
30F1						14	2	1						17
31E0								3				1		4
31E3								2						2
31E4								7						7
31E5								36	1			2		39
31F1					6	41	7							54
31F2						2	1							3
32E3								2			1			3
32E4								7						7
32E5								203						203
32E6								4	13					17
32F1						2	1							3
32F2					3	9								12
32F3					1									1
32F4								1						1
33E2											1			1
33E3								1			1		1	3
33E4								2						2
33F1						2								2
33F2					5	2								7
33F3					4	3								7
33F4						1								1
34E4													1	1
34E5								1						1
34F2					1	9	1							11

Table 3: Plaice tag and recapture records from the Celtic Sea. Data arranged by ICES statistical rectangle (continued).

	Release Rectangle													
Recapture Rectangle	26E8	27E9	30E7	30E8	30E9	30F0	30F1	32E5	32E6	34E5	35E6	36E6	38E6	Grand Total
34F3					2	5	1							8
35E4											1	1		2
35E6											49			49
35F0						1								1
35F2					1	5	1							7
35F3					1	4								5
35F4						1								1
35F5							1							1
36E4								1				1		2
36E5											1		1	2
36E6										1	27	55	5	88
36F2						1								1
36F3						1								1
36F4						1								1
37E3													1	1
37E5											1		8	9
37E6											4	14	54	72
37E7												1		1
37F0					1	2								3
37F1					1									1
37F5													1	1
38E4													1	1
38E5													9	9
38E6								1			1		513	515
38E9						1								1
38F1						1								1
38F2					1	3								4
38F4						1								1
39E4												1		1
39F2						1								1
39F3					1									1
40E9						1								1
40F0						2								2
41E9						1								1
41F4								1						1
42F5													1	1
42F6											1			1
43F7													1	1
Grand Total	7	12	1	147	944	615	26	333	17	1	94	78	597	2872

E.4 Analysis of the effort data of the French fleet operating in the Celtic sea

Contribution to the EU project DST2, June 2001

Ludger Evers, Verena Trenkel and Stephanie Mahevan, IFREMER Nantes, France

E.4.1 Introduction

This paper summarises the results of the analysis of the French Celtic sea catch and log-book data for the years 1991-1998. The analysis had two main aims : 1. identification of fishing métiers by grouping boats that have similar catch profiles and 2. definition of homogenous fishing zones and seasons. The results are intended as building blocks for the multi-area and multi-species assessment model for the Celtic sea case study.

The catch data was available per fishing trip and fishing boat while time spent fishing (fishing effort) was available per statistical rectangle for each fishing trip (fishing sequence).

E.4.2 Identification of métiers

The definition of fishing métiers proposed in this section is based on the species composition of the catch. The métiers can then be used to define fleets with homogeneous catch profiles. In this sense of fleet, one ship can belong to several fleets.

Principal Component Analysis

For this purpose the relative estimations of catch associated with each statistical rectangle are used. This relative estimation, which sum to 1 per species and per trip, is multiplied by the total catch of that species during the trip and the current price to obtain the value of the catch of one specific species in one specific rectangle. This total estimation is finally divided by the value of the total catch in that rectangle to obtain the percentage in value of each species per rectangle.

The resulting matrix is used for a PCA using the *covariance* matrix. The PCA is weighted and the total value of the catch is used as weight.

Analysis using all data

	Comp. 1	Comp. 2	Comp. 3	Comp. 4	Comp. 5	...
Proportion of variance explained	0.2874	0.1990	0.1078	0.0697	0.0579	...
Cumulative proportion	0.2874	0.4865	0.5942	0.6640	0.7219	...

Figure 1 shows the *biplots* for all the data.

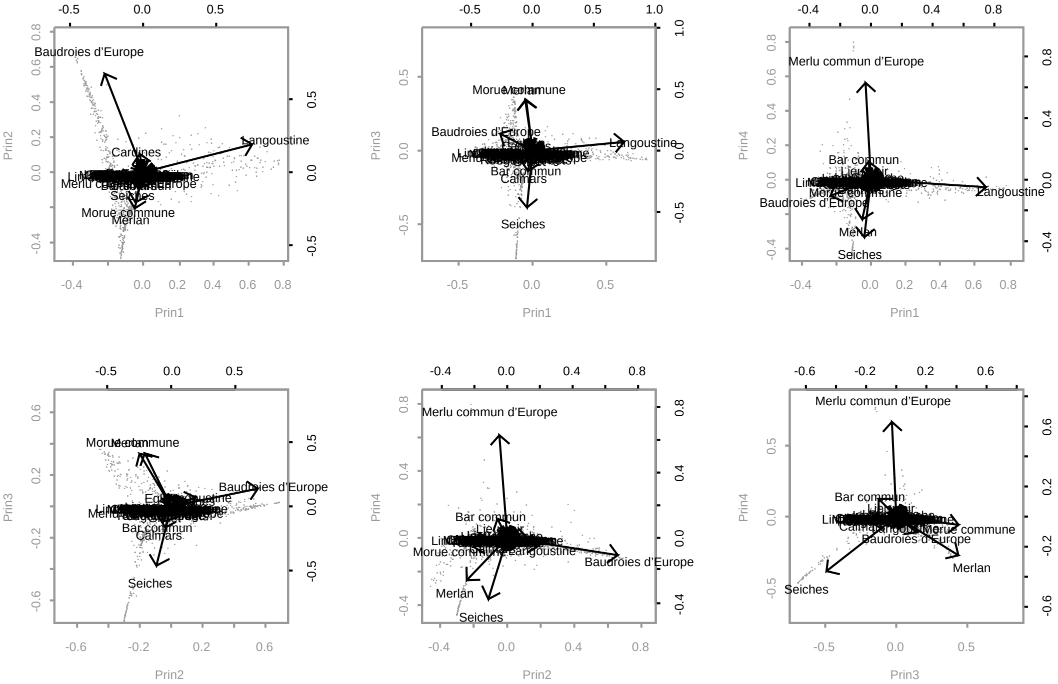


Figure 1: *Biplots* of the first four principal components using all data.

Analysis per fleet: coastal fleet and offshore fleet

As both coastal and offshore fisheries are observed in the Celtic sea it seems to be necessary to analysis both fleets separately to preserve coastal métiers.

A trip was defined to be coastal if the vessel had a length of less than 10m *or* if the duration was no longer than two days (48h hours).

Coastal fleet The following table and figure 2 show the results:

	Comp. 1	Comp. 2	Comp. 3	Comp. 4	Comp. 5	...
Proportion of variance explained	0.3839	0.1615	0.1075	0.0713	0.0538	...
Cumulative proportion	0.3839	0.5454	0.6529	0.7243	0.7781	...

Offshore fleet The following table and figure 3 show the results:

	Comp. 1	Comp. 2	Comp. 3	Comp. 4	Comp. 5	...
Proportion of variance explained	0.3056	0.2065	0.1003	0.0694	0.0551	...
Cumulative proportion	0.3056	0.5121	0.6124	0.6817	0.7368	...

The different results confirm the decision to divide into a coastal and a offshore fleet.

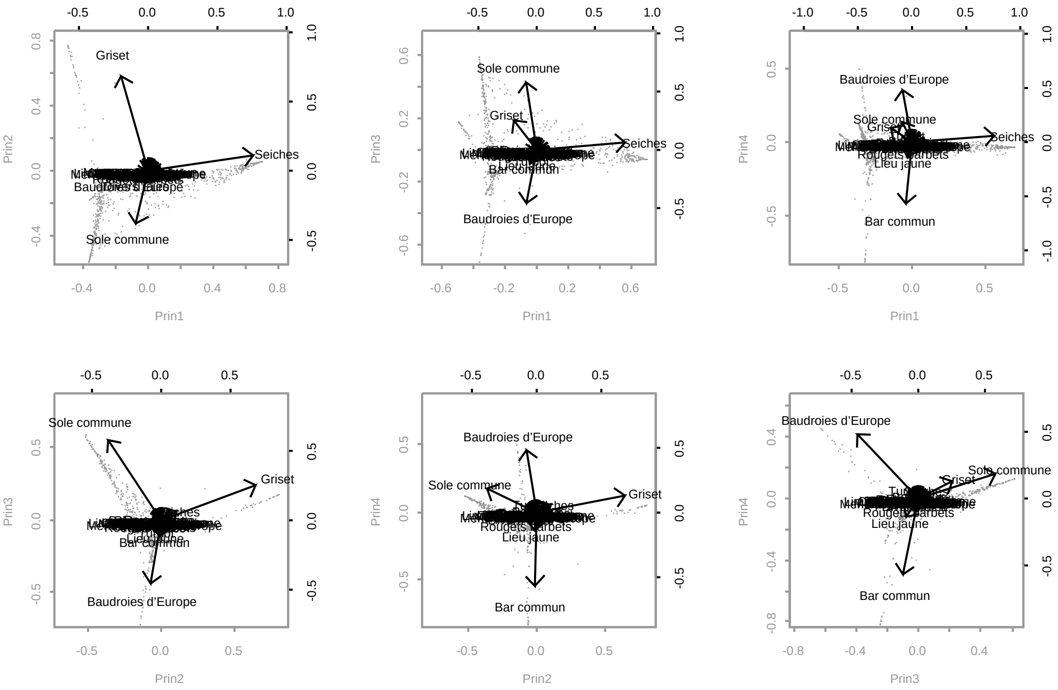


Figure 2: *Biplots* of the fist four components for the coastal fleet.

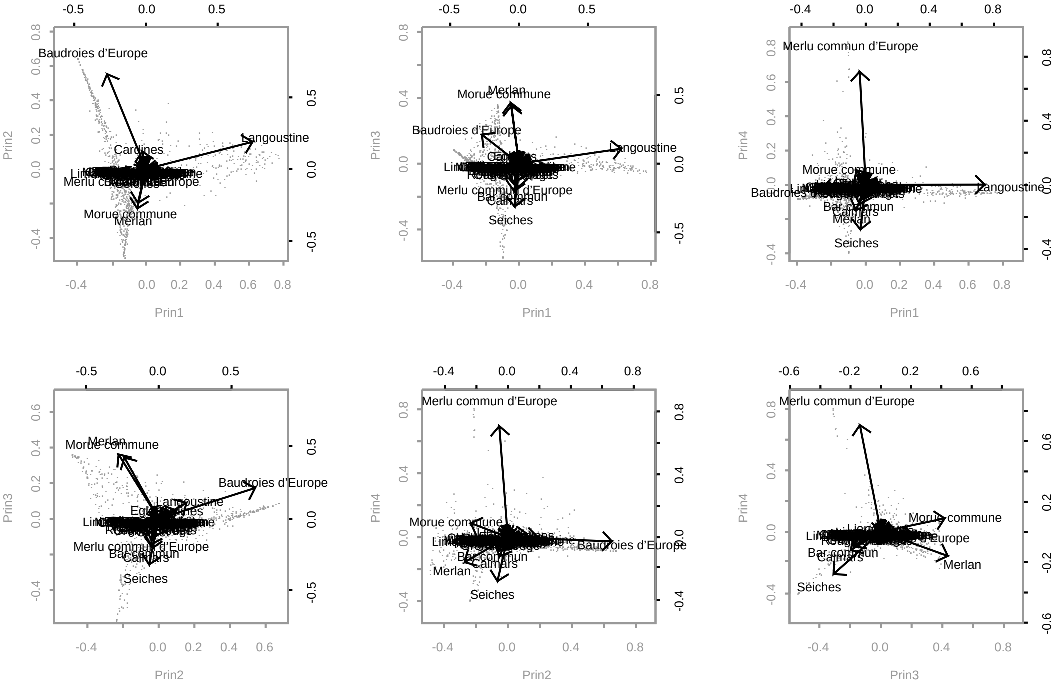


Figure 3: *Biplots* of the fist four components for the offshore fleet.

Cluster analysis

A cluster analysis can be used to obtain the métiers. The first four components of each fleet were analysed separately using that technique.

As the data set is too big (too many observations) a two step approach is used:

1. A hierarchical cluster analysis using complete linkage was applied to several samples of 10,000 observations. All samples clearly showed for the coastal fleet a partition into four clusters and for the offshore fleet a partition into six clusters having more or less the same cluster centres.

2. The k-means clustering method was applied to the whole data set using the six/four clusters obtained in the step before as initial class centres.

The following coastal métiers were found (characterised by the dominating species): Black seabram (small métier), sole, cuttlefishes and anglerfish. The offshore métiers can be characterised by the following species: anglerfish, whiting/cod, hake, nephrops, cuttlefishes and mixed fishery. The métiers cuttlefishes and anglerfish for the coastal and the are offshore fleet have each different catch profiles, so they are not put together.

Figure 4 shows the spatial distribution of métiers and indicates a serious problem with the approach. In the northwest of the Celtic sea (rectangles 31D4-34D4 and 36D6-37D7) only the métier "cuttlefish" is predicted although there is no cuttlefish to be found in that part of the Celtic sea.

This phenomenon can be explained in the following way: In these rectangles none of the principal species is caught. These rectangles are dominated by ling. As ling is no métier of its own these rectangles were classified into the métier "cuttlefish" as this métier had the highest ling "residual".

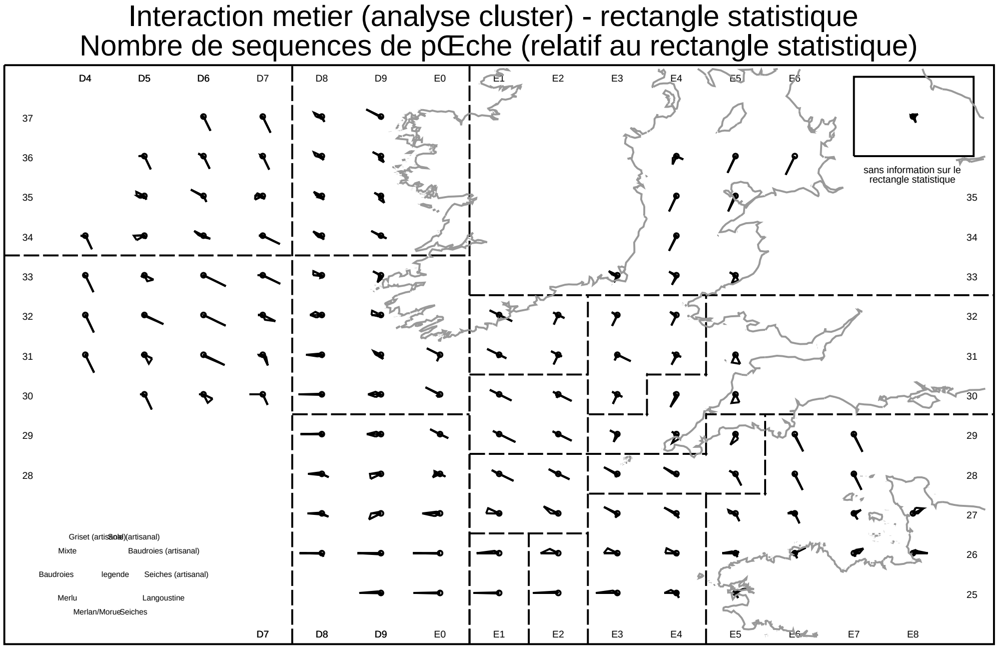


Figure 4: The spatial distribution of métiers which were obtained by cluster analysis.

Final definition of métiers

As the cluster analysis led to some métiers being estimated to be present in rectangles were they cannot occur, some reassignements were carried out manually based on the métier definitions found in the cluster analysis. The different métiers were characterised by one of the following (group of) species:

1. hake, haddock, ling, pollack and saithe (gadoids I)
2. whiting and cod (gadoids II)
3. nephrops
4. anglerfish
5. cuttlefishes
6. flat fish, especially sole

If none of the above groups could unify more than 35%, the observation was classified into the métier "mixed fishery".

Figure 6 shows the composition of the final métiers. Figure 5 shows a strong interaction between the rectangle and the métier.

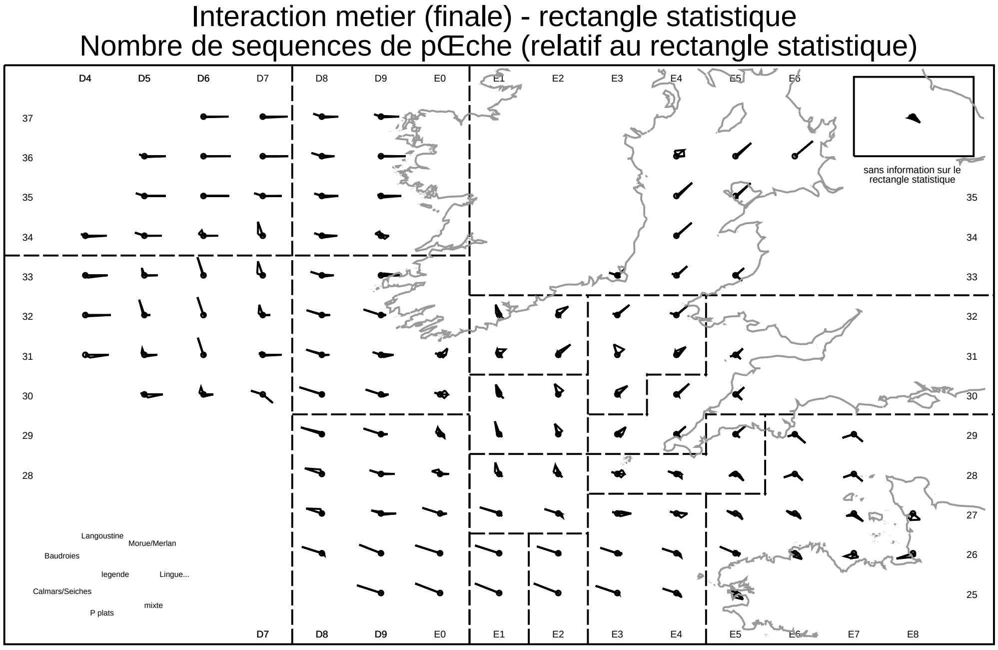


Figure 5: The spatial distribution of the different metiers.

