



A simple statistical method for catch comparison studies

René Holst^{a,1}, Andrew Revill^{b,*,1}

^a National Institute of Aquatic Resources, Technical University of Denmark (DTU-Aqua), Box 101, DK-9850 Hirtshals, Denmark

^b Centre for Environment Fisheries & Aquaculture Science (CEFAS), Pakefield Road, Lowestoft, NR33 0HT, UK

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ABSTRACT

For analysing catch comparison data, we propose a simple method based on Generalised Linear Mixed Models (GLMM) and use polynomial approximations to fit the proportions caught in the test codend. The method provides comparisons of fish catch at length by the two gears through a continuous curve with a realistic confidence band. We demonstrate the versatility of this method, on field data obtained from the first known testing in European waters of the Rhode Island (USA) 'Eliminator' trawl. These data are interesting as they include a range of species with different selective patterns.

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1. Introduction

The catch comparison experimental method has some advantages, which makes it preferred to selectivity trials for many purposes. This includes handling of the gears, commercial-like performance of the gears and conveying and interpretation of results. The same technique is also used in calibration experiments for trawl surveys.

The analysis of data from catch comparison experiments is however far less developed than that of selectivity experiments. See Millar and Fryer (1999) for a thorough review of the main achievements in statistical methods for the analysis of data from selectivity experiments. This imbalance may likely be explained by the fact that data from catch comparison experiments do not permit a model-based analysis in the sense of estimating the underlying selective properties by which the data were generated.

The more traditional approach for analysing catch comparison data uses paired tests by length classes. Paired *t*-tests have often been used in such studies, regardless of the data being discrete and potentially non-symmetric, thus violating the assumptions that underpin this test. The Wilcoxon test provides an alternative that does not rely on any distributional assumptions, but is dis-

advantaged by reduced power. Irrespective of the particular test, continuous curves along the length scale are more useful in describing the properties of interest, i.e. the catch efficiency at length of one gear relative to that of another gear.

Besides the intuitive appeal of making inference in terms of smooth curves with confidence bands rather than a succession of test conclusions, the approach proposed here works on the unscaled count data. In the case of sub-sampled catches the test-based methods use scaled up counts and thereby underestimate the variances and potentially produce erroneous conclusions. Our method does not suffer from this deficiency but uses the sub-sampling ratios as known offsets in the estimation and thereby obtain more realistic variance estimates.

A more recent curve fitting method/approach was proposed by Fryer et al. (2003). They used a two-stage mixed effects model similar to that commonly used for selectivity analysis (Millar and Fryer, 1999). Smooth curves were fitted for individual hauls using generalised additive models (Hastie and Tibshirani, 1990). For each length class in turn, the fitted values were input to Fryer's model of between-haul variation, giving a mean estimate over hauls. Joining up the mean estimates then gives a smooth mean curve. Imputations are used to fill in "empty" length classes. They justify their use of non-parametric smoothers by the complicated relationships of the observed proportions. We argue that the expected relationships derived from common assumptions about the selective properties makes low-order polynomials feasible approximations, with the order depending on the relative position and distance between the selective properties of the two gears. There is no requirement on

* Corresponding author. Tel.: +44 1502 562244.

E-mail address: andrew.revill@cefas.co.uk (A. Revill).

¹ Both the authors contributed equally.

similar coverage of length classes across hauls. The model can be fitted using standard statistical software which have routines for generalised linear mixed models.

2. Method

The GLMM method: catch comparison experiments generate binomial data and it is thus of interest to estimate the expected proportions at length of the total catch caught in the test codend. The absence of a non-selective control means that it is not possible to estimate the absolute selectivities of the two codends, by which these proportions are determined. The logit of the expected proportions at length may adequately be approximated by a low-order polynomial in length. For a single haul the curve may be fitted by a GLM. For a cruise, i.e. a collection of related hauls, the mean curve may exhibit random variation between hauls in addition to that variation accounted for by fixed effect covariates (Fryer, 1991). For such data a Generalised Linear Mixed Models (GLMM) can be used to obtain a pragmatic and reliable curve for the expected proportions-at-length and obtain realistic variance estimates by modelling the sampling structure.

