DYNAMIC PRODUCTION MODEL FOR SHRIMP STOCK ASSESSMENT: A CASE STUDY OF NORTHERN SHRIMP (*PANDALUS BOREALIS*) IN HÚNAFLÓI, ICELANDIC WATERS

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ABSTRACT

The northern shrimp (*Pandalus borealis*) fishery in the Húnaflói area developed in the late last century but collapsed in 1999 because of the increasing of cod (*Gadus morhua*) abundance. This study aims to estimate the shrimp biomass before the collapse and predict the equilibrium yield and spawning stock biomass if the shrimp stock recovers. A length distribution model, a dynamic production model, and a yield per recruit model were used with the input data on length and weight of shrimp, survey abundance index from the annual spring and autumn surveys and catch data from the commercial shrimp fishery. The maximum likelihood criterion and least-squares criterion were used for fitting the models. The size of *Pandalus borealis* in the Húnaflói area was small compared to other areas such as the Flemish Cap, Barents Sea or Jan Mayen. The growth parameters were in the range of the others with $L_\infty =$ 24.9 mm (carapace length), $K = 0.29$ and $t_0 = -0.33$. The shrimp biomass was estimated with a dynamic production model 1989 and 1999 by tuning it with the abundance index from the surveys and the commercial catch. The average biomass was estimated at about 10,000 tonnes. The expected yield and spawning stock biomass were obtained from the prediction model assuming a recovery of shrimp stock in Húnaflói. An equilibrium yield and spawning stock biomass were also modelled in order to estimate the sustainable harvest levels in the future. Both models agreed on a long term annual yield of 2500 tonnes.

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1   INTRODUCTION

Shrimp is one of the most important commodities in the world market. In 2004, the value of shrimp products was 16.5% of the total value of internationally traded fishery products and was even more important in several key markets (FAO 2006). In recent years, Vietnam has been one of the top shrimp exporting countries. The shrimp fishery in Vietnam has a one thousand year history from the country's settlement and development. The shrimp resources in Vietnamese waters are diverse, with 225 species belonging to 21 families, of which species of the family Penaeidae are 34% or 77 (MOFI 1996). Shrimp has been targeted by the trawl fishery and has contributed significantly to marine production because of its high value. Shrimp catches were 91,850 metric tonnes of total catches of 1,647,233 metric tonnes of marine products and 17% in monetary value of the marine capture fisheries in 2003 (MOFI 2005).

However, based on the results from previous studies, the estimated total shrimp biomass in Vietnamese waters was about 80,773 metric tonnes (MOFI 1996). Why the catch is higher than the estimated biomass is difficult to say. Based on this contradiction, how are we to make the right decision for the sustainable utilisation of this resource? This resource might also be overfished because of decreasing CPUE of the shrimp fleet. It is, therefore, necessary to re-estimate the shrimp biomass. New studies have to take into account the need to combine the results from the surveys with the data from the commercial fisheries.

The northern shrimp (*Pandalus borealis* Kroyer, 1838) is widely distributed in the North Atlantic and North Pacific. Their habitat is in the depth range of 20 to 1 380 m on clay and mud bottoms. Their maximum total lengths are 120 mm (♂) and 165 mm (♀) (FAO 1980). Studies in Greenland show that larvae, juveniles and adults of *P. borealis* have different distributions at a small spatial scale. Larvae and juveniles are distributed in shallow waters or near the coast and the adult shrimp occurr in deeper waters. The northern shrimp has diurnal vertical migrations, ascending in the water column in the evening and returning to the sea bottom in the morning, probably for feeding purposes (Parsons *et al.* 1998, Garcia 2007).

P. borealis has become an important target of the fisheries of the North Atlantic. The main fisheries are now concentrated off Greenland, in the Gulf of St. Lawrence, the Bay of Fundy and the Gulf of Maine. Intensive shrimp fisheries were also present in Icelandic and Norwegian waters. It is also fished in Kattegat and Skagerak by Danish trawlers and in the northern and central North Sea by Danish, Norwegian, British, German and Dutch trawl fleets (FAO 1980).

With the Icelandic name Stóri Kampalampi, the northern shrimp was exploited for the first time in an experimental fishing in northwest Icelandic waters in 1924 (Garcia 2007). This did not continue but a commercial fishery was started again in 1935 when processing facilities on land became available in Ísafjörður. According to a review paper by Garcia (2007), the shrimp fishery extended to Arnarfjordur in 1938 and other inshore areas around Iceland later on. The shrimp catches increased from less than 2000 tonnes during the period 1955-1968 to 2500-7800 tonnes in 1969-1984 (Garcia 2007).

The Icelandic offshore shrimp fishery began in 1974 and became the most important shrimp fishery after 1984 when total landings were between 68% and 94% of annual shrimp catches. It played an important role in increasing catches from a maximum of 7300 tonnes in 1973 (only of inshore fishery) to 76,000 tonnes in 1995 (Garcia 2007).

The first trawl survey for stock assessment of offshore shrimp was conducted in 1987 and the results from these surveys are the base for establishing total allowable catch (TAC) in the offshore shrimp fishery (Garcia 2007). Standardised inshore shrimp surveys in autumn and spring have been carried out since 1988 (Skúladóttir *et al.* 2001).

In this connection, the northern shrimp *(Pandalus borealis)* in the Icelandic waters, with the relevant data from both surveys and fishing fleet, was a good case study for the author to conduct with the knowledge gained from the UNU-FTP training course. The lessons from the project have been the comprehensive experiences for the author in order to contribute to research and shrimp stock assessment in Vietnamese waters.

Because of timeconstraints, the study was only concentrated on the Húnaflói area in the northern part of Iceland. The data for analysis were based on length distribution and biomass index from the surveys and the total landings from the shrimp fleet. This is convenient since it is also difficult to estimate age of fished resources in Vietnamese waters.

Húnaflói is one of the inshore shrimp fishing grounds. The first survey for shrimp in this area was in 1961, but not much shrimp was found at that time (Hallgrímsson 1961). More successful experimental shrimp fishing surveys were conducted again in 1965 (Hallgrímsson 1983) when a local fishery for shrimp was established. According to official statistics, the shrimp landings in this area had two peaks with total catches of 2969 tonnes in 1984-1985 and 2618 tonnes in 1995-1996. Nevertheless, the shrimp landings have decreased significantly since then and collapsed in 1999.

What happened to the shrimp stock in Húnaflói? Temperature, substratum and salinity are importance factors that impact the distribution of *P. borealis* (Shumway 1985). The range of temperature tolerance is between -1.6°C and 8°C, the salinity preference of northern shrimp varies from $33^{0}/_{00}$ to $35^{0}/_{00}$ but shrimp still occur in some areas with lower salinity such as $23.4^{0}/_{00}$ (Garcia 2007). Bottoms of soft, muddy or sandy silt are preferred. The northern shrimp stock in the Gulf of Maine is at the southern limit of its range and its growth, development rates and reproductive success have been affected by temperature changes (Idone 2006).

The growth rates of shrimp depend on temperature and seem to increase with higher temperatures. Skúladóttir *et al. (*2007) compared the growth rate of shrimp in some areas and pointed out that shrimp in Gullmarsfjord showed the fastest growth where bottom temperature was around 5°C. Flemish Cap shrimp also showed fast growth at temperatures of 3.2°C whereas in the Barents Sea it showed the lowest growth with the coldest temperature at $1-2^{\circ}$C. Increased sea temperatures have been observed in northern Iceland since approximately the time the stock in Húnaflói collapsed. The increase in the temperature itself is unlikely to have caused the collapse directly as the temperatures were still well within the range of preferred temperatures for the shrimp. So why did the stock collapse?

Northern shrimp are preyed upon by many fish species (Parsons *et al*. 1998, Garcia 2007) such as cod (*Gadus morhua*), Greenland halibut (*Reinhadtius hippoglossoides*) and redfish (*Sebastes marinus*) and also by sea birds and some marine mammals. Shrimp stocks seem to be especially vulnerable to predation by cod and the currently high shrimp fisheries in Greenland and Newfoundland developed only after the cod stocks in these regions collapsed (Vilhjalmsson *et al*. 2004). The opposite has indeed happened in Iceland. Almost all the shrimp stocks in Iceland did collapse in the wake of a more northernmore distribution of cod (Skúladóttir *et al*. 2001).

Figure 1: The northern shrimp (*Pandalus borealis*) (Idoine 2006).

Studies on *P. borealis* in Icelandic waters have been conducted since 1960. Skúladóttir *et al.* (1989) reported the stock size of *P. borealis* in the Isafjardardjup area based on VPA and swept area methods. The length distribution of shrimp was used to obtain the mean length-at-age together with proportion and catch data in order to calculate the number in each year-class.

The offshore stock of *P. borealis* was evaluated in 1994 including a predation factor by cod stock using a stock production type model (Stefansson *et al*. 1994). The model was composed of three parts with a part describing the recruitment as a function of spawning stock, a part describing how the stock size at the end of the year developed from the stock size at the beginning of the year, intermediate catches, natural mortality, growth and recruitment, and a part describing the number consumed by cod.

In order to formulate an age structured production model for shrimp stock, Ratz and Skúladóttir *et al.* (2000) used VPA with the Extended Survivors Analysis (XSA) to assess the historical stock, spawning stock size in numbers and weight, as well as exploitation rates of *P. borealis* on the Flemish Cap.

Skúladóttir (2004) calculated yield and spawning biomass per recruit for northern shrimp at the Flemish Cap. The study used a length-based model with fishing pattern by length, Von Bertalanffy growth equation, and maturity of females by length and three sets of natural mortality (*M*).

Considering the shrimp in the Húnaflói area in two periods, the objectives of this study were to estimate the shrimp biomass before the collapse and predict the equilibrium yield and spawning stock biomass in the next 20 years when the shrimp stock recovers.