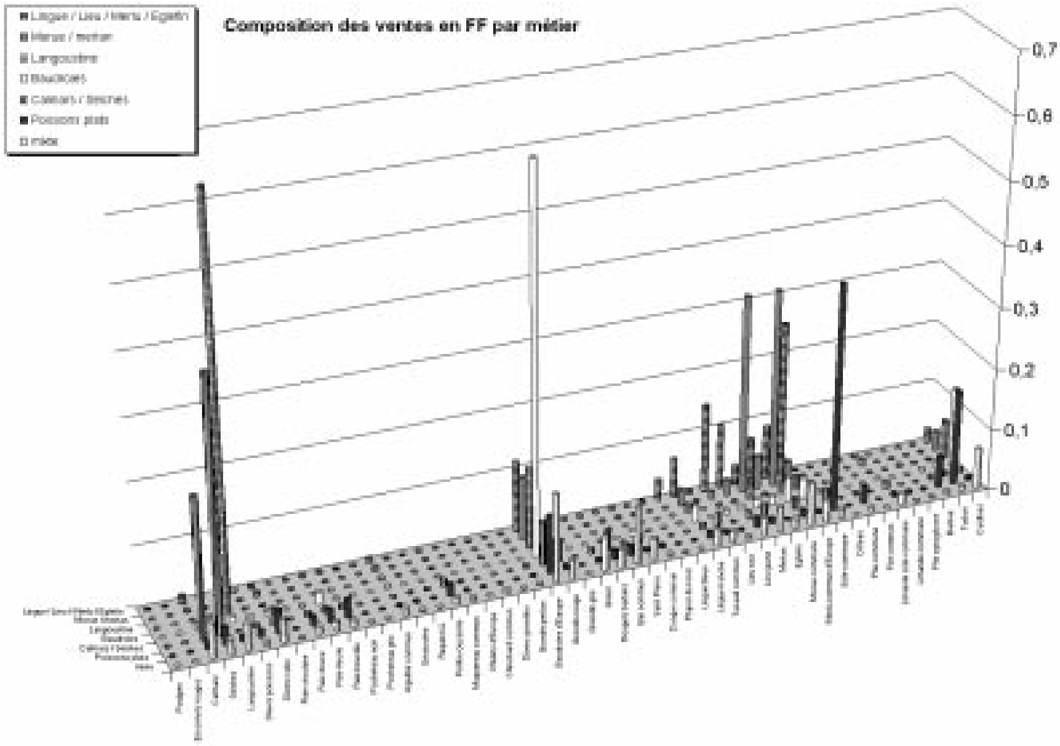


Figure 6: The catch profiles per métier.

Combinations of métiers*

The following combinations of métiers during one trip were found:

	gadoids I	gadoids II	nephrops	anglerfish	cuttlefish	flat fish	mixed
only this métier	18,4 %	4,5 %	31,7 %	41,7 %	92,0 %	95,0 %	52,5 %
gadoids I	0,0 %	23,6 %	4,6 %	10,9 %	0,8 %	0,4 %	6,1 %
gadoids II	34,5 %	0,0 %	19,9 %	17,1 %	1,8 %	1,0 %	14,0 %
nephrops	6,6 %	19,5 %	0,0 %	13,4 %	0,1 %	0,9 %	12,7 %
anglerfish	21,9 %	23,5 %	18,8 %	0,0 %	0,9 %	1,2 %	11,4 %
cuttlefish	1,4 %	2,2 %	0,1 %	0,8 %	0,0 %	0,2 %	2,9 %
flat fish	0,3 %	0,6 %	0,5 %	0,5 %	0,1 %	0,0 %	0,4 %
mixed	16,8 %	26,3 %	24,3 %	15,6 %	4,4 %	1,3 %	0,0 %

(Trips involving more than two sequences count several times).

E.4.3 Combination of gears

Different gears are nearly never combined during one trip:

		1	2	3	4	5	6	7	8	9	10	11
	only this gear	25112	1598	6268	1251	67705	1932	71	18	1292	21	84
1	unspecified	—	0	2	0	12	0	0	0	0	0	0
2	gill nets	0	—	3	3	0	0	0	0	0	0	0
3	trammel nets	2	3	—	56	31	0	1	0	0	0	0
4	tangle nets	0	3	56	—	0	0	0	0	0	0	0
5	bottom trawl with doors	12	0	31	0	—	0	0	0	137	0	0
6	twined bottom trawl	0	0	0	0	0	—	0	0	0	0	0
7	several bottom trawls	0	0	1	0	0	0	—	0	0	0	0
8	pair. trawl (2 vessels)	0	0	0	0	0	0	0	—	4	0	0
9	pel. pair. trawls (2 vessels)	0	0	0	0	137	0	0	4	—	0	0
10	pel. pair. trawls (mesh<20mm)	0	0	0	0	0	0	0	0	0	—	0
11	several pair. trawls	0	0	0	0	0	0	0	0	0	0	—

E.4.4 Analysis of presence/absence

Firstly only presence/absence of fishing activity in a given rectangle is modelled. Using the variables

Y_{ijk}	number of sequences in the rectangle R_i that took place in the month M_j of the year A_k
$Z_{ijk} = 1_{\{Y_{ijk}>0\}}$	indicator of presence of effort in the rectangle R_i in the month M_j of the year A_k.

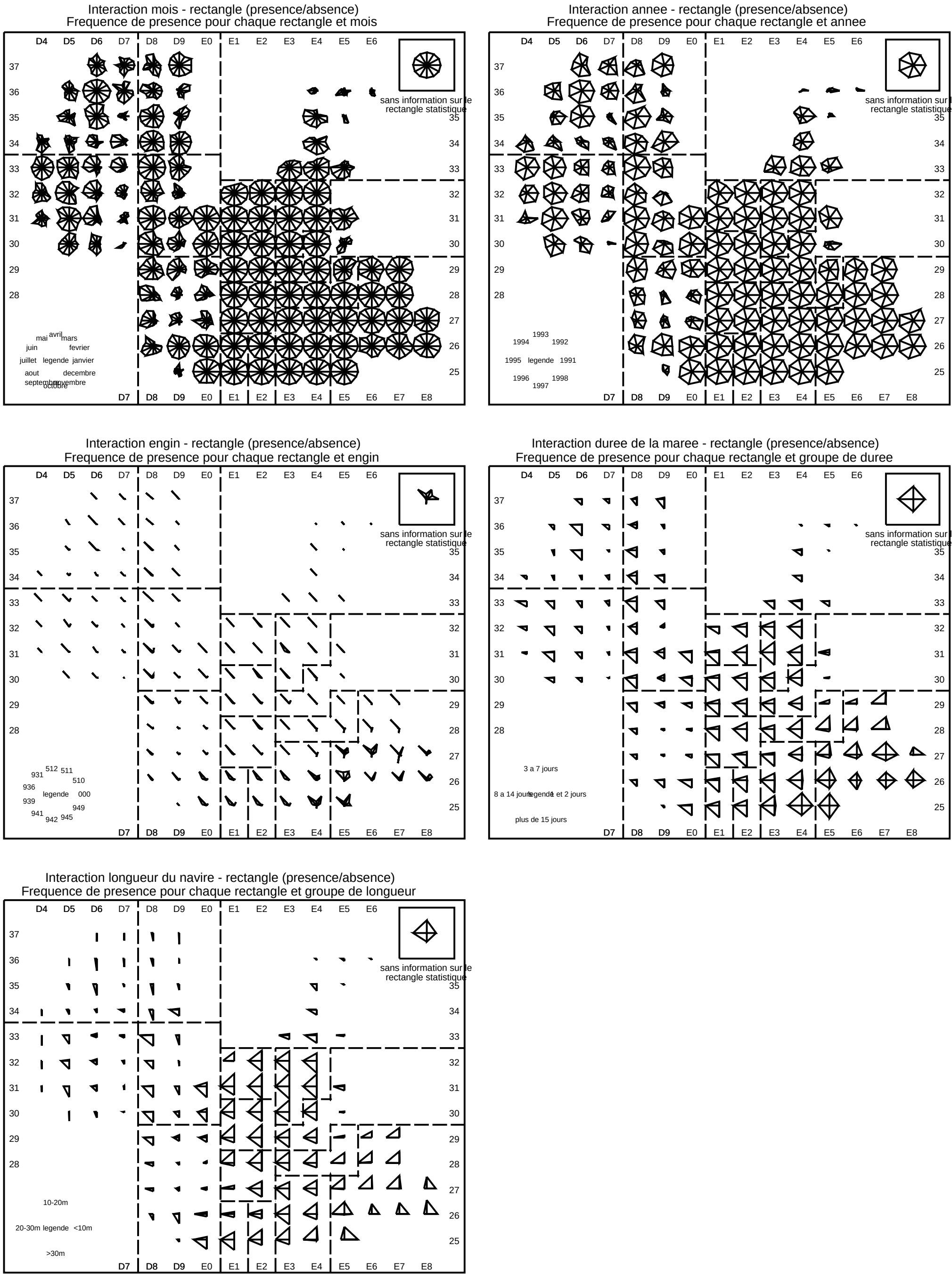
we try to model

$$logit\left(P\left(Z_{ijk}=1\right)\right) = logit\left(P\left(Y_{ijk}>0\right)\right) = X'\beta$$

using logistic regression.

Descriptive analysis

The descriptive analysis (Figure 7) shows a huge spatio-temporal interaction, as well as huge interaction between the additional factors and the statistical rectangle.


Interaction mois - rectangle (presence/absence)
Frequence de presence pour chaque rectangle et mois

Interaction annee - rectangle (presence/absence)
Frequence de presence pour chaque rectangle et annee

Interaction engin - rectangle (presence/absence)
Frequence de presence pour chaque rectangle et engin

Interaction duree de la maree - rectangle (presence/absence)
Frequence de presence pour chaque rectangle et groupe de duree

Interaction longueur du navire - rectangle (presence/absence)
Frequence de presence pour chaque rectangle et groupe de longueur

Figure 7: Interaction between rectangle, month, year and different factors (presence)

Spatio-temporal models

Main effects model using ICES divisions

$$logit\left(P\left(Z_{ijk}^{sec}=1\right)\right)=\beta_0+\gamma_i^{sec}+\kappa_j+\nu_k$$

This model doesn't have a high spatial resolution and does not take into account any interactions. Therefore is doesn't explain a high proportion of the deviance.

Goodness of fit			
AIC			8998.757
SC / BIC			9240.532
$-2\ln(L)$			8932.757
Global test for $H_0 : \beta = 0$			
Test	DF	χ^2	p-value
logratio	32	2913.7193	< .0001
score	32	2345.8065	< .0001
Wald	32	1003.1341	< .0001

In this model all the main effects are significant:

Effet		DF	Wald χ^2	p-value
division	γ^{sec}	14	135.0799	< 0.0001
month	κ	11	140.1073	< 0.0001
year	ν	7	825.5876	< 0.0001

Model with interactions using the ICES divisions

As a huge spatio-temporal interaction has been discovered in the descriptive analysis, it seems to be necessary to incorporate interactions: In the model

$$\begin{aligned}logit\left(P\left(Z_{ijk}^{sec}=1\right)\right) &= \beta_0+\gamma_i^{sec}+\kappa_j+\nu_k+\\ &\quad(\gamma^{sec}\kappa)_{ij}+(\gamma^{sec}\nu)_{ik}+(\kappa\nu)_{jk}+\\ &\quad(\gamma^{sec}\kappa\nu)_{ijk}\end{aligned}$$

all the interactions except the third order interaction are significant:

Effect		DF	Wald χ^2	p-value
division	γ^{sec}	14	135.0799	< 0.0001
mois	κ	11	56.0199	< 0.0001
year	ν	7	33.6520	< 0.0001
division:month	$(\gamma^{sec}\kappa)$	154	281.7132	< 0.0001
division:year	$(\gamma^{sec}\nu)$	98	323.5574	< 0.0001
year:month	$(\kappa\nu)$	77	130.0565	0.0002
division:month:year	$(\gamma^{sec}\kappa\nu)$	1078	262.7502	1.000

So the best fitting model is

$$\begin{aligned}logit\left(P\left(Z_{ijk}^{sec}=1\right)\right) &= \beta_0+\gamma_i^{sec}+\kappa_j+\nu_k+\\ &\quad(\gamma^{sec}\kappa)_{ij}+(\gamma^{sec}\nu)_{ik}+(\kappa\nu)_{jk}\end{aligned}$$

Its goodness of fit criteria are the following:

Goodness of fit			
AIC			8782.915
SC / BIC			11435.116
$-2\ln(L)$			8058.915
Global test for $H_0 : \beta = 0$			
Test	DF	χ^2	p-value
logratio	361	3787.5614	$< .0001$
score	361	3300.5538	$< .0001$
Wald	361	1210.4824	$< .0001$

The logratio statistic for the comparison between this model and the main effects model is 873.842 having 329 DF which results in a p-value lower than 0.001. Although interactions are now taken into account, this model still doesn't explain more than one third of the deviance. This is due to the heterogeneity of the ICES divisions and autocorrelations.

Main effects model using statistical rectangles

The model

$$logit\left(P\left(Z_{ijk}=1\right)\right)=\beta_0+\gamma_i+\kappa_j+\nu_k$$

explains also only about 40% of the deviance. But its higher spatial resolution makes it significantly better than the marginal model using the ICES divisions. The corresponding logratio-test has a statistic of 1666.105 for 102 DF and therefore a p-value of less than 0.0001.

Goodness of fit			
AIC			7536.652
SC / BIC			8525.733
$-2\ln(L)$			7266.652
Global test for $H_0 : \beta = 0$			
Test	DF	χ^2	p-value
logratio	134	4579.8240	$< .0001$
score	134	4058.6944	$< .0001$
Wald	134	1432.9831	$< .0001$

Also in this model, all effects are significant.

Effect		DF	χ^2 de Wald	*p-value*
Statistical rectangle	γ	116	1321.6280	< 0.0001
month	κ	11	147.7925	< 0.0001
year	ν	7	172.5355	< 0.0001

Model with interactions using the statistical rectangle

For numeric reasons or reasons of asymptotics, this model cannot be computed using logistic regression; the three asymptotically equivalent tests Wald test, logratio test and score test from the "global" hypothesis $H_0 : \beta_0 = 0$ don't give the same results:

test	DF	χ^2	*p-value*
logratio	7978.3260	2299	< 0.0001
score	6829.3397	2299	< 0.0001
Wald	1064.7548	2299	1.0000

Heterogenity of ICES divisions

The marginal model using the statistical rectangle can be used to verify the homogeneity of the ICES divisions. For that reason the hypothesis that all spatial parameters γ_i are equal will be tested. The Wald test for $H_0 : \{\gamma_i = \gamma_j \forall i, j$ of the same division $\}$ gives for each division and overall the following results:

division	Wald χ^2	DF	p-value
7A1	236.0445	8	< 0.0001
7B1	98.03134	7	< 0.0001
7C1	128.9021	11	< 0.0001
7E1	19.01295	12	0.0882
7E2	2.220325	3	0.5280
7F1	34.78794	4	< 0.0001
7G1	4.238084E-28	3	1.0000
7G2	2.673959	4	1.0000
7G3	5.243762	3	0.1547
7H1	0.312870	1	0.5759
7H2	4.173992E-28	7	1.0000
7H3	2.278404E-29	3	1.0000
7J1	190.8397	13	< 0.0001
7J2	118.6446	9	< 0.0001
7K1	209.9677	14	< 0.0001
overall	1017,280	102	< 0.0001

Only the sectors having a nearly permanent presence cannot be shown to be significantly heterogeneous. Hence the hypothesis of homogeneity of ICES divisions seems to be doubtful.

Geomorphologic models

Geomorphologic differences among the ICES divisions could explain the spatial variation in the presence of effort. Therefore the spatial information will be withdrawn of the model and replaced by the depth and the type of sediment. The type of sediment is a sequence of eight percentages indicating which percentage of the surface of the corresponding rectangle is covered by the corresponding sediment. The eight types of sediment used are: rocks, banks, sand waves, pebbles, shelly sands, fine sands, muddy sands, shelf muds and plain[1]

Model using only the geomorphologic characteristics

We use the model

$$\mathit{logit}\left(P\left(Z_{ijk}=1\right)\right) = \beta_0 + \beta_1 \cdot \mathrm{prof}_i + \iota_1 \cdot \mathrm{sedi}_i^1 + \cdots + \iota_8 \cdot \mathrm{sedi}_i^8 + \kappa_j + \nu_k$$

where prof_i indicates the depth and sedi_i^1 à sedi_i^8 the proportions of each of the eight sediments in the rectangle R_i.

In this model all the parameters except plain are significant:

Effect		DF	Wald χ^2	p-value
depth	β_1	1	45.4943	< 0.0001
rocks	ι_1	1	14.2546	0.0002
banks	ι_2	1	31.0119	< 0.0001
sand waves	ι_3	1	135.9991	< 0.0001
pebbles	ι_4	1	8.8216	0.00300
shelly sands	ι_5	1	27.1570	< 0.0001
fine sands	ι_6	1	12.1227	< 0.0001
muddy sands	ι_7	1	121.2068	0.0005
shelf muds	ι_8	1	141.7638	$< 0; 0001$
plain	ι_{10}	1	1.8957	0.1686
month	κ	11	112.7768	< 0.0001
year	ν	7	132.0389	< 0.0001

But also this model does not explain a high proportion of the deviance:

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[1] The sum of these percentages is not 1, but the percentage of the rectangle covered by sea.

Goodness of fit			
AIC			9619.528
SC / BIC			9831.997
$-2\ln(L)$			9561.528
Global test for $H_0 : \beta = 0$			
Test	DF	χ^2	p-value
logratio	28	2284.9482	$< .0001$
score	28	1587.3446	$< .0001$
Wald	28	825.0943	$< .0001$

Model using the depth, the sediments and the ICES division

The information concerning the sediments seems to be taken into account just as a replacement for the spatial information. Therefore the ICES division is added to the model which can now be written:

$$logit\,(P\,(Z_{ijk} = 1)) = \beta_0 + \beta_1 \cdot \text{prof}_i + \iota_1 \cdot \text{sedi}_i^1 + \cdots + \iota_{10} \cdot \text{sedi}_i^{10} + \gamma^{div}_{\text{devision}_i} + \kappa_j + \nu_k$$

with secteur$_i$ the sector to which the ith rectangle belongs. The information about the rectangle cannot be added, the model would then be overparameterised.

The different sediments rest significant:

Effect		DF	Wald χ^2	p-value
ICES devision	γ^{sec}	14	675.8444	< 0.0001
depth	β_1	1	27.2310	< 0.0001
rocks	ι_2	1	180.2688	< 0.0001
banks	ι_3	1	212.0376	< 0.0001
sand waves	ι_4	1	87.6734	< 0.0001
pebbles	ι_5	1	45.2211	< 0.0001
shelly sands	ι_6	1	8.3537	0.0038
fine sands	ι_7	1	14.9451	0.0001
muddy sands	ι_8	1	9.8567	0.0017
shelf muds	ι_9	1	49.0659	< 0.0001
plain	ι_{10}	1	0.9102	0.3401
month	κ	11	128.3154	< 0.0001
year	ν	7	150.0580	< 0.0001

Goodness of fit			
AIC			8443.845
SC / BIC			8758.886
$-2\ln(L)$			8357.845
Global test for $H_0 : \beta = 0$			
Test	DF	χ^2	p-value
logratio	42	3488.6312	$< .0001$
score	42	2789.9296	$< .0001$
Wald	42	1210.7882	$< .0001$

The model provided a significantly better fit compared to the model without ICES divisions (logratio statistic of 1203.683 having 14 df, therefore a p-value inferior to 0.0001. Compared to the model without sediments and depth the logratio test statistic is 574.912 having 10 df, therefore a p-value of less than 0.0001.

