

# **ICES SGASAM REPORT 2006**

**ICES RESOURCE MANAGEMENT COMMITTEE  
ICES CM 2006/RMC:10**

## **REPORT OF THE STUDY GROUP ON AGE- LENGTH STRUCTURED ASSESSMENT MODELS (SGASAM)**

**BY CORRESPONDENCE**



**International Council for the Exploration of the Sea**  
**Conseil International pour l'Exploration de la Mer**

**International Council for the Exploration of the Sea  
Conseil International pour l'Exploration de la Mer**

H. C. Andersens Boulevard 44-46  
DK-1553 Copenhagen V  
Denmark  
Telephone (+45) 33 38 67 00  
Telefax (+45) 33 93 42 15  
[www.ices.dk](http://www.ices.dk)  
[info@ices.dk](mailto:info@ices.dk)

Recommended format for purposes of citation:

ICES. 2006. Report of the Study Group on Age-length Structured Assessment Models (SGASAM), By correspondence. ICES CM 2006/RMC:10. 73 pp.

For permission to reproduce material from this publication, please apply to the General Secretary.

The document is a report of an Expert Group under the auspices of the International Council for the Exploration of the Sea and does not necessarily represent the views of the Council.

© 2006 International Council for the Exploration of the Sea.

## Contents

---

<b>Executive summary .....</b>	<b>1</b>
<b>1 Introduction .....</b>	<b>2</b>
1.1 General .....	2
1.2 Terms of Reference .....	2
1.3 Structure of Report .....	3
1.4 Participants .....	3
<b>2 Developments in Methodologies .....</b>	<b>3</b>
2.1 Stock Synthesis 2.....	3
2.2 LCS.....	4
<b>3 Implementation of improved process-based models in age-length structured models .....</b>	<b>4</b>
3.1 Use of tagging data in age-length structured models.....	5
3.2 Evolutionary effects of exploitation .....	5
<b>4 Comparing the performance of different models .....</b>	<b>5</b>
4.1 A length-structured model for the European hake ( <i>Merluccius merluccius</i> ): assessing the impact of discretisation assumptions in a growth matrix model .....	6
<b>5 Use of age-length structured models for the assessment of stocks with limited age-disaggregated data.....</b>	<b>7</b>
5.1 <i>Nephrops</i> .....	7
5.2 Northeast Atlantic spurdog.....	8
5.3 Northern Hake and Sprat .....	9
5.4 Bay of Biscay Hake .....	10
<b>6 Investigating the effects of potential management measures.....</b>	<b>10</b>
6.1 EU Projects using age-length structured models for management Strategy Evaluation.....	10
6.1.1 BECAUSE.....	10
6.1.2 UNCOVER.....	11
6.2 Changes in exploitation pattern and pressure .....	11
6.2.1 YPR estimates for northeast Arctic cod.....	11
6.2.2 Maximum landings size for Northeast Atlantic spurdog .....	12
6.3 Using age-length structured models to predict the length structure in the catch under different management scenarios.....	12
<b>7 Conclusions and Recommendations.....</b>	<b>13</b>
<b>8 References and Working Documents.....</b>	<b>14</b>
8.1 References .....	14
8.2 Working Documents.....	16
<b>Annex 1: List of participants .....</b>	<b>17</b>
<b>Annex 2: Working Document 1.....</b>	<b>18</b>
<b>Annex 3: Working Document 2.....</b>	<b>44</b>

**Annex 4: Working Document 3..... 51**

## Executive summary

---

Low anticipated participation meant that the third meeting of the ICES Study Group on Age-length Structured Assessment Models (SGASAM) was held by correspondence in December 2006. Nine scientists (mainly with expertise in age-length structured modelling and stock assessment) from five countries provided written contributions to the report. Work was presented relating to all 5 of the Terms of Reference.

### *Developments in methodologies and applications*

Much of the work presented in this report makes use of the size-transition matrix approach to length-structured population modelling. However, an increasing number of applications are being developed which make use of the Lagrangian approach in which the population is modelled as a group of 'super-individuals' each with its own growth characteristics and abundance. This method has advantages in that it allows for growth to depend not just on the current size, but on growth in previous time-steps i.e. fast growing fish remain fast growing. However, these types of models are, in general, much more computationally demanding as many 'individuals' need to be modelled to make up the population.

### *Incorporating process submodels*

The incorporation of age-length structure is particularly useful for comparing the effect of different assumed process models. Work was presented on the use of tagging data in age-length structured models. Additionally a number of presentations were made at this year's ICES ASC which made use of (age-) length structured models to consider the evolutionary effects of exploitation level and pattern. Age-length structured models are therefore likely to be important to the work of the new ICES Study Group on Fisheries Induced Adaptive Change (SGFIAC).

### *Model comparison*

Age-length structured models are being used in a number of EU projects as 'operating models' to generate data (assumed to be the 'true' situation) which are then used to compare the performance of alternative assessment models and management scenarios.

Comparing the performance (in terms of 'goodness-of-fit' to data) of models with different levels of complexity and/or different process models is a necessary part of the development of an appropriate assessment model, although generally such comparisons are conducted on an ad hoc basis. In this report a more systematic investigation into the sensitivity of results to assumptions about the growth matrix model is presented.

### *Case studies with limited age-structured data*

The development of (age-) length-structured assessment models for a number of species with limited age-disaggregated data are already in progress. A number of independent pieces of work have investigated (age-) length-structured models for hake and these are being driven by the uncertainties in the ageing of this species. Other case studies presented consider length-based models for *Nephrops* and spurdog for which no routine ageing is carried out. These exploratory assessments have generally been welcomed by the assessment WGs, although there is a need for updated growth data for both of these species.

### *Investigating management measures*

Models which incorporate length structure are particularly useful for investigating the effect of certain management measures. Examples presented included the effect of introducing a maximum landing size on spawning biomass, the effect on length structure of different closed seasons, and comparison of YPR estimates in age- and age-length based models.

The present report was written by correspondence because the expected number of participants at the meeting was quite low, and this seems to indicate that SGASAM should not be continued as a separate study group, at least for the time being. However, the considerable amount of ongoing work which has been presented to SGASAM indicates that there should be a 'home' within one of the methods-oriented WGs or SGs in ICES for work on these issues. SGASAM thus recommends that the future of work on age/length and length structured models within ICES be discussed e.g. at the 2007 Working Group on Methods of Fish Stock Assessments (WGMG) meeting. Also, a theme session on such models could be held at the 2008 ICES ASC.

## **1 Introduction**

---

### **1.1 General**

There have been two previous meetings of the Study Group on Age-length Structured Assessment Models (SGASAM). Although age-length structured modelling has advanced considerably since this SG was first convened, it was agreed at the last meeting in March 2005 (ICES, 2005) that it remained important to have a specialist forum within ICES for evaluating the use and development of length- and age-length structured assessment models.

There are many stocks within the ICES area for which it is acknowledged that age-structured assessments are inappropriate and the incorporation of length-structure into the population model considered important. Such stocks include those when:

- it is considered that length-based models give a better representation of biological and fishery processes;
- age-based data are unreliable or unavailable, but length-structured data are readily available;
- age is not considered to be a good proxy for length.

SGASAM addresses issues concerned with introducing length structure into stock assessment models, particularly model complexity, incorporation of sub-process models, numerical implementation and model fitting and practical use of such models. More extensive discussion of the difficulties associated with incorporating length-structure into assessment models can be found in Section 2 of ICES 2003a.

### **1.2 Terms of Reference**

The **Study Group on Age-length Structured Assessment Models [SGASAM]** (Chair: H. Dobby, UK) will meet at ICES Headquarters from 27 November - 1 December 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 submodels 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).

SGASAM will report by 31 December 2006 for the attention of Resource Management Committee.

### **1.3 Structure of Report**

This year's meeting of SGASAM was held by correspondence as it was anticipated that this would allow for greater participation in the meeting. The report provides a summary of recent work which was available to the SG. Relevant work was presented on all of the ToRs.

A description of general methodological developments in age-length structured modelling (ToR a) is given in Section 2. (More specific developments relating to particular stocks, biological process and management measures are described in later sections.) Section 3 addresses ToR b), implementing improved process-based models in age-length structured model frameworks, while work related to ToR c) is summarized in Section 4. A number of applications of models incorporating length-structure for stocks with limited age-disaggregated data are presented in Section 5. The discussions include consideration of appropriate process models, data availability and current usage of such models with regard to formal stock assessment. Section 6 presents ongoing work on a number of examples where age-length structured models have been used to investigate the effects of possible management measures.

### **1.4 Participants**

A list of those who contributed to this report can be found in Annex 1.

## **2 Developments in Methodologies**

---

Tor 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.

### **2.1 Stock Synthesis 2**

Stock Synthesis 2 (SS2) is an assessment model in the class termed integrated analysis. SS2 is built with a population submodel operating by forward simulation, an observation submodel to estimate expected values for various types of data, and a statistical submodel to characterize the goodness-of-fit of the data and to obtain the best-fitting parameters with associated variance. It 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 (Dave Fournier, Otter Research Ltd.) 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 1990s.

In SS2, data includes catch by fleet in weight or numbers, fishery and survey age and length composition, mean length-at-age, age composition conditional on length/gender, survey abundance, fishery CPUE, mean body weight, and percentage discard by weight. There is no specific limit to the number of fisheries or surveys. The time-step is typically annual, but multiple seasons of varied duration can be defined. The population of each gender can be divided into a set of phenotypic morphs, each with unique growth and natural mortality parameters. 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. Expected values for data from each morph are accumulated within each gender to match the level at which observed data are collected. Growth parameters can be estimated internally to take into account the effects of size-selectivity and ageing imprecision on observed length-at-age. Fishery age and length data can be specific to discard or retained samples, so provide necessary information to allow the model to estimate retention functions. Model parameters

can be a function of environmental data or vary randomly or in time blocks. SS2 includes routines to estimate MSY and levels of exploitation that correspond to various standard fishery management targets. A user-selected harvest policy is used to conduct a forecast as part of the final phase in running the model.

SS2 integrates population estimation with inferences about population productivity and uses both to conduct forecasts about future stock conditions. The model defines annual recruitment as deviations from an estimated spawner-recruitment curve. This establishes a linkage between estimation of abundance during the data-available period to inferences about historical and unfished conditions. Some applications have started the time-series as early as 1876 to span an unfished condition, through an era with only catch data available, through a data-rich period and into a forecast period. By treating future recruitments as parameters to be estimated in this final phase, the model seamlessly transitions from the last year with data into the first year of the forecast. 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. In addition, SS2 is designed to produce a set of parametric bootstrap data sets. Comparable confidence regions on model parameters and derived quantities have been observed using the inverse Hessian, parameter profiles, MCMC, and re-running the model on the bootstrap data.

In 2005, SS2 was used to assess the status of about 20 groundfish stocks off the west coast of the U. S. At a workshop in November 2005, its general capabilities were compared to CASAL (Bull *et al.*, 2005), Multifan-CL (Fournier *et al.*, 1998), and A-SCALA (Maunder and Watters, 2003). Subsequently, exploratory applications to Pacific tuna assessments were initiated. In 2006, SS2 was introduced to the CSIRO assessment group in Australia and about 6 assessments were conducted. Also, a graphical user interface was developed by Alan Seaver as part of the NOAA Fisheries Assessment Toolbox (<http://nft.nefsc.noaa.gov/>). The detailed model output can be viewed using the GUI interface, a customized Excel spreadsheet, or a program in R developed by Ian Stewart.

At this time, SS2 is being upgraded based upon user-feedback and needs analysis from the 2005–2006 applications. A new release is expected in February 2007.

## **2.2 LCS**

A new length based assessment model called Lcs is currently under development at IMR, Norway and uses an approach similar to that used by Stock Synthesis 2 for incorporating growth. The method uses a ‘Lagrangian’ approach where the population consists of a group of ‘super-individuals’ each with its own growth characteristics and abundance which are projected forwards in time. The method has been applied to the Northern hake stock and also North Sea sprat, and further details can be found in Section 5.3 and WD 1.

## **3 Implementation of improved process-based models in age-length structured models**

---

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

A population model which incorporates age-length structure allows for detailed investigations into stock dynamics and is considered particularly useful for comparing the effect of incorporating different process models. A comprehensive discussion of the feasibility of incorporating process-based submodels into age-length model frameworks is given in last year’s report of this SG (ICES, 2005).

This ToR follows on from previous ToRs of this SG and also from work carried out under the remit of the Study Group on Growth, Maturity and Condition in Stock Projections



(SGGROMAT, ICES 2004). One of the intentions of including this ToR was to attract greater interest in this SG from biological process modellers. Although, this did not prove entirely successful, a number of examples of more complex process models in age-length structured frameworks were presented to the SG and are outlined below. Further, process modelling work has been conducted within the EU projects BECAUSE and UNCOVER, which are discussed in Section 5.1. In both of these projects, age-length structured models are implemented using the Gadget (Globally applicable Area Disaggregated General Ecosystem Toolbox, Begley and Howell 2004, [www.hafro.is/gadget](http://www.hafro.is/gadget)) framework.

### 3.1 Use of tagging data in age-length structured models

Tagging (i.e. mark-recapture) data have been widely used to study fish migration in a qualitative way. An example of application of tagging data to estimate migration using an age-length structured multi-area Gadget model is given by Hannesson *et al.* (2004). Tagging data have also been applied in age-structured assessment models (e.g. Tjelmeland and Lindstrøm, 2005).

Age-length structured models are useful in studies involving tagging data, both for migration and stock assessment, because the observations contain more information about length than about age. When the fish is tagged, the length (although with some uncertainty) is recorded. Age-structured models usually apply an age-length key to convert the length distribution of the tagged fish to an age-distribution. The recaptured fish may have either no information on length (when detectors are used), the length may be known, or the length and age is known. The time period between mark and recapture is known. Thus use of age-length structured models allows for using direct observations rather than transformed data when fitting models to observations.

Useful extensions to the current handling of tagging data in Gadget would be:

- Allowing a tagging experiment to include several population groups (e.g. immature and mature);
- Including tagging mortality.

### 3.2 Evolutionary effects of exploitation

Another possible area of application of age-length structured models is studies of evolutionary (genetic) effects of exploitation on living marine resources. This is an area of research which has attracted a lot of attention in recent years. At the ICES ASC in 2006, several length- and age/length-based approaches for studying evolutionary effects of exploitation level and size-selective harvesting on population dynamics were presented. Most of those studies considered the evolutionary effects on maturation and growth (e.g. Boukal *et al.*, 2006). Open questions about fisheries-induced evolution will be addressed in ICES's new Study group on Fisheries-induced Adaptive Change (SGFIAC), which will commence its work in 2007.

## 4 Comparing the performance of different models

---

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

At the 2005 SGASAM meeting, two alternative ways in which age-length structured model frameworks could be used to investigate the performance of models with different levels of complexity:

- as operating models to generate data and then apply other simpler assessment models and evaluate their performance with regard to the 'true' stock;

- for comparing different submodels or models with different levels of complexity within the same framework and evaluating their performance in terms of ‘goodness-of-fit’ to the underlying data.

Section 6.1 provides a description of some projects where Gadget models are being used as operating models to test other assessment models and explore alternative management regimes while the work outlined in this section focuses on the comparison of results from models with different levels of complexity within an age-length structured framework.

#### **4.1 A length-structured model for the European hake (*Merluccius merluccius*): assessing the impact of discretisation assumptions in a growth matrix model**

Current assessment models are usually age-structured and not spatialised (Fournier and Archibald, 1982; Pope, 1972; Shepherd, 1999; Virtala *et al.*, 1998). These two assumptions may lead to unreliable assessment for the European hake, since the required length-age conversion is questioned for this species (Kocher; Amara 2005; de Pontual *et al.*, 2003), seasonal concentrations of the populations related to the species's biology occur (Poulard, 2001), and the stock is exploited by several fleet fishing in specific zones. For these reasons, we have chosen to develop a spatialised length-structured matrix model for the European hake. To date, very few studies have looked at the impact that the discretisation of time and length classes may have on the ability of the population model to reproduce the underlying “reality” and correctly estimate parameters. In this study; we try to identify some critical points in the discretisation of a continuous process and try to quantify the impact of different assumptions to find a more flexible model. To do that, we fit a growth matrix model on quasi-continuous individual growth data and statistically analyse the discrepancy between observed and estimated frequencies-at-length, and observed and estimated growth rate. This analysis demonstrates the importance of both time-step and classes' width in a matrix model: these choices are strongly interdependent and should depend on the objectives of the model. In addition, the analysis puts into relief some robust assumptions making the model more flexible.

The complete length-based model has three main objectives: to improve the knowledge of the stock and its exploitation, to make a diagnostic of their current state, to simulate the evolution of the population and the fishing activity under various scenarios. It has a quarterly time-step, classes of 1 cm wide. The distribution area is divided into several compartments. Fishing activity and population distribution are assumed uniformly distributed within these zones.

A state model details the main biological processes and fishing activity dynamics. The biological submodel is based on four main processes: a stochastic recruitment, growth, migration and natural mortality. The fishing activity submodel is based on métiers. We assumed that the fishing mortality generated by each métier is the product of a selectivity factor (computed by a double half-gaussian), a year factor following a random walk and a seasonal factor. Recruitment, growth and migration are supposed to occur successively at the beginning of the time-step in an insignificant time, then fishes die from natural (distinct for mature and immature) and fishing mortality.

An observation model details the observation process. Each observation (catch, survey abundance index tagging date) is assumed to be inexact; following a statistical distribution, whose mean value is the model estimate.

Unknown parameters are estimated by maximum likelihood. The number of unknown parameters being very elevated, a major caution is necessary on the identifiability of the parameters and on the choice of the optimisation algorithm. A multidimensional integration is necessary to compute the likelihood since the model includes simultaneously process (year factor random-walk and stochastic recruitment) and observation errors (de Valpine 2004; de

Valpine and Hastings, 2002). This integration requires specific methodology (MCMC chain, particles filter, EM algorithm...), however a preliminary sensitivity analysis to reduce the number of unknown parameters (not sensitive parameters would be estimated by a simpler method) will be necessary.

Further details can be found in Drouineau *et al.* (WD 3).

## **5 Use of age-length structured models for the assessment of stocks with limited age-disaggregated data**

---

Tor 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).

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. This section describes a number of examples where (age-) length-structured methods have been developed for species for which age-disaggregated data are unavailable or unreliable due to age-reading uncertainties.

### **5.1 *Nephrops***

At last year's meeting of SGASAM, presentations were made on the development of age-length structured models for *Nephrops* stocks in Iceland and around Scotland.

A preliminary assessment of Firth of Forth *Nephrops* using a sex-disaggregated, size-structured population model was presented last year to this SG, with further details in Working Documents submitted to the *Nephrops* Working Group (Dobby, 2003; 2004). The model, which assumes sex and maturity specific growth and catchability, with size transition matrices derived from assumed von Bertalanffy growth parameters appeared to fit the data (commercial catch-at-length and TV survey biomass) well and indicate similar stock trends to previous XSA assessments. A further presentation of this work was given at this year's Workshop on *Nephrops* (ICES, 2006a) where a number of concerns were raised over particular aspects of the model and its assumptions, particularly the assumed growth transition matrix.

Size transition matrix models such as this; require either assumptions or estimates of the distribution of growth increments. Growth parameters relate the loss of individuals with length to disappearance with time/age which is the mortality signal and as a consequence, estimates of fishing mortality are confounded with the growth parameters which should therefore be estimated externally (e.g. Punt *et al.*, 1997) unless there are good age-length or growth data to which the model can be fitted. For the *Nephrops* stocks around Scotland, growth parameters are derived from length frequency analysis of historical survey data. Although previous *Nephrops* WGs have used von Bertalanffy growth parameters derived from these data to 'slice' catch-at-length distribution data into nominal age-classes, WKNEPH considered that the available data were currently insufficient for the estimation of size-transition matrices.

WKNEPH recognized the potential of such size-based approaches and noted that several other invertebrate stocks are currently assessed in this way, including Southern rock lobster (*Jasus edwardsii*) stocks off New Zealand and Australia (Breen *et al.*, 2002; Starr *et al.*, 2003) and Paua (*Haliotis iris*) (Breen *et al.*, 2003; Breen and Kim, 2004). They therefore recommended the initiation of an EU coordinated approach to updating growth information on *Nephrops* with the aim of being able to better parameterize such length-based models.

No updates were available to this SG on the development of the age-length structured assessment model for Icelandic *Nephrops*.

## 5.2 Northeast Atlantic spurdog

Over the past decade, a good deal of work has gone into improving the assessment of Northeast Atlantic spurdog. The methods employed during the 2002 meeting of the Study Group on Elasmobranch Fishes (ICES, 2002) and DELASS project (Heessen, 2003) included catch curve analysis and separable VPA using length distributions sliced according to growth parameters from the scientific literature, and a Bayesian assessment using a stock production model, with a prior for the intrinsic rate of increase set by demographic methods. More recent approaches (ICES, 2006b) have tried to make more use of the available length frequency data.

The use of a size-transition matrix model was first investigated at the 2002 meeting SGEF and further developed at more recent meetings of the Working Group on Elasmobranch Fishes (ICES, 2003b and ICES, 2006c). The sex specific size-transition matrix is parameterized from historical growth data and assumed fixed through time. The population dynamics process, such as recruitment and fishing mortality are assumed to depend only on length and in addition were initially assumed independent of sex. Unlike many models of this type, this spurdog model could almost be called a 'closed life cycle' model as a stock-recruitment relationship is incorporated which constrains the estimates of total recruitment. The fecundity of mature females has been shown to be related to size (Gauld, 1979) and so the total annual recruitment in year  $t$  is constrained by

$$R_t = \sum_{l_i > 70 \text{ cm}} 0.5 * (a + bl) p_{f,l} N_{l,t}^f$$

where  $N_{l,t}^f$  is the number of females in year  $t$  with length  $l$  and  $p_{f,l}$  is the proportion mature at length  $l$ . The parameters  $a$  and  $b$  which define the length-fecundity relationship, are fixed within the model and estimated from Gauld (1979). The gestation period of spurdog is known to be 22 months, so it is assumed that during any year only half of the females will give birth.

The model was fitted to sex-specific commercial catch-at-length frequency data (from UK (E&W) market sampling), total landings and a survey index of abundance. Problems were encountered with the fit of the model to the sex-specific catch-at-length data with persistent under-prediction for the females and over-prediction of the males. This may be due to the fact that the fishery targets mature females and therefore the fishing mortality at length for females may be higher than that for males. Further exploration of this model therefore needs to be carried out with sex specific fishing mortality. Additional problems were encountered with under-prediction of large individuals which was a result of the assumed  $L_\infty$  (based on historical) being significantly lower than individuals recorded in the commercial length frequency data. WGEF has highlighted the need for updated growth data (ICES, 2006c).