Tools for GLM analyses are implemented in most general statistical packages today, whereas tools for GLMM analyses are less standardised and less widely available. This work used the `glmm-PQL` function in MASS package of the R statistical software. It implements the penalised quasi likelihood function (Breslow and Clayton, 1993). Insignificant terms were removed based on the Wald's test.

Repeat GLMM analyses were also made on the same source data using the SAS PROC NLMIXED routine (Wolfinger, 1999). This routine implements a proper likelihood method for mixed models. The key syntax required for GLMM analyses for both R and SAS software packages is provided as an appendix to this work.

The polynomial GLMM method proposed here is justified by considering a model for the process by which data were generated. For ease of presentation we consider a single haul and therefore suppress reference to haul indices in the following. The two gears being compared are indexed t (test) and c (control). It is assumed that their selection properties can adequately be described by logistic curves. The conditional probability that a length ℓ fish is retained by codend i given it has entered it, is thus given by

$$r_i(\ell) = \frac{\exp(\alpha_{i,0} + \alpha_{i,1} \cdot \ell)}{1 + \exp(\alpha_{i,0} + \alpha_{i,1} \cdot \ell)} = \frac{\exp(\eta_{i,\ell})}{1 + \exp(\eta_{i,\ell})}, \quad i = t, c.$$

The split parameter, i.e. the probability that a fish “chooses” the test codend given it chooses one them, is denoted by π . The sub-sampling ratios q_t and q_c are the proportions taken out for measurements from the catch bulk of the test and control codend respectively. The logit of the expected proportion ϕ of the total catch caught in the test codend is then given by

$$\begin{aligned} \logit(\phi(\ell; \boldsymbol{\theta})) &= \log \left(\frac{\pi \cdot q_t \cdot r_t(\ell)}{(1 - \pi) \cdot q_c \cdot r_c(\ell)} \right) \\ &= \logit(\pi) + \log \left(\frac{q_t}{q_c} \right) + \log \left(\frac{r_t(\ell)}{r_c(\ell)} \right) \\ &= \logit(\pi) + \log \left(\frac{q_t}{q_c} \right) + \eta_{t,\ell} - \eta_{c,\ell} \\ &\quad - \log \left(\frac{1 + \exp(\eta_{t,\ell})}{1 + \exp(\eta_{c,\ell})} \right), \end{aligned}$$

where $\boldsymbol{\theta} = (\alpha_{t,0}, \alpha_{t,1}, \alpha_{c,0}, \alpha_{c,1}, \pi)^T$.

This shows that when $\logit(\phi(\ell; \boldsymbol{\theta}))$ is approximated by some k 'th order polynomial in ℓ :

$$\logit(\phi(\ell; \boldsymbol{\theta})) \approx p_k(\ell; \boldsymbol{\beta}) = \log \left(\frac{q_t}{q_c} \right) + \beta_0 + \beta_1 \cdot \ell + \dots + \beta_k \cdot \ell^k,$$

the intercept term β_0 absorbs the split and the intercepts $\alpha_{t,0}$ and $\alpha_{c,0}$. Inference about the efficiency of the test gear relative to that of the control gear is therefore subject to an assumed value of the split, say $\pi = 50\%$. Polynomial terms of order higher than 1 account for the non-linear component $\log(1 + \exp(\eta_{t,\ell})/1 + \exp(\eta_{c,\ell}))$ of $\logit(\phi(\ell; \boldsymbol{\theta}))$.

When data are collected during say H hauls, a mixed effects model approach may be used to account for the variability between the hauls. For a random intercept model the polynomial associated with haul h becomes

$$p_k^{(h)}(\ell; \boldsymbol{\beta}) = \log \left(\frac{q_t^{(h)}}{q_c^{(h)}} \right) + \beta_0 + \beta_1 \cdot \ell + \dots + \beta_k \cdot \ell^k + b_h,$$

with $q_t^{(h)}$ and $q_c^{(h)}$ being sub-sampling ratios for haul h for test and control respectively and where $b_h \sim N(0, \sigma^2)$. The model is readily extended to more complex variance-component structures (Longford, 1994).

