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14–18 March 2005

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Contents

Executive summary

The second meeting of the ICES Study Group on Age-length Structured Assessment Models (SGASAM) was held at ICES Headquarters from 14-18 March 2005. There were 12 participants (mainly with expertise in age-length structured modelling and stock assessment) from 10 countries. The main objective of SGASAM is to investigate and evaluate the use of length-structured and age-length structured population models in fish stock assessment. The terms of reference for this meeting related to both model development and species-specific applications.

Developments in methodologies and applications

An increasing number of age-length structured models are being developed (e.g. GADGET, CALEN, Stock Synthesis) and applied to a wide variety of species with differing life-histories. The acceptance of these for use in stock assessment is increasing, particularly outside of the ICES area. There is growing interest in the development of simpler length-structured models for the assessment of species for which age-structured data are unavailable and in particular, a number of length-structured models have been developed which make use only of length-structured survey data to obtain information on stock trends. These are clearly useful for stocks for which commercial catch data may also be unreliable.

Incorporating process sub-models

Process models previously developed by the ICES Study Group on Growth, Maturity and Condition in Stock Projections were specifically considered. Many of these are length-dependent and some, particularly for growth and maturity, have already been included into existing age-length structured modelling frameworks (e.g. GADGET). Further improvements to the implementation of these process models in age-length structured population models (important for the assessment of species where biological and fishery processes are better represented by length) will require greater co-operation between process modellers and age-length structured population modellers. It is therefore recommended that process modellers be encouraged to attend any further meetings of this SG.

Investigating complexity

The SG identified two different ways in which age-length structured model frameworks could be used to investigate the performance of models with different levels of complexity. One approach was to consider age-length structured models as operating models to generate data sets and then evaluate other simpler models (e.g. VPA, biomass dynamic) in terms of their performance against the underlying 'true' system and perhaps also in terms of relative performance against alternative management regime. The second approach was the comparison of different sub-models within the same framework and comparing their performance in terms of 'goodness of fit' to the underlying data. There is a need for development of formal statistical methods to carry out these comparisons.

Case studies

The alternative to more complexity is the development of simpler length-based approaches for species for which age-disaggregated data are sparse or unavailable. A number of species for which there are age-reading uncertainties (and hence limited age-based data) were considered by the SG and the development of length-structured models is already in progress for some of these. The SG felt that continuing work on such simpler approaches is important and would be particularly useful for the assessment of species such as Nephrops, redfish, anglerfish and some elasmobranchs.

1 Introduction

1.1 Participants

Helen Dobby, United Kingdom (Scotland)
Hilaire Drouineau, France
Dorleta Garcia, Spain
Daniel Howell, Norway
Sung-Tae Kim, Republic of Korea
Kasper Kristensen, Denmark
Peter Lewy, Denmark
José De Oliveira, United Kingdom (England and Wales)
Mike Smith, United Kingdom (England and Wales)
Ian Stewart, USA
Lorna Taylor, Iceland
Dmitry Vasilyev, Russia

In addition a written contribution was received from Nick Davies and Dave Gilbert, NIWA, Wellington, New Zealand.

The full contact details of the participants can be found in Annex 1 of this report.

1.2 Terms of Reference

The **Study Group on Age-length Structured Assessment Models** [SGASAM] (Chair: H. Dobby, UK) met at ICES Headquarters from 14–18 March 2005 to:

a. review developments in methodologies and applications of length- and age-length structured population models in ICES areas and elsewhere, and provide a forum for dissemination of information regarding these methods;
b. investigate the feasibility of incorporating process-based growth, maturity, condition and fecundity models into existing model frameworks;
c. evaluate the utility of age-length structured model frameworks for investigating the performance of models with different levels of complexity;
d. explore the potential of applying age-length based models to stocks of anglerfish, hake, redfish and sprat.

SGASAM will report by 15 April for the attention of Resource Management Committee and ACFM.

1.3 Scientific justification by ICES

Despite the existence of a diversity of available model types, for largely historical and institutional reasons, catch-at-age models are by far the most widely used approach in stock assessment within the ICES context. However, in many cases a catch-at-age model may not be the most appropriate assessment model and improvements may be made to the assessment by using either a length-structured or age-length structured population model. The reasons for adding length-structure to population models fall broadly into three classes:

- it is thought that such models are a better representation of biological and fishery related processes;
- problems with age determination do not permit the use of age-structured models or make such models less reliable;
- age is not considered to be a good proxy for length.

This Study Group addresses the problems that come from introducing length structure (in addition, to age structure) and see how these problems may be solved in practical use. Specifically, SGASAM investigates and evaluates the use of length-structured and age-length structured population models in fish stock assessment. Age-length structured models may have a higher degree of complexity. The final choice of model will depend upon the question being asked and often require a trade-off between a desire for complexity and the availability of data.

A more extensive discussion of the importance of incorporating length-structure into assessment models can be found in Section 2 of ICES 2003a.

1.4 First meeting of SGASAM

A large number of diverse presentations were reviewed at the first meeting of SGASAM (ICES 2003a). These highlighted the considerable amount of modelling work in progress around the world on length-structured and age-length structured assessment techniques, and on processes relevant to such models. It was considered that age-length structured models provided a flexible structure which can be used to investigate the feasibility of particular process models and conversely that new process sub-models may provide valuable improvement to overall model performance.

It was evident that it is not only choices about model complexity that are important, but also how the model is implemented numerically. As with all models in discrete time which describe continuous dynamics, the choice of discretization scheme can affect simulation results and parameter estimates. The SG group recommended that such artefacts be further investigated.

A number of case studies were presented in which length structure had been incorporated into the assessment model. However, none of the age-length structured assessments presented at this meeting had been formally used as the basis for scientific advice. This may be due to the inherent complexity of more sophisticated models, which is often exacerbated by the lack of documentation, difficulty in constructing, running and interpreting the model. The development of user-friendly interfaces for running models, producing diagnostics and analysing model results was considered by the SG to be an important step in increasing acceptance. When there is no current accepted methodology, it appeared to the SG that there may be greater acceptance of new models than in situations with a long history of using conventional tools. It was therefore agreed that identifying stocks for which age-length based models may be more appropriate should be a high priority and that the results compared to those from more conventional methods.

1.5 Structure of the report

Some of the general recommendations made at the first meeting of SGASAM have been addressed by intersessional work, some of which has been presented at the current meeting and is discussed in Section 2 of this report. Section 3 addresses ToR b, looking at the feasibility of incorporating particular process sub-models into currently available model frameworks. The discussions related to ToR c are documented in Section 4. Section 5 addresses ToR d by providing some discussions on the possibility of applying age-length based models to particular stocks, including discussions on appropriate process models, data availability and where applicable the current usage of such models is noted.

A discussion of the main conclusions of the meeting can be found in Section 6 and a list of recommendations in Section 7.

2 Presentations and working documents

ToR a) review developments in methodologies and applications of length- and age-length structured population models in ICES and elsewhere, and provide a forum for dissemination of information regarding these methods.

2.1 Maximum likelihood estimation in a single species model

Kasper Kristensen and Peter Lewy, DIFRes, Copenhagen, Denmark

In the study by Kristensen *et al*. (2005) a new consistent approach to length-based, single-species fish stock assessment is presented. The method combines continuous size-spectra modelling with statistical modelling of length composition data and performing statistical inference. CPUE data by length from individual research survey hauls are used as raw data and not the mean CPUE, and thus the stochastic variation between individual hauls is determined from analysis of data. Stock parameters are estimated by maximum likelihood, and likelihood ratio tests by size are used to localize model problems.

A simple size spectra model was derived assuming that each recruit is assigned its own growth pattern and that the mortality is size selective. Sub-models for growth, fishing mortality, survey catchability and variance structures are included in the model. The parameters including relative recruitment are estimated by maximum likelihood. As data for individual hauls are used, it is possible to test a hierarchy of crucial hypotheses.

The model is applied to research survey length distribution data from the Danish vessel DANA for Eastern Baltic cod in ICES Division 25. The use of size based scientific survey data only is particularly relevant when the age determination is uncertain and the quality of catch data poor. Hence the model is relevant for the Baltic cod for which these problems apply. Data consist of cod catches from 299 selected hauls taken in 9 Baltic International Trawl Surveys. The period 2000–2004 was considered because a new survey gear was introduced in 2000. The survey is performed twice a year.

Estimably in the model was examined by re-estimating known parameters from simulated data-sets. Quite surprisingly it turned out that even in a model with a time varying catchability all model parameters were estimable.

The results for Baltic cod showed that the negative binomial distribution was accepted by a Kolmogorov-Smirnov test. Various visualizations of the data indicated that the proposed variance structure described the data in a satisfying manner. Furthermore, the mean length distributions in the surveys determined by the spectra-model fit the observed length-distributions reasonably well. A test of the validity of the model is to compare the predicted and observed relative length distributions of yearly commercial catches, which were not included in the model. The comparison showed that the predicted distributions fitted well to the observed. Mean fishing mortality seems to be of the same order of magnitude for the present model and the ICES Baltic Sea WG.

With respect to applicability of the model for Baltic cod it is difficult to compare the results with the ICES age-based assessment. This is because that the ICES working group covers all Divisions 25- 32, while the present model only cover Division 25. Further, the time period considered, 2000-2004, is rather limited for comparisons. Finally, the model assumes that recruitment takes place instantaneously once a year. We think that this should be improved either by assuming that recruitment takes place twice a year or by including continuous recruitment.

2.2 Integrated analysis of fishery and survey size, age, and abundance information

Richard Methot, NOAA Fisheries Service, Office of Science and Technology

presented by Ian Stewart, NOAA Fisheries Service, Northwest Fisheries Science Center

Integrated analysis is a class of stock assessment models that include a population sub-model operating by forward simulation, an observation sub-model to estimate expected values for various types of data, and a statistical sub-model to characterize the goodness of fit of the data and to obtain the best-fitting parameters with associated variance. The integrated analysis model, SS2, includes a rich feature set including age and size-based population dynamics and observational phenomena such as ageing imprecision. The model is coded in ADMB (www.otter-rsch.com) and incorporates and expands the feature set of the Stock Synthesis model developed in 1988 and used for most west coast groundfish assessments during the 1990's. In SS2, there is no specific limit to the number of fisheries or surveys. Data includes fishery and survey age and length composition, mean size-at-age, survey abundance, mean body weight, and percentage discard by weight. Annual recruitment is modelled as deviations from a spawner-recruitment curve. The population is modelled as a set of phenotypic morphs, each with an assigned gender and unique growth and natural mortality parameters. Growth parameters can be estimated internally to take into account the effects of size-selectivity and ageing imprecision on observed size-at-age. Model parameters can be a function of environmental data or vary randomly over time. Numbers-at-age for each morph are tracked independently, so that size-specific fishing mortality will have a differential effect on the survivorship of each morph. Recruitment is apportioned among areas and growth morphs. For example, different morphs can be assigned to different areas to mimic a cline in size-at-age while also allowing diffusion of each morph along the cline. Parameter estimation occurs in a Bayesian context and the Monte Carlo Markov Chain algorithm is used to provide non-parametric confidence regions on parameters and derived quantities.

Program and documentation available from: Richard.Methot@noaa.gov.

2.3 A yield per recruit model for brown shrimps (*Crangon crangon*) with temperature dependent development and growth rates

Mike Smith, CEFAS, Lowestoft, UK

A yield per recruit model incorporating temperature dependent development and growth rates has been developed and applied at the ICES WG on *Crangon* Fisheries and Life History (Temming and Damm, 2002; ICES, 2003c). The model takes the seasonal pattern of daily egg production as its input and projects these cohorts forward with daily time steps over a period of 4 years. Temperature dependent egg and larval development rates are used daily to calculate the proportion of development achieved and when this equals or exceeds unity the cohort passes to the next stage.

On completing larval development all animals are assigned an initial length of 5mm and stochasticity is introduced to the model. A growth function based on the first derivative of the von Bertalanffy model with temperature dependent anabolic and catabolic components is used to model daily growth increments. Each daily cohort is split into 50 (or more) 'micro-cohorts' each with a stochastically generated growth parameter that is retained throughout its lifetime. Moult duration is also modelled as a temperature dependent process, but is used only to regulate spawning frequency and is not coupled with growth.

Natural mortality is size (or stage) structured and varies by season on a monthly scale. Information from the literature was used to provide estimates of the level of mortality by size and seasonal trends were based on temperature regimes and the availability of key predator species.

Females make up by far the majority of the catch, although some males are caught around the size of selection. The model has therefore been implemented as female only and selection considered as knife-edged using alternative values (45mm or 50mm). Fishing mortality varies seasonally with the overall level set as a proportion of total mortality (estimated using length converted catch curves) and the seasonal pattern following that of fishing effort for the national fleets concerned.

Slightly different implementations have been produced and applied by German and UK working group participants. The models have been applied to explore the potential dynamics of the *Crangon* population with particular regard to the timing of recruitment and spawning as well as the contributions to the population, egg production and landings of summer and winter spawned cohorts (ICES, 2003c). They have also been applied using a scenario modelling to approach to examine the possible effects of changes in the pattern of fishing mortality for a range of growth model parameters (ICES, 2003c ; 2005 *in prep*.). Results were found to be relatively robust for a range different growth parameters. It was acknowledged that results were likely to be highly dependent on the seasonal pattern of natural mortality and that this aspect needed further attention. Simulated length frequency data from the UK version were used as the basis for investigating the performance of modal progression analyses and simple graphical methods for estimating growth parameters (ICES, 2005 *in prep*.).

The temperature dependent growth model based on the first derivative of the von Bertalanffy model represents an example of a process driven model and shows some interesting behaviour. At a constant temperature the model produces growth that corresponds to the von Bertalanffy model algebraically derived from the parameters. However, if temperature is varied around the same average temperature then the model produces growth that (while oscillating) converges towards a lower L_∞ (and has a higher K).

Also of some possible interest to the group are some results obtained from the stochastic implementation of the model. Growth increment is a function of length and subsets of a cohort are each assigned a stochastic growth parameter. With moderate variance in growth rate (CV on stochastic growth parameter = 0.3) this results in a skewed distribution about the mean size at age. This is contrary to commonly made assumptions that the distribution of individual sizes about mean size at age is symmetrical.

This is an example of a simulation model that considers biological and process models explicitly and sometimes in considerable detail. The models can generate a wide variety of outputs at various scales. The model has not been fitted to observations directly, but rather parameters for individual sub-models have been fitted independently or values drawn from the literature have been used. The model provides interesting insights in to the population dynamics of *Crangon* and has been usefully applied to address some issues of relevance to *Crangon* fisheries.

2.4 Simple models of a cod population – complexity and inconsistent data sources

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2.4.1 Abstract

An age-length structured statistical modelling framework Gadget, (**G**lobally applicable **A**rea **D**is-aggregated **G**eneral **E**cosystem **T**oolbox). is used to consider different levels of model complexity, both in the structure of the model and in the range and aggregation level of the likelihood data. Models of varying complexity can provide a useful source of information on the model flexibility required to minimise incompatibilities between data sources. Inappropriate model structure can lead to datasets appearing to be inconsistent. Consideration of model complexity along with inconsistencies in the data sources can help identify the most appropriate scales at which processes should be modelled.

2.4.2 Introduction

Gadget is an age-length structured statistical modelling framework (Begley, 2005). Models can be fully parameterised and run as simulation models or parameters can be estimated using maximum likelihood estimation. A variety of different data types from many different sources can be used and these are combined in an objective function which is a sum of weighted negative log likelihood components. If there is inconsistent information from these different data sets, then the solution will be pulled in different directions by the different components, resulting in different parameter estimates. This means that the weighting can affect the resulting parameterisation. In order to avoid the problem of *ad hoc* weights, which can bias estimation, a statistical methodology is used to calculate the weights using the inverse of the minimum sum of squares.

2.4.3 Models

All the models have a similar basic structure: 2 stock components (immature and mature) with 12 ages on a single area. There are either 4 or 12 time-steps per year and either 19 or 20 years. All commercial catch is in one fleet and there are also 2 surveys. In one model, the mature predate on the immature.

The data consist of landings, length distributions, age-length distributions and age distributions from the catch and surveys, the ratio of mature to immature from the spring survey, survey indices and stomach data as biomass ratios (both by prey species and length distribution with cod). The survey abundance indices are calculated by slicing the length distributions into 3 groups, with these groups representing age 1, age 2 and age3+. This enables the spring and autumn surveys to be combined without resorting to pre-processing the data. At all times the likelihood data are based purely on observations, rather than using processed data such as catch numbers at age, or survey numbers at age. In particular, it should be noted that it is statistically inappropriate to include the same data twice in the objective function.

Estimated biological parameters are: growth, maturation, selection patterns of the fleets and selection through consumption. In addition, recruitment as numbers at age 1 and the number at age for the initial population are estimated.

2.4.4 Combining different data sources

As part of the protocol to estimate weights, each likelihood component is heavily weighted in turn and the model optimised. This makes the influence of the other likelihood components negligible in the optimisation. In the case of the survey indices, the equivalent indices from the 2 surveys are heavily weighted simultaneously. From each run the resulting likelihood score of the heavily weighted component is an unbiased estimate of the minimum sum of squares (as the objective function being used here is a sum of squares). From this procedure, it can be seen that the fit of the model to the data is highly dependent on the weights and that the datasets are inconsistent in the framework of this model. It is also apparent that the resulting parameter estimates are affected by the weights e.g. the trend in recruitment from the different length groups from the survey indices are very different. It should be noted that inconsistencies between datasets are more easily detected when unprocessed data are used than in models which rely on heavily processed data such as catch in numbers at age.

2.4.5 Model comparisons

Model comparisons were made between 4 models on monthly time-steps and more generally between the monthly and quarterly models. The models with 12 time-steps per year are: 1) a baseline cod model with age and length likelihood data and no predation, 2) the same model with consumption, 3) a model equivalent to 1 with no age data but with fixed growth and 4) equivalent to 1 with more aggregated length likelihood components. In model 4, length distributions and age-length distributions are aggregated in 10cm groups rather then 2cm and 4cm for the length distributions and age-length distributions respectively for the other models. The purpose of these models was to investigate the ability of the model to optimise consistently to different model structures and levels of data availability rather than to conduct formal statistical tests of the models.

The quarterly models are similar to model 1 above but with 4 time-steps per year. Models were created on 1cm or 2cm length intervals and with the betabinomial parameter (used to calculate the transition matrix for the length update) either fixed or optimised.

Estimation of the parameters by the 4 models with 12 time-steps is mostly consistent. The only major difference is in the estimation of the selection pattern of the survey indices. By aggregating the survey length distribution into 10cm length groups a considerable amount of information is lost and a different selection pattern estimated.

Preliminary model runs indicate that the number of time-steps in a year affects the fit of the model to the survey indices, with the sum of squares typically greater for the less flexible 4 time-step model than the 12 time-step model. It is important to note that not only are the sse higher, but that the estimated slopes are less appropriate with 4 than 12 time-steps. The difference in the ability of the 4 time-step model to fit to the survey indices may be due to it's reduced temporal flexibility as there is only one time-step between the surveys rather than 6 in the 12 time-step model.