At the 2005 meeting of WGEF, an exploratory assessment was attempted for spurdog, based on an approach developed by Punt and Walker (1998) for school shark (*Galeorhinus galeus*) off southern Australia. The population model is basically age- and sex-structured, but incorporates biological process models that are length dependent. These include pup-production (see above), maturity, growth and gear selectivity. A length-at-age relationship with fixed parameters taken from the literature is used to convert between age and length, although other implementations of this model have used variable growth (Punt *et al.*, 2001).

Parameter estimates include total virgin biomass, survey selectivity by size category, commercial selectivity-by-category for both the Scottish fleet and England and Wales fleet, and constrained recruitment deviations (1905–2005). The commercial selectivity-at-length parameters are assumed to have remained constant since 1905 (first year in model) which is likely to be an oversimplification given the changes in the fleets that may have taken place

over this period. The model gives a reasonable fit to the available data with no obvious residual trends. Further details can be found in ICES (2006c).

### 5.3 Northern Hake and Sprat

A Working Document (Skagen, WD1) was presented describing a newly developed computer program for length based assessment called lcs. This program has a self-contained, parametric forward-projecting operating model, and estimates parameters by fitting the estimated survey and catch data to observed values. The operating model is designed as a set of 'super-individuals', each with its own growth parameters, and time and length at entrance to the population, that are subsequently reduced according to mortalities at length. These parameters characterizing each super-individual are drawn according to defined distributions. Hence, the variability in length-at-age is accounted for by the distribution of growth properties and entrance time/length among the super-individuals. This 'Lagrangian' approach is an alternative to the state space approach used in e.g. Gadget. The Lagrangian approach has some advantages and disadvantages compared to the state space approach. It allows some non-Markovian features (fast growing fish remain fast growing over time), but is probably more computationally demanding, and the results may be sensitive to the number of super-individuals applied to each year class.

Since it is self-contained and defined only by its parameters, the operating model can be used as a data generator. The program has the option to output such generated data. It also has the facility to use such generated data for a new assessment, and generate new data from that assessed stock and so forth (called 'cyclic estimation' in the paper). This is suggested as a hard test on internal consistency.

The program is still under development, the user interface is still primitive and it has not been extensively tested, but it is presented to the SGASAM to report on the progress so far.

Emphasis so far has been on gaining experience on the limitations of using only length-based data to estimate the model parameters in an assessment context. Studies have been made with artificial data, and data sets for Northern hake and North Sea sprat. In both these example stocks there are known problems with ageing of the fish, causing problems with age-based assessments. The program is designed to leave it to the user to decide which parameters to estimate. This allows for gross over-parameterization, and an important part of the assessment process becomes to decide on constraints that are necessary to obtain a reliable solution.

The development of the lcs model has confirmed that it is technically possible to construct an operating model for assessing a stock with the 'Lagrangian' type of population. A further comparison with state space type algorithms would be desirable.

Cyclic estimation with noise free data reproduces the data. This may be used as one check on program bugs.

Estimates of fishing mortality and biomass are far more noisy than in age-structured assessments. The noise in the mortality signal is expanded and it is confounded with growth variation. The stock number in a time-length cell originates from previous recruitments (or initial numbers). Due to the stochasticity in growth and initial size, each recruitment is distributed on a number of such time-length cells. The propagation of each recruitment into new cells later on is determined by the growth rate, while the abundance in the cell (i.e. how much is left of the recruitment) is determined by the cumulated mortality over the time it takes to reach that cell. That time again depends on the growth rate. The number in a time-length cell of data are therefore the resultant of recruitment, growth and mortality, as well as of catchability in the case of survey data.

The signal about mortality is the rate of decline of stock abundance with length. However, this signal is confounded with the growth rate. If the growth parameters are 'known', the slope can be translated into a raw  $Z$  estimate as:

$$-Z \sim d/dl (\ln N) * k*(L_{inf}-l).$$

With  $k$ -values typically in the order of 0.5, the term  $k*(L_{inf}-l)$  is much larger than unity, except when the length is close to  $L_{inf}$ . Hence, the slope  $d/dl(\ln(N))$  is much smaller than  $Z$ , so noise in the slope is amplified when translated into  $Z$ . The model framework is sufficiently flexible to allow fitting to a good deal of the noise in the data, but since this amplifies the noise, the results may become quite artificial. Attempts were made to filter away some of the high-frequency noise, and that stabilized the parameter estimates, but the validity of such measures has to be considered more closely.

In the hake study, estimates were made by fitting to survey indices at length, with and without additional fit to total annual catches. A penalty function on the year-to-year variation in  $F$  had to be applied in order to avoid zero  $F$ -values in some years. In the sprat study, with similar data sets, no stable assessment was obtained with the few attempts made so far.

The effect of the number of super-individuals per year on the estimates was examined only briefly. This number seems to matter, but to what extent this is an expression of over-parameterization is currently not clear.

#### **5.4 Bay of Biscay Hake**

One of the most relevant discussions around the European hake (*Merluccius merluccius*) is nowadays the big uncertainty in the age determination, due to the relevance of it in the assessment of the Hake. Furthermore, there are some recent results of the tagging experiments conducted in the Bay of Biscay in 2002 (De Pontual, Groison *et al.*, 2006) showing that the growth of hake is higher than the one used by now in the ICES assessment (Lucio, Murua *et al.*, 2000).

Taking those suggestions into account, it is clear that it would be very useful to implement a length-based model in the assessment of Hake and the first attempt had been done within the BECAUSE European project, trying to include trophic interactions of the ecosystem as well. For that the Gadget framework is being used, and it is possible to say that the preliminary results obtained with this are more or less reasonable and comparable with the results given by the Working Group on the Assessment of Southern Shelf Stocks of Hake, Monk and Megrim, applying the XSA analysis.

A more detailed discussion of this work is presented in Andonegi *et al.* (WD 2).

## **6 Investigating the effects of potential management measures**

---

Tor 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)

### **6.1 EU Projects using age-length structured models for management Strategy Evaluation**

#### **6.1.1 BECAUSE**

Several age-length structured multispecies, multi-area models have been set up in the Gadget framework during the EU project BECAUSE (2004–2007) (<http://www1.uni-hamburg.de/BECAUSE/>). For the Barents Sea, a cod-capelin-herring-minke whale model has

been set up. Several multispecies Gadget models have also been developed for stocks in Icelandic waters, while Gadget models are under construction for the Bay of Biscay/Iberian peninsula (see Section 4.4) and selected regions in the Mediterranean, with the focus on hake. Predation is modelled as a length-only dependent process in all of these models. Since information about prey age generally is not available, use of age-length structured models allows for using direct observations rather than transformed data when fitting models to observations. In addition fishing is modelled as a length-based process, and compared with length-based data in fitting the models, thus avoiding the uncertainty that would be introduced by using age-based data.

The multispecies models set up in BECAUSE will be run into the future to explore various multispecies management and environmental scenarios. The models, conditioned on the historical data, will be used to evaluate the possible response of the modelled stocks to these different scenarios. For example the long term catches (in numbers and age/length) of cod under different multispecies fisheries strategies, or the availability of food to marine mammals under different management regimes for fish stocks can be investigated using these tools.

### **6.1.2 UNCOVER**

In the EU project UNCOVER (UNderstanding the mechanisms of stock reCOVERy) (2006–2010), (<http://www.uncover.eu/>), Gadget models from BECAUSE will be used as operating models when testing the performance of assessment models as well as exploring management scenarios. UNCOVER focuses on developing recovery strategies for fish stocks. For this project the Gadget models (as well as other models, depending on the geographical area in question) will be used as “operating models” in an “operating model - assessment model - management rule” cycle. The Gadget model is treated as the “true” situation; catches and surveys (with errors) are taken from that true population and fed into the assessment model. The catches for the coming year are then computed from the stock assessment and the management rule, and used as inputs to operating model for the next year of the simulation. This process allows for more realistic evaluation of different management scenarios, including investigating the uncertainties resulting from the stock assessment process. It also allows for the performance of different assessment models to be evaluated. For both situations it is valuable to use an age-length structured model as the operating model. The operating model should be detailed enough to provide the data required by a range of different assessment models; by using an age-length structured model either age- or length-based assessment models could be used. Further, the use of a biologically detailed operating model, which is in many respects structurally different from the simpler assessment model, provides a more realistic scenario than using the same class of model for both parts of the cycle.

Length-based process information (e.g. fecundity as a function of fish length/weight, length-dependent mortality of larvae...) will be implemented in existing Gadget models during UNCOVER.

## **6.2 Changes in exploitation pattern and pressure**

### **6.2.1 YPR estimates for northeast Arctic cod**

Age-length structured models can also be used to study the effect of size-selective fishery on a population. An example of such a study is the work by Kvamme and Bogstad (2007). They compared traditional age-based yield-per-recruit (YPR) estimates for northeast Arctic cod with alternative, though comparable, YPR estimates calculated using an age-length structured model. The model *Fleksibest* (Frøysa *et al.*, 2002), which has now been incorporated in Gadget, was used as the age-length structured model in this study.

In the age-length structured model, growth, fishing mortality and natural mortality depend only on length, not on age. Such a model considers possible changes in size-at-age caused by

e.g. a length-selective fishery, and thus, by comparing the different YPR estimates, the importance of considering the stock's length structure are assessed. The results showed that length- and weight-at-age in stock and catches were affected by both exploitation pattern and pressure. Such changes are not considered in traditional YPR estimates, for which weight-at-age is fixed and strictly speaking only representative for the current fishery. As a result, the traditional age-based YPR estimates were somewhat higher than the age-length based estimates for exploiting smaller fish than at present, and the other way round for exploitation of larger fish.

Both models indicated a gain in YPR for only reducing exploitation pressure (age-structured model: 13%, age-length structured model: 20%) or both reducing exploitation pressure and postponing exploitation (age-structured model: 23–31%, age-length structured model: 33–48%) as compared to the current fishery on this stock.

The study could be extended to consider the effect of including length-structure on MSY estimates. One would then need to include a stock-recruitment relationship as well as possible density-dependent effects.

### **6.2.2 Maximum landings size for Northeast Atlantic spurdog**

The stock of Northeast Atlantic spurdog is considered to be depleted with all experimental assessments indicating that the stock is at a historical low. In addition to the usual management measures such as TACs, WGEF has also considered other regulatory methods that may allow the stock recover.

Demographic studies on elasmobranchs have shown low fishing mortality on mature females is beneficial to population growth rates (Cortés, 1999; Simpfendorfer, 1999). Hence, measures that afford protection to mature females may be an important element of a management plan for the species. As with many other elasmobranch species, female spurdog attain a larger size than males, and larger females are more fecund (See section 4.2).

The length-structured population model which was used in the catch-at-size analysis described above (Section 4.2) can also be used as a simulation tool with fixed input parameters. WGEF has conducted some exploratory simulations were conducted to investigate the effects of altering exploitation pattern and rate on stock status and in particular the effect of enforcing a maximum landing size (ICES, 2006b and 2006c).

Length frequency data from commercial catches (UK market sampling) and research vessel surveys around the coast of Britain indicate that at lengths of up to about 65 cm, the sex ratio of spurdog is approximately 1: 1, with males predominant at lengths of 70–80 cm, and females predominant at lengths of >85 cm. The population was initially assumed to be in equilibrium with fishing mortality at levels similar to those derived from previous exploratory assessments. Simulations were carried out with a range of maximum landings sizes from 70–90 cm to compare recovery rates of biomass, recruitment and landings. All simulations assumed a 100% survival of discards and also that fishing mortality (effort) on the large individuals was not re-allocated to the smaller length-classes. It is not known to what extent these assumptions are true and therefore the effects need to be further investigated. Additional sensitivity analysis could include the effect of incorporating stochasticity into recruitment and exploring different exploitation strategies.

## **6.3 Using age-length structured models to predict the length structure in the catch under different management scenarios**

The Sofala Bank shrimp fishery in Mozambique is in part regulated by means of a closed season at the end and beginning of each year (Palha de Sousa *et al.*, 2006). The value of the catch is dependant on the size of shrimp caught, with large individuals fetching a higher price,



and small individuals being difficult to sell. Costs in the industry have recently increased as a result of higher fuel prices. Other management regimes which increase the mean size at capture are therefore being considered - such regimes also improve protection for the stock by allowing the shrimp to reach larger size before being caught, and thus improving the breeding chances of the shrimp. This fishery mainly targets two species, each with different sizes and recruitment times. Both species have short lifespans (relatively few individuals survive for more than one year after recruiting to the fishery), and age-based data are not collected. As a result age-structured models are not well suited to this fishery. A Gadget age-length structured model (two species, each split by male and female) has been used to conduct simulation experiments on the likely effects of several different short mid-season closures on the catch distribution in the second half of the season. In future this model could be used to evaluate the possible effects of other management scenarios before their implementation.

The fishery is characterized by highly variable catch rates and size distributions over the course of a year. The start of the fishing season is generally characterized by high catch rates, with some large individuals caught. Catch rates in the fishery drop during the middle of the season, and begin to recover somewhat towards the end of the season, when new recruits are coming into the fishery. The current high price of fuel, combined with the low catch rates, is making the middle part of the season much less profitable than in previous years. The suggestion has therefore arisen that a mid-season closure could reduce costs in the industry, while maintaining the overall catch and possibly improving the size distribution and thus the profitability of the fishery.

An age-length structured Gadget model was developed, and optimized to fit the historical data. Simulation experiments were then undertaken in which the fishing pattern in the last year of the historical model was altered to that which would have been expected if different closed seasons had been in place. Various possible mid-season closures were compared with the model results with no mid season closure. The resulting predicted catch rates and catch length distributions for the different scenarios were then examined. The results of the simulations indicated that a mid-season closure would likely result in significantly improved catch rates and length distribution in the second half of the fishing season.

Work is currently in progress to implement Vessel Monitoring Systems (VMS) on all industrial fishing boats in the Sofala Bank shrimp fishery. This would allow for the possibility of more precise targeting of closures, with particular areas closed at particular times to protect the smaller shrimp. The effects of such possible closures could be simulated using the same model that was used in the experiments described above, helping to identify the management regime that would make the best use of the introduction of VMS.

## **7 Conclusions and Recommendations**

---

The work described in the three SGASAM reports shows that there is considerable interest in age/length and length-structured models. Single-species applications to a wide range of stocks with quite different biology and availability of data were presented, as well as multispecies and mixed fisheries applications. The methods being used include traditional size-transition matrix approaches, but also Lagrangian ensemble approaches which lump together individuals sharing similar life-histories (growth parameters) and track the collection of 'super-individuals' through time.

Models are being developed for use in the formal stock assessment process but also for wider research purposes. An increasing number of (age-) length based assessments have been presented to ICES assessment WGs, though the use of these models as the primary assessment method is still infrequent within the ICES region when compared to other parts of the world (e.g. US Pacific coast, Australia). Age-length structured models have also been shown to be

particularly useful for exploring potential management measures and as data generators for comparing alternative stock assessment methods.

The present report was written by correspondence because the expected number of participants at the meeting was quite low, and this seems to indicate that SGASAM should not be continued as a separate study group, at least for the time being. However, the considerable amount of ongoing work which has been presented to SGASAM indicates that there should be a 'home' within one of the methods-oriented WGs or SGs in ICES for work on these issues. SGASAM thus recommends that the future of work on age/length and length structured models within ICES be discussed e.g. at the 2007 WGMG (Methods) meeting. Also, a theme session on such models could be held at the 2008 ICES ASC.

## 8 References and Working Documents

---

### 8.1 References

- Begley, J., and Howell, D. 2004. An overview of Gadget, the Globally applicable area-Disaggregated General Ecosystem Toolbox. ICES C. M. 2004/FF:13.
- Boukal, D. S., de Roos, A. M., and Persson, L. 2006. How does stochasticity affect evolutionary regime shifts in age and size at maturation? ICES CM 2006/H:05.
- Breen, P. A., Kim, S. W., Starr, P. J., and Bentley, N. 2002. Assessment of the red rock lobsters (*Jasus edwardsii*) in area CRA 3 in 2001. New Zealand fisheries assessment report 2002/27.
- Breen, P. A., Kim S. W., and Andrew, N. L. 2003. A length-based Bayesian stock assessment model for the New Zealand abalone *Haliotis iris*. Marine and Freshwater Research, 54(5): 619–634.
- Breen, P. A., and Kim, S. W. 2004. The 2004 stock assessment of paua (*Haliotis iris*) in PAU 5A. New Zealand Fisheries Assessment Report 2004/40.
- Bull, B., Francis, R. I. C. C., Dunn, A., McKenzie, A., Gilbert, D. J., Smith, M. H. 2005. CASAL (C++ algorithmic stock assessment laboratory): CASAL user manual v2.07–2005/08/21. NIWA Technical Report 127. 272 p.
- Cortés, E. 1999. A stochastic stage-based population model of the sandbar shark in the Western North Atlantic. *In: Life in the slow lane: Ecology and conservation of long-lived marine animals* Ed by J. A. Musick. American Fisheries Society Symposium, 22: 115–136.
- de Pontual H., Bertignac, M., Battaglia, A., Bavouzet, G., Moguedet, P., and Groison, A. L. 2003. A pilot tagging experiment on European hake (*Merluccius merluccius*): methodology and preliminary results. ICES J. Mar. Sci 60(6): 1318–1327.
- de Pontual, H., Groison, A. L., Piñeiro, C., and Bertignac, M. 2006. Evidence of underestimation of European hake growth in the Bay of Biscay, and its relationship with bias in the agreed method of age-estimation. ICES J. of Marine Science, 63, 1674–1681.
- de Valpine, P. 2004. Monte-Carlo state space likelihoods by weighted posterior kernel density estimation. Journal of the American Statistical Association 99(99): 523–536.
- de Valpine, P., and Hastings, A. 2002. Fitting population models incorporating process noise and observation error. Ecological Monographs 72(1): 57–76.
- Dobby, H. 2003. Investigation a size-transition matrix approach to the assessment of *Nephrops*. Working Document for the Working Group on *Nephrops* Stocks, March 2003.

- Dobby, H. 2004. More thought on a length-based approach to the assessment of Firth of Forth *Nephrops*: incorporation of auxiliary data. Working Document for the Working Group on *Nephrops* Stocks, 2004.
- Fournier, D., and Archibald, C. P. 1982. A general theory for analysing catch at age data. *Canadian Journal of Fisheries and Aquatic Sciences* 39: 1195–1207.
- Fournier, D. A., Hampton, J., and Sibert, J. R. 1998. MULTIFAN-CL: a length-based, age-structured model for fisheries stock assessment, with application to South Pacific albacore, *Thunnus alalunga*. *Can. J. Fish. Aquat. Sci.* 55, 2105–2116.
- Frøysa, K. G., Bogstad, B., and Skagen, D. W. 2002. Fleksibest - an age-length structured fish stock assessment model. *Fisheries Research*, 55: 87–101.
- Gauld, J. 1979. Reproduction and fecundity of the Scottish-Norwegian stock of Spurdog, *Squalus acanthias* (L). International Council for the Exploration of the Sea CM, H: 54, Copenhagen, Denmark.
- Hannesson, S., Jakobsdottir, A., Begley, J., Taylor, L., and Stefansson, G. 2004. On the use of tagging data in statistical multispecies multi-area models of marine populations. ICES C. M. 2004/FF:30.
- Heessen, H. J. L. (ed). 2003. Development of elasmobranch assessments, DELASS. Final Report of DG Fish Study Contract 99/055, 603p.
- ICES. 2002. Report of the Study Group on Elasmobranch Fishes. ICES CM 2002/G:08.
- ICES. 2003a. Report of the Study Group on Age-length structured assessment models. ICES CM 2003/D:07.
- ICES. 2003b. Report of the Working Group on Elasmobranch Fishes. ICES CM 2003/G:09.
- ICES. 2004. Report of the Study Group on Growth, Maturity and Condition in Stock Projections. ICES CM 2004/D:02.
- ICES. 2005. Report of the Study Group on Age-length Structured Assessment Models. ICES CM 2005/D:01.
- ICES. 2006a. Report of the Workshop on *Nephrops* Stocks (WKNEPH), 24–27 January 2006, ICES Headquarters. ICES CM 2006/ACFM:12. 85 pp.
- ICES. 2006b. Report of the Working Group on Elasmobranch Fishes (WGEF), 14–21 June 2005, Lisbon, Portugal. ICES CM 2006/ACFM:03. 232 pp.
- ICES. 2006c. Report of the Working Group on Elasmobranch Fishes (WGEF), 14–21 June 2006, ICES Headquarters. ICES CM 2006/ACFM:31. 291 pp.
- Kacher, M., and Amara, R. 2005. Distribution and growth of 0-group European hake in the Bay of Biscay and Celtic Sea: a spatial and inter-annual analyses. *Fisheries Research* 71(3): 373–378.
- Kvamme, C., and Bogstad, B. 2007. The effect of including length structure in yield-per-recruit estimates for Northeast Arctic cod. *ICES Journal of Marine Science* 64:xxx-xxx.
- Lucio, P., Murúa, H., and Santurtún, M. 2000. Growth and reproduction of hake (*Merluccius merluccius*) in the Bay of Biscay during the period 1996–1997. *Ozeanografika*, 3: 325–354.
- Maunder, M. N., and Watters, G. M. 2003. A-SCALA: An age-structured statistical catch-at-length analysis for assessing tuna stocks in the eastern Pacific Ocean. *IATTC Bul.* 22: 433–582.
- Methot, R. D., and I. G. Taylor. Technical Description of the Stock Synthesis II Assessment Program. Program and documentation available from: [Richard.Methot@noaa.gov](mailto:Richard.Methot@noaa.gov).