Summary

For all models, the *overall test* was significant having a p-value of less than 0.0001.

Although the model using the statistical rectangle has a better spatial resolution and although the ICES divisions are not homogeneous, the model with interactions using the ICES division seems to be superior to the other models. No model explains more than 40% of the total deviance, which might be due to an temporal and/or spatial autocorrelation.[2]

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[2] cf. section **??**

Finally one has the choice either to neglect the “local” effects or to neglect the interactions.

Spatial and seasonal regrouping

The results of the seasonal and spatial regroupments can be found in figures 8 and 9.

E.4.5 Analysis of the total fishing time

Data and notation

The total fishing time[3] per rectangle, month and year will be modelled in this chapter. This variable is called T_{ijk}, where i indicates the rectangle R_i, j the month and k the year.

To avoid problems with the asymptotics a “classic” linear model is used. But a transformation $\tau : t \mapsto \log(t+1)$ is necessary to obtain (more or less) normal distributed residuals (cf. figure 10).

This transformation leads to the multiplicative model

$$\log(T_{ijk}+1) = \gamma_i + \kappa_j + \nu_k \Longleftrightarrow T_{ijk}+1 = e^{\gamma_i} \cdot e^{\kappa_j} \cdot e^{\nu_k} =: \tilde{\gamma}_i \cdot \tilde{\kappa}_j \cdot \tilde{\nu}_k$$

Like in the analysis of presence/absence all rectangles having overall less than 26 sequences were excluded. Only sequences where the statistical rectangle was specified were used.

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[3] i.e. the sum of the fishing times of all vessels corresponding to that category

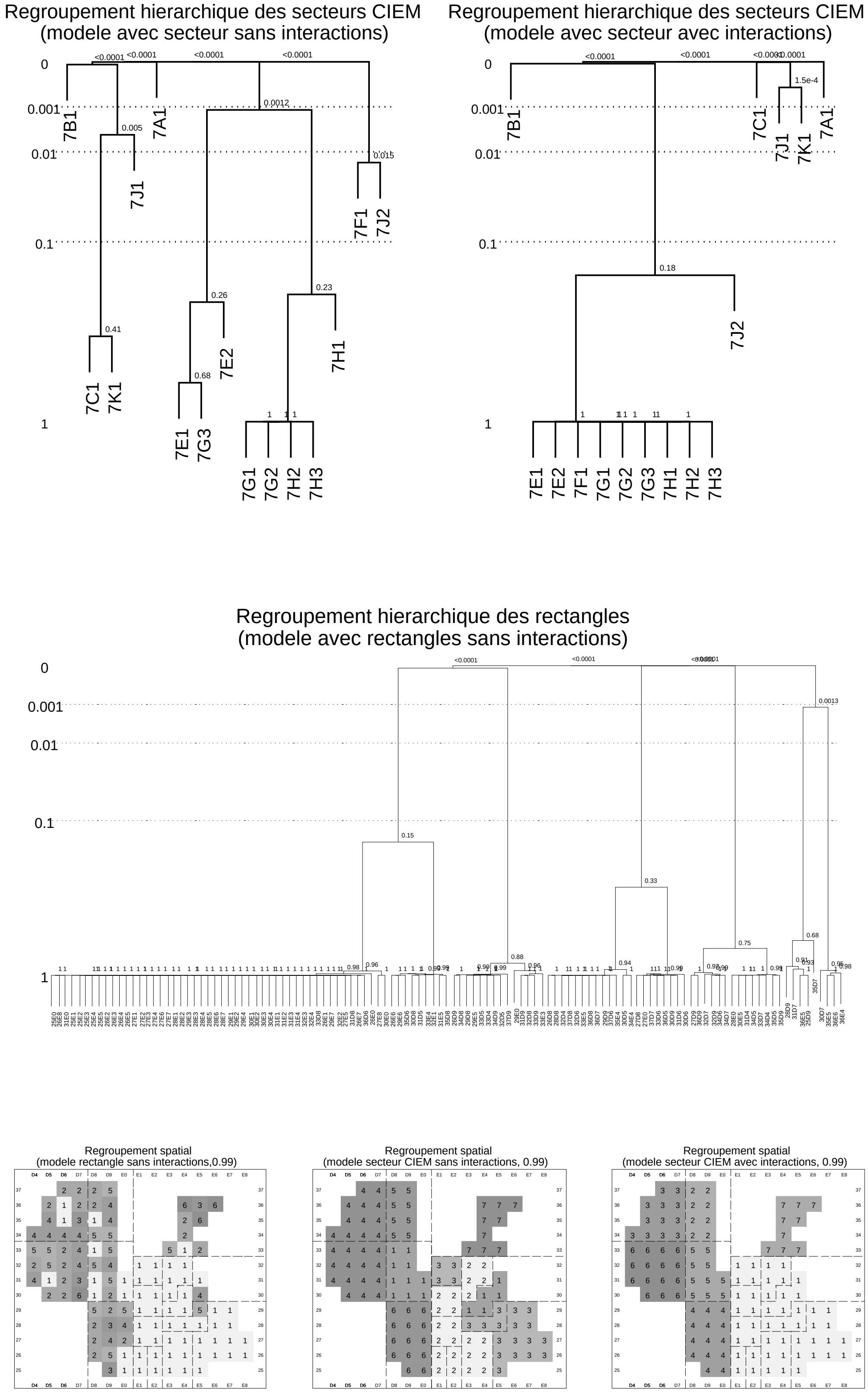
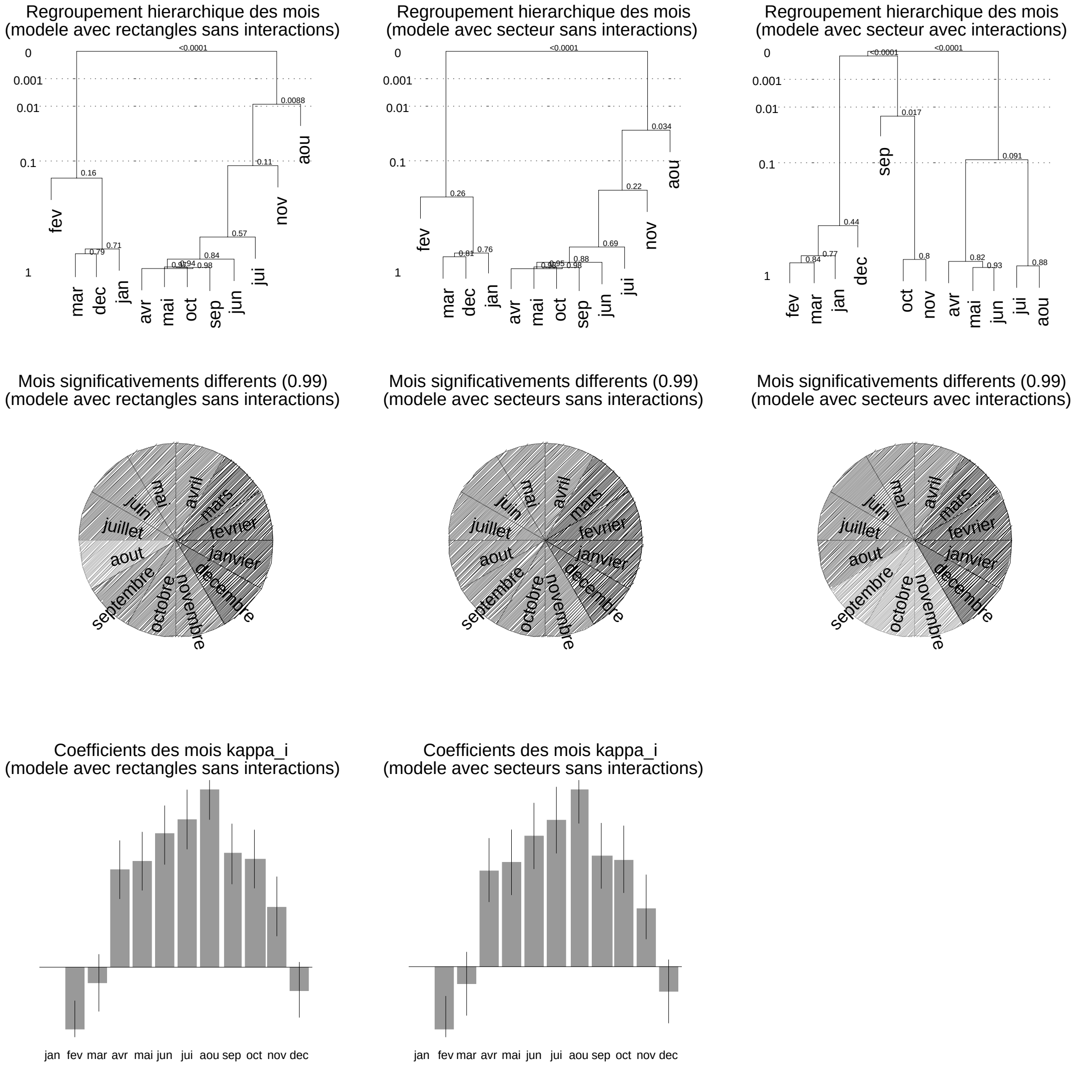


Figure 8: Hierarchical spatial regroupment using the different models and significantly (niveau $1-\alpha=0.99$) different regions


Regroupement hierarchique des mois (modele avec rectangles sans interactions)

Regroupement hierarchique des mois (modele avec secteur sans interactions)

Regroupement hierarchique des mois (modele avec secteur avec interactions)

Mois significativements differents (0.99) (modele avec rectangles sans interactions)

Mois significativements differents (0.99) (modele avec secteurs sans interactions)

Mois significativements differents (0.99) (modele avec secteurs avec interactions)

Coefficients des mois kappa_i (modele avec rectangles sans interactions)

Coefficients des mois kappa_i (modele avec secteurs sans interactions)

Figure 9: Hierarchical seasonal regroupment using the different models and significantly (niveau $1-\alpha=0.99$) different seasons

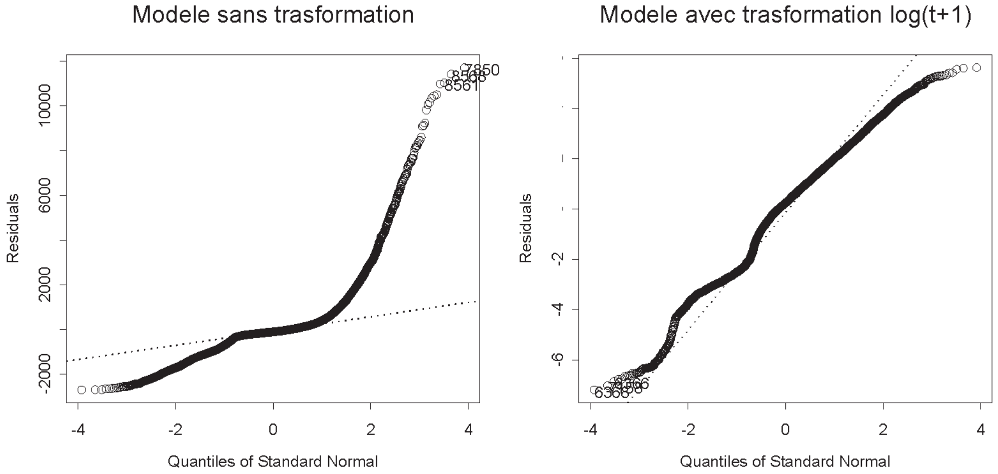


Figure 10: qq-plot of the residuals before and after the $\log(t+1)$ transformation for the main effects model using the ICES division.

Descriptive analysis

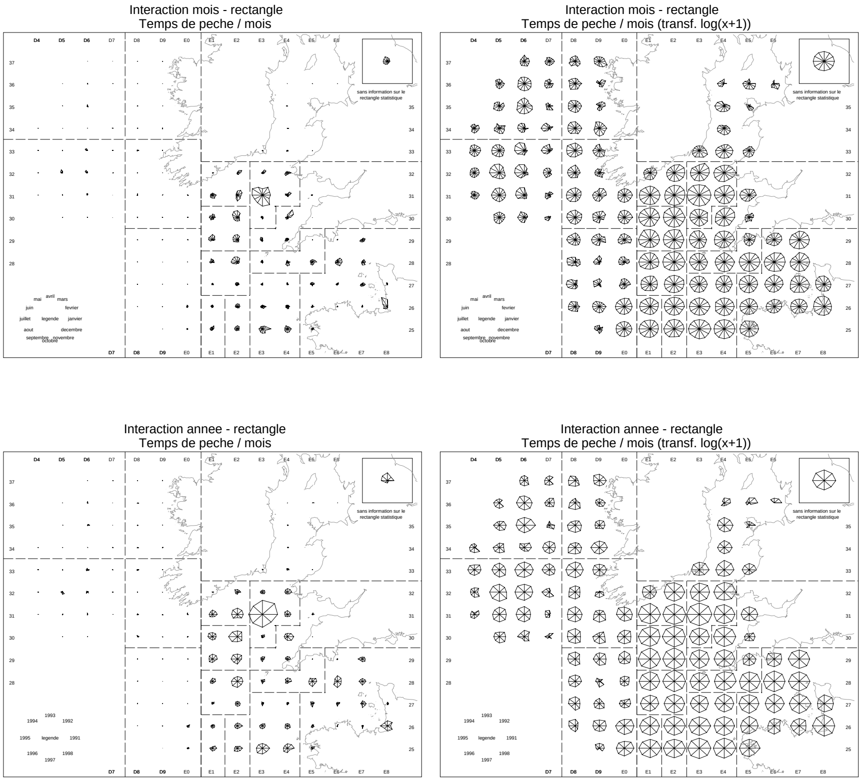


Figure 11: Interaction between the rectangle the year and the month (total fishing time)

Figure 11 shows a strong interaction between the rectangle on the one hand and the month and the year on the other hand.

Spatio-temporal models

Model for rectangle without interactions					
Goodness of fit					
AIC	12056.5559				
SC / BIC	13045.6363				
R^2	0.647				
Global test for $H_0 : \beta = 0$					
	DF	sum sq	mean sq	F statistic	p-value
model	134	58928.3141	439.7635	152.1356	< 0.0001
residuals	11097	32077.0140	2.8906		
total	11231	91005.3281	8.1030		

Model for ICES division without interactions					
Goodness of fit					
AIC	16264.844				
SC / BIC	16506.619				
R^2	0.478				
Global test for $H_0 : \beta = 0$					
	DF	sum sq	mean sq	F statistic	p-value
model	32	43493.838	1359.182	320.375	< 0.0001
residuals	11199	47511.490	4.242		
total	11231	91005.328	8.103		

The main effects model can once more be used to test the homogeneity of the ICES divisions. Once again, this assumed homogeneity cannot be found in the data. The Wald test for H_0 : $\{\gamma_i = \gamma_j \forall i, j$ of the same division$\}$ nearly always rejects this hypothesis:

division	*sum sq* hyp	DF	*mean sq* hyp	F statistic	p-value
7A1	2037.155631	8	254.644454	88.093908	< 0.0001
7B1	711.233764	7	101.604823	35.150053	< 0.0001
7C1	1579.016507	11	143.546955	49.659877	< 0.0001
7E1	943.335500	12	78.611292	27.195471	< 0.0001
7E2	885.702435	3	295.234145	102.135857	< 0.0001
7F1	1963.102426	4	490.775606	169.783163	< 0.0001
7G1	12.839437	3	4.279812	1.480595	0.21760
7G2	310.067536	4	77.516884	26.816862	< 0.0001
7G3	735.067920	3	245.022640	84.765254	< 0.0001
7H1	6.552447	1	6.552447	2.266810	0.13220
7H2	265.368571	7	37.909796	13.114843	< 0.0001
7H3	144.552385	3	48.184128	16.669235	< 0.0001
7J1	2488.542626	13	191.426356	66.223691	< 0.0001
7J2	1290.356704	9	143.372967	49.599686	< 0.0001
7K1	2061.582514	14	147.255894	50.942979	< 0.0001
overall	15434.476404	102	151.318396	52.348396	< 0.0001

Models with interactions

These are models of the type

$$\begin{aligned}\log(T_{ijk}+1) &= \beta_0 + \gamma_i + \kappa_j + \nu_k + \\ &\quad (\gamma\kappa)_{ij} + (\gamma\nu)_{ik} + (\kappa\nu)_{jk} + \\ &\quad (\gamma\kappa\nu)_{ijk}\end{aligned}$$

where either the ICES division or the statistical rectangle is used.

All interactions except the interaction of all the three factors are significant with a p-value of less than 0.001. In the model using the statistical rectangle the interaction of month and years has a p-value of only 0.0220.

Model rectangle with interactions					
Goodness of fit					
AIC					8407.069
SC / BIC					25258.070
R^2					0.827
Global test for $H_0 : \beta = 0$					
	DF	sum sq	mean sq	F statistic	p-value
model	2299	75241.542	32.728	18.544	< 0.0001
residuals	8932	15763.786	1.765		
total	11231	91005.328	8.103		

Model ICES division with interactions					
Goodness of fit					
AIC					15441.103
SC / BIC					18093.304
R^2					0.542
Global test for $H_0 : \beta = 0$					
	DF	sum sq	mean sq	F statistique	p-value
model	361	49365.782	136.747	35.698	< 0.0001
residuals	10870	41639.543	3.831		
total	11231	91005.324	8.103		

The model using the statistical rectangle and taking into account the interactions — which could not be fitted in the presence/absence analysis — best describes the data.

Spatial and seasonal regrouping

The results of the seasonal and spatial regroupments can be found in figures 12 and 13.

Spatio-temporal models with an additional factor

In this chapter the impact of different supplementary factors which allow to define several fleets is examined. The following factors are used:

- the gear used (cf. table of French gear codes:),
- the length of the vessel (four classes: <10m, 10-20m, 20-30m, >40m)
- the length of the trip (four classes: 1/2 days, 2-7 days, 8-14 days more than 14 days)
- the métier.

As the models using the statistical rectangle showed better goodness of fit statistics than the models using the ICES division, the statistical rectangle is used as spatial resolution.

Table 1 shows the goodness of fit characteristics of the different model. When comparing the different factors it has to be taken into account that for each factor another data set (especially having another length) is used for the analysis. Looking at the AIC and the R^2 one can observe that the métier is not a very good additional factor. The fact that the gear and the vessel length explain a big part of the variance confirms the approach of the EU data regulations to define fleets by vessel length and gear.