Demonstrating the flexibility of polynomials: low-order polynomials may well approximate to the range of data likely encountered in a wide range of catch comparison scenarios. A polynomial fitted to data deviates from the “true” curve partly by the bias introduced by being an approximation and partly by the binomial errors. The bias depends on the ‘wiggleness’ of $\logit(\phi)$ (as determined by the parameter $\boldsymbol{\theta}$) and the degree of the polynomial. The use of polynomial approximations is only useful if the bias can be made negligible by polynomials of relatively low-order. For known values of the parameter vector $\boldsymbol{\theta}$ and a fixed k , the bias from the assumed model curve $\logit(\phi)$ may be quantified by the maximum absolute difference between the curve and the polynomial of degree k , which fits it the best; i.e. the polynomial of degree k with minimal maximum absolute difference to the curve it is approximating.

Since these so called minimax polynomials (Denman, 1966) are very difficult to obtain, Chebychev polynomials of the first kind are used as alternatives (Abramowitz and Stegun, 1972). These are virtually the same, but much easier to compute (Press et al., 1992). Thus, the potential of the method by finding the minimal required polynomial orders for a broad range of possible scenarios is possible. An exhaustive coverage is outside the scope of this article and instead we demonstrate the validation by three different settings. The three scenarios all describe the comparison of catches from fishing gears with widely differing L50's and selection ranges (SR) as might be encountered in most field experiments. Low-order polynomials can efficiently describe a wide range of likely catch comparison data (Fig. 1, Table 1). The maximum absolute differences between true catch comparison curves and various approximating polynomials under the three scenarios are detailed in Table 1, while the corresponding curves are plotted in Fig. 1.

3. Demonstration data

The GLMM method is demonstrated here using newly obtained unpublished data collected from a catch comparison study undertaken in the North Sea (Location 54–55°N and 001°W–001°E) during 2–8 December 2007. The catches of fish (measured to 1 cm below) from both the Experimental trawl (Eliminator trawl) (Fig. 2) and from the Control trawl (a typical North Sea demersal fish trawl) are compared. The parallel hauls method was used to collect the data, whereby two vessels towed the trawls along parallel tracks, keeping as close together as was practicable and safe (usually within 0.5

