Analyses of length and age distributions using continuation-ratio logits

Anna Rindorf and Peter Lewy

Abstract: Sampling of length and age distributions of catches is important for the assessment of commercially fished stocks. This paper presents a new method for statistical analyses and comparisons of length and age distributions based on generalised linear models of continuation-ratio logits. The method allows statistical testing of the effects of both continuous and discrete variables. Further, by utilising the smoothness of length and age distributions as a function of length, the method provides more accurate estimates of these distributions than traditional methods. The observations are assumed to be multinomially distributed, but cases in which the variance exceeds that of this distribution may also be analysed. The implementation of the method in existing statistical analysis software is straightforward and is demonstrated using length and age distributions of the lesser sandeel, *Ammodytes marinus* Raitt.

Résumé : L'échantillonnage des distributions de fréquence des longueurs et des âges dans les captures est une étape importante dans l'évaluation des stocks des pêches commerciales. On trouvera ici une nouvelle méthode pour l'analyse statistique et la comparaison des distributions de fréquence des longueurs et des âges basée sur des modèles linéaires généralisés des logits cumulatifs supérieurs (continuation-ratio logits). La méthode permet d'éprouver les effets de variables tant continues que discontinues. De plus, en utilisant le lissage des distributions de fréquence des longueurs et des âges en fonction de la longueur, elle génère des estimations plus précises de ces distributions que ne le font les méthodes traditionnelles. On assume au départ que les distributions sont de type multinomial, mais on peut aussi analyser des cas où la variance dépasse celle de cette distribution. L'insertion de cette méthode dans les logiciels courants d'analyse statistique se fait sans problème, ce qui est illustré par l'utilisation des distributions de fréquence des longueurs et des âges du Lançon nordique, *Ammodytes marinus* Raitt.

[Traduit par la Rédaction]

Introduction

Length and age compositions of numerous commercially fished stocks are analysed on a regular basis to assess recruitment, stock biomass, and other aspects of the state of the stock. Samples for this purpose are obtained by either commercial-catch sampling, research surveys, or both. In a typical sampling programme, catch of a species is sampled by recording the total number or weight of the species caught, the length distribution of a subsample of the catch, and the age at length of a subsample of the length sample (Cotter 1998).

The multinomial distribution is frequently used to describe length and age distributions, and most authors compare these distributions by aid of the χ^2 test of homogeneity (Baird 1983; Zwanenburg and Smith 1983; Engås and Soldal 1992). However, the χ^2 distribution has the disadvantage of being an inaccurate approximation when the expected number of outcomes in a category is less than five (Cramér 1946), and the variance in the collected data is often greater than can be described by the multinomial distribution (Smith and Maguire 1983; Williams and Quinn 1998).

The calculation of catch in numbers at age from numbers at length is usually based on an age–length key. The traditional key is based on a two-way table of age and length in which the entries are number of fish at length and age (Fridriksson 1934). This key does not take the knowledge of fish growth into account. However, this relationship has been included in some investigations by assuming the length distribution of a particular age group to be normal (Schnute and Fournier 1980; Labonté 1983; Gudmundsdóttir et al. 1988).

This paper presents a new method to statistically analyse and compare samples of age and length distributions from different geographical areas, time periods, laboratories, etc. The object of the analyses is to enable the estimation of age and length distributions with the lowest possible uncertainty. One important step on the way is deciding whether or not to pool distributions from different strata. This multinomially based method provides a statistical tool for this decision that is comparable with the analysis of variance (ANOVA) in the case of normal distributed data.

The method is based on continuation-ratio logits as presented by Agresti (1990) and as previously applied by Kvist et al. (2000) to analyse age distributions. However, the method presented here has several additional advantages over previous applications. It can take the smoothness of length distributions into account even in cases where the length distribution is skewed or polymodal, and can be used in cases where the variance of the observations exceeds that

Received June 13, 2000. Accepted February 7, 2001. Published on the NRC Research Press Web site on May 7, 2001.
J15816

A. Rindorf.[1] University of Copenhagen, c/o Danish Institute for Fisheries Research, Charlottenlund Castle, DK2920 Charlottenlund, Denmark.
P. Lewy. Danish Institute for Fisheries Research, Charlottenlund Castle, DK2920 Charlottenlund, Denmark.

[1] Corresponding author (e-mail: ar@dfu.min.dk).

DOI: 10.1139/cjfas-58-6-1141

of the multinomial distribution. The method utilises the knowledge of increasing mean fish age as a function of size without any assumptions being made regarding growth apart from the mean length of older fish being greater than that of younger. Further, it can easily be implemented in existing statistical-analysis software, and the effect of both categorical and continuous variables on the distribution can be tested. Methods to obtain the accuracy of estimated length or age distributions are provided as well. The method is demonstrated using survey data on length and age composition for the lesser sandeel, *Ammodytes marinus* Raitt.

Analysing ordinal multinomially distributed variables by continuation-ratio logits

Generalised linear models are a convenient tool for statistical analysis of variables following distributions in the exponential family (McCullaugh and Nelder 1989). Applying these to multinomial data enables model-selection, estimation, and testing techniques developed for generalised linear models to be employed. It is thus possible to simultaneously analyse several different length or age distributions. This implies that problems inherent in small samples can be reduced. Further, the ordinal nature of length and age measurements makes the application of the continuation-ratio logits, as presented by Agresti (1990), possible. This has several advantages when analysing length and age distributions, as shall be shown in the following.

Continuation-ratio logits can be used for any multinomial variable for which the outcomes are ordinally scaled. Assume that we have observations in ordinally scaled groups i and let p_i be the probability of the outcome falling in group i. The continuation-ratio logits are then defined as (Agresti 1990):

$$\log\left(\frac{p_i}{p_{i+1}+\ldots+p_n}\right), \quad i=1,\ldots,n-1$$

This logit corresponds to the binomial logit

$$\log\left(\frac{\pi_i}{1-\pi_i}\right)$$

where

$$\pi_i = \frac{p_i}{p_i+\ldots+p_n} = P(\text{index} = i \mid \text{index} \geq i)$$

for $i = 1,\ldots, n–1$. That is, π_i is the probability of the outcome being of index i conditional on the outcome being of index i or greater.

The continuation-ratio logits can be modelled separately or simultaneously in a generalised linear model of a binomially distributed variable, since the likelihood of a multinomial trial can be expressed as $\prod_{i=1}^{k-1} b[\pi_i, n_i, n_{i+}]$, where n_i is the number of outcomes in category i, n_{i+} is the number of outcomes in category i or greater, π_i is the conditional probability described above, and k is the number of outcome categories (Agresti 1990). Maximising the multinomial likelihood is thus equal to maximising the product of likelihoods of the conditional binomial distributions of each index. As shown by Agresti (1990), this implies that the continuation-ratio logit of each index may be modelled separately.

The continuation-ratio logits of the different outcomes are not independent observations. However, owing to the relationship between the multinomial likelihood and the likelihood of the conditional binomial distributions, maximising the multinomial likelihood is equivalent to maximising the product of the conditional binomial trials simultaneously. Thus, any software implementing maximum-likelihood techniques to analyse binomial data may be used to analyse ordinal multinomial data. This includes software designed for analyses of generalised linear models, such as SAS® and S-Plus® (McCullaugh and Nelder 1989; SAS Institute Inc. 1996; Mathsoft Inc. 1997). However, the original multinomial data must first be transformed into a data set containing the conditional binomial observations and the index of the outcome. For instance, if the multinomial data are as seen in the first two columns of Table 1, the data set to be analysed in the binomial model contains the index i, the number of outcomes in this category, n_i, and the number of outcomes of this order or greater, n_{i+} (Table 1, columns 1, 2, and 4).

