

A. Stock assessment appendices for Atlantic Surfclams in the US EEZ

Appendix A1: Surfclams in New York and New Jersey state waters¹

¹Many thanks to Jeff Normant of the New Jersey Division of Fish and Wildlife and Debra Barnes and Jennifer O'Dwyer of the New York State Department of Environmental Conservation for data and assistance with this report.

The states of New York and New Jersey support surfclam fisheries in their territorial waters not covered by the NEFSC clam survey. The two states have carried out their own annual or semi-annual surveys of the resource since 1992 and 1988, respectively. Commercial and survey data from state waters are important in this assessment of the federally managed EEZ stock given the biological linkage between state waters and the EEZ, the productivity and importance of fisheries in state waters, and the possibility of environmental effects in southern surfclam habitat. New York and New Jersey state waters have historically been excellent habitat for surfclams, but there is evidence of declining recruitment to the population in both states. The percentage of landings harvested from state waters has been falling since 2001 (Figure 1).

The New York and New Jersey state surveys

The New Jersey State survey is conducted annually by the New Jersey Department of Environmental Protection from a commercial clam vessel with a commercial hydraulic dredge, most recently the F/V Ocean Bird. The survey has been conducted since 1988, and has followed a stratified random sampling protocol since 1994. The survey area is divided into regions covering the whole New Jersey coast, and each region has 3 one mile wide strata, parallel to the coast, covering surfclam habitat out to the 3-mile limit of state waters (Figure 2). Each survey does between 250 and 330 five minute tows, measuring the tow volume in bushels, then counting and measuring a known volume of surfclams for population estimates and length frequencies. Grab samples of the sediment are also taken.

Data from the state of New Jersey available for this appendix includes annual state surfclam survey numbers and lengths through 2012 and grab samples for juvenile surfclams through 2011. Surfclam landings from New Jersey state waters are available from 1989-2012.

The New York surfclam survey is conducted by the New York Department of Environmental Conservation approximately every three years. They use a commercial clam vessel, most recently the F/V Ocean Girl, with a hydraulic dredge. The survey area is divided into four regions which span the southern shore of Long Island. The three westernmost regions are subdivided into three mile wide strata (Figure 3). The most recent surveys have taken place in the summer or fall, had an average of 236 stations, and used a random stratified sampling technique. Tows are three minutes long, the total volume of each tow is measured in bushels, and half a bushel of surfclams from each tow is measured and counted for population estimates and length frequencies. A picture of the dredge used is shown in Figure 4.

Data from New York State are from the 2002, 2005, 2006, 2008 and 2012 state surfclam surveys. Total numbers, densities and length frequencies are available for all years and ages are available for all years except 2012. Surfclam landings from New York state waters are available through 2011.

Results

Both states have seen a significant decrease in the population of surfclams (Figure 5). The peak population of surfclams in New Jersey in recent years seems to have occurred in 1996, a few years before the peak in biomass in the EEZ in 1998-1999. The data available to us from New York do not go back far enough to see evidence of a concurrent population peak.

Despite the decline in numbers of clams in surveys since 2002, landings in New York stayed relatively high through 2006 (Figure 6). There was a very large harvest limit set in 2004 (930,000 bushels) and it was almost reached, making the landings from New York from that year almost double what they had been in years before. In 2010 and 2011, landings were around 200,000 bushels annually.

Surfclam landings for human consumption from New Jersey state waters have fallen from a high of about 700,000 bushels in 2003 to less than 100,000 in 2005 and to near zero levels since 2006. Since the early 2000s, a few tens of thousands of bushels of surfclams have been harvested annually from “prohibited waters” (where they are not allowed to be sold for human consumption due to contamination) to be sold as bait (Figure 7). About a third of the surfclam standing stock in New Jersey is in prohibited waters (Figure 8).

In the 2000s, the length composition of surfclams in New Jersey was narrow and composed of only larger surfclams, indicating a lack of new recruitment. However, recent survey data shows some smaller clams recruiting to the population (Figure 9). The 2011 NEFSC clam survey also showed evidence of some recruitment off New Jersey and New York.

Surfclams from the New York surveys conducted in 2005 and 2006 were larger on average than those collected in 2002, yet some smaller clams were seen in the 2008 and 2012 surveys, mirroring the bump in recruitment seen in the New Jersey and NEFSC surveys (Figure 10).

Surfclam densities have historically been high in the inshore areas surveyed by New Jersey and New York states compared to offshore areas south of Georges Bank surveyed by NEFSC (Figure 12). However, inshore densities appear to be falling recently towards levels typical of more unproductive offshore areas (Figure 11). However, the comparisons in Figure 11 are approximate due to differences in dredge design, capture efficiency and size selectivity. Numbers have been falling in all strata in New Jersey (Figure 13).

Recently it appears surfclams in New York and New Jersey have been unable to resupply their aging populations with new recruits. This could be happening because there is not enough successful spawning occurring and the supply of larvae is not there, or because smaller surfclams are dying before they are available to a survey or commercial dredge.

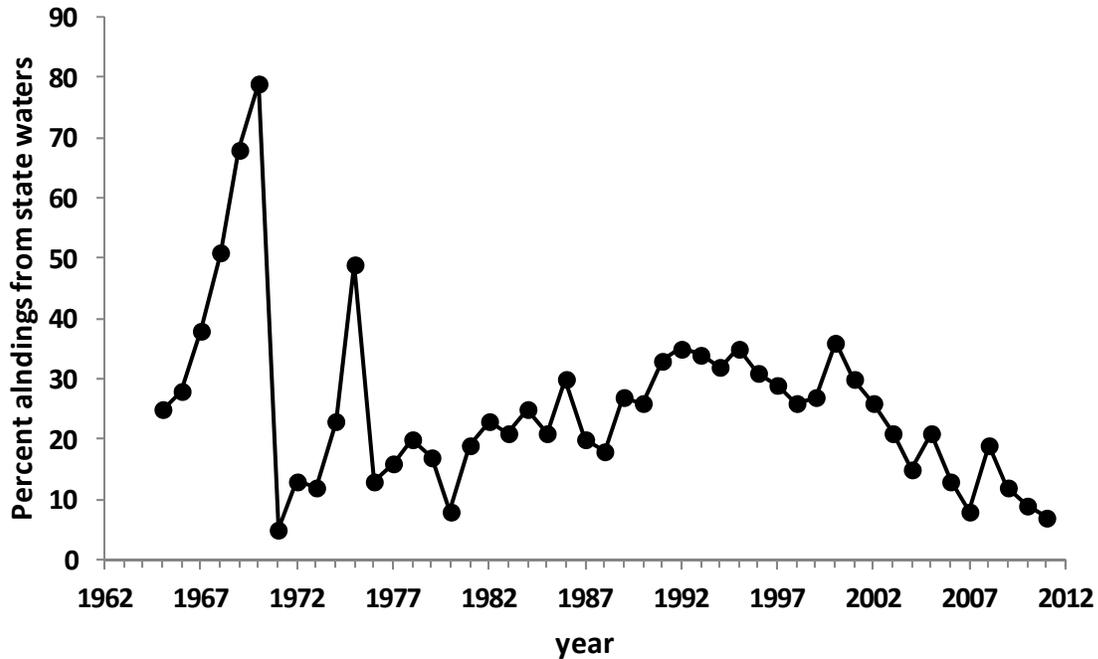
In New Jersey, grab sample data collected regularly since 1994 from the area of the survey show that juvenile surfclams are setting successfully out of the plankton (Figure 14). Some years have been better than others with occasional larger sets such as the ones seen in 2005 and 2009, a typical pattern for bivalve recruitment. This data does not show any downward trend in juvenile surfclams that might explain the decline in older surfclams of fishable size.

Surfclam age frequencies from the New York surveys in 2002, 2005, 2006 and 2008 (Figure 15) show that surfclams of all ages are present with recognizable ~1996, ~1991 and ~1988 year classes which can be followed. The 2008 data also reflect the recent recruitment seen in the survey size frequencies in both New York and New Jersey. Age data from the Long Island region of the NEFSC survey are not available, but recognizable year classes seen in the New Jersey region included one in 1992.

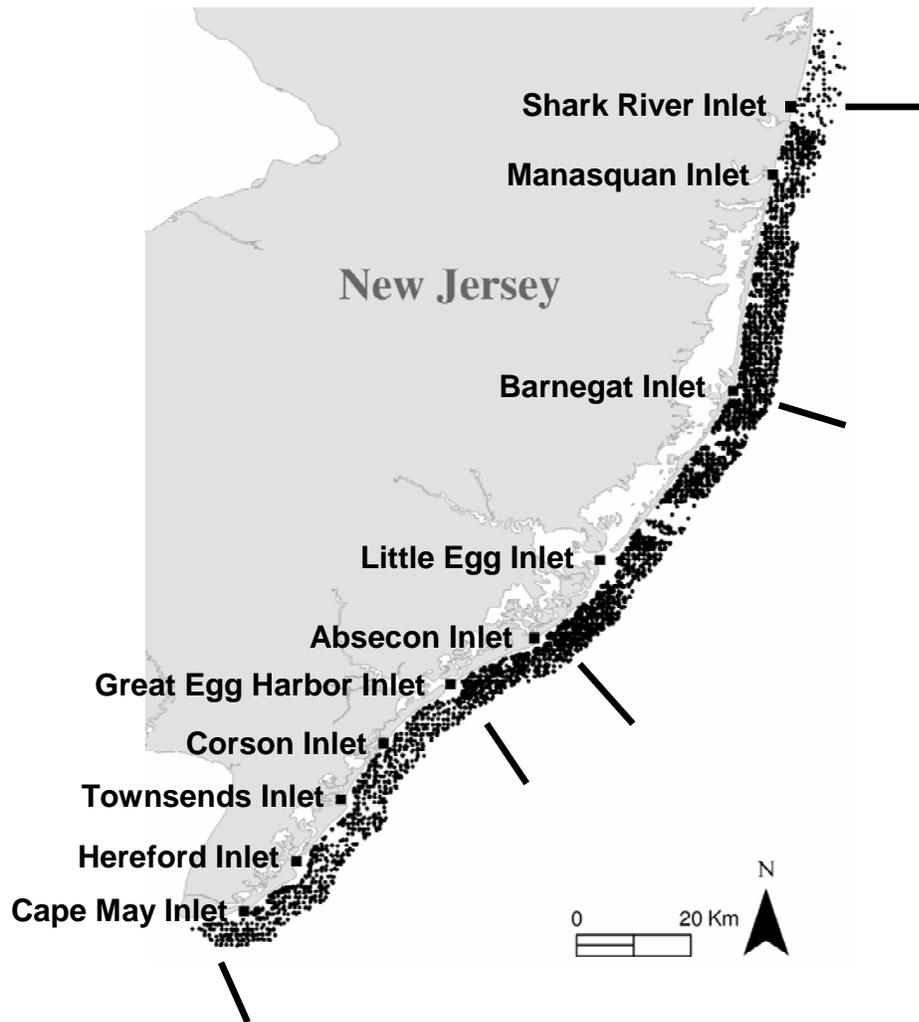
Length-at-age data from the New York surveys (figure 16) indicate there was no significant change in growth rate from 2002 through 2008, but all regions and strata were lumped together so spatial changes may be masked.

Exploitation rates (landings / survey abundance) were calculated for surfclams in both NJ and NY state waters (Figure 17). The data suggest that exploitation rates in NJ waters decreased from about 4% in 1996 to 2% in 1997-1998 then increased to about 6% in 2002 before falling to zero by 2005 as the fishery for human consumption all but ceased. The limited data for NY indicate that exploitation increased from 2002 to 2008 (landings data were not available for NY in 2012). These simple exploitation rates provide useful information about relative trends in fishing mortality, but they assume all the surfclams in the path

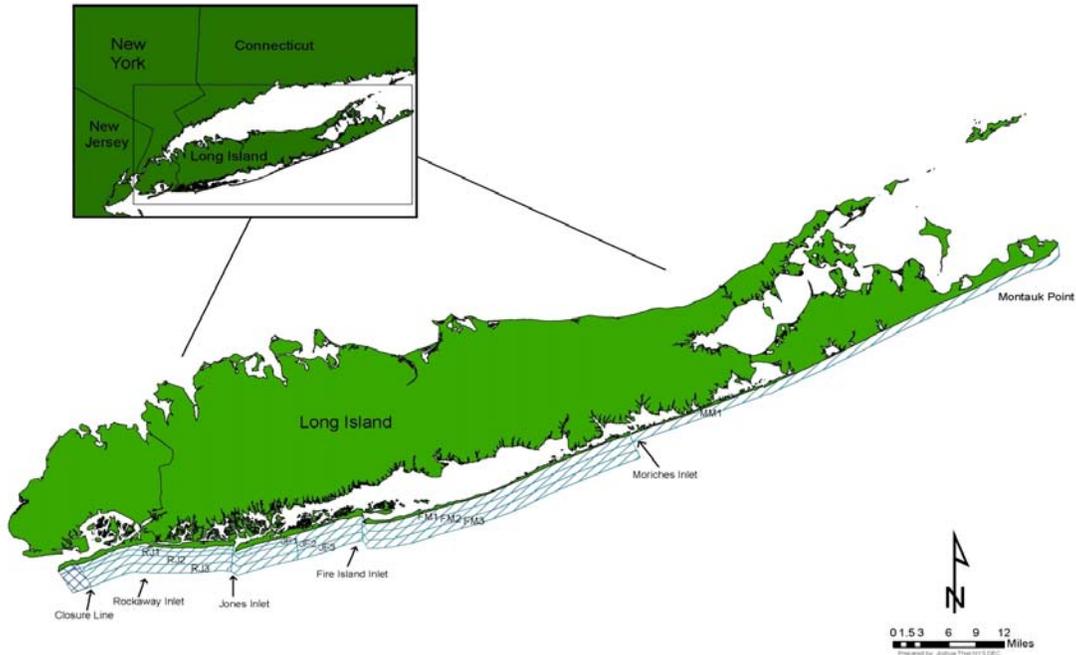
of the survey dredge are captured, which is almost never true. The capture efficiency of a clam dredge is almost always less than one, so exploitation rates calculated here for surfclams in state waters are probably overestimated. NJ landings for use as bait were excluded because surfclams for bait are harvested in contaminated areas outside of the survey region.



Appendix A1, Figure 1. Percentage of total surfclam landings that came from state waters, which are mostly New Jersey and New York with small amounts from New England.



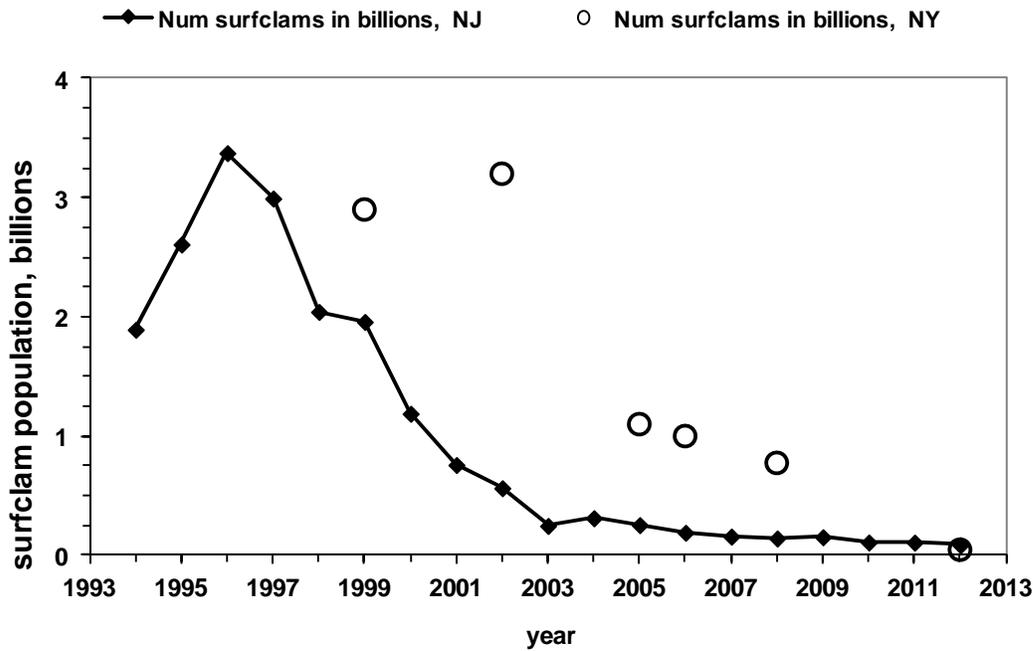
Appendix A1, Figure 2. Map showing the sampling regions for the NJ state survey, and station locations 1988-2008. Within each region there are three along-shore depth strata one mile wide. Map courtesy of Jeff Normant, NJDEP.



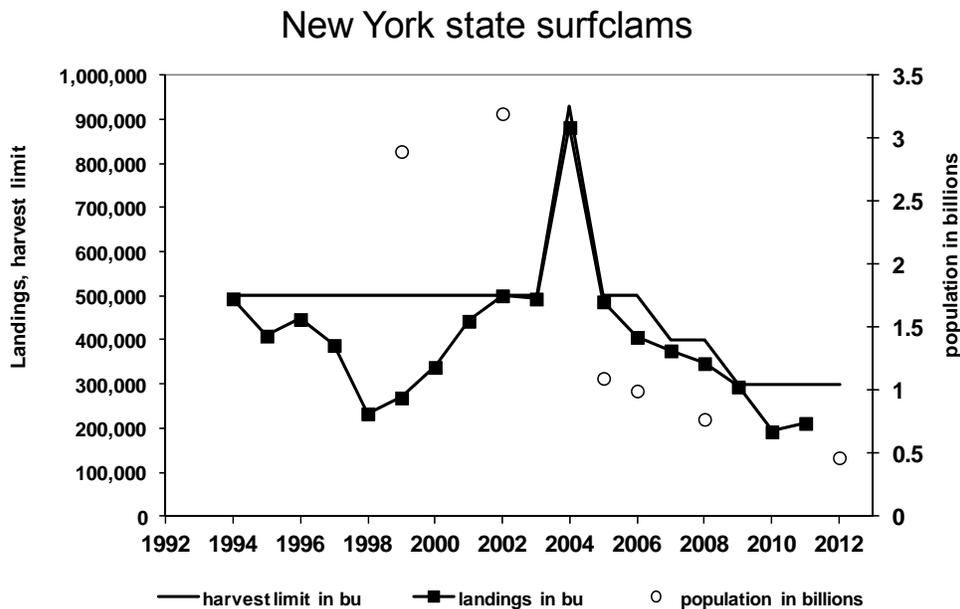
Appendix A1, Figure 3. Map showing New York state sampling regions from west to east: RJ, JF and FM, which each have 3 depth strata, and MM which has one depth stratum. Map courtesy of Wade Carden, NYSDEC.



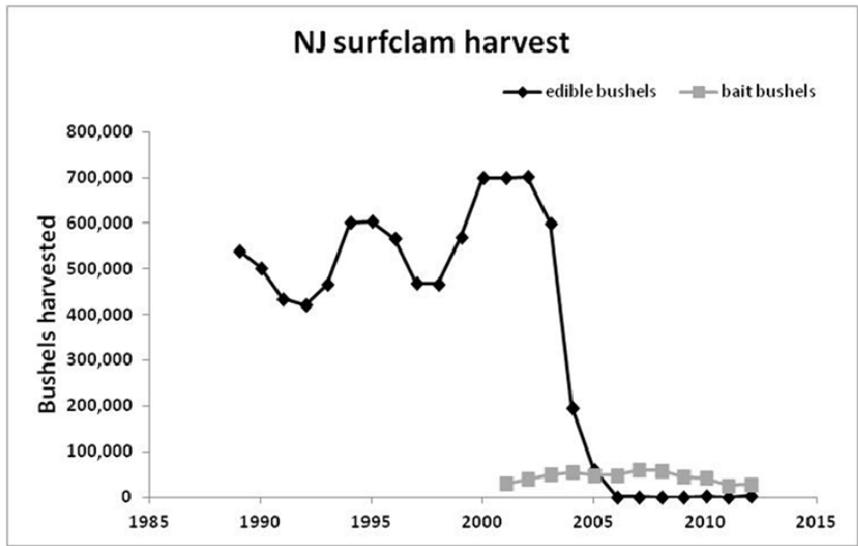
Appendix A1, Figure 4. The inshore commercial clam dredge used for the New York surveys. Photo courtesy of Jeff Normant, NJDEP; William Burton, Versar, Inc.; and Beth Brandreth, USACE.



Appendix A1, Figure 5. Survey-based population estimates for surfclams in New Jersey and New York from years when there was random stratified sampling.

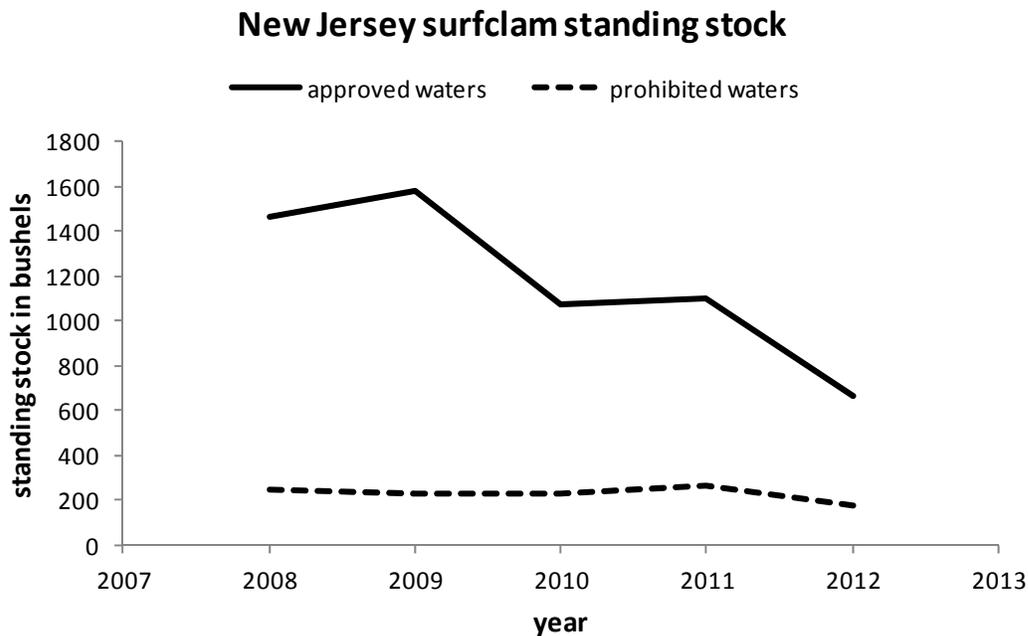


Appendix A1, Figure 6. Landings, harvest limit and population of surfclams in New York state waters. Landings and harvest limit are scaled to the left axis and population is scaled to the right axis. The harvest limit was raised to 890,000 bushels for one year in 2004.

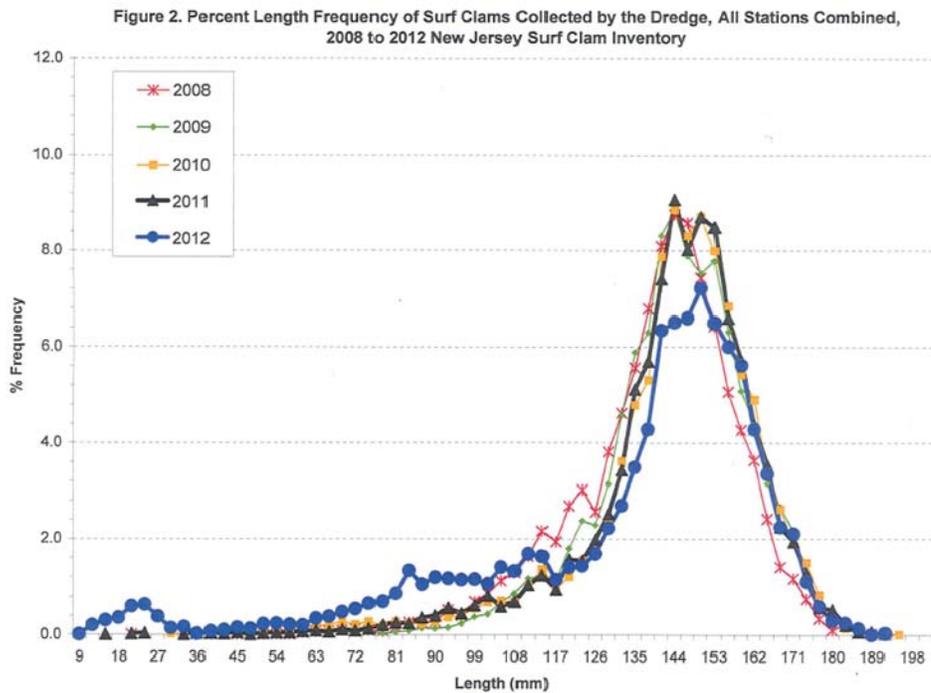


Quota for 2010-2011 season: 55,296 bushels (season OCT –MAY)
 Quota for 2011-2012 season: 49,152 bushels

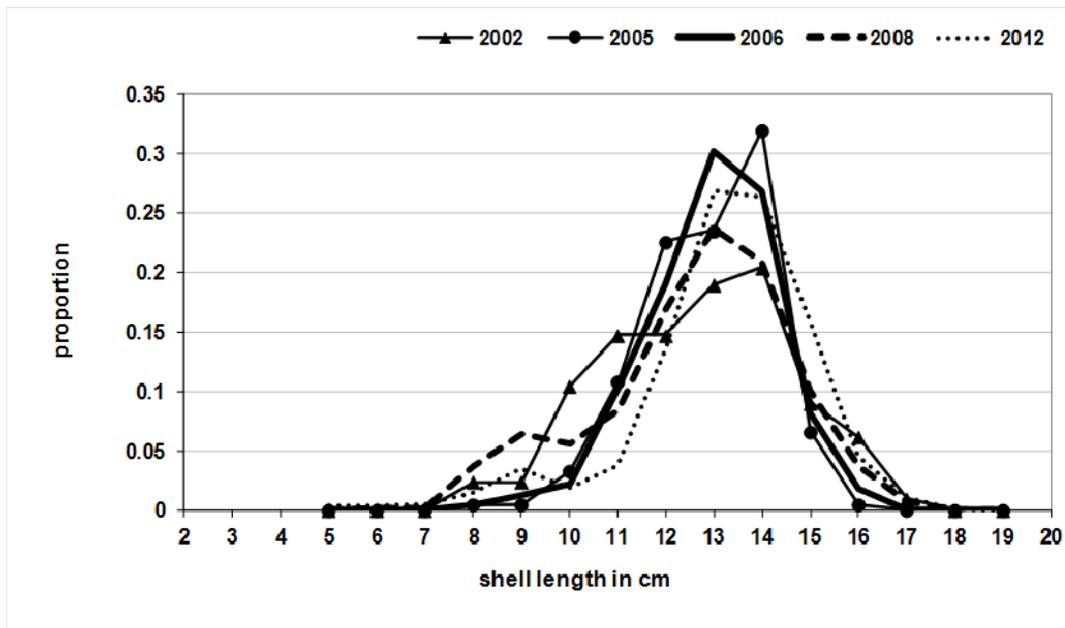
Appendix A1, Figure State - 7. Bushels of surfclams harvested from New Jersey “approved” (surfclams for human consumption) and “prohibited” (surfclams for bait only) waters.



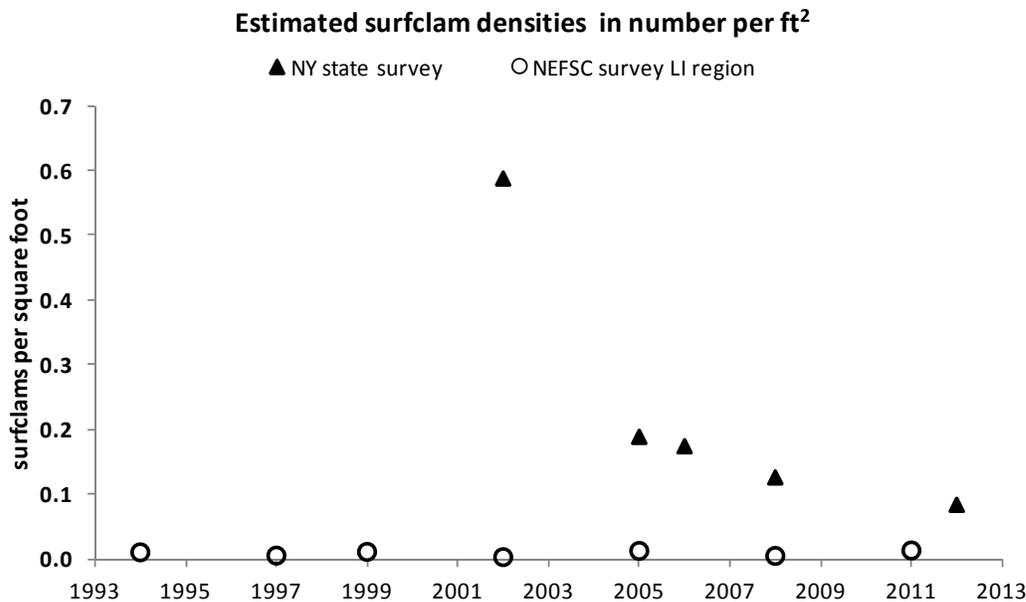
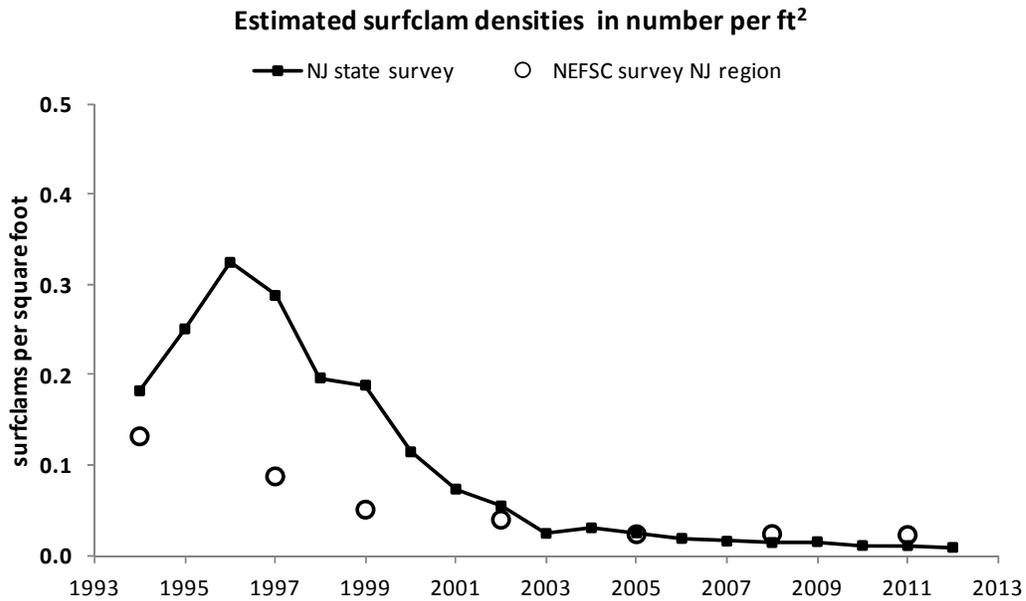
Appendix A1, Figure 8. Standing stock in industry bushels from New Jersey state waters. Clams from approved waters can be sold for human consumption, while clams from prohibited waters are sold for bait only.



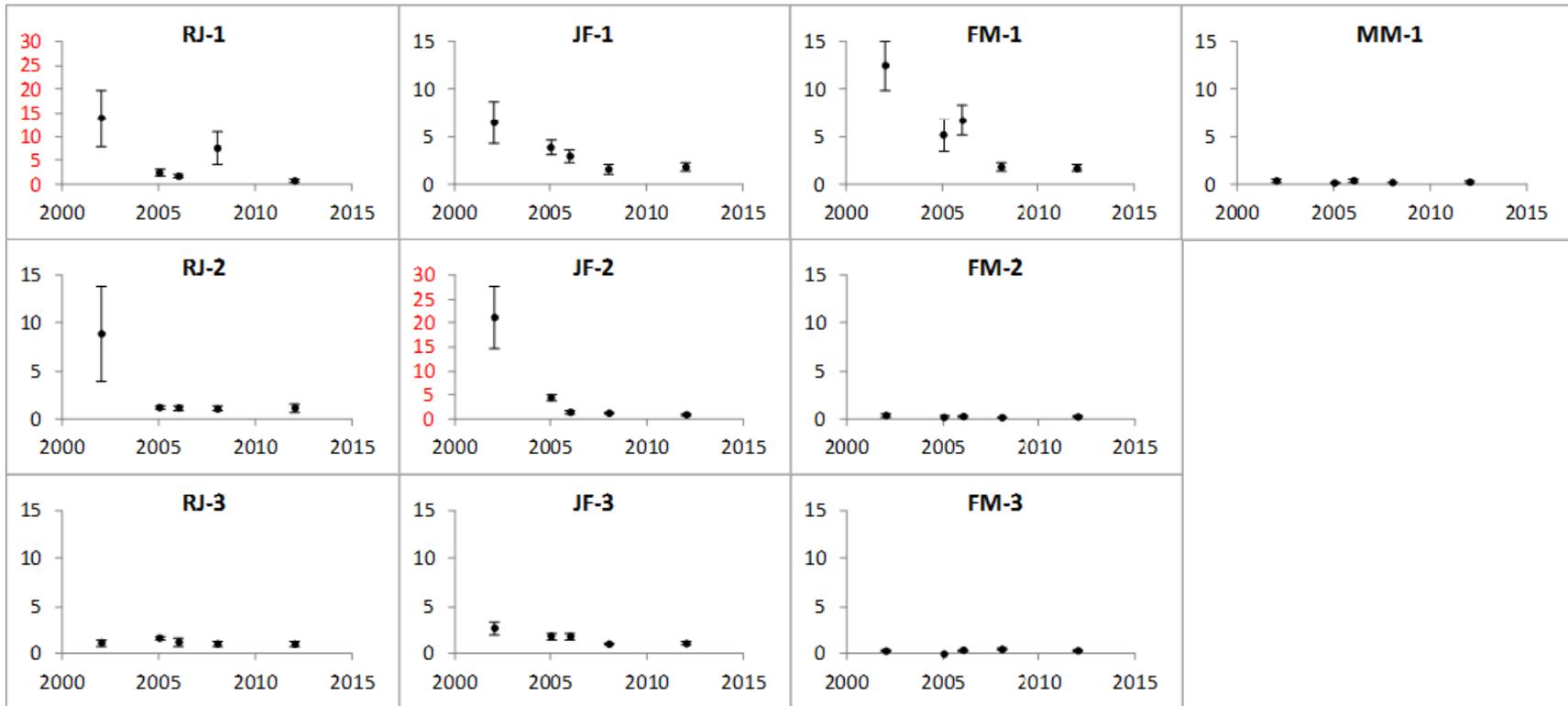
Appendix A1, Figure 9. Length frequencies from the 2008-2012 annual New Jersey state surfclam surveys. Figure courtesy of Jeff Normant, NJDEP.



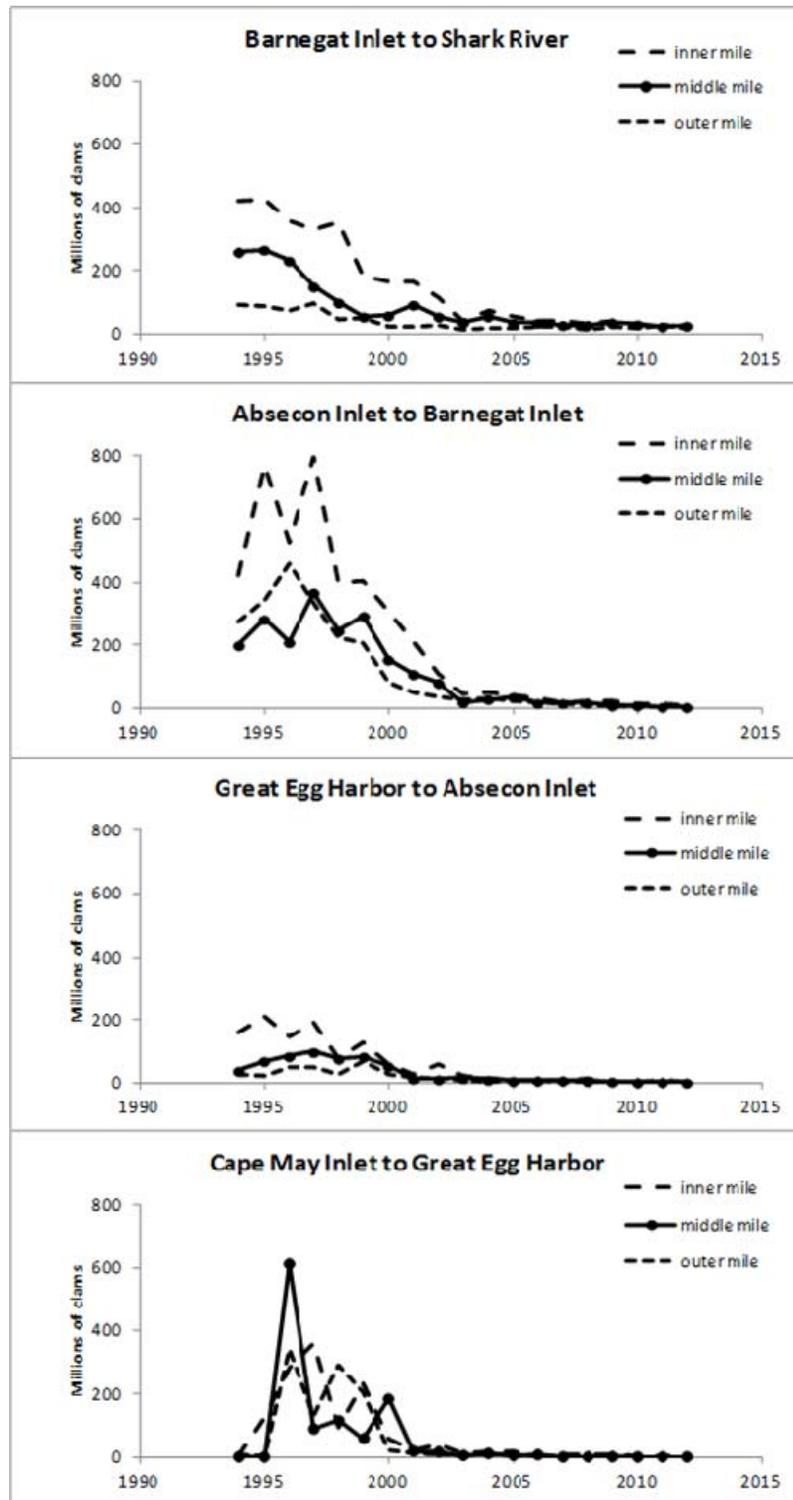
Appendix A1, Figure 10. Length frequencies from the 2002, 2005, 2006, 2008 and 2012 New York state surfclam surveys.



Appendix A1, Figure 11. A rough comparison of surfclam density estimates (total estimated number of clams over the area surveyed in square feet) from the NJ State survey and the NJ region of the NEFSC survey in federal waters (top) and the NY state survey and LI region of the NEFSC survey in federal waters (top). All sizes of clams were included, and an adjustment was made to the NEFSC data to account for a dredge efficiency of 0.256. No adjustments were made to the NY or NJ data. The comparisons are approximate due to differences in dredge design, capture efficiency and size selectivity

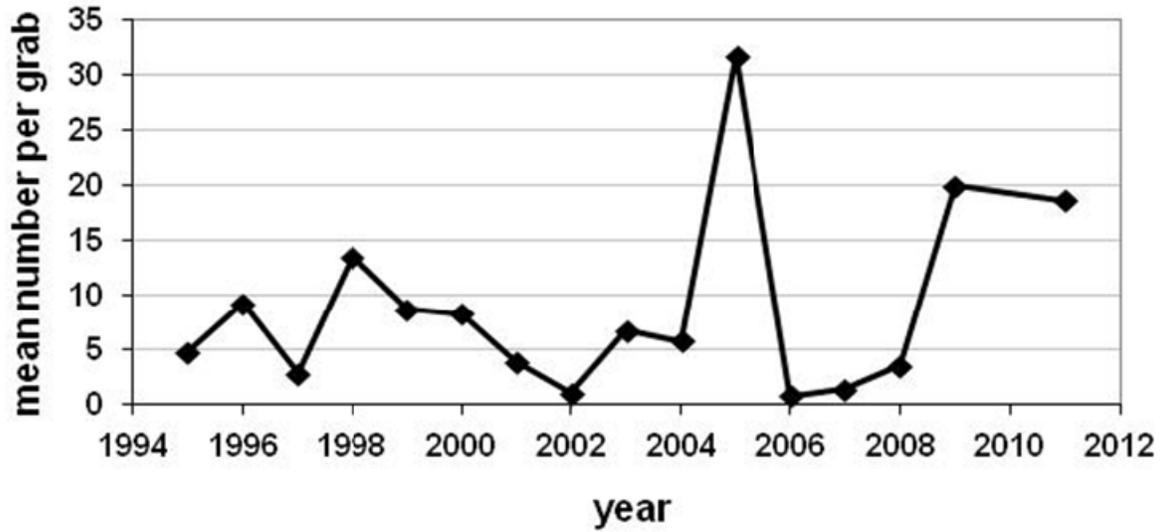


Appendix A1, Figure 12. New York State Surfclam Survey - Estimated density of clams, in individuals per m², per stratum by survey year. Strata cover the waters off the south side of Long Island. Plots are laid out in order with the left plots representing the westernmost strata, which are broken down into inner, middle and outer miles (numbers 1-3), covering the three-mile limit of State waters. The easternmost stratum has only the inner substratum. RJ = Rockaway Inlet to Jones Inlet, JF = Jones Inlet to Fire Island Inlet, FM = Fire Island Inlet to Moriches Inlet, MM = Moriches Inlet to Montauk Point.

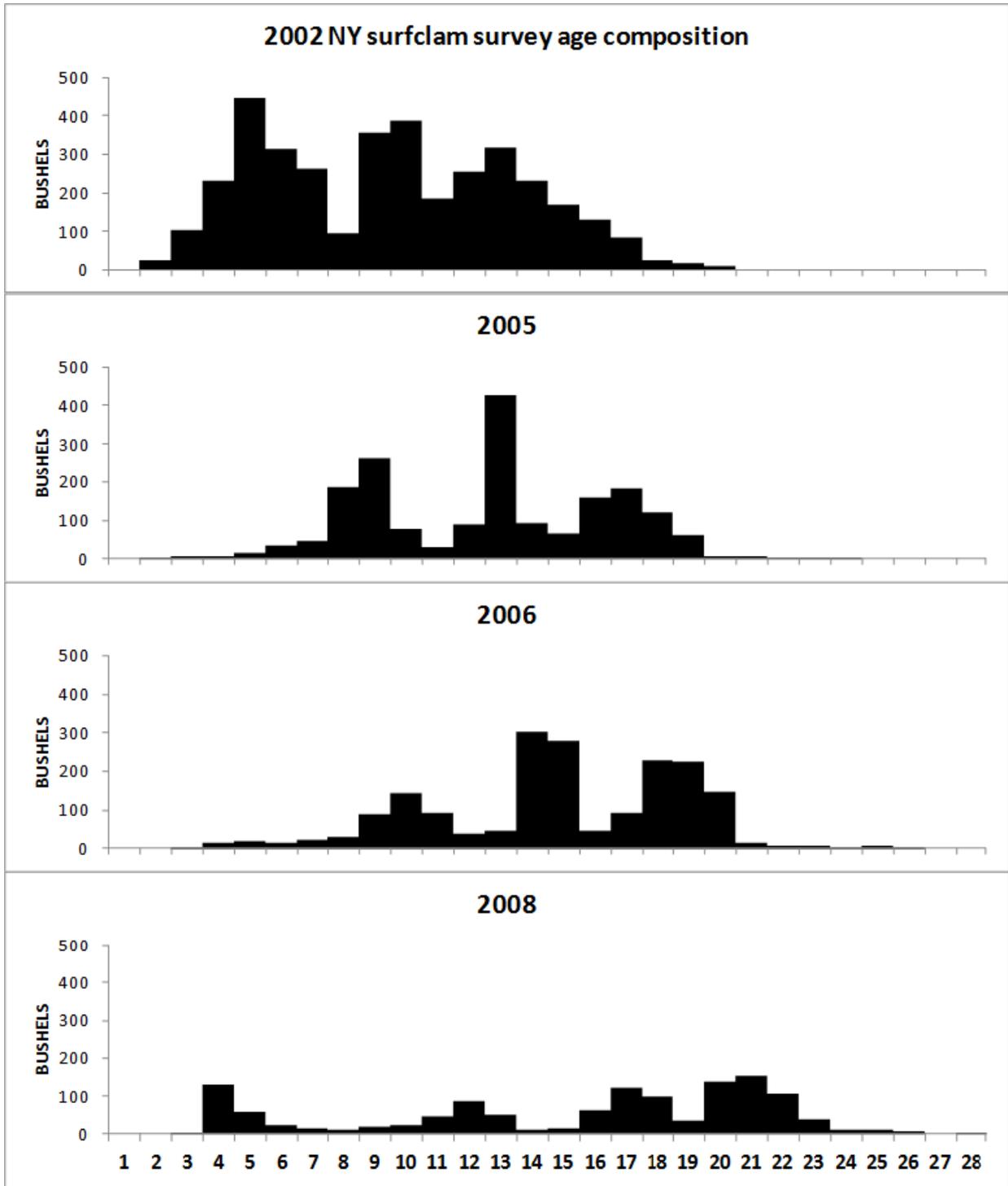


Appendix A1, Figure 13. New Jersey State survey - estimated number of clams per stratum by survey year. Plots are laid out in order with the top plot representing the northernmost stratum. Strata are further broken down into inner, middle and outer miles, covering the three-mile limit of State waters.

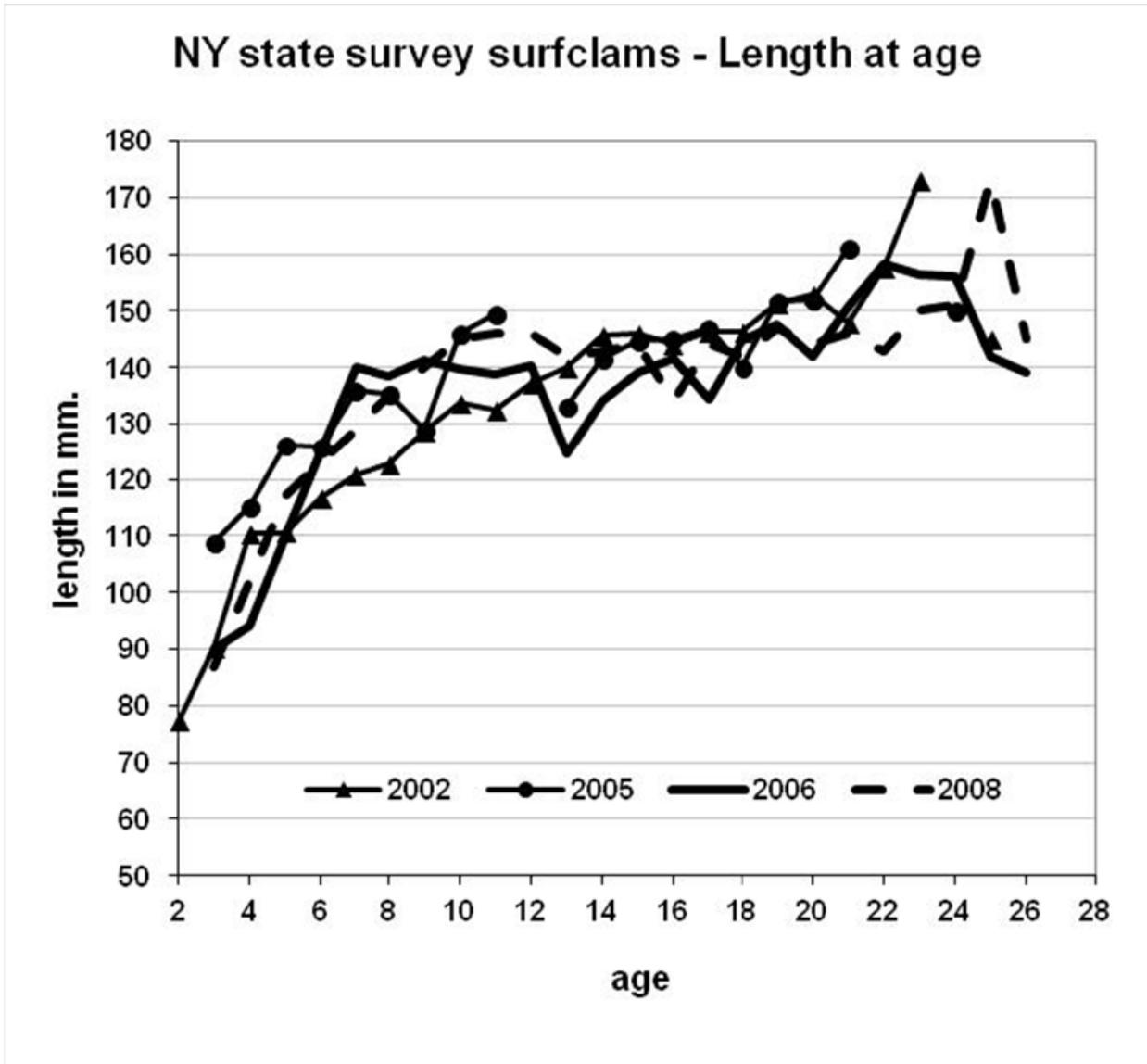
Juvenile surfclams per grab sample - NJ



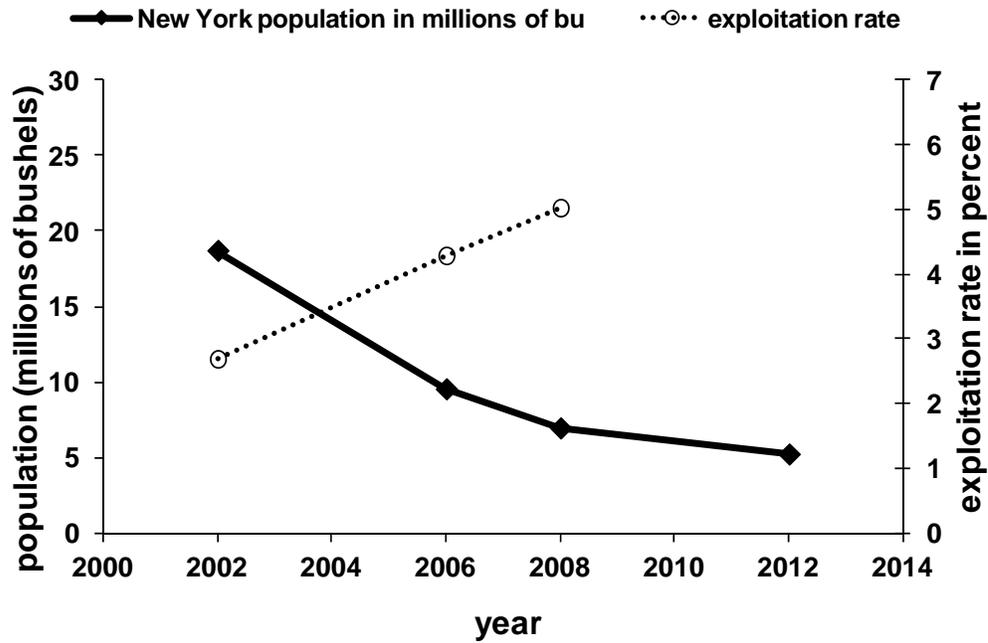
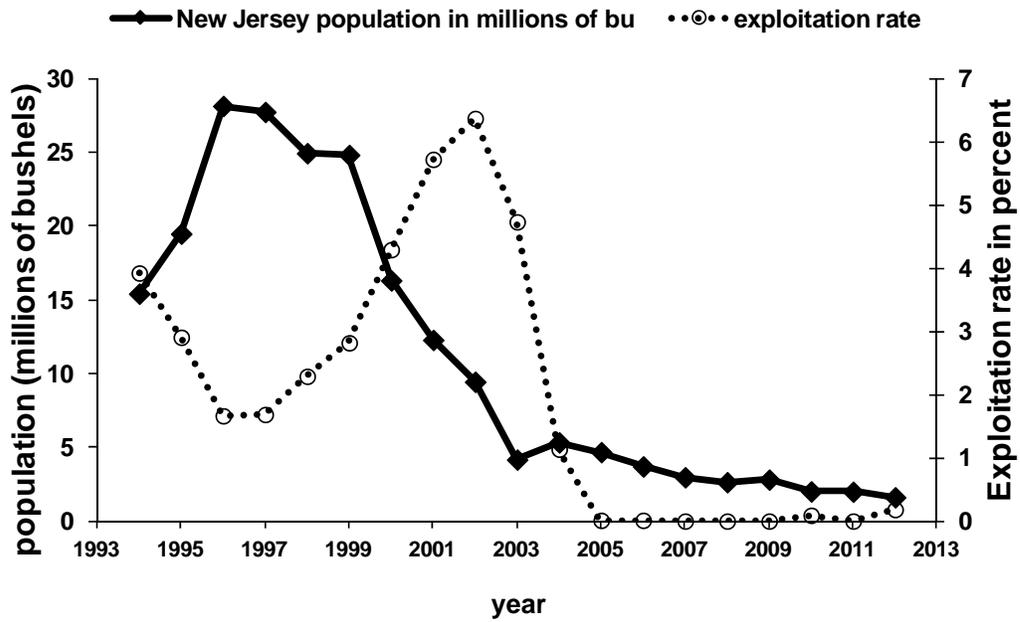
Appendix A1, Figure 14. As part of the annual survey, the state of New Jersey takes sediment grab samples, which contain recently settled juvenile surfclams. The clams are generally less than 10mm. About 300 grabs are taken every survey, and the area sampled is 1/10 of a square meter.



Appendix A1, Figure 15. Age compositions from the 2002, 2005, 2006 and 2008 New York State surfclam surveys, in bushels at age.



Appendix A1, Figure 16. Surfclam length at age from the 2002, 2005, 2006 and 2008 New York State surveys.

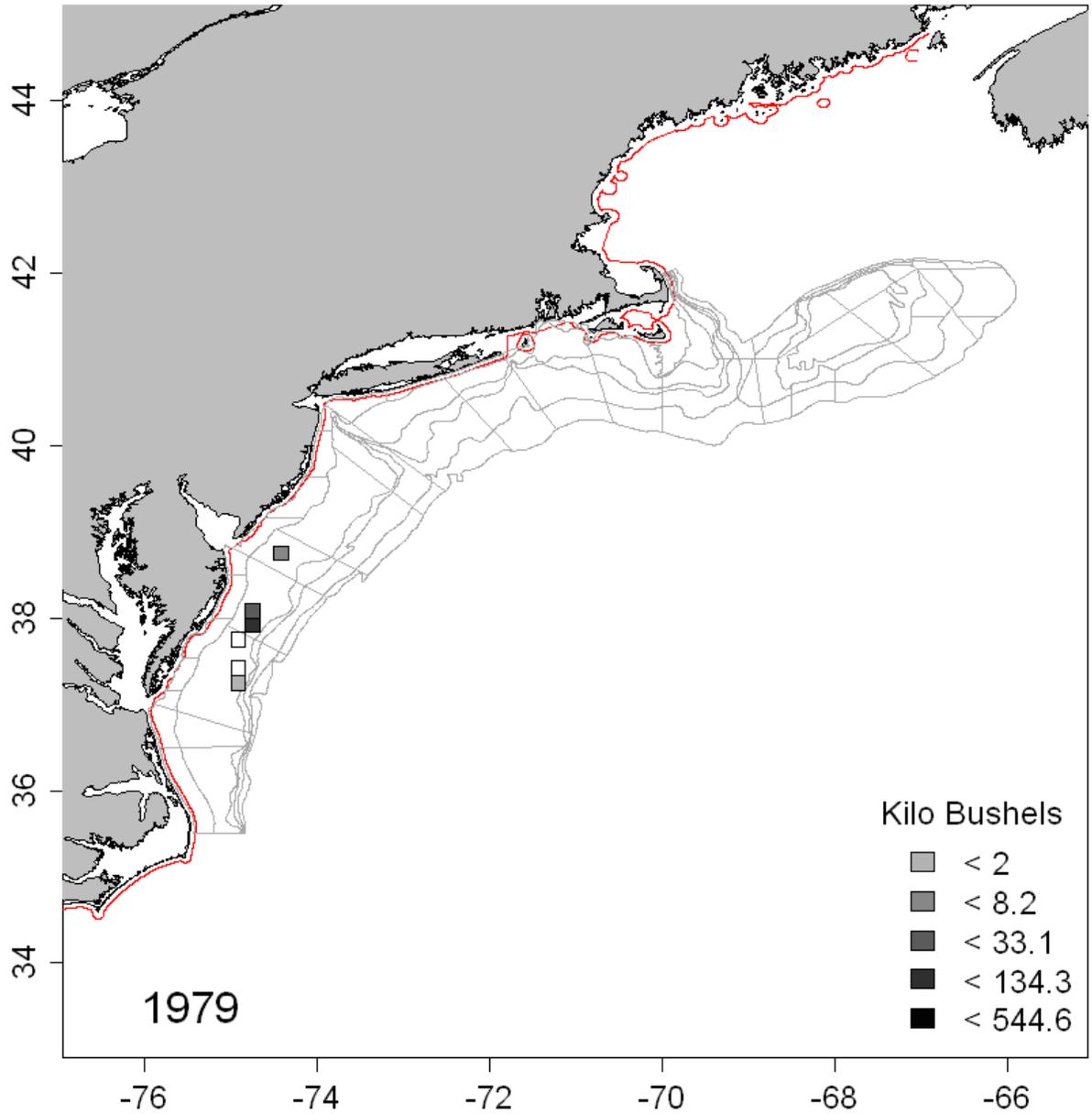


Appendix A1, Figure 17. Exploitation rates (expressed as landings as a percentage of estimated biomass) and population biomass for New Jersey (top) and New York state surfclams.

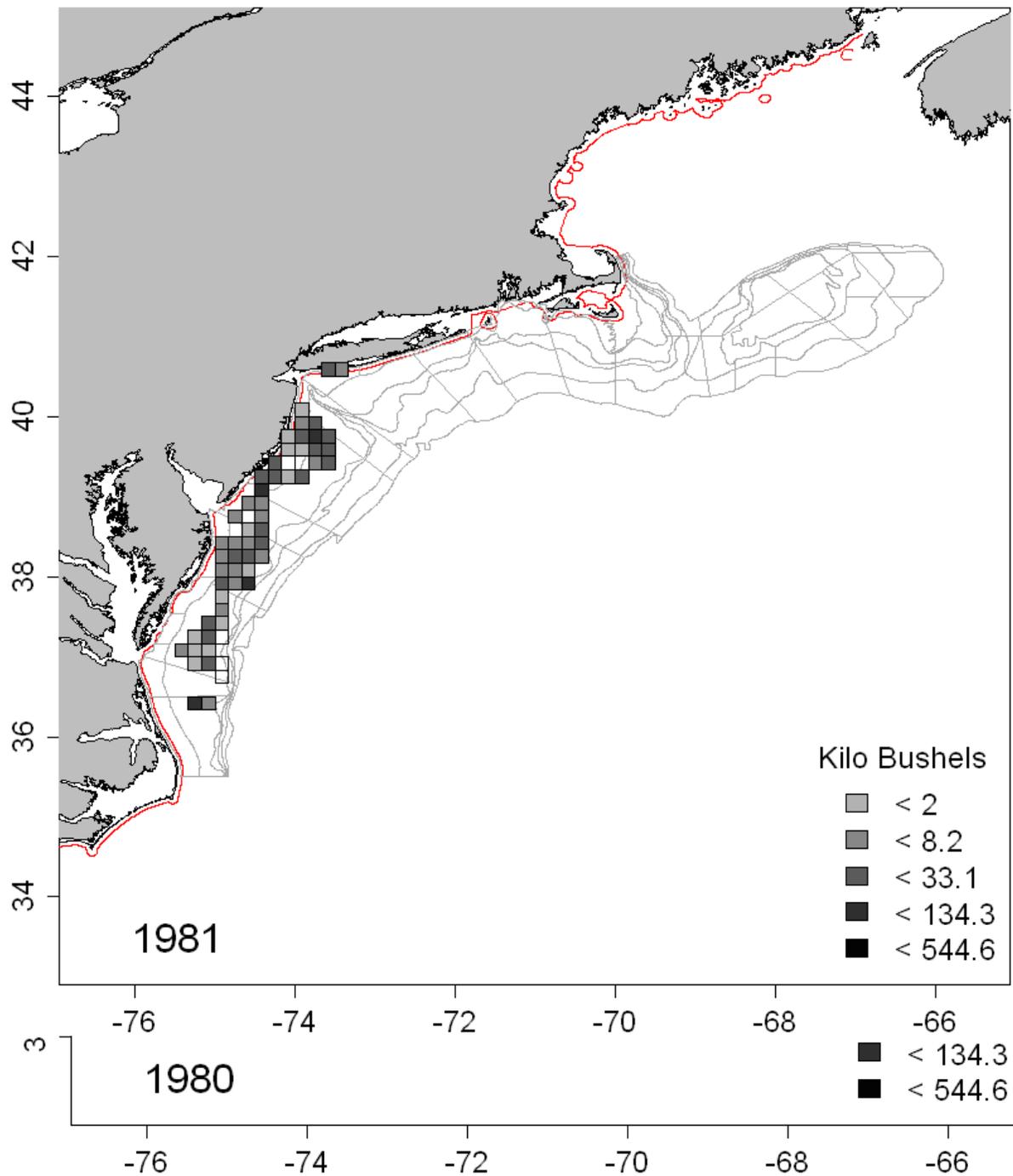
Appendix A2: Maps of commercial harvest through time

Appendix A2, Figure 1. Landings, time fished and LPUE by ten-minute square from 1979 – 2011 (Following pages).

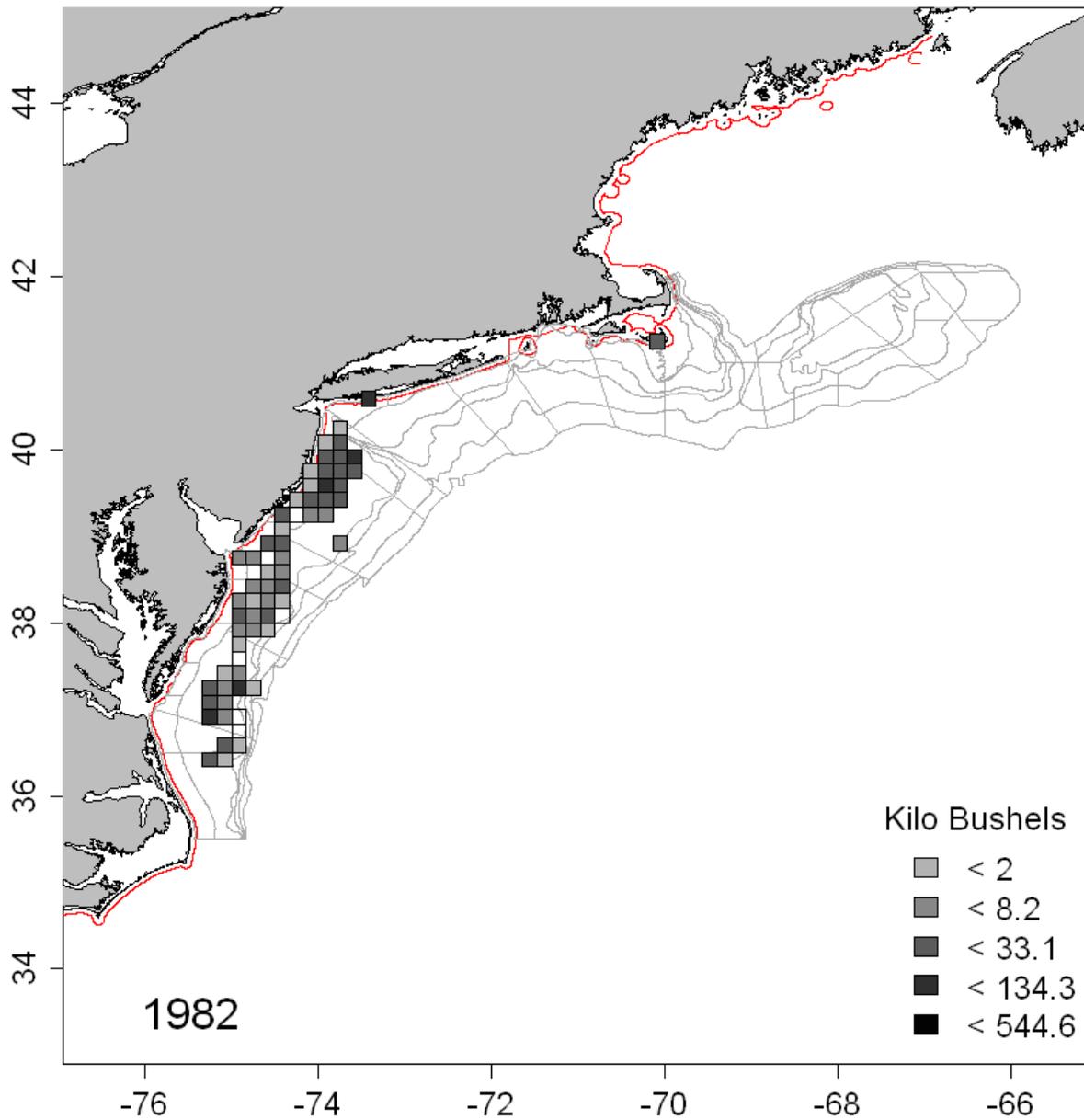
Surfclam catch by ten-minute square



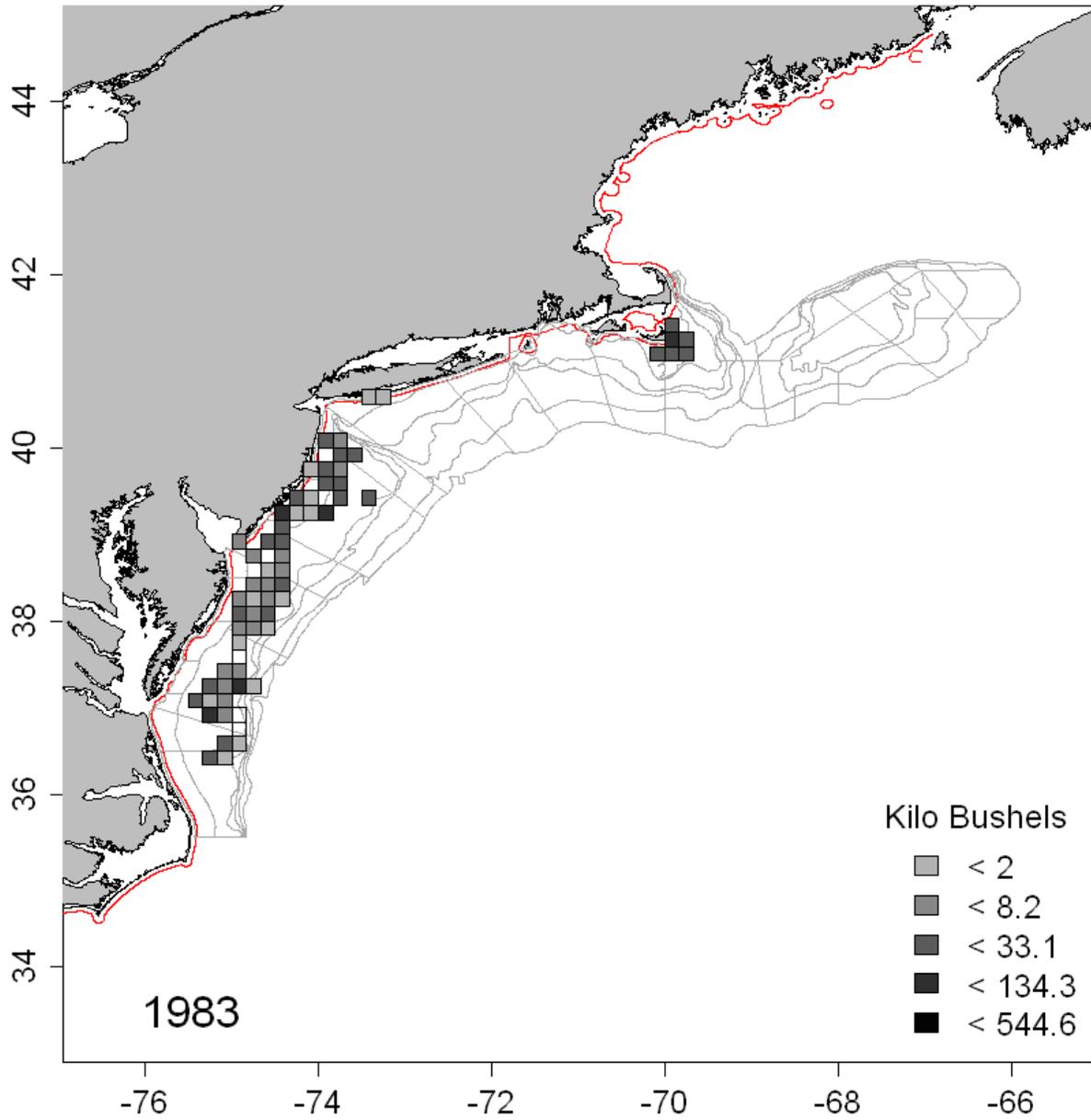
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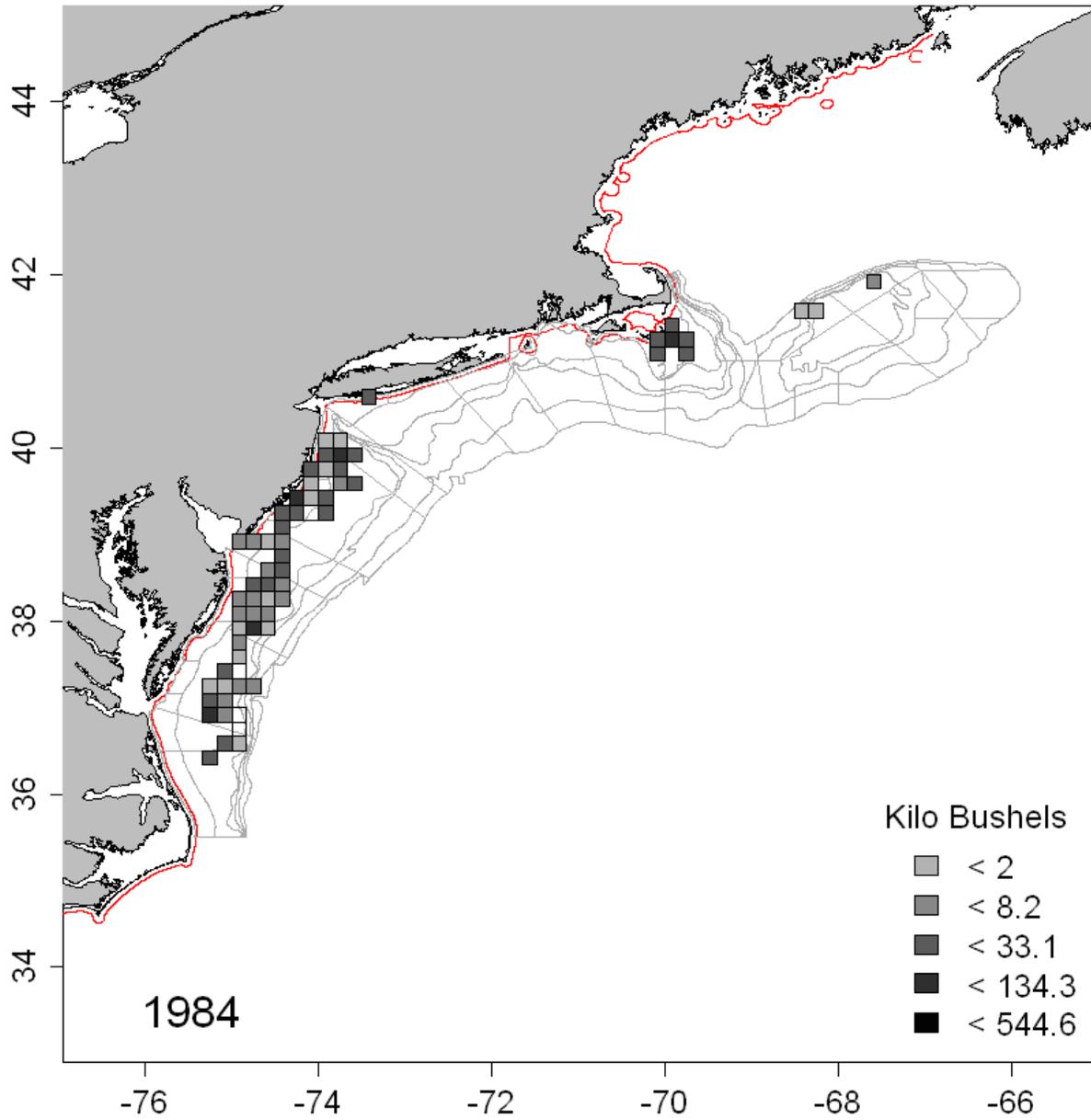
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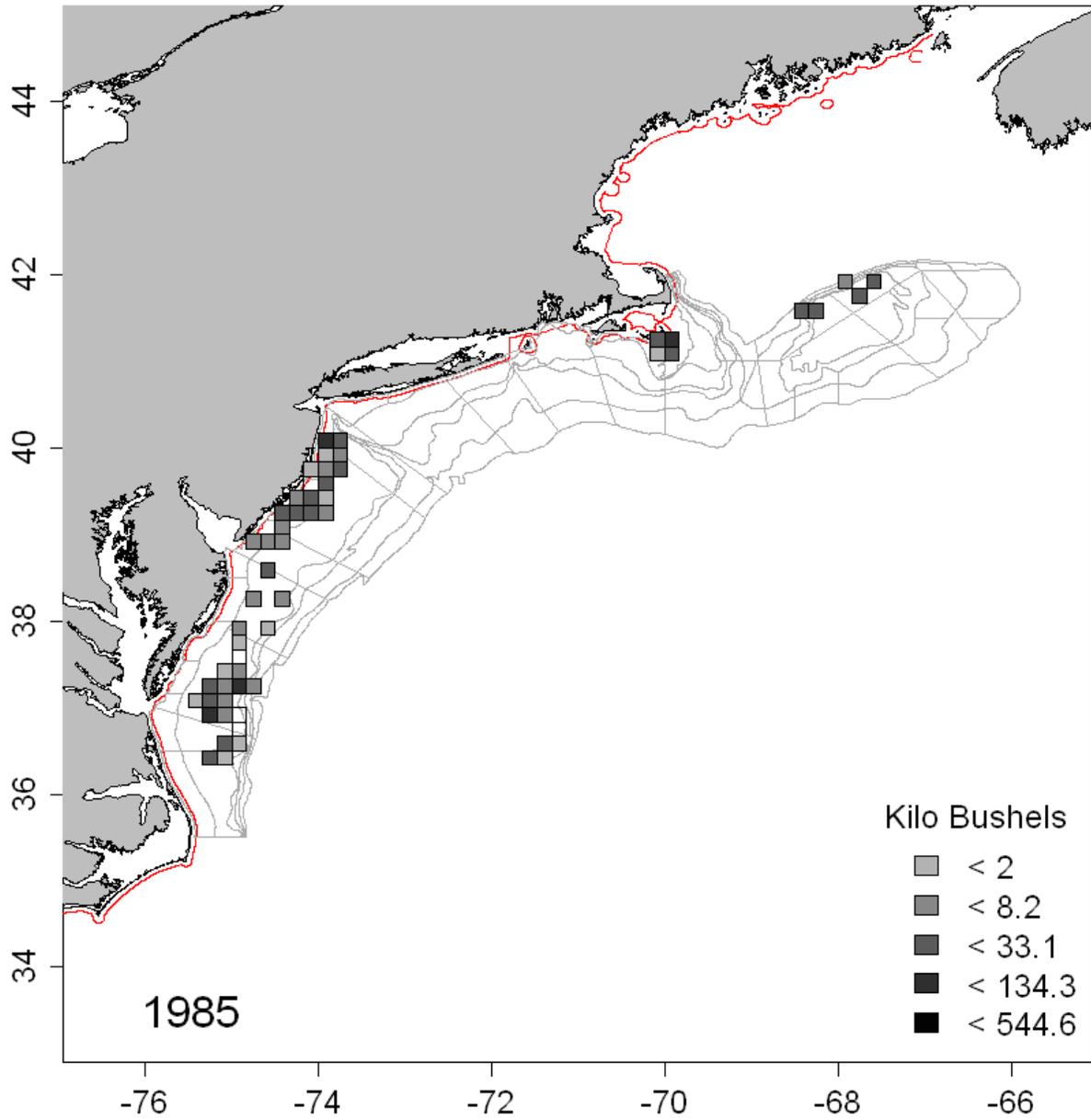
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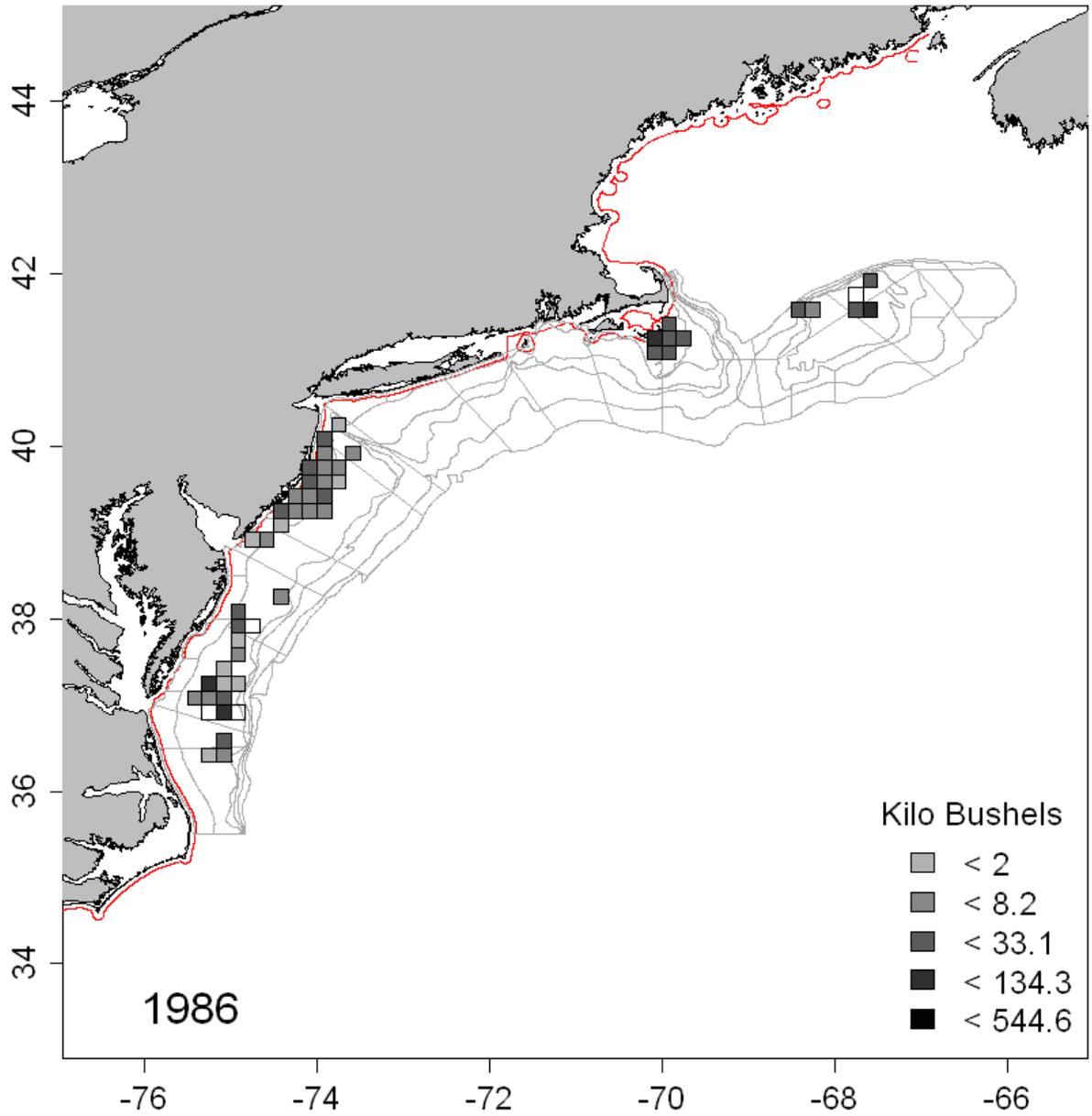
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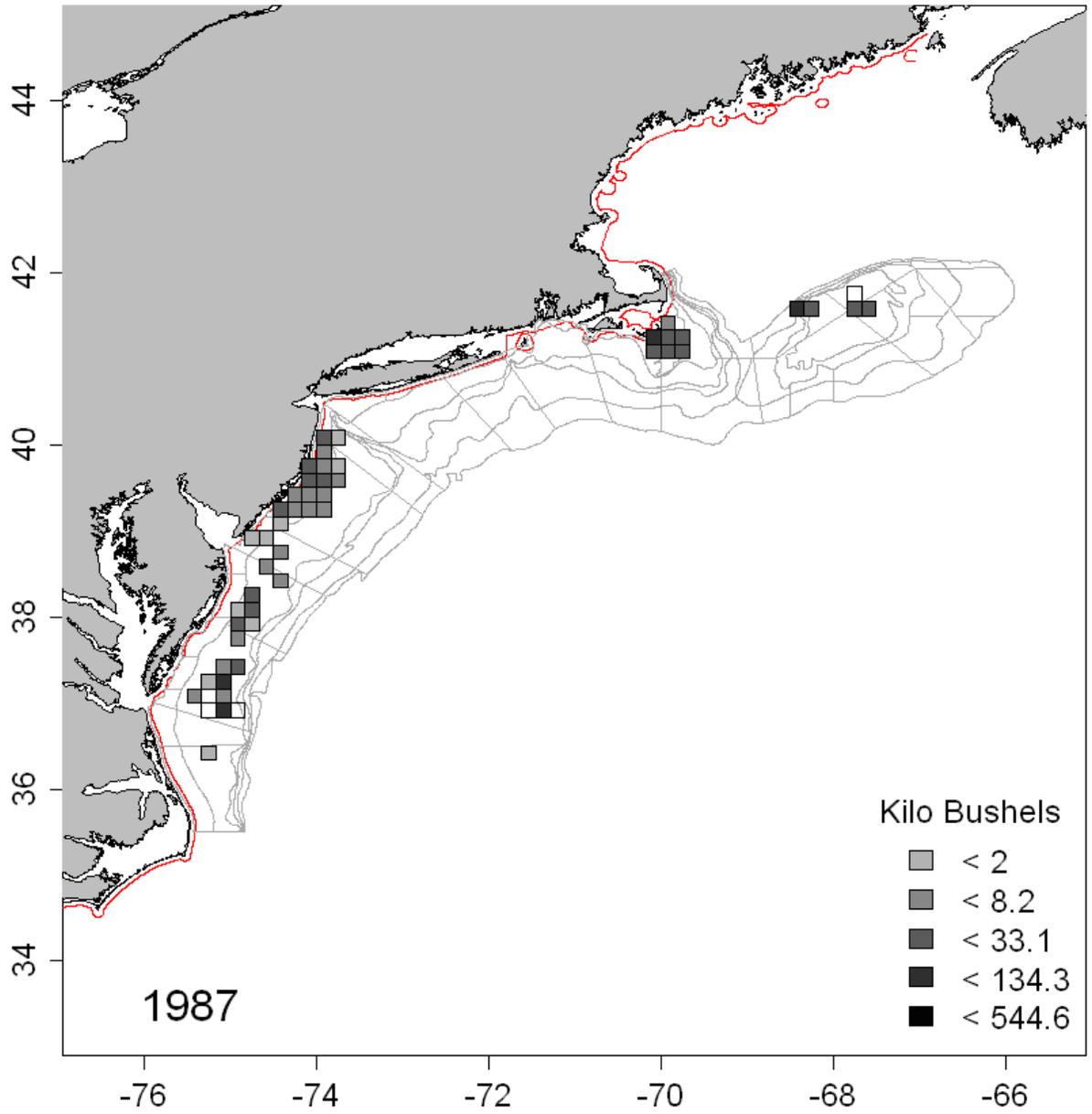
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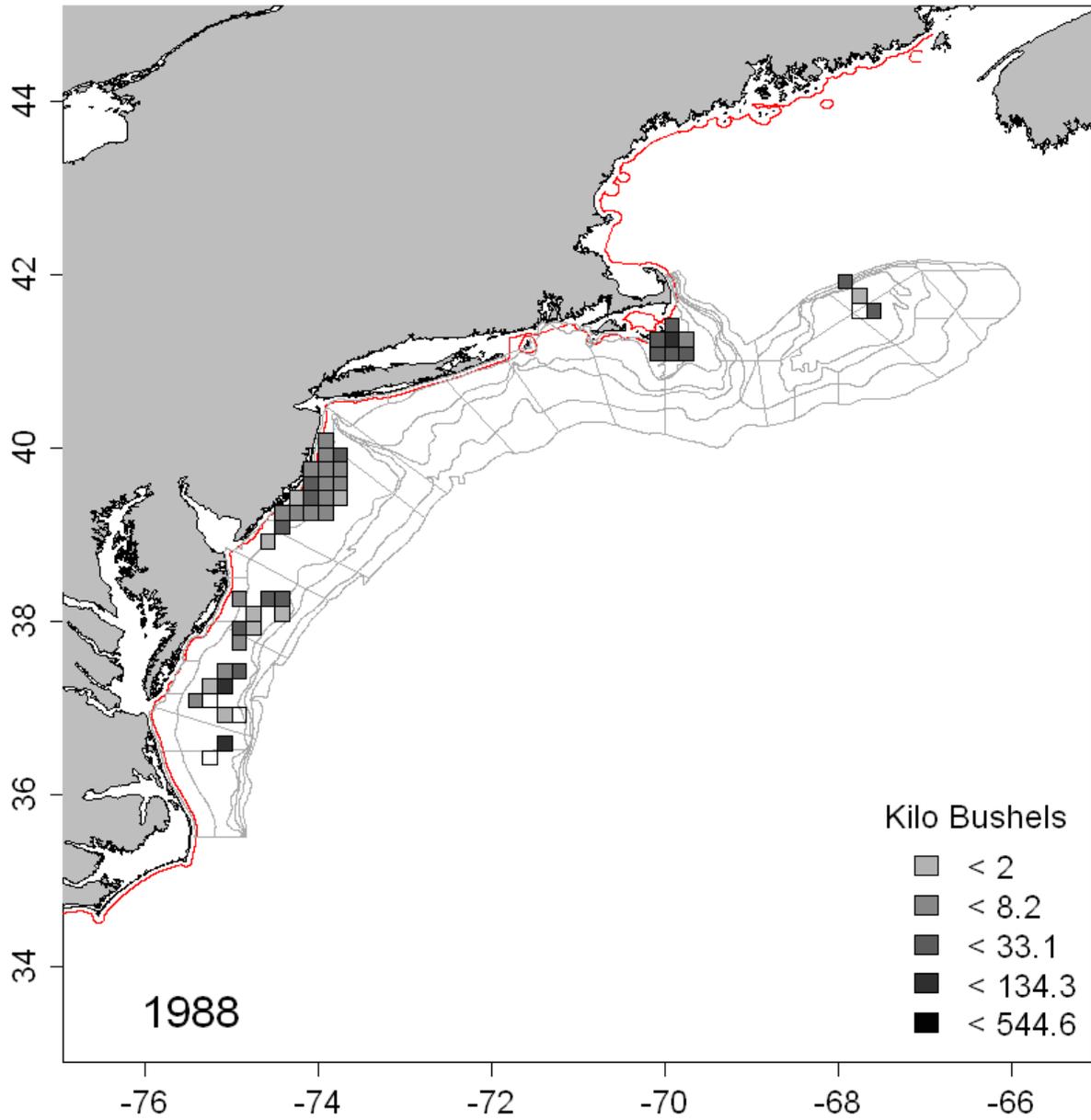
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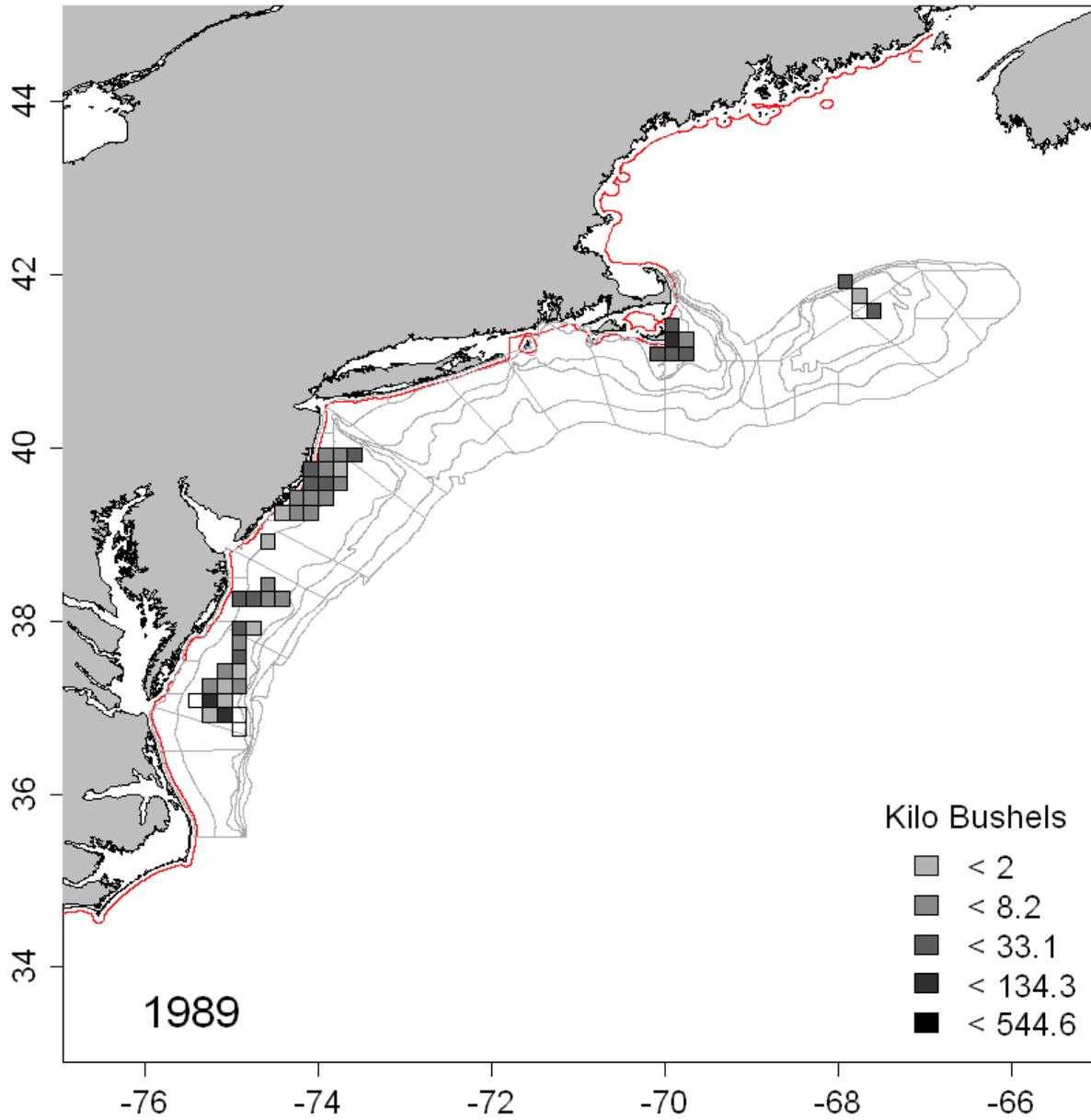
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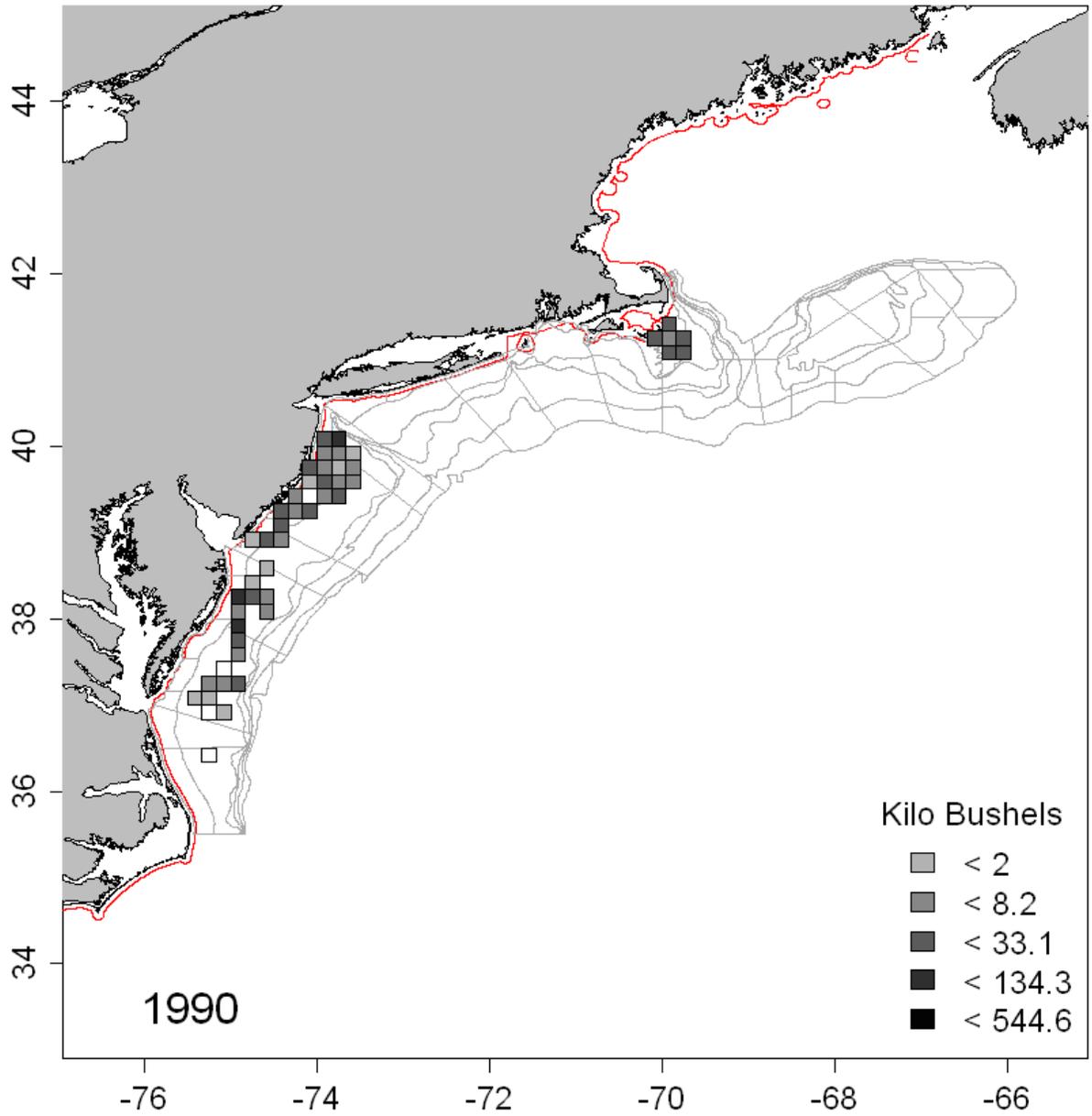
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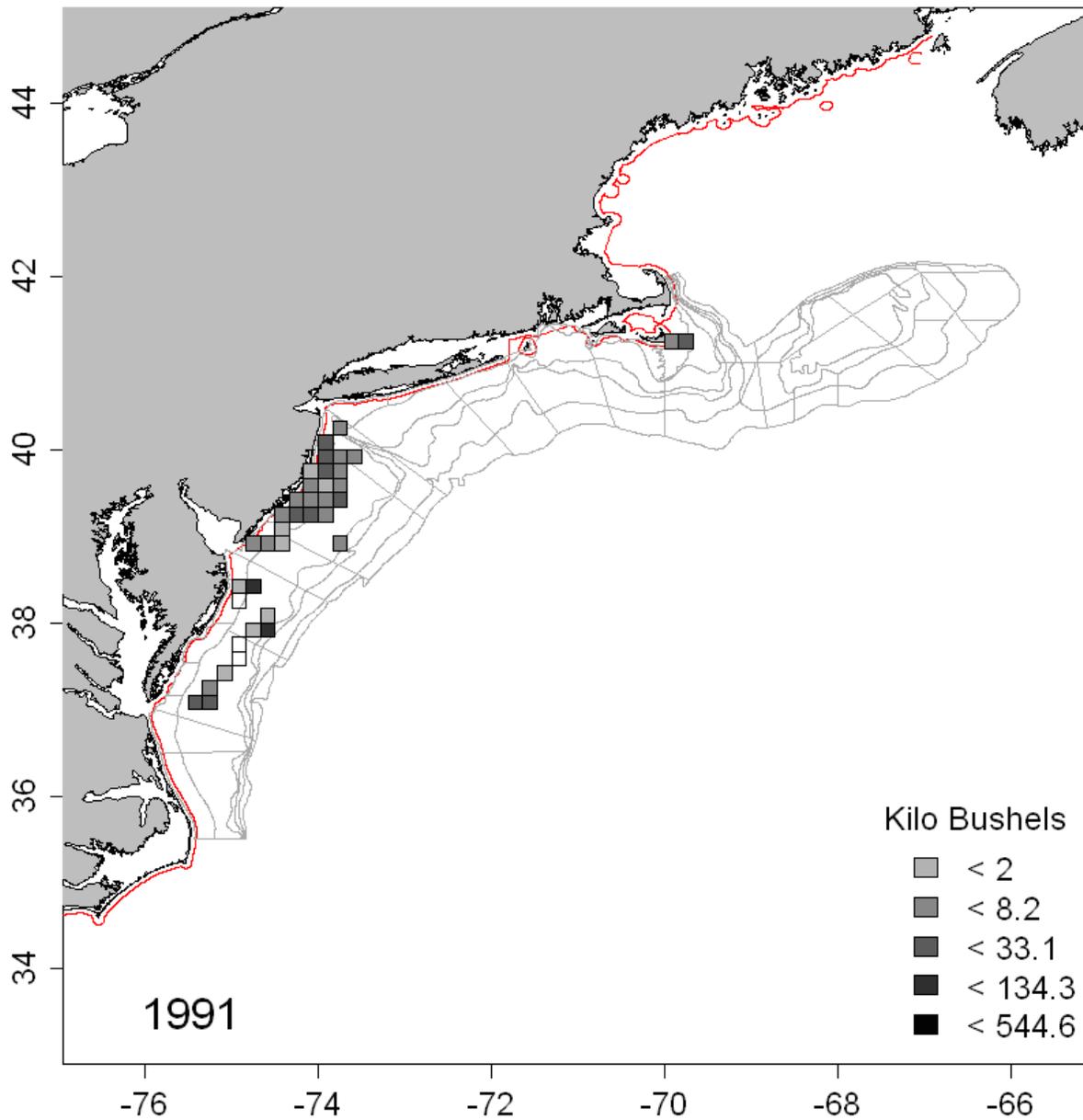
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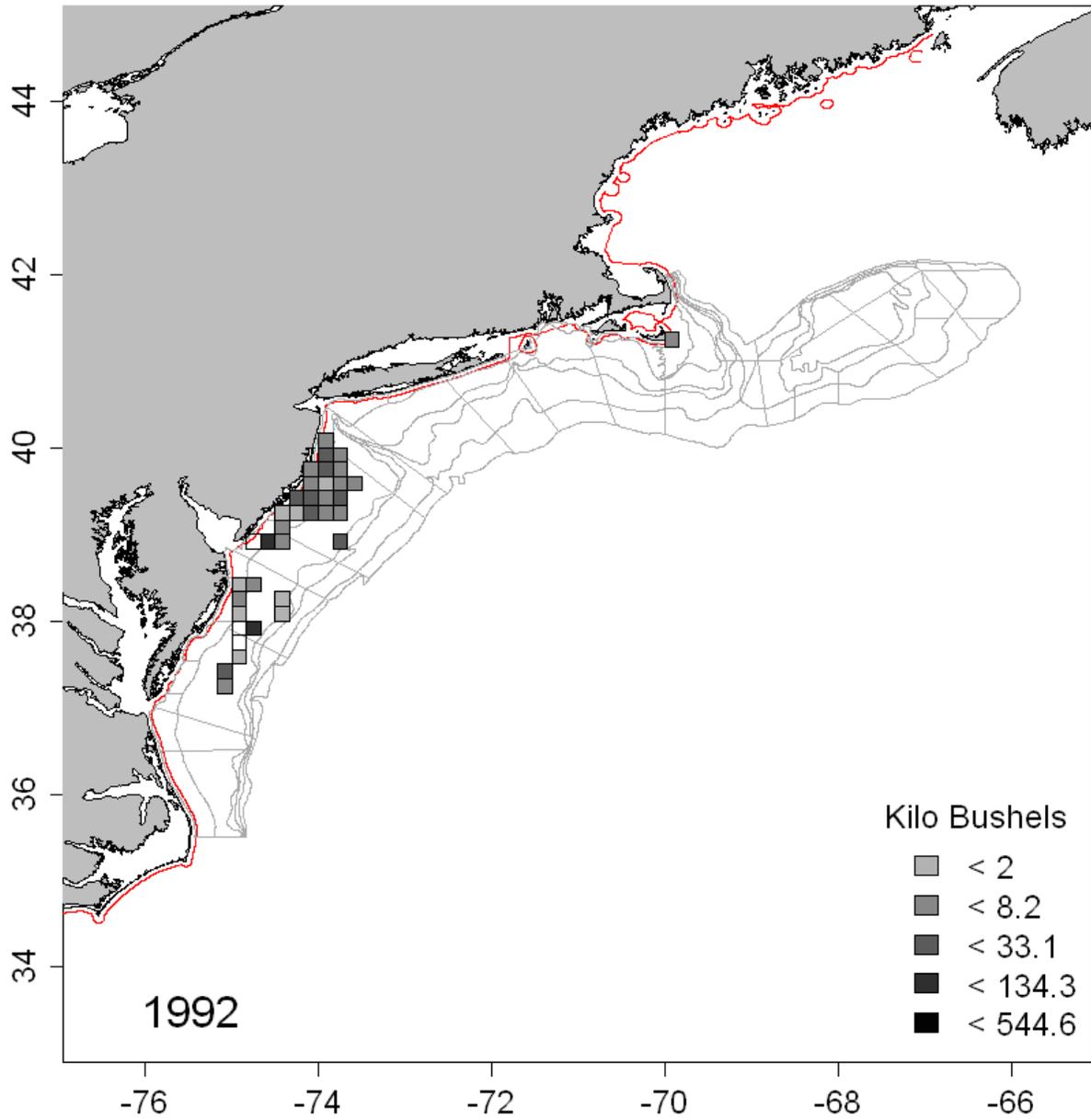
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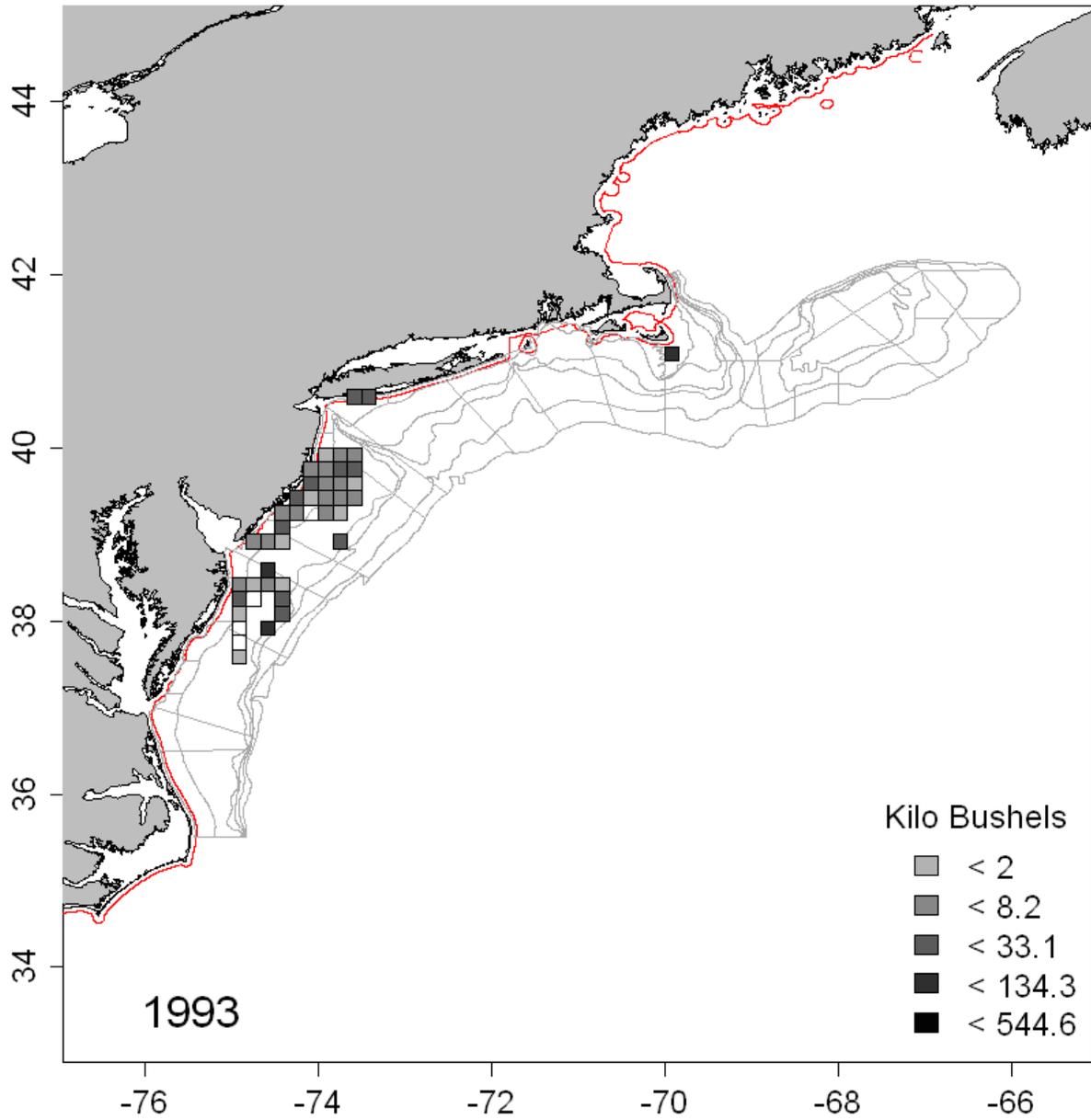
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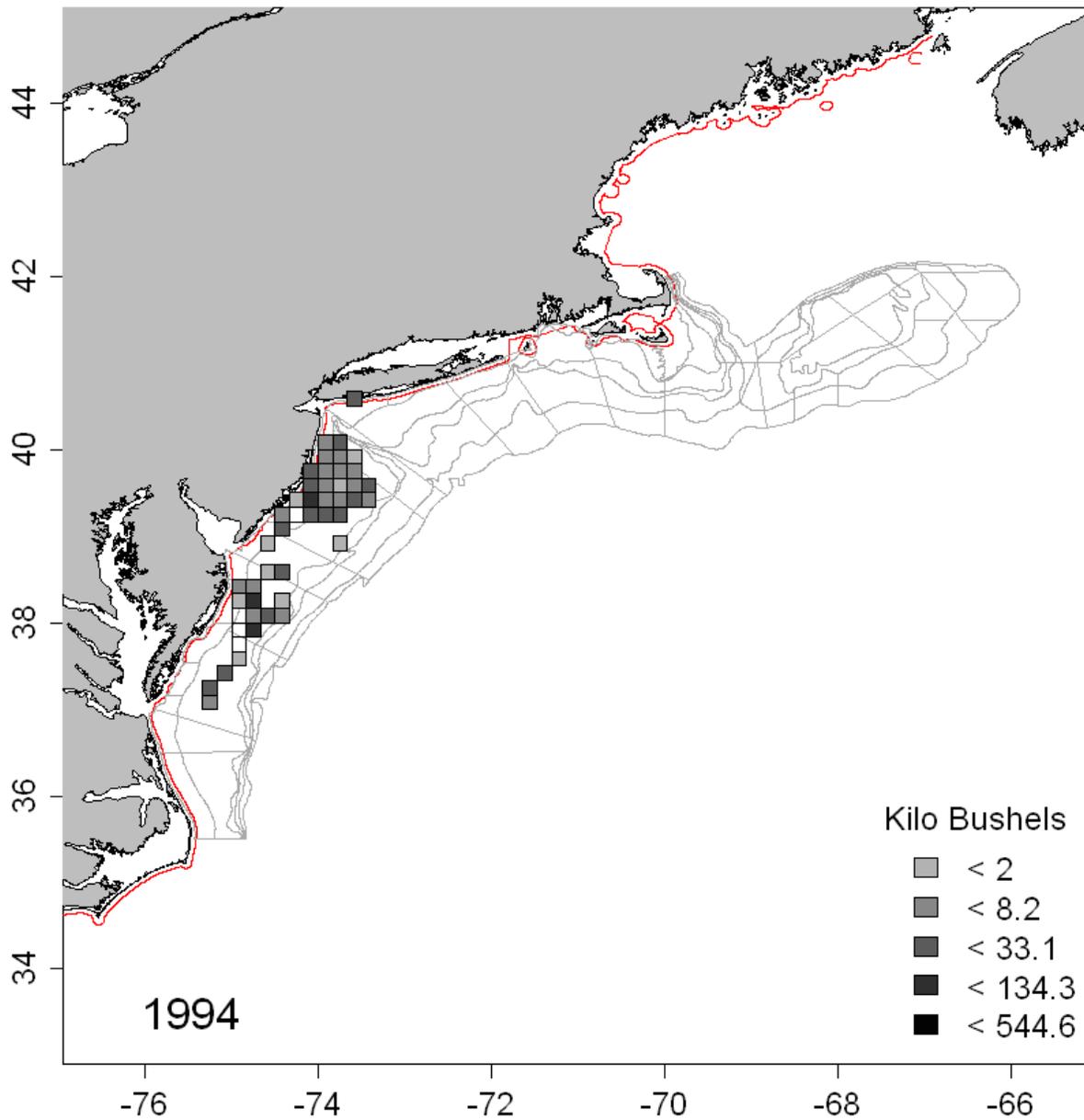
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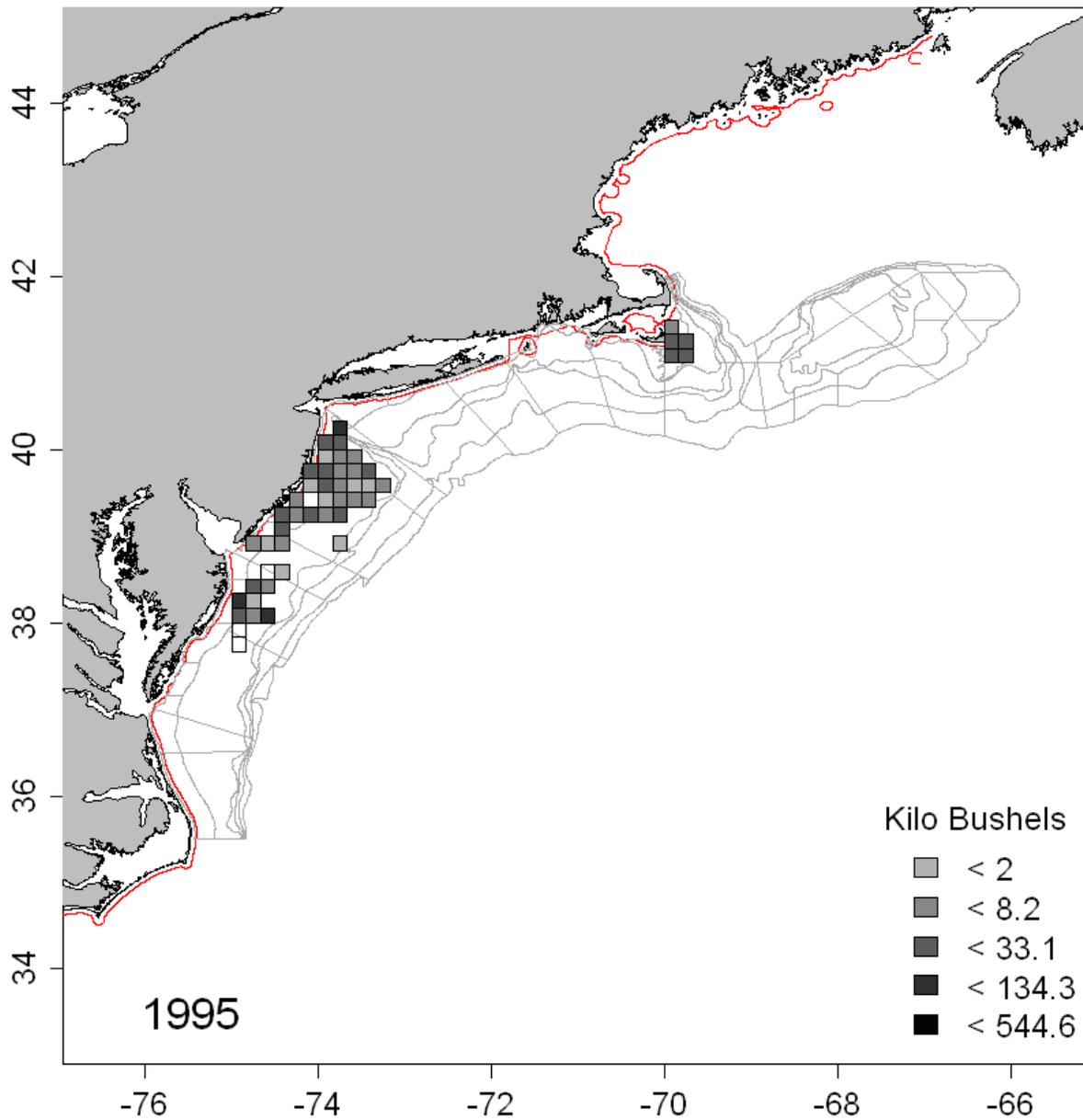
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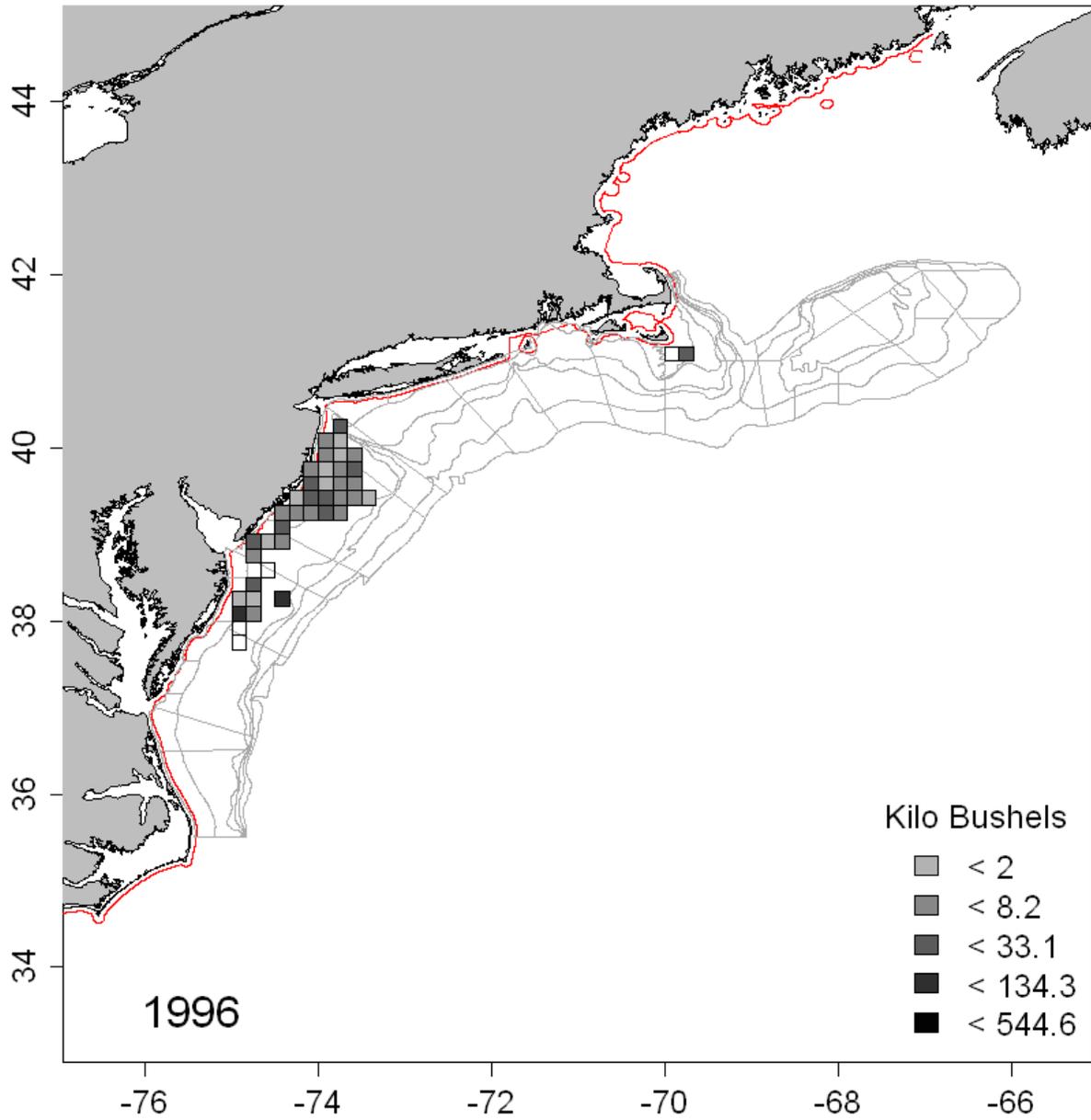
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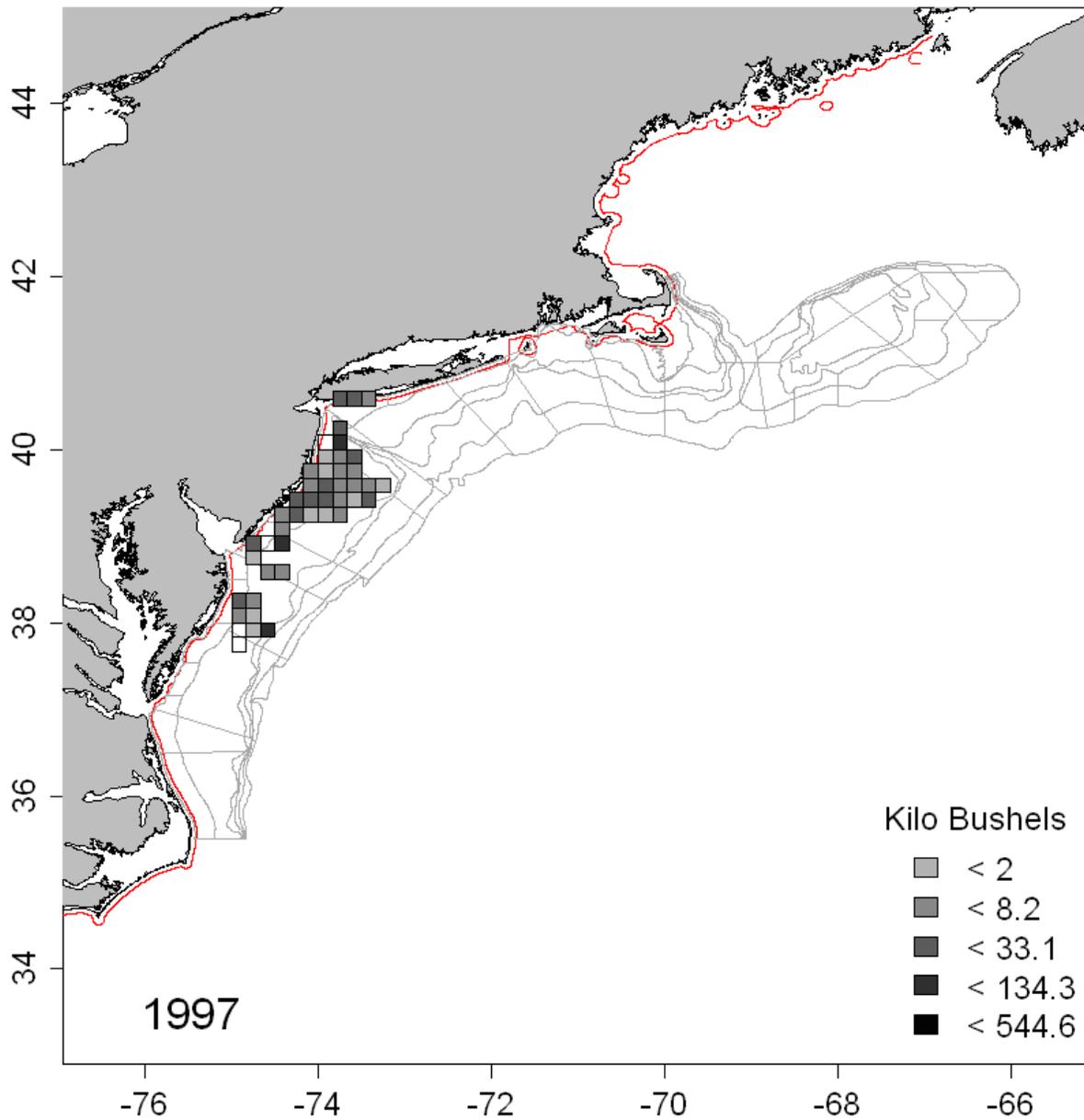
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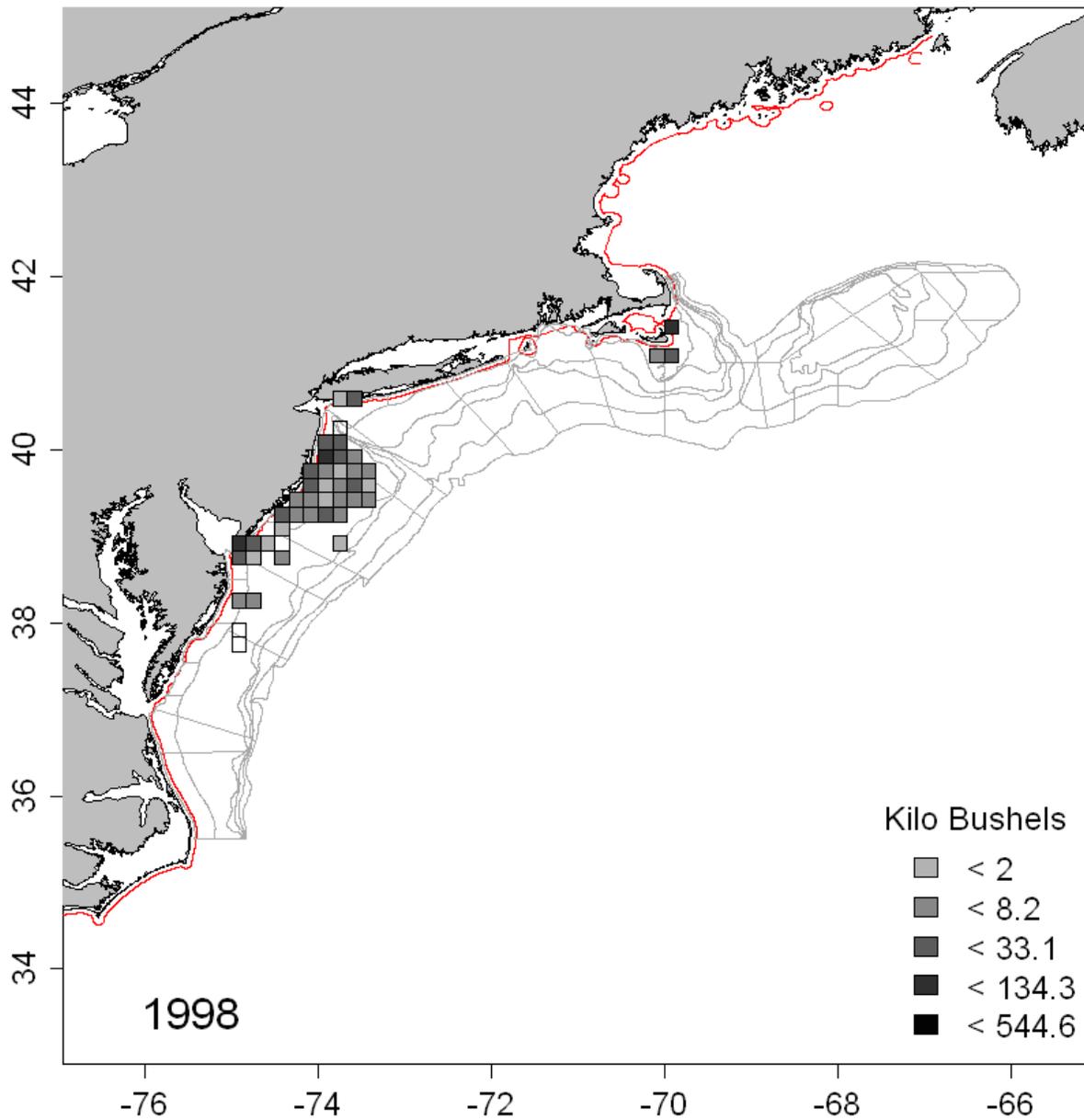
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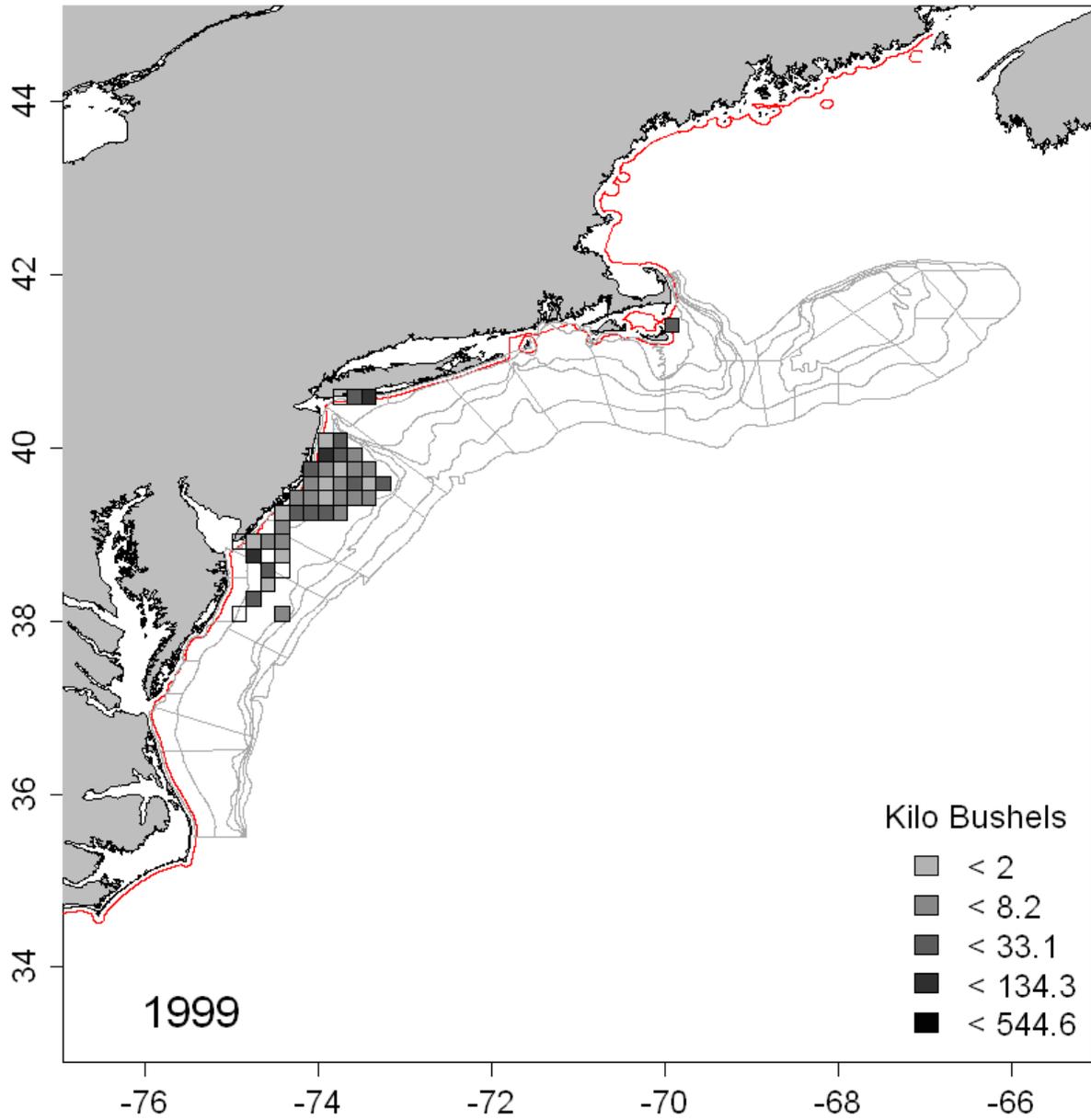
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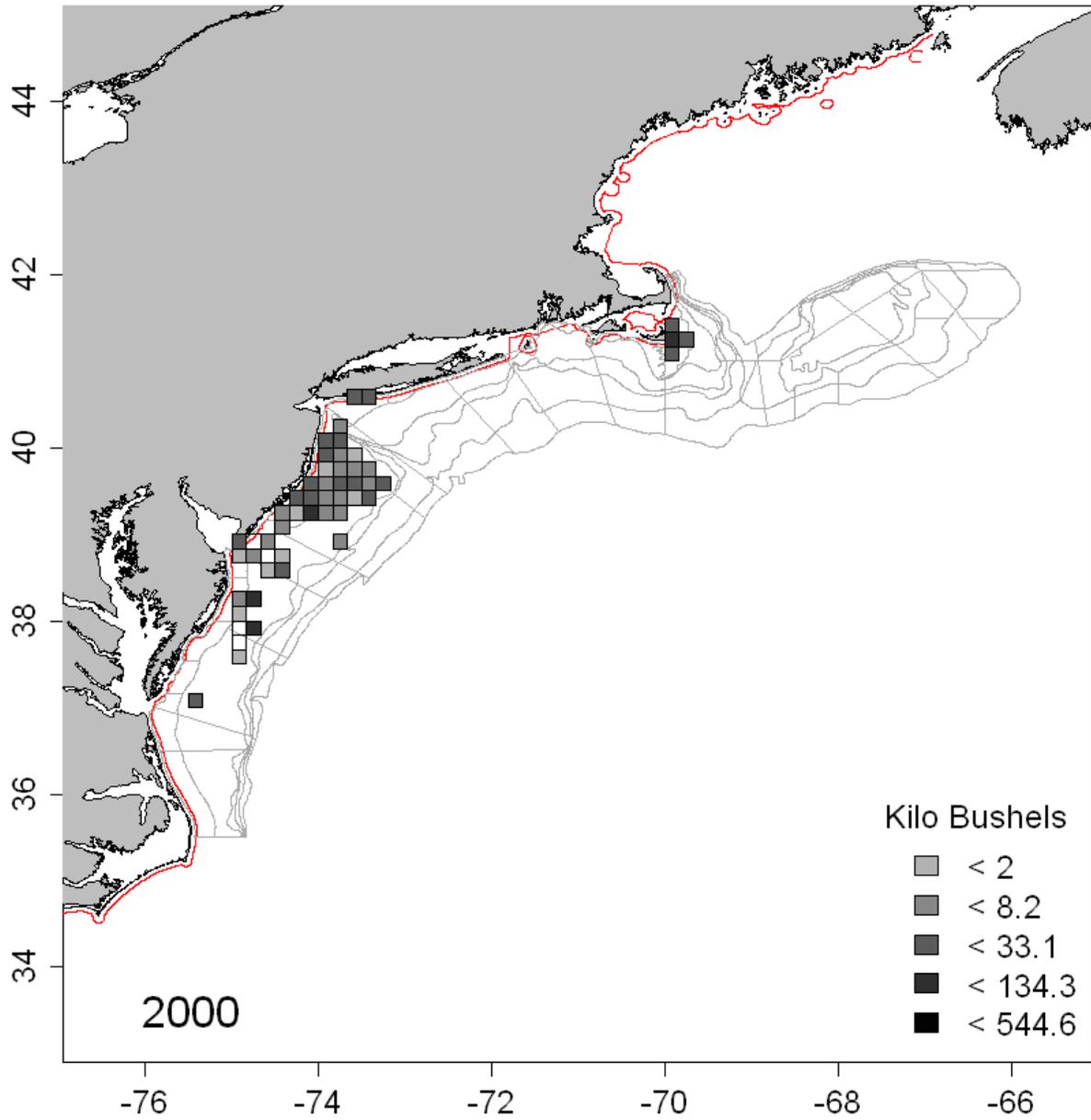
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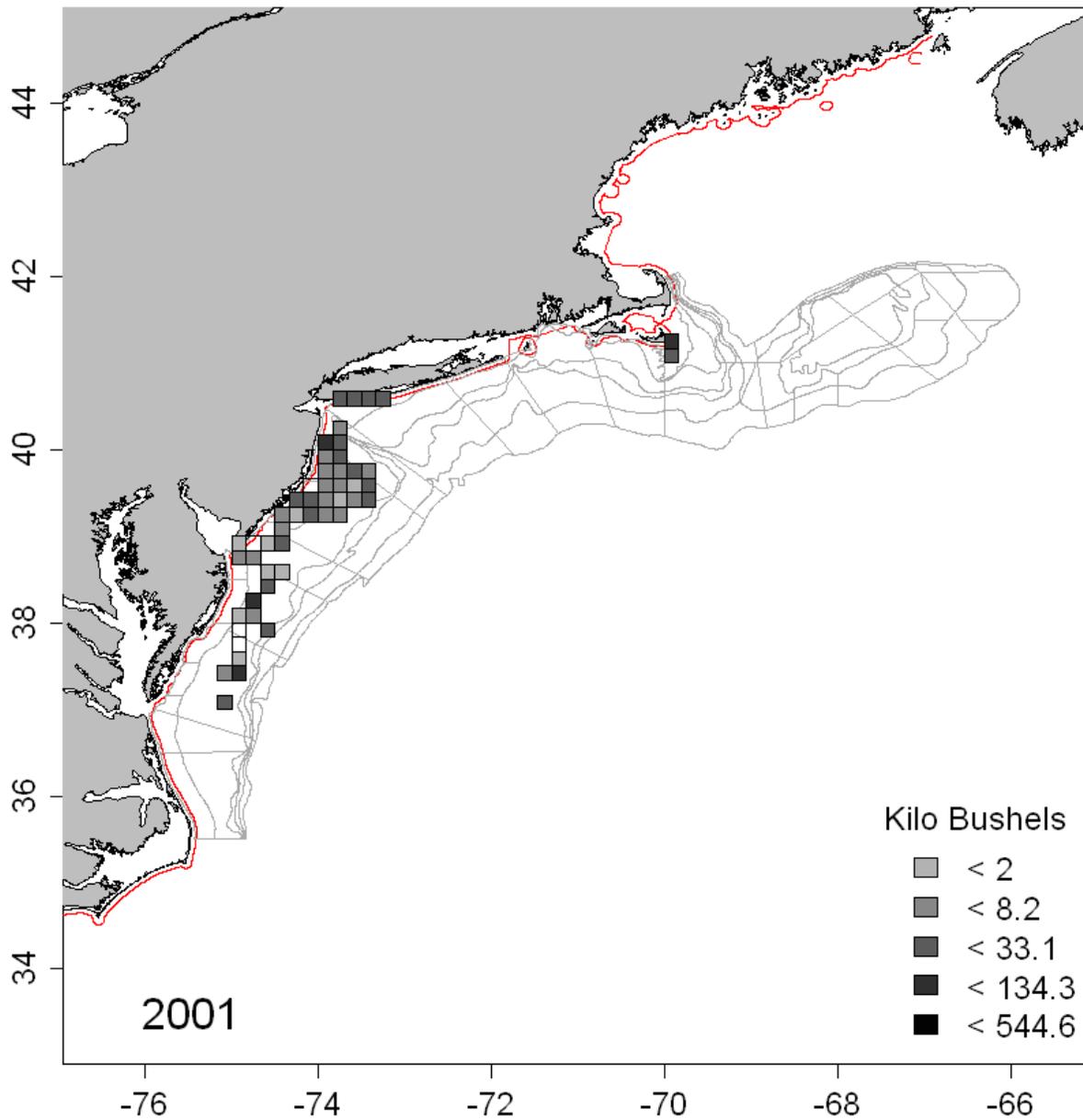
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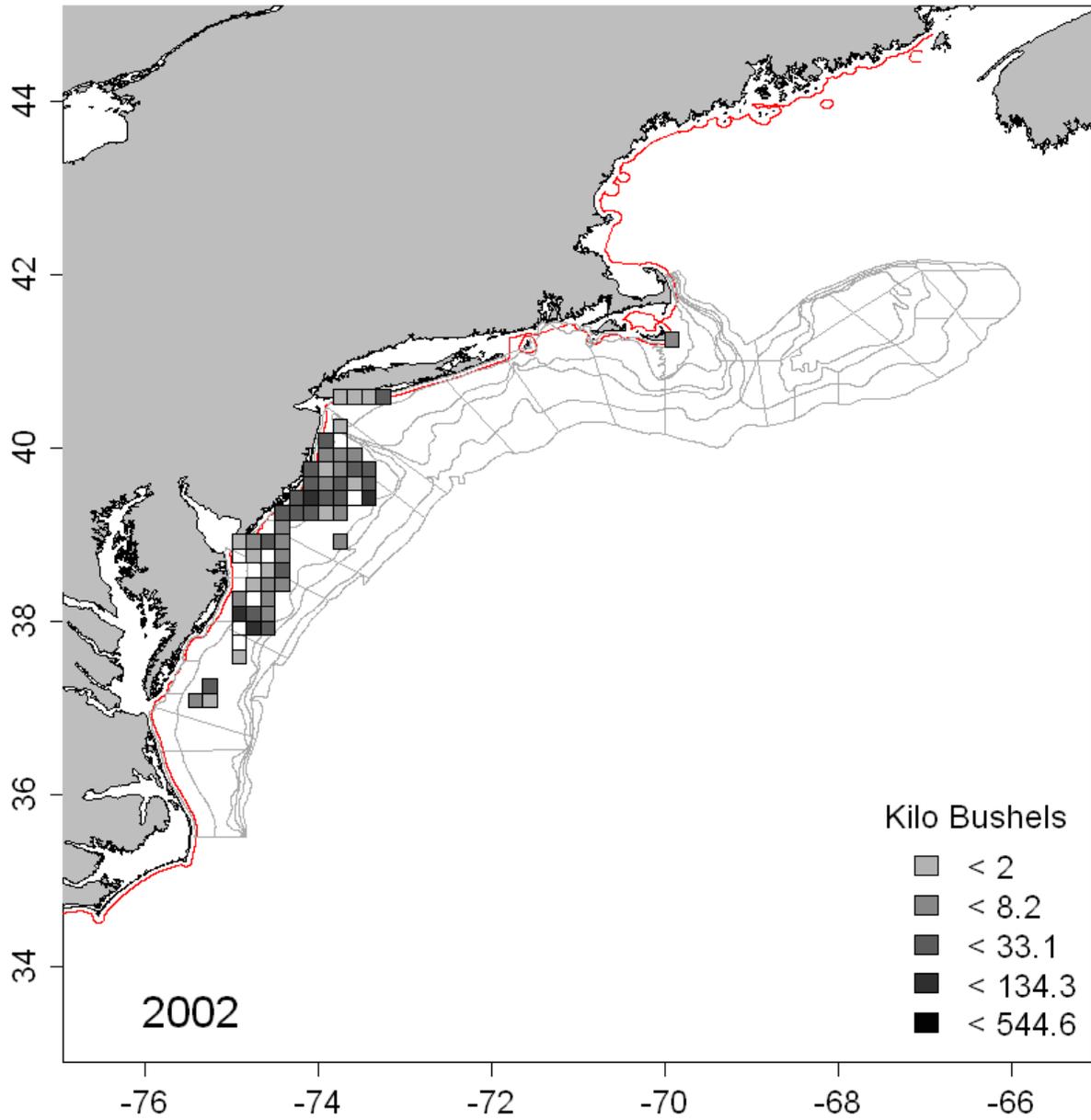
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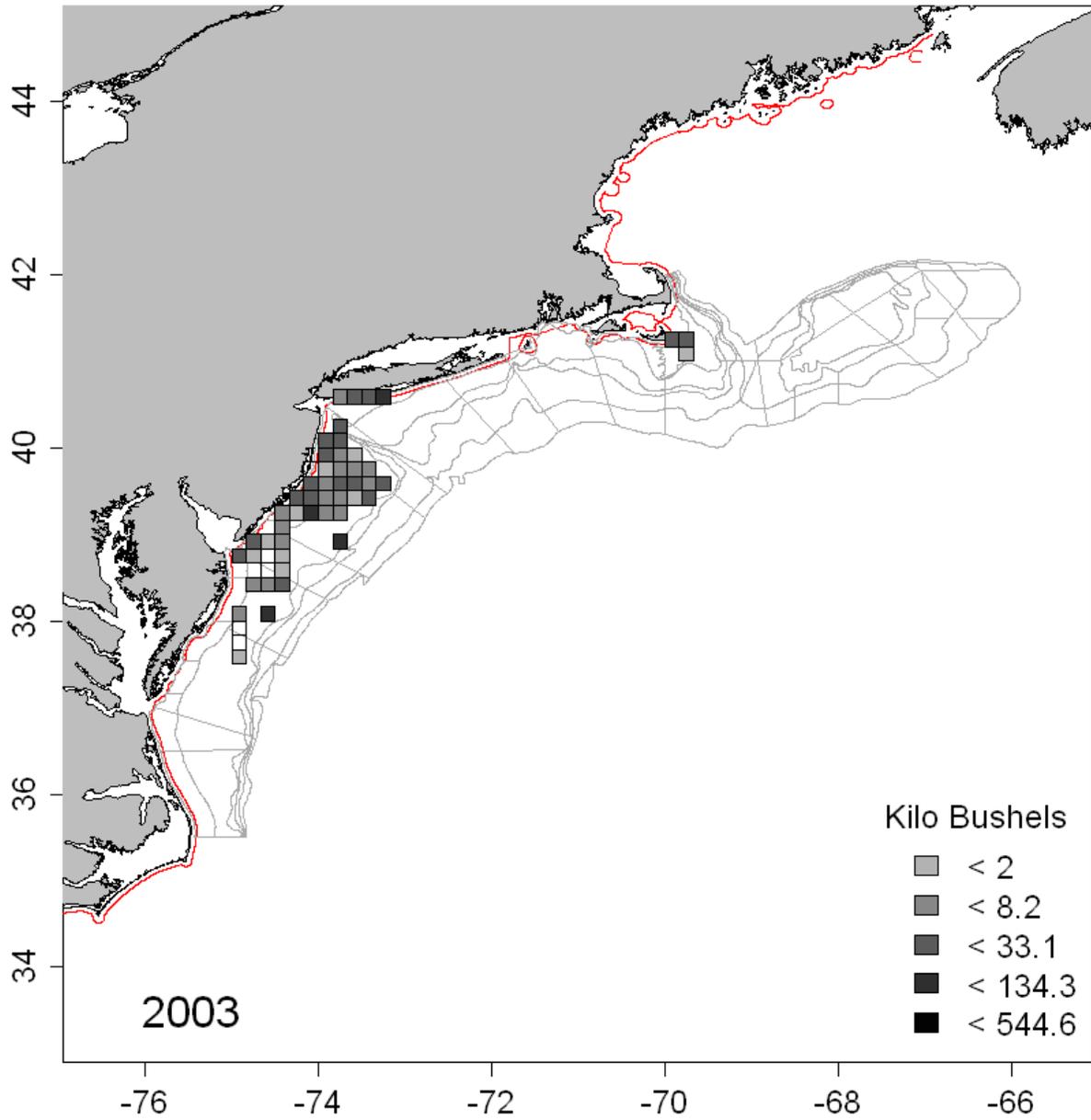
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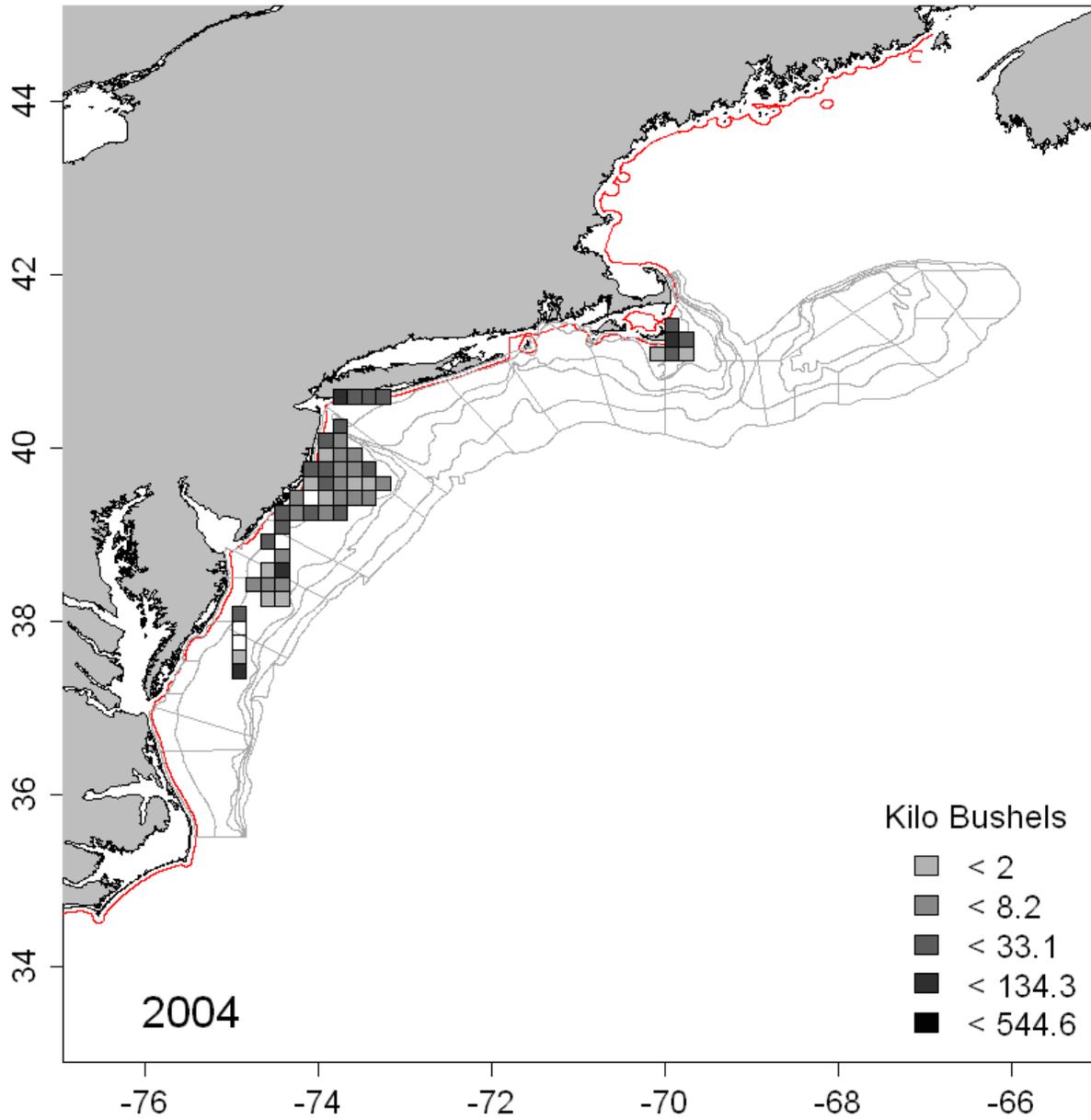
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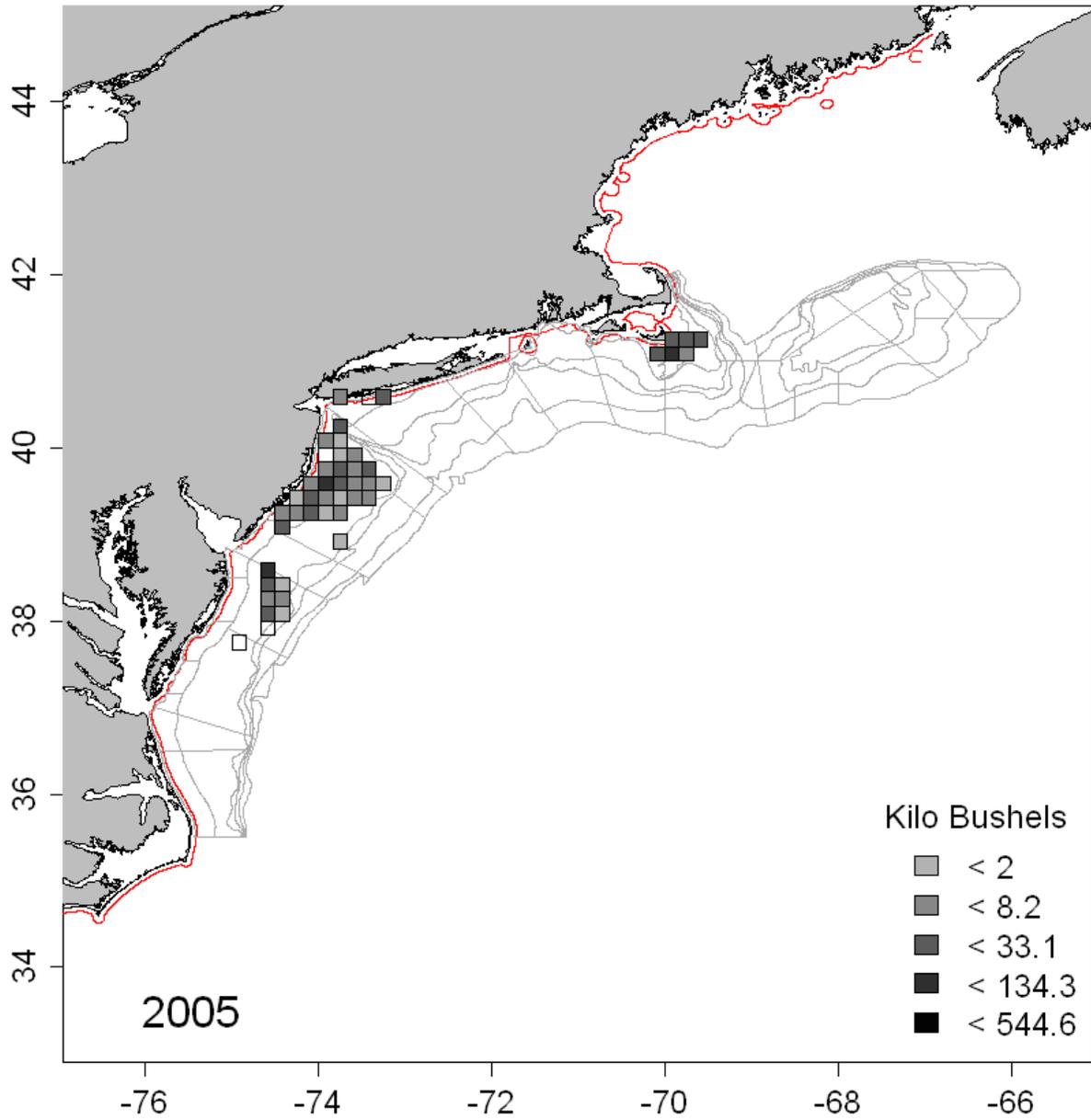
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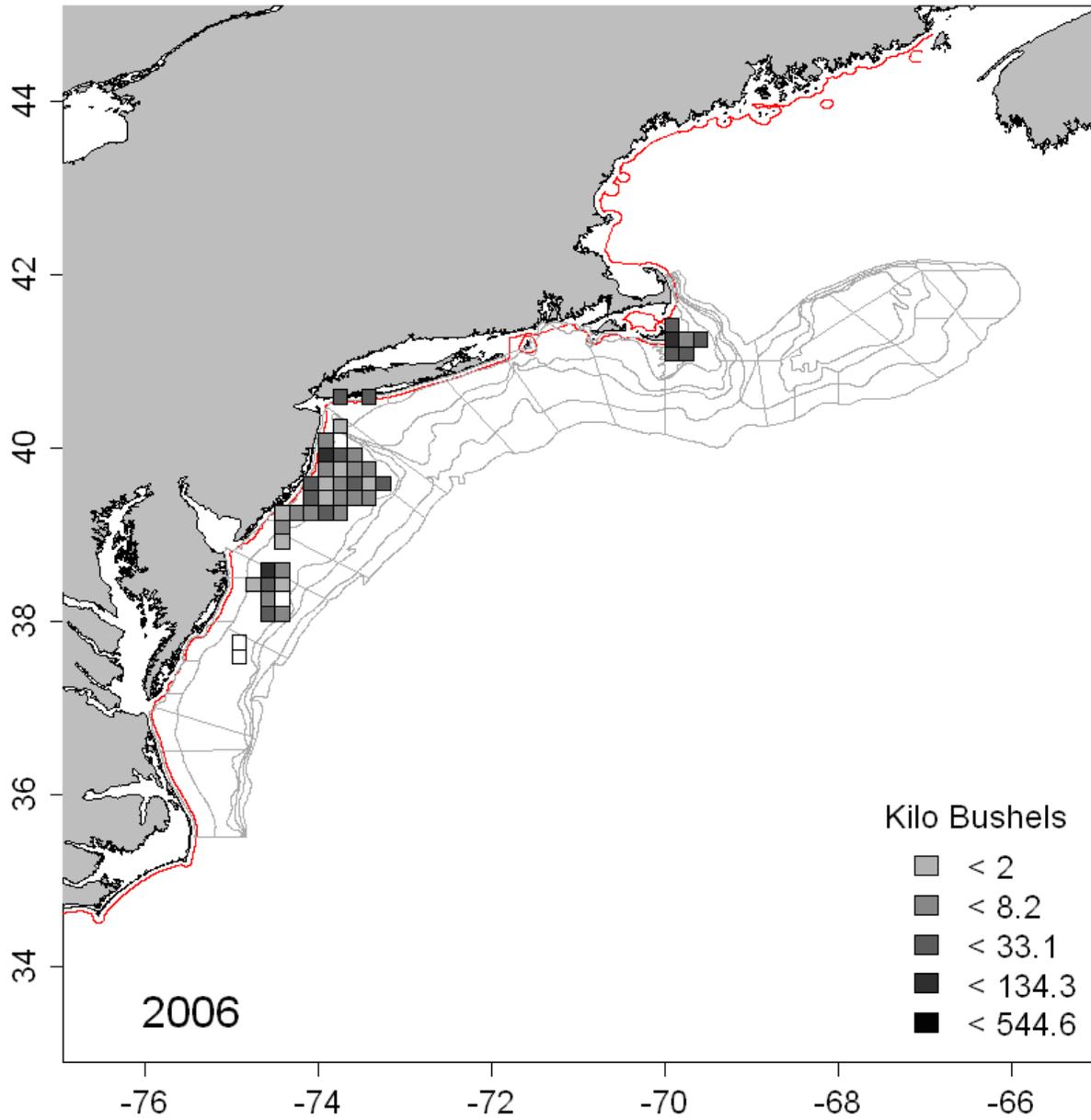
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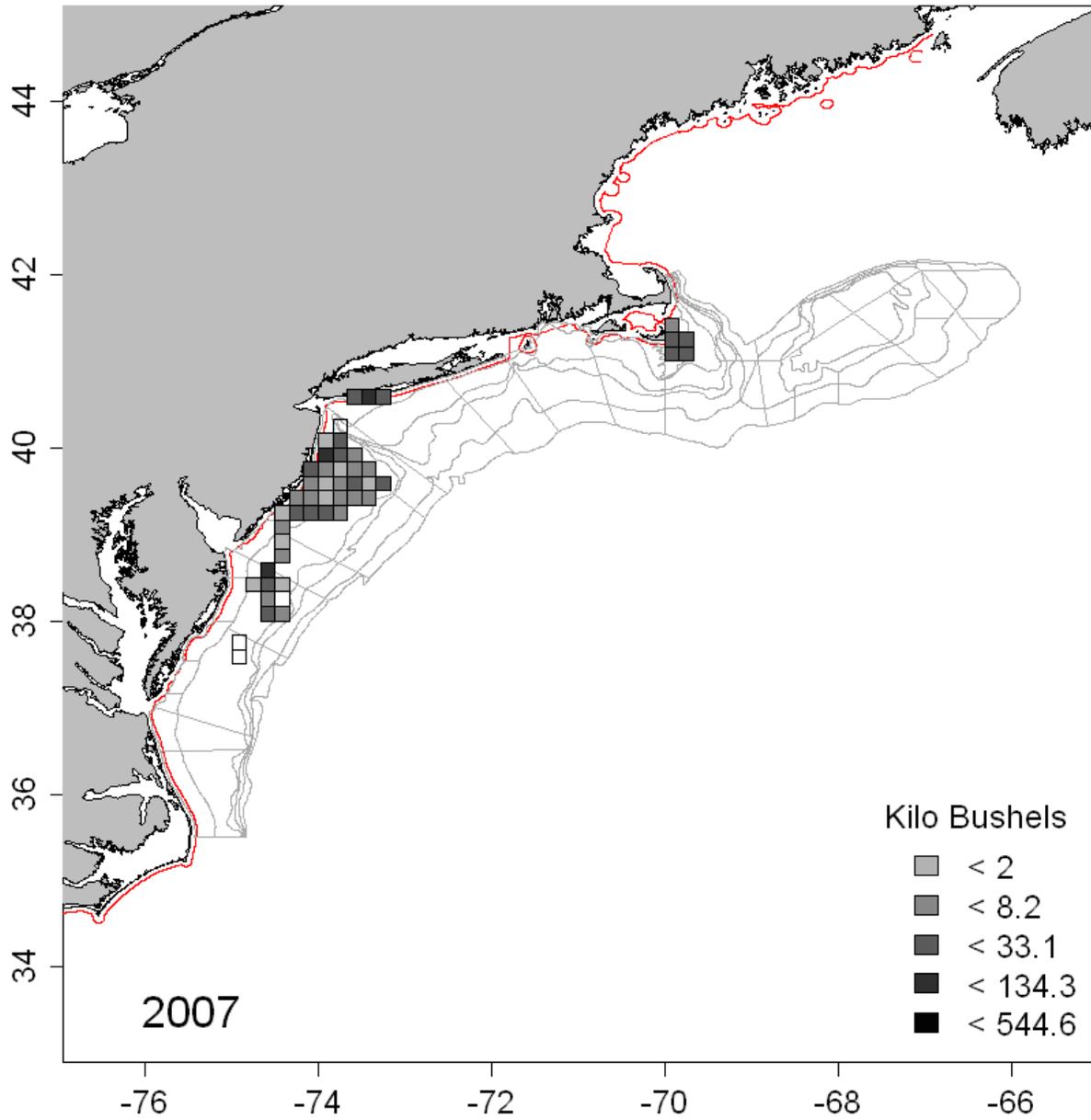
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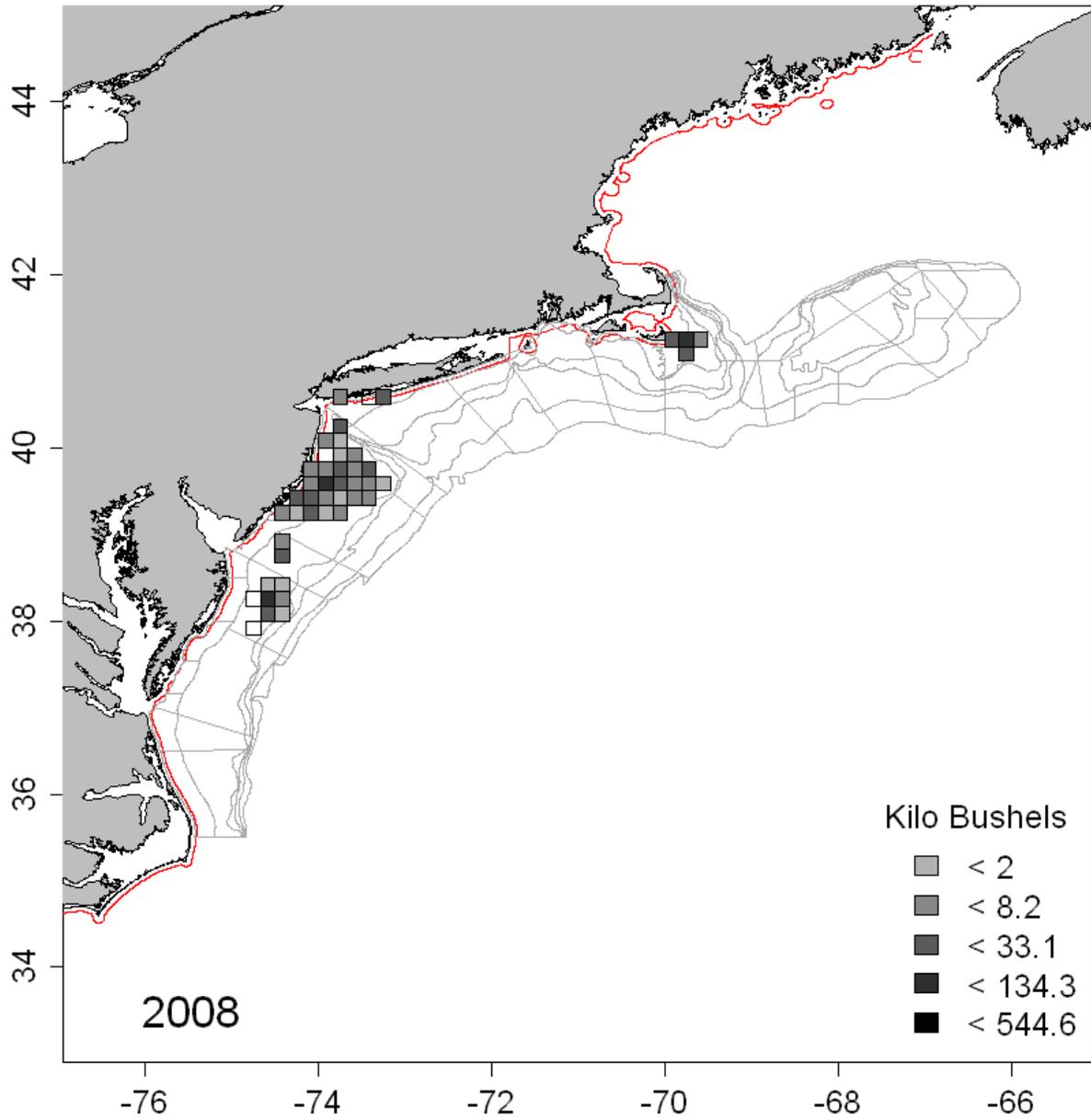
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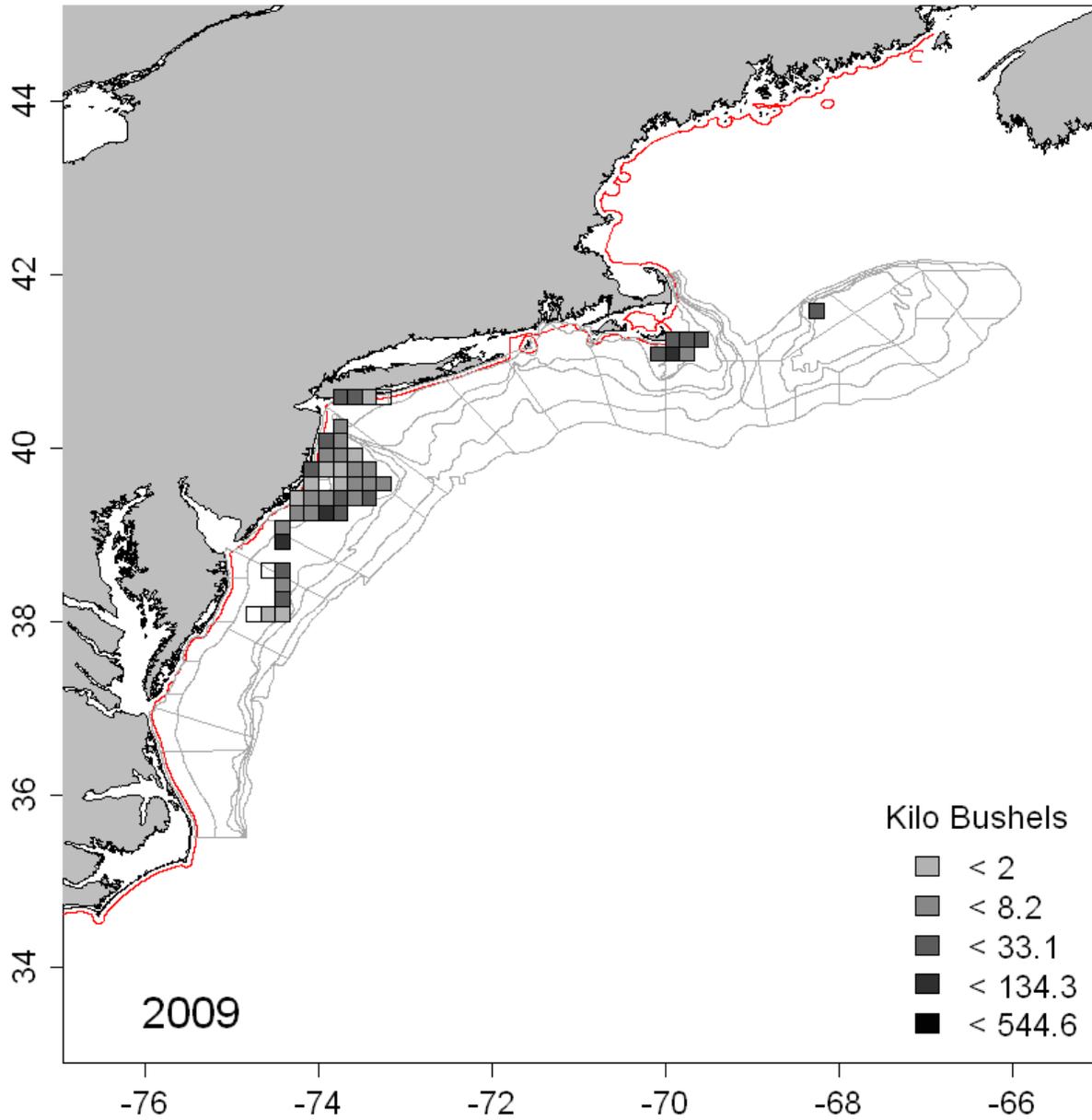
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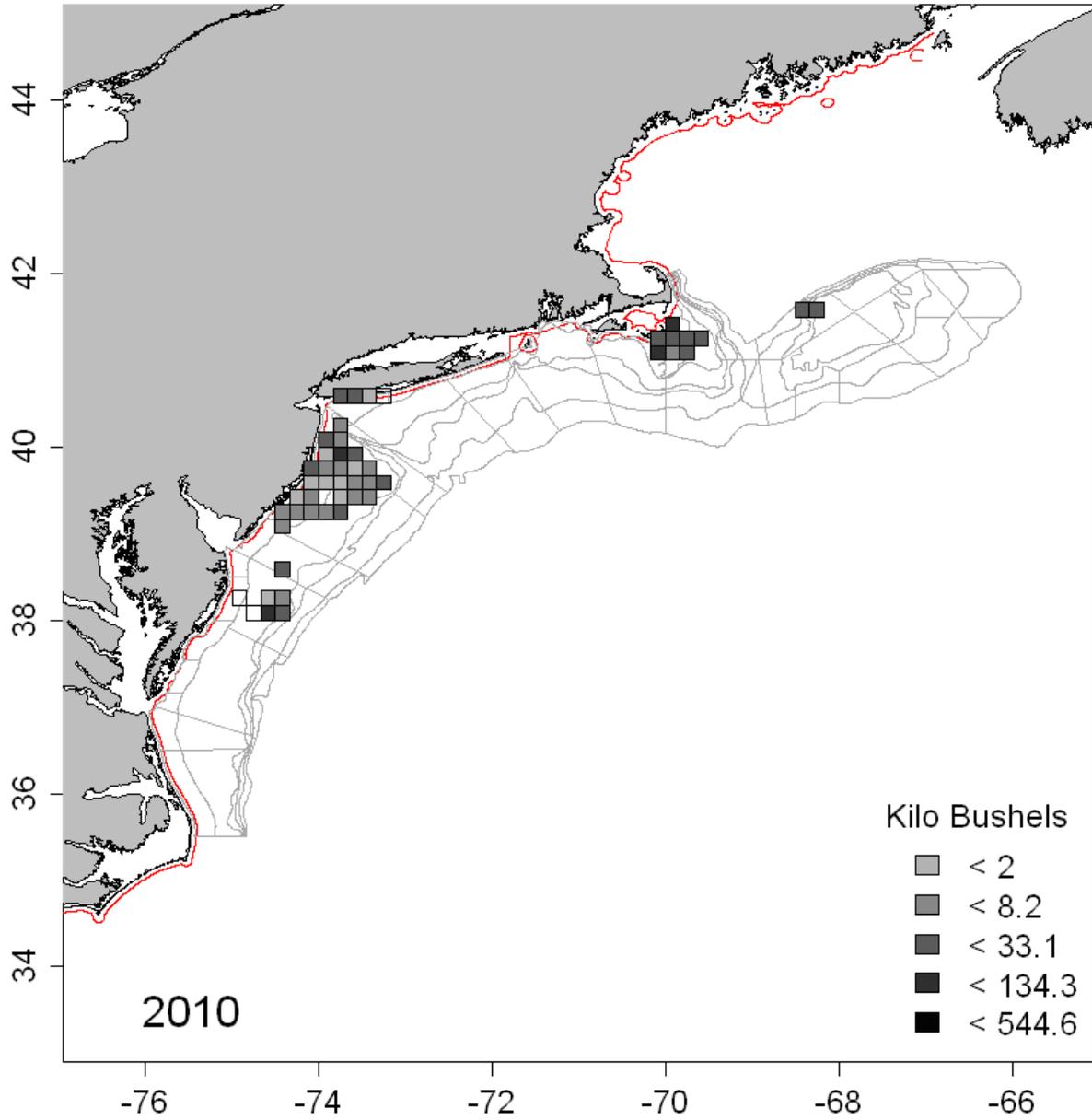
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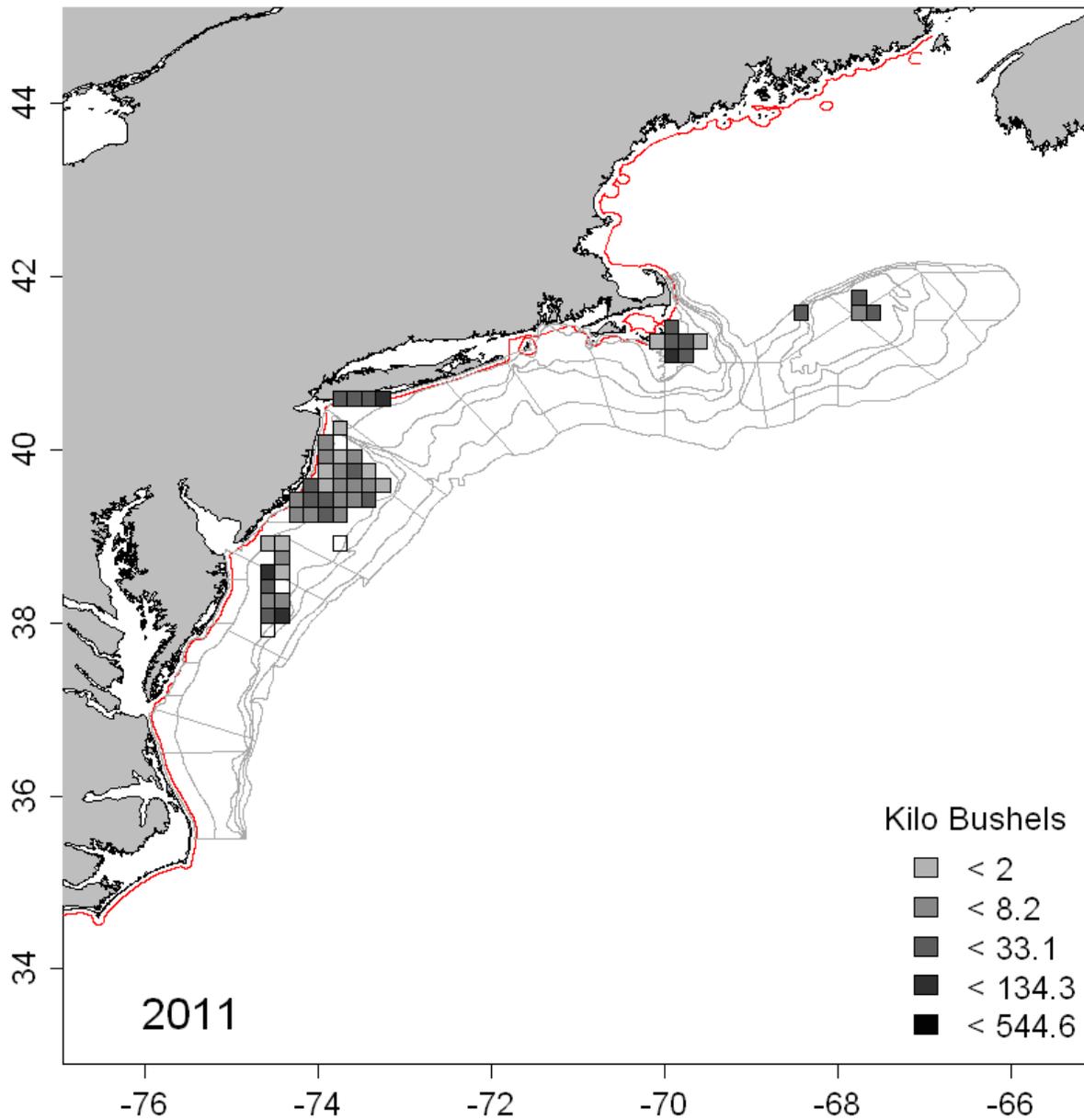
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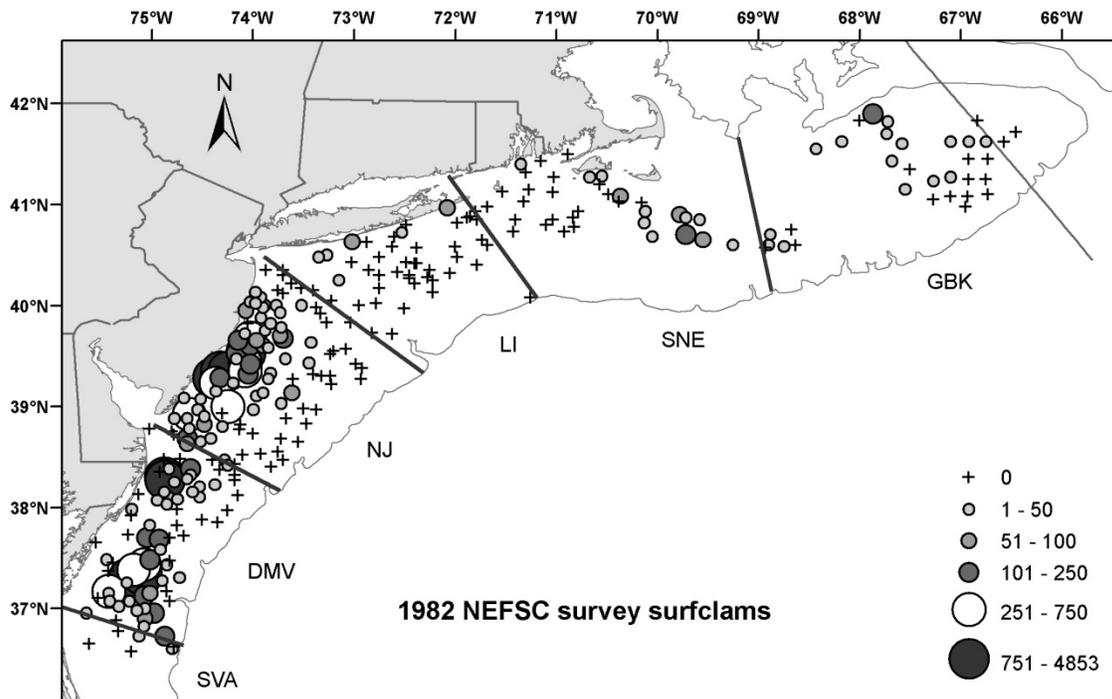
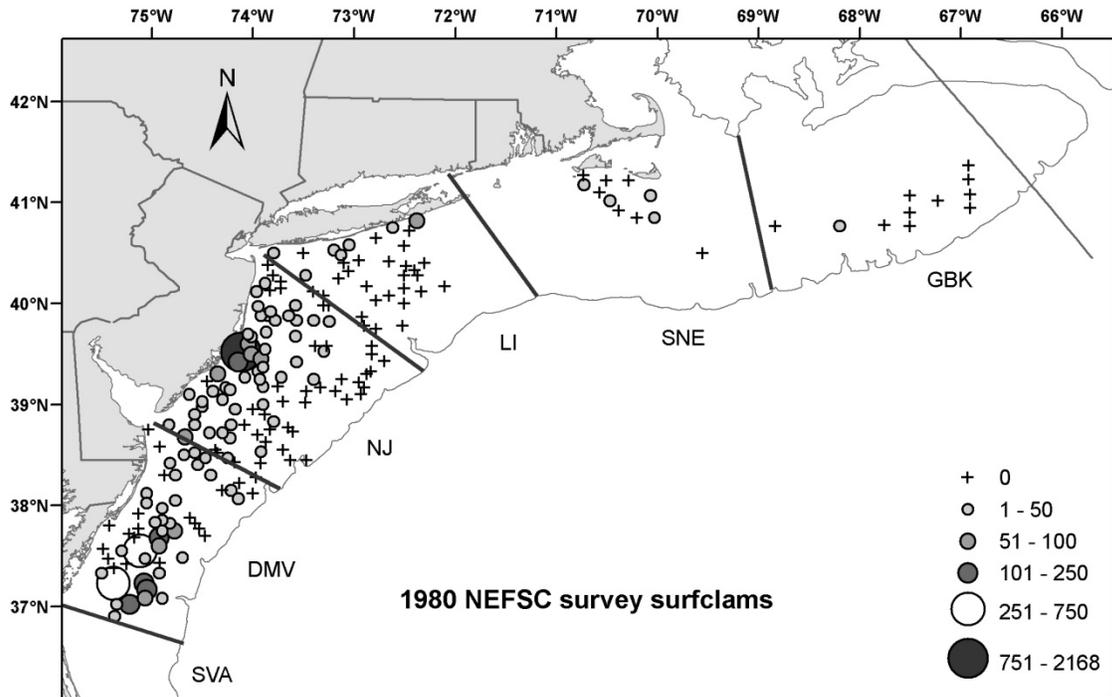