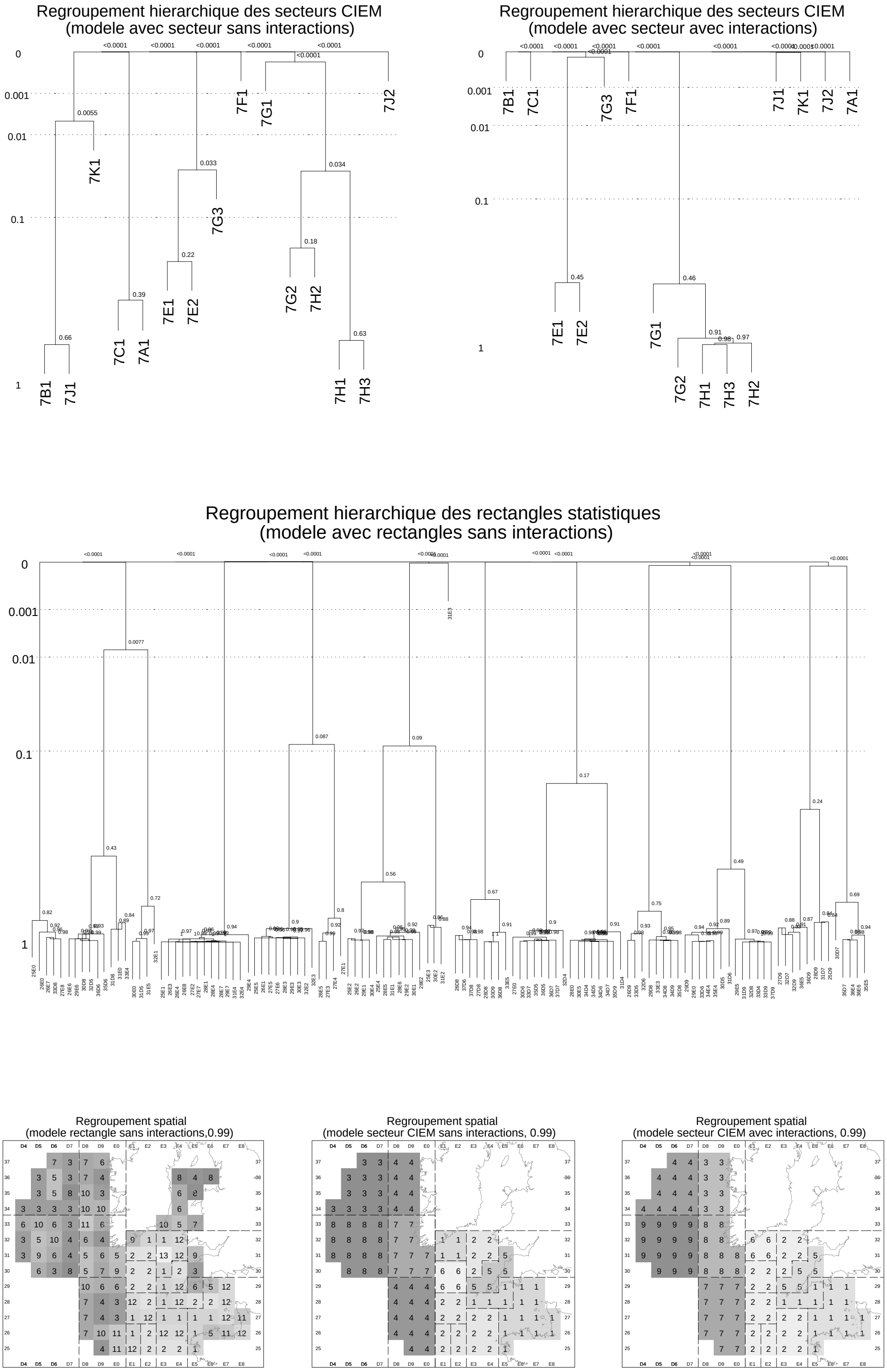


Figure 12: Hierarchical spatial regroupment using the different models and significantly (niveau $1 - \alpha = 0.99$) different regions

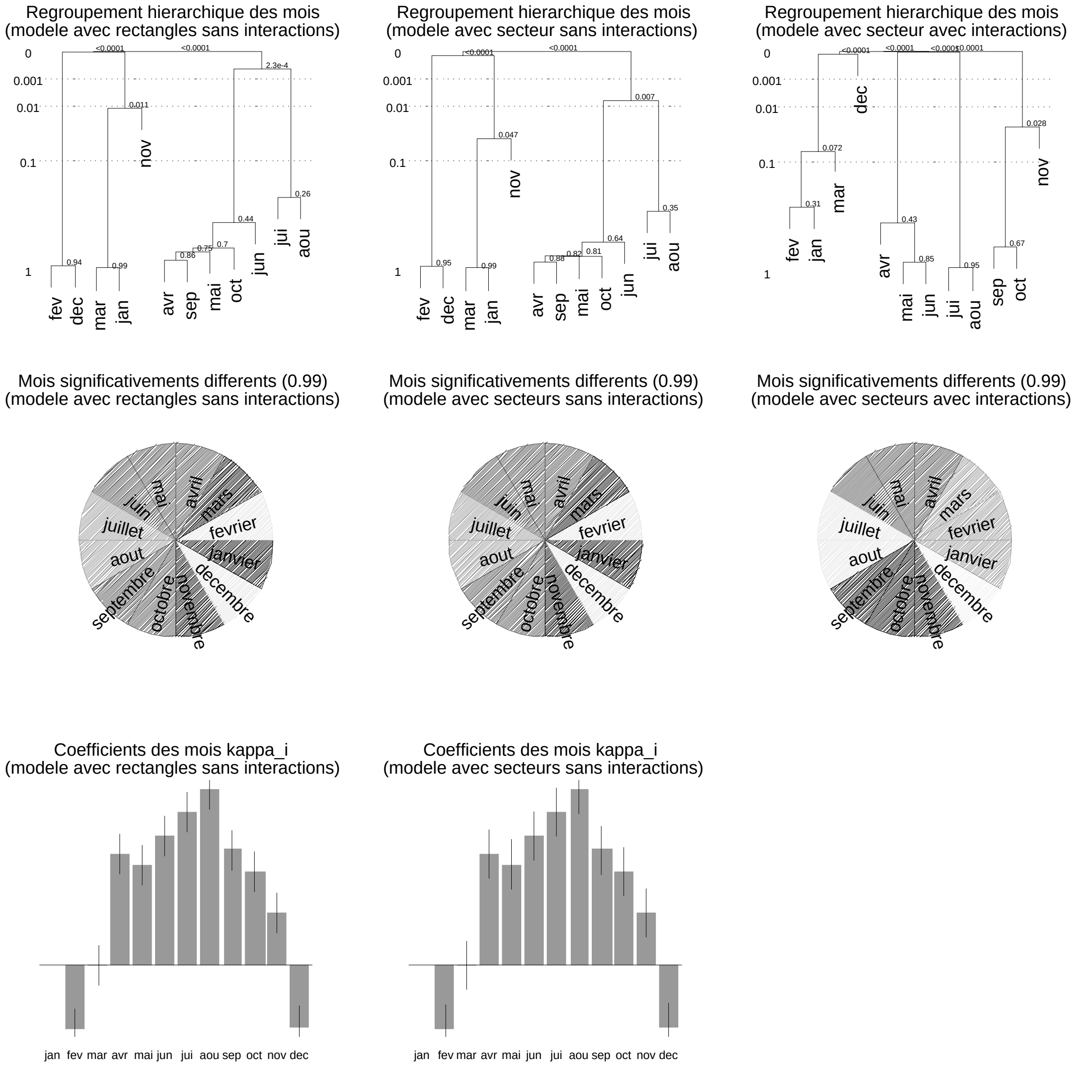


Figure 13: Hierarchical seasonal regroupment using the different models and significantly (niveau $1-\alpha = 0.99$) different seasons

Factor	gear		vessel length		trip duration		métier	
Models without interactions with (and in parenthesis without) the factor								
DF	144	(134)	137	(134)	144	(134)	140	(134)
AIC	22107.12	(122334.77)	52883.16	(85538.21)	39116.75	(85732.16)	104219.75	(118620.07)
F statistic	1162.05	(43.25)	228.8	(101.99)	295	(101.76)	248.12	(166.25)
R^2	0.57	(0.05)	0.41	(0.23)	0.47	(0.23)	0.31	(0.22)
$\Delta SSE/\Delta DF$		18429.96		19064.72		7753.15		5904.54
Models with interactions with (and in parenthesis without) the factor								
DF	3649	(2299)	2704	(2299)	2704	(2299)	3109	(2299)
AIC	-340855.28	(124912.90)	-63093.30	(82405.68)	-53920.14	(80414.12)	13193.03	(82405.67)
F statistic	121.6	(3.27)	55.1	(7.16)	50.11	(7.61)	52.49	(7.16)
R^2	0.79	(0.06)	0.78	(0.28)	0.76	(0.29)	0.68	(0.25)
$\Delta SSE/\Delta DF$		236.78		397.25		374.59		124.86

Table 1: Summary of the different models for fishing time using an additional factor

Analysis of the correlation structure of the residuals

In the fitted models it was assumed that the residuals are uncorrelated. An analysis of the residuals shows however, that there might be both temporal and spatial correlations present. In order to explore this, a new class of models is investigated.

Spatial and temporal autcorrelation

Spatial and temporal autocorrelations are tested using the Durbin-Watson test with the following test statistics

$$DW = \frac{\sum_{i=2}^{n}(\varepsilon_i - \varepsilon_{i-1})^2}{\sum_{i=1}^{n}\varepsilon_i^2} \approx 2(1-\hat{\rho}).$$

The following table gives the mean of the Durbin-Watson test statistics for each type of autocorrelation and for the different models:

	Rectangle statistique		Secteur CIEM	
	sans interaction	avec interactions	sans interaction	avec interactions
Autocorrélation temporelle	1.067248	1.704054	0.77108	0.87282
Autocorrélation spatiale nord-sud	1.145113	1.357657	1.19962	1.32491
Autocorrélation spatiale ouest-est	1.345609	1.52522	1.47923	1.61295

Both temporal and spatial autocorrelations in residuals are significant. Thus it seems necessary to explore a new class of model for this data. This will be done as the next step.

E.4.6 Table: French species names ↔ English species names

French name	Latin name	English name
Aiguillat commun	Squalus acanthias	Spiny dogfish
Bar commun	Dicentrarchus labrax	Sea bass
Barbue	Scophthalmus rhombus	Brill
Baudroies d'Europe	Lophius budegassa	Black anglerfish
Calmars	Lutaria spp	Otter shells
Cardines	Lepidorhombus wiffiagonis	Megrim
Céteau	Microstomus kitt	Lemon sole
Chinchard commun	Trachurus trachurus	Horse mackerel
Congre commun	Conger conger	Europeen conger
Divers grondins	-	Various gurnards
Divers poissons	-	Various fishes
Divers raies	-	Various rays
Eglefin	Melanogrammus aeglefinus	Haddock
Emissoles	Mustelus mustelus	Smoothhound
Encornets rouges	Illex coindetii	Broadtail shortfin squid
Flet commun	Platichtys flesus	European flounder
Griset	Spondyliosoma cantharus	Black seabream
Grondin gris	Eutrigla gurnardus	Grey gurnard
Grondin perlon	Trigla Lucerna	Tub gurnard
Grondin rouge	Aspitrigla cuculus	Red gurnard
Langoustine	Pecten maximus	Common scallop
Lieu jaune	Pollachius pollachius	Pollack
Lieu noir	Pollachius virens	Saithe
Limande commune	Limanda limanda	Common dab
Limande sole commune	Microstomus kitt	Lemon sole
Lingue bleue	Molva diperygia	Blue ling
Lingue franche	Molva molva	Bing
Maquereau commun	Scomber scombrus	Mackerel
Merlan	Merlangius merlangus	Whiting
Merlu commun d'Europe	Merlucius merlucius	Hake
Morue commune	Gadus morhua	Atlantic cod
Mulets d'Europe	-	Mullets
Petite roussette	Scyliorhinus canicula	Smallspotted catshark
Phycis de fond	Phycis blenoides	Greater forkbeard
Plie commune	Pleuronectes platessa	Plaice
Plie cynoglosse	Glyptocephalus cynoglossus	Witch flounder
Pocheteau gris	Raja batis	Blue skate
Pocheteau noir	Raja oxyrinchus	Long-nose skate
Poulpes	Eledone cirrosa	Octopus
Raie bouclée	Raja clavata	Biscuit ray
Raie circulaire	Raja circularis	Sandy ray
Raie douce	Raja montagui	Spotted ray
Raie fleurie	Raja naevus	Cukoo ray
Requin hâ	Galeorhinus galeus	Tope
Rougets barbets	Mullus surmuletus	Striped red mullet
Saint Pierre	Zeus faber	John Dory
Seiches	Sepia officinalis	Common cuttelfish
Sole commune	Solea vulgaris	Sole
Tacaud commun	Trisopterus luscus	Pouting bib
Turbot	Psetta maxima	Turbot

E.5 Revised species list for Celtic Sea GADGET model

(presented at 2001 meeting in Reykjavik)

During the dst^2 plenary meeting in Nantes (June 2000), a preliminary food-web was sketched out (figure 1), based on local knowledge and listing nine commercial species which would be included in the Celtic Sea GADGET model. It was agreed that this would be revised and possibly expanded at future meetings, following examination of the available survey and stomach contents data for the region.

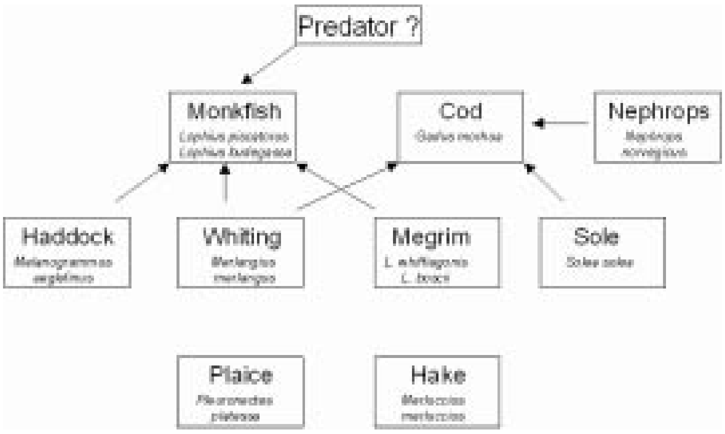


Figure 1: Tentative food-web proposed during the plenary meeting in Nantes, June 2000.

As a first step towards refining/revising the species list, the importance of the different 'chosen' species was examined in terms of their biomass in trawl surveys, their commercial importance (in tonnes landed) and their value (in UK £). The 'selected' species represented only a very small proportion of total fish biomass (figure 2a) and total fishery landings (figure 2b). The 'selected' species represented a high proportion of total value (figure 2c).

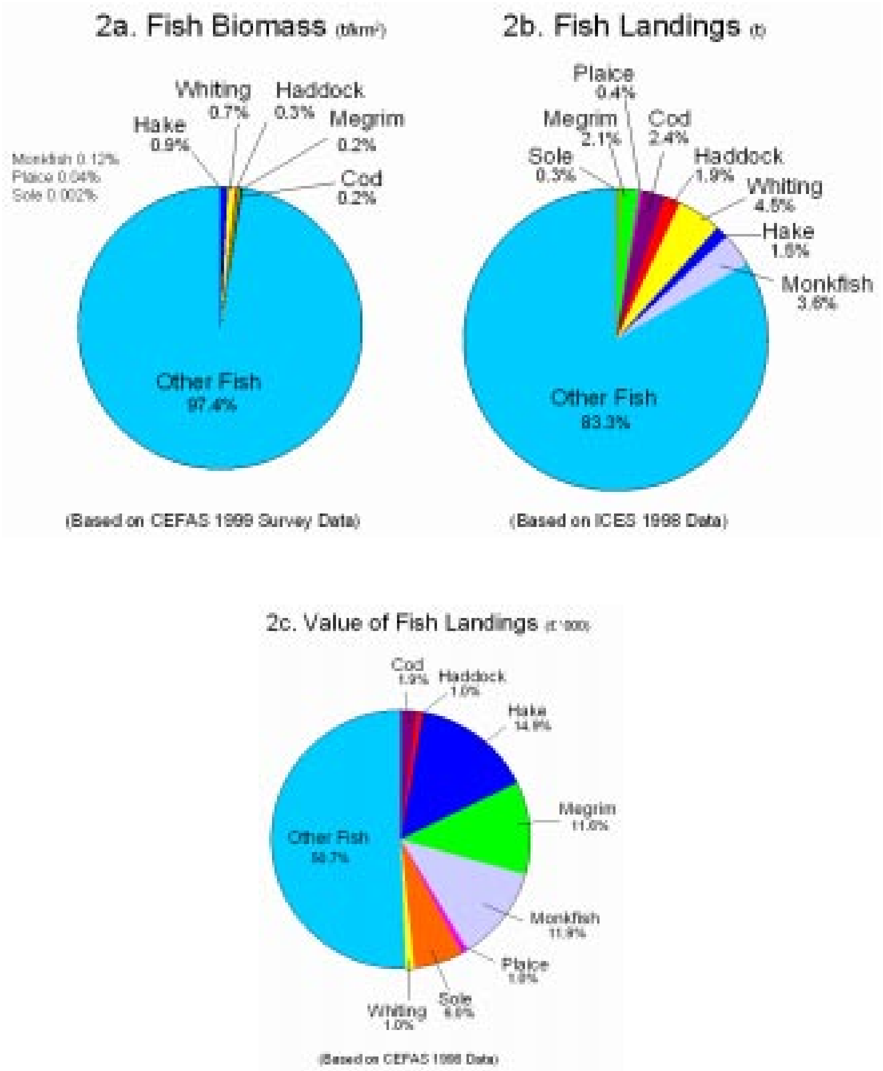


Figure 2: The importance of the nine species proposed during the plenary meeting in Nantes (2000), in terms of total biomass in trawl surveys (a), commercial landings (b) and commercial value (c).

To establish the nature and magnitude of interactions between different components of the Celtic Sea ecosystem, a preliminary model was constructed using ECOPATH software (figure 3). Stomach contents data were collated for 62 fish species (from the literature), and these fishes were then categorised into 'functional groups' according to Bray-Curtis similarity coefficients. The preliminary Ecopath model comprised 18 fish groups (including the 8 'selected' fish species as mono-specific categories), 2 groups of marine mammals, 14 invertebrate groups, 2 primary producers, 2 bacteria groups and detritus. Biomass estimates were based on published literature or CEFAS survey data for the Celtic Sea. PB, QB and unassimilated production values were taken from the literature and/or other models.