2.4.6 Increasing complexity

Simple models can be used to identity ways in which it may be desirable to increase the structural complexity. The fit of the model to the data may contain patterns and inconsistencies between likelihood components can be identified. An example of the former is when the fit of the model to catch sampling data contains patterns, with certain time-steps having greater likelihood scores. In this case, increasing model complexity by disaggregating the fleet may improve model performance. Inconsistencies between likelihood components identified using the sequential weighting procedure, may also be reduced by increasing model flexibility.

2.4.7 Conclusions

In some respects, growth in the quarterly model will be expected to be better than the monthly model, as the betabinomial transition matrix has greater scope to spread the growth over several length groups. For this fish stock, with the population modelled on 1cm intervals in time-steps of 1 month, most fish will grow either 0 or 1 cm and to model the population on a scale finer than 1cm would be time consuming and data are not available. While data are not required it is preferable not to model on a scale which cannot be validated against data. On the other hand, these initial runs suggest that the reduction in temporal flexibility results in a considerably poorer fit to the survey indices. It should also be noted that in some potential multispecies applications of a model of cod in Icelandic waters, in particular with capelin, 4 time-steps a year is inadequate to represent the processes.

Considering model complexity more generally: While the simplest approach is to model a single area, inconsistencies between surveys at different times of the year may be due to changes in distribution or behaviour. These factors coupled with area dependent catchability and the relative distribution of substocks mean that multiarea models may be necessary to reduce inconsistencies. Simpler ways in which model structural complexity can be increased to reduce inconsistencies are, e.g. fleet disaggregation, variable growth rates and different growth parameters for immature and mature stock components.

The selection of models presented here, show that the statistical estimation of weights is possible. With slight changes to either model structural complexity or the availability of data the resulting weighting scheme is consistent as is the final parameter estimation. Age data are not necessarily required, and data can be aggregated although care is required that the level of aggregation does not lead to substantial loss of information. Preliminary results from the 4 time-step model indicate, however, that the increase in model stiffness may be increasing the inconsistencies between the surveys.

2.5 Development and fitting of a spatial length-structured model for the European hake

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Presented by Hilaire Drouineau

The European hake represents the second French landed species in value (DPM/OFIMER 2003). Actually, the Northern stock is in an alarming state (Fpa superior to Flim and SSB inferior to SSBlim, ICES 2004d) and a recovery plan came into effect in April 2004, because of an alarming biological state.

Several sources of uncertainties remain in the assessment of this stock and alternative stock assessment models are needed. In this respect, a statistical spatial length-based model is considered for several reasons:

i. Uncertainty on growth and difficulty to age (De Pontual, Bertignac *et al*., 2003)
ii. Heterogeneities of both population and exploitation spatial distribution
iii. Many unknown parameters (biological or of fishing activities), with unknown distribution.

Those three reasons lead us to consider the construction of a spatial statistical length-based model.

An appropriate structure should be selected for each process. It means that the model should be a trade-off between the desired complexity and the availability of data, and that the impact of each assumption should be quantified.

Two previous studies were realised preliminary to the model construction.

The first was aimed at evaluating the impact of the discretisation process in a growth model with individual variability. This analysis demonstrates the major impact of discretisation of both time and length. Gamma and lognormal seem to be the more flexible distribution functions to describe inter-individual growth variability, especially when variance is fixed as a proportion of the mean increment. Finally, it confirms that it is more appropriate to consider that individuals are uniformly distributed within length classes than to place them in the middle of the class.

The second reviewed different optimisation algorithms which can be used for maximum likelihood estimation. Three types of algorithm were considered. Each presents specific advantages and disadvantages. Genetic algorithms in particular seem a promising tool and should be tested.

A first model is actually coded to serve as baseline of work and to test and compare different structures. Preliminary studies on mortality (fishing and natural), recruitment and migration, analogous to the study previously presented, are going to be realised to quantify the impact of different hypotheses. The quality of fitting of different model structures (quantified for example by the AIC index) will allow to compare these structures, and also to compare different optimisation algorithm.

The final model should make possible to assess the hake population on real data, while estimating unknown parameters, and to quantify some management scenarios, and especially spatial measures. This level of complexity requires the use of a large of amount of data. We hope to have at our disposal:

iv. Catch data by class, quarter, fleet and zone
v. Survey indices of abundance by class, quarter and zone
vi. Tagging-recaptures data: a campaign is actually realised in the Bay of Biscay but a campaign on a larger area would be required
vii. If possible, nominal effort by fleet, quarter and zone.

Finally, estimated parameters may be used in other model, especially ISIS-Fish simulator tool aimed at evaluating the impact of various management scenarios. A more complete description of this presentation can be found in Working Document 2 (Annex 2)

2.6 Some applications of length-structured models

Helen Dobby, FRS, Aberdeen, UK

2.6.1 Exploratory size-structured assessment of Firth of Forth *Nephrops*

Historically *Nephrops* stocks have been assessed using a variety of methods, ranging from analytic age-based and length-based methods to the analysis of long-term CPUE (or other fishery data) and the analysis of fishery independent survey data. Current methods make use of previously estimated von Bertalanffy growth parameters to generate ‘slicing points’ in the catch-at-length frequency data and divide these data into nominal ‘age classes’. These ‘catch-at-age’ data are then used in XSA to conduct an age-based assessment. Clearly this method does not take account of the variability in individual growth rate and hence the variability in length-at-age. Each nominal ‘age class’ therefore contains a mixture of year classes with the effect that estimates of recruitment tend to be smoothed out, perhaps leading to difficulties in identifying biological reference points and detecting stock trends.

A more biologically satisfying way to model *Nephrops* population dynamics is to implement a size-transition matrix approach (a modified catch-at-size analysis, Sullivan *et al*. 1990). The population is described by a vector of numbers-at-length which is projected forwards in time using a size transition matrix obtained from a stochastic growth model with known parameters. In this model all population dynamics processes (e.g. recruitment, fishing mortality) are assumed to be dependent on length only. Parameter estimates and historical trends in stock abundance (annual recruitment, mean and standard deviation of recruitment distribution, selectivity parameters, temporal component of fishing mortality) are then obtained by fitting the model to the observed data. In contrast to the age-based assessments currently used, this length-based approach carries out the assessment of males and females simultaneously. The population model links the males and females by assuming identical numbers recruit to the male and female populations and also that the fishing mortality fluctuates in a similar way. The reduced fishing mortality on the mature female population due to reduced emergence from burrows during the spawning season is modelled by introducing a quarterly dependent ‘catchability’ parameter (fixed from year to year) which calculates female fishing mortality as a proportion of the male fishing mortality. A more complete description of this model can be found in Dobby (2002 and 2004).

The resulting estimates of biomass and fishing mortality are very similar to those obtained from the XSA assessment which may not be surprising since the assessment uses the same catch-at-length data. However, although the estimated recruitment has the same trends, it shows much greater fluctuations, possibly due to the application of length-slicing to obtain the age-structured data. Incorporation of TV survey biomass data alters the perception of the stock biomass in that estimates are increased in early years, but then show a downward trend which was not observed in runs based only on the commercial data. Possible explanations for this mismatch are that commercial catchability may have increased (not accounted for in the model) or that the low values in the TV survey data may have been due to weather conditions rather than any particular downward trend in stock biomass.

2.6.2 An analysis of length-structured survey data

The standard assessment techniques used by ICES Working Groups (e.g. XSA, Darby and Flatman, 1994; ICA, Patterson and Melvin, 1996) rely largely on reported catch-at-age data with survey indices generally only being used as supplementary data to ‘tune’ final year parameter estimates. If reduced TACs are not accompanied by a reduction in actual fishing effort then discarding and misreporting of catches is more likely to occur. The reported catch data in these cases is therefore not likely to reflect actual catches and assessments relying on these data are likely to give a very misleading picture of the stock.

Recent development work at FRS on stock assessment methods has been directed towards making the best possible use of information obtained from research vessel surveys. SURBA (Needle 2002) is a recent implementation of a survey-based assessment model developed by Cook (1997) which assumes a separable model for fishing mortality. Estimates of the age and year effects of fishing mortality and year class effects are obtained by assuming that survey catchability is known and then fitting the model estimates to the observed survey index at age. The need to specify a fixed survey catchability means that abundance estimates are relative and until independent methods of estimating these values are developed the model can only be used to indicate population trends. Options currently being explored are: i) using the catchabilities obtained from traditional VPA type analysis (Needle 2004) and ii) obtaining independent estimates based on gear parameters.

One such stock for which reported catch is unlikely to reflect true catch is the Northern Shelf anglerfish and at their meeting last year, the Working Group on the Assessment of Northern Shelf Demersal Stocks (WGNSDS, ICES 2004a) felt unable to present an assessment largely because of this reason. Uncertainties in the age-readings of anglerfish make the assessment of this stock particularly challenging and in previous years a method utilising a size-structured model and catch-at-length data has been developed (Dobby 2000, 2002). Due to the ageing difficulties, age information is not routinely collected on surveys and this document begins an exploration of whether the size-structured approach can be adapted to make use only of survey data. Furthermore, such an approach would be useful for other stocks with more limited data availability and for which ageing is not possible (e.g. deep-water species, elasmobranchs), but which are routinely measured on research surveys.

The basic population model is the same as that described above for Nephrops (and in WD’s referenced above), but parameter estimation relies only on a comparison between estimated and observed length-structured survey indices. Estimates of the survey indices ($\hat{I}_{l,y}$) are obtained from the product of catchability (q_l) and modelled population numbers at length at the time of the survey

$$\hat{I}_{l,y} = q_l \hat{N}_{l,y} e^{-pZ_{l,y}}$$

$\hat{N}_{l,y}$ are the modelled population numbers at length at the beginning of year *y*, *p* is the time of the survey (as a fraction of a year) and $Z_{l,y}$ is the total mortality rate of length class *l* in year *y*. Survey catchability is assumed to be a function of length and currently must be derived externally and input to the model in the form of an array. Like the age-based model (SURBA) described earlier, without appropriate values for survey catchability at length, the estimates of recruitment and abundance obtained from this method will be relative rather than absolute.

Although the motivation behind the development of this approach was to facilitate the assessment of Northern Shelf anglerfish and other traditionally non-assessed stocks, the application described here will be to West of Scotland haddock. This stock was chosen because it's status is considered to be relatively well known and it also exhibits particularly strong fluctuations in year-class strength which appear as relatively strong signals in the survey data.

The particular assumptions of this model are very simple: no structuring by sex, growth parameters assumed known and fixed, annual time step, commercial selectivity pattern is logistic. Although the sensitivity of the results to these assumptions has not yet been fully explored, resulting stock trends have been compared to those resulting from an application of SURBA and also to the results of the TSA assessment (based on commercial catch data) (Fryer 2002) conducted at the 2004 WGNSDS (ICES 2004a). The estimated trends in stock biomass and recruitment show relatively good consistency between methods, but the estimates of fishing mortality are rather different and much more variable from year to year for the survey-based approaches than for the commercial catch-based assessment. Possible reasons for this include the generally noisy survey data, but it may also be the case that the commercial catch data does not include a complete estimate of discards.

Further work on this approach needs to focus on how to obtain more consistent estimates of fishing mortality as well as testing the model on other species without such clear year-class signals.

2.7 A closed life-cycle model for NE Arctic cod

Bjarte Bogstad, Daniel Howell and Morten Nygaard Åsnes, IMR, Bergen, Norway

Northeast Arctic cod (*Gadus morhua*) is a species with considerable knowledge available on the main population dynamics processes (growth, maturation, fecundity, recruitment, natural mortality, fishing mortality). An age-length structured Gadget model exists for this stock, modelling all fish from age 1+, and dividing immature and mature fish. This makes for an ideal case study for exploring process sub-models. The model is described in Bogstad et. al. 2004.

Two such models, for cannibalism and fecundity, were presented. Cannibalism is modelled as dependent on the length of predator and prey, and is subject to prey switching based on the relative abundance of capelin and small cod. Fecundity is modelled based on the length and condition factor of the mature cod. In each case the use of more data (stomach content or first time/repeat spawners) is available and could be used to enhance the models. Alternative comparisons between different process formulations (e.g. SSB) are also possible. The model is then able to evaluate the differences such changes would make to the estimated population.

The differences in using the model as a tool to explore the process sub-models, and using it as an assessment model were highlighted. For an assessment, estimating model parameters may dominate over the choice of functional form for any given process sub model.

2.8 An example of the effect of including length structure in yield-per-recruit estimates

C. Kvamme and B. Bogstad, presented by Daniel Howell

An analysis was conducted comparing how the results of a yield-per-recruit analysis varied according to the choice of model structure. An age-structured and an age-length structured model were compared. In a fishery large fish within a cohort are likely to enter the fishery earlier than the smaller fish of the same age. This results in a change in the mean weight at age of a year class of fish, depending on the fishing pressure and the selectivity of the fishery. An age-based approach may not capture this feature, and may thus yield misleading yield-per-recruit calculations. In particular it may underestimate the benefits to be gained by delaying exploitation to older, larger, fish.

The example presented considered Northeast Arctic cod. It was shown that moderate or high fishing pressures, with fishing on medium or small fish, would produce significant reductions in the mean weight at age of the stock. This translated to marked differences in the yield-per-recruit curves in the model in which length structure was included. It was estimated that changing the fishing pattern to target older, larger, fish would produce a 20% increase in yield per recruit. It was recommended that such analyses should incorporate length structure.

2.9 First steps towards a dynamic length structured model for edible crabs – two alternative probabilistic growth models

Mike Smith, CEFAS, Lowesoft, UK

This short presentation considered two alternative models for probabilistic growth models for edible crabs (*Cancer pagurus*). Growth was considered as two processes; annual moult frequency (the probability of moulting in a given year or the proportion of crabs moulting in any given year) and moult increment (the amount by which a crab increases in size during moulting).

The process of moult frequency was considered using the reverse logistic models of Zheng *et al.* (1995; 1997; 1998) and the log linear model used by Bennett (1974). Both models were fitted by least squares minimisation assuming normal errors. Towards the lower limit of the sizes observed (tagging data from Bennett, 1974) the logistic model is inappropriate because crabs may moult more than once per year and because of the symmetric nature of the function. Fits using a logistic model gave estimates of the size at which moult frequency approaches zero that were considered rather low. Fitting using the log-linear model gave estimates of the size at which moult frequency approaches zero that were more reasonable, although still possibly somewhat low, but gave very high moult frequencies if extrapolated to smaller sizes. A number of reasons for under-estimation of moult frequency (especially at large size) when using tagging data were postulated including; increased tag loss during moulting; low sample size at high and low sizes; size dependent selection at low and high sizes (Hancock and Edwards, 1967); higher natural mortality rate during moulting (Hancock and Edwards, 1967) and differential migration (possibly to spawning areas) by crabs that have moulted and therefore also mated (Hancock and Edwards, 1967).

Moult increment was considered to be well represented by the tagging data. It was modelled using absolute measurements with a gamma error (Zheng *et al.*, 1995; 1997; 1998) and using increment as percent of pre-smoult size assuming normal errors (Bennett, 1974). Both models fitted the data well, were highly significant and behaved similarly over most of the range of commercial catch data (slight differences in the transition matrix were apparent for large females). However, it was interesting to note how different the behaviour of the models was if extrapolated. The absolute increment and gamma error model was clearly inappropriate at very small sizes, while the relative increment model with normal errors was loosely plausible at all sizes, but had very wide confidence intervals at high size (especially for males).

2.10 An overview of Gadget age-length structured models at IMR Bergen

Daniel Howell, IMR, Bergen

There are currently four different Gadget age-length structured models in use at IMR, Bergen. These are Northeast Arctic cod, Barents Sea Redfish, Barents Sea Capelin and Sofala Bank shrimp. These models cover a wide range of different life histories, environments, data availabilities and fishing regimes. In addition the models are intended for a range of different uses. In terms of life cycles the models vary in life span from long lived (>30 years for redfish) to short lived (mostly 1 year for shrimp). Some stocks (cod, redfish) spawn multiple times, capelin only once. Redfish show fairly stable population numbers, cod have occasional large peaks, while capelin have major crashes. Data ranges from very good for cod, to less abundant or reliable data for the other stocks. Management can aim at stable quotas (cod, redfish), highly variable quotas (capelin) or largely based on closed areas or times (shrimp).

The purpose for each model also varies. The redfish model is intended as an assessment model, and to assess the effects of including or excluding age readings from the data. Cod is part of the assessment process, and a key component of a multi-species model in development for the Barents Sea under the BECAUSE EU project (Anon 2005), of which capelin will form a part. The shrimp model is aimed at giving earlier predictions of the coming year's stock size, and as a tool to explore the possible effects of different management scenarios. Of these models the cod was described in another talk (Section 2.7), while the shrimp model was presented here.

The fishery for large shallow-water shrimp on the Sofala bank of Mozambique represents a significant contribution to the export earnings of the country. The fishing is largely concentrated on two species, *P. Indicus* and *M .monoceros*, with a number of minor species also caught. The Gadget model consists of both major species, each split by sex to give a four stock model. These species are short lived and fast growing, with larger specimens commanding a price premium. The shrimp spawn in open water, the larvae migrate to coastal mangroves, and adults return to open water, where the main fishing occurs. The migration to the fishing grounds is split over several months, and the early stages of this migration are partially protected by the closed season. The success of the fishery depends on the size of the year class and the timing of recruitment. Shrimps having more time to grow before being caught give a much higher value than shrimps caught at smaller size. The model aims at providing a tool towards refining the management techniques to maximize the value realized by the stock. To this end a simple value-per-recruit analysis was conducted.

2.11 Growth and Spawning of Japanese tiger shrimp(*Penaeus japonicus*) in Korea

SungTae, Kim. National Fisheries Research and Development Institute, South Sea Fisheries Research Institute, R. O. Korea

The sex ratios of Japanese tiger shrimp show a higher proportion of males than females. The spawning seasons is from: May to November (Main from June to September) It's biological minimum size is BL(body length) about 150mm. Fecundity equation for body length is $F=0.0011\ BL^{2.50}$ ($R^2=0.79$). Relative growth: Female, BW(Body weight)=$0.000012\ BL^{2.98}$ ($R^2=0.96$); Male BW= $0.000019BL\ ^{2.88}$ ($R^2 = 0.94$). I estimated that Japanese tiger shrimp of life span is about 1–2years olds.

2.12 Measuring the robustness of an age-structured model (CASAL) using an age-length-structured operating model (CALEN)

Nick Davies and Dave Gilbert, National Institute of Water and Atmospheric Research Ltd, Wellington, New Zealand.

A written contribution was received on the development of an approach for systematically quantifying the robustness of conventional age-structured models using an age-length-structured model. Some preliminary results are also outlined. Details can be found in Annex 3.

3 Feasibility of incorporating process-based growth, maturity, condition and fecundity models into existing model frameworks

3.1 Introduction

This TOR relates to TOR c at the Study Group on Growth, Maturity and Condition in Stock Projections (SGGROMAT, ICES 2004b), to "implement suitable process-based models in medium-term projection methodologies and conduct sensitivity analyses to examine the likely effects of these new approaches on management advice." The focus of *this* group is to concentrate on actual process-based models, and the feasibility of including them into existing model frameworks.