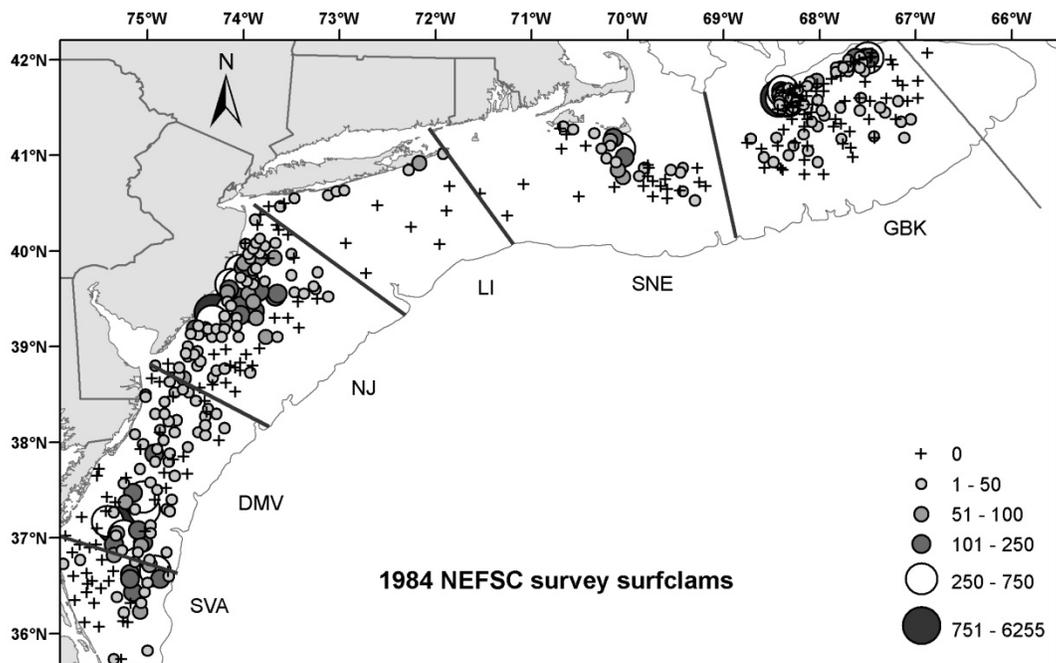
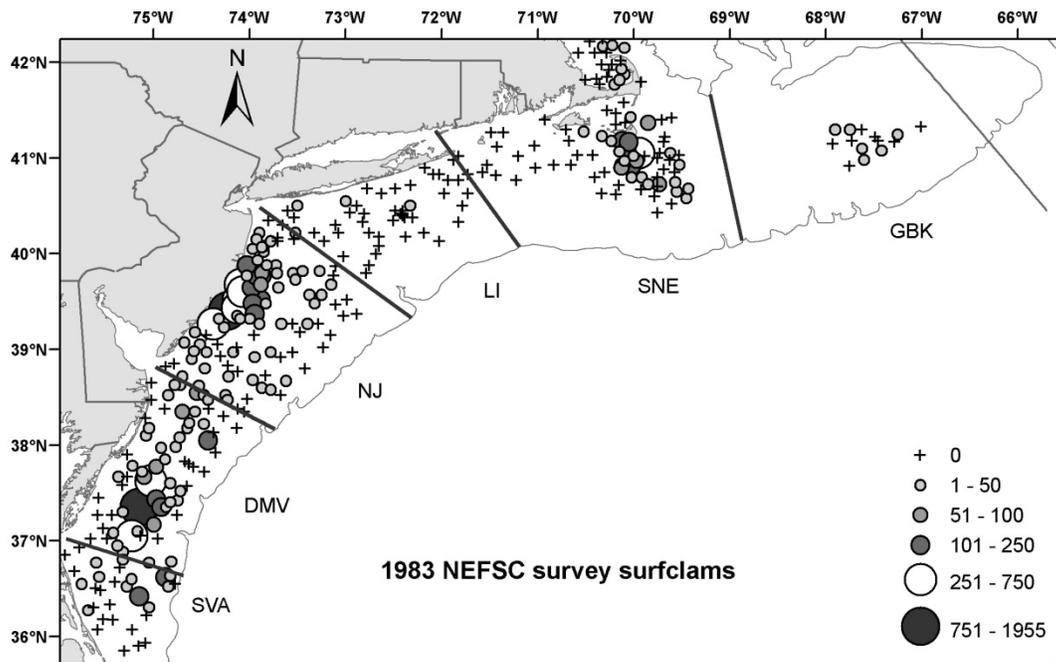
Surfclam catch by ten-minute square

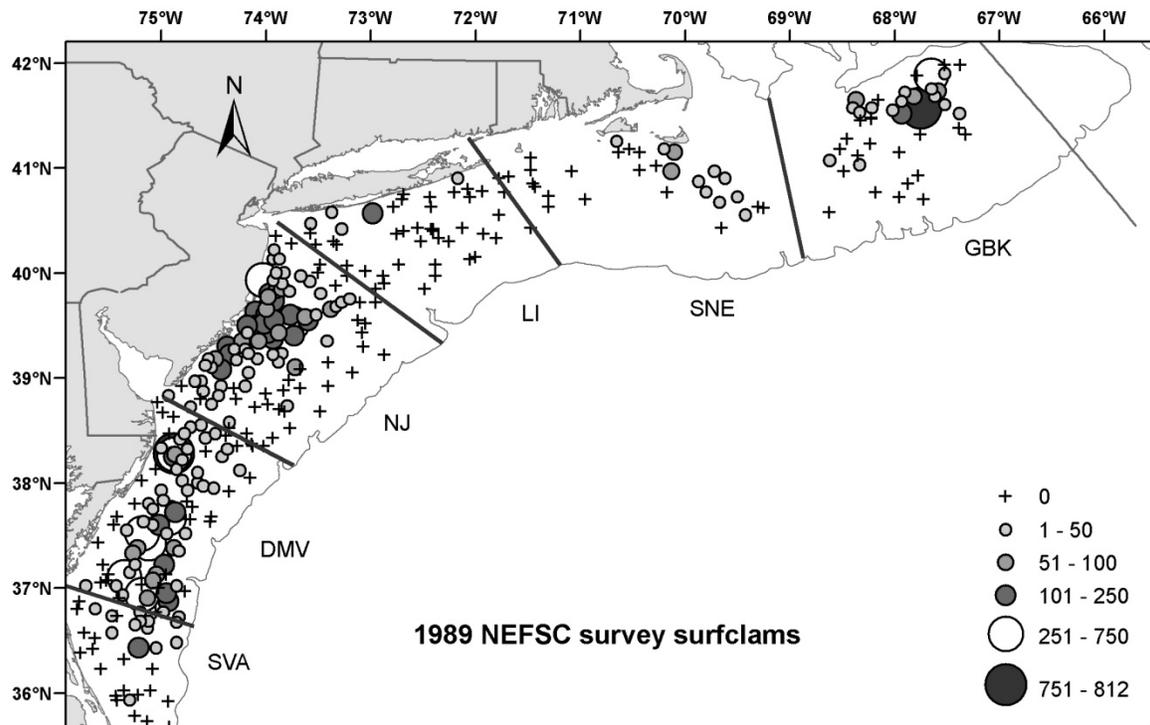
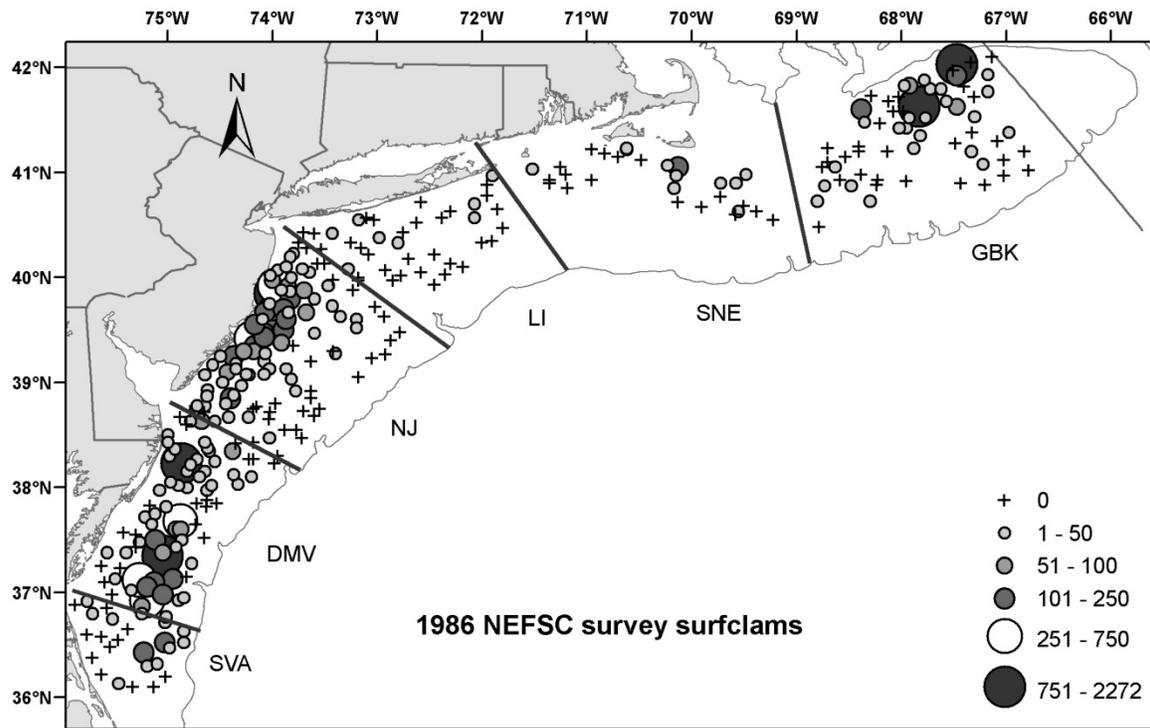


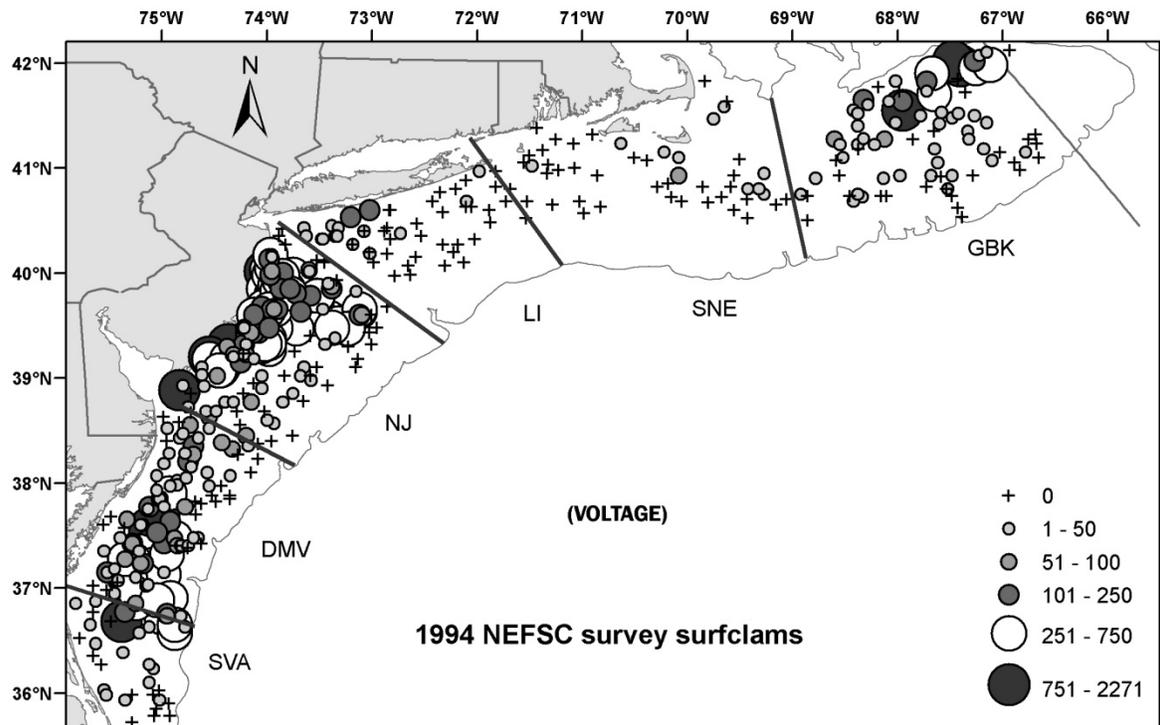
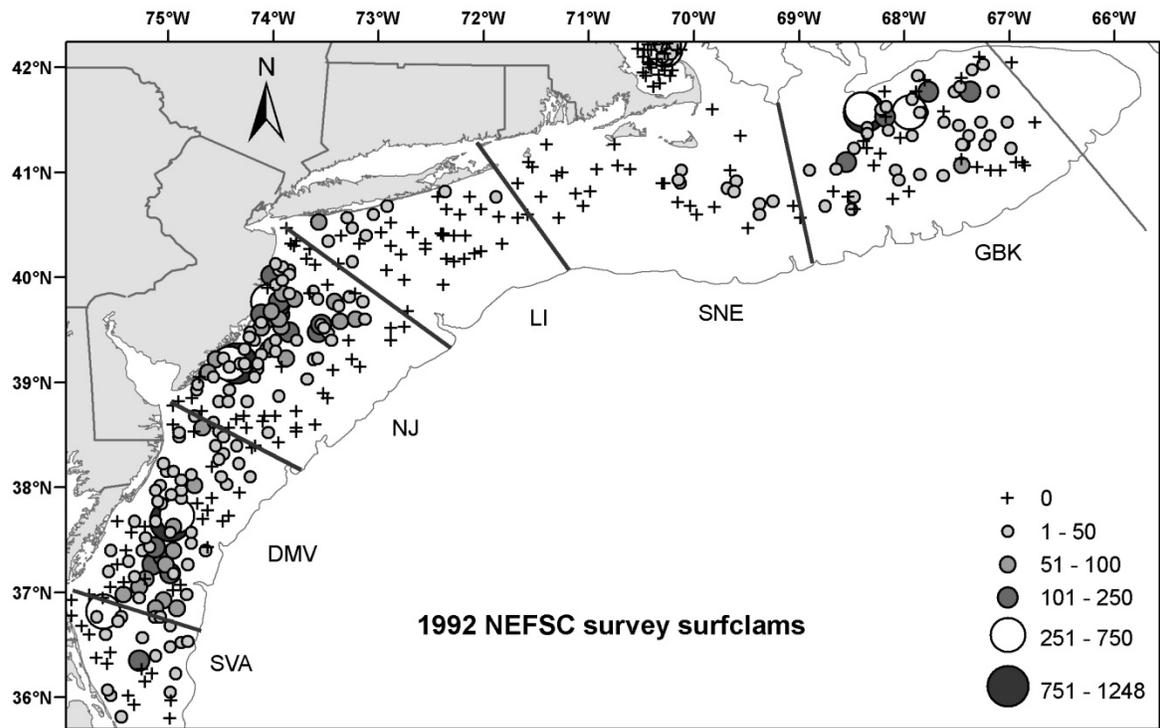
Appendix A3: Maps of NEFSC clam surveys

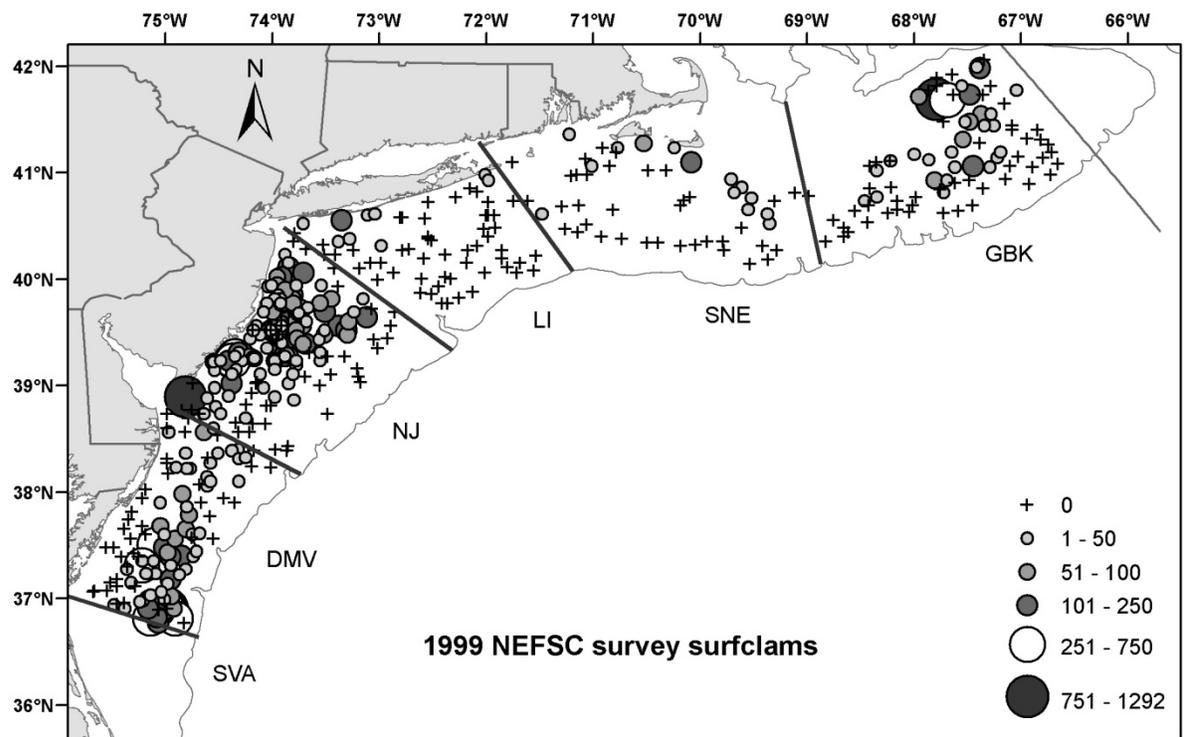
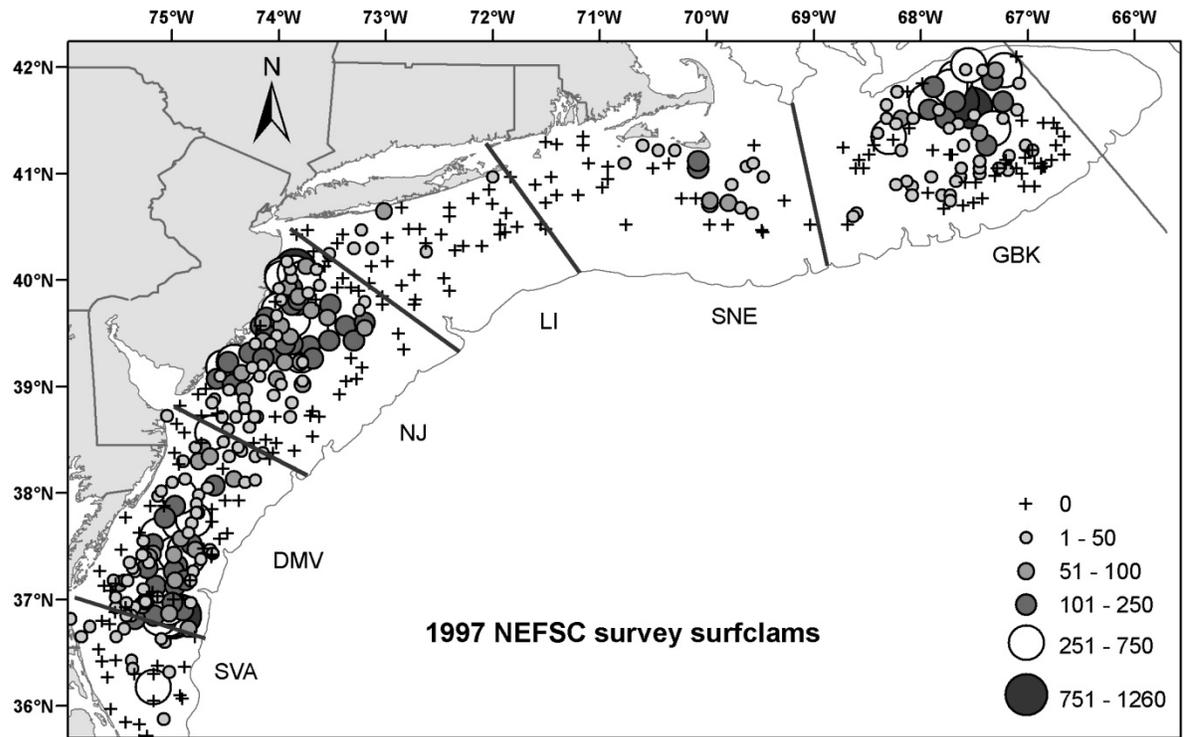
(Following pages) Maps of NEFSC clam survey surfclam catches since 1980. Symbols represent number per tow of clams of all sizes. The maximum number of clams caught in a tow is the highest number in the legend.

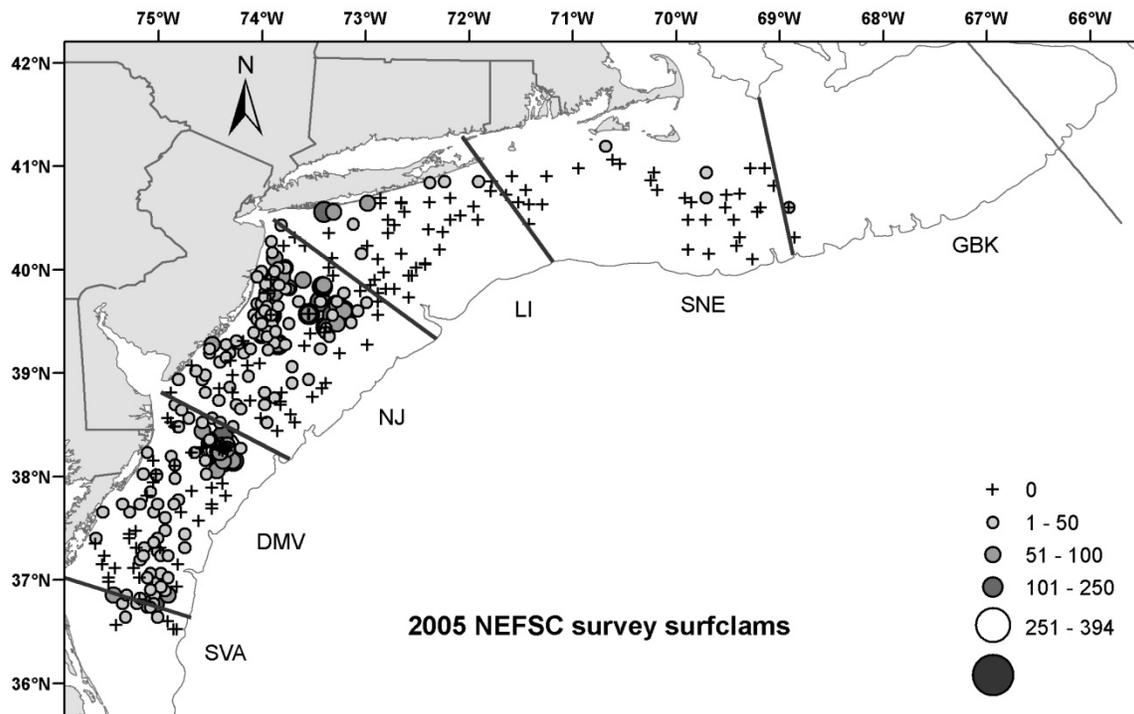
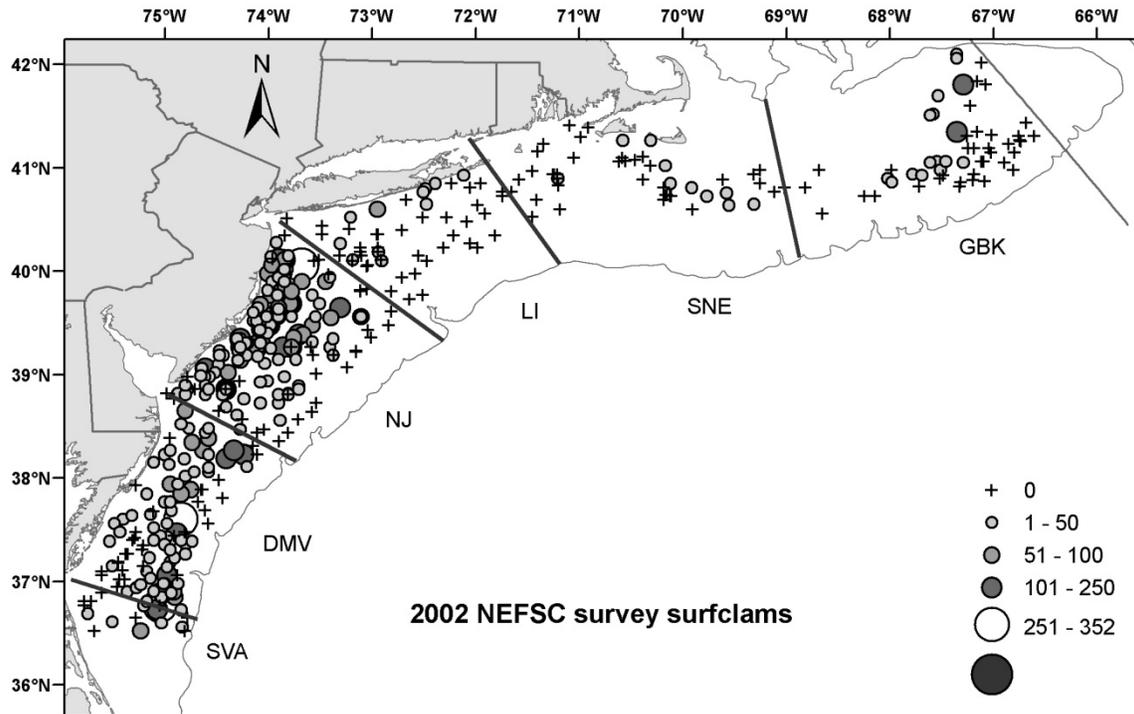


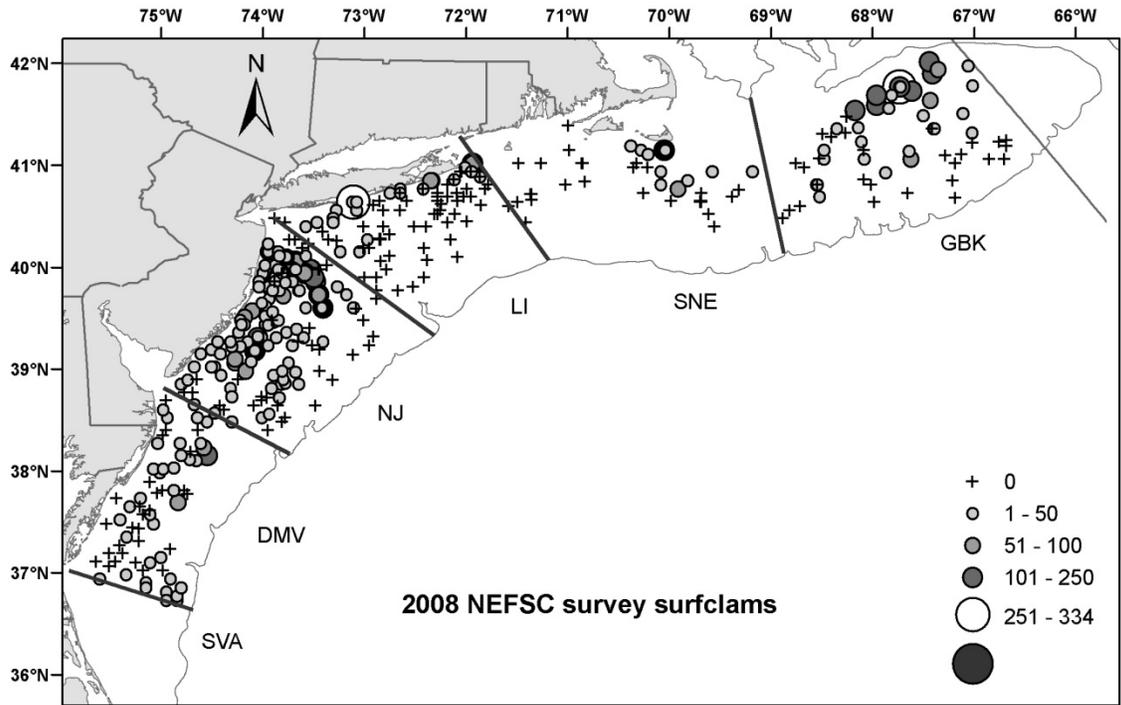


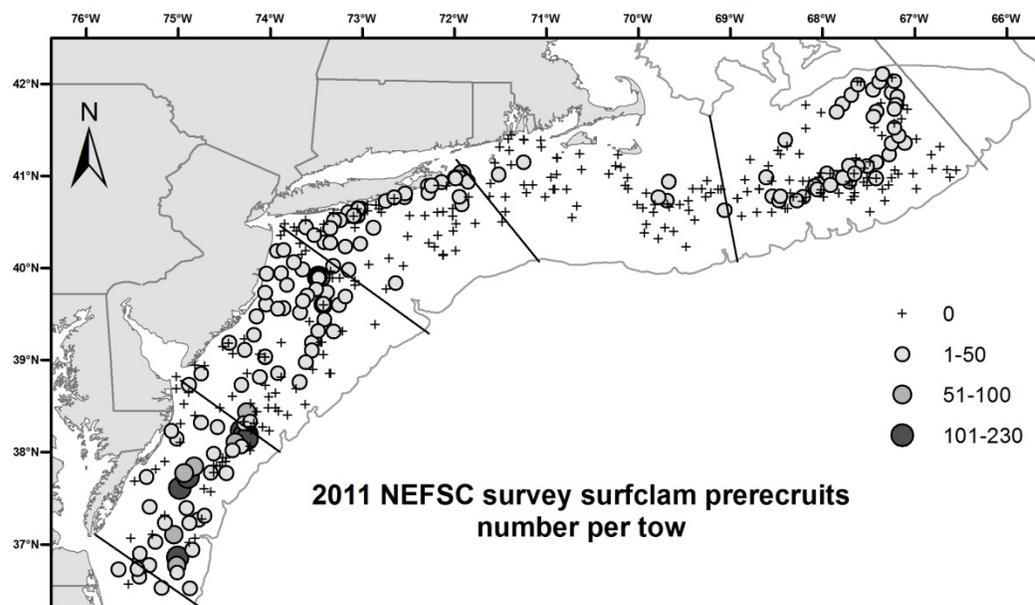
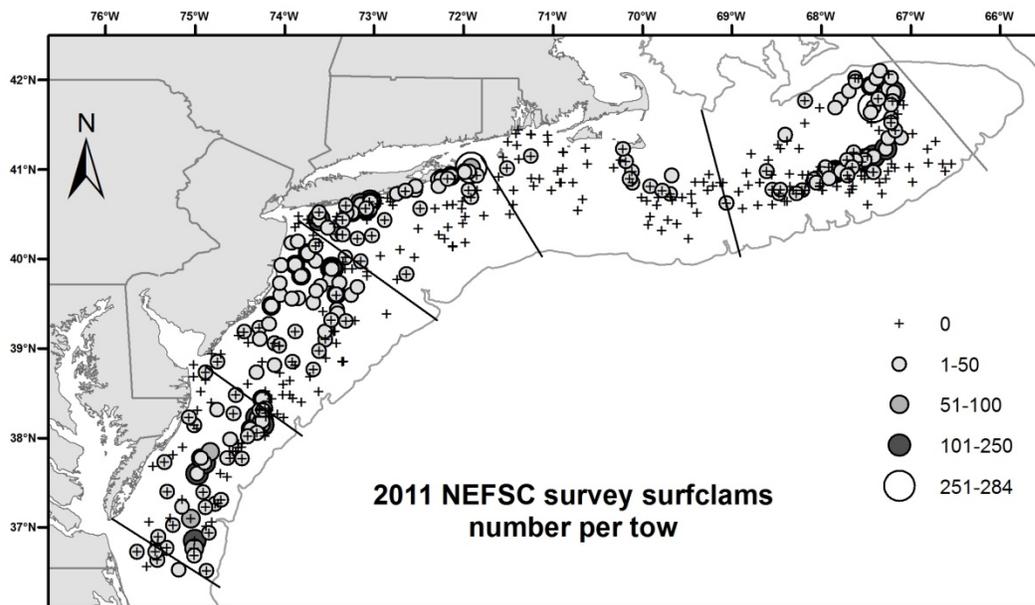












Appendix A4: KLAMZ methods

KLAMZ Assessment Model – Technical Documentation

The KLAMZ assessment model is based on the Deriso-Schnute delay-difference equation (Deriso 1980; Schnute 1985; Quinn and Deriso 1999). The delay-difference equation is a relatively simple and implicitly age structured approach to counting fish in either numerical or biomass units. It gives the same results as explicitly age-structured models (e.g. Leslie matrix model) if fishery selectivity is “knife-edged”, if somatic growth follows the von Bertalanffy equation, and if natural mortality is the same for all age groups in each year. Knife-edge selectivity means that all individuals alive in the model during the same year experience the same fishing mortality rate.⁵ Natural and fishing mortality rates, growth parameters and recruitment may change from year to year, but delay-difference calculations assume that all individuals share the same mortality and growth parameters within each year. The KLAMZ model includes simple numerical models (e.g. Conser 1995) as special cases because growth can be turned off so that all calculations are in numerical units (see below).

As in many other simple models, the delay difference equation explicitly distinguishes between two age groups. In KLAMZ, the two age groups are called “new” recruits (R_t in biomass or numerical units at the beginning of year t) and “old” recruits (S_t) that together comprise the whole stock (B_t). New recruits are individuals that recruited at the beginning of the current year (at nominal age k).⁶ Old recruits are all older individuals in the stock (nominal ages $k+1$ and older, survivors from the previous year). As described above, KLAMZ assumes that new and old recruits are fully vulnerable to the fishery. The most important differences between the delay-difference and other simple models (e.g. Prager 1994; Conser 1995; Jacobson et al. 1994) are that von Bertalanffy growth is used to calculate biomass dynamics and that the delay-difference model captures transient age structure effects due to variation in recruitment, growth and mortality exactly. Transient effects on population dynamics are captured exactly because, as described above, the delay-difference equation is algebraically equivalent to an explicitly age-structured model with von Bertalanffy growth.

The KLAMZ model incorporates a few extensions to Schnute’s (1985) revision of Deriso’s (1980) original delay difference model. Most of the extensions facilitate tuning to a wider variety of data that anticipated in Schnute (1985). The KLAMZ model is programmed in both Excel and in C++ using AD Model Builder⁷ libraries. The AD Model Builder version is faster, more reliable and probably better for producing “official” stock assessment results. The Excel version is slower and implements fewer features, but the Excel version remains useful in developing prototype assessment models, teaching and for checking calculations.

The most significant disadvantage in using the KLAMZ model and other delay-difference approaches, beyond the assumption of knife-edge selectivity, is that age and length composition data are not used in tuning. However, one can argue that age composition data are used indirectly to the extent they are used to estimate growth parameters or if survey survival ratios (e.g. based on the Heinke method) are used in tuning (see below).

⁵ In applications, assumptions about knife-edge selectivity can be relaxed by assuming the model tracks “fishable”, rather than total, biomass (NEFSC 2000a; 2000b). An analogous approach assigns pseudo-ages based on recruitment to the fishery so that new recruits in the model are all pseudo-age k . The synthetic cohort of fish pseudo-age k may consist of more than one biological cohort. The first pseudo-age (k) can be the predicted age at first, 50% or full recruitment based a von Bertalanffy curve and size composition data (Butler et al. 2002). The “incomplete recruitment” approach (Deriso 1980) calculates recruitment to the model in each year R_t as the weighted sum of contributions from two or more biological cohorts (year-classes) from spawning during successive years (i.e.

$$R_t = \sum_{a=1}^k r_a \Pi_{t-a}$$

where k is the age at full recruitment to the fishery, r_a is the contribution of fish age $k-a$ to the fishable stock, and Π_{t-a} is the number or biomass of fish age $k-a$ during year t).

⁶ In some applications, and more generally, new recruits might be defined as individuals recruiting at the beginning or at any time during the current time step (e.g. NEFSC 1996). ⁶

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Population dynamics

The assumed birth date and first day of the year are assumed the same in derivation of the delay-difference equation. It is therefore natural (but not strictly necessary) to tabulate catch and other data using annual accounting periods that start on the assumed biological birthday of cohorts.

Biomass dynamics

As implemented in the KLAMZ model, Schnute's (1985) delay-difference equation is:

$$B_{t+1} = (1 + \rho) \tau_t B_t - \rho \tau_t \tau_{t-1} B_{t-1} + R_{t+1} - \rho \tau_t J_t R_t$$

where B_t is total biomass of individuals at the beginning of year t ; ρ is Ford's growth coefficient (see below); $\tau_t = \exp(-Z_t) = \exp[-(F_t + M_t)]$ is the fraction of the stock that survived in year t , Z_t , F_t , and M_t are instantaneous rates for total, fishing and natural mortality; and R_t is the biomass of new recruits (at age k) at the beginning of the year. The natural mortality rate M_t may vary over time. Instantaneous mortality rates in KLAMZ model calculations are biomass-weighted averages if von Bertalanffy growth is turned on in the model. However, biomass-weighted mortality estimates in KLAMZ are the same as rates for numerical estimates under the assumption of knife-edge selectivity because all individuals are fully recruited. The growth parameter $J_t = w_{t-1,k-1} / w_{t,k}$ is the ratio of mean weight one year before recruitment (age $k-1$ in year $t-1$) and mean weight at recruitment (age k in year t).

It is not necessary to specify body weights at and prior to recruitment in the KLAMZ model (parameters v_{t-1} and V_t in Schnute 1985) because the ratio J_t and recruitment biomass contain the same information. Schnute's (1985) original delay difference equation is:

$$B_{t+1} = (1 + \rho) \tau_t B_t - \rho \tau_t \tau_{t-1} B_{t-1} + w_{t+1,k} N_{t+1} - \rho \tau_t w_{t-1,k-1} N_t$$

To derive the equation used in KLAMZ, substitute recruitment biomass R_{t+1} for the product $w_{t+1,k} N_{t+1,k}$ and adjusted recruitment biomass $J_t R_t = (w_{t-1,k-1} / w_{t,k}) w_{t,k} N_{t,k} = w_{t-1,k-1} N_t$ in the last term on the right hand side. The advantage in using the alternate parameterization for biomass dynamic calculations in KLAMZ is that recruitment is estimated directly in units of biomass and the number of growth parameters is reduced. The disadvantage is that numbers of recruits are not estimated directly by the model. When required, numerical recruitments must be calculated externally as the ratio of estimated recruitment biomass and the average body weight for new recruits.

Numerical population dynamics

Growth can be turned on off so that abundance, rather than biomass, is tracked in the KLAMZ model. Set $J_t=1$ and $\rho=0$ in the delay difference equation, and use N_t (for numbers) in place of B_t to get:

$$N_{t+1} = \tau_t N_t + R_{t+1}$$

Mathematically, the assumption $J_t=1$ means that no growth occurs the assumption $\rho=0$ means that the von Bertalanffy K parameter is infinitely large (Schnute 1985). All tuning and population dynamics calculations in KLAMZ for biomass dynamics are also valid for numerical dynamics.

Growth

As described in Schnute (1985), biomass calculations in the KLAMZ model are based on Schnute and Fournier's (1980) re-parameterization of the von Bertalanffy growth model:

$$w_a = w_{k-1} + (w_k - w_{k-1}) (1 + \rho^{1+a-k}) / (1 - \rho)$$

where $w_k = V$ and $w_{k-1} = v$. Schnute and Fournier's (1980) growth model is the same as the traditional von Bertalanffy growth model $\{W_a = W_{max} [1 - \exp(-K(a-t_{zero}))]$ where W_{max} , K and t_{zero} are parameters}. The two growth models are the same because $W_{max} = (w_k - \rho w_{k-1}) / (1 - \rho)$, $K = -\ln(\rho)$ and $t_{zero} = \ln[(w_k - w_{k-1}) / (w_k - \rho w_{k-1})] / \ln(\rho)$.

In the KLAMZ model, the growth parameters J_t can vary with time but ρ is constant. Use of time-variable J_t values with ρ is constant is the same as assuming that the von Bertalanffy parameters W_{max} and t_{zero} change over time. Many growth patterns can be mimicked by changing W_{max} and t_{zero} (Overholtz et al., 2003). K is a parameter

in the C++ version and, in principal, estimable. However, in most cases it is necessary to use external estimates of growth parameters as constants in KLAMZ.

Instantaneous growth rates

Instantaneous growth rate (IGR) calculations in the KLAMZ model are an extension to the original Deriso-Schnute delay difference model. IGRs are used extensively in KLAMZ for calculating catch biomass and projecting stock biomass forward to the time at which surveys occur. The IGR for new recruits depends only on growth parameters:

$$G_t^{New} = \ln\left(\frac{W_{k+1,t+1}}{W_{k,t}}\right) = \ln(1 + \rho - \rho J_t)$$

IGR for old recruits is a biomass-weighted average that depends on the current age structure and growth parameters. It can be calculated easily by projecting biomass of old recruits $S_t = B_t - R_t$ (escapement) forward one year with no mortality:

$$S_t^* = (1 + \rho)S_t - \rho\tau_{t-1}B_{t-1}$$

where the asterisk (*) means just prior to the start of the subsequent year $t+1$. By definition, the IGR for old recruits in year t is $G_t^{Old} = \ln(S_t^*/S_t)$. Dividing by S_t gives:

$$G_t^{Old} = \ln\left[(1 + \rho) - \rho\tau_{t-1}\frac{B_{t-1}}{S_t}\right]$$

IGR for the entire stock is the biomass weighted average of the IGR values for new and old recruits:

$$G_t = \frac{R_t G_t^{New} + S_t G_t^{Old}}{B_t}$$

All IGR values are zero if growth is turned off.

Recruitment

In the Excel version of the KLAMZ model, annual recruitments are calculated $R_t = e^{\Omega_t}$ where Ω_t is a log transformed annual recruitment parameter, which is estimated in the model. In the C++ version, recruitments are calculated based on two log geometric mean recruitment parameters (μ , ι_t), and a set of annual log scale deviation parameters (ω_t):

$$\Omega_t = \mu + \iota_t + \omega_t$$

The parameter ι_t is an offset for a step function that may be zero for all years or zero for years up to a user-specified “change year” and any value (usually estimated) afterward. The user must specify the change year, which cannot be estimated. The change year might be chosen based on auxiliary information outside the model, preliminary model fits or by carrying out a set of runs using sequential change year values and to choosing the change year that provides the best fit to the data.

The deviations ω_t are constrained to average zero.⁸ With the constraint, for example, estimation of μ and the set of ω_t values ($1+n$ years parameters) is equivalent to estimation of the smaller set (n years) of Ω_t values.

Recruitment as a rate

Recruitment is assumed in the KLAMZ model to occur at the beginning of the year. However, it is often useful to calculate recruitment biomass as an instantaneous rate for comparison to instantaneous rates for natural mortality, fishing mortality and growth. If recruitment were a continuous process, then the instantaneous rate for year t could

⁸ The constraint is implemented by adding $L = \lambda \bar{\omega}^2$ (where $\bar{\omega}$ is the average deviation) to the objective function, generally with a high weighting factor ($\lambda = 1000$) so that the constraint is binding.

be calculated:

$$r_t = \ln\left(\frac{B_{t+1}}{B_t}\right) + M_t + F_t - G_t$$

The recruitment rate can not be calculated for the last year in the model because S_t is not available. The KLAMZ model calculates recruitment rates for all other years automatically.

Natural mortality

Natural mortality rates (M_t) are assumed constant in the Excel version of the KLAMZ model. In the C++ version, natural mortality rates may be estimated as a constant value or as a set of values that vary with time. In the model:

$$M_t = me^{\varpi_t}$$

where $m = \exp(\pi)$ is the geometric mean natural mortality rate, π is a model parameter that may be estimated (in principal but not in practical terms), and ϖ_t is the log scale year-specific deviation. Deviations may be zero (turned off) so that M_t is constant, may vary in a random fashion due to autocorrelated or independent process errors, or may be based on a covariate.⁹ Model scenarios with zero recruitment may be initializing the parameter π to a small value (e.g. 10^{-16}) and not estimating it.

Random natural mortality process errors are effects due to predation, disease, parasitism, ocean conditions or other factors that may vary over time but are not included in the model. Calculations are basically the same as for survey process errors (see below).

Natural mortality rate covariate calculations are similar to survey covariate calculations (see below) except that the user should standardize covariates to average zero over the time period included in the model:

$$\kappa_t = K_t - \bar{K}$$

where κ_t is the standardized covariate, K_t is the original value, and \bar{K} is the mean of the original covariate for the years in the model. Standardization to mean zero is important because otherwise m is not the geometric mean natural mortality rate (the convention is important in some calculations, see text).

Log scale deviations that represent variability around the geometric mean are calculated:

$$\varpi_t = \sum_{j=1}^n p_j \kappa_t$$

where n is the number of covariates and p_j is the parameter for covariate j . These conventions mean that the units for the covariate parameter p_j are 1/units of the original covariate, the parameter p_j measures the log scale effect of changing the covariate by one unit, and the parameter m is the log scale geometric mean.

Fishing mortality and catch

Fishing mortality rates (F_t) are calculated so that predicted and observed catch data (landings plus estimated discards in units of weight) “agree” to the extent specified by the user. It is not necessary, however, to assume that catches are measured accurately (see “Observed and predicted catch”).

Fishing mortality rate calculations in Schnute (1985) are exact but relating fishing mortality to catch in weight is complicated by continuous somatic growth throughout the year as fishing occurs. The KLAMZ model uses a generalized catch equation that incorporates continuous growth through the fishing season. By the definition of instantaneous rates, the catch equation expresses catch as the product:

⁹ Another approach to using time dependent natural mortality rates is to treat estimates of predator consumption as discarded catch (see “Predator consumption as discard data”). In addition, estimates of predator abundance can be used in fishing effort calculations (see “Predator data as fishing effort”).

$$\hat{C}_t = F_t \bar{B}_t$$

where \hat{C}_t is predicted catch weight (landings plus discard) and \bar{B}_t is average biomass.

Following Chapman (1971) and Zhang and Sullivan (1988), let $X_t = G_t - F_t - M_t$ be the net instantaneous rate of change for biomass.¹⁰ If the rates for growth and mortality are equal, then $X_t = 0$, $\bar{B}_t = B_t$ and $C_t = F_t B_t$. If the growth rate G_t exceeds the combined rates of natural and fishing mortality ($F_t + M_t$), then $X_t > 0$. If mortality exceeds growth, then $X_t < 0$. In either case, with $X_t \neq 0$, average biomass is computed:

$$\bar{B}_t \approx -\frac{(1 - e^{X_t})B_t}{X_t}$$

When $X_t \neq 0$, the expression for \bar{B}_t is an approximation because G_t approximates the rate of change in mean body weight due to von Bertalanffy growth. However, the approximation is reasonably accurate and preferable to calculating catch biomass in the delay-difference model with the traditional catch equation that ignores growth during the fishing season.¹¹ Average biomass can be calculated for new recruits, old recruits or for the whole stock by using either G_t^{New} , G_t^{Old} or G_t .

In the KLAMZ model, the modified catch equation may be solved analytically for F_t given C_t , B_t , G_t and M_t (see the “Calculating F_t ” section below). Alternatively, fishing mortality rates can be calculated using a log geometric mean parameter (Φ) and a set of annual log scale deviation parameters (ψ_t):

$$F_t = e^{\Phi + \psi_t}$$

where the deviations ψ_t are constrained to average zero. When the catch equation is solved analytically, catches must be assumed known without error but the analytical option is useful when catch is zero or very near zero, or the range of fishing mortality rates is so large (e.g. minimum $F=0.000001$ to maximum $F=3$) that numerical problems occur with the alternative approach. The analytical approach is also useful if the user wants to reduce the number of parameters estimated by nonlinear optimization. In any case, the two methods should give the same results for catches known without error.

Surplus production

Annual surplus production is calculated “exactly” by projecting biomass at the beginning of each year forward with no fishing mortality:

$$B_t^* = (1 + \rho) e^{-M} B_{t-1} - \rho e^{-2M} B_{t-2} - \rho e^{-M} J_{t-1} R_{t-1} + R_t$$

By definition, surplus production $P_t = B_t^* - B_t$ (Jacobson et al. 2002).

Per recruit modeling

Per recruit model calculations in the Excel version of the KLAMZ simulate the life of a hypothetical cohort of arbitrary size (e.g. $R=1000$) starting at age k with constant M_t , F (survival) and growth (ρ and average $J(\bar{J})$) in a population initially at zero biomass. In the first year:

$$B_1 = R$$

In the second year:

$$B_2 = (1 + \rho) \tau B_1 - \rho \tau \bar{J} R_1$$

In the third and subsequent years:

¹⁰ By convention, the instantaneous rates G_t , F_t and M_t are always expressed as numbers ≥ 0 .

¹¹ The traditional catch equation $C_t = F_t (1 - e^{-Z_t}) B_t / Z_t$ where $Z_t = F_t + M_t$ underestimates catch biomass for a given level of fishing mortality F_t and overestimates F_t for a given level of catch biomass. The errors can be substantial for fast growing fish, particularly if recent recruitments were strong.

$$B_{t+1} = (1 + \rho) \tau B_t - \rho \tau^2 B_{t-1}$$

This iterative calculation is carried out until the sum of lifetime cohort biomass from one iteration to the next changes by less than a small amount (0.0001). Total lifetime biomass, spawning biomass and yield in weight are calculated by summing biomass, spawning biomass and yield over the lifetime of the cohort. Lifetime biomass, spawning biomass and yield per recruit are calculated by dividing totals by initial recruitment (R).

Status determination variables

The user may specify a range of years (e.g. the last three years) to use in calculating recent average fishing mortality $\bar{F}_{Re\ cent}$ and biomass $\bar{B}_{Re\ cent}$ levels. These status determination variables are used in calculation of status ratios such as $\bar{F}_{Re\ cent} / F_{MSY}$ and $\bar{B}_{Re\ cent} / B_{MSY}$.

Goodness of Fit and Parameter Estimation

Parameters estimated in the KLAMZ model are chosen to minimize an objective function based on a sum of weighted negative log likelihood (NLL) components:

$$\Xi = \sum_{v=1}^{N_{\Xi}} \lambda_v L_v$$

where N_{Ξ} is the number of NLL components (L_v) and the λ_v are emphasis factors used as weights. The objective function Ξ may be viewed as a NLL or a negative log posterior (NLP) distribution, depending on the nature of the individual L_v components and modeling approach. Except during sensitivity analyses, weighting factors for objective function components (λ_v) are usually set to one. An arbitrarily large weighting factor (e.g. $\lambda_v = 1000$) is used for “hard” constraints that must be satisfied in the model. Arbitrarily small weighting factors (e.g. $\lambda_v = 0.0001$) can be used for “soft” model-based constraints. For example, an internally estimated spawner-recruit curve or surplus production curve might be estimated with a small weighting factor to summarize stock-recruit or surplus production results with minimal influence on biomass, fishing mortality and other estimates from the model. Use of a small weighting factor for an internally estimated surplus production or stock-recruit curve is equivalent to fitting a curve to model estimates of biomass and recruitment or surplus production in the output file, after the model is fit (Jacobson et al. 2002).

Likelihood component weights vs. observation-specific weights

Likelihood component weights (λ_v) apply to entire NLL components. Entire components are often computed as the sum of a number of individual NLL terms. The NLL for an entire survey, for example, is composed of NLL terms for each of the annual survey observations. In KLAMZ, observation-specific (for data) or instance-specific (for constraints or prior information) weights (usually w_j for observation or instance j) can be specified as well. Observation-specific weights for a survey, for example, might be used to increase or decrease the importance of one or more observations in calculating goodness of fit.

NLL kernels

NLL components in KLAMZ are generally programmed as “concentrated likelihoods” to avoid calculation of values that do not affect derivatives of the objective function.¹² For $x \sim N(\mu, \sigma^2)$, the complete NLL for one observation is:

¹² Unfortunately, concentrated likelihood calculations cannot be used with MCMC and other Bayesian approaches to characterizing posterior distributions. Therefore, in the near future, concentrated NLL calculations will be replaced by calculations for the entire NLL. At present, MCMC calculations in KLAMZ are not useful.

$$L = \ln(\sigma) + \ln(\sqrt{2\pi}) + 0.5\left(\frac{x-u}{\sigma}\right)^2$$

The constant $\ln(\sqrt{2\pi})$ can always be omitted because it does not affect derivatives. If the standard deviation is known or assumed known, then $\ln(\sigma)$ can be omitted as well because it is a constant that does not affect derivatives. In such cases, the concentrated negative log likelihood is:

$$L = 0.5\left(\frac{x-\mu}{\sigma}\right)^2$$

If there are N observations with possible different variances (known or assumed known) and possibly different expected values:

$$L = 0.5\sum_{i=1}^N\left(\frac{x_i-\mu_i}{\sigma_i}\right)^2$$

If the standard deviation for a normally distributed quantity is not known and is (in effect) estimated by the model, then one of two equivalent calculations is used. Both approaches assume that all observations have the same variance and standard deviation. The first approach is used when all observations have the same weight in the likelihood:

$$L = 0.5N\ln\left[\sum_{i=1}^N(x_i-u)^2\right]$$

where N is the number of observations. The second approach is equivalent but used when the weights for each observation (w_i) may differ:

$$L = \sum_{i=1}^N w_i \left[\ln(\sigma) + 0.5\left(\frac{x_i-u}{\sigma}\right)^2 \right]$$

In the latter case, the maximum likelihood estimator:

$$\hat{\sigma} = \sqrt{\frac{\sum_{i=1}^N(x_i-\hat{x})^2}{N}}$$

(where \hat{x} is the average or predicted value from the model) is used for σ . The maximum likelihood estimator is biased by $N/(N-d_f)$ where d_f is degrees of freedom for the model. The bias may be significant for small sample sizes but d_f is usually unknown.

Landings, discards, catch

Discards are from external estimates (d_t) supplied by the user. If $d_t \geq 0$, then the data are used as the ratio of discard to landed catch so that:

$$D_t = L_t \Delta_t$$

where $\Delta_t = D_t/L_t$ is the discard ratio. If $d_t < 0$ then the data are treated as discard in units of weight:

$$D_t = abs(d_t).$$

In either case, total catch is the sum of discards and landed catch ($C_t = L_t + D_t$). It is possible to use discards in weight $d_t < 0$ for some years and discard as proportions $d_t > 0$ for other years in the same model run. If catches are estimated (see below) so that the estimated catch \hat{C}_t does not necessarily equal observed landings plus discard, then estimated landings are computed:

$$\hat{L}_t = \frac{\hat{C}_t}{1 + \Delta_t}$$

and estimated discards are:

$$\hat{D}_t = \Delta_t \hat{L}_t.$$

Calculating F_t

As described above, fishing mortality rates may be estimated based on the parameters Φ and ψ_t to satisfy a NLL for observed and predicted catches:

$$L = 0.5 \sum_{t=0}^N w_t \left(\frac{\hat{C}_t - C_t}{\kappa_t} \right)^2$$

where the standard error $\kappa_t = CV_{catch} \hat{C}_t$ with CV_{catch} and weights are w_t supplied by the user. The weights can be used, for example, if catch data in some years are less precise than in others. Using observation specific weights, any or every catch in the time series can potentially be estimated.

The other approach to calculating F_t values is by solving the generalized catch equation (see above) iteratively. Subtracting predicted catch from the generalized catch equation gives:

$$g(F_t) = C_t + \frac{F_t(1 - e^{X_t})}{X_t} B_t = 0$$

where $X_t = G_t - M_t - F_t$. If $X_t = 0$, then $\bar{B}_t = B_t$ and $F_t = C_t / B_t$.

If $X_t \neq 0$, then the Newton-Raphson algorithm is used to solve for F_t (Kennedy and Gentle 1980). At each iteration of the algorithm, the current estimate F_t^i is updated using:

$$F_t^{i+1} = F_t^i - \frac{g(F_t^i)}{g'(F_t^i)}$$

where $g'(F_t^i)$ is the derivative F_t^i . Omitting subscripts, the derivative is:

$$g'(F) = - \frac{B e^{-F} [(e^F - e^\gamma) \gamma + e^\gamma F \gamma - e^\gamma F^2]}{X^2}$$

where $\gamma = G - M_t$. Iterations continue until $g(F_t^i)$ and $abs[g(F_t^{i+1}) - g(F_t^i)]$ are both less than a small number (e.g. ≤ 0.00001).

Initial values are important in algorithms that solve the catch equation numerically (Sims 1982). If $M_t + F_t > G_t$ so that $X_t < 0$, then the initial value F_t^0 is calculated according to Sims (1982). If $M_t + F_t < G_t$ so that $X_t > 0$, then initial values are calculated based on a generalized version of Pope's cohort analysis (Zhang and Sullivan 1988):

$$F_t^0 = \gamma_t - \ln \left[\frac{(B_t e^{0.5\gamma_t} - C_t) e^{0.5\gamma_t}}{B_t} \right]$$

F for landings versus F for discards

The total fishing mortality rate for each year can be partitioned into a component due to landed catch

$${}^L F_t = \frac{D_t}{C_t} F_t, \text{ and a component due to discard } {}^D F_t = \frac{L_t}{C_t} F_t.$$

Predator consumption as discard data

In modeling population dynamics of prey species, estimates of predator consumption can be treated like

discard in the KLAMZ model as a means for introducing time dependent natural mortality. Consider a hypothetical example with consumption data (mt y^{-1}) for three important predators. If the aggregate consumption data are included in the model as “discards”, then the fishing mortality rate for discards dF_t (see above) would be an estimate of the component of natural mortality due to the three predators. In using this approach, the average level of natural mortality m would normally be reduced (e.g. so that $m_{new} + {}^d\bar{F} = m_{old}$) or estimated to account for the portion of natural mortality attributed to bycatch.

Surplus production calculations are harder to interpret if predator consumption is treated as discard data because surplus production calculations assume that $F_t=0$ (see above) and because surplus production is defined as the change in biomass from one year to the next in the absence of fishing (i.e. no landings or bycatch). However, it may be useful to compare surplus production at a given level of biomass from runs with and without consumption data as a means of estimating maximum changes in potential fishery yield if the selected predators were eliminated (assuming no change in disease, growth rates, predation by other predators, etc.).

Effort calculations

Fishing mortality rates can be tuned to fishing effort data for the “landed” catch (i.e. excluding discards). Years with non-zero fishing effort used in the model must also have landings greater than zero. Assuming that effort data are lognormally distributed, the NLL for fishing effort is:

$$NLL = 0.5 \sum_{y=1}^{n_{eff}} w_y \left[\frac{\ln(E_y / \hat{E}_y)}{\sigma} \right]^2$$

where w_y is an observation-specific weight, n_{eff} is the number of active effort observations (i.e. with $w_y > 0$), E_y and \hat{E}_y are observed and predicted fishing effort data, and the log scale variance σ is a constant calculated from a user-specified CV.

Predicted fishing effort data are calculated:

$$\hat{E}_y = \zeta F_y^{\vartheta}$$

where $\zeta = e^u$, $\vartheta = e^b$, and u and b are parameters estimated by the model. If the parameter b is not estimated, then $\vartheta=1$ so that the relationship between fishing effort and fishing mortality is linear. If the parameter b is estimated, then $\vartheta \neq 1$ and the relationship is a power function.

Predator data as fishing effort

As described under “Predator consumption as discard data”, predator consumption data can be treated as discard. If predator abundance data are available as well, and assuming that mortality due predators is a linear function of the predator-prey ratio, then both types of data may be used together to estimate natural mortality. The trick is to: 1) enter the predator abundance data as fishing effort; 2) enter the actual fishery landings as “discard”; 3) enter predator consumption estimates of the prey species as “landings” so that the fishing effort data refer to the predator consumption data; 4) use an option in the model to calculate the predator-prey ratio for use in place of the original predator abundance “fishing effort” data; and 5) tune fishing mortality rates for landings (a.k.a. predator consumption) to fishing effort (a.k.a. predator-prey ratio).

Given the predator abundance data κ_y , the model calculates the predator-prey ratio used in place of fishing effort data (E_y) as:

$$E_y = \frac{\kappa_y}{B_y}$$

where B_y is the model’s current estimate of total (a.k.a “prey”) biomass. Subsequent calculations with E_y and the model’s estimates of “fishing mortality” (F_y , really a measure of natural mortality) are exactly as described above for effort data. In using this approach, it is probably advisable to reduce m (the estimate of average mortality in the

model) to account for the proportion of natural mortality due to predators included in the calculation. Based on experience to date, natural mortality due to consumption by the suite of predators can be estimated but only if m is assumed known.

Initial population age structure

In the KLAMZ model, old and new recruit biomass during the first year (R_1 and $S_1=B_1-R_1$) and biomass prior to the first year (B_0) are estimated as log scale parameters. Survival in the year prior to the first year (“year 0”) is $\tau_0 = e^{-F_0-M_1}$ with F_0 chosen to obtain catch C_0 (specified as data) from the estimated biomass B_0 . IGRs during year 0 and year 1 are assumed equal ($G_0=G_1$) in catch calculations.

Biomass in the second year of a series of delay-difference calculations depends on biomass (B_0) and survival (τ_0) in year 0:

$$B_2 = (1 + \rho) \tau_1 B_1 - \rho \tau_1 \tau_0 B_0 + R_2 - \rho \tau_1 J_1 R_1$$

There is, however, there is no direct linkage between B_0 and escapement biomass ($S_1=B_1-R_1$) at the beginning of the first year.

The missing link between B_0 , S_1 and B_1 means that the parameter for B_0 tends to be relatively free and unconstrained by the underlying population dynamics model. In some cases, B_0 can be estimated to give good fit to survey and other data, while implying unreasonable initial age composition and surplus production levels. In other cases, B_0 estimates can be unrealistically high or low implying, for example, unreasonably high or low recruitment in the first year of the model (R_1). Problems arise because many different combinations of values for R_1 , S_1 and B_0 give similar results in terms of goodness of fit. This issue is common in stock assessment models that use forward simulation calculations because initial age composition is difficult to estimate. It may be exacerbated in delay-difference models because age composition data are not used.

The KLAMZ model uses two constraints to help estimate initial population biomass and initial age structure.¹³ The first constraint links IGRs for escapement (G^{Old}) in the first years to a subsequent value. The purpose of the constraint is to ensure consistency in average growth rates (and implicit age structure) during the first few years. For example, if IGRs for the first n_G years are constrained¹⁴, then the NLL for the penalty is:

$$L_G = 0.5 \sum_{t=1}^{n_G} \left[\frac{\ln(G_t^{Old} / G_{n_G+1}^{Old})}{\sigma_G} \right]^2$$

where the standard deviation σ_G is supplied by the user. It is usually possible to use the standard deviation of Q_t^{Old} for later years from a preliminary run to estimate σ_G for the first few years. The constraint on initial IGRs should probably be “soft” and non-binding ($\lambda \approx 1$) because there is substantial natural variation in somatic growth rates due to variation in age composition.

The second constraint links B_0 to S_1 and ensures conservation of mass in population dynamics between years 0 and 1. In other words, the parameter for escapement biomass in year 1 is constrained to match an approximate projection of the biomass in year 0, accounting for growth, and natural and fishing mortality. The constraint is intended to be binding and satisfied exactly (e.g. $\lambda = 1000$) because incompatible values of S_1 and B_0 are biologically impossible. In calculations:

$$S_1^p = B_0 e^{G_1 - F_0 - M_1}$$

where S_1^p is the projected escapement in year 1 and B_0 is the model’s estimate of total biomass in year 0. The instantaneous rates for growth and natural mortality from year 1 (G_1 and M_1) are used in place of G_0 and M_0 because the latter are unavailable. The NLL for the constraint:

¹³ Quinn and Deriso (1999) describe another approach attributed to a manuscript by C. Walters.

¹⁴ Normally, $n_G \leq 2$.

$$L = \left[\ln \left(\frac{S_1^p}{S_1} \right) \right]^2 + (S_1^p - S_1)^2$$

uses a log scale sum of squares and an arithmetic sum of squares. The former is effective when S_1 is small while the latter is effective when S_1 is large. Constants and details in calculation of NLL for the constraint are not important because the constraint is binding (e.g. $\lambda=1000$).

Equilibrium pristine biomass

It may be useful to constrain the biomass estimate for the first year in a model run towards an estimate of equilibrium pristine biomass if, for example, stock dynamics tend to be stable and catch data are available for the first years of the fishery, or as an alternative to the approach described above for initializing the age structure of the simulated population in the model. Equilibrium pristine biomass \tilde{B}_0 is calculated based on the model's estimate of average recruitment and with no fishing mortality (calculations are similar to those described under "Per-recruit modeling" except that average recruitment is assumed in each year).¹⁵ The NLL term for the constraint is:

$$L = \ln \left(\frac{\tilde{B}_0}{B_0} \right)^2$$

Pristine equilibrium biomass is used as a hard constraint with a high emphasis factor (λ) so that the variance and constants normally used in NLL calculations are not important.

Estimating natural mortality

As described above, natural mortality calculations involve a parameter for the geometric mean value (m) and time dependent deviations (ϖ_t , which may or may not be turned on). Constraints on natural mortality process errors and natural mortality covariates can be used to help estimate the time dependent deviations and overall trend. The geometric mean natural mortality rate is usually difficult to estimate and best treated as a known constant. However, in the C++ version of the KLAMZ model, $m=e^\pi$ (where π is an estimable parameter in the model) and estimates of m can be conditioned on the constraint:

$$L = 0.5 \left[\frac{\ln(w/w_{target})}{\sigma_\varpi} \right]^2$$

where w_{target} is a user supplied mean or target value and σ_ϖ is a log scale standard deviation. The standard deviation is calculated from an arithmetic scale CV supplied by the user. Upper and lower bounds for m may be specified as well.

Goodness of fit for trend data

Assuming lognormal errors¹⁶, the NLL used to measure goodness-of-fit to "survey" data that measure trends in abundance or biomass (or survival, see below) is:

¹⁵ Future versions of the KLAMZ model will allow equilibrium initial biomass to be calculated based on other recruitment values and for a user-specified level of F (Butler et al. 2003).

¹⁶ Abundance indices with statistical distributions other than log normal may be used as well, but are not currently programmed in the KLAMZ model. For example, Butler et al. (2003) used abundance indices with binomial distributions in a delay-difference model for cowcod rockfish. The next version of KLAMZ will accommodate presence-absence data with binomial distributions.

$$L = 0.5 \sum_{j=1}^{N_v} \left[\frac{\ln \left(I_{v,j} / \hat{I}_{v,j} \right)}{\sigma_{v,j}} \right]^2$$

where $I_{v,t}$ is an index datum from survey v , hats “ $\hat{}$ ” denote model estimates, $\sigma_{v,j}$ is a log scale standard error (see below), and N_v is the number of observations. There are two approaches to calculating standard errors for log normal abundance index data in KLAMZ and it is possible to use different approaches for different types of abundance index data in the same model (see below).

Standard errors for goodness of fit

In the first approach, all observations for one type of abundance index share the same standard error, which is calculated based on overall goodness of fit. This approach implicitly estimates the standard error based on goodness of fit, along with the rest of the parameters in the model (see “NLL kernels” above).

In the second approach, each observation has a potentially unique standard error that is calculated based on its CV. The second approach calculates log scale standard errors from arithmetic CVs supplied as data by the user (Jacobson et al. 1994):

$$\sigma_{v,t} = \sqrt{\ln(1 + CV_{v,t}^2)}$$

Arithmetic CV’s are usually available for abundance data. It may be convenient to use $CV_{v,t}=1.31$ to get $\sigma_{v,t}=1$.

There are advantages and disadvantages to both approaches. CV’s carry information about the relative precision of abundance index observations. However, CV’s usually overstate the precision of data as a measure of fish abundance¹⁷ and may be misleading in comparing the precision of one sort of data to another as a measure of trends in abundance (e.g. in contrasting standardized LPUE that measure fishing success, but not abundance, precisely with survey data that measure trends in fish abundance directly, but not precisely). Standard errors estimated implicitly are often larger and more realistic, but assume that all observations in the same survey are equally reliable.

Predicted values for abundance indices

Predicted values for abundance indices are calculated:

$$\hat{I}_{v,t} = Q_v A_{v,t}$$

where Q_v is a survey scaling parameter (constant here but see below) that converts units of biomass to units of the abundance index. $A_{v,t}$ is available biomass at the time of the survey.

In the simplest case, available biomass is:

$$A_{v,t} = s_{v,New} R_t e^{-X_t^{New} \Delta_{v,t}} + s_{v,Old} S_t e^{-X_t^{Old} \Delta_{v,t}}$$

where $s_{v,New}$ and $s_{v,Old}$ are survey selectivity parameters for new recruits (R_t) and old recruits (S_t);

$X_t^{New} = G_t^{New} - F_t - M_t$ and $X_t^{Old} = G_t^{Old} - F_t - M_t$; $J_{v,t}$ is the Julian date at the time of the survey, and

$\Delta_{v,t} = J_{v,t} / 365$ is the fraction of the year elapsed at the time of the survey.

¹⁷ The relationship between data and fish populations is affected by factors (process errors) that are not accounted for in CV calculations.

Survey selectivity parameter values ($s_{v,New}$ and $s_{v,Old}$) are specified by the user and must be set between zero and one. For example, a survey for new recruits would have $s_{v,New}=1$ and $s_{v,Old}=0$. A survey that measured abundance of the entire stock would have $s_{v,New}=1$ and $s_{v,Old}=1$.

Terms involving $\bar{A}_{v,t}$ are used to project beginning of year biomass forward to the time of the survey, making adjustments for mortality and somatic growth.¹⁸ As described below, available biomass $A_{v,t}$ is adjusted further for nonlinear surveys, surveys with covariates and surveys with time variable $Q_{v,t}$.

Scaling parameters (Q) for log normal abundance data

Scaling parameters for surveys with lognormal statistical errors were computed using the maximum likelihood estimator:

$$Q_v = e^{\frac{\sum_{i=1}^{N_v} \left[\ln \left(\frac{I_{v,i}}{A_{v,i}} \right) \right]^2 / \sigma_{v,i}^2}{\sum_{j=1}^{N_j} \left(1 / \sigma_{v,j}^2 \right)}}$$

where N_v is the number of observations with individual weights greater than zero. The closed form maximum likelihood estimator gives the same answer as if scaling parameters are estimated as free parameters in the assessment model assuming lognormal survey measurement errors.

Survey covariates

Survey scaling parameters may vary over time based on covariates in the KLAMZ model. The survey scaling parameter that measures the relationship between available biomass and survey data becomes time dependent:

$$\hat{I}_{v,t} = Q_{v,t} A_{v,t}$$

and

$$Q_{v,t} = Q_v e^{\sum_{r=1}^{n_v} d_{r,t} \theta_r}$$

with n_v covariates for the survey and parameters θ_r estimated in the model. Covariate effects and available biomass are multiplied to compute an adjusted available biomass:

$$A'_{v,t} = A_{v,t} e^{\sum_{r=1}^{n_v} d_{r,t} \theta_r}$$

The adjusted available biomass $A'_{v,t}$ is used instead of the original value $A_{v,t}$ in the closed form maximum likelihood estimator described above.

Covariates might include, for example, a dummy variable that represents changes in survey bottom trawl doors or a continuous variable like average temperature data if environmental factors affect distribution and catchability of fish schools. Dummy variables are usually either 0 or 1, depending on whether the effect is present in a particular year. With dummy variables, Q_v is the value of the survey scaling parameter with no intervention ($d_{r,t}=0$).

For ease in interpretation of parameter estimates for continuous covariates (e.g. temperature data), it is useful to center covariate data around the mean:

$$d_{r,t} = d'_{r,t} - \bar{d}'_r$$

¹⁸ It may be important to project biomass forward if an absolute estimate of biomass is available (e.g. from a hydroacoustic or daily egg production survey), if fishing mortality rates are high or if the timing of the survey varies considerably from year to year.

where $d'_{r,t}$ is the original covariate. When covariates are continuous and mean-centered, Q_v is the value of the survey scaling parameter under average conditions ($d_{r,t}=0$) and units for the covariate parameter are easy to interpret (for example, units for the parameter are $1/^\circ\text{C}$ if the covariate is mean centered temperature in $^\circ\text{C}$).