Figure 2: Map of the study area

2   METHODOLOGY

Both the biomass estimation and prediction models used in this study are statistical models. They link to any available fisheries data sources yet do not require the existence of all of them. The data used here are:

- Length frequency distributions
- Length-weight relationships
- Annual landings
- Biomass indices from surveys

This data was analysed by models in the R software package.

2.1   Data collection

The input data for this study was collected from the MRI database including both survey and commercial fisheries data. The details can be seen in Appendix A.

Survey data for northern shrimp (*Pandalus borealis)* in the Húnaflói area are available from 1988 to 2004. Each year, two surveys were conducted, in spring and autumn

(Stefansson *et al*. 1994, Skúladóttir *et al.* 2007). Biomass indices are available from these surveys as well as length distribution measurements. Various measurements are made on the sexual stage of the shrimp but here it was separated into two groups, with internal spine (generally males) and without internal spine (mature females) (McCrary 1971).

Catch data is available from the beginning of our period (1988) until the collapse in 1998. No shrimp fisheries have been conducted in Húnaflói since that time.

2.2 Data analysis

2.2.1 *Growth parameter estimation based on length distribution data*

The length distribution data was analysed as a combination of cohort length distributions, each of which was assumed to be in the form of a Gaussian distribution (Stefansson 2007a). The location of each distribution was centred on the mean length of the corresponding cohort with a standard deviation. The Gaussian density and cumulative distribution function was:

$$f(x) = \frac{1}{\sqrt{2\pi}\sigma} e^{-(x-\mu)^2/(2\sigma^2)}$$

and the cumulative distribution was:

$$F(x) = \int_{-\infty}^{x} \phi(t)dt = \Phi\left(\frac{x-\mu}{\sigma}\right).$$

Take a fixed age group of shrimp and assume that they are distributed along the length axis according to Gaussian density, with a mean length (μ_a) and standard deviation of length at age (σ_a). For this age group the proportion of shrimp within length category l was:

$$\Phi\left(\frac{(l+\frac{1}{2})-\mu_a}{\sigma_a}\right) - \Phi\left(\frac{(l-\frac{1}{2})-\mu_a}{\sigma_a}\right)$$

And suppose the true proportion of shrimp in age group was π_a. In this case the proportion of shrimp in length group l, across all ages became:

$$\sum_a \pi_a \left\{ \Phi\left(\frac{(l+\frac{1}{2})-\mu_a}{\sigma_a}\right) - \Phi\left(\frac{(l-\frac{1}{2})-\mu_a}{\sigma_a}\right) \right\}.$$

The length distribution data of shrimp was separated to estimate the mean length of the ages of 1, 2 and 3. In order to estimate the rest of mean length at ages, the data was combined into a single estimation process. In this case, the predicted proportional length distribution was given by:

$$\widehat{y_l} = \sum_a \pi_a \left\{ \phi\left(\frac{\left(l + \frac{1}{2} \right) - \mu_a}{\sigma_a} \right) - \phi\left(\frac{\left(l - \frac{1}{2} \right) - \mu_a}{\sigma_a} \right) \right\}$$

The unknown parameters in this formula are the proportions in each age group π_a, the mean length at age μ_a, and the standard deviations σ_a. Given data (observations) on the proportions at length, those could be compared to the theoretical proportions. A formal statistical approach would be to estimate the unknown parameters by minimising the discrepancy between the observed and theoretical values. Such as sum of squares:

$$\sum (y_l - \widehat{y_l})^2$$

where y_l is the measured (observed) proportion and $\widehat{y_l}$ is the modelled proportion given above.

Using the results from the calculations described above, values for mean length at ages of shrimp were used to fit the Von Bertalanffy growth curve in order to estimate the growth parameters of the below equation:

$$L_t = L_\infty (1 - e^{-k(t-to)})$$

2.2.2 Length-weight relationship

The length-weight relationship parameters of internal spine and without internal spine shrimp were calculated based on the equation:

$$W = aL^b$$

The approach was to log-transform length and weight, followed by a simple linear regression as below:

$$\ln(W) = \ln(a) + b * \ln(L)$$

or $\quad y = a + bx$

with $\quad y = \ln(W), \ x = \ln(L)$ and $a = \ln(a)$

2.2.3 Dynamic production model

The numbers model

The growth parameters of the Von Bertalanffy equation were used to convert the length of the shrimp samples to the age structure needed for the age-based dynamic production model. The term "age-based dynamic production model" has been used to encompass a fairly wide range of models which have several common features (Stefansson 2007b). These models incorporate all the positive features of all earlier models of single-species population dynamics.

The shrimp biomass of each year was estimated based on a model of population number:

$$N_{y+1} = N_y + R_y - C_y$$

where R_y denotes the recruitment, N_y is the number of survival in year y and C_y is catch of year y.

Then the biomass was calculated:

$$B_y = \sum(N_{a,y} \, w_a)$$

Plus group

It is problematic to age-disaggregate the length distribution for the older component of the stock, where modes in the length distribution may not be easy to discern (Stefansson *et al*. 1994).

This model with true ages 1 to A (obtained from the length distribution analysis) therefore used age "A+1 as a plus group". Each year this group gets reduced by mortality but a new age group enters the plus group:

$$N_{A+1,y+1} = (N_{A,y} + N_{A+1,y})e^{-ZA}$$

When using the above equation to project stock size forward in time some assumption needs to be used for the initial population size. This applies to all ages in the first year, i.e. a single total biomass in a bulk biomass model, all true ages, as well as the plus group in a numbers model. An equilibrium assumption was used to reduce the number of parameters required. For example, in a numbers model an assumption of steady-state and no historical fishing means that the numbers at age in the first year were given as $N_{a,0} = N_{a-1,0} \, e^{-Ma}$ where Ma was an assumed number and this reduced the first-year parameter set to only the historical number of recruits.

Recruitment

In this study, recruitment is the number of individuals in an incoming year-class. Growth of older individuals, natural mortality and weight of recruits is separate. The Beverton-Holt equation was used (Stefansson 2007b):

$$R = \alpha S/(1 + S/K)$$

where the coefficient α is a multiplier for prospective recruitment and K is the size of the spawning stock that produces half the maximum recruitment.

Natural mortality

One of the important input parameters for this model was natural mortality (*M*). *M* represents all sources of mortality, except from fishing. In reality, it is not easy to obtain M. With northern shrimp (*P. borealis*), some authors set M as 0.5 without explaining it further (Fu and Quinn II 2000, Skúladóttir 2004).

In this study, the natural mortality (M) was estimated based on the growth parameters of length at infinitive (L_∞) and growth rate (K) from Pauly's equation (Pauly 1980).

$$\log M = -0.0066 - 0.279 \log L_\infty + 0.6543 \log K + 0.4634 \log T$$

The shrimp carapace length (CL) was converted to total length (TL) by the function:

TL = (CL + 1.05)/0.201   (Skúladóttir and Pétursson 1999)

Fitting the model

In order to fit the data, the model typically computed the sums of squares between each data set and the corresponding fitted values. When this model was used for estimating fishing mortality, the catches and survey indices were typically predicted from proportionality with the biomass. A complete model-fitting run consists of first initialising the parameters, followed by function definitions and finally calling the nonlinear minimisers.

The model also used the CVs as weighting factors (weights) to be assigned to sums of squares which will be minimised in order to estimate the parameters.

Assume that all of the terms corresponded to logged data. Each term was thus of the form:

$$\lambda \sum_t (\ln(x_t) - \ln(\hat{x}_t))^2$$

where the x_t's were annual landings, biomass index and recruitment factor.

The "correct" weighting factor from a statistical viewpoint was the inverse variance:

$$\lambda = \frac{1}{\sqrt{[\ln(x_t)]}} = \frac{1}{\sigma^2_{\ln(x_t)}}$$

and in the case of low variability, the standard deviations of the logged quantities were close to the coefficient of variation (CV) of the original numbers. Since the latter were convenient to think of and the former were computationally convenient, the term CV(x) was commonly used when $\sigma_{\ln(x_t)}$ was meant.

In the case of the landings data that was known quite precisely so that it was assumed CV(Y) = 0.1, reflecting a belief that 95% of the annual catch estimates are within 20% (two standard deviations) of their true value.

However, the biomass index was obtained from the survey estimation, and the fishing mortality and recruitment factors were obtained from model prediction. Therefore, it was difficult to get the precise CVs in this study, these were set as CV(I) = 0.1, CV(F) = 0.4. The CV(R) was chosen relatively high since the $\hat{R}$ was obtained from the Bevertont and Holt recruitment equation whereas the actual recruitment over this

short period would probably vary a lot as indicated by the length distribution. Thus the initial values were set according to the Beverton and Holt equation but in the iteration process these values were allowed to deviate freely from these initial values until the best fits were obtained to the other CVs.

2.2.4   Biomass prediction model

The shrimp stock in Húnaflói collapsed in 1998. The shrimp fishery was stopped but the abundance index estimated from the surveys in recent years is still very low. In this case, depensation seems to have occurred (Hilborn and Walters 2001, Jennings *et al.* 2001). "If depensation exists, fisheries managers should be extremely nervous because fished stock may not recover after being fished to very low abundance, even when fishing is stopped." (Jennings *et al.* 2001) and it could be very difficult to predict how long it takes for stock recovery (Hilborn and Walters 2001).

Notwithstanding, the shrimp stock may recover in the future if the cod disappears again from Húnaflói. We therefore tried to predict the equilibrium shrimp spawning stock biomass and the potential yield in order to estimate sustainable harvest levels in the future.