Process-based models are those models that directly model a biological process associated with a fish stock. They do not include correlation models, or models of the outcome of a process. For example a process-based maturation model would model the process of (individuals or the population) becoming mature, rather than the proportion mature. Correlation based studies are an important precursor to generating process-based models, but the two should not be confused.

The feasibility of incorporating a particular process-based sub model into stock dynamic model will depend on a number of factors: the structure of the process sub-model, the structure of the stock dynamic model, the ability to formulate the process model and the ability to estimate parameters to fit a particular situation.

An age-length structured model provides a detailed framework into which a wide range of different process-sub models could fit. Sub-models can integrate well into existing stock dynamic models provided they are formulated in terms of the parameters included in those stock dynamic models. In some cases it may be possible to integrate process-models into a purely length based model, but having a full age-length structure gives a greater flexibility, both of the process formulations and the way in which they can be compared to data. This flexibility is important because in many cases the process-based sub models will be highly specific to a given species. A number of different biologically-detailed age-length structured modelling frameworks exist into which process-based sub models can be inserted.

One of the limitations of many current age-length structured fishery models is that they compute the next time step based only on the current time step, i.e. there is no memory within the model. This prevents any model formulations that rely on factors over the course of the whole life history of the fish (such as number of spawnings, lifetime feeding history, etc). Addressing this problem would require an increase in the complexity of the models, and of the computer power required to run them.

A problem arises when the stock dynamic model is to be used to replicate an actual fish stock. The parameters controlling the different processes must be estimated, and this requires that relevant data be available. This can limit the choice of parameters which the process sub models can use. Alternatively the parameters can be fixed based on the literature or experimental data, however the latter gives a possible problem when applying the parameters to wild fish. A range of possible values could also be used for sensitivity or robustness testing.

3.2 Growth

Process — Change in length and/or weight

Depends on:

- Species, sex, maturity

- Length and weight
- Condition/food
- Population density
- Environment
- Individual genetics

Growth functions used in fisheries models may be independent of biological processes, may depend on them, or may depend on some proxy for those processes. Of the process-based models listed in TOR b, growth is the one on which most work has been done. The exact processes and driving factors to be incorporated into a model must depend on the stock dynamics of the fish modelled. For instance fluctuations in growth due to temperature will be far more significant for a short-lived fast-growing species (e.g. capelin) than a long-lived slow-growing species (e.g. redfish).

The most basic factors to be included in a growth model are the current length and/or weight. In addition it is currently possible to include temperature and condition directly, and this is done, for example in Gadget (although modelling condition is not trivial, Section 3.4). However it is not always easy to use environmental factors in practice. If the goal is to project into the future, environmental factors may be problematic as it is difficult to predict them – but they may be implemented as different environmental scenarios. Even if hindcasting is the goal, it is not always clear how, for instance, temperature measured at fixed stations relates to the temperature experienced by the fish. If the effects of condition are to be included then a feeding model is needed that can replicate the patterns of food availability. This could be a set variation in food availability or with prey modelled as part of a multi-species model. Additionally the environmental data may be a proxy for the factor actually driving the process. For example temperature could directly affect growth, could be a proxy for another factor such as currents, or could be driving food availability which in turn affects growth.

In some cases it is not currently possible to incorporate processes directly, but instead a proxy is used. The absence of a life history memory limits the different growth formulations that could be attempted. To a certain extent this can be simulated by using a cohort factor, but this is neither an ideal nor a general solution. A cohort effect may also stand in for a number of other different processes in age-length models, for example density-dependent effects. In others it may be possible to include density directly.

Using a stock synthesis model a stock can be split into a small number of different morphs. The different effects of, for example, fishing pressures on these different morphs can lead to resulting changes in overall stock structure (Section 2.8)

3.3 Maturity

Process — becoming mature

Depends on:

- species, sex
- length, weight, age
- condition/food
- environment
- population density
- life history
- individual genetics

The process involved is maturation, i.e. fish (or the population) becoming mature (Heino *et al.* 2002). Proportion mature (e.g. a maturity ogive) is not a process. Any process-based model should model maturation directly, as a probability/proportion of fish maturing based on their characteristics and/or environmental factors. At the most simple level this probability can be based on age and/or length of the fish. It is also possible at present to use the condition factor of a fish in the current time step (e.g. Gadget), although calculating that condition factor over time provides its own challenges. Other environmental and biological factors may well be involved in maturation. However it is not clear how to separate the different effects from different factors, or how to model the interaction of those factors. Estimating the parameters involved in maturation requires a data set that distinguishes between the different maturity stages to be considered. In some species it is likely that the probability of maturing is based on life history. These factors are difficult to include within current age-length structured models due to the absence of a memory. However they can be approximated using cohort effects as a proxy for life history.

Time of maturation can be used as a proxy for biological factors governing maturity, e.g. just before or after the spawning period (Burton 1994). A maturity ogive can be used as an alternative to directly modelling the maturation process.

3.4 Condition

Process — change in condition

Depends on

- species, sex, maturity
- length, weight, age
- condition/food (quantity and quality)
- spawning weight loss
- depth
- environment — e.g. temperature, salinity
- life history
- individual genetics

Condition is actually weight at length compared to some reference weight at length. Condition is thus not in itself a process, it is the effect of other processes (growth in weight, in length, feeding, spawning,…). It is currently possible to include the effects of food availability on condition (e.g. Gadget). However it is difficult to do well in practice without ecosystem/multi-species models to provide detail on prey availability, and thus provide information on food shortages. An additional factor affecting condition is weight loss due to spawning. This can be included relatively easily as part of a fecundity/spawning model.

Work on correlating condition to environmental factors is described in SGGROMAT 2004, but this is only a precursor to modelling the processes involved. In the same way that a variable maturity ogive may be applied as a proxy for the processes involved, a correlation-based condition driving function can be used in place of a process-based model.

3.5 Fecundity

Fecundity Processes:

- how many eggs does a fish lay
- how good are those eggs

Fecundity/Total Egg Production (TEP) can be based on:

- SSB

- Spawning stock structure (length, condition, age, numbers, density, first time/repeat spawners, etc)
- Population density
- Environmental conditions
- Life history
- Individual genetics

Simple SSB relationships have been developed for many species. A process-based fecundity model has been incorporated into the Gadget stock dynamic model (Bogstad *et.al.*, 2004). This model is based on the numbers, length, weight and condition of the spawning stock. More detailed process-based models have been developed based on lab experiments to relate number and quality of eggs to a range of different stock and environmental factors. Work is ongoing on incorporating these into stock dynamics models (RASER EU Framework 5 project http://raser.imr.no). A range of other processes may be considered in the future. Some of these can be evaluated now (e.g. repeat spawner/first time spawner effects which is planned for inclusion into the closed life cycle cod model presented in Section 2.7). Others would require development of models with a life history memory (e.g. life time spawning, feeding, growth).

Recruitment to a stock depends on both fecundity and subsequent survival of the eggs and then larvae. In a stock dynamics context both of these processes must be considered. The number of larvae/0group is not a process – the relevant processes are the number and quality of eggs produced, and the survival from eggs to larvae to 0group. In some cases fertilization of the eggs may become a limiting factor. This may be particularly so for animals that pair for a significant time during mating (e.g. crabs, Paul and Paul, 1990) and for sessile species (e.g. bivalves) where adult density may influence fertilisation and thereby spawning success.

Processes on eggs and lavae

- mortality on eggs and larvae
- transport of eggs and larvae

Depends on:

- Egg quality
- Size of lavae and eggs
- Spatial structure of spawning stock
- Density/egg numbers
- Life history
- Predation
- Environment (temperature, currents, salinity,…)

The mortality on the eggs and larvae must be estimated for use in a stock dynamic model. At it's most basic this modelling may simply constitute estimating a yearly mortality (e.g. Bogstad et. al. 2004). A more detailed, process-based, estimate of probability of egg survival could be based on factors such as the egg quality, density, environmental factors and predation. One way of doing this is through individual based modelling (e.g. Allain 2004). Many of the driving factors could be modelled in a single species context, although predation-induced mortality may require multi-species modelling. One such example would be the in the Barents Sea. In years where large numbers of juvenile Norwegian Spring Spawning herrings are in the Barents sea they become a major source of mortality on larvae (Hjermann *et. al.*, 2004). Age-length structure is not required to model what happens to the eggs (although it may be required to predict their numbers and/or quality). Modelling egg and larval drift may require a spatial dimension to the model.

Practical closed life cycle modelling

In a stock dynamics model it is necessary to estimate parameters according to the available data. This is a problem for fecundity and egg/larvae mortality as there are often limited data available. For instance some of the factors considered by the RASER project in estimating quantity and number of eggs (e.g. total lipid composition) may not be available for the wild stock (ICES 2004b). Process sub-models based on tank experiments may include variables on which there is little or no information for wild stocks. Such sub-models are then difficult to incorporate into stock dynamics models. Although it may be possible to use parameters from such experiments it is not clear how conditions in the experiment relate to conditions actually experienced by wild fish.

In some cases there are no direct data on egg production. This is a major problem in estimating fecundity parameters. Many of the major process (e.g. mortality on eggs and larva) occur before any data are available, and thus confound the effects of actual fecundity. It is therefore not possible to use, e.g. 0-group survey data, to estimate fecundity parameters. Where data estimating total egg production are available, estimating the parameters in fecundity becomes more practical. However the estimating the subsequent mortality on those eggs still remains a major difficulty in any model of stock dynamics.

4 Utility of age-length structured model frameworks for investigating the performance of models with different levels of complexity

This term of reference was considered by a small sub-group and generated considerable discussion regarding the different types of approaches that could be applied. The sub-group felt that it should be stated that with a limited pool of experience available, consideration could not be exhaustive and there may be some omissions. Initial discussion centred around clarifying the TOR in terms of what was meant by complexity and performance.

Differences in complexity that were identified by this Group were:

1. between modelling frameworks (e.g. VPA v biomass dynamics models),
2. between alternative sub-models within the same framework (e.g. knife edged v length dependent selection)
3. and between models using different data sets
4. or the same raw data that have been aggregated differently or to different degrees.

The Group also identified a number of different ways of considering model performance:

1. Management utility (including robustness to uncertainty)
2. Goodness of fit
3. Power to predict (e.g. hindcasting) and discriminate (trade off between Type I and Type II errors)

Presentations and Group discussions focused on the first two of these.

This Group is tasked with specifically considering the utility of age-length structured models to evaluate models of varying complexity. It is important to stress that many of the processes driving fisheries are primarily length (or age-length) structured. Selection patterns, growth, predation and natural mortality, maturity (age-length), fecundity and monetary value are immediately obvious examples of such length based processes or metrics of interest. In order to capture a high degree of reality in these it will be necessary to include length (or age-length) structured models in modelling frameworks.

Section 2.8 described comparisons between age structured, and age and length structured, yield per recruit models for Northeast Arctic cod. It was shown that including length took account of the fact that the largest fish at age enter the fishery earlier and may be rapidly removed if exploitation rate is high. Explicitly modelling in terms of length showed that removal of largest fish at age was more detrimental to the potential yield per recruit than revealed by the age structured model which assumed average length at age for all fish. This shows that the increased reality provided by age-length structured models can provide different results that may have important implications for management.

In order to investigate the performance of a particular model it is necessary to have a framework that has at least as much complexity as the model to be investigated. For example, if it is thought that spatial structure in a system is important, then to investigate the performance of a single area model, a more complex spatially disaggregated model would be required as the basis against which to evaluate the potentially less biologically realistic (simpler) model.

The Group noted a difference in approaches to model evaluation/performance that on the one hand allow hypothesis testing without a formal requirement for fitting to data (scenario modelling/simulation testing) and on the other hand approaches that focussed on the use of data for parameter estimation and goodness of fit criteria for model comparison. These methods are not exclusive and the data driven statistical approach can be considered a special case of scenario modelling.

The scenario modelling approach has generally focussed on the evaluation of management strategies (Butterworth and Punt, 1999; McAllister *et al.*, 1999). It has been used to develop strategies (e.g. for setting TACs and other regulatory mechanisms) that are robust to a variety of uncertainties. These range from uncertainties about the underlying population dynamics (process error) through uncertainties about the data collected (sampling error), fitting assessment models (estimation and model error) to uncertainty in the actual implementation of the strategies (implementation error, e.g. to what extent management measures will be achieved).

Management strategy evaluation has been applied quite widely in Southern Africa (Punt, 1992; Butterworth *et al.*, 1997; Butterworth and Geromont, 2001; De Oliveira and Butterworth, 2004), to whales by the IWC (Kirkwood, 1997) and to a number of European flatfish and gadoid stocks under collaborative EU contracts (Kell *et al.*, 1999; MATACS; MATES).

However this type of modelling framework can also carry out simulation testing of potential assessment models, for example to evaluate the performance of alternative models in terms of how well they are able to capture the underlying dynamics such as a trend in catchability.

Typically a scenario modelling framework will consist of:

- An operating model based on current knowledge of population dynamics (including length-driven processes where appropriate). This is conditioned on data where possible (modelling frameworks such as stock synthesis could be used for this purpose), but where data are lacking a range of plausible hypotheses may be used.
- Data are generated to mimic observed data, including potential problems with these data (i.e. error structure/biases are modelled). These data are aggregated to the level of complexity required for the assessment model under evaluation.
- Assessment models of different structure/levels of complexity are applied to obtain a perception of the population. The performance of different assessment models can be evaluated relative to the underlying operating model (‘true’ dynamics).
- This approach can be extended to provide full-feedback evaluation of management strategies by applying management measures, (possibly including implementation error and time-lags) based on the perception provided by alternative

sampling and assessment models, to the simulated 'true' population and projecting the model forward.

- Under such an approach the performance of different assessment and management models can be evaluated both in terms of their performance against the underlying 'true' system and, perhaps more importantly for management, in terms of relative performance against alternative management regimes. Sensitivity tests can be carried out to check for the robustness of outcomes where models and parameters are uncertain.

Up to now these applications have tended not to be age and length structured, although age and length structured models are not precluded from such simulation frameworks and Davies and Gilbert (2005) (WD3 in Annex 3) outline a simulation approach which makes use of an age-length-structured operating model.

Section 2.3 briefly described temperature dependent yield per recruit models developed by participants to the ICES working group on *Crangon* Fisheries and Life History (Temming and Damm, 2002; ICES, 2003c). These age and length structured models include process based growth models with temperature dependent anabolic and catabolic terms and have been conditioned on data taken from a wide range of literature sources. They have been used to explore the population dynamics of *Crangon* in general and have also been applied in ways that incorporate some features of the scenario modelling approach. Changes in the seasonal pattern of fishing mortality (ICES, 2003c; 2005 *in prep*.) have been evaluated, where robustness to uncertainty in estimation of growth parameters was taken in to account by using a range of alternative parameter sets. The models have also been used to simulate length frequency data with known parameters and to evaluate the performance of a range of modal progression and simple graphical methods for recovering these growth parameters (ICES, 2005 *in prep*.).

Age and length structured integrated statistical modelling frameworks (e.g. Gadget (Begley, 2005) and Stock Synthesis (Section 2.2.), SMS (Lewy and Vinther, 2004) and CALEN (ICES, 2003a)) have been used to estimate stock dynamics (history and parameters) and compare models using goodness of fit criteria and have been widely applied to more northern stocks in particular.

Within the framework of integrated statistical models, the ability of models of different levels of structural complexity to fit to observations (both from the catch and surveys) can be compared directly. Integrated statistical models can be used both to optimise to data and to simulate populations. When used as a population simulator, they can be used in a similar manner to the approach described above. In the case of Gadget, a simulation program has been written which runs in R (or Splus) and error can be added to the sampled population (dst^2, 2005).

Complexity in integrated statistical models can be considered using two main approaches:

1. fitting models of different structural complexity to the same data

Individual likelihood components can be compared directly when they are used in more than one model, although any changes in the number of parameters should be taken account of when comparing the fit to the observed data. Objective metrics such as Akaike's information criterion may be appropriate in such circumstances. In many cases, increasing structural complexity does not require more complex observed data e.g. comparing models with fixed catchability, growth or selection with models in which these processes can vary.

2. fitting a single model to a range of data

An example of this would be to compare the likelihood score of e.g. a survey index where the model was optimised with or without age-length distribution data. If the likelihood (of the fit to the survey) was improved by the additional age-length data then the increase in complexity can be considered to have provided additional information. On the other hand, if the likelihood is poorer then this highlights an inconsistency between the survey and age-length data, which may indicate that the model is inadequately representing some underlying process (whether in the data processing or the model structure). For a species with limited age information, or age reading by different methods a similar approach could be used to evaluate the consistency of the age reading, if not necessarily the consistency of the length data to the age-length data.

Sequential exclusion of likelihood components (e.g. in ADAPT, Gavaris, 1988) associated with each type of data can be used to explore sensitivity of, e.g. current stock biomass, to each source of information. Large effects from a single source may indicate areas for further research or consideration of alternative hypotheses/ model structures. An alternative method of sequentially considering the likelihood components (Section 2.4., Stefansson, 1998; 2004), is to heavily weight each component and re-optimise the model to consider each component individually. This provides information on inconsistencies between the likelihood components. The effect of different levels of structural complexity to reduce the inconsistencies between datasets can be evaluated by comparing likelihood scores, combining points 1 and 2. Both of these approaches provide insight into the relative contributions of model selection, and the choice of which data to explicitly include in assessments, to the resulting management regime.

5 Exploring the potential of applying age-length based models to stocks of anglerfish, hake, redfish and sprat

One of the recommendations made at the 2003 meeting of SGASAM was that stocks should be identified for which age-length based assessment approaches are likely to be more appropriate than existing methods. And that for these stocks age-based and age-length-based assessments should be conducted in parallel and compared. ToR d suggests a number of stocks for which age-length-based methods may be more appropriate, and these, together with a number of other species are considered in the following text.

5.1 Anglerfish

5.1.1 Southern Shelf anglerfish

Western anglerfish of Divisions VIIb-k and VIIIa,b,d,e are assessed using XSA. Ageing of both species is done reading the *illicia* cross cuts in some institutes and otoliths in others. At the last working group of reading it was demonstrated that the reading of *illicia* is consistent among institutes (Duarte *et. al*., 2004). However, the age is not validated, which could be a good reason to apply an age-length structured model. Inconsistencies arise when reading otoliths, and therefore these data are not used in estimating the catch at age matrix. For these stocks it is not clear to what extent length and/or age can be used to describe the processes of maturity, fecundity and growth. Mean weight at age has declined over time (ICES, 2004d). This, combined with the unvalidated age data, means that it is problematic to attempt to use age as a proxy for length.

Assessment of Southern anglerfish of Divisions VIIIc and IXa is done using a non-equilibrium production model, ASPIC, and combining both species (*Lophius piscatorius* and *L. budegassa*). Length data is available since 1986 and age data only since 1996 which makes difficult to apply an age structured model such as XSA, but it would be suitable to apply a length or age-length based model.