It is possible to use a survey covariate to adjust for differences in relative stock size from year to year due to changes in the timing of a survey. However, this adjustment may be made more precisely by letting the model calculate $\Delta_{v,t}$ as described above, based on the actual timing data for the survey during each year.

Nonlinear abundance indices

With nonlinear abundance indices, and following Methot (1990), the survey scaling parameter is a function of available biomass:

$$Q_{v,t} = Q_v A_{v,t}^\Gamma$$

so that:

$$\hat{I}_{v,t} = (Q_v A_{v,t}^\Gamma) A_{v,t}$$

Substituting $e^\gamma = \Gamma + 1$ gives the equivalent expression:

$$\hat{I}_{v,t} = Q_v A_{v,t}^{e^\gamma}$$

where γ is a parameter estimated by the model and the survey scaling parameter is no longer time dependent. In calculations with nonlinear abundance indices, the adjusted available biomass:

$$A'_{v,t} = A_{v,t}^{e^\gamma}$$

is computed first and used in the closed form maximum likelihood estimator described above to calculate the survey scaling parameter. In cases where survey covariates are also applied to a nonlinear index, the adjustment for nonlinearity is carried out first.

Survey Q process errors

The C++ version of the KLAMZ model can be used to allow survey scaling parameters to change in a controlled fashion from year to year (NEFSC 2002):

$$Q_{v,t} = Q_v e^{\varepsilon_{v,t}}$$

where the deviations $\varepsilon_{v,t}$ are constrained to average zero. Variation in survey Q values is controlled by the NLL penalty:

$$L = 0.5 \sum_{j=1}^N \left[\frac{\varepsilon_{v,j}}{\sigma_v} \right]^2$$

where the log scale standard deviation σ_v based on an arithmetic CV supplied by the user (e.g. see NEFSC 2002). In practice, the user increases or decreases the amount of variability in Q by decreasing or increasing the assumed CV.

Survival ratios as surveys

In the C++ version of KLAMZ, it is possible to use time series of survival data as “surveys”. For example, an index of survival might be calculated using survey data and the Heinke method (Ricker 1975) as:

$$A_t = \frac{I_{k+1,t+1}}{I_{k,t}}$$

so that the time series of A_t estimates are data that may potentially contain information about scale or trends in survival. Predicted values for an a survival index are calculated:

$$\hat{A}_t = e^{-Z_t}$$

After predicted values are calculated, survival ratio data are treated in the same way as abundance data (in particular, measurement errors are assumed to be lognormal). Selectivity parameters are ignored for survival data but all other features (e.g. covariates, nonlinear scaling relationships and constraints on Q) are available.

Recruitment models

Recruitment parameters in KLAMZ may be freely estimated or estimated around an internal recruitment model, possibly involving spawning biomass. An internally estimated recruitment model can be used to reduce variability in recruitment estimates (often necessary if data are limited), to summarize stock-recruit relationships, or to make use of information about recruitment in similar stocks. There are four types of internally estimated recruitment models in KLAMZ: 1) random (white noise) variation around a constant or time dependent mean modeled as a step function; 2) random walk (autocorrelated) variation around a constant or time dependent mean modeled as a step function; 3) random variation around a Beverton-Holt recruitment model; and 4) random variation around a Ricker recruitment model. The user must specify a type of recruitment model but the model is not active unless the likelihood component for the recruitment model is turned on ($\lambda > 0$).

The first step in recruit modeling is to calculate the expected log recruitment level $E[\ln(R_t)]$ given the recruitment model. For random variation around a constant mean, the expected log recruitment level is the log geometric mean recruitment:

$$E[\ln(R_t)] = \sum_{j=1}^N \ln(R_j) / N$$

For a random walk around a constant mean recruitment, the expected log recruitment level is the logarithm of recruitment during the previous year:

$$E[\ln(R_t)] = \ln(R_{t-1})$$

with no constraint on recruitment during the first year R_1 .

For the Beverton-Holt recruitment model, the expected log recruitment level is:

$$E[\ln(R_t)] = \ln[e^a T_{t-\ell} / (e^b + T_{t-\ell})]$$

where $a=e^\alpha$ and $b=e^\beta$, the parameters α and β are estimated in the model, T_t is spawning biomass, and ℓ is the lag between spawning and recruitment. Spawner-recruit parameters are estimated as log transformed values (e^α and e^β) to enhance model stability and ensure the correct sign of values used in calculations. Spawning biomass is:

$$T_t = m_{new} R_t + m_{old} S_t$$

where m_{new} and m_{old} are maturity parameters for new and old recruits specified by the user. For the Ricker recruitment model, the expected log recruitment level is:

$$E[\ln(R_t)] = \ln(S_{t-\ell} e^{a-bS_{t-\ell}})$$

where $a=e^\alpha$ and $b=e^\beta$, and the parameters α and β are estimated in the model.

Given the expected log recruitment level, log scale residuals for the recruitment model are calculated:

$$r_t = \ln(R_t) - E[\ln(R_t)]$$

Assuming that residuals are log normal, the NLL for recruitment residuals is:

$$L = \sum_{t=t_{first}}^N w_t \left[\ln(\sigma_r) + 0.5 \left(\frac{r_t}{\sigma_r} \right)^2 \right]$$

where w_t is an instance-specific weight usually set equal one. The additional term in the NLL $[\ln(\sigma_r)]$ is necessary because the variance σ_r^2 is estimated internally, rather than specified by the user.

The log scale variance for residuals is calculated using the maximum likelihood estimator:

$$\sigma_r^2 = \frac{\sum_{j=t_{first}}^N r_j^2}{N}$$

where N is the number of residuals. For the recruitment model with constant variation around a mean value, $t_{first}=1$.

For the random walk recruitment model, $t_{first}=2$. For the Beverton-Holt and Ricker models, $t_{first}=\ell + 1$ and the recruit model imposes no constraint on variability of recruitment during years 1 to ℓ (see below). The biased maximum likelihood estimate for σ^2 (with N in the divisor instead of the degrees of freedom) is used because actual degrees of freedom are unknown. The variance term σ^2 is calculated explicitly and stored because it is used below.

Constraining the first few recruitments

It may be useful to constrain the first f years of recruitments when using either the Beverton-Holt or Ricker models if the unconstrained estimates for early years are erratic. In the KLAMZ model, this constraint is calculated:

$$NLL = \sum_{t=1}^{t_{first}-1} w_t \left\{ \ln \left(\sigma_r + 0.5 \left[\frac{\ln(R_t / E(R_{t_{first}}))}{\sigma_r} \right]^2 \right) \right\}$$

where t_{first} is the first year for which expected recruitment $E(R_t)$ can be calculated with the spawner-recruit model. In effect, recruitments that not included in spawner-recruit calculations are constrained towards the first spawner-recruit prediction. The standard deviation is the same as used in calculating the NLL for the recruitment model.

Prior information about the absolute value abundance index scaling parameters (Q)

A constraint on the absolute value one or more scaling parameters (Q_v) for abundance or survival indices may be useful if prior information is available (e.g. NEFSC 2000; NEFSC 2001; NEFSC 2002). In the Excel version, it is easy to program these (and other) constraints in an *ad-hoc* fashion as they are needed. In the AD Model Builder version, log normal and beta distributions are preprogrammed for use in specifying prior information about Q_v for any abundance or survival index.

The user must specify which surveys have prior distributions, minimum and maximum legal bounds (q_{min} and q_{max}), the arithmetic mean (\bar{q}) and the arithmetic CV for the prior the distribution. Goodness of fit for Q_v values outside the bounds (q_{min}, q_{max}) are calculated:

$$L = \begin{cases} 10000 (Q_v - q_{max})^2 & \text{if } Q_v \geq q_{max} \\ 10000 (q_{min} - Q_v)^2 & \text{if } Q_v \leq q_{min} \end{cases}$$

Goodness of fit for Q_v values inside the legal bounds depend on whether the distribution of potential values is log normal or follows a beta distribution.

Lognormal case

Goodness of fit for lognormal Q_v values within legal bounds is:

$$L = 0.5 \left[\frac{\ln(Q_v) - \tau}{\phi} \right]^2$$

where the log scale standard deviation $\phi = \sqrt{\ln(1 + CV)}$ and $\tau = \ln(\bar{q}) - \frac{\phi^2}{2}$ is the mean of the corresponding log normal distribution.

Beta distribution case

The first step in calculation goodness of fit for Q_v values with beta distributions is to calculate the mean and variance of the corresponding “standardized” beta distribution:

$$\bar{q}' = \frac{\bar{q} - q_{min}}{D}$$

and

$$Var(q') = \left(\frac{\bar{q} CV}{D} \right)^2$$

where the range of the standardized beta distribution is $D=q_{max}-q_{min}$. Equating the mean and variance to the estimators for the mean and variance for the standardized beta distribution (the “method of moments”) gives the simultaneous equations:

$$\bar{q}' = \frac{a}{a+b}$$

and

$$Var(q') = \frac{ab}{(a+b)^2(a+b+1)}$$

where a and b are parameters of the standardized beta distribution.¹⁹ Solving the simultaneous equations gives:

$$b = \frac{(\bar{q}' - 1)[Var(q') + (\bar{q}' - 1)\bar{q}']}{Var(q')}$$

and:

$$a = \frac{b\bar{q}'}{1 - \bar{q}'}$$

Goodness of fit for beta Q_v values within legal bounds is calculated with the NLL:

$$L = (a - 1)\ln(Q'_v) + (b - 1)\ln(1 - Q'_v)$$

where $Q'_v = Q_v / (Q_v - q_{min})$ is the standardized value of the survey scaling parameter Q_v .

Prior information about relative abundance index scaling parameters (*Q-ratios*)

Constraints on “Q-ratios” can be used in fitting models if some information about the relative values of scaling parameters for two abundance indices is available. For example, ASMFC (2001, p. 46-47) assumed that the relative scaling parameters for recruit and post-recruit lobsters taken in the same survey was either 0.5 or 1. If both indices are from the same survey cruise (e.g. one index for new recruits and one index for old recruits in the same survey), then assumptions about q-ratios are analogous to assumptions about the average selectivity of the survey of the survey for new and old recruits.

Q-ratio constraints tend to stabilize and have strong effects on model estimates. ASMFC (2001, p. 274) found, for example, that goodness of fit to survey data, abundance and fishing mortality estimates for lobster changed dramatically over a range of assumed q-ratio values.

To use q-ratio information in the KLAMZ model, the user must identify two surveys, a target value for the ratio of their Q values, and a CV for differences between the models estimated q-ratio and the target value. For example, if the user believes that the scaling parameters for abundance index 1 and abundance index 3 is 0.5, with a CV=0.25 for uncertainty in the prior information then the model’s estimate of the q-ratio is $\rho=Q_1/Q_3$. The goodness of fit calculation is:

$$L = 0.5 \left(\frac{\ln(\rho/\tau)}{\sigma} \right)^2$$

where τ is the target value and the log scale standard deviation σ is calculated from the arithmetic CV supplied by the user.

Normally, a single q-ratio constraint would be used for the ratio of new and old recruits taken during the

¹⁹ If x has a standardized beta distribution with parameters a and b , then the probability of x is

$$P(x) = \frac{x^{a-1}(1-x)^{b-1}}{\Gamma(a,b)}.$$

same survey operation. However, in KLAMZ any number of q-ratio constraints can be used simultaneously and the scaling parameters can be for any two indices in the model.

Surplus production modeling

Surplus production models can be fit internally to biomass and surplus production estimates in the model (Jacobson et al. 2002). Models fit internally can be used to constrain estimates of biomass and recruitment, to summarize results in terms of surplus production, or as a source of information in tuning the model. The NLL for goodness of fit assumes normally distributed process errors in the surplus production process:

$$L = 0.5 \sum_{j=1}^{N_p} \left(\frac{\tilde{P}_j - P_j}{\sigma} \right)^2$$

where N_p is the number of surplus production estimates (number of years less one), \tilde{P}_t is a predicted value from the surplus production curve, P_t is the assessment model estimate, and the standard deviation σ is supplied by the user based, for example, on preliminary variances for surplus production estimates.²⁰ Either the symmetrical Schaefer (1957) or asymmetric Fox (1970) surplus production curve may be used to calculate \tilde{P}_t (Quinn and Deriso 1999).

It may be important to use a surplus production curve that is compatible with recruitment patterns or assumptions about the underlying spawner-recruit relationship. More research is required, but the asymmetric shape of the Fox surplus production curve appears reasonably compatible with the assumption that recruitment follows a Beverton-Holt spawner-recruit curve (Mohn and Black 1998). In contrast, the symmetric Schaefer surplus production model appears reasonably compatible with the assumption that recruitment follows a Ricker spawner-recruit curve.

The Schaefer model has two log transformed parameters that are estimated in KLAMZ:

$$\tilde{P}_t = e^\alpha B_t - e^\beta B_t^2$$

The Fox model also has two log transformed parameters:

$$\tilde{P}_t = -e \left(e^{e^\alpha} \right) \frac{B_t}{e^\beta} \log \left(\frac{B_t}{e^\beta} \right)$$

See Quinn and Deriso (1999) for formulas used to calculate reference points (F_{MSY} , B_{MSY} , MSY , and K) for both surplus production models.

Catch/biomass

Forward simulation models like KLAMZ may tend to estimate absurdly high fishing mortality rates, particularly if data are limited. The likelihood constraint used to prevent this potential problem is:

$$L = 0.5 \sum_{t=0}^N (d_t^2 + q^2)$$

where:

²⁰ Variances in NLL for surplus production-biomass models are a subject of ongoing research. The advantage in assuming normal errors is that negative production values (which occur in many stocks, e.g. Jacobson et al. 2001) are accommodated. In addition, production models can be fit easily by linear regression of P_t on B_t and B_t^2 with no intercept term. However, variance of production estimate residuals increases with predicted surplus production. Therefore, the current approach to fitting production curves in KLAMZ is not completely satisfactory.

$$d_t = \begin{cases} Ft - \Phi & \text{if } Ft > \Phi \\ 0 & \text{otherwise} \end{cases}$$

and

with the threshold value κ normally set by the user to about 0.95. Values for κ can be linked to maximum F values using the modified catch equation described above. For example, to use a maximum fishing mortality rate of about $F \approx 4$ with $M=0.2$ and $G=0.1$ (maximum $X=4+0.2-0.1=4.1$), set $\kappa \approx F/X(1-e^{-X})=4 / 4.1 (1-e^{-4})=0.96$.

Uncertainty

The AD Model Builder version of the KLAMZ model automatically calculates variances for parameters and quantities of interest (e.g. R_b , F_b , B_b , F_{MSY} , B_{MSY} , $\bar{F}_{Re cent}$, $\bar{B}_{Re cent}$, $\bar{F}_{Re cent} / F_{MSY}$, $\bar{B}_{Re cent} / B_{MSY}$, etc.) by the delta method using exact derivatives. If the objective function is the log of a proper posterior distribution, then Markov Chain Monte Carlo (MCMC) techniques implemented in AD Model Builder libraries can be used estimate posterior distributions representing uncertainty in the same parameters and quantities.²¹

Bootstrapping

A FORTRAN program called BootADM can be used to bootstrap survey and survival index data in the KLAMZ model. Based on output files from a “basecase” model run, BootADM extracts standardized residuals:

$$r_{v,j} = \frac{\ln \left(I_{v,j} / \hat{I}_{v,j} \right)}{\sigma_{v,j}}$$

along with log scale standard deviations ($\sigma_{v,j}$, originally from survey CV’s or estimated from goodness of fit), and predicted values ($\hat{I}_{v,j}$) for all active abundance and survival observations. The original standardized residuals are pooled and then resampled (with replacement) to form new sets of bootstrapped survey “data”:

$${}^x I_{v,j} = \hat{I}_{v,j} e^{r \sigma_{v,j}}$$

where r is a resampled residual. Residuals for abundance and survival data are combined in bootstrap calculations. BootADM builds new KLAMZ data files and runs the KLAMZ model repetitively, collecting the bootstrapped parameter and other estimates at each iteration and writing them to a comma separated text file that can be processed in Excel to calculate bootstrap variances, confidence intervals, bias estimates, etc. for all parameters and quantities of interest (Efron 1982).

Projections

Stochastic projections can be carried out using another FORTRAN program called SPROJDDF based on bootstrap output from BootADM. Basically, bootstrap estimates of biomass, recruitment, spawning biomass, natural and fishing mortality during the terminal years are used with recruit model parameters from each bootstrap run to start and carryout projections.²² Given a user-specified level of catch or fishing mortality, the delay-difference equation is used to project stock status for a user-specified number of years. Recruitment during each projected year is based on simulated spawning biomass, log normal random numbers, and spawner-recruit parameters (including the residual variance) estimated in the bootstrap run. This approach is similar to carrying out projections based on parameters and state variables sampled from a posterior distribution for the basecase model fit. It differs from most current approaches because the spawner-recruit parameters vary from projection to projection.

²¹ MCMC calculations are not available in the current version because objective function calculations use concentrated likelihood formulas. However, the C++ version of KLAMZ is programmed in other respects to accommodate Bayesian estimation.

²² At present, only Beverton-Holt recruitment calculations are available in SPROJDDF.

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Appendix A5: KLAMZ model results

KLAMZ modeling

The KLAMZ model for the entire surfclam stock during was the main modeling approach and primary basis for providing management advice in the last assessment (NEFSC 2010). KLAMZ model results are provided here to build a bridge between the previous assessment and the current one. KLAMZ results are also provided for the Northern and Southern areas.

The KLAMZ assessment model is based on the Deriso-Schnute delay-difference equation (Deriso 1980; Schnute 1985; see complete technical documentation in Appendix A4). The delay-difference equation is a relatively simple and implicitly age structured approach. It gives the same results as explicitly age-structured models (e.g. Leslie matrix model) if fishery selectivity is “knife-edged”, if somatic growth follows the von Bertalanffy equation, and if natural mortality is the same for all age groups in each year. Natural and fishing mortality rates, growth parameters and recruitment may change from year to year.

There are two age or size groups in KLAMZ, “new” and “old” recruits that, together, comprise the whole stock. New recruits are individuals that recruited at the beginning of the current year. Old recruits are all older individuals in the stock that recruited at the beginning of previous years.

KLAMZ delay-difference models in this assessment were for surfclam biomass dynamics during 1981-2011 and were generally similar to models used in the last surfclam assessment (NEFSC 2010). The first year with survey data was 1982, however, the model has an estimable parameter for biomass in 1981 that defines the initial age structure. Landings data are available for earlier years. A number of changes, primarily to input data, for this assessment are described below under “Building a bridge”. As in the last assessment, the natural mortality rate is $M=0.15 \text{ y}^{-1}$ (Appendix A4).

Growth patterns were assumed to vary over time in all models because of recent slow growth in the DMV and NJ regions and because of changes in the distribution of the stock among regions which have different SLMWT and von Bertalanffy growth patterns. In the KLAMZ model, the growth parameter $J_t = w_{t-1,k-1}/w_{t,k}$ (where $w_{t,k}$ is the mean body weight of a surfclam at the age of recruitment k in year t) may vary from year to year. The growth parameter J_t represents the combined effects of the traditional von Bertalanffy growth parameters W_∞ and t_0 . This approach was adequate for surfclams because much of the variation in growth appeared to be in maximum size W_∞ (Table A16 Assessment report).

Model configuration

NEFSC clam survey data in the KLAMZ model were for new and old recruits. Surveys were assumed to occur in the middle of the year because the NEFSC clam survey is carried out during late May-early July. As in the previous assessment, survey data used in the KLAMZ model were trends, after holes (unsampled survey strata in some years) were filled to the extent possible by borrowing data from the previous and successive surveys. Some years were not used in whole stock or Northern area modeling because GBK was undersampled (Figure 1). For example, GBK was not sampled at all in 2005.

Survey trend data (stratified mean kg/tow) for surfclams 120-129 mm SL were assumed to track trends in biomass of new recruits. Survey data for surfclams 130+ mm were assumed to track trends in the entire stock (old recruits).

Following NEFSC (2009), swept area biomass estimates were included in the assessment model to measure scale, but not trends, in biomass. Swept area biomass estimates were not efficiency corrected in this case because the prior on survey efficiency (see TOR 2) was intended to carry forward model uncertainty in scale. Goodness of fit to the swept area biomass data was given nil weight in the overall objective function. However, the likelihood of the estimated scaling parameter for swept area biomass was calculated based on a log normal prior distribution with mean 0.234 and arithmetic CV = 1.32 and the likelihood was added to the objective function used in fitting the model. The CV was estimated by bootstrapping all available data on survey dredge efficiency (see TOR 2). The CV is relatively broad and the prior information had a little effect in determining the overall scale of surfclam biomass and fishing mortality estimates. Experience has shown that surfclam stock assessment data, aside from the

swept are area biomass estimates, are uninformative about the overall scale of biomass but do provide information about trends. Thus, the model tended to be uncertain regarding overall scale, for which there was limited data beyond the somewhat uninformative (high CV) prior distribution on survey dredge efficiency.

Following NEFSC (2003) surfclam recruits were estimated in the KLAMZ model as a random walk with steps constrained by a variance parameter. A smooth, random walk process is probably not ideal from a biological perspective because of the evidence in survey age composition data for strong year classes, but the approach was necessary because of the lack of annual recruitment data. The random walk approach keeps the recruitment estimate in year t at the same level as in year $t-1$, unless there is a good reason, in terms of goodness of fit, to change it. For surfclams in the KLAMZ model, the random walk approach helped avoid excessive variation in recruitment, enhanced model convergence, and ensured that some recruitment was estimated for each year.

In modeling surfclam population dynamics with random walk recruitment, it is important to tune the “random walk recruitment variance” σ_R^2 which measures variability in the size of successive steps taken during the random walk (i.e. variance in $[\ln(R_1/R_2), \ln(R_2/R_3), \ln(R_3/R_4), \text{etc.}]$, where R_t is the recruitment estimate for year t). As σ_R^2 approaches zero, recruitment estimates become smooth and tend towards a constant value with no changes from year to year. As σ_R^2 becomes large, estimated recruitments will change randomly and more widely from one year to next.

Following NEFSC (2007), initial KLAMZ model runs assumed high CV for steps in the random walk. The assumed CV was gradually decreased in subsequent runs until the model was just able to fit the survey data without pattern in residuals and the model was able to fully converge (the Hessian matrix was invertible). In addition, the CV for fit to the survey data (residual CV) was compared to CV for the actual survey data to determine if the model was fitting the survey data more closely than should be expected based on the precision of the survey data (implying that σ_R^2 was too large). Finally, it was determined that the fit to the “old” recruit time series should be better than the fit to the new recruit time series as the older recruits were based on a broader set of size classes and thus more data. The goal was basically to find the model that would adequately explain the survey data for surfclams, but not over fit the new recruit time series.

Recruitment estimates for surfclam from the KLAMZ model are complicated to interpret because of the constraints on variability and limited survey data. Under these conditions, recruitment estimates for surfclam from the KLAMZ model should probably be regarded as “nuisance” parameters of less interest than biomass and fishing mortality estimates. Recruitment estimates for surfclams at best reflect long term average trends. However, recruitment estimates in the KLAMZ model are aliased with model misspecification, survey noise, survey year effects, natural mortality and variability in growth.

Results-whole stock

The KLAMZ model fit survey biomass trend data reasonably well (Figure 2). The model fit the whole stock survey data index better than the index for new recruits, as expected based on the CV for the two sets of survey data (CV for the recruit index are higher).

The survey scaling parameter for efficiency corrected swept area biomass was $Q=0.16$, which is close to the mode of the prior distribution of survey dredge efficiency. This indicates that the trend data, landings and model estimates did not provide sufficient information on scale to shift the model away from the relatively uninformative prior information about Q for swept area biomass estimates.

Model results (Figure 3 - 4) suggest that surplus production was high before the late 1990's and steadily declined afterwards to negative levels during 2001-2011 as somatic growth and recruitment rates declined. Biomass increased until the late 1990s when surplus production was less than catch.

Bootstrap and delta method CV for biomass, and recruitment estimates were $< 25\%$ indicating that estimates were reasonably precise (Table 1). The bootstrap CV for fishing mortality were high because the denominator, the estimated fishing mortality values, were often close to zero. Delta method CV are probably the

better measure of uncertainty in this case.

Internal retrospective analysis

Retrospective analyses were carried out with the base case KLAMZ model for terminal years 2000-2011 (Figure 5). There was little evidence of a retrospective problem in either biomass or fishing mortality estimates. The model tends to fluctuate somewhat in scale because the scale of the model is uncertain, but the trend is consistent through time. Changes in scale tended to occur when data from an additional NEFSC clam survey (as in the case of 2002, 2008 and 2011) was dropped.

Historical retrospective analysis

Biomass and fishing mortality estimates from surfclam stock assessments carried out since 1998 were compared to determine the stability of stock estimates used to provide management advice (Figure 6). The scale of the model fit is considerably higher than in past assessments. This is primarily due to changes in the way survey efficiency was estimated and the increased variance in the prior distribution for survey Q . The most important aspect of the historical retrospective analysis is the substantial differences between base case biomass and fishing mortality estimates and estimates from the previous assessment. The factors responsible for these changes are explained below.

Performance of historical projections

The current model differed from historical projections. Comparisons in trend were used because the scale of the model in the last assessment was much lower (Figure 6). In the last assessment the projected biomass in 2011 was approximately 6% lower than biomass in 2008. Using the current whole stock KLAMZ model, biomass in 2011 was approximately 14% lower than biomass in 2008 (Table 2). The discrepancy can be explained by differences in estimated trend between the models, caused by differences in the fit to the survey data (see below).

Building a bridge

Differences between estimates in the base case model in this assessment and the last assessment due to modifications to data and modeling procedures. These are discussed below, one step at a time (Figure 7). The most important factors contributing to differences between the base case model biomass estimates in this assessment and estimates in the previous assessment are: additional variance in the prior distribution for survey Q (Step 3), and additional variance allowed in the fit to the recruit time series (Step 2, Step 13).

Step 1 was to run the KLAMZ model using updated data from the last assessment to determine if any new bugs had crept into the model code. The model was able to estimate parameters, but produced steep gradients and did not converge. Step 2 was to allow more freedom in the variance of the random walk recruitment parameter, σ_R^2 , which allowed a better fit to the survey data for both old and new recruits. This step reduced the magnitude of the gradients, but still did not produce an invertible hessian matrix. Step 3 was to incorporate the new prior distribution for survey Q , which increased the variance in the prior by an order of magnitude from the last assessment. Step 4 was to include the new selectivity estimates for the survey dredge. The fifth step was to incorporate new SLMWT relationships. Step 6 was to add the updated growth estimates. The model converged for the first time after this step. The seventh step was to decouple the surveys (in previous estimates there was overlap in size classes between the old and new recruits). The eighth step was to include discards in the fishery data being used (a correction to an oversight). The ninth step was to remove data from 1983 from the whole stock model due to poor coverage on GBK. Step 10 was to incorporate changes in sensor data criteria used to identify and discard “bad” survey tows for use in estimating efficiency corrected swept area biomass. The eleventh step was to fix a bug in the routine to borrow data from adjacent years to fill holes in the survey time series. Step 12 was to fix a bug in the growth estimates added in step 6. Finally step 13 was to adjust the σ_R^2 parameter to minimize the overall Likelihood function. Convergence was generally tenuous throughout this process. The model was sensitive to starting conditions and generally produced large gradients even when the hessian matrix was invertible.

Results-Southern Area

The KLAMZ model for the southern area (SVA to SNE) incorporated all of the data available. All survey

years were included for new (120 – 129 mm SL) and old (130+ mm SL) recruits. Swept area biomass for all years in which dredge sensors were deployed (1997 and after; Figure 8) were included as well. Catch data between 1982 and 2011 were used.

Other model parameters were selected according to the methodology established in the whole stock model. Growth parameters and juvenile ratios (see above) were calculated for the appropriate subset of the data for the whole stock (animals from SVA to SNE). The σ_R^2 parameter (see above) was chosen to minimize a concentrated Likelihood function that ignored the recruitment model component. The recruitment model component is always minimized by a σ_R^2 equal to zero because it prefers a recruitment model with fewer parameters (see Appendix A4).

Changing the σ_R^2 parameter had a substantial affect on the overall model (Figure 9). The trend of the model fit was relatively unaffected, but the scale changed by as much as a factor of three depending on the value of σ_R^2 chosen.

The model fit the survey data reasonably well (Figure 10). Trends in the overall fit were similar to the fit for the whole stock, indicating that the population biomass peaked in the late 1990's. The southern area, however, indicates a steeper decline since then (Figure 11).

Surplus production (Figure 12) was positive until the mid 1990's and has been negative since then, until 2011. The upward trend in surplus production over the last six years has been driven by strong recruitment.

The scale parameter for the KLAMZ model, survey Q , was 0.55. This value is considerably higher than the survey Q estimated for the whole stock (0.16). The discrepancy is a result of uncertainty in our extra-model estimates of survey dredge efficiency (see above) and is reflected in the prior distribution which has a CV of 134%. The KLAMZ model is therefore given very little information about scale and that uncertainty is evident in the trouble KLAMZ has in establishing a consistent scale.

Bootstrap runs (n=500) for the southern area KLAMZ model runs were fairly consistent though there were a few extreme outliers (Figure 13). This is reflected in the bootstrap CV which were generally high (Table 3) and driven by outliers which tended to be unconverged cases (~3%). Delta method CV were generally below 20%.

Internal Retrospective

Retrospective analysis indicates a shift in scale, but not trend, as survey years are removed from the model (Figure 14). The model tends to fluctuate somewhat in scale because the scale of the model is uncertain, but the trend is consistent through time. Changes in scale tended to occur when data from an additional NEFSC clam survey (as in the case of 2002, 2008 and 2011) were dropped.

Results-Northern Area

The KLAMZ model for the northern area (GBK) incorporated a subset of the data available. There were some years where coverage on GBK was poor (1982, 1983) and other years where GBK was not sampled (2005). Swept area biomass for all years in which dredge sensors were deployed and GBK was sampled (1997 and after, excluding 2005; Figure 15) were included as well. Catch data was sparse, as GBK was not fished for 20 years between 1989 and 2008.

Other model parameters were selected according to the methodology established in the whole stock model. Growth parameters and juvenile ratios were calculated for the appropriate subset of the data for the whole stock (animals from GBK). The σ_R^2 parameter (see above) was chosen to minimize a concentrated likelihood function, that ignored the recruitment model component. The recruitment model component is minimized by a σ_R^2 equal to zero, because it prefers a recruitment model with fewer parameters (see Appendix A4). This choice could not be made naively however, as it is possible to overfit the recruitment index at the expense of other data. In this case the

minimum of the concentrated likelihood occurred at $\ln(\sigma_R^2) = -4$, which would have resulted in the goodness of fit to the recruitment time series being less than the goodness of fit implied by the CV of the index itself. The σ_R^2 parameter was gradually increased until the goodness of fit to the index was greater than the goodness of fit implied by the survey CV ($\ln(\sigma_R^2) = -4.65$; Figure 16). Changing the σ_R^2 parameter had little effect on the overall model (Figure 17).

The model fit the survey data reasonably well (Figure 16). Based on the fit to the survey data, the northern area has been growing since the cessation of fishing there in 1989. The upward trend in growth seems to be tapering off and has been essentially flat for approximately the last 5 years (Figure 18).

Surplus production (Figure 19) was positive from the late 1980's until 2010. The decline in surplus production is probably due to declining recruitment since 1995 (Figure 19).

The scale parameter for the KLAMZ model, survey Q , which is analogous to survey dredge efficiency in efficiency corrected swept are biomass calculations was 0.14. This value was comparable to the survey Q estimated for the whole stock (0.16). The estimated Q was close to the mean of the prior distribution and indicated that the data provided to the KLAMZ model for the Northern area probably provided very little information about scale. The prior distribution we used was highly uninformative and ($CV = 134\%$ see TOR 2 above) and was not likely to influence the estimate of survey Q very much in the presence of data that informed scale. The fact the estimated survey Q did not differ from mean of the prior probably means that the data were not informative regarding scale.

Bootstrap runs ($n=500$) for the Northern area KLAMZ model runs were fairly consistent (Figure 20). This is reflected in the bootstrap CV which were generally tight (Table 4). Delta method CV were generally very high ($\sim 100\%$). The discrepancy between delta method CV based on the Hessian matrix and the bootstrap CV is probably due to differences between the two methods. The delta method uncertainty reveals a flat likelihood and thus a wide CV in the area immediately around the converged solution. If however the “flatness” of the likelihood surface is confined to a relatively small parameter space, the bootstrap solutions might all arrive at nearly the same solution and thus produce a relatively narrow CV. Some evidence for this is provided by the high rate of convergence in the bootstrap runs (100% converged) and by the fact that profiles over various values of σ_R^2 (Figure 17) and survey Q (Figure 21) indicate that the solution is fairly stable over these parameters. There is simply not enough information in these data to provide a strongly peaked likelihood surface.

Internal Retrospective

Retrospective analysis indicates a shift in scale, but not trend as survey years are removed from the model (Figure 22). There are no indications of retrospective problems in the Northern area KLAMZ model.

Appendix A5. Table 1. Bootstrap and delta method CV for whole stock KLAMZ runs.

Year	Biomass		F		Recruitment	
	Bootstrap cv	Delta cv	Bootstrap cv	Delta cv	Bootstrap cv	Delta cv
1981	27.58	28.27	50.62	28.40	24.45	46.92
1982	25.43	19.80	51.56	19.88	22.57	41.23
1983	23.79	14.73	53.04	14.81	22.82	27.38
1984	22.60	13.31	54.64	13.39	21.47	28.36
1985	21.74	13.57	56.53	13.64	20.58	26.08
1986	21.01	14.40	58.40	14.48	20.53	27.24
1987	20.57	15.31	59.28	15.38	20.62	25.93
1988	20.23	15.98	59.53	16.06	20.76	21.73
1989	19.91	16.27	59.44	16.34	21.25	23.75
1990	19.78	16.33	58.92	16.41	21.13	23.80
1991	19.71	16.31	57.99	16.38	19.89	22.66
1992	19.42	16.27	56.90	16.34	18.26	21.67
1993	18.80	16.44	57.21	16.50	19.44	19.49
1994	18.54	16.36	57.44	16.41	17.34	22.45
1995	18.05	16.05	57.04	16.09	17.15	22.85
1996	17.58	15.92	56.69	15.96	19.28	20.31
1997	17.30	15.99	56.86	16.02	19.02	23.32
1998	17.15	16.09	56.15	16.12	19.53	22.66
1999	17.07	16.20	55.91	16.24	19.90	25.74
2000	17.07	16.30	55.70	16.34	19.89	26.17
2001	17.09	16.41	55.72	16.46	19.21	24.45
2002	17.12	16.54	56.11	16.60	19.84	27.88
2003	17.20	16.64	57.09	16.70	20.79	29.18
2004	17.33	16.76	58.46	16.83	21.33	29.29
2005	17.49	16.91	59.91	16.97	21.21	28.56
2006	17.63	17.05	61.53	17.13	20.67	26.88
2007	17.75	17.22	63.41	17.30	20.78	23.39
2008	17.79	17.34	64.94	17.42	20.33	28.27
2009	17.82	17.52	66.30	17.59	21.00	28.79
2010	17.84	17.82	67.19	17.89	22.59	25.45
2011	17.88	18.12	67.41	18.19	NA	NA
mean	19.23	16.72	58.32	16.78	20.45	26.40

Appendix A5. Table 2. Mean, median and quantiles of relative biomass change from 2008 to 2011, comparing projections from the last assessment to the current KLAMZ model results.

Statistic	change from 2008 to 2011	
	Proj 2009	This Assessment
Q10%	-7.54%	-14.63%
Mean	-5.72%	-13.55%
Median	-5.63%	-13.50%
Q90%	-3.80%	-12.50%

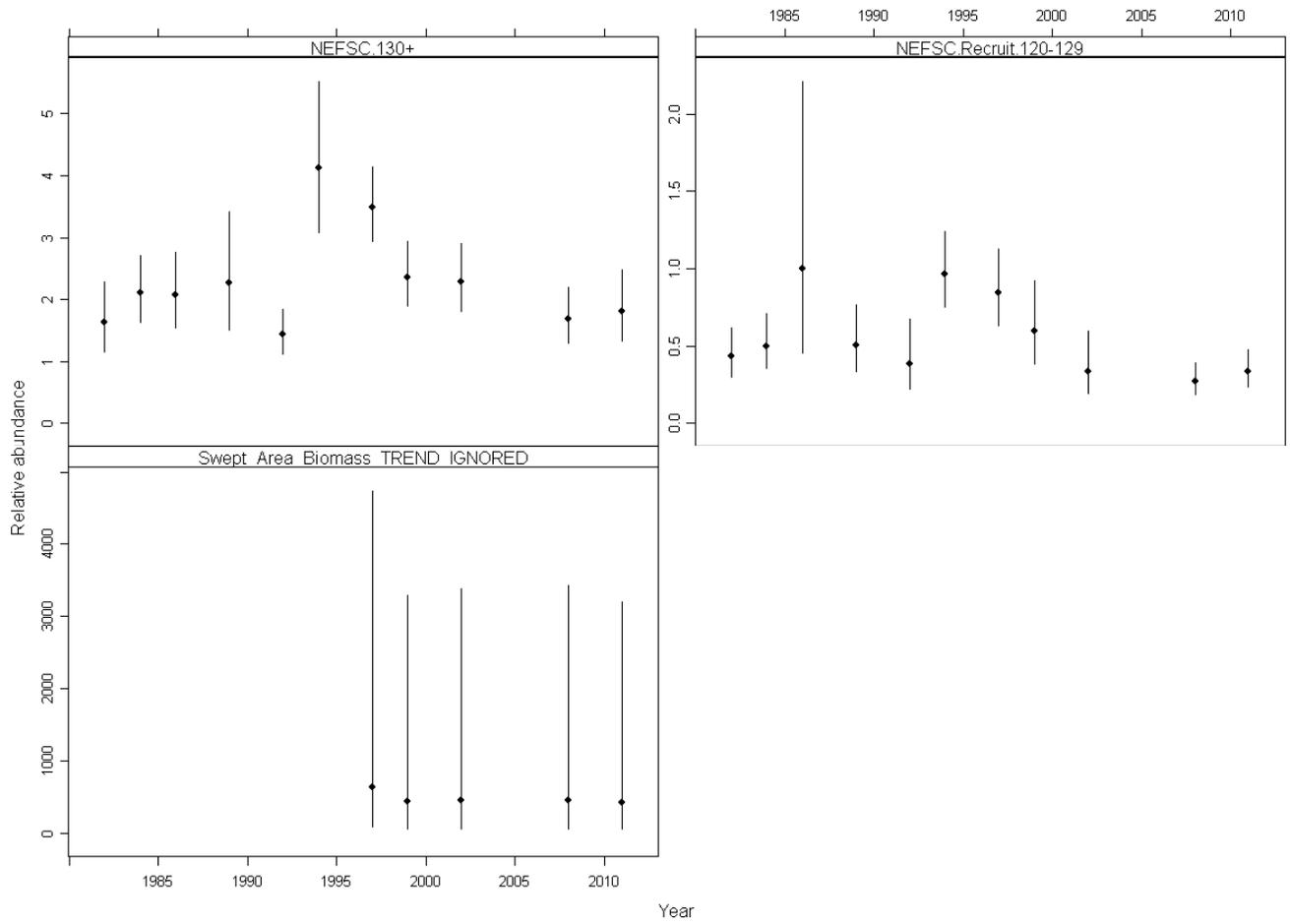
Appendix A5. Table 3. Bootstrap and delta method CV for southern area KLAMZ runs.

Year	Biomass		Fishing Mortality		Recruitment	
	Bootstrap CV	Delta CV	Bootstrap CV	Delta CV	Bootstrap CV	Delta CV
1981	56.48	5.46	25.60	5.56	59.88	16.53
1982	57.17	6.30	24.28	6.42	55.42	15.85
1983	57.74	7.78	23.75	7.91	54.17	15.11
1984	58.08	9.10	23.61	9.24	53.81	14.71
1985	58.59	10.15	23.68	10.32	53.84	14.26
1986	59.07	11.00	23.87	11.17	57.68	13.82
1987	60.19	11.61	24.04	11.82	60.74	13.37
1988	61.47	12.10	24.16	12.33	62.41	12.86
1989	62.89	12.47	24.19	12.72	56.66	12.61
1990	63.19	12.72	24.10	12.96	51.71	12.26
1991	62.69	12.82	23.90	13.03	47.89	11.84
1992	61.13	12.75	23.63	12.97	43.65	11.31
1993	58.90	12.60	23.42	12.82	45.27	10.88
1994	57.26	12.41	23.30	12.59	41.87	11.00
1995	55.59	12.24	23.12	12.39	40.87	10.97
1996	54.10	12.06	22.91	12.19	42.47	10.90
1997	53.12	11.87	22.70	11.99	47.17	11.21
1998	52.97	11.79	22.53	11.93	51.52	11.27
1999	53.34	11.77	22.57	11.92	54.75	11.36
2000	54.14	11.83	22.67	11.99	56.99	11.38
2001	55.16	11.93	22.82	12.13	58.42	11.32
2002	56.43	12.11	23.08	12.36	55.56	11.37
2003	57.89	12.38	23.44	12.67	52.08	11.36
2004	59.41	12.71	23.87	13.04	48.71	11.06
2005	60.83	13.12	24.26	13.46	49.87	11.70
2006	62.18	13.45	24.75	13.89	51.36	11.98
2007	64.03	13.92	25.43	14.46	53.19	12.00
2008	66.27	14.55	26.14	15.14	51.26	12.98
2009	68.06	15.09	27.00	15.70	50.15	13.63
2010	69.15	15.57	27.88	16.18	50.43	14.33
2011	69.29	15.97	28.85	16.66	NA	NA
mean	59.57	11.99	24.18	12.26	51.99	12.51

Appendix A5. Table 4. Bootstrap and delta method CV for GBK area KLAMZ runs.

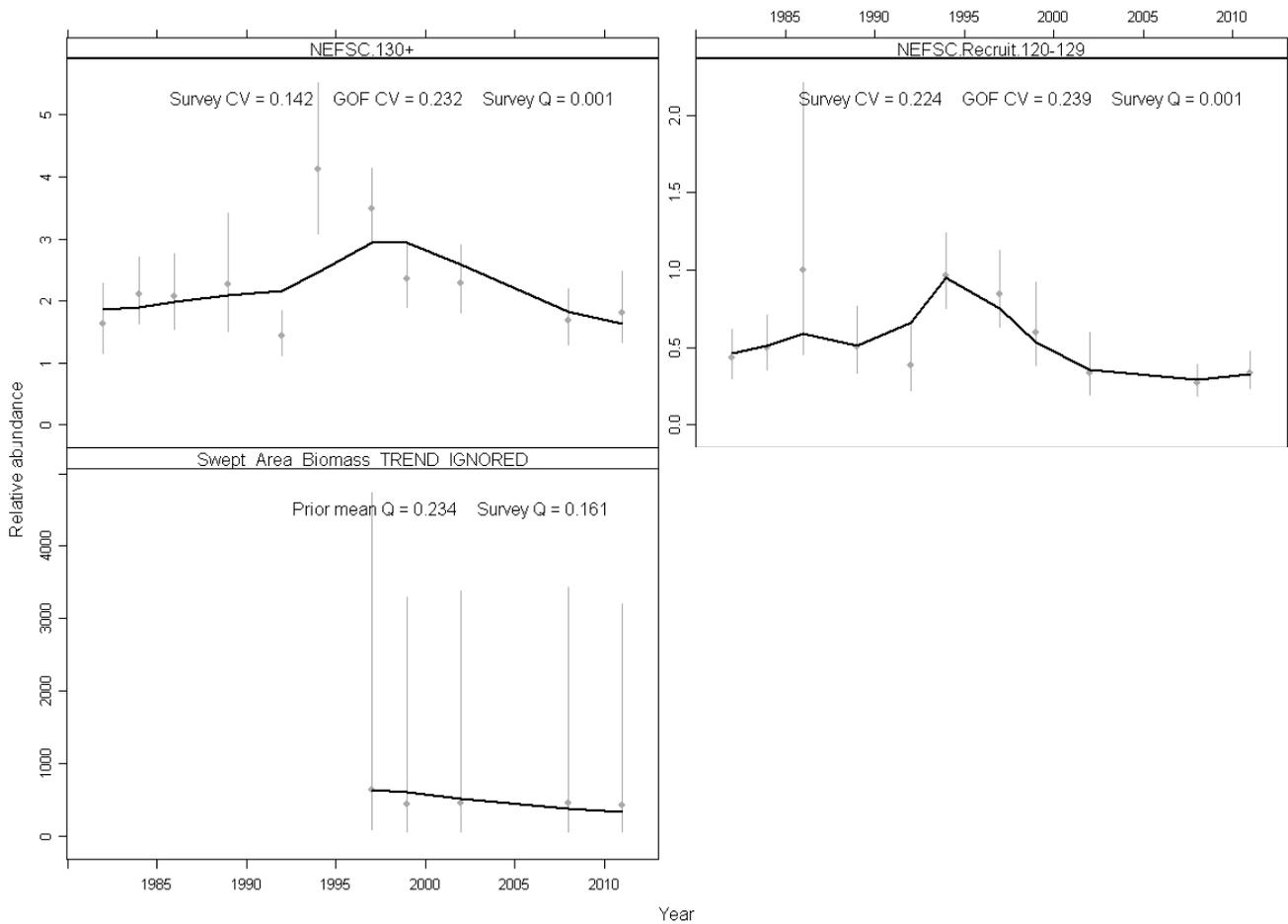
Year	Biomass		Fishing Mortality		Recruitment	
	Bootstrap CV	Delta CV	Bootstrap CV	Delta CV	Bootstrap CV	Delta CV
1981	70.64	99.01	NA	NA	27.70	97.13
1982	65.04	99.13	NA	NA	27.76	97.14
1983	59.55	99.15	NA	NA	27.69	97.43
1984	54.31	99.16	46.48	97.38	25.06	97.97
1985	49.38	99.14	41.49	96.97	23.96	97.70
1986	44.58	99.14	37.18	96.54	24.20	97.53
1987	39.84	99.16	33.47	96.08	24.57	97.44
1988	35.41	99.18	30.24	95.70	24.62	97.44
1989	31.50	99.21	27.50	95.45	24.61	97.55
1990	28.19	99.23	25.27	95.27	24.41	97.81
1991	25.57	99.24	NA	NA	24.70	97.83
1992	23.53	99.22	NA	NA	22.19	98.03
1993	21.99	99.19	NA	NA	21.33	98.45
1994	20.72	99.12	NA	NA	19.37	98.45
1995	19.62	99.01	NA	NA	17.95	98.76
1996	18.40	98.87	NA	NA	18.18	98.43
1997	16.99	98.72	NA	NA	14.43	98.30
1998	15.49	98.55	NA	NA	15.30	98.41
1999	14.03	98.35	NA	NA	14.53	98.02
2000	12.70	98.10	NA	NA	15.37	98.22
2001	11.65	97.76	NA	NA	16.78	97.74
2002	10.93	97.38	NA	NA	18.34	97.42
2003	10.65	97.02	NA	NA	20.15	97.26
2004	10.82	96.63	NA	NA	21.50	97.11
2005	11.36	96.18	NA	NA	22.32	97.25
2006	12.13	95.92	NA	NA	23.11	97.72
2007	12.98	95.69	NA	NA	25.04	97.79
2008	13.84	95.55	NA	NA	25.17	98.13
2009	14.67	94.86	14.67	98.91	26.83	96.86
2010	15.46	94.10	15.45	99.08	30.11	95.66
2011	16.28	93.27	16.23	99.16	NA	NA
mean	26.07	97.88	28.80	97.05	22.24	97.70

SC_2012_update2009 - Survey observations with 95% CI



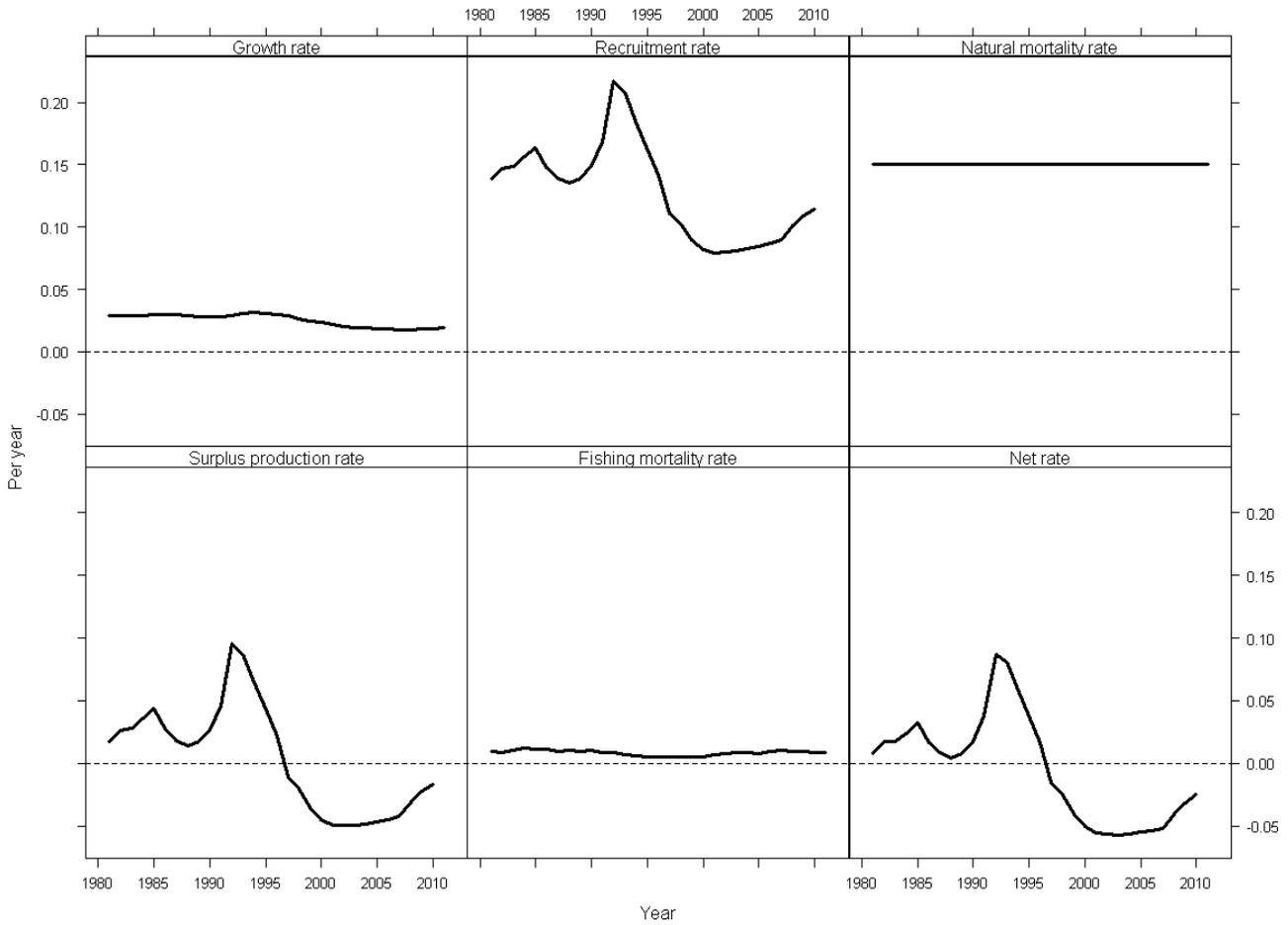
Appendix A5. Figure 1. Whole stock survey data and swept area biomass estimates with approximate 95% confidence intervals.

SC_2012_update2009 - Survey observations, 95% CI and fitted values

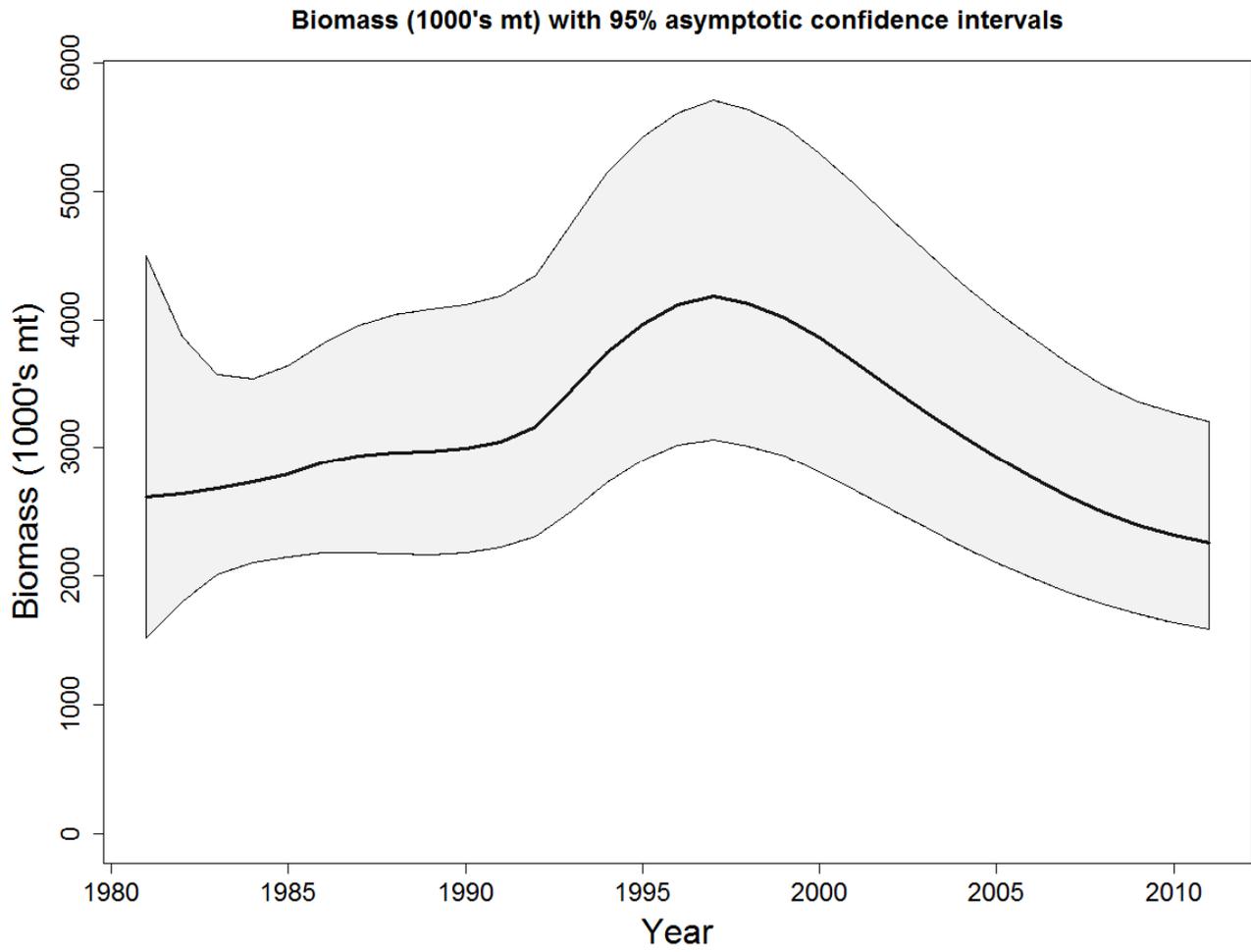


Appendix A5. Figure 2. Whole stock survey data and swept area biomass estimates with approximate 95% confidence intervals and KLAMZ model fits with goodness of fit statistics and estimated catchability parameters.

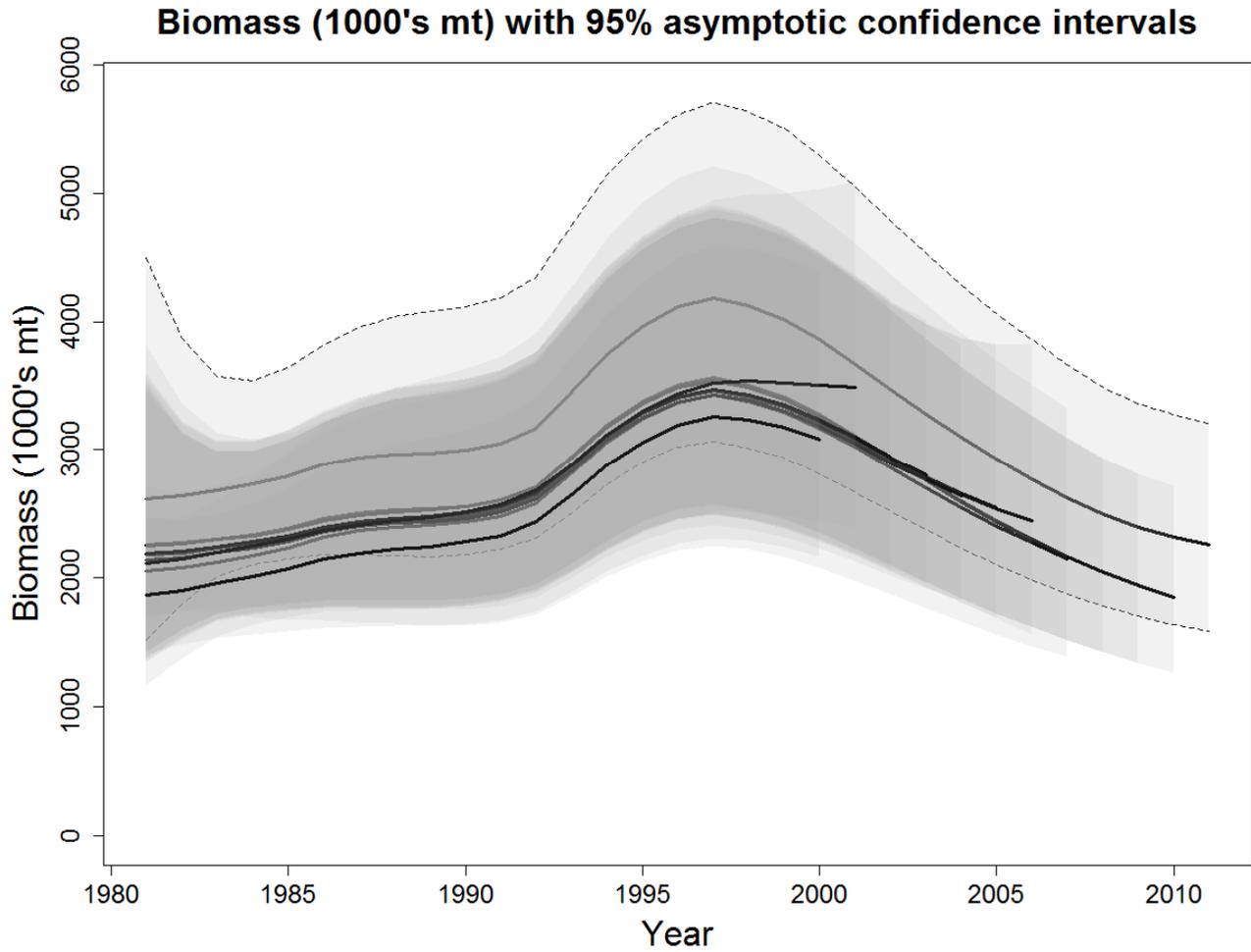
SC_2012_update2009 - Population dynamics as rates



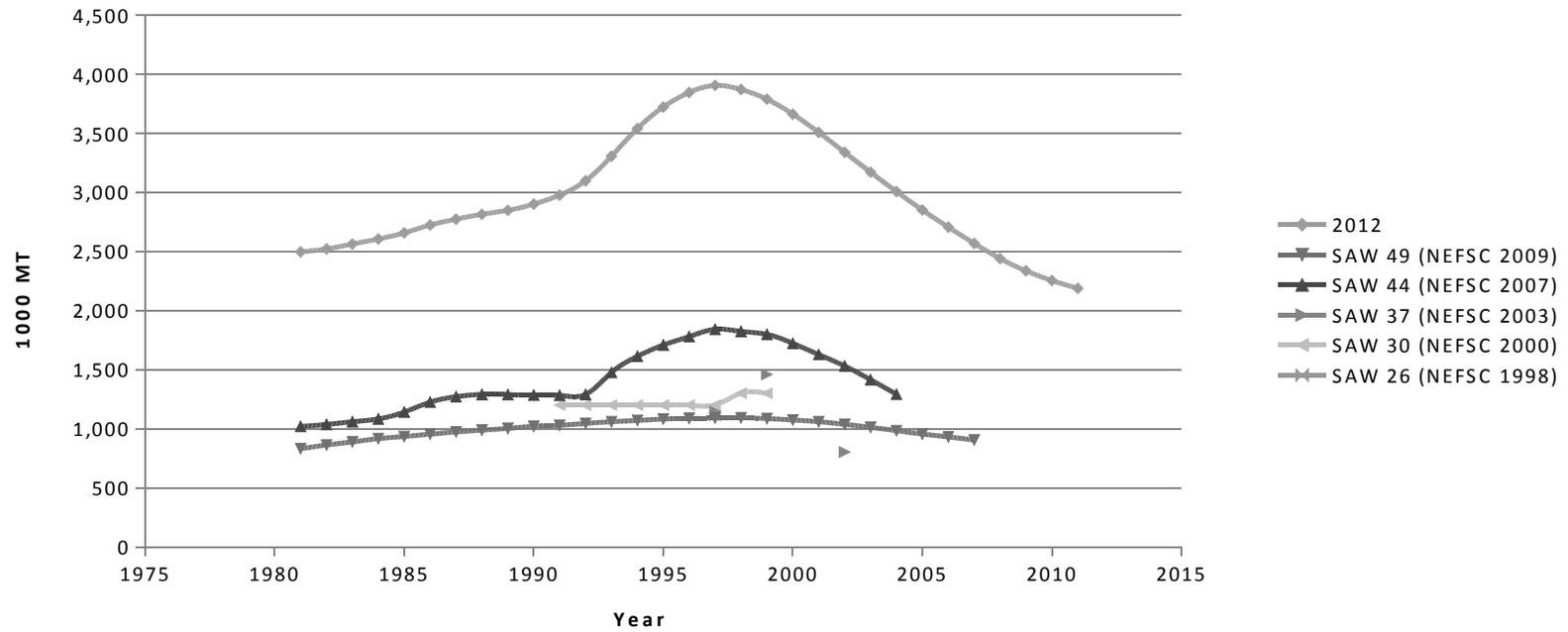
Appendix A5. Figure 3. Some population dynamics, shown as rates, estimated in KLAMZ for the whole stock.



Appendix A5. Figure 4. Total biomass (1000 mt) estimated for the whole stock.

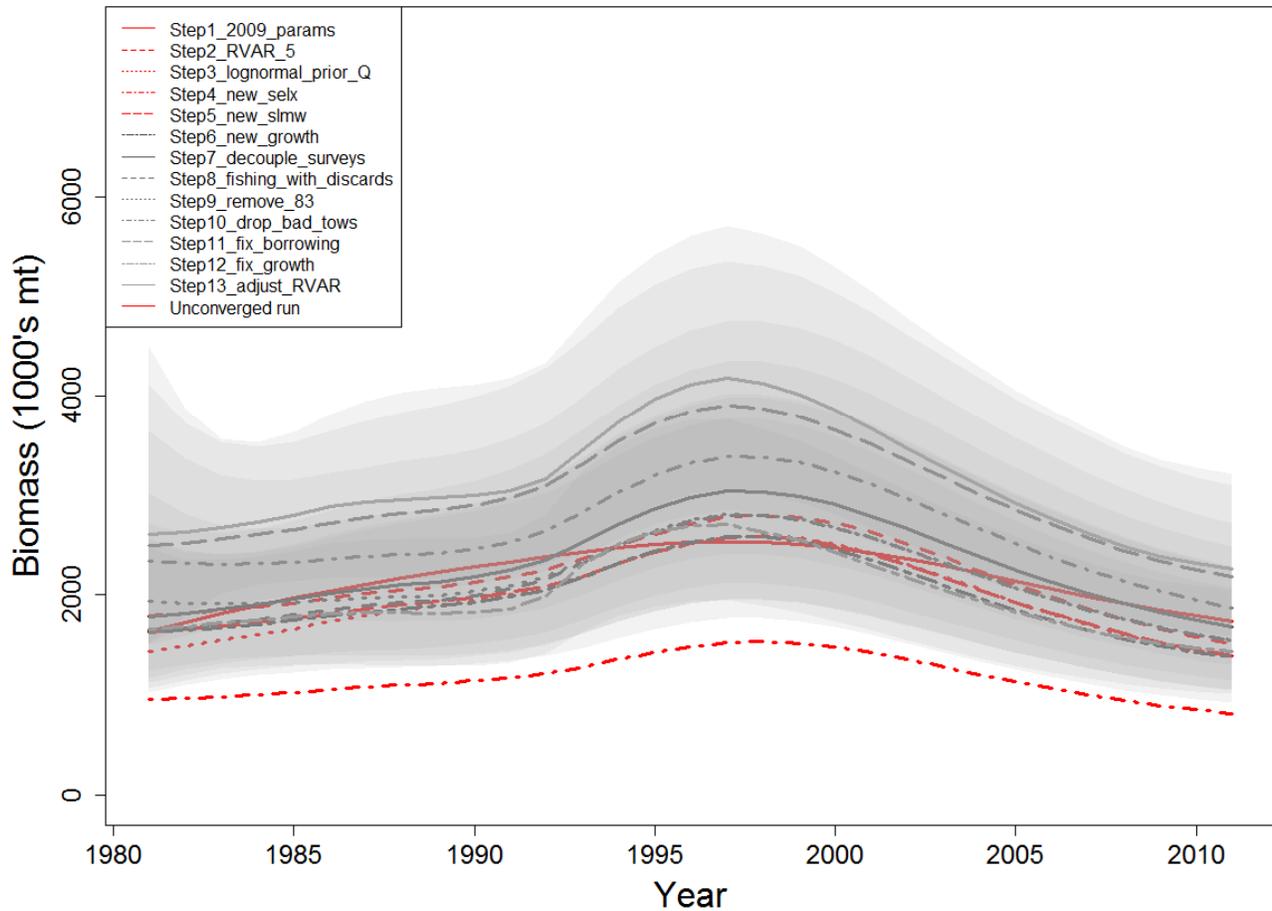


Appendix A5. Figure 5. Retrospective patterns in total biomass for the years 2000-2011 using the base case whole stock KLAMZ model.



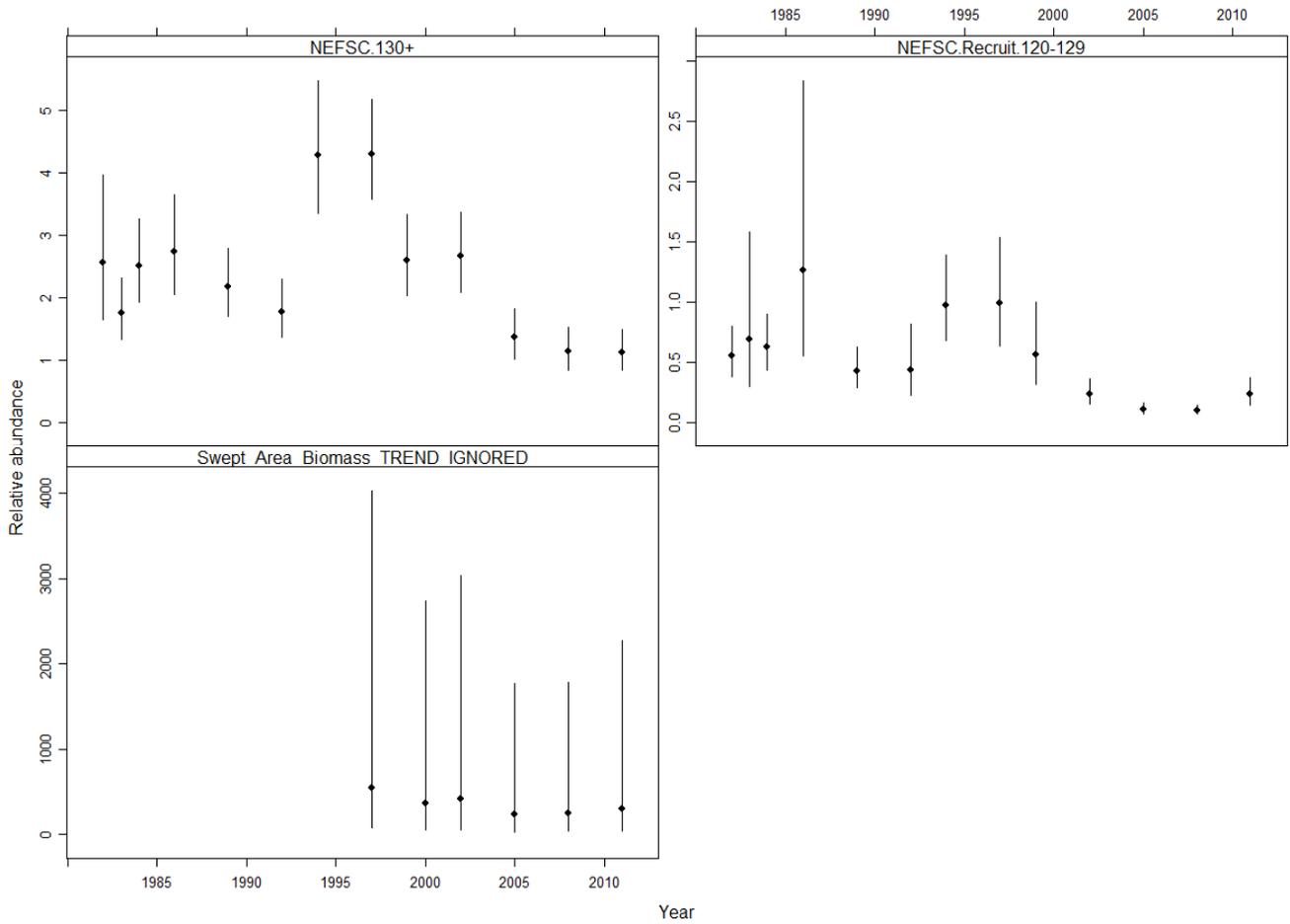
Appendix A5. Figure 6. Historical retrospective pattern in basecase whole stock KLAMZ models.

Biomass (1000's mt) with 95% asymptotic confidence intervals



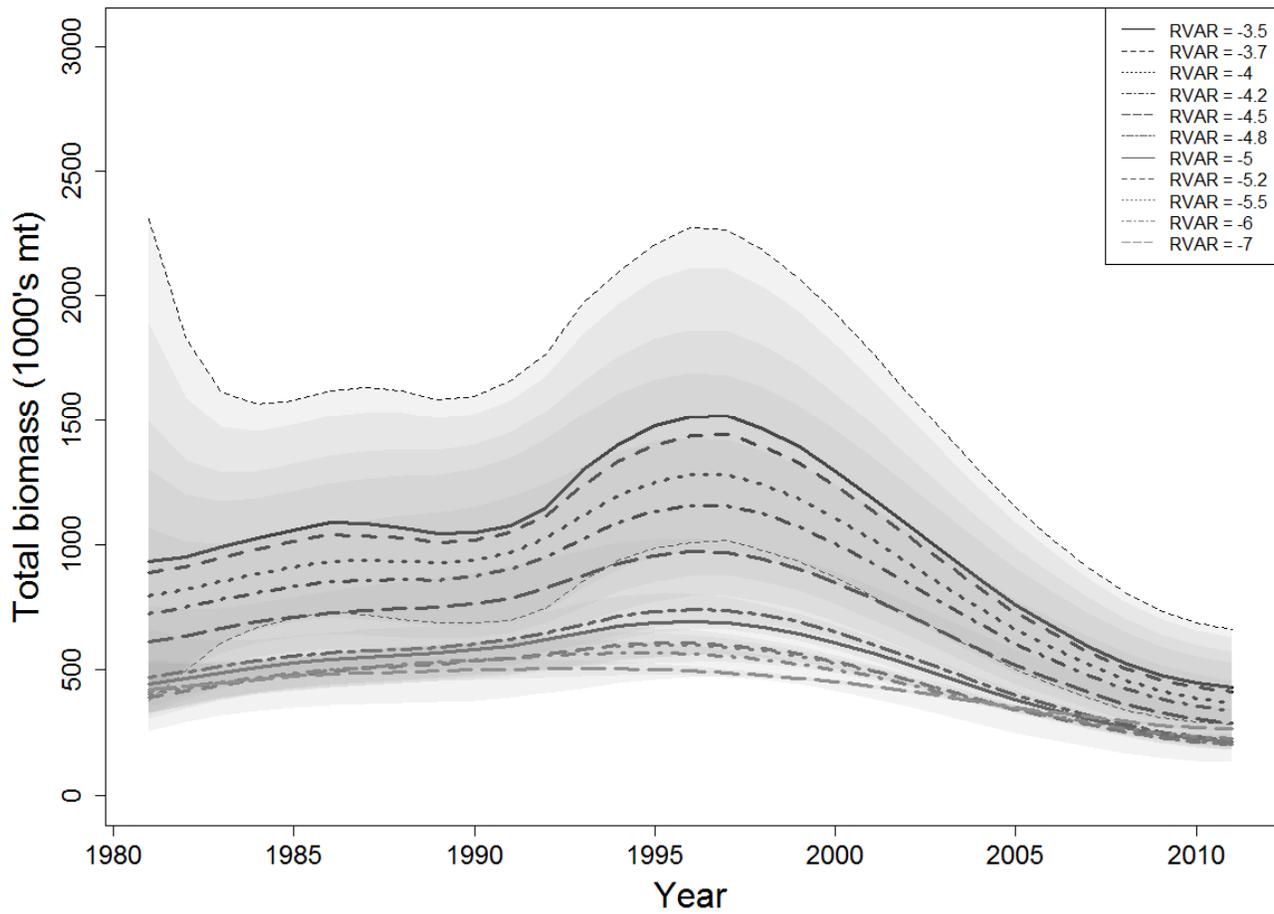
Appendix A5. Figure 7. Build a bridge. The steps involved in updating the KLAMZ model from the 2009 assessment to the current base case whole stock KLAMZ version. Not all runs converged (red lines) and so asymptotic confidence intervals based on the delta method were not always available.

SC_2012_update2009 - Survey observations with 95% CI



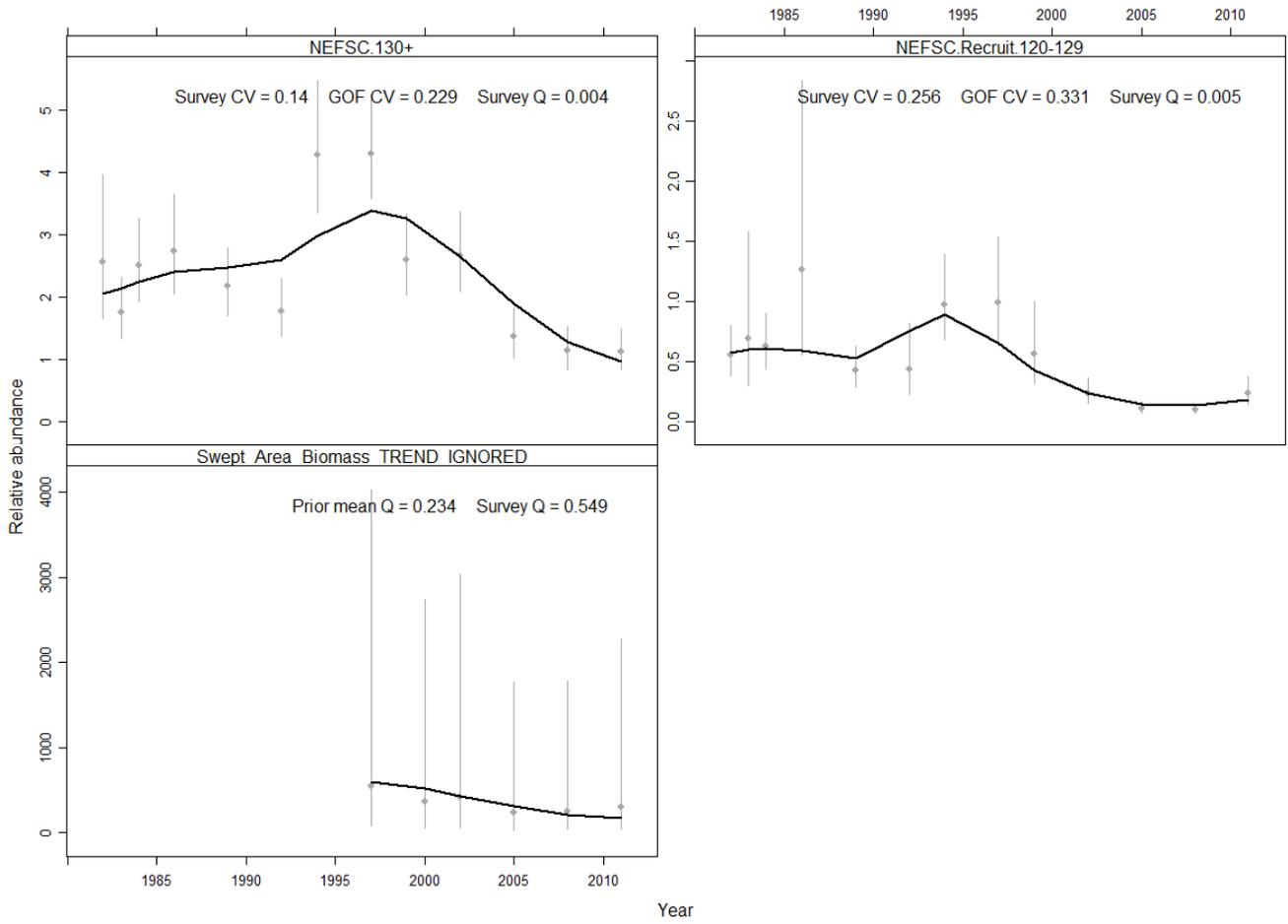
Appendix A5. Figure 8. The data with approximate 95% confidence intervals used to model the southern area (SVA to SNE) with KLAMZ.

Total biomass (1000's mt) with 95% asymptotic confidence intervals

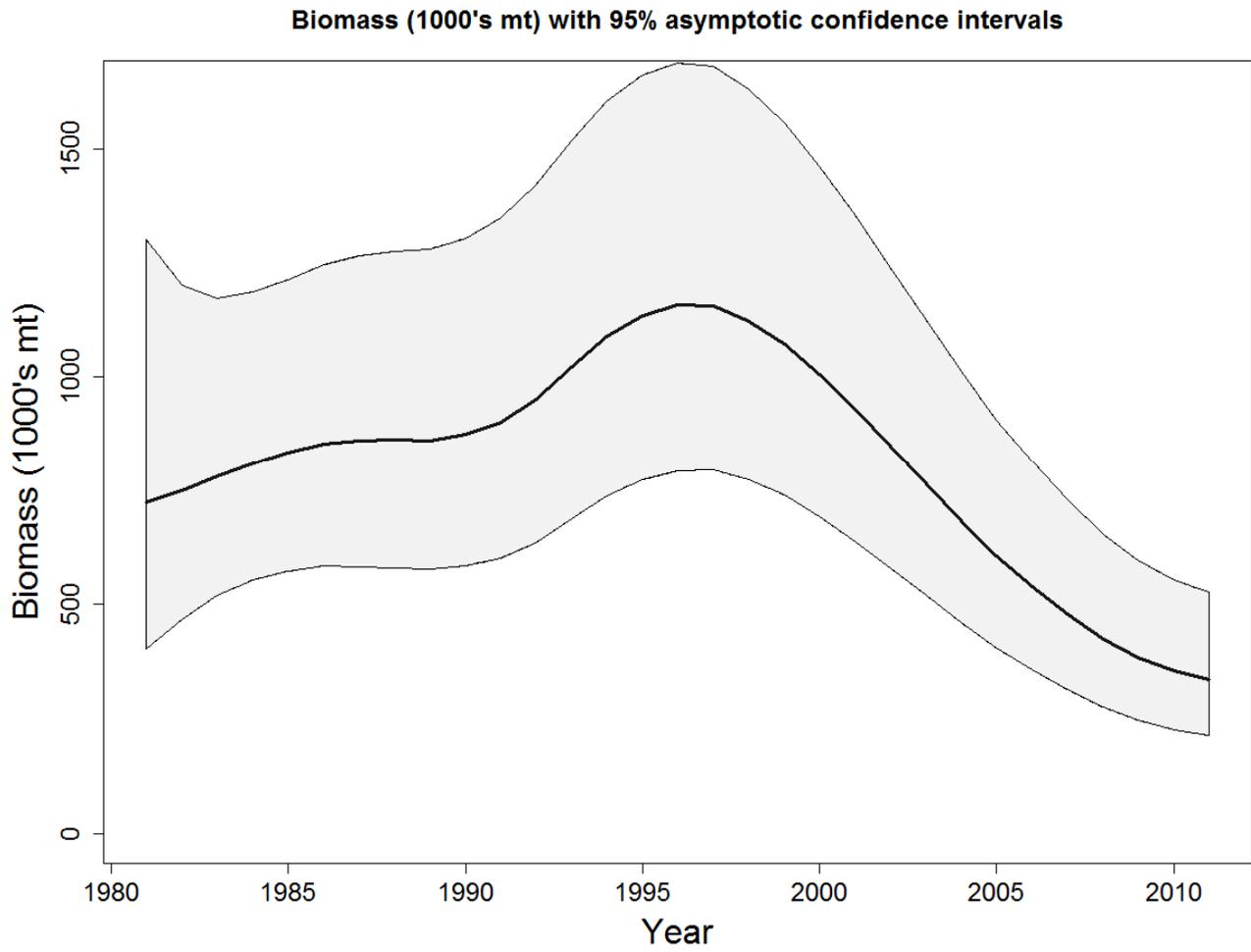


Appendix A5. Figure 9. Sensitivity to σ_R^2 the variance in the random walk recruitment parameter (RVAR).

SC_2012_update2009 - Survey observations, 95% CI and fitted values

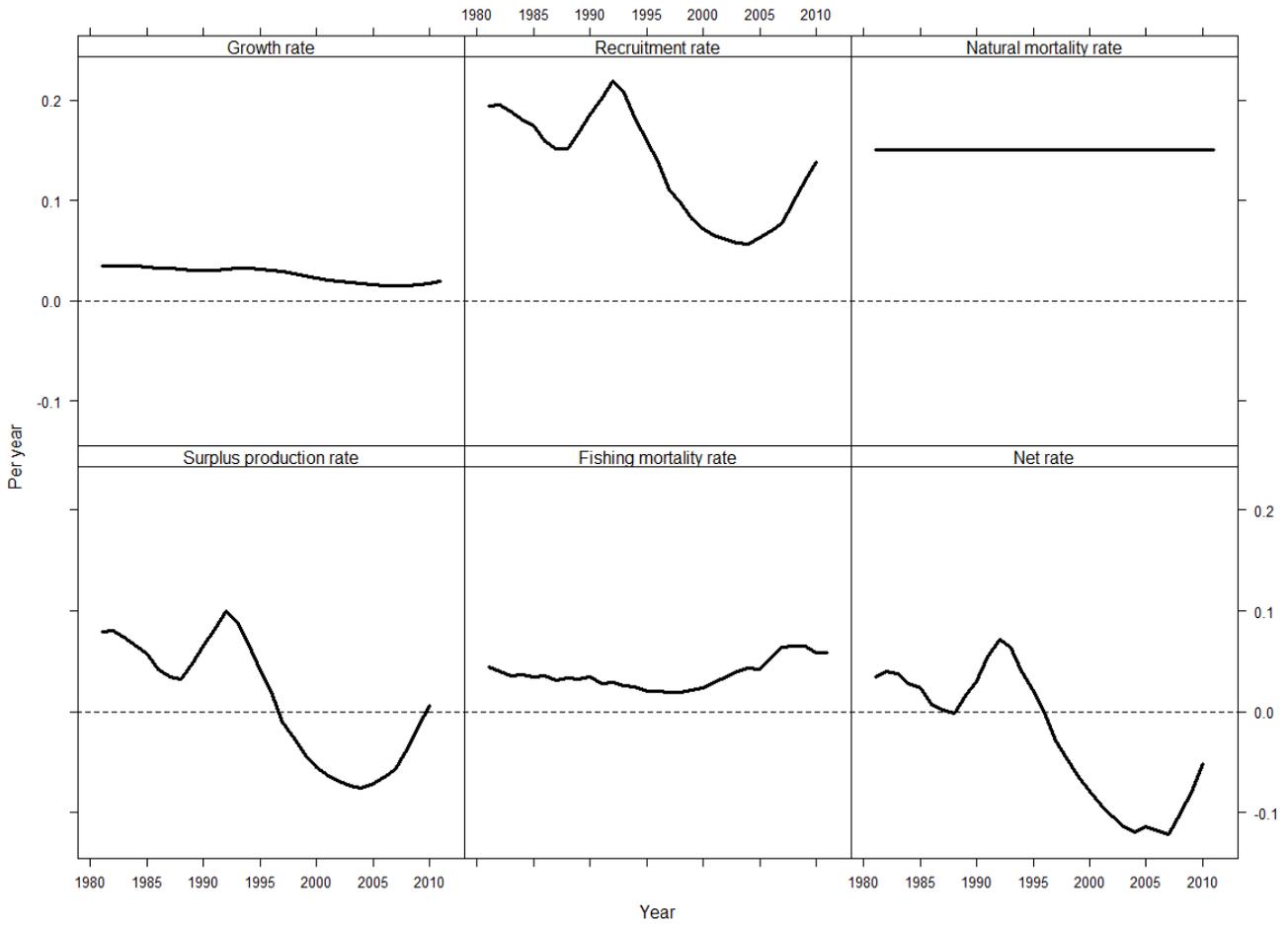


Appendix A5. Figure 10. KLAMZ model fit to the southern area.



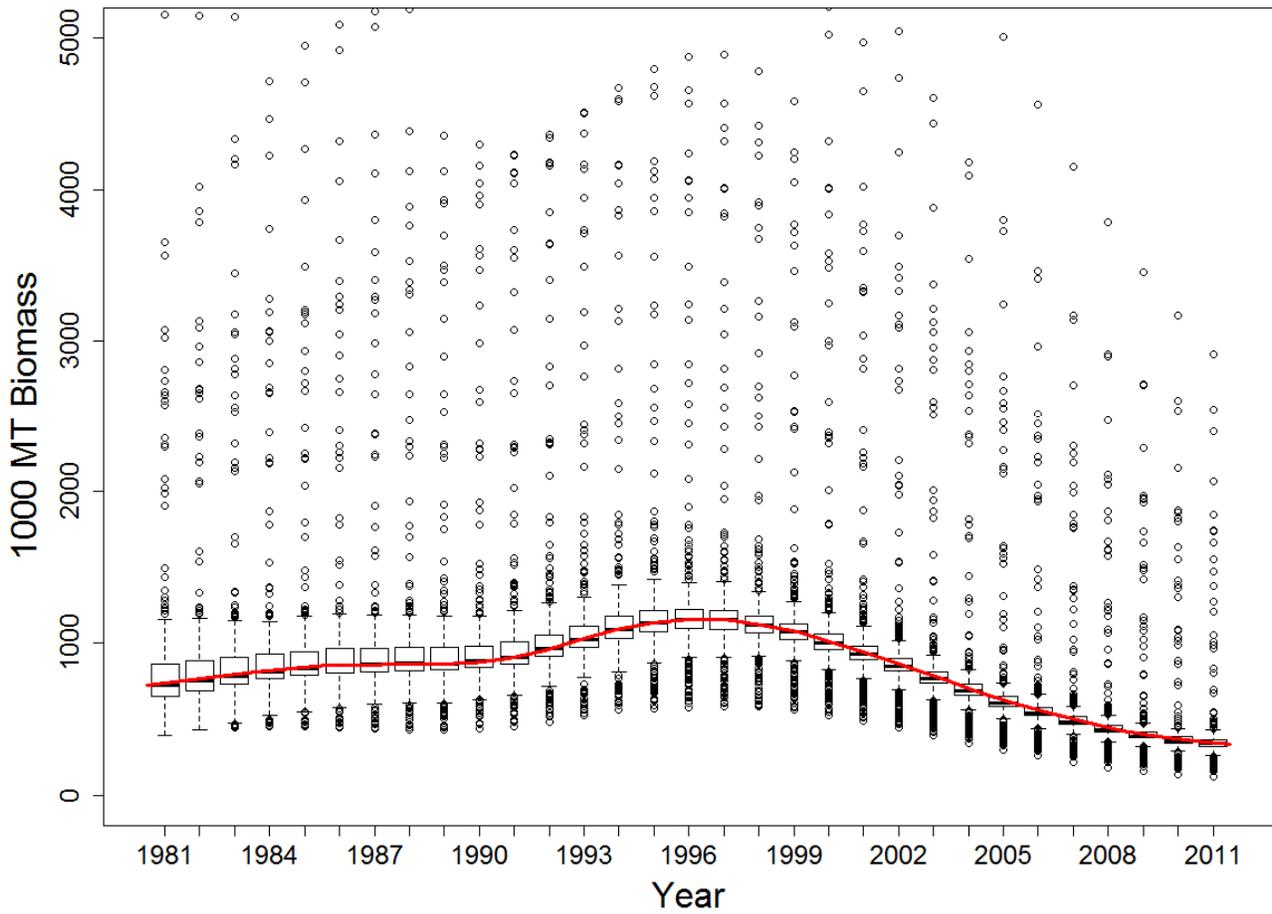
Appendix A5. Figure 11. Biomass (1000 mt) estimated using KLAMZ for the southern area.

SC_2012_update2009 - Population dynamics as rates



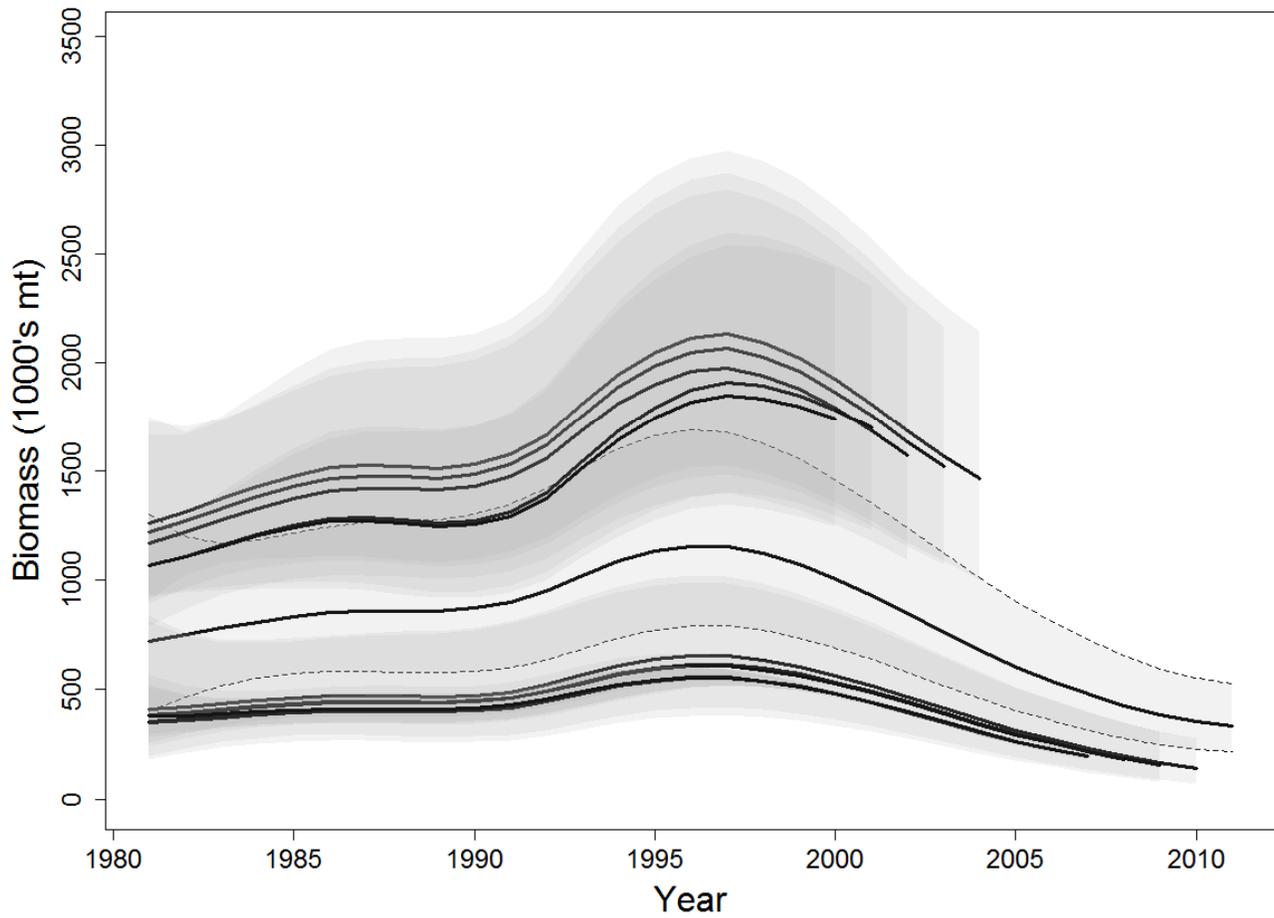
Appendix A5. Figure 12. Population dynamics as rates over time for the southern area.

Bootstrap realizations of basecase KLAMZ run



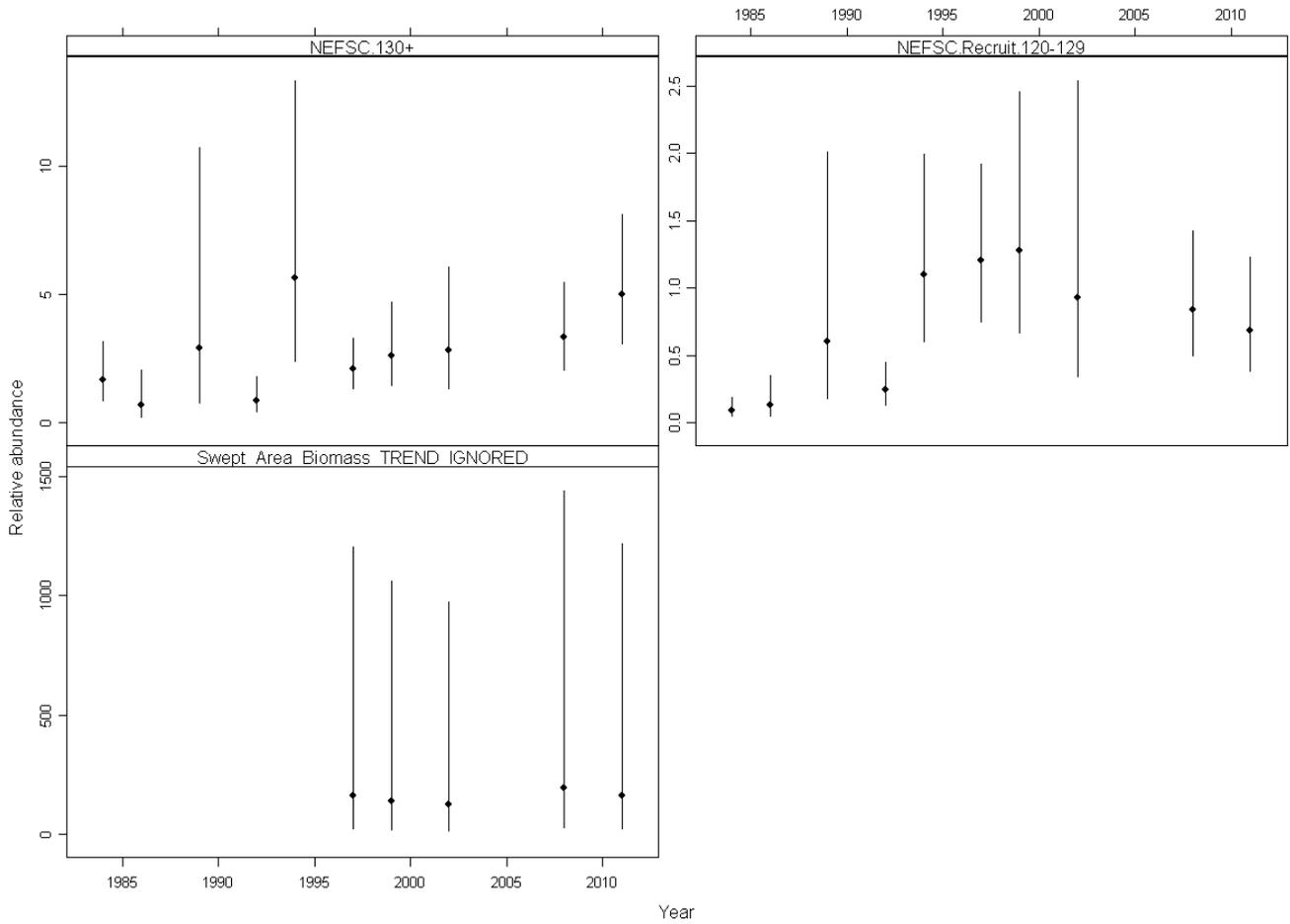
Appendix A5. Figure 13. Bootstrap iterations of the KLAMZ model biomass estimates for the southern area. The base case is shown in red.

Biomass (1000's mt) with 95% asymptotic confidence intervals



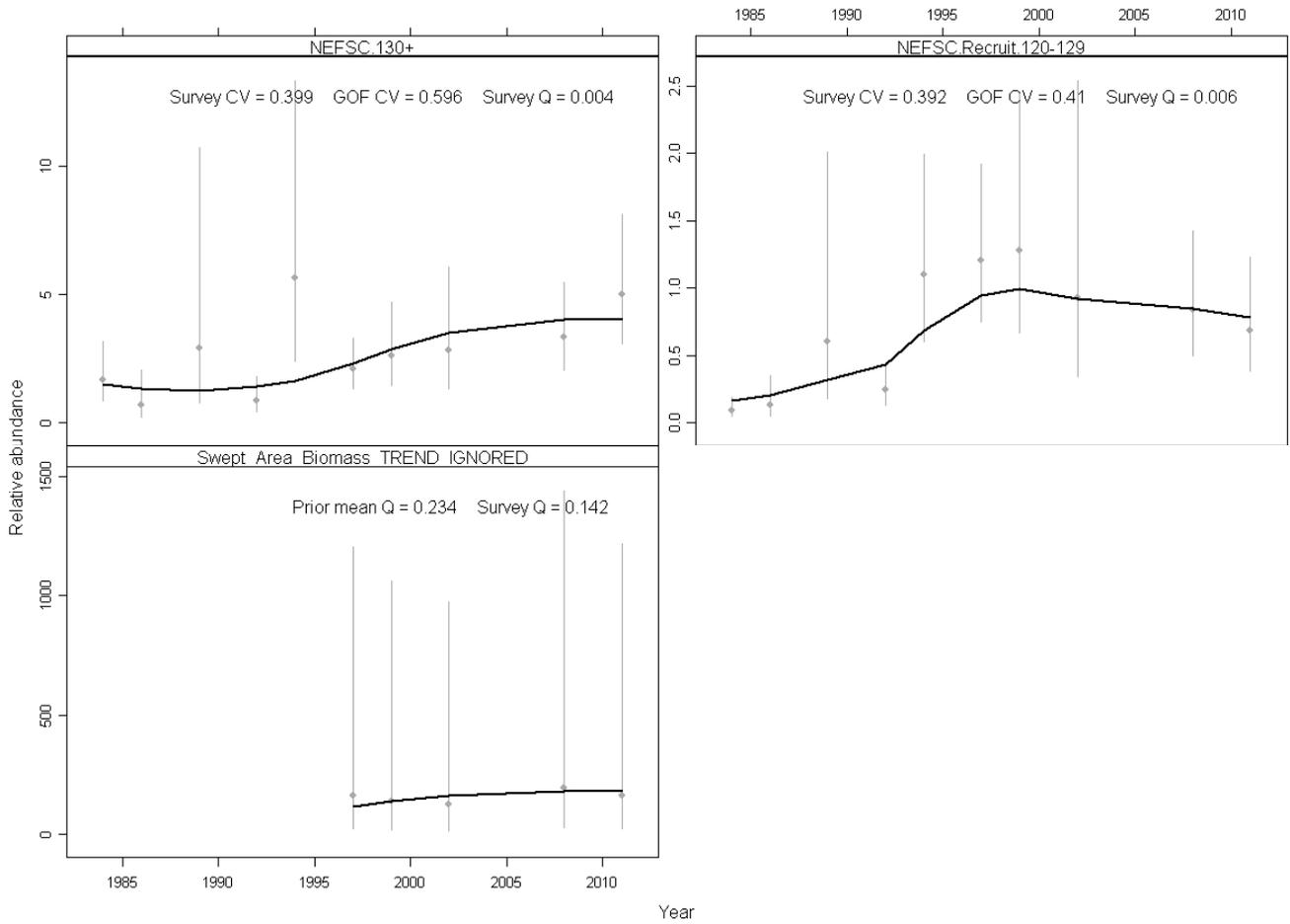
Appendix A5. Figure 14. Retrospective patterns in total biomass for the years 2000-2011 using the base case southern area KLAMZ model.

SC_2012_update2009 - Survey observations with 95% CI



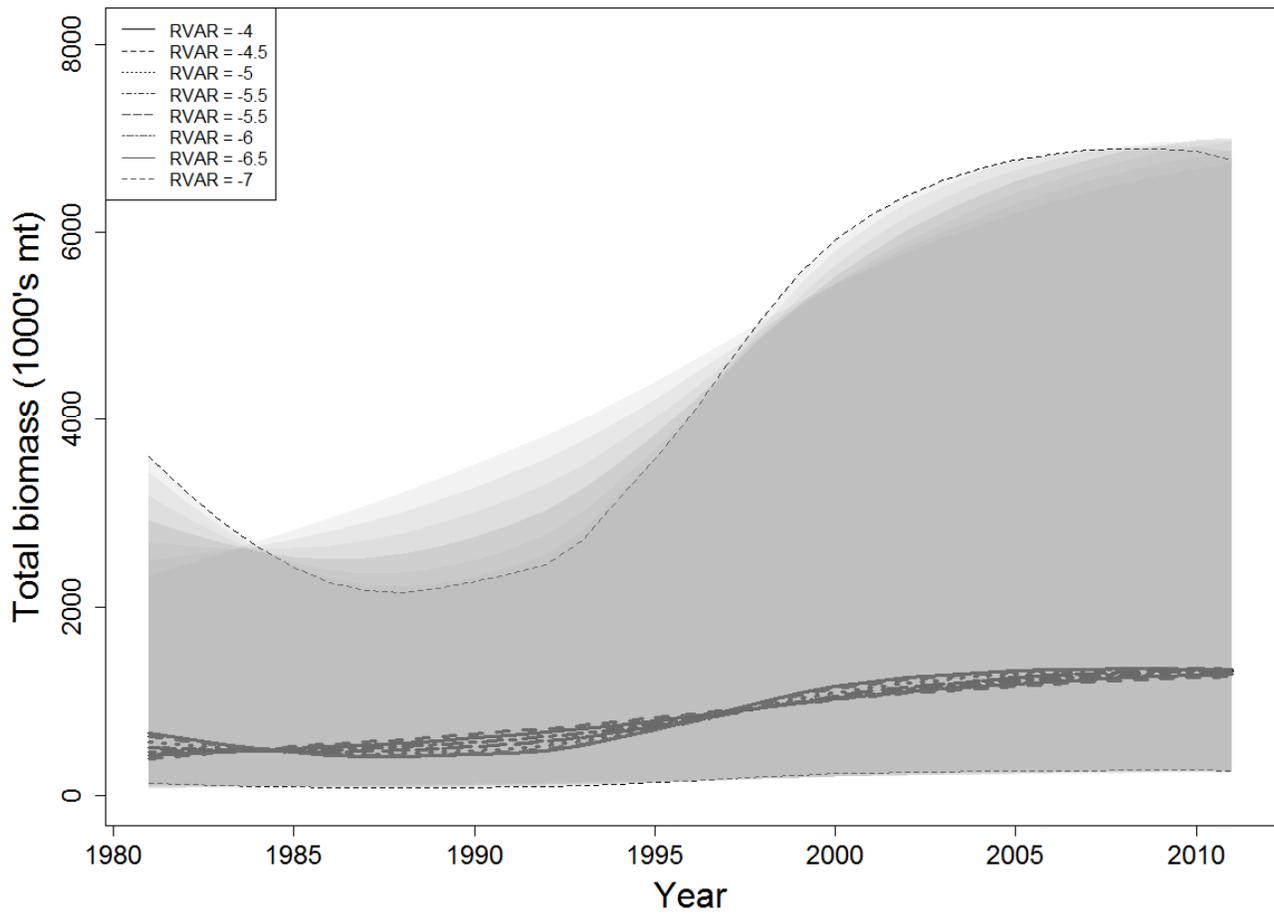
Appendix A5. Figure 15. The data with approximate 95% confidence intervals used to model the northern area (GBK) with KLAMZ.

SC_2012_update2009 - Survey observations, 95% CI and fitted values



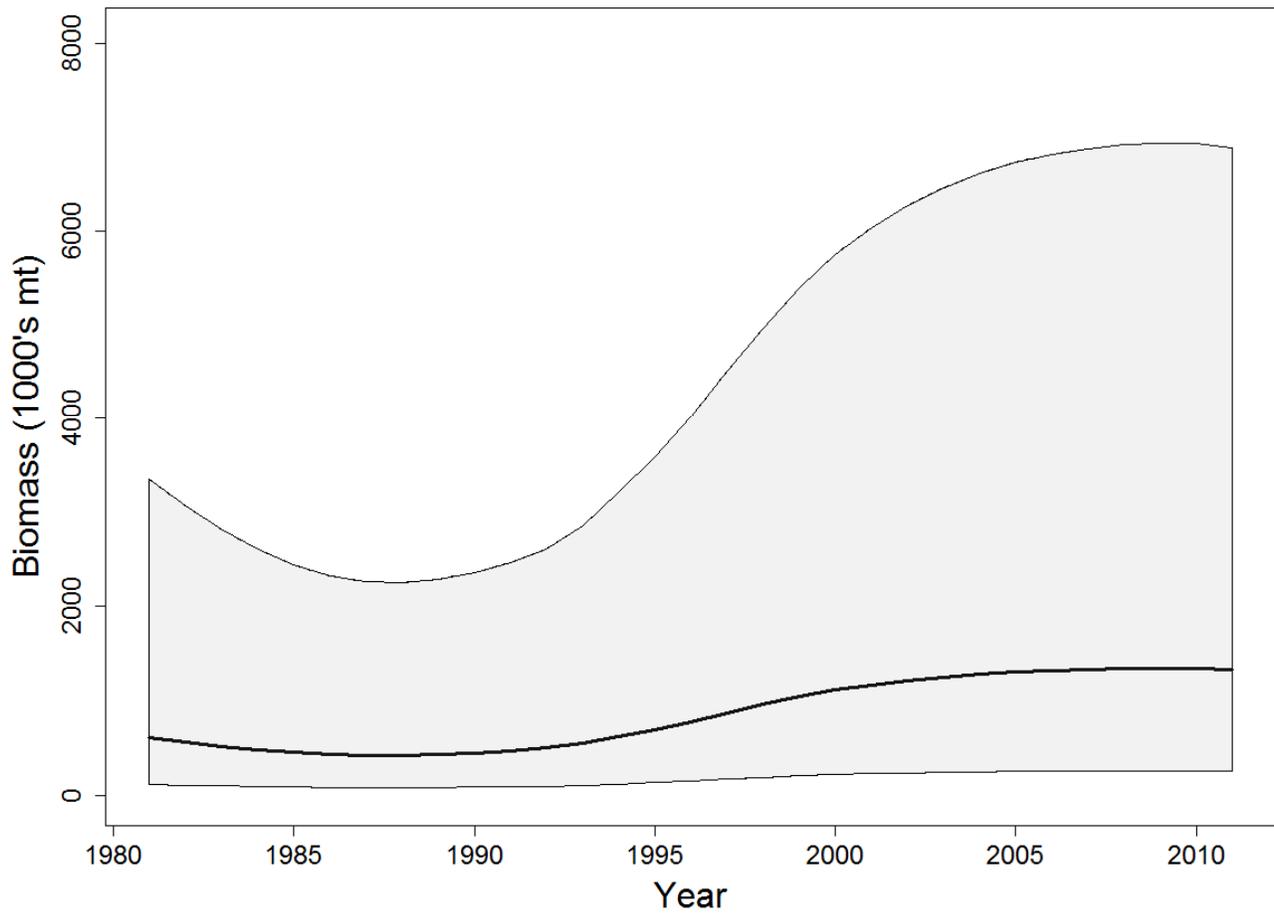
Appendix A5. Figure 16. KLAMZ model fit to the northern area (GBK).

Total biomass (1000's mt) with 95% asymptotic confidence intervals



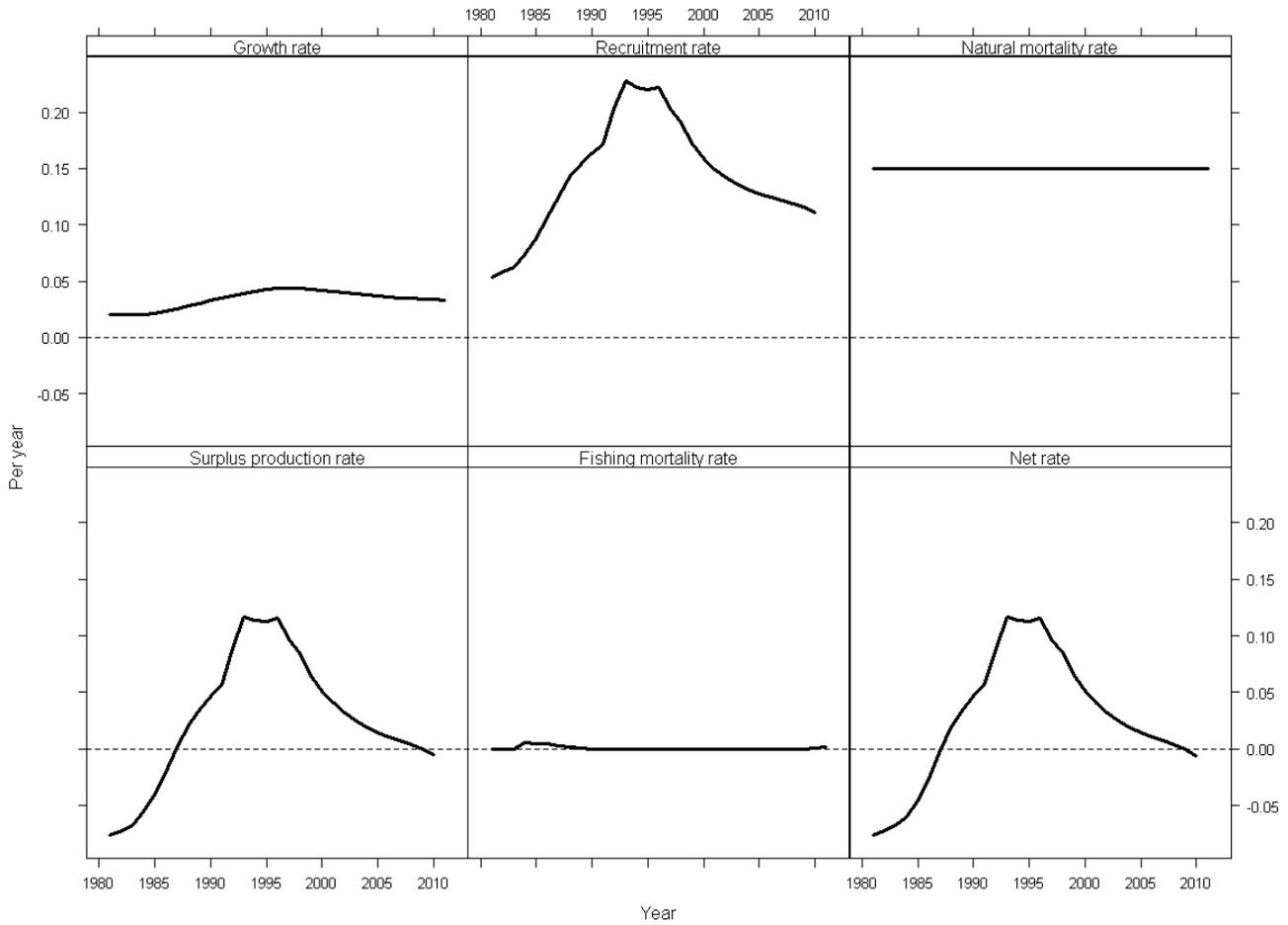
Appendix A5. Figure 17. Sensitivity to σ_R^2 in total biomass for northern area KLAMZ model fit.

Biomass (1000's mt) with 95% asymptotic confidence intervals



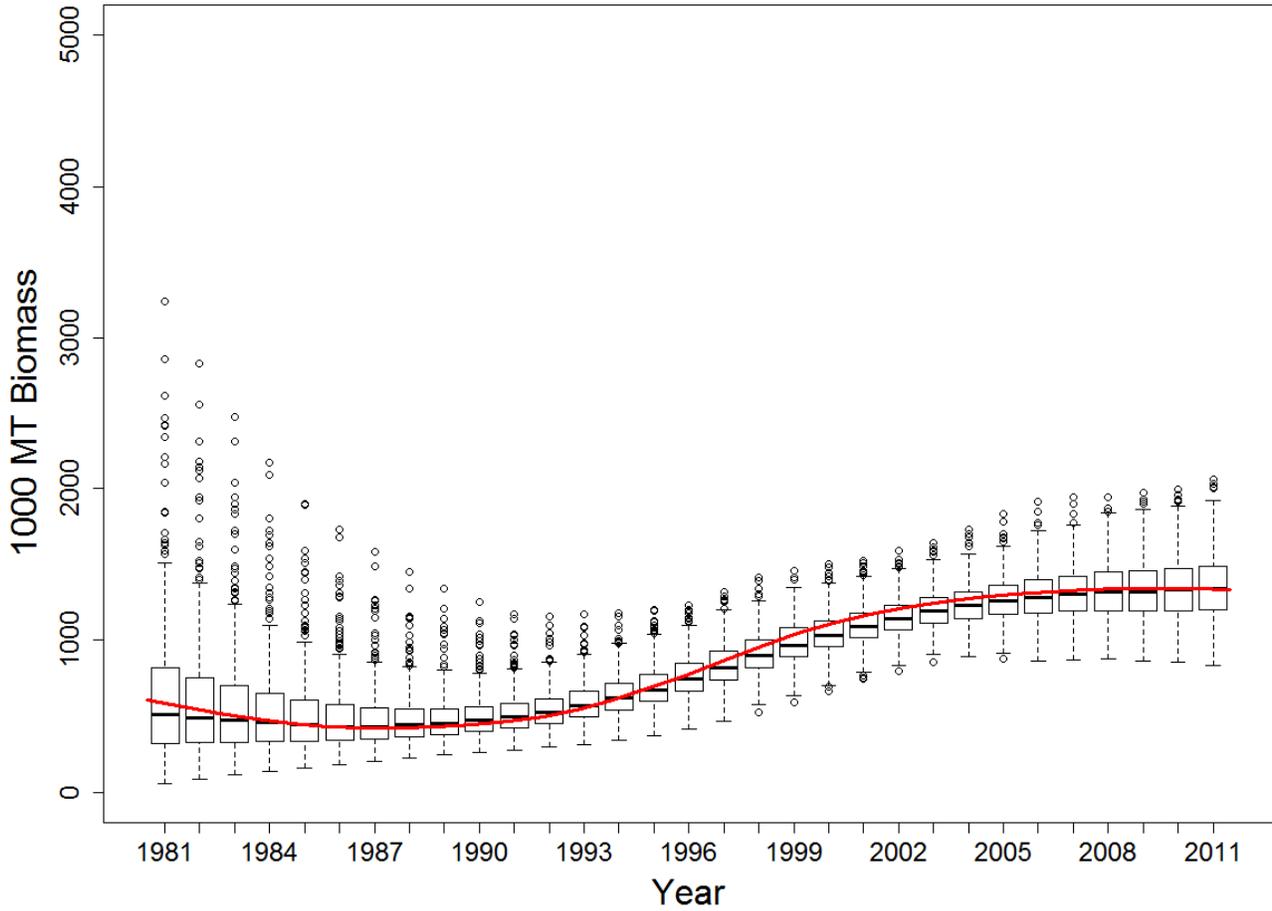
Appendix A5. Figure 18. Trend in biomass in the northern area.

SC_2012_update2009 - Population dynamics as rates



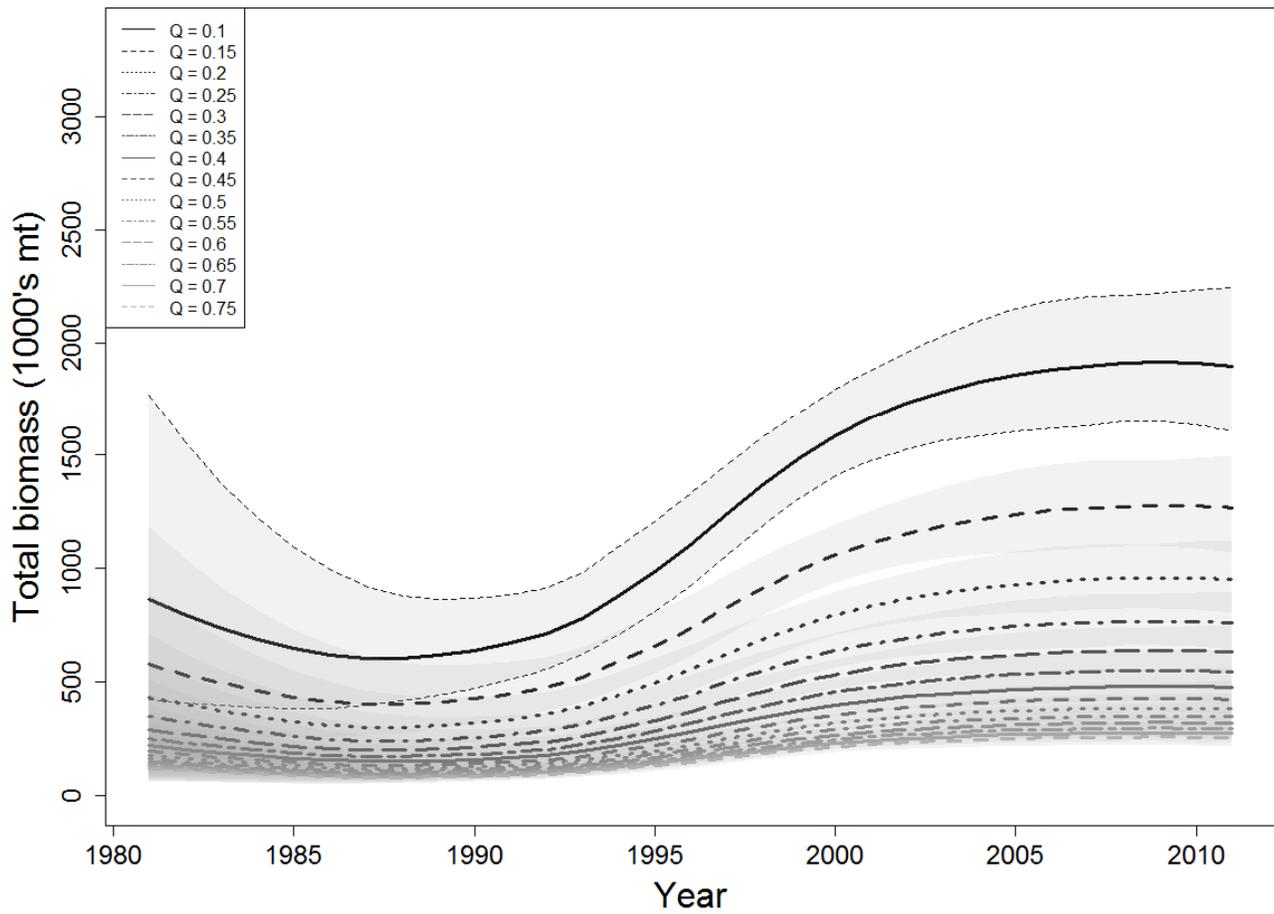
Appendix A5. Figure 19. Population dynamics as rates from KLAMZ model on northern area.

Bootstrap realizations of basescase KLAMZ run



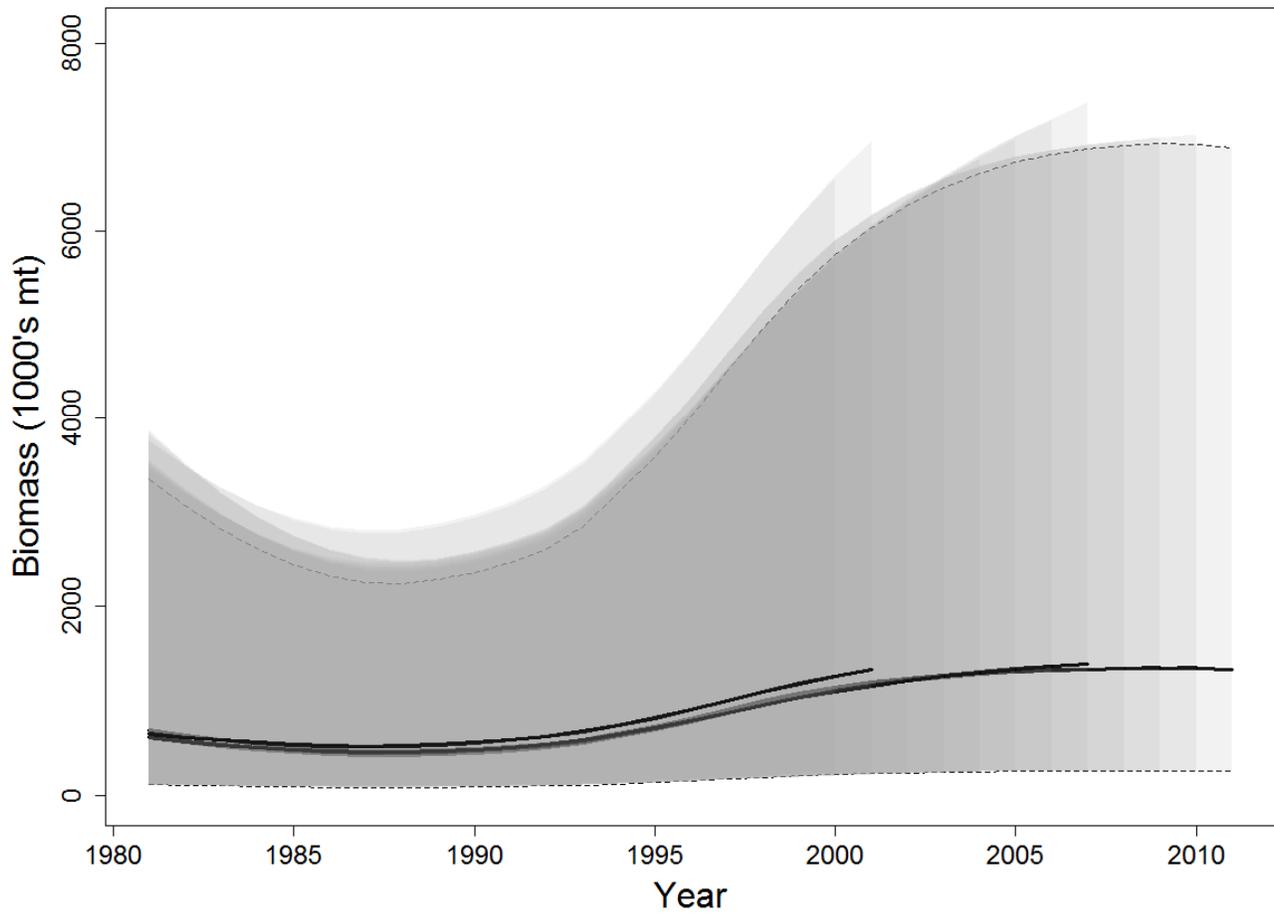
Appendix A5. Figure 20. Bootstrap iterations of the KLAMZ model biomass estimates for the northern area. The base case is shown in red.

Total biomass (1000's mt) with 95% asymptotic confidence intervals



Appendix A5. Figure 21. Profile over survey Q for the northern area.