The average shrimp recruitment between 1989 and 1995 was 3866 million (from the dynamic production model) and this number, therefore, was assumed for the virgin stock after recovery. The yield per recruitment and spawning stock per recruitment were estimated for a range of fishing mortalities from 0 to 2.

The stock projecting was done using the stock equation (Stefansson 2007c):

$$N_{ay} = N_{a-1, y-1} e^{-Z_{a-1, y-1}}$$

The catch in numbers at age is given by the catch equation:

$$C_{ay} = (F_{ay}/Z_{ay})(1 - e^{-Z_{ay}})N_{ay}$$

and the total catch in weight is given by:

$$Y_y = \sum_a w_{ay} C_{ay} \sum_a w_{ay} C_{ay}$$

The simplest catch projection was based on a constant future fishing mortality, i.e.:

$$F_{ay} = F_{a,y-1}$$

This was a special case of assuming a constant selection pattern and only setting the overall fishing mortality, i.e.:

$$F_{ay} = F_{y,sa}$$

where sa is usually set to the same selection pattern as obtained from the assessment.

Based on the results from the yield per recruit model, the F_{max} and $F_{0.1}$ were chosen for the prediction model in order to get the equilibrium yield and predicted fishing mortality in future. The yield and spawning stock biomass were predicted for 20 years using the stock equation as shown above with the incoming recruitment each year determined by the Beverton and Holt function.

The R programs for this study are shown in Appendix B.

3   RESULTS

3.1   Growth parameters of *P. borealis* in the Húnaflói area

3.1.1   *Length distribution analysis*

The shrimp carapace length distribution data was initially analysed for both spring and autumn surveys from 1988 to 2004. The length frequency of *P. borealis* samples was sliced for both surveys in order to find the modes of distribution. However, only the spring surveys were later used because of peaks in the length frequency distribution corresponding to cohort distribution were more distinct than in the autumn surveys. Figure 3 shows the spring cohort distribution and three peaks assumed for ages of 2, 3 and 4 which were chosen to obtain the mean carapace length by Gaussian distribution analysis.

The mean carapace length obtained at these ages was used as input data in the model and fitted to the length distribution of all the years in order to find the mean carapace length at age 1 and older than 4. Figure 4 shows the length distribution that was fitted and the mean carapace length at ages 1 to 5. The results of the length distribution analysis are also shown in Table 1.

Table 1: The mean carapace length (mm) of shrimp in the Húnaflói area estimated from survey data in 1988-2004 using a length distribution model.

Age	Mean carapace length	Standard deviation	Proportion
1	7.94	1.27	0.076
2	12.37	1.47	0.278
3	15.17	1.40	0.343
4	17.80	1.36	0.243
5	19.64	1.36	0.059
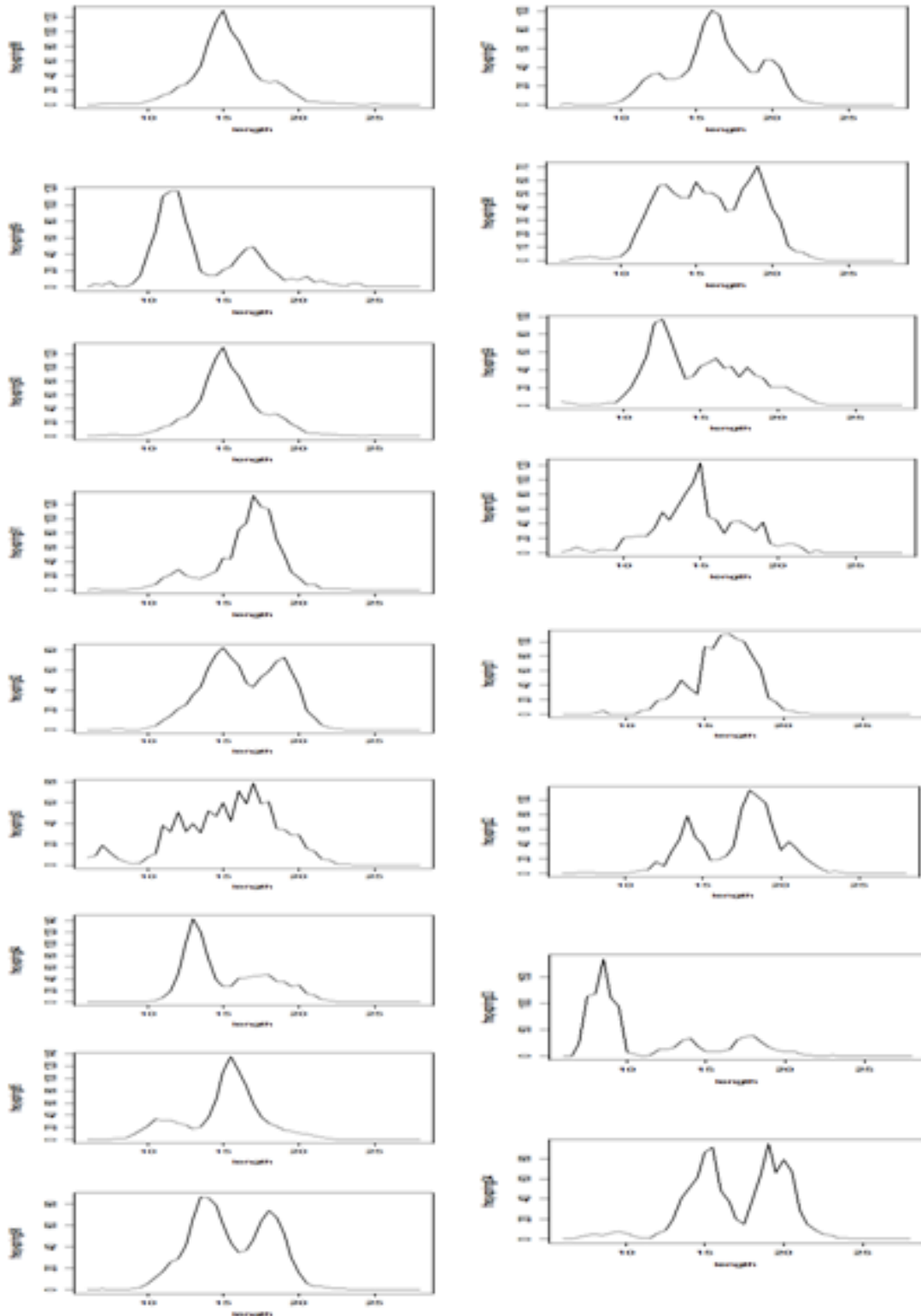
Figure 3: The length frequency slices of spring cohorts of *P. borealis* plotted from the spring surveys data in 1988-2004 in the Húnaflói area.
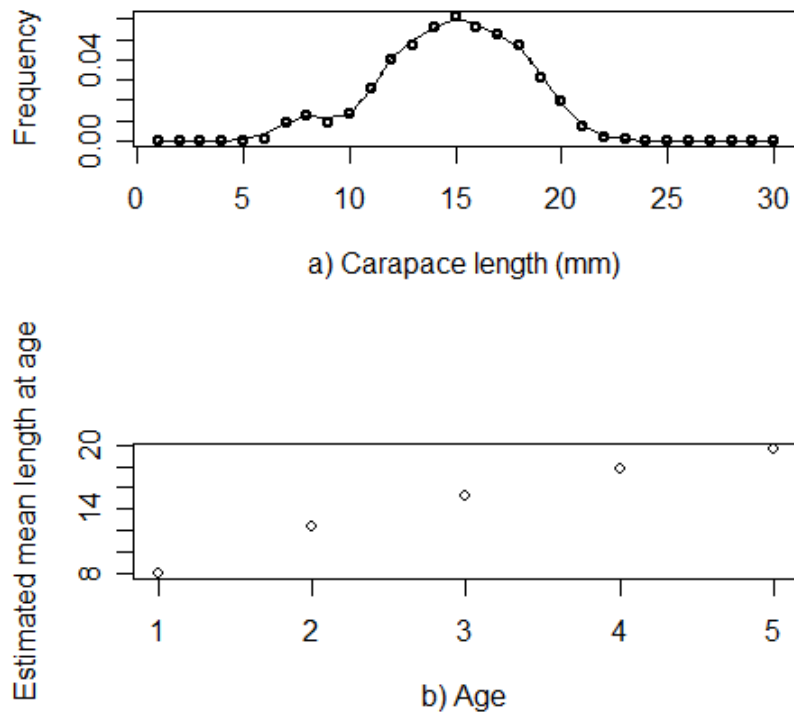
Figure 4: The results of length distribution analysis. a) The length distribution that was fitted. The dots are length frequency fitted by the line that outcome from the model. b) The mean length at ages (mm) estimated from the model

3.1.2 Growth parameters of Von Bertalanffy function

The mean carapace length at ages obtained from the length distribution analysis were then fitted to the Von Bertalanffy growth curve model to estimate the growth parameters (Figure 5). The SSE was 0.079 and growth parameters were: $CL_\infty = 24.9$ mm, $K = 0.29$, $t_0 = -0.33$.
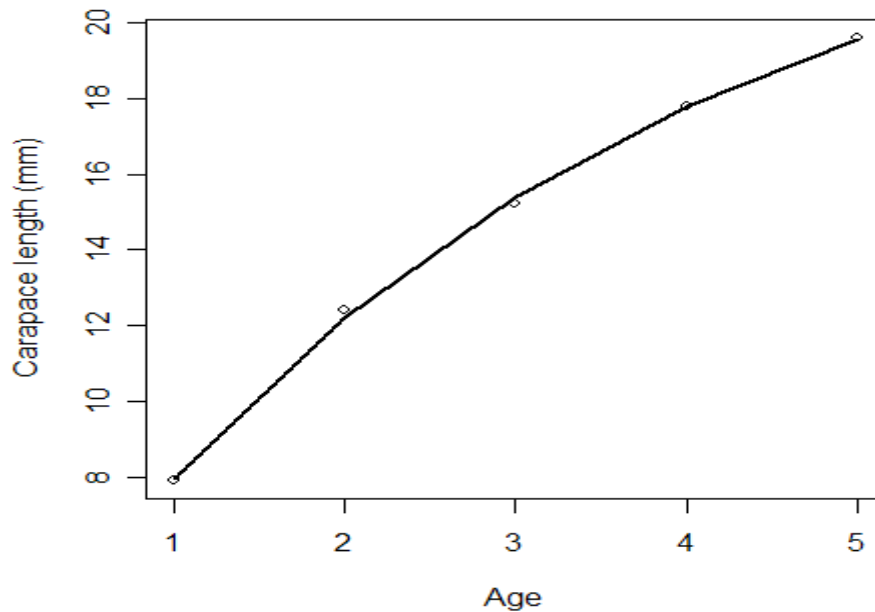
Figure 5: The mean carapace length fitted the growth curve