5.1.2 Northern Shelf anglerfish

Despite an EU-funded project on the subject (Anon, 2001), the biology and growth of anglerfish are still not well understood and age-readings of anglerfish are still considered uncertain. This would therefore seem to suggest that basing an assessment on length-structured rather than age-structured data would make more sense. In addition, the fishery for Northern Shelf anglerfish (Division IIIa, Subarea IV and Subarea VI), expanded rapidly in the mid 1990s implying that the length-at-age distributions are unlikely to be in equilibrium and therefore age is unlikely to be a good proxy for length. Based on these reasons, Northern Shelf anglerfish seem to be a potential stock for an age-length structured assessment. (A length-structured assessment of anglerfish has already been implemented and used at previous Northern Shelf WGs, ICES 2003 b).

Due to the difficulties in ageing, age-based survey data are generally not available and have been collected only on infrequent dedicated anglerfish surveys. However, length frequency data are available from a number of surveys and from commercial landings. Anecdotal information from the fishing industry indicates that TACs are currently very restrictive and that this has resulted in increased misreporting and possibly discarding (of which there are no estimates). Recent reported commercial landings data are unlikely to be representative of actual catches (ICES 2004a) and furthermore if there is systematic misreporting by size category, then the length frequency samples may also be unreliable. Therefore any (age-length structured) assessment would have to be able to either account for extremely biased commercial data in the most recent years or cope with no commercial data at all.

5.1.3 Northern hake

The principal reason put forward to justify the use of a length-structured assessment model for hake is the difficulty to age correctly the individuals. In the more recent Hake otolith exchange programme a decreased consistency has been observed in recent years between the hake age determination readers. In addition the last Workshop on European Hake Age Reading the results indicate that ageing fish older than 3 years is not possible with an acceptable level of precision (Piñeiro *et al*., 2005). The parameters currently used in the von Bertalanffy growth model, and the age-length key, are questioned by the first results of a French tagging campaign (De Pontual *et al*. 2003). As a consequence, the age-length conversion is a major source of uncertainty in the current assessment model and a length-structured model might provide more accurate assessments, by avoiding this conversion.

An amount of data, as large as possible, is desirable to fit the model, especially for a spatialized model which seem appropriate for this species (large distribution area, migrations (ICES 2003d) (Quéro and Vayne 1997), different fishing units with different fishing areas (ICES 2003d). Three survey data sets are available, covering the Bay of Biscay (FR-RESSGASCS, FR-EVHOES) and the Celtic Sea (FR-EVHOES, UK-WGCFS). However no single survey provides complete spatial or temporal coverage. Catch data are also available, even if some precautions have to be taken with the quality of the data, for example by integrating uncertainty as a likelihood component. The integration of other data sources such as tagging data or fishing effort by fleet would also provide valuable information to improve the estimation of fishing mortalities. Such a tagging experiment took place in the Bay of Biscay since 2004 after a pilot experiment in 2002, and will be re-conducted in 2005. A larger tagging experiment would provide valuable information on migrations, growth, natural mortality... Some data on particular biological processes, notably fecundity (Murua and Lucio 1998, RASER) and maturation (Martin 1991; Lucio *et al*., 2000, RASER) are also available and may be used to detail some aspects of the biological cycle.

The Working Group on the Assessment of Southern Shelf Stocks of Hake, Monk and Megrim (ICES 2004d) pointed out that several sources of uncertainty remain for Hake stocks, including concerns about the growth and age estimations. Therefore, the Working Group support the project of conducting a large-scale tagging experiment to validate age determination, improve the knowledge of stock limits, spatio-temporal stock dynamics and estimates of mortality rates.

To conclude, a length-based model would be an important improvement because of the great uncertainty on both aging techniques and growth. Available data are sufficient to build a first model. Additional data would be valuable for this stock. With sufficient improvement in spatial coverage it would be possible to construct a more realistic detailed model taking spatial structure into account.

5.2 Redfish

Age readings for different redfish species have been considered unreliable (ICES, 1996), and are often limited in their availability. This limited availability makes it difficult to construct catch at age data. As a result there is a desire to avoid age-structured models when investigating these species. One method of doing this is to move to an age-length structured model, which can incorporate length data directly. Such an age-length structured model exists for golden redfish (*Sebastes marinus*) in Icelandic waters (Bjornsson and Sigurdsson 2003; ICES, 2004e). This model has been successfully used to assess the existing state of the stock, and to project possible stock levels into the future. An additional redfish model is under development for *S. marinus* in the Barents Sea (Section 2.10). In both cases it is possible to include age-length data alongside length data, or to exclude age data entirely. Including available age data seems to produce improvements in model performance (Bjornsson and Sigurdsson, 2003).

5.3 Sprat

Sprat are a short-lived species and age-readings from many stocks are considered to be uncertain. Furthermore there is evidence of varying growth rates (due to environmental conditions) in Baltic sprat and this may be another reason for applying an age-length structured assessment model. The SG was unable to comment on the availability of the data required for the implementation of such an assessment. The Herring Assessment Working Group (HAWG, ICES 2004 c) recommended that the Methods WG should consider assessment methods for short-lived species.

5.4 *Nephrops*

5.4.1 *Nephrops* in Icelandic waters

An age-length structured model is desirable for Nephrops in Icelandic waters as there is no direct ageing method for this species. The assessment is currently conducted using a standard age based assessment, with catch at age created by slicing the catch at length data. There tends to be little contrast in the length distribution with which to validate the slicing procedure. Only males are assessed as very few females are landed, with the rest discarded as they are not marketable. The stock is spatially disaggregated with different stock trends in the three main areas and the fishery is seasonal with most of the catch landed within a period of 3 months in summer.

There are no foreseen problems in constructing an age-length model in terms of data availability. An annual trawl survey has been conducted since 1987, providing length frequency data by sex and maturity stage and either survey abundance indices or survey CPUE. Catches, sampled at sea and in harbour (although for most years one or other of these dominates) also provide length frequency data by sex. Log books have been compulsory since 1991 and prior to then log book records are available from a subset of the fleet for a much longer time period. Tagging experiments have been used to estimate growth rates.

No model has been developed yet, as work until now has focused on data preparation and correction or clarification of data in the institute database. Aspects of the population dynamics considered desirable to include in initial models are: multiple stocks with seasonal fishing effort estimated for each stock and seasonal catchability.

5.4.2 *Nephrops* around Scotland

Age determination techniques for *Nephrops* are both expensive and labour-intensive and it is therefore unlikely that age-based data will be routinely available in the foreseeable future (ICES 2004g). The main source of information on the structure and dynamics of *Nephrops* stocks is the length composition of catches (by sex) and supplementary data from surveys. It therefore seems more appropriate to adopt a length-structured approach to modelling the population dynamics rather than creating age-structured data by slicing the length distributions and conducting an age-based assessment. A preliminary length-structured assessment of Firth of Forth Nephrops has already been conducted and Section 2.6.1 gives details of the model structure. Spatially structured stock dynamics may also be important, though this has yet to be considered.

5.5 North Sea whiting

The model described by Kristensen *et al.* (2005) was applied to North Sea whiting using length-structured data from IBTS for 1991–2004. The reason why whiting was considered is that the 2004 assessment of this stock was rejected by the ICES Working Group on demersal stocks in the North Sea (ICES 2005a) because of inconsistencies between IBTS, EFGS and SFGS surveys. Further analysis has suggested that there may not be inconsistencies in the surveys between 1991 and 2004 (Henrik Sparholt, personal communication). Quarterly survey data were available for the first part of this series (1991–1997). It was therefore decided to consider the period 1991–2004 in the model.

The model used for North Sea whiting deviates from Kristensen *et al*. (2005) with respect to the assumptions on recruitment and survey catchability. For whiting, recruitment is assumed to take place instantaneously on March 1, April 1 and May 1. The (relative) number of recruits was estimated individually for each of these three months for each year. Based on preliminary trials with the model the survey catchability was modelled in the following way: As in the paper (Kristensen *et al*. 2005) catchability is assumed to depend on two factors, a time-dependent and a length-dependent factor (the selection pattern). The first factor was assumed to depend on the quarter while the selection pattern was assumed to be the same for the first three quarters, but different from the last quarter. The mean of L_∞ was fixed to 60 cm.

The model fit is indicated in Figure 1. In general, predicted length distributions appears to fit well to the observed data. The growth parameter in the von Bertalanffy growth equation was estimated to 0.32, which seems to be in line with values found in the literature. Total biomass and recruitment are shown and compared to the estimates of the ICES working group (ICES 2004f) for 2003 in Figures 2 and 3. Figure 2 shows that except for the last two years the biomass estimates seems to agree well. The recruitment at age one from the 2003 working group and the recruitment at age zero from the model to some extent have the same trends. In general the two models produce comparable results.

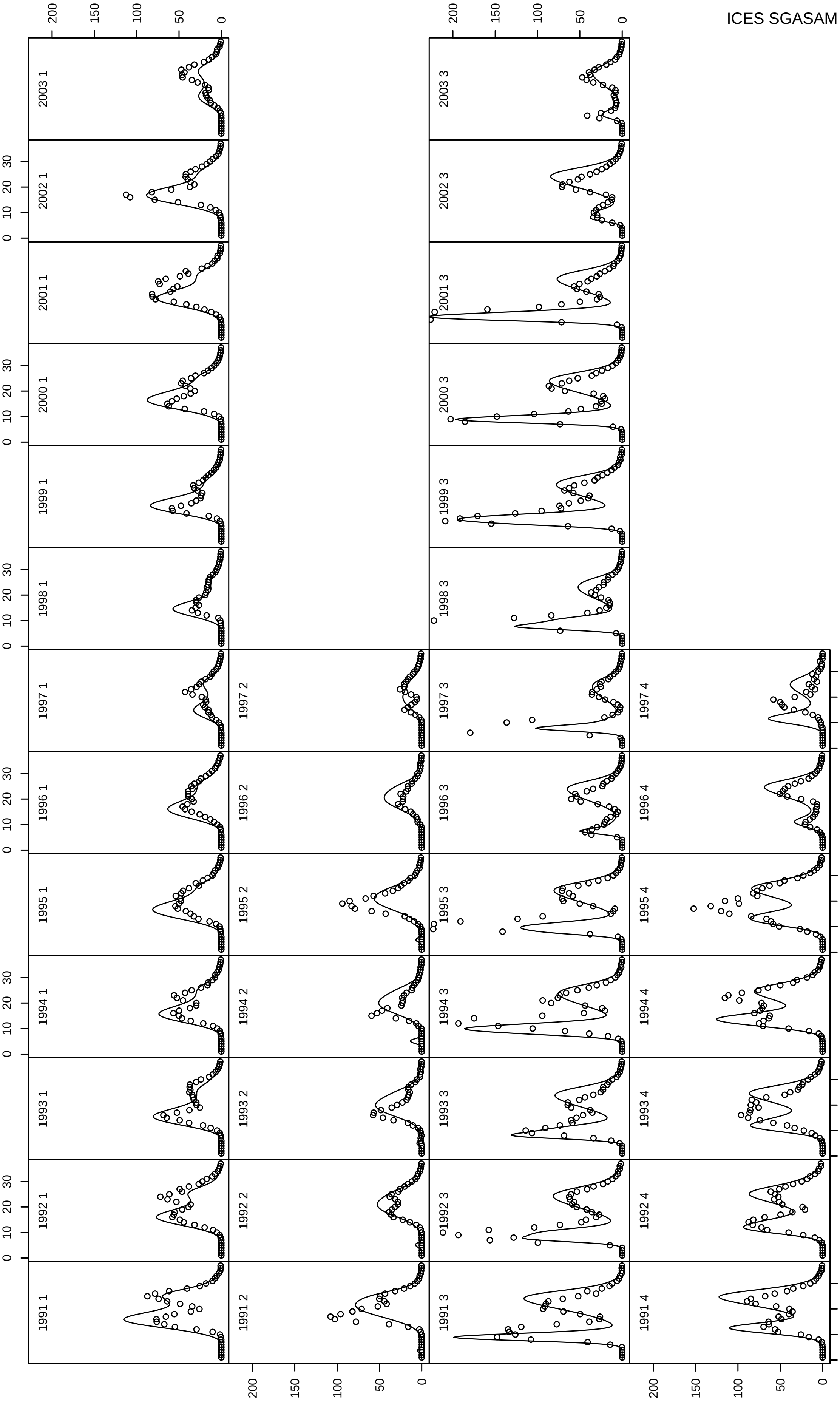

Figure 1: Observed CPUEs (circles) and expected CPUEs (solid line) per 1 cm length group at each survey.

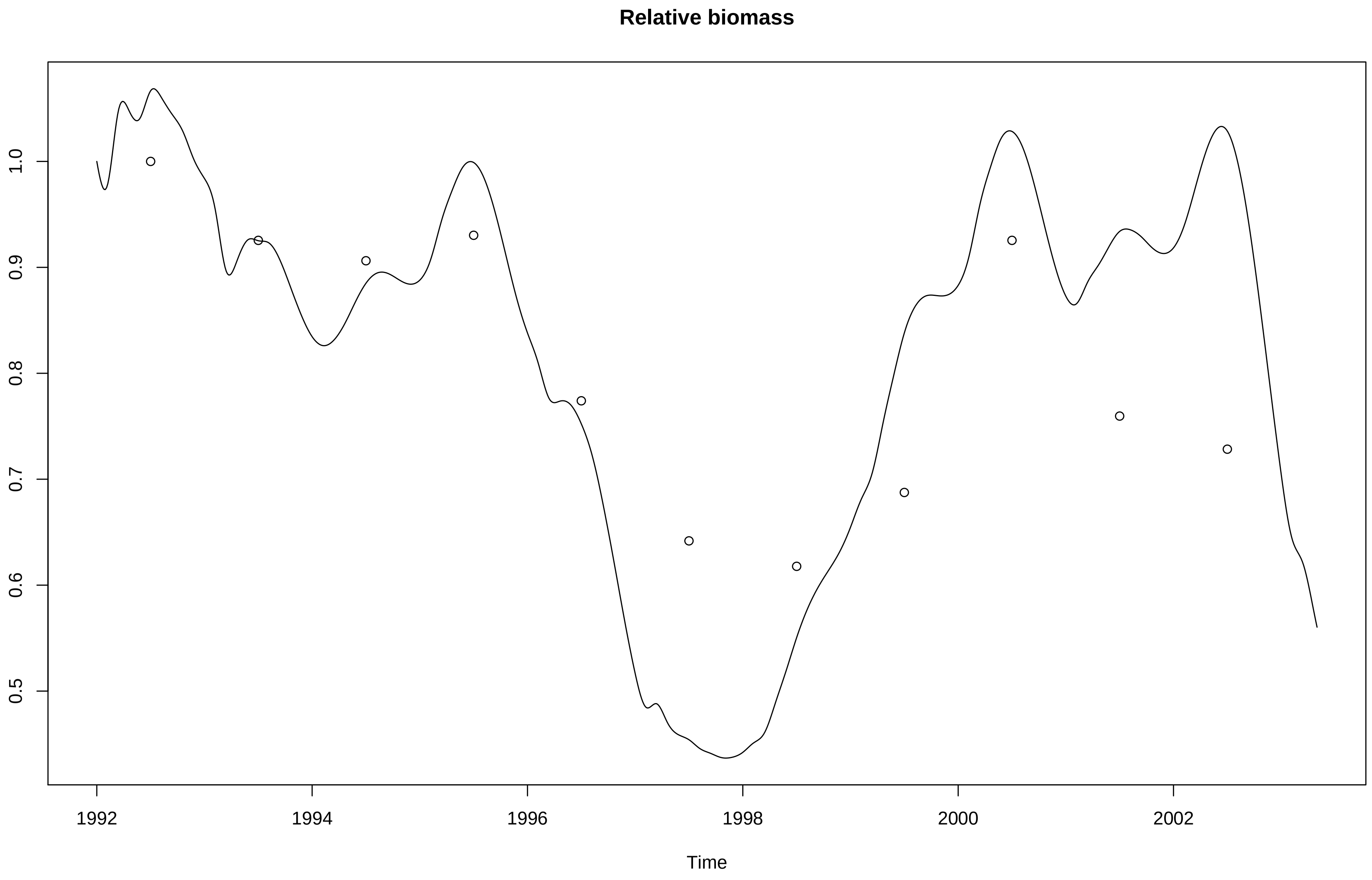

Figure 2: Relative total biomass estimated by the length based model (solid line) and the ICES assesment working group, WGNSSK (circles).

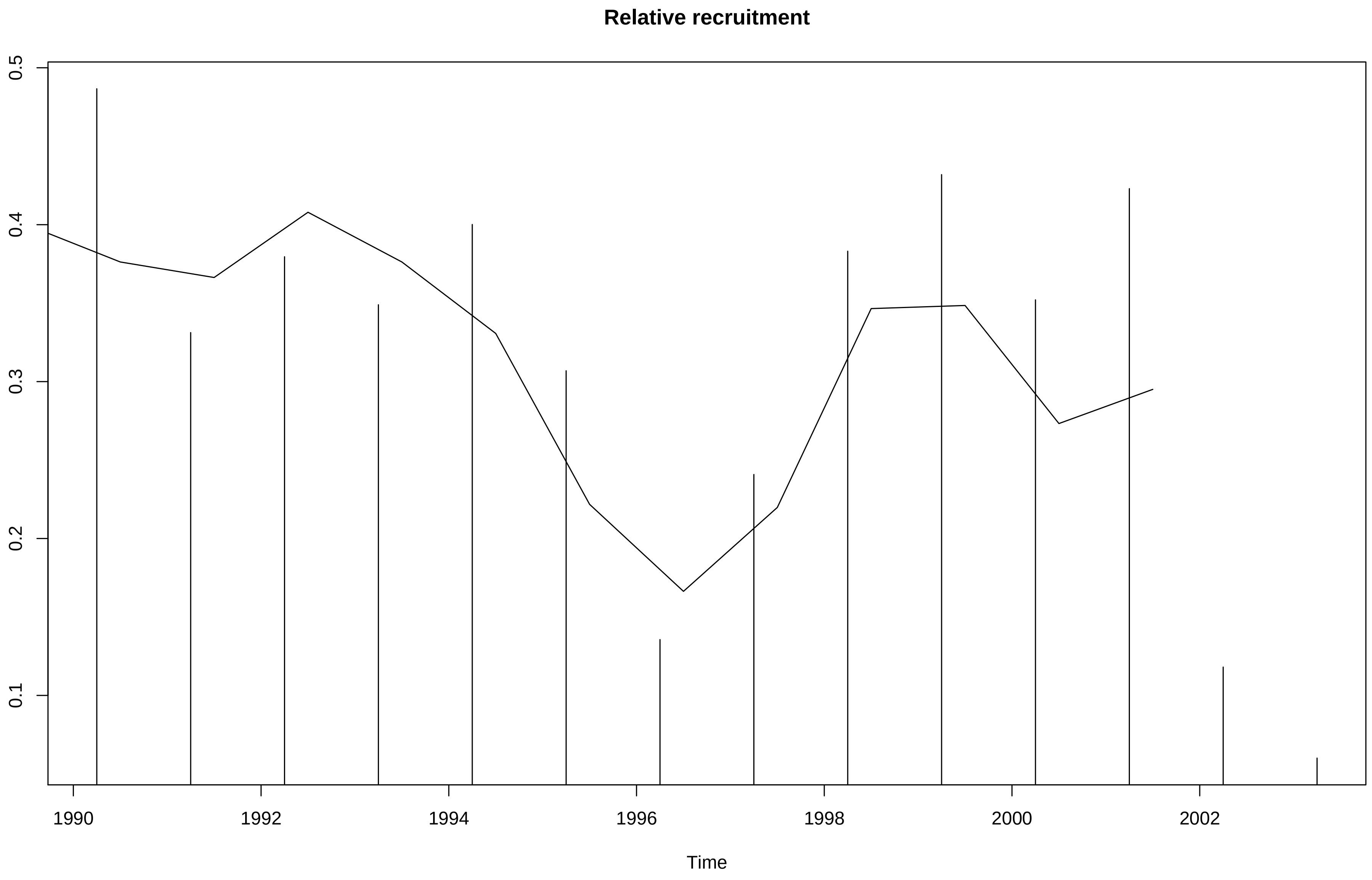

Figure 3: Relative recruitment estimated by the length based model (vertical lines) and the ICES assesment working group, WGNSSK (solid line).