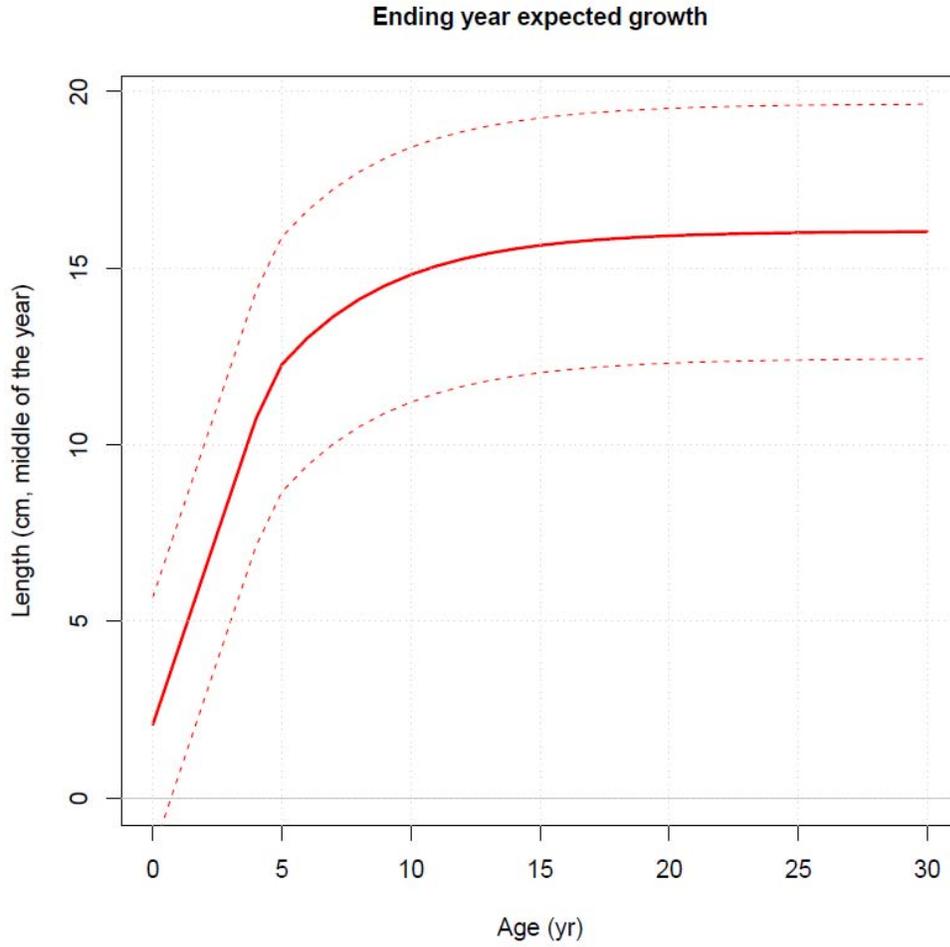
Biomass (1000's mt) with 95% asymptotic confidence intervals

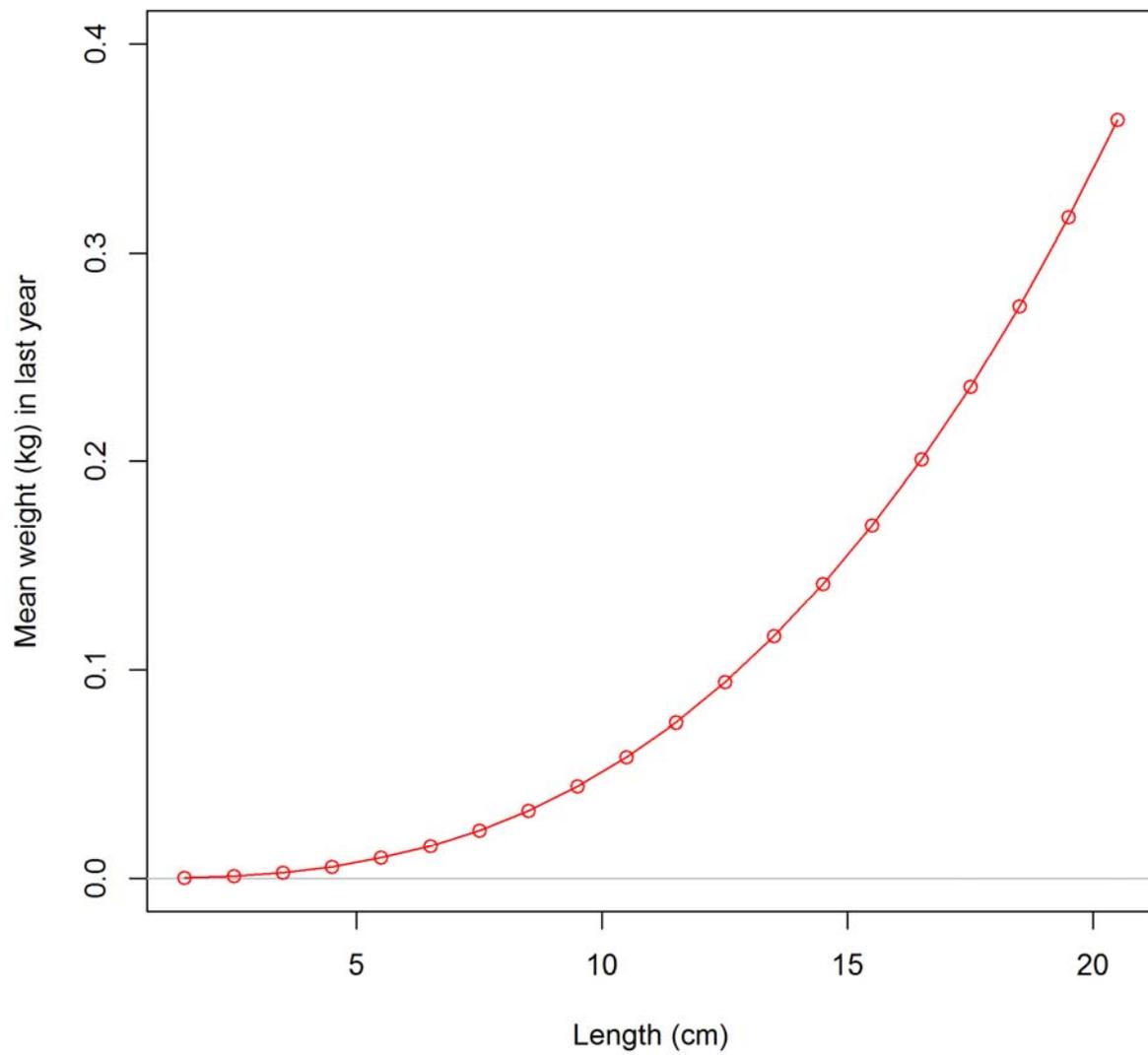


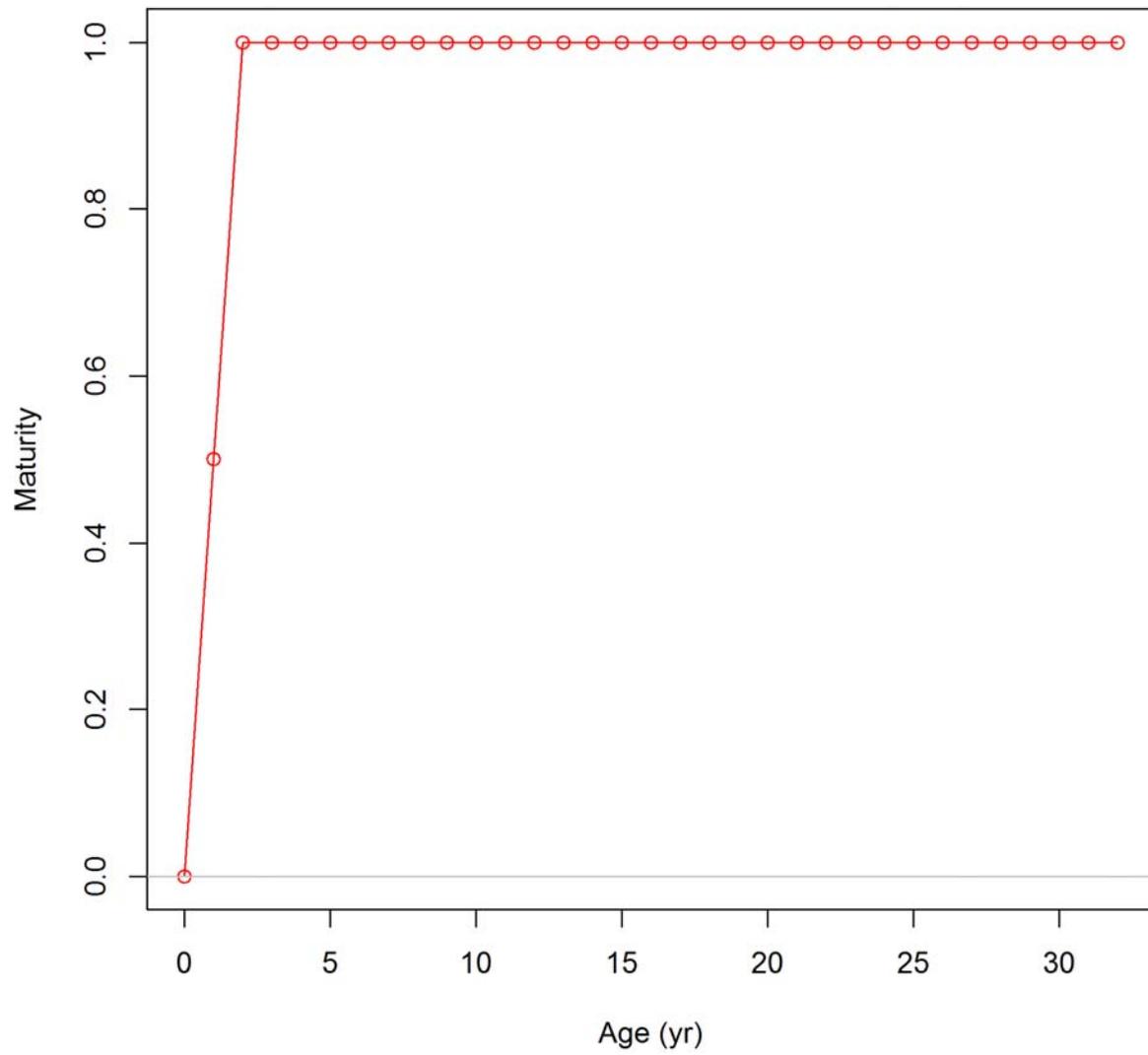
Appendix A5. Figure 22. Retrospective patterns in total biomass for the years 2000-2011 using the base case northern area KLAMZ model.

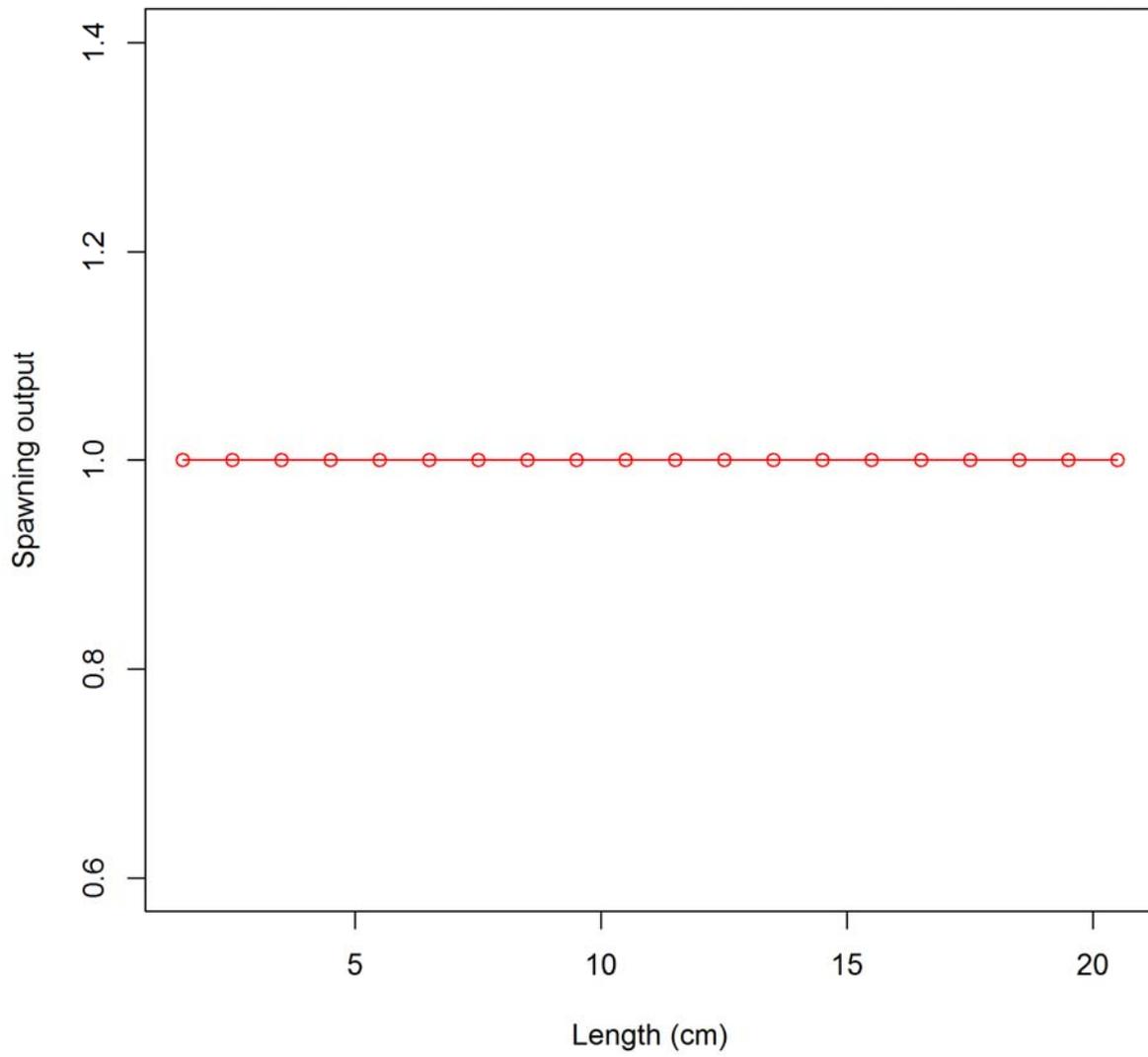
Appendix A6: SS3 diagnostics for the southern area

Plots created using the 'r4ss' package in R
Stock Synthesis version: SS-V3.24f
StartTime: Thu Dec 6 12:28:02 2012
Data_File: Surfclam_South-1.dat
Control_File: Surfclam_South-1.ctf

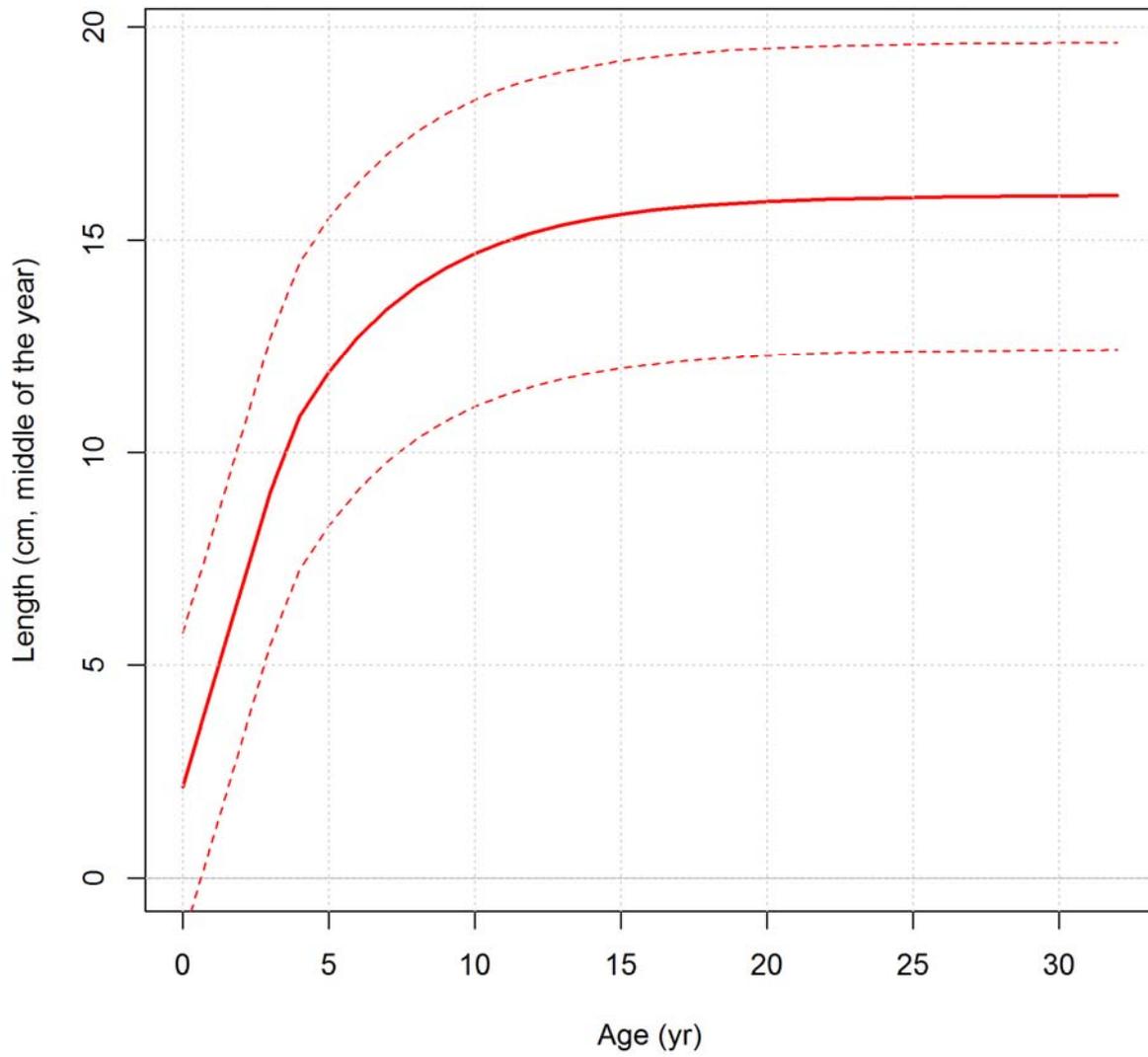


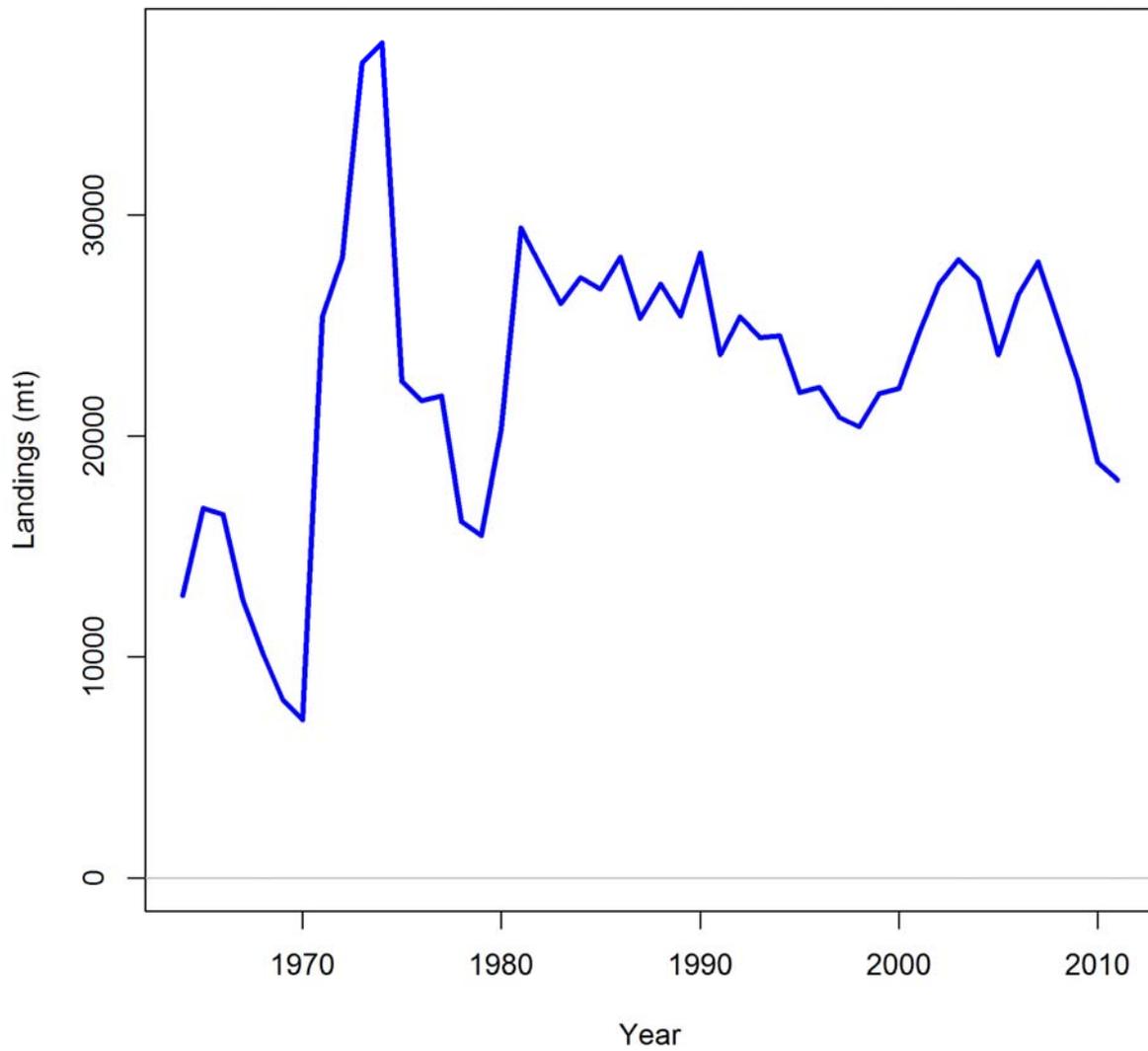


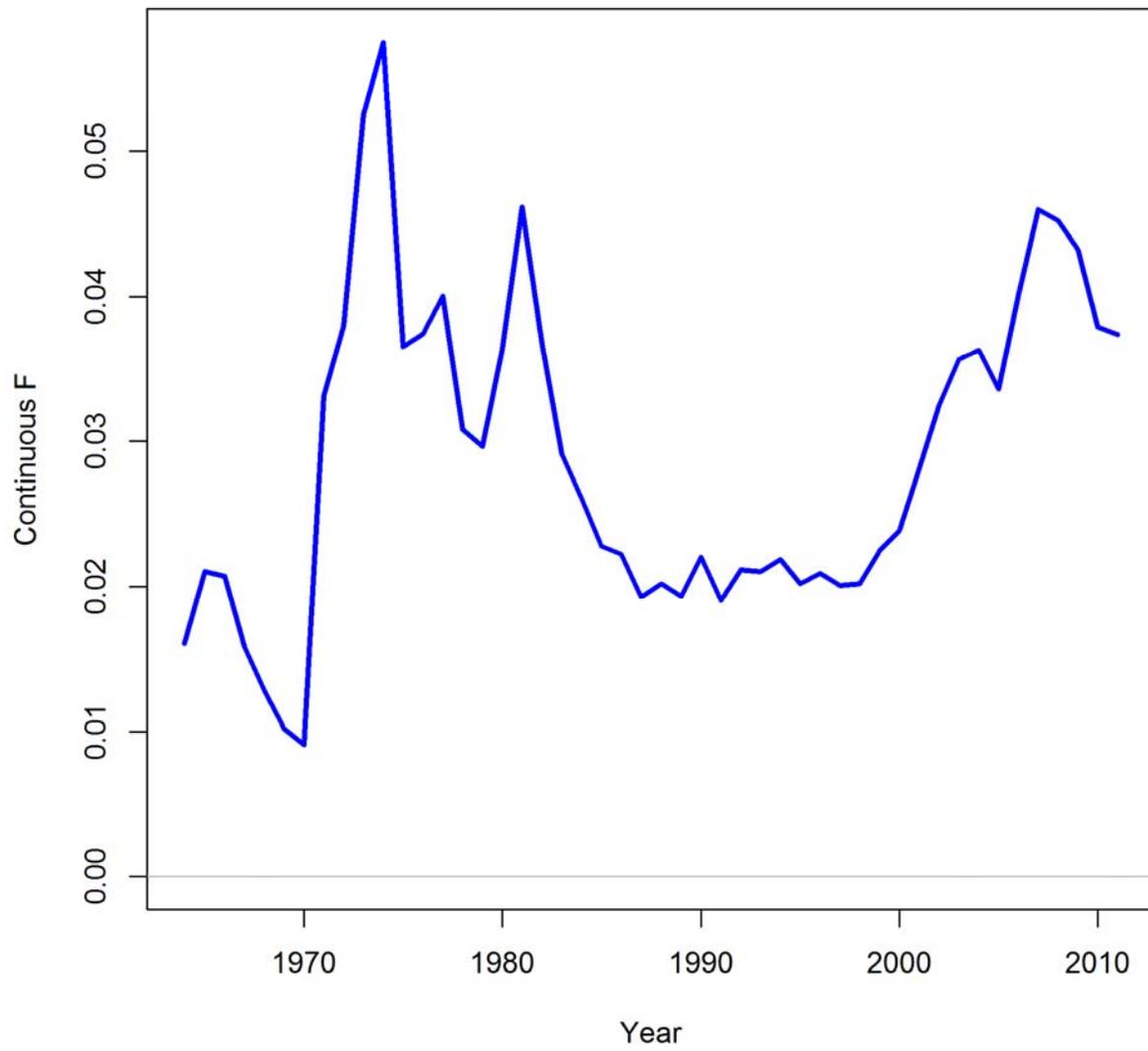




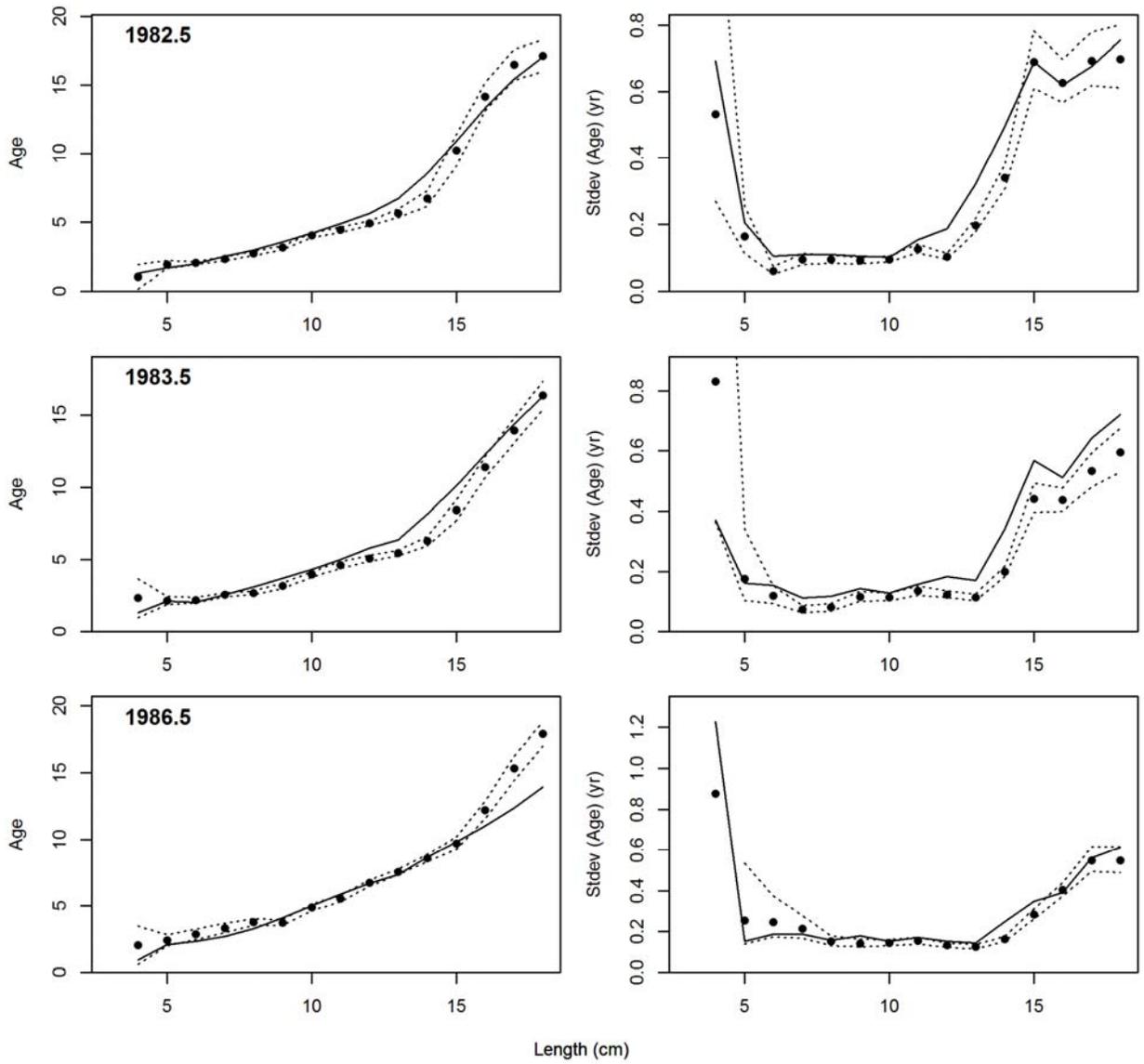
Ending year expected growth



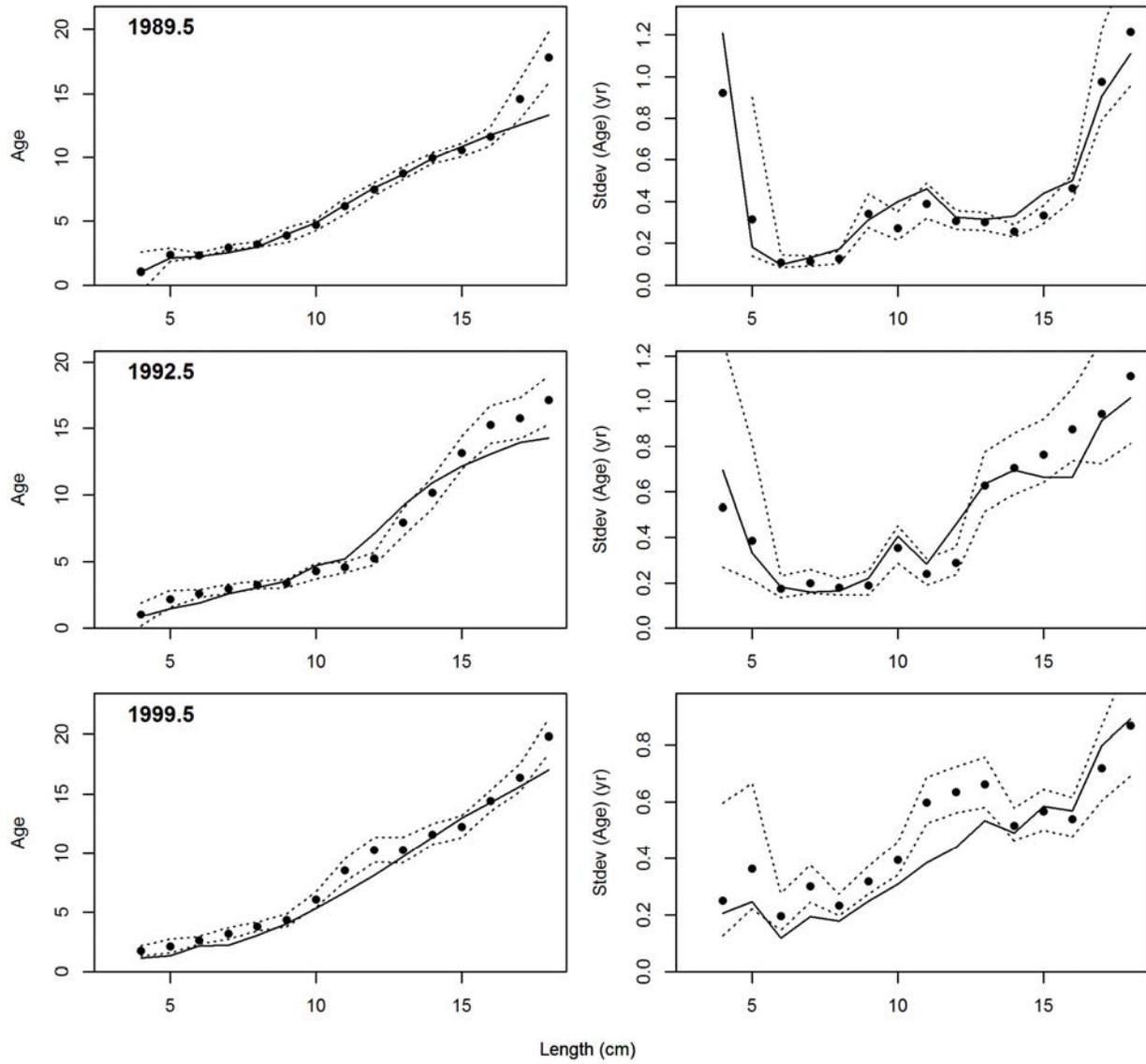




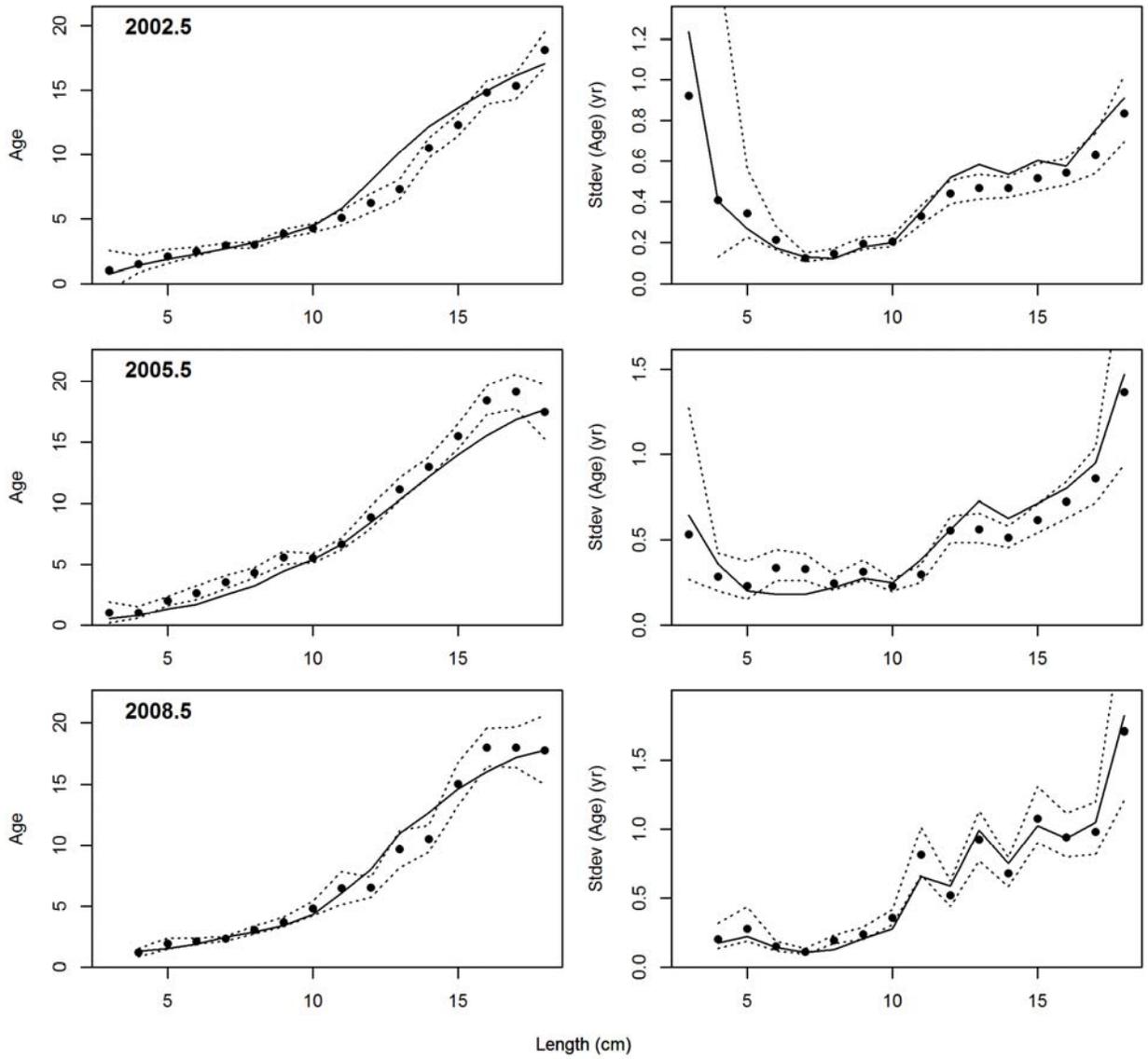
Andre's conditional AAL plot, sexes combined, whole catch, NperTow+mm



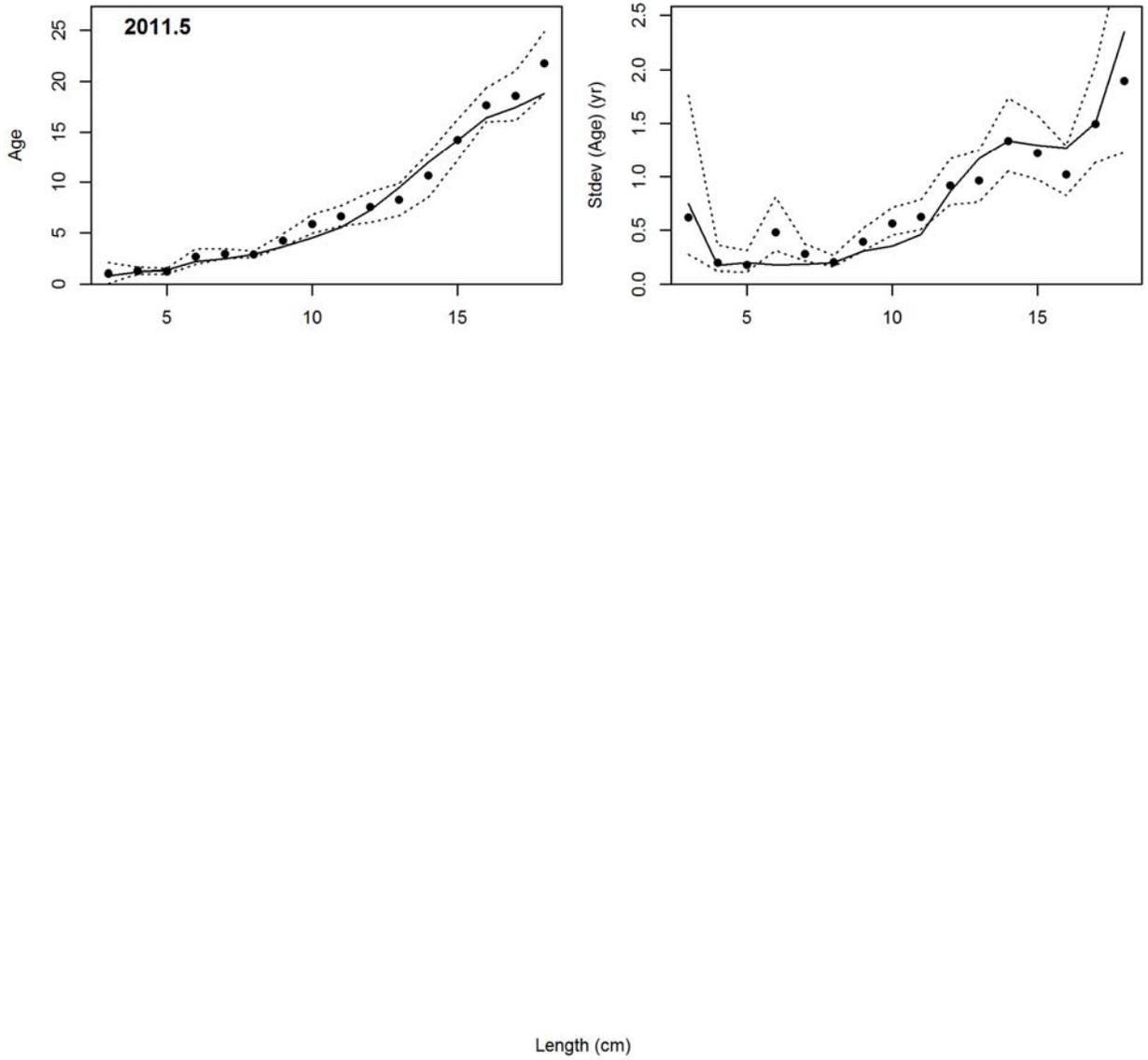
Andre's conditional AAL plot, sexes combined, whole catch, NperTow+mm



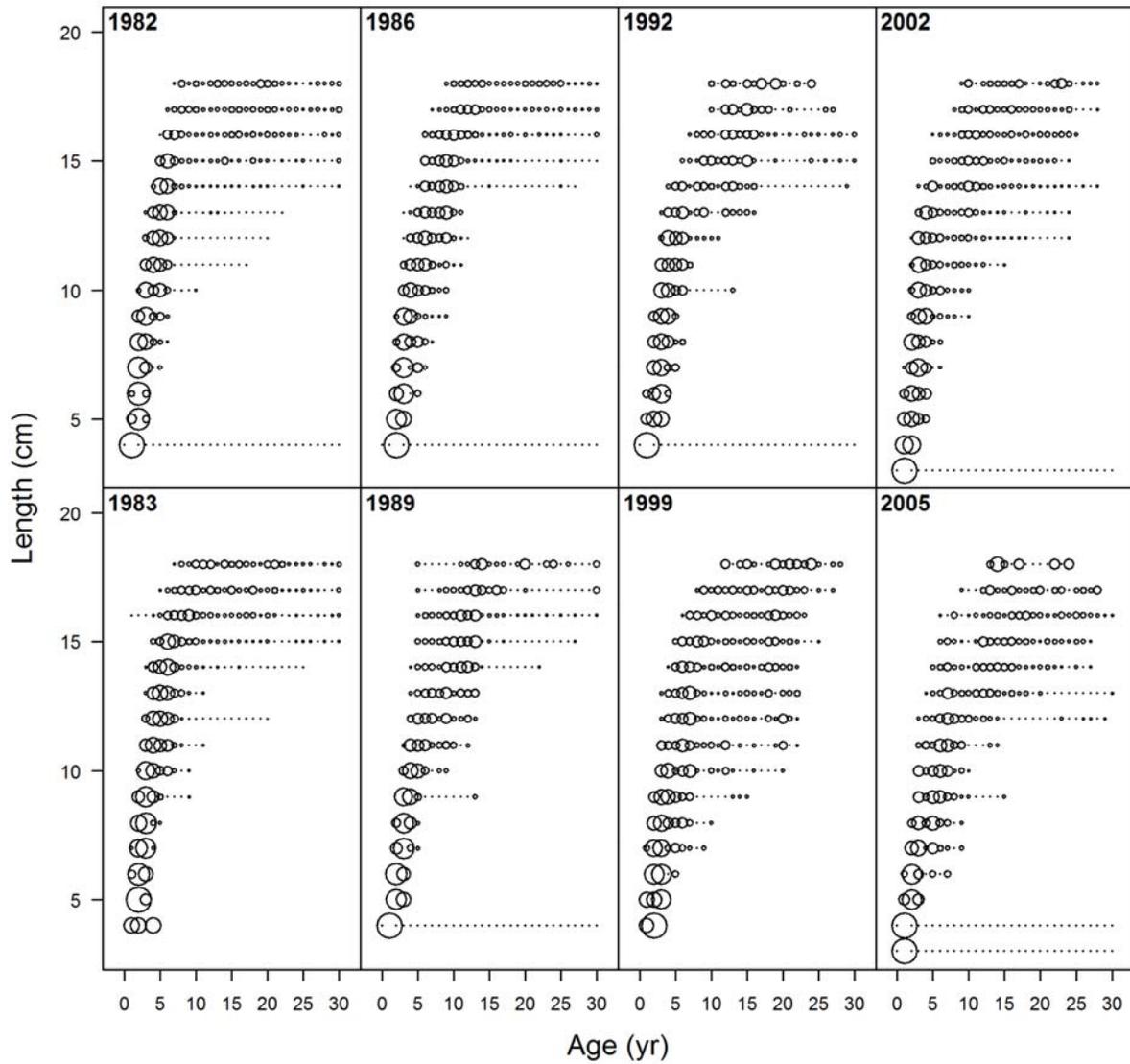
Andre's conditional AAL plot, sexes combined, whole catch, NperTow+mm



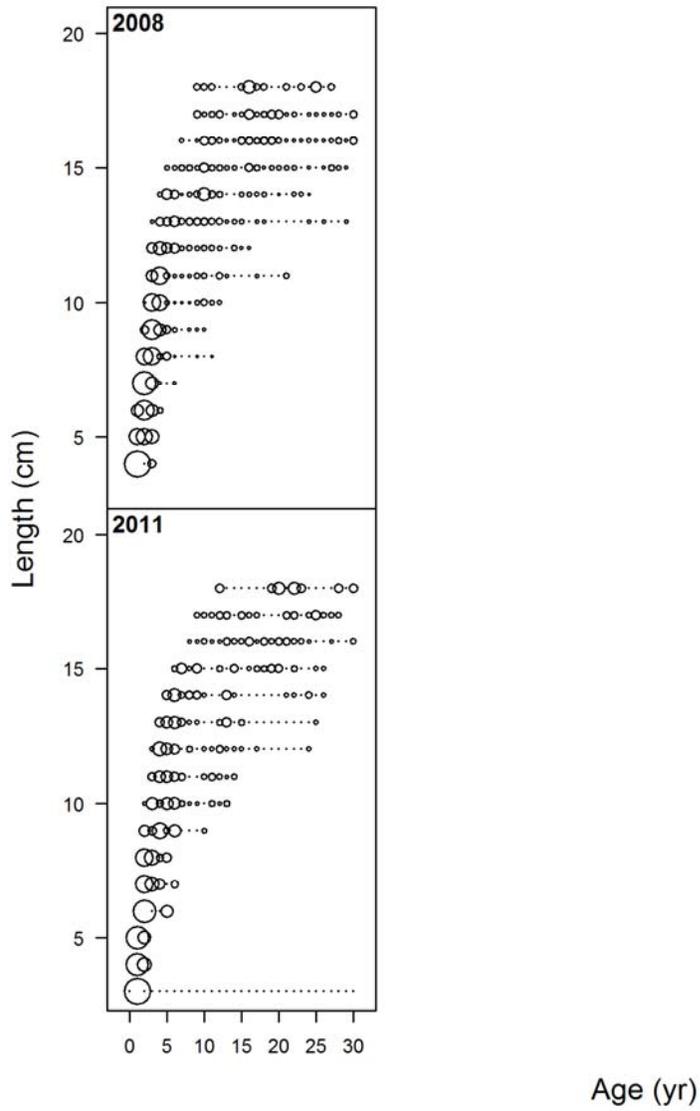
Andre's conditional AAL plot, sexes combined, whole catch, NperTow+mm



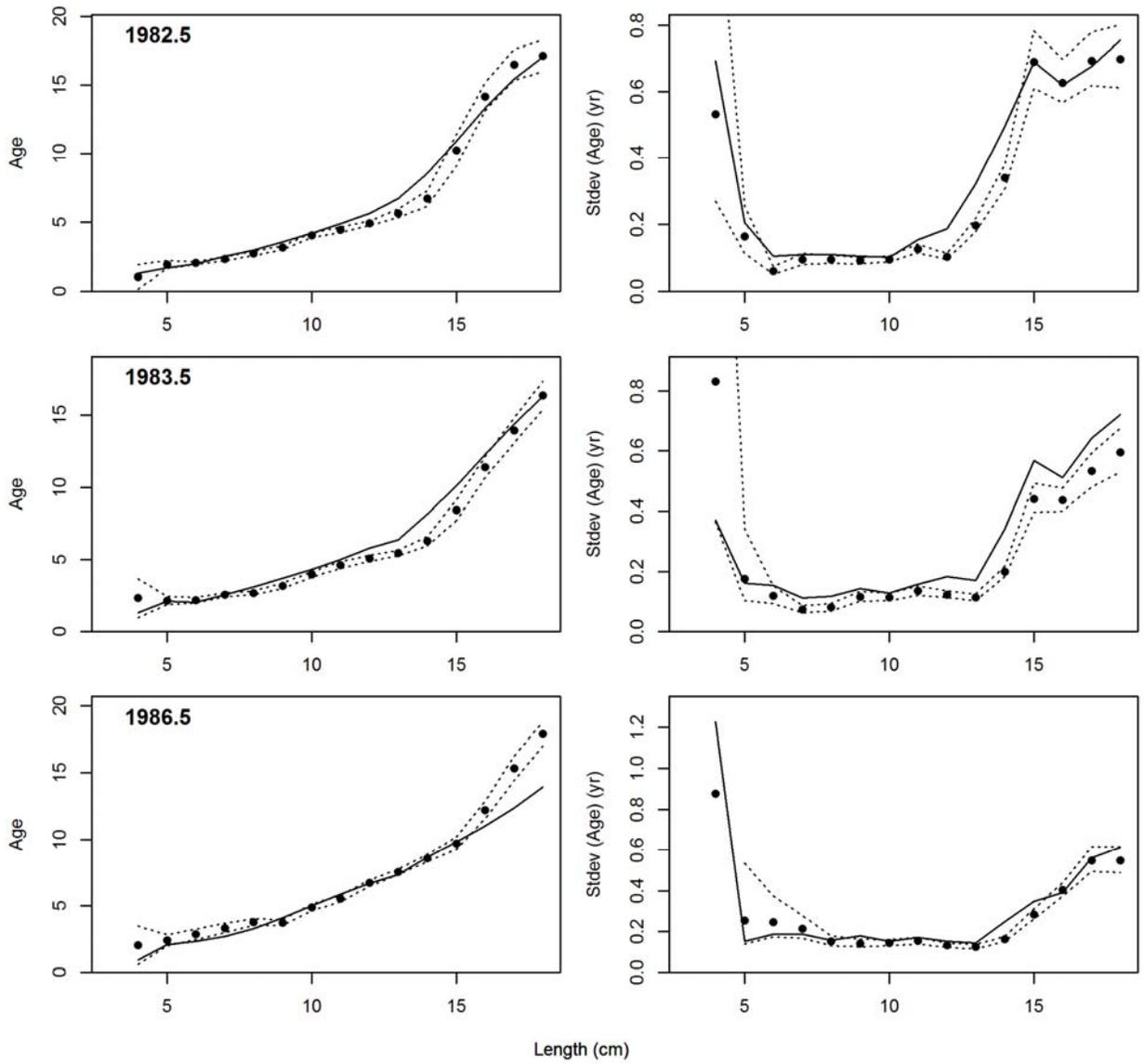
conditional age-at-length data, sexes combined, whole catch, NperTow+mm (max=1)



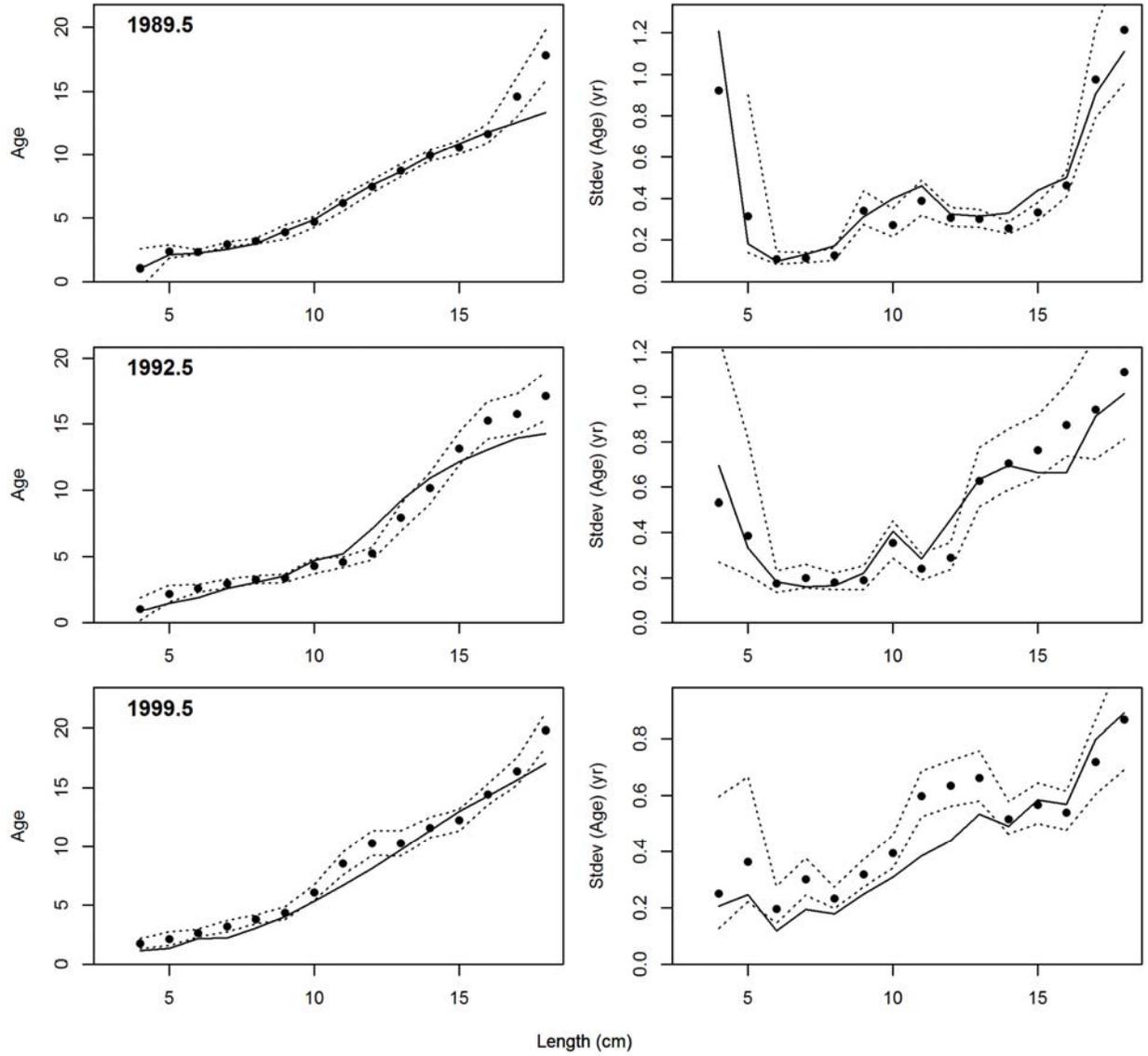
conditional age-at-length data, sexes combined, whole catch, NperTow+mm (max=1)



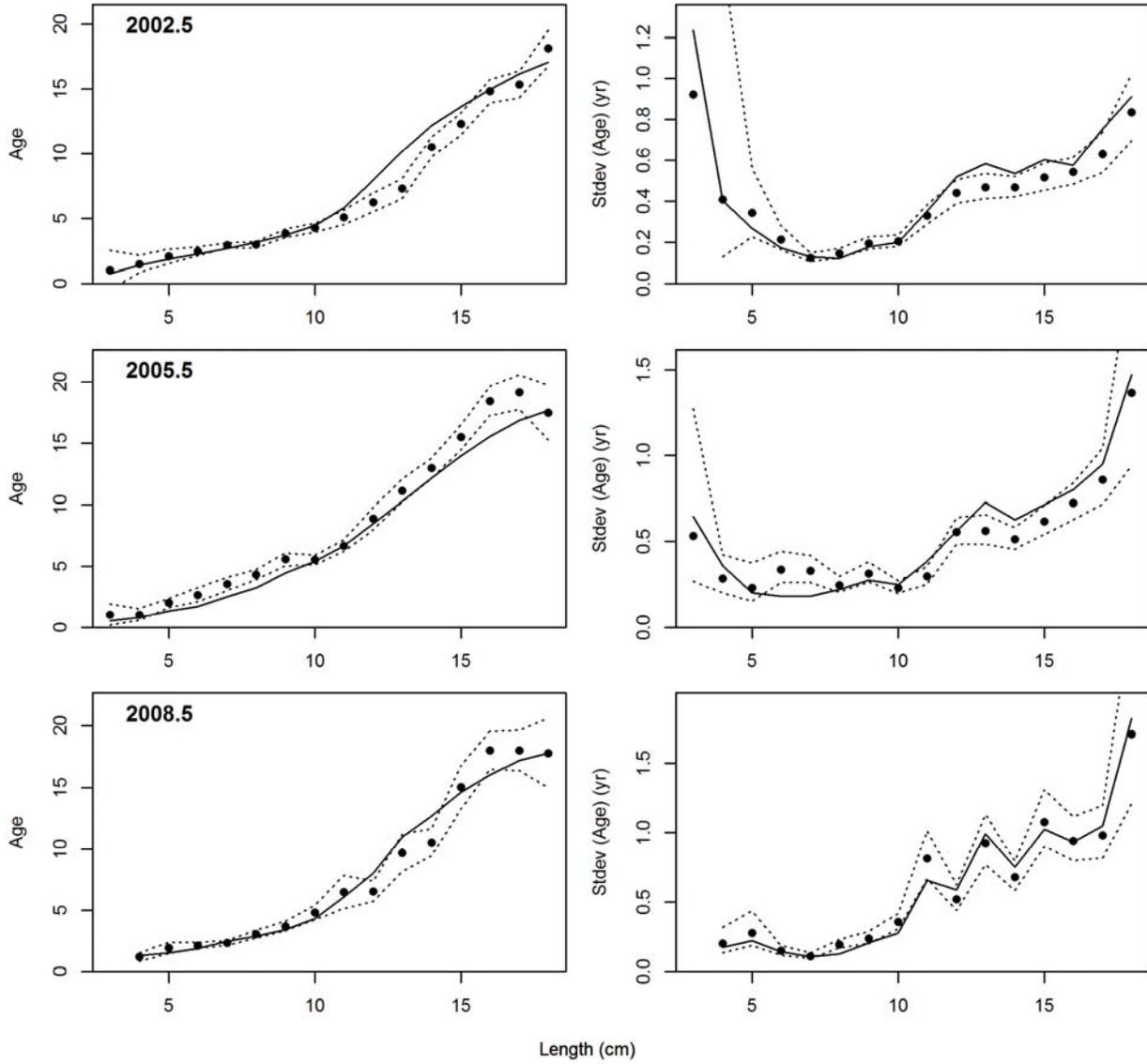
Andre's conditional AAL plot, sexes combined, whole catch, NperTow+mm



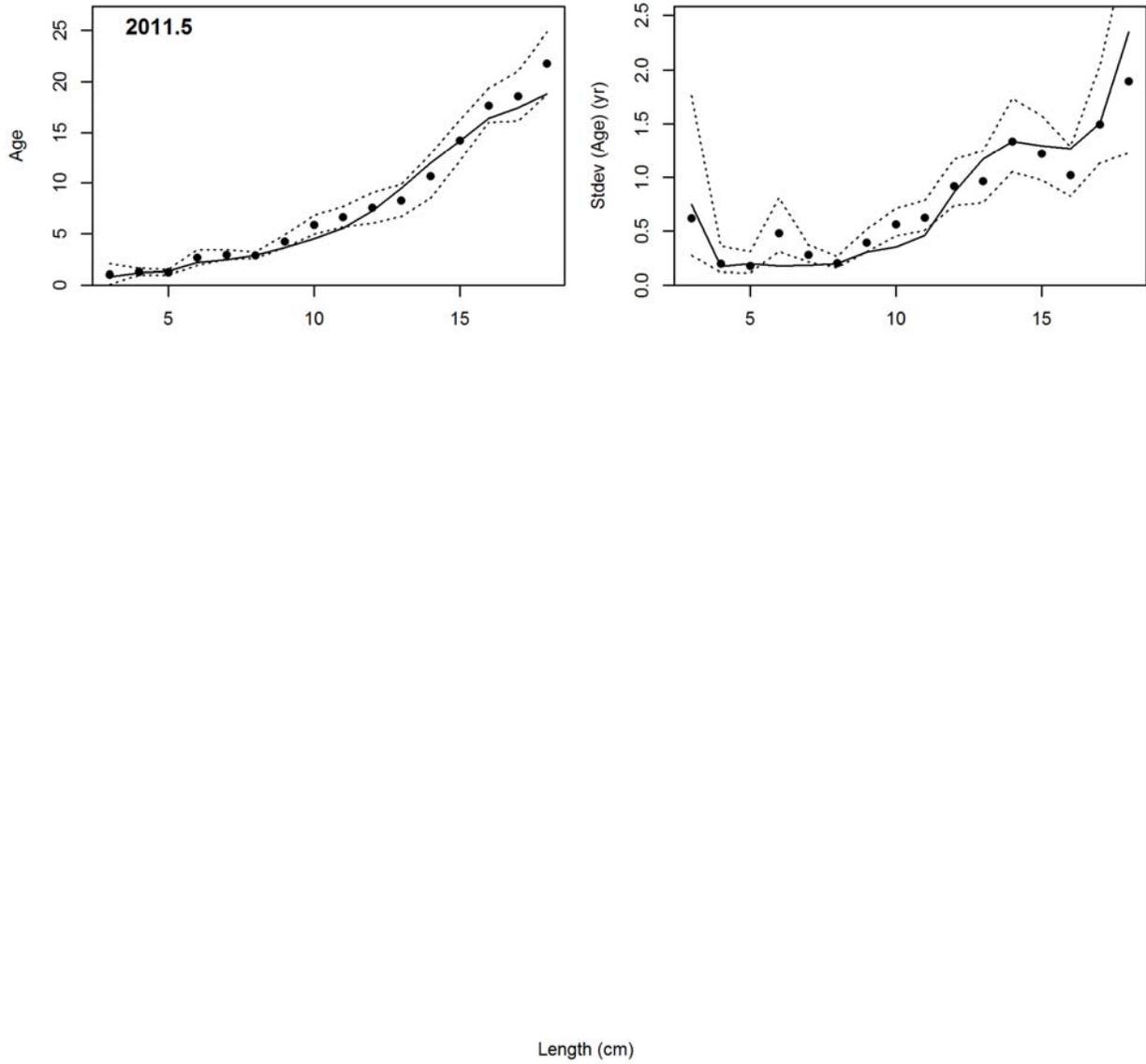
Andre's conditional AAL plot, sexes combined, whole catch, NperTow+mm



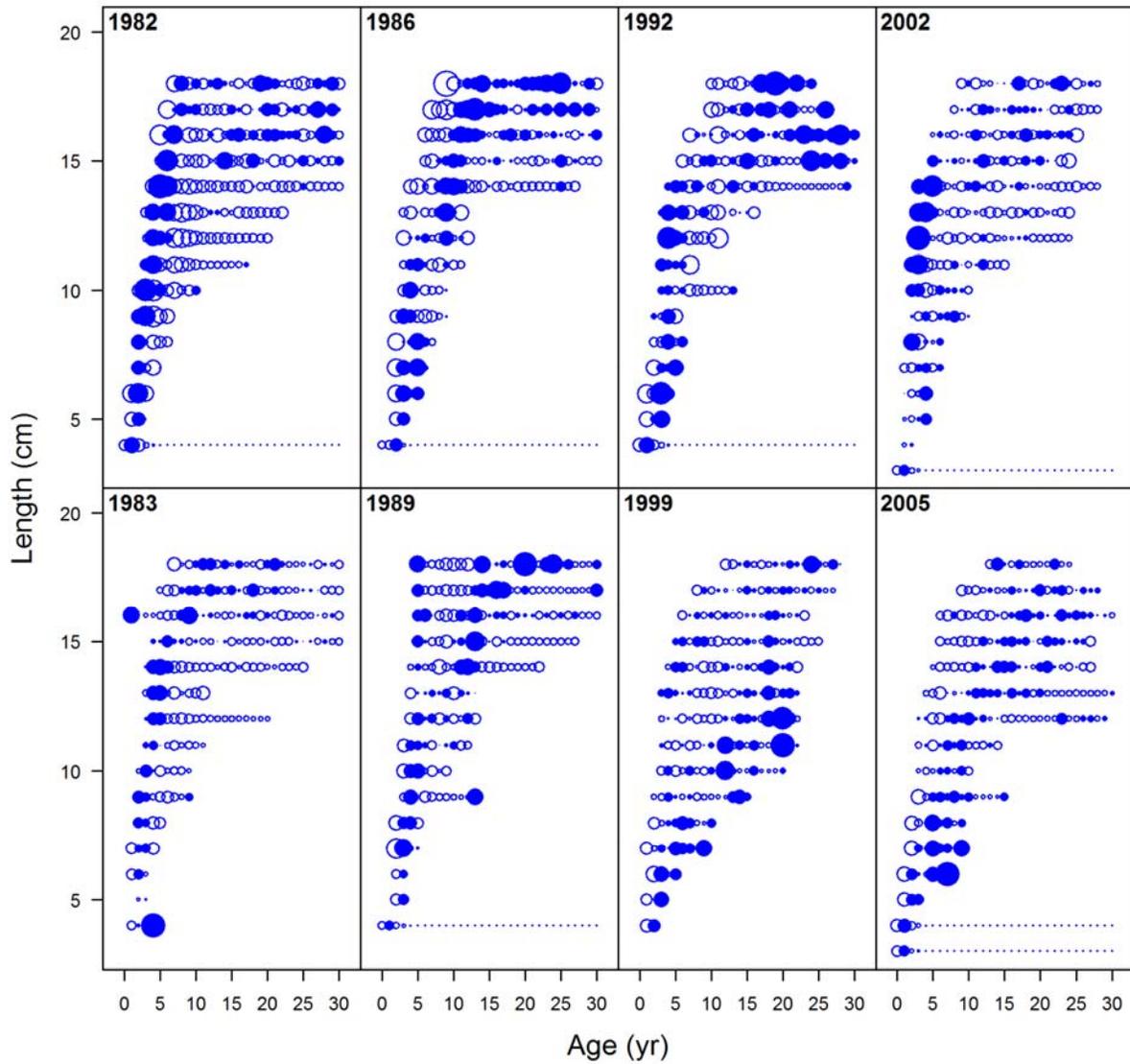
Andre's conditional AAL plot, sexes combined, whole catch, NperTow+mm



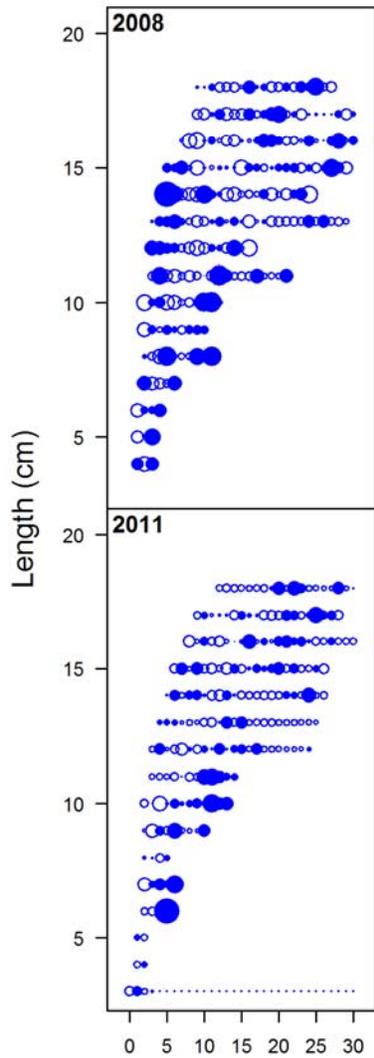
Andre's conditional AAL plot, sexes combined, whole catch, NperTow+mm



Pearson residuals, sexes combined, whole catch, NperTow+mm (max=10.83)

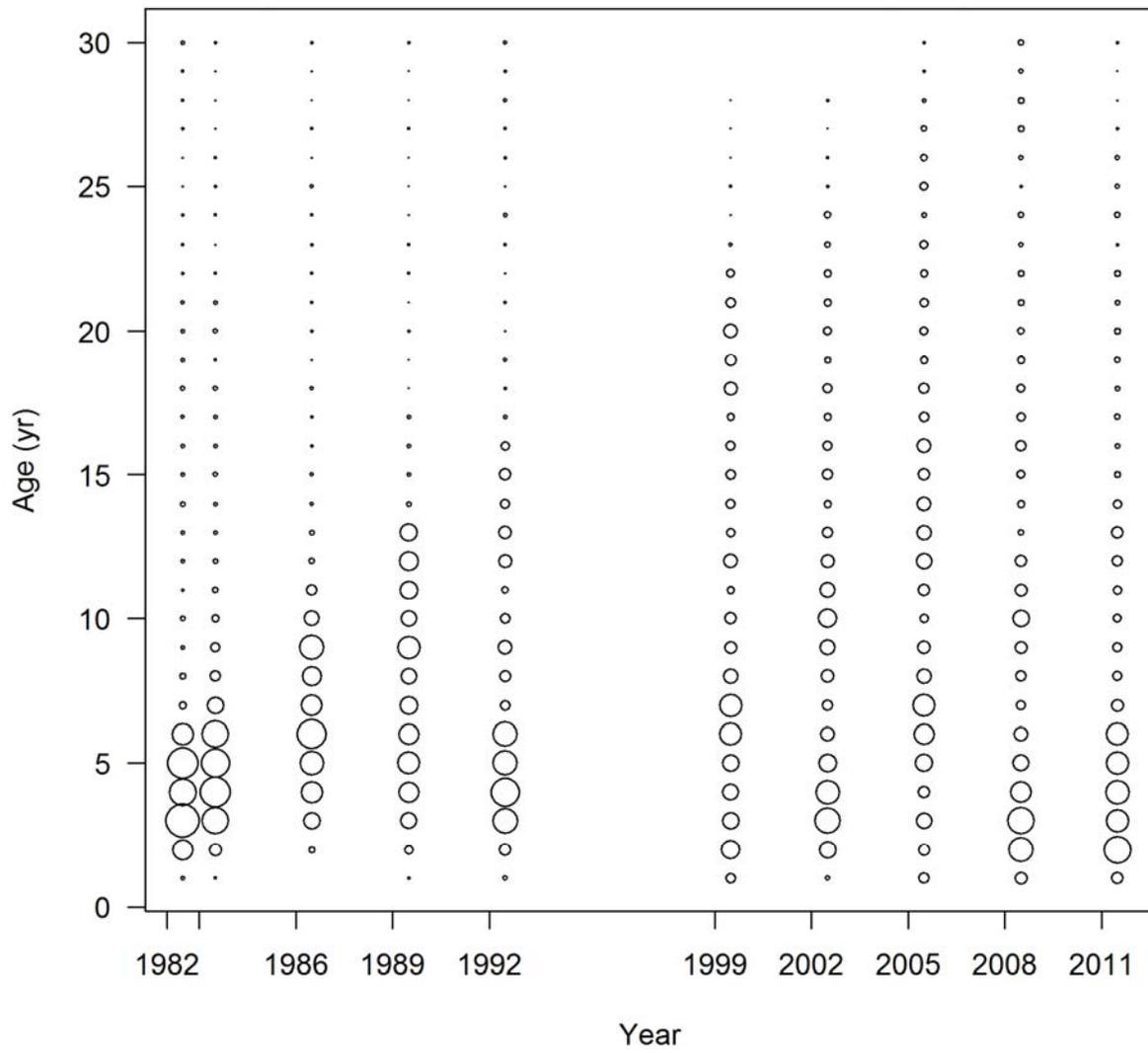


Pearson residuals, sexes combined, whole catch, NperTow+mm (max=10.83)

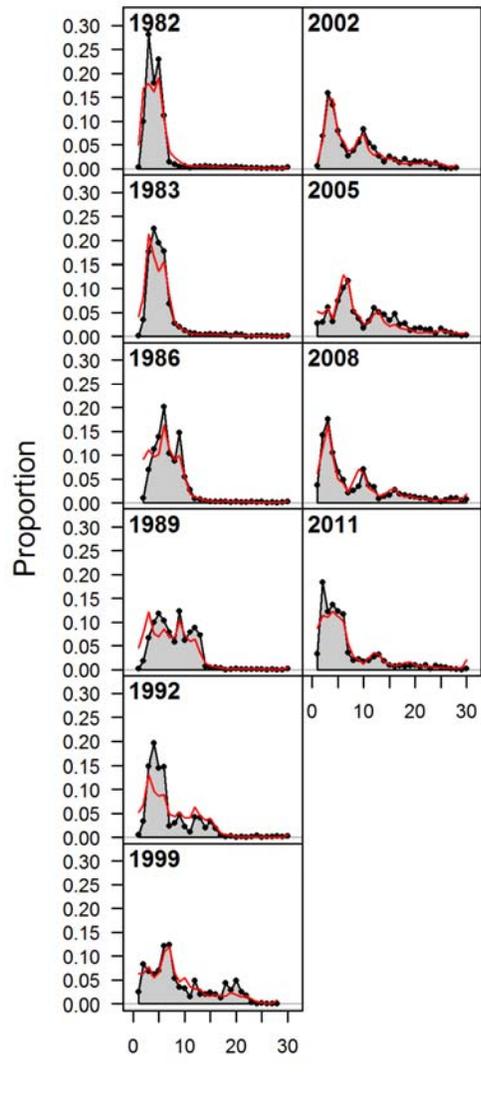


Age (yr)

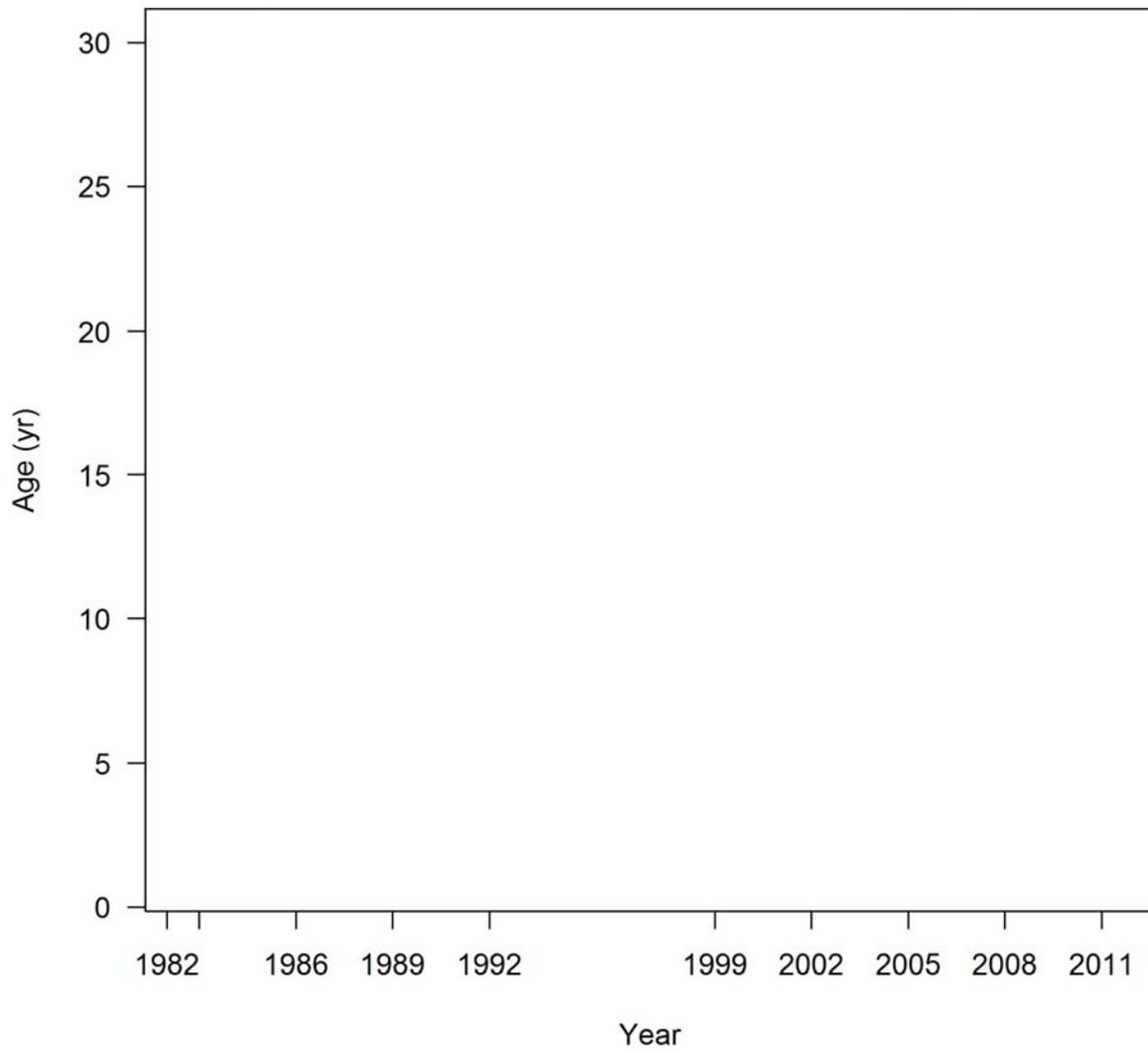
ghost age comp data, sexes combined, whole catch, SWAN (max=0.28)



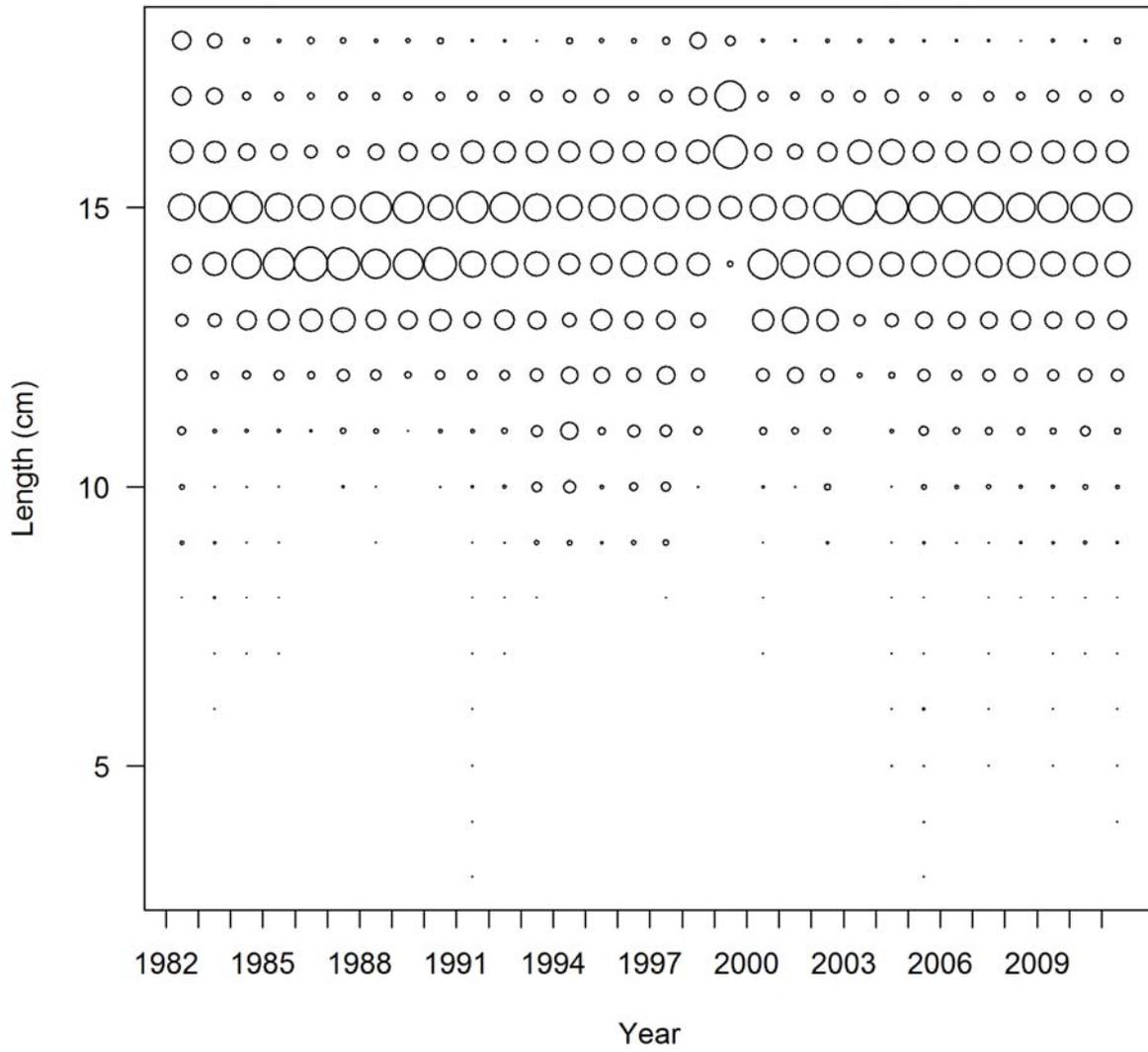
ghost age comps, sexes combined, whole catch, SWAN



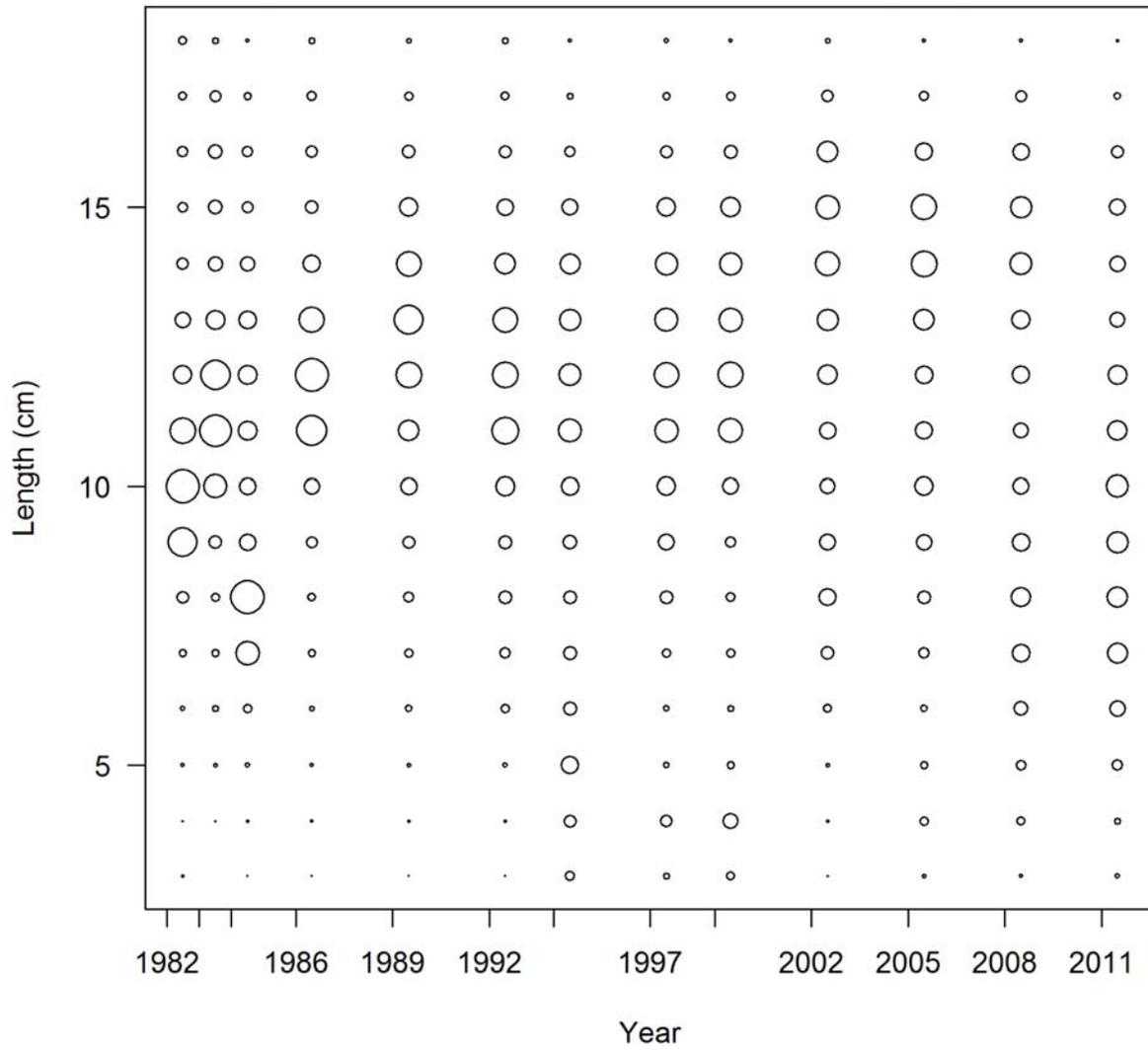
Pearson residuals, sexes combined, whole catch, SWAN (max=NA)



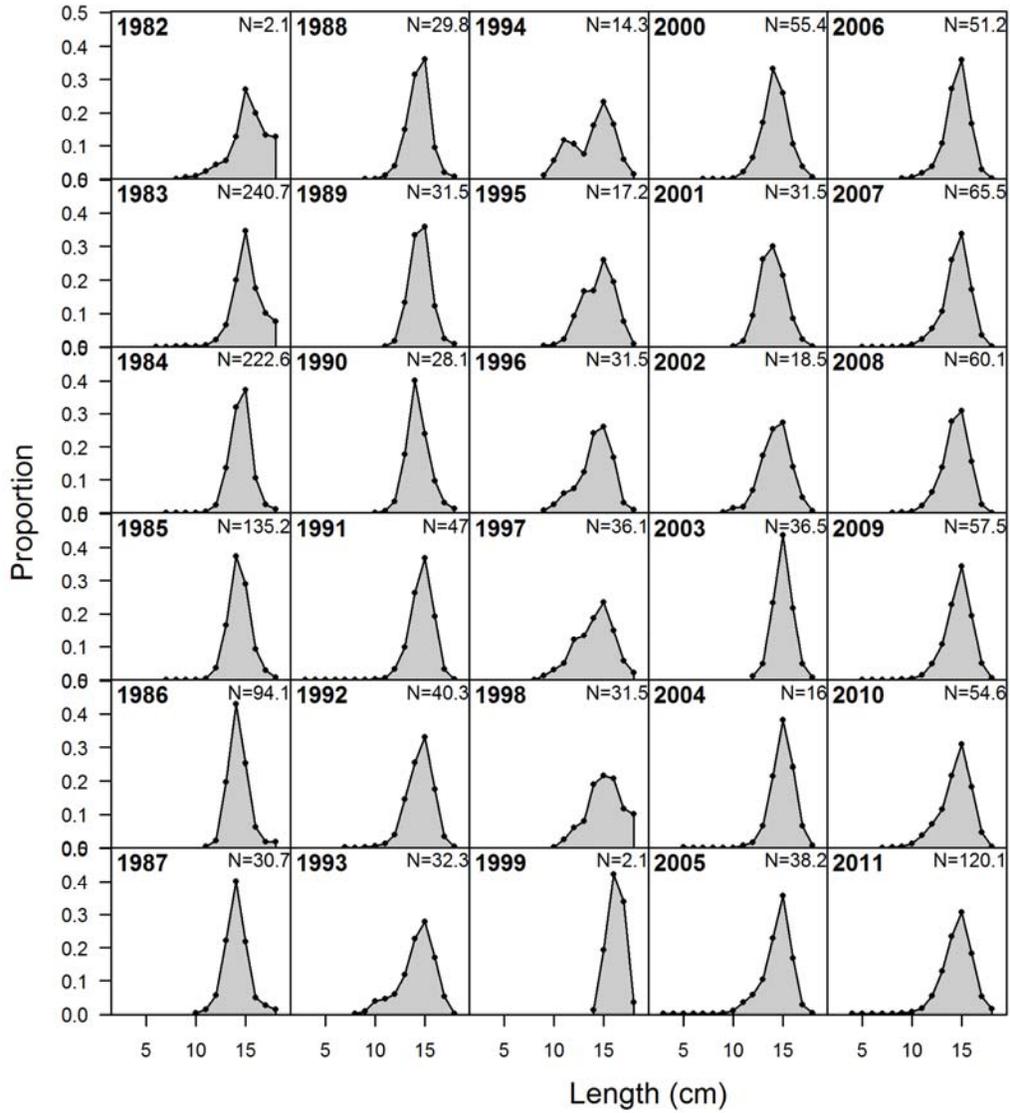
length comp data, sexes combined, whole catch, Fishery (max=0.44)



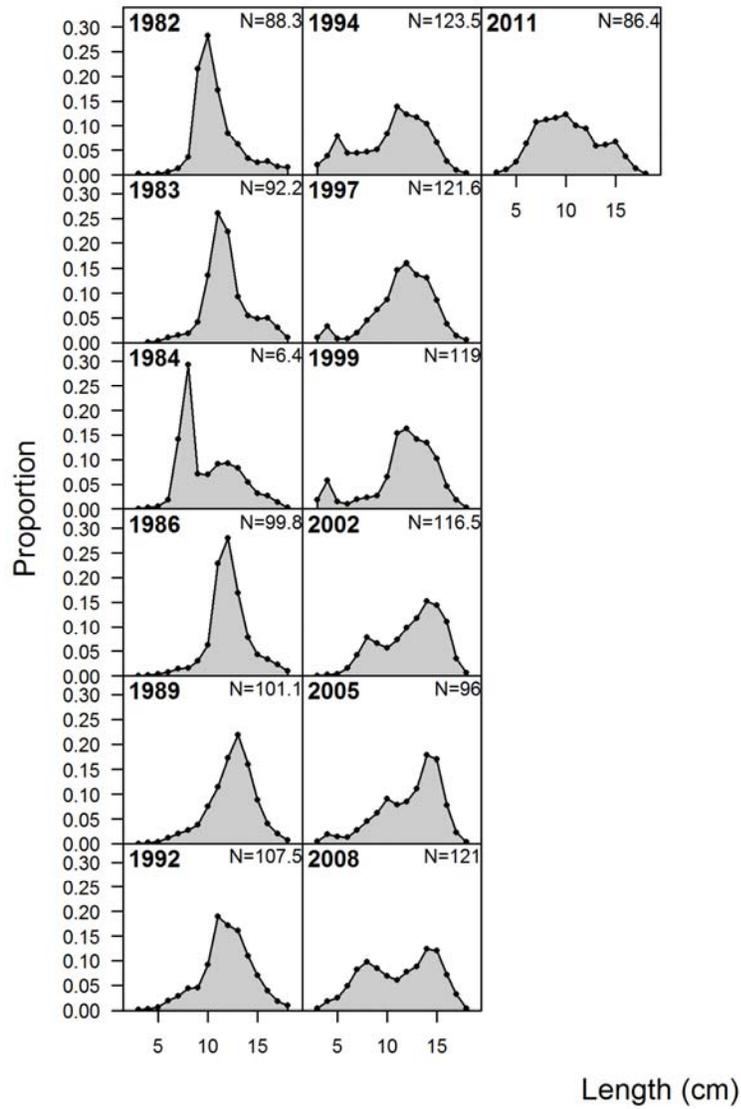
length comp data, sexes combined, whole catch, NperTow+mm (max=0.29)



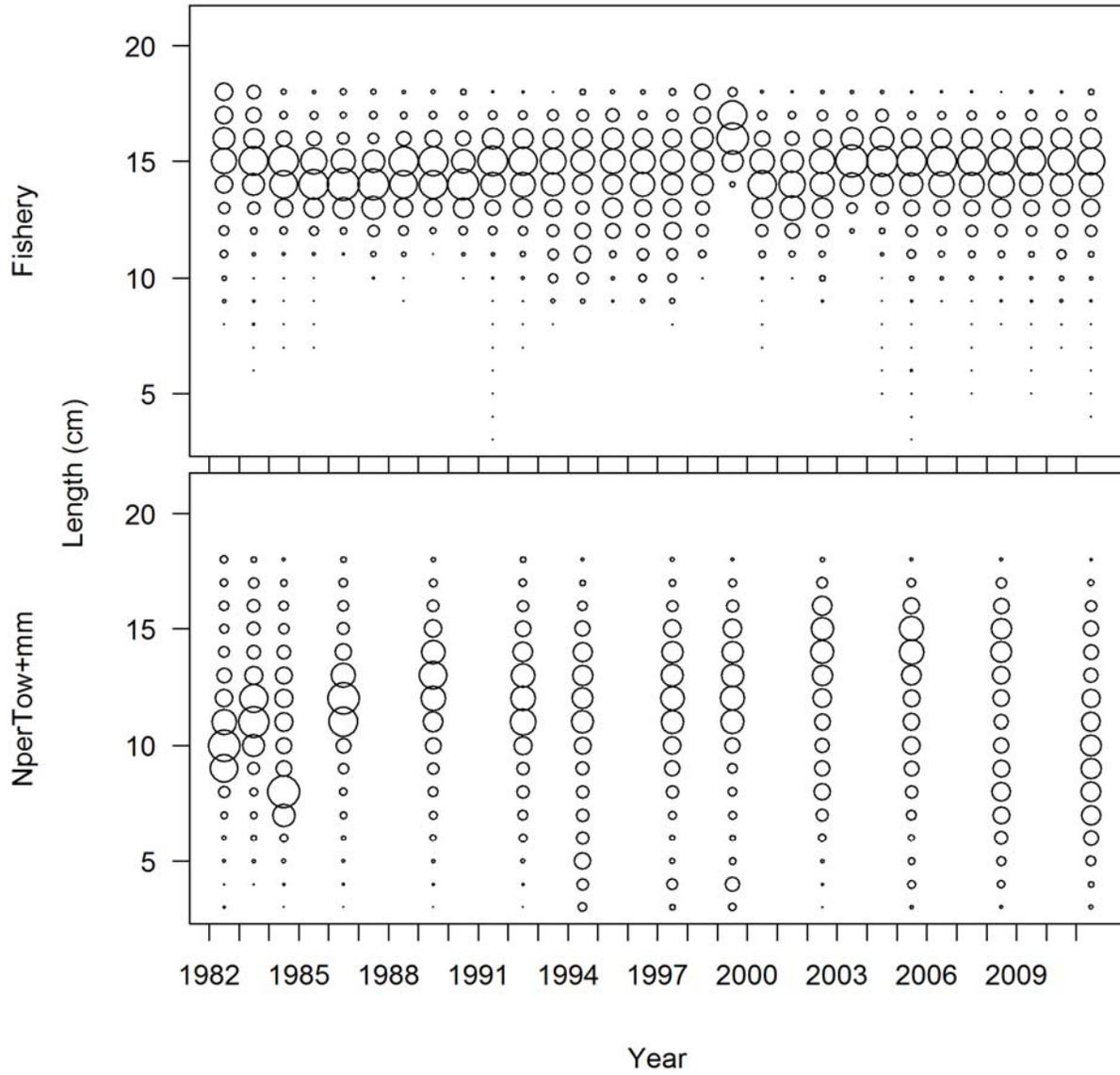
length comp data, sexes combined, whole catch, Fishery



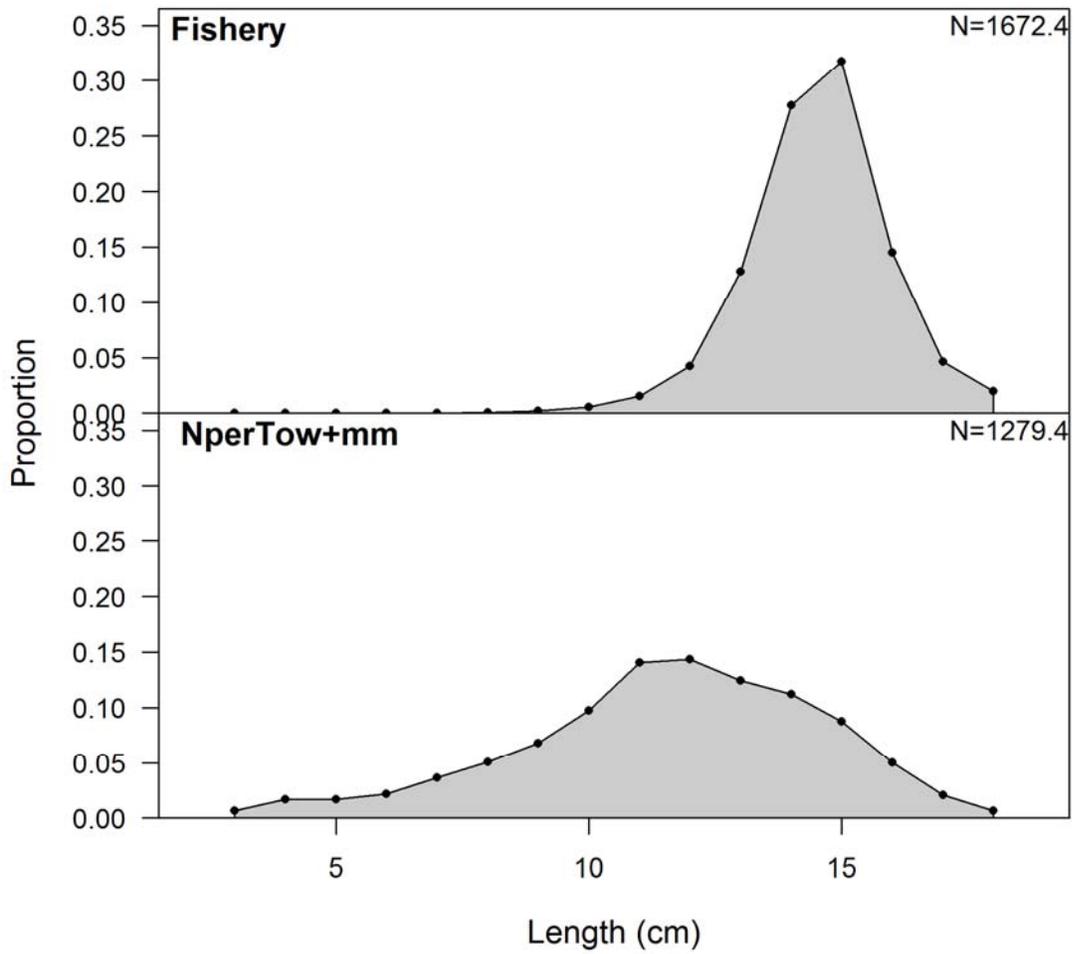
length comp data, sexes combined, whole catch, NperTow+mm



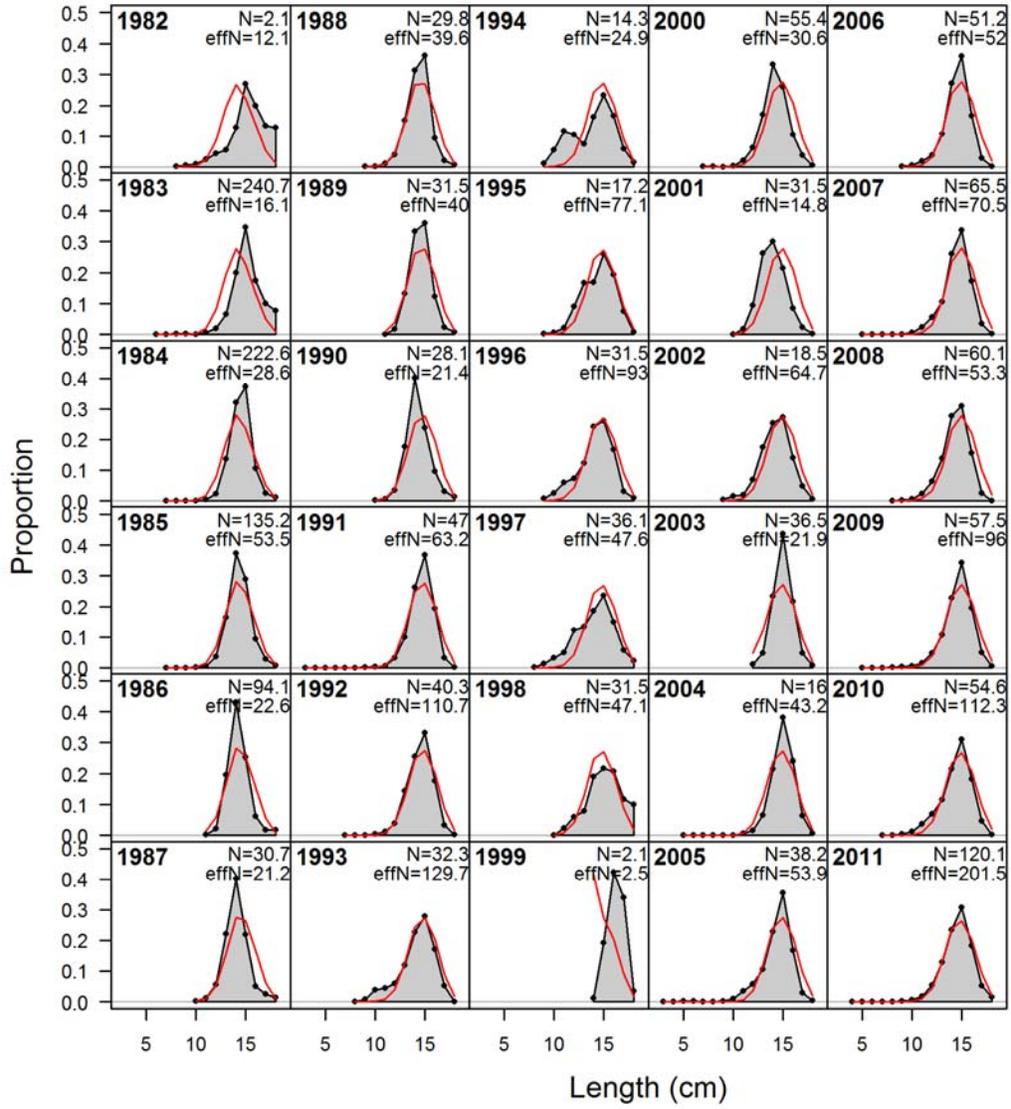
length comp data, sexes combined, whole catch, comparing across 1



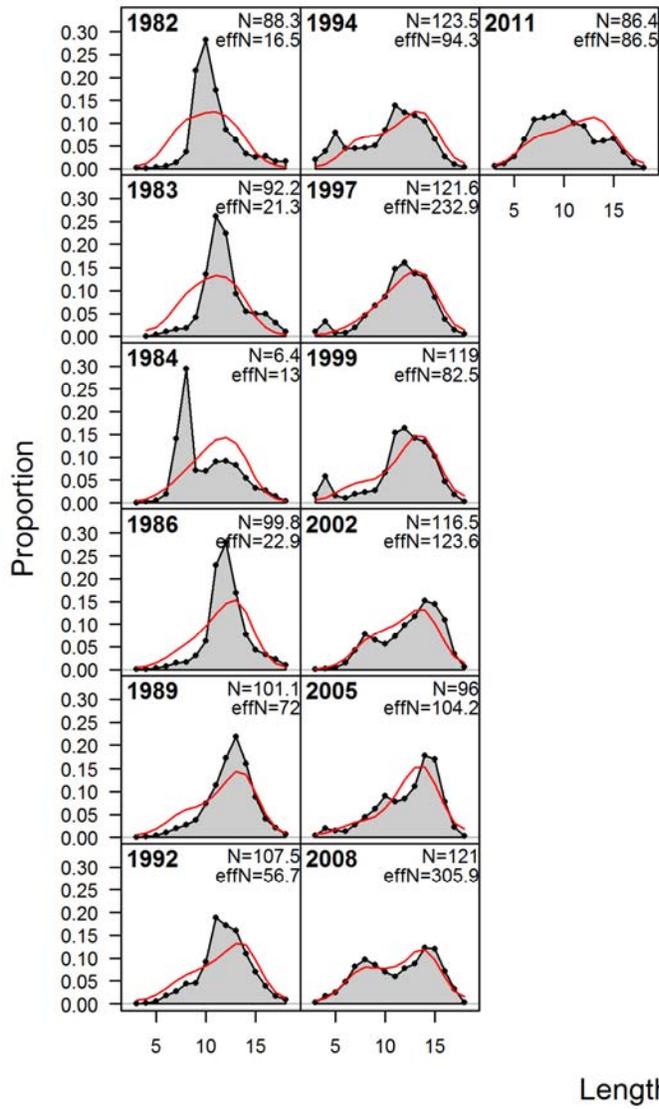
length comp data, sexes combined, whole catch, aggregated across time l



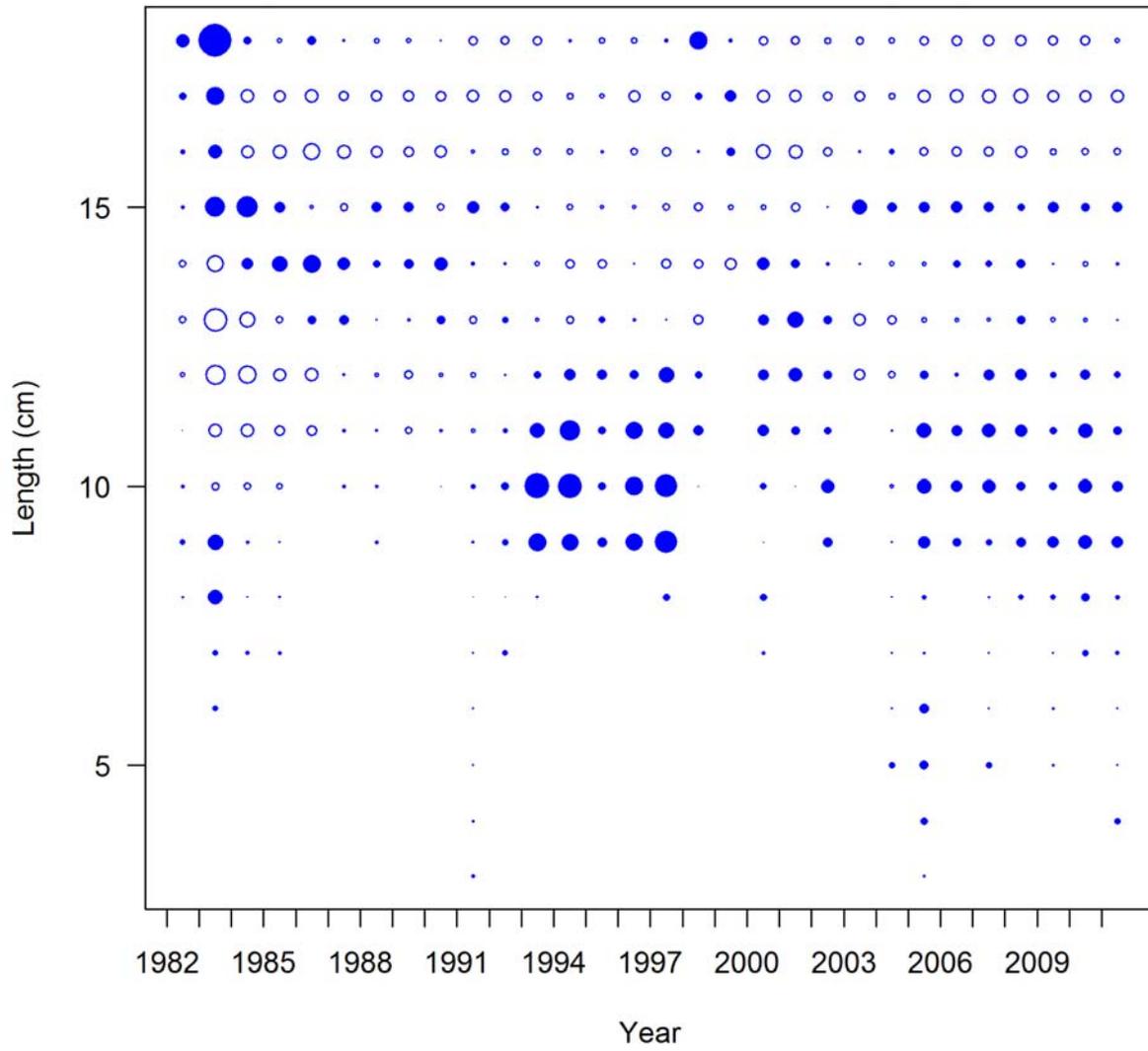
length comps, sexes combined, whole catch, Fishery



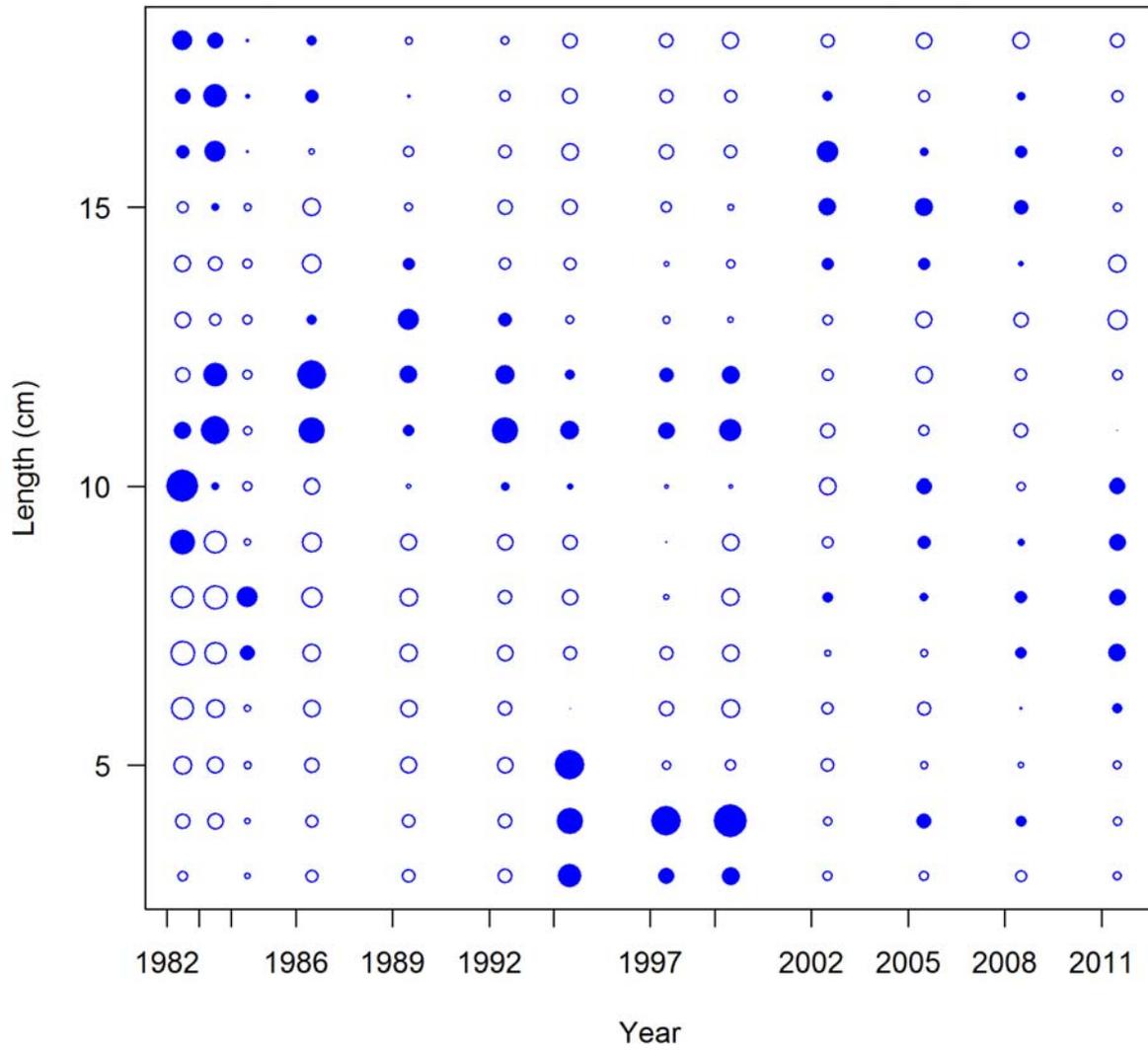
length comps, sexes combined, whole catch, NperTow+mm



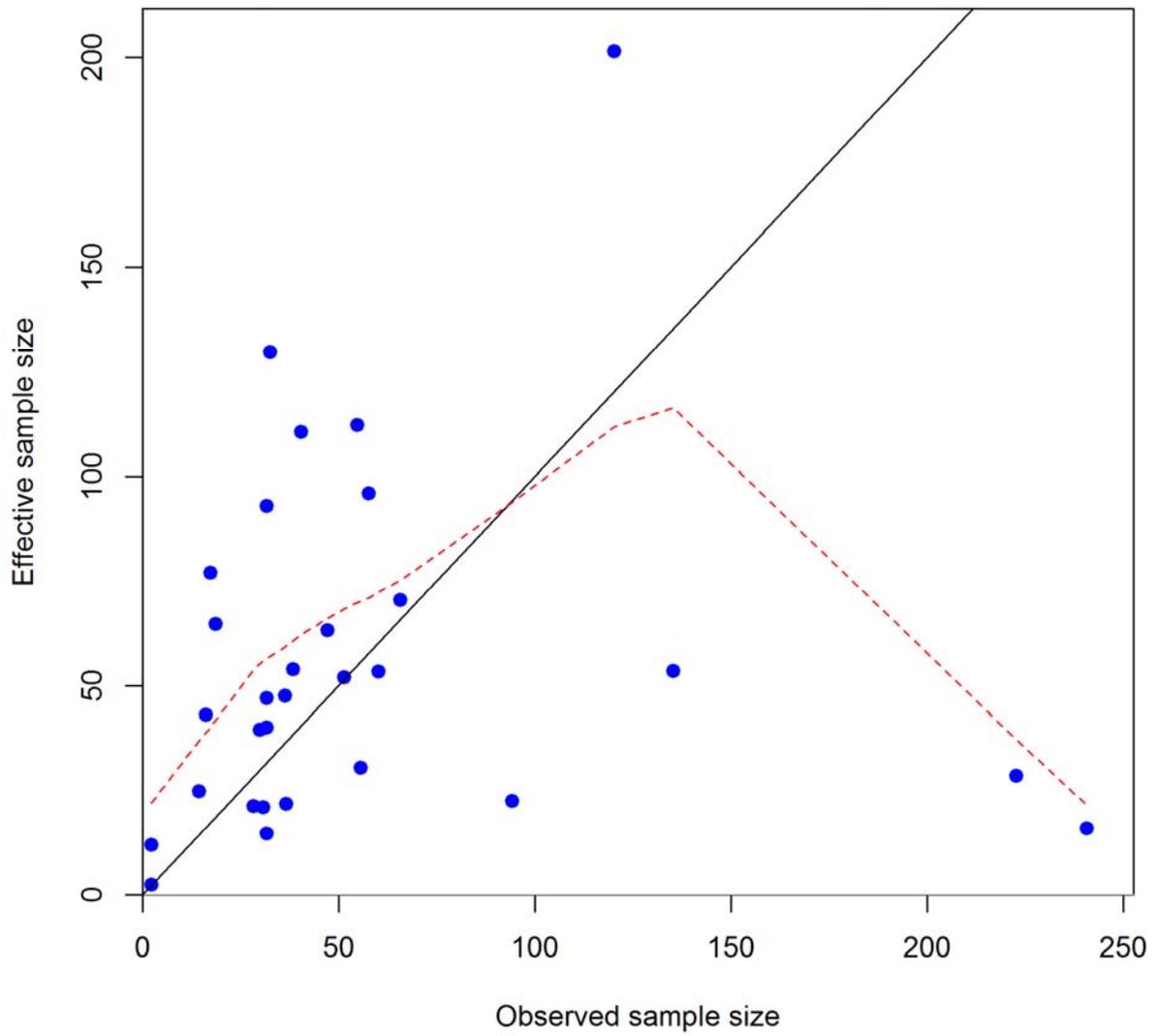
Pearson residuals, sexes combined, whole catch, Fishery (max=11.27)



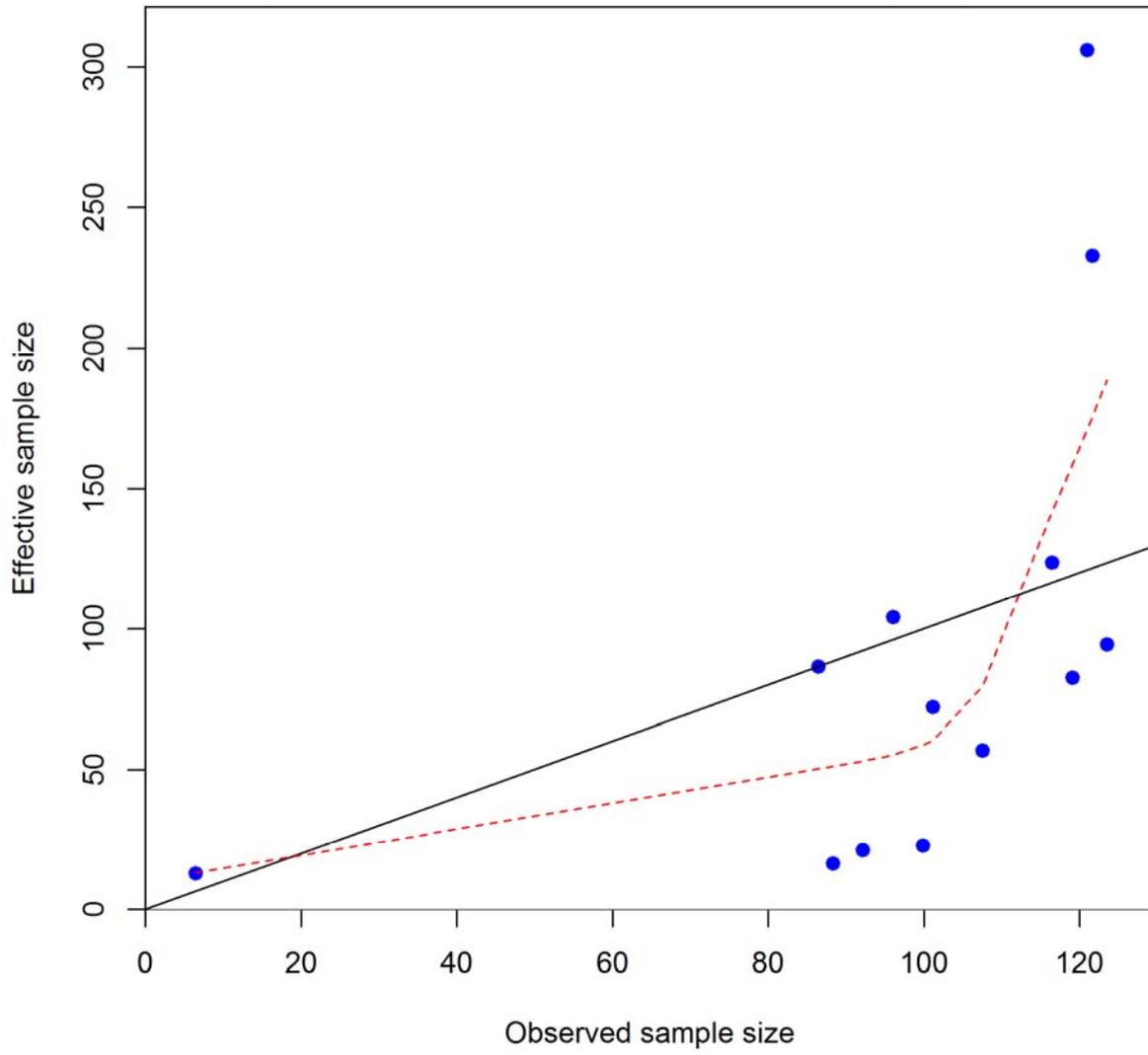
Pearson residuals, sexes combined, whole catch, NperTow+mm (max=5.01)



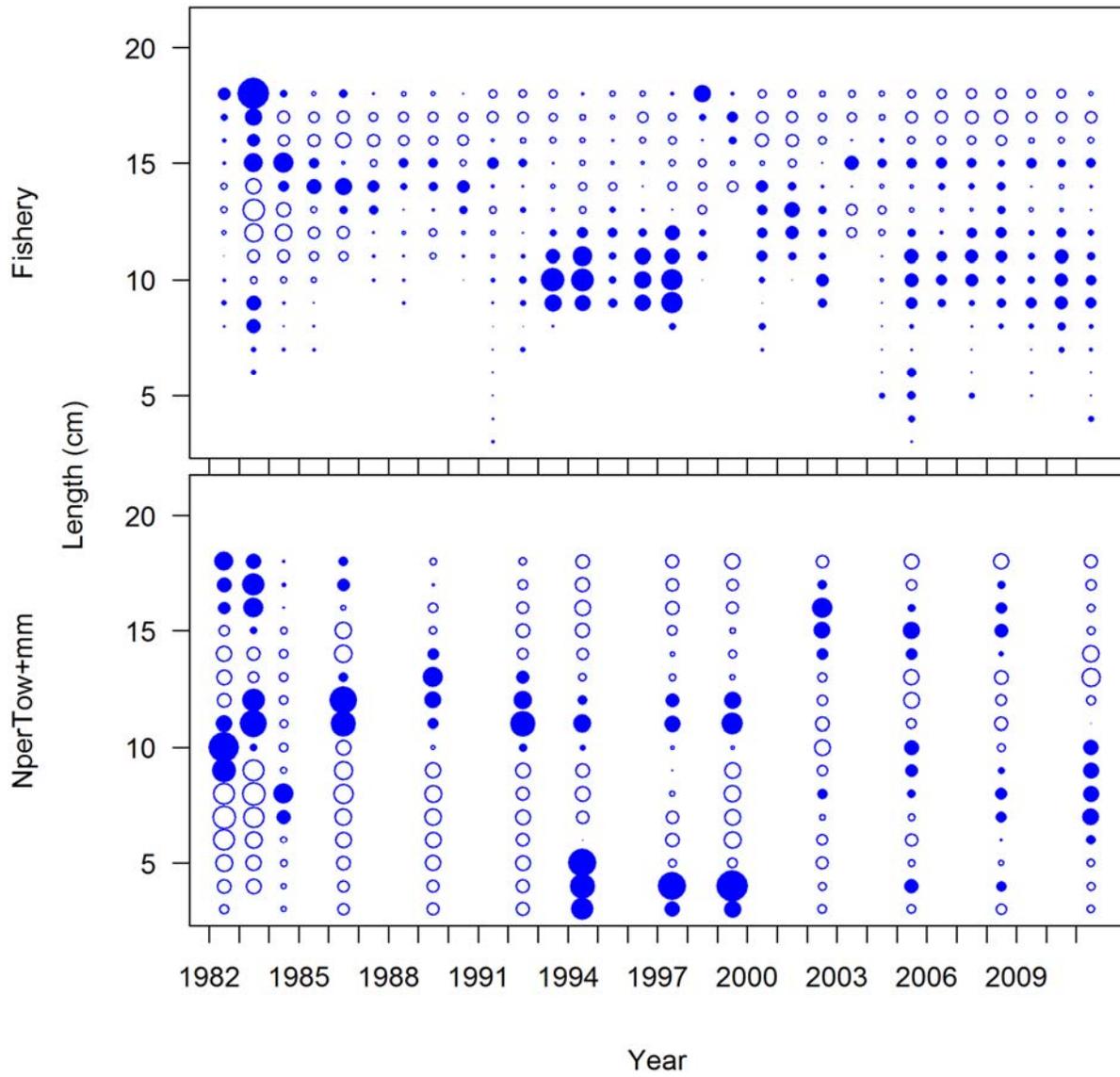
N-EffN comparison, length comps, sexes combined, whole catch, Fishery



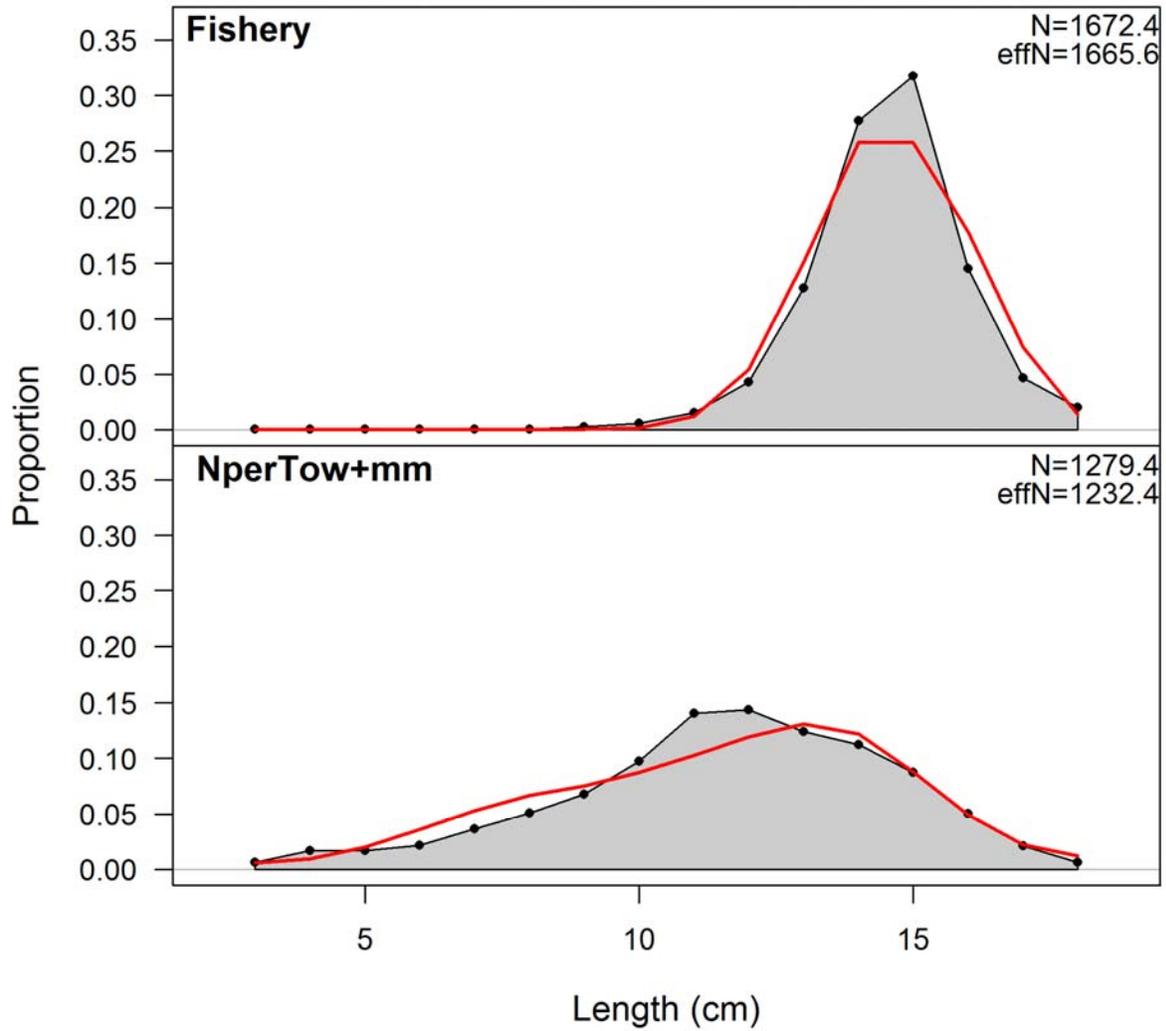
N-EffN comparison, length comps, sexes combined, whole catch, NperTow+mm



