Observers Statement to the NEWREP-NP Special Permit Expert Panel Review Workshop

W.K. De La Mare

INTERNATIONAL
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Introduction

I keep my written comments brief, but we are ready to expand on them should the Panel have any queries on any of the points we raise. Supporting material is provided in an appendix.

The Scientific Committee review process should be based on the quantitative analysis of expected research outcomes. We urge the Panel to encourage use of tested and agreed methods of quantitative evaluation so that proponents can demonstrate the contribution of information from proposed research activities in addressing the research articulated in the research objectives. This approach is particularly important in those cases where the objectives are targeted at conditioning RMP ISTs. Most of our specific comments are made from this perspective, paying particular attention to the demonstrations relating to the selection of sample sizes and the use of statistical catch at age analysis (SCAA).

Comments on specific objectives and methods

There is little change in substance in many of the sub-objectives of NEWREP-NP from JARPN II, and hence they remain vague and have little role in determining the design of the lethal sampling program. Generally lacking are demonstrations of how the lethal data will lead to these objectives being attained. In particular, the objectives are not accompanied by quantitative performance criteria that will enable future evaluations as to whether the objectives are being met.

I (iv): Improve RMP trials by incorporating age data in their conditioning

The proponents refer to IWC (2016):

> *If the Implementation Simulation Trials for the western North Pacific common minke whales are to be revised in the future, the age data should be included in the conditioning proces*s (IWC, 2016c).

However the Expert Panel provided important context in relation to this statement:

> *The specific assumptions underlying SC/F16/JR43 will need to be refined before the age data are included in the conditioning process. In particular, consideration should be given to (a) using alternative selectivity patterns, (b) using a spatial structure that better matches that underlying the trials, and (c) fitting to the actual abundance estimates rather than the output from trials. In terms of selectivity, it would be expected that the selectivity pattern would be dome-shaped for the inshore areas, at least for the case in which there is a single O-stock. Ageing of commercial data could be used to inform the pre-1987 selection pattern, which is currently pre-specified based on values estimated for North Atlantic minke whales. See Item 9.1.1 for additional discussion of the age data.*

In several places the proponents refer to the age and genetic comparisons of inshore and offshore minke whales. Sample size evaluations relating to these comparisons have not been presented relating to the proportional allocation of the take of minke whale offshore proposed in sub-areas 8 and 9. No demonstrations are provided on the power of the existing and proposed data to discriminate between the alternative stock hypotheses using SCAA. Under JARPN II permits were issued for the take of around 50 minke whales per year off Ayukawa (sub-area 7CS). However the number taken has often been less half that number. This is relevant to the recommendation above about using an appropriate spatial structure and estimated rather than assumed selectivity/availability functions.

The selection of sample size is justified on the ability to detect a step-change in recruitment using SCAA. It is not explained how or when these particular data and analyses would be expected to be used in conditioning RMP ISTs. No performance measures relating to the choice of the effect size that it will make a material difference to ISTS have been provided, nor any direct analysis of the probability of detecting an effect of that size. The median of a large number of projections does not provide enough information on the properties of estimates based on using different sample sizes; only Fig 1 of Annex 12 provides calculations of the standard deviations of the estimates. These show that the different selected sample sizes make no substantial difference to the estimates of the standard deviation of female births.

The demonstrations also apply to scenarios not included in the research proposal; namely the collection of age and sightings data over periods greater than 10 to 20 years, Only with 100 years of data is there some modest correspondence between the 'true' and median of the estimated scenarios, and even then the step change in

recruitment is not well estimated. The demonstrations in Fig 2 shows that the estimated aggregated effect sizes on the medians of the trials with 10 to 20 years of data are small compared with the standard deviations given in Fig 1.

Of course the real world will not have 200 replicates and so medians do not give insight into the properties of the range of potential outcomes. Evaluation of the methods need to examine the population of estimated trajectories, for example, by plotting trajectories individually and/or as boxplots by year. A more directly related performance measure should be provided such as the distribution of the ratios of estimated to true percentage change in recruitment over time.

Models that have density dependence only in recruitment will give the greatest effect size when generating simulated age distributions. However, pure density dependence in recruitment is highly unlikely; energetics models (de la Mare and Miller, 2016) indicate density dependence in mortality is likely to be highly important, and will have less obvious effects on age structure since all cohorts are affected simultaneously, particularly for juveniles. This process is likely to be more important for recruitment to the mature population than births. This class of effect should also be included in the simulations.

The simulations provided in Annex 12 of the proposal have omitted likely important elements of the 2016 Panel's recommendations. Additionally, the SCAA should allow for the effects of known historic regime shifts, particularly since the timing of such shifts have been established from oceanographic and fisheries data (e.g. Hare and Mantua, 2000).

In summary, the information provided does not include sufficient diagnostics about the tests to enable a reasonable judgement about the properties of SCAA in meeting the objective (see appendix). Likely scenarios relating to density dependence, spatial variation in age structure and the estimation of selectivities should also be examined. Consequently, it is not possible to determine from the information provided whether the lethally collected age data and methods of analysis are necessary or sufficient for achieving Objective 1.

II (ii): Estimation of biological and ecological parameters in North Pacific sei whales for RMP Implementation

The selection of sample size for the sei whale component is based on obtaining an estimate of natural mortality (M) using SCAA. As for the minke case, the simulated scenario omits important factors, particularly relating to the likely dome shaped selectivity for the earlier commercial catches. It is also appears to be assumed that MSYR is known and fixed at 0.04 and that M is independent of age and density.

The first question is what is the utility of estimating M and why is this relevant to sei whales but not minke whales? The parameter of interest in conditioning ISTs is MSYR. If MSYR is assumed to have a specific value the estimate of M is conditioned on that value, M and MSYR are correlated (see Fig 1). The appropriate question is whether the additional age data are likely to improve estimates of MSYR. Some simulation analyses on this subject are given in the appendix. These analyses illustrate that the prospects of reliably estimating MSYR and/or M from the amount of data proposed is remote. This is not that surprising since this was also attempted in JARPA with results that lacked useful precision.

The other use of the analysis in conditioning ISTS is closely linked to the estimation of MSYR and that is scenarios relating to the recovery of sei whales from heavy exploitation prior to 1976. The results in the appendix suggest that this important factor is unlikely to be well informed by the proposed data. The third illustration from the Appendix is the types of diagnostics needed to evaluate the likely properties of SCAA.

Consequently, it is not possible to determine from the information provided whether the lethally collected age data are necessary or sufficient for achieving Objective 2.

General comment on statistical catch at age analyses

Given the increasing emphasis on the use of SCAA, the Scientific Committee should establish standards for the implementation and presentation of these methods, including diagnostics for both applications to existing data and the prospective evaluation of future data collection.

References

de la Mare, W. K and Miller, E. 2016. Further examination of the relationship between MSYR1+ and MSYR mature based on individual based energetic models. SC/66b/RMP04.

The Government of Japan. 2016. Proposed Research Plan for New Scientific Whale Research Program in the western North Pacific (NEWREP-NP).

IWC 2016. Report of the Scientific Committee. SC/66b/Rep1.

Hare, S. R. and Mantua, N. J. 2000. Empirical evidence for North Pacific regime shifts in 1977 and 1989. Progress in Oceanography 47:103–145
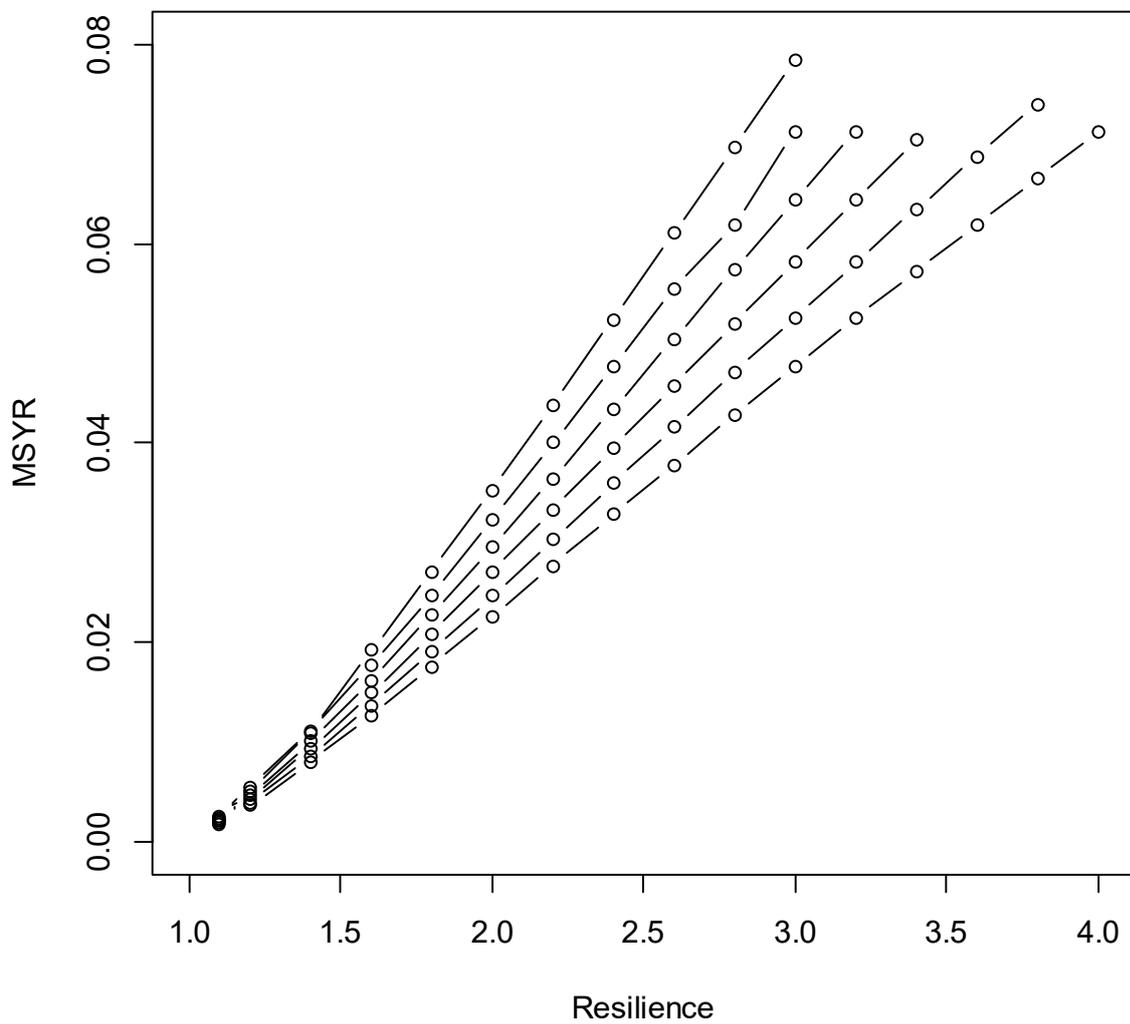
Fig 1. Relationship between MSYR, resilience and natural mortality (in this case with M also density dependent). Resilience is the density dependence term that affects births, Recruitment is the combined effects of births and mortality. The lowest curve corresponds to M = 0.02, the upper curve has M = 0.07.

Appendix   Simulated performance of a statistical catch at age analysis

Introduction

Statistical catch at age analysis models (SCAA) have become a mainstay of a number of analyses seeking to estimate a range of parameters of management interest by fitting population models to a range of data types, typically combining catch-at-age data with time series of abundance data. The important developments in this space have been driven by Punt and Polacheck (2005. 2006, 2007 and 2008) and in a series of update and model improvements (Punt; 2011, Punt et al. 2014). Much of this development was originally to address the issue of whether catch-at-age data from southern hemisphere minke whales carried a signature of population trends that pre-date their exploitation and that may have arisen from the depletion of other baleen whales – particularly blue whales earlier last century; the much discussed 'krill surplus'. This question was addressed by using SCAA models to fit population models that allow for changes in carrying capacity (K) over time. SCAA models generally need to estimate tens to hundreds of parameters and to be computationally tractable they rely on maximisation of log-likelihood functions by numerical methods that make use of auto-differentiation.

These models are beginning to be relied upon to utilise the catch-age-data from JARPA, JARPAII, NEWREP-A and NEWREP-NP to meet those programs' objectives of providing information relevant to management and the development of ecosystem models. Therefore it is timely to use simulation methods to improve our knowledge of the reliability of estimates arising from these models and to develop methods for the prospective evaluation of the likely outcomes from collecting further abundance and age-data.

A second issue is that if the models are to be used for the derivation of management related information, the SC should follow its normal practice and have them independently validated. The model presented here has been developed independently and makes no use of any code used in the existing SCAAA model. Consequently inter-comparison of the two model implementations using simulated data could be used to assist in their validation.

The model used in the simulations here is built using an object oriented class template library written in C++ originally developed for stock-assessment and management strategy evaluations (Logan *et al.* 2005). The class template models can be instantiated with variables declared as double precision or as auto-differentiable while using identical source code for model implementation. This readily allows for multiple instances of the model so that for simulation testing it is easy to set up one instance of the model for data generation and an entirely independent instance to be used for fitting to data. The details of the model are given in the Appendix.

The fitted model uses an auto-differentiation class template library developed by Justin Cooke. Testing showed that the fitted model with auto-differentiation produces identical numerical results to the data-generating simulation model when the same parameter values are used. The fitting procedure recovers the 'true' values of the data generating model parameters when fitted using perfect information. Although the model presented here has the sexes pooled, the class library also contains two sex versions of the model and so the model can be readily extended. However, for the purposes of this paper which is to begin to define the issues relevant for SCAA modelling, a pooled sex model is sufficient.