3.2   Length-weight relationship

Based on length and weight data of shrimp with internal spine and without internal spine, the length-weight relationship parameters of the equation:

$$W = aL^b$$

was calculated with the results as below:

The shrimp with internal spine: a = 0.000933   and   b = 2.875
The shrimp without internal spine: a = 0.000887   and   b = 2.960

3.3   Biomass of *P. borealis* from 1989-1999

The carapace length of L infinitive was converted to total length by using the conversion factor TL = (CL + 1.05)/0.201 (Skúladóttir and Pétursson 1999). The natural mortality obtained from Pauly's function was 0.5. The growth and length-weight relationship parameters were used to calculate the weight at age. The gear selectivity patterns were kept at 0 for 1 year olds (no fishing at this size), 0.2 for 2 year olds, 0.5 for 3 year olds and 1 for the older groups. The 50% of mature age (that is they become females) was chosen as 3 years old as this is the time the inshore shrimp males start to turn into females. At the age of 4 most of them have become females (Skúladóttir and Pétursson 1999).

The output of the dynamic biomass model was estimated with SSEI, SSEY, SSEF and SSER in Figure 6. The biomass of *P. borealis* is presented in Table 2. The fit was generally good to the catch and survey index data (Figures 6a and 6b) except that the model could not follow the high increase in the survey index in 1991.
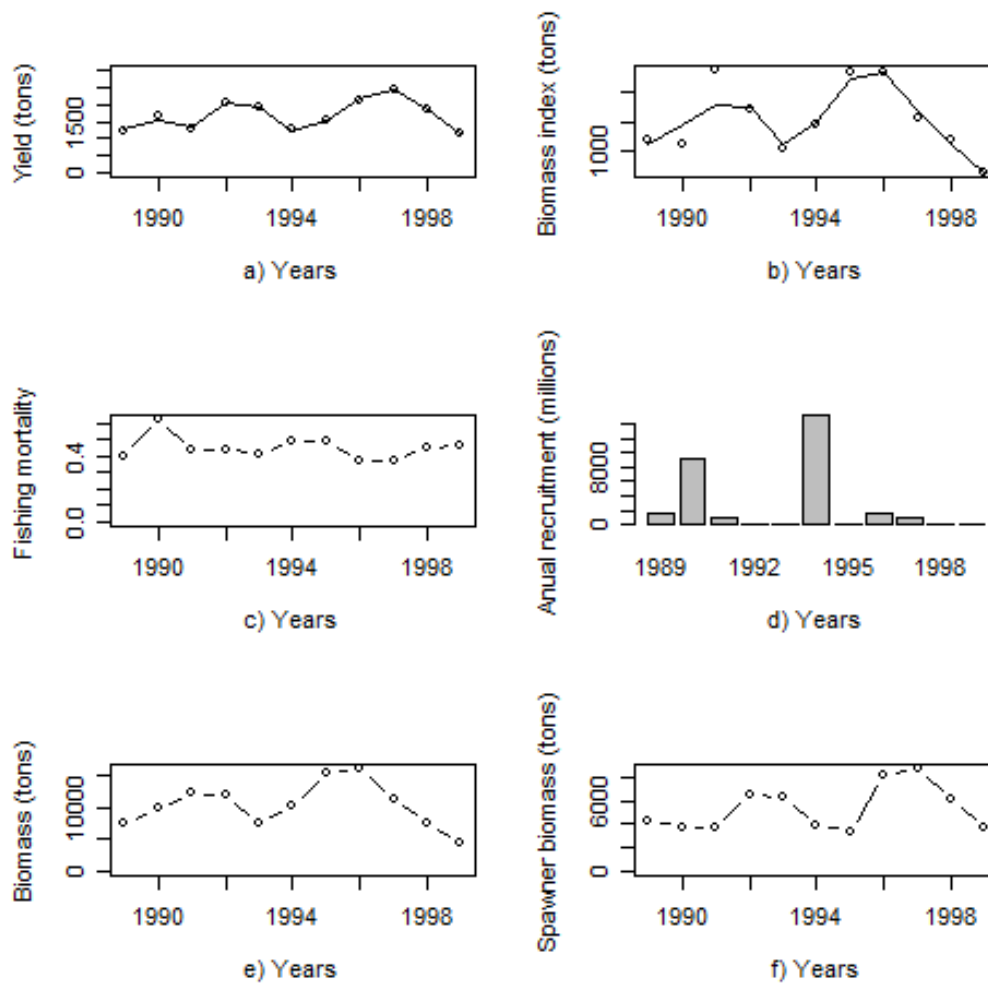
SSEI SSEY SSER SSEF
 0.17 0.01   363.38 0.46

Figure 6: The output of the dynamic biomass model. 6a) and 6b) present the annual catch from the commercial fishery and biomass index from the surveys with the lines fitted from the model. 6c, d, e, f) the prediction of fishing mortality, recruitment, biomass and spawner biomass estimated from the model for 1989-1999.

From the output of the model, the recruitment (Figure 6d) has high fluctuations, with peaks in 1990 and 1994 but is low in other years. The fishing mortality is rather stable between 0.4 and 0.6 (Figure 6c). The stock biomass and spawning stock biomass decreased rapidly 3 or 4 years before the collapse (Figures 6e and 6f). The stock biomass reached a peak in 1996 with 16,054 tonnes but went down to 4297 tonnes in 1999 and has been very low in recent years (see the biomass index in Appendix A).

Table 2: The biomass of *P. borealis* in the Húnaflói area (1989-1999)

Year	Biomass (tonnes)
1989	7507
1990	9818
1991	12271
1992	11934
1993	7515
1994	10190
1995	15273
1996	16054
1997	11349
1998	7615
1999	4297

3.4   Prediction model

The equilibrium yield and spawning stock biomass were estimated for fishing mortalities ranging from 0 to 2. If we assume that the shrimp stock in Húnaflói recovers (the cod goes away) and the recruitment in a virgin stock is 3866 million, then the predicted yield increases from 1137 tonnes at F = 0.2 to 2647 tonnes at F = 1.86 whereas the spawning stock biomass decreases from 9653 tonnes at the beginning (no fishing) to 2025 tonnes at F = 2. The output of the prediction model is shown in Figure 7 and Table 3.
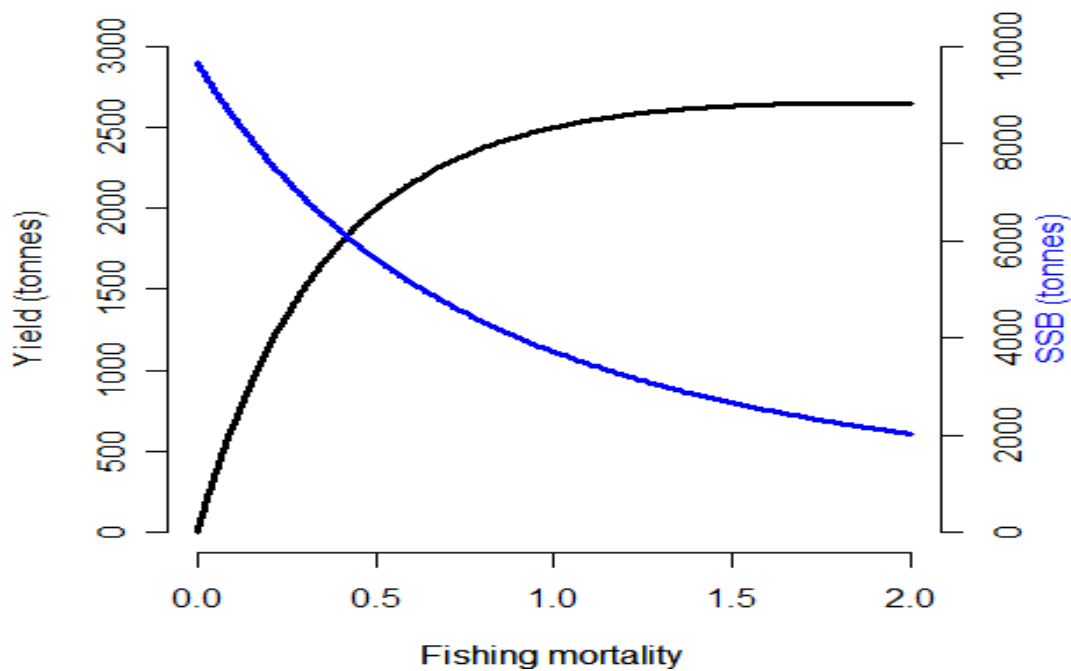
Figure 7: The yield and spawning stock were estimated from the yield per recruit model with fishing mortality ranging from 0 to 2.

Table 3: The yield and spawning stock biomass with different F values estimated from the yield per recruit model.