If the data show greater variance than can be accounted for by the binomial variance, this may be incorporated in the generalised linear model by estimating a dispersion parameter (McCullaugh and Nelder 1989). The only constraint imposed by this method is that the dispersion parameter must be the same for all the observations included in the model, and thus for all conditional distributions, when multinomial data are analysed as described above.

Including the conditional probabilities of all indices simultaneously in one generalised linear model, it is possible to use the index as a continuous explanatory variable. The value of the conditional logit of group i can then be expressed by

$$\log\left(\frac{\pi_i}{1-\pi_i}\right) = \lambda(i)$$

where $\lambda(i)$ is a smooth function of i. The function $\lambda(i)$ can, for example, be modelled by a local nonparametric smoother or a polynomial in i. Alternatively, one model may be estimated for each ordinal group separately, if one does not wish to include the smooth relationship between the conditional probability and the index of the group. The effect of categorical factors on the conditional probability of group i may also be estimated by generalised linear models.

The model provides estimates of the conditional probabilities, $\hat{\pi}_i$, as well as the variances of these estimates. The estimated unconditional probabilities, $\hat{p}_i$, can be calculated from the conditional probabilities by applying the formula:

$$\hat{p}_1 = \hat{\pi}_1$$

$$\hat{p}_i = \hat{\pi}_i \cdot \left(1 - \sum_{j=1}^{i-1} \hat{p}_j\right) = \hat{\pi}_i \cdot \prod_{j=1}^{i-1} (1-\hat{\pi}_j), \quad i > 1$$

Approximations of the variance of $\hat{p}_i$ are easily obtained, if the variance of $\hat{\pi}_i$ has been estimated and if the conditional probabilities, $\hat{\pi}_i$, are modelled independently of each other. In this case, the estimates are uncorrelated and the variance

Table 1. A multinomial data set with the ordinally scaled outcomes, *i*, and the corresponding data set for analysis in a generalised linear model of a binomially distributed variable with the explaining variable *i* and the observed conditional probabilities π_i.

Outcome (i)	No. of observations of i (n_i)	Observed probability of i (p_i)	No. of observations of index i or greater (n_{i+})	Conditional probability of i (π_i)
1	10	0.19	54	0.19
2	25	0.46	44	0.57
3	14	0.26	19	0.74
4	3	0.06	5	0.60
5	2	0.04	(2)[a]	(1)[a]

[a] As the conditional probability of the highest outcome is always one, the value in parentheses was not included in the analyses.

of these can be approximated by the first order Taylor approximation:

$$(1) \qquad V(\hat{p}_1) = V(\hat{\pi}_1)$$

$$V(\hat{p}_i) \approx \hat{\pi}_i^2 \hat{A}_i^2 \sum_{j=1}^{i-1} \frac{V(\hat{\pi}_j)}{(1-\hat{\pi}_j)^2} + \hat{A}_i^2 V(\hat{\pi}_i), \quad i > 1$$

where

$$\hat{A}_i = \prod_{k=1}^{i-1} (1 - \hat{\pi}_k)$$

Correspondingly, the covariance between the unconditional probabilities, COV($\hat{p}_i$, $\hat{p}_j$), can be calculated.

If the conditional probabilities of all groups are analysed simultaneously and one or more parameters are common to all groups, the predicted conditional probabilities, $\hat{\pi}_i$, are correlated. This complicates derivation of analytical approximations to the variance of $\hat{p}_i$. In this case, simulation studies provide a convenient method for estimating the variance.

A simulation procedure that can be used for this purpose is the parametric bootstrap (Davison and Hinkley 1997). In this type of analysis, observations are simulated from the parameter estimates obtained from the fitted model. The simulated observations are then used to re-estimate the parameters. This is done by repeating the entire procedure of model fitting on a number of simulated data sets. The parameter estimates obtained provide estimates of the simulated variance and mean of these parameters.

Estimation of the probabilities and their variance in the multinomial distribution

The estimated probabilities obtained by the traditional multinomial approach, $\tilde{p}_i$, are calculated as

$$\tilde{p}_i = \frac{n_i}{\sum_{j=1}^{k} n_j}$$

where n_i is the number of outcomes in category *i* and *k* is the number of outcome categories. Thus, this probability does not take the overdispersion potentially present in the data into account. The variance of the estimate is calculated as

$$(2) \qquad V(\tilde{p}_i) = \frac{\tilde{p}_i(1-\tilde{p}_i)}{\sum_{j=1}^{k} n_j}$$

These estimates are referred to as the multinomial estimates in the following discussion.

Application of the method

Data analysed

The data used to demonstrate the method consist of catches of the lesser sandeel from three surveys conducted in the Firth of Forth east of Scotland in 1997 and 1998 (Fig. 1). Positions were initially chosen according to prior knowledge of sandeel distribution in the area and the same positions were dredged in both years. A modified scallop dredge was used each year to catch the sandeels while they were buried in the sediment (Winslade 1974). In 1998, the third survey was conducted using a van Ven grab to collect additional sandeels for ageing. This survey was performed at positions 2, 5, 7, and 8 (see Fig. 1*b*) within a week of the dredge survey.

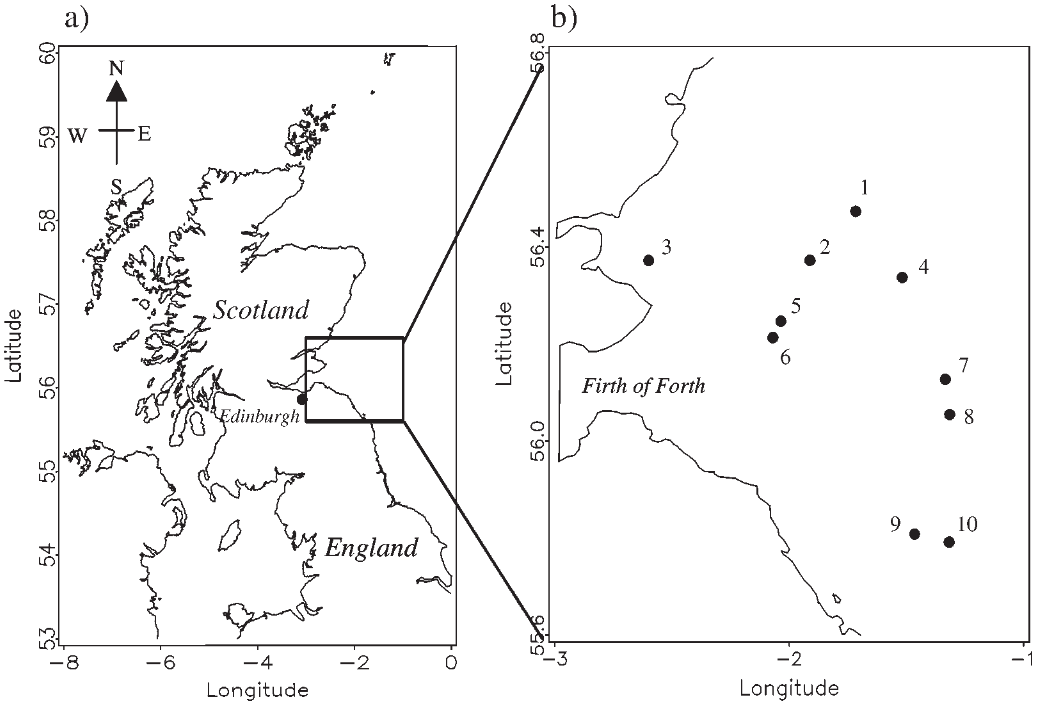
At each station, an average of five dredge hauls of 15-min duration were carried out in both years. The total content of sandeels in all hauls was weighed separately. If time permitted, the entire content was counted and length measured to the nearest 0.5 cm below. Otherwise, a random subsample was counted, measured, and weighed.