The model presented here provides for more flexible estimation of some of the relationships included in the existing SCAA models. In particular Punt *et al.* (2014) used piece-wise linear functions to describe changes in K and the shape of age-dependent natural mortality as well as a discontinuous function for 'dome shaped' commercial age-specific catch selectivity. The difficulty with piece-wise linear and other discontinuous functions is that they do not have continuous derivatives at the joints, which makes it difficult to estimate the position of the joints using auto-differentiation. The positions of the joints are not included in the estimation procedure in the existing SCAA models.

The model can also incorporate time variations in K modelled using a dome-shaped curve derived from multiplying a logistic function with a reversed logistic function. This combined function has continuous differentials (see Appendix for definition). The same functional form is used for dome-shaped selectivities. Age dependence in natural mortality is modelled using a continuous function of the general form due to Siler (1979), but with an additional parameter to defer increasing mortality with age (see Appendix). Here, as in the existing SCAA the value of MSYL is kept fixed.

A more subtle difficulty arises in the existing SCAA and other models that use a Pella-Tomlinson (P-T) stock-recruitment relationship. With a P-T model, population levels somewhat above K lead to negative recruitment. The existing SCAA includes the usual practice of resetting negative recruitment values to zero and penalising the likelihood function. However, this also destroys the continuity of the function. In the models presented here all of the functions to be fitted, including the stock-recruitment relationship, are continuous and so estimating all of their parameters is feasible when using auto-differentiation. The population dynamics model, the functional forms for model components and other variable functions and the likelihood functions used in fitting are all given in the Annex.

The scenario tested here is based on western north Pacific sei whales and the types of data collected under JARPN, JARPN II and prospectively under NEWREP-NP. These initial tests are idealised because all animals in the catch are aged without error and the catch-at-age distributions represent random samples from the selected population. Age-specific selectivities are also constant over time for both commercial and special permit catches. There are two series of absolute abundance estimates, one corresponding to the existing survey and the second to the prospective NEWREP-NP surveys. Neither series is assumed to be unbiased, each has its own correction factor estimated during minimisation as a time-invariant constant.

All the simulated data conform to the assumptions used in fitting the model. Consequently the performance of the estimation procedure is evaluated under ideal circumstances. The list of all the estimated parameters is given in Table 1. However, recruitment multipliers are not estimated in scenarios where there is no variability in K, thus correctly assuming that there is negligible recruitment variability. There are multiple restarts for the search with randomly dithered starting values for the parameters, centred in these trials on their true values, with increasing stringency for the convergence criteria. This is to reduce the possibility of landing on a local minimum. This is particularly important for multiple replicates in simulation testing because it is not feasible to examine the fit of every estimate in the same way as one would do for fitting a model to a single dataset. With complex multi-parameter likelihood functions it is likely that the morphology of the surface may exhibit local minima or twisting valleys, both of which make it possible for searches to converge even though there is a different set of parameter values that have a better minimum.

Table 1. Parameters estimated during fitting of model to simulated data. The searches for parameters are all constrained to a range by using a logit function to transform the parameters. In this way the transformed parameters are unbounded during the numerical search, but after the inverse transform the estimated values will lie in the bounded region. The column Order refers to the order in which the parameters are estimated in the fitting procedure, with 0 indicating that the parameter has a fixed value. The harvest rate nuisance parameters and stock size can be estimated first with the other parameters held at their starting values. After the first pass all the parameters are estimated together. This is can be more efficient because it gives the nuisance parameters roughly correct values before searching over the entire parameter space.

Parameter	Lower bound	Upper bound	Order
Initial total biomass (tonnes)	550 000	1 500 000	1
Stock recruit compensation	1.05	5.0	0
Density dependence in natural mortality	0.0	1.0	0 or 1
Siler coefficient 1	0.03	0.2	1
Siler coefficient 2	0.5	4.0	1
Siler coefficient 3 (floor on M)	0.02	0.12	1
Siler coefficient 4	0.1	0.5	1
Siler coefficient 5	40	65	1
Peak value for difference in K (as multiple of K)	-	-	0
First inflection year for K scaling	-	-	0
Number of years to first 95% point on K scaling	-	-	0
Extra years to second 95% point on K scaling	-	-	0
Extra years to second inflection for K scaling	-	-	0
First inflection for commercial age selectivity	3	15	1
Additional age to lower 95% commercial age selectivity	1	12	1

Additional age to upper 95% commercial age selectivity	1	40	1
Additional age to second inflection commercial selectivity	1	20	1
Inflection for special permit age selectivity	0.2	4.0	1
Additional age for 95% point for special permit selectivity	0.2	5.0	1
Survey bias for existing survey	0.5	5.0	1
Survey bias for future special permit surveys	0.2	5.0	1
Harvest rates (for every year with a non-zero catch	0.	0.1	1
Year class multipliers	0.1	2.	0

In the results presented here it is clear that with the amount of data assumed to be available that finding global minima are difficult and so the comparisons of likelihood function values will be misleading. However, in the time available further refinement of the search control algorithm was not possible. Nonetheless, the results as presented demonstrate the types of information needed to understand the basic properties of the analyses and in particular their strengths and weaknesses. Only one set of results are shown but I intend to develop further the search algorithm and to examine some of the issues mentioned in my observer's statement. These are not meant to represent an exhaustive set of potential performance statistics, but they provide some preliminary ideas should the Scientific Committee take up the recommendation that SCAA requires standardised performance measures and diagnostics.

Aggregated results for both fitted and true model having age-dependent but density independent natural mortality – resilience takes specified values.

The example examines the fits of a model to a single true population with MSYR = 0.04. The fitted population has resilience fixed at levels corresponding to MSYR from 0.01 to 0.06. Thus the trials provide estimates of natural mortality conditioned on different assumptions about MSYR. Table 2 below shows the aggregated results. The differences between the assumed and estimated values of MSYR arise from the dependence of MSYR on the estimated values of the age-dependent natural mortality parameters.

The first set of figures (1 through 16) show the results summarised for the range of MSYR values. The plots of the likelihood profiles indicate that convergence in the global minimum is problematic, but suggest that power to distinguish between alternative values of MSYR may be poor.

Table 2. Properties of estimates given assumed values of MSYR. The first sub-table are the estimates of M and MSYR and Delta K from a nominal 25 trials, although some are deleted where obvious convergence failure has occurred. The second sub-table is the mean marginal total negative log-likelihood profiles from the nominal 25 replicates subdivided by the different data sources.

Assumed MSYR	Siler 3	SD	CV	Bias	MSYR	SD	CV	Bias
0.01	0.0118	0.0030	0.2554	0.2362	0.0132	0.0006	0.0441	0.3288
0.02	0.0122	0.0033	0.2678	0.2432	0.0259	0.0022	0.0831	0.6483
0.03	0.0137	0.0083	0.6049	0.2738	0.0368	0.0015	0.0409	0.9194
0.04	0.0186	0.0155	0.8312	0.3724	0.0486	0.0033	0.0673	1.2161
0.05	0.0201	0.0181	0.9011	0.4026	0.0608	0.0049	0.0809	1.5193
0.06	0.0220	0.0126	0.5716	0.4394	0.0792	0.0069	0.0867	1.9803

Assumed MSYR	Number of replicates	Total	Survey 1	Future surveys	Commercial ages	Special permit ages
0.01	24	2610.342	17.30525	52.17239	793.8576	1642.431
0.02	24	2629.451	13.36123	31.94484	817.0063	1694.410
0.03	22	2510.688	12.72337	24.61974	745.1055	1665.021
0.04	25	2583.564	11.75114	25.53154	820.2850	1663.561
0.05	22	2632.665	11.11808	24.27947	862.6439	1674.712
0.06	25	2696.897	11.22860	24.30935	908.3805	1689.614

All
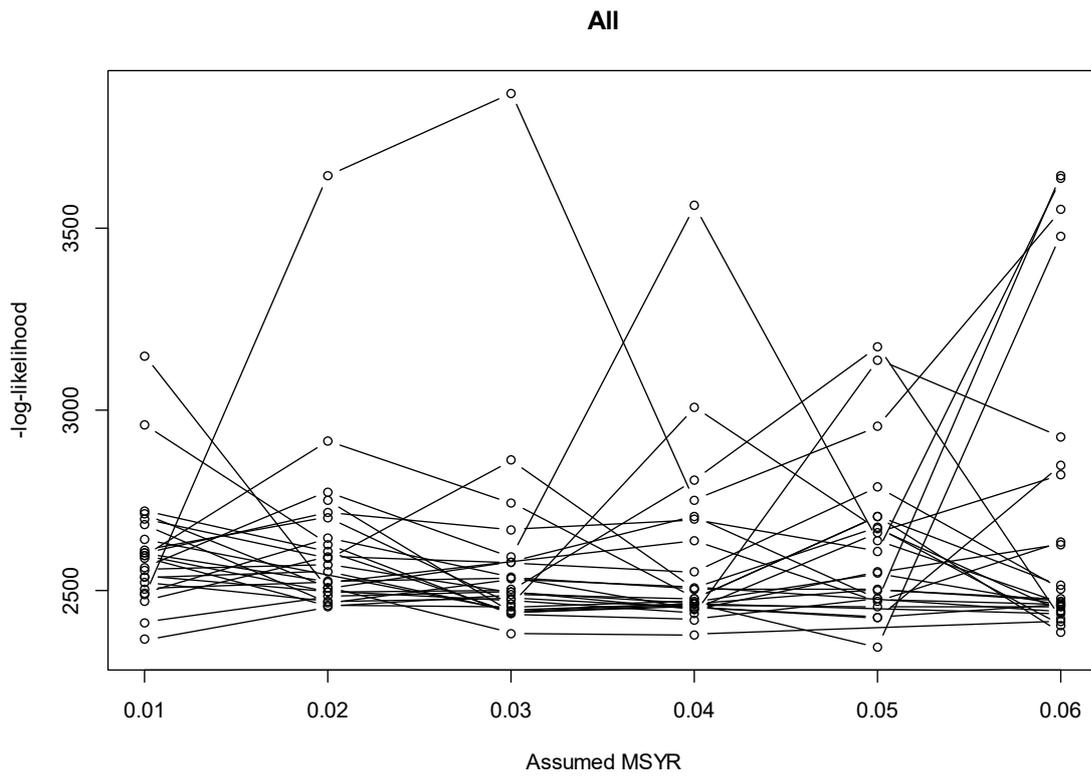
Fig 1. Likelihood profiles for the combination of all data types vs assumed MSYR values.

Early abundance surveys
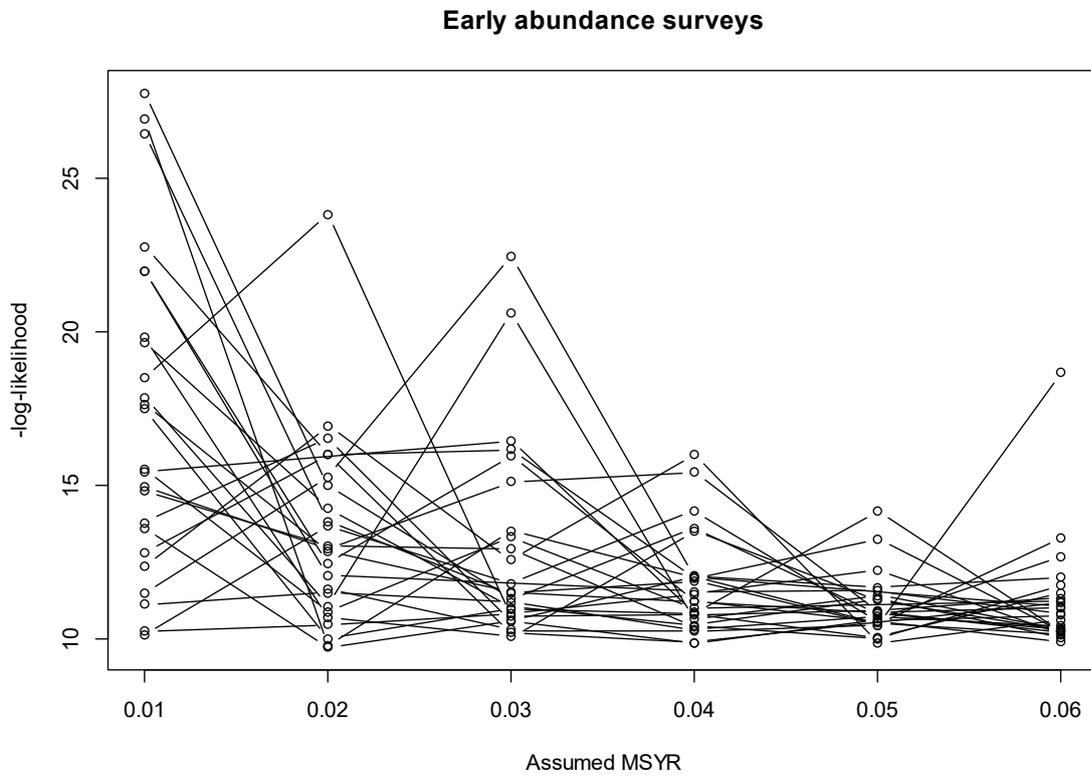
Fig 2. Likelihood profile contribution from the fit to the early abundance surveys vs assumed MSYR values.