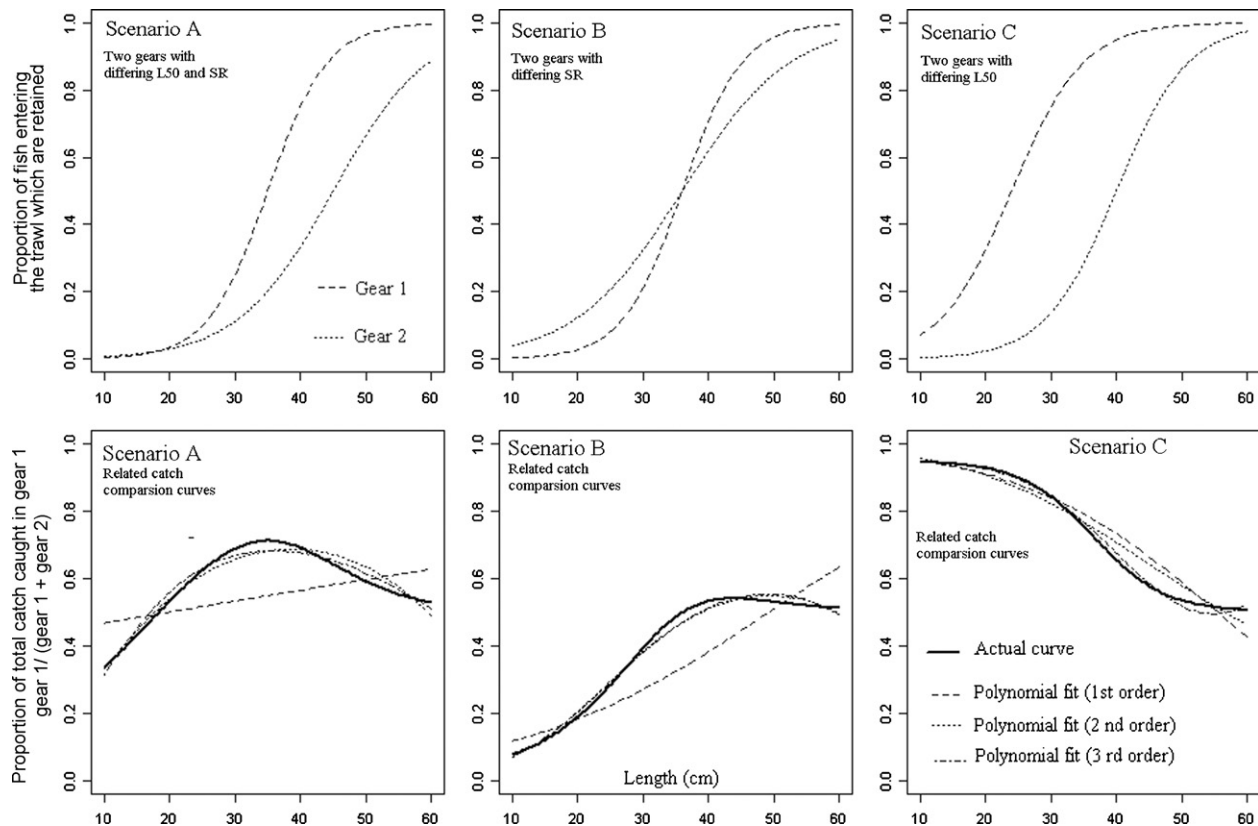


Fig. 1. Demonstrating the flexibility of low-order polynomials to provide good approximations of catch comparison curves derived from a range of scenarios. Top row: three typical scenarios showing how the selectivity of two gears might differ. Bottom row: the related catch comparison curves from the two gears in each scenario. Curves show the back transformed Chebychev polynomials (1–3rd order) fit of the data relative to the actual true curve.

Table 1

The maximum bias obtained when using low-order polynomials to provide estimations of the catch comparison curve in three varying scenarios.

Scenario	Test		Control		Maximum bias $ \phi(\ell) - p_k(\ell) _\infty$		
	L50 (cm)	SR (cm)	L50 (cm)	SR (cm)	$k = 1$	$k = 2$	$k = 3$
A	35	10	45	16	0.132	0.043	0.028
B	36	10	36	18	0.123	0.020	0.024
C	24	12	40	12	0.089	0.065	0.021

nautical miles). Both trawls were fitted with rock-hopper ground-gear, new and identical cod ends, each with a mesh size of 80 mm. The data from the twelve consecutive paired hauls (4–5 h in duration) have been analysed. Basic details on the sea trials and catches are provided in Table 2 and Fig. 3.

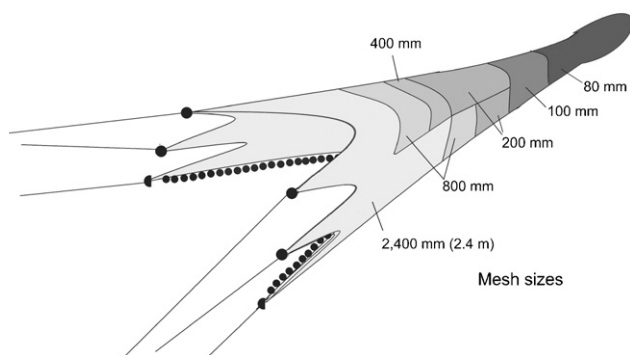


Fig. 2. Overview of the Eliminator trawl (Manufactured by Superior Trawls, R.I., USA). See Beutel et al. (2008) for detailed net plan.

4. Fitting the GLMM to the demonstration data

For each of four fish species, the polynomial regression GLMM (with random intercepts) was used successfully to fit curves for the

Table 2

Vessel and fishing gear details used in the catch comparison study.