In 1997, a random subsample of 10 sandeels was taken from each length group of the dredge catch at each position (provided that the catch exceeded 10 sandeels), and age determinations were made from otoliths of these fish at the Danish Institute of Fisheries Research. In 1998, the ages of only a small number of sandeels from the scallop-dredge catches were determined at the Danish Institute. To supplement these samples, sandeels collected in the grab survey were also used in calculating the age–length relationship. The ages of these samples were determined at the Institute of Fisheries Research Services, Marine Laboratory (Scotland, U.K.) and kindly supplied by S. Greenstreet.

Analysing length distribution of catch using continuation-ratio logits

The observations analysed in this model were distributions of the observed lengths grouped in 1-cm classes for each of the hauls taken. Thus, there were five length distributions at each position, on average. The number of fish in each length group was assumed to be multinomially distributed. The object of the model developed was to examine whether the length distribution of the catch varied from year to year and (or) from position to position. As these length

Fig. 1. (*a*) Map showing the location of the study area. (*b*) Enlargement of the inset in *a*, showing the locations of dredging positions 1–10.



categories are ordinal, the conditional probabilities can be modelled as described above.

Initially, the original multinomial data set was transformed into a data set containing the index of the outcome (length in this case), the number of outcomes in the category in trial *j*, the number of outcomes of this index or greater in trial *j*, and the additional variables year and dredging position. This is equivalent to the transformation illustrated in Table 1. If no fish of index *i* or greater were recorded in trial *j*, the conditional probabilities of index *i* and greater were missing in the trial. The length-dependent continuation-ratio logits were analysed in a generalised linear model of this binomial data set.

The minimum length observed was 7 cm and the maximum length for which conditional probabilities were calculated was 18 cm. The model of the continuation-ratio logits included a seventh degree polynomial in length and categorical parameters describing the effects of year and position:

$$\text{(3)} \qquad \log\left(\frac{\pi_{l,y,\text{pos}}}{1-\pi_{l,y,\text{pos}}}\right) = \lambda_{y,\text{pos}}(l) = \sum_{n=0}^{7} b_n(y,\text{pos})l^n$$

where

$$b_n(y,\text{pos}) = b_n + b_{n,y} + b_{n,\text{pos}} + b_{n,y,\text{pos}}$$

and *l* indicates length in group *l*, *y* indicates year, pos indicates position, and *b* indicates parameters to be estimated in the model. The seventh degree polynomial was chosen as the highest-order polynomial for which no convergence problems arose. These problems are due to lack of contrast in the data, which makes it difficult or impossible to find a global minimum of the deviance. The model was fitted using the SAS® GENMOD procedure (SAS® version 6.12 for Windows®; SAS® Institute 1996). The dispersion parameter was estimated by Pearson's X^2 statistic divided by the degrees of freedom. This parameter measures the deviation between the variance between samples (hauls) measured and the variance between samples expected in the multinomial distribution. A value of one indicates that the between-haul variation is completely described by random variation within five samples from a multinomial distribution. The model was reduced by eliminating insignificant factors from the model (*F* test, 5% level). Values of r^2 were calculated as the deviance explained by a particular factor divided by the total deviance.

The length proportions, $\hat{p}_{l,y,\text{pos}}$, estimated from the reduced generalised linear model (including the significant effects of year and position) were used to perform a parametric bootstrap analysis. The number of replicates was 1000, that is, 1000 independent multinomially distributed length composition data sets for all hauls were generated by simulation, using the estimated length distribution at the given year and position, as well as the total number of fish lengths measured in the particular haul, as input. For each of these 1000 equivalent data sets, a generalised linear model of the conditional probabilities was used to estimate the length proportions, $\hat{p}_{\text{sim},l,y,\text{pos}}$. The dispersion parameter in these models was fixed at one (no overdispersion). From the 1000 replicates, the mean, $\hat{p}_{l,y,\text{pos}}$, and the variance of the estimates were calculated.

The original data were slightly overdispersed, as data showed greater variance around the model than could be accounted for by the multinomial variance. The estimation of the length distributions from the original data included this problem by introducing a dispersion parameter (McCullaugh and Nelder 1989). However, this overdispersion was not taken into account when simulating data or when building generalised linear models of the simulated data. Therefore the resulting variances estimated from the simulated data may be somewhat lower than the variances in the original data. However, the comparison between the variance calculated from the simulations and the variance in the original data does not affect the multinomial variance, as the dispersion parameter is assumed to be one in both cases.

The approximated analytically derived value of the variance of each length proportion, $\hat{p}_{l,y,\text{pos}}$, was calculated using eq. 1. These variances were compared with the simulated variances. Further, the estimated probabilities and the variances of these obtained by the traditional multinomial approach were calculated as well. These last two estimates do not take the variance between hauls (the overdispersion) into account.

Analysing age distributions for given length using continuation-ratio logits

As the number at age in a sample is also an ordinal multinomial variable, the model may equally well be applied to age distributions. In this case, the observations in the conditional binomial distribution are the number of fish of age *a*, given the age is *a* or greater. The relationship between the length of the fish and the continuation-ratio logit of the probability of being of a given age in a length group has been shown analytically by Kvist (1999) to be simple in certain cases (the results are summarised in the Appendix). Thus, if the length distribution of an age group follows a normal distribution, the relationship between length and the continuation-ratio logits can be approximated by a second-degree polynomial. A skewed length distribution such as a gamma distribution will lead to an approximately linear relationship between the continuation-ratio logits and length.

As the survey took place in early spring before the age-0 group settled in the area, only the age-1, -2, and -3+ groups were considered in the analyses. The primary aim of this model was to smooth the age distribution over lengths and not the age distribution at a given length. Therefore, to facilitate the interpretation of results, it was decided to model age groups separately and thus not smooth over multinomial orders as described in the section on length distributions.

As age determinations made by the two different laboratories may differ, and slight changes in age structure may have taken place in the 2 weeks between the surveys, a laboratory effect was included in the model. We assumed that this effect was independent of length, resulting in the full model:

$$\log\left(\frac{\pi_{a|l,y,\text{pos}}}{1-\pi_{a|l,y,\text{pos}}}\right) = c_a + c_{a,y} + c_{a,\text{pos}} + c_{a,y,\text{pos}} + d_{a,\text{lab}}$$

$$+ (g_a + g_{a,y} + g_{a,\text{pos}} + g_{a,y,\text{pos}})l$$

$$+ (h_a + h_{a,y} + h_{a,\text{pos}} + h_{a,y,\text{pos}})l^2$$

where *a* denotes age, *l* denotes length, $\pi_{a|l}$ denotes the conditional proportion of age *a* for given length *l*, lab denotes the laboratory at which the otoliths were read, and *c*, *d*, *g*, and *h* denote parameters to be estimated in the model.

Estimation of parameters in the model is performed by minimising the deviance. However, when length groups at either end of the length spectra with an observed probability of 0 or 1 were included, convergence problems occurred, owing to the inability of the minimisation routine (SAS® GENMOD (SAS® Institute 1996)) to detect a global minimum in deviance (McCullaugh and Nelder 1989). Therefore, these length groups were excluded from the data. This had virtually no effect on the estimated parameters and conditional probabilities, while eliminating the problems in the minimisation procedure. This meant that fish smaller than 8 cm or greater than 16 cm were excluded from calculations analyzing the probability of being age 1. Fish smaller than 11 cm were excluded from the analysis of the continuation-ratio logits of the age-2 group.