6 Conclusions

Age-length structured models have important roles to play in research into stock dynamics and in formal advice on stock management because length (or age and length) is a primary driver for many key processes in fisheries systems and the majority of data underlying stock assessments are length (or age-length) structured.

An increasing number of age-length structured models have been, and are being, developed (e.g. Gadget, SMS, CALEN, Stock Synthesis) and take up of some of these models is occurring on a wider scale. Additionally there has been some increase in the use of age-length structured methods for the provision of ICES advice (Section 5). This trend seems likely to continue due to a desire to include more realism and process-based models in modelling and assessment frameworks and it is facilitated by ongoing increases in computing power.

Development of age-length structured models is going on around the world. In some countries there is a greater acceptance of such models in an advice context than within ICES. These models have been commonly applied to species that are difficult to age, such as pelagic tunas (e.g., Fournier *et al.* 1998, Hampton and Fournier 2001), and invertebrates (e.g. Bergh and Johnston 1992, Zheng *et al*. 1995, Punt *et al*. 1997, Lai and Bradbury 1998) Increasingly, these types of models are used for comparison to, and as a replacement for traditional exclusively age-structured methods in North America (Presentation 2.2), Norway (ICES 2004g), Iceland (ICES 2004e), as well as elsewhere in the world.

Age-length structured models are generally more complex to set up and use, partly due to their greater inherent degree of flexibility. This flexibility means that a greater number of structural models can be created within any given modelling framework. Some models are only easily usable by the scientist(s) who developed them. However in other cases documentation has improved to the point where modelling packages are beginning to be used by a range of different institutes (e.g. Gadget). This improved documentation of the models, and dissemination of modelling techniques should be encouraged. Where these models are to be used in an assessment context an independent review of the model is desirable.

In a research context the high degree of complexity and flexibility provided by age-length structured models is an advantage, allowing for a wide range of different models to be compared under a number of diagnostics. Following investigative analyses it may be possible to recommend a single model, together with appropriate diagnostics, for use in formal assessment and advice (Section 2.4, Section 4). The model used in the advisory process may be less complex, and more focussed towards providing robust management advice, than some of those considered during the exploratory phase. The selected model could then be used for a number of years to ensure consistency in the assessment.

Having age-length structure in a model allows for detailed investigations into stock dynamics. Age-length structure is especially important where there is a desire to include process-based modelling, while the high degree of flexibility in age-length structured models allows for many different scenarios to be considered. Such investigations can be focussed on using process sub-models to improve modelling and understanding of a particular stock. Age-length structured models also provide a framework in which alternative process sub-models can be compared.

Many length or age-and-length based models use the raw data directly. Fisheries data are typically collected on a length basis. In principle therefore models should use this length-based data directly, and not have to rely on external aggregation or conversions. The advantage of doing that in the context of a statistical model is that this makes it possible to investigate possible bias problems and to identify inconsistencies in the data.

By using raw data directly many of the problems involved in combining data from different sources (e.g. different countries, fleets or individual boats) but of the same type into one data set will be reduced because the number of observations and the variations associated with the data sets automatically will be included in standard estimation methods. In principle the statistical use of raw data removes the problems involved in relative weighting between different types of data. However in practice the fact that all models contain mis-specification means that relative weighting of different data types is often used. There was disagreement over whether this relative weighting is a valid technique or not.

In practice for many stocks the inclusion of all assessment data in dis-aggregated form would pose logistically intractable problems in an ICES assessment working group forum in the short term. However there are cases where this is already being done (Icelandic redfish ICES 2004e, NE Arctic cod ICES 2004g), and the adoption of such methods should be encouraged where possible.

7 Recommendations

It is clear that age-length structured models can address a range of issues that more traditional age-structured models cannot. A large, and increasing amount of effort is being invested in the development of age-length structured models. It is important that such effort be allocated efficiently, with duplication of effort reduced to a minimum, and knowledge shared between groups.

7.1 General recommendations

- Continue to develop and monitor developments in age-length structured models
- Promote links and sharing of knowledge on age-length structured models between different scientists and groups working within and outside ICES
- Where ACFM believes that a stock may benefit from an age-length structured approach links should be promoted between the assessment working group and methods working groups
- Promote the use of age-length structured models where:
    - Age data is limited or problematic
    - There is a desire to include process-based models with high length dependency
    - Modelling stock dynamics by length is considered more realistic
    - Their ability to handle raw data directly reduces problems associated with combining or aggregating data
- Improve process-based sub models for inclusion in age-length structured models
- Promote comparisons between models (e.g. of different complexity or different process-based sub models), and the use and development of formal statistical methodologies to conduct these comparisons.

7.2 Third Study Group meeting

It remains important to have a forum for evaluating the use of length- and age-length structured assessment models outside of the ICES Methods WG. The development of age-length structured models is important if there is a need for added complexity - in that length may be required to better model particular biological or fishery processes, but also in cases where age-determination is problematic and only length-structured data may be available. Accordingly, the SGASAM should consider both more complex (biologically detailed) models and simpler length-based approaches and proposes that the Resource Management Committee makes the following recommendation:

The **Study Group on Age-length Structured Assessment Models** (SGASAM) should meet for a third time at a location to be decided for 5 days in late 2006 to:

a. provide a forum for dissemination of information regarding developments in methodologies and applications of length- and age-length structured models in ICES areas and elsewhere;

b. implement improved process-based models for predation, growth, maturation, fecundity and condition in age-length structured model frameworks;

c. compare the performance of models with different process-based sub-models and/or different levels of complexity, and use and develop formal statistical methods to conduct these comparisons;

d. evaluate the use of age-length structured models for the assessment of stocks for which age-disaggregated data are sparse or unreliable (e.g. *Nephrops*, elasmobranchs, hake, anglerfish redfish)

e. investigate the utility of age-length structured models for investigating the effects of potential management measures (e.g. technical measures such as mesh size changes)

Supporting Information

Priority:	In order to maintain and improve the quality of ICES advice, continual developments of new and more relevant modelling tools that take into account new scientific ideas is essential.
Scientific Justification and relation to Action Plan:	Assessment methods within ICES are still largely age-based, but it is increasingly acknowledged that the incorporation of length-structure into population models is important when: • it is thought that such models give a better representation of biological and fishery related processes • age-based data are unavailable or unreliable making the use of age-structured models inadvisable, but length-structured data are readily available • age is not considered to be a good proxy for length Age-length structured modelling has advanced considerably since the first meeting of SGASAM (June 2003). However, the members agreed that there was still a need for a further meeting of this SG. Further developments to process-model formulation and the implementation of these models in age-length structured models should be conducted under the remit of this group, continuing work begun by SGGROMAT. In contrast, the development of simpler length-structured assessment models is also important (for species where age-disaggregated data are sparse or unreliable) and is not being carried out elsewhere in ICES. Comparison of the performance of these models (in terms of robustness and goodness of fit) is an important part of the evaluation process. In general, the remit of this group addresses Action Numbers 3.5 and 3.6.
Resource Requirements:	No specific resource requirements.
Participants:	Participants should include assessment scientists, age-length structured modellers and also process modellers.
Secretariat Facilities:	None
Financial:	No financial implications
Linkages To Advisory	ACFM

Committees:	
Linkages To other Committees or Groups:	The work of this group would be of relevance to the WG on Multispecies Assessment proposed at the meeting of SGMSNS 2005. It is hoped that this SG will advance some of the work initiated by the SGGROMAT (now disbanded).
Linkages to other Organisations:	
Secretariat Marginal Cost Share:	

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8.2 Working documents

WD 1. Kristensen, K., Lewy, P. and Beyer, J. E. Maximum likelihood estimation in a size spectra model

WD 2. Mahevas, S., Bertignac, M., Fertin, A., Drouineau, H. and Vettoretti, A. Preliminary studies for the development and fitting of a statistic spatial length-based model for the European hake

WD 3. Davies, N. and D. Gilbert. Measuring the robustness of an age-structured model (CASAL) using an age-length-structured operating model (CALEN).

Annex 1: Working Document 1

Maximum likelihood estimation in a size spectra model

Maximum likelihood estimation in a size-spectra model

Kasper Kristensen, Peter Lewy, and Jan E. Beyer

Abstract: Length based stock dynamics models are appealing because fundamental processes are likely to depend on the size of the individuals rather than the age. Here we derive a simple single species size spectra model by assuming that each recruit is assigned its own growth pattern and that the mortality is size selective. We focus on the estimation of spectra-model parameters from length data obtained from scientific trawl surveys only. Using data for individual hauls makes it possible to test a hierarchy of crucial hypotheses. It is assumed that the observed length data follows a negative binomial distribution where the variance is a power function of the mean. The use of size based scientific survey data only is particularly relevant when the age determination is uncertain and the quality of catch data poor. The model is applied to the Baltic cod for which these problems apply.

Key words: spectra-model, negative binomial distribution, maximum likelihood estimation.

1. Introduction

In this methodological study, we present a new consistent approach to length-based, single-species fish stock assessment by combining continuous size-spectra modelling with statistical modelling of length composition data, and performing statistical inference. In order to put this approach into perspective it is useful to distinguish between the two lines from which the length-based assessment methods have developed. The first component of our study is based on the body-size line emerging from ecology, motivated by various problems when dealing with size under the other more traditional age-structured line of fisheries. The second component is the statistical description of data.

In ecology, body-size has been given crucial importance for determining life-history characteristics (Werner and Gilliam 1984), and size-spectra modelling has evolved, further motivated by Sheldon's empirical findings for the pelagic ecosystem (Sheldon et al. 1972; Kerr 1974; Platt and Denman 1977) using the von Foerster's (partial differential) continuity equation (von Foerster 1959). Focus has mainly been on analysis of steady-state characteristics of community spectra (Benoit and Rochet 2004). An important point, however, is that the governing continuity equation represents a common starting point for modelling the dynamics of the number density continuous with respect to size and time whether we are considering an ecosystem, fish communities or a single cohort. The advantage of considering a single species is that growth, mortality and recruitment are well defined and the dynamics simple. Characteristics of single cohort dynamics have been derived in special cases based on the continuity equation (Sickle 1977; DeAnglis and Mattice 1979; DeAnglis et al. 1980; Kirkpatrick 1984). However, to our knowledge only Smith et al. (1998) have combined continuous size-spectra modelling with maximum likelihood estimation, MLE. Smith et al. (1998), considering size-dependent mortality and the von Bertalanffy growth equation (VBGE) with variability among individuals in both parameters determining growth rate (Sainsbury 1980), applied a size spectrum model to observations on growth increments and empirical size frequency distributions. One limitation of the size spectra approach of Smith et al. (1998) is that changes in mortality and recruitment over time were not described as the stock was assumed to be in steady state. Beyer and Lassen (1994), considering also VBGE but only with individually varying asymptotic lengths and size-specific mortalities changing with time, applied a cohort-based spectrum simulation model to obtain size-specific temporal dynamics of a single species without applying MLE or similar techniques.

In analyses of fish stock dynamics age has been considered the important variable. In cases where the age is unknown length-based methods have been applied to determine the age (Pauly and Morgan 1987). Length-based estimation methods have developed from either modal class progression analysis (Petersen 1892) or from separating length frequencies into normally distributed components (Pearson 1894). These methods are limited by the fact that it is seldom possible to determine the number of age modes from length frequencies alone (Macdonald and Pitcher 1979). Further, the empirical information on size-dependent growth and mortality was not utilized in any consistent way as only estimated mean size-at-age were used and not the variation in size-at-age. Sullivan (1992); Frøysa et al. (2002); Schnute and Fournier (1980) combined standard, age-structured stock dynamics models with growth models and applied the derived models to length based catch observations. Sullivan (1992) and Frøysa et al. (2002) approximated for each length group the discrete probabilities that fish either do not grow or grow into the neighbor length intervals. Alternatively, growth parameters were estimated assuming that mean length-at-age follows a specified distribution around a VBGE-curve (Schnute and Fournier 1980; Fournier et al. 1998; Fu and Quinn

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2000). These age-length structured approaches include both recruitment and temporal dynamics but age-related approximations are needed in order to combine age-structured stock and growth parameters. For instance, Schnute and Fournier (1980) and Fournier et al. (1998) need to calculate the age dependent fishery selectivity and hence must account for length overlap between adjacent age groups. This problem has been solved by theoretical approximations, which may not be justified. The approaches of Sullivan (1992), Frøysa et al. (2002) and Fu and Quinn (2000) can be considered as exclusively size based approaches, but another problem arises in the first two approaches which assume that the probabilities of growing into neighboring length intervals are constant over time. Even if fish growth remains unchanged this assumption is violated if the size specific mortality varies over time. With respect to the discrete approach of Fu and Quinn (2000) this problem is partly avoided as the mortality affects the length distribution of the stock after the growth in a time step has taken place.

Statistical modelling of length composition data represents the other component, that is, in our case, the statistical properties of the observed catch per unit effort, CPUE, by length groups in scientific surveys. In this respect it is a problem that the stochastic variations of CPUE by lengths appear to be based on arbitrary choices between the normal (Sullivan 1992), the log normal (Frøysa et al. 2002; Fu and Quinn 2000), the conditional multinomial (Frøysa et al. 2002; Schnute and Fournier 1980; Smith et al. 1998) and the gamma (Frøysa et al. 2002) distributions or other minimization criteria (Schnute and Fournier 1980; Fu and Quinn 2000). The importance of the choice of distribution is rarely investigated, though this may greatly affect the results. It is further standard tacitly to assume independence between length-groups, an assumption which rarely is tested.

Focus in this paper is on the importance of statistical modelling with the aim of obtaining a consistent interpretation of CPUE data by length. Like Beyer and Lassen (1994) we consider a size spectrum model continuous in time and size with individually varying mean asymptotic length (L_∞) and with time and size dependent mortalities. However, this model has been formulated in closed form and has been combined with a statistical model of the variation of the observed CPUEs by length. We use the length based CPUE from individual hauls as raw data and not the mean CPUE, and thus the stochastic variation between individual hauls is determined from analysis of data. Stock parameters are estimated by maximum likelihood, and likelihood ratio tests by size are used to localize model problems. Further, simulation experiments are performed in order to demonstrate the estimability of the model parameters.

The use of scientific survey length composition data only for analysing stock dynamics is particularly relevant when the age determination is uncertain, when the quality of catch data is poor or when such data are not available. The model is applied to research survey length distribution data for Eastern Baltic cod for which these problems apply (Reeves 2003).

2. Modelling the number density of a population

In the present model the life history of an individual is considered determined by growth and mortality. Each individual is assumed to follow its own growth pattern while the mortality depends on the size of the individual and of the time. Recruitment is assumed to take place once a year instantly at a certain time. For a single cohort let R_0 denote the number of individuals born at the same time t_0 with the same size L_0. The fish growth is modelled using the Von Bertalanffy growth equation. All individuals are assumed to have the same growth parameter k while L_∞ varies individually following a common distribution with density u. For an individual fish in the cohort with a given L_∞ the length at time t is:

$$L(t, L_\infty) = L(t, L_\infty | k, t_0, L_0) = L_\infty - (L_\infty - L_0)e^{-k(t-t_0)} \qquad [1]$$

At time t the individuals that have size less than x are exactly the ones with an L_∞ belonging to the set

$$\{L_\infty : L(t, L_\infty) \leq x\} = [0, G(x)] \qquad [2]$$

where

$$G(x) = G(x|k, t_0, L_0) = \frac{x - L_0 e^{-k(t-t_0)}}{1 - e^{-k(t-t_0)}} \qquad [3]$$

Let $z(x, t)$ denote the size and time dependent total mortality.Then the number of survivors with size contained in the interval $[0, x]$ at time t is given by

$$R_0 \int_0^{G(x)} \exp\left(-\int_{t_0}^{t} z(L(s, L_\infty), s)\, ds\right) u(L_\infty)\, dL_\infty$$

By differentiation with respect to x of this expression we obtain the number density n based on one cohort:

$$n(x, t) = R_0 \exp\left(-\int_{t_0}^{t} z(L(s, G(x)), s)\, ds\right) u(G(x))G'(x)$$

It should be kept in mind that both L and G depend on k,t_0 and L_0. To find the number density based on m cohorts we simply add the corresponding number densities. Suppose the recruitment times before time t are $t_1, t_2, \ldots, t_m$ with recruitment sizes $R_1, R_2, \ldots, R_m$. Then the number density at time t is:

$$n(x, t) = \sum_{i=1}^{m} R_i \exp\left(-\int_{t_i}^{t} z(L_{t_i}(s, G_{t_i}(x)), s)\, ds\right) u(G_{t_i}(x))G'_{t_i}(x) \qquad [4]$$

It may be noted that equation [4] easily could be extended to continuous recruitment by replacing the sum with an integral. An extended equation thus obtained could alternatively have been derived directly from solutions $n(x, t, L_\infty)$ to the size-structured von Foerster equation for a given value of L_∞ and then mixing all these solutions with respect to the probability density $u(L_\infty)$.

3. Statistical model

3.1. Formulation

The number densities from the previous section are now used to formulate a statistical model for catch data. The data

we wish to describe consists of hauls made on random positions. Several hauls are made approximately simultaneously with half year intervals with the same gear. Individual fish are measured with one cm accuracy.
We end up with a matrix N_{ij} of counts for the j'th length-group at the i'th haul. The time of the i'th haul is denoted t_i.
The survey catchability is defined as the function $q(x,t)$ indicating the fraction of the total number of individuals of size x in the entire population we expect to catch in a given haul taken at time t. Then the mean value of the number of fish in a given length group C_j at a given haul (i) is

$$E(N_{ij}) = \int_{C_j} q_\theta(x,t_i) n_\theta(x,t_i)\, dx \qquad [5]$$

We consider a simple statistical model with a corresponding hierarchy of hypothesis ($M \supset H_1 \supset H_2 \supset H_3$).