	Experimental trawl	Control trawl
Vessel	Our Lass II (WY 261)	Jubilee Quest (GY 900)
Vessel length and main engine power	21.5 m, 480 kW	21.2 m, 347 kW
Usual home port	Whitby, UK	Grimsby, UK
Trawl type	Eliminator trawl	108 foot Jackson trawl
Trawl manufacturer	Superior Trawls, R.I., USA	Jackson Trawls, Scotland
Otter boards	3 m NETS	88 inch Perfect Patent B
Ground gear	Rock-hoppers	Rock-hoppers
Door spread and sweep length	28, 38 fathom	30, 38 fathom
Headline height	5–6 fathom	3 fathom
Towing speed	2.5–3 knots	2.5–3 knots
Cod end mesh size	80 mm	80 mm

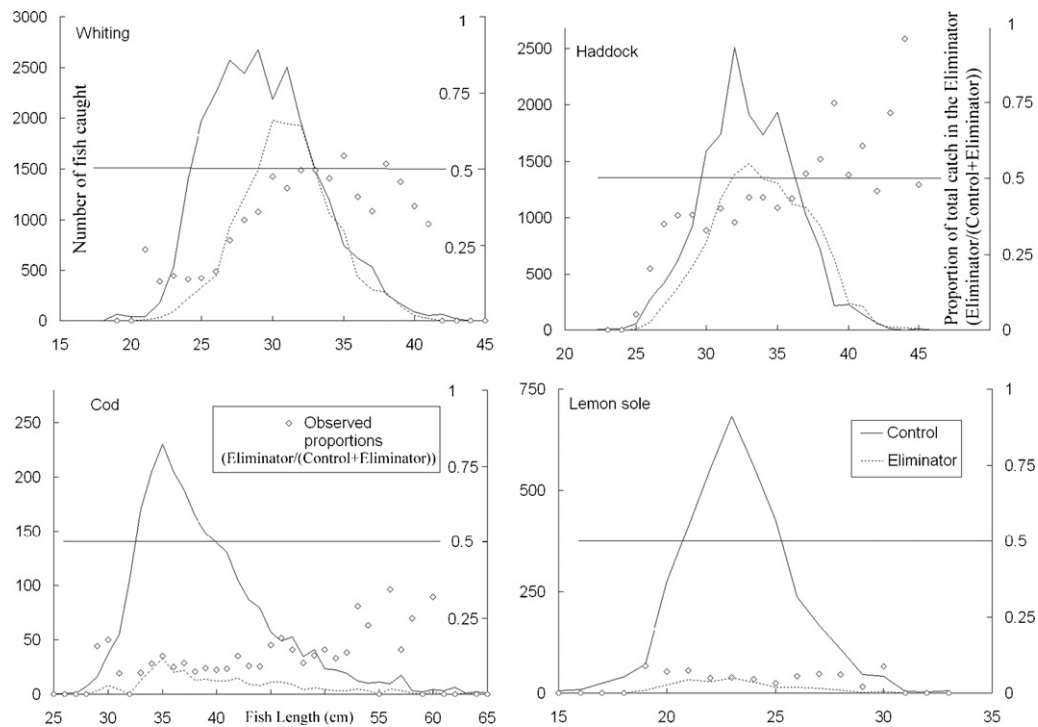


Fig. 3. Pooled catch length–frequency distributions and the observed proportions of the total catch caught in the Eliminator trawl.

expected proportions of the total catch caught by the experimental (Eliminator) trawl. Exploratory plots of the observed proportions were used as initial guidelines for choosing a sufficient polynomial order and reasonable starting values. The length variable was not centralised, but it might have facilitated the estimation in a few instances where it was necessary to pick other starting values for the parameters. The analyses proceeded by fitting third order polynomials followed by subsequent reductions until all terms showed significance. The R function `glmmPQL` was used to fit the GLMM model. Reductions were based on Wald's test, with removal of one term at a time, similarly to ordinary use of Wald's test for conventional GLM analyses. Parameter estimates with standard errors of the final fits are detailed in Table 3.

Similar, but not identical results were obtained using the SAS routine PROC NLMIXED. The difference is attributed to the different methods for integrating out the random effects.