Permit abundance data
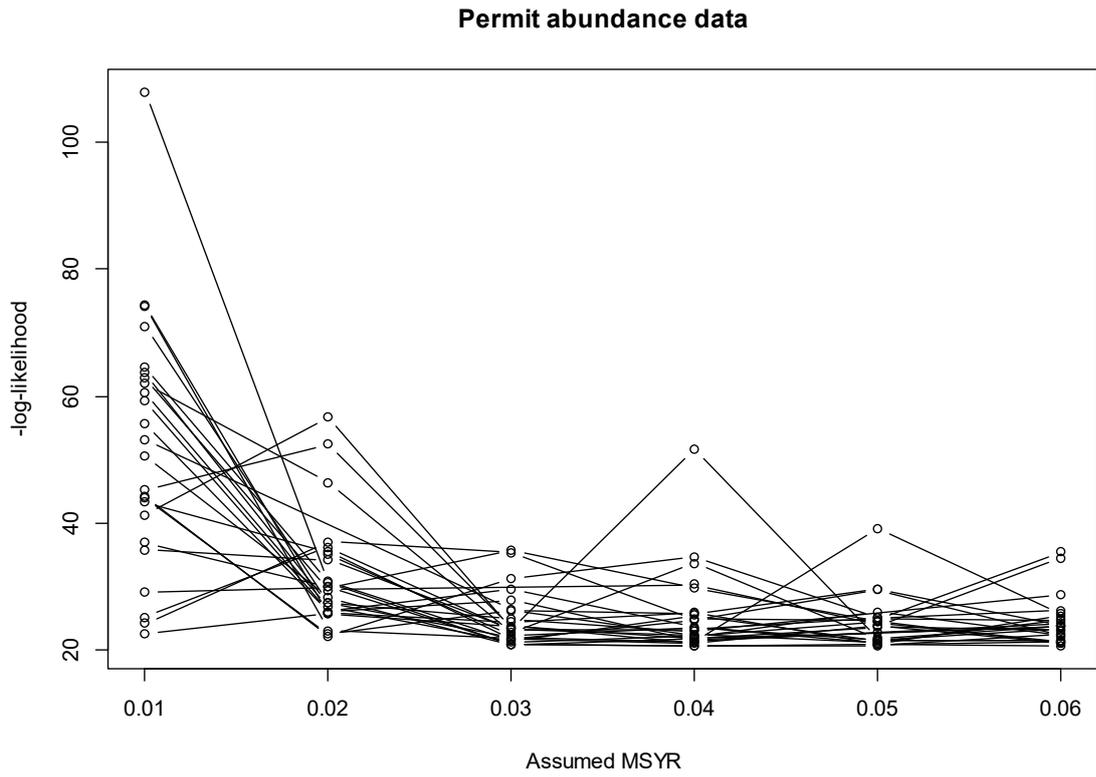
Fig 3. Likelihood profile contribution from the fit to the later abundance surveys vs assumed MSYR values.

Commercial age data
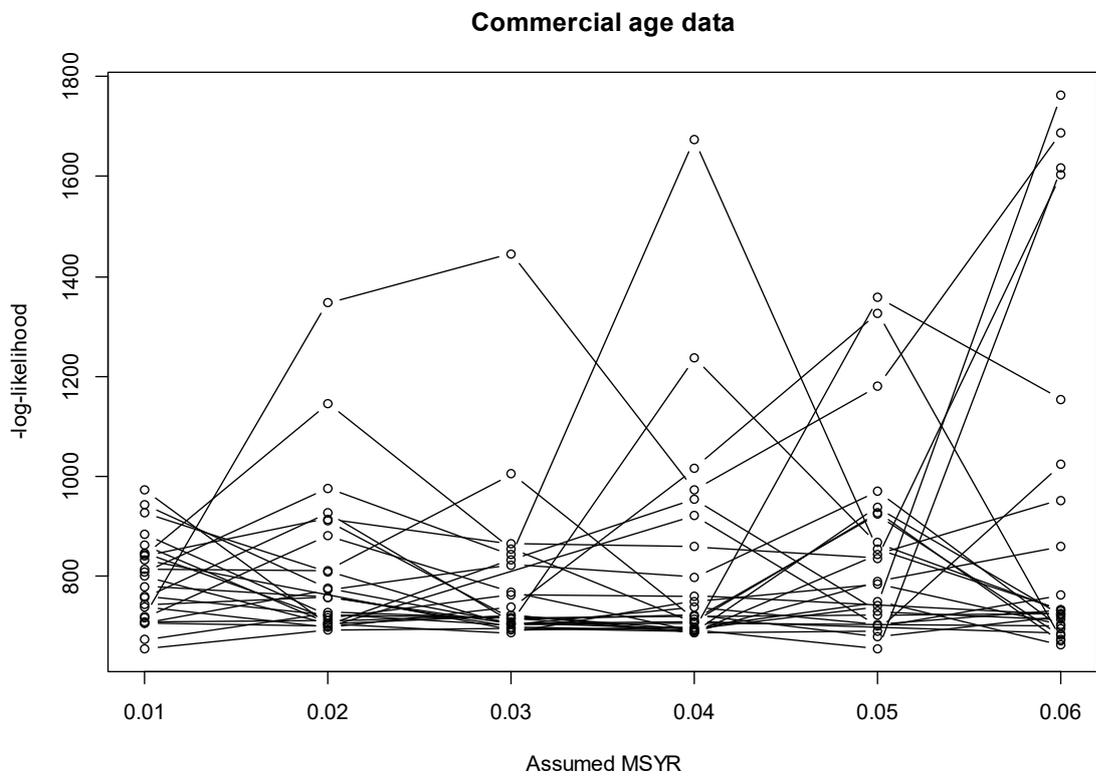
Fig 4. Likelihood profile contribution from the fit to the commercial catch-at-age vs assumed MSYR values.

Age data
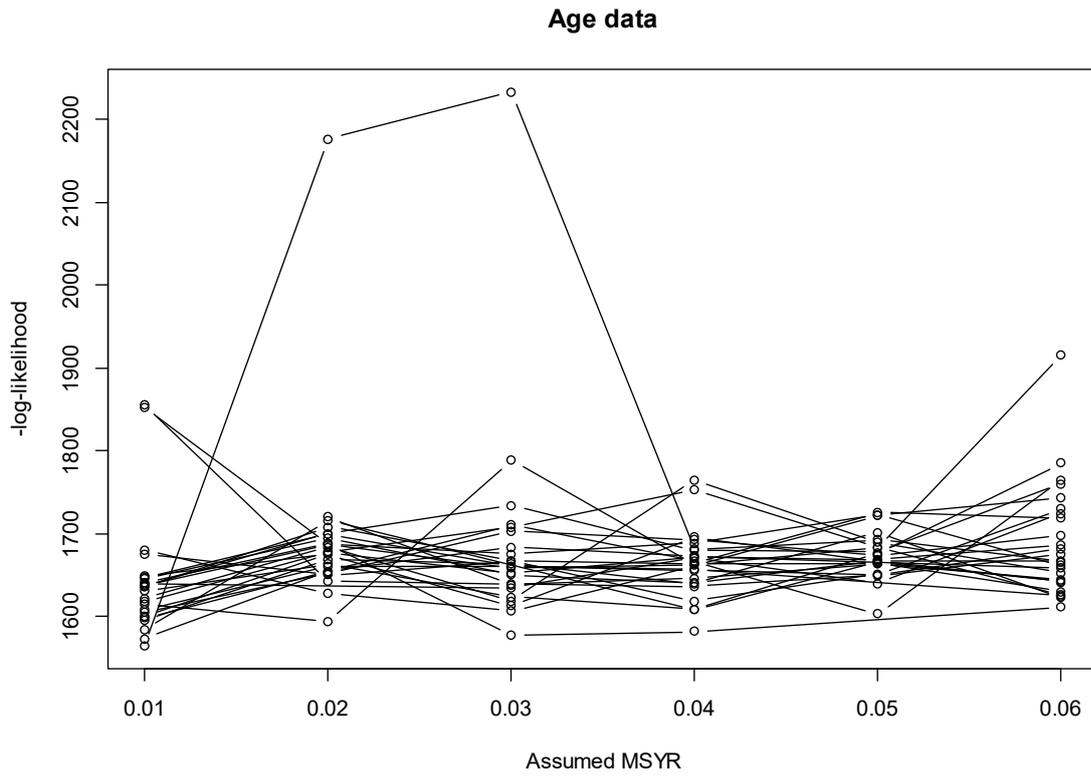
Fig 5. Likelihood profile contribution from the fit to the permit catch-at-age vs assumed MSYR values.

Commercial age selectivity A1_50
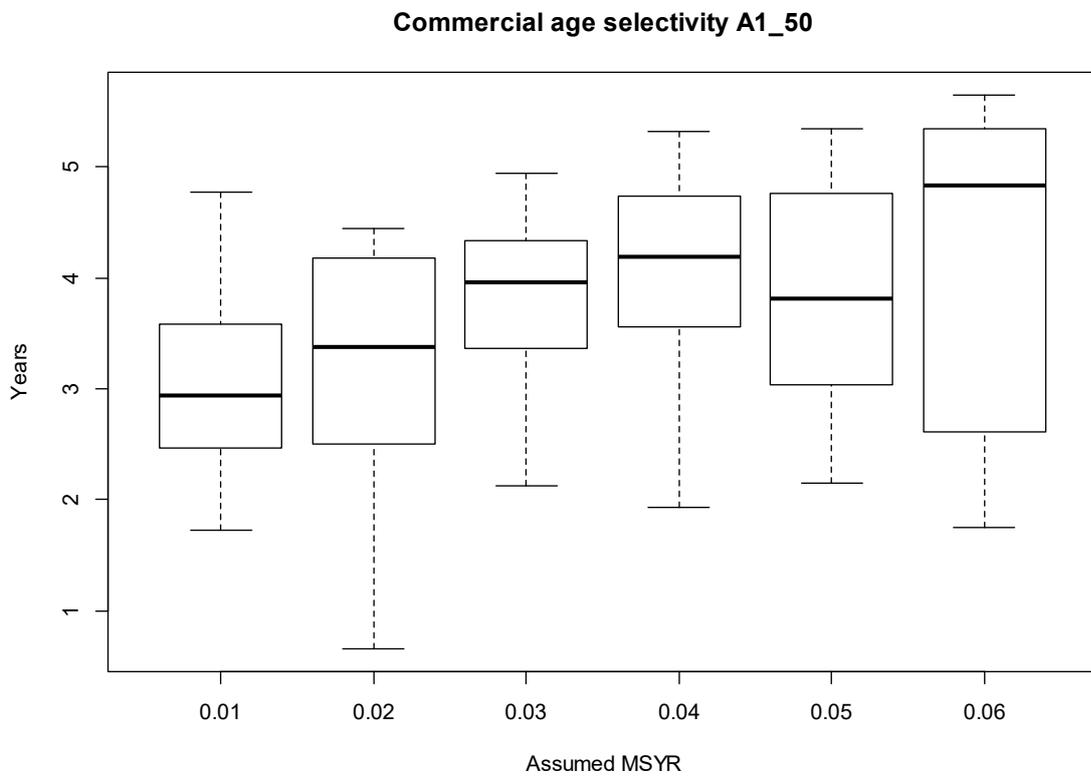
Fig 6. Distributions of estimates of the youngest age at 50% recruited for the commercial catch-at-age

Commercial age selectivity A1_95
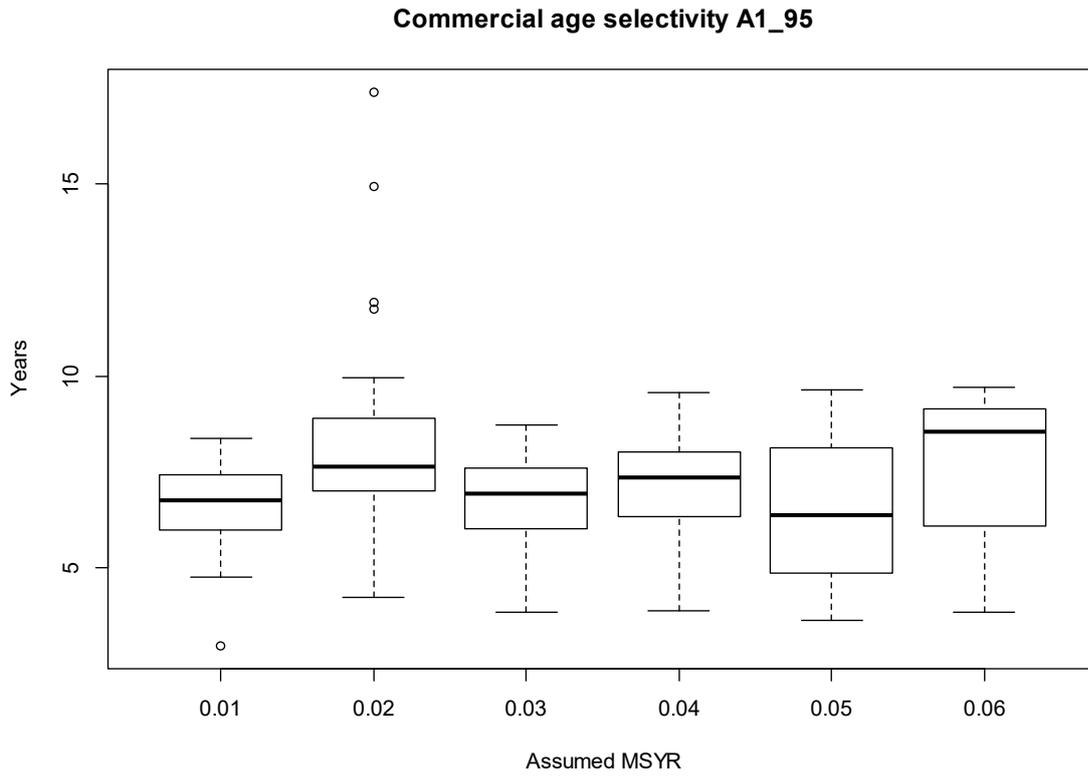
Fig 7. Distributions of estimates of the youngest age at 95% recruited for the commercial catch-at-age