Estimation of the length distribution by age

The estimated length distribution for a given age group, $\hat{p}_{l|a}$, can be estimated by

$$(4) \qquad \hat{p}_{l|a} = \frac{\hat{p}_l \hat{p}_{a|l}}{\sum_l \hat{p}_l \hat{p}_{a|l}}$$

where $\hat{p}_{a|l}$ denotes the estimated probability of being *a* years old for a given length *l*, and $\hat{p}_l$ denotes the estimated probability of being length *l*. As the length distribution may differ with year and position, a length distribution was estimated for each of the year–position combinations for which more than 100 sandeels were measured. The average length distribution over positions of an age group in a given year was calculated as a weighted average, using the mean number caught at each position as weights.

Results

Length distributions

Observed length distributions, estimated multinomial length distributions, and 95% confidence limits of the estimates for two of the dredging positions are displayed in Fig. 2. The results of testing the significance of the parameters in the full model of length distribution (eq. 3) show that the parameters $b_n(y,\text{pos})$ for $n = 6$ and $n = 7$ were not significantly different from zero, which means that the continuation-ratio logit could be described by a fifth degree polynomial in length (Table 2). The fifth degree parameter, b_5, does not vary with year and position. The part of the polynomial that is fourth degree or less varies with year, position, or their crossed effect, indicating that the length distribution is not simply changed towards larger or smaller fish at all positions from 1 year to the next. Note that the polynomial parameters estimated are not of particular interest, but are merely tools used to model the fact that length distributions are usually smooth functions of length. The predicted length distributions for different positions are correlated and, therefore, there is a gain in the precision of the predictions from incorporating this into the model as opposed to examining each position separately. The proportion of the total deviance explained by the model is high (93%). The rather high number of parameters estimated (91) should be compared with the multinomial alternative of estimating 271 probabilities (one for each length group at each year and position). The deviation between positions is greater than the deviation between years (15% as opposed to 8.8% of total deviance). It is interesting to note that the greater part of the variation between

Fig. 2. Length distributions at dredging positions 1 (*a*) and 6 (*b*) in 1998; + signs indicate the observed probability, the solid line indicates the probability estimated by the multinomial distribution, and the hatched lines indicate the 95% confidence limits of the estimate (calculated using eq. 2).

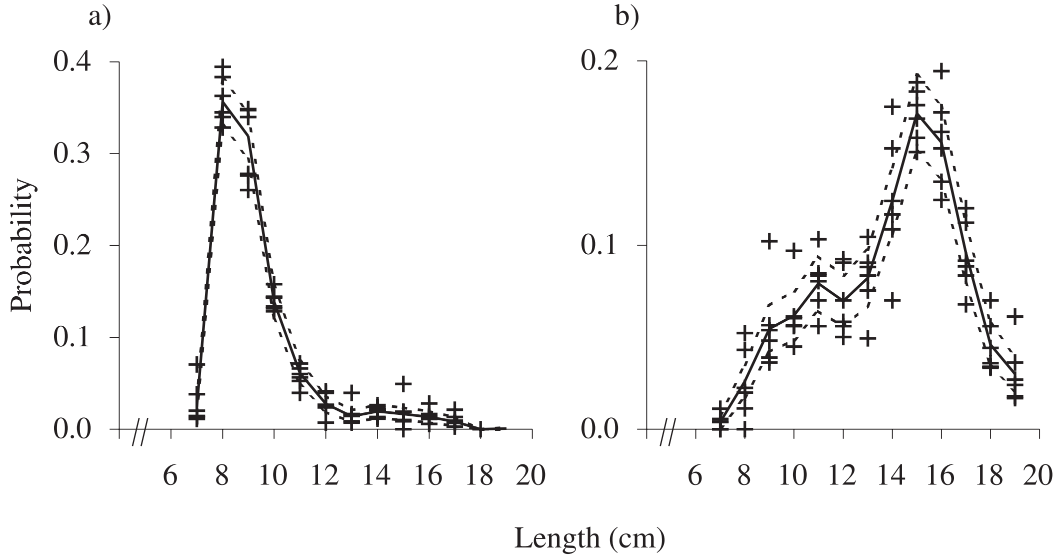


Table 2. Generalised linear model of the continuation-ratio logit of the probability of being of length *l*.

Source	Deviance	df	*F* (Type 1)	*P* > *F*	r^2	Cumulative r^2
Total	24 045	1036				
$f_1(l)$	13 901	5	1585	0.0001	0.578	0.578
$f_2(l,\text{year})$	2 120	4	292	0.0001	0.088	0.666
$f_3(l,\text{position})$	3 616	36	55	0.0001	0.150	0.817
$f_4(l,\text{year},\text{position})$	2 654	36	41	0.0001	0.110	0.927
$b_{4,\text{pos}}l^4$	74	9	4.7	0.0001	0.003	0.930
$b_{4,\text{y}}l^4$	1	1	0.8	0.3594	0.000	0.930
$b_{4,\text{y,pos}}l^4$	13	9	0.8	0.6290	0.001	0.931
$b_{5,\text{y}}l^5$	1	1	0.8	0.3608	0.000	0.931
$b_{5,\text{pos}}l^5$	36	9	2.3	0.0170[a]	0.001	0.932
$b_{5,\text{y,pos}}l^5$	9	9	0.6	0.8310	0.000	0.933

Note: $f_1(l) = \sum_{n=0}^{5} b_n l^n$, $f_2(l,\text{year}) = \sum_{n=0}^{3} b_{n,y} l^n$, $f_3(l,\text{position}) = \sum_{n=0}^{3} b_{n,\text{pos}} l^n$, and $f_4(l,\text{year},\text{position}) = \sum_{n=0}^{3} b_{n,y,\text{pos}} l^n$. See text for definition of b_n.

[a] The parameters no longer have a significant effect when the model is reduced.

positions can be explained by a greater proportion of smaller or larger fish at some positions in both years, rather than by a general trend towards larger fish in one of the years. The data were slightly overdispersed (dispersion parameter = 1.45).

The estimated conditional probabilities, $\hat{\pi}_{l,y,\text{pos}}$, the corresponding observed values, and the 95% confidence limits of the estimates are plotted against length in Fig. 3 for the two dredging positions for which the multinomial length distribution is seen in Fig. 2. Correspondingly, the unconditional length distributions predicted by the model for the same two positions are shown in Fig. 4, along with the simulated confidence limits of this prediction. The confidence limits obtained by the suggested model are clearly smaller than the confidence limits of the multinomial probability usually employed (Fig. 2).

Comparison of simulated and approximated variance

The length distributions estimated by applying the model to the simulated data did not differ significantly from the input length distributions from which the simulations were derived (the probability of difference in no case exceeded 0.50), indicating that the method provides unbiased estimates of the length proportions. The relative difference between the standard deviation of the predicted length distribution approximated by eq. 1 and the standard deviation calculated from the simulations is shown in Fig. 5*a*. If the covariances assumed in eq. 1 to be zero are in fact negative, then the approximated standard deviation will be an overestimate compared with the true value for all groups but the smallest. The relative difference between the variances is below 0.5 for the 7 and 8 cm length groups, but increases rapidly with length, indicating substantial negative correlation between the estimated conditional probabilities.