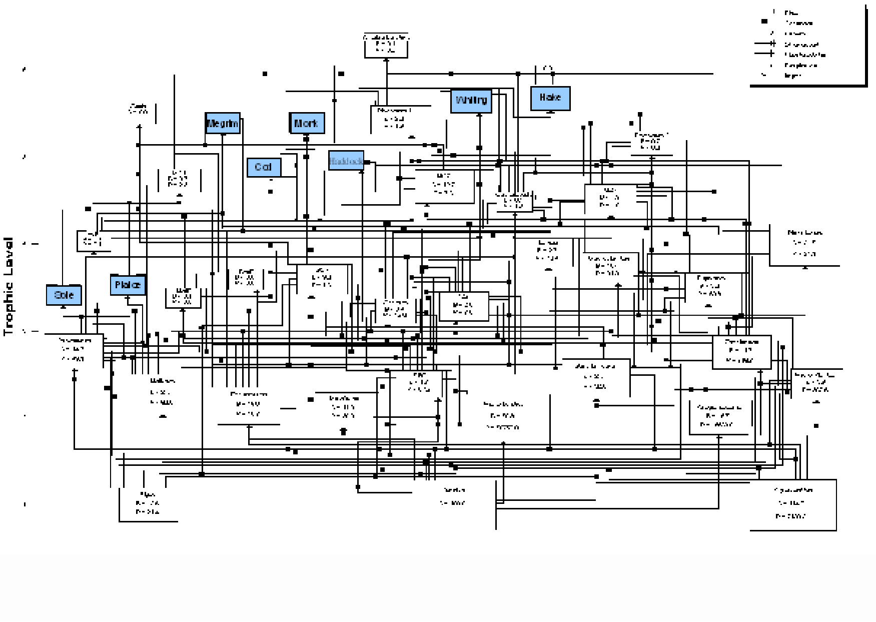


Figure 3: Preliminary ECOPATH model for the Celtic Sea ecosystem, including 8 species chosen during plenary meeting in 2000 (shaded). All fluxes >0.001 t/km2.

Analysis of individual fluxes between components within the system (in t/km2/yr) revealed that most predation by and on the 'selected species' involvesd other animals in the ecosystem (figure 4), i.e. the chosen species do not interact strongly with each other. Plaice and sole did not interact at all with the other 'selected' fish species, either as prey or as predators. Use of prey overlap indices (sensu Hurlbert 1978, Loman 1986), revealed that hake, megrim and whiting have similar prey, whilst use of predator overlap indicies revealed that haddock, whiting and cod have similar predators (Tables 2a and 2b).

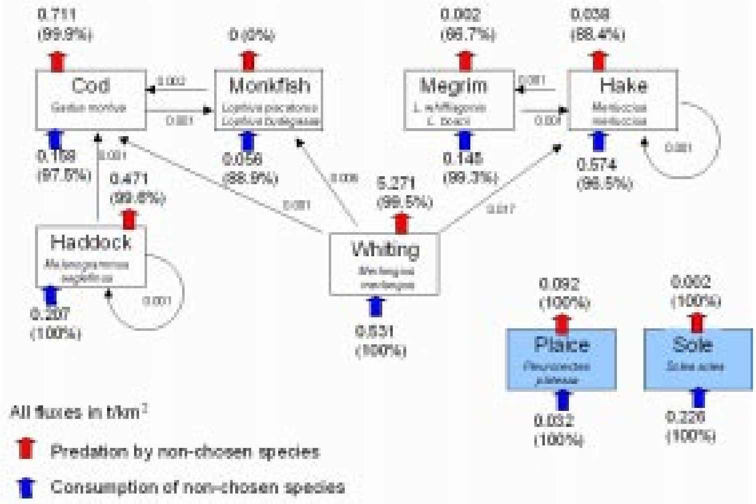


Figure 4: Strength of interactions (in t/km2/yr) between the 8 species chosen during plenary meeting of 2000, as modelled using ECOPATH.

2a. Predator Overlap

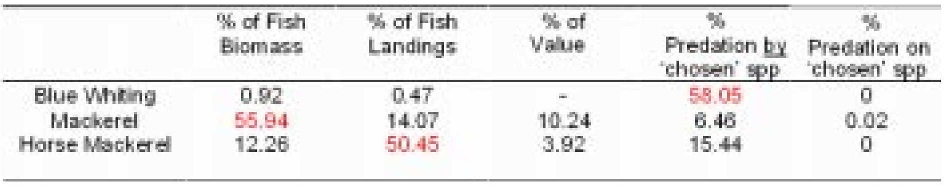
	Cod	Haddock	Monkfish	Megrim	Hake	Whiting	Plaice
Haddock	0.993						
Monkfish	0	0.003					
Megrim	0.305	0.302	0.040				
Hake	0.221	0.129	0	0.086			
Whiting	0.950	0.910	0	0.291	0.466		
Plaice	0	0	0	0.002	0	0.047	
Sole	0	0.001	0.065	0.313	0	0	0.005

2b. Prey Overlap

	Cod	Haddock	Monkfish	Megrim	Hake	Whiting	Plaice
Haddock	0.340						
Monkfish	0.614	0.279					
Megrim	0.591	0.220	0.720				
Hake	0.380	0.134	0.501	0.917			
Whiting	0.355	0.130	0.481	0.911	0.997		
Plaice	0.054	0.230	0.003	0.007	0	0	
Sole	0.011	0.088	0	0.020	0	0.003	0.308

Table 2: predator (a) and prey (b) overlap indices calculated for fish species chosen during plenary meeting of 2000.

Construction of the ECOPATH model also revealed that there are strong interactions (in terms of t/km2/yr) between the 'selected' species, blue whiting and mackerel. Blue whiting (Micromesistius poutassou) represents an important food for numerous ichthyophagous fishes (Du Buit, 1994), whilst mackerel and horse-mackerel represent a high proportion of fish biomass in trawl surveys and commercial landings (Table 3). It was concluded (meeting in Nantes, January 2002) that blue-whiting, horse-mackerel and mackerel should be included in the Celtic Sea GADGET model, in addition to the nine species originally proposed.



	% of Fish Biomass	% of Fish Landings	% of Value	% Predation by 'chosen' spp	% Predation on 'chosen' spp
Blue Whiting	0.92	0.47	-	58.05	0
Mackerel	55.94	14.07	10.24	6.46	0.02
Horse Mackerel	12.26	50.45	3.92	15.44	0

Table 3: The importance of blue whiting (Micromesistius poutassou), mackerel (Scomber scombrus) and horse mackerel (Trachurus trachurus) in terms of total biomass in trawl surveys, commercial landings and commercial value, together with the strength of interactions between these and the 8 fishes originally proposed during plenary meeting of 2000.

References:

Du Buit, M.H. (1994) Blue whiting in food webs in the Celtic Sea. Journal of Fish Biology, 45,
Hurlbert, S. H. 1978. The measurement of niche overlap and some relatives. Ecology 59:67-77.
Loman, J. 1986. Use of overlap indices as competition coefficients: tests with field data. Ecol. Modelling, 34:231-243

E.6 The effect of different survey designs in the Celtic Sea

Do different survey designs provide the same picture of community structure?

Verena M. Trenkel[1], John Pinnegar[2], Marie-Jöelle Rochet[1], Brian Rackham[2], Steve Warnes[2]

[1]Laboratoire MAERHA, IFREMER, Rue de l'Ille d' Yeu, BP 21105, 44311 Nantes cedex 3, France.

[2]Centre for Environment, Fisheries & Aquaculture Science, Lowestoft Laboratory, Lowestoft, NR33 0HT, UK.

Running Title: The effect of different survey designs in the Celtic Sea

Abstract

Many scientific surveys have been designed for the purpose of obtaining abundance indices for particular target fish populations. This implies that the sampling methods are appropriate to provide such data, surveys are conducted at the right time of year and cover the entire stock area. Recently, scientific attention is shifting towards the assessment of whole fish assemblages but using essentially the same set of survey data. However, it is unclear how suitable the data that has been collected for single-species assessments might be for this new multi-species purpose? How much does the assessment depend on survey design and technical set up? These questions are to be investigated for the Celtic sea groundfish community using data from three surveys conducted in different seasons and using different gears: an autumn groundfish survey (IFREMER, GOV trawl), a spring/autumn groundfish survey (CEFAS, Portuguese High-Headline trawl) and a spring beam trawl survey (CEFAS). Comparisons for single species abundance index estimates for the whole area do not show survey effects in general. In addition community assessments using indicators such as biodiversity, proportion of non-commercial species were similar for all data series.

Keywords: Survey, trawl, Celtic Sea, abundance, biomass, biodiversity.

Introduction

Scientists trying to measure the impact of fishing on communities are often forced to rely on research vessel data which in general has been collected for a very different purpose, i.e. for single species stock assessment. Yet there is increasing need for the assessment of multispecies communities including non-commercial species (see overview for non-commercial species in Greenstreet and Rogers 2000, Greenstreet, Spence et al. 1999). Historically sampling gears were chosen in order to provide representative data only on a few commercial species and were often timed to coincide with spawning aggregations (e.g. (Warnes & Jones 1995)) in order to reduce the sampling effort necessary. The fisheries of the Celtic Sea are are very diverse and represent several distinct fleets (métiers), characterised by different gears and different target species (Biseau 1998; Marchal & Horwood 1996; Laurec *et al.* 1991). Given these circumstances, it has now become imperative to establish how sensitive conclusions drawn from scientific trawl-surveys are within a wider multispecies context.

Gear selectivity and the availability of individuals due to survey timing are two major factors which can lead to potential differences between survey data sets (REF). In addition, the behaviour and design of the research vessel itself might be expected to act on species selectivity (Pelletier 1998). Studies can be designed to estimate the selectivity of trawls for individual species, e.g. as a function of length and body shape, (Godø & Walsh 1992) or gear characteristics (Engås & Godø 1989), both of which can in-turn vary with depth, sediment type and other environmental conditions (Godø & Engås 1989). Alternatively, single species abundance estimates and community indicators can be estimated by comparing data for the same geographic location but obtained with different surveys. Comparison of abundance estimates allows us to identify species that are particularly sensitive to different survey or gear designs. Previous studies have demonstrated that the relative species composition described for a particular area can be very sensitive to the sampling methodology applied (Merrett et al. 1991, Kulbicki and Wantiez 1990, Wantiez 1996) however community indicators such as total biomass or species diversity tend not to vary significantly (Wantiez 1996).

The Celtic sea groundfish community is surveyed annually by one French survey taking place in autumn, one English groundfish survey and recently by an English beamtrawl survey aimed at describing the epibenthos, the latter two occurring in spring. In the early years of the English groundfish survey sampling was carried out in spring and autumn. Data will henceforth be referred to as : French, Uk-spring, Uk-autumn and Uk-beamtrawl. Using the Uk-spring and Uk-autumn series it is possible to assess the effect of survey timing (seasonality), whereas all data series can be used to study the impact of survey design in the wider sense. Previous analysis of survey and fisheries data have shown that there have been significant long-term changes in the composition of fish communities in the Celtic Sea (Pinnegar *et al.* in press). Furthermore, species are not distributed uniformly in either space or over different seasons (Warnes & Jones 1995).

Material and methods

CELTIC SEA

The Celtic Sea is an area of continental shelf which supports many important and valuable fisheries and is bordered by Ireland in the North, the UK in the East and the 47° N Latitude line in the South. In the present study we consider that portion of the Celtic Sea sampled by all the three research vessel surveys, and which covers approximately 36300 square nautical miles. The study is restricted to fish species, since the identification of invertebrates was not carried out to the same taxonomic level by all surveys. Fish belonging to the *Argentinidae* and *Callionymidae* were only identified to the genus level, as over the course of the series individual species had not always been identified. The data series are of variable duration and longevity (Table 1).

ENGLISH GROUNDFISH SURVEYS

The original objective of the UK survey, which commenced in 1981, was to investigate the distribution and biology of the Western mackerel stock; the spring suvery targetting spawning adults and winter surveys targeting pre-recruit mackerel (Warnes & Jones 1995). At this time there had been a great expansion in the fishery for mackerel and there were concers about over-explotation of the stock (Lockwood & Shepherd 1984). Subsequently (after 1982), with increasing need for fishery independent data on the state of demersal stocks, the objectives were widened to include the biology, distribution and abundance of all species which could be sampled representatively by bottom trawl.
On the earliest cruises, the surveys covered much of the west coast of the British Isles, through the Bay of Biscay to the northern coast of Spain. This area of coverage proved to be too ambitious and from the winter cruise of 1987 it was decided to reduce the survey area from 47° 30' N to 52° 30' N and from 3° W to 12° W (Warnes & Jones 1995). The elimination of the Bay of Biscay from the survey involved some sacrifice of information and this is an important area for pre-recruit hake and horse mackerel.

The standard bottom trawl used in the English Celtic Sea surveys is a modified Portuguese High-headline Trawl (Table 1, Figure A1 in appendix). This gear is relatively robust and was chosen because of the unevenness of the bottom substratum in the Celtic sea. Since 1990 Scanmar equipment has been used to monitor trawl parameters (Table 1), and accoustic transponders are attached to the trawl doors.

The English spring survey is currently used to 'tune' VPA assessments for whiting, megrim, hake and mackerel.

ENGLISH BEAM TRAWL SURVEY

In 2000 and 2001, during the routine groundfish survey, additional data were collected througout the Celtic Sea using a 2m beam-trawl. The purpose of this exercise was to sample fish and benthic invertebrates for studies of epibenthic diversity (Ellis *et al.* in press).

The gear used (Table 1) followed the modified 2m trawl of Jennings *et al.* (1999), and was designed to operate in relatively deep waters, on a range of substrates, from large research vessels and in rough seas. The net was fished from the stern ramp of the RV *Cirolana,* and distance covered was measured retrospectively using sextant software, linked to the ships Differential Global Positioning System (DGPS). Each tow was 5 minutes in duration at a speed of approximately 1 kn, and the 5 minute period was timed from the moment that the net made contact with the seabed. In most areas the amount of warp released was three times the water depth, although a ratio of 2.5 was used at the deepest sites.

FRENCH GROUNDFISH SURVEY

The French groundfish survey was initiated to monitor changes in commercially important demersal species, in particular whiting, in the Bay of Biscay. The autumn period was chosen in order to obtain estimates of recruits. In recent years however the survey area has been extended to include the Celtic sea and the objectives were widened to cover all fish and shellfish species, although benthic species are not well captured by the chosen survey gear.

The survey started in 1990 with the vessel Thalassa and samples were taken on a systematic grid covering the South and Central Celtic sea. During 1992 to 1996 the area was not fully surveyed. In 1997 the vessel was replaced, the survey area extended further North and a stratified design implemented according to depth contours (31-80, 51-120, 121-160, 161-200 and 201-400 m) and geographic region (South, Center and North). The ten strata are divided into units of 25 square nautical miles. Stratified random sampling of these units is implemented. Overall 50-60 hauls are carried out each year. The GOV 36/47 trawl used corresponds to the standard IBTS (international bottom trawl surveys coordinated by ICES) configuration (Anonymous 1996) with the only difference being that no Exocet kite is used and additional floats have been added instead (Table 1). Gear geometry is monitored using Scanmar acoustic transponders attached to the net wings.

The French autumn survey is currently used to 'tune' VPA assessments for cod, megrim, whiting and hake.

STATISTICAL ANALYSIS

Total abundances by species were estimated using the swept area method where mean numbers per haul and per unit area are calculated and then multiplied by the total area sampled. Swept area is defined as net wing-spread multiplied by distance covered. For the French data abundances were estimated per stratum and then summed. No corrections were made for differences in catchability between species and biomass estimated were calculated in a similar manner.

When comparing the surveys results, the autumn results of one year (year t) were always compared with the spring results of the following year (year t+1). This procedure was adopted due to biological reasons. The new recruits will first show up in the autumn surveys and then in the spring surveys of the following year.

The overall effect of seasonality was tested by means of a two-way analysis of variance (ANOVA) using the UK-spring and UK-autumn survey data from 1982-1988, with species and season as factors on the log-transformed abundance estimates. Only species for which non-zero abundance estimates were available for all years were included in the comparison. Log-transformation was carried out to ensure normality of abundance estimates. For individual species, the effect of seasonality was investigated by using Wilcoxon paired rank tests on the transformed abundance estimates.

Survey effects (due to gear and season) were studied using data from the UK-spring PHHT survey and the French autumn GOV survey. Trends over time (positive or negative) in species abundance were investigated using the correlation between abundance and time (year) for each data series (rank test on Spearman's correlation coefficient rho). A comparison of test results indicates whether the two surveys suggest similar patterns of abundance for a particular species. Differences in length-specific survey selectivity were compared by looking at the mean length of each species in each given year.

Survey effects were also investigated for several community indicators: the ratio of benthic to pelagic species, the proportion of piscivores (for species classification see appendix), the proportion of non-commercial species, average individual weight and length. Average individual weight and length were estimated for all species combined. As a diversity indicator Δ_1 was chosen. This parameter gives the probability that two individuals chosen at random from the community belong to different species. Overal length selectivity was compared using size spectra, based on the number of individuals per size category irrespective of species. Further details concerning these indicators can be found in Rochet & Trenkel (in prep). Confidence intervals for community indicators were based on 500 parametric bootstrap samples (Gamma distributions for abundance estimates) as described in (Trenkel & Rochet submitted). Since the English beam trawl data series is very short (it starts in 2000), only general statistics have been calculated.

Results

Seasonality

A significant effect of seasonality was detected for both the fish community as a whole as well as for individual species based on analysis of variance of the log-transformed abundance estimates (Table 2). Only twenty-four species could be included in the comparison as for all other species there were years with no observations.

Pairwise comparisons of the Uk-spring and Uk-autumn abundance estimates revealed significant differences for eight species out of the 24 tested (Wilcoxon paired rank test with $p<0.05$). The species concerned were Merluccius merluccius, Merlangius merlangus, Micromesistius poutassou, Pollachius virens, Scomber scombrus, Trachurus trachurus, Trisopterus esmarkii and Zeus faber. The relationships between the two sets of abundance estimates for the nine most abundant species are illustrated in figure 1.

It is concluded from the present analysis that most differences which might be found between the UK-spring and the French autumn surveys should be attributable to differences in survey gear and design rather than to the survey season.

Survey design effect : Single species

Taking all the available data, 98 fish species were noted for the UK-spring and 69 for the UK-autumn survey. In contrast, the French survey registered 89 fish species and the UK-beam trawl survey only 52 fish species (only two years of data). These numbers include many rare species that appeared only intermittently in any given time-series.

Another way of looking at the species "selectivity" of a particular survey is to compare the list of the most abundant species (Table 3). The lists of the ten most abundant species (average over 1997-2000) for the French and the Uk-spring abundance series were nearly indentical although the species did not occur in the same order. The beam trawl survey data was dominated by *Arnoglossus imperialis* and contained in general more small benthic species compared to either the French GOV and UK PHHT surveys.