Commercial age selectivity A2_95
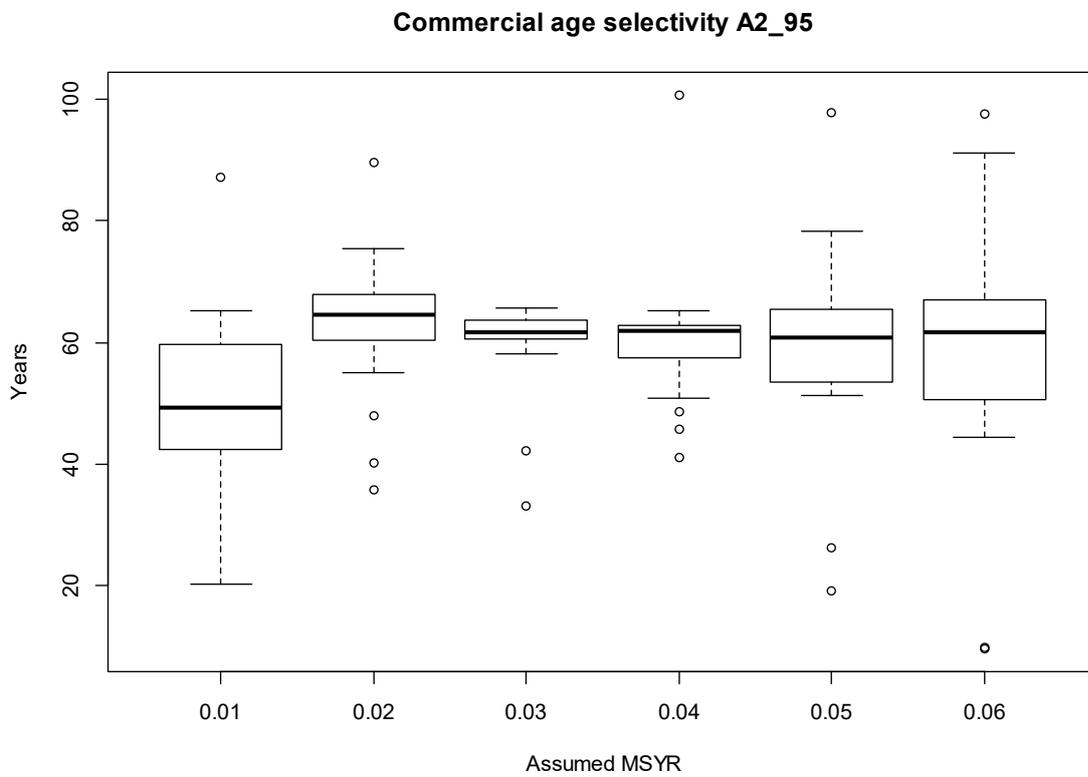
Fig 8. Distributions of estimates of the oldest age 95% recruited for the commercial catch-at-age

Commercial age selectivity A2_50
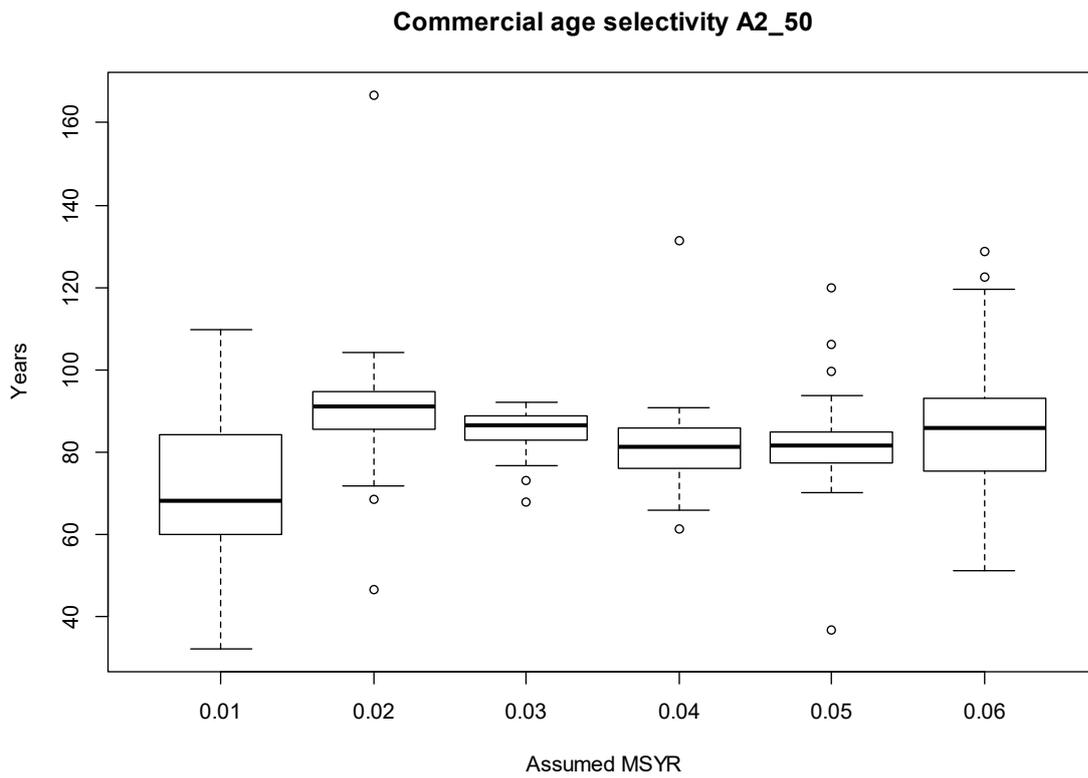
Fig 9. Distributions of estimates of the oldest age 50% recruited for the commercial catch-at-age

Siler mortality parameter 1
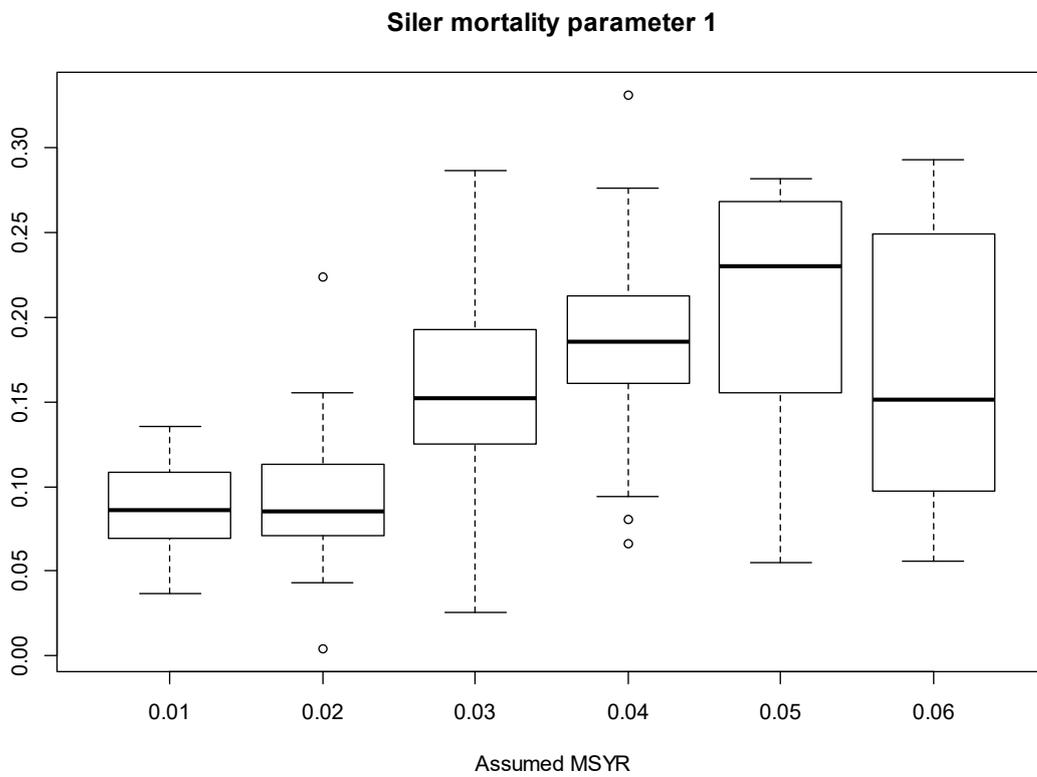
Fig 10. Distributions of estimates of Siler mortality parameter 1 (mortality at birth).

Siler mortality parameter 2
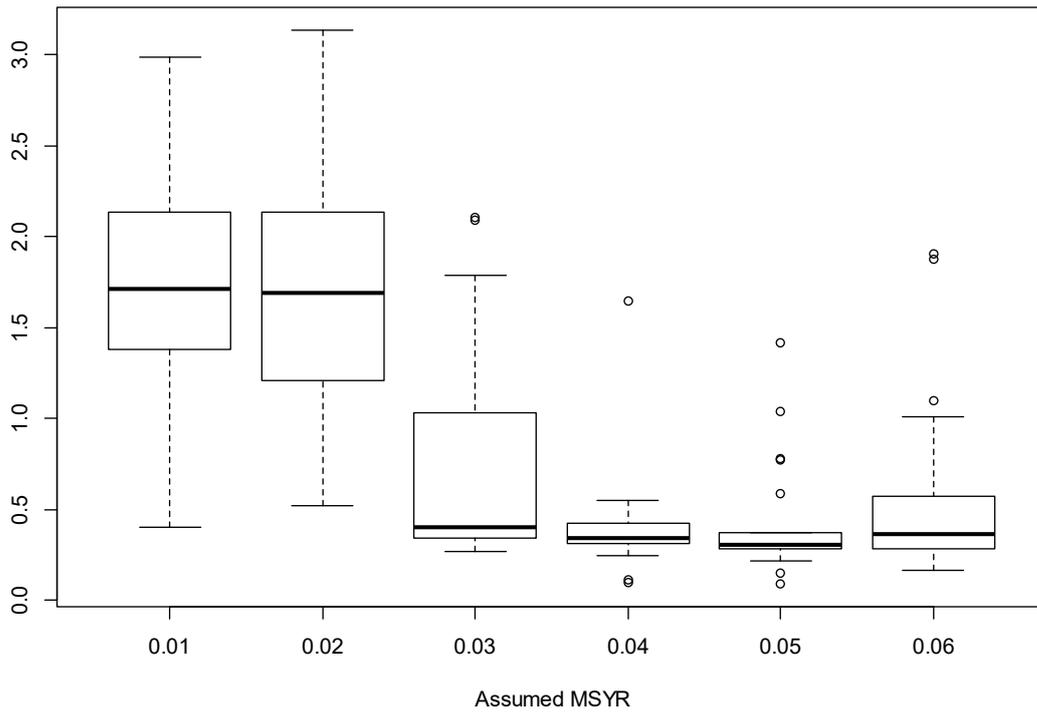
Fig 11. Distributions of estimates of Siler mortality parameter 2 (rate of transition from juvenile to adult mortality).

Siler mortality parameter 3
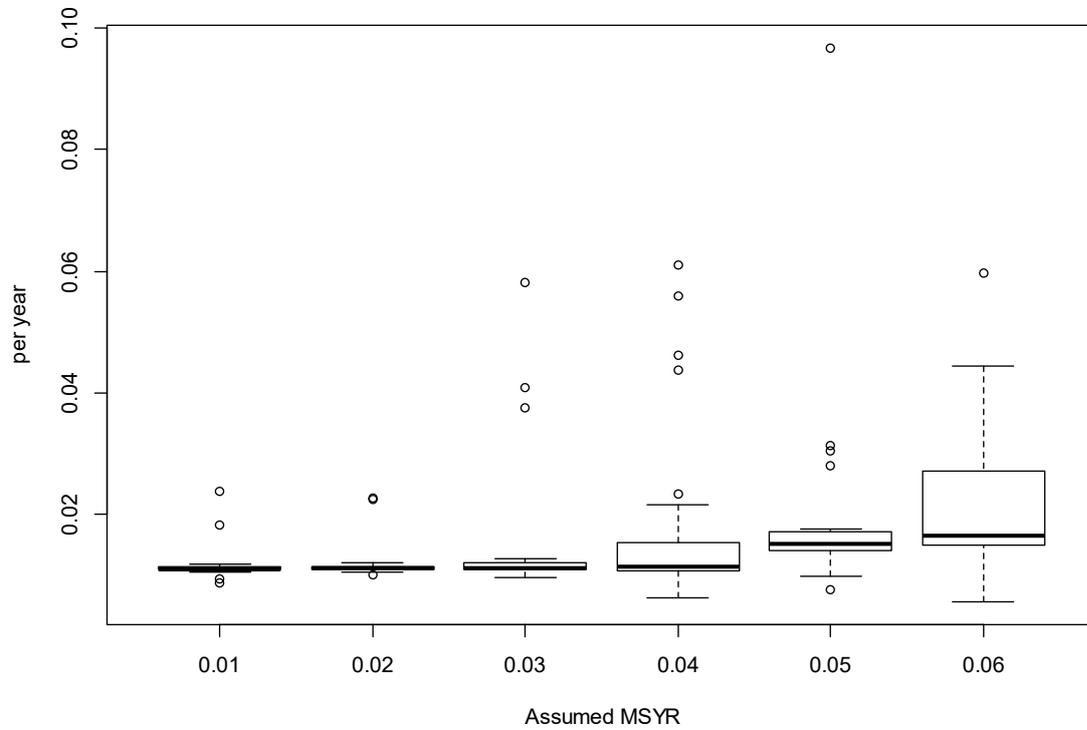
Fig 12. Distributions of estimates of Siler mortality parameter 3 (adult mortality).