Comparing the simulated standard deviation of the model predictions with the standard deviation of the unsmoothed multinomial probabilities (Fig. 5*b*), the traditional method

Fig. 3. Probability of being a given length conditional on being at least this length, $\hat{\pi}_{l,y,\text{pos}}$, at dredging positions 1 (*a*) and 6 (*b*) in 1998; the + signs indicate the observed probability, the solid line indicates the probability predicted by the model, and the hatched lines indicate the 95% confidence limits of the predicted mean.

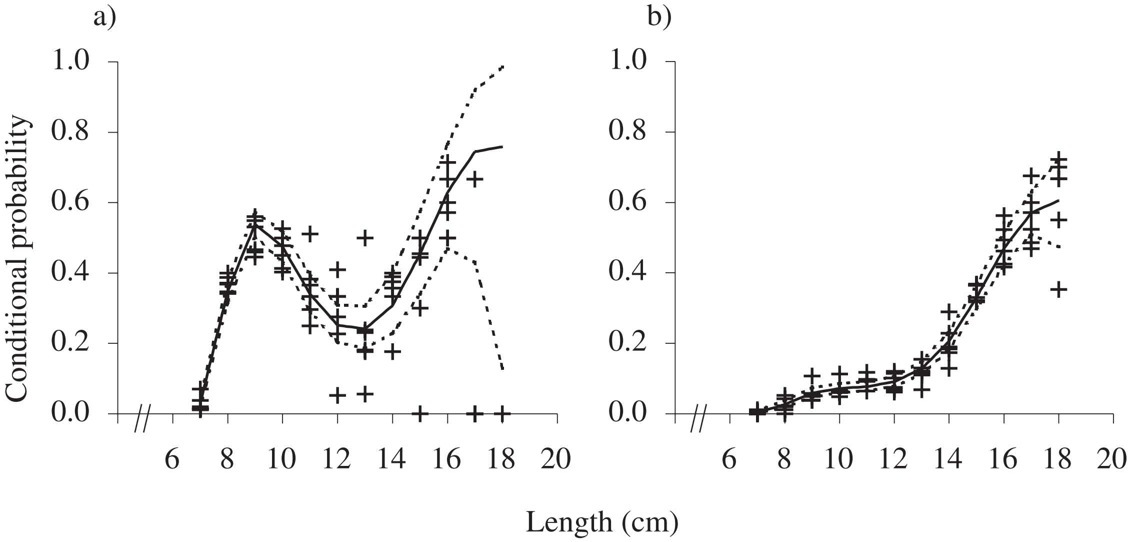
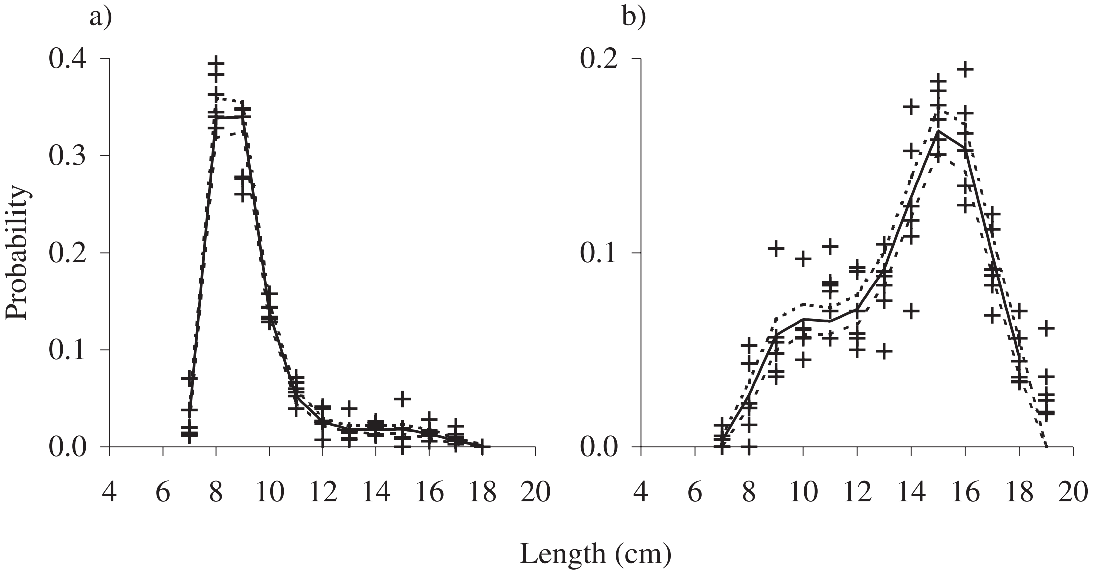


Fig. 4. Length distribution at dredging positions 1 (*a*) and 6 (*b*) in 1998; the + signs indicate the observed probability of being length *l*; the solid line indicates the probability predicted by the model, and the hatched lines indicate the 95% confidence limits of the mean (simulated).



consistently provides estimates with higher standard deviation. The reduction in standard deviation ranges from a minimum of 22%, on average, for the smallest length group to a maximum of 54%, on average, for the 14 cm length group, indicating the advantage of utilising the knowledge of the smoothness of the catch as a function of length.

Age distribution for given length

Leaving out insignificant effects, the model of the conditional probability of being age 1 became

$$\log\left(\frac{\pi_{1|l,y,\text{pos}}}{1-\pi_{1|l,y,\text{pos}}}\right) = c_1 + c_{1,y} + c_{1,\text{pos}} + g_1 l$$

Thus there was no significant effect of length squared or laboratory. The reduced model describes the data well, explaining 91% of the total deviation (Table 3; Fig. 6). In each length group, the number of sandeels for which age was determined varies, with a mean of 16 for the 8–12 cm length groups and a mean of three for the 13–16 cm length groups. The observed value of p = 1 in Fig. 6*a* at 14 cm is derived on the basis of one fish for which age was determined. Further, the logits of 0 and 1 are not defined, and these can therefore not be plotted in Fig. 6*b*. However, these values are included in the model-fitting process and thus the slope of the line appears somewhat high.

By far the most important factor influencing the conditional probability is length (67%), demonstrating the importance of including this information in the model. The year

Fig. 5. Relative differences in standard deviation by length (indicated by + signs), calculated as ($\mathrm{std}_{\mathrm{estimated}} - \mathrm{std}_{\mathrm{simulated}}$) / $\mathrm{std}_{\mathrm{simulated}}$; the solid line indicates the average relative difference. (*a*) The value of $\mathrm{std}_{\mathrm{estimated}}$ calculated by assuming covariances to be zero (eq. 1). (*b*) The value of $\mathrm{std}_{\mathrm{estimated}}$ calculated by the multinomial distribution (eq. 2).