- Palha de Sousa, L., Brito, A. Abdula, S. Penn J., and D. Howell, 2006. The industrial shallow water shrimp fishery at Sofala Bank in Mozambique in 2005. Instituto de Investigação Pesqueira (IIP), Mozambique (unpublished report).
- Pope, J. G. 1972. An investigation of the accuracy of virtual population analysis for the calculation of fishing mortality from catch at age data. International Commission for the Northwest Atlantic Fisheries Research Bulletin 9: 65–74.
- Poulard, J. C. 2001. Distribution of hake (*Merluccius merluccius*, Linnaeus, 1758) in the Bay of Biscay and the Celtic sea from analysis of French commercial data. Fisheries Research 50: 173–187.
- Punt, A. E., Kennedy, R. B., Frusher, S. D. 1997. Estimating the size-transition matrix for Tasmanian rock lobster, *Jasus edwardsii*, resources. Mar. Freshwat. Res. 48, 981–992.
- Punt, A. E., and Walker, T. I. 1998. Stock assessment and risk analysis for the school shark (*Galeorhinus galeus*) off southern Australia. Marine and Freshwater Research 48, 719–31.
- Punt, A. E., Pribac, F., Walker T. I., and B. L. Taylor. 2001. Population modelling and harvest strategy evaluation for school and gummy shark, Report of FRDC 99/102. CSIRO Marine Research, Hobart.
- Shepherd, J. G. 1999. Extended survivors analysis: an improved method for the analysis of catch-at-age data and abundance indices. ICES J. Mar. Sci 56(5): 584–591.
- Simpfendorfer, C. A. 1999. Demographic analysis of the dusky shark fishery in Southwestern Australia. *In: Life in the slow lane: Ecology and conservation of long-lived marine animals* (J. A. Musick, ed.). American Fisheries Society Symposium, 22: 149–160.
- Starr, P. J., Bentley, N., Breen, P. A., Kim, S. W. 2003. Assessment of red rock lobsters (*Jasus edwardsii*) in CRA 1 and CRA 2 in 2002. New Zealand Fisheries Assessment Report 2003/41. 119 pp.
- Tjelmeland, S., and Lindstrøm, U. 2005. An ecosystem element added to the assessment of Norwegian spring-spawning herring: implementing predation by minke whales. ICES Journal of Marine Science 62: 285–294.
- Virtala, M., Kuikka, S., and Arjas, E. 1998. Stochastic virtual population analysis. ICES Journal of Marine Science 55(6): 892–904.

## 8.2 Working Documents

- WD 1. Skagen, D. W. Estimating population abundance and mortalities from length structured catch and survey data. Approaches, the program **Ics** and case studies with North Sea sprat and Northern hake.
- WD 2. Andonegi, E., Quincoces, I., Garcia, D., Arregi, I., and U. Ganzedo. First implementation of a GADGET model for the analysis of the Bay of Biscay Hake population.
- WD 3. Drouineau, H., Mahevas, S., Bertignac, M., and Fertin, A. Assessing the impact of discretisation assumption in a growth matrix model.

## Annex 1: List of participants

NAME	ADDRESS	TEL/FAX	E-MAIL
Eider Andonegi	AZTI Txatxarremendi ugarte z/g 48395 Sukarrieta (Bizkaia) Spain		<a href="mailto:eandonegi@suk.azti.es">eandonegi@suk.azti.es</a>
Bjarte Bogstad	Institute of Marine Research P. O. Box 1870 Nordnes N-5817 Bergen Norway	+47 55 23 86 81 (Tel) +47 55 23 86 87 (Fax)	<a href="mailto:bjarte.bogstad@imr.no">bjarte.bogstad@imr.no</a>
Helen Dobby (Chair)	Fisheries Research Services Marine Laboratory P. O. Box 101 375 Victoria Road Aberdeen AB11 9DB United Kingdom	+44 1224 876544 (Tel) +44 1224 295511 (Fax)	<a href="mailto:h.dobby@marlab.ac.uk">h.dobby@marlab.ac.uk</a>
Hilaire Drouineau	IFREMER rue de l'Ile d'Yeu B. P. 21105 F-44311 Nantes Cédex 03 France	+33 2 40 37 43 06 (Tel) +33 2 40 37 40 75 (Fax)	<a href="mailto:Hilaire.Drouineau@ifremer.fr">Hilaire.Drouineau@ifremer.fr</a>
Dorleta Garcia	AZTI Txatxarremendi ugarte z/g 48395 Sukarrieta (Bizkaia) Spain	+34 946 02 9400 (Tel) +34 946 870 006 (Fax)	<a href="mailto:dgarcia@suk.azti.es">dgarcia@suk.azti.es</a>
Daniel Howell	Institute of Marine Research P. O. Box 1870 Nordnes N-5817 Bergen Norway	+47 55 23 86 79 (Tel) +47 55 23 86 87 (Fax)	danielh@imr.no
Richard Methot	NOAA/NMFS Northwest Fisheries Science Center 2725 Montlake Boulevard East Seattle, WA 98112 USA		richard.methot@noaa.gov
Inaki Quincoces	AZTI Txatxarremendi ugarte z/g 48395 Sukarrieta (Bizkaia) Spain		iquincoces@suk.azti.es
Dankert W. Skagen	Institute of Marine Research P. O. Box 1870 Nordnes N-5817 Bergen Norway	+47 55 23 84 19 (Tel) +47 55 23 86 87 (Fax)	dankert@imr.no

**Annex 2: Working Document 1**

---

Working Document  
SGASAM 2006

**Estimating population abundance and mortalities from length structured catch and survey data.****Approaches, the program lcs and case studies with North Sea sprat and Northern hake**

*Dankert W. Skagen*

Institute of Marine Research

Bergen, Norway

November 2006

**Introduction**

Many features than enter a fish stock assessment, like gear selectivity, area distribution and maturation are probably more linked to size than to chronological age. When growth is highly variable, relating such features to length rather than age may relieve some problems in the interpretation of the data. On the other hand, when a year class structure can be applied, the one-to-one correspondence between age and time simplifies the calculation of rates, in particular mortalities. Hence, taking length dependencies into account is probably best done when the stock and fisheries data are disaggregated both on length and age.

Age data are not always available, however, either because they are too expensive to get, ageing is technically problematic, or because the recruitment takes place throughout most of the year, making the year class structure unclear. Still, as long as there are samples taken from the fishery or at surveys, length data are in practice always available.

The link between abundance at length and mortality is not unique. Hence, with only length disaggregated data at hand, there is less information in the data, which limits the opportunity to draw inferences from the data. There is still a scope for methods that rely only on length disaggregated data, but the limitations of such methods must be taken into account when designing a management regime for that situation.

In order to estimate measures of exploitation, e.g. mortalities, changes in population abundance have to be related to a time scale. With only length data, there are several ways to approach the problem of relating lengths to time.

1. Slicing: Based on growth rate assumptions, the lengths are converted to age by assuming that each age corresponds to a length interval. Ordinary age structured methods can then be applied. The boundaries between the length intervals can be sharp, or one may assume that each age has a distribution of lengths.
2. Equilibrium methods: One may assume that the length distribution at a given time represents the growth and decline of a cohort of fish born at one instant (or equivalently – that the recruitment is uniform and the population is at equilibrium). A VPA can then be constructed on that cohort (Jones' Length Cohort Analysis – Jones 1984). This gives a fair idea of the level of mortality relative to growth rate as well as of yield-per-recruit, which can be useful for e.g. evaluation of technical regulations. However, since these are equilibrium methods, year class structure or the recruitment variability can not be evaluated. The method is commonly used in cases where the recruitment can be assumed to be relatively stable, or when the species is very short lived.
3. Within the framework of 'statistical models' i.e. methods where a self-contained population model is fitted to the data, the population may be constructed by age, and supplemented with a length structure. This is done by projecting the year classes forwards in time and model the size of the fish as part of the projection, along with abundance, mortality and other characteristics of the time course. The growth will normally be treated as stochastic in order to reproduce the smoothness of the length distributions.

Within the third alternative, two basic approaches can be outlined.

1. To transform vector of lengths in one time-step into a new vector at next time-step as a stochastic process, typically by applying a transition matrix (a 'state space' approach).
2. To project forwards trajectories representing 'super-individuals', each with its own growth characteristics and abundance. The ensemble of such 'super-individuals' constitutes the population (a 'Lagrangian' approach).

The former is used in several age-length structured models, like Bormicon/Gadget/Fleksibest (Frøysa *et al.*, 2002). The latter is less common but some examples exist (Methot). Both have advantages and disadvantages. In practice, the state space approach becomes very unwieldy unless the Markov property can be assumed, i.e. the growth in the next time-step depends on the present size, but not on the growth in previous time-steps. The 'Lagrangian' approach has the advantage that it is a more direct way of expressing the variability between individuals with respect to growth, and of preserving the age structure in the model. The effect of e.g. exploitation on the size distributions (Rosa Lee's phenomenon – Lee 1912) can be modelled directly. Likewise, prolonged recruitment seasons can easily be implemented. The main disadvantage is that the number of trajectories needed easily becomes large. With the large memory capacity and high speed of modern computers, this is less of a problem than previously.

The present program called lcs uses the Lagrangian approach. This is partly to allow future inclusion of non-Markovian behaviour of the growth, but also to get some more experience with this way of constructing a population model.

The program is not fully developed for routine use. The purpose at the present stage is to study the approach from a methodological perspective rather than providing a full-fledged routine assessment tool. The core elements of the program are a population model, a model for generating model catch and survey observations, an objective function and a minimization routine to find the best model fit. However, the user interface is primitive and output is restricted to a few tables. Likewise, only a simple, logistic catchability model and a similar model for fishing mortality at length are implemented so far.

## Outline of the method

### Program structure

The program has a population model, which calculates the whole population, as an ensemble of ‘super-individuals’, in numbers by length class and time-step. From this population, observables like catches and survey indices at length and time are calculated, using the catch equation and a model with catchabilities as parameters, respectively. These ‘observables’ are compared with the actual observations in an objective function. A minimization routine searches over the space of parameters and calls the objective function for each parameter set, to find the parameter set that gives the best value of the objective function, i.e. the best model fit. This is regarded as the estimate of the population according to the data. The lay-out is shown in Figure 1.

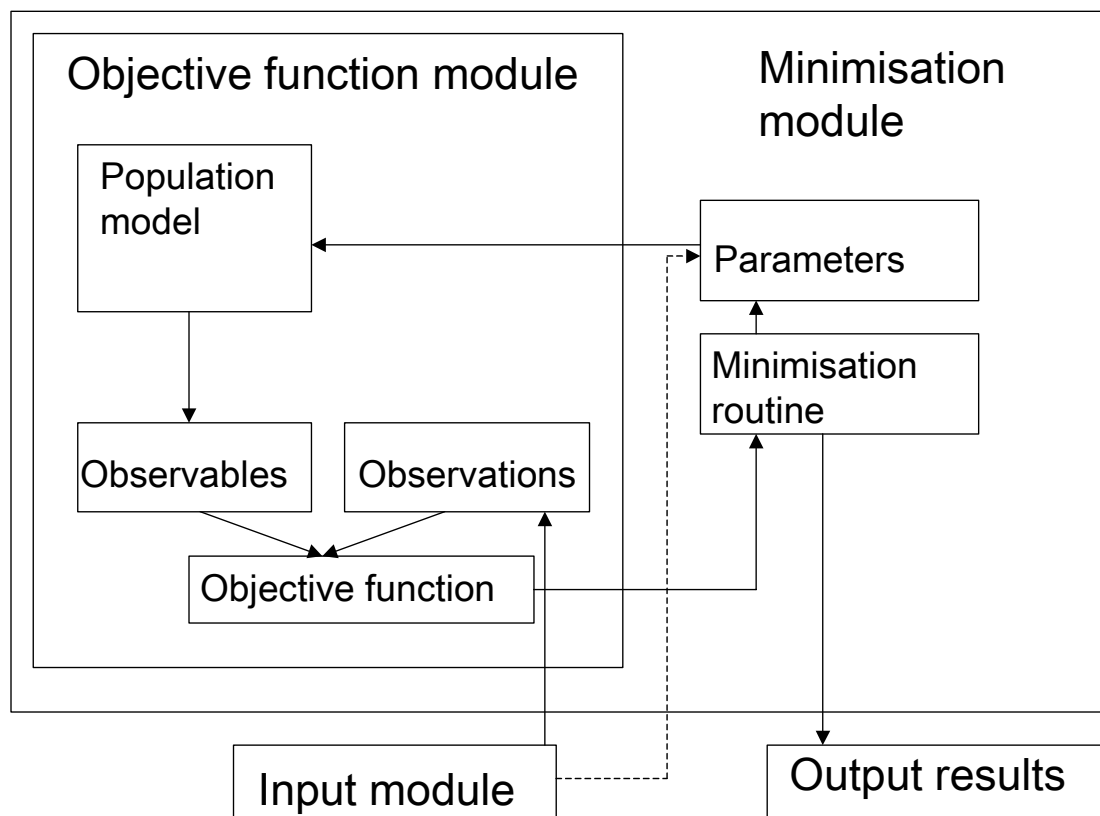


Figure 1: Layout of main elements.

### Population model

A parametric model population is defined uniquely by the model structure and the parameters. By the ‘Lagrangian’ approach, the stock is represented as an ensemble of trajectories. Each trajectory is characterized by an initial time and length, its growth parameters, and the number of fish that it represents, and it is projected forwards in time.

Growth is modelled according to the von Bertalanffy equation:



The growth in a time interval  $\Delta t$  is:

$$L(t+\Delta t) = (L_{inf} - L(t)) * (1 - \exp(-k\Delta t)),$$

where  $L$  is length,  $t$  is time and  $L_{inf}$  and  $k$  are parameters.

Equivalently, the time it takes to grow from  $L$  to  $L+\Delta L$  is

$$\Delta t = -(1/k) * \log[(L_{inf} - (L + \Delta L)) / (L_{inf} - L)]$$

Each trajectory has a randomly drawn  $L_{inf}$  that is kept fixed over time, and a randomly drawn  $k$ -value that can be modified over time.

When projecting the stock forwards in time, the abundance in numbers  $N$  represented by a trajectory is reduced by mortality as:

$$N(t + \Delta t) = N(t) * \exp\{-F(t, L) + M(t, L) * \Delta t\}$$

where  $F$  and  $M$  are fishing mortality and natural mortality respectively.

Mortalities are modelled as separable, i.e. the product of a year factor  $F_y(y)$  and a length selection factor  $S(L)$ . The length factor of the fishing mortality is at present assumed to be time-independent, and is expressed as a logistic function:

$$S(L) = 1 / (1 + \exp(-b * (L - L50)))$$

with parameters  $L50$  and  $b$ .

However, the program is designed to allow for more elaborate models without having to re-write other parts of the code.

In the program, mortalities are allocated to discrete length classes, and are calculated according to the length in the middle of each length class.

It was found to be practical to project the stock forwards in discrete time-steps, and to keep the length as a continuous variable. Internally, the time-steps are quarters of the year. For each time-step, the length and the abundance at the start and at the end of the time-step are calculated for each trajectory. This design allows for feedback between e.g. current stock abundance and growth rate, because the total abundance is calculated at each time-step and is available for deciding e.g. the growth rate in the next time-step. However, mortalities (and catchabilities) at length as parameters are defined for discrete length classes. The mortality applied is the mortality defined for the length class where the current length for the trajectory belongs. If a trajectory passes into a new length class during a time-step, successive length class mortalities are applied according to the time spent in each length class.

The lowest length class represents fish in that length class and smaller, and the upper length class represents fish in that length class and larger. Since the length is a continuous variable, problems with transfer into and out of such pooled length classes are avoided, the only assumption is that mortalities and catchabilities are homogenous within each length class.

Annual recruitments in numbers are parameters. Each year, a set of new trajectories are initialised. Each of these trajectories has a randomly drawn  $L_{inf}$ ,  $k$ -value, time of entry and length at entry. The initial number of fish is evenly distributed on these new trajectories. Hence, the probability structure with respect to initial abundance at length and time is represented by how the initial lengths and time are distributed among the trajectories. Length at entry and time at entry (relative to 1 January) are assumed to be bivariate normally

distributed, with truncation for each. This construction allows for recruitment across the new year, and for a gradual entrance into the stock, which may be necessary to get a realistic representation of the length distribution of newly recruited fish.

Implicitly, this population model has an age-length structure, because each trajectory can be referred to a certain entry time (i.e. year class), but the ages are not supposed to be represented in the observations data.

The population abundance at length (i.e. by length class) in each time-step is obtained by summing trajectory abundance numbers across all trajectories that are in the length class in question in that time-step. Likewise, catches at length can be summed across trajectories. This is done at the stage where each trajectory is projected through the time-step, to take into account that growth during the time-step implies that the catches can be allocated to a succession of length classes.

### **Deriving observables from the model**

Fitting the model to data are done by deriving 'observables' from the model, and compare them with the corresponding observed data.

#### Survey indices at length

Model survey indices  $I_{mod}$  at length are derived from the population at length at the appropriate time-steps through a catchability model:

$$I_{mod}(L,t) = q(N_{mod}(L,t),L,t)$$

where  $I_{mod}(L,t)$  is the model derived survey index observable,  $N_{mod}(L,t)$  is the stock abundance at length in the quarter of the year where the survey takes place, and  $q$  is a function of  $N$ , length and time.

At present, only the simple relation

$$q(N_{mod}(L,t),L,t) = q(L)*N_{mod}(L,t),$$

is implemented., where the  $q(L)$  is a logistic function of  $L$ ,

#### Catches at length

Model catch data at length are derived with the estimated fishing mortalities and stock numbers by length.

#### Aggregate data:

Annual catches in biomass can be included in the objective function and compared with model values obtained as the SOP of catch numbers at length and catch weights at lengths. The catch weights at length are input.

Aggregate survey biomass and survey spawning biomasses are included the same way.

Acoustic survey  $S_a$  values are derived by the model as

$$I_{mod} = \sum N_{mod}(L,t) * s, \text{ summed over a specified length range}$$

where

$$s = 4.0 * \pi * 10.0^{(\text{sigma}/10.0)}$$

and

$$\text{sigma} = Ts1 * \log_{10}(L) - Ts2$$

where the target strength  $T_s = T_s I * \log_{10}(L) - T_s 2$

### The objective function

The fit of the model to the data are expressed as an objective function, which is the sum of partial objective functions for each source of data.

The fit of the model to the survey data  $I_{obs}$  is expressed by the objective function

$$\Phi_I(\theta) = \sum_{all\ data\ entries} w(L) * (\log(I_{mod}(L; \theta)) - \log(I_{obs}(L)))^2$$

which is a function of the vector  $\theta$  of all the parameters. The weighting  $w(L)$  in principle represents the inverse variance of the measurement error at length, but is taken as input here.

The fit of the model to catch numbers at length  $C(L)$  is expressed by the partial objective function:

$$\Phi_C(\theta) = \sum_{all\ data\ entries} w(L) * (\log(C_{mod}(L; \theta)) - \log(C_{obs}(L)))^2$$

An additional term in the objective function, which is a penalty on year-to-year fluctuations in fishing mortality, can be included. This option is discussed further below.

Furthermore, the observed and modelled survey values at length can be substituted by smoothed values, obtained as  $I_{smooth}(L, y) = \sum_{i=y-1, y+1; j=L-1, L+1} I(i, j)$ . This was done to explore the effect removing the most high-frequency random noise in the data.

### Overview of parameters and indices

Indexing:

- First and last year
- First and last length class
- Length class interval
- Number of trajectories per year class

Parameters:

- Initial numbers by length class in the first year
- Annual recruitment
- Annual fishing mortality
- Natural mortalities by length, fixed over time
- Parameters in Logistic selection at length function
- Linf: Mean, SD and truncation
- k-value: Mean, SD and truncation
- Entry time (fraction of year): Mean, SD and truncation
- Entry length: Mean, SD and truncation
- Correlation between entry time and entry length
- Parameters in Logistic catchability at length function

### Deciding on parameters to estimate

When applying the parametric population model in the stock assessment context, the approach is to estimate the parameters of interest (i.e. abundance and exploitation rates) by fitting the model population with such parameters to observed data. This allows liberty in the construction of the population model, and it allows for using the data that are at hand. It has to be recognized, however, that the amount of parameters that can be estimated is limited by the information inherent in the available data. With shortage of data, quite strong assumptions may have to be made to get a unique estimate of the still free parameters. For practical

purposes, not the least in a case where one may have to rely on survey data only, some way to allow the user to specify assumptions becomes very useful. Therefore, the program has the facility to allow the user to specify which parameters are to be actually estimated, and which parameters just are fixed at the given input values.

### **Optimisation**

The final estimates of the population and the mortalities are taken to be those that are derived with the set of parameters that minimizes the objective function. To find the minimum, a simple searching routine is used. This routine changes each parameter in succession one step up and one step down, and keeps the best value. The step sizes are reduced successively, and at each step size the search process is repeated until the objective function does not improve any more. The sequence of the parameters is random, and changed for each new round of search. The convergence criterion is that the objective function does not become smaller by changing any of the parameters by the smallest step.

Alternatively, quasi-Newton methods may be used, but such procedures have not been implemented yet. So far, the present procedure is preferred because it is simple and has proven to be very robust in other assessment programs like AMCI (Skagen, unpublished).

### **Using lcs as a data generator and cyclic estimations**

As for any statistical catch-at-age type model, lcs generates observables from an underlying self-contained population model. To estimate parameters, the model, represented by the observables, is fitted to actual observations. However, the generated observables by themselves are a set of artificial observations from a known model population, and can be used as an artificial data set for other purposes. Lcs has the facility to output such artificial data in the format that is used by lcs. It should not be a big job to convert such files to formats that are used as input to other assessment programs.

A further extension of the use of the program as a data generator is to make the program assess the stock that it generated itself. Hence, with an initial set of parameters, data are generated by the model. Noise is added to these data. The program is then used to estimate parameters by fitting to these data. The estimated parameters define a new population, from which data again are derived, and so forth. This procedure is referred to later on as cyclical iterative runs. To be internally consistent, one would require that the parameter estimates in this iterative procedure would remain close to the original set. Hence, this procedure will act as a quality check on the program and assumptions, in particular that the model gives a fair reproduction of the data.

## **Worked examples**

### **Artificial data**

Data sets with artificial data generated by the model were examined. They were generated with model parameters as summarized in Table 1.