The relationship between single species estimates (for the 9 most abundant species) based on French and Uk-spring series, varied from positive to negative (Figure 2). In general, there was some agreement between the estimates. Trends over time in species abundance were found to differ depending on the series being considered, but for most species there was no overall trend (Table 4). Abundance of *Capros aper* was found to significantly increase in the French series but there was no significant trend in the UK-spring series (note that the French series has missing years). *Trisopterus minutus* was significantly decreasing in both surveys. Time trends obtained with the Uk-spring and Uk-autumn abundance estimates showed good agreement; all species appeared stable over the study period (1982-1988).

Survey design effects : Community

Community indicators were calculated for the three longer data series (French. UK-spring, UK-autumn). Mean individual weight and length were smaller for the autumn data series compared to Uk-spring (Figure 3), however this difference was not significant as confidence limits were large for all estimates. The ratio of benthic to pelagic fish abundance showed good overall agreement between surveys (Figure 4), however a marked outlier was noted for 1995, due largely to very low catches of mackerel in the UK-spring suvey for that particlar year (Pinnegar *et al.* in press). Note that the benthic:pelagic ratio increases after 1995 and this coincides with reduced catches of horse mackerel in recent years in the Uk-spring survey.

The proportion of non-commercial species also showed good overall agreement between surveys and seemed to be on the increase over the whole period (Table 4). Diversity indices Δ_1 were broadly similar for all series but were unreliably estimated (Figure 6).

All community indices were tested for time trends (Table 5). Both the benthic:pelagic ratio and the proportion of non-commercial species were found to significantly increase over the 18 year period (Uk-spring data). However, although increases were detected, the tests were not significant for the shorter time series (French and Uk-autumn).

Table 1: Sampling and net construction details for Celtic Sea surveys

	uk groundfish	uk beam trawl	french groundfish
Institute	CEFAS	CEFAS	IFREMER
vessel (period, length, kW)	Cirolana (1970, 72.5m, 2 ´820 kW)	Cirolana (1970, 72.5m, 2 ´820 kW)	Thalassa 90-91 Nouvelle Thalassa (1997, 74 m, 2200 kW
time period	1982, 84-2000 S 1982-88 A	2000-2001	1990-91, 1997-2000
time of year	S = March A= November/December	March	October/November
towing speed (kt)	4	1	4
tow duration (min)	60	5	30
gear	PHHT	2m Steel Beam	36/47 GOV
number of tows	34-93	31 (2000), 61 (2001)	50-60
av. swept area per tow (km2)	0.11	0.0005	0.068
horizontal opening (m)	14.3	2	18.4
vertical opening (m)	4.4	0.3	4.1
door type m2/kg	5.6/1440	-	4.5/1350
ground rope	18.3	-	
head line (m)	16	-	36
bobbins no./diam. (cm)	/35.6cm	-	
Mesh size codend liner (mm)	20	4	20
Warp-length/water depth	3.8	3.0	
Tickler chain	16.5m	Chain mat	

Table 2: Analysis of variance for season effect of UK groundfish surveys on log-transformed abundances for all species for species with non-zero abundance estimates for all years.

	Df	SSQ	Mean SSQ	F-Value	Pr(F)
Species	23	2083.78	90.60	92.18	0
Year	7	25.6	3.66	3.72	0.0007
Season	1	4.995	5.00	5.08	0.025
Species:Season	23	116.47	5.06	5.15	0
Residuals	281	276.18	0.98		

Table 3: Ten most abundant (in numbers and biomass) species in 1997-2000 in Celtic sea as estimated from French autumn groundfish survey, UK spring groundfish survey and Uk beam trawl survey (2000-2001).

Numbers

	Rank									
Survey	1	2	3	4	5	6	7	8	9	10
French	Micromesistius poutassou	Capros aper	Trachurus trachurus	Trisopterus minutes	Trisopterus esmarkii	Argentina spp.	Scomber scombrus	Merluccius merluccius	Aspitrigla cuculus	Melanogrammus aeglefinus
Uk-spring	Capros aper	Trachurus trachurus	Scomber scombrus	Micromesistius poutassou	Trisopterus minutus	Sprattus sprattus	Gadiculus argenteus	Merluccius merluccius	Lepidorhombus whiffigonis	Argentina spp.
Uk beam trawl	Arnoglossus imperialis	Buenia jeffreysii	Lepidorhombus boscii	Callionymymidae	Pomatoschistus norvegicus	Microchirus variegatus	Lepidorhombus whiffiagonis	Aspitrigla cuculus	Trisopterus minutus	Gobiidae

Biomass

	Rank									
Survey	1	2	3	4	5	6	7	8	9	10
French	Trachurus trachurus	Micromesistius poutassou	Capros aper	Trisopterus minutes	Scomber scombrus	Argentina spp.	Melanogrammus aeglefinus	Trisopterus esmarkii	Merluccius merluccius	Lepidorhombus whiffigonis
Uk-spring	Scomber scombrus	Trachurus trachurus	Capros aper	Micromesistius poutassou	Merluccius merluccius	Pollachius pollachius	Argentina spp	Lepidorhombus whiffigonis	Trisopterus minutes	Beryx spp.
Uk beam trawl	Lepidorhombus boscii	Lophius piscatorius	Arnoglossus imperialis	Callionymidae	Gadus morhua	Lophius budegassa	Lepidorhombus whiffiagonis	Microchirus variegatus	Aspitrigla cuculus	Scyliorhinus canicula

Table 4: Spearman rank correlations coefficient rho for trend of species abundance estimates with time and p-value for rank tests of significant abundance trends.

	period 1982-1988				period 1990-2000			
	Uk spring		Uk winter		Uk spring		French autumn	
species	rho	p-value	rho	p-value	rho	p-value	rho	p-value
Argentina spp	0.49	0.31	0.54	0.25	0.05	0.9	-0.37	0.37
Capros aper	0.77	0.1	0.66	0.16	0.52	0.1	0.94	0.04
Lepidorhombus whiffigonis	0.37	0.44	0.1	0.92	-0.63	0.05	0.66	0.16
Merluccius merluccius	0.43	0.37	0.14	0.8	-0.31	0.32	-0.37	0.37
Micromesistius poutassou	-0.31	0.44	-0.43	0.31	0.57	0.07	0.54	0.25
Scomber scombrus	0.43	0.37	0.31	0.52	-0.06	0.83	0.26	0.61
Trachurus trachurus	0.09	0.9	0.31	0.52	-0.63	0.05	0.37	0.44
Trisopterus esmarkii	-0.71	0.1	-0.6	0.16	-0.25	0.43	0.31	0.52
Trisopterus minutes	-0.14	0.7	-0.71	0.1	-0.79	0.01	-0.89	0.04

Table 5: Spearman rank correlations coefficients rho and p-value for time trends of various community indicators for Celtic sea groundfish community derived from estimated abundances for Uk spring, winter and French autumn surveys.

Indicator	period 1982-1988				period 1990-2000				period 1982-2000	
	UK spring		UK autumn		UK spring		French autumn		UK spring	
	rho	p-value	rho	p-value	rho	p-value	rho	p-value	rho	p-value
mean individual weight	-0.09	0.80	0.54	0.20	-0.09	0.80	-0.6	0.16	-0.12	0.61
benthic: pelagic	0.65	0.16	0.18	0.69	0.45	0.15	-0.26	0.52	0.84	$<$0.001
proportion non-commercial	0.66	0.16	-0.11	0.76	0.48	0.13	0.03	1	0.85	$<$0.001
biodiversity	0.46	0.27	-0.29	0.46	0.2	0.56	-0.6	0.16	040	0.10
mean individual length	-0.14	0.70	0.36	0.41	-0.40	0.39*	-0.8	0.12*	0.35	0.41

*1997-2000 only

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ANNEXE

Trophic groups from Whitehead et al. 1986 and Greenstreet 1996. PEPA = pelagic planktivore; PEPI= pelagic piscivore; DEBE= demersal benthivore; DEPI= demersal piscivore; NA=not available.

Species	Code	trophic group
ALOSA ALOSA	ALOS-ALO	PEPA
AMMODYTIDAE	AMMO-SPP	PEPA
ANGUILLA ANGUILLA	ANGU-ANG	DEBE
ARGENTINIDAE	ARGE-SPP	PEPA
ARNOGLOSSUS IMPERIALIS	ARNO-IMP	DEBE
ARNOGLOSSUS LATERNA	ARNO-LAT	DEBE
ASPITRIGLA CUCULUS	ASPI-CUC	DEBE
BELONE BELONE	BELO-BEO	DEPI
BERYX SPP.	BERY-SPP	NA
BLENNIUS OCELLARIS	BLEN-OCE	DEBE
CALLIONYMIDAE	CALL-SPP	DEBE
CAPROS APER	CAPR-APE	DEBE
CEPOLA RUBESCENS	CEPO-RUB	DEBE
CHIMAERA MONSTROSA	CHIM-MON	DEPI
CLUPEA HARENGUS	CLUP-HAR	PEPA
COELORINCHUS COELORHINCHUS	COEL-COE	NA
CONGER CONGER	CONG-CON	DEPI
CORYPHAENOIDES RUPESTRIS	CORY-RUP	PEPA
DASYATIS PASTINACUS	DASY-SPP	DEPI
ECHIODON DRUMMONDI	ECHI-DRU	DEBE
ENGRAULIS ENCRASICOLUS	ENGR-ENC	PEPA
ETMOPTERUS SPINAX	ETMO-SPI	DEPI
EUTRIGLA GURNARDUS	EUTR-GUR	DEPI
GADICULUS ARGENTEUS	GADI-ARG	PEPA
GADUS MORHUA	GADU-MOR	DEPI
GAIDROPSARUS VULGARIS	GAID-SPP	NA
GALEORHINUS GALEUS	GALE-GAL	DEPI
GALEUS MELASTOMUS	GALE-MEL	DEPI
GLYPTOCEPHALUS CYNOGLOSSUS	GLYP-CYN	DEBE
GOBIUS SPP	GOBI-SPP	PEPA
HELICOLENUS DACTYLOPTERUS	HELI-DAC	DEBE
HEXANCHUS GRISEUS	HEXA-GRI	PEPI
HIPPOGLOSSOIDES PLATESSOIDES	HIPP-PLA	DEBE
LAMPANYCTUS CROCODILUS	LAMP-CRO	PEPA
LEPIDORHOMBUS BOSCII	LEPI-BOS	DEPI
LEPIDORHOMBUS WHIFFIAGONIS	LEPI-WHI	DEPI
LIMANDA LIMANDA	LIMA-LIM	DEBE
LOPHIUS BUDEGASSA	LOPH-BUD	DEPI
LOPHIUS PISCATORIUS	LOPH-PIS	DEPI
MACRORHAMPHOSUS SCOLOPAX	MACR-SCO	PEPA
MACROURIDAE	MACR-SPP	PEPA
MALACOCEPHALUS LAEVIS	MALA-LAE	DEBE
MAUROLICUS MUELLERI	MAUR-MUE	PEPA
MELANOGRAMMUS AEGLEFINUS	MELA-AEG	DEPI
MERLUCCIUS MERLUCCIUS	MERL-MCC	DEPI
MERLANGIUS MERLANGUS	MERL-MNG	DEPI
MICROSTOMUS KITT	MICR-KIT	DEBE
MICROMESISTIUS POUTASSOU	MICR-POU	PEPA
MICROCHIRUS VARIEGATUS	MICR-VAR	DEBE
MOLVA DYPTERYGIA	MOLV-DYP	DEPI

Species	Code	trophic group
MOLVA MACROPTHLMA	MOLV-MAC	DEPI
MOLVA MOLVA	MOLV-MOL	DEPI
MULLUS SURMULETUS	MULL-SUR	DEBE
MUSTELUS ASTERIAS	MUST-AST	DEPI
MUSTELUS MUSTELUS	MUST-MUS	DEPI
MYCTOPHIDAE	MYCT-SPP	NA
NEZUMIA AEQUALIS	NEZU-AEQ	NA
PAGELLUS BOGARAVED	PAGE-BOG	PEPI
PETROMYZON MARINUS	PETR-MAR	NA
PHRYNORHOMBUS REGIUS	PHRY-REG	NA
PHYCIS BLENNOIDES	PHYC-BLE	DEBE
PLEURONECTES PLATESSA	PLEU-PLA	DEBE
POLLACHIUS POLLACHIUS	POLL-POL	DEPI
POLLACHIUS VIRENS	POLL-VIR	DEPI
RAJA BATIS	RAJA-BAT	DEBE
RAJA BRACHYURA	RAJA-BRA	DEBE
RAJA CIRCULARIS	RAJA-CIR	DEBE
RAJA CLAVATA	RAJA-CLA	DEBE
RAJA FULLONICA	RAJA-FUL	DEBE
RAJA MONTAGUI	RAJA-MON	DEBE
RAJA NAEVUS	RAJA-NAE	DEBE
RAJA NIDAROSIENSIS	RAJA-NID	DEBE
RAJA OXYRINCHUS	RAJA-OXY	DEBE
RAJA UNDULATA	RAJA-UND	DEBE
RANICEPS RANINUS	RANI-RAN	DEBE
SARDINA (CLUPEA) PILCHARDUS	SARD-PIL	PEPA
SCOMBER SCOMBRUS	SCOM-SCO	PEPI
SCOPHTHALMUS RHOMBUS	SCOP-RHO	DEPI
SCYLIORHINUS CANICULA	SCYL-CAN	DEPI
SCYLIORHINUS STELLARIS	SCYL-STE	DEPI
SEBASTES VIVIPARUS	SEBA-VIV	NA
SPRATTUS (CLUPEA) SPRATTUS	SPRA-SPR	PEPA
SQUALUS ACANTHIAS	SQUA-ACA	DEPI
SYNAPHOBRANCHUS KAUPI	SYNA-KAU	DEBE
SYNGNTHIDAE	SYNG-ACU	DEBE
TORPEDO NOBILIANA	TORB-NOB	DEPI
TORPEDO TORPEDO	TORB-TOR	DEPI
TRACHURUS TRACHURUS	TRAC-TRU	PEPI
TRIGLA LUCERNA	TRIG-LUC	DEPI
TRISOPTERUS ESMARKI	TRIS-ESM	PEPA
TRISOPTERUS LUSCUS	TRIS-LUS	DEPI
TRISOPTERUS MINUTUS	TRIS-MIN	DEPI
ZEUS FABER	ZEUS-FAB	DEPI

Figure A1

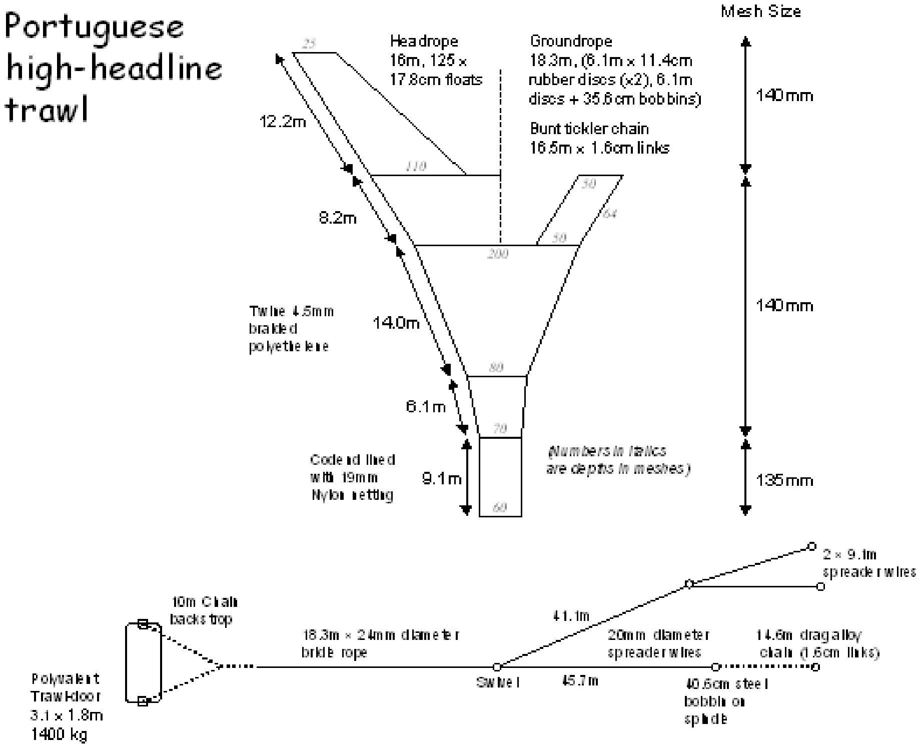

Portuguese high-headline trawl
Mesh Size
25
Headrope 16m, 125 × 17.8cm floats
Groundrope 18.3m, (6.1m x 11.4cm rubber discs (x2), 6.1m discs + 35.6cm bobbins)
Bunt tickler chain 16.5m x 1.6cm links
140mm
12.2m
110
30
64
8.2m
50
200
140mm
Twine 4.5mm braided polyethelene
14.0m
80
6.1m
70
Codend lined with 19mm Nylon netting
9.1m
60
(Numbers in italics are depths in meshes)
135mm
2 × 9.1m spreader wires
10m Chain backstrop
41.1m
18.3m × 24mm diameter bridle rope
20mm diameter spreader wires
14.6m drag alloy chain (1.6cm links)
Polyvalent Trawldoor 3.1 x 1.8m 1400 kg
Swivel
45.7m
40.6cm steel bobbin on spindle

Figure 1 Comparison of estimated annual abundances for Uk-autumn (year t) and Uk-spring (year t+1) surveys.

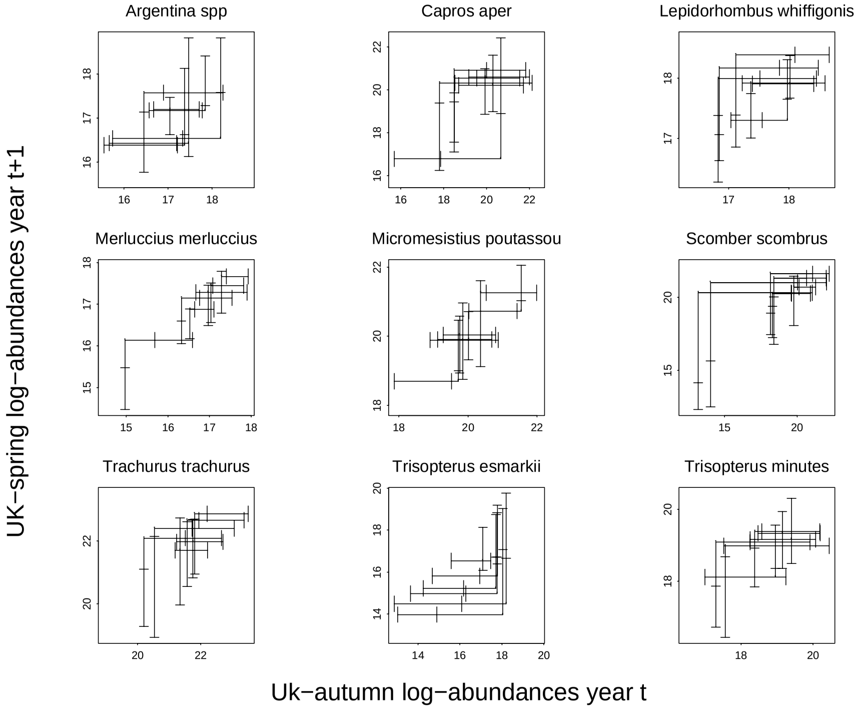


Figure 2 Comparison of estimated annual abundances for French autumn (year t) and Uk-spring (year t+1) surveys.