Siler mortality parameter 4
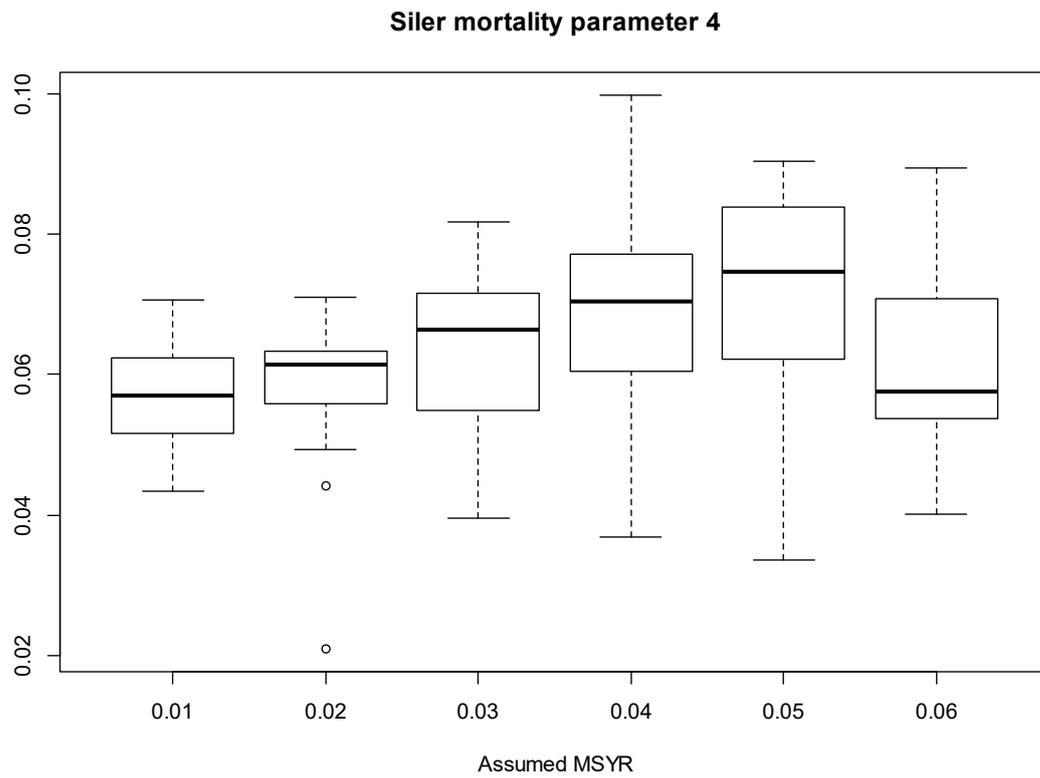
Fig 13. Distributions of estimates of Siler mortality parameter 4 (rate of mortality increase in older animals).

Siler mortality parameter 5
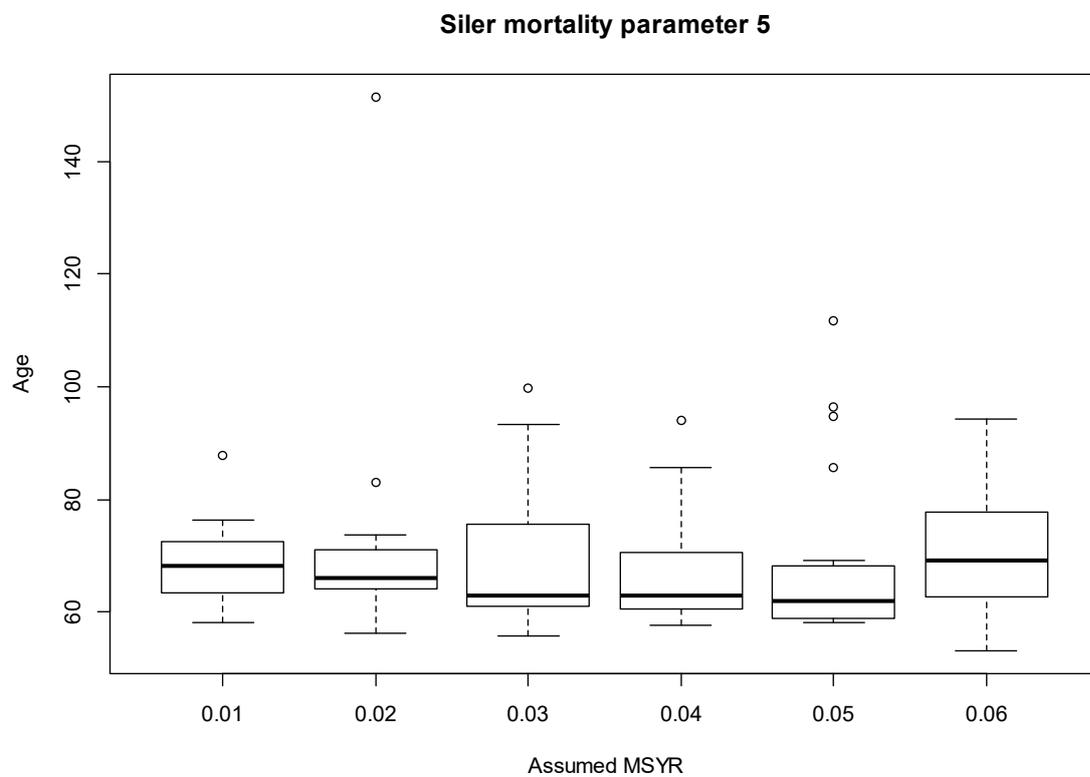
Fig 14. Distributions of estimates of Siler mortality parameter 5 (transition age to higher mortality in older animals).

MSY rates
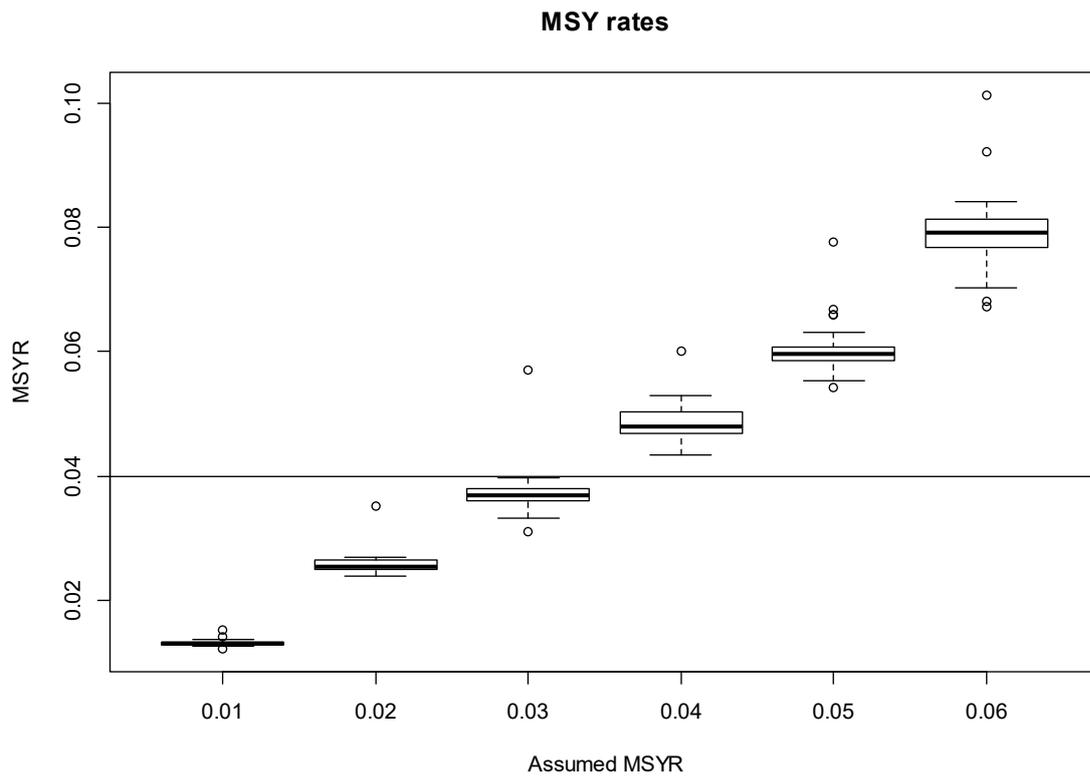
Fig 15. Distributions of estimates of MSYR.
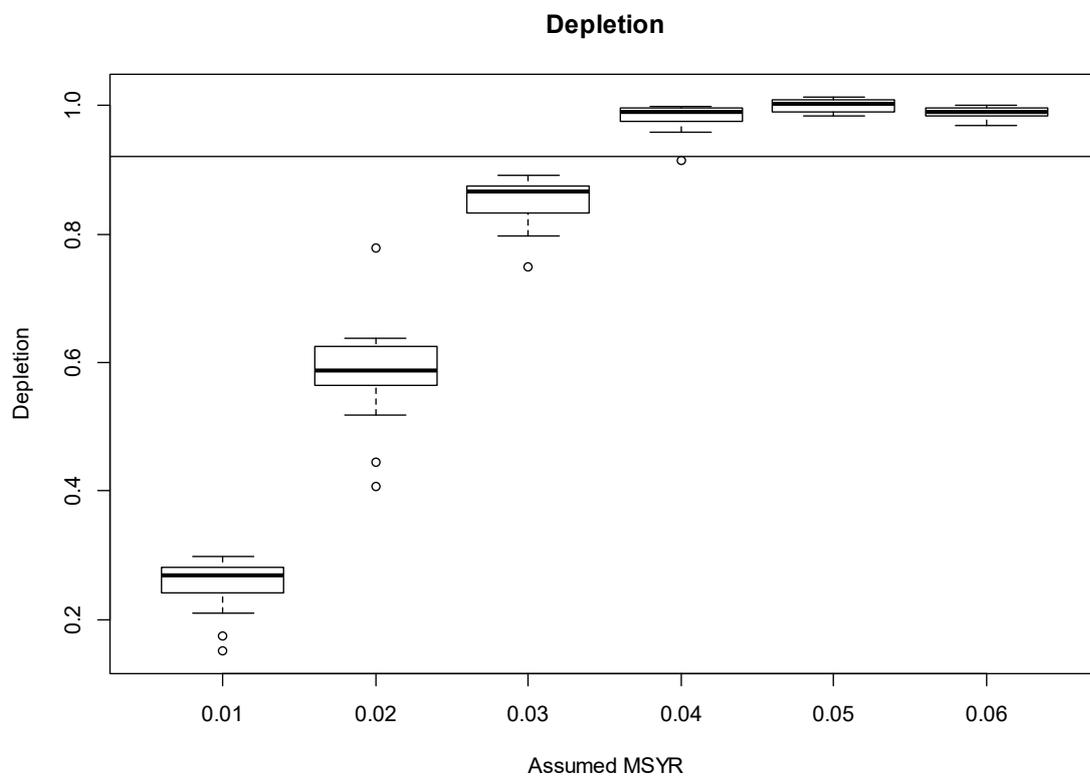
Depletion

Fig 16. Distributions of estimates of depletion (K/N$_{2028}$).