**Table 1: Parameters for artificial data.**

Years: 1990 2003

Lengths: 10 to 30 cm, steps of 2 cm

Trajectories per year class: 100 (unless stated otherwise)

Recruitment by year: near periodic, as shown in Figure 3

Annual fishing mortality: Two alternatives, as shown in Figure 4

Natural mortality by length class:

10	0.50
12	0.40
14	0.30
16 and larger:	0.20

Logistic selection function in fishery:

a: 25

b: 0.07

Growth parameters

Mean Linf: 30

SD Linf: 3

Truncation Linf: 1 SD

Mean k: 0.5

SD k: 0.1

Truncation k: 1 SD

Mean entry time 0.4 /year (fraction of year)

SD entry time .2

Truncation entry time 1 SD

Mean entry length: 12

SD entry length 2

Trunc entry length 1 SD

Correlation entry time and entry length: 0.1

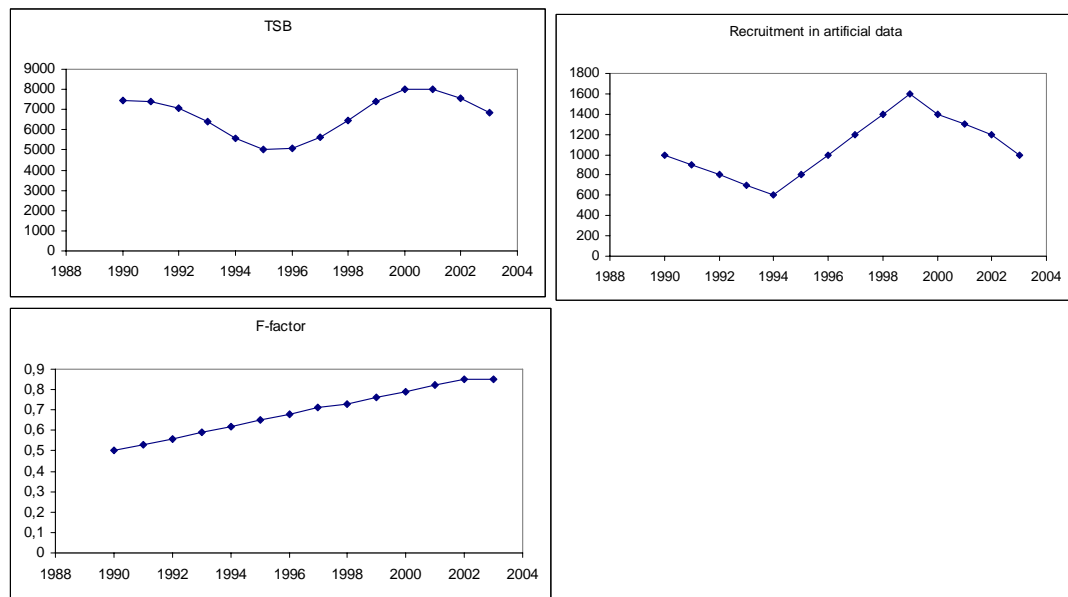
Logistic survey catchabilities at length

a: 15

b: 0.07

Level: 0.1

The time course of the recruitment and total biomass is shown in Figure 2



**Figure 2: Artificial data (Total biomass, annual recruitment and year factor for F. The year factor is the fishing mortality per year for fully recruited fish.**

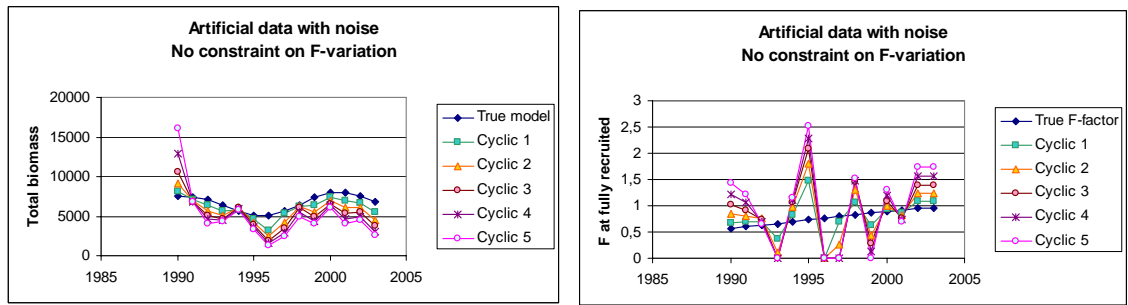
### Results and comments

The model was run with the artificial data. The parameters estimated were initial numbers at length, recruitments and annual F-factors. Likewise, the parameters for selection at length in the fishery were estimated. The growth parameters, including time and length at entry,  $k$ -values and  $L_{inf}$  were kept fixed at the correct values, as were the survey catchabilities.

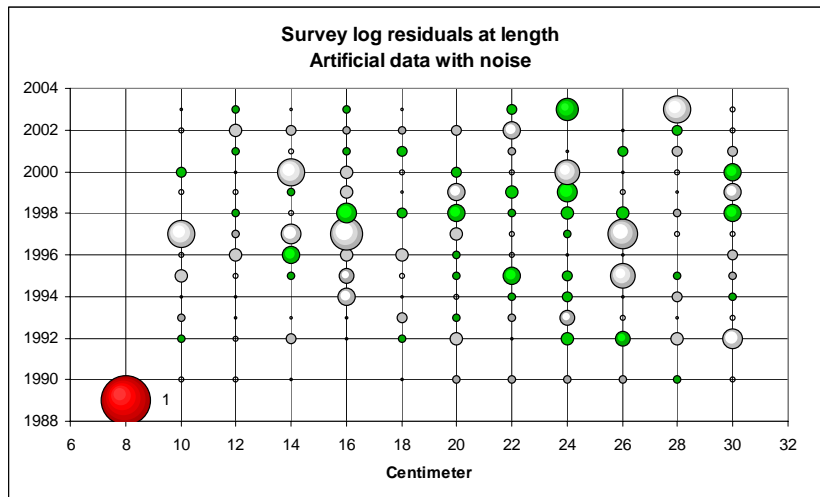
As a first test, new data were generated based on the model according to the parameters, with no noise. After 5 cyclic iterations, there were no deviations from the original and the fit was perfect ( $SSQ < 10^{-7}$ ).

Second, with the same model, new data were generated as above, but supplemented with noise as a random year multiplier (normally distributed with  $C.V = 0.2$ ) and a random noise multiplier (normally distributed with  $C. V. = 0.2$ ).

During cyclic iterations, the results deviated markedly and progressively. It is remarkable that the annual fishing mortality estimates went into wild oscillations, and the  $F$  in some years just became 0. The direct cause of this is not clear, in the noisy survey data, the year 1996 had a negative year effect, but in general, it probably just is a manifestation of the general problem that the model has too many opportunities to improve the fit to the data. A plot of the residuals in the first cyclic iteration is shown in Figure 4, but it is hard to infer any cause of the problem there. The option to constrain year-to-year variation in the annual fishing mortality was introduced because of such problems.



**Figure 3: Cyclic iterative model runs, with noisy artificial data. Left: Total biomass at the start of the year. Right: F year factor.**

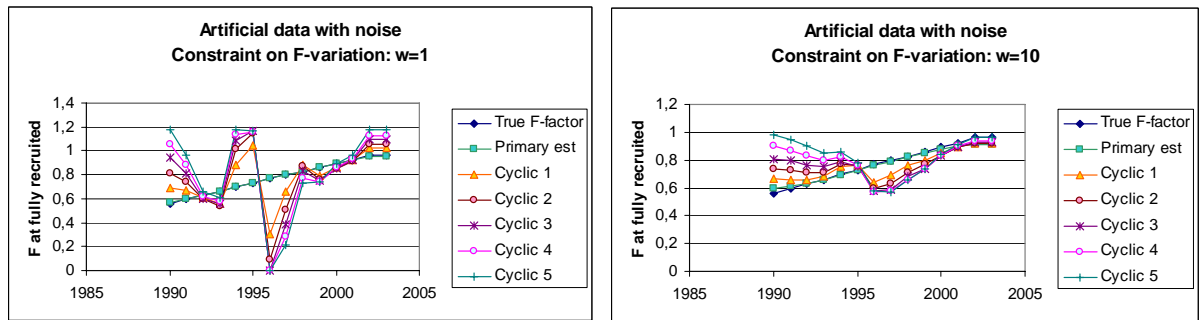


**Figure 4: Log residuals in the step in the cyclic iteration with noisy data where F in 1996 goes to 0. Green: Obs>model, White: Obs<model. Red: Indicates the scale (value = 1.0).**

The other remarkable finding is that both fishing mortality and abundance tend to deviate progressively, but in different directions in different years. This may indicate that the response of the fit to noise is not symmetrical. That may be expected since a log-normal likelihood function is used, but if that is the case, it happens even with noise that by itself is deliberately log-normal. A similar problem has been encountered in age-structured models as a possible contribution to retrospective bias, (see e.g. Skagen, 2001)

**Effect of constraints on year-to-year variation in F**

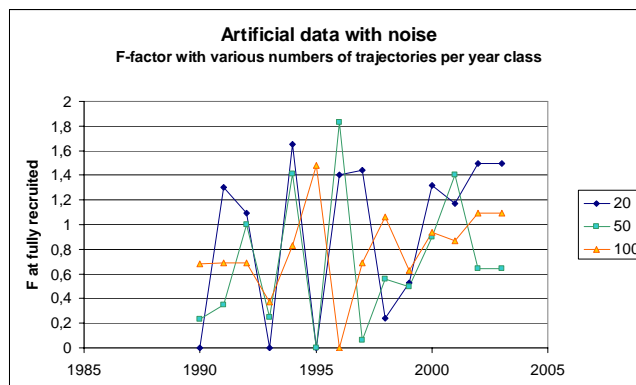
A term in the objective function penalising variation from year-to-year in the fishing mortality was introduced to avoid the wild fluctuations in F seen above. Figure 5 shows the outcome of this exercise with weak and strong weights on the penalty term. The inference from these figures is that such a penalty may reduce the fluctuations, but it does not guarantee that the trends in the results are correct.



**Figure 5: Effect of constraining the year-to-year variation in fishing mortality, with a weak and strong penalty term with weak and strong weighting as indicated.**

### The number of trajectories per year class

The impact of this number was explored briefly using the artificial data set with noise, with no penalty on F-variation. The results diverge wildly, mostly so with a low number of trajectories. This is probably related to the poor estimates of the model parameters in general, and the result here may not be generally applicable.

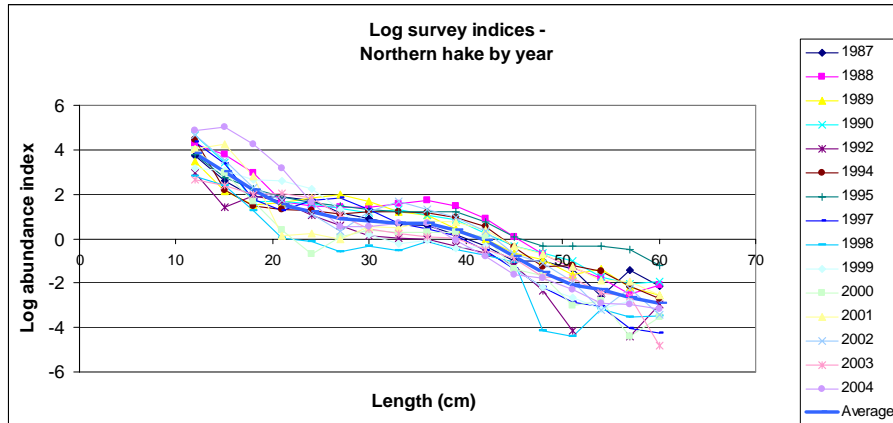


**Figure 6: Estimates of annual F with various numbers of trajectories per year class. Artificial data with noise.**

### Northern hake case study

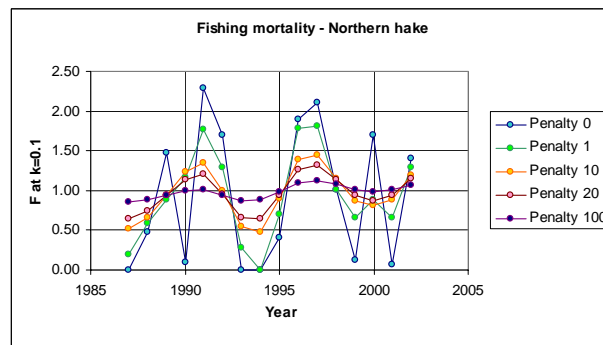
The data for Northern hake was a set of survey data from the French EVHOE survey, kindly provided by Verena Trenkel, IFREMER. This was survey indices by 3 cm length classes, covering the years 1987–2003 with some exceptions. Figure 7 shows the indices at length for each year. They seem fairly regular and consistent, but have a heap between 30 and 40 cm which may be difficult to explain with the current operating model.





**Figure 7: Survey index at length for Northern hake.**

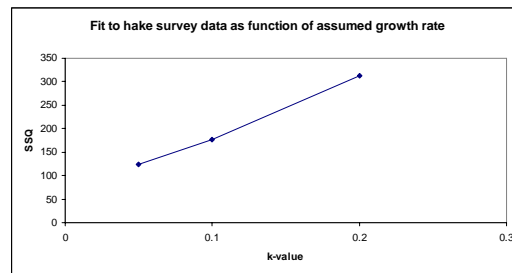
The data were analysed with lcs with various alternative growth rates and with various degrees of constraints on the year-to-year variation in  $F$ . Without any penalty, the annual fishing mortality became extremely variable. With some penalty, the mortalities stabilize, but with some fluctuations and a slight upward trend (Figure 8).



**Figure 8: Annual fishing mortality for Northern hake (data set 3) with various levels of constraint on year-to-year variation in  $F$ , assuming growth rate parameter  $k=0.1$ .**

A major problem with the assessment of this stock is uncertainty in the ageing. Hence, the growth rate is poorly known, and several alternatives are plausible.

The choice of growth rate is crucial for the estimated levels of mortality, as should be expected. It also matters for the variability of  $F$ , a low growth rate leads to larger variation in estimated  $F$ s. Attempting to estimate the mean  $k$  failed, as the searching routine found the trivial minimum at an extremely rapid growth. This made all fish move to the plus length in the first time-step, allowing for a perfect fit to each year class. Hence, exploratory runs were made with a range of fixed growth rates. The model fit was improved by assuming slow growth (Figure 10), which is no real guidance because slow growth (and correspondingly low mortality) probably makes it easier to fit to the noise in the data.

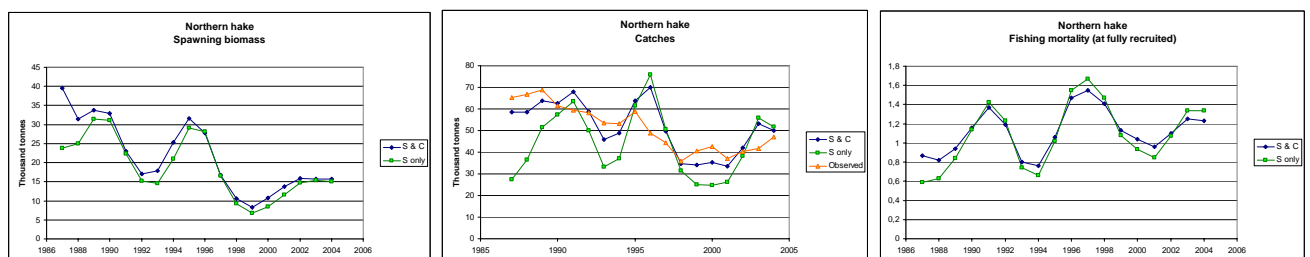


**Figure 9: Model fit (total sum of squares) to Northern hake data (data set 3) at various levels of growth rate parameter  $k$ .**

For a ‘final’ assessment, a  $k$ -value of 0.1 was used, together with a  $L_{inf} = 120$ . With that growth rate, hake should reach about 80 cm in 10 years. A penalty with weight 10 on the  $F$ -variation was applied in these calculations to obtain apparently meaningfully stable estimates of  $F$ . Entry time was fixed early in the year and entry length (mean and SD) estimated. Natural mortality was kept fixed at 0.2 per year. A flat catchability at length was assumed for the survey, and the selection at age in the fishery was kept fixed with  $L_{50}$  at 25 cm.

Data on total yearly catch was also available. An alternative run was made using these data in addition to the survey, with a weighting of 10 on the catch data. This made some difference in the early period, but less so in the recent period.

The main results of these assessments are shown in Figure 10.



**Figure 10: Northern hake. Main results of trial assessment, with and without including total catch in the assessment.**

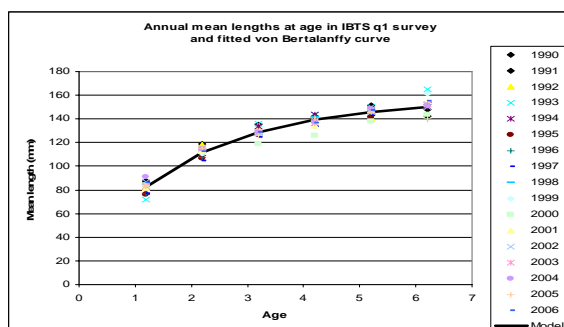
### Sprat case study

The data used were indices at length from the IBTS first quarter bottom trawl survey for 1990 to 2005. This survey takes place in January – February, which is the recruiting season for sprat in the North Sea. Hence, it is quite likely that the representation of the smallest sizes can vary from year-to-year, depending on how early the recruitment takes place. The survey is not directed towards sprat.

Age data are available from this survey. Although the ageing is problematic, this allows for estimating the growth parameters using length-at-age data. The reliability of these estimates is of course conditional on the reliability of the ageing.

In addition, total catch per year was available. Again, these data may be questionable, because in this industrial fishery, there is no incentive for sorting the catch by species and there has at least in some periods been incentives to misreport by species.

An estimate of the growth parameters was made using the mean length-at-age per year from the survey data (Figure 11). The result is shown in the figure below, and gave 156 mm for *Linf* and 0.49 for *k*. These values were used for a key run with lcs.



**Figure 11: Estimation of growth parameters for sprat.**

An initial run was set up fitting the model to all survey indices at length and to the total annual catches. The latter term was given a high weight so that effectively, the model was constrained by requiring that it should reproduce the reported catches. Initial numbers, recruitments and annual fishing mortalities were left as free parameters. Selection at age in the fishery was a logistic function with fixed parameters – L50 was set at 80 mm.

Mean *Linf* and *k* were fixed as described above, while the SDs of these parameters were estimated. Likewise, the time and length at entry, and their respective SDs were estimated. No correlation between time and length at entry was assumed. Parameters in a logistic function for survey catchability were estimated.

With these settings, it turned out that the end result was quite sensitive to the starting values for the optimisation. This was taken as a strong indication that the model was over-parameterized.

Ignoring the catches in the objective function stabilized the estimate, i.e. the results could be reproduced with different initial values for the search. The estimated catches were far above those reported, however, which seems somewhat unlikely because it may be more likely that sprat is over-reported.

On the other hand, without the catch data there is no information on absolute levels in the data. Hence, the catchability of the survey should be fixed, and the likely level may be guided by a comparison between modelled and reported catches. The discrepancy between reported and modelled catches varies considerably from year-to-year, however, indicating a conflict between survey information and reported catches.

**Limitations of this type of models**

**Confounding of recruitment, growth and mortality**

In a length based assessment, several parameters are confounded in the sense that various combinations of parameters lead to nearly the same model fit. The stock number in a time-length cell originates from previous recruitments (or initial numbers). Due to the stochasticity in growth and initial size, each recruitment is distributed on a number of such cells. The placement of each recruitment in cells at any time is determined by the growth rate, while the abundance in the cell (i.e. how much is left of the recruitment) is determined by the cumulated mortality over the time it takes to reach that cell. That time again depends on the growth rate.

The number in a time-length cell of survey data are therefore the resultant of recruitment, growth and mortality, as well as of catchability in the case of survey data.

On that background, the problem of over-parametrization can be expected to be more prominent with length structured models than with age-structured models. The signal about mortality is not a direct signal on  $Z$  as in age structured data, but on  $Z/k$ . It is unlikely that it shall be possible to estimate both growth rates and mortalities from a set of indices at length. In practice, the growth parameters – both  $Linf$  and  $k$ , have to be assumed.

#### **Lack of absolute abundance data in the case with only survey data**

The origin of this program was a request from the EU project FISBOAT to develop a length structured assessment tool that would use only survey data. Unless there are reliable catch data or some survey data can reliably be considered as absolute estimates of the stock, all information in a set of survey indices at length (and age for that sake) are relative measures, and the scaling of the population estimates to absolute values comes from the catch data. The survey indices are scaled according to the catchabilities. All recruitments and initial stock numbers can be scaled with a common multiplier without altering the model fit, by adjusting the catchabilities accordingly. In order to produce a unique solution, some scaling parameter needs to be fixed. In practice, this could be the catchability level for one of the surveys, so that stock numbers are scaled to the values of that survey index. If catch data are available, they normally will provide the necessary scaling, but bias in the catch data will of course carry over to the abundance estimates.

#### **Influence of noise in the data**

The data (survey indices) at a given time will show a certain length distribution. The mortality signal is embedded in the slope of that length distribution on a log scale:

$$d/dl(\ln N) = dN/dl * 1/N = -Z/[k*(Linf-l)],$$

The slope of these curves depends to some extent on the representation of large and small year classes, but the variation from year-to-year in the shape of these distributions is relatively small. As an example, Figure 2 below shows the yearly length distributions on a log scale in a set of survey indices for Northern hake.

If the growth parameters are ‘known’, the slope can be translated into a raw  $Z$  estimate as

$$-Z \sim d/dl(\ln N) * k*(Linf-l).$$

With  $k$ -values typically in the order of 0.5, the term  $k*(Linf-l)$  is much larger than unity, except when the length is close to  $Linf$ . Hence, the slope  $d/dl(\ln N)$  is much smaller than  $Z$ , so noise in the slope is amplified when translated into  $Z$ .

The assumptions made in the present model (specified growth rates, time and length at recruitment and logistic function for selection as well as catchabilities) as well as the use of only survey data, imply that most of the freedom to respond to noise in the data are at the year factor in the separable fishing mortality model, and to some extent in the annual recruitments. In the examples below, it is shown how noise in the survey indices can lead to extremely irregular estimates of the mortality.

The fluctuations in fishing mortality translate into fluctuations in stock numbers, but with strong damping because of the spread in growth. On the other hand, high frequency noise in the data cannot be accommodated by changing catchabilities and growth rates, when these are assumed to be constant over time.

Therefore, the assessment will become an analysis of the data under quite strict conditions to a much larger extent than in age-structured catch-at-age analysis, and results in terms of fishing mortality and biomass are only comparable when the conditioning is consistent. The over-parametrization goes one step further; because with sparse and noisy data, the link between the level of stock abundance and the level of fishing mortality may be too close to allow a unique estimate of each of them. Furthermore, single parameters may drift away. Typically, the  $F$  or recruitment in one year may go towards zero. For the fit to the survey, other year classes give a sufficient population at length to fit to the survey data. That may help to get rid of residuals, but leads to unrealistic results.

The recipe may be to fix the fishing mortality, say in the last year, and to take all estimates relative to that. The trends seem to be reasonably well preserved, but the absolute levels, both of fishing mortality and of SSB remain undetermined.

Because of the confounding of parameters, some combinations of constraints may give better fit than others. It is not obvious that this can be used as a guidance to the best data fit. First, there may be trivial optima for extreme values of parameters, typically for a near zero fishing mortality and extremely large recruitments. But also the ability to accommodate irregularities in the data may be sensitive to the choice between confounded parameters. In the sprat example, including a constraint on the annual catches, to conform to the reported catches, destabilizes the assessment. This may be surprising at first sight but may perhaps because the strong constraint restricts the space of feasible parameter values in such a way that local optima appear.

#### **Damping of the noise in fishing mortalities**

From the considerations above, it follows that the best fit to noisy data may be obtained with highly variable fishing mortalities, which hardly reflect true fluctuations in the exploitation rate.