Fishing mortality	Yield (tonnes)	Spawning stock biomass (tonnes)
0	0	9653
0.2	1137	7658
0.4	1780	6214
0.6	2151	5146
0.8	2369	4339
1.0	2498	3716
1.2	2573	3226
1.4	2617	2833
1.6	2639	2513
1.8	2647	2247
2.0	2645	2025

Along the range of fishing mortality, two reference points were obtained, $F_{max} = 1.86$ and $F_{0.1} = 0.85$. These two values of fishing mortality were used as input data for the prediction model in order to estimate the prediction yield and spawning stock biomass for the next 20 years.

The output of the prediction model is shown in Figure 8 and Table 4.

Table 4: The prediction yield and spawning stock biomass obtained from the prediction model.

Year	Yield (tonnes)	Spawning stock biomass (tonnes)
1	2516	6037
2	2200	4214
3	2127	3173
4	920	2516
5	827	2814
6	3309	3516
7	3559	4163
8	1076	3471
9	3045	4822
10	4631	6791
11	1958	6330
12	4463	6631
13	3002	5431
14	1738	4352
15	2146	4782
16	1915	5648
17	2793	5480
18	2712	5887
19	2809	6123
20	2949	5577
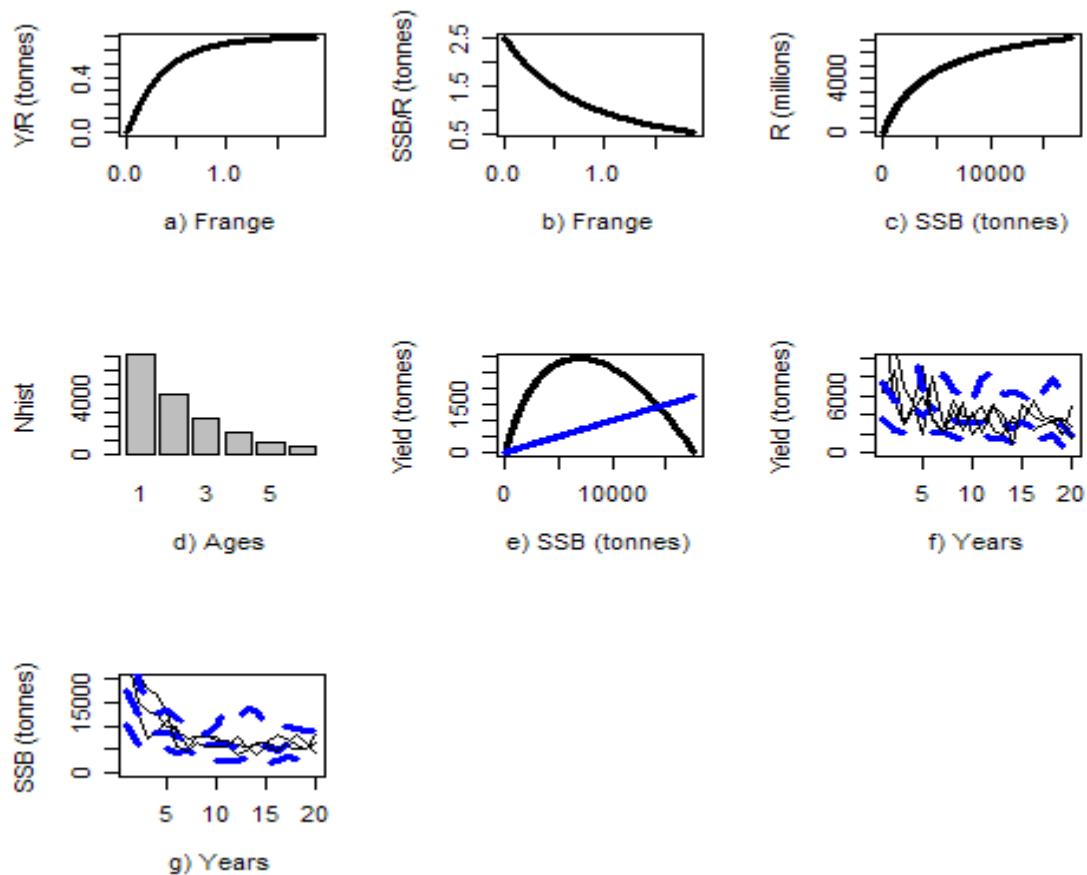
Figure 8: The output of the prediction model: 8a) and 8b) present the yield per recruitment (Y/R) and spawning stock per recruitment (SSB/R) along with the range of fishing mortality, 8c) shows the Berveton-Holt recruitment curve, 8d) represents the number of virgin stock, 8e) the equilibrium yield curve with fishing mortality at $F_{0.1}$, 8f) and 8g) present the yield and spawning stock biomass fluctuation along the time series with three proportion patterns at 0.05, 0.5 and 0.95.

4   DISCUSSION

In this study, uncertainties of parameter estimations were solved by setting criteria to judge the quality of fit between the models' predictions and the observed data (Haddon 2001). The mean carapace length at age was fitted by a maximum likelihood criterion with normal probability distribution and followed by a least-squares criterion (SSE) in order to minimise the sum of residual error squared of growth parameters (see sections 2.2.1 and 3.1). The set of coefficient of variation (CV) while fitting the dynamic production model with the least-squares criterion (see section 2.2.2) helped ensure the estimated parameters were precise (see section 3.3).

The carapace length of *P. borealis* in spring samples ranged from 6 mm to 25 mm in Húnaflói (see Appendix A). This size is small compared to Jan Mayen shrimp which can reach a length up to 38 mm (Aschan *et al.* 1996) or Flemish Cap shrimp (28 mm) (Skúladóttir *et al.* 2007). The L_∞ was obtained from the length distribution model and,

therefore, was smaller than the L_∞ of these other areas. The carapace length of L_∞ of Húnaflói shrimp was 24.9 mm. This length is small compared to 32.50 mm of Flemish Cap shrimp or 37.57 mm of Barents Sea (Skúladóttir *et al.* 2007) but is larger than the L_∞ for shrimp in Kachemak Bay (Alaska) which varied from 23.8 mm to 24.25 mm (Fu and Quinn II 2000).

The growth rate K of Húnaflói shrimp obtained from the model was 0.29. This value was in range of the K value of northern shrimp in the Flemish Cap, Barents Sea, Sweden waters (Skúladóttir 2007), Jan Mayen (Aschan *et al.* 1996) and Kachemak Bay (Fu and Quinn II 2000).

Table 5: The growth parameters of *P. borealis* in some areas.

Location	L_∞	K	References
Húnaflói	24.9	0.29	
Flemish Cap[1]	32.5	0.26	[1] Skúladóttir *et al.* (2007)
Barents Sea[1]	37.6	0.14	
Sweden[1]	27.9	0.60	
Kachemak Bay[2]	24.6	0.37	[2] Fu and Quinn II (2000)
Jan Mayen[3]	33.2	0.19	[3] Aschan *et al.* (1996)

Pauly's equation was used for estimating the natural mortality (M) of *P. borealis* in Húnaflói area with the results of M = 0.5. "Although Pauly's equation was developed for fish, it is also applicable to shrimp (Pauly and Munro 1984). This equation provides equally reasonable estimates of M in shrimp because shrimp and fish generally share the same habitats, resources and predators, and therefore, they are not likely to differ widely in their vital parameters. Even if shrimp differed from fish stocks by having a slightly higher or lower natural mortality, the method would still provide estimates of M that are more reasonable than many of those found in the literature" (Martinez *et al.* 2002). When using the three sets of M (0.3, 0.5, 0.7) for estimating the yield per recruit of shrimp in the Flemish Cap, the result of M=0.5 was the same as expected in 2004 (Skúladóttir 2004). This value has also been used for running simulation-estimation experiments in a length-based model for *P. borealis* in Kachemak Bay, Alaska (Fu and Quinn II 2000).

One of the factors affecting estimates of spawning stock biomass in age structured populations is the age at 50% maturity (in this case when they become females). In this study this factor was chosen as 3 years old based on a study on the population of northern shrimp in Icelandic waters using the maximum length and maturity ogive of females by Skúladóttir and Pétursson (1999). Northern shrimp is hermaphroditic, after being male for some years the shrimp change sex to become female. In the Gulf of Maine, Idoine (2006) reckoned that *P. borealis* matures first as males at roughly 2½ years of age and then transforms to females at about 3½ years of age and most shrimp do not live past the age of 5. Skúladóttir *et al.* (2007) reported the age at sex change of shrimp in the Flemish Cap was 5 years for the 1990 year-class, but the 1991 and 1992 year-classes changed sex at age 4. However, the age at sex change of *P. borealis* in Jan Mayen was higher than the others, from 5-9 years old (Aschan *et al.* 1996).

The yields of the shrimp fishery in Húnaflói from 1988 to 1998 started at 1216 tonnes in 1988 and got 1148 tonnes in the last year before it collapsed with three peaks in 1991 (2021 tonnes), 1995 (2132 tonnes) and 1996 (2438 tonnes) (Figure 6a). The fishing mortality from the dynamic biomass model was rather stable between 0.4 and

0.6 (Figure 6c). The fluctuation of catches were therefore similar to fluctuations in shrimp biomass. Our results on shrimp biomass in Húnaflói (section 3.3) was directly proportional to the survey index so that it reflected clearly the shrimp abundance. The shrimp biomass in 1999 was only a quarter of the peak in 1996. That meant the number of shrimp recruited in this time did not compensate for the loss. The shrimp recruitment had two peaks in 1990 and 1994 (Figure 6d) and was very low in the other years.