(M) In our *main statistical model* N_{ij} are assumed independent negative binomial distributed with identical parameters within each sampling time (t) and length-group (j) i.e. the random variables $\{N_{ij} : t_i = t\}$ are identically distributed with mean $\mu_{t,j}$ and variance $\sigma^2_{t,j}$ ($\sigma^2_{t,j} > \mu_{t,j}$). To be able to estimate parameters in this model we need at least two hauls for each sampling time.
The likelihood function is given by

$$L((\mu_{t,j}),(\sigma^2_{t,j})) = \prod_i \prod_j \frac{\Gamma(N_{ij}+\nu_{t_i,j})}{\Gamma(\nu_{t_i,j})\Gamma(N_{ij}+1)} \pi_{t_i,j}^{\nu_{t_i,j}} (1-\pi_{t_i,j})^{N_{ij}}$$

where the probability parameter is $\pi_{t_i,j} = \frac{\mu_{t_i,j}}{\sigma^2_{t_i,j}}$ and the size parameter is $\nu_{t_i,j} = \frac{\mu^2_{t_i,j}}{\sigma^2_{t_i,j}-\mu_{t_i,j}}$. Note that for a given sampling time t the maximum likelihood estimate $\hat{\mu}_{t,j}$ is just the group average while $\hat{\sigma}^2_{t,j}$ can not be written on closed form.

(H1) To reduce the number of parameters in the main model we state the *variance structure hypothesis*

$$\sigma^2_{t_i,j} = a_{t_i} \mu_{t_i,j}^{b_{t_i}} + \mu_{t_i,j} \qquad [6]$$

This variance structure is mainly proposed from empirical investigations (even though we can give a mechanistic argumentation in the case $b_{t_i} = 2$ which is out of scope for this paper). Note that the additional $\mu_{t_i,j}$-term ensures that $\sigma^2_{t_i,j} > \mu_{t_i,j}$ which is required by the negative binomial distribution.

(H2) The *size-spectra model with time dependent catchability* is simply a mean value hypothesis in the previous models obtained by letting $q(x,t) = p_t s(x)$ in [5] and assuming the variance structure [6]:

$$\mu_{t_i,j} = p_{t_i} \int_{C_j} s_\theta(x) n_\theta(x,t_i)\, dx$$

The relevance of letting the catchability be time dependent will be justified.

(H3) Finally we may consider the *time independent catchability model* by assuming that $p_t = p$ in (H2):

$$\mu_{t_i,j} = p \int_{C_j} s_\theta(x) n_\theta(x,t_i)\, dx$$

Setting up a hierarchy of hypothesis like this have several benefits. First of all it lets us perform successive statistical tests to validate the spectra-models. But more importantly it helps us to localize model problems. For example the model (H2) is composite of three different assumptions regarding the statistical distribution, a variance structure and a mean-value structure. If the (H2)-hypothesis have problems fitting the data it will be possible to find out which of the three assumptions are critical by considering successive likelihood ratios.

3.2. Validating the main model

To validate the main model (M) we need to use a randomization technique because the random variables N_{ij} have a discrete distribution.
For each sampling time and length combination we estimate the parameters $\hat{\mu}_{t_i,j}$ and $\hat{\sigma}^2_{t_i,j}$ in the negative binomial distribution by maximum likelihood. Denote by $\hat{F}_{t_i,j}$ the corresponding distribution function. If N_{ij} was a true realisation of a negative binomial random variable with mean $\hat{\mu}_{t_i}$ and variance $\hat{\sigma}^2_{t_i}$ then the variables

$$U_{ij} \sim Unif([\hat{F}_{t_i,j}(N_{ij}-1), \hat{F}_{t_i,j}(N_{ij})])$$

would be independent uniformly distributed on $[0,1]$ (this statement is proven in appendix A.1).
We may verify this by a qq-plot. Plotting the U_{ij}'s as function of μ_{t_i} should not show any vertical patterns.

3.3. Identifiability

Some care is needed to avoid that the spectra models (H2) and (H3) get overparameterized. Since the statistical models are determined by the mean values [5] we need to dispel all obvious parameter bands appearing here. First of all notice - by inserting formula [4] in [5] - the band between the parameter vector (p_t) and the vector of recruitment sizes $(R_1,\ldots,R_m)$: if we multiply and divide the two vectors respectively with the same constant the model is unchanged. This is taken care of by fixing R_1 to 1. With this convention it is possible to estimate the parameters in both statistical models based on the parametrization given in the following section. This claim has been verified by re-estimating known parameters in simulated datasets.

3.4. Parametrization

The survey-selection function is chosen as a symmetric sigmoid curve

$$s_\theta(x) = \frac{1}{1+\exp(-\alpha(x-l^s_{50}))} \qquad [7]$$

The mortality z is split into two components - the natural mortality and the fishing mortality

$$z(x,t) = m(x) + f(x,t)$$

where m is assumed known and according to Beyer and Lassen (1994)

$$m(x) = M_\infty \left(\frac{x_\infty}{x}\right)^\gamma$$

and f is assumed to split into the product of a piecewise constant function of time and a sigmoid function of size

$$f(x,t) = \frac{\sum_{i=1}^{n} F_\infty^{(i)} 1_{(\tau_{i-1}<t<\tau_i)}}{1+\exp(-\beta(x-l_{50}^{f}))}$$

New individuals are recruited to the size of L_0 at the input times $t_i = i + \Delta t$, $i = 1995, \ldots, 2003$ where Δt is the common recruitment date. The corresponding recruitments are $R_{1995}, ..., R_{2003}$.

For the distribution of L_∞ (u) we use a t-distribution with three parameters $mean$, $scale$ and the number of degrees of freedom df. Small values of df leads to heavy tails in the distribution while large values of df makes the distribution approach the normal.

The parameters of the statistical model (H2) are summarized in the vector θ:

$$\begin{aligned}\theta = (\quad & R^*_{1995} = R^*_{1996} = R^*_{1997} = R^*_{1998} = 1,\\ & R_{1999}, R_{2000}, R_{2001}, R_{2002}, R_{2003},\\ & \Delta t,\\ & p_{Mar\ 2000}, \ldots, p_{Mar\ 2004},\\ & k, \mu^*_{L_\infty}, scale_{L_\infty}, df_{L_\infty},\\ & L_{50}^{(survey)}, \alpha^{(survey)}, L_{50}^{(fishery)}, \alpha^{(fishery)},\\ & F_\infty^{(<2001)}, F_\infty^{(2001-2002)}, F_\infty^{(2002-2003)}, F_\infty^{(2003<)},\\ & M^*_\infty = 0.2, x^*_\infty = 100, \gamma^* = 0.25 \quad)\end{aligned} \qquad [8]$$

A “*” indicates that the parameter is fixed.

3.5. Model-predictions

Once we have obtained the estimate $\hat{\theta}$ we can compute model predictions of the relative biomass and length distribution of the commercial catches.

Assuming an allometric relationship between fish weight- and length i.e. $W = qL^3$ for some constant q, the total biomass in the system at time t is given by

$$B(t) = q\int_0^\infty x^3 n(x,t)\,dx \qquad [9]$$

The constant q becomes irrelevant at this point because $n(x,t)$ is only known up to a multiplicative constant.

We may compute the *number density* of the fishery catch during the time period I by the formula

$$c_I(x) = \int_I f(x,t)n(x,t)\,dt \qquad [10]$$

This formula makes it possible to compare the catches for a given length group between different time periods.

In order to compare results to those from age-based models it is useful to convert length-specific mortalities to age-specific mortalities. For a cohort with the recruitment time t_0, the overall mortality for the cohort at time t is given by $z_{cohort}(t) = \frac{-N'(t)}{N(t)}$ where $N(t)$ is the total number of individuals in the cohort at time t. Hence

$$z_{cohort}(t) = \frac{\int_0^\infty z(L(t,L_\infty),t)\exp\left(-\int_{t_0}^{t} z(L(s,L_\infty),s)\,ds\right)u(L_\infty)\,dL_\infty}{\int_0^\infty \exp\left(-\int_{t_0}^{t} z(L(s,L_\infty),s)\,ds\right)u(L_\infty)\,dL_\infty} \qquad [11]$$

4. Data

Our data consist of cod catches from 299 selected hauls obtained from the Baltic International Trawl Survey (BITS). Only positions inside ICES division 25 are considered. All the hauls are taken with TVL-trawl by the Danish vessel DANA. The duration of a haul is approximately 30 minutes.

The survey is performed twice a year - the spring survey, which takes place around first of March, and the autumn survey, which takes place around first of November. The actual haul times are distributed over a one month interval around these dates and we associate an average date with each survey - the so-called sampling time.

A brief overview of the data is given in Table 1. The length of each fish has been measured to an accuracy of 1 cm. We define the CPUE for a given 1 cm length group as the average number of fish caught at a given time and a given length group per haul. The CPUEs per length group are illustrated in Fig. 1 which also shows Von Bertalanffy growth curves (with parameters given in the caption) in order to follow the cohorts through time. The positions of the peaks in the length distributions are reasonably well described by the growth curves. Figure 1 also indicates to what extent it is possible to estimate recruitment. The earliest year class with a clear data signal is the 98-year class, hence it is natural to use the 98-year class as reference. Furthermore, we must assume constant recruitment prior to that time. Hence the recruitment-sizes from 95 to 98 are set to one.

Survey	Number of hauls	Number of fish caught
Mar 2000	8	1920
Nov 2000	29	6345
Mar 2001	50	13670
Nov 2001	33	8631
Mar 2002	41	14749
Nov 2002	35	16805
Mar 2003	41	7467
Nov 2003	24	5917
Mar 2004	38	10887

Table 1. Number of hauls and fish caught by survey.

5. Results

5.1. Validating the main statistical model

The model (M) includes both a distributional assumption and an assumption about independence. These are considered

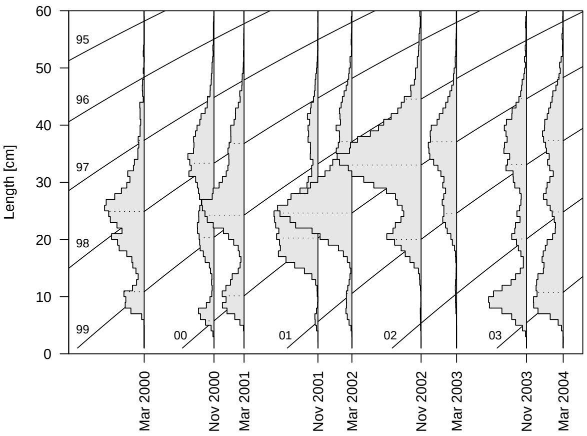

Fig. 1. CPUE per 1 cm length group at the 9 sampling times and Bertalanffy curves with initial size 1 cm at first of August. Each Bertalanffy curve is marked with the year classes from 1995 to 2003. Except for the initial time t_0 all curves have the same parameters $k = 0.12\, year^{-1}$ and $L_\infty = 135\, cm$.

separately.

For each of the 9 surveys and 59 length groups the MLEs $\hat{\mu}_{t_i}$ and $\hat{\sigma}^2_{t_i}$ have been obtained. By transforming with the estimated distribution function - and randomizing as described in section 3.2 - we obtained 299×59 residuals U_{ij} which should follow a uniform distribution on the unit interval. A qq-plot indicates that this holds true (Fig. 2a). The same residuals U_{ij} were also plotted against μ_{t_i} (Fig. 2b) showing no systematic patterns.

To demonstrate the importance of choosing a distribution with over-dispersion the same plots were made with the negative binomial distribution replaced by the Poisson distribution (Fig. 2c and d). The Poisson distribution obviously did not meet the criterion of uniformity.

The model (M) assumes independence between length-groups. To validate this assumption the empirical correlations between length groups were visualized (Fig. 3) and it appeared that strong correlations exist between neighboring length groups.

In the light of the length-group dependencies it did not make sense to perform a formal Kolmogorov-Smirnov test on the randomized residuals ($U_{i,j}$) to test whether these residuals followed a uniform distribution. Instead we chose to partition the residuals into corresponding 1 cm length groups (i.e. considering U_{ij} for fixed j) and performing the statistical test for each of the length groups in order to test the distributional assumption. Indeed this lead to acceptance for every group.

We will ignore the length-group dependencies throughout this study.

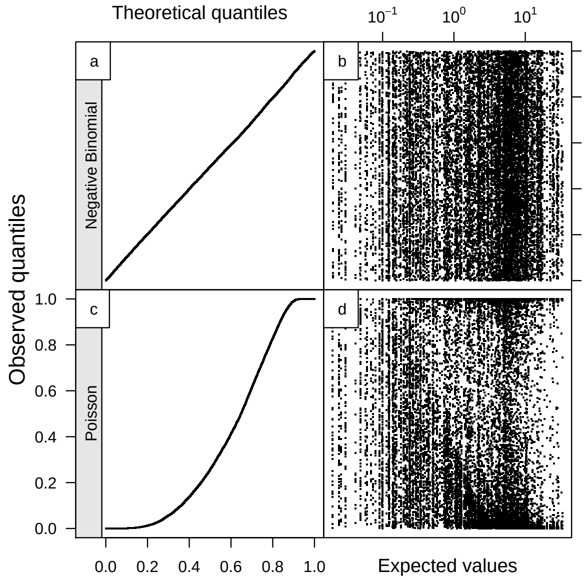

Fig. 2. a) qq-plot for the negative binomial distribution. The observed randomized quantiles are plotted against the theoretical quantiles. b) The observed randomized quantiles for the negative binomial distribution as a function of the estimated mean value parameter. c) qq-plot for the randomized quantiles based on the Poisson-distribution. d) The observed randomized quantiles for the Poisson distribution as a function of the estimated mean value parameter in the Poisson distribution.

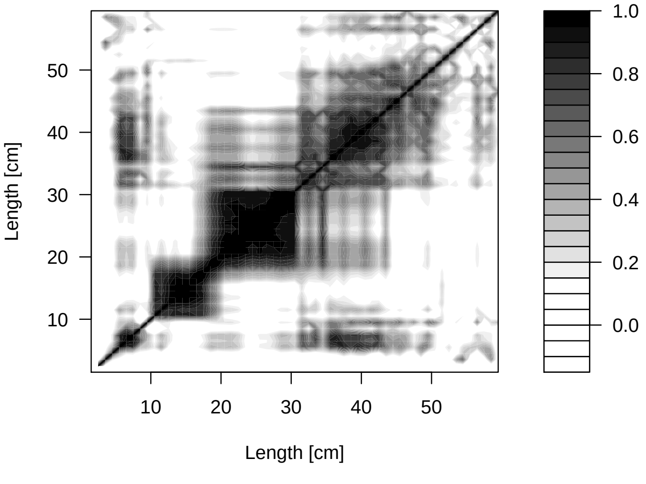

Fig. 3. Empirical correlations between number of fish caught in different length-groups during the autumn survey 2001.

5.2. Examining the variance structure

For computational reasons it is most effective to be able to reduce the number of parameters in the main model (M). The variance structure proposed in (H1) almost eliminates half of the parameters.

The reasonability of this hypothesis is justified in Fig. 4 which shows 9 independent analyses - one for each sampling time. The parameter estimates $(\hat{\mu}_{t,j}, \hat{\sigma}^2_{t,j})$ from the full statistical model (M) are plotted for each sampling time together with

the curve $\sigma^2 = \hat{a}_t \mu^{\hat{b}_t} + \mu$ where $\hat{a}_t$ and $\hat{b}_t$ are the MLEs from the variance structure model (H1) at time t.
Inspecting the exponents b_t on Fig. 4 we see that they are all quite close to 2. But a formal test rejects this hypothesis.

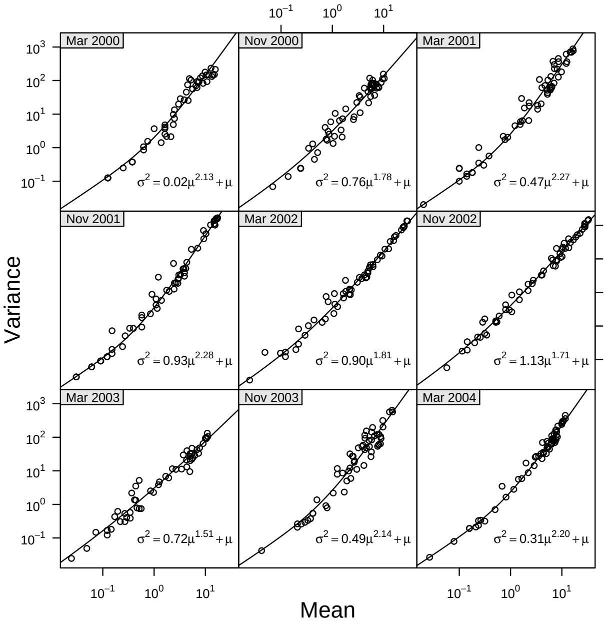

Fig. 4. The circles represent the MLEs $\hat{\sigma}_i^2$ vs $\hat{\mu}_i$ from the main model (M). The solid line indicates the function $\sigma^2 = \hat{a}_t \mu^{\hat{b}_t} + \mu$ where $\hat{a}_t$ and $\hat{b}_t$ are the MLEs from the variance structure model (H1) at time t.

5.3. Spectra-model estimation

Assuming the hypothesis (H1) we now consider the size-spectra model (H2) with time-dependent catchability.
The maximum likelihood estimate $\hat{\theta}$ for θ [8] was obtained. Based on $\hat{\theta}$ the expected CPUEs $\mu_{t_i,j}$ were computed and compared to the observed mean CPUEs (Fig. 5). We conclude that the model (H2) describes the CPUEs well, despite some confusion with the 2003-yearclass which during the Nov 2003 survey appeared to be of larger size than newly recruited individuals usually are in the autumn-survey (Fig. 1). The highest parameter correlations were found to be as high as 0.98 among and between certain recruitment parameters $\{R_i\}$ and catchability parameters $\{p_i\}$. Also within each survey the variance-structure parameters $\{a_i\}$ and $\{b_i\}$ were highly correlated (up to 0.95).

Assuming constant catchability over time we estimated parameters based on (H3) and obtained a plot equivalent to Fig. 5, which showed that it was impossible for the model to explain the increasing CPUE for the 2000-cohort during year 2002. For this reason we chose not to present the results obtained under this hypothesis.

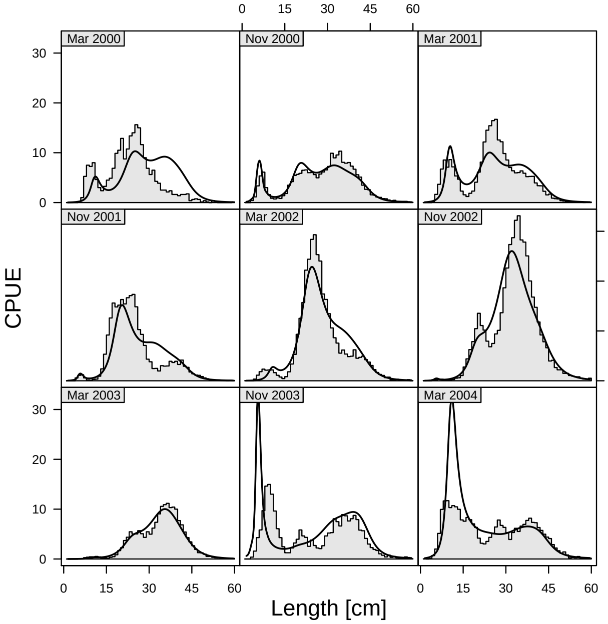

Fig. 5. Observed CPUEs and expected CPUEs per 1 cm length group at each sampling time obtained from model (H2) .