There are several possible ways to handle this problem. A simple, but probably not irrelevant solution is to make the assumption that fishing mortality is relatively stable from year-to-year (unless there are external indications of the opposite). This may be implemented by including a penalty on the year-to-year change of the annual fishing mortality in the objective function. The form of the penalty function is:

$$SSQ_P = w_p * \sum_{Years} (F(y-1) - F(y))^2$$

where  $w_p$  is the weight given to this function. A high weight implies that the fishing mortality is forced towards being constant. A lower weight allows for some deviation from year-to-year if this is justified by an improved overall fit to the data. Hence, the choice of penalty weight should reflect the signal-to-noise ratio in the data, taking into account the number of terms that go into this sum compared to the number of terms that go into the fit of survey indices by length class.

Another alternative may be to relate the modelled population to smoothed survey indices. To show the utility of this kind of noise filtering, each survey observation was substituted in the objective function by a 3 year – 3 length classes average:  $I_{smooth}(y,L) = \sum_{y-1,y+1;L-1L+1} I_{orig}(y,L)$ . In order to not conceal real trends, the same smoothing was done to the modelled indices.

The experience so far with artificial data are that the smoothing of the survey indices is clearly insufficient to avoid undue influence of random noise in the data. Applying a penalty on the year-to-year variation in  $F$  takes most of the noise away, and combining it with smoothing of the survey indices removes even more of the noise from the results. When the true fishing mortality is variable, these variations become damped, however.

## Summary of experience

The development of the lcs model has confirmed that it is technically possible to construct an operating model for assessing a stock with the ‘Lagrangian’ type of population.

Both from theoretical considerations and practical experience with artificial and real case studies, it is clear that parameter estimation by fitting to data are far less simple with length structured models than with typical age structured assessment tools. This is partly because the parameters are more confounded, partly because the noise in the data are amplified when converted to signals about stock dynamics, and partly because the model has enough flexibility to accommodate noise in the data with quite unrealistic estimates of some parameters.

Therefore, using length based operating models in stock assessment requires stronger conditioning of the model than with typical age-structured methods, and the choice of constraints, and criteria for choosing constraints are by no means clear and simple. If these obstacles can be overcome, however, length based methods should be a useful alternative in situations where reliable age-structured data are unavailable.

## Acknowledgements

Dr Verena Trenkel at IFREMER, France, kindly provided the survey data set for Northern hake and Lotte Worsøe Clausen provided the sprat data. Part of the work was funded by the EU-project Fisboat, funded by the European Union (*Contract reference*).

## References

- Frøysa, K. G., Bogstad, B., Skagen, D. W. 2002. Fleksibest – an age-length structured fish stock assessment model. *Fisheries research* 55: 87–101.
- Jones, R. 1984. Assessing the effects of changes in exploitation patterns using length composition data (with notes on VPA and cohort analysis) *FAO Fish. Tech. Pap.*, 256: 118 pp.
- Lee, R. M. 1912. An investigation into the methods of growth determination in fishes *Cons. explor. mer, Publ. de circonstance* 63.
- Method, R. D., and Taylor, I. G. xxxx. Technical description of the Stock Synthesis II Assessment Program. Program and documentation available from [Richard.Methot@noaa.gov](mailto:Richard.Methot@noaa.gov)
- Skagen, D. W. 2001. Some possible causes of ‘retrospective bias’ in an ICA-like assessment model. Working document, ICES Methods WG, December 2001.
- Skagen, D. W. 2005. AMCI, Version 2.4: Model description, Instructions for installation and running, File formats Unpublished. Program and documentation is available from the author.

## Annex 1. Technical description of the program

---

The program is written in Fortran 77. No external libraries or other proprietary software is needed. The code is available from the author. The building blocs are outlined below.

### *Main blocks*

#### **Input module (subroutines readpar, readdata)**

Read parameter file  
Read data file

*Output:*

*Bounds :*

*Number of years, number of time-steps per year*

*Number of length classes, length class interval*

*Number of trajectories per year*

*List of parameters*

*List of active parameters*

*Key to interpretation of parameters*

*Observed data*

#### **Objective function module (subroutine objfunc)**

Call updpar (update active parameters)

Call pop

Call getsurv

Call calcobj: Calculate sum of squared differences between log observed and observable values by type of data (partial objective functions)

Survey observables are derived in the subroutine getsurv

Model catches are generated in subroutine pop.

Each partial objective function is calculated in a separate subroutine called by calcobj, which also aggregates data as necessary.

*Output: Partial objective function = sum of squares*

*Total objective function*

#### **Optimisation (subroutine manopt)**

Searches for better values among the active parameters, as expressed by the objective function

Calls objfunc

*Output: Best fit parameters*

#### **Printout module (subroutine print)**

*Output:*

*Prints survey indices (observed and observables)*

*Prints stock numbers at length for each time-step*

*Prints catches at length for each time-step*

### *Secondary blocks*

#### **Population module (subroutine pop):**

*Input: Parameter list*

Organise initial data for each trajectory

Get pre-set parameters from parameter list:

Natural mortality at length

Annual fishing mortality that are pre-set

Draw growth parameters (Linf and k) for each trajectory

Year loop

Loop over trajectories for the year

Get initial time, length and number for each trajectory

For the first year: Init. time = 1, numbers acc. to initial length distribution  
 For later years: Random initial time and length, recruitment equal in all trajectories initiated that year.  
 Set up list of when each trajectory will enter ('becomes active')  
 end year/trajectory loop

Project trajectories forward

Year loop  
 Get selection at age for the year  
 Set up table of fishing mortalities for the year  
 Time-step loop within the year  
 Identify trajectories that start in this time-step. Initialise length and number for those trajectories  
 Loop over active trajectories in the time-step  
 Transfer length and number at the end of previous time-step to the start of this time-step  
 Calculate length at end of the time-step  
 Calculate number at end of the time-step and catch during the time-step, using mortalities for the length classes that are passed underway  
 Sum numbers and catches at length over trajectories  
 end trajectory loop  
 end time-step loop  
 end year loop

*Output:*

*Numbers at length for each time-step*  
*Catches at length for each time-step*  
*Fishing mortalities at length as applied for each time-step*

#### **Survey module (subroutine getsurv)**

*Input:* *Catchabilities at length from parameter list*  
*Numbers at length from population module*

Calculate model survey indices:

Get catchabilities at length (parameters)  
 Calculate survey indices at length:  $I(L) = q(L) \cdot N(L)$  for each time-step with survey

*Output:* *Survey indices observables.*

#### **General framework** (stated on top of the parameter file)

- First and last length class, Length class step  
 The range of lengths is the outer range also for data, but lengths may be missing in the data files. Length class step is assumed to be universal; both internally and on length disaggregated data.
- First and last year, Number of time-steps per year.  
 Data may be annual. If so, the model values (in practice catches) will be aggregated. Survey data are allocated to a specific season for the survey.
- Number of trajectories per year
- Time for spawning (fraction of years)

#### **Parameter handling:**

All parameters are assembled in a parameter list. When input, each parameter is associated with a parameter type, which indicates what it is supposed to represent. A parameter index array keeps reference to position in the parameter list for each type. The appropriate parameters are picked from the list according to the reference in the index array in the parametric model routines where they are used.



To each parameter is associated an active flag, which indicates how the parameter shall be regarded with respect to estimation. The flag can take the values:

0: Fixed: The parameter is taken as input, and kept as it is

1: Active: The parameter value is adapted by the optimisation process, to get the value corresponding to the best model fit. Hence, these are the parameters to be estimated.

2: Passive: The value of the parameter is always set equal to the parameter above on the list. This is the way to keep a group of parameters equal, and change them *en bloc* if needed.

The active parameters are kept in an 'active parameter list'. This list is the only structure that is seen and can be changed by the optimisation module. The ordinary parameter list, which is seen by the model part of the program, is updated with the current values of the active parameter list each time it is used.

### Parameter types:

- Growth parameters:
  - $k_0$ : Basic growth rate parameter: Mean and SD
  - $L_{inf}$ : Mean and SD
- Starting values
  - Time of the year of entry: Mean, SD and truncation (negative random values are permitted)
  - Length at entry: Mean, SD and truncation
  - Correlation between time and length at entry

Initial numbers are with a length distribution; later recruitments are either with a length distribution, distribution of entry time or both.

- Abundances:
  - Initial numbers at length
  - Number of each subsequent recruitment.
- Mortalities:
  - Natural mortality at length (constant for the time being)
  - Selection at length, either for each length or parameters in a selection function.
  - Annual fishing mortalities scaled to a range of lengths
- Catchabilities (assumed to be constant over time)
  - Catchabilities at length by fleet, either for each length or parameters in a selection function
  - Catchabilities for biomass survey indices, by fleet.

## Annex 2. Files and file formats

---

You need two files to make an assessment with lcs, and a third file to specify how new data are generated if you want to do that.

- A parameter file with the background information, choices of options and a list of parameters with suggested values. With each parameter there is a flag, indicating whether the parameter is to be estimated.
- A file with observations data.
- Optional: A file with specifications on how to generate data.

The names of these files are stated when the program is started. The program finds the rest of the information it needs on the files.

When new data are generated by the program, these data are kept internally. Optionally, they may be copied to a file called *newfile.out*.

The files are ASCII format, and are read in ‘free format’ by FORTRAN, i.e. spaces or commas are regarded as separators. Tabulators may sometimes cause problems, and are not recommended. Empty lines at the end of the file may cause the program to crash.

The various categories of parameters or data are separated by keyword lines, followed by specific headers. Details are given below. When the parameter file is read, a certain number of parameters of each category is expected, (for example one fishing mortality for every year, no more and no less), and if something is missing or redundant, the program normally crashes.

You may add comments on the files, but only after the actual numbers on the line. Extra lines are not permitted.

A typical problem with Fortran is that reading files easily crashes if the files are not entirely correct. Some common causes for problems with the input files for lcs:

- Empty lines at the end of the file
- Tabulators
- Commas instead of decimal points
- Blanks at the start of lines with keywords
- Data and type numbers not in position 6

A small piece of advice: All these problems cause the program to crash. If you run the program in a separate dos-window, or in a terminal window under unix, you will get a reference to the program line where the error appears. It may be useful to consult the source file just to see where it happens – these errors can be difficult to spot by just looking at the file.

### The parameter file

#### **Header:**

First line:	First year Last year Number of seasons per year Spawning season
Second line:	Lowest length Highest length Length class interval
Third line:	Number of trajectories (‘super-individuals’) per year class
Fourth line:	Weight to constraint on year-year variation in F
Fifth line:	Flag for smoothing of survey data.

Example:

```

1990 2005 4 1
50.0 160.0 5.0
30
10.0
0

```

Each set of parameters starts with the keyword:

```

Parameter type X
X is the type number

```

Then follows the values with the general format:

```

Number Identifier Value Flag

```

**Number:** Each parameter is given a number – in sequence. These numbers are used to only identify parameters on output files. In particular, on the *par.out* file that holds current active parameters, only the number, the internal active number and the current value are given.

**Identifier:** Can be either year or length, as appropriate. Where none of these are relevant, no identifier is used.

**Value:** Proposed (starting) value for the parameter

**Flags on the parameter file:**

- Flag = 0: Use the specified value.
- Flag = 1: Let the optimisation process find a best value
- Flag = 2: Let the parameter have the same value as the parameter above on the list.

This is the way to change related parameters *en bloc*.

When the parameter is to be estimated (flag=1 or 2), the value stated on the file is just a suggestion that acts as a starting value in the optimisation process. It should not be totally out of the way, but since the final estimates are independent on these starting values, there is absolutely no need to spend effort on making the values close to the right ones. In the other case (flag = 0), the stated value is used. When using lcs to generate data, the parameter values are your specification of the underlying population and model, which are used as they are, or substituted with estimates if that is what you ask for.

**Parameter types:**

- 1 Initial numbers by length
- 2 Annual recruitment by year
- 3 Annual F-factor by year
- 4 Annual natural mortality by length
- 5 Selection in fishery
  - L50 for fishing mortality

Slope for fishing mortality

Reference length for selection = 1

#### 6 Trajectory parameters

Mean Linf

SD Linf

Truncation Linf

Mean k

SD k

Truncation k

Mean entry time

SD entry time

Trunc entry time

Mean entry length

SD entry length

Trunc entry length

Correlation time-length

#### 7 Selection parameters for survey fleets (one set for each fleet)

Fleet 1

Survey q: L509

Survey q: Slope

Survey q level

Fleet 2

.

.

#### **The data file:**

The data are all on one file, so this file contains a diversity of data. Each set of data are characterized by a *setnumber*, which is the reference to the data set, and a *type* number, which tells which type of data this is. On the file, a new set of data are signalled by the keyword *Data*. To each set there is a header, and then the data themselves.

#### **Headers :**

Data Setnumber.

Type typeno

Fleet name (*a name for the data series*).

*If type =1-6:*

`weight-to-obj.-func` Resolution (*smallest measurable value*)

`Data` and `Type` are keywords and **must** appear with that spelling (Capital first letter) in position 1: 4. That signals a new data set on the file.

`Setnumber` identifies a data set. Each set of data needs a specific number, which is the reference to the data everywhere. A `fleet` name is associated with each abundance data set, and kept in an array `fleetlist` for future reference. The `setnumbers` for weights and maturities indicate the abundance data set where these weights and maturities apply. Each abundance data set of type 2 needs its specific set of weights, hence weights that refer to survey biomasses (Type 12 data) must identify the fleet where it applies. This is done by using the same set number as for the survey biomass series it refers to. If there are several such fleets, there must be a set of weights for each. The other types of weights and maturities apply universally, so the set number is a dummy, and can be 0 for convenience.

Each of the data sets with types 1–6 generate a partial objective function. The weighing of this objective function is set by `weight-to-obj.-func` after the type number. If the type number is higher, no such number is needed.

In the objective function, zero values are accepted. To avoid problems with logarithms, a small number is added to both the observed value and the corresponding model value. This small number is the `resolution` given on the data file. It should represent the smallest value that can be measured. See the description of the objective functions for more detail.

#### ***Data types***

##### Abundance data

- 1: Survey index at length
- 2: Survey biomass
- 3: Survey spawning biomass
- 4: Survey  $S_a$  value
- 5: Catches in number at length
- 6: Yield biomass

##### Weights and maturities

- 11: weight at length in the catch
- 12: weight at length in survey (survey-specific)
- 13: weight at length at spawning
- 14: maturity at length

**Type specific headers**

The first line(s) for each data type (after the headers described above) are instructions about how to read the file.

The format is given in the example below. Text in bold are fleet specific instructions, *text in italics is explanations*:

```
Data 1

Type 1

IBTS Q1 Fleet name

1 1 Weight in obj. func; Resolution (smallest measurable unit)

1 Season when the survey takes place

50.0 160.0 5.0 Lowest and highest length and length interval

0 Flag for smoothing the input data (surveys at length only)

    1990      11      10      .....      98      79      65      28      14

    .

    .

    2005      1      21      .....      36      19      12      7      2
```

The type specific headers for each type are:

1: Survey index at length:

```
1 Season when the survey takes place

50.0 160.0 5.0 Lowest and highest length and length interval

0 Flag for smoothing the input data (surveys at length only)
```

2: Survey biomass

```
1 Season when the survey takes place

80.0 160.0 5.0 Lowest and highest length and length interval
```

3: Survey spawning biomass

*None*

4: Survey  $s_A$  value

```
1 Season when the survey takes place

50.0 160.0 5.0 Lowest and highest length and length interval

Ts value (a and b in the formula:  $T_s = a:\log(l) - b$ )
```

5: Catches in number at length

```
50.0 160.0 5.0 Lowest and highest length and length interval
```

6: Yield biomass

*None*

11: weight at length in the catch

50.0 160.0 5.0 *Lowest and highest length and length interval*

12: weight at length in survey (survey-specific)

50.0 160.0 5.0 *Lowest and highest length and length interval*

13: weight at length at spawning

50.0 160.0 5.0 *Lowest and highest length and length interval*

14: maturity at length

50.0 160.0 5.0 *Lowest and highest length and length interval*

The lower length is the lower bound of the lowest length class of the data. The highest length is the lower bound of the plus-length, i.e. fish above this length is all pooled into one length class starting at the highest length here.

The range of lengths for the model, as well as the length class intervals are given in the parameter file. The statements on the data file are primarily indicating how the following table is to be read. However, for aggregated surveys data, the length span here is the one that will be used by the objective function. In the example above, the lower length for type 2 is set at 80. This indicates that the biomass value will be calculated only for fish above 80, which then presumably is how the observed survey biomass was made as well.

The length intervals must be the same everywhere. The reference is the length interval given on the parameter file. It is included on the data file for control – if it deviates from the standard a warning is given and the program stops.

Internally in the program, each data set is kept in a separate array, and the data sets are numbered consecutively as they appear on the data file. The book-keeping is through a list *keydata*, where the type and associated weights and maturities are listed for each abundance data set.

## Annex 3: Working Document 2

---

Working Document  
SGASAM 2006

### *First implementation of a GADGET model for the analysis of the Bay of Biscay Hake population*

*Eider Andonegi<sup>a</sup>, Iñaki Quincoces<sup>a</sup>, Dorleta García<sup>a</sup>, Igor Arregi<sup>b</sup> and Unai Ganzedo<sup>b</sup>*

*Azti-Tecnia Foundation*

*<sup>a</sup>: Txatxarramendi Ugarte z/g, 48395, Sukarrieta, Bizkaia.*

*<sup>b</sup>: Herrera Kaia z/g - 20110 Pasaia, Gipuzkoa,*

*Basque Country, Spain*

#### INTRODUCTION

At present an increasing uncertainty is taking shape on the validity of the European hake (*Merluccius merluccius*) age determination criteria used until now, mainly after considering the results of the last hake tagging experiments conducted in 2002 in the Bay of Biscay (De Pontual, Groison *et al.*, 2006). This study suggested that the growth of hake is higher than expected from the von Bertalanffy growth parameters obtained by (Lucio, Murua *et al.* 2000) and used in the ICES assessment since 1993 (ICES, 2004). Furthermore in the last hake otolith exchange workshop held in 2004, it was shown that although the age reading is similar up to age 3 among readers, this is not the case for older fishes.

In order to analyse the effects of different growth patterns in the assessment of Northern Hake (Bertignac, 2004) presented a simulation study, in which an ALK corresponding to a twice faster growth pattern was applied to derive the catch-at-age matrix and the abundance indices inputted in a XSA analysis. This study showed that the change in growth affects the absolute levels of estimates of fishing mortality and stock biomass from stock assessment while overall trends are very similar, meaning that our perception of the stock is broadly the same using both ALKs. However, the simulation also showed that a stock with such growth rates would be more reactive to changes in fishing levels, which would affect catch forecasts and advice.

The Working Group on the Assessment of Southern Shelf Stocks of Hake, Monk and Megrim (WGHMM), carried out two different assessments in 2005 and 2006, one using the normal ALK and another one using the simulated one. The results in both years were similar to those obtained in the 2004 simulation.

A length-based model would be an important improvement due to the great uncertainty on hake growth pattern. A first attempt of fitting a length-based model to Northern Hake have been done within the BECAUSE European project, though this is not covering all the



Northern stock area. The main aim of this project is to provide an alternative method to the assessment of the stock and to try to include trophic interactions in order to take ecosystem properties into account in fisheries management by means of a multispecies GADGET model with hake as the main natural predator.

## MATERIAL AND METHODS

### Model spatial distribution:

The covered area by the model, the Bay of Biscay, extends from 48°N to 43°N and from 11°W to the coastlines of France and Northwestern Spain, which correspond to the ICES fishing Divisions VIIIa,b,d. The Northern Hake stock considered by the working group comprises also ICES Division IIIa and Subareas II, IV, VI and VII. Biogeographically the region corresponds to a subtropical/boreal transition zone (from Finisterre to Brittany) (OSPAR, 2000). The topographical diversity is reflected in the ecological richness of the region, which includes a wide range of fish species many of these of commercial interest.

### Model time range:

The model time range was from 1987 to 2003. Although the catch-at-age data available for this stock went up to 1978, the available length frequency distributions for the considered area started in 1993 but it was decided to start the model in 1987, starting year for EVHOE index, in order to allow the model to obtain more stable estimates in the first year with length frequency distributions from commercial fisheries.

### Model initial conditions and parameters:

To initialize the Bay of Biscay population of hake into the GADGET model the numbers-at-age in the first year (1987) and the number of recruits for every modelled year (1987–2003) are needed. This data were taken from the ICES WGHMM 2006 XSA estimates. All the values were scaled, since the population studied does not comprise the whole area of Northern Hake stock assessed by the WGHMM. The way to scale those values was very simple: once calculated the proportion that the landings of hake in the VIIIa,b,d referred to the total landings in the whole stock were for each year, these proportions were applied to the total abundances, getting the total amount of individuals in the area for each year and age.

The hake growth was modelled through the von Bertalanffy growth function using as input the available Age Length Keys for the model time-series. As the readings were done with the “traditional” ageing criteria the growth pattern inputted in the model is the “slow” one. The von Bertalanffy growth function parameters were calculated with the INBIO package for R (Sampedro, Trujillo *et al.*, 2005) fixing the  $L_{\infty}$  to a value of 100 cm.

Sexual maturity is still not implemented in the model and a combined maturity ogive was calculated with the length vs. maturity data available for the time span of the model with the INBIO package and used to transform final biomass at length estimates into mature and immature biomass and finally into annual SSB.

GADGET considers the fishing fleets as a predator into the model, so the model has implemented different predation suitability functions that in case of the fishing fleets or the scientific surveys are similar to the selectivity patterns of the fleets and/or surveys. The suitability functions' equations selected were different for the fishing fleet and for the survey, for the commercial fleet an exponential L50 function was chosen

$$S(l, L) = \frac{1}{1 + e^{-4\alpha(l-l_{50})}}$$

and for the survey Andersen suitability function.

$$S(l, L) = \begin{cases} p_0 + p_2 e^{-\frac{(\ln \frac{L}{l} - p_1)^2}{p_4}} & \text{if } \ln \frac{L}{l} \leq p_1 \\ p_0 + p_2 e^{-\frac{(\ln \frac{L}{l} - p_1)^2}{p_3}} & \text{if } \ln \frac{L}{l} > p_1 \end{cases}$$

#### Likelihood data

When GADGET works as an optimizing toolbox, it does the optimization maximizing the likelihood function which is integrated by different likelihood components. In this case, these likelihood components are the length distributions of the commercial fleet and the survey, the abundance indices from the survey and the CPUEs.

Total landings, length distribution of the landings and fishing efforts of the commercial fisheries were provided by the different institutes that are part of the BECAUSE project (from 1987 to 2003).