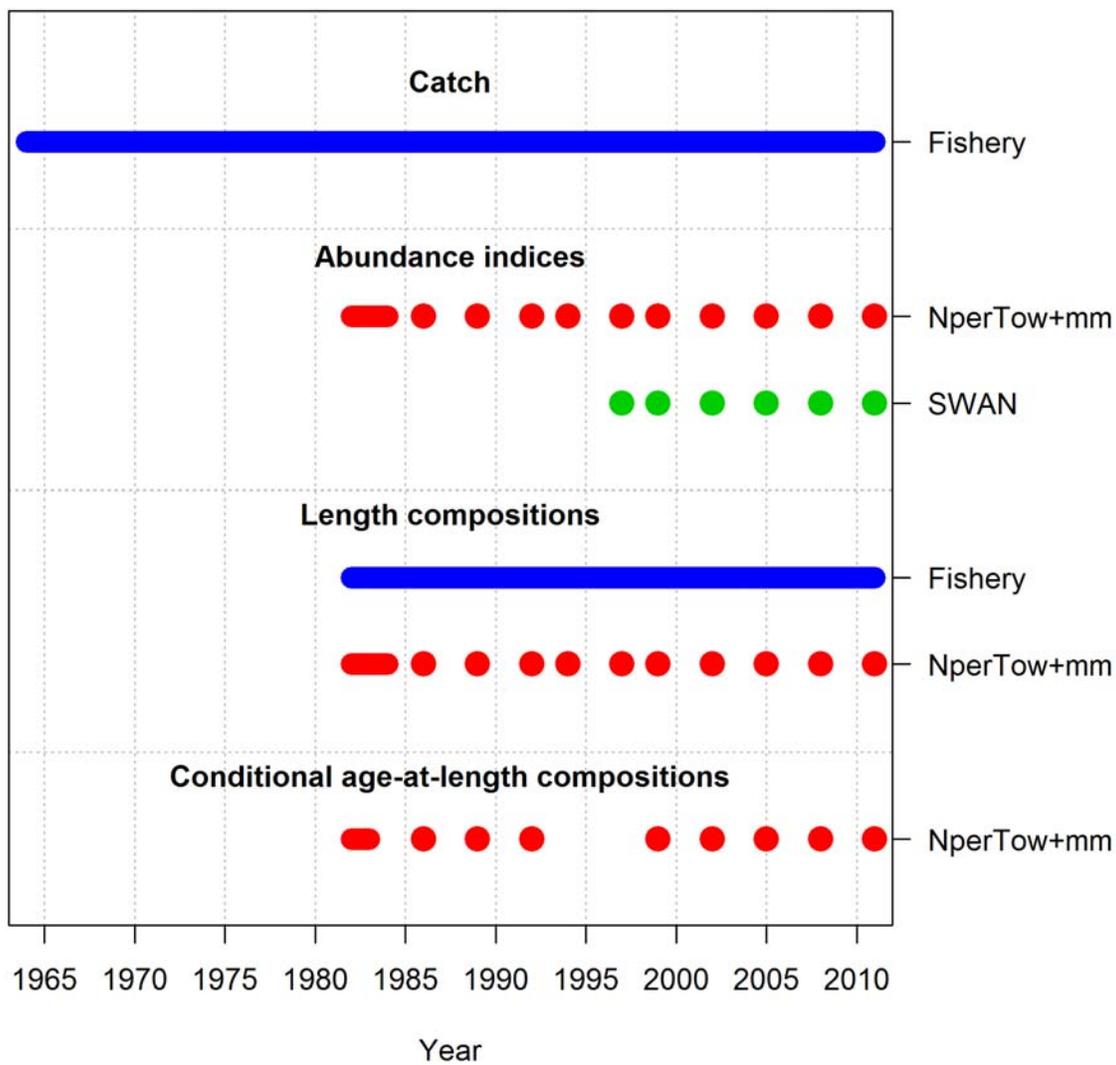
Pearson residuals, sexes combined, whole catch, comparing across



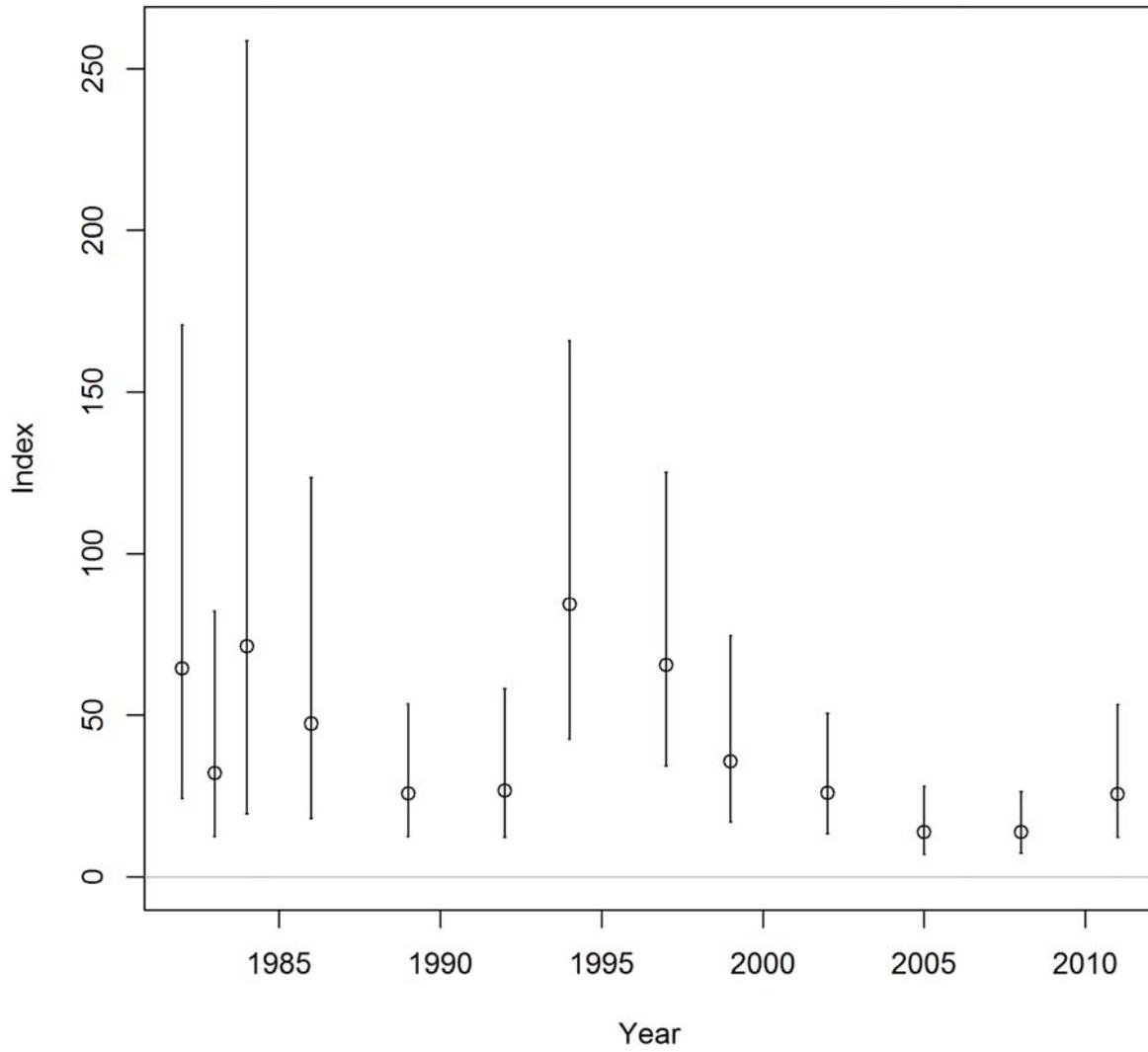
length comps, sexes combined, whole catch, aggregated across time by



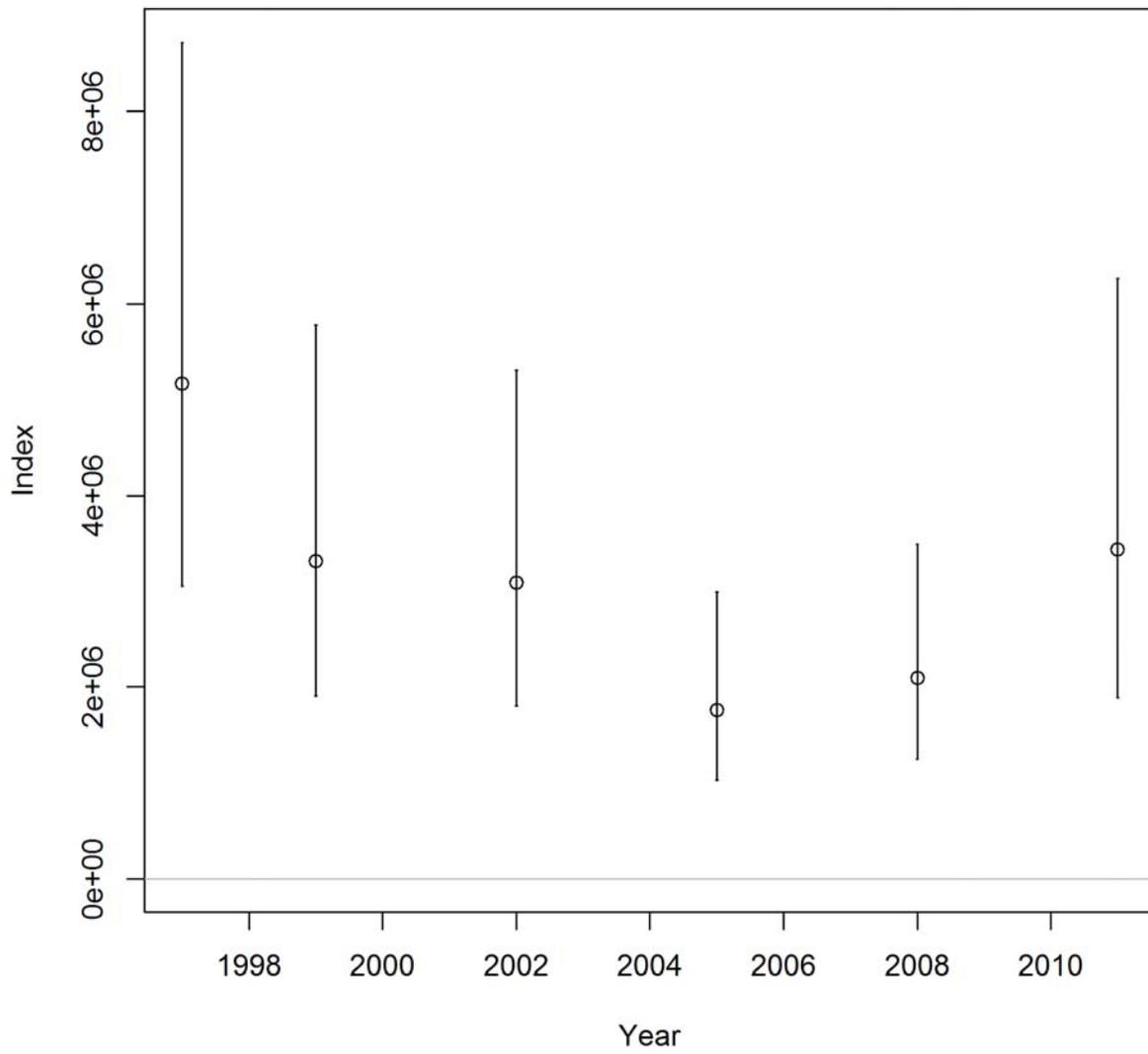
Data by type and year



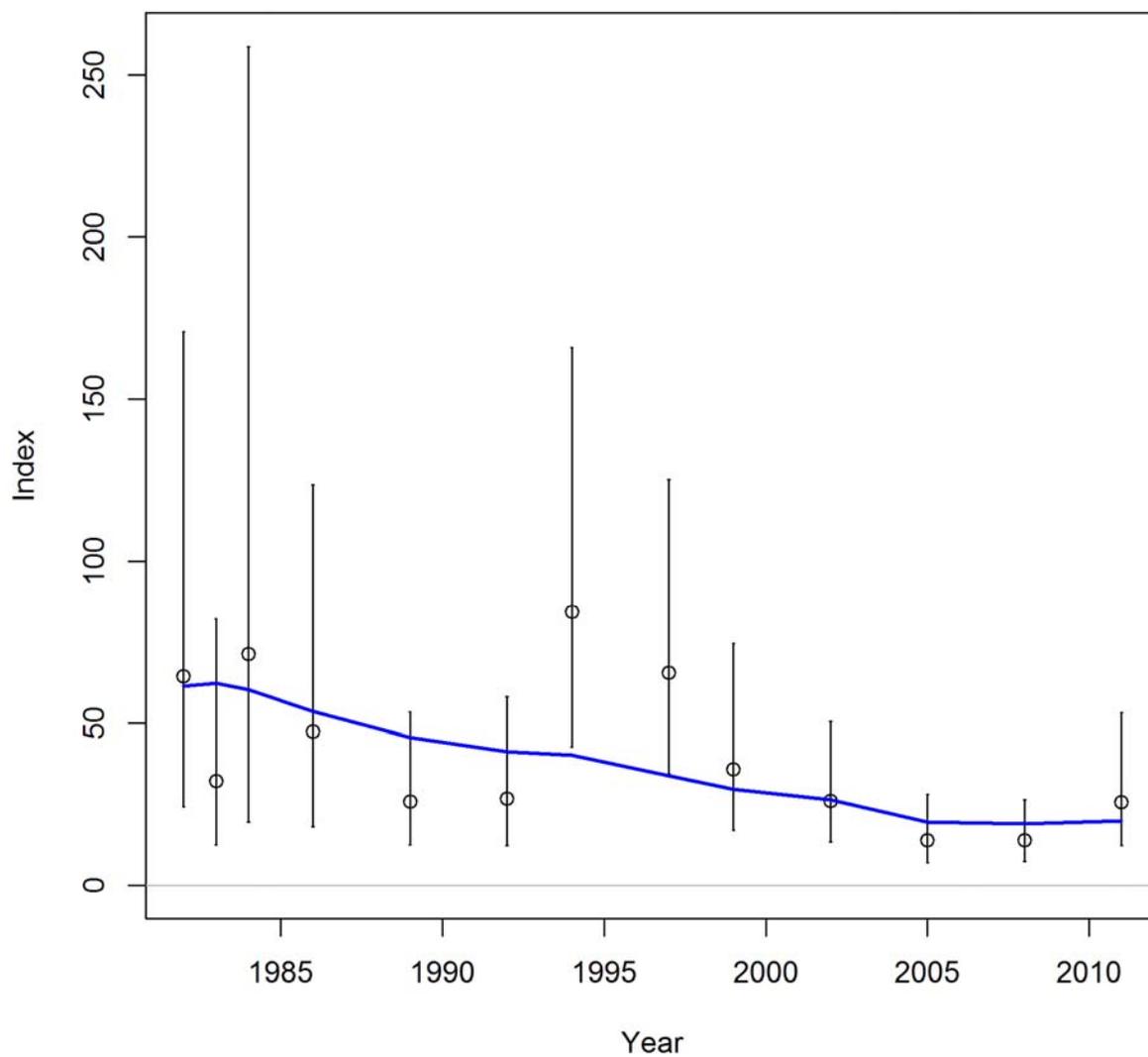
Index NperTow+mm



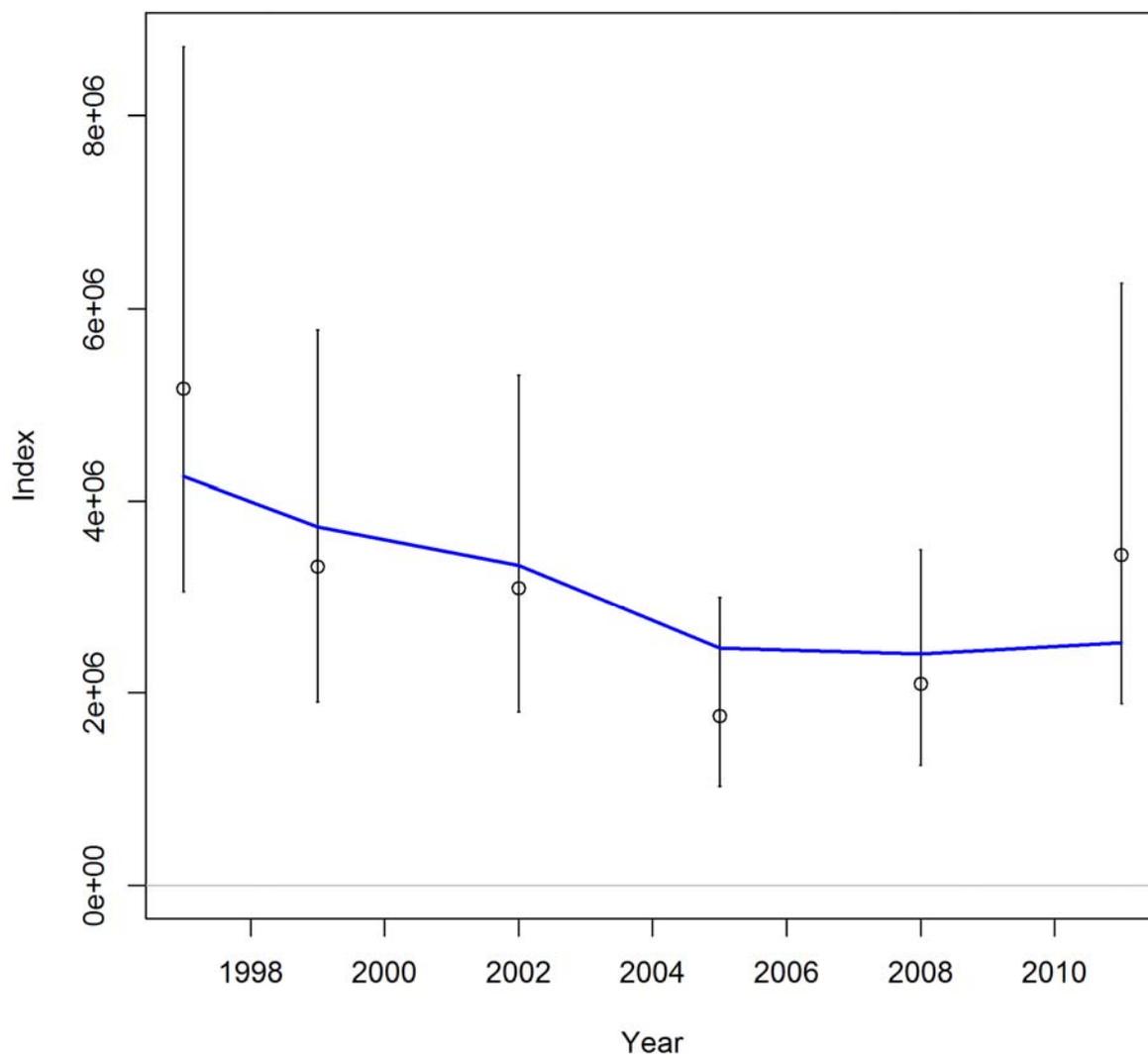
Index SWAN



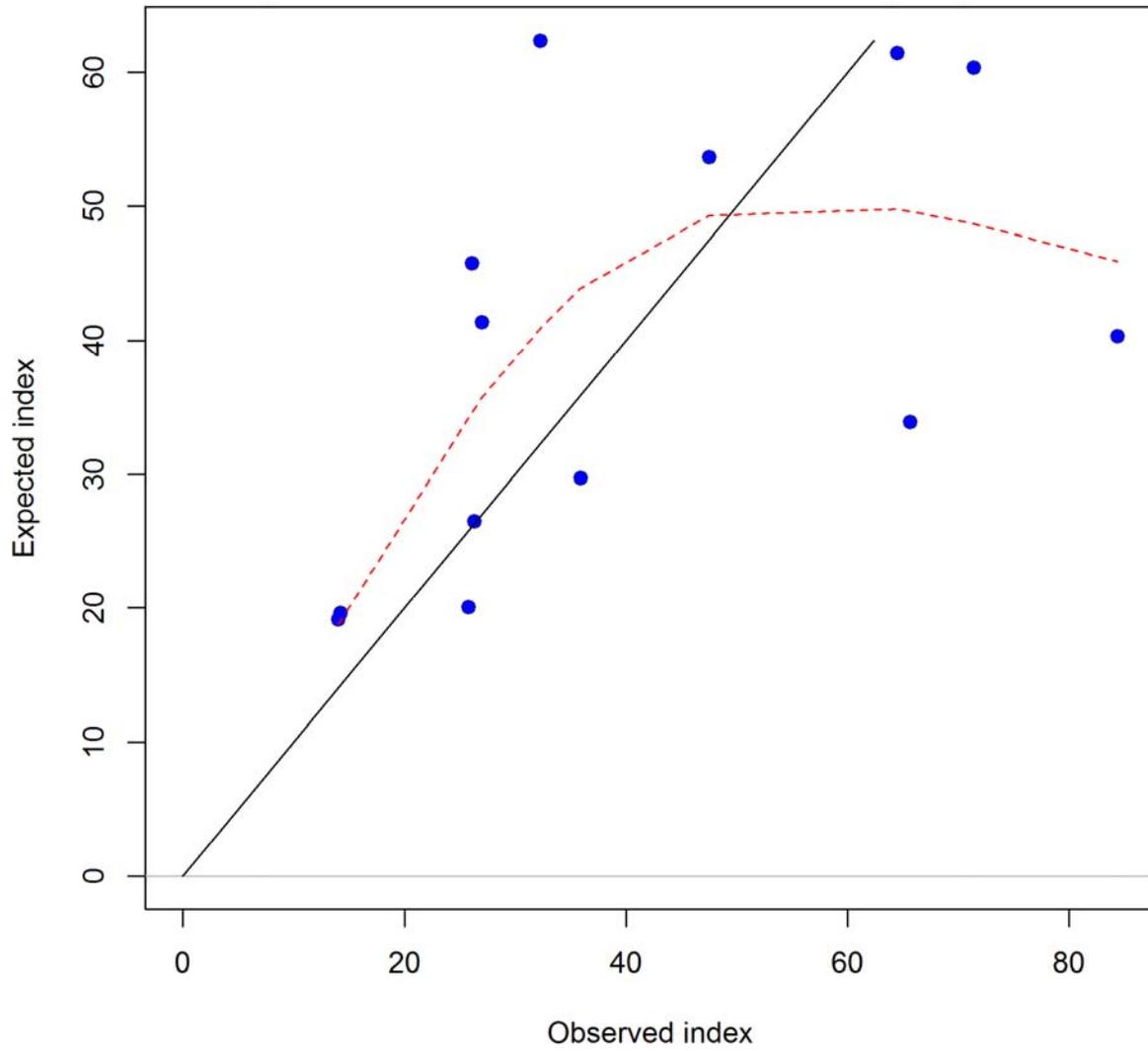
Index NperTow+mm



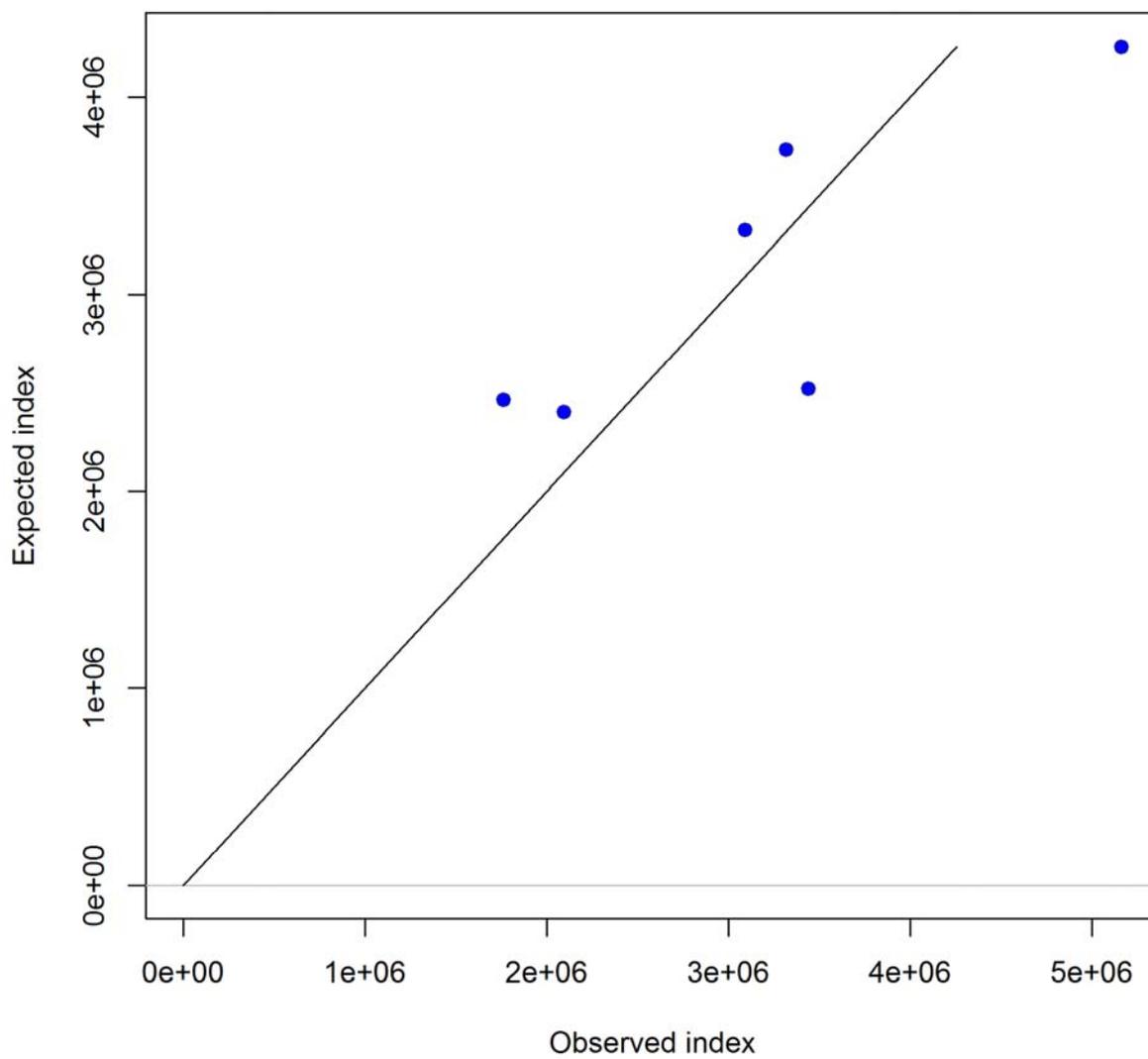
Index SWAN



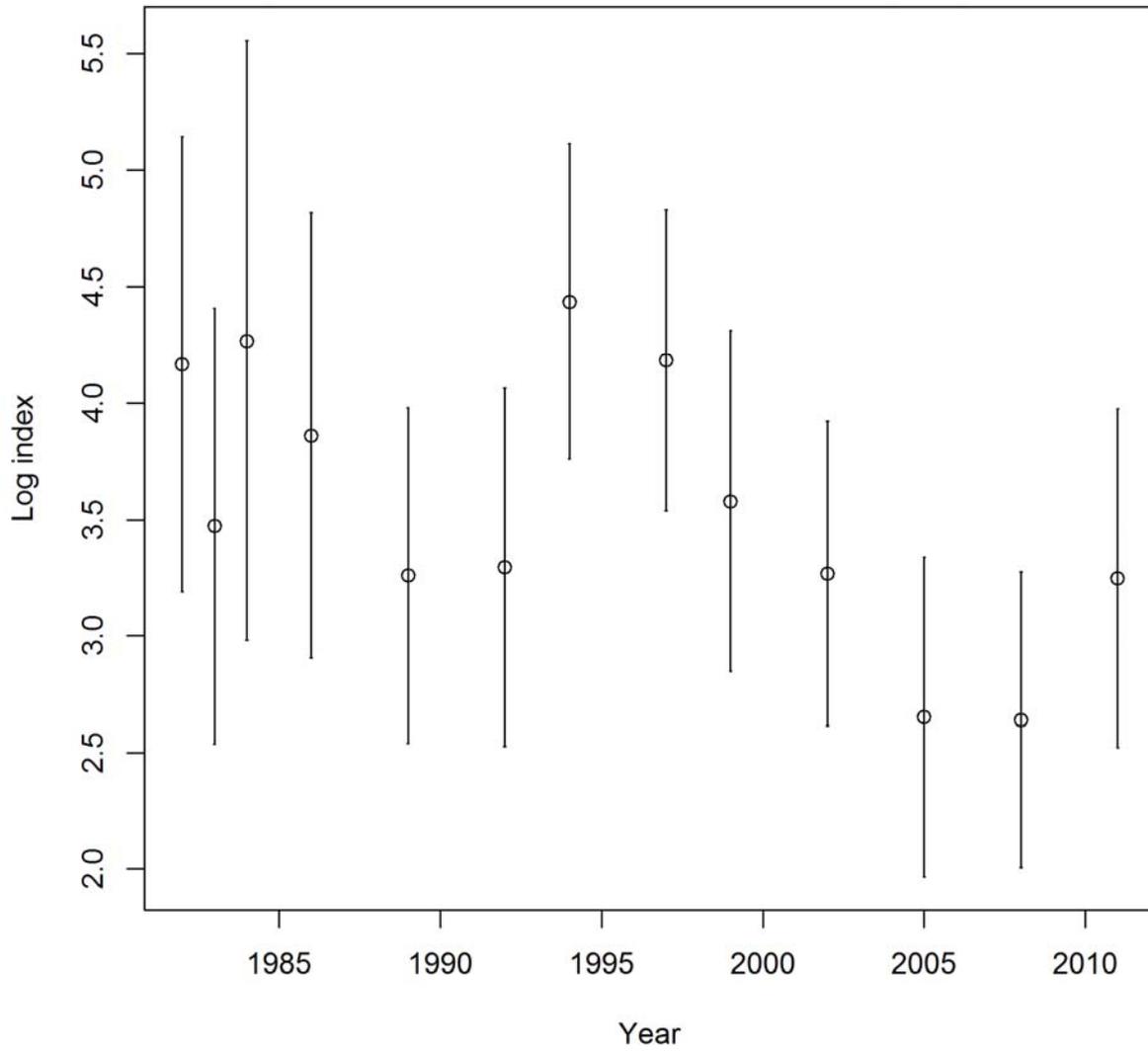
Index NperTow+mm



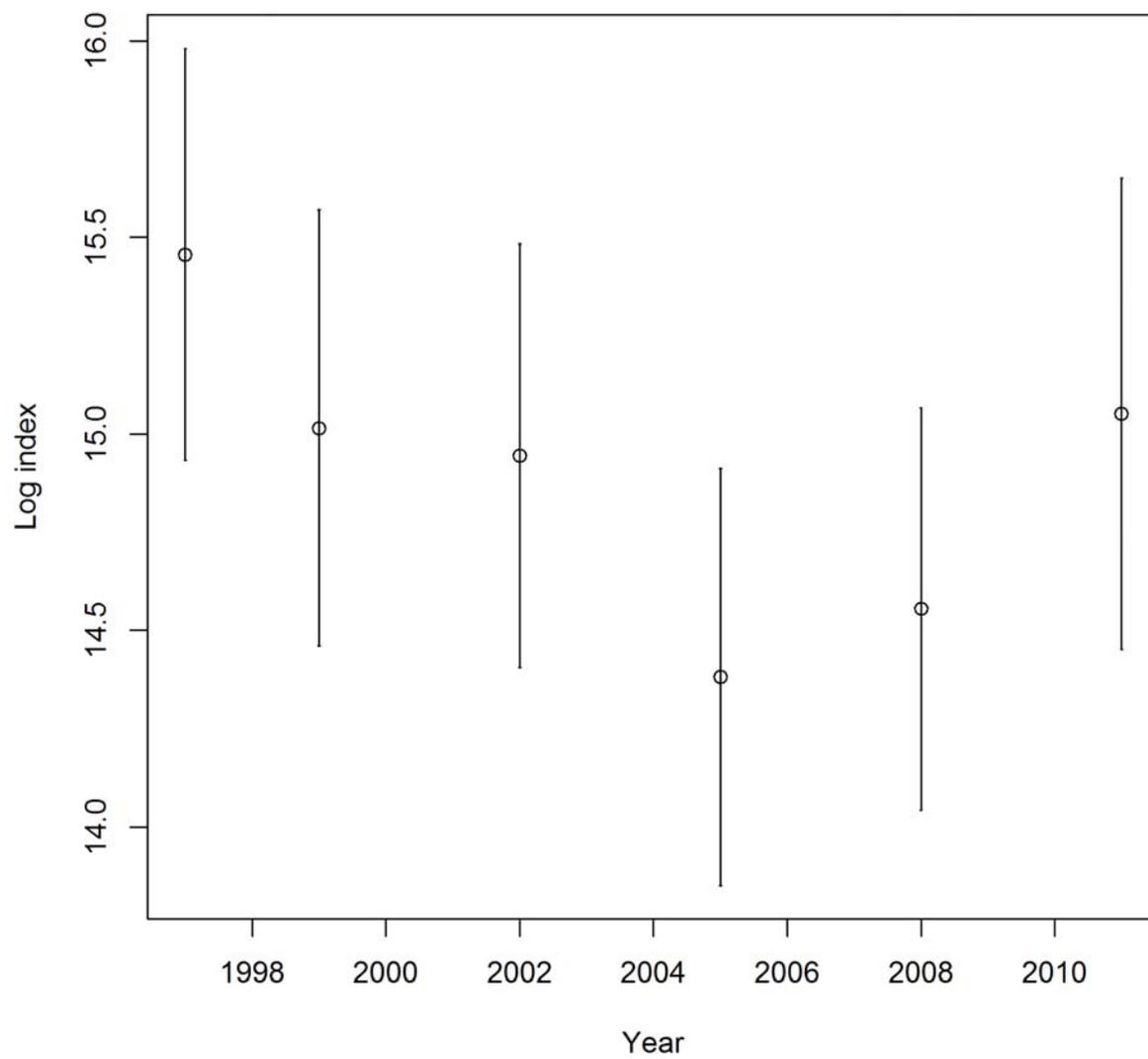
Index SWAN



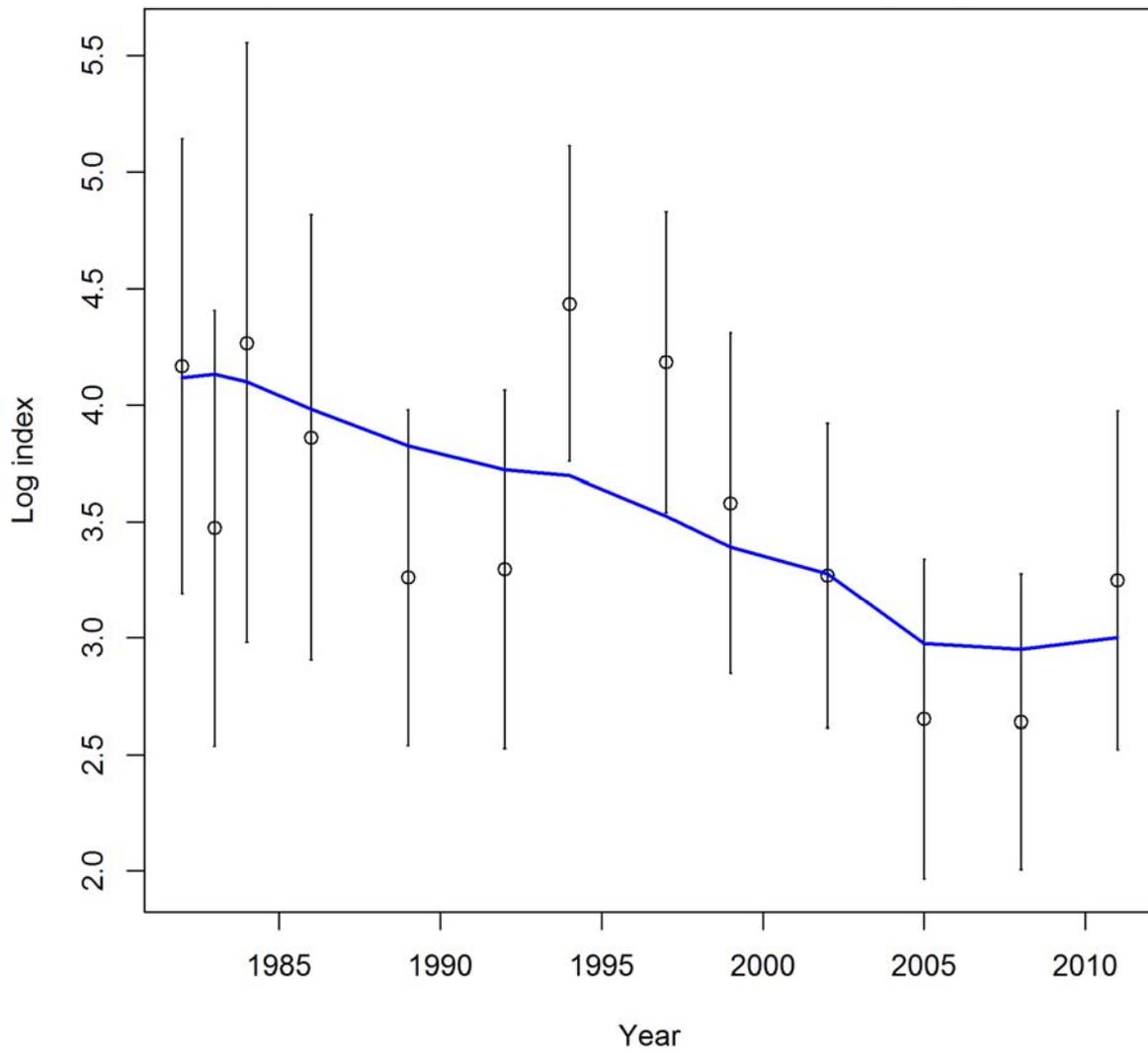
Log index NperTow+mm



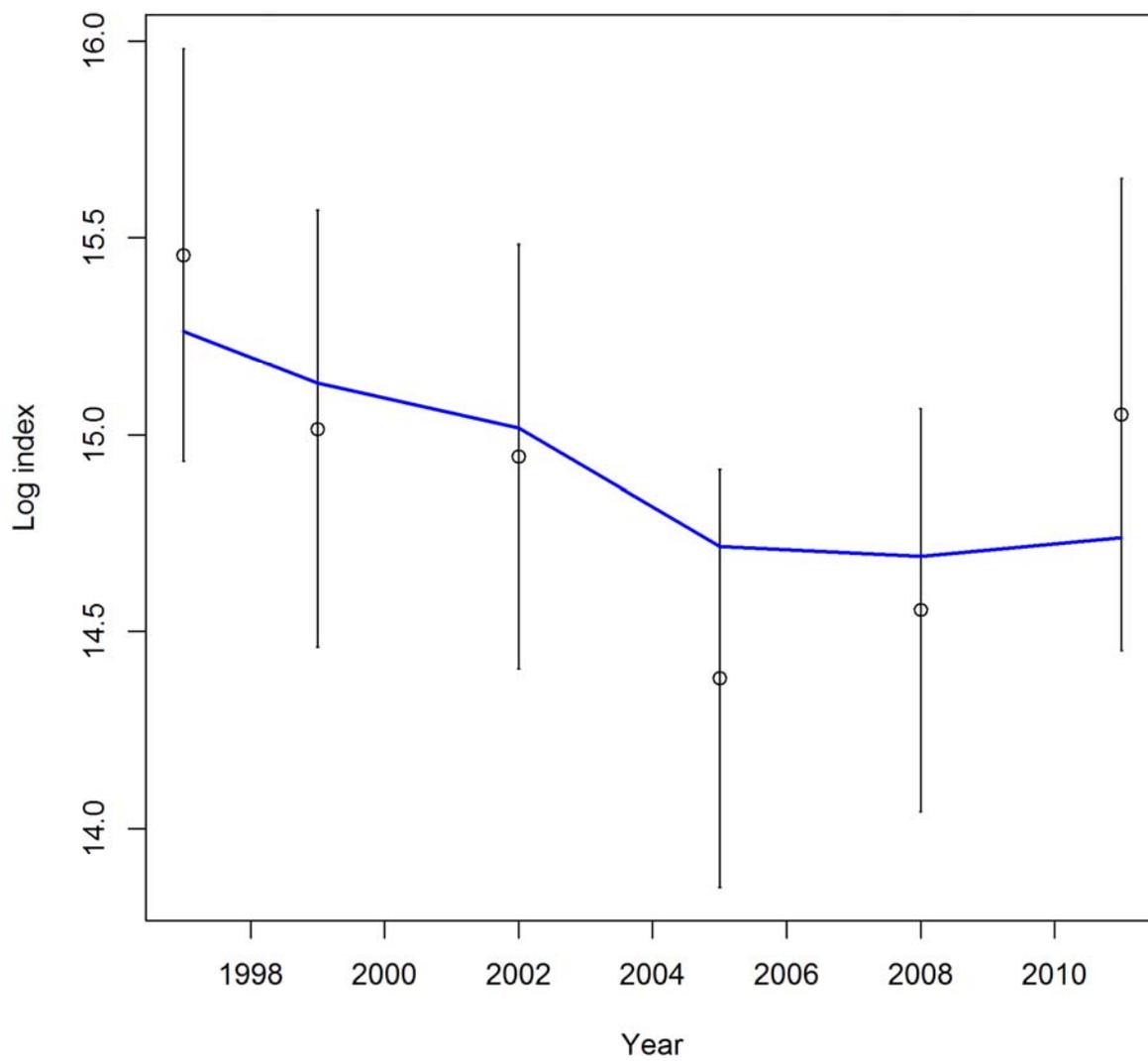
Log index SWAN



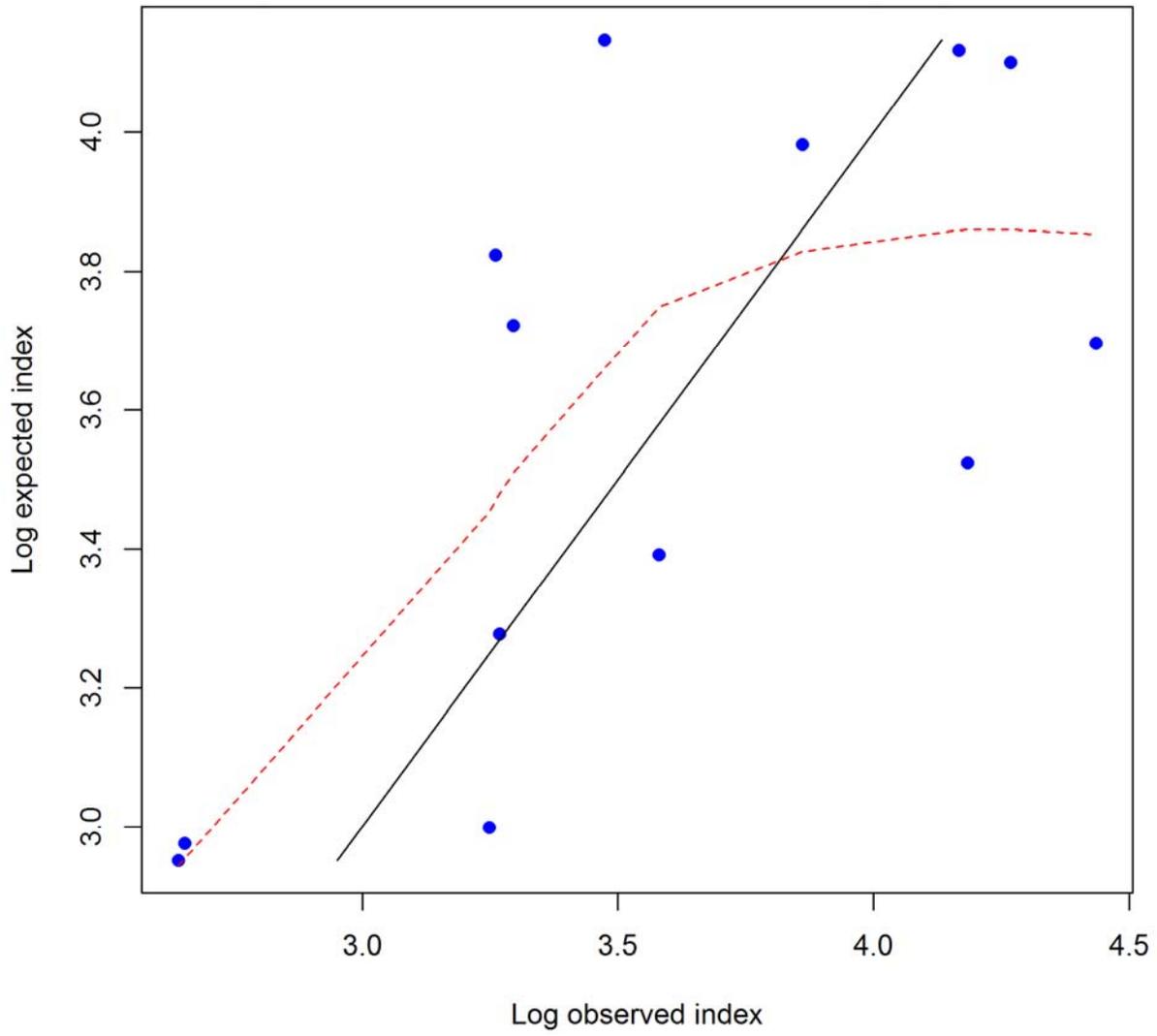
Log index NperTow+mm



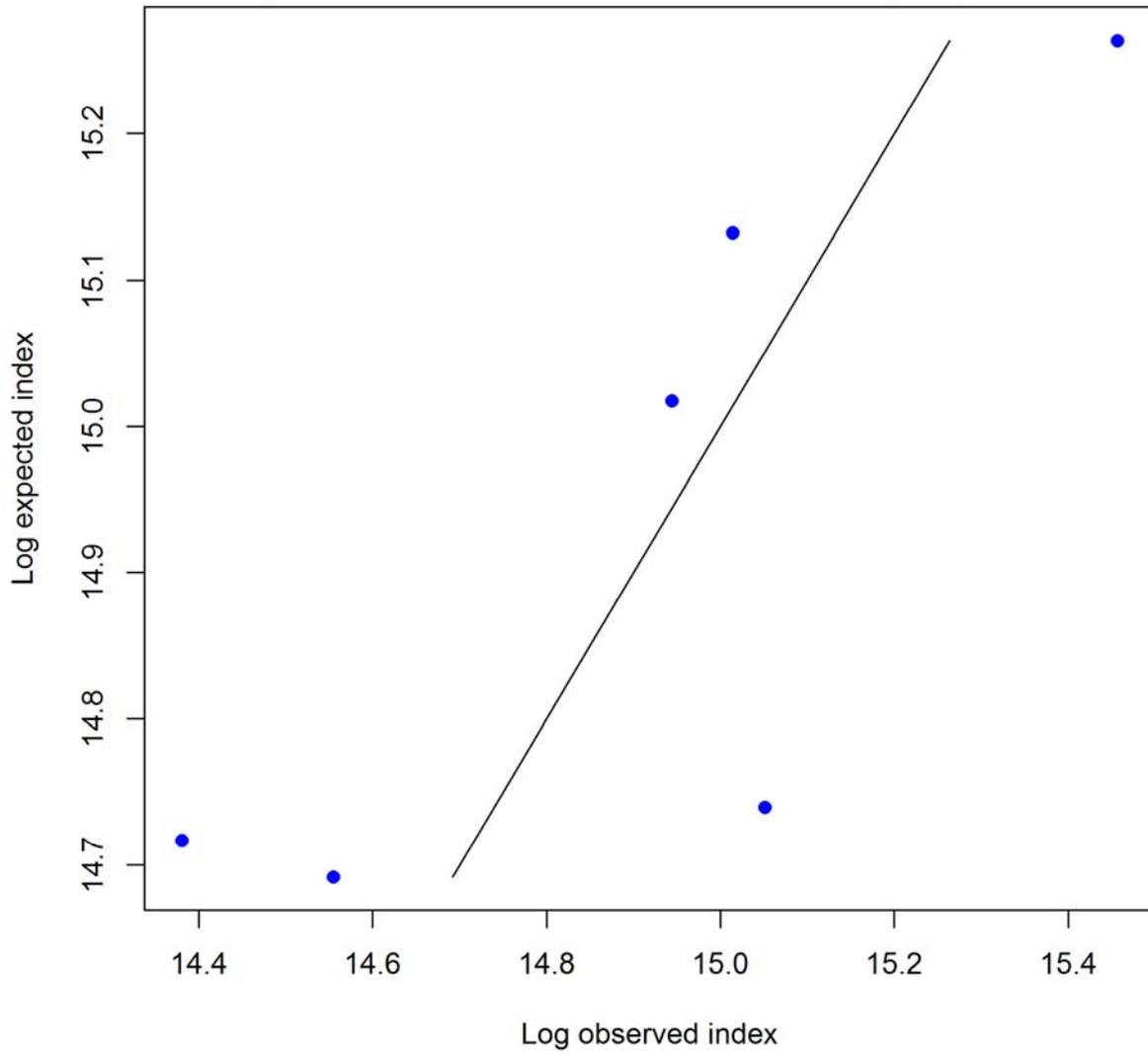
Log index SWAN



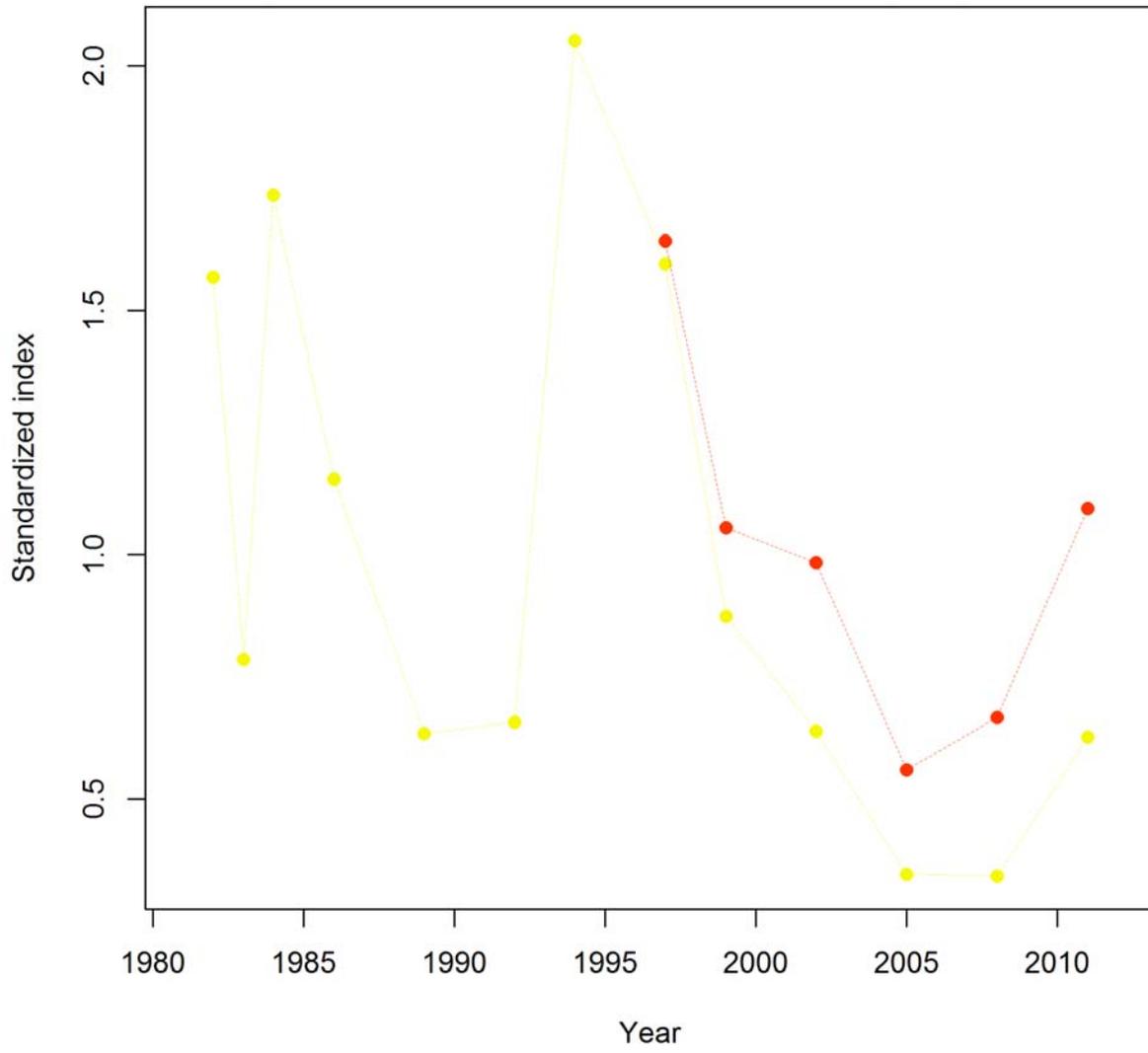
Log index NperTow+mm



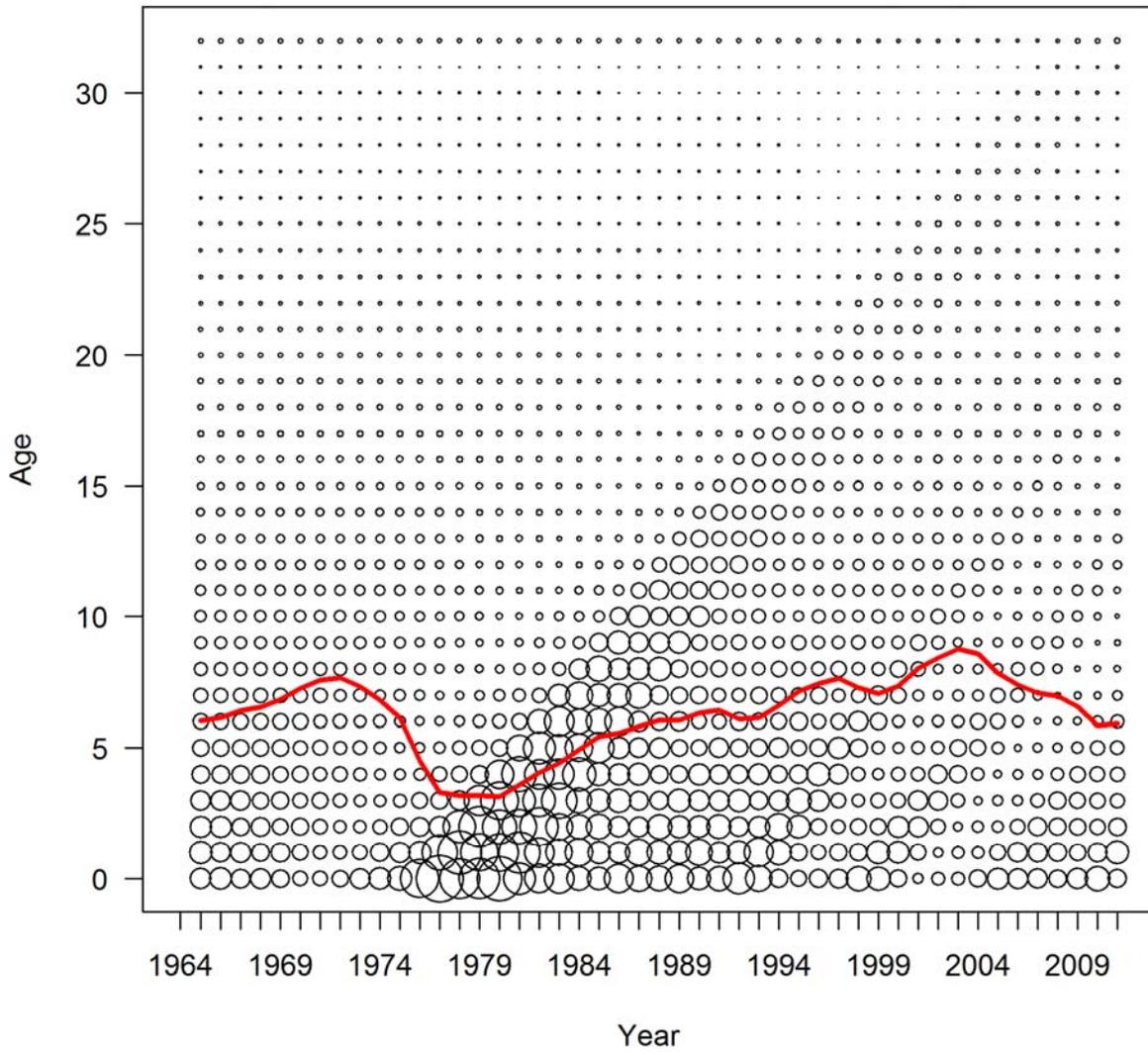
Log index SWAN



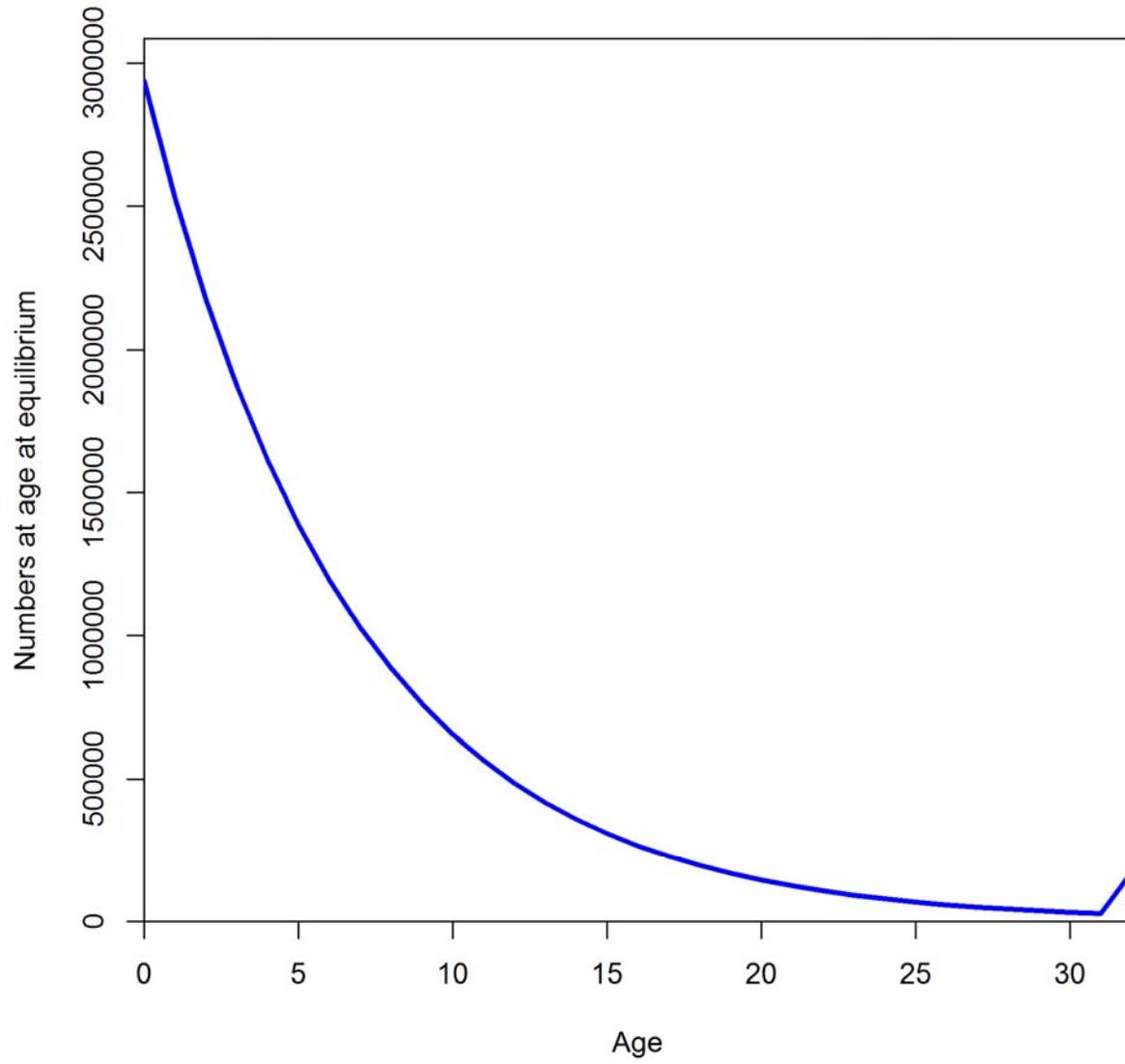
All cpue plot



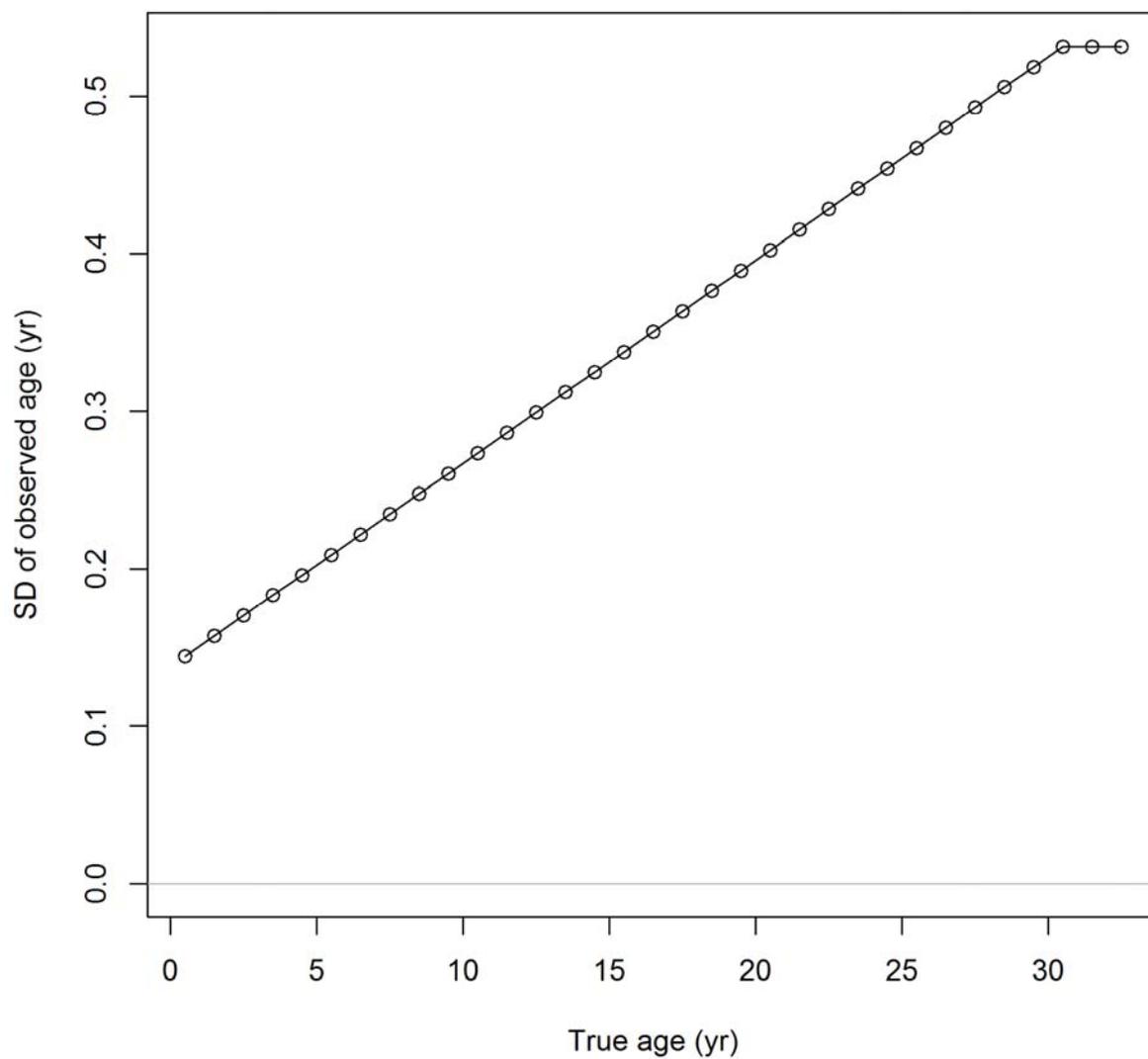
Middle of year expected numbers at age in thousands (max=9887690)



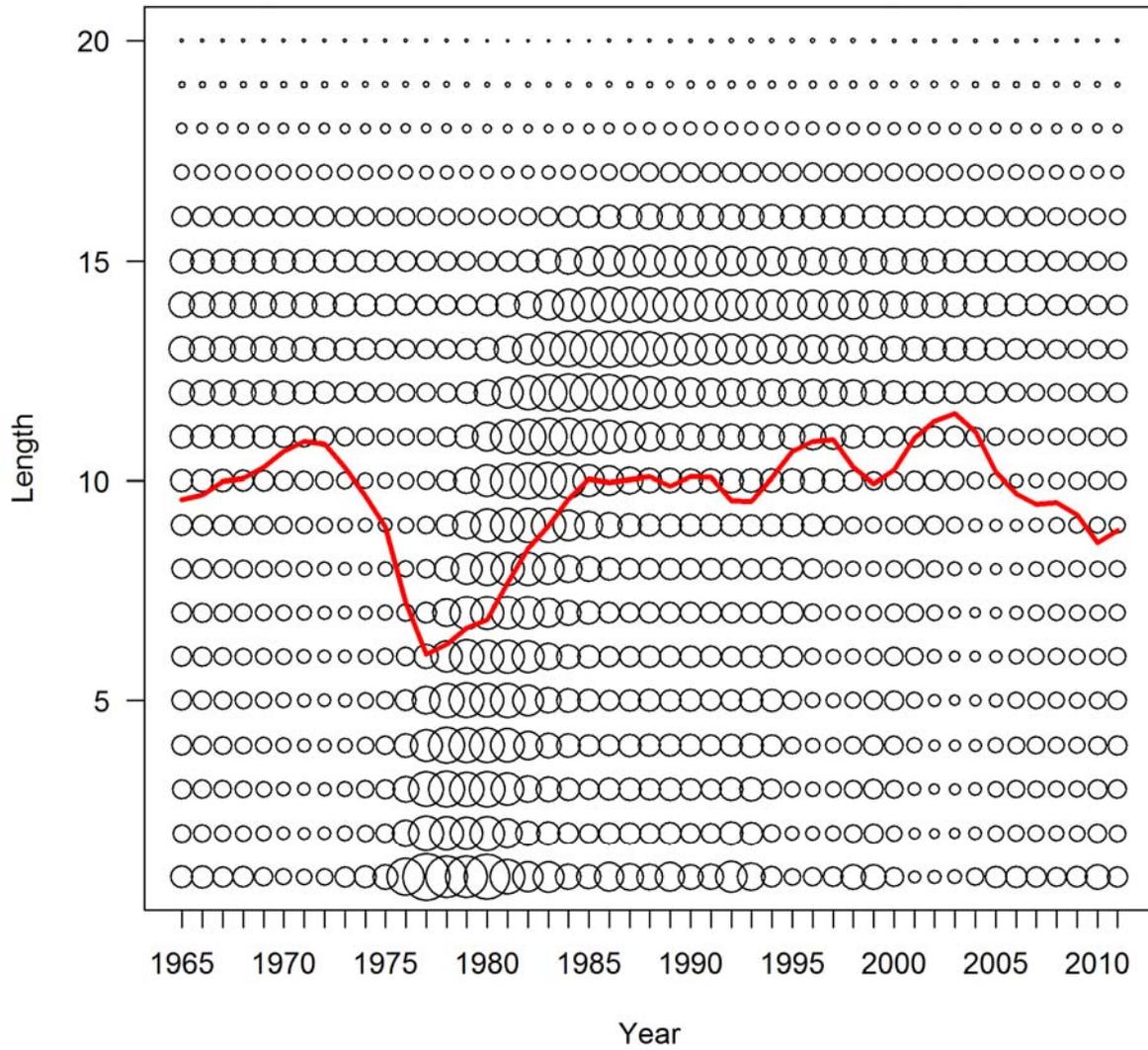
Equilibrium age distribution

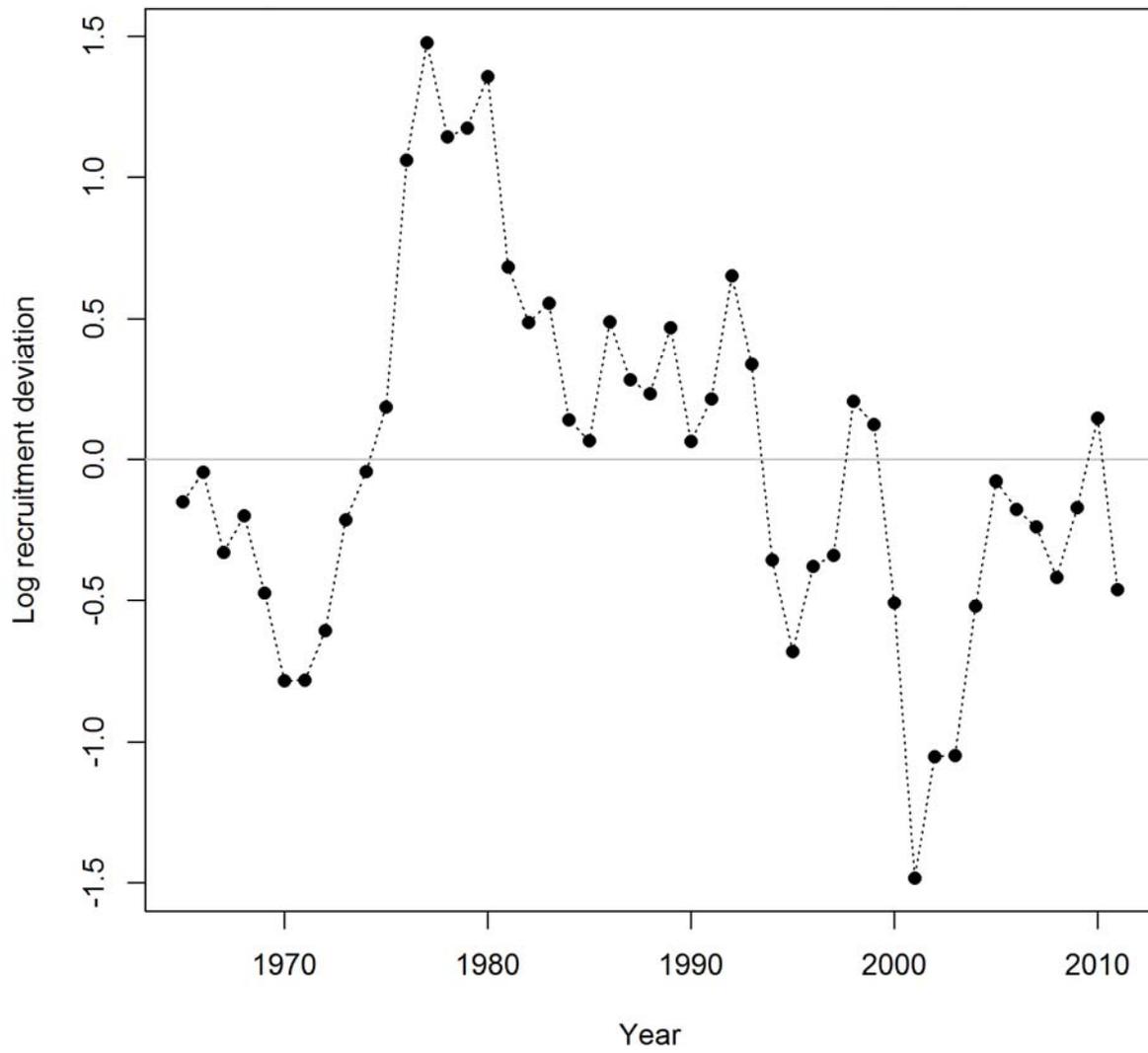


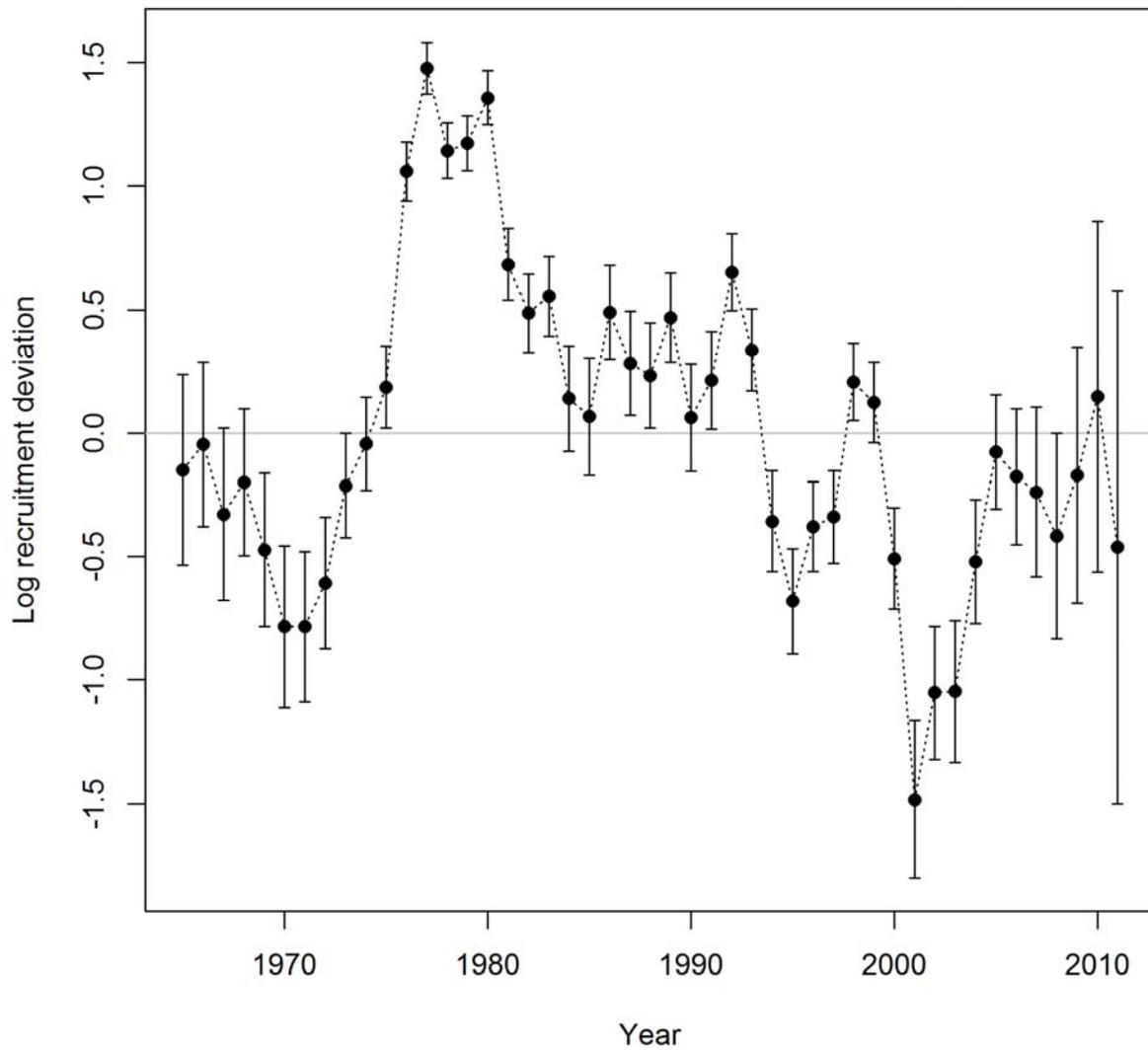
Ageing imprecision



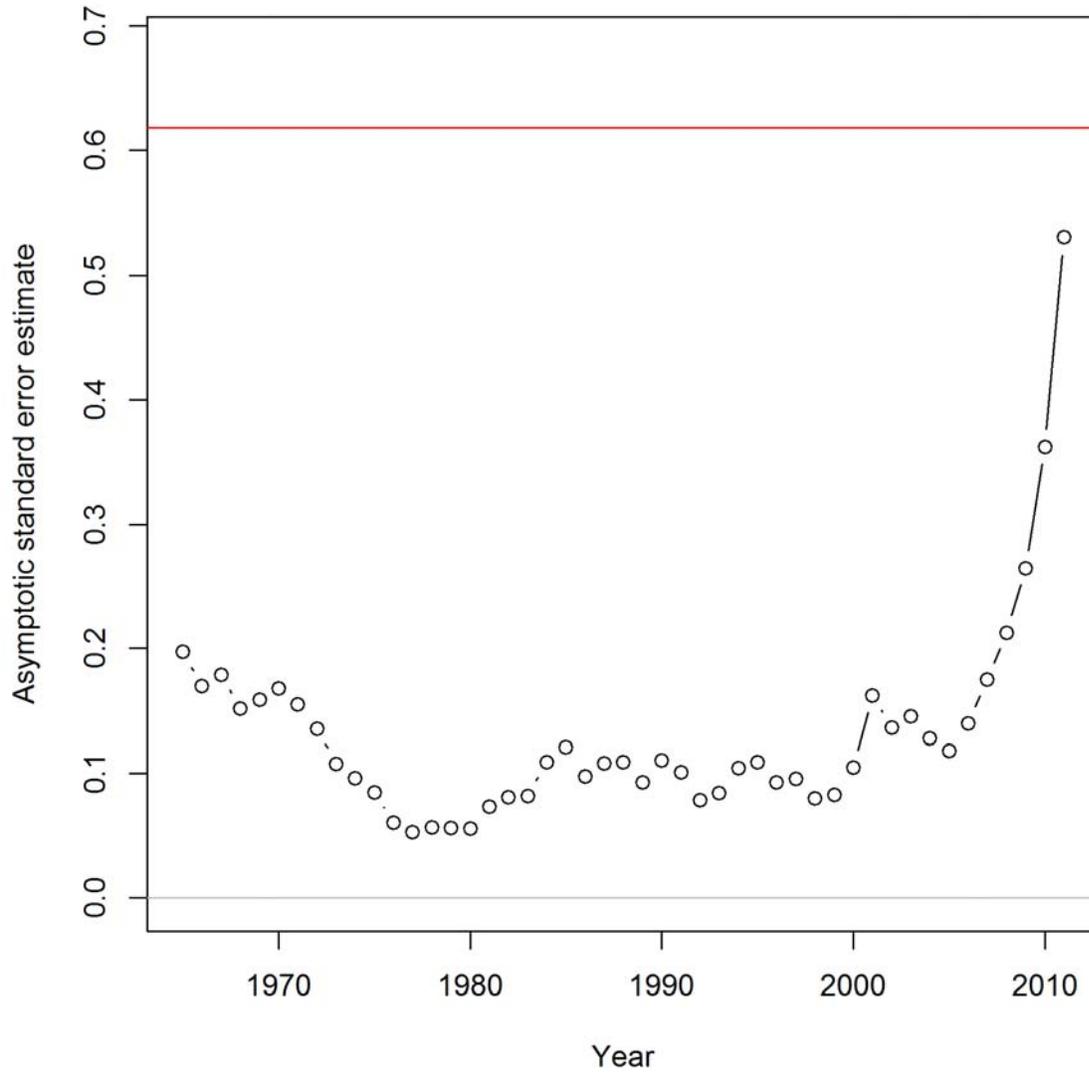
Middle of year expected numbers at length in thousands (max=5122360)

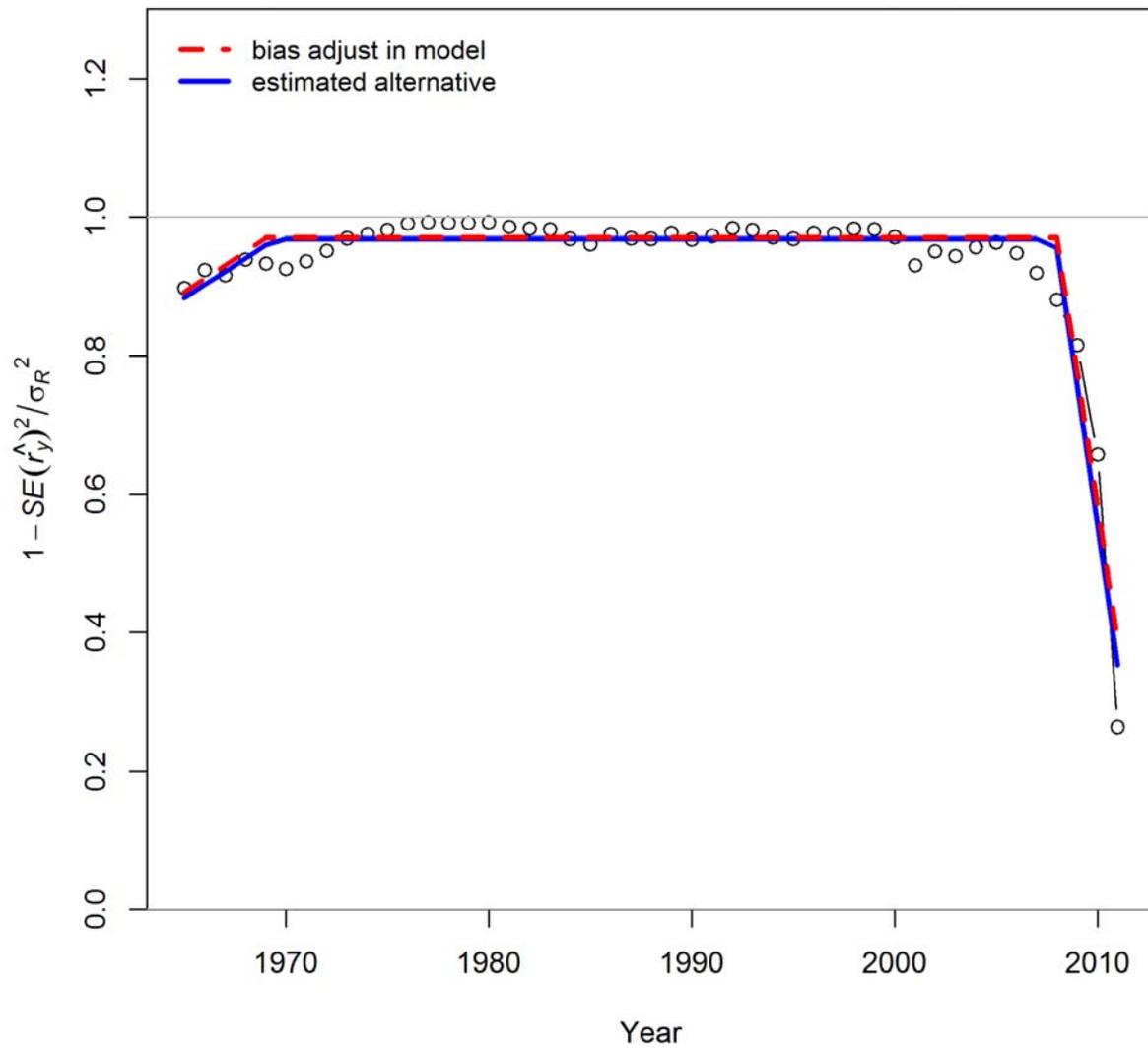




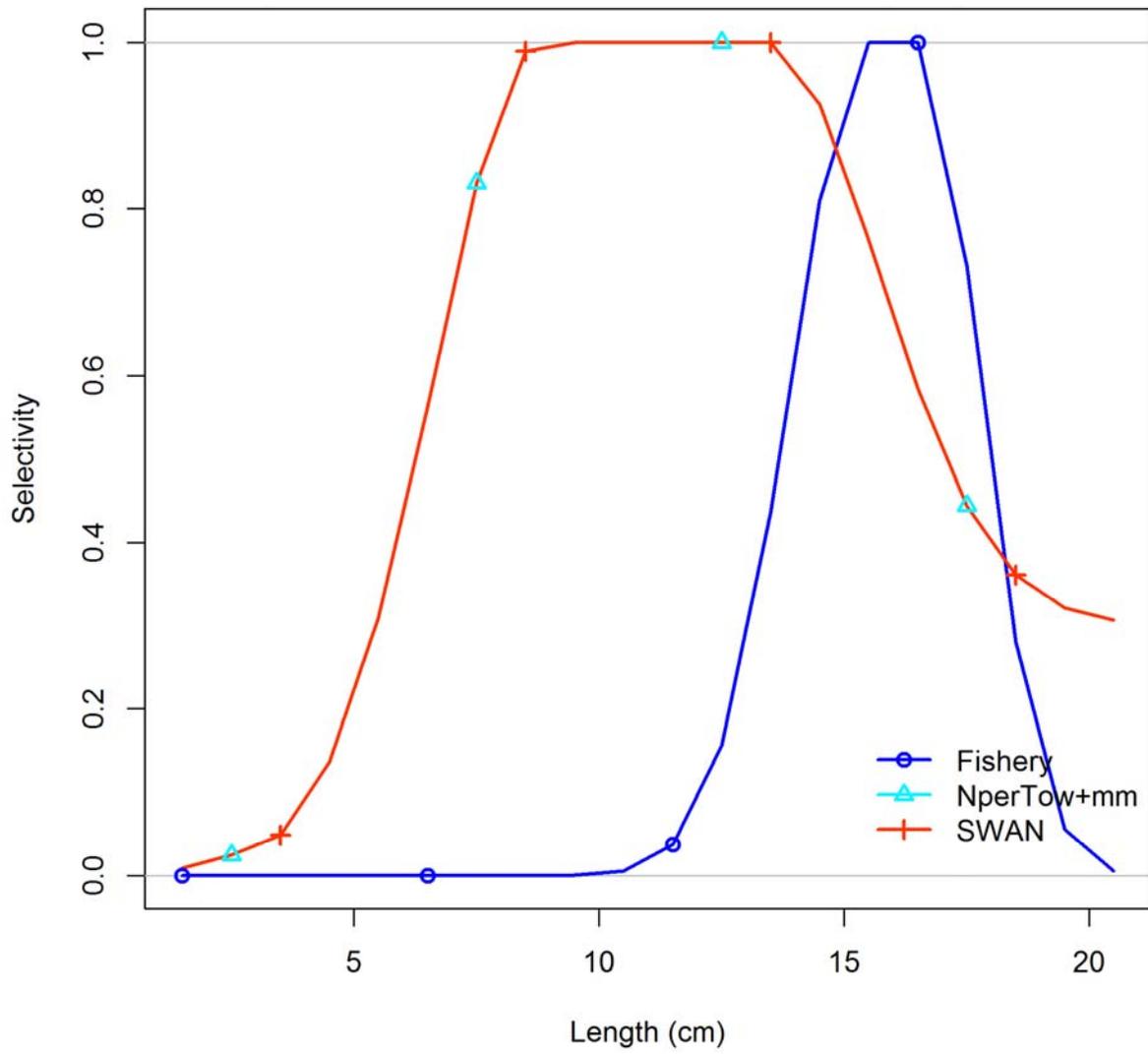


Recruitment deviation variance check

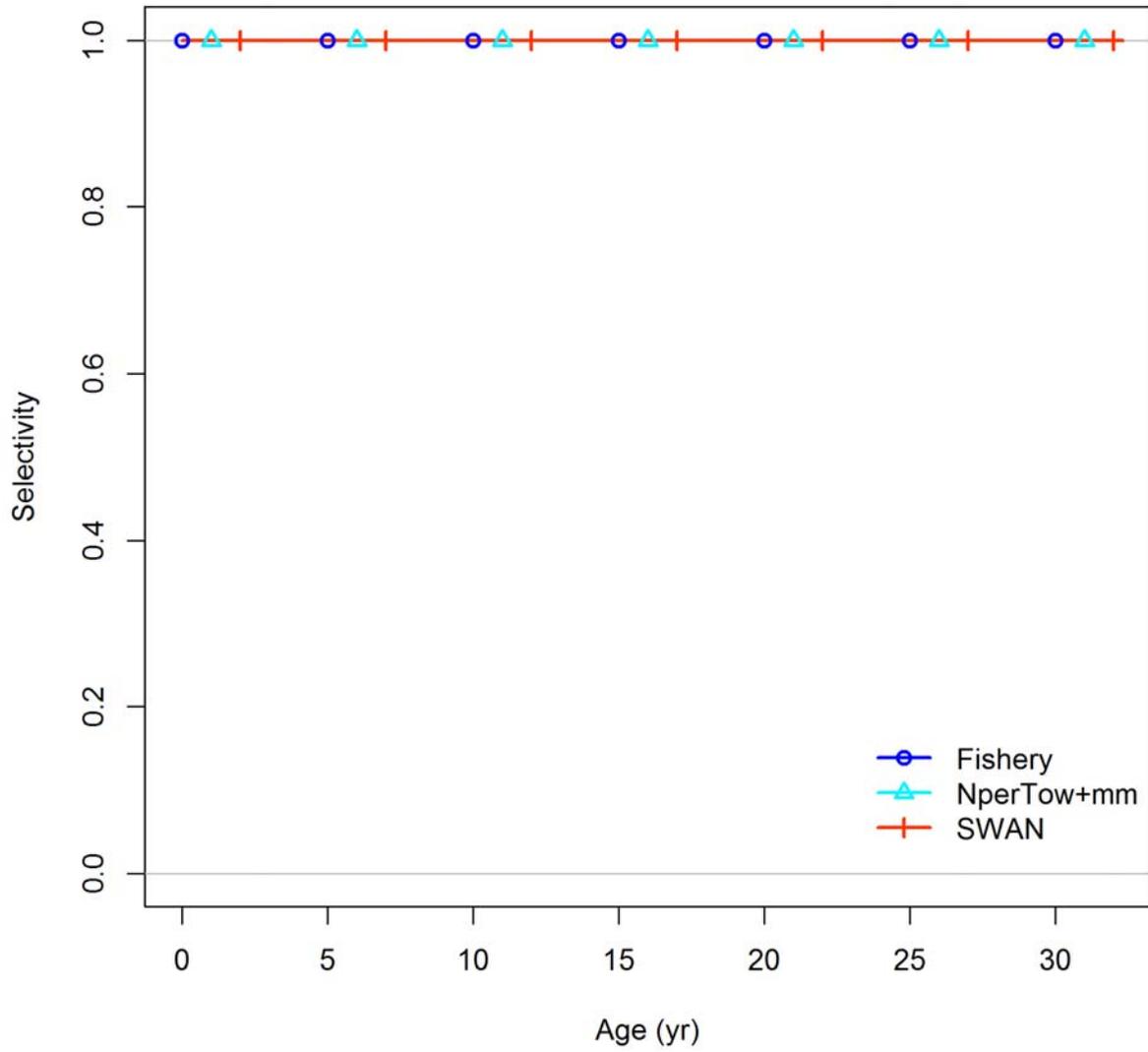




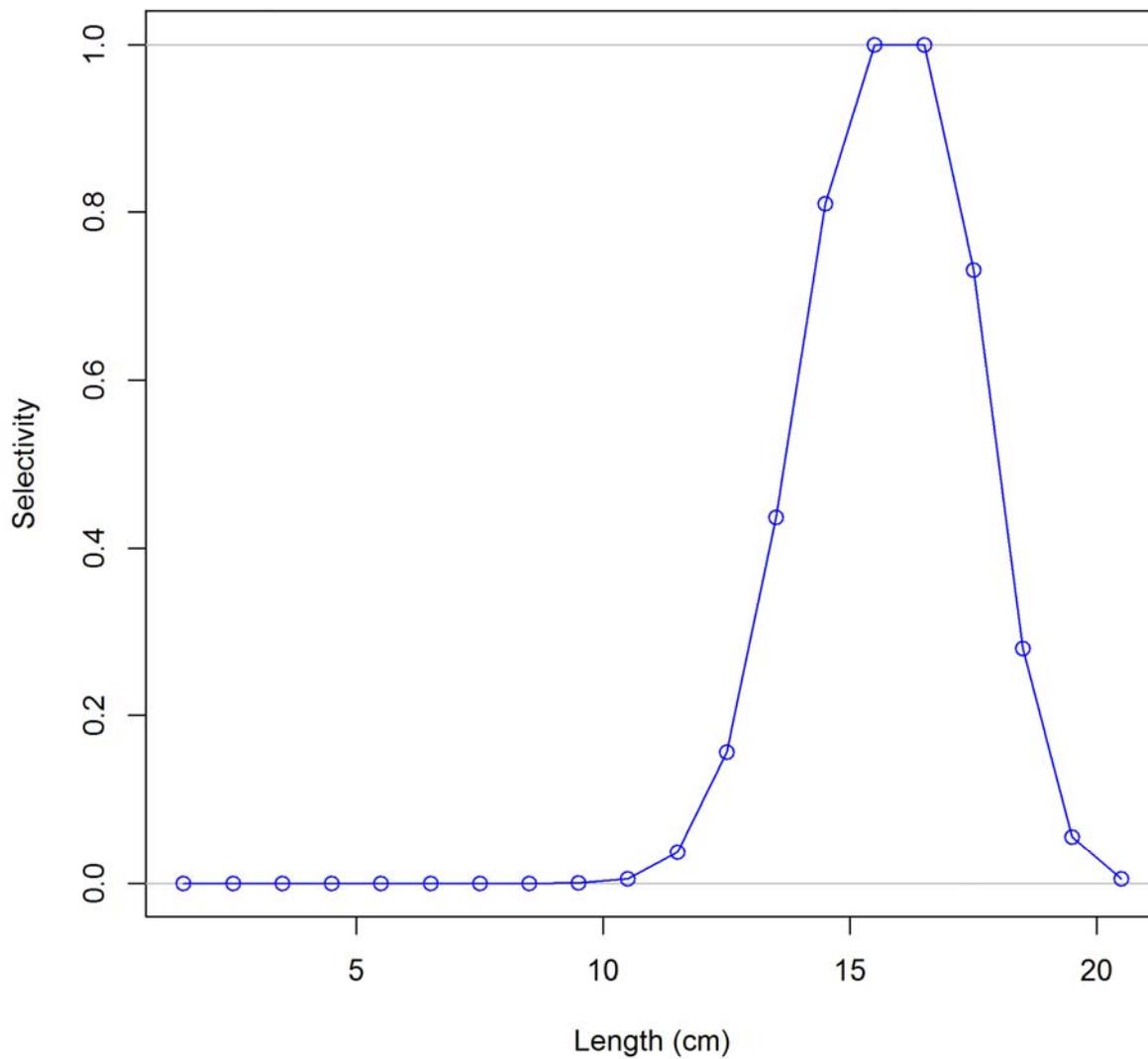
Length-based selectivity by fleet in 2011



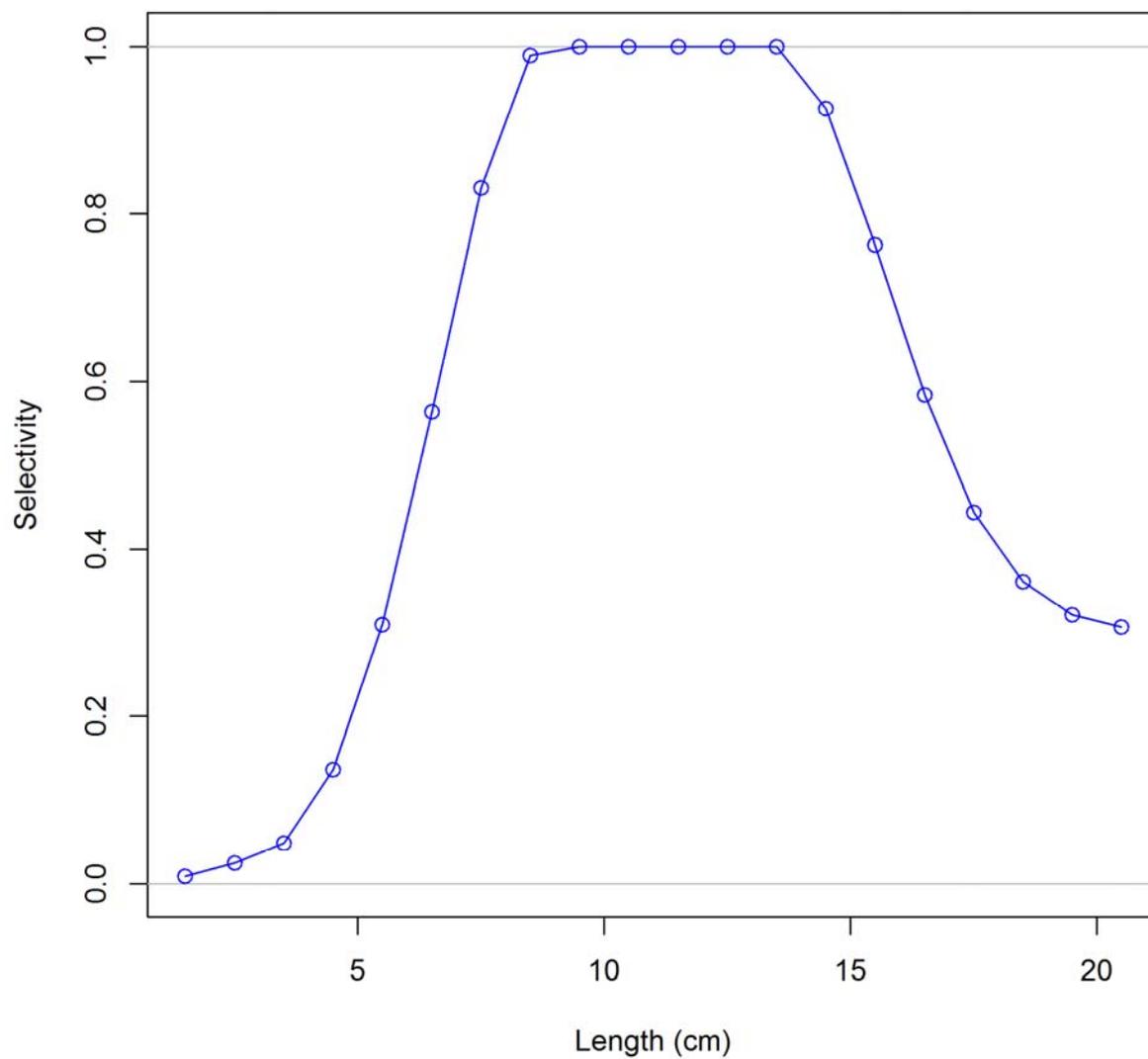
Age-based selectivity by fleet in 2011



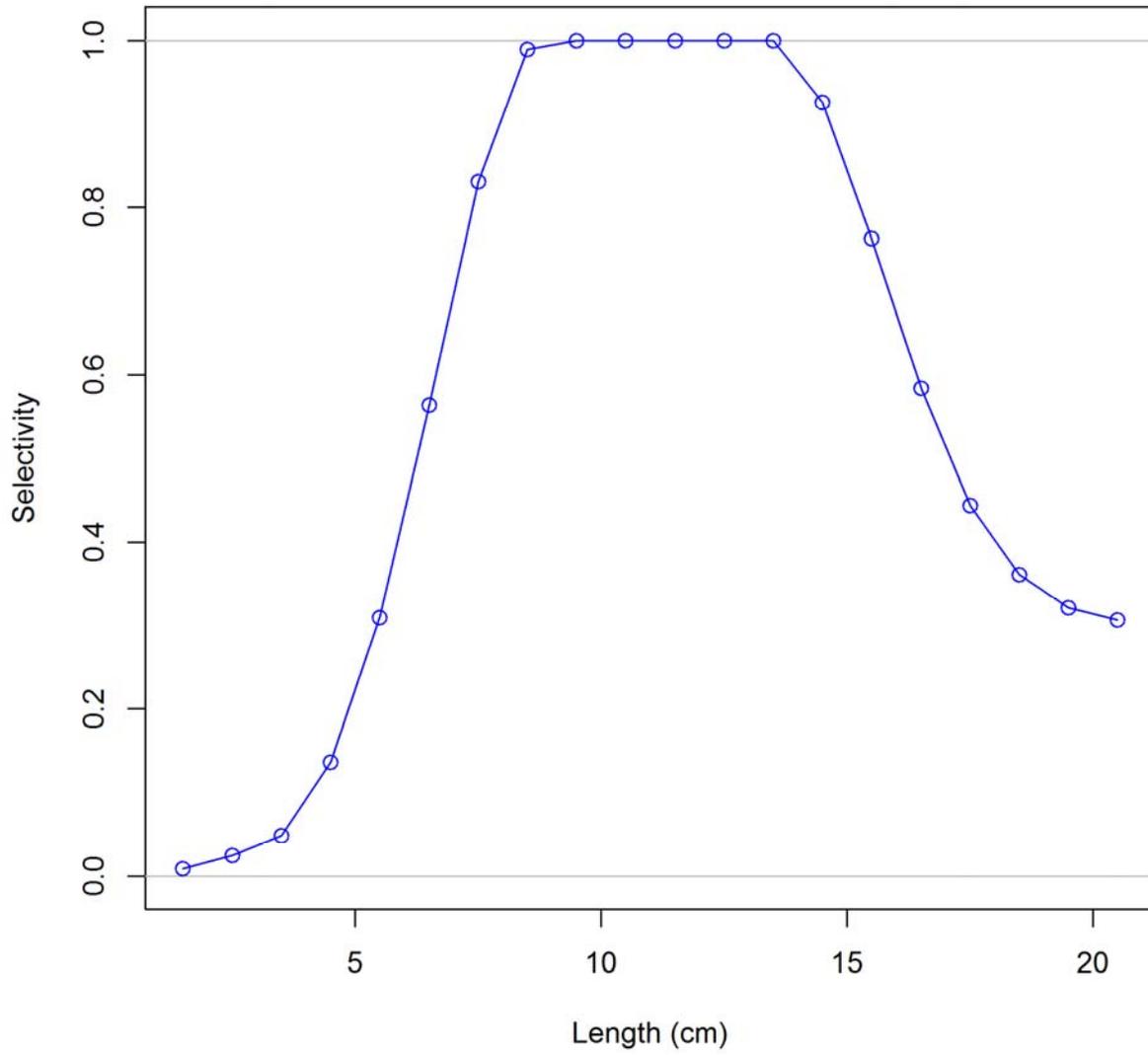
Ending year selectivity for Fishery



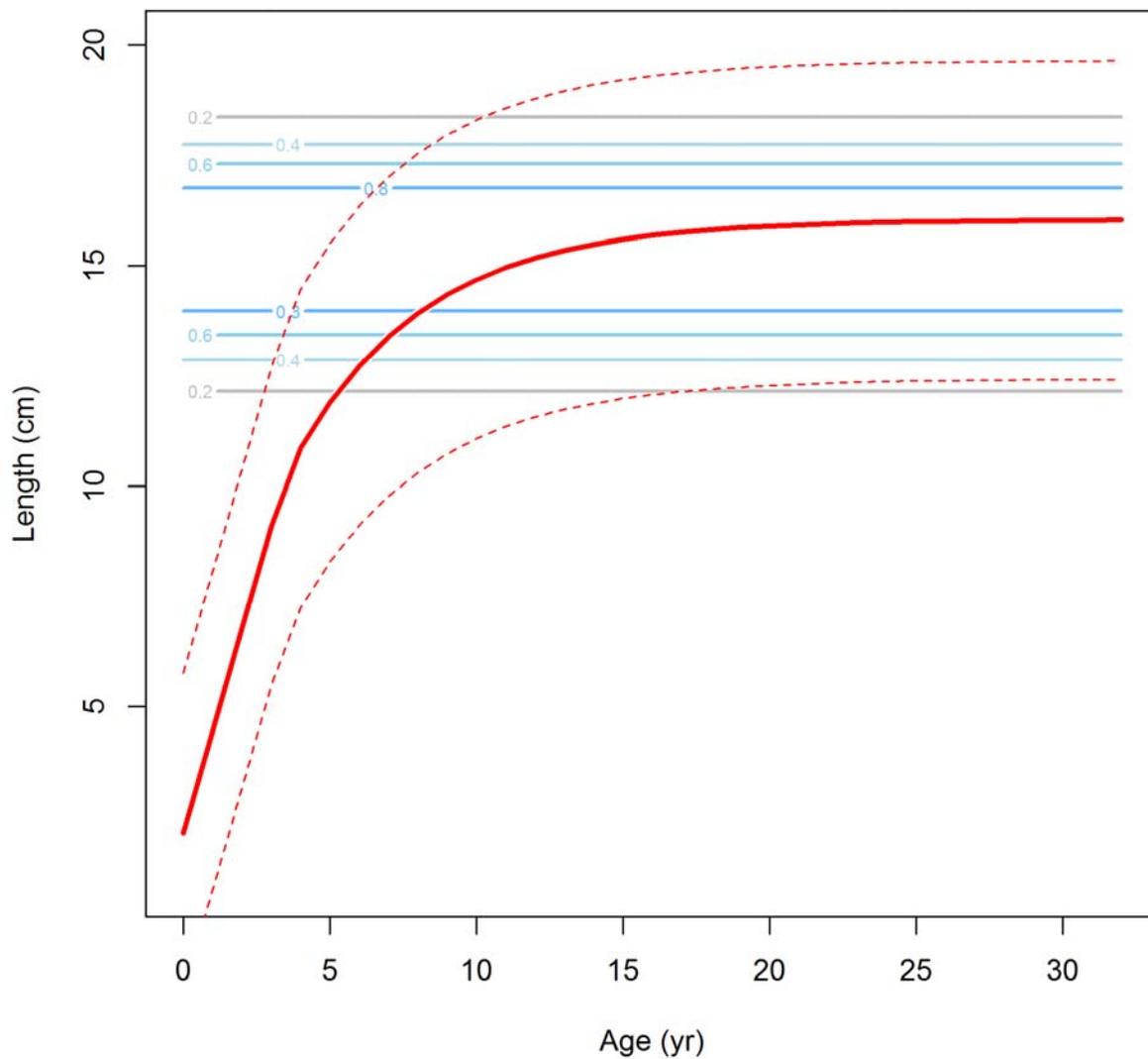
Ending year selectivity for NperTow+mm



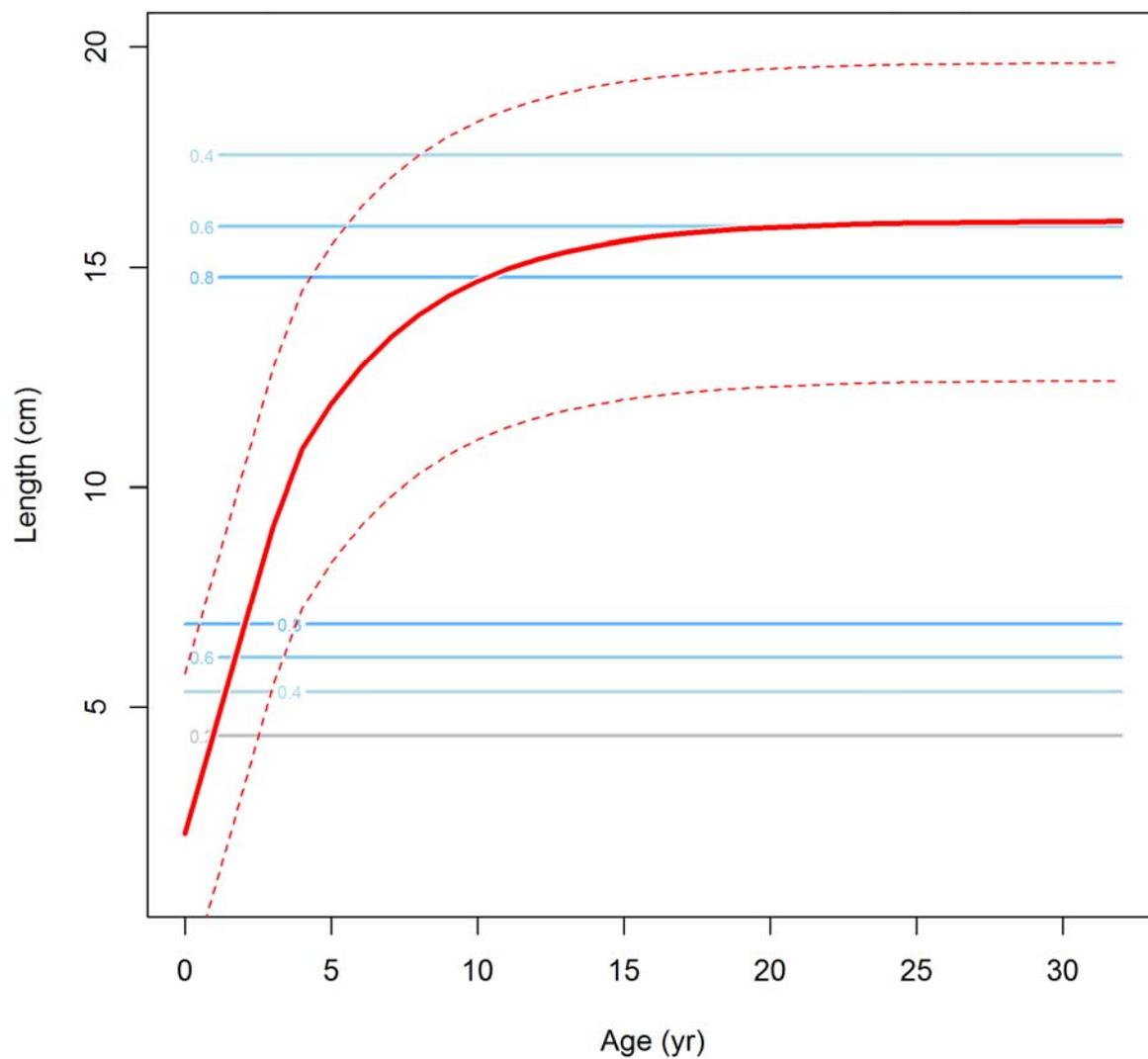
Ending year selectivity for SWAN



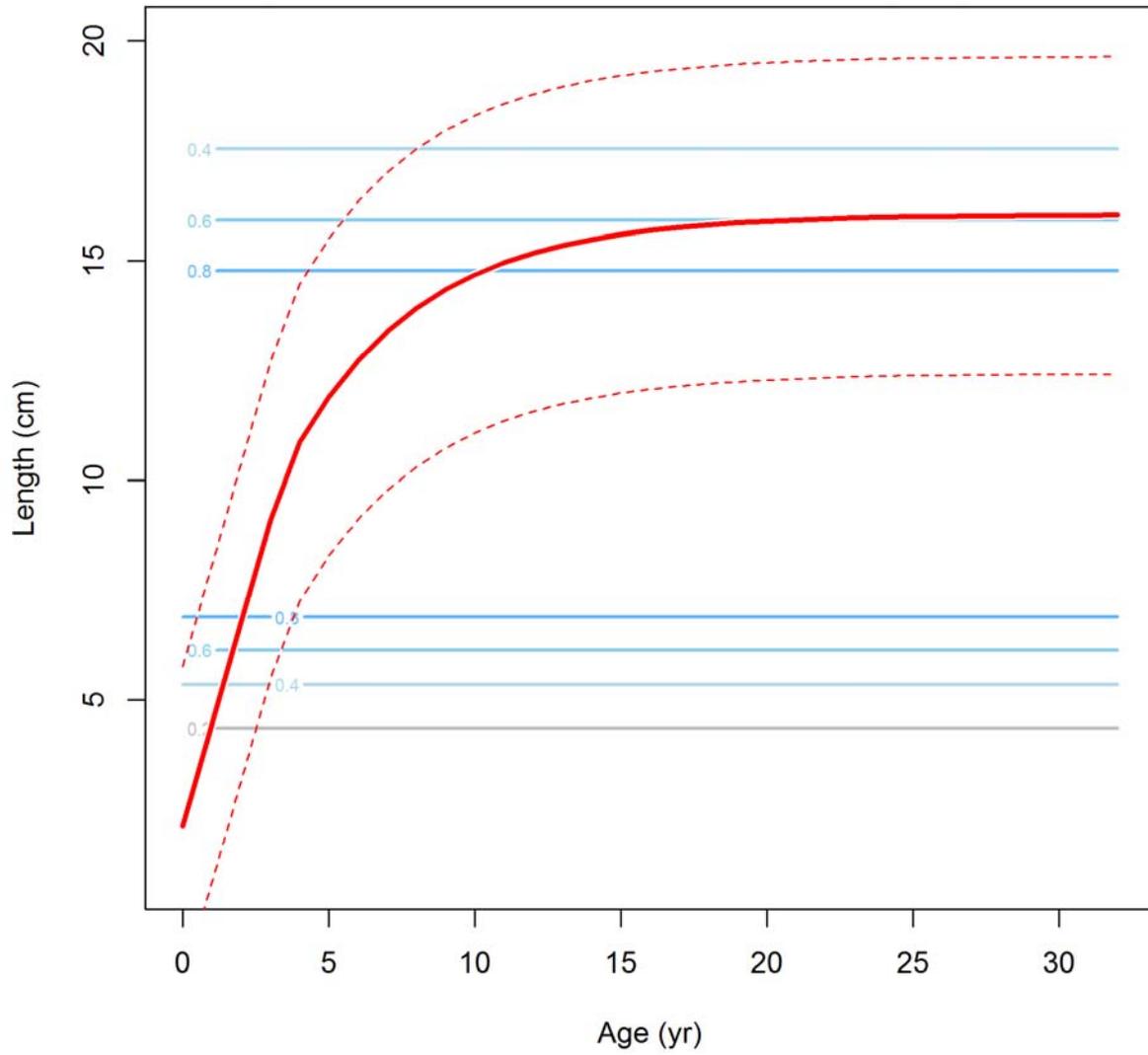
Ending year selectivity and growth for Fishery

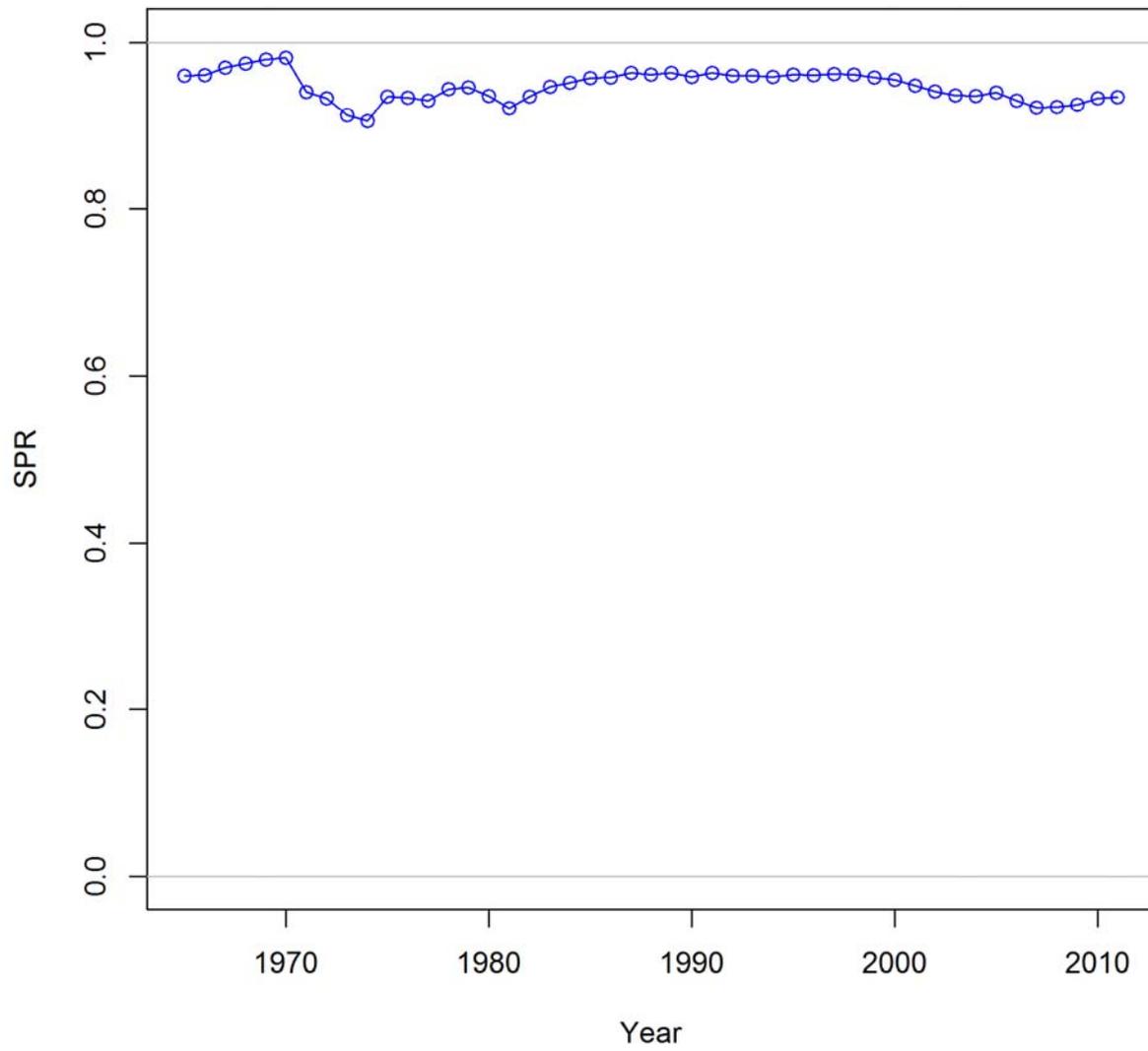


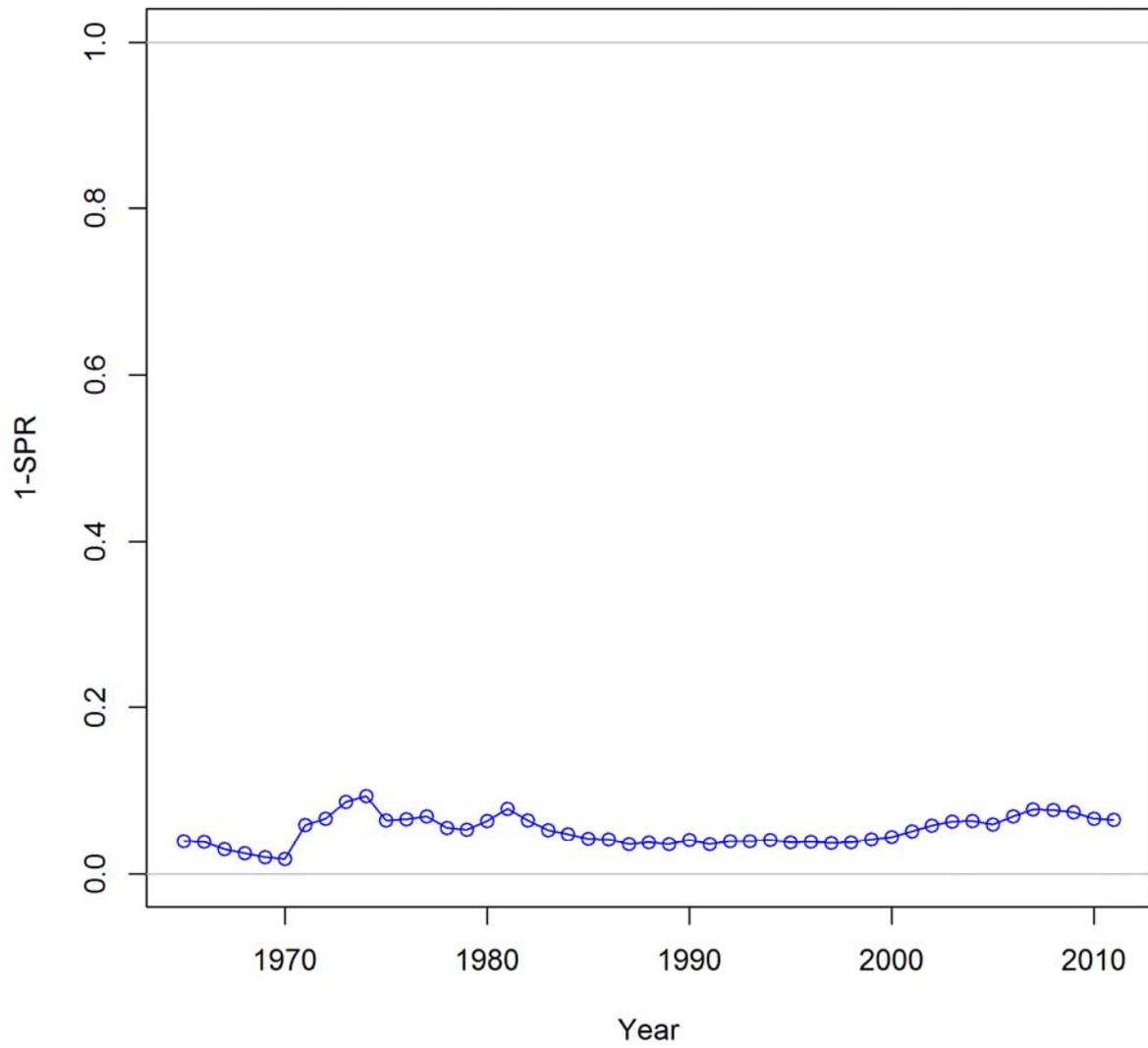
Ending year selectivity and growth for NperTow+mm

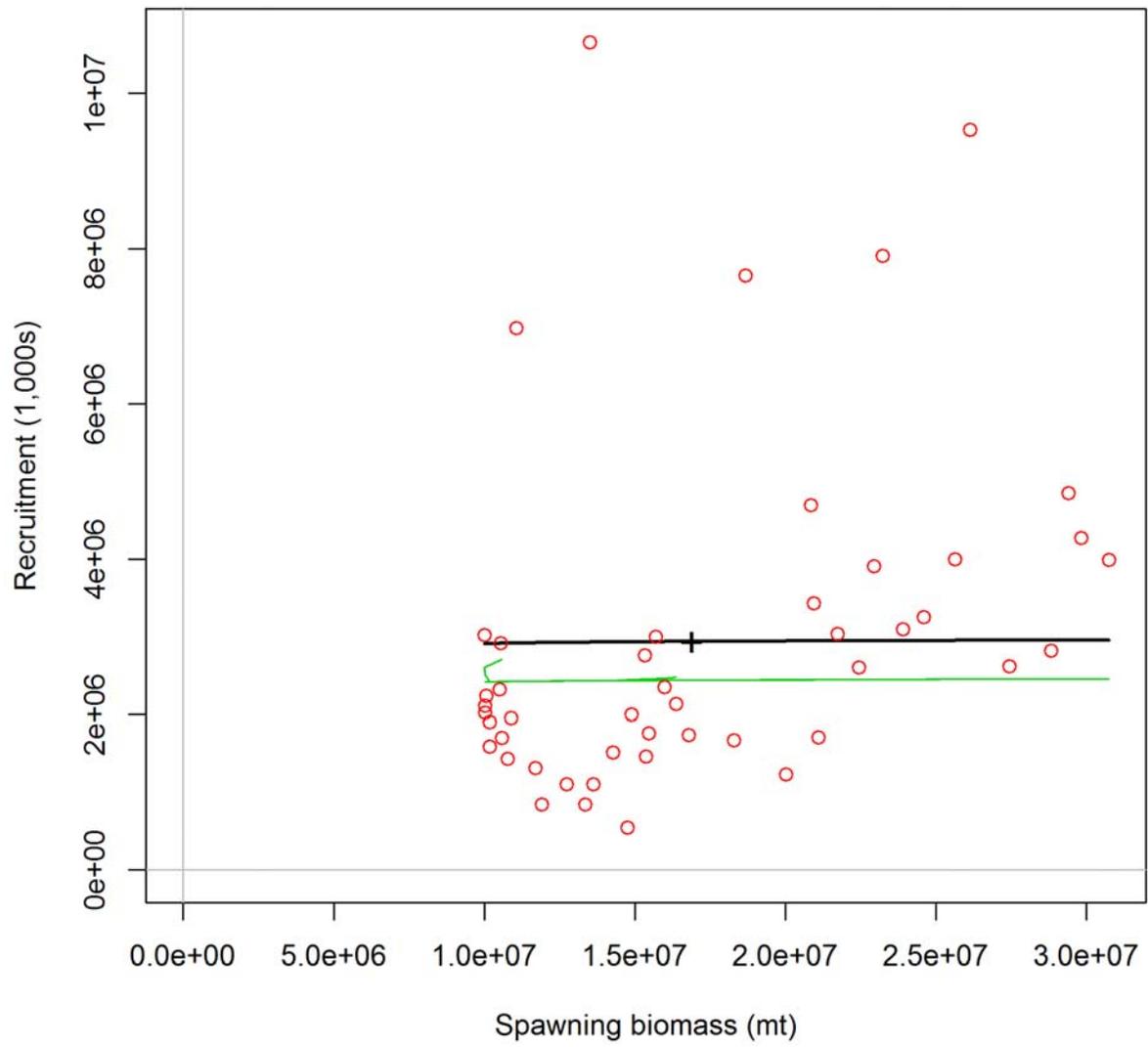


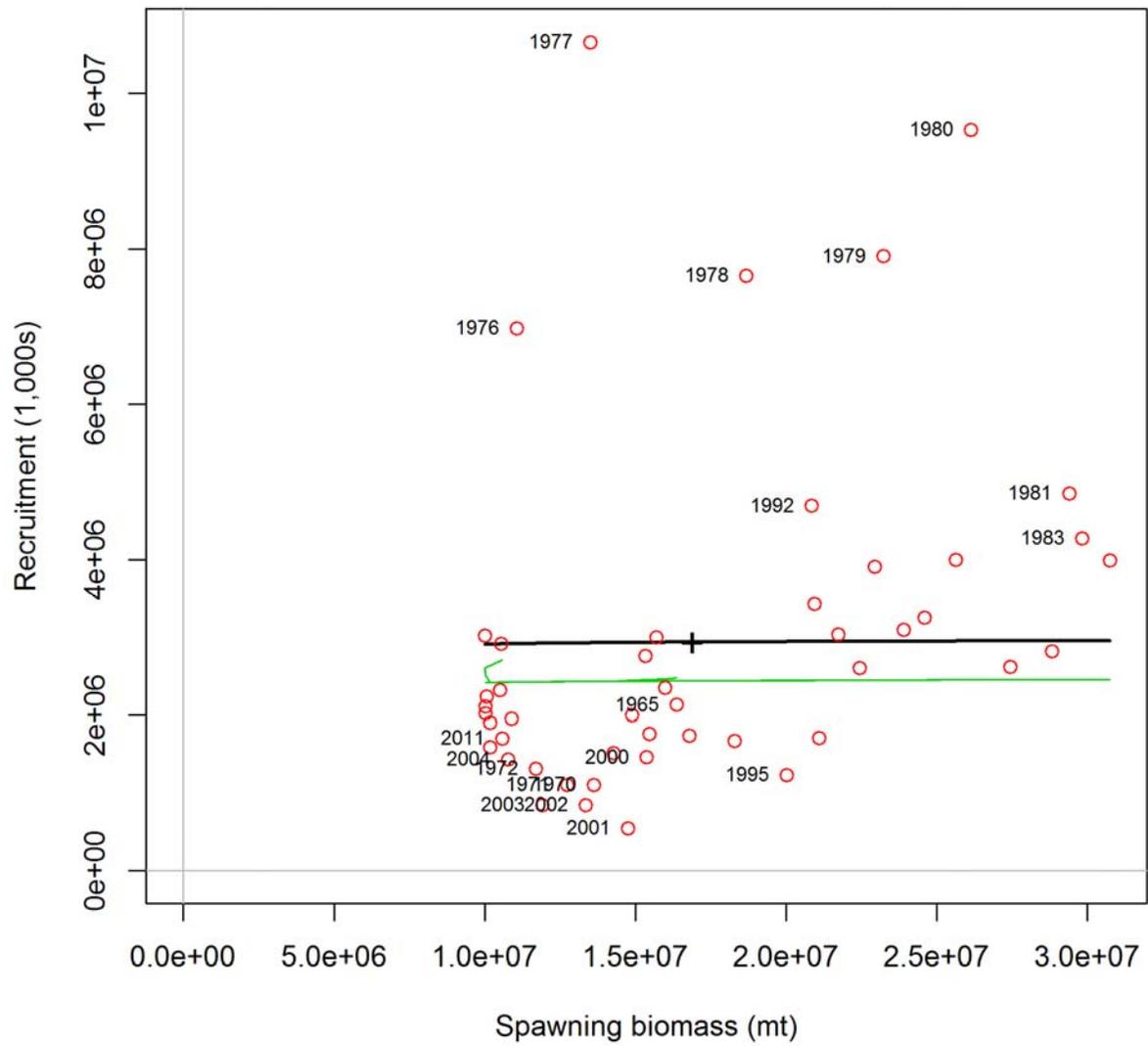
Ending year selectivity and growth for SWAN