The best polynomial curve for both cod (*Gadus morhua*) and haddock (*Melanogrammus aeglefinus*) was the logit-linear curve (Table 3 Fig. 4) indicating that fish length was a significant factor in the curve fit. Here “best” is used in the pragmatic sense of the minimal degree polynomial curve that captures the main trends

indicated by the observed proportions. The best polynomial curve for whiting (*Merlangius merlangus*) was a logit-quadratic curve and confirmed that both fish length and length² were significant factors in the fit (Table 3 Fig. 4). For lemon sole (*Microstomus kitt*), the best curve was the logit-constant, confirming that fish length was not a factor in the curve fit (Table 3; Fig. 4).

5. Discussion

GLMM catch comparison analysis: the work here has demonstrated that a GLM polynomial regression of relatively low-order provides a simple, proper and adequate tool for estimating the mean proportions of the total catch caught in the test codend at length from catch comparison data. Extra variability induced by sampling over multiple hauls is appropriately handled within the framework of GLMM.

The widespread use of catch comparison experiments emphasises the need for improved methods to replace the test based method that are most commonly used for analysing this type of data. These methods suffer from various deficiencies and have probably only survived by tradition.

A length-based curve is preferable for several obvious reasons. Catch comparison data do however not permit a proper modelling of the underlying process and direct estimation of the true expected proportion cannot be achieved. A previous work has proposed to use non-parametric smoothers in combination with linear mixed effects model. The choice of using smoothers was motivated by an assumed complicated shape of the expected proportion. Our work suggests that polynomial regression of reasonably low-order has sufficient flexibility to capture the variety of shapes that the expected proportion can attain with an acceptable level of accuracy. In our work we have studied the shapes of the expected proportion derived from a broad range of different selectivity configurations (not reported). These suggested that low-order polynomials

Table 3
GLMM parameters from trials with the Eliminator trawl.

Species	Model	Parameter	Estimate	Standard error
Cod	Linear	β_0	−4.77	0.507
		β_1	0.0551	0.0102
Whiting	Quadratic	β_0	−26.4	4.41
		β_1	1.58	0.292
		β_2	−0.0236	0.00479
Lemon sole	Constant	β_0	−3.34	0.427
Haddock	Linear	β_0	−3.42	0.749
		β_1	0.0976	0.0211