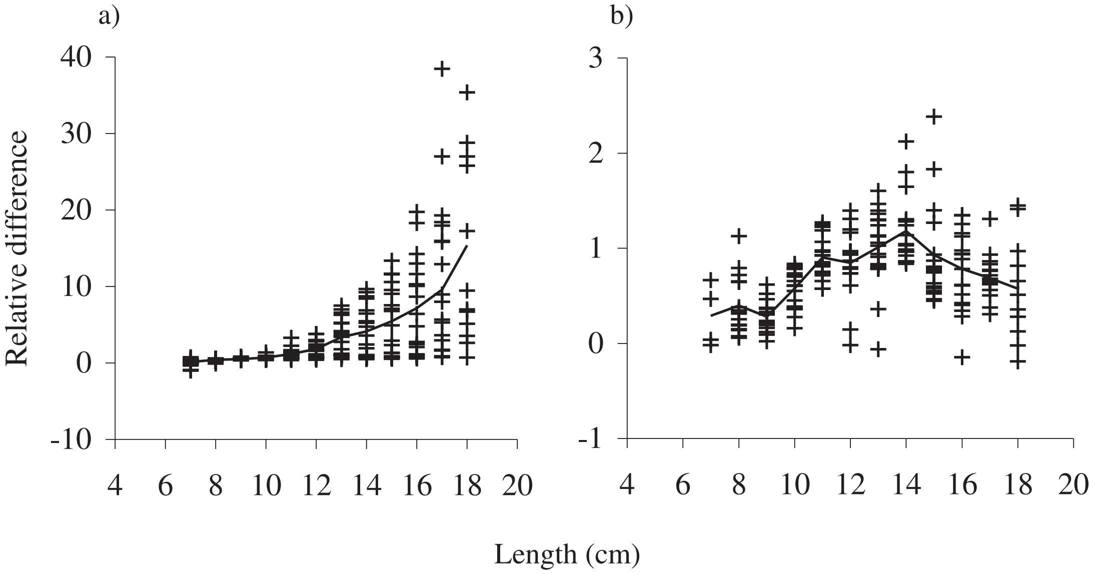


Table 3. Model of probability of being age 1.

Source	Deviance	df	*F* (Type 1)	*P* > *F*	r^2	Cumulative r^2
Total	2791	403		0.0001	0.671	0.671
$g_1 l$	1872	1	2225	0.0001	0.197	0.867
$c_{1,\mathrm{y}}$	549	1	653	0.0001	0.039	0.906
$c_{1,\mathrm{pos}}$	108	9	14	0.0059[a]	0.003	0.909
$d_{1,\mathrm{lab}}$	7	1	7.7	0.0027[a]	0.007	0.915
$c_{1,y,\mathrm{pos}}$	19	7	3.2	0.0660	0.005	0.920
$g_{1,y} l$	13	9	1.8	0.3215	0.000	0.921
$h_1 l^2$	1	1	1.0	0.0356[a]	0.004	0.925
$h_{1,\mathrm{y}} l^2$	12	6	2.3	0.2133	0.000	0.925
$g_{1,\mathrm{pos}} l$	1	1	1.6	0.2666	0.000	0.926
$g_{1,y,\mathrm{pos}} l$	1	1	1.2	0.8213	0.001	0.927
$h_{1,\mathrm{pos}} l^2$	4	9	0.6	0.9878	0.000	0.927
$h_{1,y,\mathrm{pos}} l^2$	1	6	0.2			
Residual	203	335				

[a] The parameters no longer have a significant effect when the model is reduced.

effect is the second most important factor (20%). Therefore, the same age–length key should not be applied in the 2 years. The lack of evidence of a second-degree effect of length indicates that the length distribution by age is either skewed (resembling a gamma distribution) or that the variances of the length distributions of the age-1 and age-2 groups are similar (Appendix). The percentage reduction in standard deviation obtained by using the model ranges from 35% (at 12 cm) to 71% (at 14 cm).

For the age-2 group, length once again explains more than half the variation in the probability (r^2 = 0.517, P < 0.0001). As for the age-1 group, year effect is the second most important parameter, with an r^2 of 0.139. In contrast with the model of the conditional probability of being age 1, the reduced model showed significant laboratory effects (r^2 = 0.018, P < 0.0002), perhaps owing to the increased difficulty in determining the age of older fish. When a significant crossed effect between year and length is included as well (r^2 = 0.010, P < 0.0068), the proportion of the total deviation explained is somewhat less than in the model of age 1.

Length distribution by age

The length distributions estimated by eq. 4 for sandeels in the age-1 and age-2 groups in 1997 and 1998 are unimodal and smooth, and the distribution for the 2 year olds is slightly broader than the distribution for the 1 year olds (Fig. 7). The distributions of the age-1 group in both years and of the age-2 group in 1997 are symmetrical and may be approximated by normal distributions. The distributions of the age-2 group in 1998 and the age-3+ groups in both years are very skewed, but the distributions of the age-2 and age-3+ groups in 1998 also show a tendency to bimodality.

Fig. 6. Probability of being age 1 (*a*) and the logit of this probability (*b*) as a function of length at dredging position 5 in 1997. The + signs indicate the observed values (calculated by haul), the solid line indicates the values predicted from the model, and the hatched lines indicate the 95% confidence limits of the predicted values.

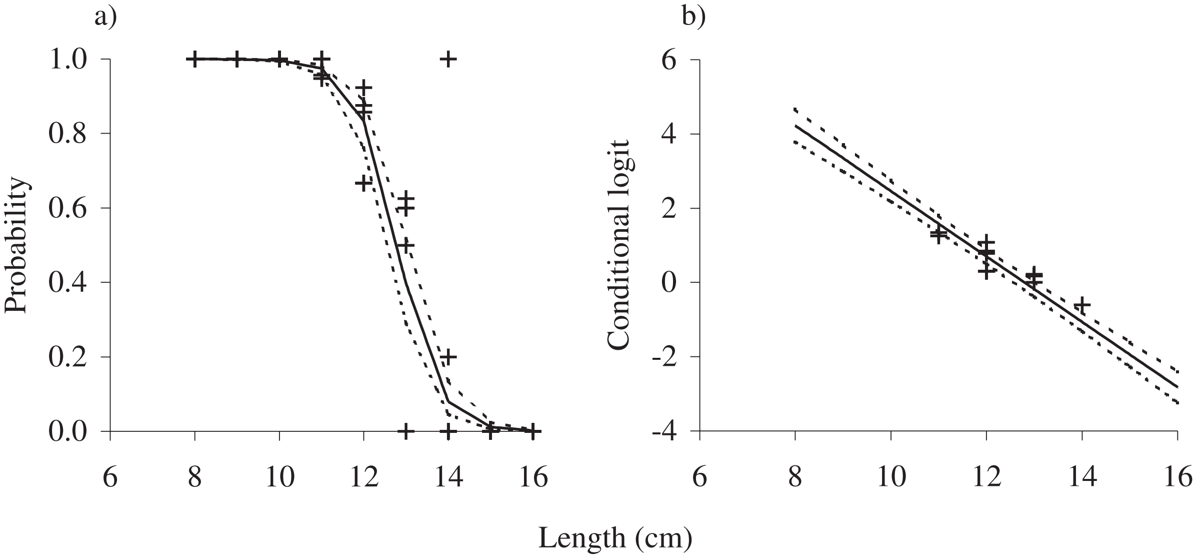
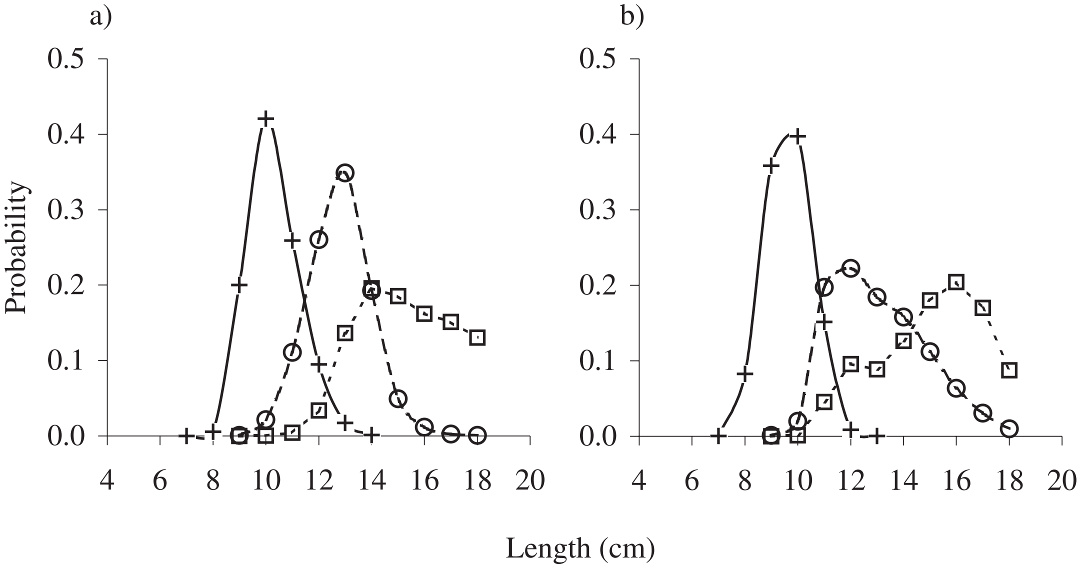


Fig. 7. Estimated length distribution of age-1 (+), age-2 (○), and age-3+ (□) sandeels in (*a*) 1997 and (*b*) 1998.