The general distribution of northern shrimp is affected by environmental factors such as temperature, substratum and salinity (Shumway 1985, Idone 2006, Garcia 2007, Skúladóttir 2007). However, these factors in Húnaflói were within the range of the shrimps' tolerance and could therefore not be the cause of shrimp collapse in Húnaflói. The trawl surveys from 1988 to 2006, however, show increases in cod (*Gadus morhua*) numbers. Stefansson *et al.* (1994) have shown that the northern shrimp biomass had a negative relationship with cod biomass in Icelandic waters. In this study the average numbers of cod per haul from annual spring and autumn surveys (Appendix A) could well explain the shrimp recruitment failure. In 1989 the low cod density encouraged the shrimp juveniles recruited to the stock in 1990. Then the shrimp recruitment peaked again in 1994 because the density of cod was low. However, after 1994 the cod abundance increased rapidly and peaked in 1998 leading to depensatory effects on shrimp recruitment (Hilborn and Walters 2001, Jennings *et al.* 2001) and the shrimp stock collapsed consequently (Figure 9).
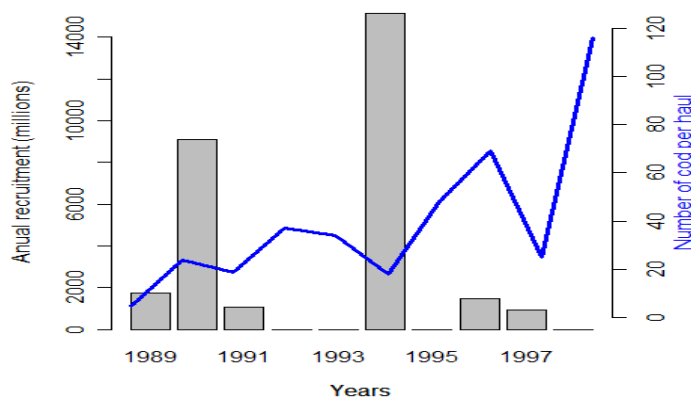
Figure 9: The annual recruitemnt estimated from the dynamic production model (barplot) and the average number of cod per haul (line) from the surveys data (Source: MRI)

Skúladóttir *et al.* (2007) noted that the biomass of shrimp has increased greatly in the Flemish Cap since 1997 after the collapse of the cod. In the case of Húnaflói, it is assumed that the shrimp stock will recover to the virgin abundance if the numbers of cod in Húnaflói decline again. The yield per recruit model runs along with fishing mortality (F) range in order to find the F_{max} and $F_{0.1}$ for the equilibrium yield (section 3.4). At F=0 (no fishing) that meant no catch. When F is increased from zero the catches increase dramatically as implied by a steep slope of the yield per recruit curve at the origin (Figure 10). While F increases, the slope is reduced until it becomes zero at F=F_{max}. The fishing mortality at which the slope of the yield per recruit has become one tenth of the slope at the origin is denoted $F_{0.1}$. At this fishing mortality, the

marginal gain in yield is only 10% of the initial marginal gain when fishing is started. This point is very important in the economic context and becomes an economically optimum fishing mortality below F_{max}.
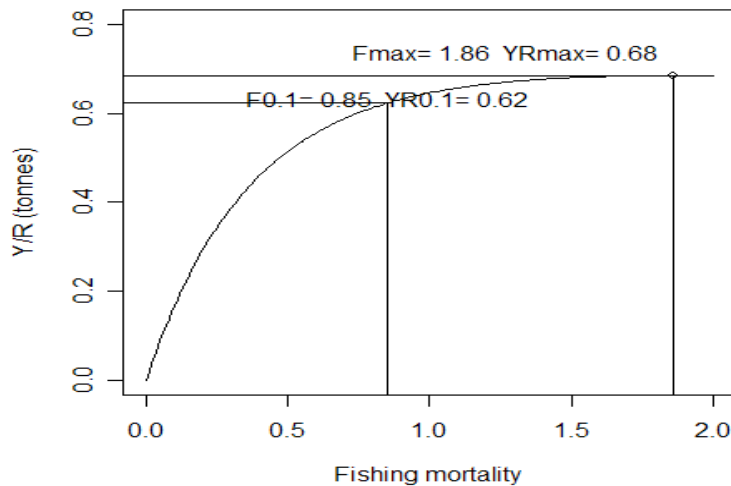
Figure 10: The F_{max} and $F_{0.1}$ estimated from the yield per recruit model with the range of fishing mortality from 0 to 2.

While the yield per recruit model predicted the yield and spawning stock biomass with a given fishing mortality, the yield and spawning stock biomass model aimed to predict the range of the yield and the spawning stock biomass with time. With fishing mortality at $F_{0.1}$, the two models had similar predictions, with an average annual long term yield of 2500 tonnes (section 3.4).

5   CONCLUSION

The size of *P. borealis* in the Húnaflói area is small compared to some other areas such as the Flemish Cap, Barents Sea or Jan Mayen. The growth parameters were on the range while compared with the others.

The natural mortality calculated was 0.5 based on Pauly's equation and this agreed with other studies. During the fishing years (1988-1998), the fishing mortalities were estimated to be rather stable between $0.4 - 0.6$, the average biomass was 10,000 tonnes.

The recruitment was highly variable. Further studies on shrimp juvenile distribution and predator-prey relationship between shrimp and other demersal fish species such as haddock are needed in order to reduce the uncertainty of recruitment parameters in the Húnaflói area.

If/when the shrimp stock recovers in the Húnaflói area, the annual catch should be at the level of 2500 tonnes.

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APPENDIX A: DATA

Table 5: The biomass index and average number of cod (*Gadus morhua*) per haul from surveys in Húnaflói area (Source: MRI).

Year	Biomass index (tonnes)	Number of cod per haul
1989	1186	5
1990	1110	24
1991	2393	19
1992	1715	37
1993	1030	34
1994	1453	18
1995	2377	48
1996	2372	69
1997	1559	25
1998	1180	116
1999	620	41
2000	204	167
2001	67	147
2002	9	133
2003	4	182
2004	8	111
2005	No data	
2006	3	114

Table 6: The annual catch of the shrimp commercial fishery in Húnaflói area (Source: MRI).

Year	Yield (tonnes)
1988	1216
1989	1691
1990	1308
1991	2021
1992	1888
1993	1264
1994	1549
1995	2132
1996	2438
1997	1848
1998	1148

Table 7: The length distribution of *Pandalus borealis* from annual spring surveys (Source: MRI).

Length	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004
6	0	0	0	0	0	7	1	0	0	0	0	4	1	0	0	0	0
6.5	0	4	0	1	0	9	0	0	0	1	0	3	4	0	0	0	0
7	1	2	1	0	0	19	0	1	1	0	2	1	8	0	1	24	2
7.5	2	6	2	0	0	12	1	1	0	0	2	0	4	0	1	114	4
8	2	0	2	0	1	6	0	2	0	0	3	1	1	1	1	118	5
8.5	1	0	1	0	0	3	0	3	0	0	2	1	5	5	0	185	4
9	1	4	1	1	0	1	0	8	1	0	1	3	4	0	0	111	6
9.5	2	14	2	2	0	2	0	15	2	1	2	3	4	0	0	94	8
10	5	43	5	5	2	8	1	23	6	4	3	11	21	0	0	7	6
10.5	8	69	8	8	4	11	3	34	12	9	8	21	22	0	2	3	3
11	13	111	13	17	9	38	8	31	17	16	20	36	23	5	4	0	1
11.5	16	117	16	21	14	32	19	32	26	26	32	55	23	7	5	1	1
12	25	117	25	29	21	51	49	27	29	32	45	93	34	19	16	12	6
12.5	28	79	28	20	25	32	104	24	42	34	56	97	56	21	10	13	9
13	37	54	37	17	35	40	144	18	66	27	57	78	45	29	29	16	20
13.5	53	19	53	16	43	31	121	21	87	27	51	53	63	47	46	29	40
14	88	14	88	21	63	52	74	36	86	30	47	30	81	36	78	34	51
14.5	115	14	115	26	76	47	38	66	79	38	47	33	97	28	49	17	61
15	130	21	130	45	83	60	27	111	61	58	59	44	124	93	40	9	86
15.5	102	25	102	44	73	42	27	136	44	87	51	48	50	90	18	9	91
16	88	37	88	85	65	71	41	112	35	101	51	53	45	109	19	9	48
16.5	66	47	66	94	47	59	42	87	37	96	47	42	27	111	24	13	38
17	45	49	45	133	43	79	45	59	47	68	37	44	42	104	37	31	20
17.5	34	37	34	117	53	59	46	38	64	54	38	32	44	100	88	37	15
18	31	23	31	114	59	61	47	27	74	45	53	43	38	80	113	38	39
18.5	32	17	32	71	69	35	36	22	68	35	61	34	30	63	104	26	63
19	26	8	26	49	73	34	35	16	52	35	71	31	42	22	95	16	95

19.5	18	10	18	25	59	29	27	14	30	48	56	21	13	17	61	11	66
20	12	9	12	17	44	29	29	11	16	48	39	21	9	6	32	8	79
20.5	5	13	5	7	19	16	15	10	6	40	30	21	12	5	43	9	67
21	4	6	4	8	12	13	12	6	3	20	11	15	12	1	33	3	28
21.5	3	8	3	2	5	6	5	4	3	9	7	12	8	1	22	2	15
22	3	4	3	2	2	5	3	2	2	4	6	7	0	0	14	0	9
22.5	2	3	2	1	1	1	1	1	1	2	3	3	4	0	7	0	5
23	1	1	1	2	0	1	1	1	1	1	1	1	0	0	2	1	4
23.5	1	4	1	0	0	0	0	0	0	0	0	0	0	0	3	0	1
24	0	4	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1
24.5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
25	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0