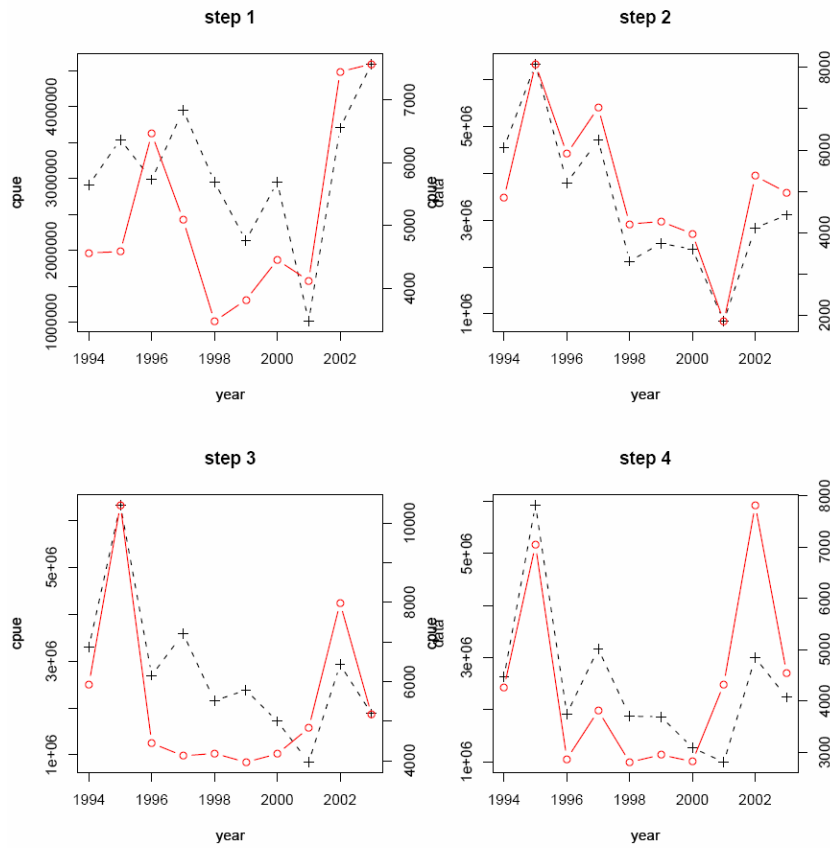
The whole commercial fishery catching fish in the area was split in two different fleets, since in 2001, due to the emergency plan for recovery of Northern Hake, the fishery selectivity changed.

The survey data (EVHOE) were provided by the French institute (IFREMER) and it covered all the time period of the model. This survey was separated in two periods as well, caused by the change in the survey design that took place in 1997. These surveys provide information on fish biomass and abundance in autumn each year, by length.

All these observed data that have been introduced into the model are aggregated by quarter. This is the minimum temporal disaggregation that can be used in GADGET to fit the needed parameters and simulate the population. Unfortunately, the data are not available at a monthly basis that is the best way to input it in a GADGET model.

**RESULTS**

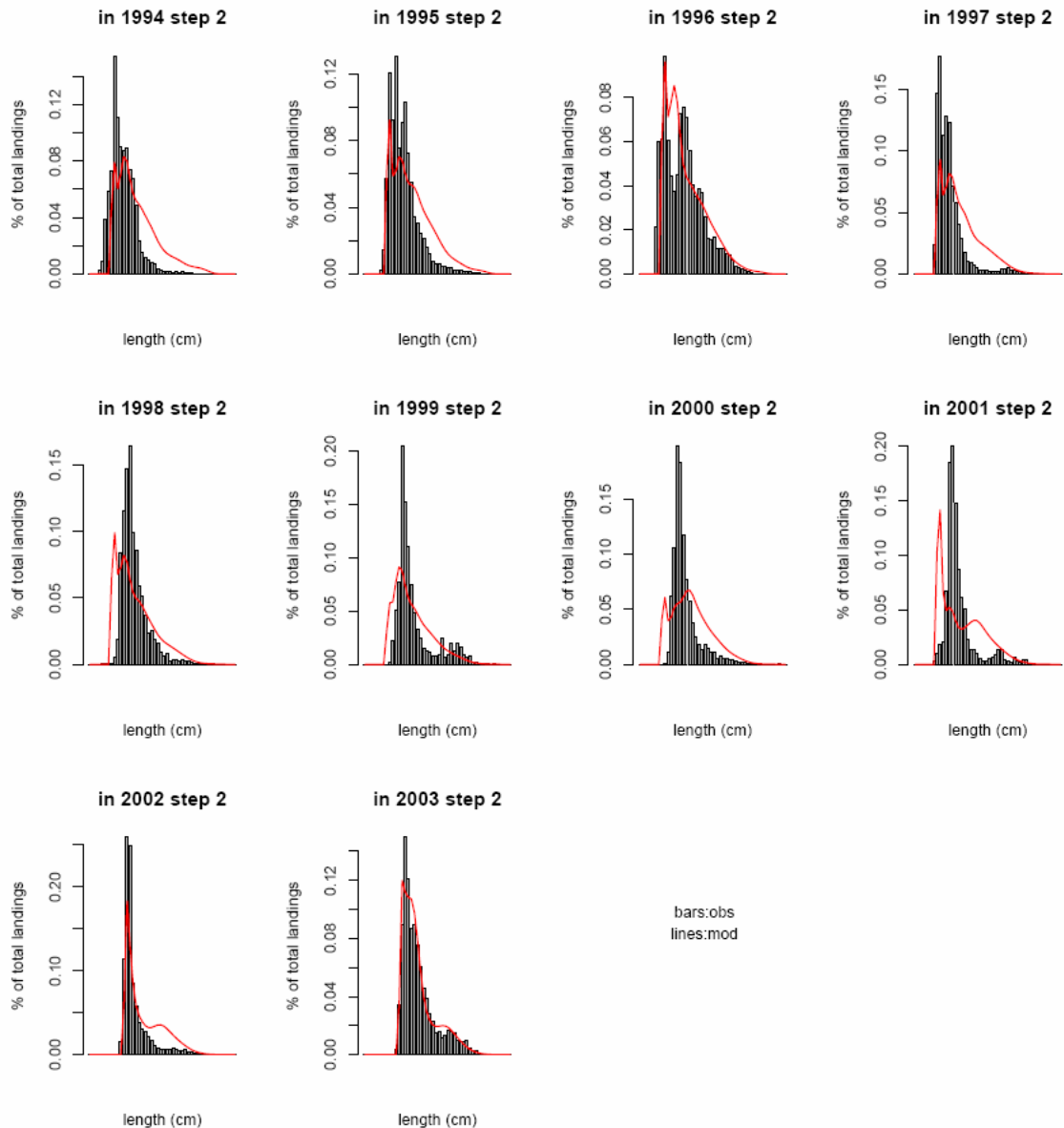
Even if the Bay of Biscay could be defined as a medium level of richness of data (being a rich data area i.e. the North Sea and a low level one the Mediterranean Sea) a stable GADGET model was obtained for Bay of Biscay Hake. The model fitted quite well to the data and the results were reasonable and comparable with those obtained in the WGHMM by means of an analysis performed with an age structured model as XSA.



**Figure 1: Modelled and Observed CPUEs of commercial fisheries. The observed ones are plotted in red and the modelled ones in black.**

When plotting the observed commercial CPUE index against to the predicted by the model (Figure 1) is clear that the best fit is in the second trimester and that even the fit is not so good in the remaining trimesters the general tendencies are reflected in the model.

The observed and predicted length distributions in the second step are shown in Figure 2. In general the fit of both distributions is fairly good, being the fit in 2003 remarkably good. There was a change in the minimum legal size that was set in 27 cm in 1989. But it is evident from the figures obtained from the model and the observed data that this was not being totally enforced until 2002, when the emergency plan was implemented. This causes a change in the suitability function parameters for the commercial fleets modelled.



**Figure 2: Observed (bars) and predicted (red lines) length distributions for the period 1994–2003.**

In Figure 3 the results obtained by the working groups using the XSA for the whole stock of Northern Hake and those obtained with the GADGET model for the Bay of Biscay Hake are compared. The reference XSA estimated fishing mortality, mean fishing mortality for ages 2 to 6, the first panel plot, is more variable and there are some opposed tendencies but it must be taken into account that the modelled population is not the same. In the case of the SSB and the biomass, the general trend of both results is very similar. And about the recruitment, it is also shown that the general trend of the outputs of both models is more or less similar, and the numbers are at least reasonable.

Temptative KEY run BoB hake summary plots XSA vs GADGET

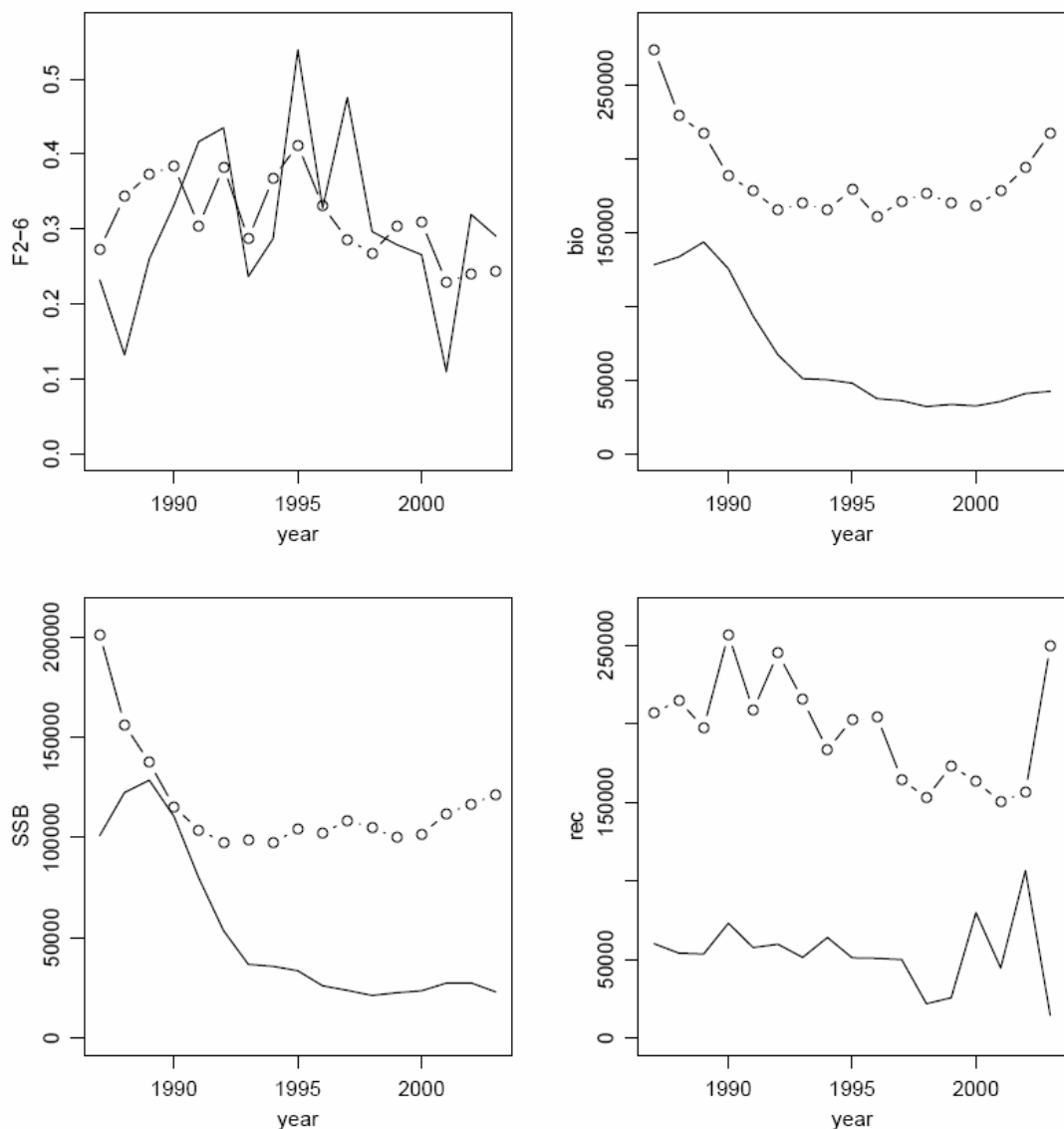


Figure 3: Comparison between the results from the XSA used in the ICES assessment WGHMM (lines and spots) and the results from the GADGET model for the Bay of Biscay Hake (lines). N.

## CONCLUSIONS

This first attempt of fitting an age-length assessment model for the Northern Hake of Bay of Biscay seems to give quite good results and a solid basis for implementing an age-length based model for the whole stock of Northern Hake as considered in the WGHMM. An extended and more elaborated model would be a potential alternative assessment model to the current one.

To avoid relying in age reading to derive a growth model, the GADGET can fit the needed growth parameters from the available length distributions, an attempt was done but it did not fit properly, probably due to the impossibility for the model to find the necessary cohorts in the length distributions and follow them along the time.

Since the former approach was impossible to use a growth model was specified to obtain a proper fit. The advantage of this approach is that alternative growth models can be tested without much extra work changing only the growth model parameters. As mentioned above, in future work, the same model with alternative growth models from (De Pontual, Groison *et al.*, 2006) will be implemented.

## REFERENCES

- ICES. 2004. "Report of the ICES Advisory Committee on Fishery management and Advisory Committee on Ecosystems." *ICES Advice* 1 Book 2;part 3: 625–973.
- Bertignac, M. 2004. "A preliminary simulation study of the implications of possible changes in growth on the assessment of Northern stock of Hake and management advice." Working Document presented to ICES WGHMM 2004.
- De Pontual, H., A. L. Groison, *et al.* 2006. "Evidence of underestimation of European hake growth in the Bay of Biscay, and its relationship with bias in the agreed method of age estimation." *ICES Journal of Marine Science* 63: 1674–1681.
- Lucio, P., H. Murua, *et al.* 2000. "Growth and reproduction of hake (*Merluccius merluccius*) in the Bay of Biscay during the period 1996–1997." *Oceanografika* 3: 325–354.
- OSPAR. 2000. "Quality Status Report 2000 for the Region IV: Bay of Biscay and the Iberian Coast."
- Sampedro, M. P., V. Trujillo, *et al.* 2005. Software Estimación Incertidumbre de Parámetros Biológicos, Instituto Español de Oceanografía.

## **Annex 4: Working Document 3**

---

### **Assessing the impact of discretisation assumptions in a growth matrix model**

Authors:

DROUINEAU Hilaire (author for correspondence)

address: IFREMER department EMH, rue de l'Ile d'Yeu, B. P. 21105 44311 - Nantes Cedex 3, France

e-mail: hilaire.drouineau@ifremer.fr

tel: +33 (0)2 40 37 43 06

fax: + 33 (0)2 40 37 40 75

MAHEVAS Stéphanie

address: IFREMER department EMH, rue de l'Ile d'Yeu, B. P. 21105 44311 - Nantes Cedex 3, France

e-mail: stephanie.mahevas@ifremer.fr

tel: + 33 (0)2 40 37 41 81

BERTIGNAC Michel

address: IFREMER, STH / LBH, Centre Ifremer de Brest, BP 7029280 Plouzané, France

tel: + 33 (0)2 98 22 45 25

e-mail: michel.bertignac@ifremer.fr

FERTIN Arnold

address: Université de Tours, IRBI UMR CNRS 6035, Parc Grandmont, 37200 Tours, France

tel: + 33 (0)2 47 36 69 81

e-mail: arnold.fertin@etu.univ-tours.fr

## Abstract

---

Most of the traditional assessment models are age-structured. However, many biological and exploitation processes are more length dependant than age dependant, and the required length-age conversion of available data are often doubtful. Consequently, length-structured or age-length structured models have undergone considerable development in recent years. The growth transition matrix used to model the mean growth and growth variability of the population, is of primary importance in a length-structured matrix model. Building this growth transition matrix is not trivial and it is necessary to assess the impact that various assumptions may have to identify robust model structures. In this study, we assess the effects of time and length discretisation, of the distribution of individuals within length classes and of the statistical distribution used to describe growth variability, by fitting a growth matrix model on individual quasi-continuous simulated growth data. The study demonstrates the major importance of the choices of the time-step and of the classes' width which are strongly interdependent. Furthermore, the use of a gamma distribution for the growth increments and/or a uniform distribution of individuals within length classes makes the model more robust.

## Introduction

---

From deterministic - single cohort analysis (Pope, 1972) to multi cohort analysis, age-structured models (Fournier and Archibald, 1982; Shepherd, 1999; Virtala *et al.*, 1998) are widely used for fisheries stock assessments. While these models have proved to be useful in estimating population abundance and assessing stocks, several limitations have been pointed out. One limit, often mentioned, is related to the need to convert catch at size into catch at age, which is often carried out using an age-length key. In this case, the difficulties in determining the age at length result in uncertainty in catches at age. Moreover, since the ageing techniques are very expensive, few fishes can be aged, increasing further the sampling error and variability in the age-length key. Another source of uncertainty is the size-dependant selectivity function which is not explicitly taken into account in age-structured model. Large variations in size within an age class could thus result in incorrect estimates of fishing mortality by age. Consequently, length-structured models or age-length structures models have undergone considerable development in recent years (Banks *et al.*, 1991; De Leo and Gatto 1995; DeLong *et al.*, 2001; Fournier *et al.*, 1998; Froysa *et al.*, 2002; Schnute 1987; Schnute *et al.*, 1989a; Schnute *et al.*, 1989b; Sullivan *et al.*, 1990). Indeed, the required data to fit these kinds of model are catches at length and length formal processes (like selectivity and maturity) are explicitly modelled without any transformation.

Different mathematical frameworks can be used to model length structured population dynamics, whether population states are assumed discrete or continuous and the projection time is discrete or continuous. Continuous approaches match better biological processes which are, most of the time, continuous. However, the disadvantage of this approach is the complexity, using differential equations which do not necessarily have analytical solutions. In addition, available data are generally aggregated reducing the advantages of continuous model. By contrast, discrete approximations simplify model implementation and are easy to compute. Discrete approaches require discrete assumptions on continuous processes. They necessitate however decisions on the size of the length and time intervals, the way growth increments are modelled (stochastically or deterministically) and on the distribution of individuals into each classes.

Fish growth is a major process of fish biology (Laslett *et al.*, 2002) and is part of the information necessary to estimate stock size and fishing mortality in stock assessments models (Anda-Montañez *et al.*, 1999). It is largely accepted that it is of primary importance to describe jointly mean growth and individual variability in growth in stock assessment process (Chen *et al.*, 2003; Laslett *et al.*, 2002). Two approaches are classically considered to model



the variability in growth. The most common model is a mean growth by length class given by the growth function and a stochastic distribution for individual variability around the mean (Cruywagen 1997; De Leo and Gatto 1995; Froysa *et al.*, 2002; Sullivan *et al.*, 1990). Another way to describe growth variability is to integrate individual variability in the growth function with stochastic parameters (Pilling *et al.*, 2002; Sainsbury 1980; Smith *et al.*, 1998; Smith and Botsford, 1998). The correlation between the two parameters  $L_{\infty}$ ,  $K$  of the von Bertalanffy function represents a major difficulty for this type of model and no general solution has yet been proposed. A good estimation of growth parameters is especially important in length-based models to compute a realistic growth transition matrix (Sullivan, 1992; Sullivan *et al.*, 1990). Several approaches can be used to estimate the growth and its variability. Length-at-age can be back-calculated using information contained in fish hard parts, but this approach is often imprecise due to difficulties in detecting growth increments. A second approach is the tagging. This technique is very expensive as many fishes have to be tagged in order to be successful. Tagging experiments on hake are currently carried out in the Bay of Biscay and preliminary results appear promising (de Pontual *et al.*, 2003; de Pontual *et al.*, accepted). Captive studies can also be used. However their results could be questioned given the differences in life conditions between captivity and the ocean.

To date, very few studies have looked at the impact of the discretisation of time and length classes may have on the ability of the population model to fit data and estimate parameters. In this study we provide a methodology to assess the impact of different choices of discretisation of the time, of the individual size distribution and of the growth process in a length structured model. A graphical comparison of frequencies at length obtained with the matrix model according to different assumptions was first practised to detect some possible artefact. Then, we fitted the matrix model to simulated individual growth data to assess the effect of the different assumptions. Real individual based growth data are rarely available, so we had to generate frequencies with using a quasi-continuous individual based model. Tagging data at a large scale would be a valuable improvement in such study. This methodology is useful to find a flexible growth model which will be integrated into a length-based assessment model.

## 1. A length growth structured model

---

A matrix formulation of a model in discrete time is derived to describe the growth of the population. The length-structured abundance in number at time  $t+1$  is given by the following equation:

$$N(t+1) = G(\Delta t)N(t)$$

$N(t)$ : vector of abundance per class at time  $t$ ,

$G(\Delta t)$ : matrix of probabilities of transition between length classes

We assume a constant growth transition matrix over time (i.e. no seasonality has been taken into account). The population is supposed to grow according to a von Bertalanffy growth function. The von Bertalanffy function is parametrized by the three parameters  $L_{\infty}$ ,  $K$  and  $T_0$ ,  $l(t) = L_{\infty} \times (1 - e^{-K(t-T_0)})$ . The mean growth increment for a period  $\Delta t$  for a fish of size  $l$  during  $\Delta t$  is given by the following equation  $\Delta l = (L_{\infty} - l) \times (1 - e^{-K \times \Delta t})$ . The population growth variability is represented by a statistical distribution of the growth increments around this mean (Cruywagen 1997; De Leo and Gatto, 1995; Froysa *et al.*, 2002; Sullivan *et al.*, 1990).

Two assumptions of variance of the growth increments are considered. The variance is a functional form of the mean increment in both cases:

- i)  $V(X_i) = C.E(X_i)$  the variance of a growth increment is assumed to be proportional to its mean whatever the class (Sullivan 1992 ; Sullivan *et al.* 1990),

- ii)  $V(X_i) = C \cdot E(X_i)^2$  the variance is assumed to be proportional to the square of its mean whatever the class (DeLong *et al.* 2001),

with  $X_i$  the random variable describing the growth increment of fishes in class  $i$ .