5.4. Spectra-model predictions

From the parameter-estimates based on (H2) different kinds of model characteristics were computed - namely the estimated biomass, mortality and recruitment. Furthermore, the predicted commercial landings were compared to the observed ones.

The biomass relative to year 2000, i.e. $\frac{B(t)}{B(2000)}$ where $B(t)$ is computed by formula [9], is shown in Fig. 6c. The increasing trend during 2001-2003 was mainly caused by the strong 2000-year-class (Fig. 6b). The predicted length probability distributions of the yearly commercial landings in the period from primo 2000 until ultimo 2003 where computed by formula [10] and compared to the observed distributions (Fig. 6d). The predictions fits the observations quite well for all years. However when considering the absolute commercial landings over the same period there is a clear decreasing trend which is not replicated by the model.

The age-specific fishing mortalities were computed (Table 2) based on formula [11]. These mortalities were remarkably low compared to the size-specific mortalities (Fig. 6a). The reason for this is that only the fraction consisting of the fastest growing individuals of an age-group is exposed to the high size-specific mortalities. This phenomenon is maintained by the increasing size-dispersion within a cohort implied by the underlying stochastic growth model.
Another consequence of the extreme size-selective mortality is the emergent property that old individuals grow surprisingly slowly. This is illustrated in Fig. 7 which shows the modes of the single cohorts as function of time. From that Figure we can conclude that for the typical length-distribution of fish within a given survey - which consists of three peaks - the first and

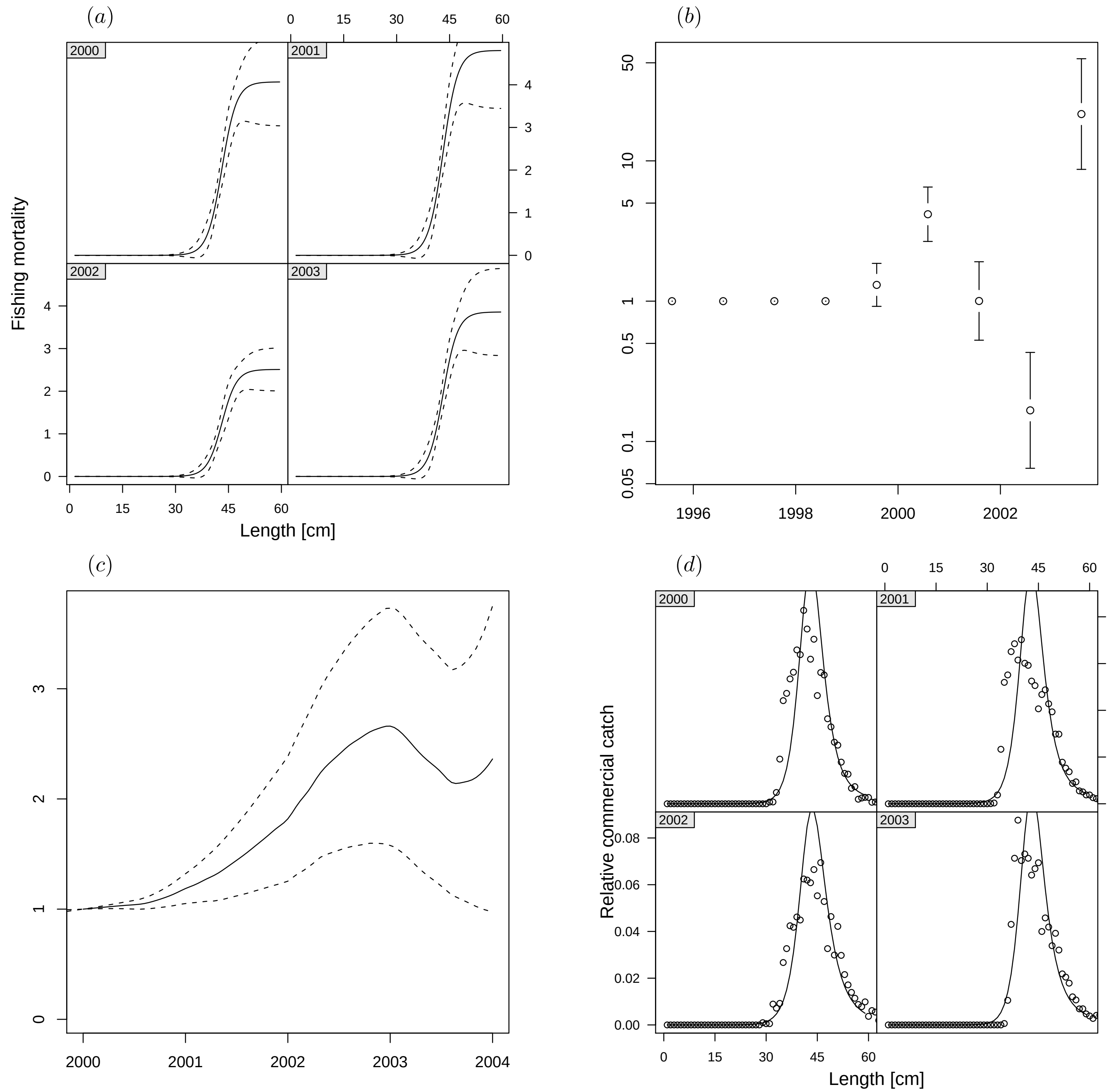

Fig. 6. (a) Estimated fishery mortality (solid lines) and 95% confidence limits (dashed lines) by fish-size. (b) Estimated recruitment R_t by year and 95% confidence limits. (c) Estimated relative biomass (solid line) and 95% confidence limits (dashed lines). (d) Observed relative length distributions for the commercial catches (circles) and predicted relative length distributions for the fishery based on the spectra-model (solid line).

second peaks consist primarily of the 0-group and 1-group respectively, while the third peak consists of all other age-groups.

5.5. Hypothesis testing

The hierarchy of hypotheses ($M \supset H_1 \supset H_2 \supset H_3$) allows us to apply standard likelihood ratio testing (Table 3). Unfortunately all tests were rejected despite the convincing fits on Fig. 4 and 5.

This motivated a study of the log-likelihood differences by length group as shown in Fig. 8. Fig. 8a shows that the difference between the log-likelihood of the variance structure model and the main model has two peaks covering the two size-intervals $[0, 25cm]$ and $[25cm, 60cm]$ respectively. The two peaks cannot be below the threshold simultaneously. However if we remove from the analysis fish shorter than 20 cm the second peak will definitely get smaller. To show this we tried to discard all length-groups below 20 cm and refit all models. The corresponding hypothesis tests are given in Table 4. From

	0	1	2	3	4	5	6
Mar 2000	0.01	0.09	0.42	0.93	0.74		
Nov 2000	0.00	0.05	0.25	0.83	0.84	0.55	
Mar 2001	0.01	0.09	0.44	1.04	0.85	0.56	
Nov 2001	0.00	0.06	0.26	0.87	0.85	0.55	0.39
Mar 2002	0.01	0.06	0.27	0.57	0.46	0.29	0.21
Nov 2002	0.00	0.04	0.19	0.65	0.74	0.48	0.33
Mar 2003	0.01	0.09	0.44	1.10	0.98	0.65	0.45
Nov 2003	0.00	0.05	0.24	0.81	0.90	0.62	0.43
Mar 2004	0.01	0.08	0.41	0.92	0.77	0.52	0.37

Table 2. Age-specific fishing mortality

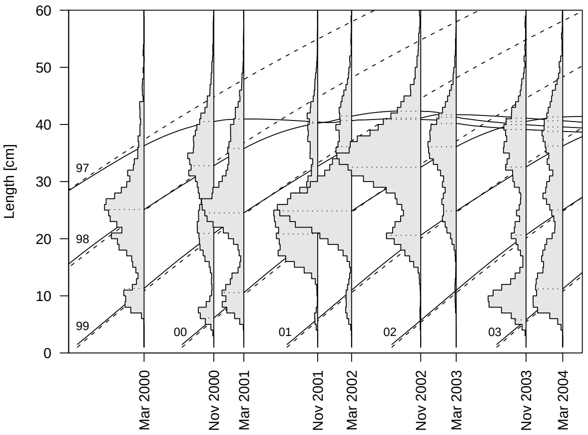

Fig. 7. Estimated modes of the individual cohorts (solid line) and von Bertalanffy curves from Fig. 1 (dashed line).

this table it appears that the second peak in both Fig. 8a and 8b can be brought below the threshold by removing the small fish. The test for time-independent catchability (H3) could not be accepted.

	$-\log L$	$-2\log Q$	nparms	df	p
M	34613.3		1062		
H1	35087.5	948.4	549	513	0
H2	35814.1	1453.2	44	505	0
H3	35965.2	302.2	36	8	0

Table 3. Successive asymptotic likelihood ratio tests.

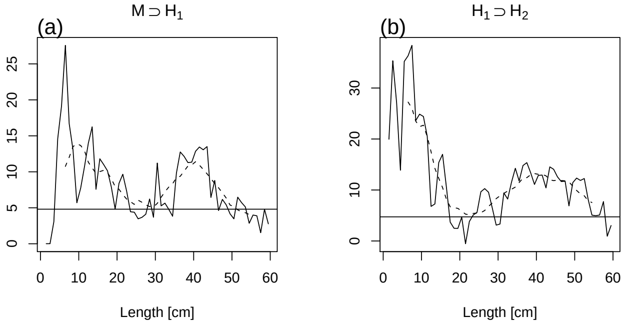

Fig. 8. Difference in log-likelihood contributions by length group (solid line) for (a) Models (M) and (H1). (b) Models (H1) and (H2). The dashed lines are smoothened versions of the solid lines to show the trend. A large value indicates a bad fit of the submodel compared to the super-model. The horizontal lines are thresholds based on the quotient of the relevant χ^2-quantile and the number of length groups, chosen such that test would be accepted if the average likelihood difference were less than the threshold.

	$-\log L$	$-2\log Q$	nparms	df	p
M	25356.5		702		
H1	25530.5	348.0	369	333	0.27
H2	25706.9	352.8	44	325	0.14
H3	25848.3	282.8	37	7	0.00

Table 4. Successive asymptotic likelihood ratio tests obtained by refitting all models without length-groups below 20 cm.

6. Discussion

Length-based stock assessment models based on scientific survey data are particularly relevant when catch-data are unreliable e.g. because of misreporting, or when individual age determination is uncertain or even impossible.

In the present work a simple continuous time size-spectra-model was derived and a statistical model was formulated based on the negative binomial distribution. This was done to estimate parameters in the spectra-model based on length data by haul for a single species.

Estimability in the model was examined by re-estimating known parameters from simulated data-sets. Quite surprisingly it turned out that even in a spectra-model with a time varying catchability (H2) all model-parameters were reestimable.

The spectra-model was applied to a Baltic cod dataset obtained from the Baltic International Trawl Survey. Various visualizations of the data indicated that a negative binomial distribution combined with the proposed variance structure described the data in a satisfying manner (Fig. 2 and 4). Furthermore, the mean-value structure determined by the spectra-model fit the observed length-distributions reasonably well (Fig. 5) and predicted the relative length distributions of yearly commercial catches (Fig. 6) even though this data-source was not part of the parameter-estimation.

The use of single haul information made it possible to test the four hypotheses. In the Baltic cod case the negative binomial distribution was accepted by a Kolmogorov-Smirnov test performed marginally for each length-group.

The variance structure was rejected even though it visually seemed to be a good choice (Fig. 4). By examining log-likelihood differences between the main model and the variance structure (Fig. 8a) it became apparent that fish of sizes below 25 cm had a different variance structure to fish above 25 cm. With this in mind we have later realized that the points above the curve on

Fig. 4 generally correspond to small fish while points below the curve corresponds to large fish. A solution would thus be to double the number of parameters in the variance structure.
Also the spectra-model (H2) was rejected because of the problems with describing fish shorter than 20 cm (Fig. 8b). This suggests the need to include dispersion in the recruitment period e.g. by modelling recruitment as a continuous process.
The rejection of (H3) points us to an important question regarding the Baltic cod dataset which remains unanswered: How is it possible for the observed CPUE for the 2000-year-class to increase through the entire period from the recruitment time until autumn 2002? One possible explanation is that the overall survey catchability increased during the period. This was the motivation for the formulation of hypothesis (H2). Such a change could be caused by hydrographical variations especially regarding oxygen conditions on the bottom. Another possibility could be migration.

Our estimates of the fishing-mortality by length (Fig. 6a) were remarkably high for large fish (up to 3 for certain periods) and very size-selective. However only a fraction of the individual cohorts were exposed to those high mortalities and therefore the corresponding age-specific mortalities were all below 1.1 (Table 2). The size-selective mortality had the effect of slowing down the movement of the peaks in the spectrum as illustrated in Fig. 7 in contrast to Fig. 1.
A main assumption of the statistical model was independence between length groups. This assumption is not fulfilled by the data. In fact if a large number of fish is caught in a given length group and in a given haul then it is very likely that the number of fish caught in the adjacent length groups is high as well. This relationship has been verified on the data by computing the empirical correlation matrices from each survey (Fig. 3 shows the autumn 2001 survey). These matrices show high (positive) correlations (90%-100%) for length groups separated by less than 10-15 cm.
Obviously the assumption of independence exaggerates the statistical information in the data. This implies that our parameter-estimates are too well determined and that the hypotheses in general tend to be rejected. In order to validate the quality of the estimated confidence intervals obtained from the Hessian matrix, several bootstrap experiments were performed. Half of the hauls where taken out at random and parameters were estimated from the reduced dataset. This procedure was repeated 100 times and the conclusion was that our confidence bounds for certain parameters should be twice as large (after correcting with the $\sqrt{2}$-factor coming from reducing the data-set).

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A. Appendix

A.1. Randomization

Let N be a discrete random variable on $\mathbb{N}_0$ with distribution function F and let the conditional distribution $U|N = n$ be uniform on the interval $[F(n-1), F(n)]$. Then the distribution of U is uniform on $[0, 1]$.
To prove this let g be the density of U. The conditional density of $U|N = n$ is given by

$$g(u|n) = \frac{1}{P(N = n)} 1_{(u \in (F(n-1), F(n)])}$$

Hence the unconditional density is

$$\begin{aligned} g(u) &= \sum_{n=0}^{\infty} g(u|n) P(N = n) \\ &= \sum_{n=0}^{\infty} 1_{(u \in (F(n-1), F(n)])} \\ &= 1 \end{aligned}$$

for any $u \in [0, 1]$.

Annex 2: Working document 2

Preliminary studies for the development and fitting of a statistic spatial length-based model for the European hake

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Introduction

The European hake represents the 2nd French landed species in value (DPM/OFIMER 2003). Actually, the Northern stock is in an alarming state (Fpa superior to Flim and SSB inferior to SSBlim, ICES 2004) and a recovery plan came into effect in April 2004, because of an alarming biological state.

Several source of uncertainties remain in the assessment of this stock and alternative stock assessment models are needed. In this respect, a statistical spatial length-based model is considered for several reasons:

i. Hake growth is poorly known (De Pontual, Bertignac *et al*. 2003) and aging is very difficult. As a consequence, a length-structured should be more appropriate to avoid the age-length conversion.
ii. European hake is largely distributed over North East Atlantic, and large-scale migrations are supposed to occur. In addition, many different fleets working in specific area exploit it. More, spatial management measures, especially marine protected areas, are often presented as promising alternative or complementary management measures to the simple catch regulation (Botsford, Castilla *et al*. 1997). A spatialized model is necessary to take into account the spatial heterogeneities of both population and fishing activity, and to evaluate spatialized management measures.
iii. Maximum likelihood estimation is an appropriate method to estimate unknown parameters (biological or of fishing activities), with unknown distribution.

The considered model can be written on a matrix form:

$$N(t+1) = Sr(t)[R(t) + M(t)\ G(t)N(t)]$$

With:

f. N(t) strength at time t
g. Sr(t) survival rate at time t
h. M(t): migration probabilities at time t
i. R(t): recruitment at time t
j. G(t): growth transition matrix at time t

An appropriate structure should be selected for each process. It means that the model should be a trade-off between the desired complexity and the availability of data, and that the impact of each assumption should be quantified.

Two previous studies were realised preliminary to the model construction. The first was aimed at evaluating the impact of the discretisation (both time and length) of continuous processes, especially growth. The second compared different optimisation algorithm usable for the maximum likelihood estimation.

Analysis of the impact of the discretisation process in a growth model with individual variability

Different mathematical frameworks can be used to model structured population dynamics, whether population states are assumed discrete or continuous and the projection time is discrete or continuous (Caswell 2000). The complexity of mathematical objects used to model continuous process (such as differential equations) and sometime the difficulties to find simple analytical solutions leads to the use of discrete approximations, which are furthermore easy to implement on computers. The main drawback of discrete model lies in the required division of continuous variables into discrete classes and time into time steps. This imposed to make assumptions on individuals within classes and on process during time steps.

Many population models describe the population growth process using a mean growth: the growth in each length class is supposed to be equal to the growth at the midpoint. Such models could produce large errors in growth rates. A largely used solution is to consider a mean growth by length class, given by the growth function, and a stochastic distribution for individual variability around the mean (Sullivan 1990; DeLeo *et al* 1995; Cruywagen 1997; Delong *et al* 1998; Froysa *et al* 2002).

The purpose of this study is to identify some critical points in the discretisation of a continuous process and to quantify the impact of different choices of discretisation of the time, the individual size distribution and the growth process in a length structured model. A preliminary qualitative study leads us to eliminate some irrelevant hypotheses. Then a quantitative analysis was practised to quantify the impact of the different hypotheses.

Qualitative approach

A part of this analysis was presented during the last study-group meeting (ICES 2003). The model consisted in a population only submitted to growth. It can be written on a matrix form:

$$\boldsymbol{N(t+1)=G\left(t\right)N(t)]}$$

Simulations consisted in projecting cohorts through 10 years simulations. The mean growth was supposed to follow a Von Bertalanffy equation, and growth increments were distributed around this mean following beta-binomial, normal, lognormal and gamma distribution. Two types of length classes were built: classes of same duration in time and classes of same length interval (5 and 10 cm). For the cohort projection, the individuals within a class were either located in the middle of the class or uniformly distributed within the class. Finally different hypotheses were considered for the variance of the distribution of growth increments, as a function of the mean.

Visual comparisons shows the great impact of time and length dicretisations on the resulting frequencies. It also demonstrates that the normal, lognormal and gamma distribution were relevant distribution to describe inter-individual growth variability. Finally, a uniform distribution within classes, especially in case of large length classes, and a variance decreasing with growth increments seemed to be preferable.