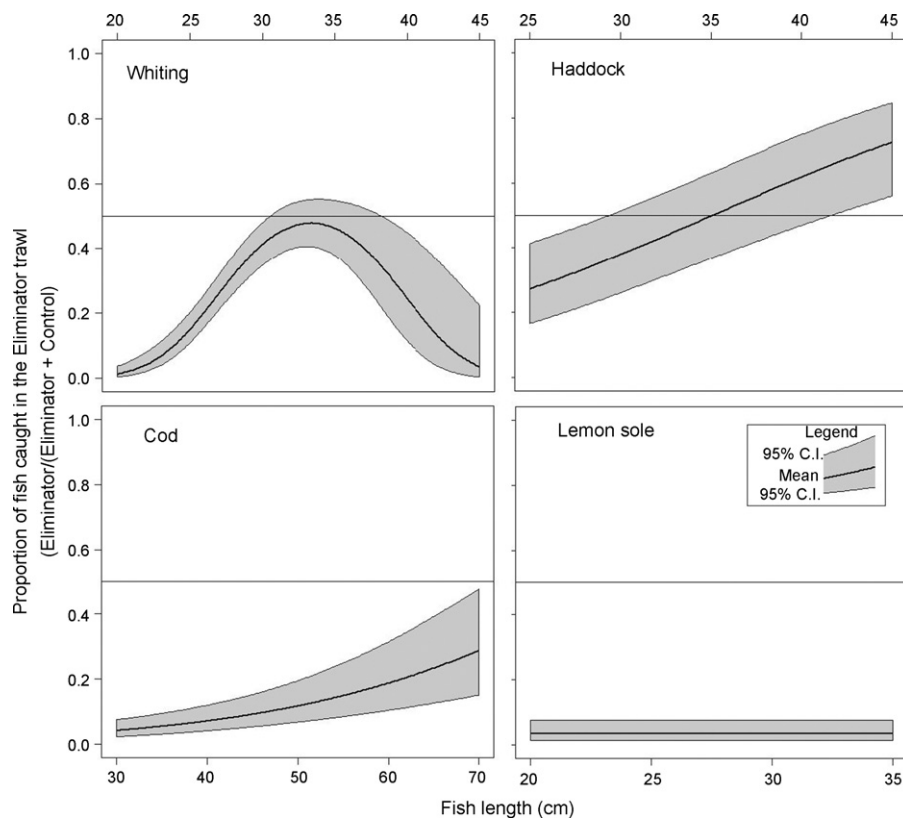


Fig. 4. GLMM modelled proportion of the total catches caught in the Eliminator trawl. Interpretation: a value of 0.5 indicates an even split between the two trawls, whereas a value of 0.25 indicates that 25% of the total fish at that length were caught in the Eliminator trawl and 75% were caught in the control trawl.

may well approximate the rather simple, smooth and un-wiggly shapes.

Chebyshev polynomials were used to assess the minimum order required to achieve acceptable accuracy and indicated that 4th order polynomials would suffice for all purposes, 3rd order would be necessary and adequate for most cases and in some cases a 1st or 2nd order would be enough. When applying the method to the Eliminator trawl data, terms of order higher than two were not significant for any of the species. Our interpretation is that the corrections contributed by higher order terms were dominated by binomial errors and therefore turned out insignificant. For ease of presentation it is useful to constrain the fits to random intercept polynomials. The fits might potentially be improved further by considering random effects on more or all polynomial terms. Inspection of fits for individual hauls will be helpful in revealing what structures are adequate and necessary. Many GLMM fitting procedures, including the R procedure *glmmPQL* and in particular SAS PROC NL MIXED, do however show difficulties in fitting models with more random effects. Changes in variance component structure mainly affect the variance of the parameter estimates rather than the estimates themselves.

For any particular dataset the shape of the fitted polynomial is entirely driven by the data within the observed range of lengths. This polynomial merely serves as a proxy for the “true” curve and therefore the continuation of the polynomial outside the observational range does not relate to the shape of true curve outside this range. Avoiding extrapolations is therefore particularly important when using this method.

The virtue of the GLMM method presented here is the simplicity with which realistic estimates with negligible bias and reliable variance estimates can be obtained. Tools for GLMM type analyses

have become widely available in many general statistical packages. The Chebyshev polynomials indicate that this method may have broader value, i.e. for a range of other likely catch comparison experiments and we suggest that further evaluations of the GLMM method could usefully be explored through simulation exercises.

Demonstration data: the results from these previously unpublished sea trials, support the findings of US workers (Beutel et al., 2008) in that the Eliminator trawl has the potential to selectively harvest haddock and whiting in a mixed-demersal fishery while allowing cod and other species to escape. In these North Sea trials, the number of cod caught were reduced by 89% and accounted for 2% (weight) of the marketable fish caught in the Eliminator, contrasted by 10% weight in the control trawl. North Sea stocks of cod are overexploited and at risk of being fished unsustainably, whereas haddock stocks have full reproductive capacity with a biomass above precautionary limits. The Eliminator trawl may therefore have potential utility within the ongoing Northern European cod recovery programme.

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Appendix A. GLMM codes for R and SAS® statistical software packages

R code

```
glmmPQL(fixed=test/(test+ctrl)~1+lgt+I(lgt^2)+offset(log(q.T/q.C)),
        random=~1|haul,
        family=binomial,
        weights=test+ctrl, data=my.R.data)
```

SAS code

```
proc nlmixed data=my.sas.data METHOD=GAUSS;
  qoffs= log(q.T/q.C)
  temp=exp(a2*lgt*lgt+a1*lgt+a0+b0+qoffs);
  r=temp/(1+temp);
  PARMS a2=0.001 a1=0.07 a0=-5 varb0=1;
  MODEL test~BINOMIAL(total,r);
  RANDOM b0~NORMAL(0,varb0) SUBJECT=haul;
```

RUN;

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