**Table 1: List of the abbreviations and their significations. Bold terms correspond to assumptions on the quasi-continuous model. Other terms correspond to assumptions on the matrix model.**

Abbreviation	Signification	Possible Values
v	Hypotheses of variance of the growth increments $X$	1: $V(X)=C E(X)$ 2: $V(X)=C E(X)^2$
$\Delta t$	Time-steps of the matrix model	12: monthly time-step 4: quarterly 1: yearly
$\Delta l$	Size of the length classes in the matrix model	1: 1 cm 5: 5 cm
Lm	Statistical distribution of the growth increments in the matrix model	0: gamma 1: normal 2: log-normal
ODEp	Distribution of the individual within length classes in the matrix model	0: center 1: uniform
CV	Coefficient of variation of the growth increments in the quasi-continuous model	0.2 1 2
K	Growth rate in the quasi-continuous model	0.1, 0.2
Ls	Statistical distribution of the growth increments in the quasi-continuous model	0: gamma 1: normal 2: log-normal
$\alpha$	Parameter of the Beta-Binomial	0.1, 1, 10, 50
$\beta$	Parameter of the Beta-Binomial	1, 10, 50, 100
Kest	Estimated growth rate when fitting the matrix model on frequencies at length generated by the quasi-continuous model	
BIC	Bayesian Information Criterion when fitting the matrix model on frequencies at length generated by the quasi-continuous model	
Lbic	Neperian logarithm of the absolute value of $BIC$	
LK	Neperian logarithm of the absolute value of the difference between Kest and <b>K</b>	

The mean coefficient of variance  $CV(X_i) = \sqrt{V(X_i)} / E(X_i)$  is used (Table 1) to characterize the level of variability in a simulation. Note that  $CV^2$  is equal to  $C$  for each  $X_i$  with the second hypotheses of variance.

Different statistical distributions are used to describe growth increments distribution: a Beta-Binomial distribution and three different continuous distributions (respectively, normal, log-normal, gamma).

The Beta-Binomial (Table 2) is an extension of the binomial distribution often used to describe a multivariate data set and known as appropriate to describe overdispersion (Ennis and Bi 1998). For each length class, the Beta-Binomial distribution is used to model the growth increments (Stefansson, 2001) counting the number of classes jumped during one time-step using the following algorithm:

- 1) calculate the length reached by the midpoint using the growth function during one time-step
- 2) calculate the associated number of classes jumped by the midpoint
- 3) calculate the relative position of the length reached by the midpoint within the class reached by the midpoint
- 4) the mean growth is then equal to the sum of the two previous values (2. + 3.)

The Gamma distribution (Table 2) is a two-parameters distribution, entirely defined by its two first moments. It is largely used in modelling thanks to its flexibility in describing many functional forms. More specifically in our context, it can describe growth for small and large fish. The normal and log-normal (Table 2) statistical distributions were also considered.

**Table 2: Distribution, mean and variance of the beta-binomial (Beta), normal (N), log-normal (LN)**

**and Gamma (G) statistical distributions. With  $\Gamma(x) = \int_0^{\infty} e^{-u} u^{x-1} du$  the gamma function and n the**

**number of classes crossed in the Beta-Binomial distribution, In the simulations, either  $\alpha$  or  $\beta$  of the Beta-Binomial was fixed, the other parameters was calculated with the relationship**

$$\beta = \frac{n - E_i(X)}{\alpha E_i(X)}$$

		Distribution	E	V
discrete	Beta	$P(X=x) = \binom{n}{x} \frac{\Gamma(\alpha+x)\Gamma(\beta+n-x)\Gamma(\alpha+\beta)}{\Gamma(\alpha+\beta+n)\Gamma(\beta)\Gamma(\alpha)}$	$E(X) = n \frac{\alpha}{\alpha+\beta}$	$V(X) = n \frac{\alpha\beta}{(\alpha+\beta)^2} \left(1 + \frac{n-1}{1+\alpha+\beta}\right)$
	N	$f(x) = \frac{1}{\sigma \times \sqrt{(2 \times \pi)}} \times e^{-\frac{1}{2} \times \left(\frac{x-\mu}{\sigma}\right)^2}$	$E(X) = \mu$	$V(X) = \sigma^2$
continuous	LN	$f(x) = \frac{1}{\sigma \times x \times \sqrt{(2 \times \pi)}} \times e^{-\frac{1}{2} \times \left(\frac{\log(x)-\mu}{\sigma}\right)^2}$	$E(X) = e^{\mu + \frac{\sigma^2}{2}}$	$V(X) = (e^{\sigma^2} - 1) \times e^{2\mu + \sigma^2}$
	G	$f(x) = \frac{1}{\beta^\alpha} x^{\alpha-1} e^{-\frac{x}{\beta}}$	$E(X) = \frac{\alpha}{\beta}$	$V(X) = \frac{\alpha}{\beta^2}$

The coefficients of the growth matrix are calculated according to the following equations:

- i) if fishes are assumed to be at the midpoint of the departure class i, denoted  $m_i$ , then the probability of transition to class j is given by the following single integral:

$$g_{ij} = \int_{lowerboundj - m_i}^{upperboundj - m_i} f(x) dx$$

- ii) if fishes are assumed to be uniformly distributed within the departure class i, then the value of the following double integral is the probability of transition from class i to class j:

$$g_{ij} = \int_{lowerboundi}^{upperboundj} \left( \int_{lowerboundj - y}^{upperboundj - y} f(x) dx \right) dy$$

with  $f$  the considered density function of the growth increments.

Several ways of constructing classes can be considered: i) classes of equal width in length ; ii) classes of equal width in time ; iii) classes associated with biological stages of the life cycle ; iv) classes resulting from an optimisation of a specific criterion. The first type of length class construction is the most common in the literature (De Leo and Gatto 1995; Froysa *et al.*, 2002; Sullivan *et al.* 1990). We have not found any application with the second types. The third method is usual in stage-structured models. This requires available knowledge of the relationship between life cycle and size is available in order to use a length-structured approach. (Vandermeer, 1978) proposed an algorithm corresponding to the fourth approach, based on the minimization of the sum of two errors, sampling error and distribution error, improved by (Moloney, 1986). Some details on this algorithm are given in (Caswell 2000). But this approach has several drawbacks, requiring data on individual growth, and only modelling the probability of staying in the departure class. For these reasons, we assume length classes of equal width in length when growth variability is described with a continuous distribution. We consider two types of length classes for the continuous distributions (Table 1). On the other hand, we build classes of equal duration when assuming a Beta-Binomial distribution, since the probability to cross a class is considered constant whatever the class.

In this study we consider two von Bertalanffy growth rates (Table 1). The first rate corresponds to a slow growing species, whereas the alternative corresponds to a faster growing species.

Finally, three different time-steps are considered in this analysis: monthly, quarterly and an annual (Table 1).

Let us denote  $M(v, Lm, \Delta t, \Delta l, ODep)$  a matrix model with a hypothesis of variance  $v$ , a statistical distribution of growth increments  $Lm$ , a time-step  $\Delta t$ , length classes of size  $\Delta l$ , and an option of distribution of individuals within classes  $ODep$  (Table 1).

## 2. Data

---

Individual growth data are necessary to assess the impact of both time and length discretisation assumptions in the growth dynamics model. However, no such data are available: consequently we simulate individual growth data. We used a monthly time-step to mimic time continuous growth. Shorter time-steps were also tested, but the differences in frequencies-at-length were minor. Let us denote  $S(v, K, CV, Ls)$  a simulation set of individual growth trajectories performed with the variance hypothesis  $v$ ,  $K$  as parameter of the von Bertalanffy curve, a coefficient of variation  $CV$  and a statistical distribution  $Ls$ . A set of 10000 individual trajectories over a 10 years period is simulated for each combination of assumptions of growth variability ( $v, K, CV, Ls$ ) using a monthly time-step (Table 1). These simulations aim at mimicking individual growth observations. For each set, the initial length of individuals is generated according to a normal distribution with mean 5 cm and standard deviation of 1.

## 3. Methods

---

Each single or combined discretisation assumption can affect the matrix model. We perform two full experimental designs (one for each hypothesis of variance) to assess the impact of the different discretisation assumptions and of their combinations. The four varied factors are  $Lm, \Delta t, \Delta l$  and  $ODep$  with respectively 3, 2, 3 and 2 modalities (Table 1) leading in 648 experiments for each experimental design. One experiment corresponds to a ten-year's cohort projections with the matrix model  $M$  for a set of parameters ( $v, Lm, \Delta t, \Delta l, ODep$ ). The initial length distribution of the cohort is the same as the initial length distribution of individuals presented above, i.e. a normal distribution of mean 5 cm and standard deviation of 1. Each experimental design (i.e. each variance assumption (1) and (2)) is analysed independently.

First, the distribution of the model projections by length classes are plotted for different time-steps. Graphical comparisons of the frequencies at length obtained were provided to detect

possible artefacts of the model. The mean length and the standard deviation of the individuals were computed at different time-steps to compare the growth rates and associated variability.

Second, each matrix model  $M(v, \bullet, \bullet, \bullet, \bullet)$  is fitted on each set of observations assuming the same variance hypothesis  $S(v, \bullet, \bullet, \bullet)$ . The parameter  $K$  of the von Bertalanffy growth curve and the constant  $C$  of the variance structure are estimated by minimizing the sum of squared error:

$$LS = \sum_{i=1}^I \sum_{t=1}^T (f_{est}(t,i) - f_{obs}(t,i))^2$$

with  $f_{obs}(t,i)$  the simulated frequencies of individuals within class  $i$  at time-step  $t$ ,  $f_{est}(t,i)$  the frequencies of individuals within class  $i$  at time-step  $t$  estimated by the matrix model,  $I$  the number of class and  $T$  the number of time-step. The minimization of the function  $LS$  was carried out using a genetic algorithm coupled with automatic differentiation algorithm provided in the Autodif library (Otter Research Ltd. 2000). The genetic algorithm was used in a first step in order to provide a solution closed to the global optimum of the function in a reasonable time. Then, the Autodif algorithm (Otter Research Ltd. 2000) was used, starting from the solution provided by the genetic algorithm.

The adequacy of the model is quantified using two criteria:

The discrepancy between the  $K$  estimated ( $K_{est}$ ) by the matrix model and the  $K$  used to generate the observations data ( $K$ ). It quantifies the goodness of the estimation of  $K$

The Bayesian Information Criterion ( $BIC$ ) is computed using the formula  $BIC = 2 \times -2 \text{Log}L + 2 \times \log(n)$  with  $\text{Log}L = n \times \log(\sqrt{2 * \pi}) + \frac{1}{2} \times \left[ n \times \left( \log \frac{n-1}{LS} - 1 \right) + 1 \right]$  and  $n$  the number of observations (number of time-steps X number of classes). The  $BIC$  is here a measure of the matrix model ability to fit the data. The  $BIC$  balances the discrepancy between data and predictions (measured by  $LS$ ) by the number of estimated parameters and the number of observations (which depends on the time-step and the size of the classes in the matrix model).

A statistical analysis of the criteria is carried out to quantify the effect of each hypothesis. First, each criterion is analysed separately using linear models step fitted on the transformed criterion, respectively  $\log(|BIC|) = LBic$  (the absolute value is necessary for the logarithmic transformation because the  $BIC$  were negative) and  $\log(|K - K_{est}|) = LK$ , where  $LBic$  and  $LK$  will refer to the two transformed variables. An adequate model is characterized by a high  $LBic$  and a low  $|K - K_{est}|$ . The variability of  $LBic$  and  $LK$  is explained by the assumption on the matrix model and on the quasi-continuous model, and by the first order interactions. Theoretically, a full experimental design allows inclusion of all the main effect and first order interaction in the model, so that the models may be written under the general form:

$$LBic \sim \sum_i \alpha_i + \sum_i \sum_{j < i} \beta_{i,j}$$

$$LK \sim \sum_i \alpha_i + \sum_i \sum_{j < i} \beta_{i,j}$$

with  $\alpha_i$  the effect of the assumption  $i$ ,  $\beta_{i,j}$  the effect of the interaction between assumption  $i$  and assumption  $j$ .

The coefficients of an effect are constrained to sum to 0.

These linear models enable to quantify the impact of the assumptions on the quality of the estimation of  $K$  and the quality of the reproduction of frequencies separately, but we are also interested in selecting the most appropriate model with regard to both objectives. A multiple regression tree (De'Ath, 2002) is built for each hypotheses of variance to explain the variations of the two transformed variables, previously centred and reduced, by the different explanatory variables (i.e. different assumptions). The tree is grown by repeated binary partitioning of the data, maximizing the Euclidean distance between the two groups centroid and minimizes the total Euclidean distance to the centroid within each group. Each partition is characterized by an explanatory variable and the rank of the explanatory variable selections in the tree reflects the magnitude of impact of the variable on both responses. For each hypotheses of variance the model is:

$$\frac{(Lbic - mean(Lbic))}{sd(Lbic)}, \frac{(LK - mean(LK))}{sd(LK)}$$

$$\sim \Delta t + \Delta l + Lm + CV + K + ODep + Ls$$

For the significance of the abbreviation see 2.2.1 and 2.2.2. Bold terms correspond to assumptions for the quasi-continuous model. Other terms correspond to assumptions on the matrix model.

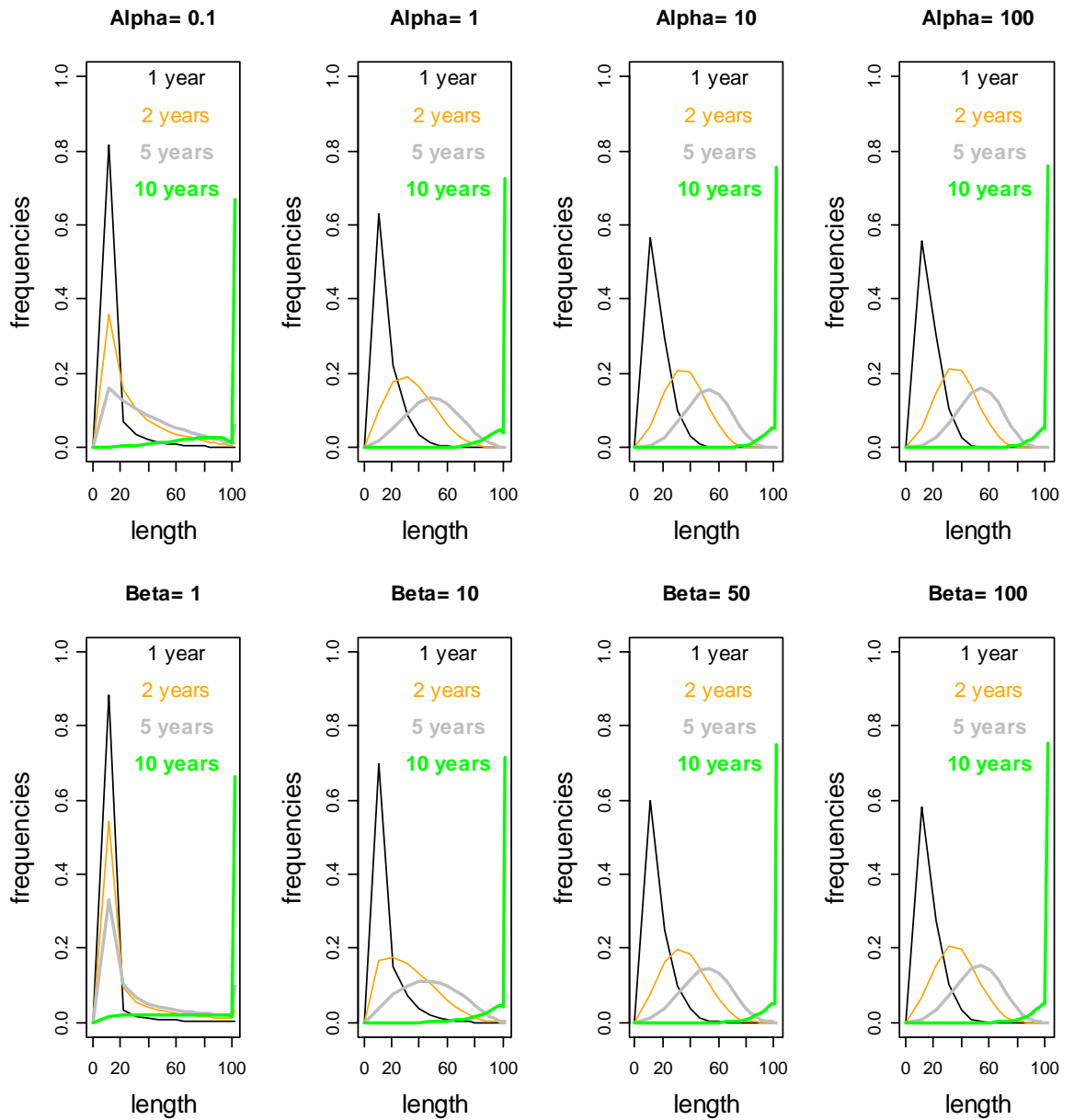
The code to run the simulations is written in C++ using the Autodif library (Otter Research Ltd. 2000).

## 4. Results

---

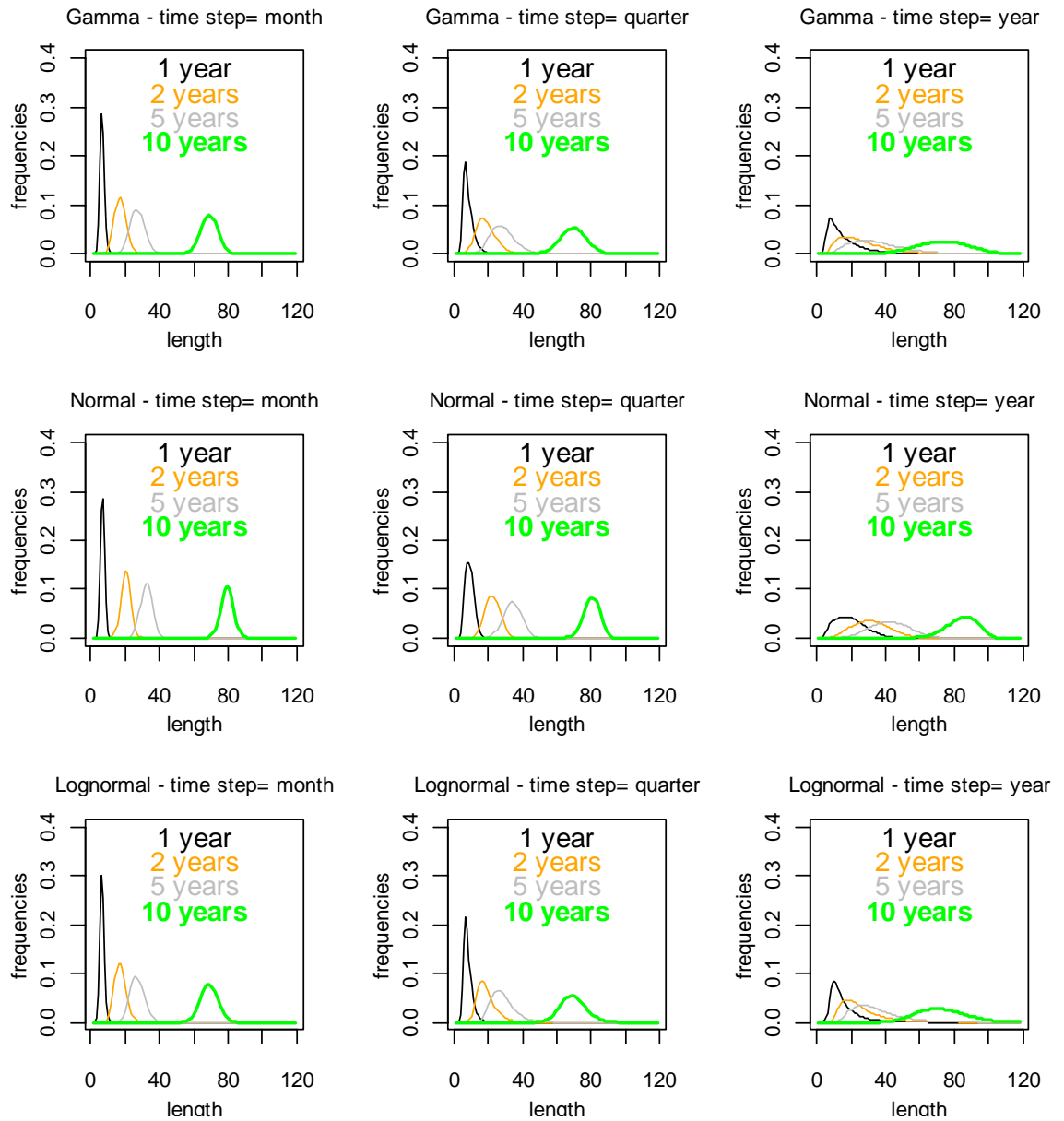
### 4.1 Graphical comparisons of cohort projections

The frequencies at length for a Beta-Binomial assumption are rather closed when fixing alpha or beta (Figure 1). For small values of alpha and beta, a mode appears either on the first or in the final class. It means that the individuals grow very slowly and suddenly reach the final class. For larger values of alpha and beta, the frequencies are nearly identical for any value of alpha and beta, demonstrating a lack of flexibility of the Beta-Binomial distribution. With larger time-steps, the frequencies are more flat, meaning that the individuals are more dispersed, and they tend to grow more slowly. However, the growth is faster than the expected growth whatever time-step has been chosen. This simple graphical analysis of frequencies assuming a Beta-Binomial distribution of growth increments shows a lack of flexibility of this distribution to describe growth variability. Furthermore important artefacts are observed for small values of alpha and beta after 10 years of simulation. This leads us to conclude that the Beta-Binomial distribution is not the most appropriate to model growth variability.



**Figure 1: Frequencies at length at different time (1 year, 2 years, 5 years and 10 years) provided by the matrix model assuming a Beta-Binomial distribution of the growth increments for different values of alpha and beta,  $\Delta t=0.25$ ,  $O_{Dep}=1$ ,  $K=0.1$ . On the first row Alpha is set to a value (0.1, 1, 10, 100) and Beta is calculated according to the equation given in Table 2. On the second row, Beta is set to a value (0.1, 1, 10, 100) and Alpha is deduced from the same equation (Table 2).**





**Figure 2: Frequencies at length provided by the matrix model assuming continuous distributions with different time-steps,  $v=2$  -  $C=1.000$  -  $K=0.1$  -  $\Delta l=1$  cm -  $Odep=1$ .**

The graphical analysis of the continuous distributions suggests they are more appropriate (Figure 2). The gamma and log-normal distributions lead to very similar results whatever the other assumptions. No major artefacts were detected. Consequently, we further focus on continuous statistical distributions to describe growth increments variability, and all the assumptions were considered to assess the impact of discretisation assumptions.

## 4.2 Experimental designs analysis

To comply with the linear models assumption, some first order interaction was removed from the linear models. Insignificant effects were also removed from the final models the final form of the model can be found in Table 3 and Table 4. The  $R^2$  of the linear models are 0.996 (hypothesis (1)) and 0.995 (hypothesis (2)) for the *LBIC*, and 0.708 (hypothesis (1)) and 0.674 (hypothesis (2)) for the *LK*

#### 4.2.1 Fitting observed frequencies-at-length (Table 3)

The results are very similar for both hypotheses of variances. The significant effects of interaction factors are minor compared to the main effects and do not influence the results. Among the main effects, most factors are significant, but few have a large estimated value. The width of the length classes and the time-steps are the two factors which most influence the discrepancy between the frequencies at length. The best fits are obtained with a monthly time-step and 1 cm length classes. Results also demonstrate that a high level of inter-individual variability and a high growth rate are more easily fitted by the matrix models.