Quantitative approach

The qualitative approach lead to a large reduction in the number of hypotheses, but a quantification of the remaining ones was required. To quantify such impact it was necessary to use quasi-continuous simulation that mimic continuous processes as “reference”.

Growth simulation of N individuals according to the previous model with time steps equal to one month was carried out. Each possible assumption of individual variability with several hypothesis of variance levels was used to generate several instances of plausible “realities”. The individuals were re-attributed to the corresponding length class at the end of the 10 years simulation. Let us denote S(*s,v) a simulation set provided with a stochastic distribution of individual reality s and a variance hypothesis v.*

Cohorts were then projected with the discretized model for each arrangement of hypotheses (table 1).

Table 1: Different hypotheses considered for the dicretized model.

TIME STEPS DT	LENGTH CLASSES DL	DISTRIBUTION OF GROWTH S	DISTRIBUTION WITHIN A CLASS POS	VARIANCE V
Quarter	1cm	Normal	Proportional to mean increment	Middle
Half-year	5cm	Gamma	Proportional to (mean increment)²	
	10cm	Log-normal		

The total distance between the frequencies obtained by quasi-continuous simulations and discretized model was then calculated for each pair of quasi-continuous model and discretized model. A statistical analysis was conducted with the distance as explained variable and dt, dl, s, pos and v as explicatory variables. The estimated coefficients makes possible to quantify the impact of each type of hypotheses.

This analysis demonstrates the major impact of discretisation of both time and length. It demonstrates that gamma and lognormal are more flexible distribution, especially when variance is fixed as a proportion of the mean increment. It also confirms that it is more appropriate to consider that individuals are uniformly distributed within length classes than to consider they are all located in the middle of the class.

In the future, it will be interesting to fit the discretized model to the reference model and to quantify the impact of each hypothesis on the estimated variance. It would seem also interesting to analyse the impact of those hypotheses on the Akaike Information Criteria.

Review of different optimisation algorithm

Maximum likelihood method is based on the optimisation of the likelihood function regarding unknown parameters.. Two main qualities are necessary for an optimisation algorithm to be efficient. First, it should converge towards the global optimum of the function, avoiding local optimum. Secondly, the speed of convergence should be as small as possible. This study aimed to compare three types of algorithm usable for maximum likelihood estimation.

Gradient-based method

This method is the most often used. It consists in choosing an initial vector of parameters and then iteratively constructing a new vector in the steepest direction. This type of algorithm presents two main disadvantages:

i. Choosing the steepest direction requires to calculate or approximate the derivatives of the function for each parameter.

ii. The results depend of the initial vector; it means that local optimums are not necessarily avoided (figure 1).

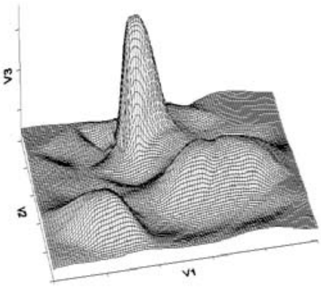

Figure 1: In case of complex objective function, the algorithm may converge a local optimum.

Simplex

The method relies on the choice of N+1 initial sets of parameters (N = number of parameters to estimate) called Simplex. Each set is evaluated. The worst is modified to construct a new Simplex. This method do not avoid local optimum and the speed decrease quickly when the number of parameters to estimate increase.

Genetic Algorithm

Genetic algorithm relies on the principle of natural selection. It is aimed at exploring the entire space search. Each parameter is coded through a binary string called gene. We will call “bit” a character of string. A chromosome is a set of parameters (and so a potential solution). Each chromosome is characterised by its fitness (in our case likelihood) which quantify how reliable is the solution. A population consists in a group of chromosome. A genetic algorithm tries to iteratively improve the average fitness of the population while keeping enough “diversity” to explore the entire search space. Three successive operations are realised to create a new generation: reproduction, crossover and mutation (figure 2).

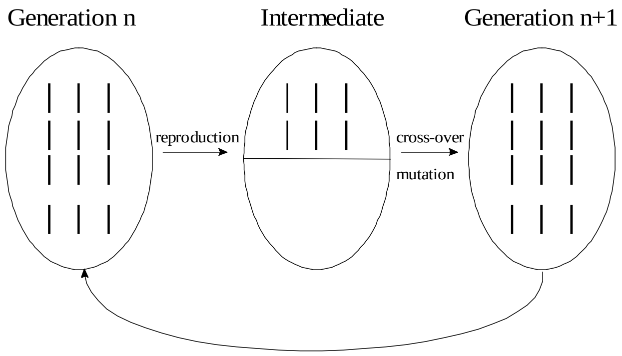

Figure 2: Successive operations realised to construct a new generation.

Reproduction consists in selecting the best chromosomes (the one with the highest fitness). The probability to reproduce is often set to be proportional to the fitness in order to conserve some inferior chromosomes and so to keep diversity (by opposition to a purely elitist reproduction: only the best are kept).

Crossover is the operator necessary to create new gene associations. The crossover acts at the “bit” level, so that genes can be modified and that new diversity is created (figure 3).

Mutation is the change of a bit. It leads to modify the value of parameters and so to explorer new possible values (figure 3).

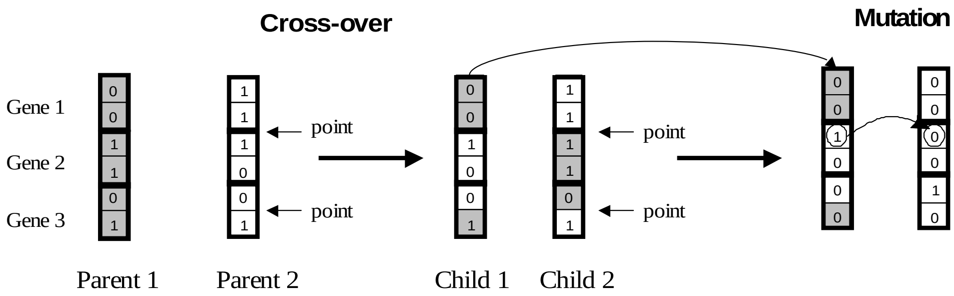

Figure 3: Cross-over and mutation are two operators aims at evaluating new possible parameter's value association (cross-over) and to create new parameter's value (cross-over and mutation).

Two main advantages are usually put forward:

i. The speed of convergence in case of complex objective function
ii. The exploration of the entire search space and so the avoidance of local optimum.

Even if it does not exist any objective stopping criteria, genetic algorithm are interesting tools, and should be tested.

Perspectives

A first model is actually coded to serve as baseline of work and to test and compare different structures. Preliminary studies on mortality (fishing and natural), recruitment and migration, analogous to the study previously presented, are going to be realised to quantify the impact of different hypotheses. The quality of fitting of different model structures (quantified for example by the AIC index) will allow to compare these structures, and also to compare different optimisation algorithm.

The final model should make possible to assess the hake population on real data, while estimating unknown parameters, and to quantify some management scenarios, and especially spatial measures. This level of complexity requires the use of a large of amount of data. We hope to have at our disposal:

i. Catch data by class, quarter, fleet and zone
ii. Survey indices of abundance by class, quarter and zone
iii. Tagging-recaptures data: a campaign is actually realised in the Bay of Biscay but a campaign on a larger area would be required
iv. If possible, nominal effort by fleet, quarter and zone.

Finally, estimated parameters may be used in other model, especially ISIS-Fish simulator tool aimed at evaluating the impact of various management scenarios.

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Annex 3: Working document 3

Measuring the robustness of an age-structured model (CASAL) using an age-length-structured operating model (CALEN)

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Introduction

A population dynamics model was developed that describes population state by a matrix of numbers at age and length, i.e., an integrated age-length structured model, called CALEN (Davies *et al*. 2002, Gilbert *et al*. 2005 *in prep*). Functional forms were developed for processes that best fitted Hauraki Gulf/Bay of Plenty snapper population data including commercial and research estimates of proportions at age and length, commercial estimates of proportions at age, tag-recapture estimates of numbers by length class, and a catch per unit effort relative abundance index, together with SST data. In the model, both length- and age-length-dependent growth processes were required to explain the data. Annual mean growth and annual year class strength were both found to be positively related to SST, but during different seasons, and the model accommodates these relationships.

Conventional age-structured models take no account of the length-, and age-length-related processes implicit in the CALEN model, and it is likely that bias will be introduced into population biomass and yield estimates in certain circumstances. To address this source of uncertainty the CALEN model was used, with assumed parameters, to simulate observations for input to an age-structured model, which is then used to estimate the CALEN parameters. Subsequent differences between the parameter estimates will be assessed in terms of the robustness of the age-structured model to length-dependent processes inherent in the CALEN model.

This report describes the development of an approach for systematically quantifying the robustness of conventional age-structured models and outlines some of the preliminary results.

Simulation approach

An evaluation of the robustness of a population model involves assessing its performance under particular states of nature using Monte Carlo simulation. Observed data from a theoretical “true” population showing various states of nature are simulated with random variability to which the estimator model is fitted and estimates for the “true” population are derived and compared to the known values. Robustness of the estimator model to predetermined states of nature is determined by including the relevant processes in the operating model. In the context of the age-length structured operating model, these population structural processes include annual growth variability and length-dependent fishing mortality. These processes have been estimated in conditioning the operating model by fitting to observed distributions of catch-at-age-length.

A simulation framework has been developed for making deterministic and stochastic comparisons between the CALEN operating model and age-structured estimators (AMOD, Gilbert *et* *al*. 2000 and CASAL, Bull *et al*. 2004), including an initial stage of calibrating simplified versions of the models to produce equivalent results.

Three stages were identified in developing the simulation approach:

1. defining the operating model's structural and statistical assumptions;
2. calibrating the operating model and age-structured estimator; and,
3. deterministic and stochastic simulations.

The first stage aims to specify CALEN such that realistic states of nature are simulated from it as an operating model. This is preferable if one is to extend interpretations of the accuracy of the age-structured model (relative to the operating model) to making recommendations regarding its utility for stock assessment.

The second stage involves demonstrating the integrity of the models by obtaining identical results when fitting CALEN and the age-structured estimator to observed data with identical structural and statistical assumptions in each. This is termed 'calibration' because it provides a baseline, or state of zero differences, between the models.

The third stage makes comparisons between the operating model and estimator to demonstrate the effects of the different structural and statistical assumptions in the operating model, deterministically and stochastically. Of course, variations of the CALEN operating model must be obtained from fits to the observed data in each instance.

Deterministic comparisons may be defined as:

- operating model simulation data is generated without error and the age-structured estimator is fitted to it.

This comparison measures bias in the age-structured estimator point estimates (maximum likelihood estimates) that are caused by structural or statistical (fitting assumption) differences. The results of the second stage provide identical simplified operating and estimator models for comparison in the first instance. Thereafter, additional features will be added to the operating model to identify the relative effect of these features on the accuracy of the estimator using deterministically simulated data.

Stochastic comparisons may be defined as:

- operating model simulation data is generated with error and the age-structured estimator is fitted to it.

This comparison measures estimator bias, and also compares estimator precision relative to operating model precision as determined from comparing estimator precision to the precision of the operating model fitted to the same simulation data.

Age-structured models

Two types of estimator models were developed for the simulations:

- AMOD (simple age-structured, with capability for estimating a relationship between environmental variables and year class strength, SST-YCS); and,
- CASAL (age-structured with length-specific fishing mortality, no capability for SST-YCS estimation).

AMOD was included because of its historical role in New Zealand snapper stock assessments and it provided a means of evaluating the integrity of the CASAL estimator against an existing assessment model. AMOD has a SST-YCS relationship that is identical to that of the operating model. This offered a means of evaluating the lack of this process in the CASAL age-structured estimator.

A framework for the deterministic and stochastic comparisons is described below:

Deterministic comparisons (single calculation of data without observation error)

At each stage the specified CALEN model is used as an estimator to obtain the "true" state of nature from the data (or that subset of the data that is relevant to the specifications). The simulations are then carried out from the "true" parameters.

The comparisons will be cumulative, with the differences compounding with each stage of the operating model development (Table 1). At various points, where the estimator is capable of emulating the operating model development, this functionality will be included in the estimator. A "before-and-after" comparison of each of these steps may be required. This is proposed for the comparison that will show how well CASAL can approximate growth variability.

Table 1: List of deterministic comparisons between the operating model (CALEN) and estimator models (AMOD and CASAL).

OPERATING MODEL (CALEN)	AMOD	CASAL
1. Simplified equivalent to AMOD (no growth variability, fixed selectivity equivalent to AMOD selectivity at age, etc) - no SST-YCS relationship	no SST-YCS relationship	no SST-YCS relationship, age-specific fishing mortality
2. as above	Not required	no SST-YCS relationship, length-specific fishing mortality
3. Simplified equivalent to AMOD (no growth variability, fixed selectivity equivalent to AMOD selectivity at age, etc) - include SST-YCS relationship	SST-YCS relationship estimated	as above with all YCS's estimated
4. Add variability around mean growth and selectivity at length	as above	as above
5. Add SST-growth variability	as above	as above
6. As for 5. but exclude SST-YCS relationship	no SST-YCS estimated	as above, include observed mean weight-at-age
7. Full structural and statistical assumptions	SST-YCS relationship estimated	as above

Versions of CALEN and AMOD as detailed in Table 1 were compared under a range of model assumptions and denoted as follows:

no SST-YCS relationship, flat selectivity's	**SSToff, selflat**
no SST-YCS relationship, estimated selectivity's	**SSToff, selest**
SST-YCS relationship, flat selectivity's	**SSTon, selflat**
SST-YCS turned on, estimated selectivity's	**SSTon, selest**

For the SSTon and SSToff options, parameters for the SST-YCS relationship were, or were not, estimated respectively. Hence, for SSToff runs, YCS for an estimation period were assumed to be 1.0. For the selflat and selest options: selectivity's for longline, single trawl and Danish seine were either assumed to be 1.0, or were estimated, respectively.

In each option, both CALEN and AMOD were fitted to the same set of observations: catch-at-age, CPUE, trawl survey relative recruitment indices and tagging programme estimates of biomass. The **SSTon, selest** comparison forms the basis of a calibrated set of operating and estimator models having near-zero differences. Biomass trajectories for the models were compared, and the various likelihood terms examined.

Stochastic comparisons (i.e. 1000 datasets simulated with observation error)

CASAL is unable at present to include SST-YCS estimation, therefore a stochastic comparison must be made that excludes this functionality in CALEN, i.e. operating model 6. in the deterministic comparisons above. This comparison will specifically examine the impact of the differences between the population state matrix in CALEN and CASAL.

A second stochastic comparison will be made with the full CALEN operating model specified.

Table 2: Specifications of the stochastic simulations using the CALEN operating model and the age-structured estimators (AMOD and CASAL).

OPERATING MODEL (CALEN)	AMOD	CASAL
1. Full structural and statistical assumptions, but exclude SST-YCS relationship - assume mean YCS for these years.	no SST-YCS estimated	no SST-YCS relationship, length-specific fishing mortality, include observed mean weight-at-age
2. Full structural and statistical assumptions, include SST-YCS relationship.	SST-YCS relationship estimated	as above, also do MCMC's for a small number of datasets to obtain Bayesian median estimators

Comparison 1. will test the ability of CASAL to replicate growth variability and the interaction of this and length-specific fishing mortality. This provides a test of the impact of the differences between the population state matrix in CALEN and the state vector in CASAL. AMOD will test the effect of assuming constant growth when growth is varying.

Comparison 2. will measure the differences with both models operating to their full structural and statistical specifications. CASAL will test the effect of estimating free YCSs when there is a SST-YCS relationship.

Comparisons will primarily be between the "true" and estimated values of B_y, B_0, B_{70}, $B_{current}/B_0$ and *MSY*. Where these differ substantially we may examine true and estimated values for other variables.

Preliminary results

Essentially identical estimates (Figure 1) have been produced from fitting the AMOD and simplified CALEN models to the same set of observations under a range of options for structural assumptions relating to YCS and selectivity.

This demonstrates equivalence between the two models achieving the calibration stage of the simulation framework, and forms the basis for the deterministic comparisons under differing structural assumptions that will be carried out in the next step of the project.

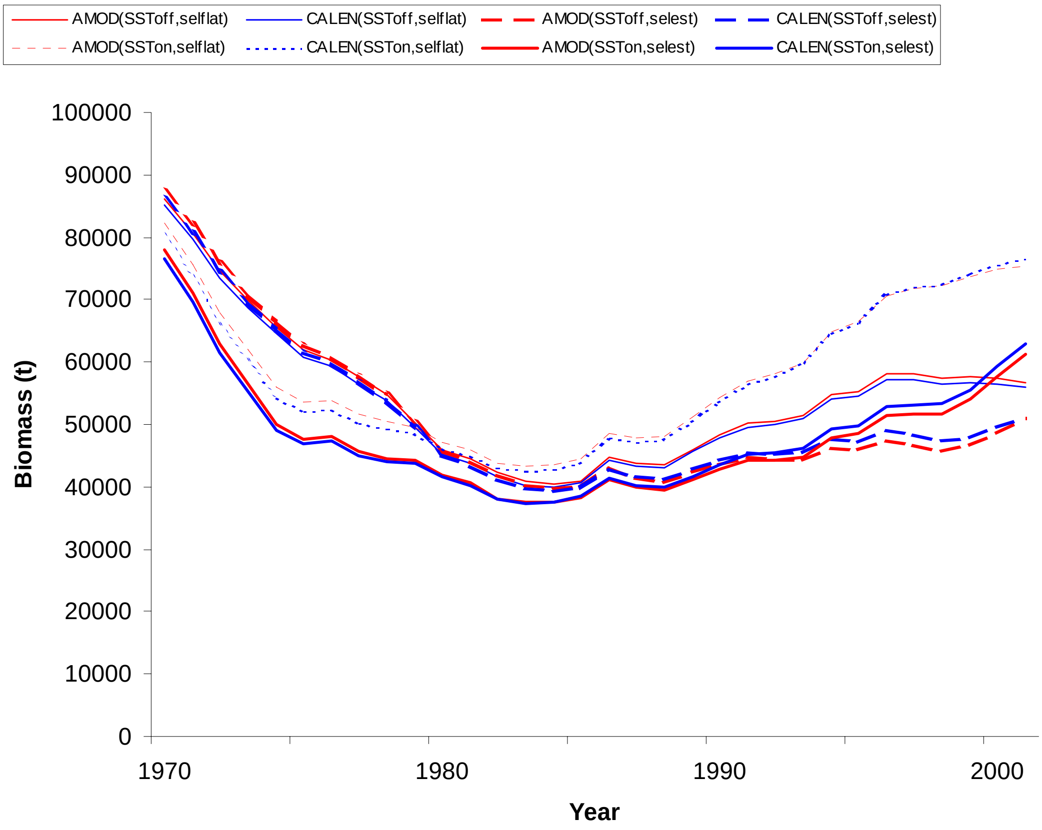

Figure 1: Biomass trajectories of the CALEN and AMOD models under four options of structural assumptions relating to YCS and selectivity (see text).

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