APPENDIX B: MODELS' PROGRAMMES BY R SOFTWARE PACKAGE

Length distribution analysis

```
############################
#Length distribution analysis
############################
# functions.r - a collection of functions to assist with fitting to a length distribution

# predle - a function to predict a length distribution from a set of parameters

predle<-function(pi,mu,sigma,lmin,lmax){
 if(length(sigma)!=length(mu))sigma<-c(sigma,rep(sigma[nsigma],length(mu)-
nsigma))
 nl<-lmax-lmin+1
 if(length(pi)!=length(mu)){
  pi<-c(pi,1-sum(pi))
  pi<-abs(pi)                # Make sure all are positive
  pi<-pi/sum(pi)              # Readjust, just in case
 }
 fit<-rep(0,nl)              # Compute the fitted values
 for(lgrp in lmin:lmax){
  fit[lgrp]<-sum(pi*(pnorm((lgrp+0.25-mu)/sigma)-pnorm((lgrp-0.25-mu)/sigma)))
 }
 return(fit)
}

# sseprop - a function to evaluate the fit of different vectors of proportions

sseprop<-function(pvec,mu,sigma,dat,lmin,lmax){          # The pvector is input - the
mu and sigma are fixed
 pi<-c(pvec,1-sum(pvec))       # na-1 values - the last is computed
 pi<-abs(pi)                # Make sure all are positive
 pi<-pi/sum(pi)              # Readjust, just in case
 fit<-predle(pi,mu,sigma,lmin=lmin,lmax=lmax)      # Compute the fitted values
 sse<-1e6*sum((dat-fit)^2)
 return(sse)
}

# ssemu - a function to evaluate the fit of different mu vectors.

ssemu<-function(muvec,pi,sigma,dat,lmin,lmax){
 fit<-predle(pi,muvec,sigma,lmin=lmin,lmax=lmax)      # Compute the fitted values
 sse<-1e6*sum((dat-fit)^2)
 return(sse)
}

# ssesigma - a function to evaluate the fit of different sigma vectors.

ssesigma<-function(sigmavec,pi,mu,dat,lmin,lmax){
```

```
  sigma<-c(sigmavec,rep(sigmavec[nsigma],length(mu)-nsigma))
  fit<-predle(pi,mu,sigmavec,lmin=lmin,lmax=lmax)      # Compute the fitted values
  sse<-1e6*sum((dat-fit)^2)
  return(sse)
}
```

ssevonB - a function to evaluate the SSE when estimating the parameters of a von Bertalanffy

```
ssevonB<-function(beta,agrps,sigma,dat,lmin,lmax){
  Linf<-exp(beta[1])
  k<-beta[2]
  muvec<-Linf*(1-exp(-k*(agrps)))
  fit<-predle(pi,muvec,sigma,lmin=lmin,lmax=lmax)      # Compute the fitted values
  sse<-sum((dat-fit)^2)
  return(sse)
}
```

ssefull - a placeholder for a function to use when estimating all parameters in a length distribution

```
ssefull<-function(b,dat,lmin,lmax){
  pvec<-b[1:(na-1)]
  mu<-b[na:(2*na-1)]
  sigma<-b[(2*na):(2*na+nsigma)]
  pvec<-ifelse(pvec<0,-pvec,pvec)
  pi<-c(pvec,1-sum(pvec))
  pi<-abs(pi)                       # In case something stupid happened in the minimizer
  pi<-pi/sum(pi )                   # Proportions - routinely making sure they add to 1
  fit<-predle(pi,mu,sigma,lmin=lmin,lmax=lmax)      # Compute the fitted values
  sse<-sum((dat-fit)^2)
  cat("SSE=",sse,"\n")
  return(sse)
}
```

init.r - A generic file for initializing variables for fitting length distributions

Step 1: Read in the data and extract into two vectors, le and freq

```
lmat<-read.table("data/le-fre.dat",header=T)   # Read the data file        - *** change
file name as needed
le<-lmat$le                      # Extract the observed lengths - *** change column
name as needed
freq<-lmat$freq                   # Extract the obs frequencies  - *** change column
name as needed
```

Set a few important values (note that lengths are in integer cm (or mm) groups)
```
na<-5                    # Define the number of ages    - *** change if needed
```

```
nsigma<-4                        # Number of sigma parameters to be estimated - ***
change as needed
lmin<-1                   # Smallest possible length    - *** change if needed
lmax<-30                  # Kargest possible length     - *** change if needed

# Initialize variables - the user may change any of these and *** needs to change
some

p0<-rep(1/na,na-1)               # Set the initial values for proportions in each but last
age group
mu<-c(7.5,12.5,15.5,18,21) # Mean lengths at age - *** definitely change this!
sigma<-rep(1,nsigma)             # Standard dev. of length at age  - *** definitely
change this!

# Final initialization - a regular user does not change this

lgrps<-lmin:lmax                 # The complete list of allowable length groups
agrps<-1:na                    # The complete list of age groups
nl<-length(lgrps)              # Number of length groups
dat<-rep(0,nl)
dat[le]<-freq/sum(freq)           # The data vector - with zero values where there are
no obs.
pi<-c(p0,1-sum(p0))             # Proportions - routinely making sure they add to 1
pi<-abs(pi)                  # In case something stupid happened above
pi<-pi/sum(pi)                 # Proportions - routinely making sure they add to 1




fm<-nlm(sseprop,p0,mu=mu,sigma=sigma,dat=dat,lmin=lmin,lmax=lmax) # Find the
best proportions for the initial values of mu, sigma
p1<-fm$estimate
pi<-c(p1,1-sum(p1))
pi<-abs(pi)               # Make sure all are positive
pi<-pi/sum(pi)            # Readjust, just in case
# Now estimate the sigma vector
sigma0<-rep(1,nsigma) # Note that we are only estimating 4 sigma values...
fm<-nlm(ssesigma,sigma0,pi=pi,mu=mu,dat=dat,lmin=lmin,lmax=lmax)
sigma1<-fm$estimate
sigma<-c(sigma1,rep(sigma1[nsigma],length(mu)-nsigma))
# Estimate the mu vector
mu0<-mu
fm<-nlm(ssemu,mu0,pi=pi,sigma=sigma,dat=dat,lmin=lmin,lmax=lmax)
mu1<-fm$estimate
mu<-mu1
####### Repeat the process
# First 2nd-time estimate the proportions
p0<-pi[1:(na-1)]    # Initialize with previous...only estimate na-1 props
fm<-nlm(sseprop,p0,mu=mu,sigma=sigma,dat=dat,lmin=lmin,lmax=lmax) # Find the
best proportions for this particular set of mu, sigma
```

```
p1<-fm$estimate
pi<-c(p1,1-sum(p1))
pi<-abs(pi)                # Make sure all are positive
pi<-pi/sum(pi)             # Readjust, just in case
# Now 2nd-time estimate the sigma vector
sigma0<-sigma[1:nsigma]              # Only estimate 4 sigma values...initialize with
previous
fm<-nlm(ssesigma,sigma0,pi=pi,mu=mu,dat=dat,lmin=lmin,lmax=lmax)
sigma1<-fm$estimate
sigma<-c(sigma1,rep(sigma1[nsigma],length(mu)-nsigma))
# Finally, 2nd time estimate the mu vector
mu0<-mu                # Use previous estimate as initial value
fm<-nlm(ssemu,mu0,pi=pi,sigma=sigma,dat=dat,lmin=lmin,lmax=lmax)
mu1<-fm$estimate
mu<-mu1
##########
fit<-predle(pi,mu,sigma,lmin=lmin,lmax=lmax)       # Compute the fitted values

png("C:/hafro/project/graph/lengthdistr.png")
par(mfrow=c(2,1))

#par(mfrow=c(2,2))
plot(lgrps,dat,type='b',lwd=2,xlab="a) Carapace length (mm)", ylab="Frequency")
lines(lgrps,fit)
plot(1:length(mu),mu,xlab="b) Age",ylab="Estimated mean length at age")

#plot(1:length(sigma),sigma,xlab="Age",ylab="Estimated standard deviation at age")

#plot(1:length(pi),pi,xlab="Age",ylab="Estimated proportions at age",type='n',
   # xlim=c(0,length(pi)+1))
#for(a in 1:length(pi)){
 # lines(c(a-0.25,a-0.25,a+0.25,a+0.25),c(0,pi[a],pi[a],0))
#}
#lines(c(0.25,length(pi)+0.25),c(0,0))

print(fm)

dev.off()
```