#### 4.2.2 Ability to estimate the growth rate K (Table 4)

Again, the results are very similar for both hypotheses of variance but many more factors affect the estimation of the growth rate. As previously, classes of 1 cm greatly improve the estimation of K. More surprisingly, short time-steps do not systematically improve the estimation of the growth rate. In fact, with a monthly (or quarterly) step, individuals have a too small probability to change class (especially when classes are 5 cm wide) so that K tends to be overestimated to compensate. This highlights the links existing between size classes and time-steps (the interaction of the two factors is strongly significant). The choice of a time-step should be strongly linked to the choice of the size of classes, both choices being also constrained by the available data.

This fit demonstrates that, in contrast to the *BIC* analysis (0), a low growth rate and a weak inter-individual variability improve the estimation of K. Furthermore, if the individuals are uniformly distributed within classes, the estimation is improved, especially with a short time-step.

Finally, it highlights the fact that gamma and log-normal distributions used in the matrix model are very similar. The gamma distribution tends however to produce better fits than the log-normal even if a log-normal distribution is assumed for S. A normal assumption in the matrix model gives poor estimation of K when a gamma or log-normal distribution is assumed for S. Regarding the hypothesis of variance ((1) or (2)) of the matrix model M; the impact of the statistical distribution of growth increments differs. The three distributions for M give very similar results when a normal distribution is assumed for S with the second hypotheses of variance, but in the same situation the normal distribution gives slightly better result with the first hypothesis of variance. Among the three distributions tested, the gamma distribution appears to be the most flexible distribution to represent the variability of the growth increments.

**Table 3: Summary of the linear models explaining *LBic* of the fits by the different assumptions for each hypothesis of variance. Grey cells correspond to factors not included in the model. \*\*\* (respectively \*\*) stands for a p-value<0.01 (respectively <0.05).**

	Hypothesis 1		Hypothesis 2	
	Estimate	P-value	Estimate	P-value
(Intercept)	8.78	***	8.92	***
Lm=0	-0.01		0.03	***
Lm=1	0.02	***	-0.05	***
$\Delta t=1$	-1.15	***	-1.18	***
$\Delta t=4$	0.06	***	0.06	**
$\Delta l=1$	1.34	***	1.37	***
CV=0.2	-0.27	***	-0.21	***
CV=1	0.07	***	-0.02	
K	0.61	***	0.89	***
Ls=0	0.02		0.05	**
Ls=1	-0.05	**	-0.06	***
ODep=0	-0.01	**	-0.03	***
$\Delta t=1:\Delta l=1$	-0.07	***	-0.07	***
$\Delta t=4:\Delta l=1$	0.04	***	0.04	***
$\Delta t=1:ODep=0$	0.01	**		
$\Delta t=4:ODep=0$	0			
$\Delta t=1:CV=0.2$	0.04	***		
$\Delta t=4:CV=0.2$	-0.02			
$\Delta t=1:CV=1$	-0.01			
$\Delta t=4:CV=1$	0			
$\Delta t=1:K$			0.67	***
$\Delta t=4:K$			-0.05	
$\Delta t=1:Lm=0$			-0.02	**
$\Delta t=4:Lm=0$			-0.01	
$\Delta t=1:Lm=1$			0.03	***
$\Delta t=4:Lm=1$			0.02	**
$\Delta t=1:Ls=0$	0.04	***	-0.01	
$\Delta t=4:Ls=0$	-0.01		0	
$\Delta t=1:Ls=1$	-0.07	***	0.04	***
$\Delta t=4:Ls=1$	0.02	**	-0.01	
$\Delta l=1:K$			-0.49	***
$\Delta l=1:Ls=0$	-0.01		-0.04	***
$\Delta l=1:Ls=1$	0.02	***	0.06	***
Lm=0:CV=0.2			-0.02	
Lm=1:CV=0.2			0.03	***
Lm=0:CV=1			-0.01	
Lm=1:CV=1			0.02	
Lm=0:Ls=0	0.01			
Lm=1:Ls=0	-0.01			
Lm=0:Ls=1	-0.01			
Lm=1:Ls=1	0.02	***		
CV=0.2:K	0.24	**	0.31	**
CV=1:K	0.01		0.22	**
CV=0.2:Ls=0	-0.08	***	-0.05	***
CV=1:Ls=0	0.01		-0.01	
CV=0.2:Ls=1	0.13	***	0.08	***
CV=1:Ls=1	-0.02	**	0	
K:Ls=0	0.4	***	0.22	
K:Ls=1	-0.69	***	-0.42	***

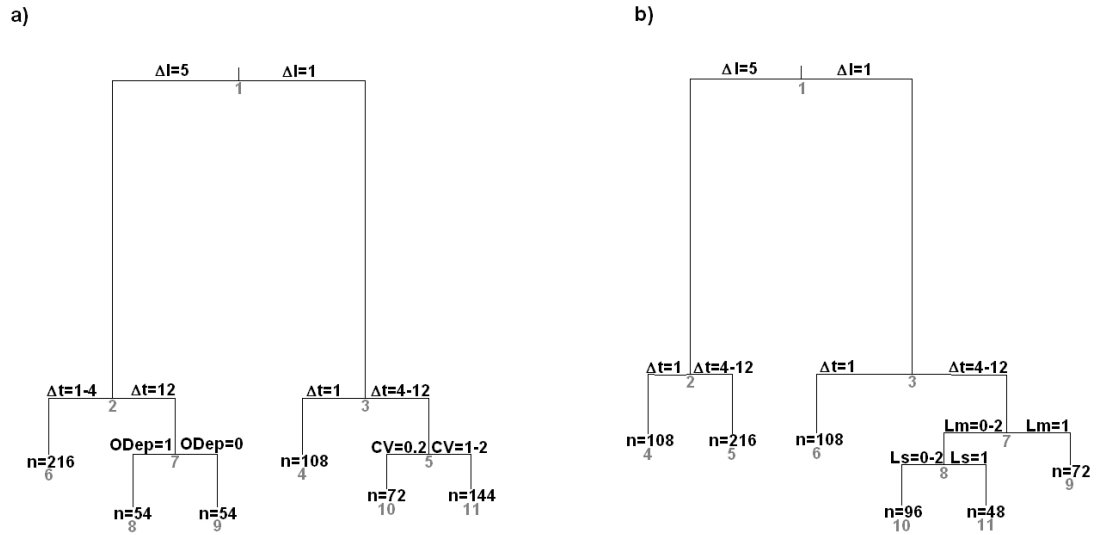
**Table 4: Summary of the linear models explaining  $LK$  of the fits by the different assumptions for each hypothesis of variance. Grey cells correspond to factors not included in the model. \*\*\* (respectively \*\*) stands for a p-value<0.01 (respectively <0.05).**

	Hypothesis 1		Hypothesis 2	
	Estimate	P-value	Estimate	P-value
(Intercept)	-4.87	***	-4.74	***
$\Delta t=1$	-0.31	***	-0.49	***
$\Delta t=4$	-0.05		0.02	
$\Delta l=1$	-0.45	***	-0.38	***
Lm=0	-0.19	***	-0.35	***
Lm=1	0.27	***	0.66	***
ODep=0	0.21	***	0.21	***
CV=0.2	-0.55	***	-0.65	***
CV=1	0.06		0.07	
K	3.9	***	4.93	***
Ls=0	-0.09		-0.40	**
Ls=1	0.14		0.64	***
$\Delta t=1:\Delta l=1$	0.1	***	0.14	***
$\Delta t=4:\Delta l=1$	0		-0.03	
$\Delta t=1:Lm=0$	0.18	***		
$\Delta t=4:Lm=0$	-0.03			
$\Delta t=1:Lm=1$	-0.22	***		
$\Delta t=4:Lm=1$	0.05			
$\Delta t=1:ODep=0$	-0.22	***	-0.22	***
$\Delta t=4:ODep=0$	-0.11	***	0.03	
$\Delta l=1:Lm=0$	-0.03			
$\Delta l=1:Lm=1$	0.12	***		
$\Delta l=1:ODep=0$	-0.21	***	-0.13	***
$\Delta l=1:CV=0.2$	-0.26	***		
$\Delta l=1:CV=1$	0.1	**		
$\Delta l=1:Ls=0$	-0.09	**	-0.23	***
$\Delta l=1:Ls=1$	0.15	***	0.35	***
Lm=0:Ls=0	-0.1	**	-0.17	**
Lm=1:Ls=0	0.22	***	0.42	***
Lm=0:Ls=1	0.2	***	0.33	***
Lm=1:Ls=1	-0.41	***	-0.68	***
K:Ls=0	-1.37			
K:Ls=1	2.55	***		
ODep=0:CV=0.2			0.13	***
ODep=0:CV=1			0.00	
Lm=0:ODep=0			-0.07	
Lm=1:ODep=0			-0.06	
Lm=0:CV=0.2			0.11	
Lm=1:CV=0.2			-0.27	***
Lm=0:CV=1			0.00	
Lm=1:CV=1			-0.03	
$\Delta t=1:CV=0.2$			-0.11	
$\Delta t=4:CV=0.2$			-0.07	
$\Delta t=1:CV=1$			-0.06	
$\Delta t=4:CV=1$			0.01	
$\Delta t=1:Ls=0$			-0.15	**
$\Delta t=4:Ls=0$			0.00	
$\Delta t=1:Ls=1$			0.18	**
$\Delta t=4:Ls=1$			-0.01	

#### 4.2.3 Multivariate regression trees analysis

Results of the multivariate regression tree analysis are presented in Table 5 and Figure 3. The first criterion to partition groups of fits is the size of the class for both hypotheses of variance. Small length classes tend to improve the estimation of  $K$  and especially the goodness of the fit of frequencies at length. Then the fits are partitioned according to time-steps for both variance assumptions: large time-steps degrade the estimation of frequencies at length, and this is amplified with wide length classes. We can notice that monthly and quarterly time-steps are opposed to yearly time-step, except when assuming the first hypothesis of variance (1) and 5

cm classes. In that case, the monthly time-steps is opposed to quarterly or yearly time-steps and the fits are then split regarding the position of individuals within classes. The next two partitions with the second hypothesis of variance (2) concerns the assumption on statistical distribution of growth increments: assuming a gamma or log-normal improves the goodness of the fit.



**Figure 3: Multivariate regressions trees of the fits of the matrix model on simulated frequencies when assuming the first hypotheses of variance (a) and the second hypotheses (b). n indicate the number of adjustments in the leaves. The grey numbers indicate the number of the nodes, more information on each node can be found in Table 5.**

**Table 5: Information on the nodes of the multivariate regressions trees (Figure 4) for both two hypotheses of variance. The best fits are the ones with the lowest LK and the highest Lbic.**

HYPOTHESES OF VARIANCE	NODE NUMBER	NUMBER OF ADJUSTEMENTS IN THE NODE	MEAN LBIC (CENTRED AND REDUCED)	MEAN LK (CENTRED AND REDUCED)	DEVIANCE
1	1	648	0.00	0.00	1294
	2	324	0.39	-0.82	328
	3	324	-0.39	0.82	117
	4	216	0.19	-1.14	118
	5	108	0.79	-0.17	21
	6	108	-0.57	0.08	9
	7	216	-0.30	1.19	435
	8	54	-0.11	-0.15	102
	9	54	1.70	-0.18	240
	10	72	-1.02	1.10	16
	11	144	0.06	1.23	167
2	1	648	0.00	0.00	1294
	2	324	0.26	-0.83	363
	3	324	-0.26	0.83	72
	4	108	-0.17	-1.46	195
	5	216	0.48	-0.51	445
	6	108	-0.51	0.10	97
	7	216	-0.14	1.19	251
	8	144	-0.48	1.20	134
	9	72	0.53	1.16	26
	10	96	-0.96	1.23	41
	11	48	0.49	1.15	69

## Discussion

This study aimed to analyse the impact of various assumptions on a length-based matrix model, especially time and length discretisation, in order to detect some artefacts caused by inappropriate assumptions in the model structure and to propose the most flexible model. Mean length was described by a von Bertalanffy growth curve, but more general growth functions can be considered as polynomial, Gompertz, Verhulst, Richards, Schnute). The inter-individual variability was modelled using a statistical distribution around this mean. Theoretically, a growth increment variance should be estimated for each length class but we made some assumptions to reduce the number of parameters to estimate. Such assumption is not critical in the model presented in this paper as the number of parameters is limited; however, our goal is to develop a complete length-based stock assessment model in which, due to the large number of parameters, such additional assumptions will be necessary. It should be noticed that assuming a relationship between the mean and variance constrains the statistical distributions. Although, a beta-binomial distribution may theoretically be used to describe growth variability, counting the number of classes crossed during a time-step, this study shows that such distribution is not the most appropriate because of a lack of flexibility.

In this analysis, we considered  $L_{\infty}$  known because it may be approximated by a function of  $L_{max}$  and it avoids the problem of the correlation between  $K$  and  $L_{\infty}$ . This assumption has already been used for example in (DeLong *et al.*, 2001). The sets of von Bertalanffy parameters used in the study are closed to the current assumed growth of the European hake ( $K=0.1$ ) (Piñeiro and Sainza, 2003) and to the newly assumed growth ( $K=0.2$ ) (Kacher and Amara, 2005; de Pontual *et al.* 2003; de Pontual *et al.*, accepted). The growth rate  $K$  and the constant of variance  $C$  were estimated by minimizing the sum of squared deviations between frequencies estimated by the matrix model and simulated frequencies-at-length.

We chose two criteria to describe the goodness-of-fit of the matrix model to frequencies generated by the quasi-continuous model. Those two criteria correspond to two modelling aims. The first objective was to reproduce and/or predict the observed data. In that case, we are less interested in the biological processes underlying the model than in its ability to reproduce observations. The other objective was to reproduce the biological process driving the model (for example growth). In that case, the quality of the estimates (precision, bias) is much more important. Selecting a model achieving these two objectives should be of major importance. However, it requires a method combining these two criteria. Indeed, in this study we show that the best fits (the ones with the lowest *BIC*) are not necessarily the ones which provide the best estimates of unknown parameters. Until now, we have not found any satisfactory quantitative methods to assess the effect of the different assumptions on both two criteria simultaneously. A possible solution would be to build a desirability function (Harrington 1965) combining criteria, but the choice of the function is rather subjective since the user must first define individual desirability functions for each response. Multivariate regression trees provide a convenient graphical tool to investigate the impact of assumptions in the matrix model on both criteria simultaneously but this is only an explanatory analysis based on hierarchical clustering.

The statistical analysis of the two criteria enables identification of robust model structures for the matrix model. It demonstrated that the choice of the time-step and of the classes' width was the key point when building a matrix model. These choices are closely linked to available data and are strongly interdependent. Small length classes significantly improved the fits and the estimation of growth rate. Reducing the time-step significantly improved the fits; however the growth rate became significantly overestimated. A compromise needs to be found to comply with the two modelling objectives of the model. Other assumptions had a significant effect on the estimation of the growth rate. The gamma distribution was the most flexible statistical distribution to describe growth increments variability. Assuming that individuals are uniformly distributed within length classes, rather than centred, also improved significantly the estimation of the growth rate.

This study was a preliminary analysis in the development of a length-based matrix model for the European hake (*Merluccius merluccius*) stock dynamics. The results will inform the selection of appropriate assumptions of time and length discretisation for this model. The European hake dynamic model will have a quarterly time-step and 1 cm wide classes since these appear to be a relevant compromise and they correspond to the time scale of available data. A gamma distribution will be used to describe the variability of growth increment and individuals will be uniformly distributed within length classes.

## Bibliography

---

- Anda-Montañez, A. D., Arreguin-Sanchez, F., and Martinez-Aguilar, S. 1999. Length-based growth estimates for Pacific sardine (*Sardinops sagax*) in the Gulf of California, Mexico. *CalCOFI Reports* 40: 179–183.
- Banks, H. T., Botsford, L. W., Kappel, F., and Wang, C. 1991. Estimation of growth and survival in size-structured cohort data: an application to larval striped bass (*Morone saxatilis*). *Journal of Mathematical Biology* 30(5): 125–150.
- Caswell, H. 2000. *Matrix Population Models: Construction, Analysis, and Interpretation*. Sinauer Associates, Sunderland, Massachusetts.
- Chen, Y., Hunter M., Vadas, R., and Beal, B. 2003. Developing a growth-transition matrix for the stock assessment of the green sea urchin (*Strongylocentrotus droebachiensis*) off Maine. *Fishery Bulletin* 101(4): 737–744.
- Cruywagen, G. 1997. The use of generalised linear modelling to determine inter-annual and inter-area variation of growth rates : the caperock lobster as example. *Fisheries Research* 29(2): 119–131.
- De Leo, G. A., and Gatto, M. 1995. A size and age-structured model of the European eel (*Anguilla anguilla* L.). *Canadian Journal of Fisheries and Aquatic Sciences* 52(7): 1351–1367.
- de Pontual, H., Bertignac, M., Battaglia, A., Bavouzet, G., Moguedet, P., and Groison, A. L. 2003. A pilot tagging experiment on European hake (*Merluccius merluccius*): methodology and preliminary results. *ICES Journal of Marine Science* 60(6): 1318–1327.
- de Pontual, H., Groison, A. L., Piñeiro, C., and Bertignac, M. accepted. Evidence of underestimation of European hake growth in the Bay of Biscay, and its relationship with bias in the agreed method of age estimation. *ICES Journal of Marine Science* 63: 000–000.
- De'Ath, G. 2002. Multivariate Regression Trees: a new technique for modelling species-environment relationships. *Ecology* 83(4): 1105–1117.
- DeLong, A. K., Collie, J. S., Meise, C. J., and Powell, J. C. 2001. Estimating growth and mortality of juvenile winter flounder, *Pseudopleuronectes americanus*, with a length-based model. *Canadian Journal of Fisheries and Aquatic Sciences* 58(11): 2233–2246.
- Ennis, D. M., and Bi, J. 1998. The beta-binomial model: Accounting for intertrial variation in replicated difference and preference tests. *Journal of Sensory Analysis* 13(4): 348–412.
- Fournier, D. A., Hampton, J., and Sibert, J. R. 1998. MULTIFAN-CL: a length-based, age-structured model for fisheries stock-assessment, with application to South Pacific albacore, *Thunnus alalunga*. *Canadian Journal of Fisheries and Aquatic Sciences* 55(9): 2105–2116.
- Fournier, D., and Archibald, C. P. 1982. A general theory for analysing catch-at-age data. *Canadian Journal of Fisheries and Aquatic Sciences* 39: 1195–1207.
- Froysa, K. G., Bogstad, B., and Skagen, D. W. 2002. Fleksibest- an age-length structured fish stock assessment model. *Fisheries Research* 55(1–3): 87–101.
- Harrington, E. C. J. 1965. The desirability function. *Industrial Quality Control* 21(10): 494–498.
- Kacher, M., and Amara, R. 2005. Distribution and growth of 0-group European hake in the Bay of Biscay and Celtic Sea: a spatial and inter-annual analyses. *Fisheries Research* 71(3): 373–378.
- Laslett, G. M., Eveson, J. P., and Polacheck, T. 2002. A flexible maximum likelihood approach for fitting growth curves to tag-recapture data. *Canadian Journal of Fisheries and Aquatic Sciences* 59(6): 976–986.



- Moloney, K. A. 1986. A generalized algorithm for determining category size. *Oecologia* 69: 176–180.
- Pilling, G. M., Kirkwood, G. P., and Walker, S. G. 2002. An improved method for estimating individual growth variability in fish, and the correlation between von Bertalanffy growth parameters. *Canadian Journal of Fisheries and Aquatic Sciences* 59(3): 424–432.
- Piñeiro, C., and Sainza, M. 2003. Age estimation, growth and maturity of the European hake (*Merluccius merluccius* (Linnaeus, 1758)) from Iberian Atlantic waters. *ICES Journal of Marine Science* 60(5): 1086–1102.
- Pope, J. G. 1972. An investigation of the accuracy of virtual population analysis for the calculation of fishing mortality from catch at age data. *International Commission for the Northwest Atlantic Fisheries Research Bulletin* 9: 65–74.
- Sainsbury, K. J. 1980. Effect of Individual Variability on the von Bertalanffy Growth Equation. *Canadian Journal of Fisheries and Aquatic Sciences* 37: 241–247.
- Schnute, J. 1987. A general fishery model for a size-structured fish population. *Canadian Journal of Fisheries and Aquatic Sciences* 44(5): 924–940.
- Schnute, J. T., Richards, L. J., and Cass, A. J. 1989a. Fish survival and recruitment: investigations based on a size-structured model. *Canadian Journal of Fisheries and Aquatic Sciences* 46(5): 743–769.
- Schnute, J. T., Richards, L. J., and Cass, A. J. 1989b. Fish growth: investigations based on a size-structured model. *Canadian Journal of Fisheries and Aquatic Sciences* 46(5): 730–742.
- Shepherd, J. G. 1999. Extended survivors analysis: an improved method for the analysis of catch-at-age data and abundance indices. *ICES Journal of Marine Science* 56(5): 584–591.
- Smith, B. D., Botsford, L. W., and Wing, S. R. 1998. Estimation of growth and mortality parameters from size frequency distributions lacking age patterns: the red sea urchin (*Strongylocentrotus franciscanus*) as an example. *Canadian Journal of Fisheries and Aquatic Sciences* 55(5): 1236–1247.
- Smith, B. D., and Botsford, L. W. 1998. Interpretation of growth, mortality, and recruitment patterns in size-at-age, growth increment, and size frequency data. *Proceedings of the North Pacific Symposium on Invertebrate Stock Assessment and Management in Can. J. Fish. Aquat. Sci.* 125: 125–139.
- Stefansson, G. 2001. An implementation of growth. Appendix E1 in dst2 progress report for 2000. *MRI Technical Report* 78: 107–112.
- Sullivan, P. J. 1992. A Kalman Filter Approach to Catch-at-Length Analysis. *Biometrics* 48: 237–257.
- Sullivan, P. J., Lai, H., and Galluci, V. F. 1990. A catch -at- length analysis that incorporates a stochastic model of growth. *Canadian Journal of Fisheries and Aquatic Sciences* 47(1): 184–198.
- Vandermeer, J. 1978. Choosing category size in a stage projection matrix. *Oecologia* 32: 79–84.
- Virtala, M., Kuikka, S., and Arjas, E. 1998. Stochastic virtual population analysis. *ICES Journal of Marine Science* 55(5): 892–904.