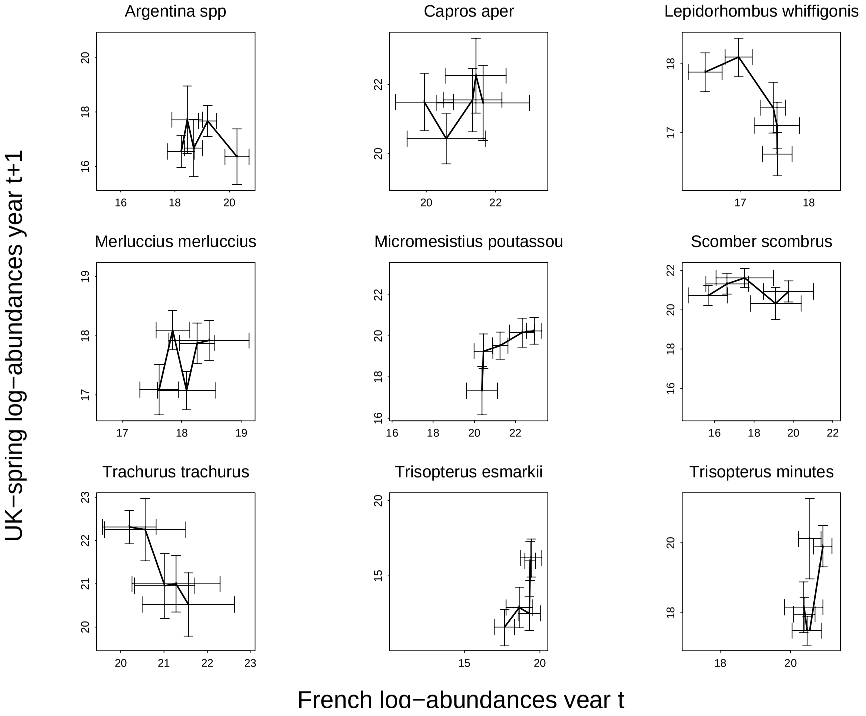


Figure 3 Mean individual weight in Celtic sea groundfish community based on Uk spring (o), Uk winter (-) and French autumn (Δ) groundfish surveys with 95% confidence intervals.

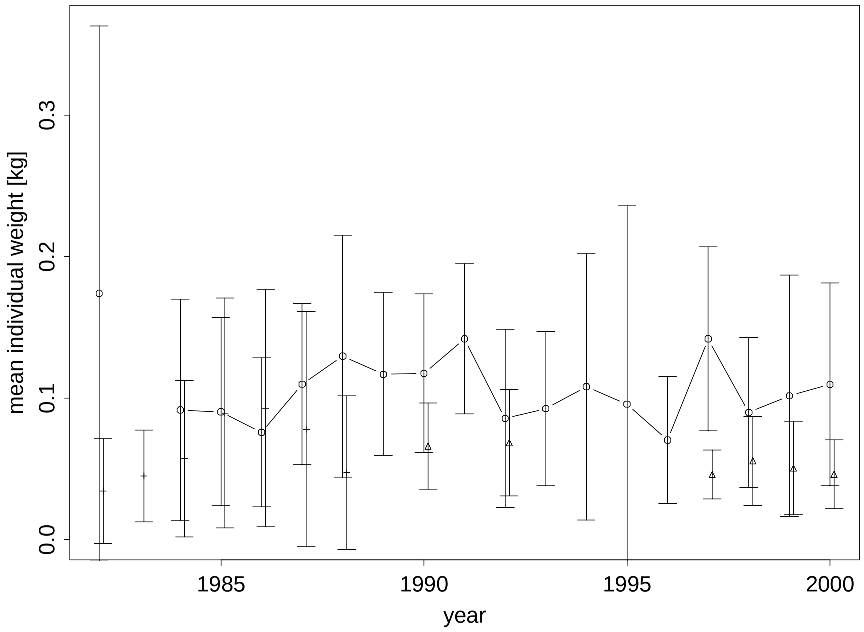


Figure 4 Ratio of demersal to pelagic abundances in Celtic sea groundfish community based on Uk spring (o), Uk winter (-) and French autumn (Δ) groundfish surveys with 95% confidence intervals.

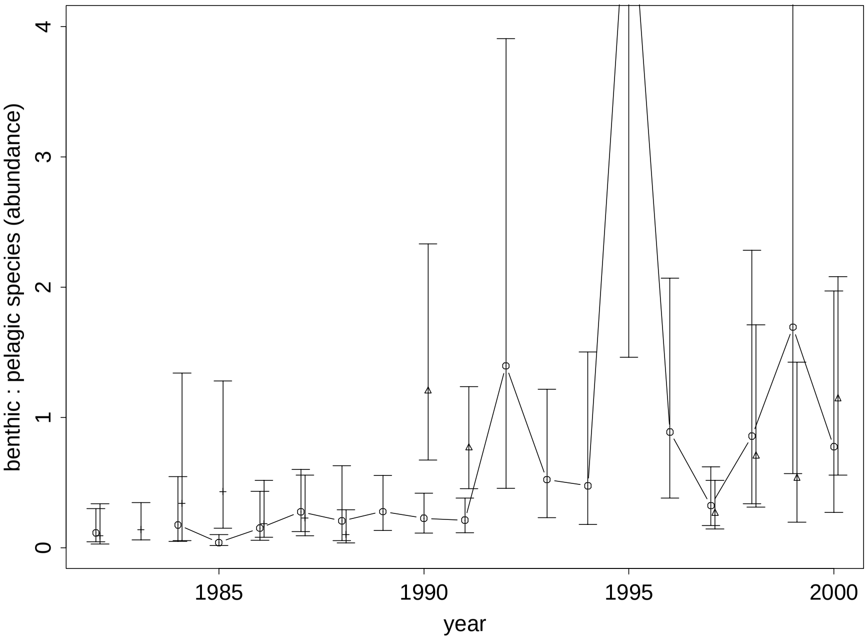


Figure 5 Proportion of non-commercial species in Celtic sea groundfish community based on Uk spring (o), Uk winter (-) and French autumn (Δ)groundfish surveys with 95% confidence intervals.

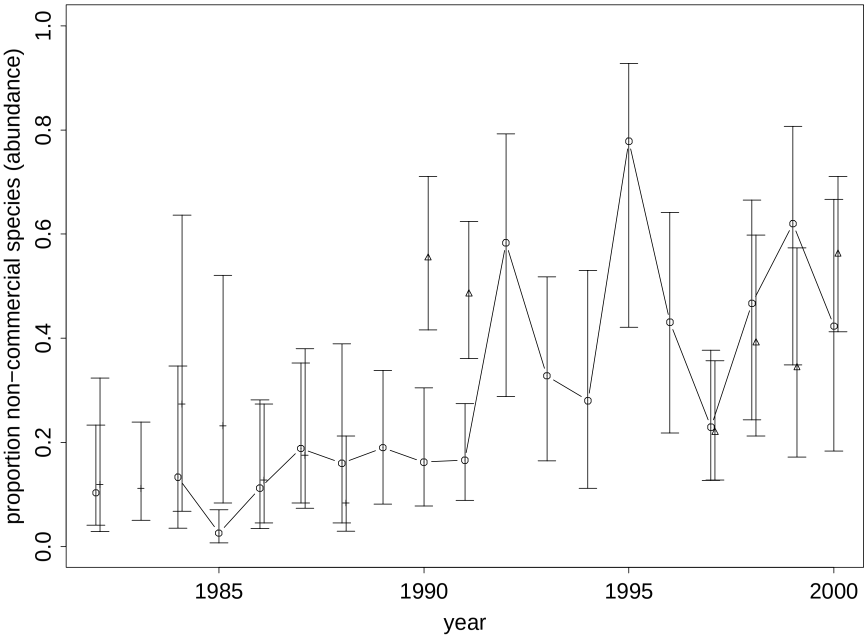
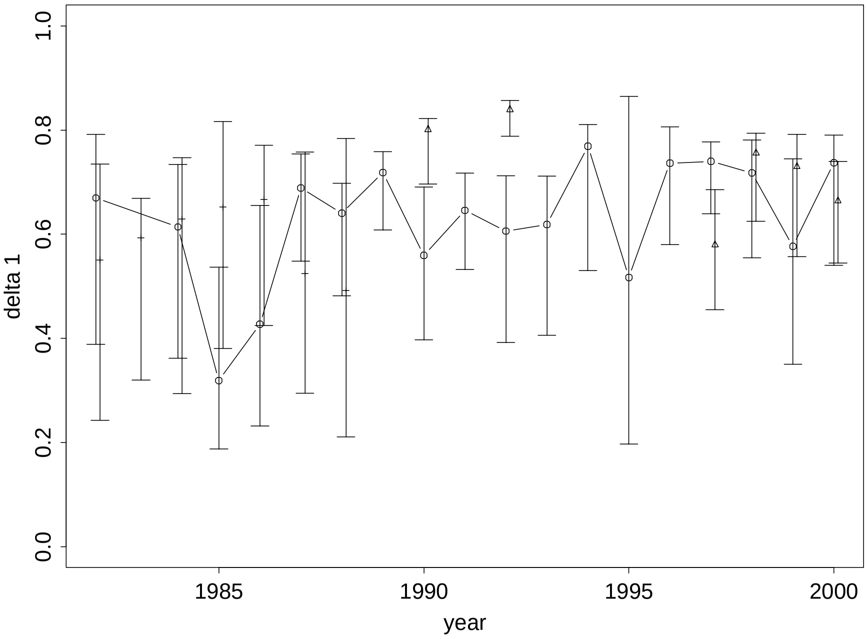


Figure 6 Biodiversity index delta of Celtic sea groundfish community based on Uk spring (o), Uk winter (-) and French autumn (Δ)groundfish surveys with 95% confidence intervals.



F Minutes: Reykjavík, June 2001

The second full dst^2 meeting took place in Reykjavík at the University of Iceland from the 19th to 22nd June, 2001.

The meeting agenda was to discuss:

Data warehouse
Biomathematical and statistical models
Status of the case studies and further work

These minutes contain summaries of some topics along with the main conclusions from the meeting.

Data Warehouse

The structure of the key part of the data warehouse was defined in 2000 and the prototype relational database is described in the first annual progress report.

Current status:

The database follows the following format:

Data are structured around sample records.

Sample	*containing who where and when*
Environment	
Water movement	
Juvenile abundance	
Landings	
Biological samples	*survey and commercial*
Sample table	
Length table	
Age table	
Miscellaneous reference data	*eg ICES assessment data*
Tagging Data	*preliminary design available*
Acoustic Data	*preliminary design available*
Stomach Content	*to be discussed*
as a possibility	
Selectivity Database	*Contact Bob Van Marlen - RIVO Netherlands*

Data are identified by unique key records. If data are input with a key record identical to an existing record, the existing record will be overwritten. This enables data to be updated but there is no warning that data are being overwritten.

The exchange format consists of a hierarchical series of flat ASCII files, with a key from the highest order table linking the tables. Data must be input in descending hierarchical order.

Each data warehouse functions as a database and is held on single computer which is linked to the Internet and can be accessed via the Internet. The prototype warehouse has been tested with Linux (Redhat 7) and W2000 operating systems

The current software requirements are:

Database	PostgreSQL
Web server	Apache
Scripting language *(to create dynamic web pages)*	PHP

The original proposal required the use of an ORB, either CORBA or XML and possibly both. These areas of development will not be pursued in the immediate future as they are not necessary with the current set up, although use of them will be reviewed later in the project.

CORBA is not required as it is unlikely that multiple location databases will be developed and as text based methods of data transmission are acceptable, it is not necessary to use XML as a link between the data warehouse and GADGET.

There are 3 levels of data warehouse user:

User	Privileges
Administrator	add, edit and delete users, update data
Writer	upload data
Reader	View and download data

The intention is that there should only be 1 authorised administrator per data warehouse and a limited number (possibly 1 or 2) of writers.

There were demonstrations of the following:

New user registration
Data uploading of pre-prepared data file (flat file)
Data access via field based hierarchical structure
Data access via SQL query typed into line

Data may be viewed or saved from the data warehouse as a text file. SQL query strings can also be saved as text files.

Although there is an interface to upload data it will also be possible to upload data from the command line, either loading each table separately or by creating a file with a hierarchical series of tables and loading them sequentially. Another option is to have a live link from an institution database into the data warehouse.

Distribution of the first version will be September 2001, including source code and the installation guide.

New items to be implemented before the first version are:

Download of dst^2 exchange format
Ability to edit, delete and add single records
Improved data browsing

New features requested:

- Scripts to upload multiple datafiles were requested as to load each table through the user interface will be time consuming.
- History log of changes to the data warehouse indicating:
    - Date of action
    - user
    - table modified
    - comment to indicate the action taken.
- Meta-data on the quality and assurance of data in the database. *eg.* Information on sampling strategy, quality control measures undertaken and any other aspects of the data

which should be taken into account when using the data.

- Ideally there should there be a template of concepts to be included in the description of the data.

Further development

The most important areas for further development are:

report views
structure of the exchange format

A key aim of the data warehouse is to facilitate the aggregation of data to be used in GADGET runs.

The data warehouse is required to aggregate data by area, time period, gear class, vessel type *etc.* into:

- length distributions
- age length tables
- age length keys
- age length distributions
- landings (weight and numbers)
- catch (tonnes)
- mean weight and length at age
- standard deviation of length at age
- proportion mature at age
- number of records contributing to the aggregation level

Initially the aggregation levels will be predefined within the data warehouse but the ideal is that these should be flexible and definable by the user at the time of data extraction.

The question of how to aggregate data relating to variance and standard deviation requires further consideration.

Interface between Gadget and Data warehouse

Three options:

1. GADGET to output aggregated data with information in the headers to enable manual editing. The header information would be taken from the query which will contain a substantial amount of the information required *eg* length groups, age, fleet, time step *etc.* Any information not derived directly from the data warehouse would be included manually, *eg* model parameters and migration matrices.
2. GADGET could be data warehouse aware and extract it's own data.
3. The data warehouse could be GADGET aware and GADGET could then be run from the data warehouse.

The last two methods are not trivial.

The current structure of the GADGET input files is complex, often including data of different types within a single file. The GADGET input files are to be modified in order to make the output of GADGET input files by the data warehouse easier to achieve. It was decided to separate the data from the modelling instructions, initial values and model parameters to facilitate data handling. GADGET control instructions and initial values will be arranged in a different file structure.

Tables could be defined to store initial parameter values in the warehouse. In the long term these could be used in the generation of GADGET input files but their initial use would be as reference tables.

Current plan for the GADGET input files:

1. Create aggregate views giving data files.

2. Add headers using the query to describe levels of aggregation.

Iceland, Norway and Denmark will co-ordinate the redesign of file structure requirements providing examples of required database outputs.

Further table definition

The acoustic table is to have an additional column of mean of raw data (which is proportional to density). This will be optional. EJS will provide a reference with a proper description of the parameter.

As any biological sampling conducted along with an acoustic survey can be identified as such in tables 5, 6 & 7 the acoustic data can be linkind with the associated samples.

The table of tagging data is to contain more information on the fish (although many of these fields will be optional). Columns additional to the table description in the first annual report are:

Day released
Day recaptured
Age recaptured
Sex recaptured
Maturity recaptured

As part of another EU project a database containing information on selectivity experiments has been established. Information on this could be of use in this project. Bob Van Marlen at RIVO (netherlands) is to be contacted in this regard.

Table 8 (miscellanous reference data) requires further clarification as it will be more complicated to design and implement.

Stomach content data requires a group of tables. An initial set of table definitions will be sent to DIFRES and will also be tested by those with stomach content data before the final table descriptions are finalised. These tables will focus on proportion by species and proportion at length within species. Pooled stomach content data will be aggregated but individual fish will be stored as individual entries.

Biomathematics and Statistics

WP4.1 Feeding and consumption

Barents Sea Model

Individual based feeding and consumption model for Barents Sea which includes cod, herring and capelin. The model encompasses spatial distribution, growth and mortality. Individual growth is simulated through bioenergetic models with movement and growth based on a model designed to deliver optimum fitness/growth.

Current Status:

Ocean circulation model There is an ocean circulation model for the Barents Sea which generates temperature and current velocities. Daily values on a 20km grid are currently available for 1988 to 1991. The intention is to increase the time period to 1993.

The intention is to focus on the period from 1990 to 1993 as cod had a choice of feeding on capelin or herring in this period.

Bioenergetic growth models Bioenergetic growth models are available in the literature for cod and herring, but not for capelin. In the model there are two forcing parameters: P feeding potential and T temperature.

The suitability of the herring model (and parameters) is being evaluated for capelin. The herring model does not provide adequate growth of capelin, but by increasing consumption at low temperatures, reducing growth dependence on body size and decreasing the activity level the model fit improved. At higher temperature consumption is kept identical to that of herring. These modifications are based on the assumption that capelin is better adapted to cold water than herring.

Drift model for larvae Movement of cod and capelin larvae is by a drift model. With simulation by advection and diffusion the fit with observed data is poor. The addition of random swimming motion does not affect the results. The addition of swimming motion of 1 or 2 body lengths in a northerly direction causes the population to move north east and improves the fit with data.

Movement of adult fish Movement for adult fish is by an adapted random walk where fish move or stay depending on fitness criteria. Habitat choice is based on adapting probabilities for movement by simulating evolution by natural selection. Individuals inherit a threshold value. If in an environment of the appropriate threshold value the individual stays, otherwise it moves. Movement north or south depends on the relationship of threshold value and environmental value using weighted random number. Seasonal effects and learning behaviour can be incorporated into this model. Evolutionary fitness is measured as maximising growth and minimising predation. Fitness landscapes are changed daily.

This method compares favourably with neural networks despite being simpler to implement, easier to understand and requiring fewer parameters.

Consumption data

Estimating consumption for cod: Consumption of herring by cod in the Barents Sea.

The Barents Sea stomach database includes data collected by IMR and PINRO. The time period covered is from 1984 to 1997 and data are available for 103,000 stomachs. Samples were mostly collected during routine bottom trawl surveys but there are some samples from other gears. Although some data are available throughout the year most of the sampling took place in winter/spring and autumn surveys.