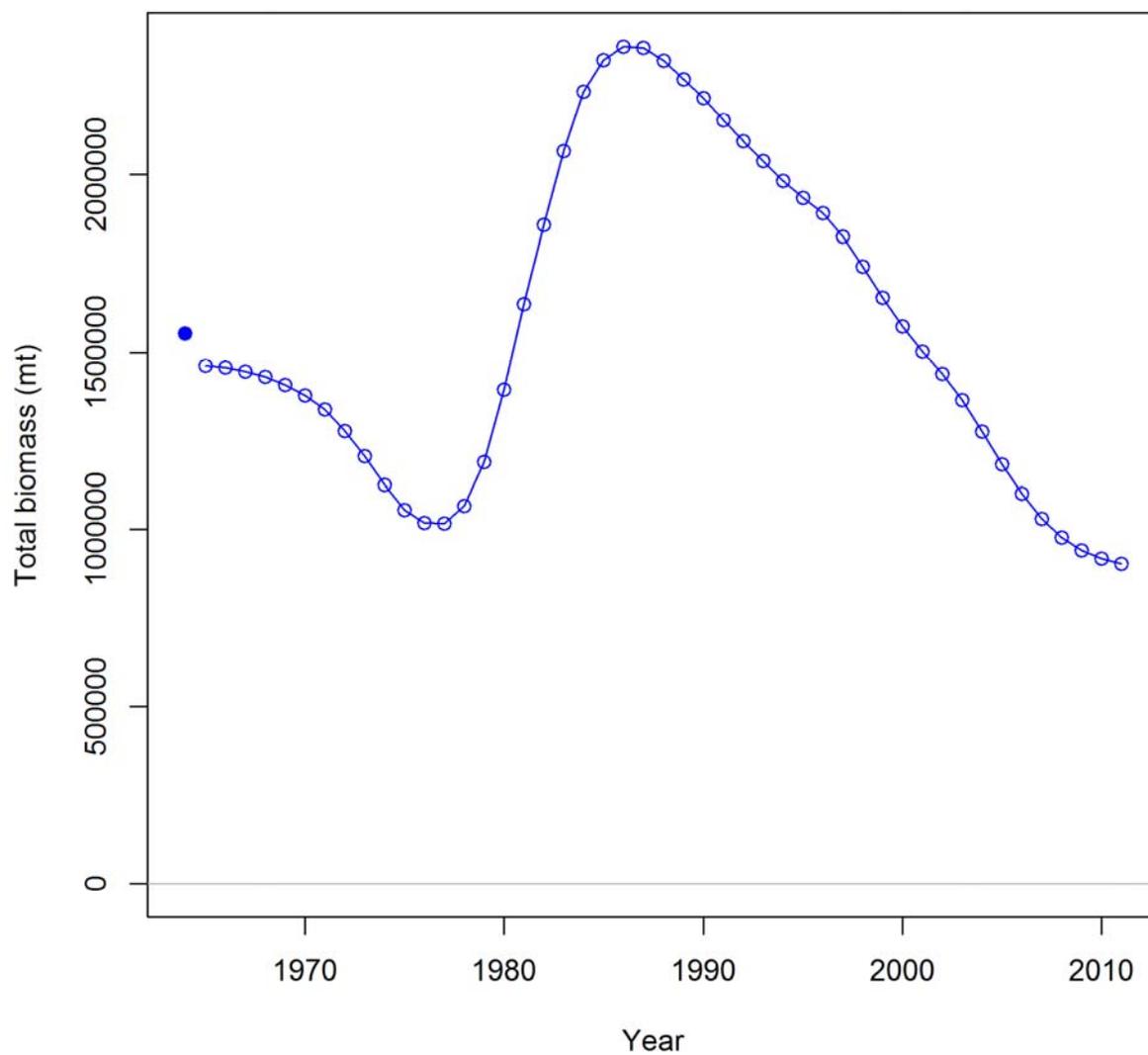


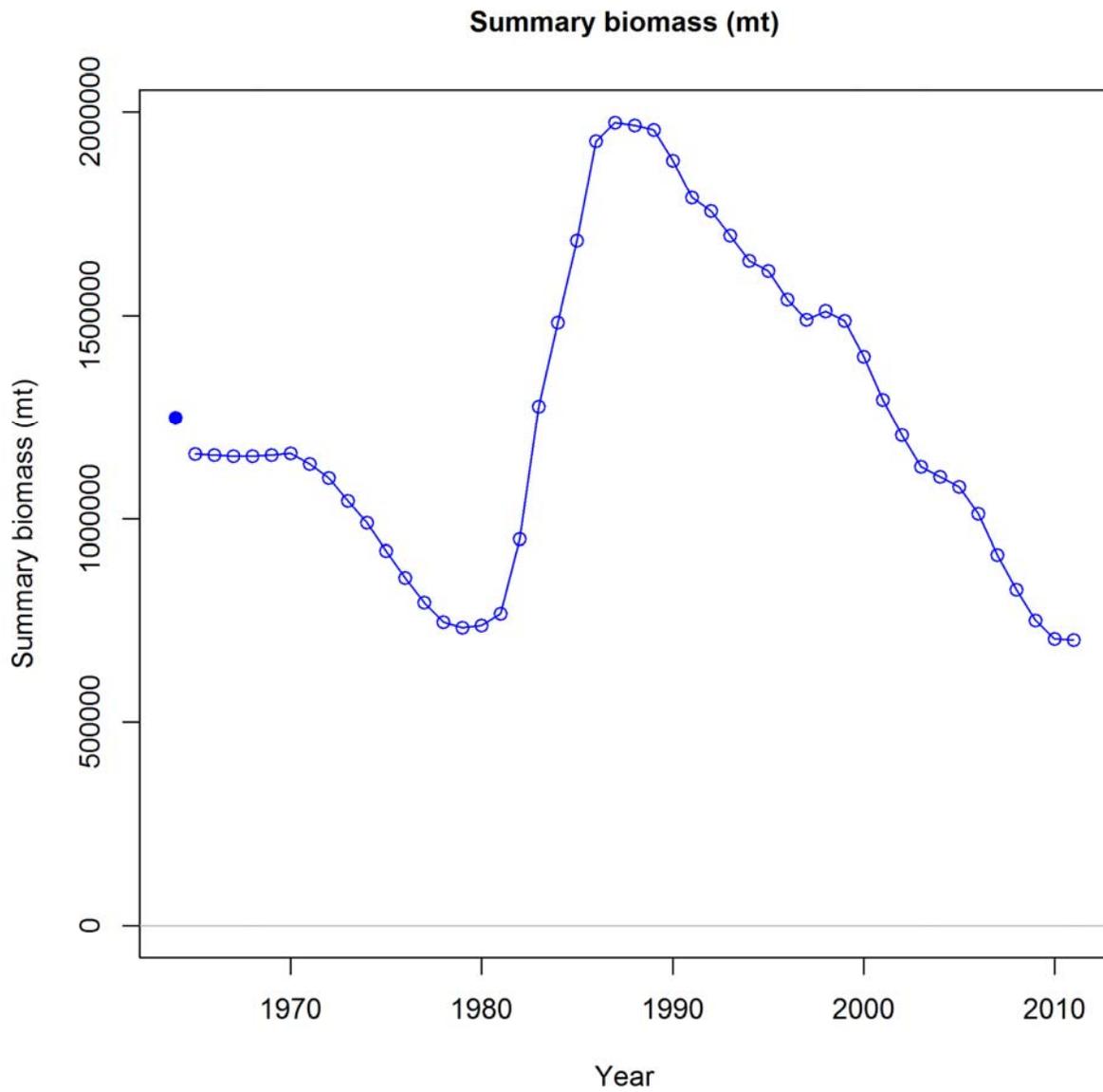




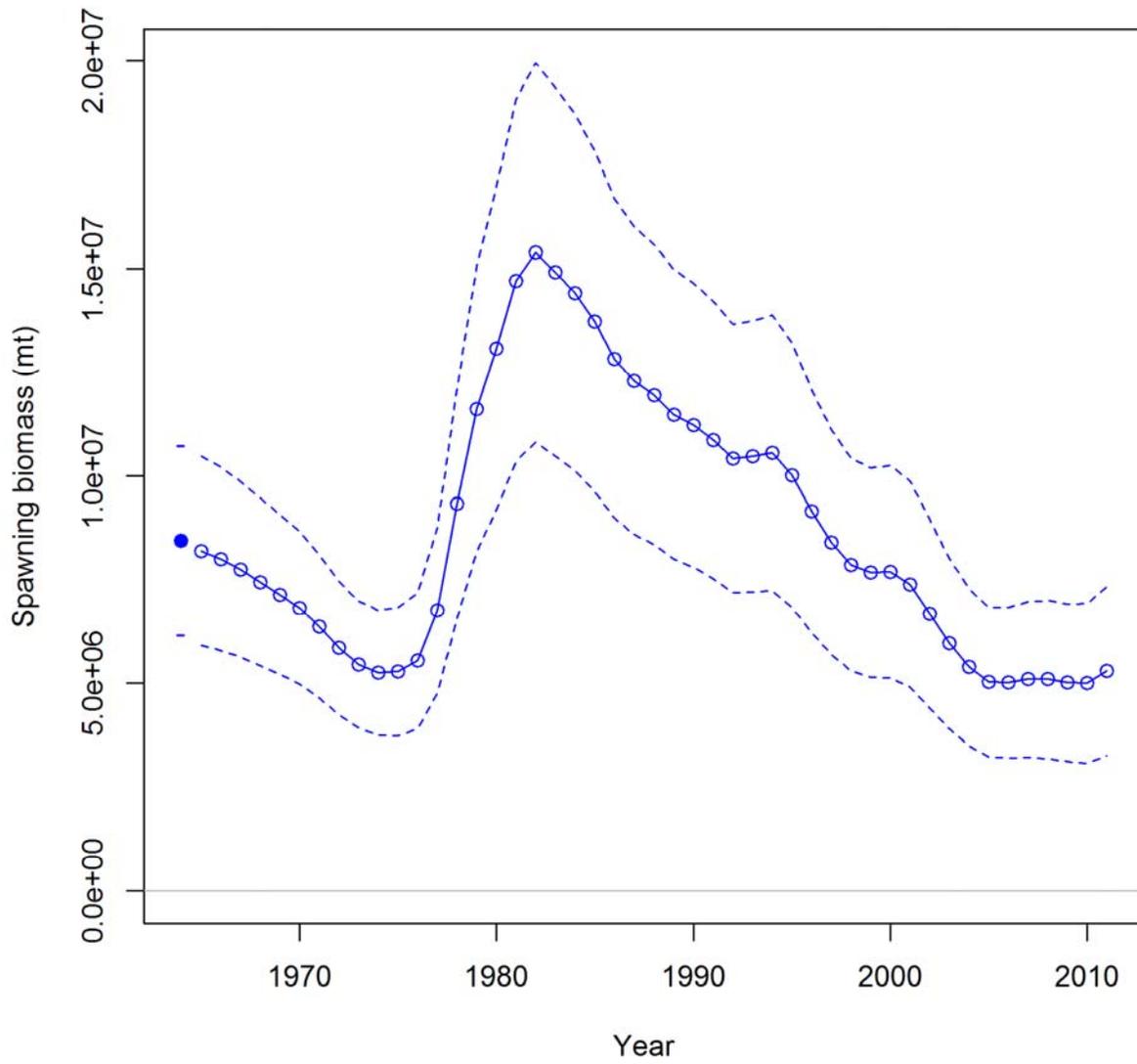


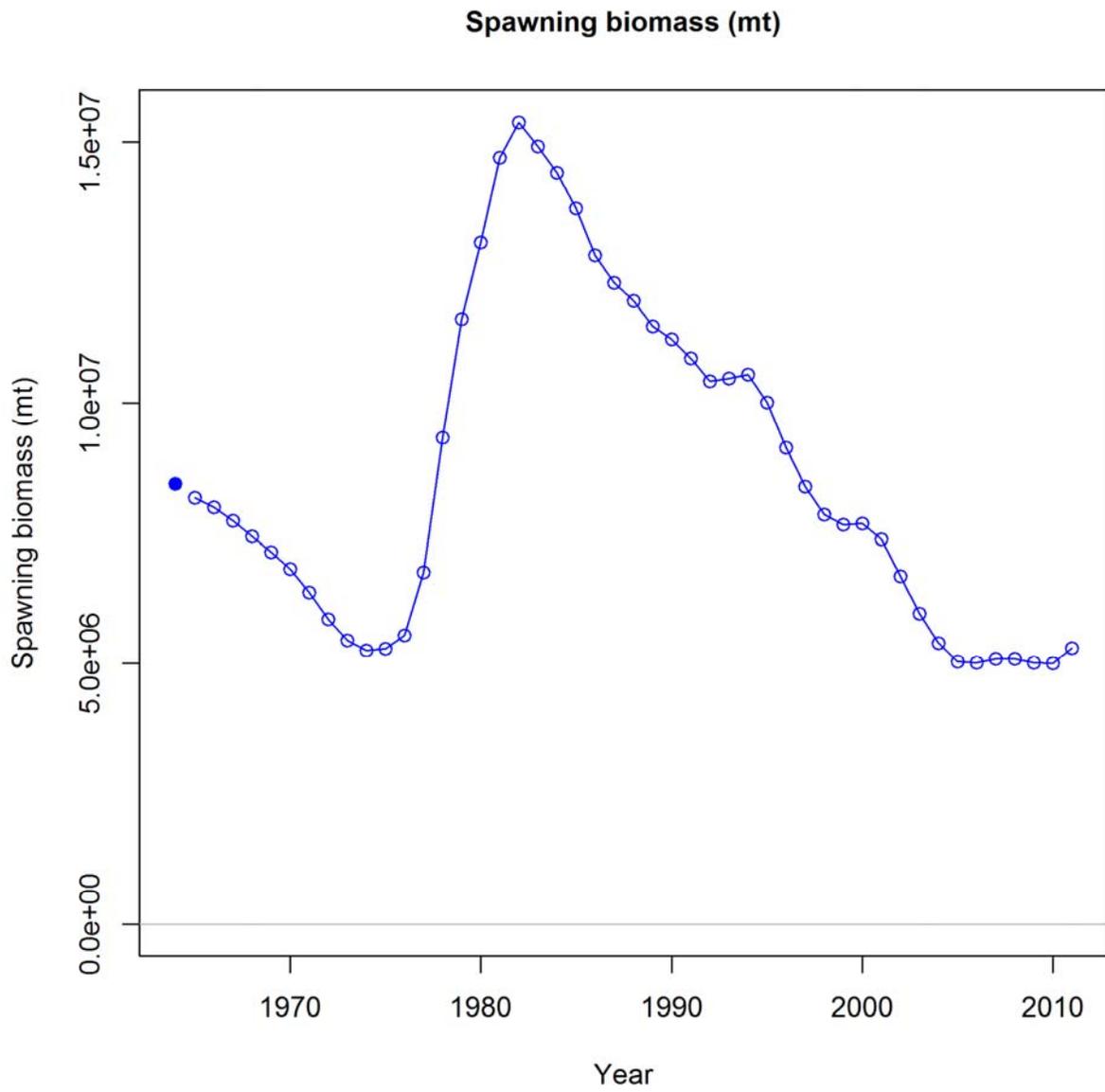
Total biomass (mt)



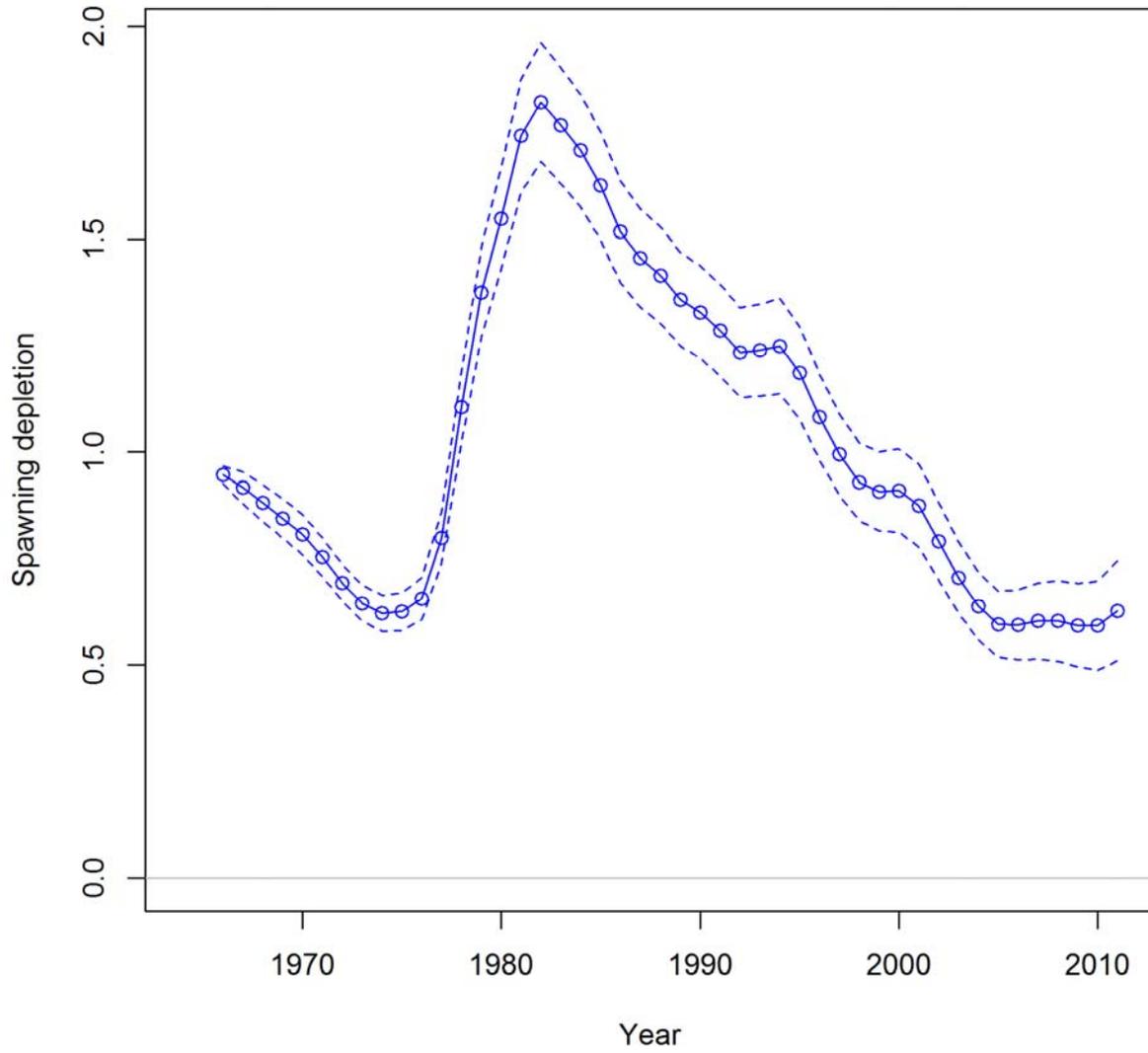


Spawning biomass (mt) with ~95% asymptotic intervals

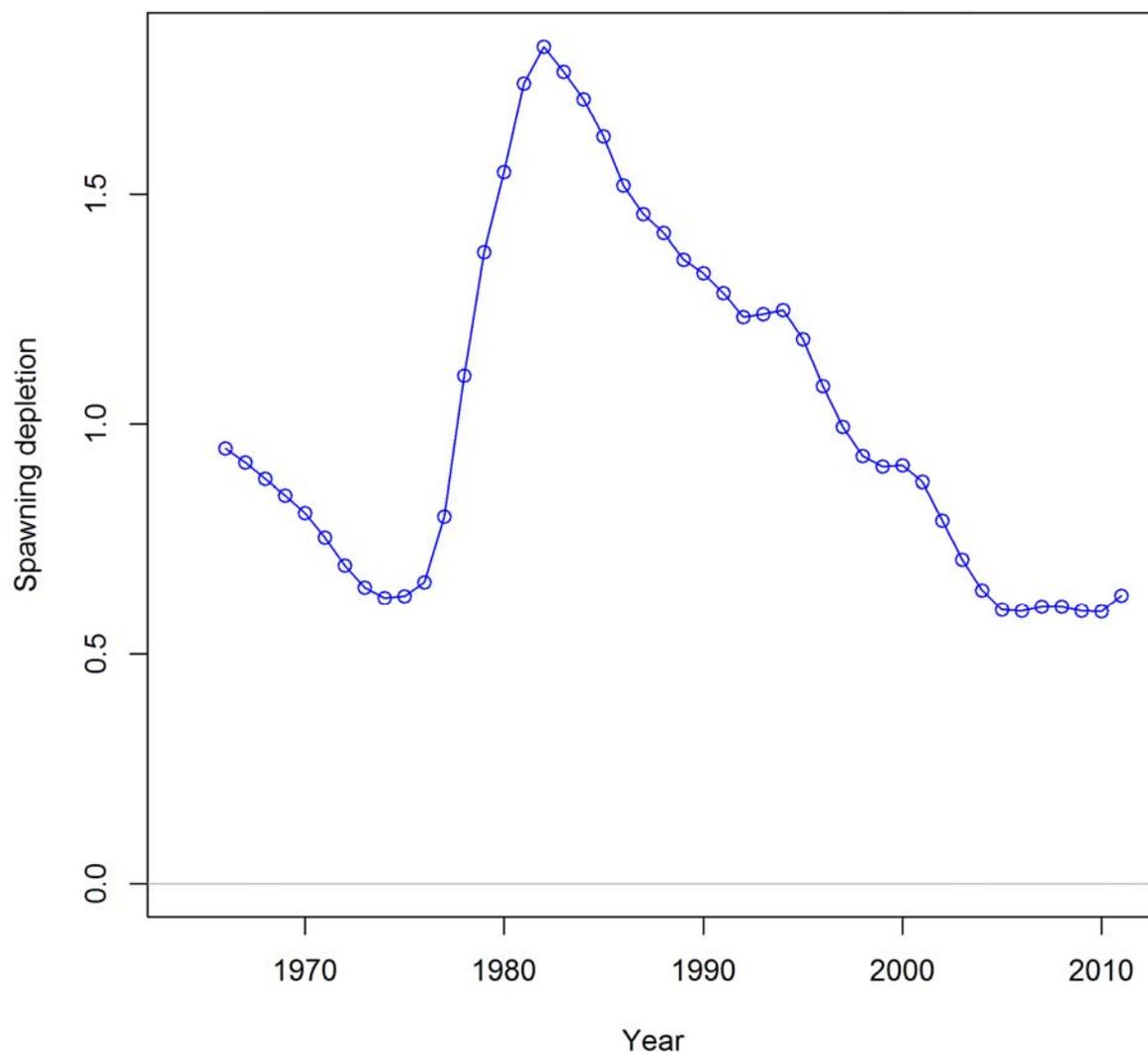




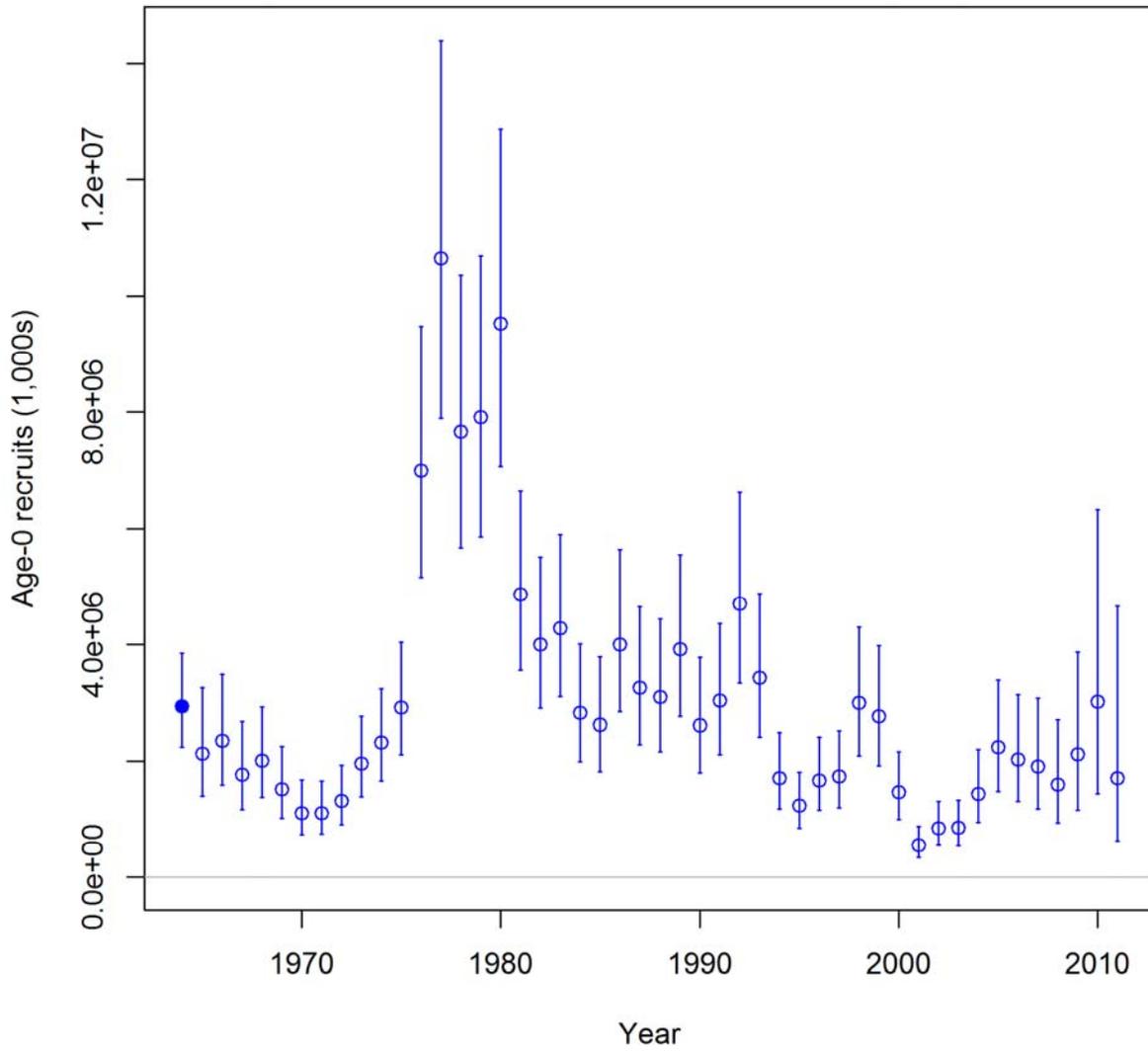
Spawning depletion with ~95% asymptotic intervals



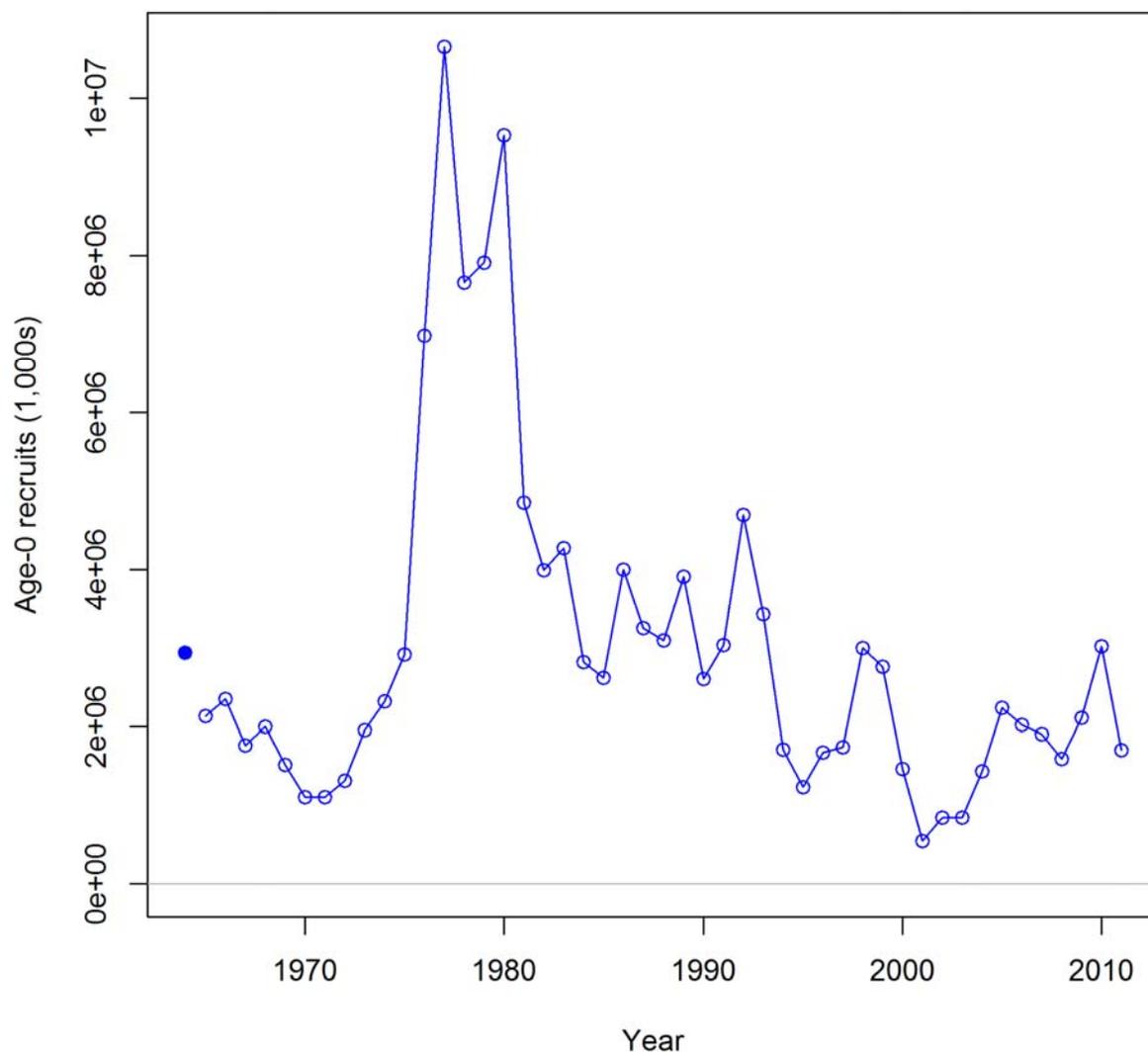
Spawning depletion

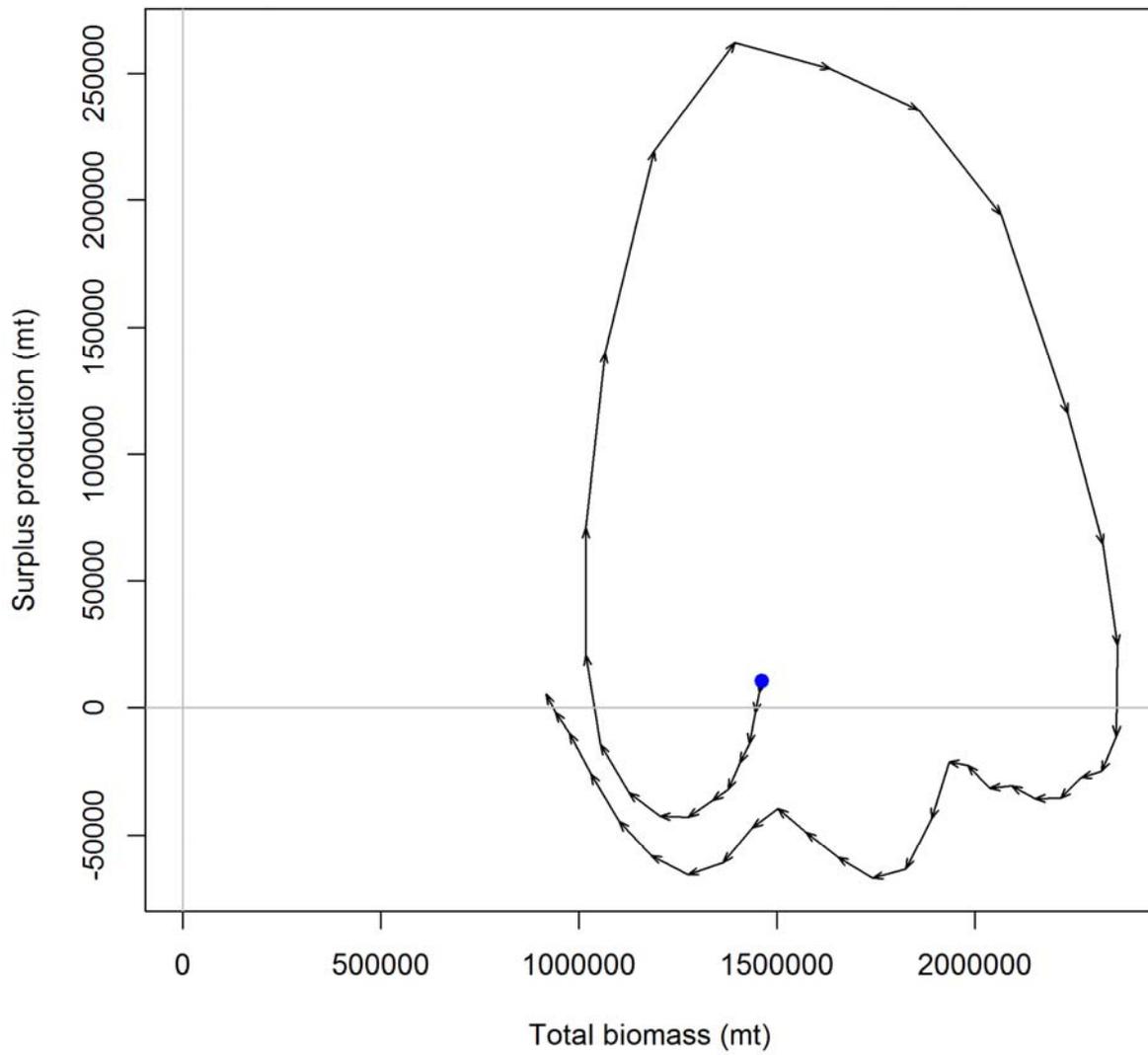


Age-0 recruits (1,000s) with ~95% asymptotic intervals



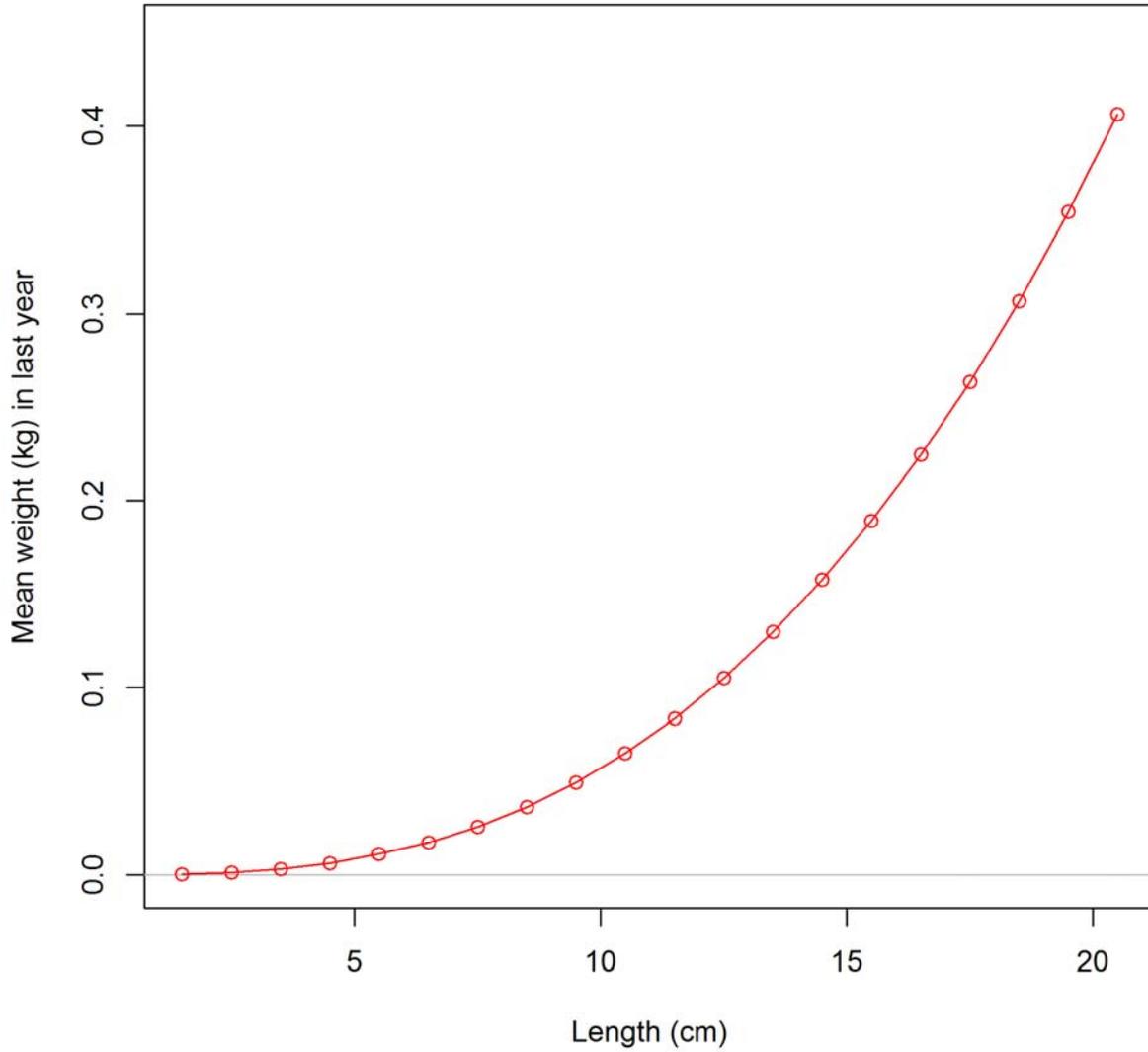
Age-0 recruits (1,000s)

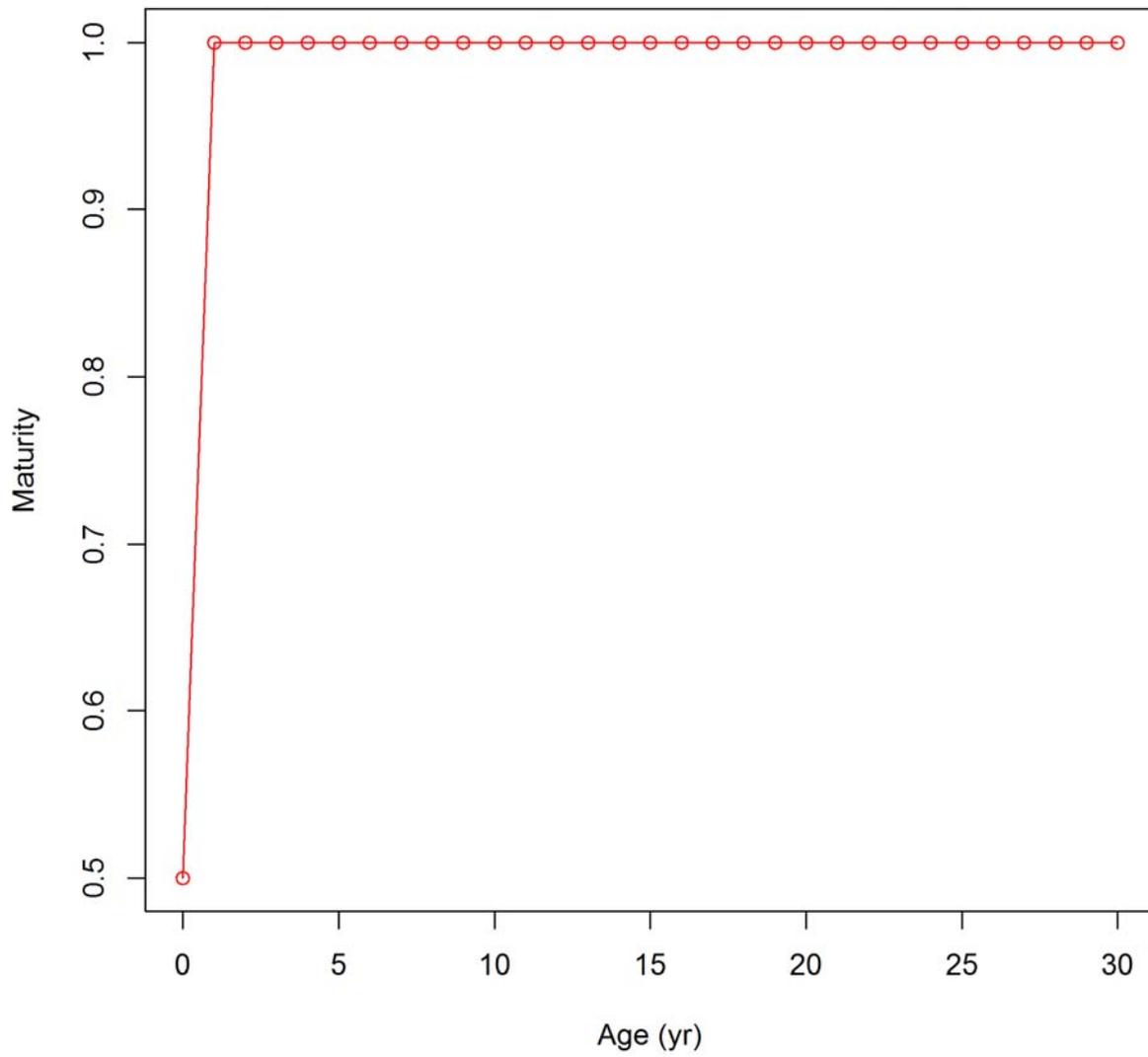


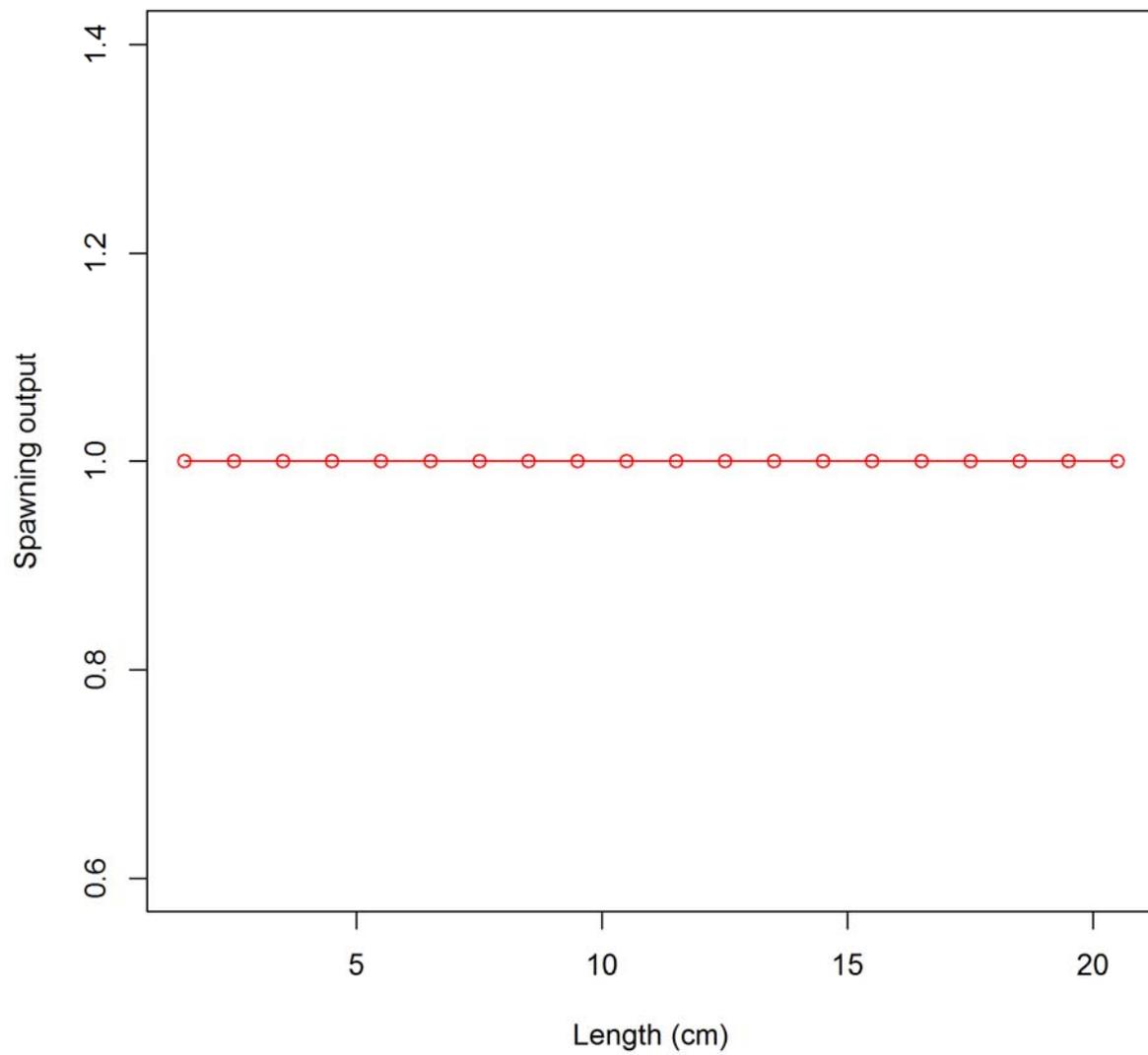


Appendix A7: SS3 Diagnostics for the GBK area

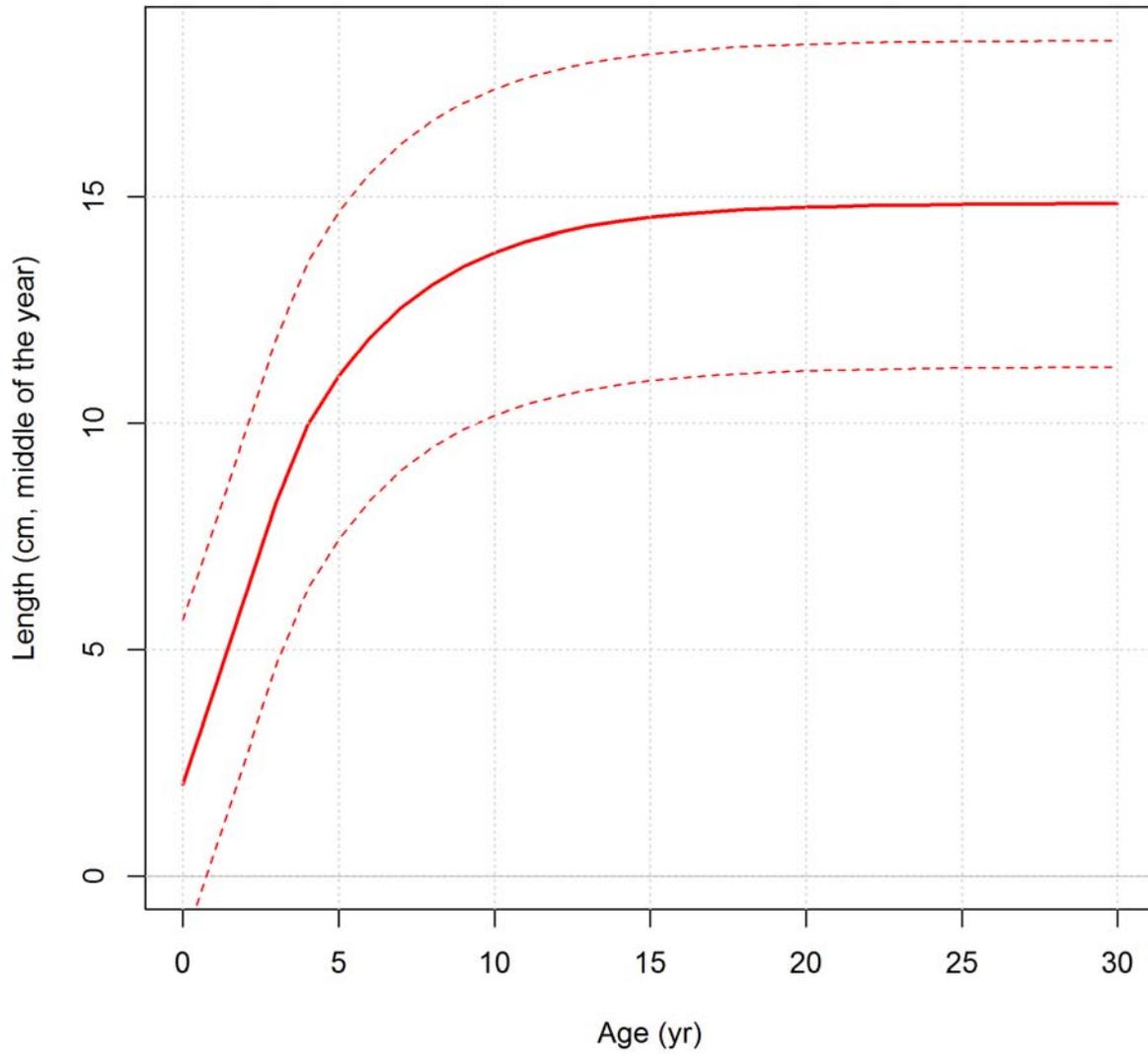
Plots created using the 'r4ss' package in R
Stock Synthesis version: SS-V3.24f
StartTime: Wed Jan 16 11:47:53 2013
Data_File: Surfclam_GBK-1.dat
Control_File: Surfclam_GBK-1.ctf

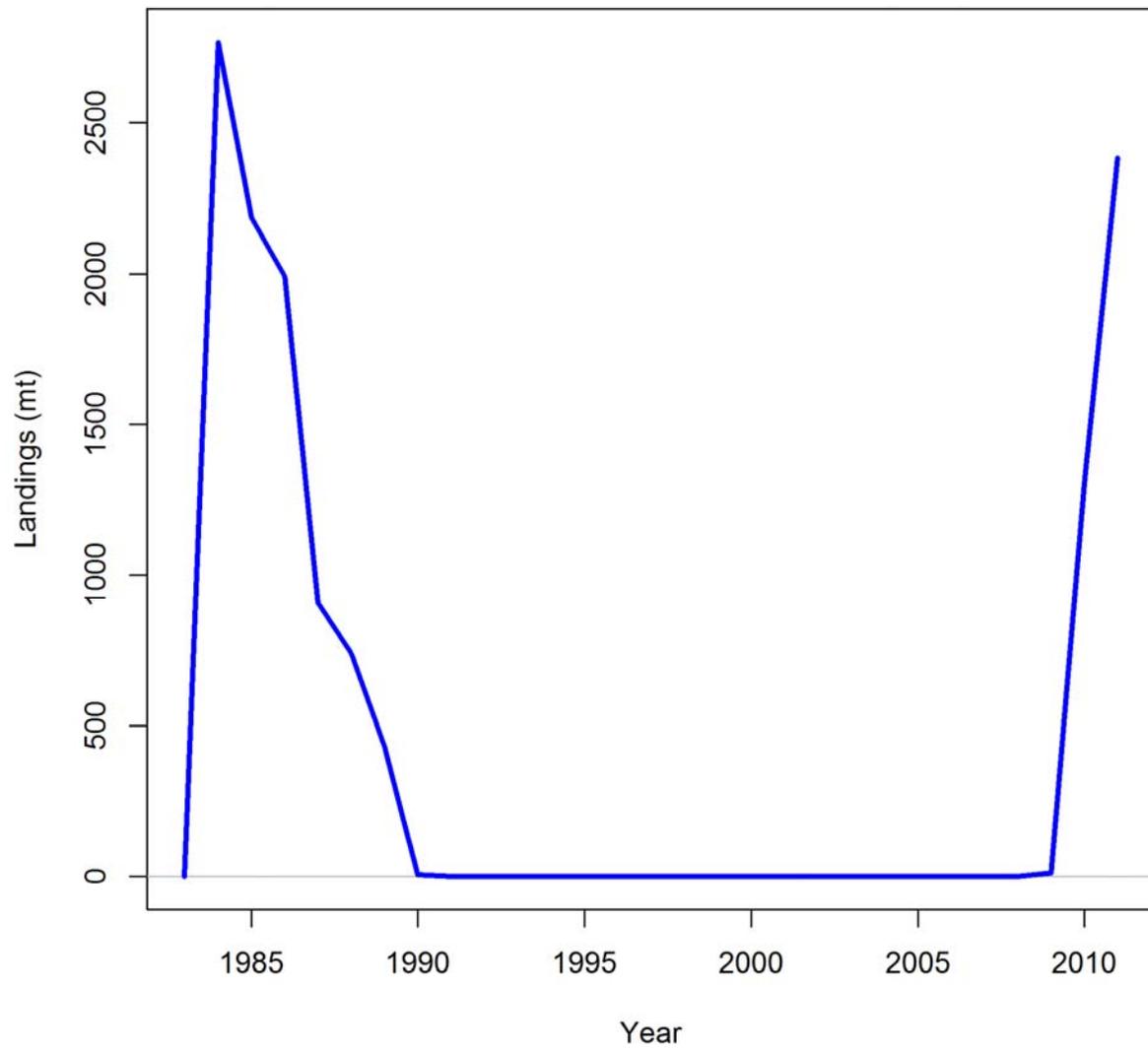


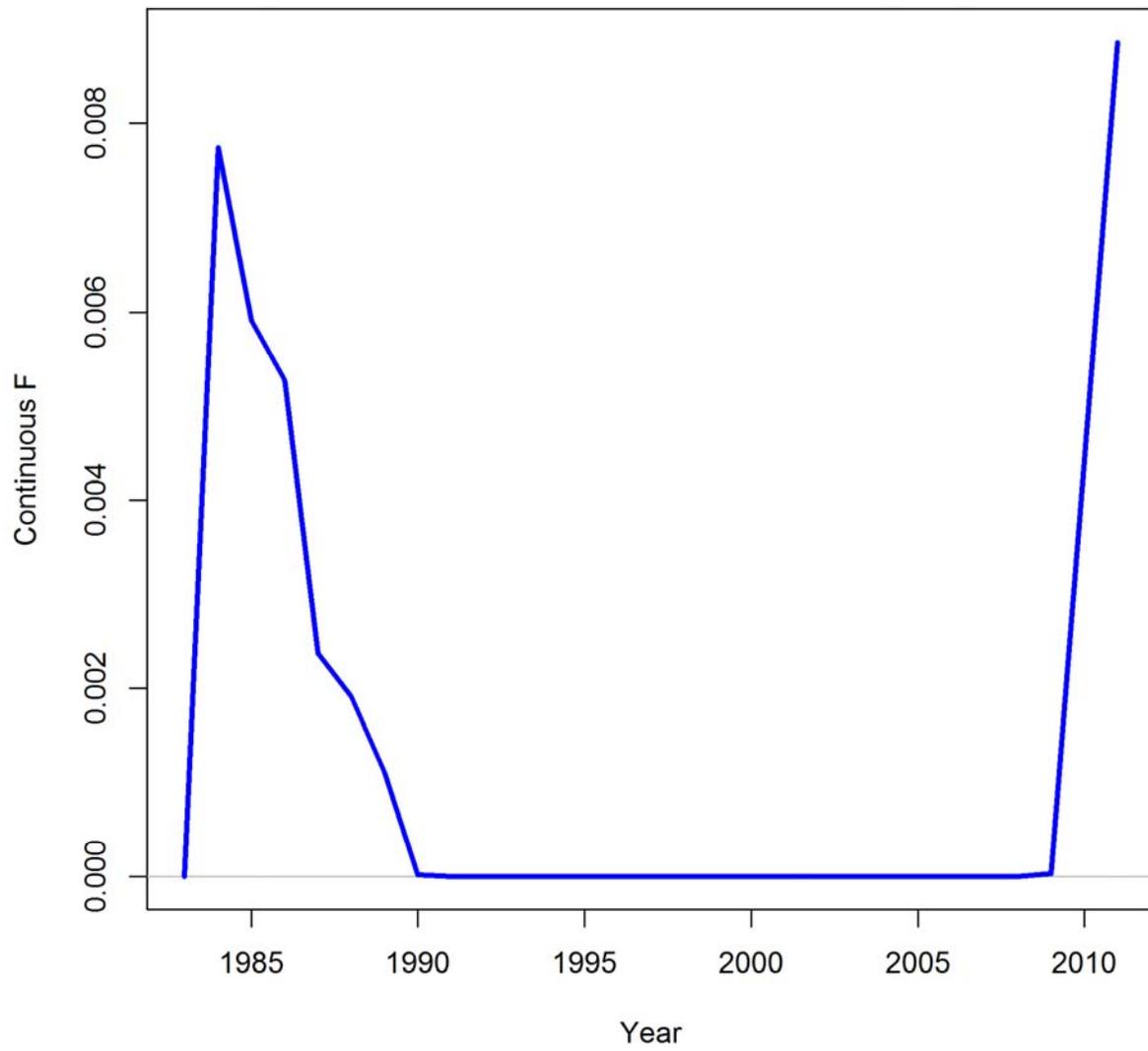




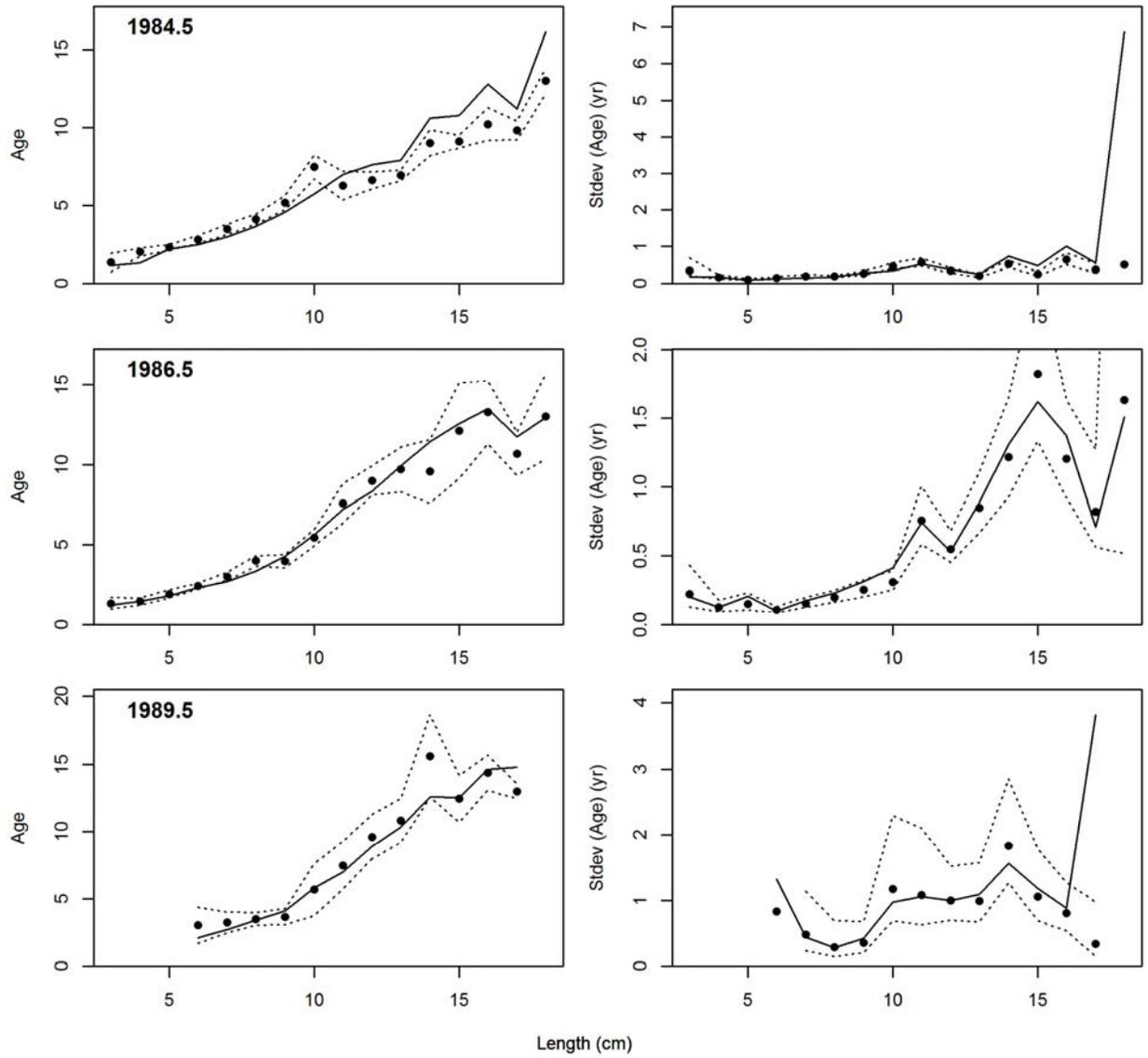
Ending year expected growth



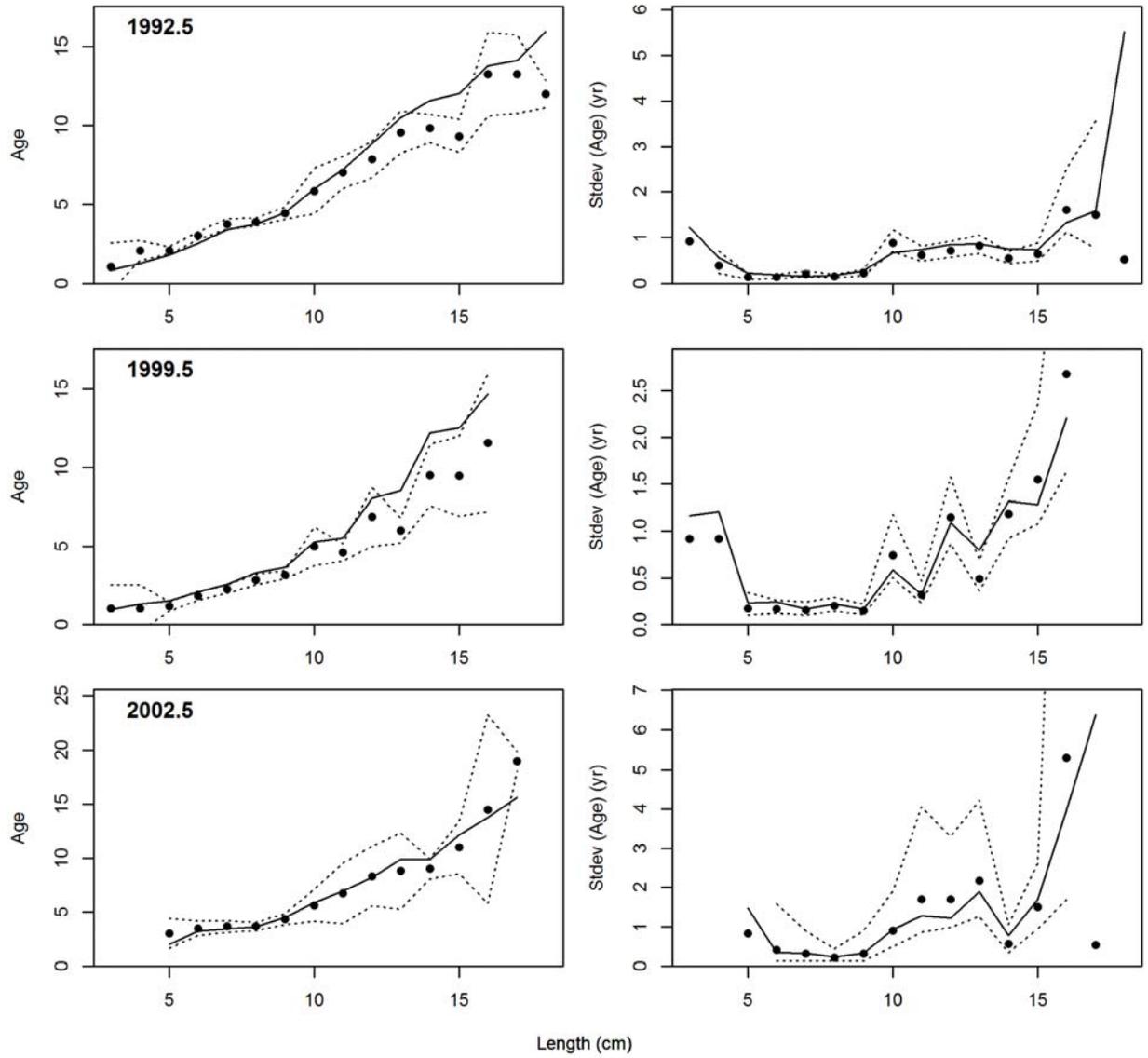




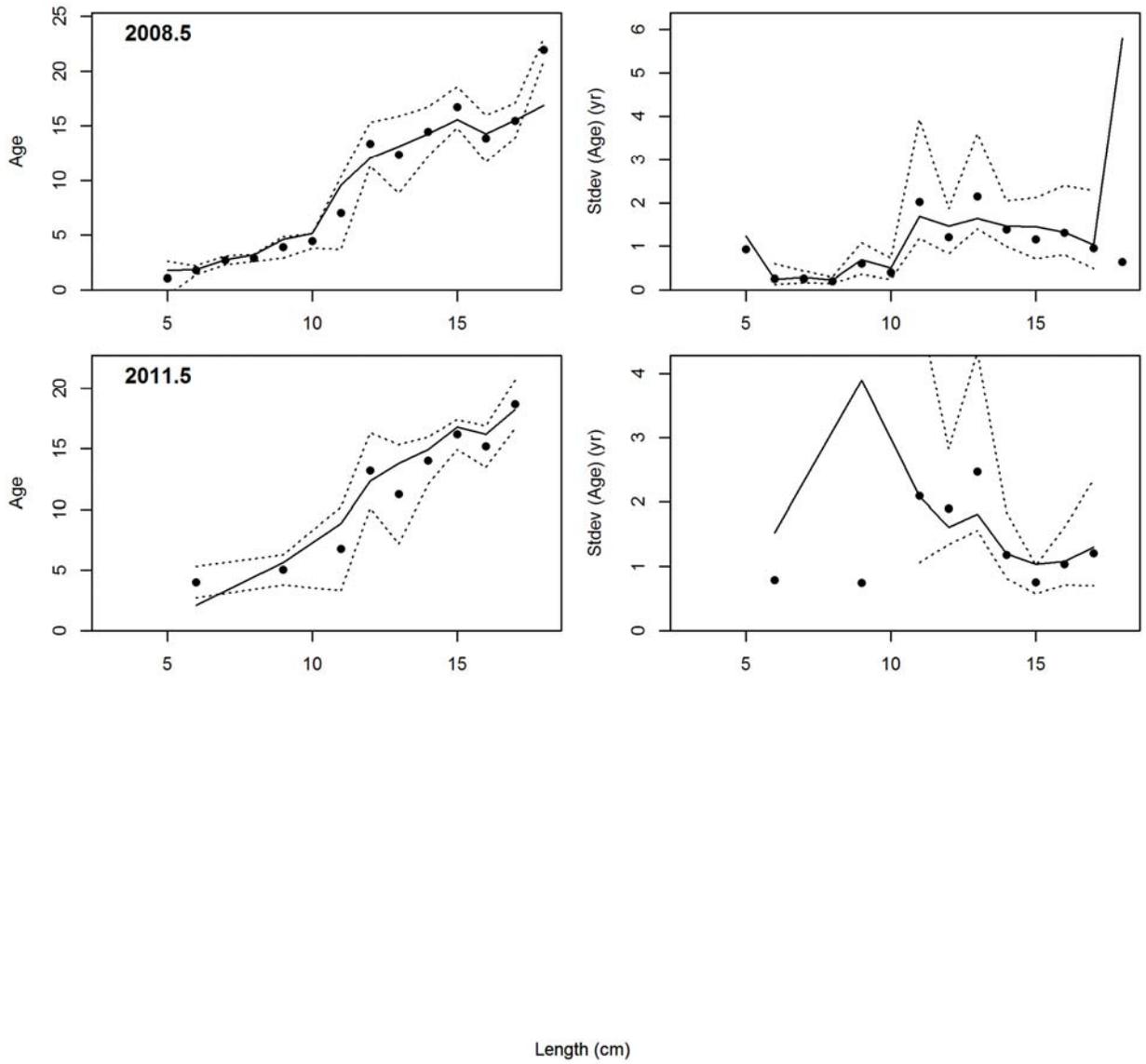
Andre's conditional AAL plot, sexes combined, whole catch, NperTow+mm



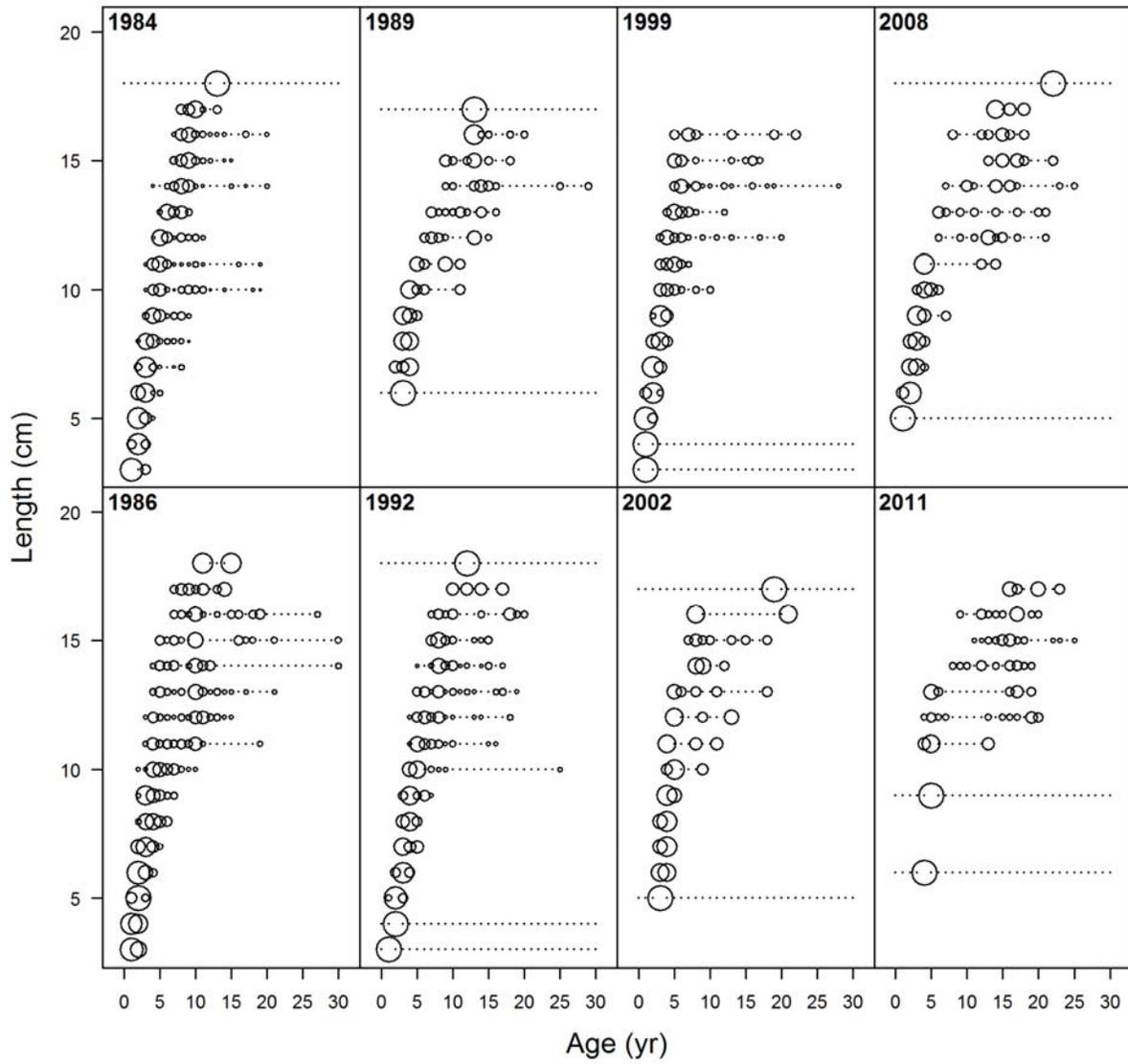
Andre's conditional AAL plot, sexes combined, whole catch, NperTow+mm



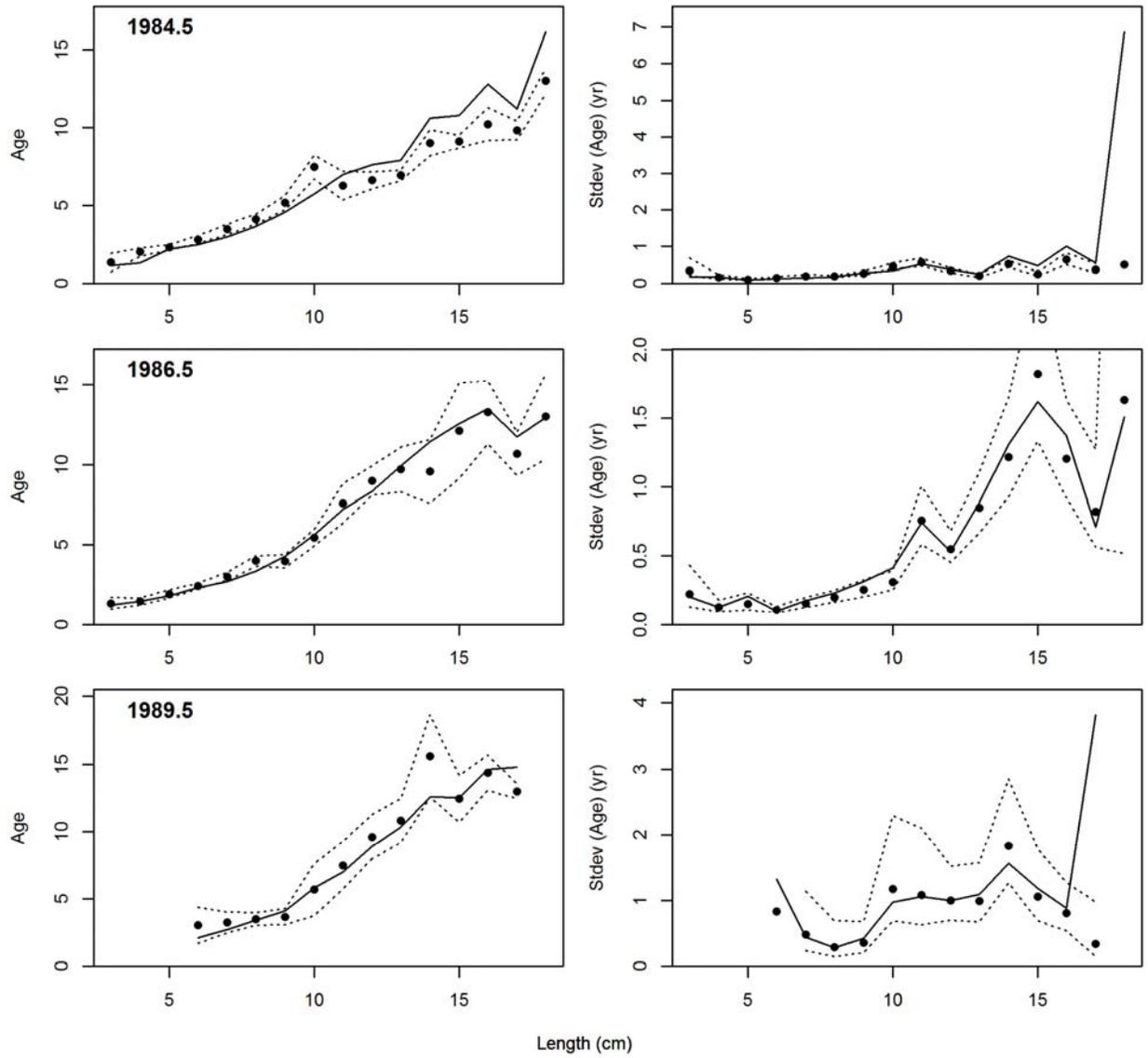
Andre's conditional AAL plot, sexes combined, whole catch, NperTow+mm



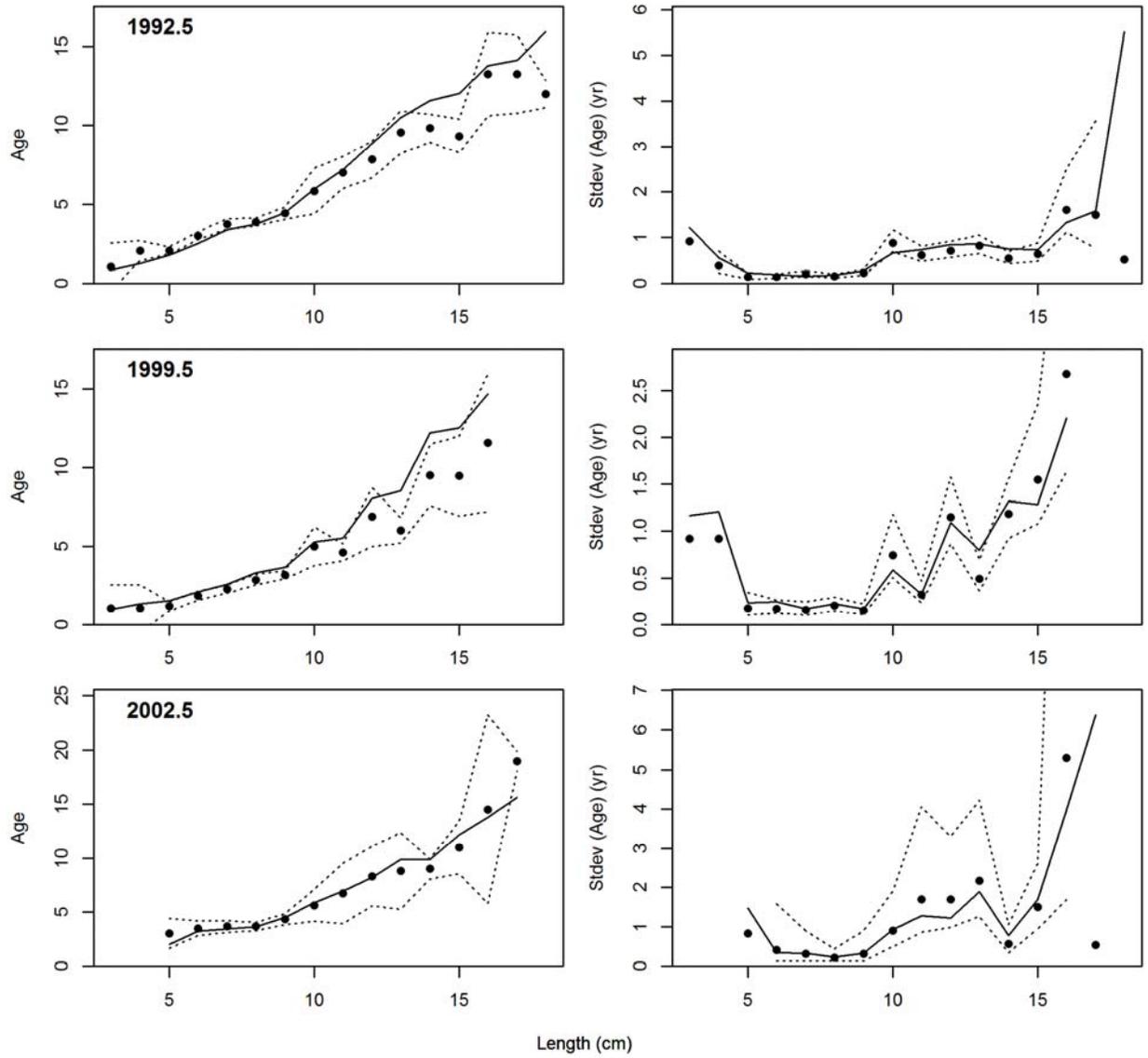
conditional age-at-length data, sexes combined, whole catch, NperTow+mm (max=1)



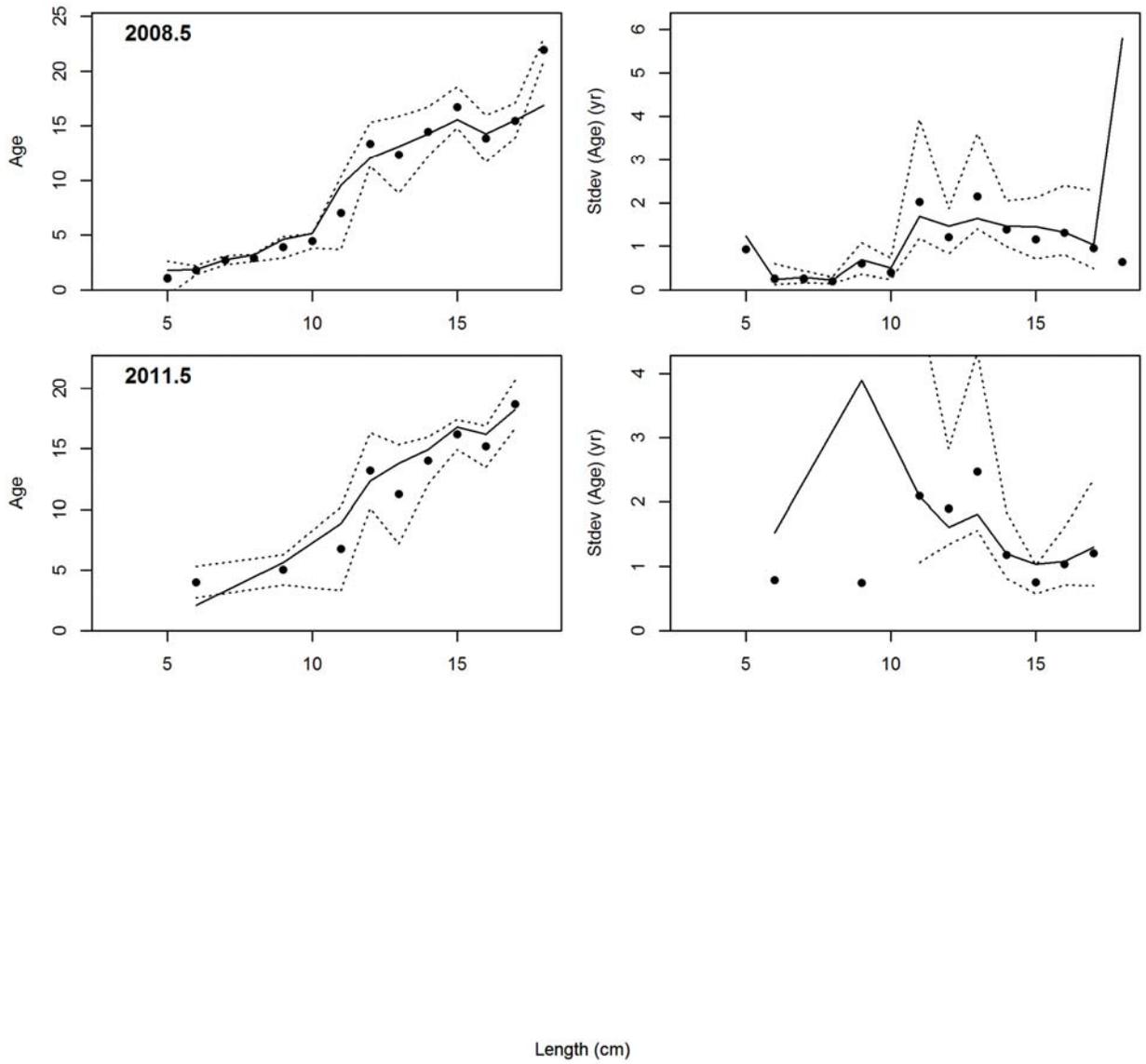
Andre's conditional AAL plot, sexes combined, whole catch, NperTow+mm



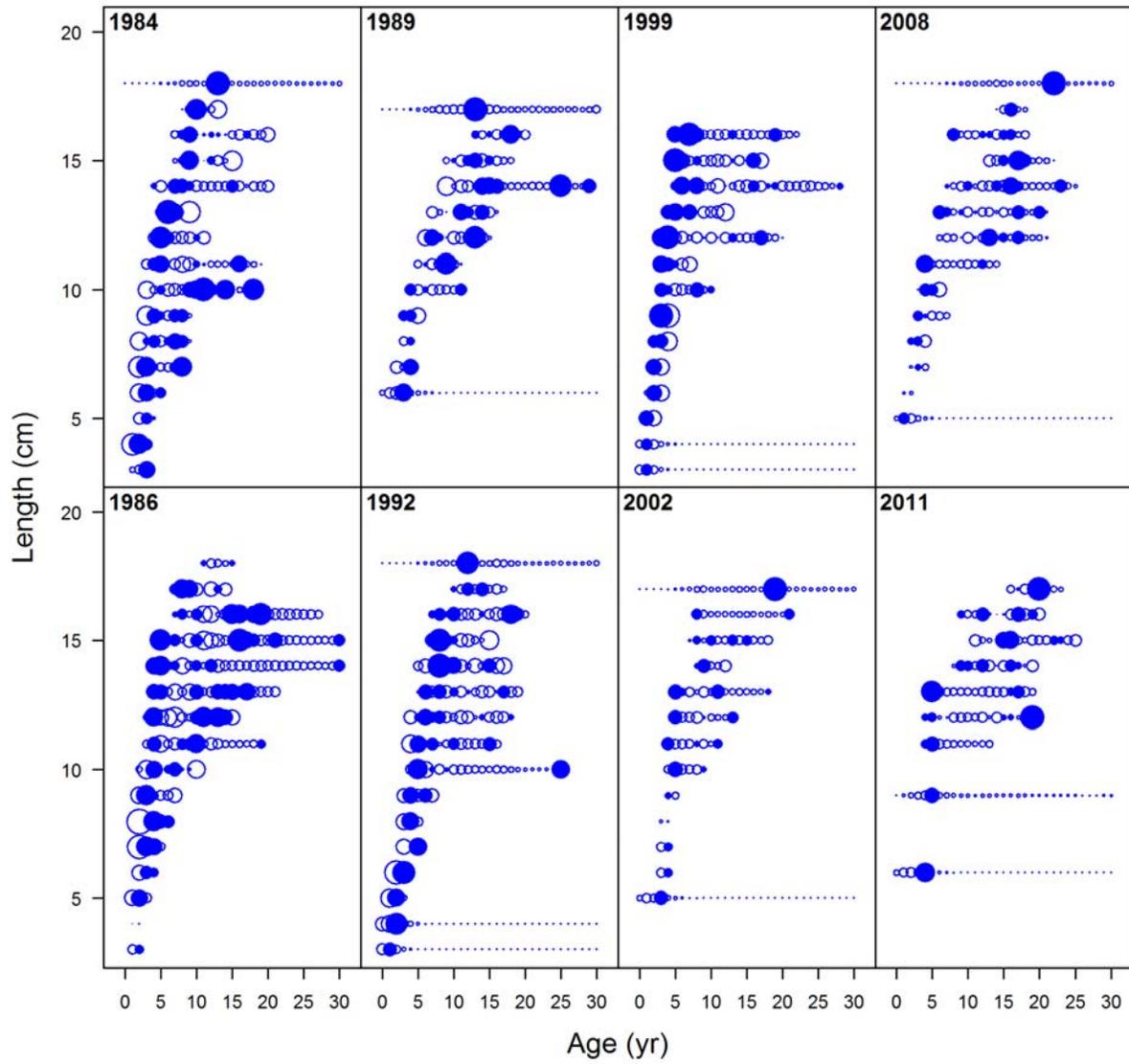
Andre's conditional AAL plot, sexes combined, whole catch, NperTow+mm



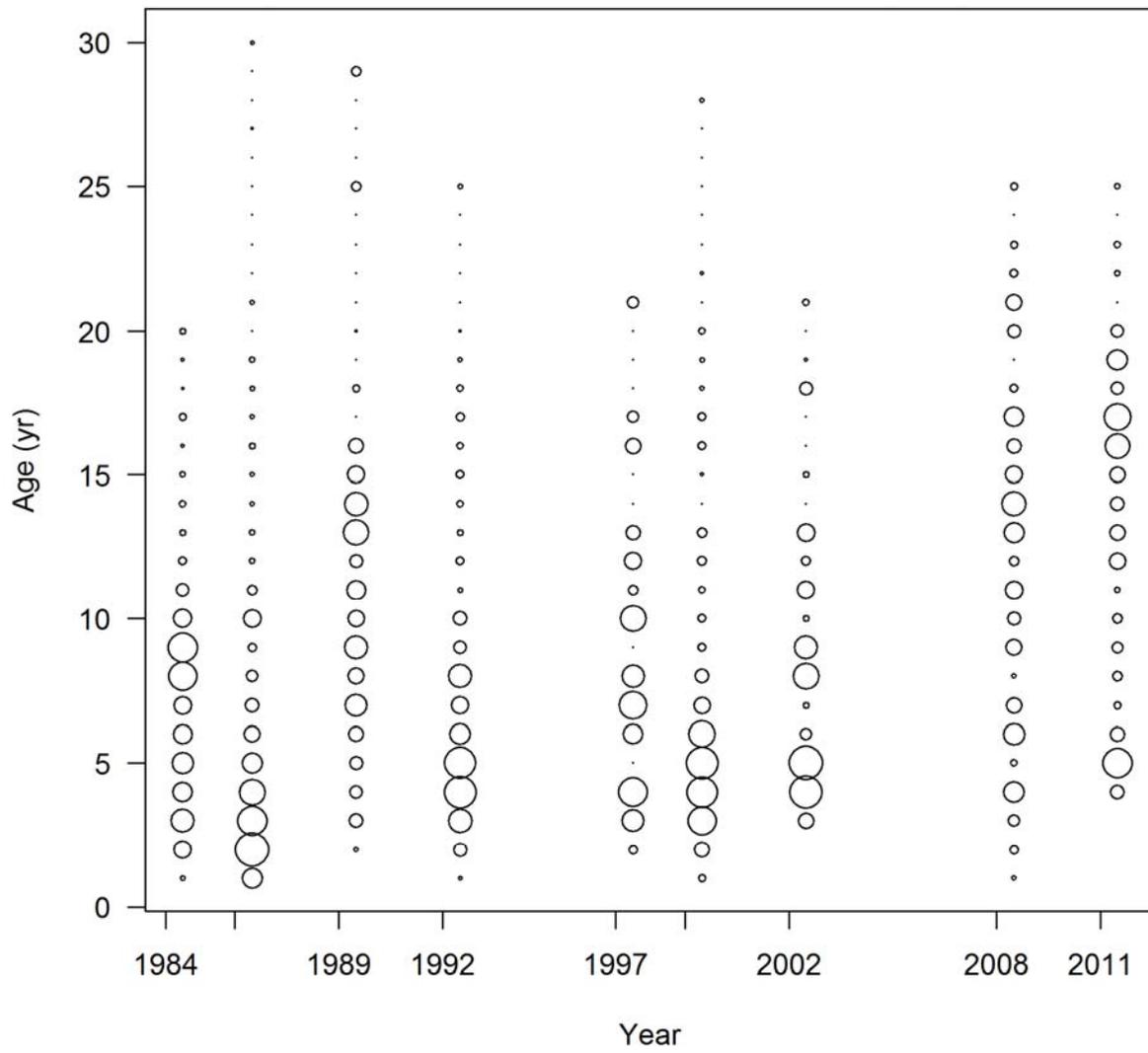
Andre's conditional AAL plot, sexes combined, whole catch, NperTow+mm



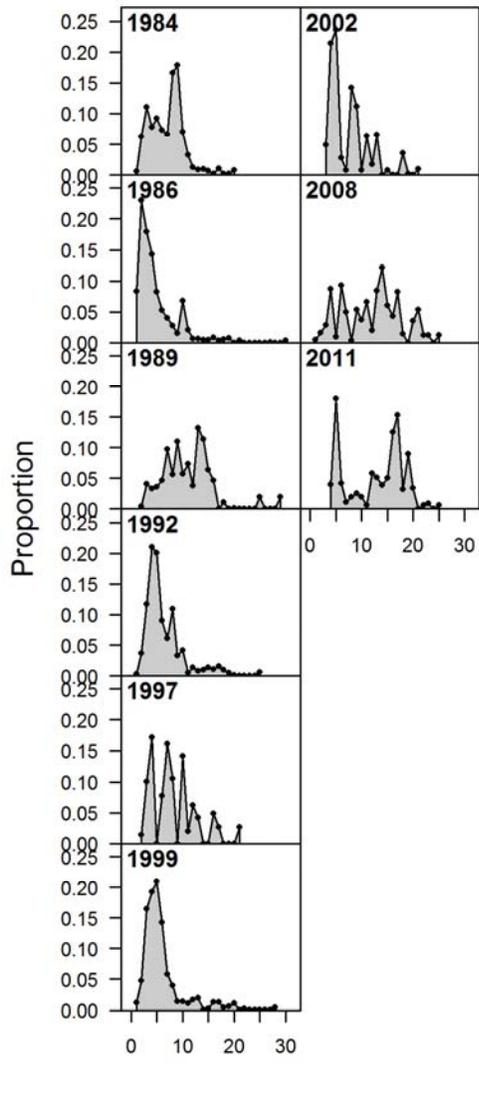
Pearson residuals, sexes combined, whole catch, NperTow+mm (max=6.03)



ghost age comp data, sexes combined, whole catch, SWAN (max=0.24)

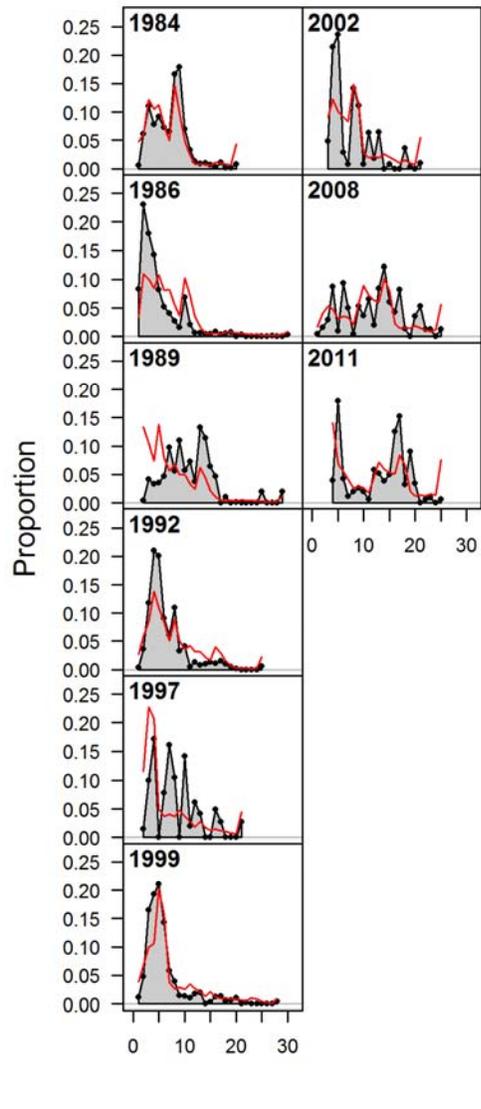


ghost age comp data, sexes combined, whole catch, SWAN



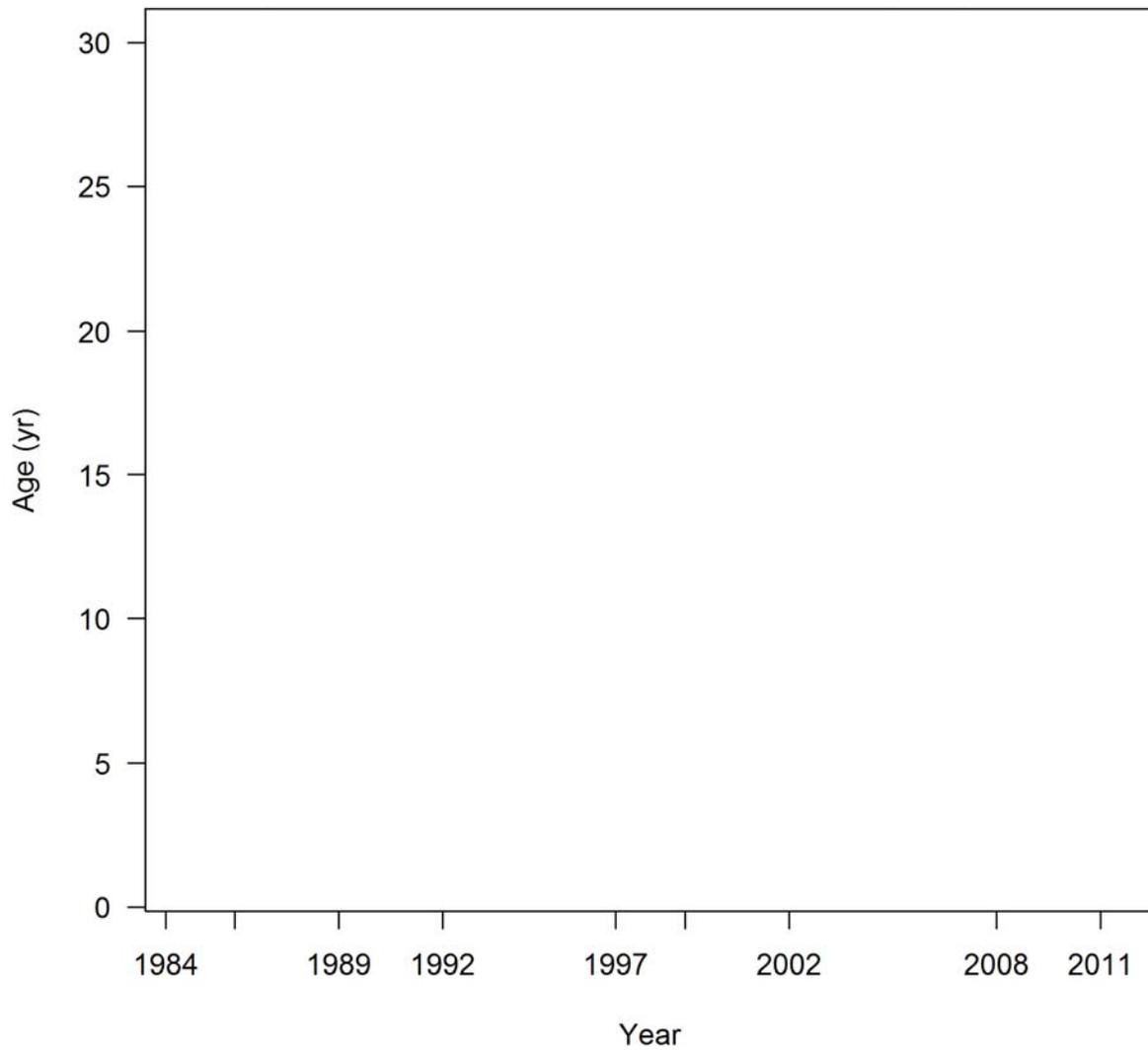
Age (yr)

ghost age comps, sexes combined, whole catch, SWAN

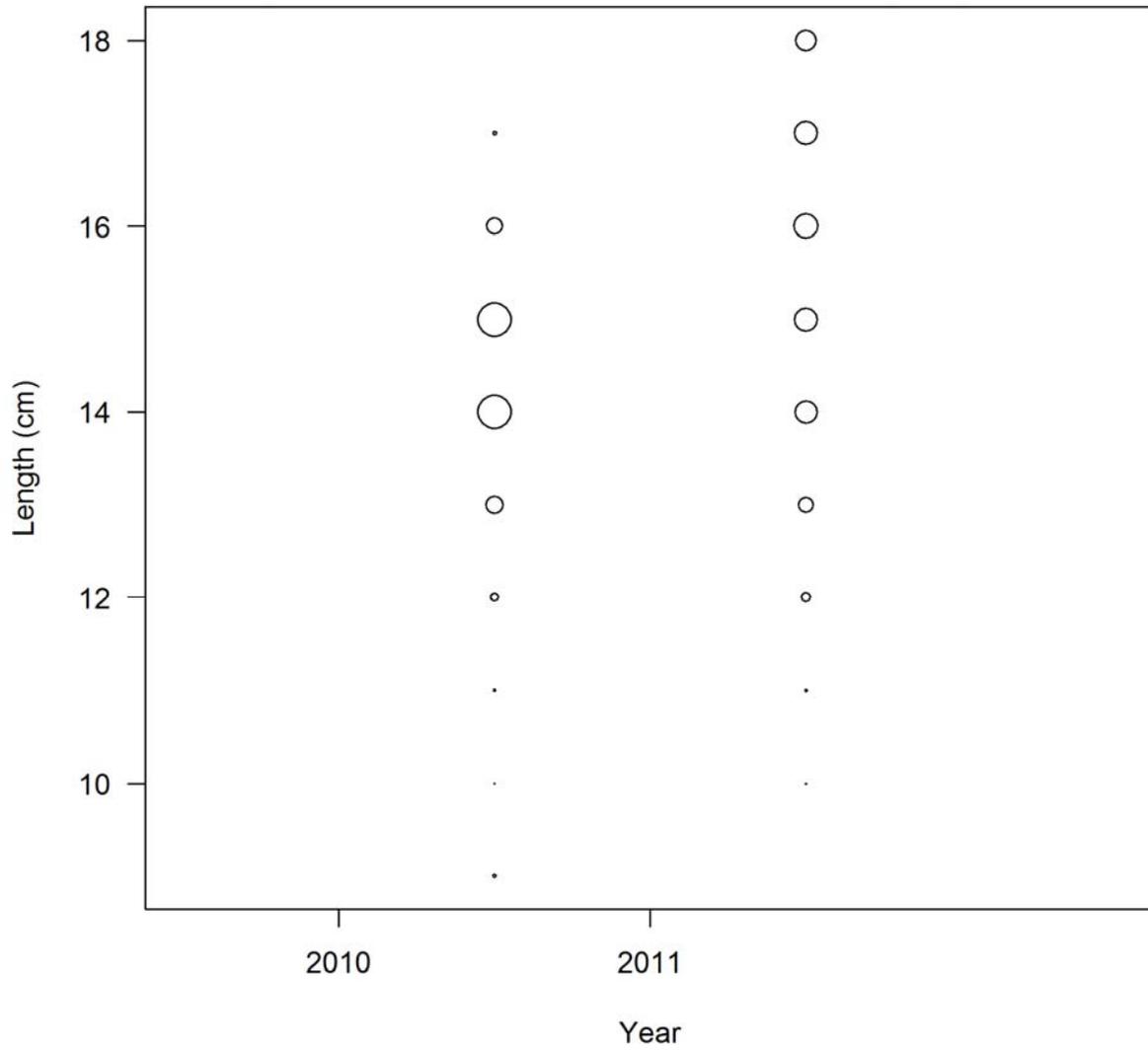


Age (yr)

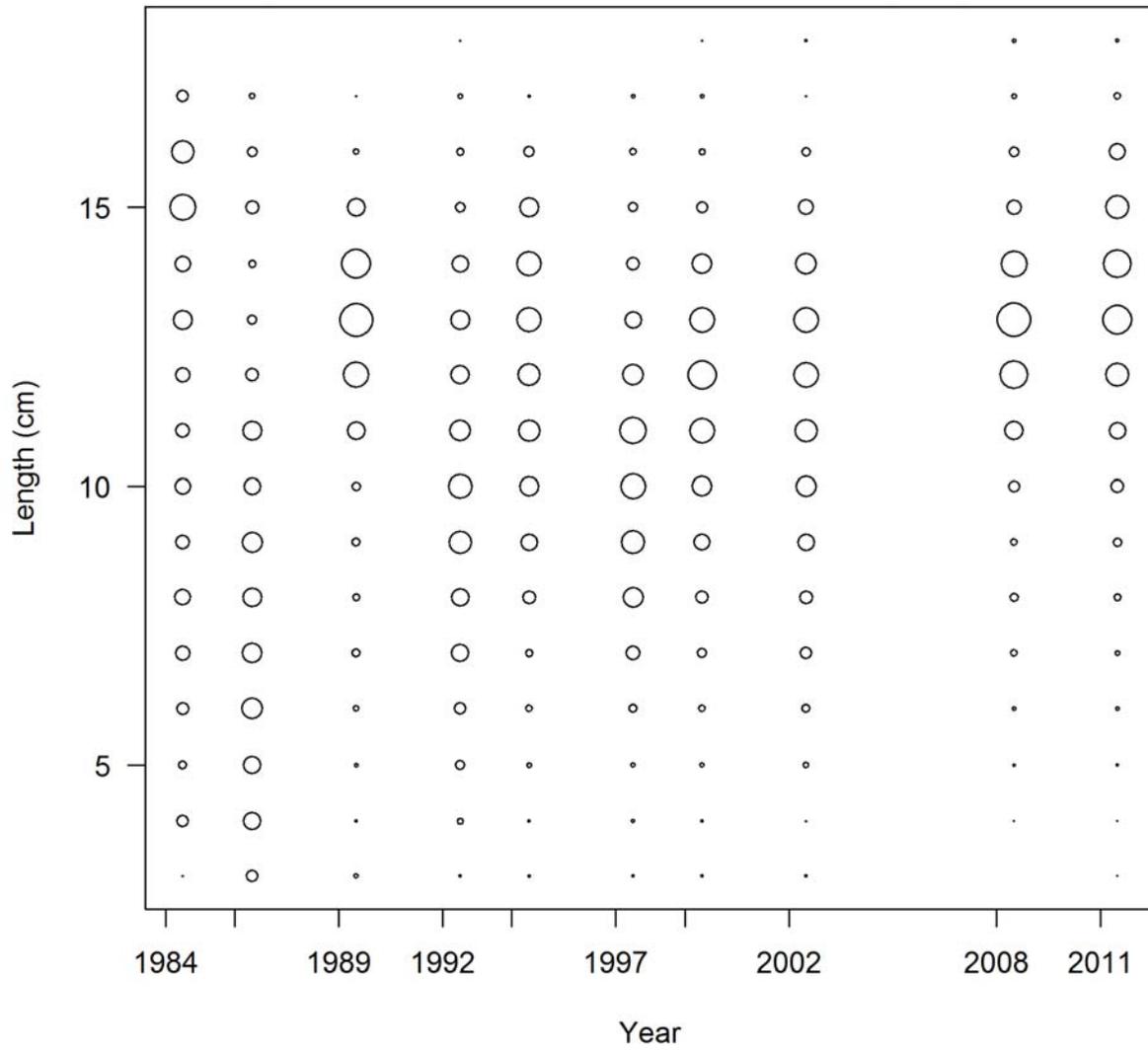
Pearson residuals, sexes combined, whole catch, SWAN (max=NA)



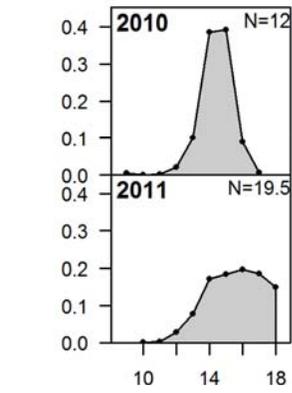
length comp data, sexes combined, whole catch, Fishery (max=0.39)



length comp data, sexes combined, whole catch, NperTow+mm (max=0.32)



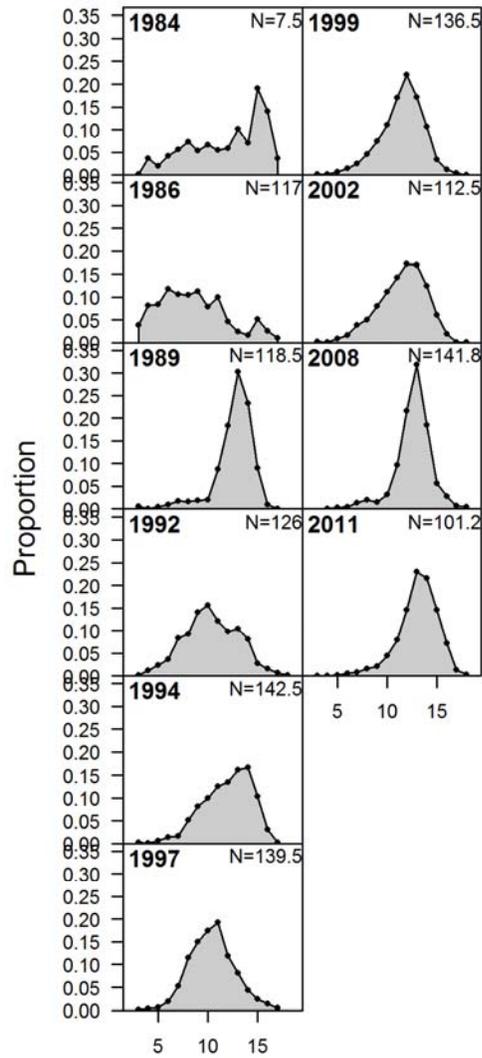
length comp data, sexes combined, whole catch, Fishery



Proportion

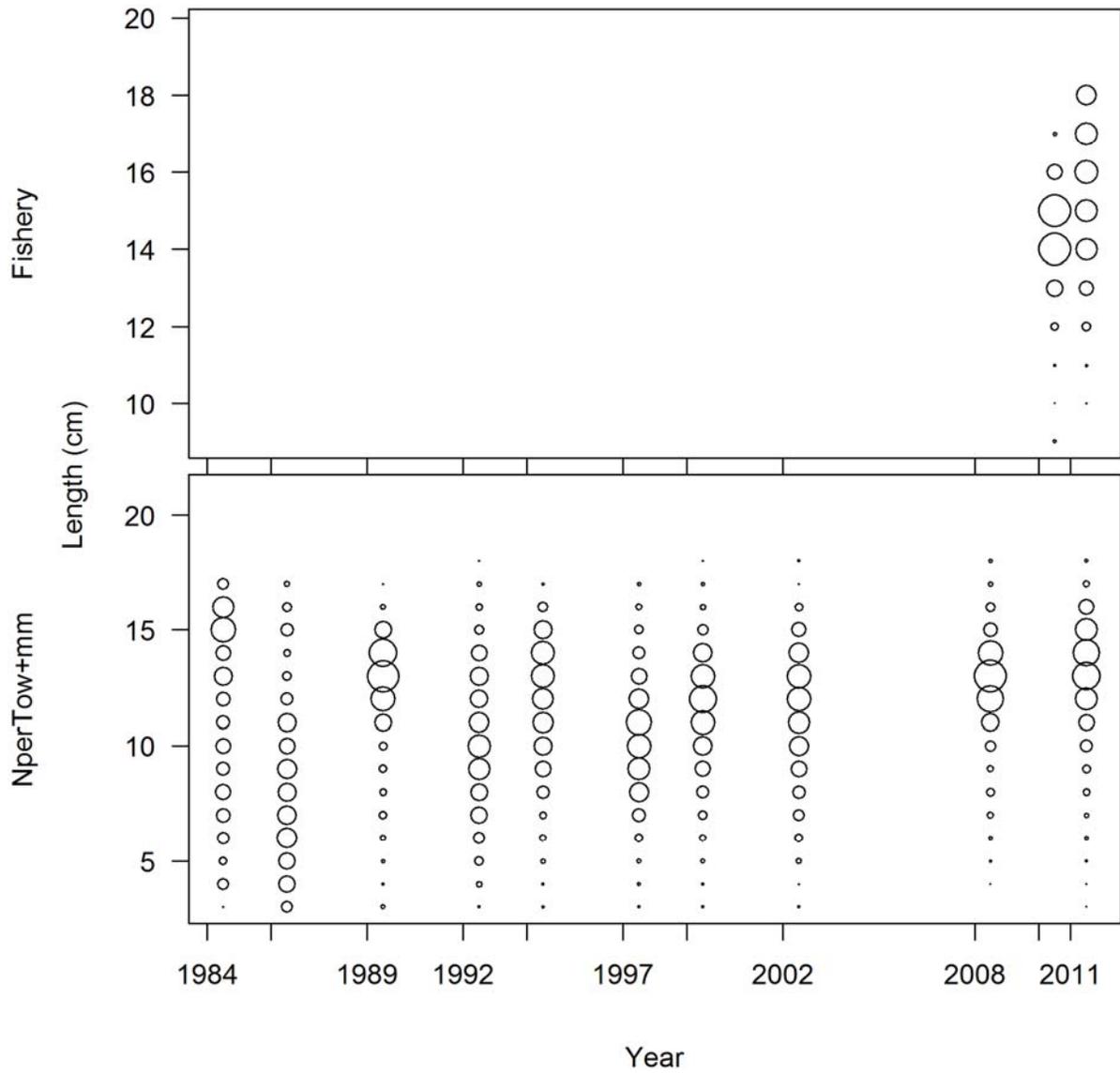
Length (cm)

length comp data, sexes combined, whole catch, NperTow+mm

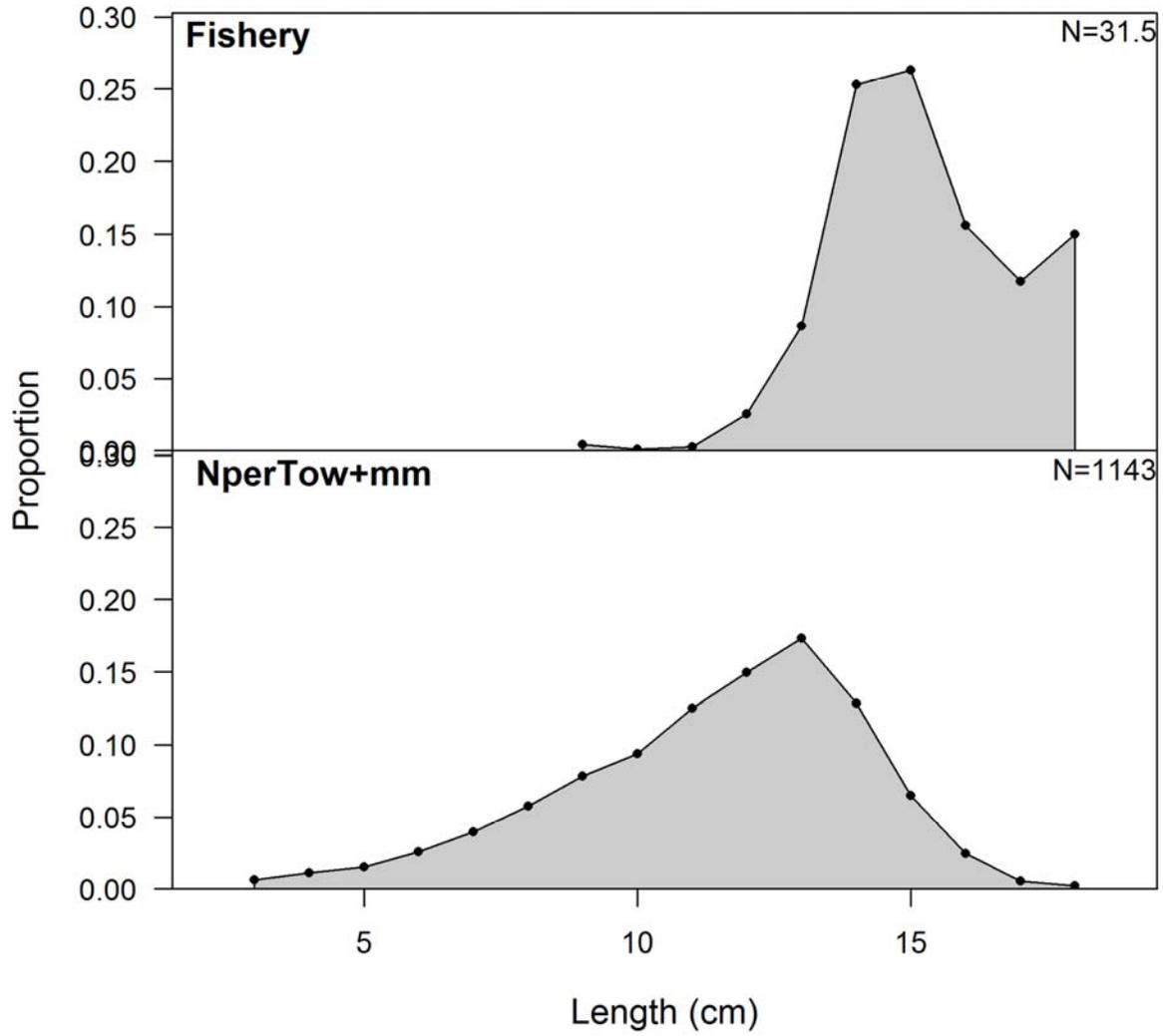


Length (cm)

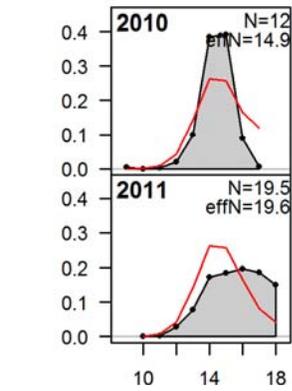
length comp data, sexes combined, whole catch, comparing across 1



length comp data, sexes combined, whole catch, aggregated across time



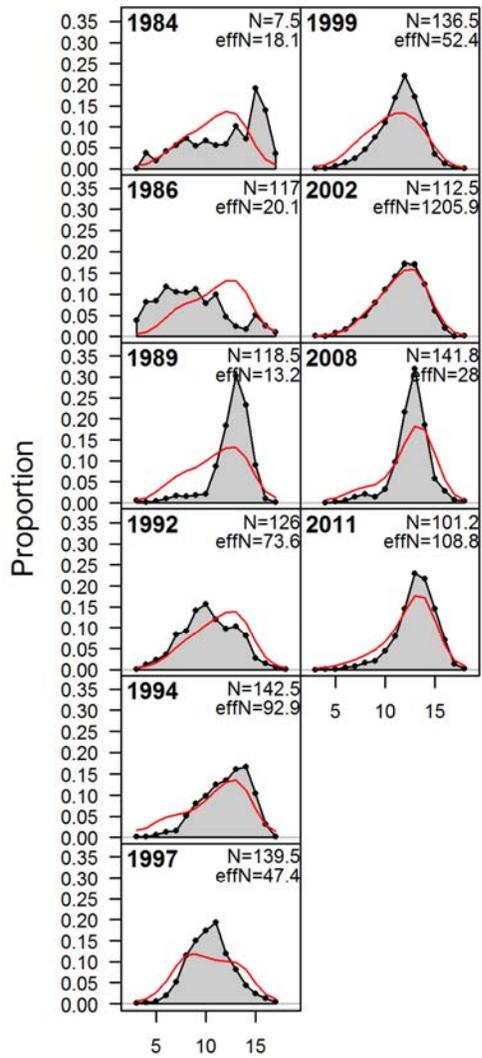
length comps, sexes combined, whole catch, Fishery



Proportion

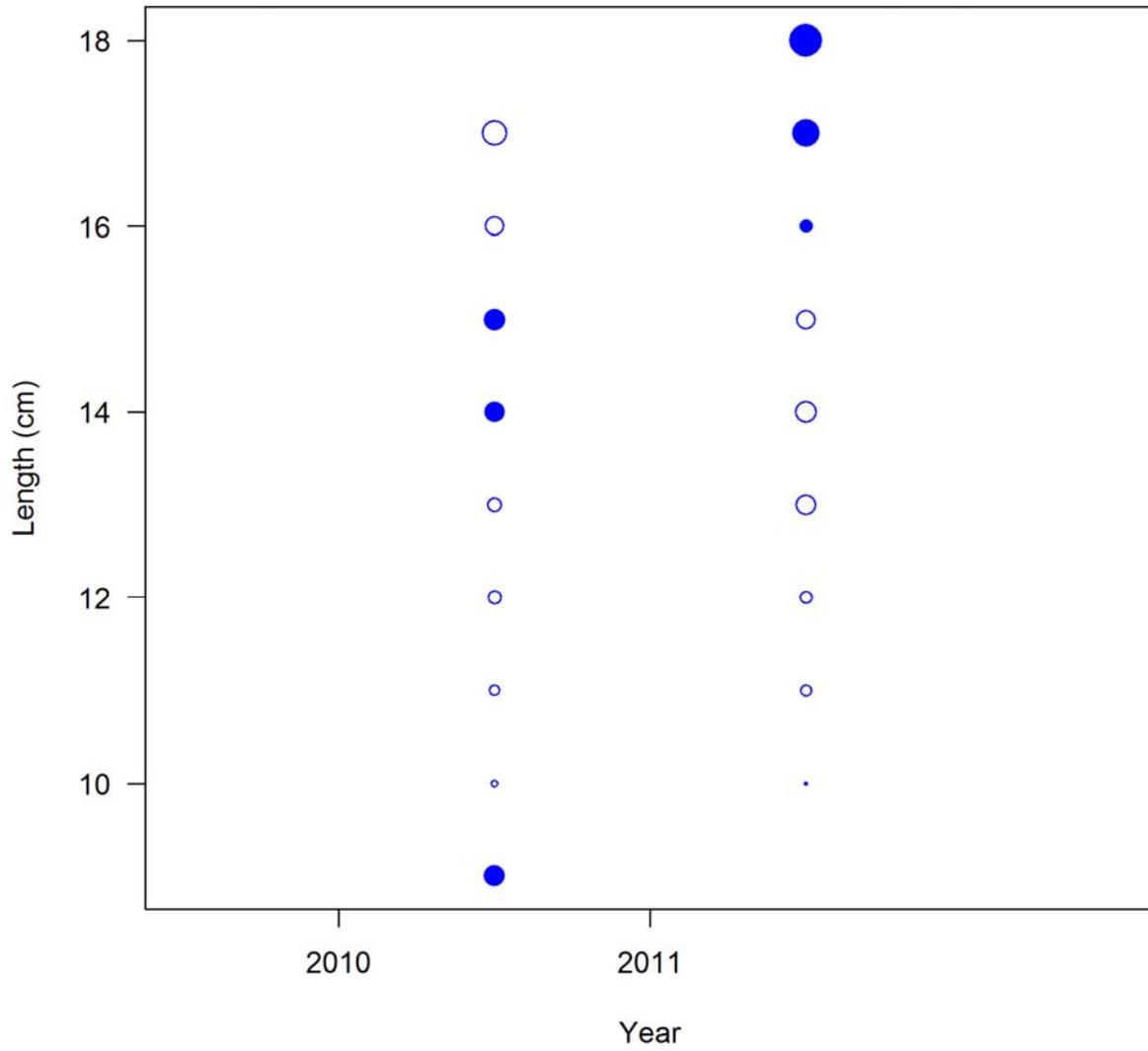
Length (cm)

length comps, sexes combined, whole catch, NperTow+mm

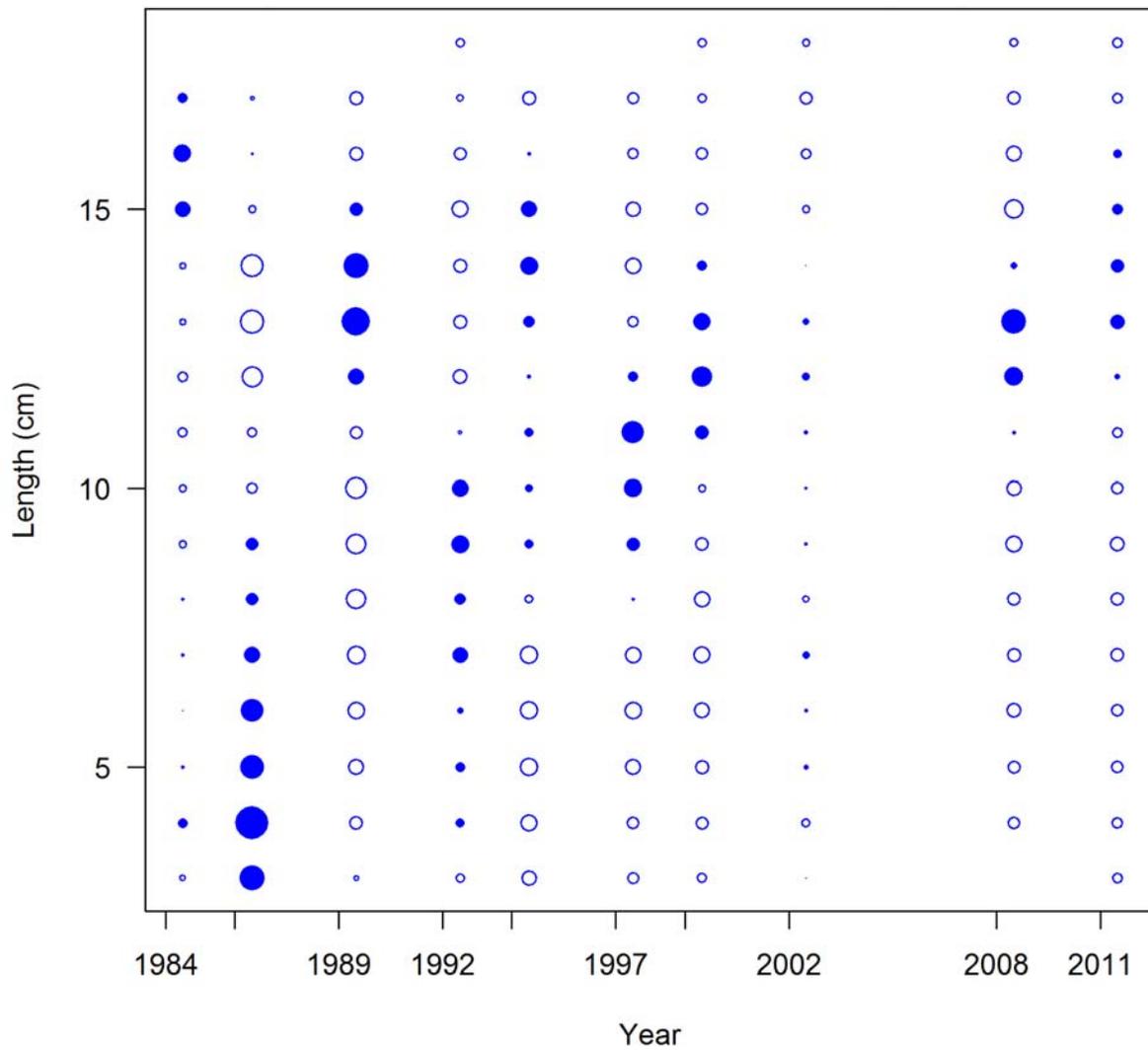


Length (cm)