Results from the individual trials for an assumed MSYR = 0.04
In addition to the aggregate statistics across trials, it is also necessary to examine the statistics for replicates within trials. Some examples of these are shown in Figs 17 through 25 for the trial where MSYR is assumed to be 0.04, which also corresponds to the 'true' value. Fig. 17 confirms that the estimated harvest rates in each year have converged on the reported catch. This can be a diagnostic of convergence failure in some replicates.
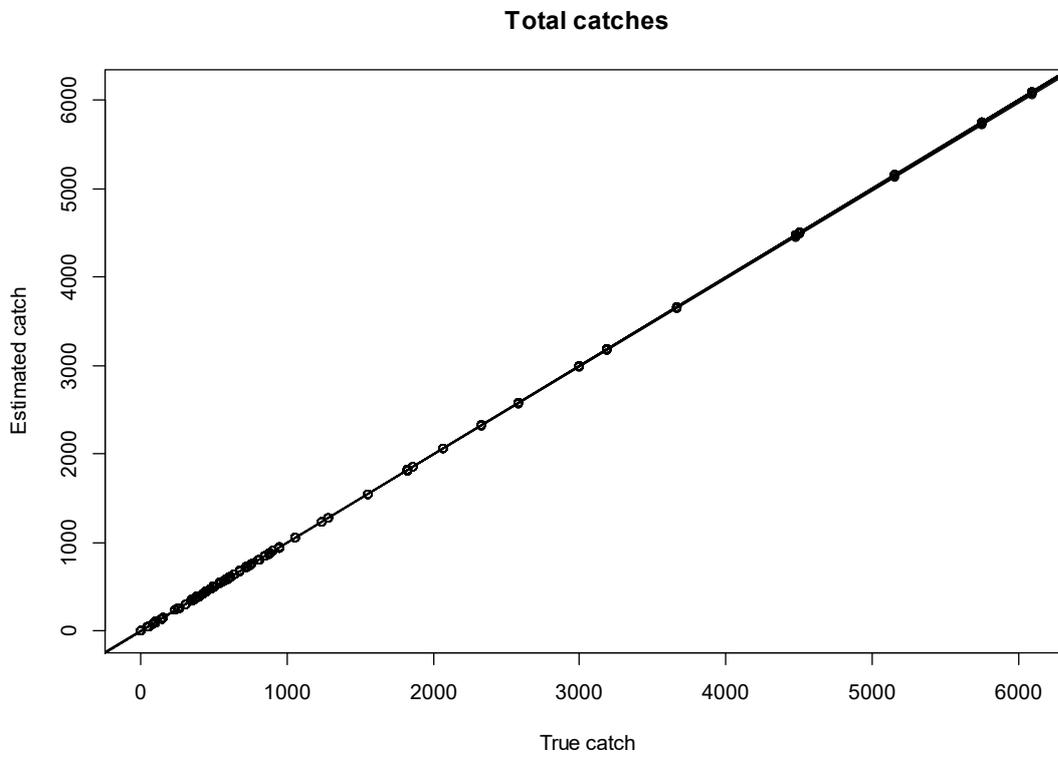
Total catches

Fig 17. Comparison of observed and expected catches from MSYR = 0.04 fit of model

Commercial age-structure
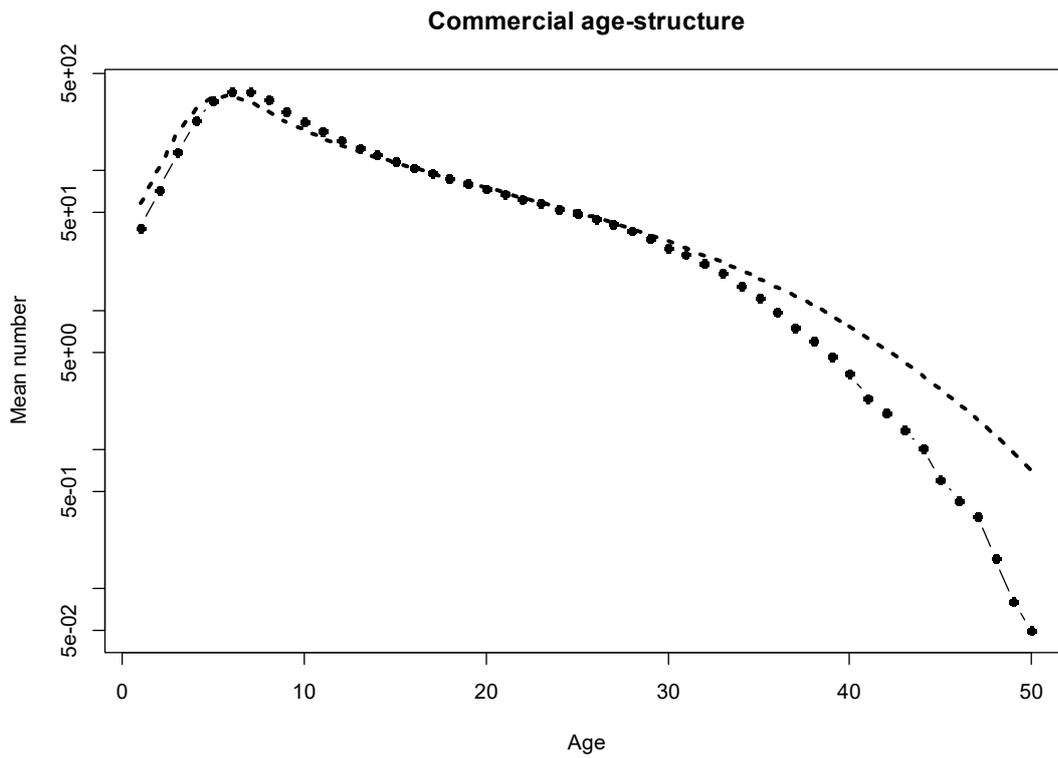
Fig 18. Mean of the expected commercial catches-at-age for the MSYR = 0.04 fit of model (dashed line) compared with the true mean catch-at-age (solid line)

Special permit age-structure
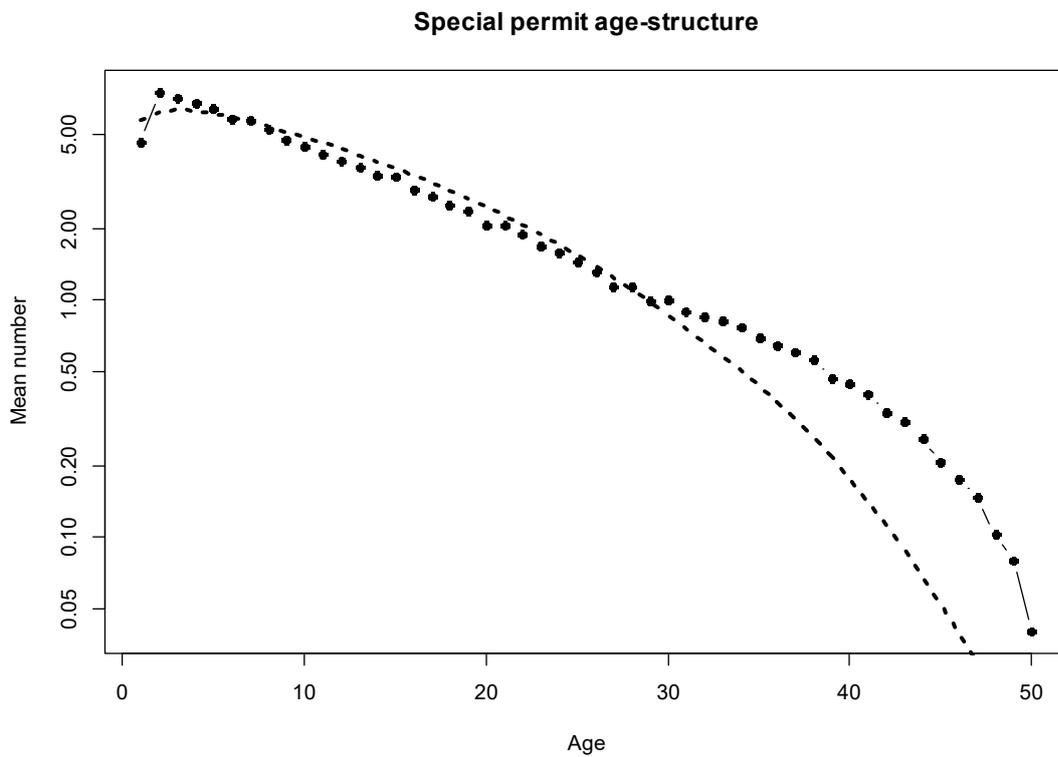
Fig 19. Mean of the special permit expected catches-at-age for the MSYR = 0.04 fit of model (dotted line) compared with the true mean catch-at-age (dashed line)

True and modelled 1+ trajectories
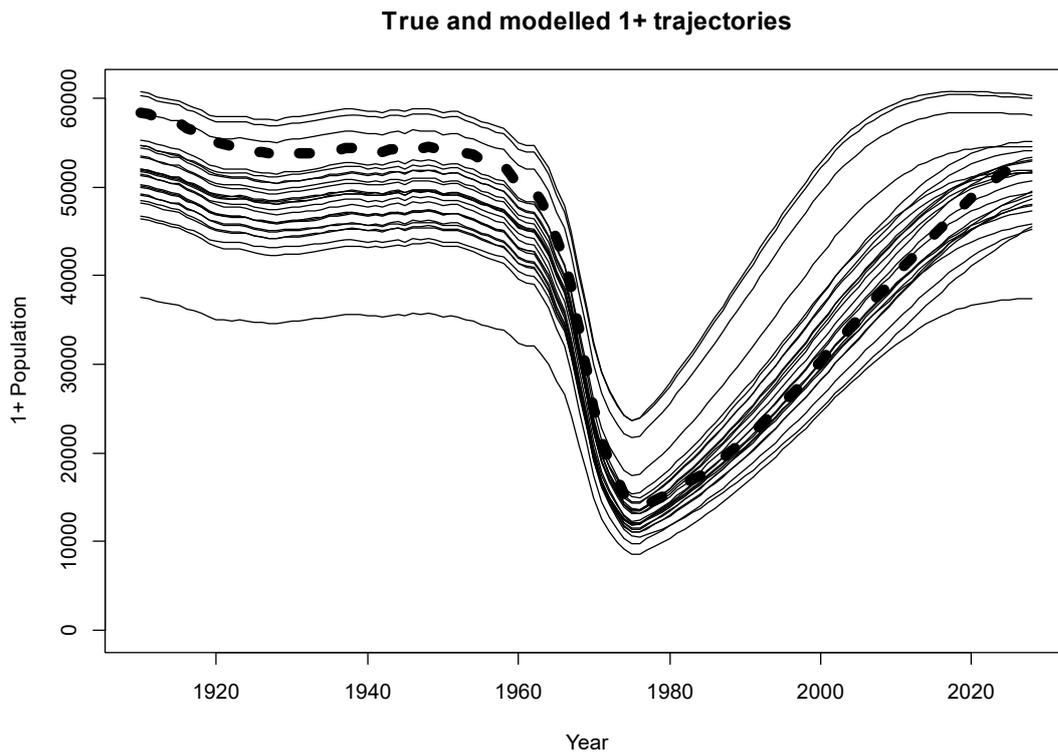
Fig 20. Estimated population trajectories for all replicates for assumed MSYR = 0.04. True trajectory is the heavy dashed line.
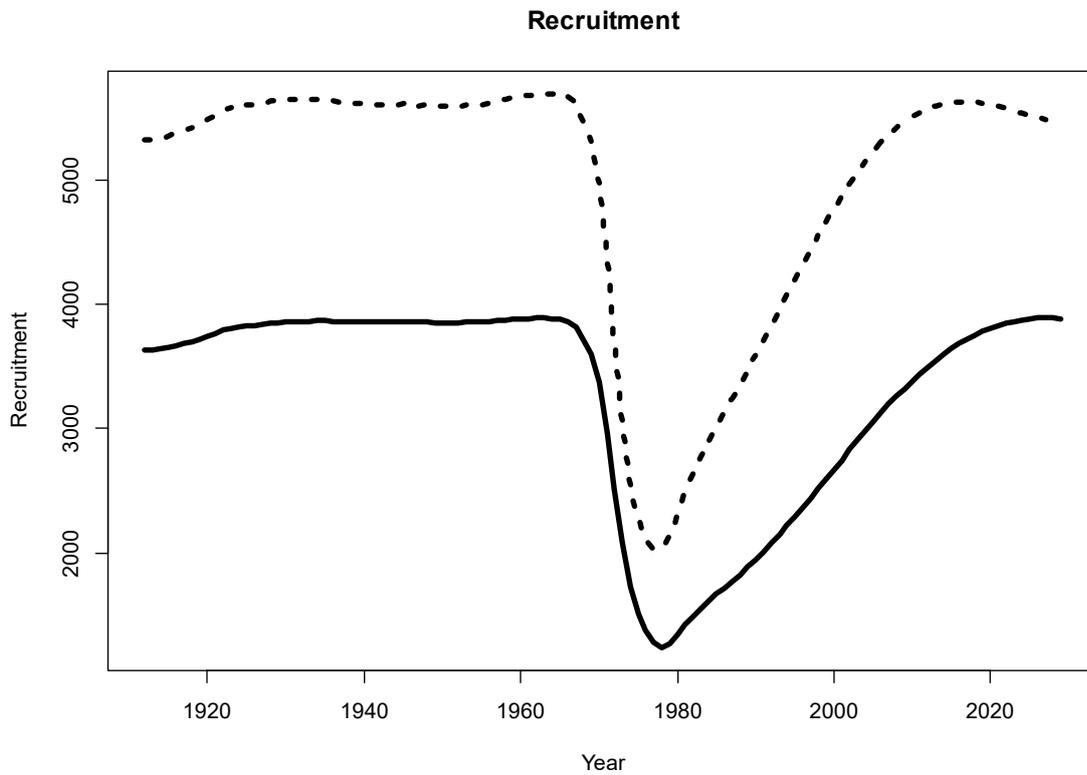
Recruitment

Fig 21. The mean estimated recruitment trajectory (dashed line) from the MSYR = 0.04 fit of model compared with mean true trajectory

Estimated/True recruitment
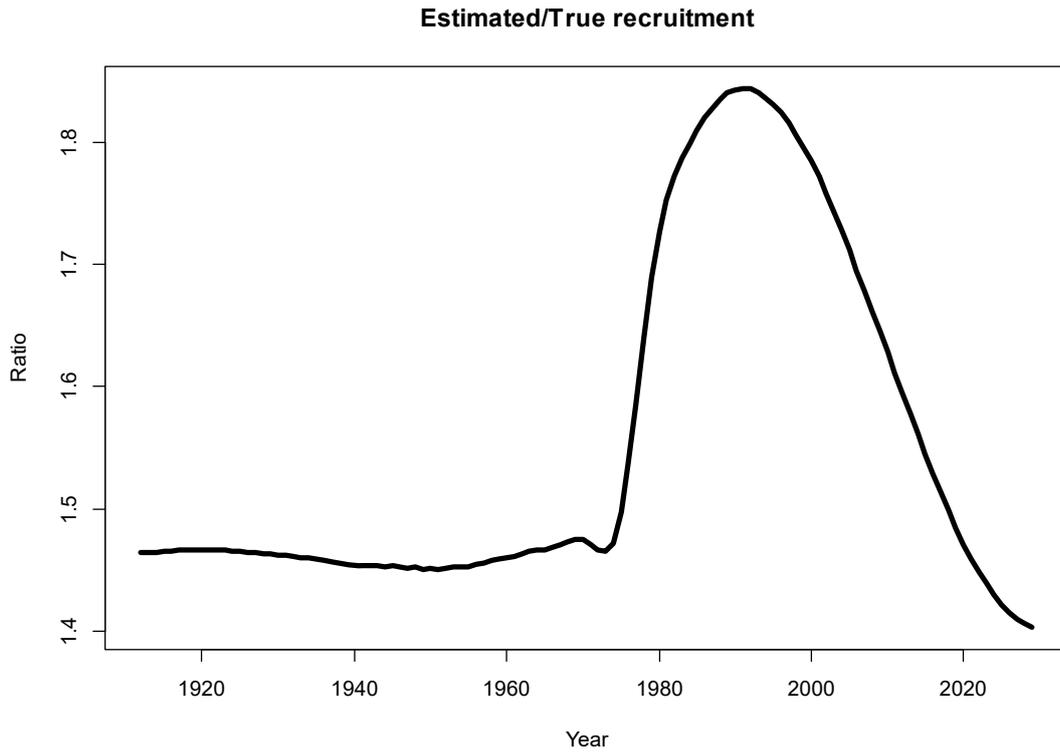
Fig 22. The estimated bias in recruitment from the MSYR = 0.04 fit of model.