Dynamic biomass model

```
###############################
#Biomass and recruitment estimation
###############################
m<-read.table("data/Yield.dat",header=T)
Y<-m$Y
m<-read.table("data/Biomass-index.dat",header=T)

I<-m$I

numyears<-length(Y)
Fmort.init<-rep(0.5,numyears)
A<-5

selpat<-c(0,0.2,0.5,1,1,1)        # Ages 1 not fished here
p50<-3
pa<-round(1/(1+exp(-2*((1:6)-p50))),2)   # Proportion mature at age

Recr.init<-rep(1000,numyears)
M<-0.5
q.init<-1
w<-c(0.41,1.47,2.92,3.68,4.84,5.85)
#Beverton-Holt parameters
 alpha<-0.006
 K<-10000

params.init<-log(c(Fmort.init,Recr.init,q.init,alpha,K))        # Initial values of all
parameters

predict<-function(Fmort,Recr){

 Rtemp<-Recr[1]
 Ninit<-Rtemp*exp(-(0:A)*M)  # First start-of-year stock size - equil.
 Nmat<-Ninit
 N0<-Ninit
 Yhat<-c()
 Bhat<-c()
 Shat<-c()
 for(y in 1:(numyears-1)){
  Z<-Fmort[y]*selpat+M
  C<-((Fmort[y]*selpat)/Z)*(1-exp(-Z))*N0
  Yhat<-c(Yhat,sum(w*C))
  Bhat<-c(Bhat,sum(w*N0))
  Shat<-c(Shat,sum(w*pa*N0))
  N1<-c(Recr[y+1],N0[1:(A-1)]*exp(-Fmort[y]*selpat[1:(A-1)]-M),
      N0[A]*exp(-Fmort[y]*selpat[A]-M)+
      N0[A+1]*exp(-Fmort[y]*selpat[A+1]-M))
  Nmat<-rbind(Nmat,N1)
  N0<-N1
 }
```

```
  Z<-Fmort[numyears]*selpat+M
  C<-((Fmort[numyears]*selpat)/Z)*(1-exp(-Z))*N0
  Yhat<-c(Yhat,sum(w*C))
  Bhat<-c(Bhat,sum(w*N0))
  Shat<-c(Shat,sum(w*pa*N0))
  dimnames(Nmat)<-list(Years=1:(numyears),Ages=c(1:A,"+"))

  return(list(Yhat=Yhat,Nmat=Nmat,Bhat=Bhat,Shat=Shat))
}


ssefcn<-function(parameters,printit=F){
  Fmort<-exp(parameters[1:numyears])
  Recr<-exp(parameters[(numyears+1):(2*numyears)])
    q<-exp(parameters[2*numyears+1])
    alpha<-exp(parameters[2*numyears+2])
    K<-exp(parameters[2*numyears+3])

  prediction<-predict(Fmort,Recr)
  Nmat<-prediction$Nmat
  C<-prediction$C
  Yhat<-prediction$Yhat
  Bhat<-prediction$Bhat
  Shat<-prediction$Shat
  Ihat<-Bhat*q
  Rhat<-alpha*Bhat/(1+Bhat/K)

            CVR<-1000
             CVY<-0.1
             CVI<-0.1
            CVF<-0.4

  SSEI<-sum((log(I)-log(Ihat))^2)
  SSEY<-sum((log(Y)-log(Yhat))^2)
  SSER<-sum((log(Recr)-log(Rhat))^2)
  SSEF<-sum((log(Fmort[2:numyears])-log(Fmort[1:(numyears-1)]))**2)

  SSE<-(1/CVI^2)*SSEI+(1/CVY^2)*SSEY+(1/CVR^2)*SSER+(1/CVF^2)*SSEF


        SSEvec<-c(SSEI,SSEY,SSER,SSEF)
        names(SSEvec)<-c("SSEI","SSEY","SSER","SSEF")


  if(printit==1){
   print(round(SSEvec,2))
  }
  if(printit==2){

   print(round(Nmat))
```

```
    print(round(Ihat,2))
    }

  return(SSE)
}

fm<-nlm(ssefcn,params.init,iterlim=500)

params.final<-fm$estimate
Fmort.final<-exp(params.final[1:numyears])
Recr.final<-exp(params.final[(numyears+1):(2*numyears)])
q.final<-exp(params.final[2*numyears+1])
alpha<-exp(params.final[2*numyears+2])
K<-exp(params.final[2*numyears+3])

prediction.final<-predict(Fmort.final,Recr.final)
Nmat.final<-prediction.final$Nmat
Yhat.final<-prediction.final$Yhat
Bhat.final<-prediction.final$Bhat
Shat.final<-prediction.final$Shat
Ihat.final<-Bhat.final*q.final

#time<-1:numyears
time<-1989:1999

#png("data/Biomass.png")
par(mfrow=c(3,2))

plot(time,Y,ylim=c(0,3000),xlab="a) Years",ylab="Yield (tons)")
lines(time,Yhat.final)
plot(time,I,xlab="b) Years",ylab="Biomass index (tons)" )
lines(time,Ihat.final)
plot(time,Fmort.final,type='b',ylim=c(0,max(Fmort.final)),xlab="c)
Years",ylab="Fishing mortality")

barplot(Recr.final,names.arg=time,xlab="d)        Years",ylab="Anual    recruitment
(millions)")

#title("Annual recruitment")

plot(time,Bhat.final,type='b',ylim=c(0,max(Bhat.final)),xlab="e)
Years",ylab="Biomass (tons)")
plot(time,Shat.final,type='b',ylim=c(0,max(Shat.final)),xlab="f)
Years",ylab="Spawner biomass (tons)")

#dev.off()

ssefcn(params.final,printit=1)
```

Prediction spawning stock biomass model

```
##############################
# Prediction yield and spawning stock biomass
############################
yrfun<-function(Fmult,M,sa,wa){
  Fmort<-Fmult*sa
  Z<-Fmort+M
  prop<-(Fmort/Z)*(1-exp(-Z))
  Ztemp<-c(0,Z[1:(length(Z)-1)])
  cumZ<-exp(-cumsum(Ztemp))
  C<-prop*cumZ
  Y<-sum(wa*C)
  return(Y)
}
srfun<-function(Fmult,M,sa,wa,pa){
  Fmort<-Fmult*sa
  Z<-Fmort+M
  Ztemp<-c(0,Z[1:(length(Z)-1)])
  cumZ<-exp(-cumsum(Ztemp))
  S<-sum(wa*pa*cumZ)
  return(S)
}
project<-function(Nhist,Fmort,sa,M,wa,alpha,K){
  N0<-Nhist*exp(rnorm(1)*CV.N)    # Rather silly - everything has the same CV etc
  Ytraj<-c()
  Straj<-c()
  for(y in years){
    Fimplem<-Fmort*exp(rnorm(1)*CV.pred)  # Implementation error
    Z<-Fimplem*sa+M
    C<-(Fimplem*sa/Z)*(1-exp(-Z))*N0
    S<-sum(wa*pa*N0)
    R<-(alpha*S/(1+S/K))*exp(rnorm(1)*CV.R) # Recr with variation
    #R<-(alpha*S/(1+S/K))            # Recr without variation
    N1<-N0*exp(-Z)
    N0<-c(R,N1[1:(length(N1)-1)])
    Ytraj<-c(Ytraj,sum(wa*C))
    Straj<-c(Straj,S)
  }
  return(list(Y=Ytraj,S=Straj))
}

selF1<-0
selF2<-0.85
selF3<-0
selF4<-1.8                       # Chosen as Fcrash

ages<-1:6
wa<-c(0.41,1.47,2.92,3.68,4.84,5.85)        # Mean weight at age
```

```
s50<-3                          # Age at 50% selection
sa<-round(1/(1+exp(-1.1*(ages-s50))),2)   # Selection at age
p50<-3
pa<-round(1/(1+exp(-2*(ages-p50))),2)   # Proportion mature at age

M<-0.5

CV.R<-0.5
CV.N<-0.5
CV.pred<-0.5

years<-1:20

alpha<-1/srfun(selF4,M,sa,wa,pa)          # Make this Fcrash
K<-5000

Frange<-(0:(selF4*100))/100      # Range for plotting
sr<-sapply(Frange,srfun,M,sa,wa,pa)
yr<-sapply(Frange,yrfun,M,sa,wa)
Srange<-K*(alpha*sr-1)
Srange<-ifelse(Srange>0,Srange,0)
Rrange<-alpha*Srange/(1+Srange/K)
Yrange<-yr*Rrange
#par(mfrow=c(3,2))
#plot(Frange,yr,type='l',lwd=3)
#plot(Frange,sr,type='l',lwd=3)
#plot(Srange,Rrange,type='l',lwd=3)

Fhist<-selF3
Zhist<-Fhist*sa+M
srhist<-srfun(Fhist,M,sa,wa,pa)
Shist<-K*(alpha*srhist-1)
Rhist<-alpha*Shist/(1+Shist/K)
Nhist<-Rhist*exp(cumsum(-c(0,Zhist[1:(length(Zhist)-1)])))
#barplot(Nhist,names.arg=ages)
#plot(Srange,Yrange,type='l',lwd=3)
#lines(Srange,0.10*Srange,lwd=3,col="blue")



# Set up the population, define functions etc
#source("functions.r")
#source("initproj.r")

Fmort<-0.8
Smat<-matrix(ncol=length(years),nrow=20)
Ymat<-matrix(ncol=length(years),nrow=20)
for(i in 1:20){
  tmp<-project(Nhist,Fmort,sa,M,wa,alpha,K)
  Straj<-tmp$S
  Ytraj<-tmp$Y
```

```
  #lines(years,Straj)
  Smat[i,]<-Straj
  Ymat[i,]<-Ytraj
}

png("data/prediction3.png")
par(mfrow=c(3,3))
#par(mfrow=c(2,3))
plot(Frange,yr,type='l',lwd=3,xlab="a) Frange", ylab="Y/R (tonnes)")
plot(Frange,sr,type='l',lwd=3,xlab="b) Frange", ylab="SSB/R (tonnes)")
plot(Srange,Rrange,type='l',lwd=3, xlab="c) SSB (tonnes)",ylab="R (millions)")

barplot(Nhist,names.arg=ages,xlab="d) Ages",ylab="Nhist")
plot(Srange,Yrange,type='l',lwd=3,xlab="e) SSB (tonnes)",ylab="Yield (tonnes)")
lines(Srange,0.10*Srange,lwd=3,col="blue")

plot(years,years,type='n',ylim=c(0,10000),xlab="f) Years",ylab="Yield (tonnes)")
fracts<-apply(Ymat,2,quantile,prob=c(0.05,.5,.95))
 for(j in 1:3){
 lines(years,Ymat[j,])
 lines(years,fracts[j,],lwd=3,col="blue",lty=2)
}
plot(years,years,type='n',ylim=c(0,20000),xlab="g) Years",ylab="SSB (tonnes)")
  fracts<-apply(Smat,2,quantile,prob=c(0.05,.5,.95))
   for(j in 1:3){
   lines(years,Smat[j,])
   lines(years,fracts[j,],lwd=3,col="blue",lty=2)
}

dev.off()
```