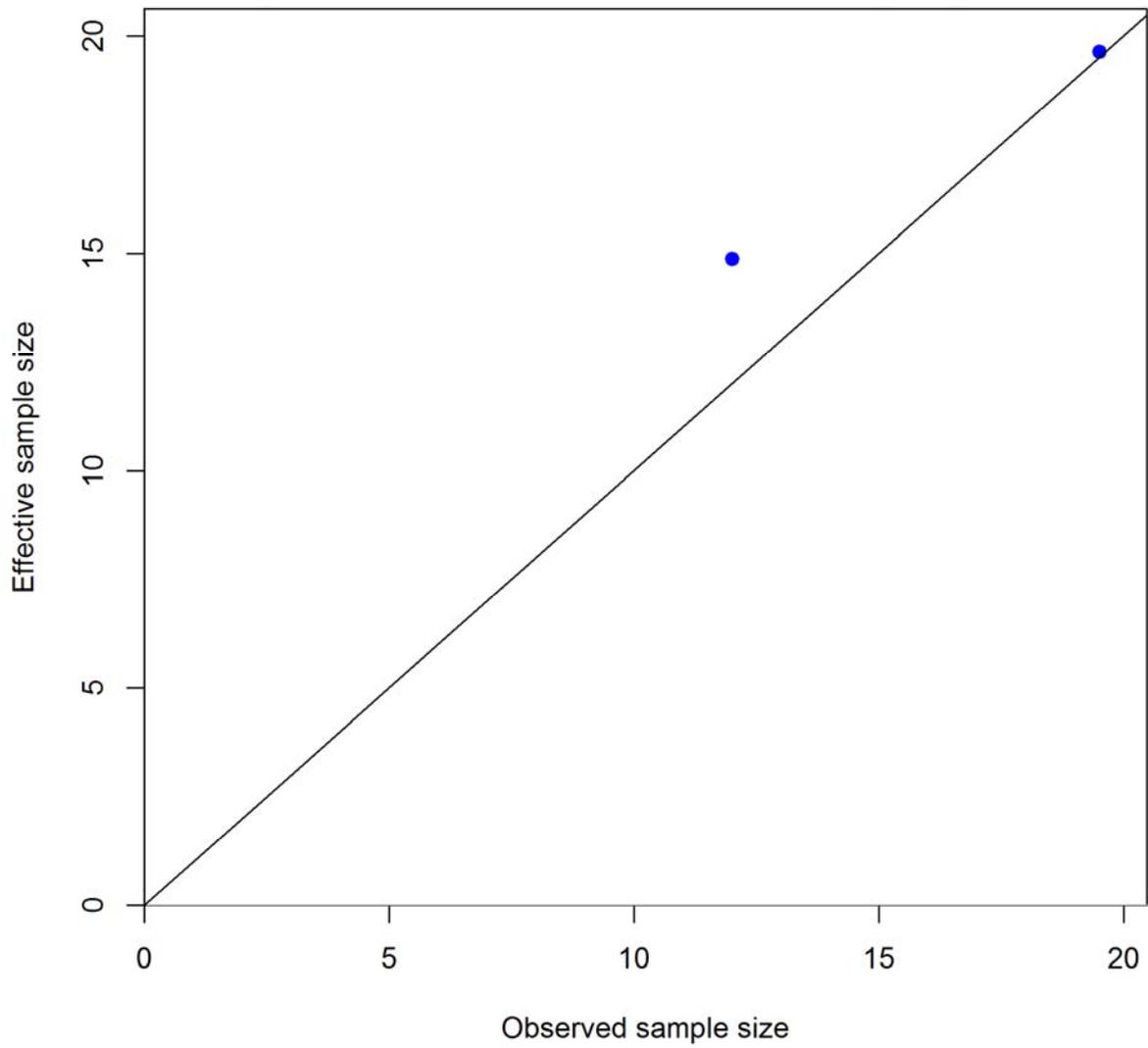
Pearson residuals, sexes combined, whole catch, Fishery (max=2.41)



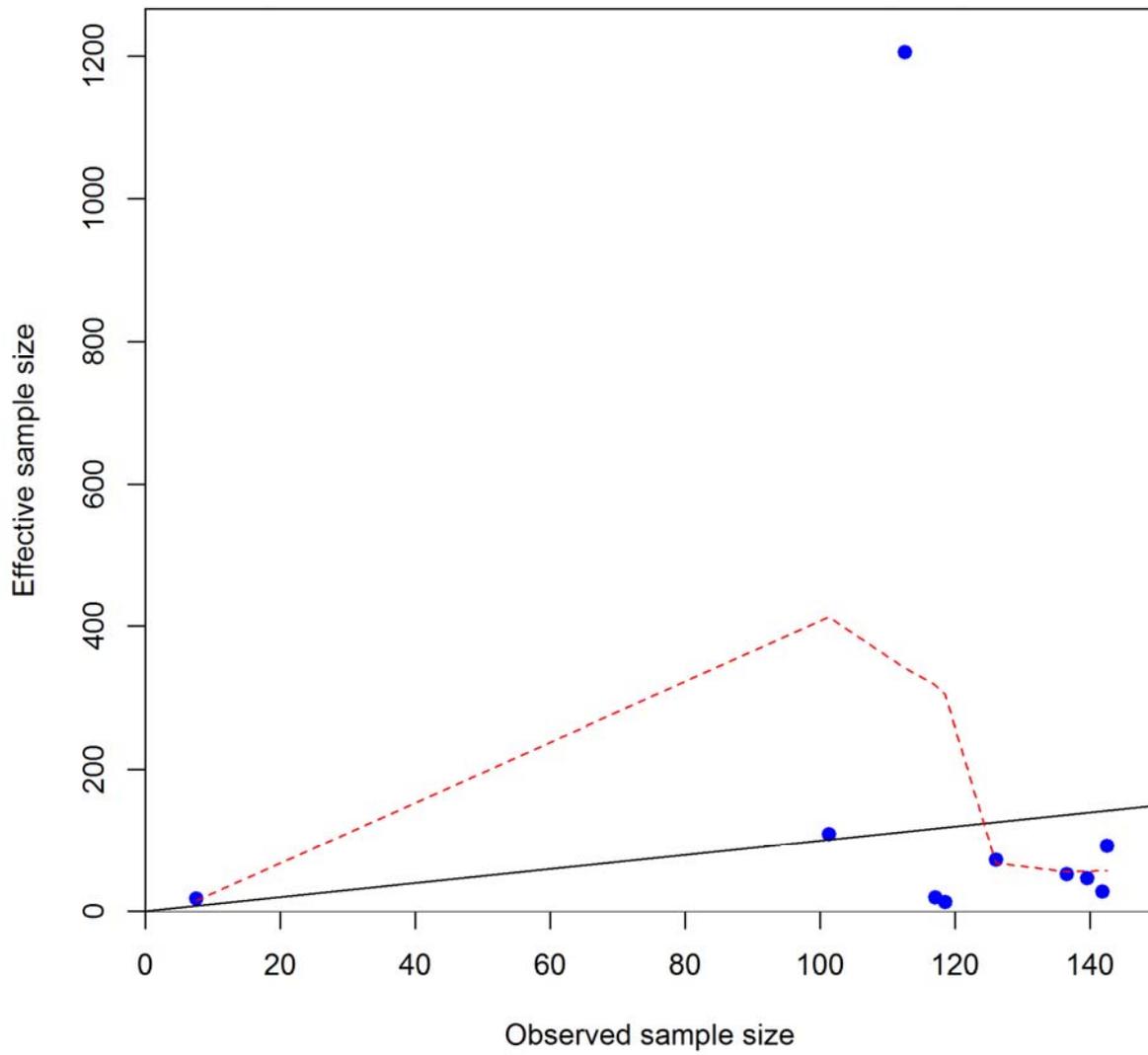
Pearson residuals, sexes combined, whole catch, NperTow+mm (max=7.5)



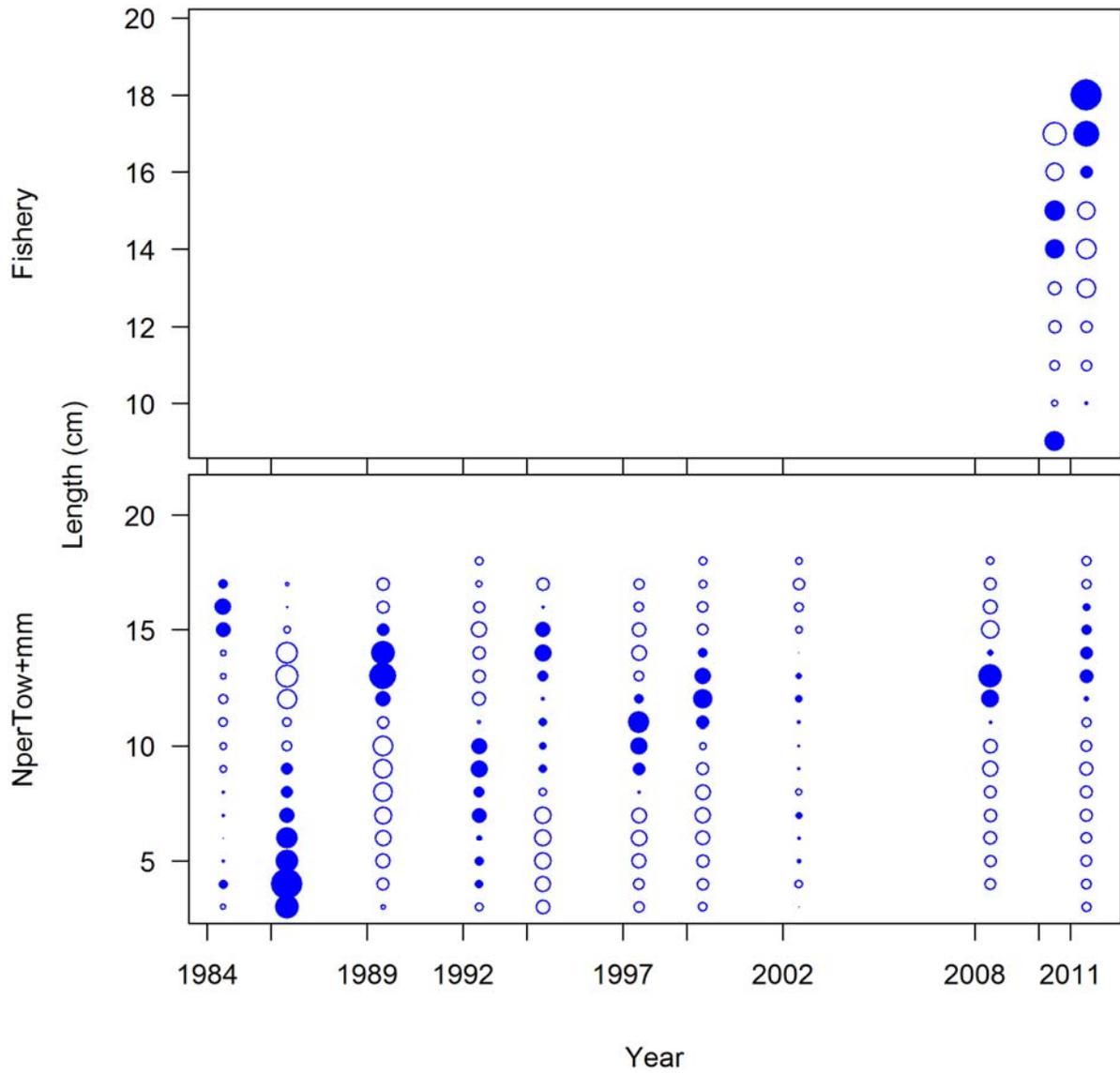
N-EffN comparison, length comps, sexes combined, whole catch, Fishery



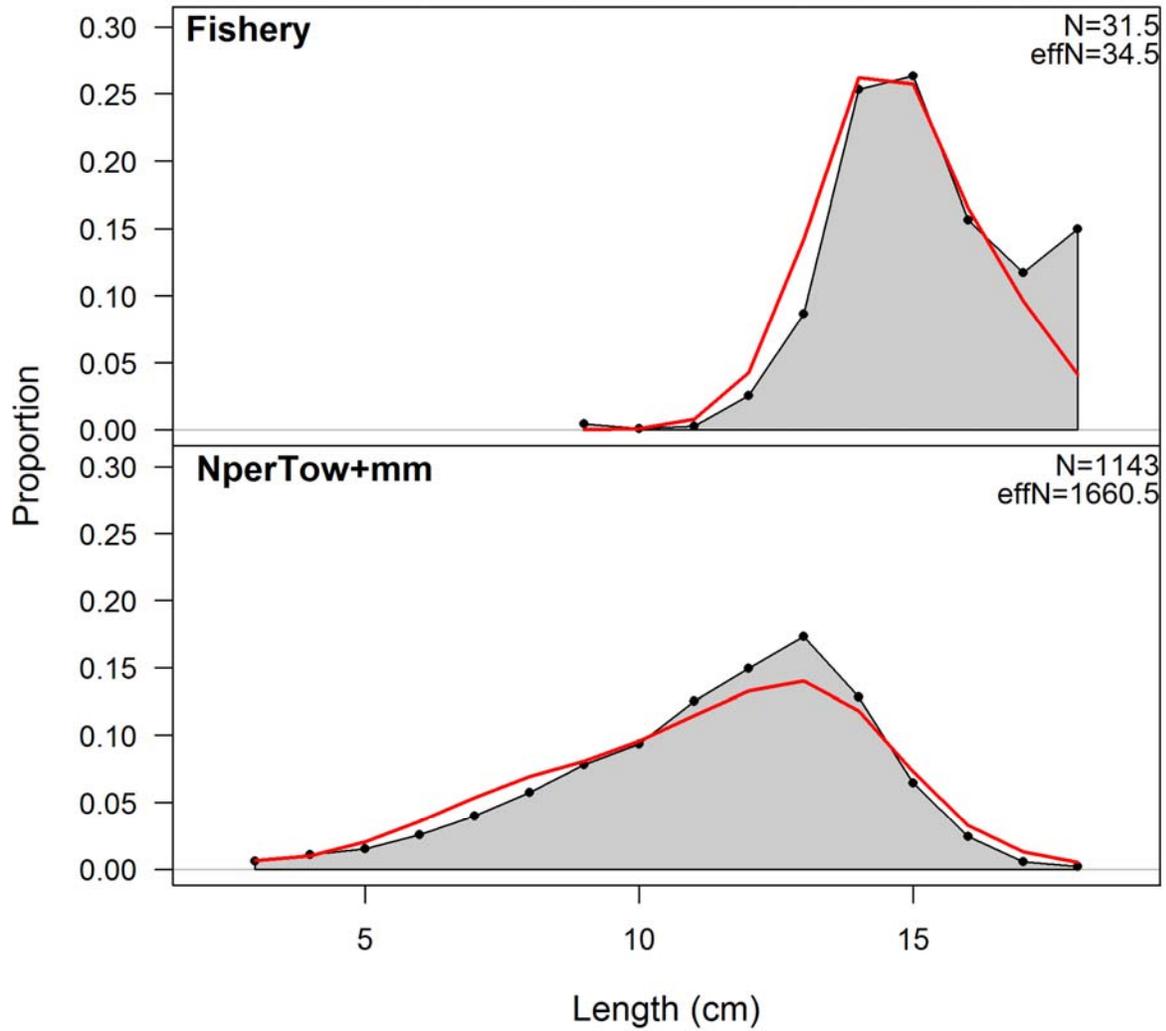
N-EffN comparison, length comps, sexes combined, whole catch, NperTow+mm



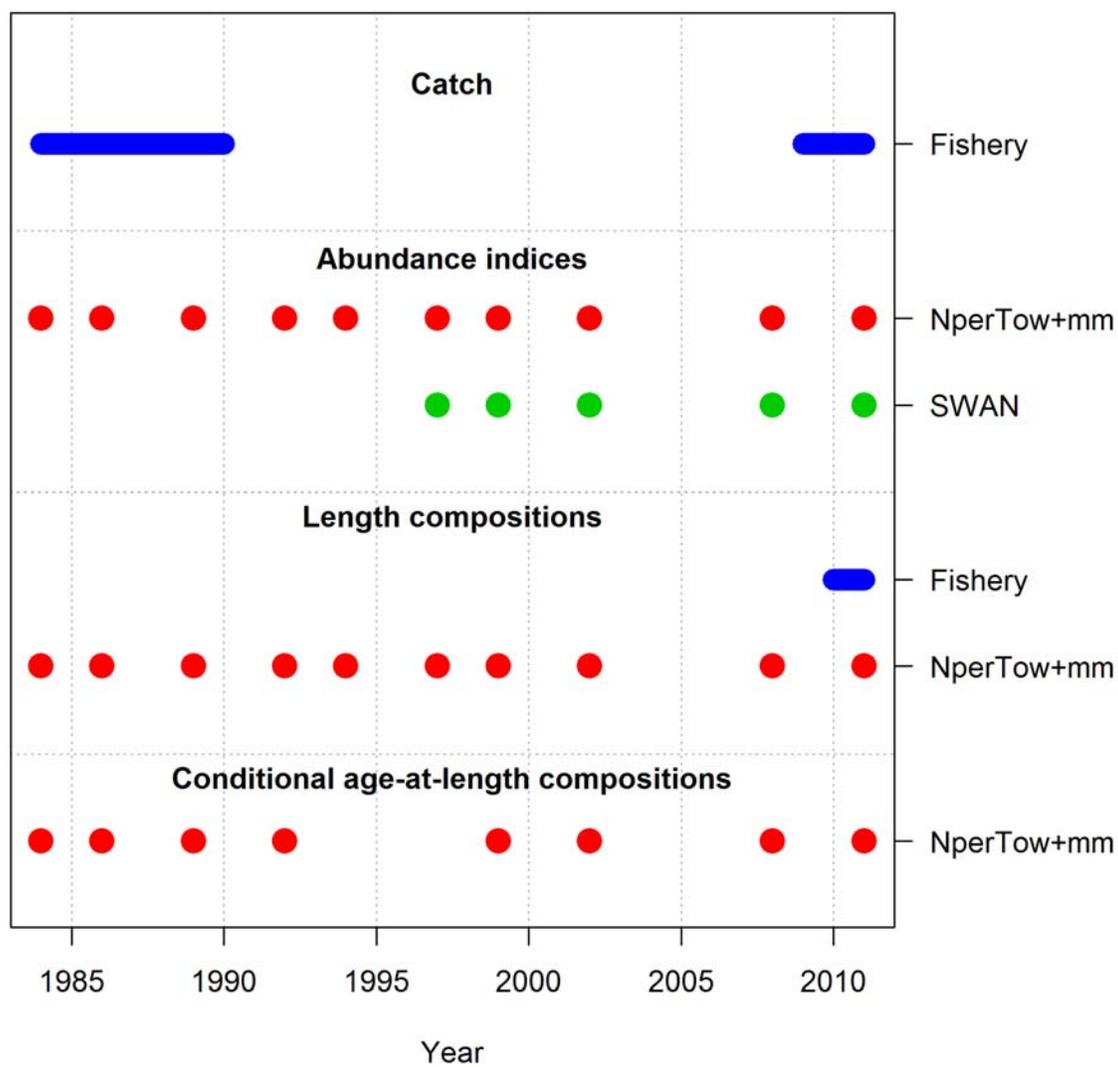
Pearson residuals, sexes combined, whole catch, comparing across



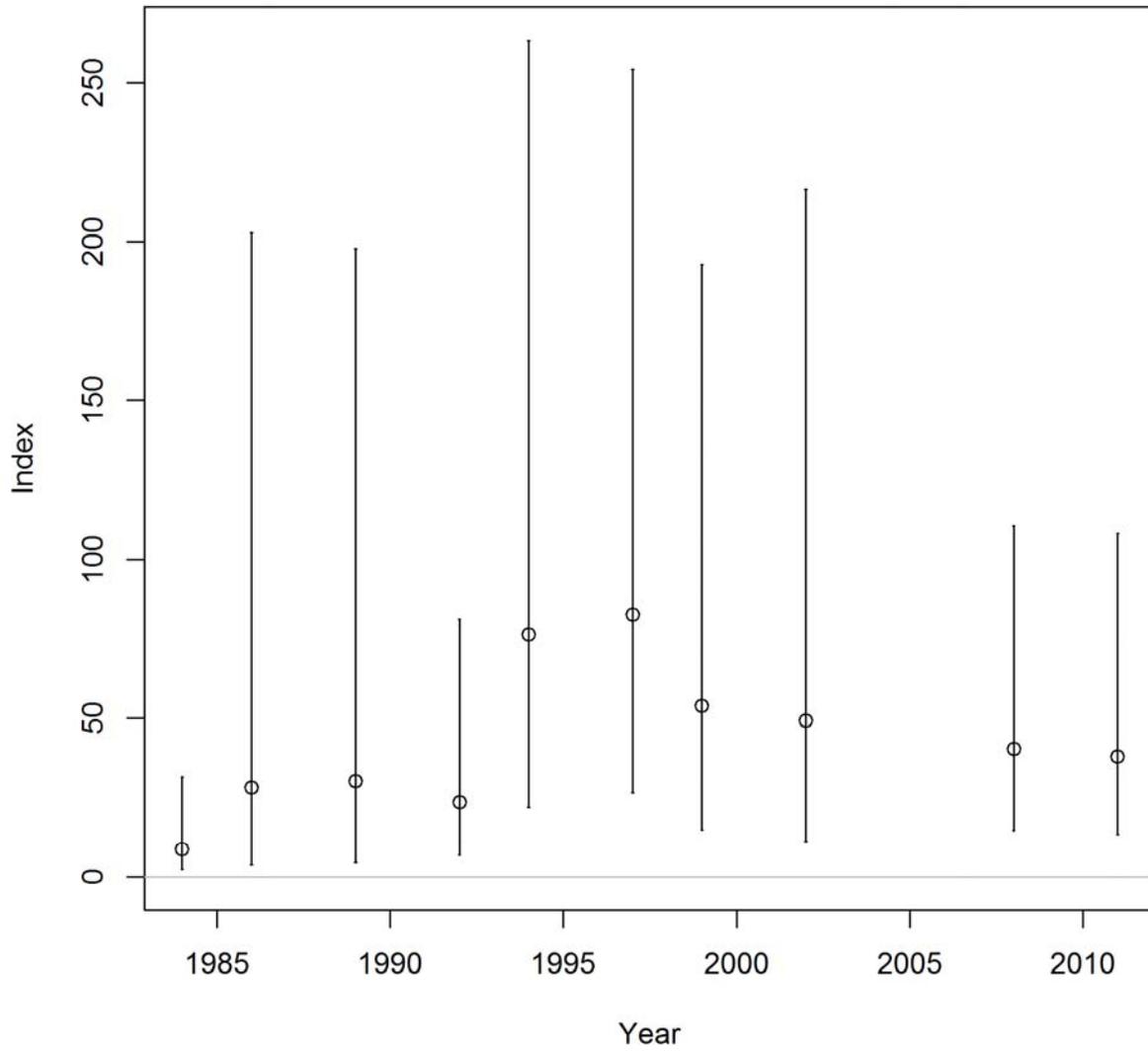
length comps, sexes combined, whole catch, aggregated across time by



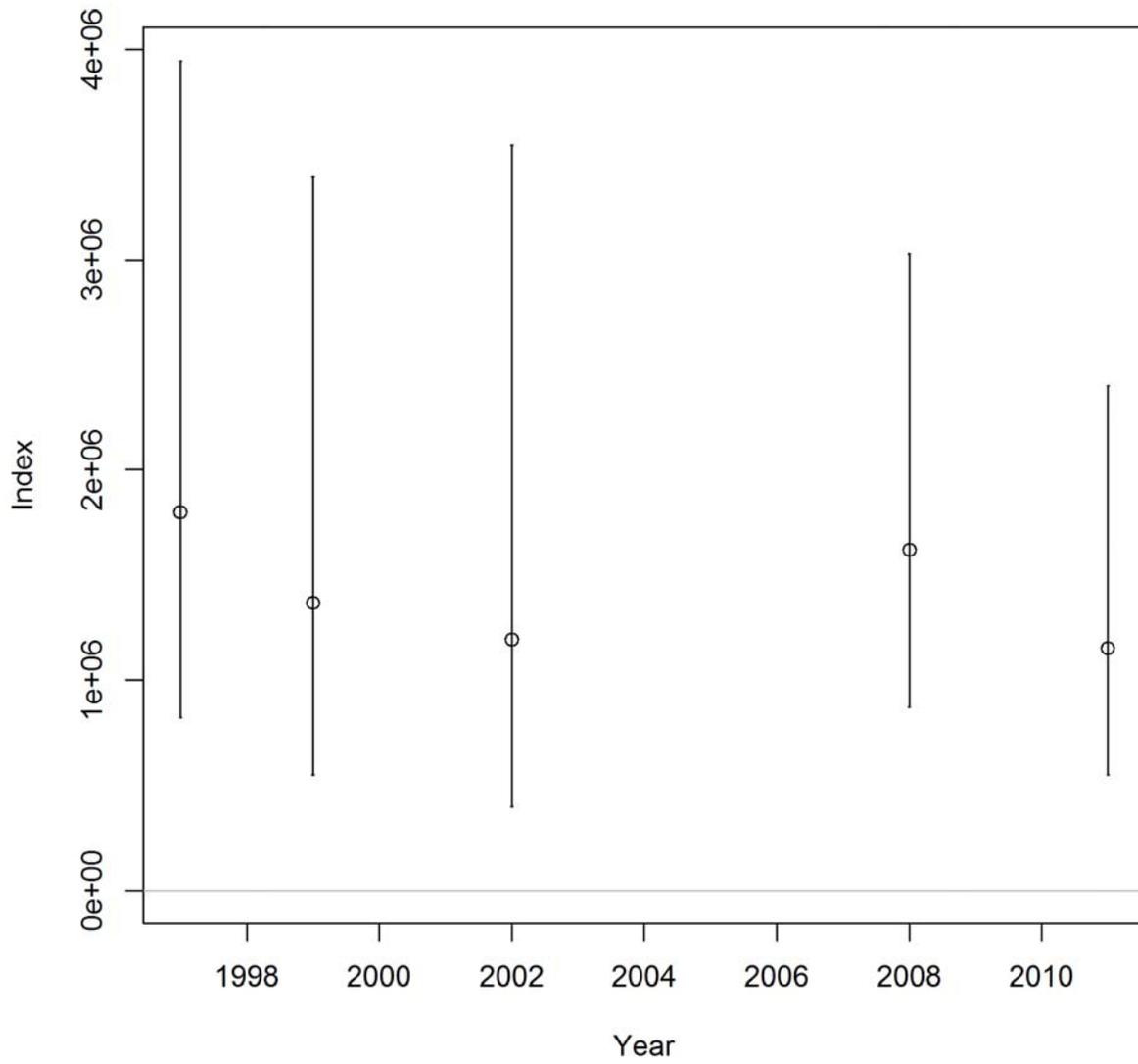
Data by type and year



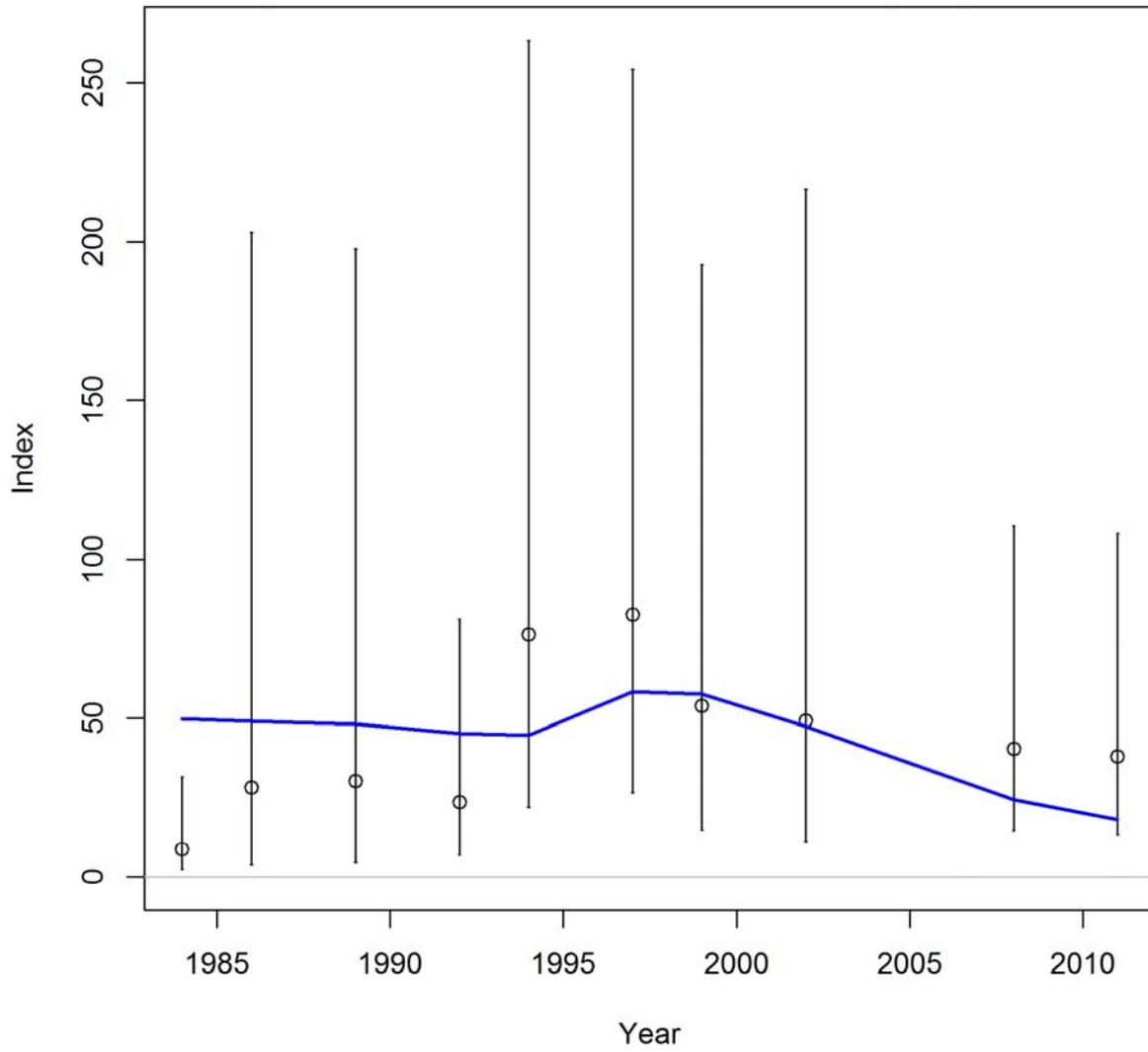
Index NperTow+mm



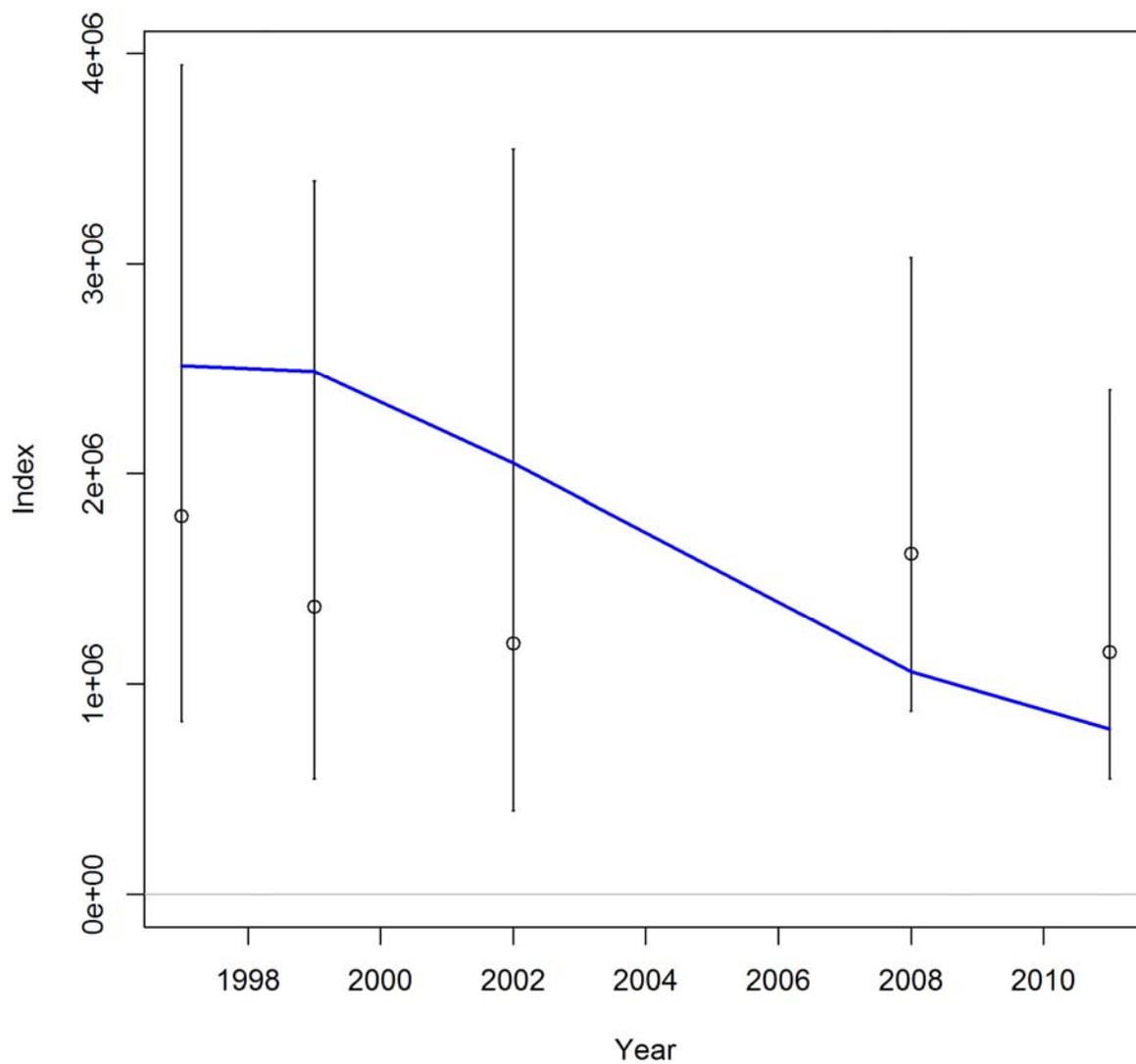
Index SWAN



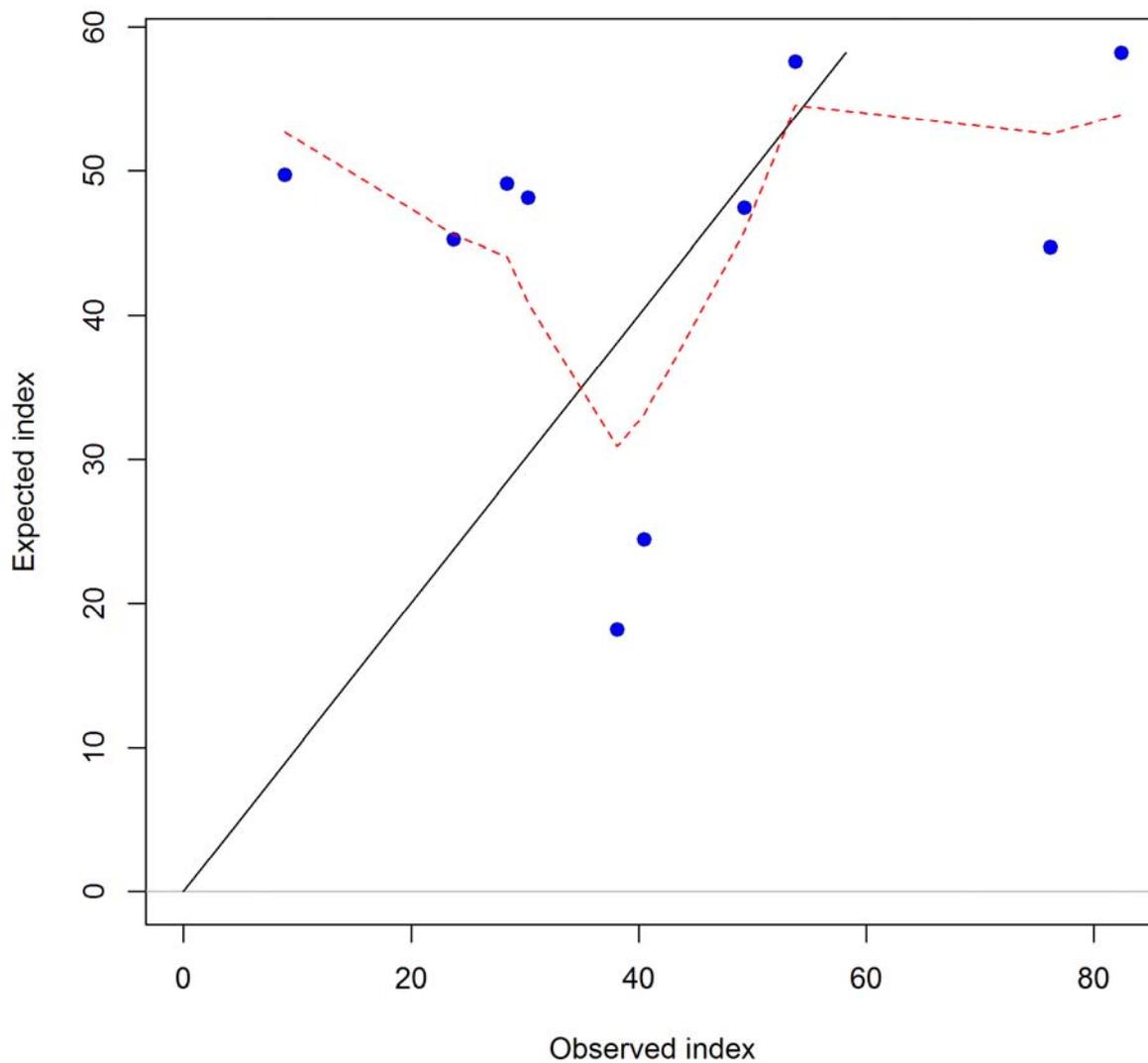
Index NperTow+mm



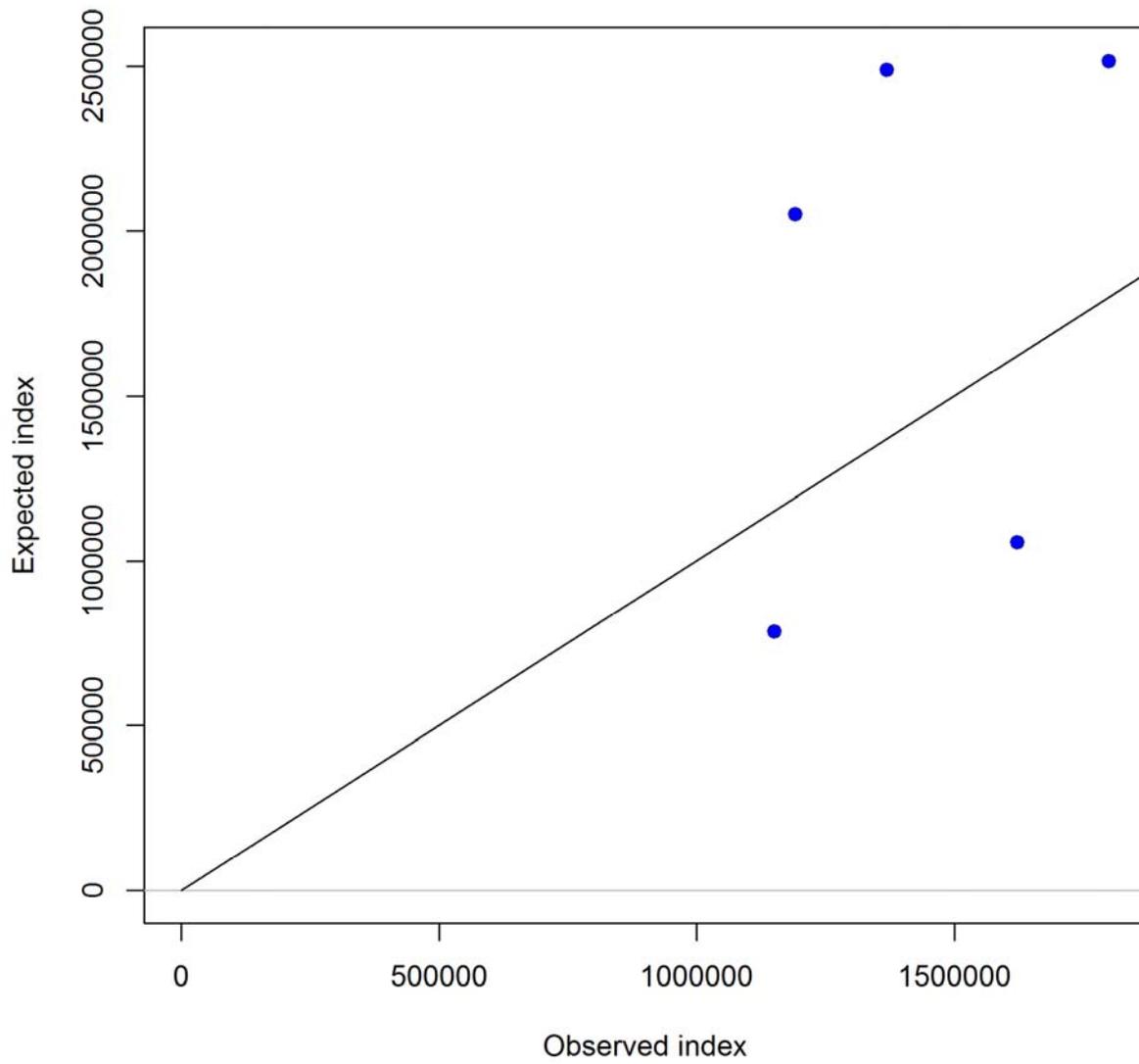
Index SWAN



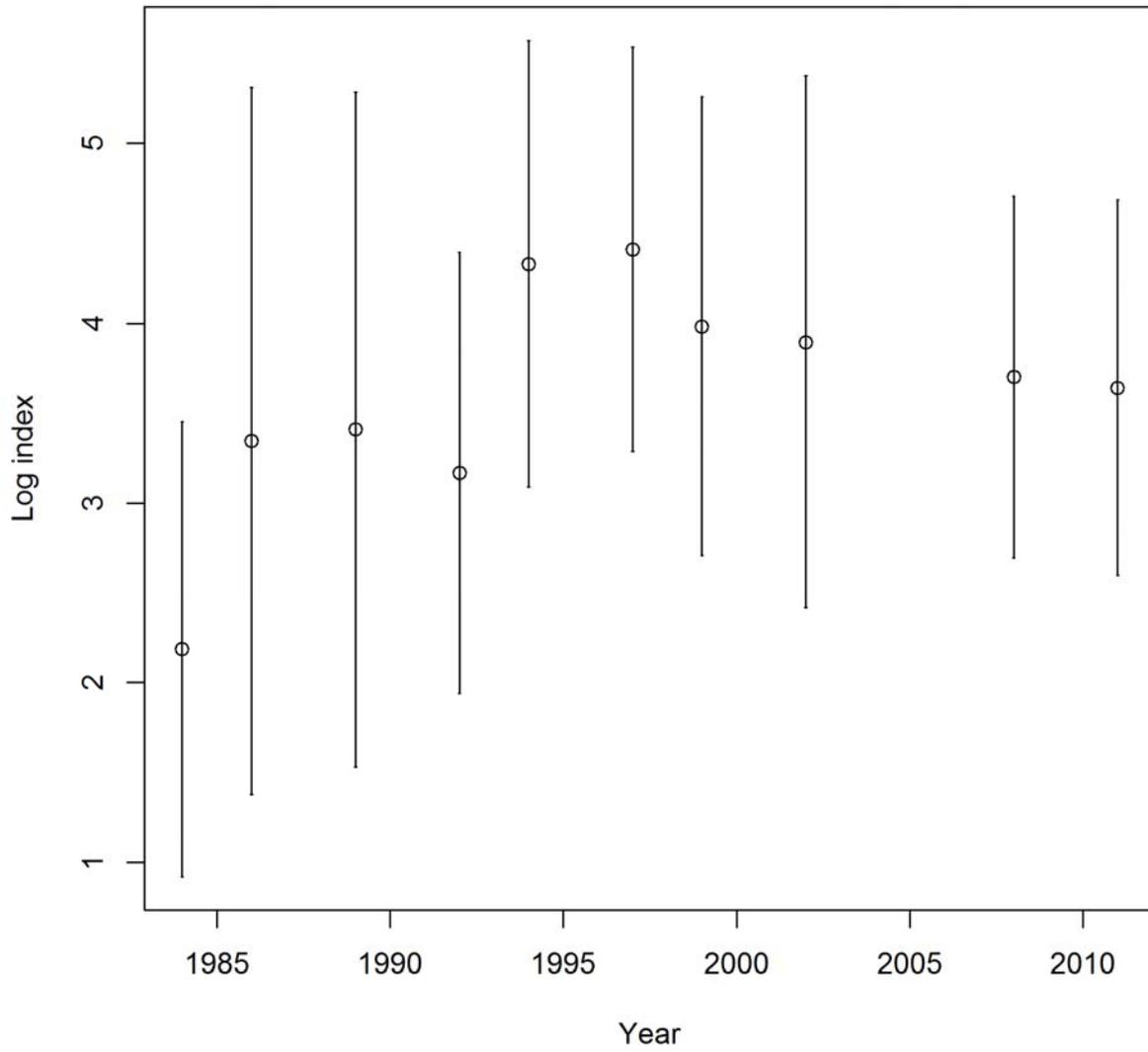
Index NperTow+mm



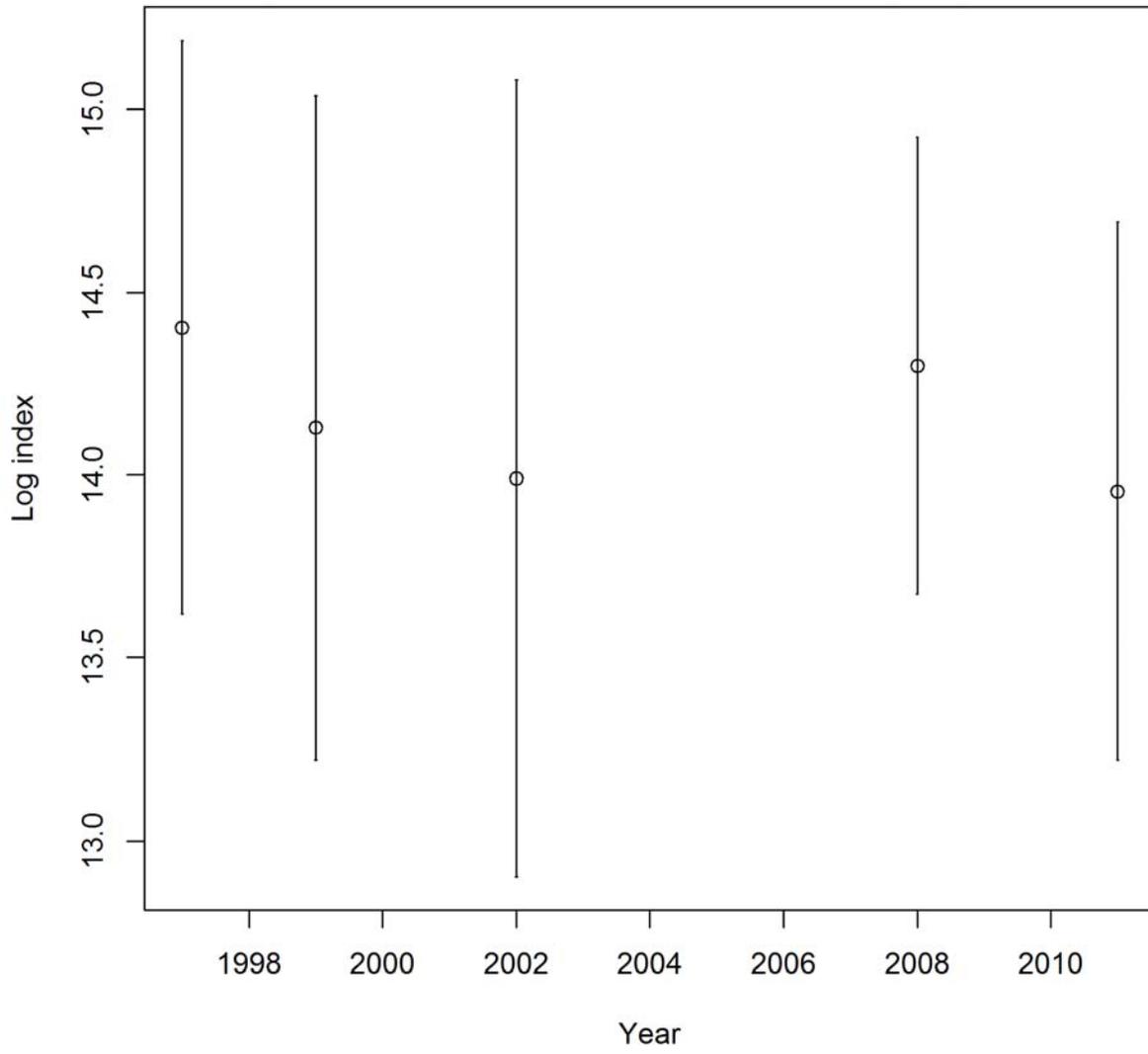
Index SWAN



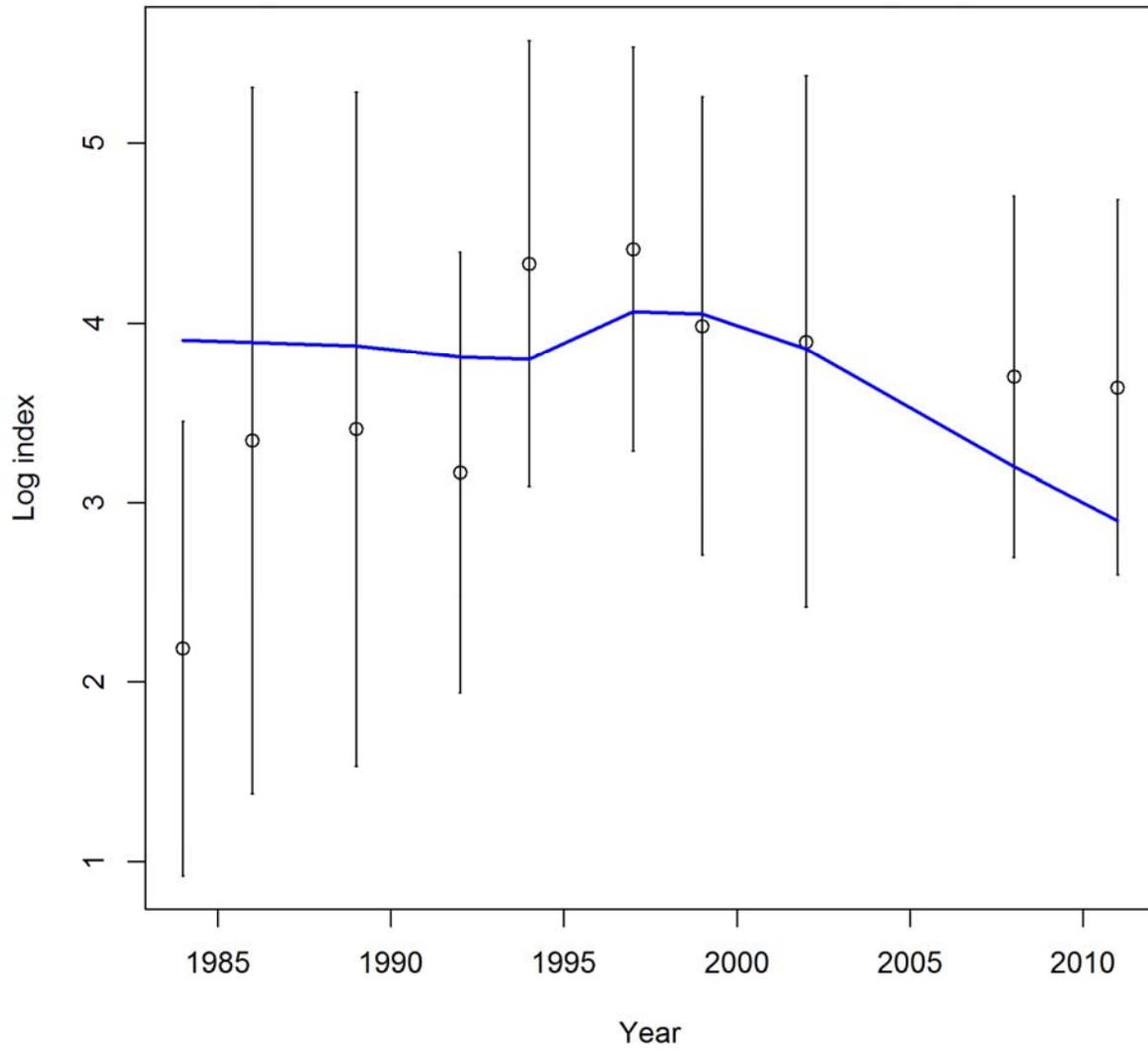
Log index NperTow+mm



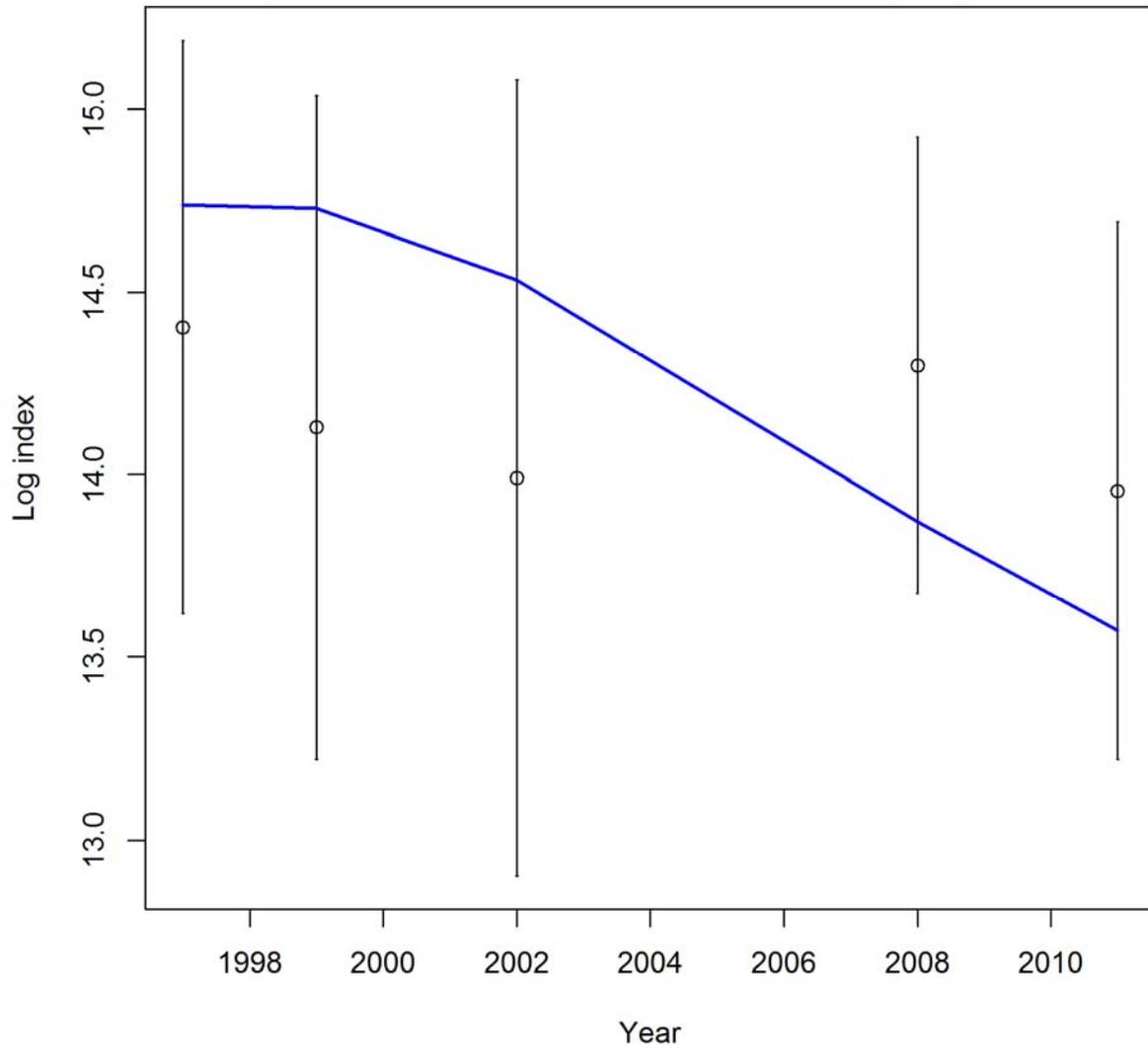
Log index SWAN



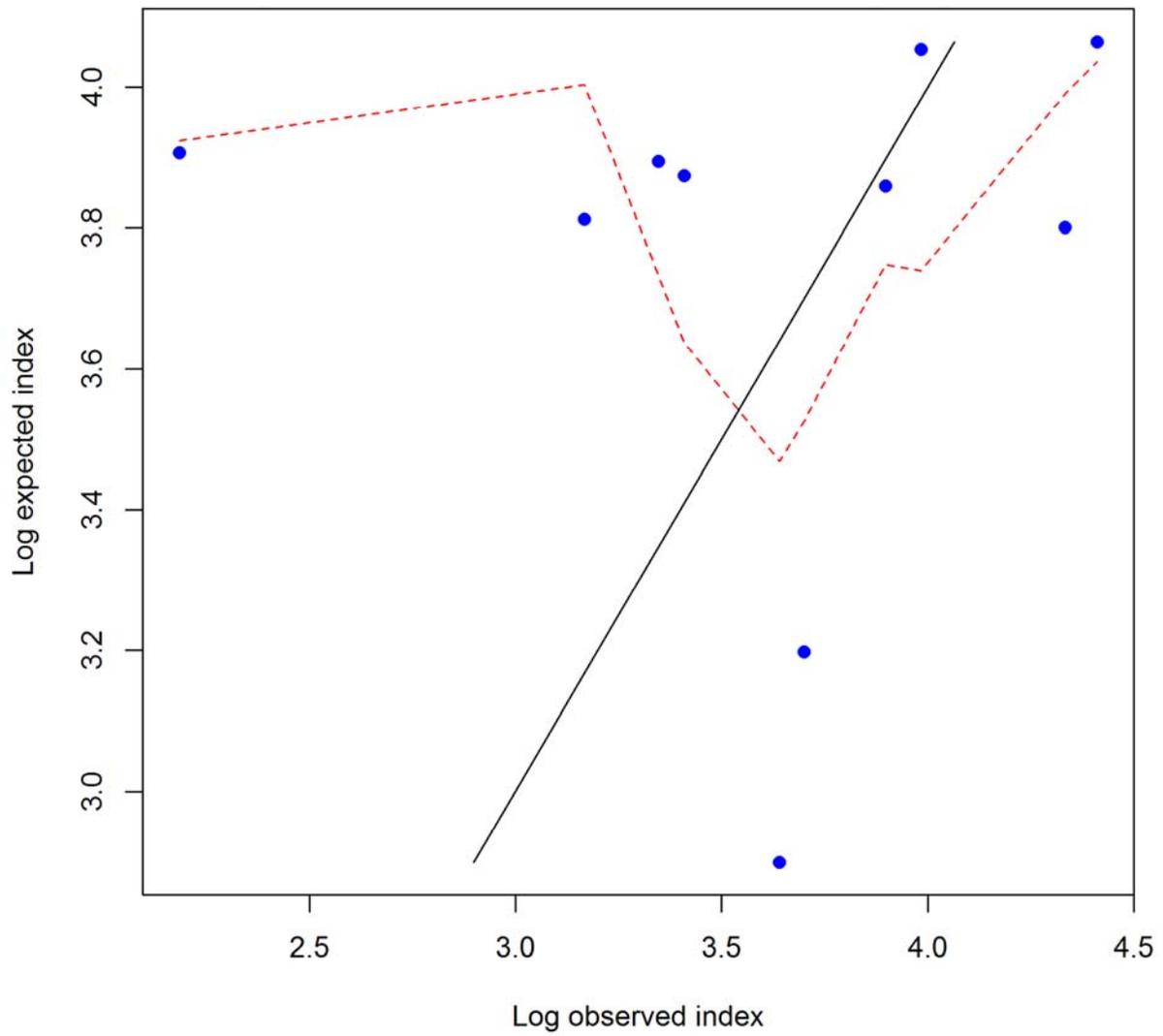
Log index NperTow+mm



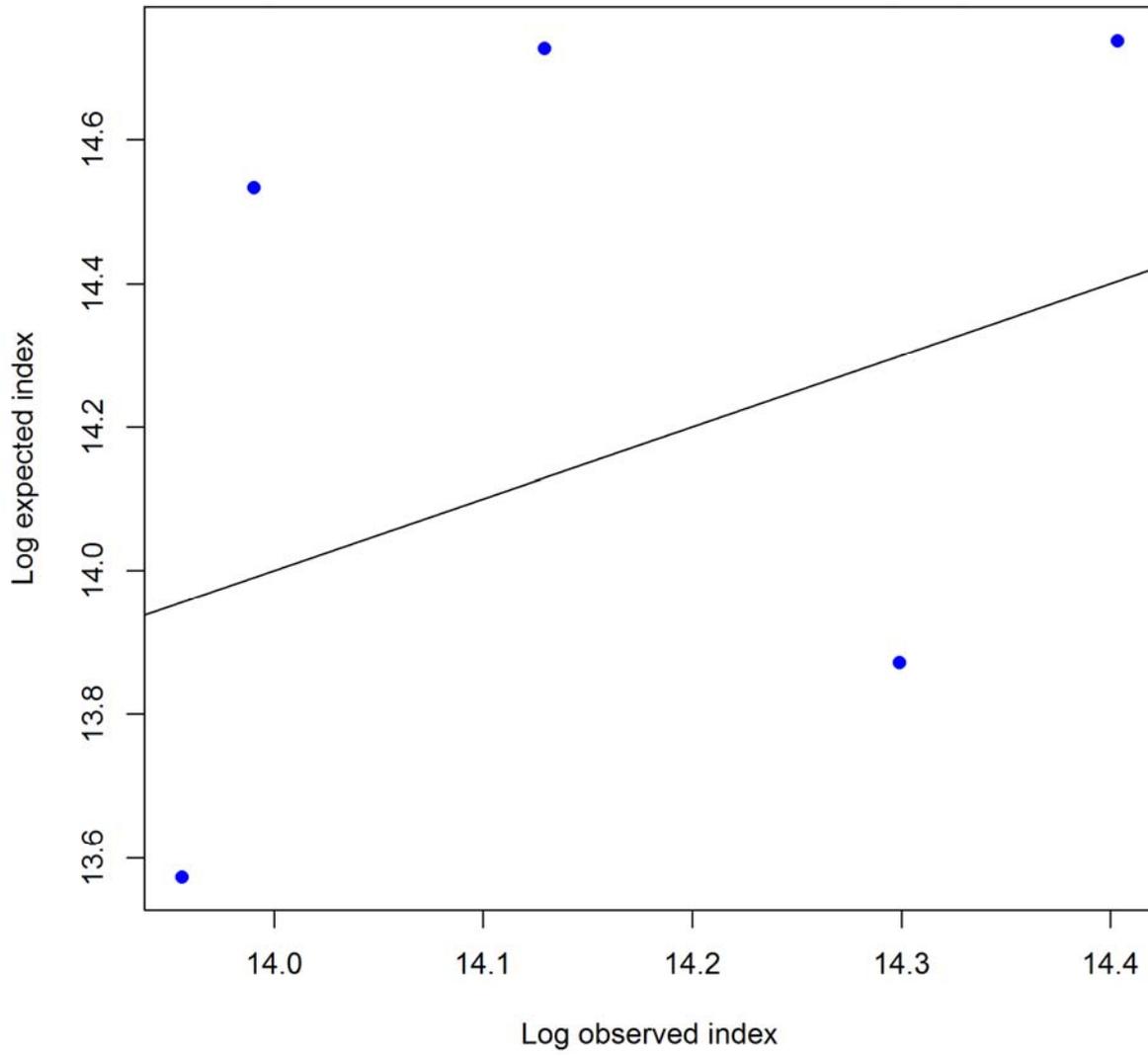
Log index SWAN



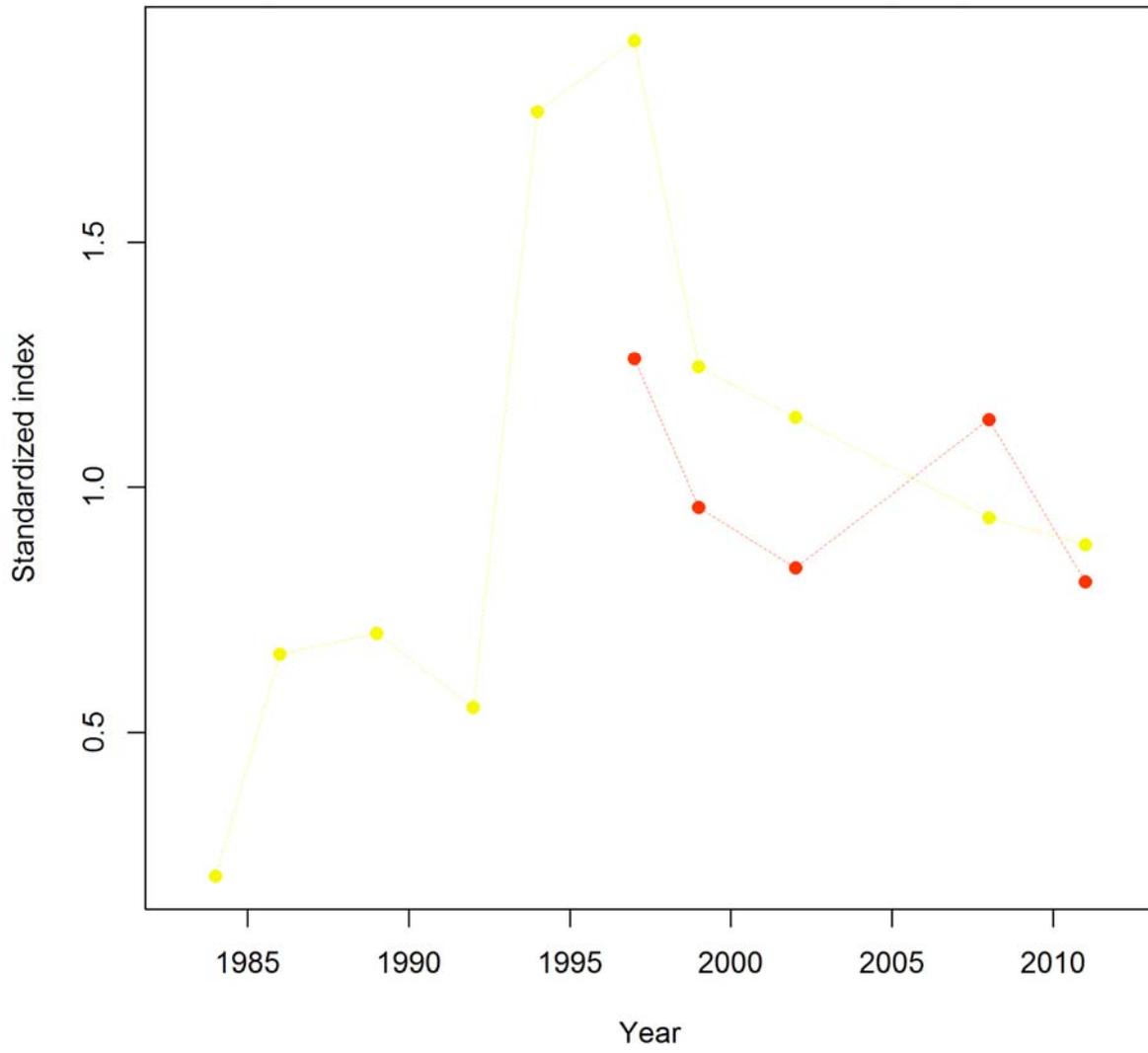
Log index NperTow+mm



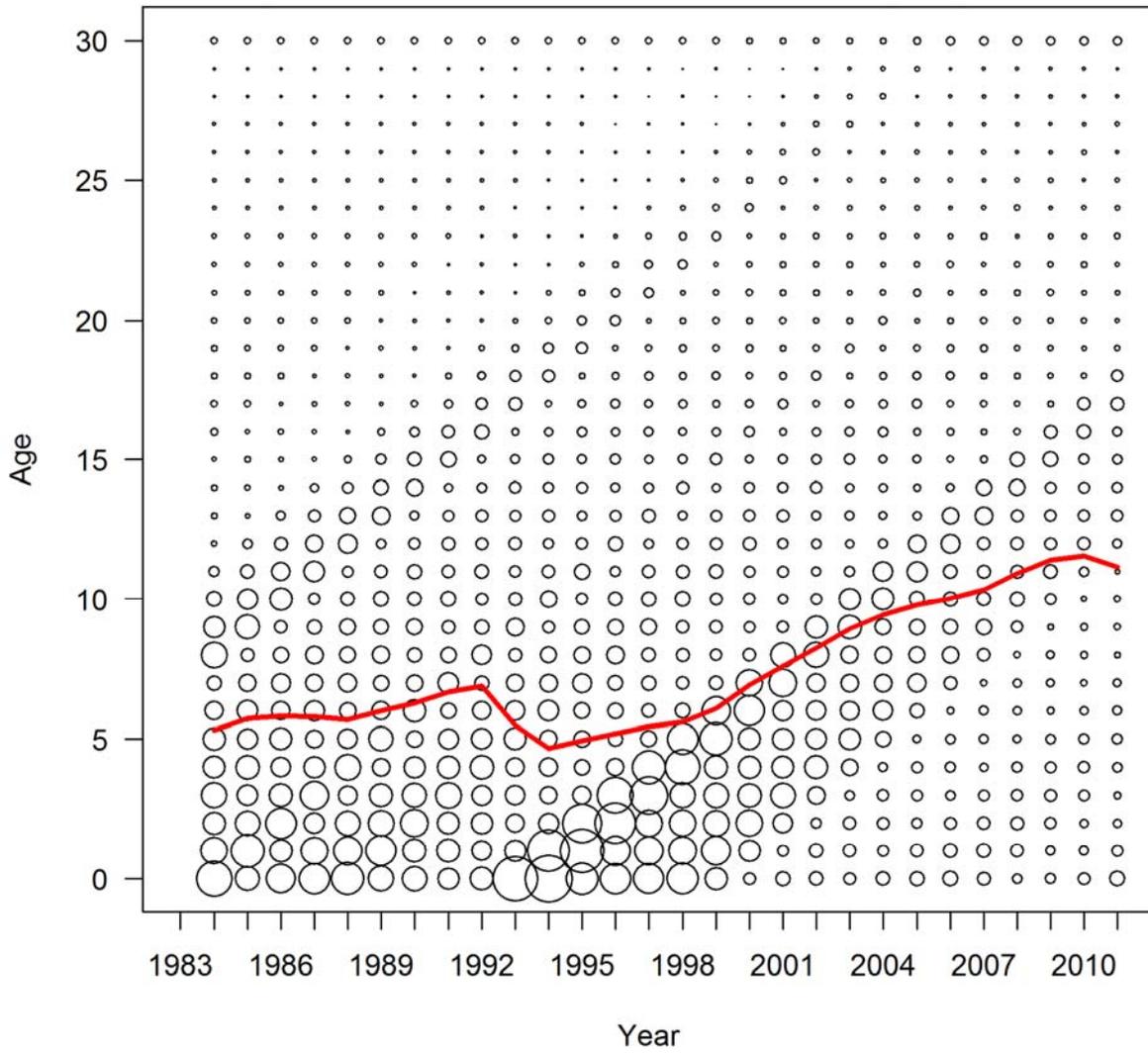
Log index SWAN



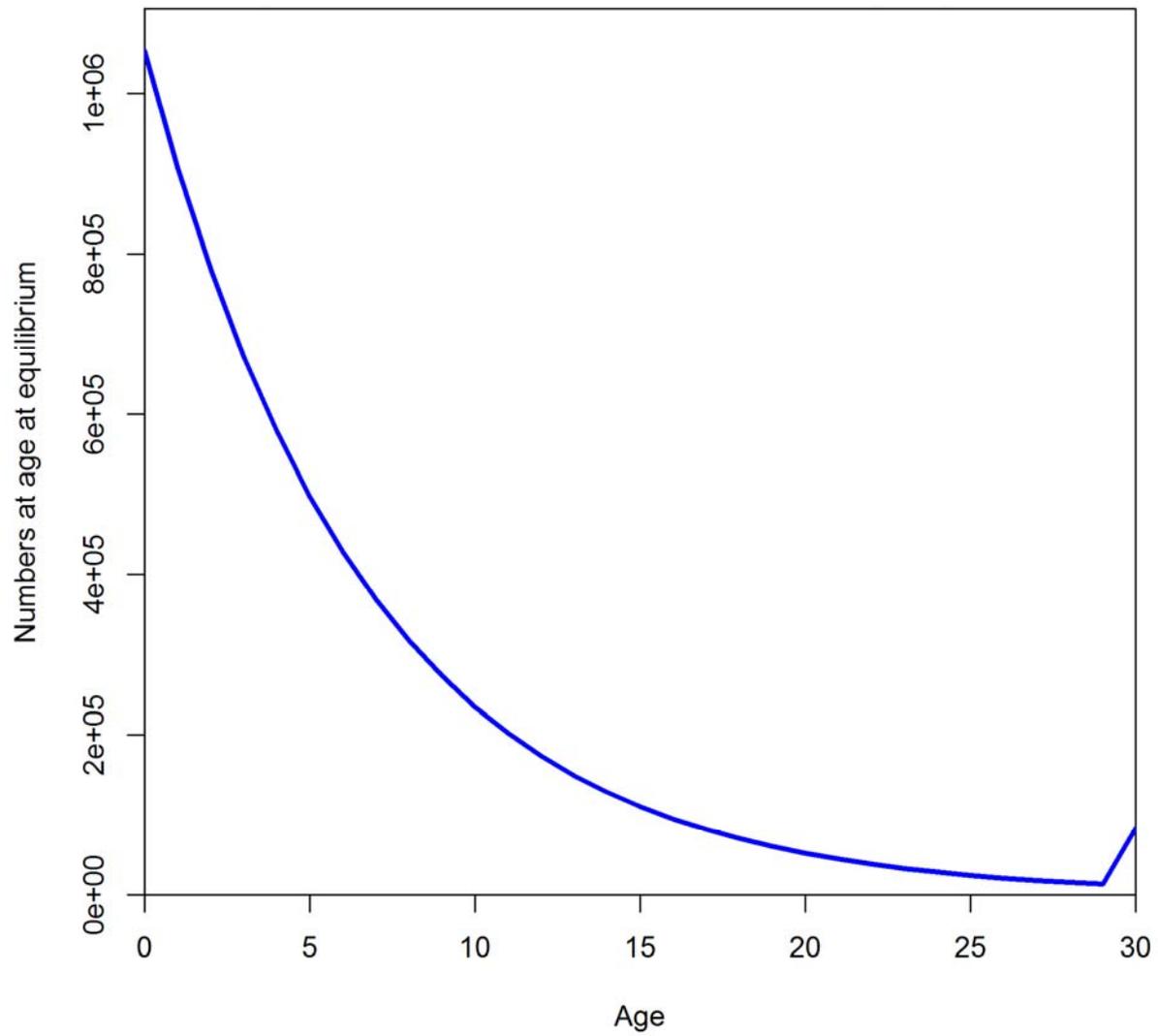
All cpue plot



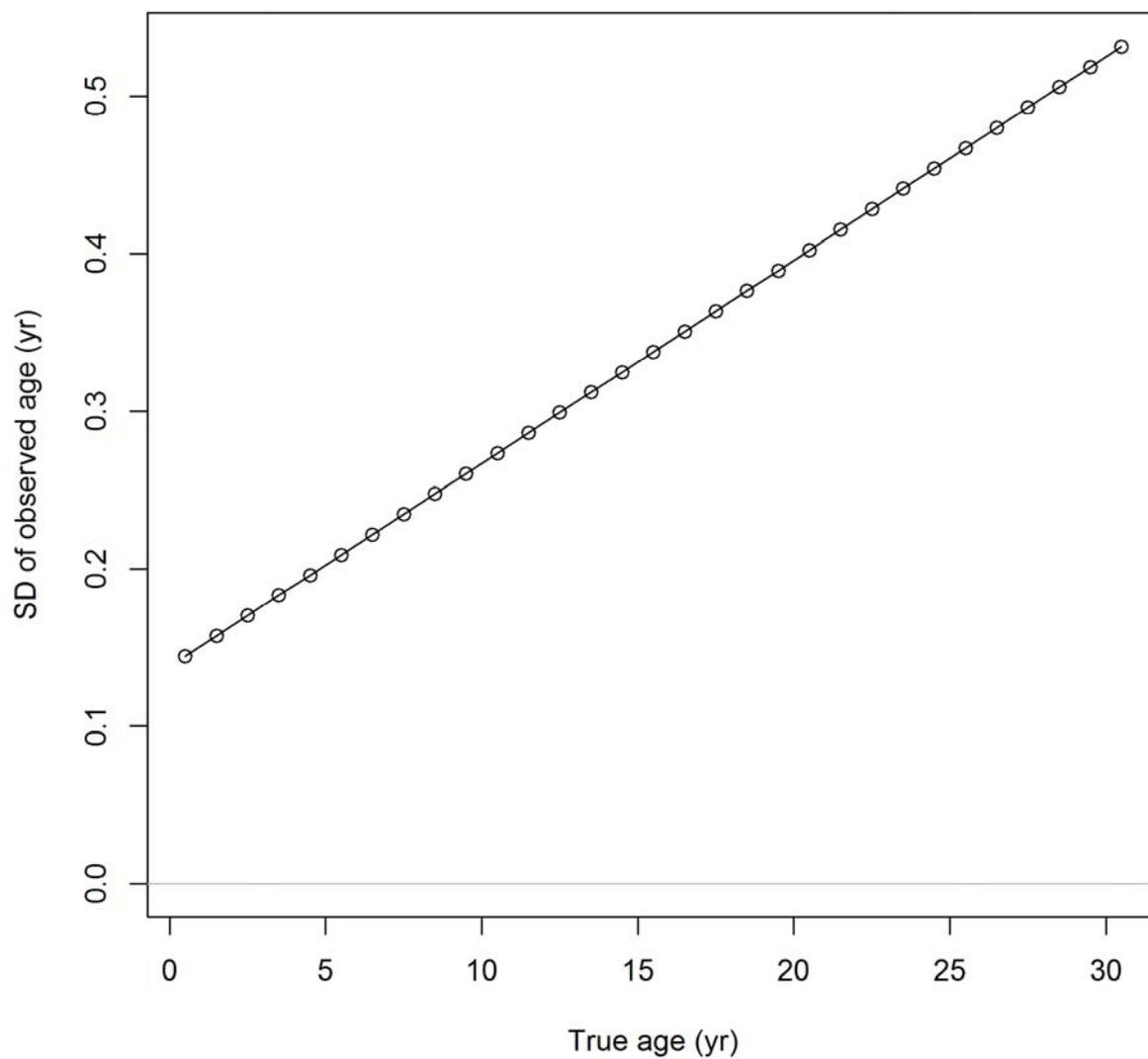
Middle of year expected numbers at age in thousands (max=3336850)



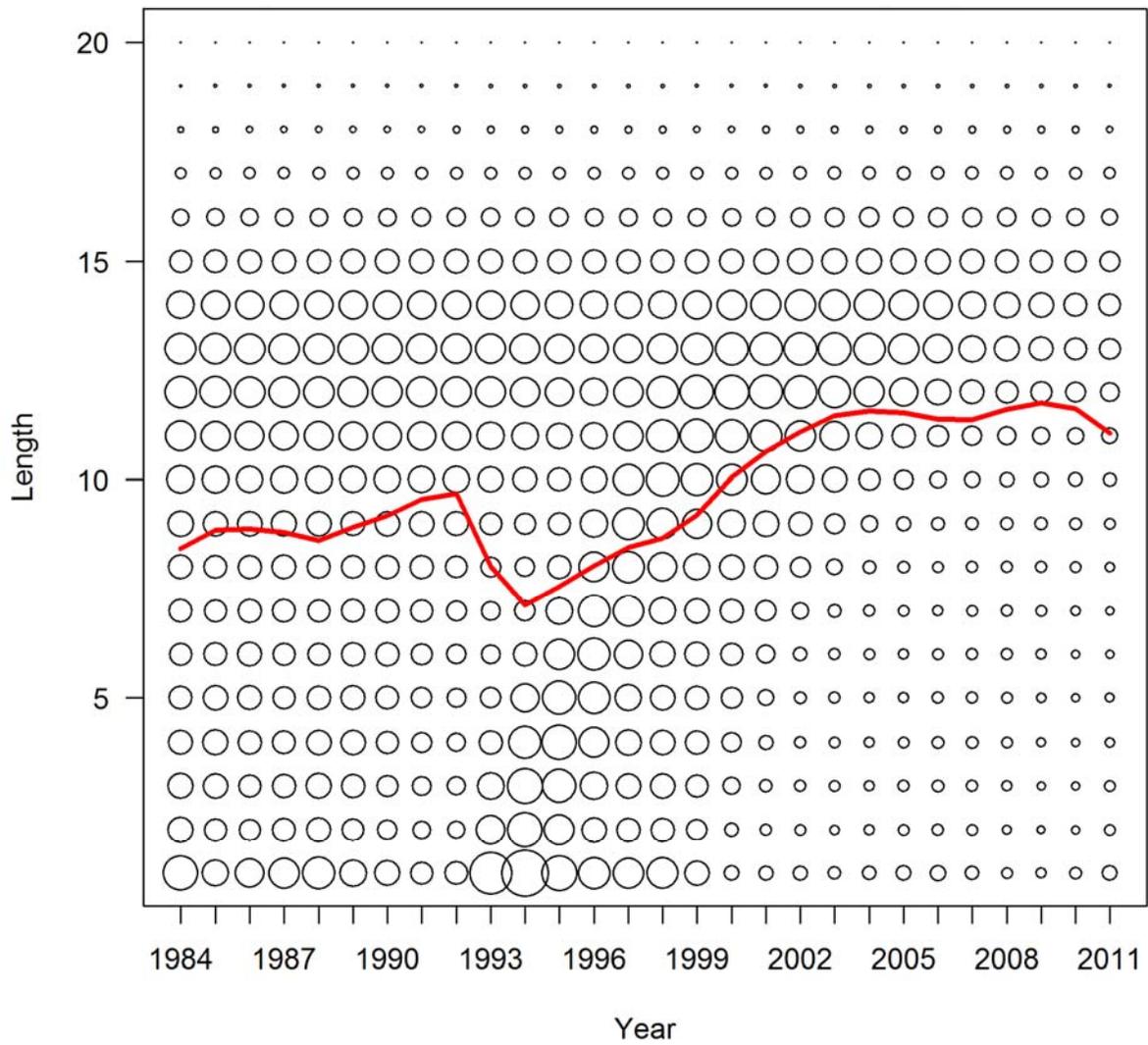
Equilibrium age distribution

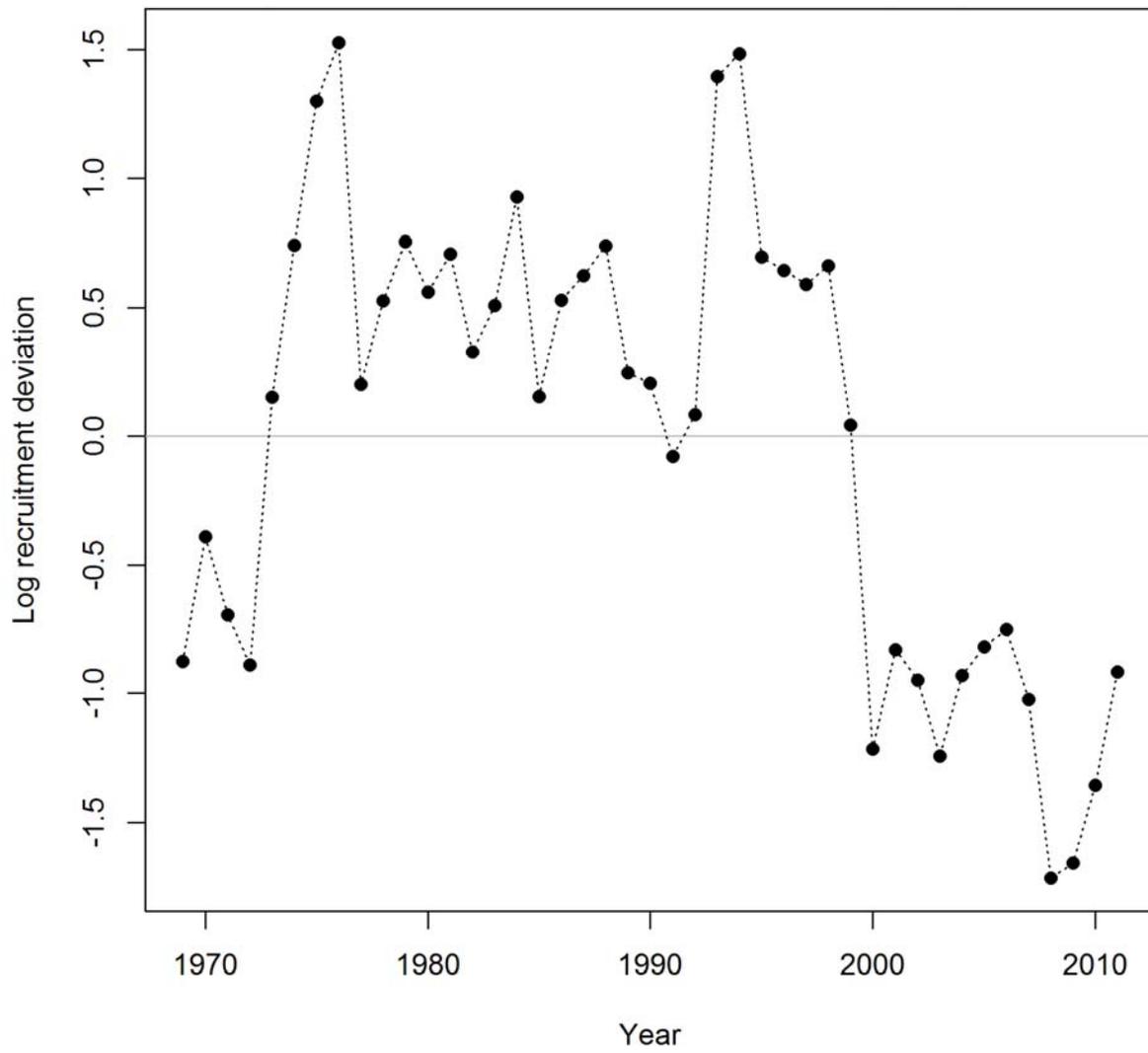


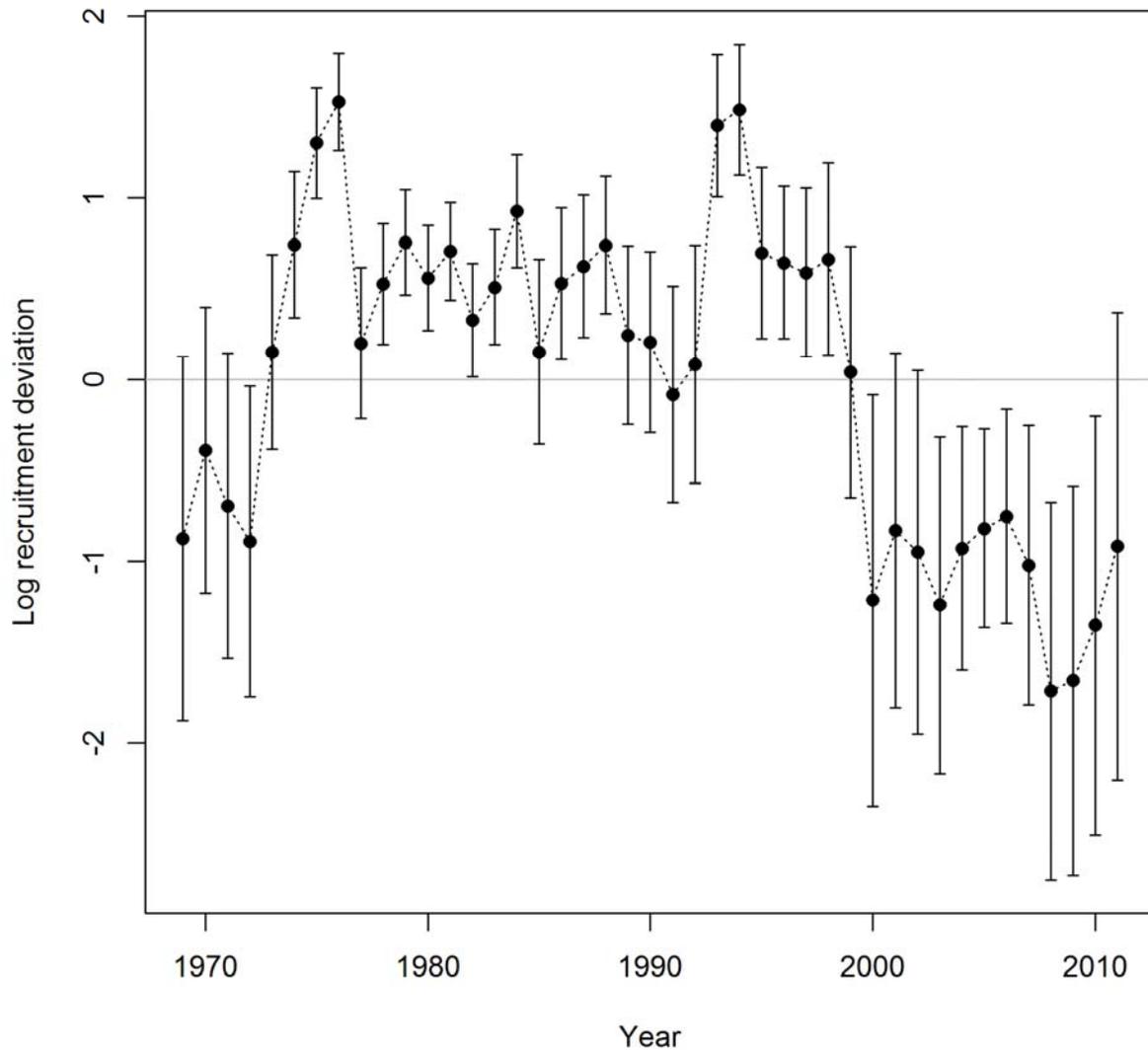
Ageing imprecision



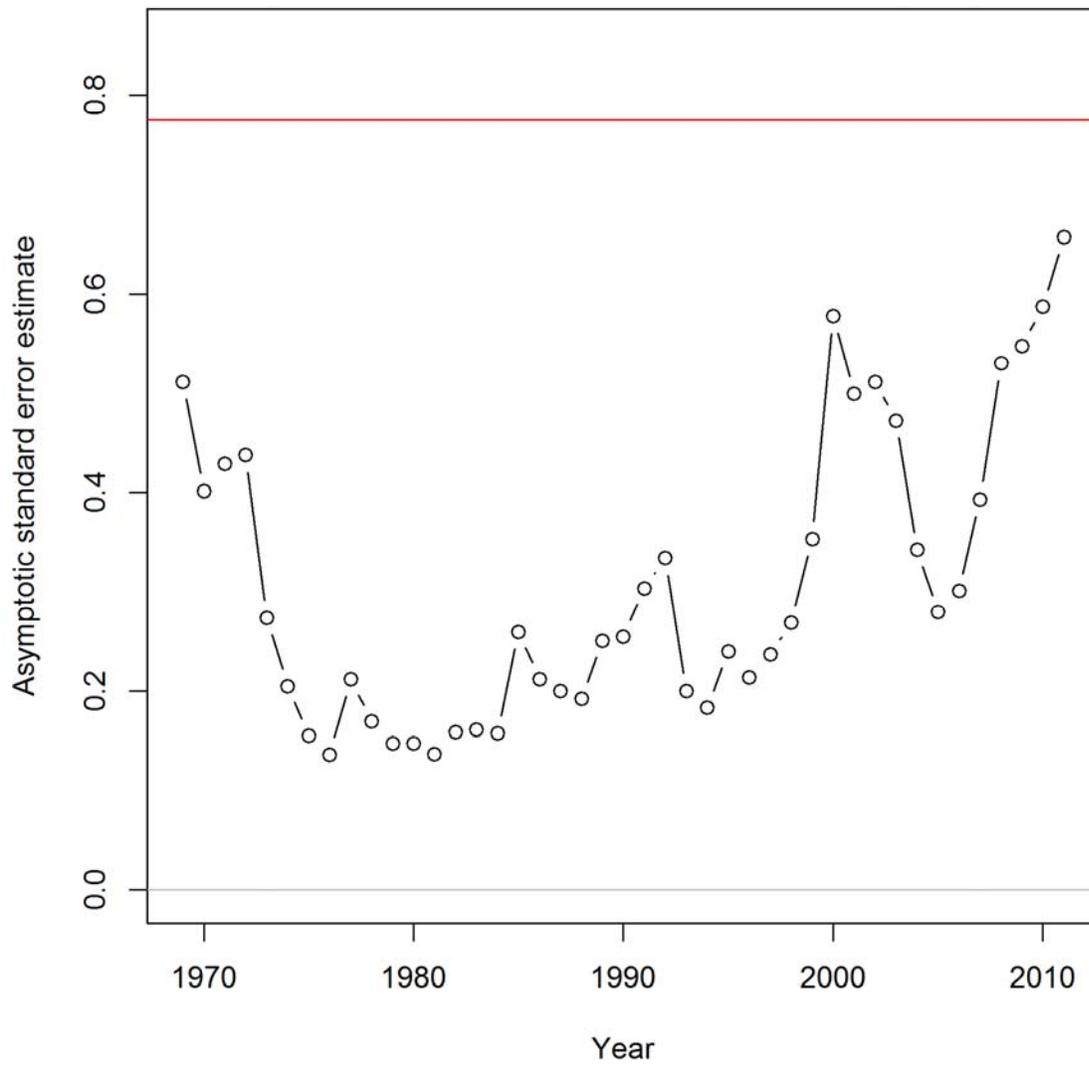
Middle of year expected numbers at length in thousands (max=1977530)

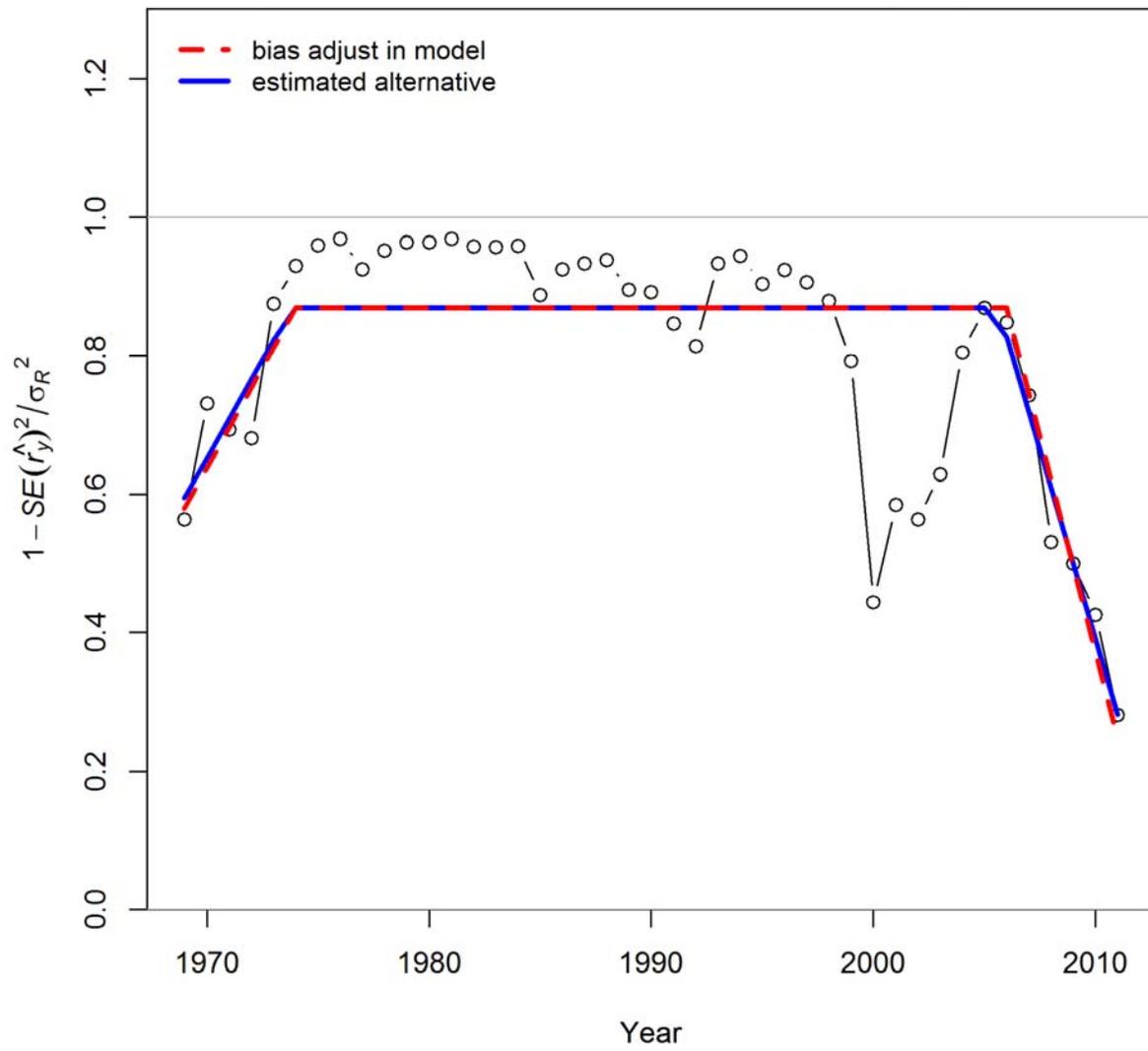




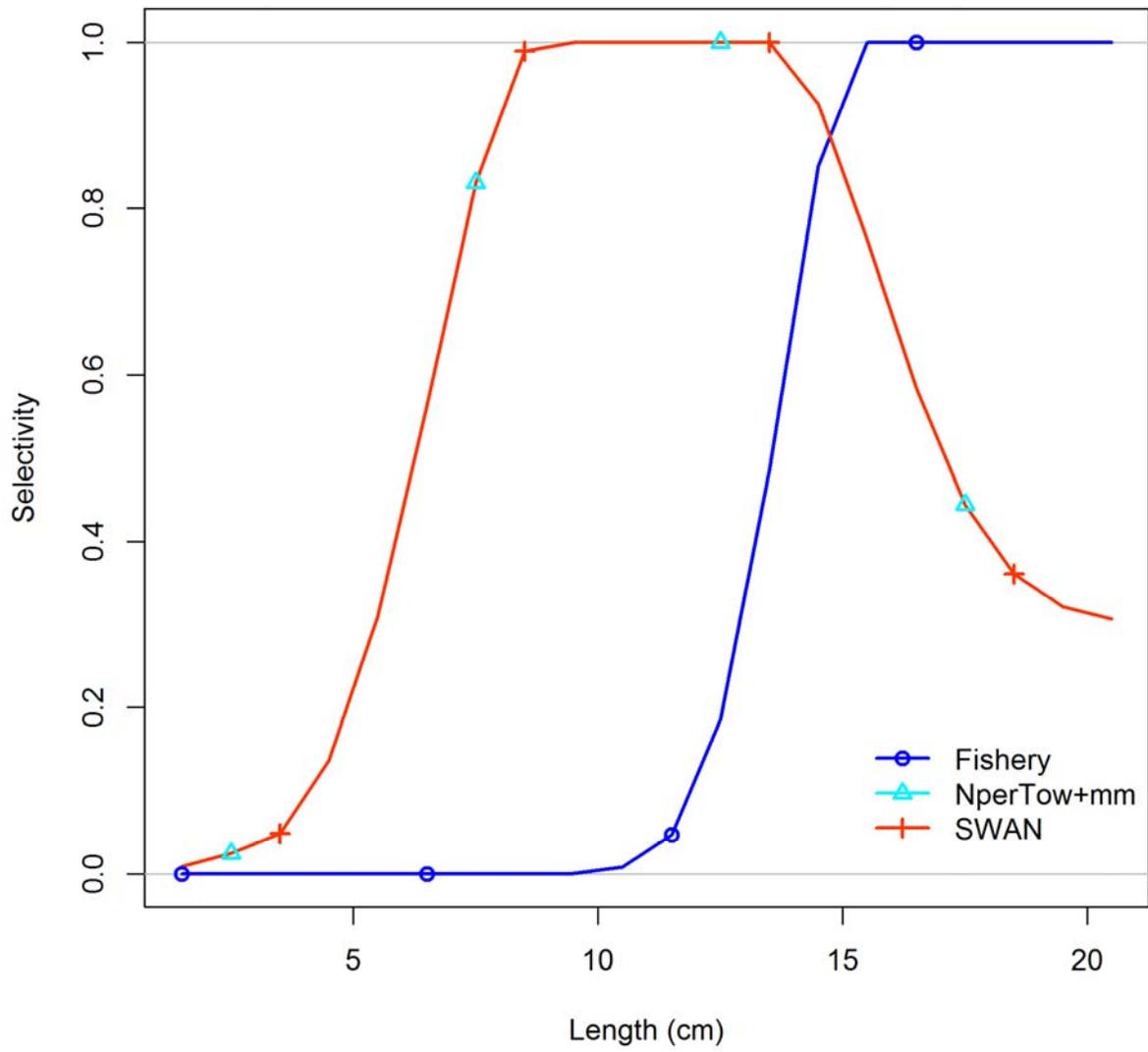


Recruitment deviation variance check

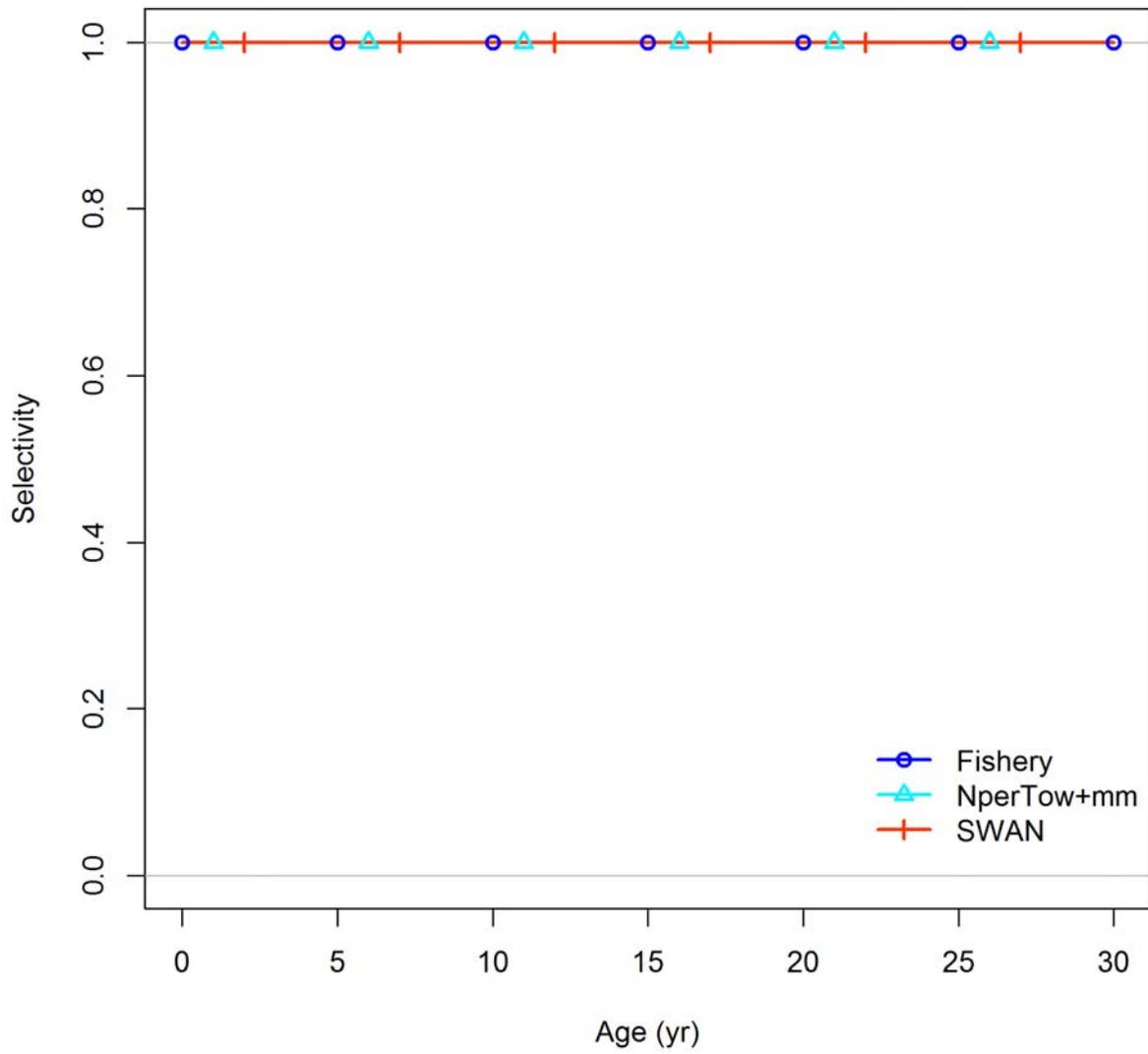




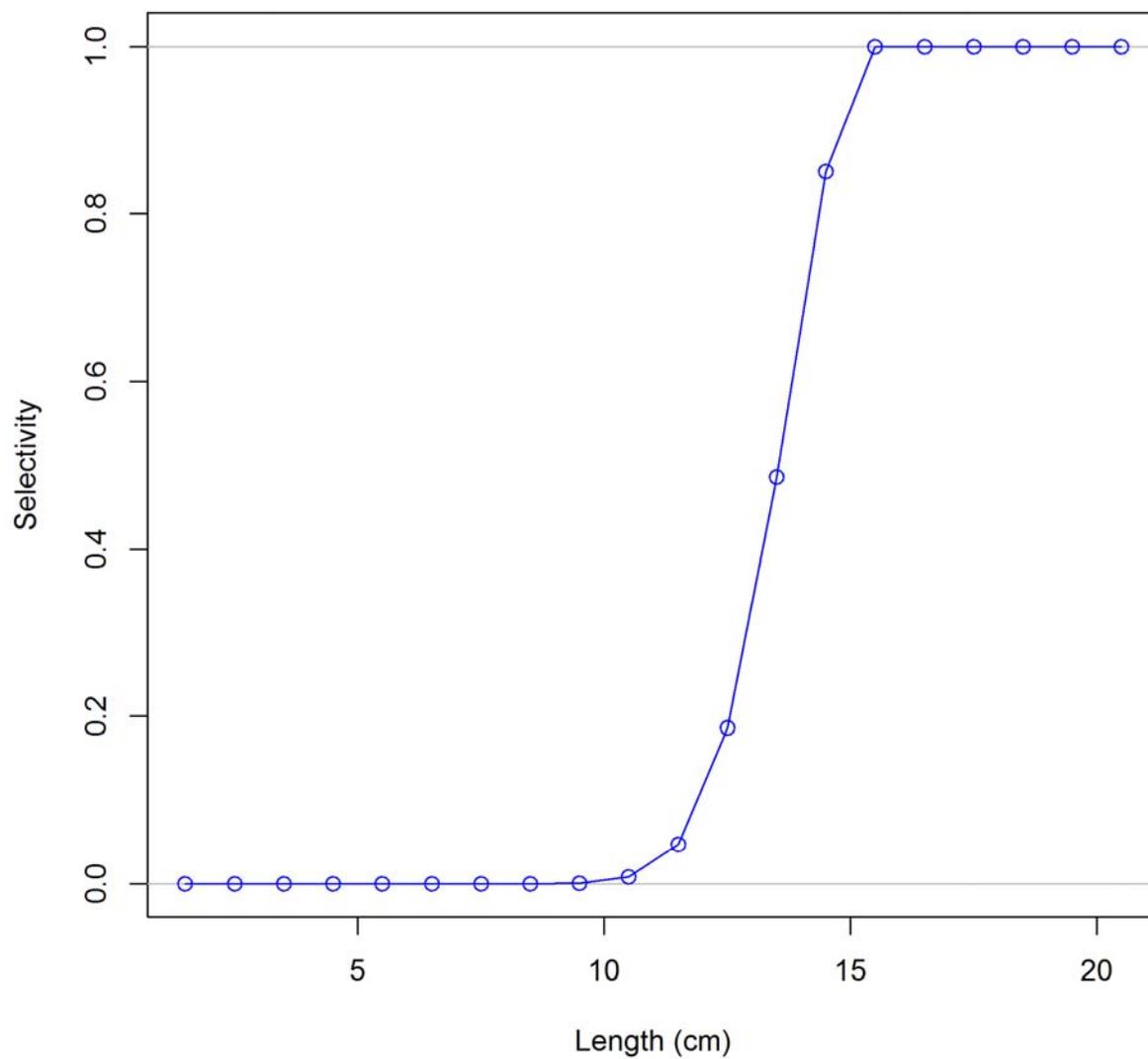
Length-based selectivity by fleet in 2011



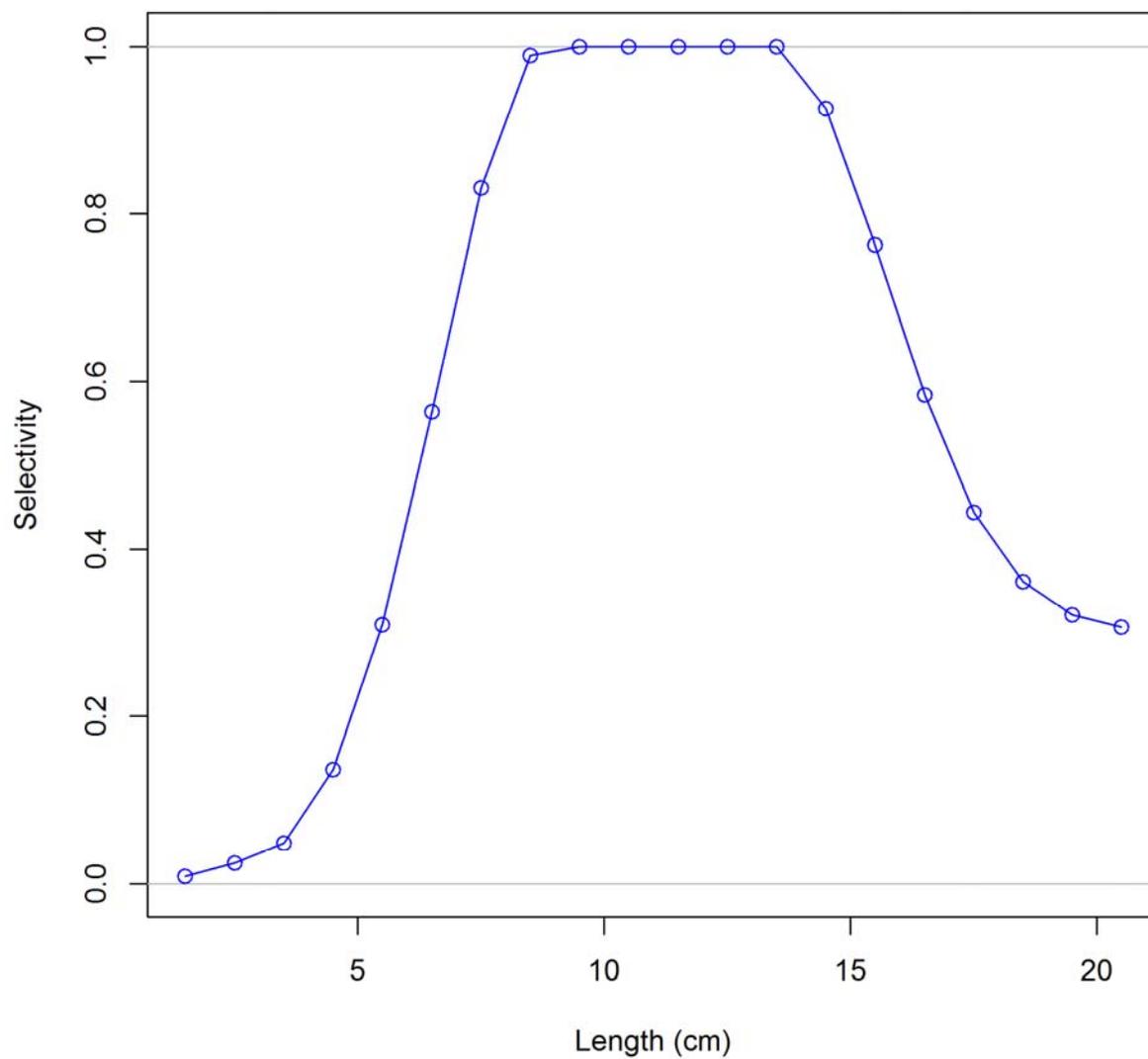
Age-based selectivity by fleet in 2011



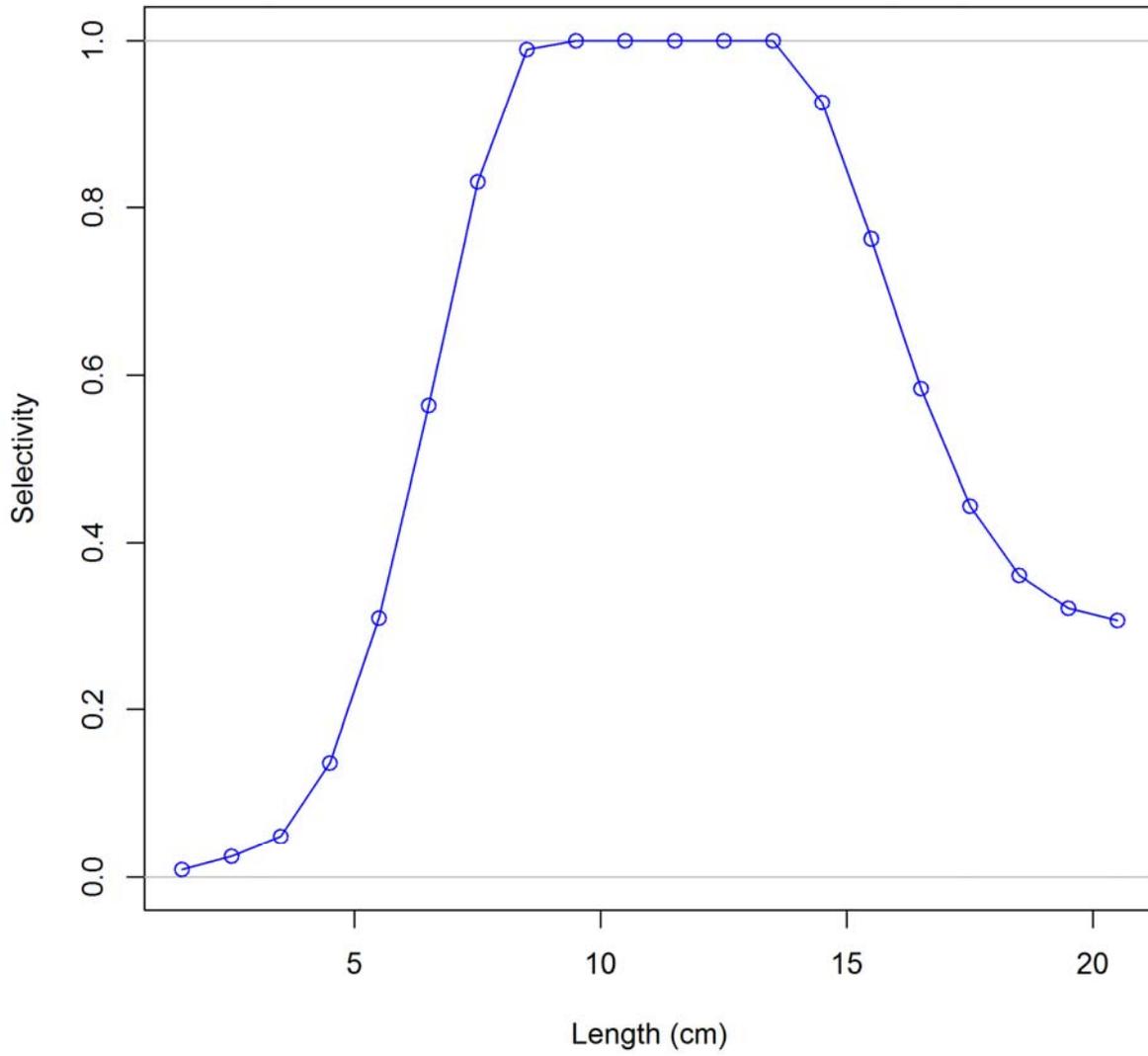
Ending year selectivity for Fishery



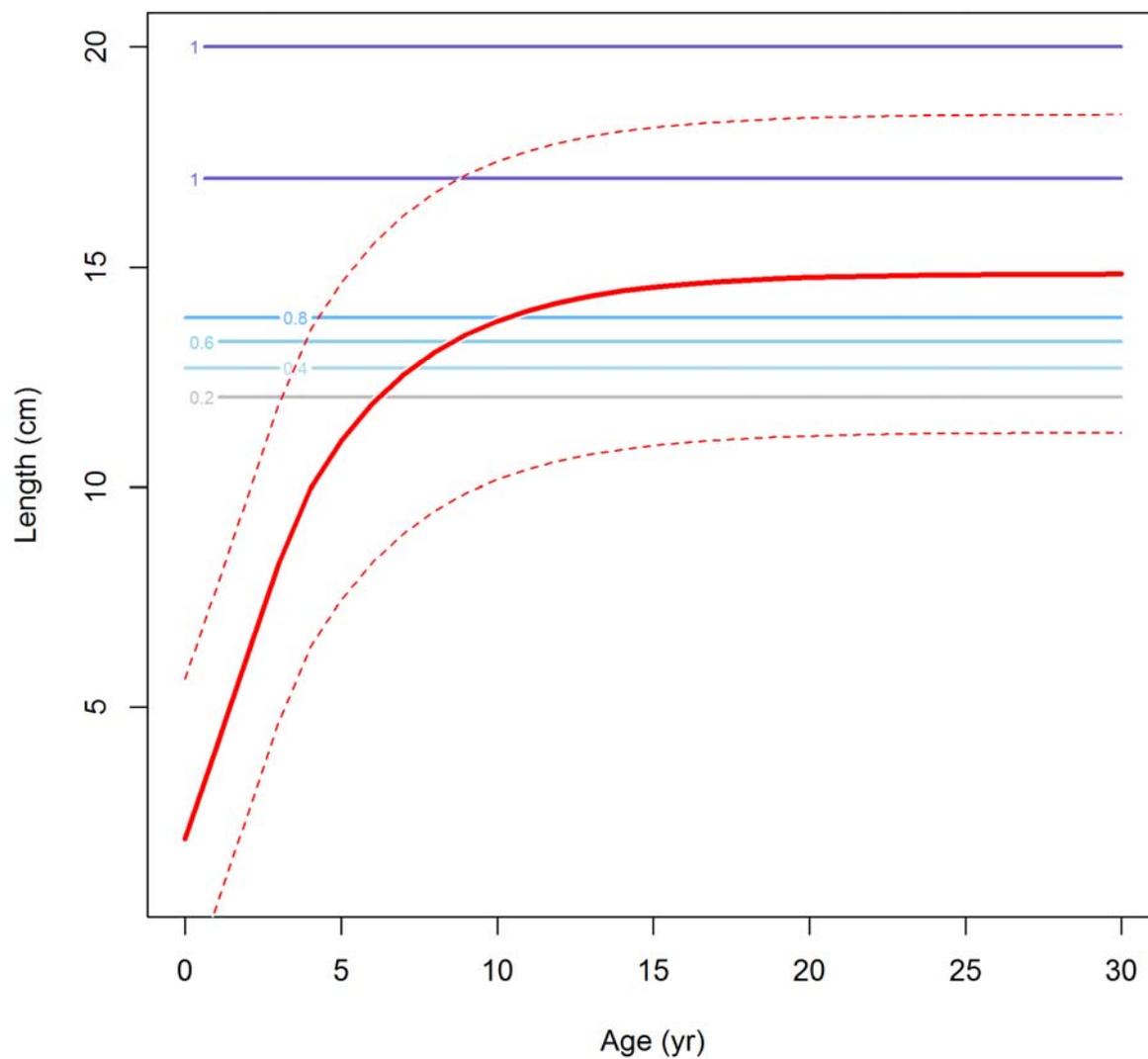
Ending year selectivity for NperTow+mm



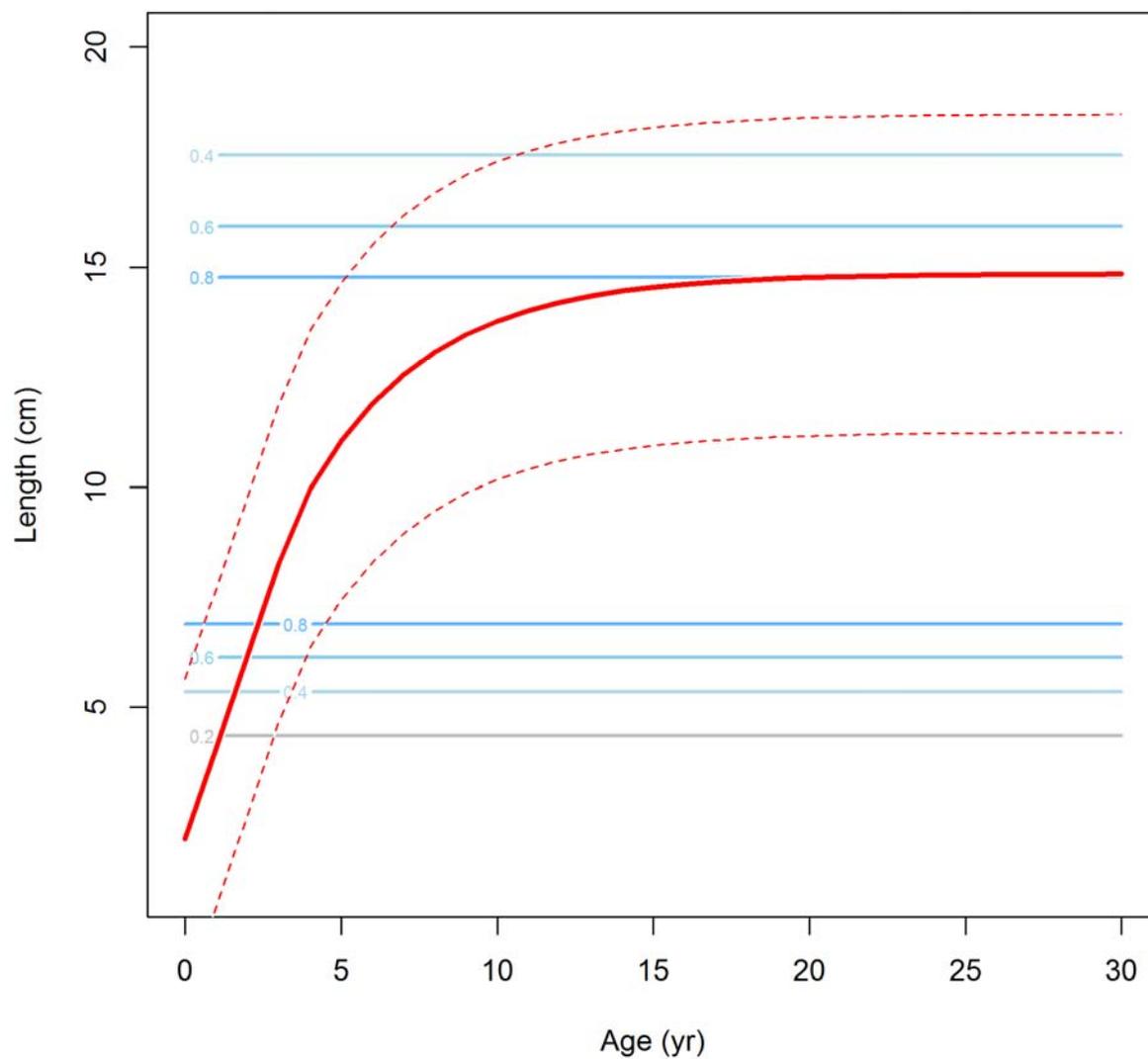
Ending year selectivity for SWAN



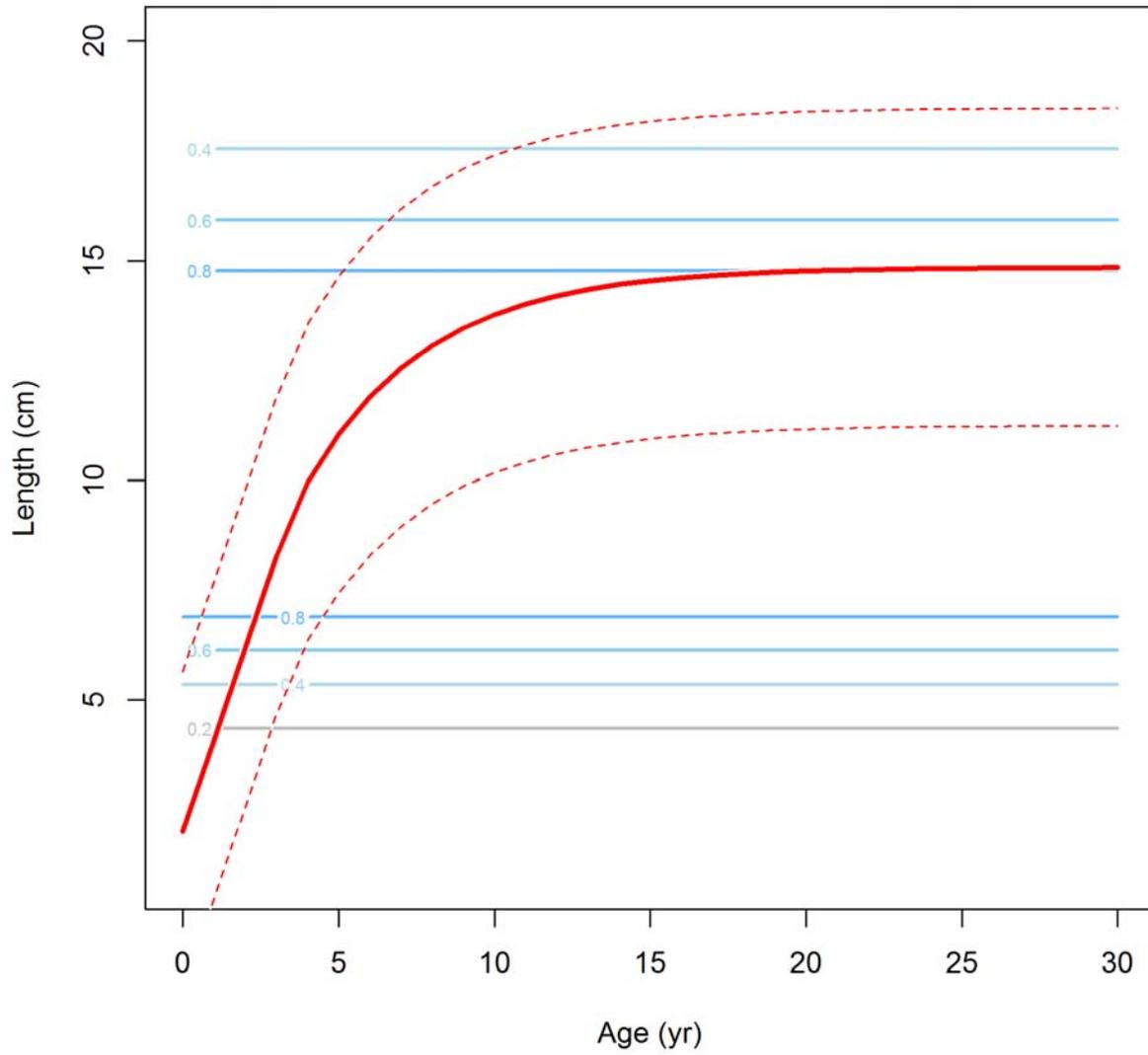
Ending year selectivity and growth for Fishery