Observed and expected survey estimates
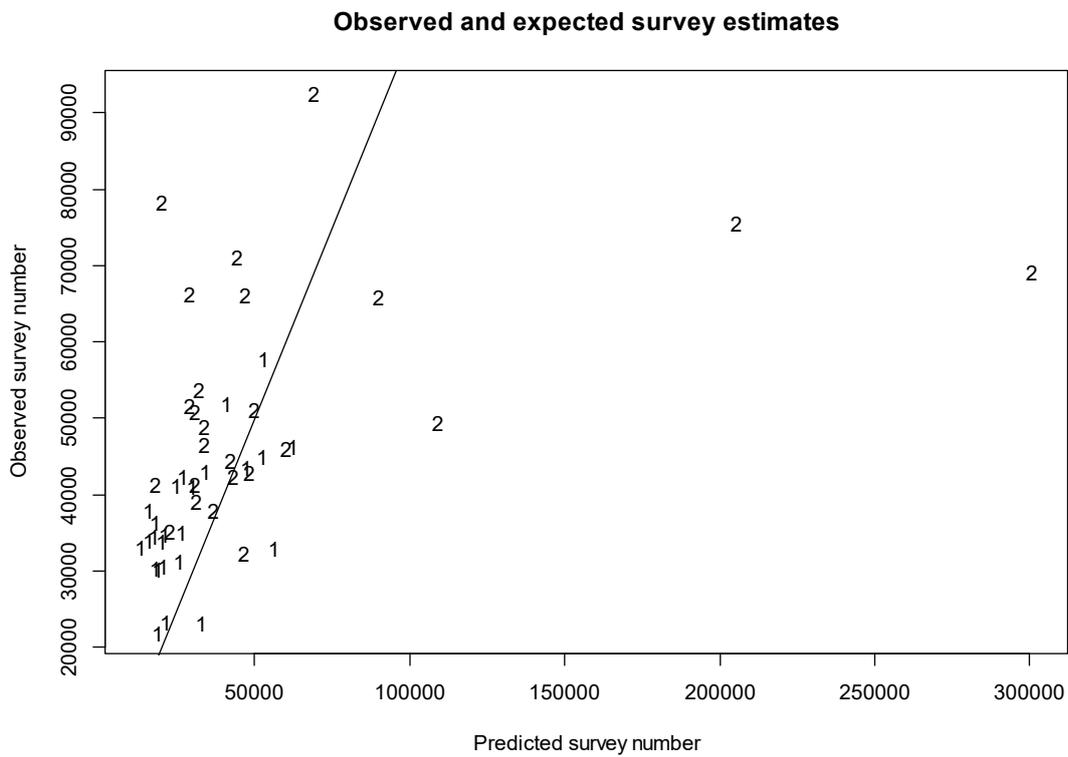
Fig 23. Observed and expected survey results from MSYR = 0.04 fit of model replicates
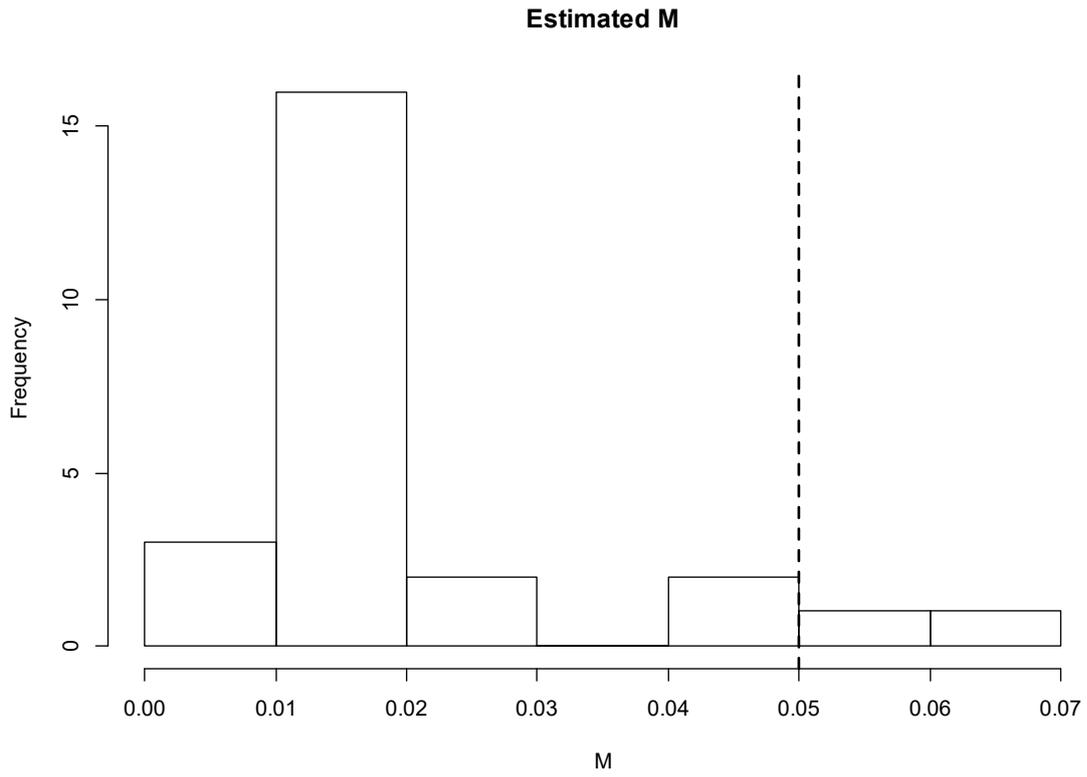
Estimated M

Fig 24. Histogram of estimates of Siler parameter 3 from MSYR = 0.04 fit of model replicates.
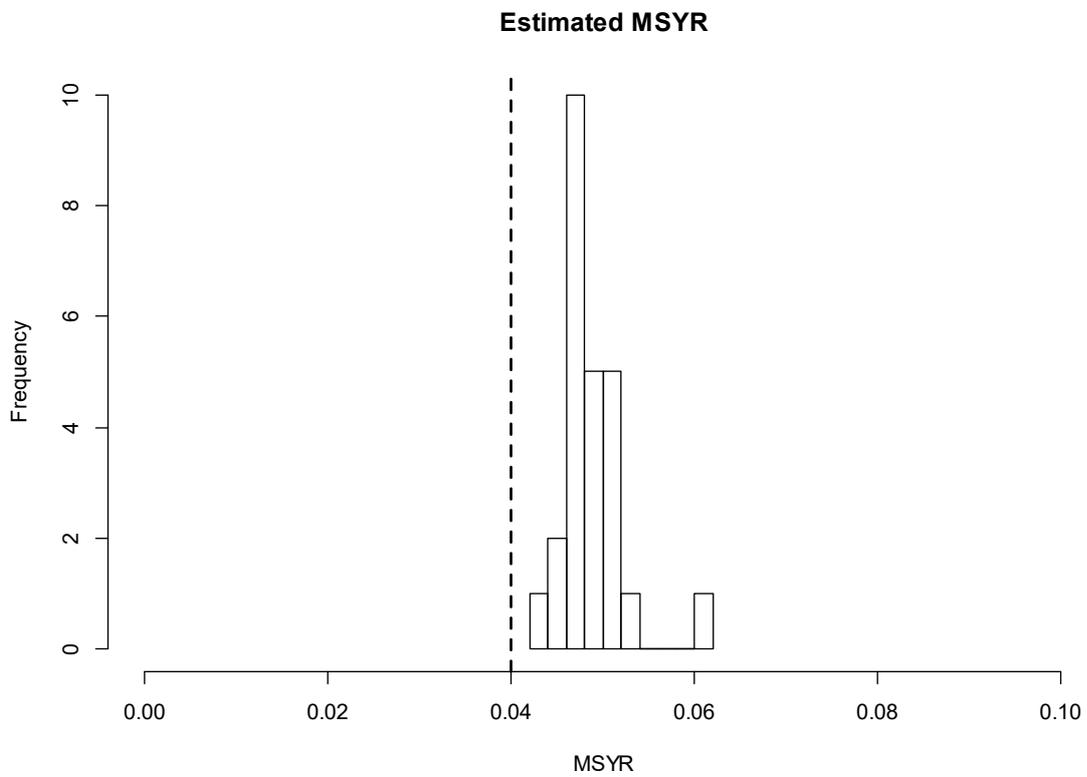
Estimated MSYR

Fig 25. Histogram of estimates of MSYR from assumed MSYR = 0.04 fit of model replicates.

References

de la Mare, W. K and Miller, E. 2016. Further examination of the relationship between MSYR1+ and MSYR mature based on individual based energetic models. (This meeting).

Logan, G. de la Mare, W., King, J. and Haggarty, D. 2005. *Management framework for Strait of Georgia Lingcod*. Research Document 2005/048, Canadian Science Advisory Secretariat, Department of Fisheries and Oceans Canada, Ottawa. 116 pp.

Press, W. H., Teukolsky, S. A., Vetterling, W. T. and Flannery, B. P. 1992. Numerical recipes in C++: the art of scientific computing. Cambridge University Press. 963pp.

Punt, A.E. 2011. Further analyses related to the application of statistical catch-at-age analysis to Southern Hemisphere minke whales. Paper SC/63/IA1 presented to the IWC Scientific Committee, May 2011 (unpublished). 20pp.Punt, A.E. and T. Polacheck. 2005. Application of statistical catch-at-age analysis for Southern Hemisphere minke whales in Antarctic Areas IV and V. Document SC/57/IA9 presented to the IWC Scientific Committee, June 2005. (unpublished). 71pp.

Punt, A. E., Bando, T., Hakamada, T. and Kishiro, T. 2014. Assessment of Antarctic Minke Whales using Statistical Catch-at-age Analysis. SC/65/IA01. Presented to the IWC Scientific Committee, June 2014.

Punt, A.E. and T. Polacheck. 2006. Further statistical catch-at-age analyses for Southern Hemisphere minke whales. Document SC/57/IA2 presented to the IWC Scientific Committee, June 2006. (unpublished). 40pp.

Punt, A.E. and T. Polacheck. 2007. Further development of statistical catch-at-age models for Southern Hemisphere minke whales. Document SC/59/IA4 presented to the IWC Scientific Committee, May 2007. (unpublished). 42pp.

Punt, A.E. and Polacheck, T. 2008. Further analyses related to the application of statistical catch-at-age analysis to Southern Hemisphere minke whales. Paper SC/60/IA2 presented to the IWC Scientific Committee, June 2008 (unpublished). 46pp.Punt

Siler, W. 1979. A competing-risk model for animal mortality. Ecology 60:750-757.

ANNEX: POPULATION DYNAMICS MODEL

Age-Structured Dynamics

The dynamics model an age-structured model derived from a class library written in C++. A list of the parameters used in the model is given in Table E.1. The basic dynamic equations are given by:

$$N_{a+1,t+1} = (N_{a,t} - C_{a,t}) S_{a,t} \qquad |0 \le a < (a_{max} - 1) \tag{A.1}$$

with:

$N_{a,t}$ number in age class a in year t,

$C_{a,t}$ catch in number from age class a in year t,

$S_{a,t}$ proportion of fish that survive after natural mortality from age a to $a+1$ in year t

$$S_{a,t} = e^{-M_{a,t}} \tag{A.2}$$

with:

$M_{a,t}$ natural mortality rate at age a in year t. Natural mortality is age dependent and denoted as depending and time because it can be specified as being density dependent. The age-dependence is given by a modified Siler age-dependent mortality function (an extra parameter is used to defer the onset of higher mortality for the older age classes):

$$M_{a,t} = \beta_1 \exp(-\beta_2 a) + \beta_{3,t} + \beta_4 \exp(a - \beta_5) \tag{A.3}$$

Density dependence in natural mortality arises from:

$$\beta_{3,t} = \beta_{3,K} + (\beta_{3,0} - \beta_{3,K}) \left(1 - \left(\frac{B_t}{K} \right)^z \right) \tag{A.4}$$

where:

     $\beta_{3,t}$ natural mortality at stock biomass B_t,

     $\beta_{3,K}$ natural mortality at carrying capacity K

     $\beta_{3,0}$ natural mortality at negligible stock size

     B_t biomass in year t

     K biomass at carrying capacity

     Z   density dependent exponent

There is a pooled age class (plus class) at $a = a_{max}$. For this class:

$$N_{a_{max},t+1} = (N_{a_{max},t} - C_{a_{max},t}) S_{a_{max},t} + (N_{a_{max}-1,t} - C_{a_{max}-1,t}) S_{a_{max}-1,t} \tag{A.5}$$

Catch-at-age by operation j in year t is estimated (and fitted to observed catch-at-age) using:

$$C_{j,a,t} = H_{j,t} s_{j,a} N_{a,t} \tag{A.6}$$

with:

$s_{j,a}$ age-specific selectivity for operation j, i.e. the proportion of age class a vulnerable to the fishery.