Whether this is caused by the actual length distribution or by sampling problems, such as problems with the accuracy of age determinations in this year, is not possible to determine from this study.

Discussion

The method suggested here has three main advantages compared with the standard use of the multinomial distribution. One is that entire multinomial distributions, such as length distributions or age distributions by length, may be modelled using generalised linear models in existing software. The theory of model selection, testing of hypotheses, estimation, and prediction developed for these models may be used directly. Further, it is likely that the χ^2 distribution is a better approximation of the distribution of the deviance than the usual test in the multinomial distribution and that the power of the test of the new method is greater than the multinomial χ^2 test, as the new method utilises the ordinal nature of the outcomes by simultaneously utilising data for all length groups contrary to the multinomial approach. However, the actual improvement in the example shown here has not been tested. Secondly, including the smoothness of the length distribution and the age distribution as a function of length is straightforward and improves the precision of the estimates. The suggested method therefore provides more accurate estimates of length and age distributions than the multinomial approach. Furthermore, estimates are unbiased. Thirdly, overdispersion is easily incorporated in the analyses, allowing the data to vary more than expected in a traditional multinomial distribution. If the variance in the collected data is greater than expected in the multinomial case, this may be addressed alternatively by analysing compound multinomial distributions in which the probabilities of the different outcomes are assumed to vary between samples (Smith and Maguire 1983) or by assuming the probabilities of the outcomes to be dirichlet distributed (Williams and Quinn 1998). However, neither of these methods incorporates the smoothness of the distributions, and they are both sensitive to the inadequacy of the χ^2 distribution in the small-sample case.

We have not been able to find other examples in which generalised linear models and continuation-ratio logit analyses have been used simultaneously for all outcomes of a multinomial distribution thus enabling the relationship between the index of the group and the probability to be modelled as smooth. However, separate fitting for each index group as suggested by Agresti (1990) has been used in analyses of age distributions (Kvist et al. 2000).

The results of a model of the continuation-ratio logits are often more easily interpreted than a model of the corresponding multinomial distribution, as a positive factor in the continuation-ratio logit model may simply be interpreted as, for example, "increasing the probability of young fish," in the case of analyses of age distributions. This was demonstrated in the reduced model of the conditional probability of being age 2, where one laboratory consistently placed a higher proportion of the fish in the age-2 group than the other laboratory. An additional advantage of the present approach compared with the traditional multinomial method is the ability to predict or interpolate length distributions or age compositions by length as well as the associated variances. This is particularly useful in cases where, in a particular intermediate-length group, either no fish were caught, all fish were of a particular age, or no ages were determined for the fish. Traditional methods are unable to estimate the proportion of a given age at this length. These problems may be approached alternatively by assuming the length distribution of the age groups to be normal (Labonté 1983; Gudmundsdóttir et al. 1988) or some other known distribution (Martin and Cook 1990). However, the method presented in this paper has the advantage of being able to describe unknown skewed or bimodal as well as normal length distributions by fitting the best possible polynomial in length to the logit, thereby letting the data dictate the age-specific length distribution. When estimates from the models of length and age distributions are combined, they provide smooth length distributions of the age groups. The data are not smoothed to the extent that problems in the input data become invisible, as is the case when length distributions at age are assumed to be normal. Further, length at age in the catch sample is sometimes known to deviate from normality, for example, if catchability increases with length. The youngest age groups in a trawl-survey catch will then have a skewed length distribution. Catchability problems, ageing problems, bimodal size at age distributions, etc., are still detected when applying the method. In the simple case in which length distributions of fish of age a and age $a + 2$ do not overlap, the relationship between the length distribution of the age group and the continuation ratio logit model is simple, as shown analytically by Kvist (1999) and summarised in the Appendix. In the data analysed here, the overlap between the age-1 and age-3+ groups is indeed limited, and so the approximation is reasonable. However, slower-growing species or species with large variations in growth rate may exhibit overlap between the length distributions of several age groups. In this case, the validity of the approximation of the continuation-ratio logit to a second-degree polynomial in length remains to be examined. Nevertheless, even if the approximation is not valid, a polynomial in length may still provide the best practical description of the continuation-ratio logit as a function of length.

When separate models of the continuation-ratio logit of the proportion at age by length are fitted, analytical calculation of the variance of the untransformed age proportions is simple. However, for length distributions in which the length-dependent logits have been analysed simultaneously, it is only possible to obtain poor approximations of the variance of the untransformed length proportions. The approximations may be appropriate for a small number of length groups, but Monte Carlo methods are needed to obtain reliable variance estimates for all length groups. Furthermore, overdispersion should be taken into account when performing the simulations, if the dispersion parameter differs from one. Thus, comparing mean lengths in one or more broader length groups by the χ^2 test of homogeneity (Baird 1983; Zwanenburg and Smith 1983; Engås and Soldal 1992) may, in many cases, provide adequate estimates for which variances are more easily calculated.

The method presented here provides estimates of age composition in a sample with a higher precision than the traditional methods. The model further provides opportunities to test for the effect of factors such as time or area, which will enable the analyst to decide when to join length distributions or age–length keys and when to apply them separately, to obtain the greatest accuracy in the results. In the past, extensive research has been devoted to obtaining age–length keys with the highest precision at the lowest possible cost (Kimura 1977; Baird 1983; Lai 1993). Analysing data in the way suggested here may alter the optimal sampling strategy and may even allow the same precision to be obtained with fewer samples and thus lower cost. The implication of this for the optimal sampling strategy remains to be determined.

Acknowledgements

Sandeel-catch data were collected and analysed as part of a project carried out with financial support from the Commission of the European Communities under study contract 95/078 and the U.K. Ministry of Agriculture, Fisheries and Food under contract CSA 4405. We thank Simon Greenstreet at the Institute of Fisheries Research Services, Marine Laboratory, Scotland, U.K., for permission to use age–length observations collected by the Scottish agency. Trine Kvist provided valuable help in developing the method and Morten Vinther and Poul Thyregod provided useful comments on an early draft of the manuscript.

References

Agresti, A. 1990. Categorical data analysis. Wiley series in probability and mathematical statistics. John Wiley & Sons, New York. pp. 306–346.

Baird, J.W. 1983. A method to select optimum numbers for aging in a stratified random approach. *In* Sampling commercial catches of marine fish and invertebrates. *Edited by* W.G. Doubleday and D. Rivard. Can. Spec. Publ. Fish. Aquat. Sci. **66**: 161–164.

Cotter, A.J.R. 1998. Method for estimating variability due to sampling of catches on a trawl survey. Can. J. Fish. Aquat. Sci. **55**: 1607–1617.