Consumption estimates are based on the gastric evacuation model of Temming and Andersen (1994). This takes into account the number of prey per time unit (as number is more appropriate than biomass in terms of feeding behaviour and mortality) and the period of time prey is in the stomach (based on weight of prey). Weight of partly digested prey combined with weight of fresh prey at a given length (along with ambient temperature) gives digestion time for that prey. Time of ingestion is calculated to give feeding pattern. This is temperature sensitive and information on temperature is available but not depth location of fish. Any predators not containing length measurable prey are not included in this analysis. Digestion rates are assumed independent of number of prey or meal size.

The time and area specific mean consumption rates for cod are calculated (as number of prey consumed per hour per fish) and can be compared with the consumption estimates from the individual based model.

A problem with consumption is that the raw data are processed by an elaborate model to generate data with which to compare the results of the individual based model.

WP 2.1 Migration and drift models

Discrete model of capelin spawning and feeding migrations

Individual based model based on neighbourhood with dynamic equations based on velocity.

Interaction with neighbours within neighbourhood based on vector sum of neighbours' velocities + noise. Individuals adapt to average speed of neighbours and the sum of directions of neighbours + noise. The size of the influential neighbourhood is defined.

With a simple model there exists 3 distinct types of behaviour:

net mass transport *eg.* migration
shoaling behaviour *eg.* feeding
random motion

These are controlled by changing ratio of noise, neighbourhood and domain size.

Non-periodic boundary condition leads to grouping at boundaries. This is dealt with by the addition of a cohesion term which represents a preferred distance (between individuals) parameter.

In directing an individual towards a point (*eg* in a feeding migration) uniform noise can be replaced with a probability density function. The noise distribution is dependent on the difference between actual velocity and that required to arrive at the preferred location, *ie* the closer their velocity to the destination, the closer to uniform the noise is. The preferred direction could be due to a feeding migration, temperature gradient, food gradient *etc.*

Boundaries can be:

periodic (not realistic)
reflective
tangential (goes along boundary)
repulsive (*eg* temperature) which does not prevent movement

The simulation of Icelandic capelin describes a set of motion steps from the feeding area in the north to the spawning area in the south and the return to the feeding are. At present the model is purely mechanistic and is an attempt to replicate observed behaviour. An initial modification would be to include isotherms to see how they affect migration routes.

It's not clear exactly how you would test the model to check the parameter values.

Continuous distributed model of fish migration

The aims of this are to aid the assessment of which type of model could be used in a more general prediction model, test which factors might control migration, test assumptions about importance of external parameters.

It is a continuous counterpart to the previous discrete model and a counterpart to the compartmentalised model.

The density of the population depends on time, location and maturity stage.

Input parameters:

Guiding velocity: direct fish to a location, align with neighbours, control speed.

Preferred direction: turn toward preferred food or spawning ground and away from frontal system, this could include a stochastic component.

Fish are guided to a specified goal, their movement is aligned to that of neighbouring fish and their maximum velocity is controlled.

Fish are turned in direction of increasing food supply and away from increasing temperature.

Fish move towards each other when density is low and away from each other when density is high, seeking ideal density.

Carrying velocity: for young fish and larvae from current models.

Velocities would be density dependent in order to stabilise density, dependent on local density.

Model scenarios:

Feeding migration: random direction when sufficient food, below threshold food level directional element could direct fish.

Spawning migration: movement towards spawning ground with motion related to neighbours, temperature barrier restrains fish temporarily, don't cross until threshold maturity level reached, guiding velocity points them to spawning area. A more complex energy/egg production index may be needed.

The mathematical model contains:

Mass balance
Momentum balance
Rate of change of maturity, dependent on energy and fish size
Mass and momentum equation gives velocity equation

The numerical model is a finite element approach to solving equations, closely related to ocean current models with lateral transport but with levels of maturity (comparable to depth levels).

Mathematical model of optimal spawning behaviour

Energy Energy level based fish development, including low energy levels causing death through to spawning behaviour if energy levels are high enough to overcome a spawning 'barrier'.

If maturity index is to reflect the relative amount of eggs then also require energy index which may reflect relative weight.

Speed Speed of motion is constrained within limits and related to energy with higher speeds consuming more energy.

Growth Fish weight depends on food intake, metabolic change, velocity, growth and egg production and carrying eggs.

Problem 1 Find optimal regime of movement, velocity and egg production such that weight of the fish at time T is maximal.

Problem 2 Find optimal regime of movement, velocity and egg production such that weight of the eggs at time T is maximal.

There are two types of final time conditions, either fixed final time or final time window (with penalties).

For evaluation, the evaluation domain is triangular bounded by maximum movement velocity with minimum egg production, minimum of both movement and egg production and minimal speed with maximal egg production.

Data and parameter models

Goodness of fit

When GADGET output has been compared with data, goodness of fit tests have indicated bad fits in most cases. These problems could be due to the likelihood functions or that the model is inadequate in these cases. Some work has been done on different types of goodness of fit tests. A possible cause of the problem is due to the complexity of GADGET as it includes models dealing with migration, feeding, growth *etc* and if one is wrong it affects the others resulting in a poor fit with the data. Some work is currently being undertaken to consider model complexity.

Analysis of length group data from groundfish surveys

The aim is to find an appropriate model for the number of fish in each length group at each station from the Icelandic groundfish survey.

Data are formed into length frequency data for individual stations following the multinomial distribution. Assuming the probability distribution at length is the same is not realistic as the data exhibit strong off diagonal correlation (*ie* there are relationships between fish of different lengths which the multinomial distribution does not explain), probably due to year classes. The data are also overdispersed.

Further distributions, including some involving the Dirichlet distribution, have been tested which match observed data but do not account for all the error.

The problems of GADGET assuming a multinomial distribution were discussed briefly. Ignoring the overdispersion is less of a problem as the point estimates will still be appropriate although the variance structure will be incorrect, however, as the model is wrong (inappropriate correlation matrix) it may generate wrong point estimates.

Implementation of growth (including beta-binomial)

There are problems with the implementation of growth in GADGET and the maintenance of number, mean length and length distribution. Individual based models are difficult to implement without arbitrary fixes. The current fixes produce unrealistic length at age distributions.

At present mean growth is precalculated and fish are distributed around the mean length (with minimum and maximum length constrained). This can generate a large cluster at the upper boundary and the distribution is then scaled to attain the correct mean. If this occurs on every timestep spikes are produced in the distribution which are maintained with each timestep. Another constraint prevents fish from growing the maximum amount in every timestep.

An alternative method of implementing growth is to propagate age groups as distributions at length which grow as a complete distribution, (*ie* model length structure at age rather than modelling growth) and data on length structure at age are available. This would be implemented by modelling the mean but keeping the CV constant, which causes the spread of the distribution to increase with age. A separate model could be used for each cohort (with mean length at age different for each cohort). This approach is more suitable for fish where future growth is dependent on early life history.

An important aspect of growth in GADGET is that feeding and fishing can affect the distribution of length at age. The approach to modelling length described above would not allow as much flexibility in incorporating biological information. In colder water, more flexibility in modelling growth is required as growth is dependent on conditions and food availability which are considerably more variable than in warmer water. This is an area of the model where alternative approaches could be developed.

Gadget Optimisation

Alternative solutions to optimisation:

Global optimisation	
Local optima	plausible local result
Artificial optima	from pre-set bounds or parameter ranges
None optimised	run out of iterations.

We should have a warning message indicating when no optimum was reached within 'X' iterations.

Existing optimisers are:

Hooke and Jeeves	default
Paramin (simulated annealing)	considerably more time consuming

Sensitivity analyses have been conducted to test the suitability of the optimisers. They were started with the global optimum, the parameters varied systematically, an optimising run was carried out for each set of values and the final value plotted against the optimised value. This was done with the Iceland haddock single area, single species example.

With Hooke and Jeeves double the standard number of iterations were allowed and if it finished without an optimum it was started again. The optimised solutions were still not always plausible. Sensitivity tests around the problems indicate that optima are being forced by the pre-set bounds (even though these are outwith plausible parameter values) which are required by the model.

Paramin always converges to same solution with the possible exception of plausible local optima caused by sparse data.

The conclusion is that using Simulated Annealing to calculate an appropriate initial value (*ie* one near the optimum) for a Hooke and Jeeves optimising run could be the most efficient way to proceed. This takes advantage of the greater power of simulated annealing to locate optima and the speed of Hooke and Jeeves when it is already close to its target value.

Although solutions on the bounds are always suspect, in some cases alternative realisations are plausible. Extra information on where to get starting values and whether solutions are likely, might be available by testing the Hessian matrix for singularity and for possibilities for solutions.

Sensitivity tests should always be done and values should not end up on bounds.

Seasonal stochastic age structured multispecies model

Stochastic model based on the ICES MSVPA model which is seasonal, time discrete, age structured and single area.

The structure is modular consisting of input/output, predation (stomach content), food intake, fishing and growth. There are likelihood functions for catch at age with catches assumed log-normal by species at age over year and quarter.

The catch variance-covariance matrix could use measured values from the EMAS project and possibly infer values for similar species. Fishing mortality currently assumes a selection model and does not model fleets separately.

Stomach content data are from the ICES stomach content database. For a given predator the average relative stomach content composition of prey species is calculated using the method from the ICES WG on stomach contents. Observed values of stomach content by prey, age, predator, year and season are bootstrapped from the samples and it is hoped to use bootstrapping to estimate the variance-covariance relationship. A problem with the stomach content data is that many of the samples were pooled. It is intended to use the Andersen and Ursin (1977) relative food composition model, alternatively the Bormicon method will be used.

Between 300 and 500 parameters are fitted through maximum likelihood functions. AD Model Builder is used with automatic differentiation with phased minimisation.

Von Bertalanffy Stochastic model of Fish growth

The Von Bertalanffy model of growth is a deterministic equation based on a growth rate related to L_∞. One method of developing this as a stochastic model, described in Smith *et. al.*, is to add a noise distribution. Three areas of uncertainty are considered:

L at time t with measurement error
L_∞ with time space variability
Curvature time and space varying

A program is available to use tag/recapture data or catch data to provide estimates of the model parameters with 95% confidence intervals.

Case Studies

Celtic Sea

Ecopath model

Nine species (monkfish, cod, nephrops, haddock, megrim, sole, whiting, plaice and hake) were initially selected for the Celtic Sea multispecies case study. The main criterion used in their selection was commercial importance. Further consideration showed that these species do not comprise a major part of the biomass, although they are important in terms of landings and their commercial value is high relative to total landings.

An Ecopath model was developed including 2 species of mammals, eighteen fish species, fourteen invertebrate species, 2 primary producers and two bacteria groups. A Bray-Curtis dendrogram was used to look at diet similarity and nine major clusters chosen. It was found that interactions between species are very small and in most cases the predators of the chosen species aren't included and the prey of these species are not included. Plaice and sole do not interact with any of the chosen species, although they may share other predators and prey.

Species identified as being particularly important by the Ecopath model were identified as being: blue whiting, mackerel and horse mackerel. Strong interactions were found between these and the nine selected species and they also constitute a high proportion of the biomass. Consideration needs to be given to the inclusion of these species in the Celtic Sea multispecies model.

Survey data

Survey data used in the Celtic Sea case study are from English and French surveys which need to be harmonised.

Surveys available are:

Institute	Survey	Years
IFREMER	Winter survey	1992, 1994, 1997-2001
CEFAS	2m Beam Survey	1998 - 2001
CEFAS	Spring Survey	1982 1984-2001
CEFAS	Winter Survey	1982-1989

A calibration study is being done to see if assessment of community depends on sampling gear/regime.

Survey data were compared using:

Ratio of biomass and abundance by survey
Community time series
Biodiversity index

GADGET implementation

The GADGET implementation will start with single area, single species models for whiting and cod, then a single area, two species model and develop into a two species multi area model prior to the development of the multispecies model.

As raw data, or data in which individual boats can be identified is confidential, some work must be done on the datasets before they can be combined, although this work will be used in deciding how to aggregate the data.

A modelling approach was used on French commercial data from 1991-1998 to identify:

Metiers
Homogeneous fishing zones
Homogeneous fishing seasons

Metiers are characterised by gear, area and time of year and have similar catch composition. Coastal (<10m and <3 days and which are not obliged to complete logbooks) and offshore (>10m and 3-10 days) were analysed separately.

PCA was used on relative catch value to calculate important species (of the 30 most important commercial species) and identify fleet metiers by similar catch proportions.

Data were used to consider different metiers within a single trip. Some trips were predominantly single metier, especially cuttlefish, flatfish and gadoid. Changes in metier were found to be more likely to be due to a change in rectangle than change in gear.

A model of total fishing time was used to identify homogeneous areas and seasons. Area divisions were tested using ICES sub divisions and ICES statistical rectangles, it was found that individual subdivisions are not homogeneous. Hierarchical regrouping of rectangles by fishing operation to separate out seasonality produces seasonal groups of winter, spring and autumn, July and August. A suitable spatial grouping is less clear.

Gear and boat length in addition to area and time were found to be good descriptors in the model of fishing time. The new EU categories with 4 length classes along with categories of mobile and passive gear were used and will be adopted.

Testing for area:

Results suggest ICES areas may be a good start.

Testing for fleet details:

Gear, length of vessel are good descriptors of fishing time.
Virtually no correlation between metier and gear

A mixed model approach was used to decompose the spatial and temporal correlation with month and ICES division as the main effects.

Temporal autocorrelation	0.82
Spatial autocorrelation (adjacent areas)	0.46
Spatial autocorrelation (diagonal neighbours)	0.33

Vessels may not be independent and this could be causing a substantial amount of the spatial and temporal correlation. Including vessel gear and length reduces the correlation.

Biological areas can be defined from survey data but there is no conclusive information. The areas will be based on “knowledge” of spawning grounds, areas of juvenile fish *etc.*

Icelandic Waters

Data

Work is being done inputting data not currently included in the ORACLE database, the period from 1960 to 1975 is still to be included.

The biological sample tables (tables 5, 6, and 7) for the data warehouse are almost complete for cod, haddock, herring, capelin and shrimp.

GADGET implementations

There are existing single species models for haddock, plaice, redfish and wolffish. GADGET has been used for plaice, redfish and wolffish as age readings are limited for these species.

Redfish can be modelled only using length. The model was tested with and without age readings giving the same results (supporting the validity of the age readings). Without yearclass data, the solution may become confused (multiple minima) but the overall management conclusions were similar. Use of age helps to define which minima are more appropriate in finding the better fit more quickly.

There is a multispecies cod - capelin - shrimp model. One use of this has been to look at the relationship between deep water shrimp and cod as cod are a major predator and seem to have caused a recent collapse of the stock. Different spatial division were considered. With standard BORMICON areas the migration parameters indicate increasing migration of cod into the deep-water shrimp areas. Applying a model with fewer areas (only north <500m, south <500m and water deeper than 500m), the suitability of shrimp for cod increases but there is insufficient explanation compared with the more detailed model. Overall the three area model is a more successful model for cod, but some interesting results from the model with more areas which can be looked at further.

North Sea and North Atlantic Herring

Data preparation

Data from UK, Denmark, Netherlands, Norway, Sweden, Germany and France are included in the dataset. The range of nations providing data is table and year dependent and the range of years varies between tables.

Most input tables for the data warehouse have been completed. An initial dataset, representing a typical spring week, has been produced for the water movement table. Data are normally available at the level of ICES rectangles, some data are from the IBTS and environment data is available by week in 10m depth intervals.

Further work requires to be done on extracting sample data and compiling lookup tables.

Model formulation

Length based population dynamics models in state space form

The discussion on the description of Bormicon & Fleksibest as state space models led to a more general discussion on the differences between Bormicon and Fleksibest and more generally the existing functional relationships.

There is some confusion about the GADGET, particularly the details of the model formulae and how they are applied within the model. This is partly due to the existing Bormicon handbook being incomplete and out of date in some aspects and also due to there being differences between Bormicon and Fleksibest.

One of the most important differences between Bormicon and Fleksibest is in the use of catch data. Fleksibest requires catch at age and length data whereas Bormicon only requires length distributions from landings (age length keys where available) along with total landings.

Functional predator prey relationships should be extended to include density dependence and prey switching. Documentation is required on the functional relationships available along with information to allow users to choose appropriate relationships. Within a multispecies model different predator prey relationships could be described by different functional responses.

Different formulations of maturity by species are possible *eg.* capelin and cod are very different. Maturity is currently a function of length, age, growth and temperature.

Future work on model formulation

Description of biological process models
Description of appropriate process errors
Description of observation models
Bayesian estimation: formulate prior distributions for all parameters
Describe estimation methods available
Describe methods for model comparison - usually likelihood ratio tests

Status of GADGET

Current status:

GADGET can now run both the Bormicon and Fleksibest formulations.
Alphanumeric parameter names have been implemented.
With the size of model length groups and time steps currently used for Northeast Arctic cod, Fleksibest cannot run the beta-binomial growth model so old growth models have been reimplemented.
Now compiles on Linux/Solaris and Windows.
Optimisation of likelihood functions can be done inside or outside GADGET using PARAMIN.

Future work on GADGET:

- Clean up design, which includes providing a more coherent function and subfunction hierarchy.
- Clean up input formats:
  - separate data and function parameters in input files
  - likelihood information no longer to be included in “main” file
  - “main” file will then list the names of the input files
  - the input files will be in 3 categories:
    - model definition files (stock files, fleet files)
    - likelihood definition file (likelihood components)
    - data files
- Output formats from Bormicon and Fleksibest should match.
- Improve PARAMIN interface.
- Document the code including diagrams and program structure.
- Improved Quality Control:
  - CVS for source code.
  - set up test procedure with standard test datasets
  - maintain coding standard
  - keep documentation up to date.

Status of deliverables

Due in 2000:

State space formulation (due Q3) needs to be completed.

Due 2001:

Deliverable	Status
Databases	will not be completed in 2001
Data warehouse design	suitable format will be available, but further development preferable
Data warehouse software	prototype will be available but more required
Mathematical estimation	some work has been done
Description of goodness-of-fit	some work has been done
Bayesian estimation	nothing been done
Parallel processing	PVM complete and work being done with CONDOR
Prototype datasets for case studies	in progress
Prototype model runs	some progress

Linking the mathematical submodels with GADGET

A sub-group meeting on the mathematical models for migration and consumption evolved into a discussion on how to incorporate information from the models with GADGET.

Output from migration modelling could be used:

to generate improved migration indices
to compare with migration from the models

Future meetings

The next full meeting is planned for June 2002, possibly at the IFREMER institure in Sète (near Montpellier).

The full project meeting for the final year will be earlier in the year and the current plan is for February 2003.

Hafrannsóknastofnun. Fjölrit
Marine Research Institute. Reports

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