$H_{j,t}$ is the proportional harvest rate of operation j in year t, specifically:

$$H_{j,t} = \frac{C_{j,t}}{\sum_{a=0}^{a_{max}} N_{a,t} s_{j,a}} \tag{A.7}$$

with:

$C_{j,t}$ total catch in number by operation j over all ages in year t

The model is coded so that time can be advanced in arbitrary increments, including zero. Catches can be removed at any time step and at as many time steps as required. Different catch series can be removed from the population at the same time step, or at different times if required. In the current application the time step used is one year.

The age-specific selectivity can be specified arbitrarily. In this current application two parametric forms of selectivity are applied, either a logistic function, or a 'dome' shape derived from the product of two logistic functions. The logistic function is given by:

$$s_{j,a} = \frac{1}{1 + e^{-g_j(a - a_{j,s50})}} \tag{A.8}$$

with:

$a_{\bullet_{s_{50}}}$ age at which 50% of a cohort is vulnerable to fishing from operation j, and

g_j a constant which determines the rate at which selectivity changes with age. Specifically:

$$g_j = \frac{\ln(19)}{\left(a_{j,s_{95}} - a_{j,s_{50}}\right)} \tag{A.9}$$

with:

$a_{j,s_{95}}$ age at which 95% of a cohort is vulnerable to fishing from operation j.

The 'dome shaped' selection function is the product of a logistic and a reverse logistic function:

$$s_{j,a} = \frac{1}{\left(1 + e^{-g_j\left(a - a_{j,s_{50}}\right)}\right)\left(1 + e^{h_j\left(a - a_{j,u_{50}}\right)}\right)} \tag{A.10}$$

Masses at age are calculated using a growth curve and a mass length relationship, that is:

$$w_{a,t} = A L_{a,t}{}^{B} + 0.5 \cdot AB(B-1) L_{a,t}{}^{B-2}\, V[L_{a,t}] \tag{A.11}$$

with:

constants A and B

$L_{a,t}$ length at age from the growth curve. This can depend on t because the growth curve can be specified to be density dependent

$V[L_{a,t}]$ variance of length at age a in year t.

It is assumed that $V[L_{a,t}]$ is well approximated by $\left(L_{\bullet,a,t}\xi_L\right)^2$, where ξ_L is a constant coefficient of variation applicable to the variability of length at age for all ages. Consequently:

$$w_{\bullet,a,t} = A L_{\bullet,a,t}{}^{B}\left(1 + 0.5 \cdot B(B-1)\xi_L{}^{2}\right) \tag{A.12}$$

The second terms in equations E.9 and E.10 are a "delta method" corrections required because an animal of mean length (i.e. from a growth curve) is not an animal whose mass is equal to the mean mass at age. However, in this application, in accordance with the common practice, $V[L_{a,t}]$ is assumed to be zero.

Length at age is given by a von Bertalanffy growth curve:

$$L_a = L_\infty\left(1 - e^{-k(a - a_0)}\right) \tag{A.13}$$

with:

L_∞ asymptotic mean length at age

k rate constant

a_0 intercept

The proportion of animals sexually mature at each age is given by an ogive

$$m_a = \frac{1}{1 + e^{-\mu\left(a - a_{\mu_{50}}\right)}} \tag{A.14}$$

with:

$a_{\mu_{50}}$ age at which 50% of a cohort is mature and

μ a constant which determines the rate at which maturity changes with age. Specifically:

$$\mu = \frac{\ln(19)}{\left(a_{\mu_{95}} - a_{\mu_{50}}\right)} \tag{A.15}$$

with:

$a_{j,s_{95}}$ age at which 95% of a cohort is vulnerable to fishing from operation j.

Stock Recruitment Relationships
Reversed logistic stock-recruit relationship
The number of recruits into age-class zero in year t is given by:

$$N_{0,t} = \frac{B_t \alpha}{1 + \exp(\beta(B_t - B_{50}))} \tag{A.16}$$

Where B_t is the mature female component of the population and B_{50} is the inflexion point of the reversed logistic. This model thus has density dependence in fecundity depending on mature biomass. Approximate yield curve due to changes in recruitment (given recruits per mature female at K (ρ_K)) is given by:

$$y = B\left(\frac{\alpha}{1+\exp\left(\beta\left(B-B_{50}\right)\right)} - \rho_K\right)$$

(A.17)

B_{MSYL} is the solution to the following equation:

$$\frac{dy}{dB} = \frac{\alpha}{D} - \frac{\alpha\beta B\left(D-1\right)}{D^2} - \rho_K = 0$$

(A.18)

where

$$D = 1 + \exp(\beta(B-B_{50}))$$

(A.19)

MSYR is close to directly proportional to alpha, which is effectively proportional to the recruits per mature female at negligible stock size. MSYL is determined by the value of beta, which can be determined by finding the root of (equation 0.4) with B fixed at MSYL. Thus the SRR is fully described by the two parameters α and β. If K is to be varied by a multiple (during minimisation), say $K' = \xi K$ then $\beta' = \frac{\beta}{\xi}$. This preserves MSYR, and MSYL retains the same value as a proportion of K'. Given the values of alpha and beta, B_{50} is given by:

$$B_{50} = K - \frac{\log\left(\frac{\alpha}{\rho_K} - 1\right)}{\beta}$$

(A.20)

This SRR has the advantage that MSYL can take a wide range of values, similarly to the Pella-Tomlinson, but with the further advantage that recruitment does not become negative at stock sizes somewhat above *K*. This is an advantage when fitting models using auto-differentiation because there are no negative recruitments that need to be set to zero, which thus avoids discontinuous derivatives that disrupt the minimisation algorithm.

Otherwise, the model can be specified with a choice of three other commonly used stock recruitment relationships (SRRs); Beverton and Holt, Ricker and Pella-Tomlinson. An additional SRR is available that allows depensation in the Beverton and Holt model. In this application only the logistic form is used. Fig A1 shows two examples of yield curves from the logistic SRR. These are very similar to the shapes of the corresponding yield curves from a Pella-Tomlinson model.
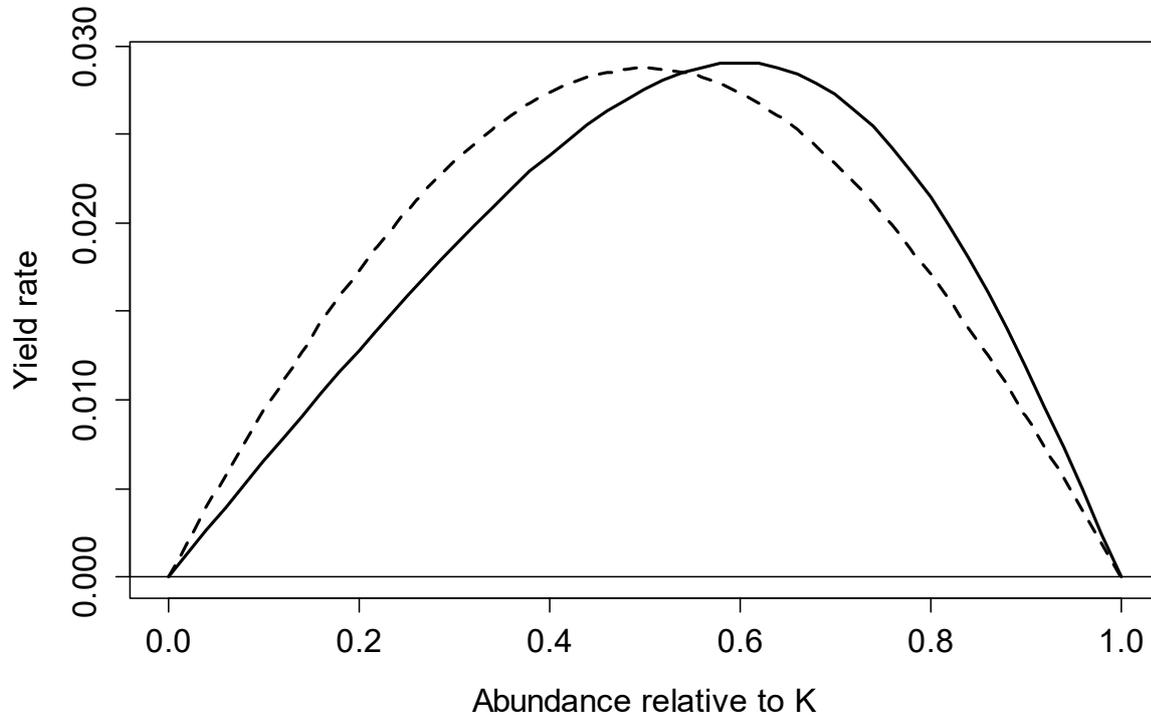
Fig A1. Two yield curves from the reverse logistic model, with MSYLs of 0.5 and 0.6.

Variability in recruitment

When required, the effects of recruitment variability can be included by multiplying the numbers of recruits by a random lognormal number ρ with an expected value of 1.0 and a specified coefficient of variation (ξ_R). The same random multiplier is used for both males and females at the same age, so that the total recruitment is variable but the sex ratio at each age is not. Recruitment variability can also be driven by multiplying K_t by a random number from log-normal distribution.

Fitting the Model to Data

The first data to be fitted is the total catch. Although in principle the catches could be taken as given and simply removed from the population, it is helpful instead to estimate an annual exploitation rate (as a proportion of the vulnerable population). This helps in the minimisation because for some trial values of population size some age-classes will go extinct, which leads to discontinuous derivatives and the failure of the search algorithm. The total catch in a given year is given by:

$$\hat{C}_t = \sum_j \sum_{a=1}^{a_{max}} \hat{h}_{j,t} \hat{s}_{j,a} \hat{N}_{a,t} \tag{A.21}$$

Where $\hat{h}_{j,t}$ is the estimated exploitation rate in year t for operation (fleet) j. These are essentially a nuisance parameters. The observed catches are assumed to have a log normal distribution with a very small, constant CV so that in the final estimates the differences between the observed and expected total catches are small. This portion of the overall likelihood function is given by:

$$-L(\mathbf{\Theta}|\mathbf{C}) = n\left(\ln(\sigma_C) + \ln(\sqrt{2\pi})\right) + \frac{1}{2} \frac{\sum_{C_t>0}\left(\ln(C_t) - \ln(\hat{C}_t) + \frac{1}{2}\sigma_C^2\right)^2}{\sigma_{C_t}^2} \tag{A.22}$$

Where n is the number of non-zero catches, σ_c is a small number, essentially the artificial coefficient of variation of the observed catch C_t. The other terms represent an additive constant, which could normally be ignored, but they are included here so that the relative contributions to the total likelihood have appropriate magnitudes. This is the same method as used in the existing SCAA. Fig 1 shows that the catches are estimated using this function with negligible error.

The variants of the model are fitted to the time series of surveys using a log-likelihood function based on the assumption that the survey estimates have log-normal distributions with an estimated coefficient of variation. The log-likelihood is given by:

$$-L(\mathbf{\Theta}|\mathbf{x}) = -\sum_{i=1}^{n} \ln(x_i) - \frac{n}{2}\ln(2\pi) - \sum_{i=1}^{n}\ln(\sigma_i) - \frac{1}{2}\sum_{i=1}^{n}\left(\frac{\ln(x_i) + \frac{1}{2}\sigma_i^2 - \ln(E[x_i])}{\sigma_i}\right)^2 \tag{A.23}$$

where:

    n   number of surveys in the series

    x_i is the ith survey estimate

    σ_i estimated standard deviation of the log-transformed survey estimate

    and $E[x_i] = q_j\hat{N}_i$ where q_j is the survey bias correction for survey series j and $\hat{N}_t$ is the modelled abundance of the 1+ population in the corresponding survey year t.

The fitting to the catch-at-age data assumes that the data have multinomial distributions, with Log-likelihood given by:

$$-L(\mathbf{\Theta}|\mathbf{n}) = -\ln N! + \sum_{i=1}^{k+1}\ln n_a! - \sum_{i=1}^{k+1}n_a \ln p_a \tag{A.24}$$

Where **n** is a vector of catches at age in a given year, N is the total sample size of catch-at-age in that year, n_a is catch in age-class a and p_a is the modelled probability of catching an animal at that age as determined by the modelled age-structure in the given year and the relevant selectivity function.

The parameter vector $\mathbf{\Theta}$, is estimated by minimising the sum over the various data types of the negative log likelihood functions using a conjugate gradient method (*frpmin* from the numerical recipes library, Press et al 1992.) using derivatives calculated by auto-differentiation.

References

Press, W. H., Teukolsky, S.A. Vetterling, W. T. and Flannery, B. T.1992. *Numerical recipes: the art of scientific computing*. Cambridge University Press.963pp.