Cramér, H. 1946. Mathematical methods of statistics. Princeton University Press, Princeton, N.J.

Davison, A.C., and Hinkley, D.V. 1997. Bootstrap methods and their application. Cambridge University Press, Cambridge, U.K.

Engås, A., and Soldal, A.V. 1992. Diurnal variations in bottom trawl catch rates of cod and haddock and their influence on abundance indices. ICES J. Mar. Sci. **49**: 89–95.

Fridriksson, A. 1934. On the calculation of age distribution within a stock of cod by means of relatively few age determinations as a key to measurements on a large scale. Rapp. P.-V. Reun. Cons. Int. Explor. Mer, No. 86. pp. 1–14.

Gudmundsdóttir, Á., Steinarsson, B.Æ., and Stefánsson, G. 1988. A simulation procedure to evaluate the efficiency of some otolith and length sampling schemes. ICES (Int. Counc. Explor. Sea) CM 1988/D:14. Available from the International Council for the Exploration of the Sea, Palaegade 2–4, 1261 K Copenhagen, Denmark.

Kimura, D.K. 1977. Statistical assessment of the age–length key. J. Fish. Res. Board Can. **34**: 317–324.

Kvist, T. 1999. Statistical modelling of fish stocks. Ph.D. thesis No. 64, Institute of Mathematical Modelling, Danish Technical University, Lyngby, Denmark.

Kvist, T., Gislason, H., and Thyregod, P. 2000. Using continuation-ratio logits to analyze the variation of the age composition of fish catches. J. Appl. Statist. **27**(3): 303–320.

Labonté, S.S.M. 1983. Aging capelin: enhancement of age–length keys and importance of such enhancement. *In* Sampling commercial catches of marine fish and invertebrates. *Edited by* W.G. Doubleday and D. Rivard. Can. Spec. Publ. Fish. Aquat. Sci. **66**: 171–177.

Lai, H.L. 1993. Optimal sampling design for using the age–length key to estimate age composition of a fish population. Fish. Bull. (Washington, D.C.), **91**: 382–388.

Martin, I., and Cook, R.M. 1990. Combined analysis of length and age-at-length data. J. Cons. Cons. Int. Explor. Mer, **46**: 178–186.

Mathsoft Inc. 1997. S-plus users guide. Data Analysis Products Division, Mathsoft Inc., Seattle, Wash.

McCullaugh, P., and Nelder, J.A. 1989. Generalized linear models. Monogr. Statist. Appl. Probab. No. 37.

SAS Institute Inc. 1996. SAS/STAT® software: changes and enhancements through release 6.11. SAS Institute Inc., Cary, N.C. pp. 231–317.

Schnute, J., and Fournier, D. 1980. A new approach to length-frequency analysis: growth structure. Can. J. Fish. Aquat. Sci. **37**: 1337–1351.

Smith, S.J., and Maguire, J.J. 1983. Estimating the variance of length composition samples. *In* Sampling commercial catches of marine fish and invertebrates. *Edited by* W.G. Doubleday and D. Rivard. Can. Spec. Publ. Fish. Aquat. Sci. **66**: 165–170.

Williams, E.H., and Quinn, T.J. 1998. A parametric bootstrap of catch-age compositions using the dirichlet distribution. *In* Fishery stock assessment models. *Edited by* F. Funk, T.J. Quinn II, J. Heifetz, J.N. Ianelli, J.E. Powers, J.F. Schweigert, P.J. Sullivan, and C.-I. Zhang. Rep. No. AK-SG-98-01 of the Alaska Sea Grant College Program, University of Alaska Fairbanks, Fairbanks. pp. 371–384.

Winslade, P. 1974. Behavioural studies of the lesser sandeel *Ammodytes marinus* (Raitt) III. The effect of temperature on activity and the environmental control of the annual cycle of activity. J. Fish Biol. **6**: 587–599.

Zwanenburg, K.C.T., and Smith, S.J. 1983. Comparison of finfish length-frequency distributions estimated from samples taken at sea and in port. *In* Sampling commercial catches of marine fish and invertebrates. *Edited by* W.G. Doubleday and D. Rivard. Can. Spec. Publ. Fish. Aquat. Sci. **66**: 189–193.

Appendix

The relationship between the length and the continuation-ratio logit of the probability of being a particular age in the catch given the length can analytically be shown to be simple (Kvist 1999). A brief summary of the derivation of the relationship is given in the following.

The probability of a fish in the sample being age a, given the fish is of length l, $p_{a|l}$, can be expressed by

$$p_{a|l} = \frac{p_{l|a}\, p_a}{\sum_a p_{l|a}\, p_a}$$

where $p_{l|a}$ is the probability of a fish in the catch being length l given the age of the fish is a and p_a is the probability of a fish in the catch being age a. Note that this relationship is not affected by stratifying age sampling by length, as long as age samples are taken at random within each length group. The probability, $p_{a|l}$, is thus proportional to the length distribution at age a and the probability of being at age a.

The continuation-ratio logit for $p_{a|l}$ is then

$$\text{(A1)}\quad \log\left(\frac{p_{a|l}}{\sum_{i\geq a+1} p_{i|l}}\right) = \log\left(\frac{p_{l|a}\, p_a}{\sum_{i\geq a+1} p_{l|i}\, p_i}\right)$$

If the length distribution at age, $p_{l|a}$, can be described by a normal distribution, eq. A1 can be written as

$$\log\left(\frac{p_{a|l}}{\sum\limits_{i\geq a+1} p_{i|l}}\right) = \log p_a - \log\sigma_a - \frac{(l-\mu_a)^2}{2\sigma_a^2} - \log\left(\sum_{i\geq a+1}\frac{p_a}{\sigma_i}\exp\left(-\frac{(l-\mu_i)^2}{2\sigma_i^2}\right)\right)$$

where μ_a and σ_a are mean and standard deviation, respectively, of the length distribution of age group a.

This is unfortunately not a simple function of l. However, if age group a can be assumed to overlap only with age group a + 1 and not with age group a + 2, the expression may be approximated by

$$\log\left(\frac{p_{a|l}}{\sum\limits_{i\geq a+1} p_{i|l}}\right) = \log p_a - \log\sigma_a - \frac{(l-\mu_a)^2}{2\sigma_a^2} - \log p_{a+1} + \log\sigma_{a+1} + \frac{(l-\mu_{a+1})^2}{2\sigma_{a+1}^2}$$

Thus, the continuation-ratio logit may be approximated by a second-degree polynomial in length, provided age group a does not overlap with age group a + 2. Furthermore, if the standard deviations of age group a and age group a + 2 are equal, the continuation-ratio logit may be expressed by a first-degree polynomial in length.

The approximation is equally simple if the length distribution of the age groups is assumed to be gamma distributed, with mean $k_a\beta_a$ and variance $k_a\beta_a{}^2$, as the expression then becomes

$$\log\left(\frac{p_{a|l}}{\sum\limits_{i\geq a+1} p_{i|l}}\right) = \log p_a - \log\Gamma(k_a) - k_a\log\beta_a + (k_a - 1)\log l - \frac{1}{\beta_a} - \log p_{a+1} + \log\Gamma(k_{a+1}) + k_{a+1}\log\beta_{a+1}$$
$$- (k_{a+1} - 1)\log l + \frac{1}{\beta_{a+1}}$$

where

$$\Gamma(k) = \int_0^\infty t^{k-1}\exp(-t)\mathrm{d}t$$

and overlap between age groups a and a + 2 is still assumed to zero. This expression is linear in log$l$ and is approximately linear in l in the range considered in the present paper.