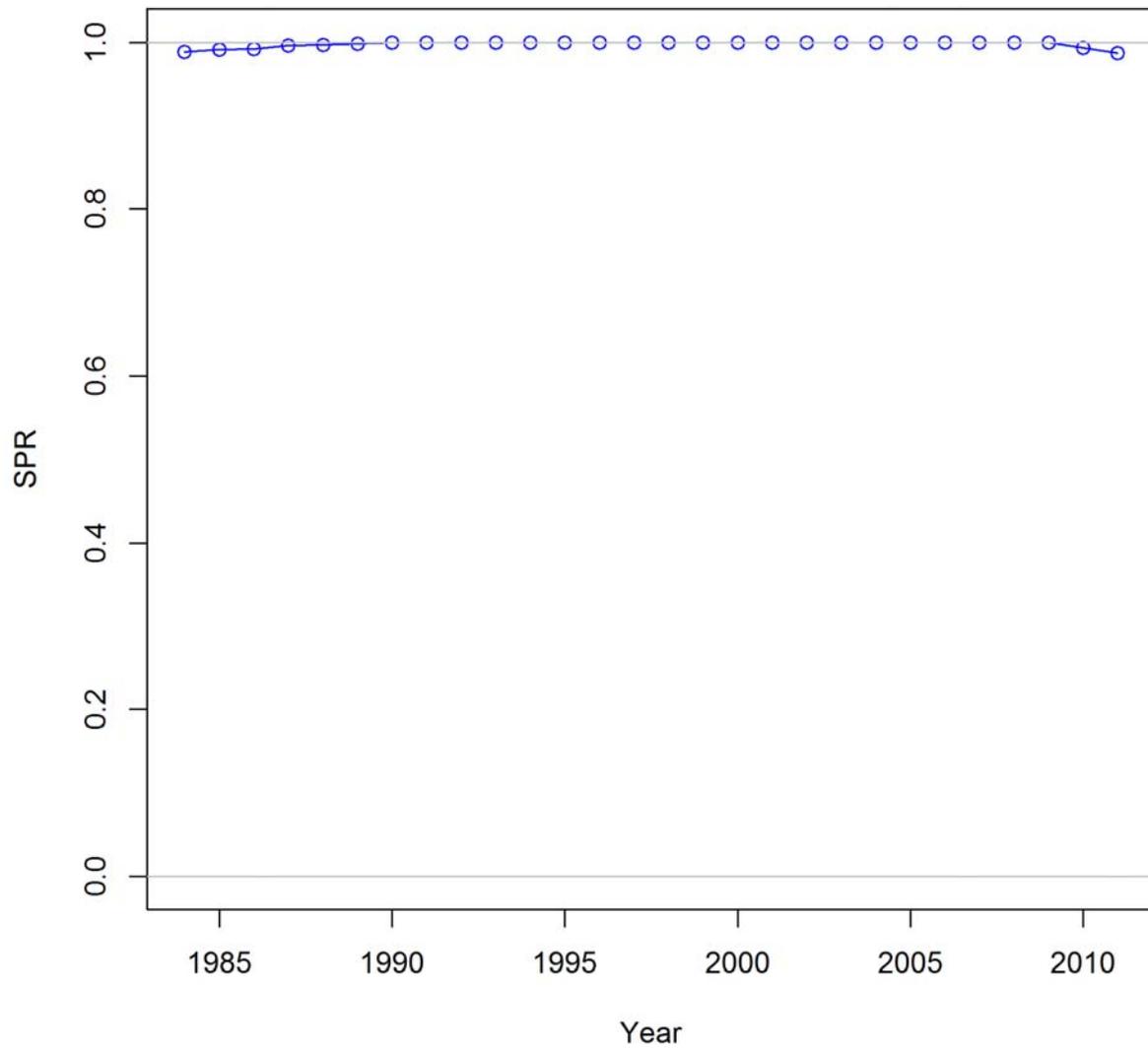


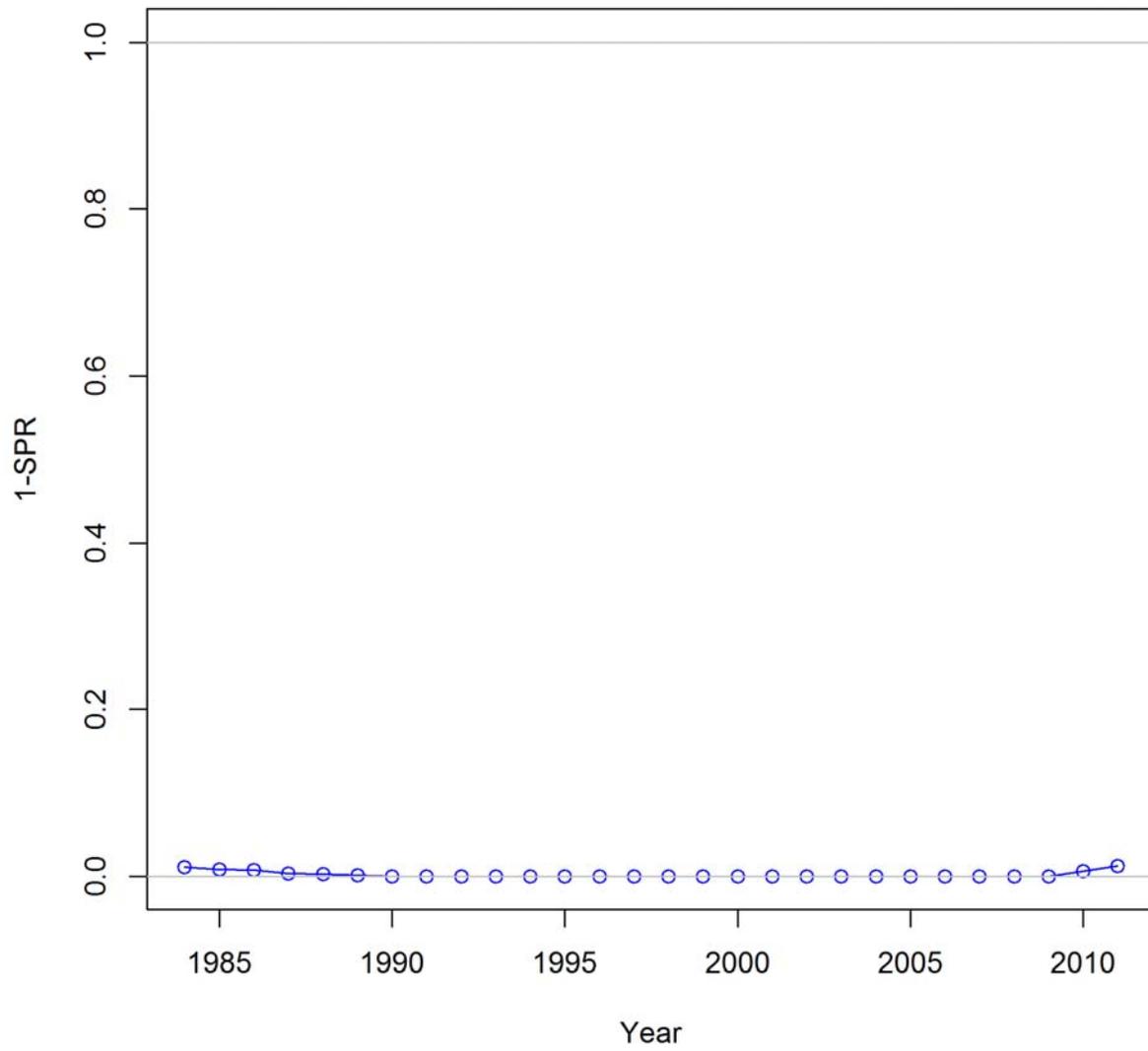
Ending year selectivity and growth for NperTow+mm

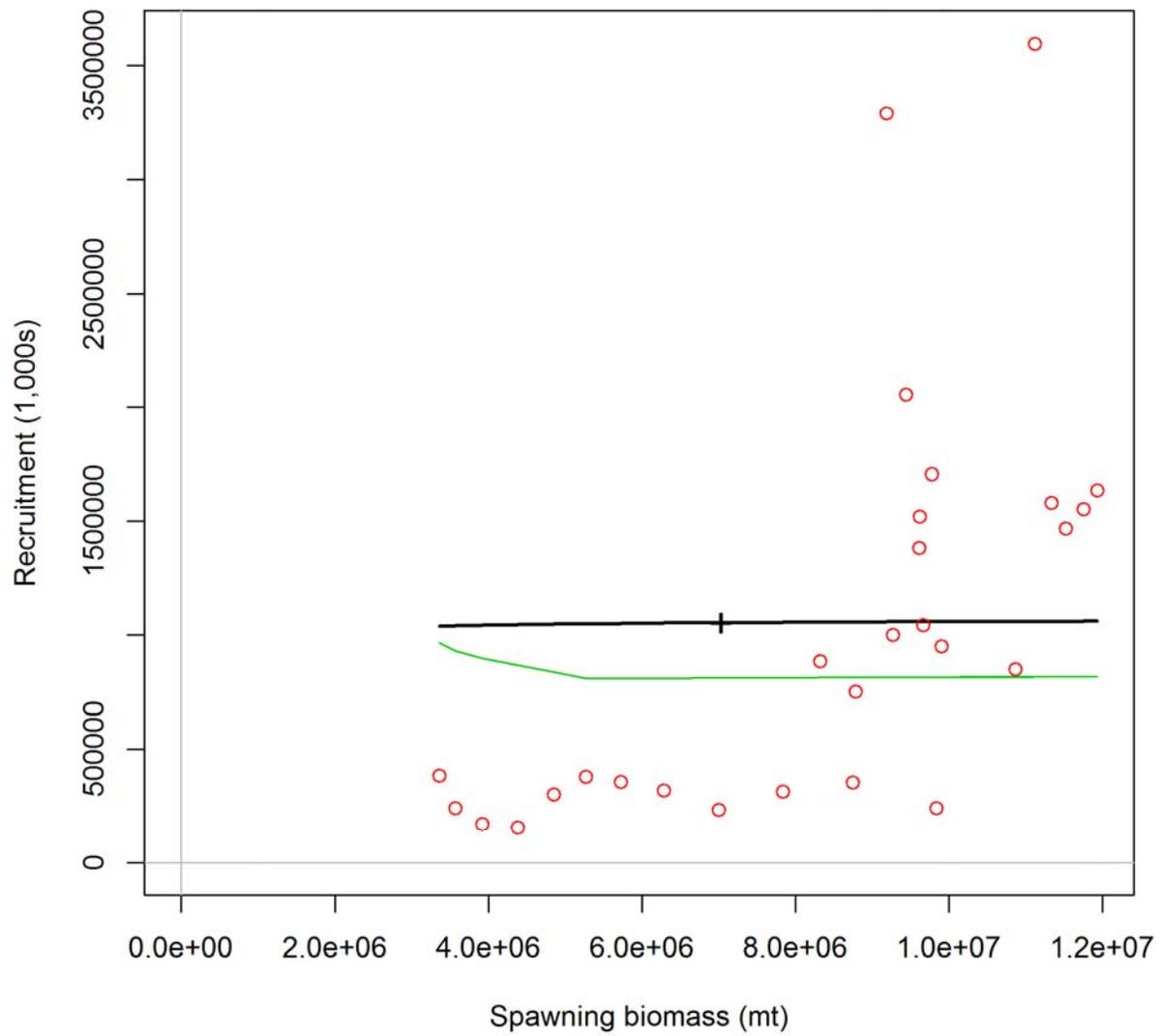


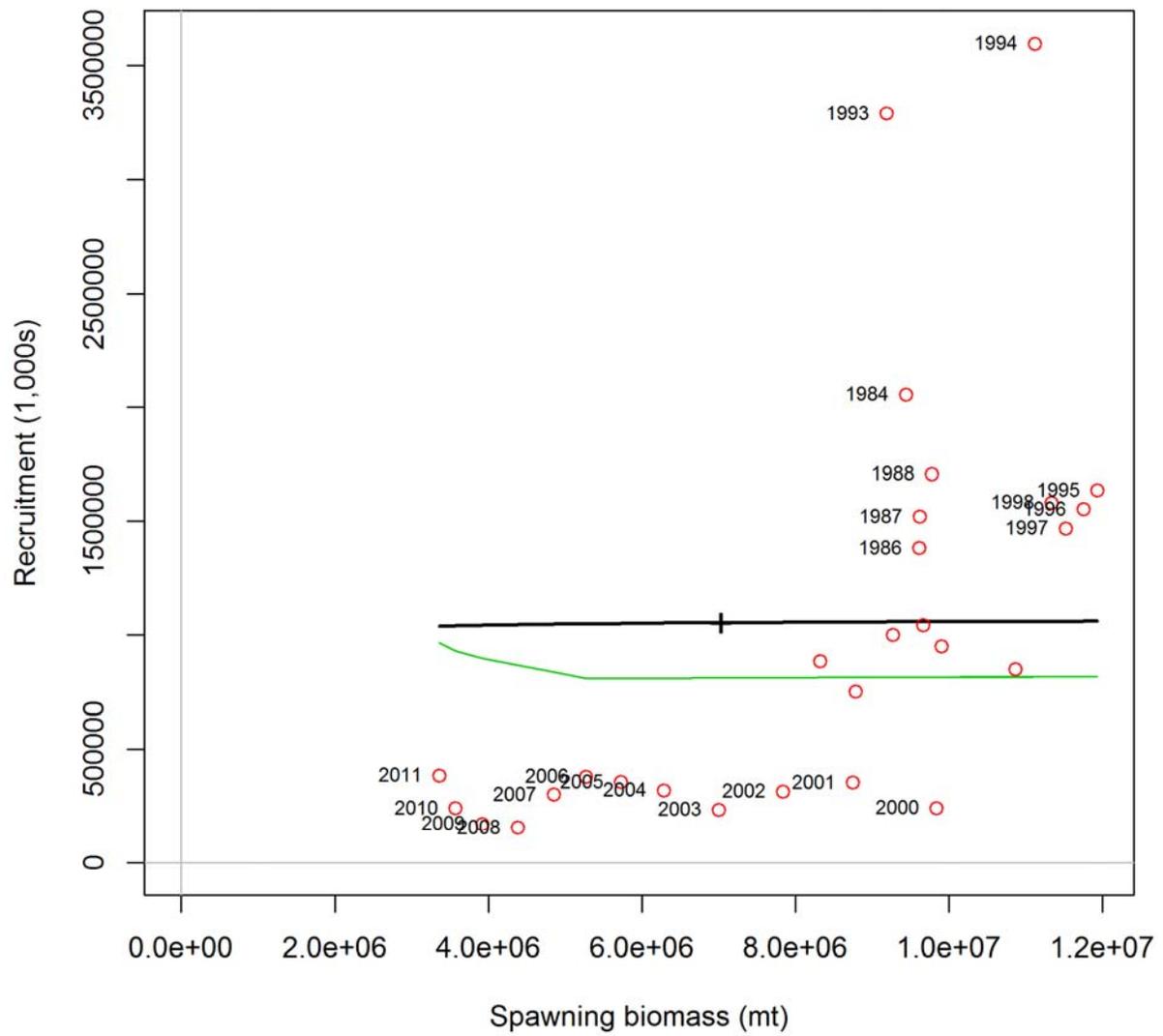
Ending year selectivity and growth for SWAN

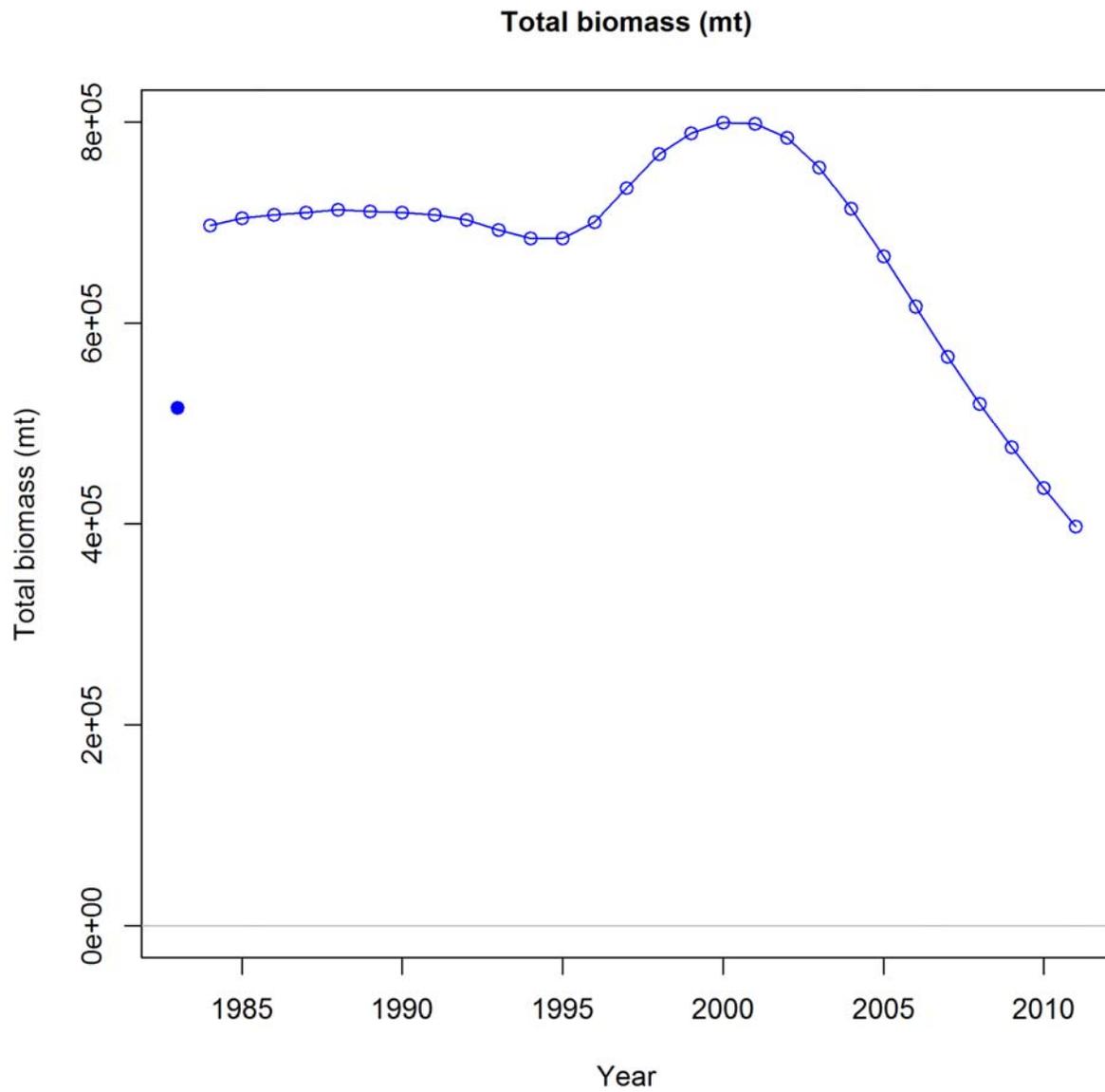




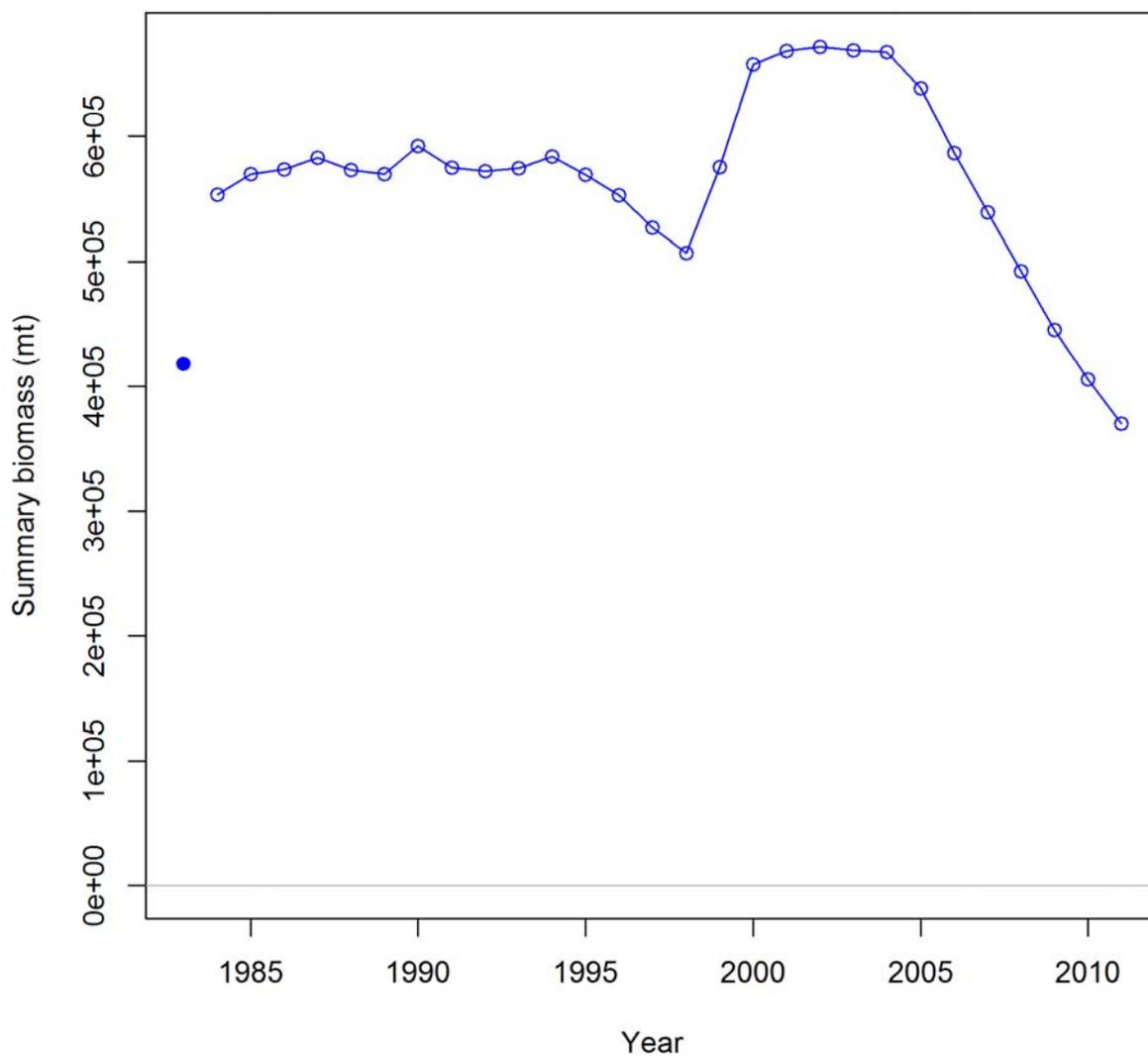




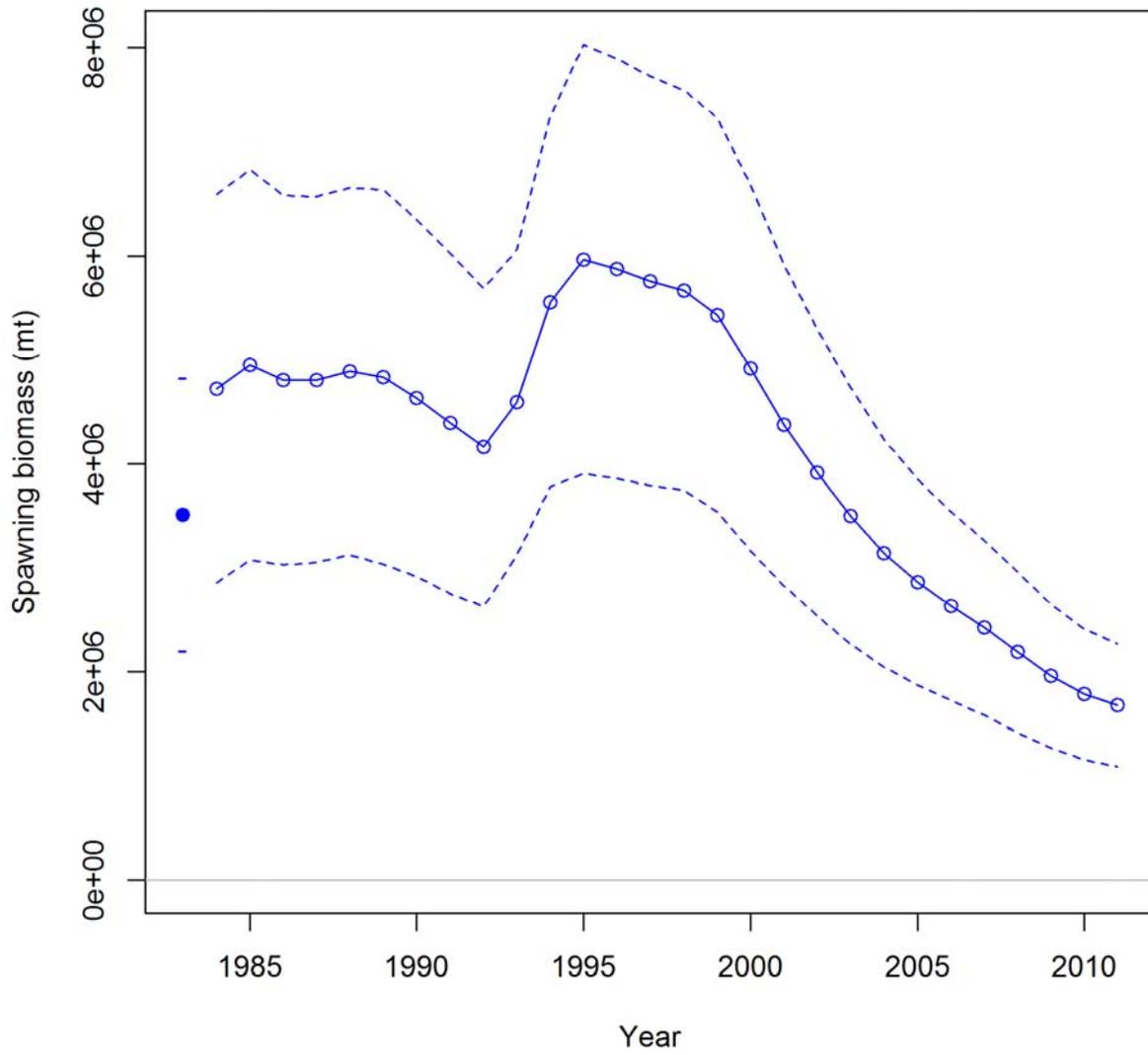




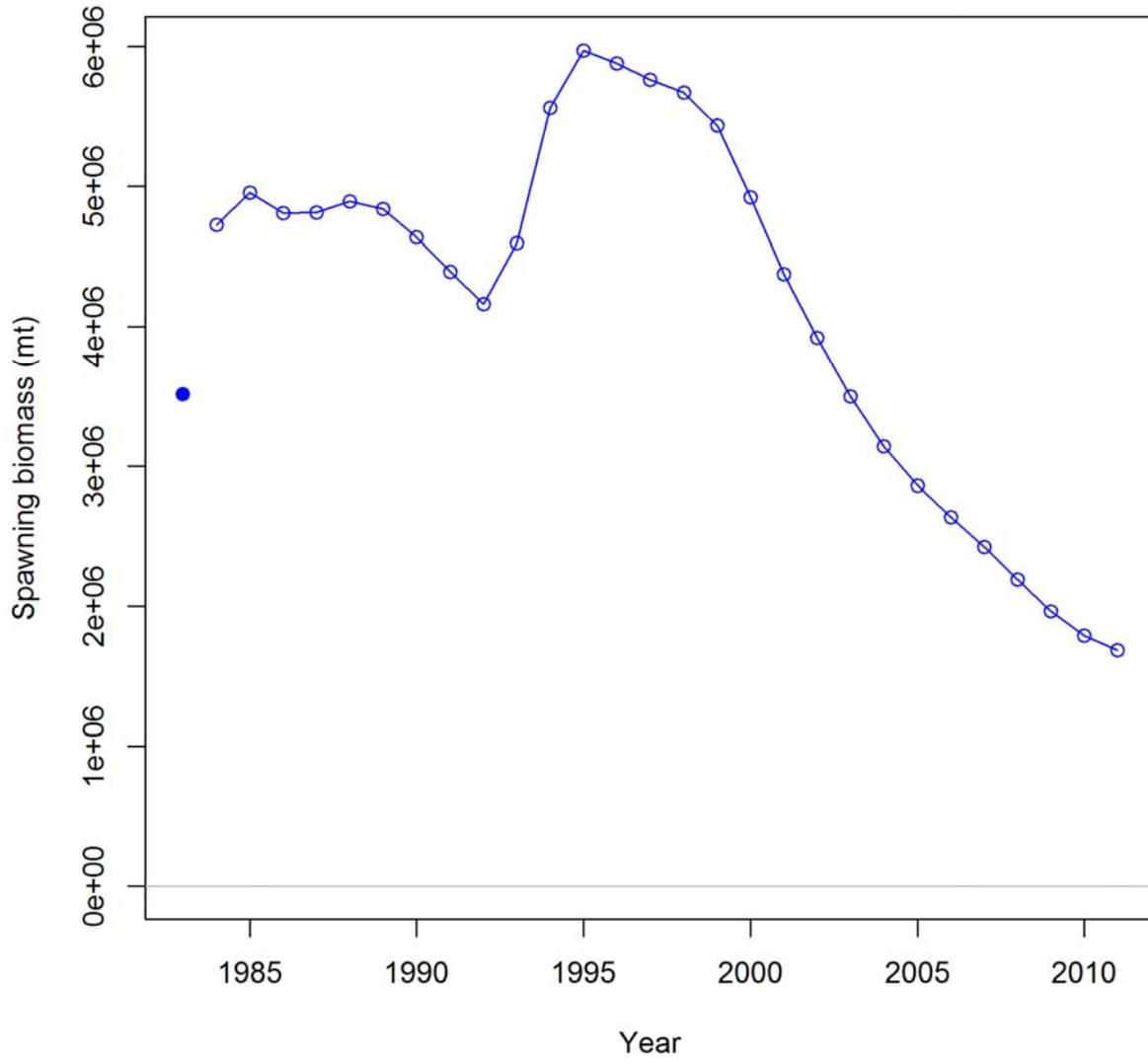
Summary biomass (mt)



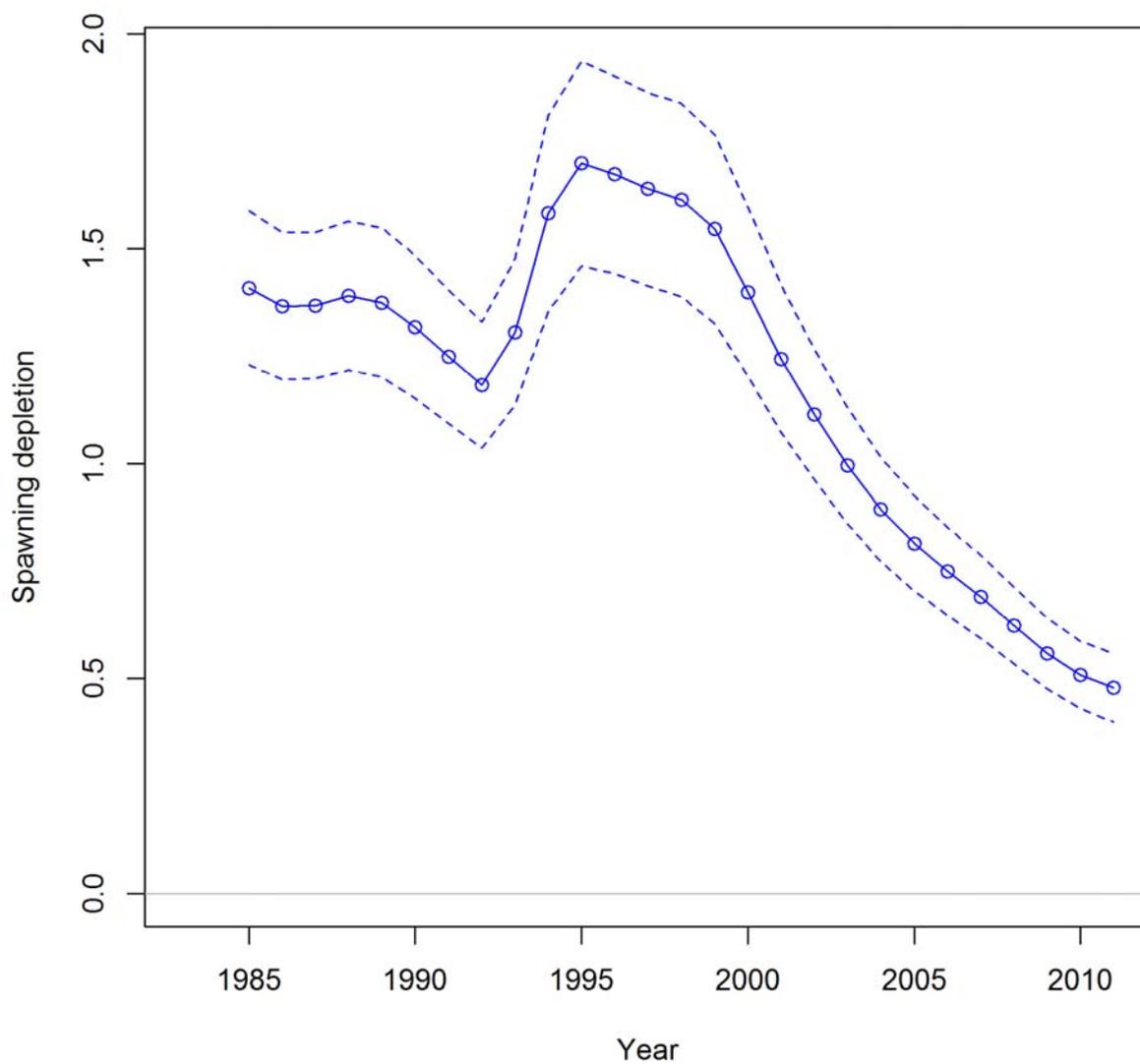
Spawning biomass (mt) with ~95% asymptotic intervals



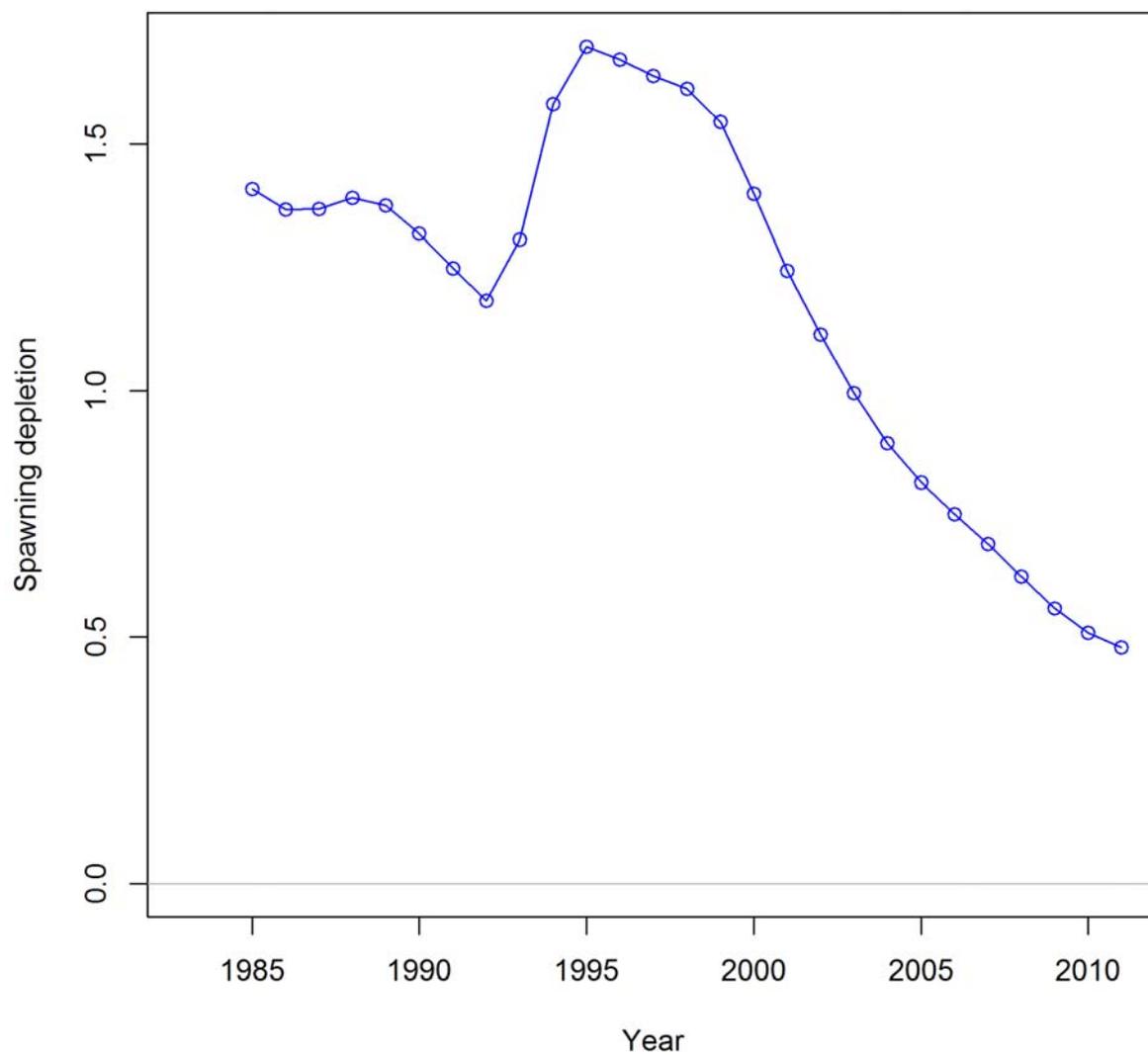
Spawning biomass (mt)



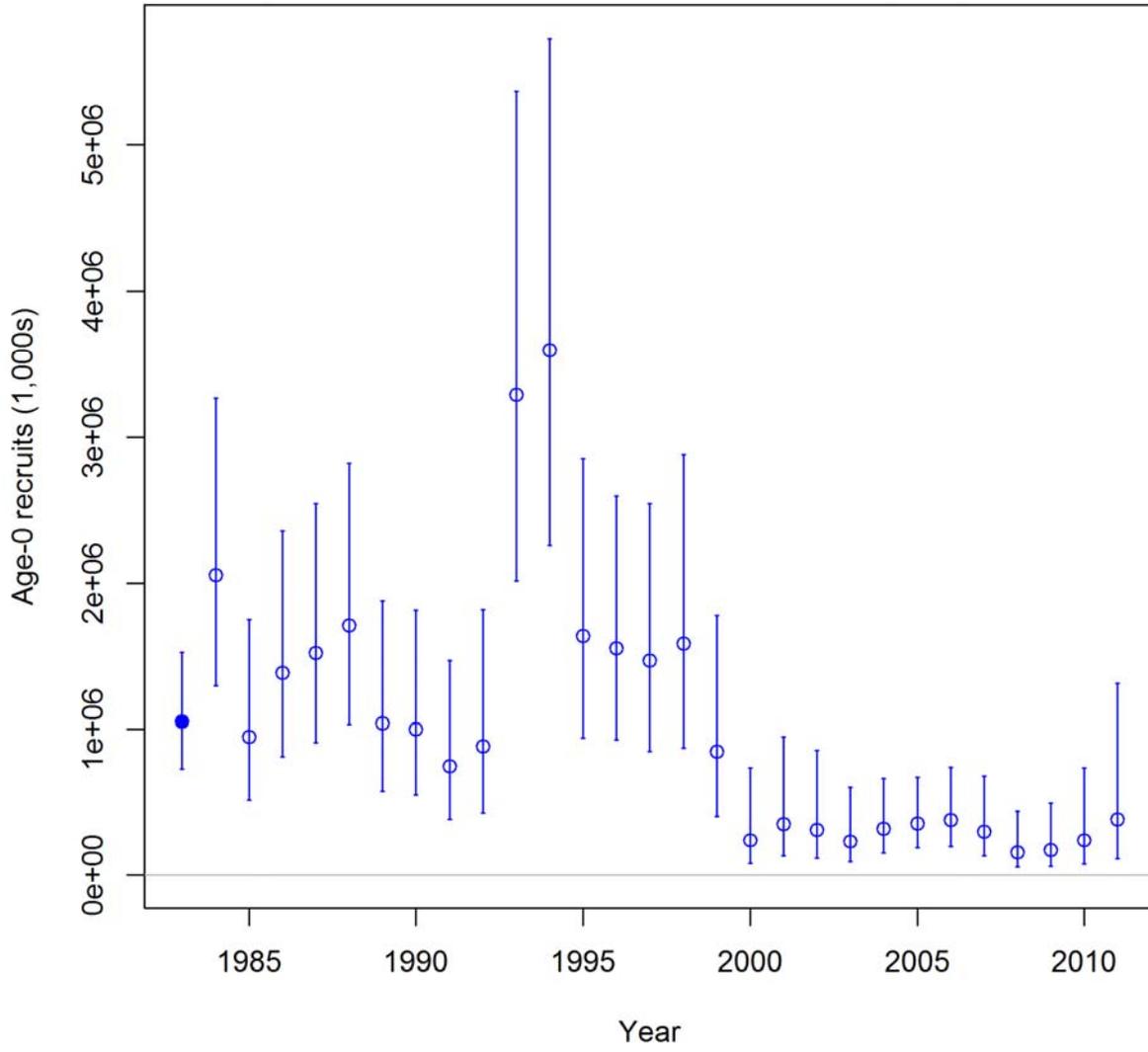
Spawning depletion with ~95% asymptotic intervals



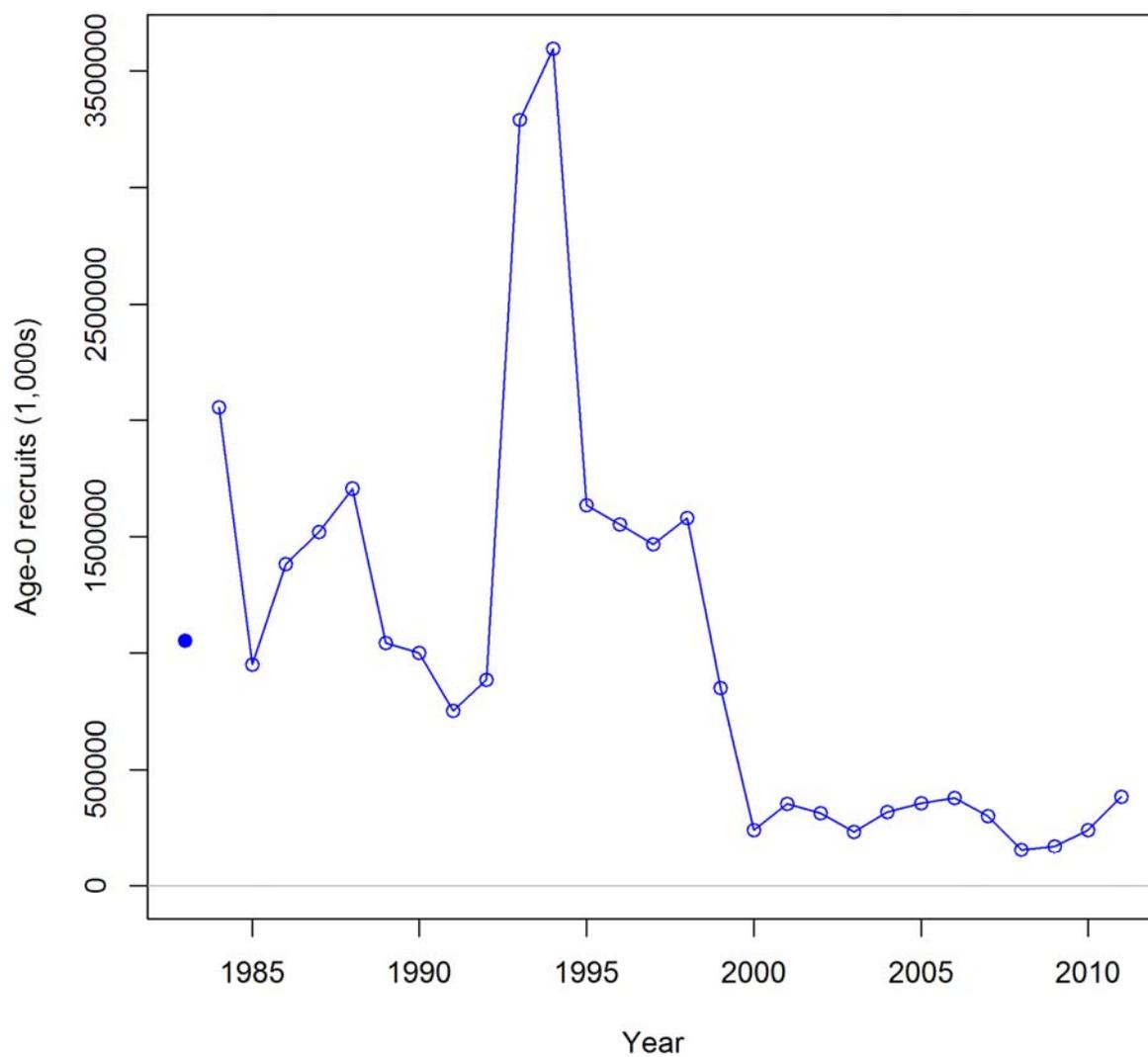
Spawning depletion

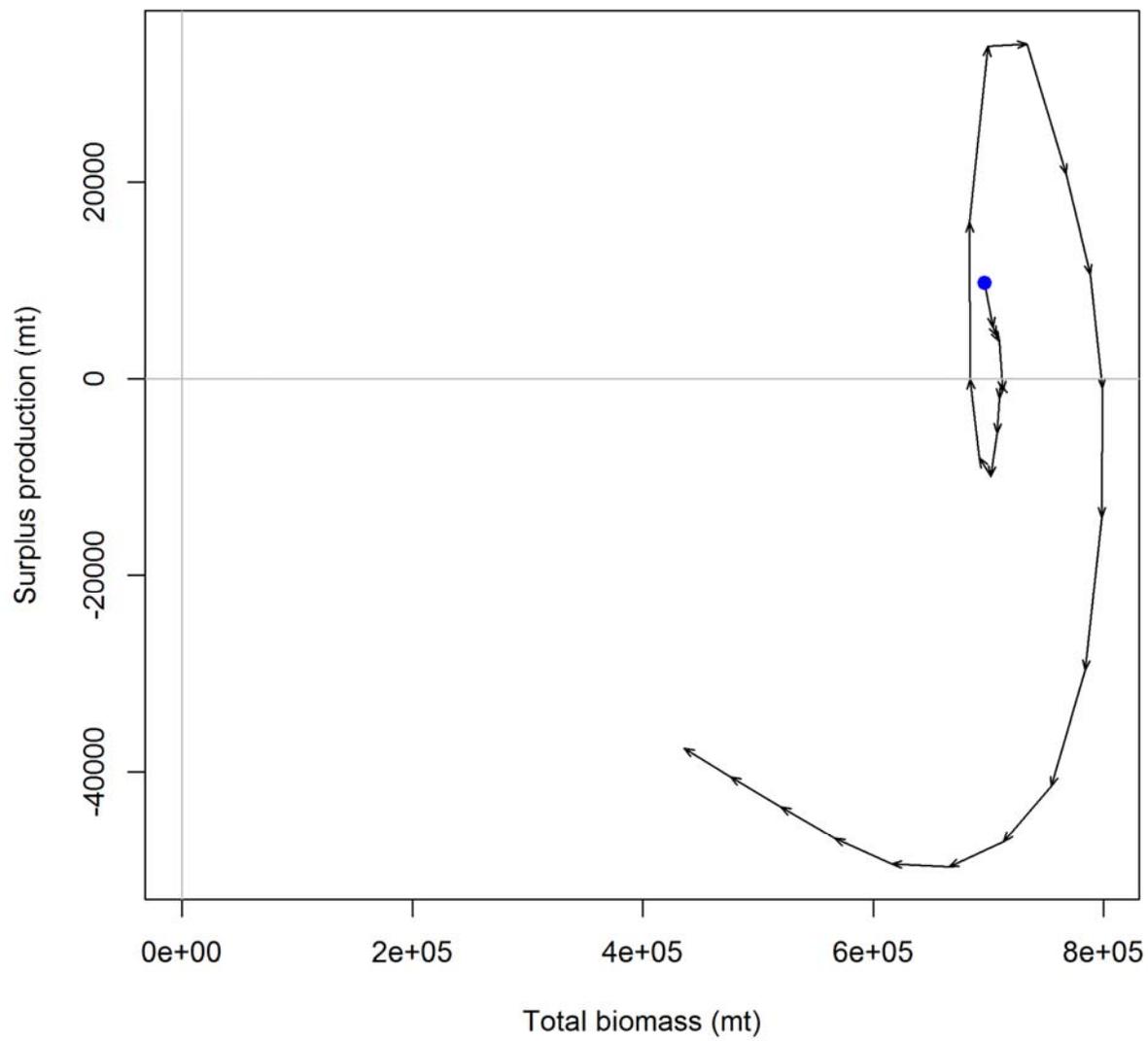


Age-0 recruits (1,000s) with ~95% asymptotic intervals



Age-0 recruits (1,000s)





Appendix A8: Swept area biomass analysis

Efficiency corrected swept-area biomass

Efficiency corrected swept area biomass and catch/biomass fishing mortality estimates have been used in past assessments to provide management advice. Although they no longer serve that purpose, they are still used to estimate scale in KLAMZ modeling.

Efficiency corrected swept area biomass and catch/biomass fishing mortality estimates were calculated with CVs for surfclams during 1997-2011 (years with dredge performance sensors deployed on surveys) on a regional basis, using the methods described in NEFSC (2010) (Table 1-2 and Figures 1-2).

Efficiency corrected swept-area biomass and fishing mortality estimates in this assessment for years prior to 2011 differ from estimates in previous assessments due to: 1) changes after the 2011 survey in the criteria used to judge a “bad” (with poor gear performance) survey tow; 2) the availability of data for 2011 that could be borrowed to help fill “holes” (unsampled strata) in the survey data for 2008; 3) new shell length meat weight relationships; 4) the updated estimate of survey dredge capture efficiency; and 5) use of a new survey dredge selectivity curve to calculate stock biomass.

A historical retrospective analysis was carried out to demonstrate the stability of efficiency corrected swept area biomass estimates. Swept-area biomass and fishing mortality calculations have changed from assessment to assessment as additional survey data accumulated and, mainly, as estimates of survey dredge efficiency were refined (Table 3, Figure 3).

Working group members were interested in seeing the ratio of swept area biomasses by region (Figure 4).

Appendix A8. Table 1. Efficiency corrected swept-area biomass estimates (1000 mt) and CVs for surfclams (120+ mm SL), by region.

	Estimate	CV										
INPUT: Nominal tow distance (dn, nm)	0.15											
INPUT: Dredge width (nm)	0.00082											
Area swept per standard tow (a, nm ²)	0.00012	10%										
Area of assessment region (A, nm²) - no correction for stations with unsuitable clam habitat												
S. Virginia and N. Carolina (SVA)	3,119	10%										
Delmarva (DMV)	4,660	10%										
New Jersey (NJ)	5,078	10%										
Long Island (LI)	2,917	10%										
Southern New England (SNE)	4,321	10%										
Georges Bank (GBK)	5,772	10%										
Total	25,867											
INPUT: Fraction suitable habitat (u)												
S. Virginia and N. Carolina (SVA)	100%	10%										
Delmarva (DMV)	100%	10%										
New Jersey (NJ)	100%	10%										
Long Island (LI)	100%	10%										
Southern New England (SNE)	100%	10%										
Georges Bank (GBK)	88%	10%										
Habitat area in assessment region (A', nm²)												
S. Virginia and N. Carolina (SVA)	3,119	14%										
Delmarva (DMV)	4,660	14%										
New Jersey (NJ)	5,078	14%										
Long Island (LI)	2,917	14%										
Southern New England (SNE)	4,321	14%										
Georges Bank (GBK)	5,079	14%										
INPUT: Biomass fraction in unsurveyed deep water												
S. Virginia and N. Carolina (SVA)	0%	10%										
Delmarva (DMV)	0%	10%										
New Jersey (NJ)	0%	10%										
Long Island (LI)	0%	10%										
Southern New England (SNE)	0%	10%										
Georges Bank (GBK)	0%	10%										
INPUT: Original survey mean catch from fishable stock (kg/tow, for tows adjusted to nominal tow distance using sensors)												
	Estimates	CV	Estimates	CV	Estimates	CV	Estimates	CV	Estimates	CV	Estimates	CV
S. Virginia and N. Carolina (SVA) 120+ mm	0.0230	42%	0.0887	42%	0.4486	59%	0.0000	0%	0.0030	100%	0.0065	100%
Delmarva (DMV) 120+ mm	2.4641	19%	1.3336	18%	2.5392	20%	0.7967	16%	0.4146	34%	0.8732	43%
New Jersey (NJ) 120+ mm	6.3488	11%	4.5417	17%	3.8543	14%	2.3883	11%	3.9031	17%	1.8693	23%
Long Island (LI) 120+ mm	0.3672	66%	0.9268	51%	0.2407	64%	2.2825	36%	0.4535	24%	1.2362	35%
Southern New England (SNE) 120+ mm	1.4769	34%	0.8400	66%	0.6545	24%	0.6508	43%	1.2236	47%	0.2323	27%
Georges Bank (GBK) 120+ mm	2.0151	21%	2.4106	32%	2.2545	43%	3.9404	23%	4.3871	21%	3.8483	25%
Swept-area biomass without efficiency correction (B, 1000 mt):												
S. Virginia and N. Carolina (SVA) 120+ mm	0.5817	47%	2.2433	47%	11.3402	63%	0.0000	20%	0.0753	102%	0.1641	102%
Delmarva (DMV) 120+ mm	93.0714	28%	50.3714	27%	95.9086	28%	30.0930	26%	15.6612	39%	32.9812	47%
New Jersey (NJ) 120+ mm	261.3123	23%	186.9338	26%	158.6390	24%	98.2987	23%	160.6465	26%	76.9379	31%
Long Island (LI) 120+ mm	8.6828	69%	21.9131	55%	5.6915	67%	53.9670	41%	10.7226	32%	29.2277	40%
Southern New England (SNE) 120+ mm	51.7246	39%	29.4211	69%	22.9215	31%	22.7916	47%	42.8541	51%	8.1361	34%
Georges Bank (GBK) 120+ mm	82.9608	29%	99.2444	38%	92.8198	47%	162.2261	31%	180.6177	29%	158.4357	32%
SVA to SNE	415	17%	291	19%	295	16%	205	17%	230	21%	147	21%
Total (including GBK)	498	15%	390	17%	387	17%	367	17%	411	17%	306	19%
INPUT: Survey dredge efficiency (e) from Patch mo												
	0.234	132%	0.234	132%	0.234	132%	0.234	132%	0.234	132%	0.234	132%
Efficiency adjusted swept area fishable biomass (B, 1000 mt)												
S. Virginia and N. Carolina (SVA) 120+ mm	2.486	140%	9.587	140%	48.463	146%	0.000	134%	0.322	167%	0.701	167%
Delmarva (DMV) 120+ mm	398	135%	215	135%	410	135%	129	134%	67	138%	141	140%
New Jersey (NJ) 120+ mm	1,117	134%	799	135%	678	134%	420	134%	687	135%	329	136%
Long Island (LI) 120+ mm	37	149%	94	143%	24	148%	231	138%	46	136%	125	138%
Southern New England (SNE) 120+ mm	221	138%	126	149%	98	136%	97	140%	183	141%	35	136%
Georges Bank (GBK) 120+ mm	355	135%	424	137%	397	140%	693	136%	772	135%	677	136%
SVA to SNE	1,775	133%	1,243	133%	1,259	133%	877	133%	983	134%	630	134%
Total (including GBK)	2,130	133%	1,667	133%	1,655	133%	1,570	133%	1,755	133%	1,307	133%
Lower bound for 80% confidence intervals on fishable biomass (1000 mt, for lognormal distribution with no bias correction)												
	Estimates	Estimates	Estimates	Estimates	Estimates	Estimates						
S. Virginia and N. Carolina (SVA) 120+ mm	0.655	2.526	12.338		0.074	0.160						
Delmarva (DMV) 120+ mm	108	59	111	35	18	37						
New Jersey (NJ) 120+ mm	305	217	185	115	187	89						
Long Island (LI) 120+ mm	9	24	6	61	12	33						
Southern New England (SNE) 120+ mm	59	32	26	26	48	9						
Georges Bank (GBK) 120+ mm	96	114	104	188	209	183						
SVA to SNE	488	341	346	241	269	172						
Total (including GBK)	586	458	455	431	482	358						
Upperbound for 80% confidence intervals on fishable biomass (1000 mt, for lognormal distribution with no bias correction)												
S. Virginia and N. Carolina (SVA) 120+ mm	9.433	36.381	190.363		1.409	3.070						
Delmarva (DMV) 120+ mm	1,464	792	1,509	472	251	535						
New Jersey (NJ) 120+ mm	4,089	2,936	2,485	1,538	2,522	1,215						
Long Island (LI) 120+ mm	148	362	97	866	170	468						
Southern New England (SNE) 120+ mm	827	502	362	370	700	129						
Georges Bank (GBK) 120+ mm	1,308	1,584	1,507	2,562	2,847	2,505						
SVA to SNE	6,461	4,535	4,580	3,192	3,590	2,302						
Total (including GBK)	7,741	6,072	6,026	5,715	6,391	4,769						

Appendix A8. Table 2. Fishing mortality estimates for surfclams based on catch and efficiency corrected swept area biomass estimates.

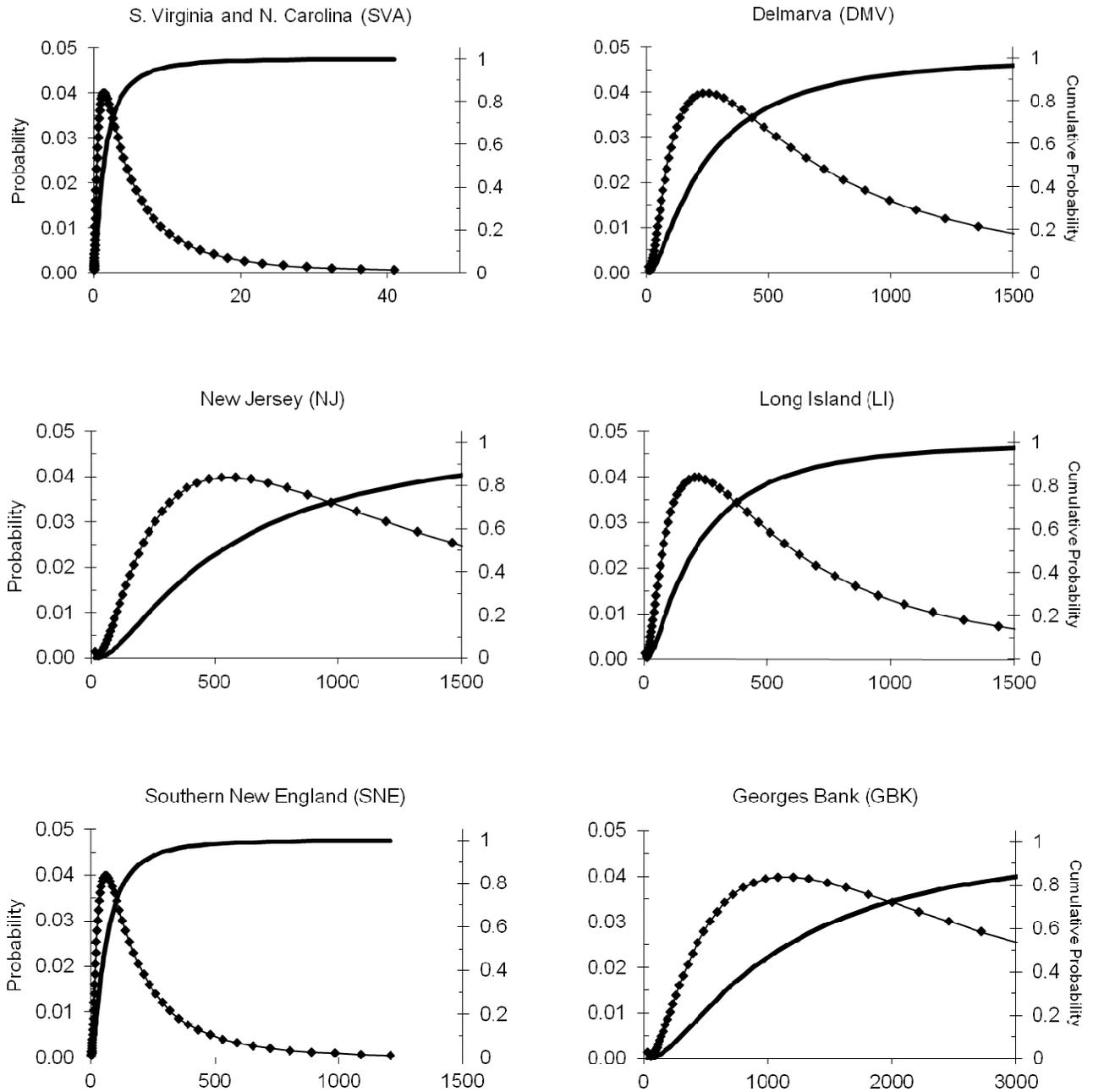
INPUT: Incidental mortality allowance	12%											
INPUT: Assumed CV for catch	10%											
INPUT: Landings (1000 mt, discard - 0)	Estimates for 1997	Estimates for 1999	Estimates for 2002	Estimates for 2005	Estimates for 2008	Estimates for 2011						
S. Virginia and N. Carolina (SVA)	0.000	0.000	0.064	0.000	0.000	0.000						
Delmarva (DMV)	1.540	0.648	4.489	1.668	3.223	1.427						
New Jersey (NJ)	16.998	18.749	18.271	16.850	17.517	11.908						
Long Island (LI)	0.073	0.157	1.130	0.759	1.317	0.437						
Southern New England (SNE)	0.000	0.016	0.052	1.885	0.423	2.420						
Georges Bank (GBK)	0.000	0.000	0.000	0.000	0.000	2.397						
Total	18.611	19.570	24.006	21.163	22.481	18.589						
Catch (1000 mt, landings + upper bound incidental mortality allowance)	Estimates for 1997	Estimates for 1999	Estimates for 2002	Estimates for 2005	Estimates for 2008	Estimates for 2011						
S. Virginia and N. Carolina (SVA)	0.000	0.000	0.072	0.000	0.000	0.000						
Delmarva (DMV)	1.725	0.726	5.028	1.868	3.610	1.598						
New Jersey (NJ)	19.038	20.999	20.463	18.872	19.619	13.337						
Long Island (LI)	0.081	0.176	1.265	0.850	1.475	0.489						
Southern New England (SNE)	0.000	0.018	0.058	2.112	0.474	2.710						
Georges Bank (GBK)	0.000	0.000	0.000	0.000	0.000	2.685						
Total	20.844	21.919	26.886	23.702	25.178	20.820						
INPUT: Efficiency Corrected Swept Area Biomass for Fishable Stock (1000 mt)	Estimates for 1997	CV	Estimates for 1999	CV	Estimates for 2002	CV	Estimates for 2005	CV	Estimates for 2008	CV	Estimates for 2011	CV
S. Virginia and N. Carolina (SVA) 120+ mm	2	140%	10	140%	48	146%	0	134%	0	167%	1	167%
Delmarva (DMV) 120+ mm	398	135%	215	135%	410	135%	129	134%	67	138%	141	140%
New Jersey (NJ) 120+ mm	1,117	134%	799	135%	678	134%	420	134%	687	135%	329	136%
Long Island (LI) 120+ mm	37	149%	94	143%	24	148%	231	138%	46	136%	125	138%
Southern New England (SNE) 120+ mm	221	138%	126	149%	98	136%	97	140%	183	141%	35	136%
Georges Bank (GBK) 120+ mm	355	135%	424	137%	397	140%	693	136%	772	135%	677	136%
SVA to SNE	1,775	133%	1,243	133%	1,259	133%	877	133%	983	134%	630	134%
Total (including GBK)	2,130	133%	1,667	133%	1,655	133%	1,570	133%	1,755	133%	1,307	133%
Fishing mortality (y ⁻¹)												
S. Virginia and N. Carolina (SVA) 120+ mm	0.0000	NA	0.0000	NA	0.0015	146%	0.0000	NA	0.0000	NA	0.0000	NA
Delmarva (DMV) 120+ mm	0.0043	135%	0.0034	135%	0.0123	135%	0.0145	135%	0.0539	138%	0.0113	141%
New Jersey (NJ) 120+ mm	0.0170	134%	0.0263	135%	0.0302	135%	0.0449	134%	0.0286	135%	0.0406	136%
Long Island (LI) 120+ mm	0.0022	149%	0.0019	143%	0.0520	148%	0.0037	139%	0.0322	136%	0.0039	138%
Southern New England (SNE) 120+ mm	0.0000	138%	0.0001	149%	0.0006	136%	0.0217	141%	0.0026	142%	0.0780	137%
Georges Bank (GBK) 120+ mm	0.0000	NA	0.0000	NA	0.0000	NA	0.0000	NA	0.0000	NA	0.0040	136%
SVA to SNE	0.0117	133%	0.0176	134%	0.0214	133%	0.0270	133%	0.0256	134%	0.0400	134%
Total (including GBK)	0.0098	133%	0.0131	134%	0.0162	133%	0.0151	133%	0.0143	134%	0.0193	134%
Lower bound for 80% confidence intervals for fishing mortality (y ⁻¹ , for lognormal distribution with no bias correction)	Estimates for 1997	Estimates for 1999	Estimates for 2002	Estimates for 2005	Estimates for 2008	Estimates for 2011						
S. Virginia and N. Carolina (SVA) 120+ mm	NA	NA	0.0004	NA	NA	NA						
Delmarva (DMV) 120+ mm	0.0012	0.0009	0.0033	0.0039	0.0144	0.0030						
New Jersey (NJ) 120+ mm	0.0046	0.0071	0.0082	0.0122	0.0078	0.0110						
Long Island (LI) 120+ mm	0.0005	0.0005	0.0131	0.0010	0.0087	0.0010						
Southern New England (SNE) 120+ mm	NA	0.0000	0.0002	0.0057	0.0007	0.0210						
Georges Bank (GBK) 120+ mm	NA	NA	NA	NA	NA	0.0011						
SVA to SNE	0.0032	0.0048	0.0059	0.0074	299.3489	0.0070						
Total (including GBK)	0.0027	0.0036	0.0045	0.0041	628.5781	0.0039						
Upper bound for 80% confidence intervals for fishing mortality (y ⁻¹ , for lognormal distribution with no bias correction)	Estimates for 1997	Estimates for 1999	Estimates for 2002	Estimates for 2005	Estimates for 2008	Estimates for 2011						
S. Virginia and N. Carolina (SVA) 120+ mm	NA	NA	0.0059	NA	NA	NA						
Delmarva (DMV) 120+ mm	0.0160	0.0124	0.0453	0.0535	0.2024	0.0091						
New Jersey (NJ) 120+ mm	0.0626	0.0968	0.1109	0.1648	0.1052	0.0458						
Long Island (LI) 120+ mm	0.0088	0.0073	0.2069	0.0139	0.1194	0.0023						
Southern New England (SNE) 120+ mm	NA	0.0006	0.0022	0.0825	0.0099	0.1090						
Georges Bank (GBK) 120+ mm	NA	NA	NA	NA	NA	NA						
SVA to SNE	0.0428	0.0645	0.0779	0.0986	0.0938	0.0447						
Total (including GBK)	0.0357	0.0480	0.0593	0.0551	0.0524	0.0175						

Appendix A8. Table 3. Historical retrospective analysis of efficiency corrected swept area biomass estimates.

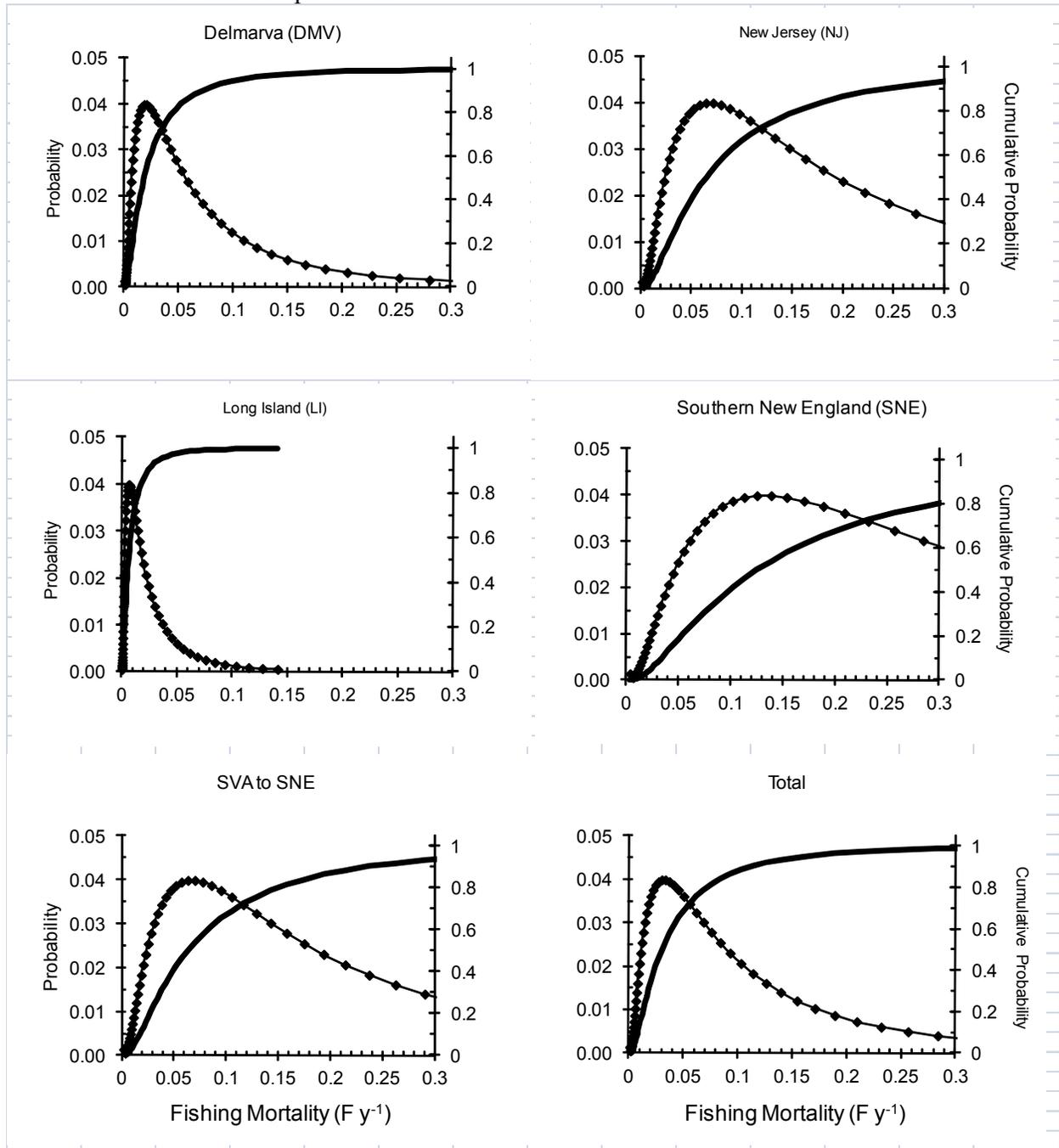
Year	SARC-26 All		SARC-30 All		SARC-37 110+ and 120+		SARC-44 120+ mm		SARC-49 120+ mm		New assessment 120+ mm	
	Biomass (1000 mt)	Survey efficiency (e)	Biomass (1000 mt)	Survey efficiency (e)	Biomass (1000 mt)	Survey efficiency (e)	Biomass (1000 mt)	Survey efficiency (e)	Biomass (1000 mt)	Survey efficiency (e)	Biomass (1000 mt)	Survey efficiency (e)
1997	1,130	0.897	1,106	0.588	1,146	0.460	1,913	0.226	1,276	0.372	2,130	0.234
1999			1,596	0.276	1,460	0.276	1,503	0.226	1,005	0.372	1,667	0.234
2002					803	0.389	1,479	0.226	1,082	0.372	1,655	0.234
2005							1,066	0.226	954	0.256	1,570	0.234
2008									1,038	0.372	1,755	0.256
2011											1,307	0.234

Year	SARC-26 All		SARC-30 All		SARC-37 110+ and 120+		SARC-44 120+ mm		SARC-49 120+ mm		New assessment 120+ mm	
	Fishing mortality	Survey efficiency (e)	Fishing mortality	Survey efficiency (e)	Fishing mortality	Survey efficiency (e)	Fishing mortality	Survey efficiency (e)	Fishing mortality	Survey efficiency (e)	Fishing mortality	Survey efficiency (e)
1997	0.0181	0.897	0.0188	0.588	0.0180	0.460	0.0109	0.226	0.0163	0.372	0.0098	0.234
1999			0.0137	0.276	0.0150	0.276	0.0146	0.226	0.0218	0.372	0.0131	0.234
2002					0.0330	0.389	0.0182	0.226	0.0248	0.372	0.0162	0.234
2005							0.0222	0.226	0.0248	0.372	0.0151	0.234
2008									0.0243	0.372	0.0143	0.234
2011											0.0193	0.234

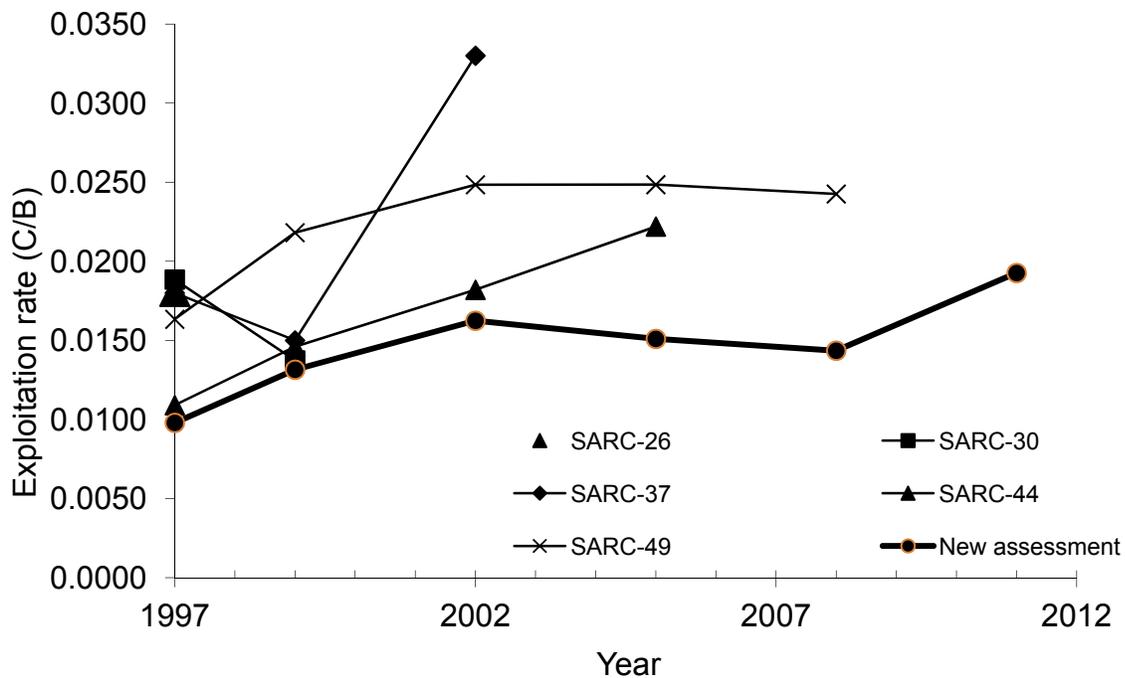
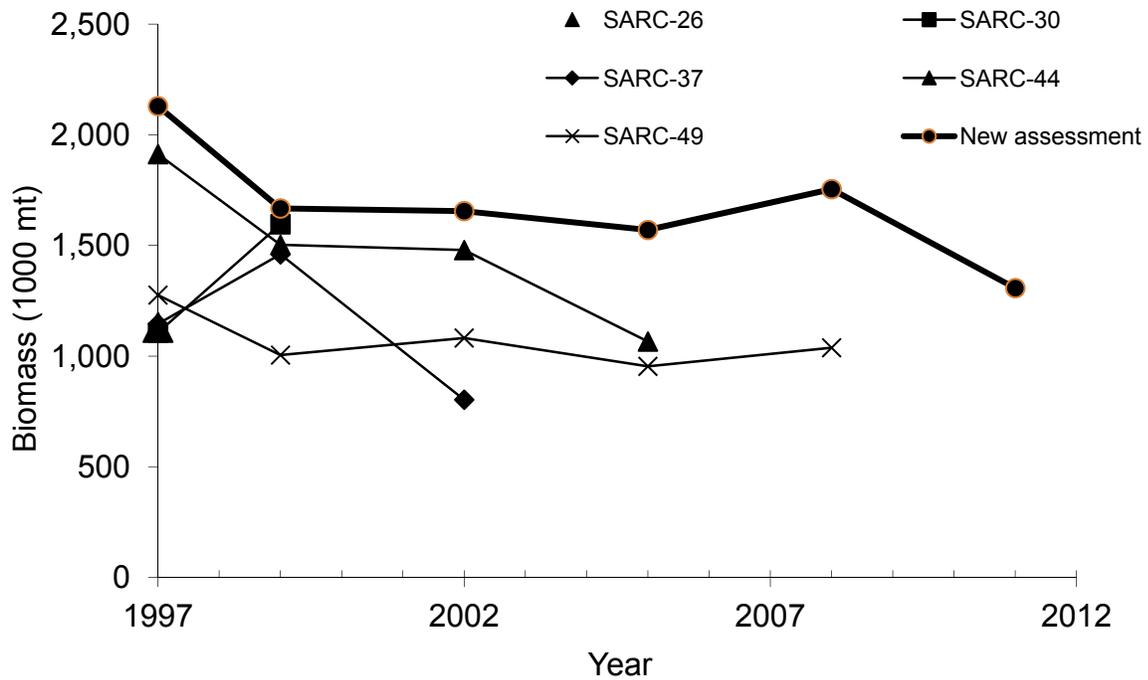
Appendix A8. Figure 1. Uncertainty in efficiency corrected swept area biomass estimates for surfclams in 2011. Note that the x-axis differs in the panel for SVA and GBK but is the same in other panels to facilitate comparisons.



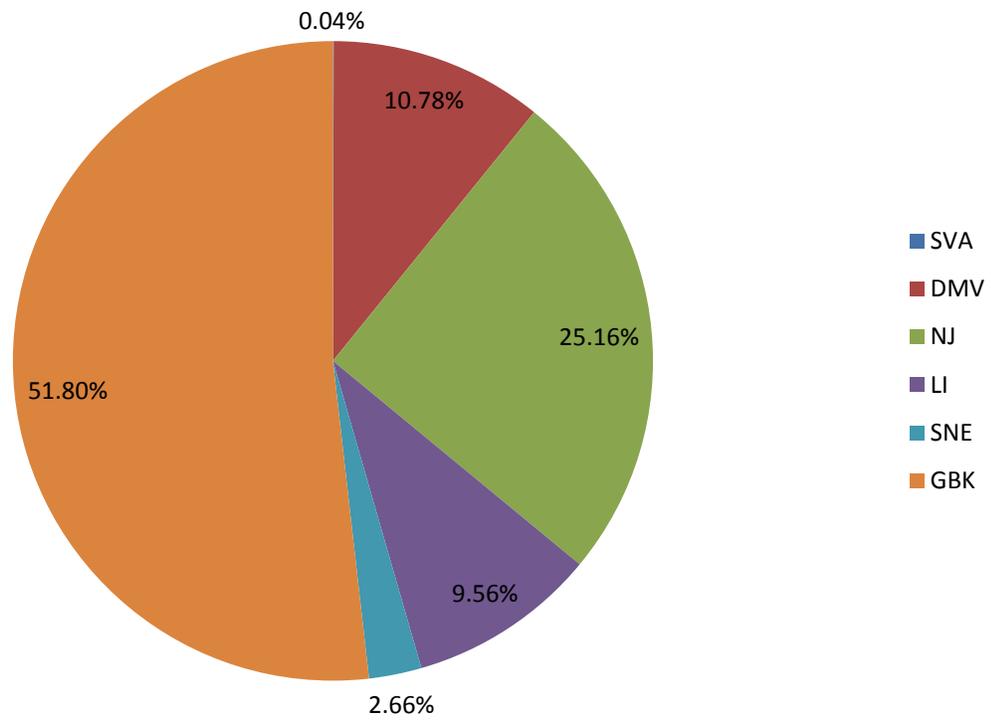
Appendix A8. Figure 2. Uncertainty in fishing mortality estimates for surfclams during 2011 based on catch data and efficiency corrected swept-area biomass. X-axes are scaled to the same maximum to facilitate comparisons.



Appendix A8. Figure 3. Historical retrospective analysis of efficiency corrected swept area biomass and exploitation rate (catch / biomass).



Appendix A8. Figure 4. Percentage of total swept area biomass by region in 2011.



Appendix A9. Additional Sensitivity Testing and Decision Table Analyses

Uncertainty in estimating the scale of biomass has been a challenge in surfclam assessments for many years. We carried out additional sensitivity analyses to determine the likely effects of potential management actions (catch levels) if the biomass scale estimated in the basecase model is substantially too high or too low. The biomass reference points used in this assessment mitigate the scale problem to some degree because the calculation used to determine biomass status $B_{2011}/(B_{1999}/4)$ is robust and does not change appreciably if the overall scale estimated by the assessment model changes, as long as trend can be estimated with relative accuracy and precision. In contrast, the calculation used to determine fishing mortality status $F=M=0.15$ is not robust to scale because it changes in proportion to the overall scale estimated by the assessment model.

In this appendix we estimate the probability of overfishing/overfished status for the entire stock and for the southern component by comparing projections against a wide range of possible biomass scales and catch levels (see TOR 4 and TOR 7 in the main document for the methods used in calculating overfished/overfishing status).

If the true catchability q for the NEFSC clam survey is higher than estimated in the basecase assessment, then the true biomass will be lower than estimated and *vice-versa*. The q estimated in the basecase model was 0.33, which was approximately equal to the 64th percentile of our prior distribution. It is possible that we misestimated q . With this in mind, one of our sensitivity tests assumes that the true q is equal to the 75th percentile of our prior distribution so that true biomass levels are substantially lower than estimated in the basecase model. Other sensitivity analyses assume that the true q is equal to the 25th percentile of our prior distribution so that the true biomass level is much higher than estimated in the basecase model. These values of q produce a wide range of biomass estimates (Table A9.1). The two sensitivity runs are hereafter referred to as “high q ” and “low q ” and will be compared to the actual assessment runs called “basecase”.

In projection scenarios we used the estimated q (0.33 = basecase) to calculate reference points. The population variables (biomass and F) estimated in the high q and low q model runs were compared to the basecase reference point to determine the status of the population. This scenario demonstrates the possible outcomes of a situation in which the assessment was incorrect regarding scale, and the true scale of the biomass is considerably higher or lower than we believe. We tested several catch levels in projection scenarios, described in the main body of the report. In order of increasing catch they are: status quo, quota and OFL (see TOR 7 and Table A9.2). These catch levels were prorated between the southern area where most fishing occurs and GBK as described in the main body of the report (TOR 7). Separate simulations were run for the southern area and GBK and the results each pair of simulations were combined to evaluate effects on the entire stock.

Because a high q results in a lower biomass, high q is more likely to result in an overfished/overfishing status determination. The scenario in which an overfished/overfishing designation was most likely to occur was when the population was fished at the OFL level, particularly when true biomass was lower than estimated using our basecase model (Figure A9.3). Under the high q -low biomass state of nature, the cumulative probability of overfished status during any of the years from 2013 – 2017 was unlikely (probability < 10%) using the status quo or quota catch levels, but was relatively likely (45%) when using the OFL catch scenario (Table A9.3). Fishing at the OFL level is not currently allowed under the surfclam FMP.

The probability of overfishing at any point during the years 2013-2017 was essentially zero (Figure A9.4) at any level of q , unless the catch was set at the OFL, when overfishing was almost inevitable in simulations.

In the low q scenario, the population was unlikely to be overfished or have overfishing occur at any point over the next five years (Table A9.3; Figure A9.5 – A9.8).

For the southern area only and high q state, the true biomass in 2011 tended to stay above the threshold (Figure A9.9). In the high q state, the annual fishing mortality trajectory fell below the F threshold, except in $F=OFL$ scenario (Figure A9.10).

Reference points are defined for the whole stock but the maximum annual probability of a hypothetical overfished condition for the southern area using the hypothetical reference point $B_{\text{threshold}}=B_{1999}/4$ for the south in any year between 2013 and 2017 was generally less than 5% except in the $F=OFL$ scenario, where it rose to about 17% (Figure A9.11). The cumulative probability of overfished status over that time period varies from 14% to 42% (Table A9.4; Figure A9.12). Overfished status was unlikely under all fishing scenarios when testing the low q state (Figures A9.13 and A9.15; Table A9.4).

The maximum annual probability of hypothetical overfishing the southern area over the years from 2013 to 2017 was zero regardless of the q used, unless fishing was set to the OFL (Figures A9.14 and A9.16; Table A9.4).

Overfished status determinations for the northern (GBK) area are not possible at this time due to a lack of reference points. The likely trajectory of the population biomass given the various states of q and fishing scenarios is available in Table (A9.2) and Figures (A9.17 – A9.18).

Overfishing the northern area is unlikely (cumulative probability through 2017 < 1%), except where fishing is set to the OFL (Figures A9.19 – A9.22; Table A9.5).

Potential effects on biomass were summarized using an additional method. We also present results based on the probability that the stock would fall below the “true” (based on the q being tested) value of $B_{1999}/4$ (Table A9.6). In this case the each state of nature (or q level) would have a unique reference point. In contrast, the method used in all other analyses summarizes results based on the probability that the stock falls below the $B_{1999}/4$ biomass level estimated in the basecase assessment, so that each q level is tested against the same reference point.

These sensitivities demonstrate that conclusions about the probability of overfishing or overfished stock status during 2011-2018 using the basecase model would likely not change under a wide range of true biomass levels and catches at the status-quo or quota levels. However, overfishing and overfished conditions are likely at the OFL which is currently not permitted in the FMP.

Table A9.1. Biomass in 2011 given the basecase and 2 sensitivity scenarios used as states of nature in decision table analysis, one in which the biomass was underestimated in the base case (low q) and one in which the biomass was overestimated (high q).

Region	$q=0.11$	$q=0.33$ Basecase	$q=0.39$
South	2,399,830	704,366	600,320
North	1,118,680	370,217	312,684
Total	3,518,510	1,074,583	913,004

Table A9.2. Biomass in projections given different sensitivity scenarios involving a range of true states of nature (biomass level) and possible management actions (catch levels).

Year	State of nature: <i>q</i> low (B high)								
	Status-quo			Quota			F=0.15		
	South	North	Total	South	North	Total	South	North	Total
2011	2,399,830	1,118,680	3,518,510	2,399,830	1,118,680	3,518,510	2,399,830	1,118,680	3,518,510
2012	2,379,060	1,027,710	3,406,770	2,379,060	1,027,710	3,406,770	2,379,060	1,027,710	3,406,770
2013	2,350,010	939,531	3,289,541	2,350,010	939,531	3,289,541	2,350,010	939,531	3,289,541
2014	2,294,130	840,714	3,134,844	2,288,940	840,714	3,129,654	2,247,970	822,088	3,070,058
2015	2,298,590	753,353	3,051,943	2,288,690	753,353	3,042,043	2,213,700	722,861	2,936,561
2016	2,382,780	683,152	3,065,932	2,368,600	683,152	3,051,752	2,264,670	645,876	2,910,546
2017	2,322,830	637,951	2,960,781	2,305,000	637,951	2,942,951	2,177,370	597,389	2,774,759
2018	2,400,280	668,168	3,068,448	2,379,180	668,168	3,047,348	2,230,390	626,192	2,856,582
2019	2,488,280	710,556	3,198,836	2,464,300	710,556	3,174,856	2,296,280	667,943	2,964,223
2020	2,574,860	756,680	3,331,540	2,548,360	756,680	3,305,040	2,362,280	713,381	3,075,661
2021	2,657,440	803,286	3,460,726	2,628,730	803,286	3,432,016	2,425,390	758,827	3,184,217

Year	State of nature: <i>q</i> high (B low)								
	Status-quo			Quota			F=0.15		
	South	North	Total	South	North	Total	South	North	Total
2011	600,320	312,684	913,004	600,320	312,684	913,004	600,320	312,684	913,004
2012	595,561	285,915	881,476	595,561	285,915	881,476	595,561	285,915	881,476
2013	587,428	260,080	847,508	587,428	260,080	847,508	587,428	260,080	847,508
2014	576,571	227,784	804,355	571,561	227,784	799,345	532,181	209,198	741,379
2015	584,775	199,284	784,059	575,246	199,284	774,530	503,376	168,882	672,258
2016	626,825	176,141	802,966	613,143	176,141	789,284	513,398	139,021	652,419
2017	625,105	160,555	785,660	607,876	160,555	768,431	485,513	120,271	605,784
2018	659,520	166,515	826,035	639,107	166,515	805,622	496,442	124,930	621,372
2019	697,259	176,256	873,515	674,032	176,256	850,288	512,770	134,134	646,904
2020	733,435	187,321	920,756	707,722	187,321	895,043	528,862	144,568	673,430
2021	767,295	198,728	966,023	739,385	198,728	938,113	543,581	154,801	698,382

Table A9.3. Decision table for the whole surfclam stock, showing cumulative probability of overfished/overfishing status in any of the 5 years during 2013-2017, using 3 three different catch scenarios and assuming three states of nature (high, basecase and low biomass levels)

Whole stock overfished status probability

Catch	Low q (high B)	Basecase	High q (low B)
Status quo	0.001	0.019	0.082
Quota	0.001	0.022	0.098
OFL	0.002	0.122	0.448

Whole stock overfishing probability

Catch	Low q (high B)	Basecase	High q (low B)
Status quo	0	0	0
Quota	0	0	0.001
OFL	0	0.99	1

Table A9.4. Decision table for the southern area, showing cumulative probability of overfished/overfishing status in any of the 5 years from 2013-2017, using 3 three different catch scenarios and assuming three states of nature (high, basecase and low biomass levels).

Southern area overfished status probability

Catch	Low q (high B)	Basecase	High q (low B)
Status quo	0	0.053	0.136
Quota	0	0.061	0.156
OFL	0	0.163	0.42

Southern area overfishing probability

Catch	Low q (high B)	Basecase	High q (low B)
Status quo	0	0	0
Quota	0	0	0
OFL	0	0.99	1

Table A9.5. Decision table for the northern area, showing cumulative probability of overfished/overfishing status in any of the 5 years from 2013-2017, using 3 three different catch scenarios and assuming three states of nature (high, basecase and low biomass levels).

Northern area overfishing probability

Catch	Low q (high B)	Basecase	High q (low B)
Status quo	0	0	0.002
Quota	0	0	0.003
OFL	0	0.99	1

Table A9.6. Decision table for the whole stock and southern area, showing cumulative probability of overfished/overfishing status in any of the 5 years from 2013-2017, using 3 three different catch scenarios, and assuming three states of nature (high, basecase and low biomass levels). In this case the biomass reference point is derived from each assessment outcome (i.e. in the low q outcome, the reference point $B_{1999}/4$ is based on the low q biomass in 1999).

Whole stock overfished status probability

Catch	Low q (high B)	Basecase	High q (low B)
Status quo	0.001	0.019	0.004
Quota	0.001	0.022	0.006
OFL	0.002	0.122	0.118

Southern area overfished status probability

Catch	Low q (high B)	Basecase	High q (low B)
Status quo	0.003	0.053	0.027
Quota	0.004	0.061	0.032
OFL	0.006	0.163	0.139

Figure A9.1 Biomass results for projections with the high q (low biomass) scenario in which true whole stock biomass was substantially lower than estimated in the basecase model. The biomass reference point is from the basecase model.

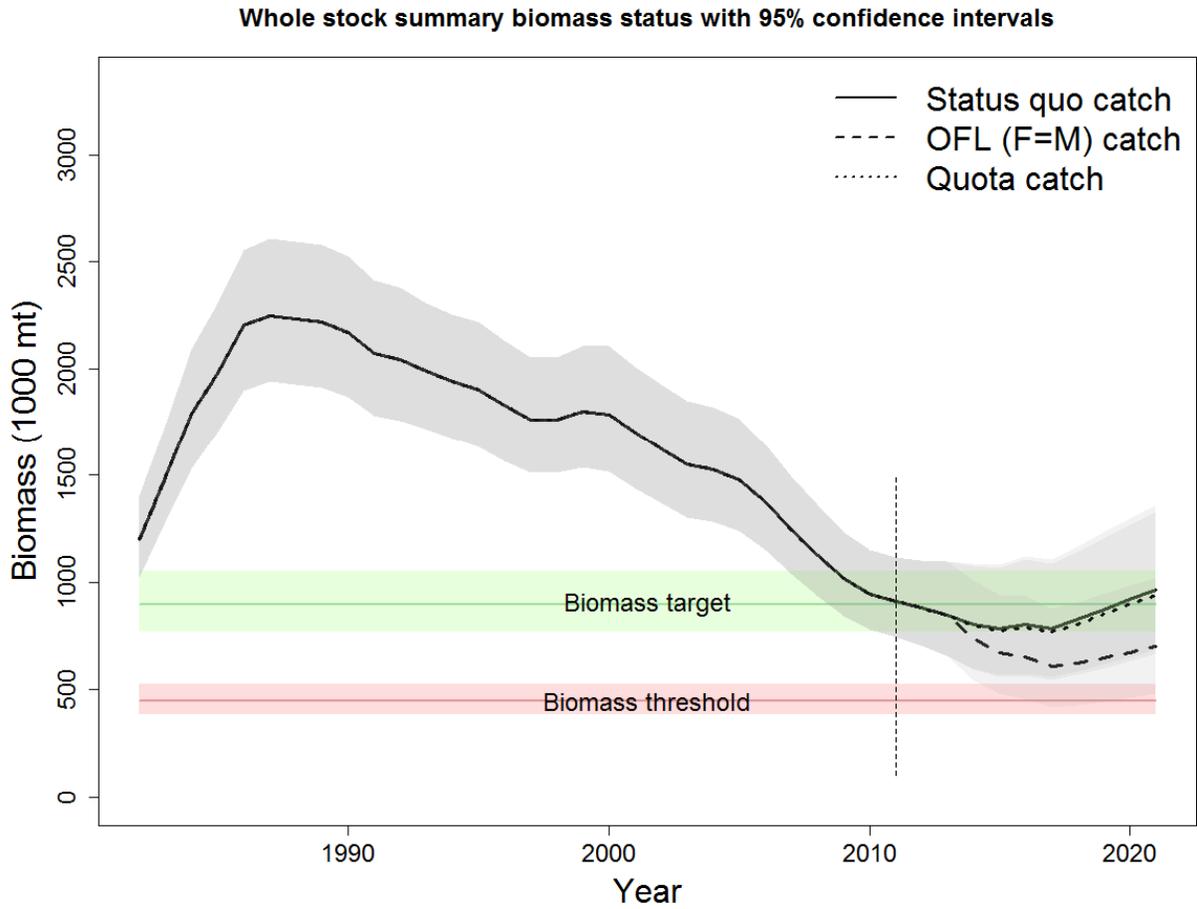


Figure A9.2. Fishing mortality results for projections with the high q (low biomass) scenario in which true whole stock biomass was substantially lower than estimated in the basecase model.

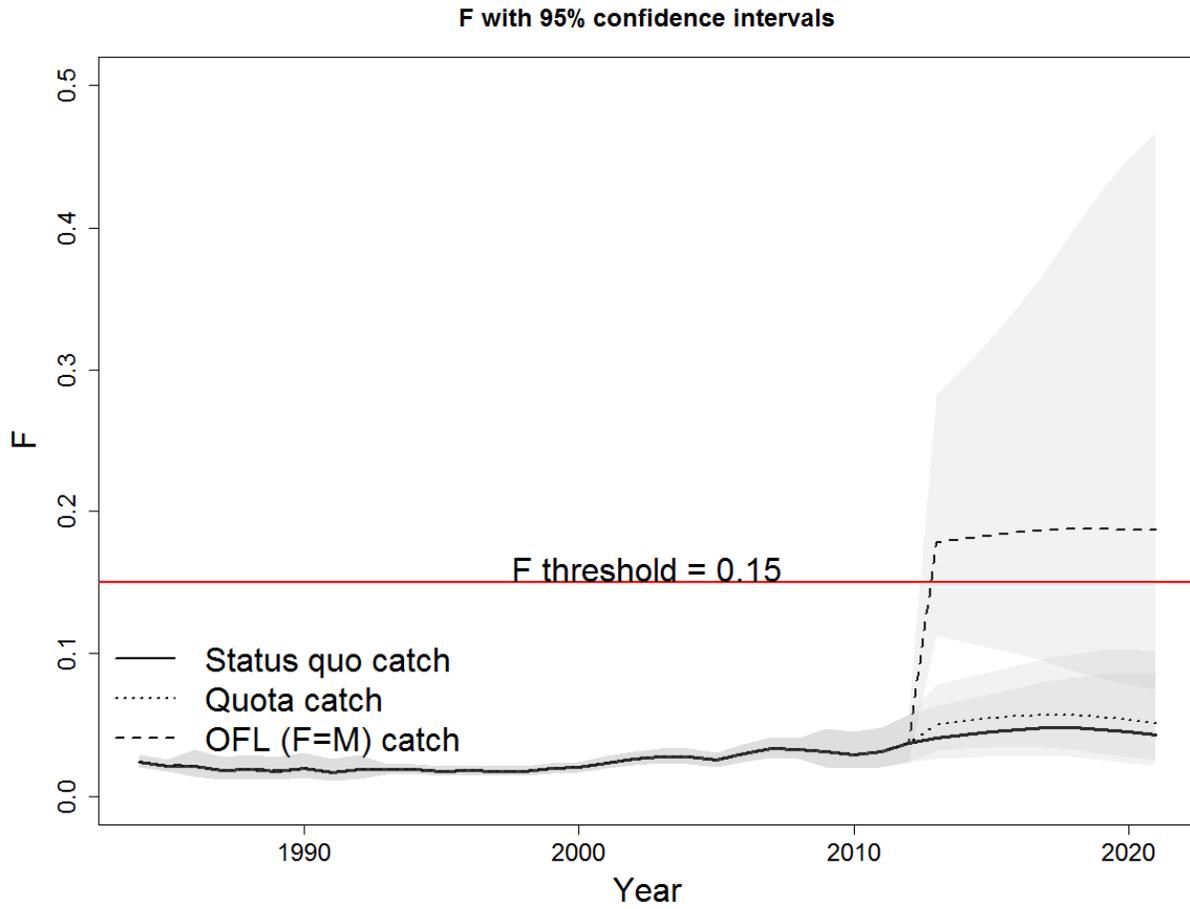


Figure A9.3. Biomass results for projections with the high q (low biomass) scenario in which whole stock biomass was substantially lower than estimated in the basecase model. Probabilities are for overfished stock status occurring given the minimum biomass projected between 2013-2017. The biomass reference point is from the basecase model.

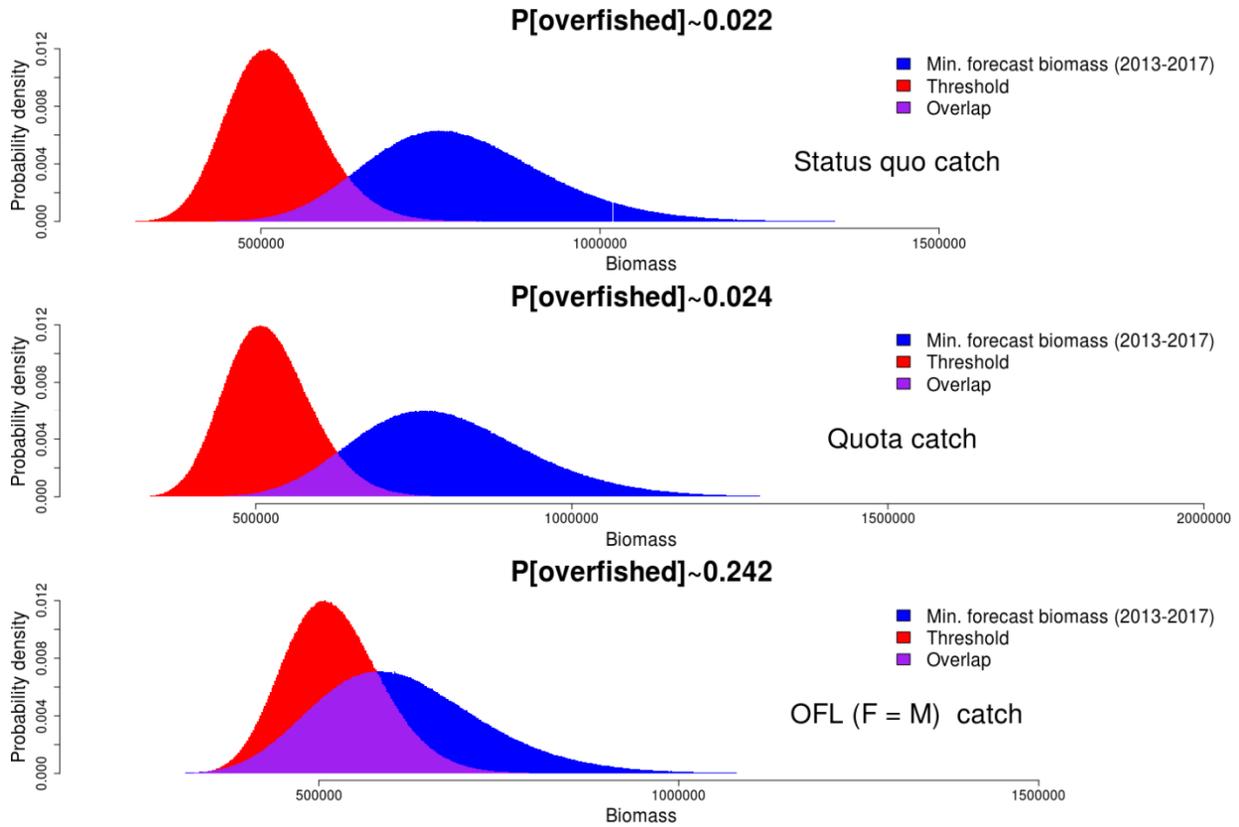


Figure A9.4. Fishing mortality results for projections with the high q (low biomass) scenario in which whole stock biomass was substantially lower than estimated in the basecase model. Probabilities are for overfishing occurring given the minimum biomass projected between 2013-2017.

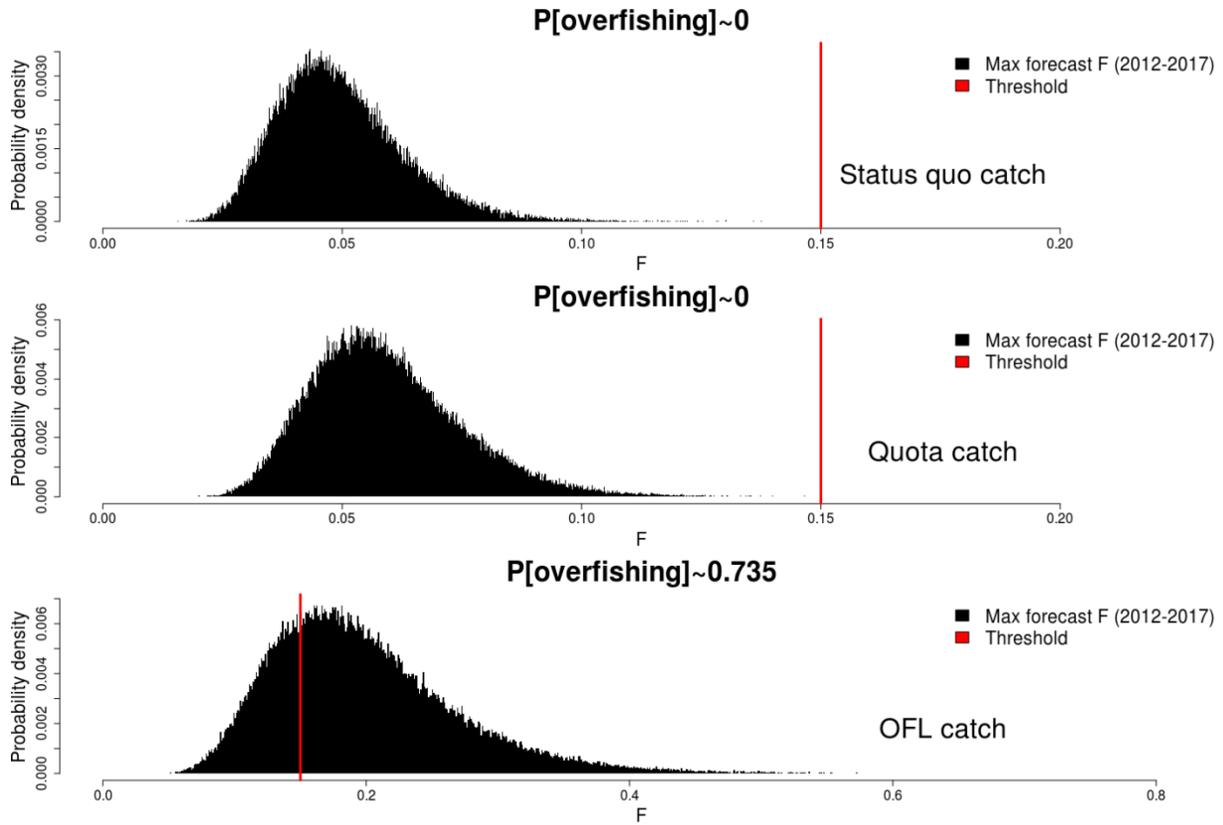


Figure A9.5. Biomass results for projections with the high q (low biomass) scenario in which true whole stock biomass was substantially larger than estimated in the basecase model. The biomass reference point is from the basecase model.

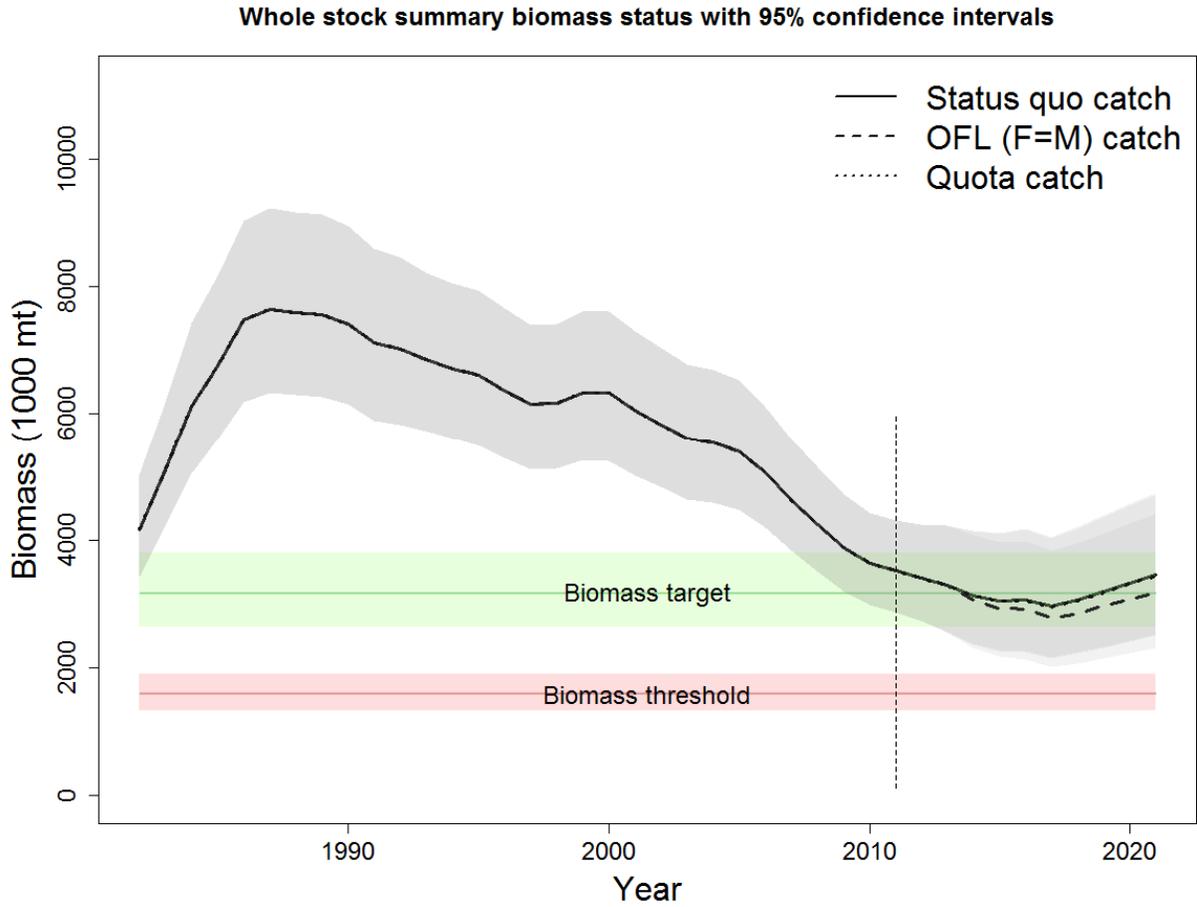


Figure A9.6. Fishing mortality results for projections with the low q (high biomass) scenario in which true whole stock biomass was substantially larger than estimated in the basecase model.

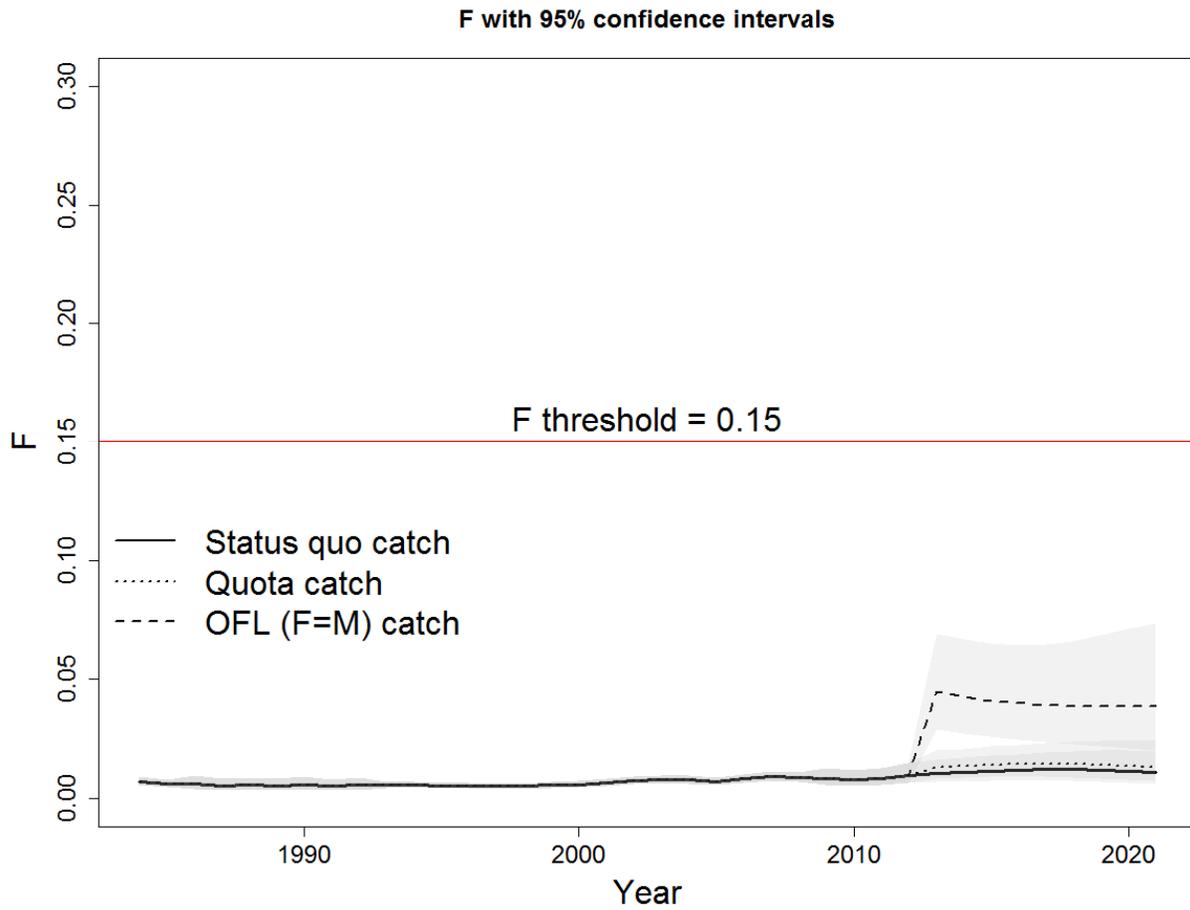


Figure A9.7. Biomass results for projections with the low q (high biomass) scenario in which whole stock biomass was substantially larger than estimated in the basecase model. Probabilities are for overfished stock status occurring given the minimum biomass projected between 2013-2017. The biomass reference point is from the basecase model.

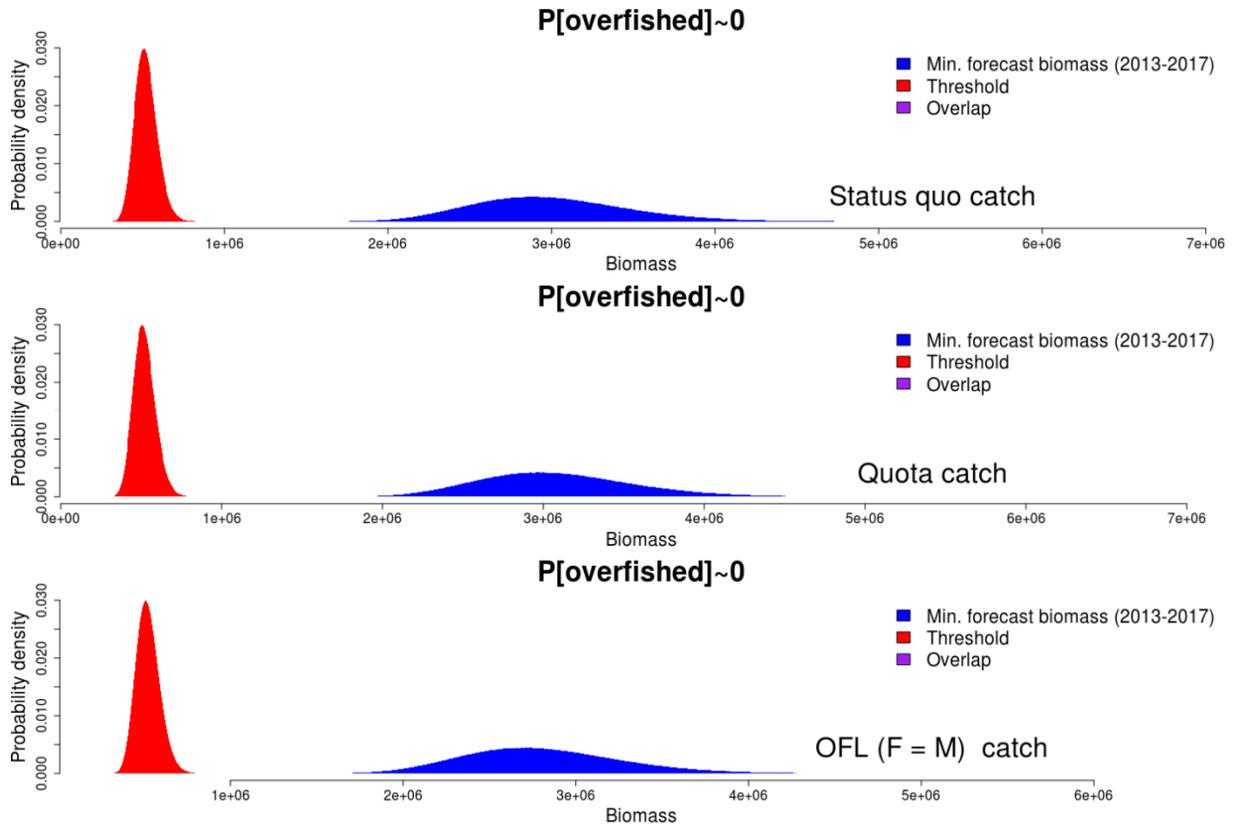


Figure A9.8. Fishing mortality results for projections with the low q (high biomass) scenario in which whole stock biomass was substantially larger than estimated in the basecase model. Probabilities are for overfishing occurring given the minimum biomass projected between 2013-2017.

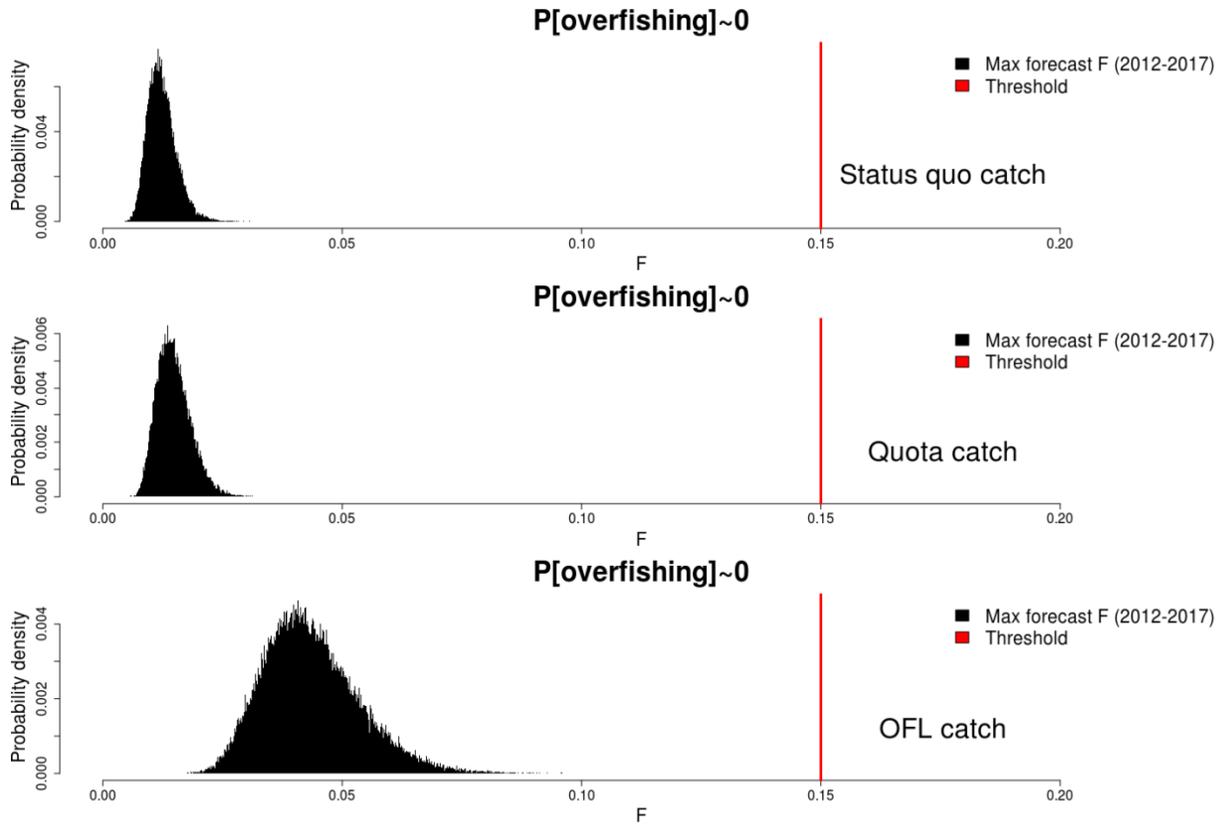


Figure A9.9. Biomass results for projections with the high q (low biomass) scenario in which true southern area biomass was substantially lower than estimated in the basecase model. The biomass reference point is from the basecase model.

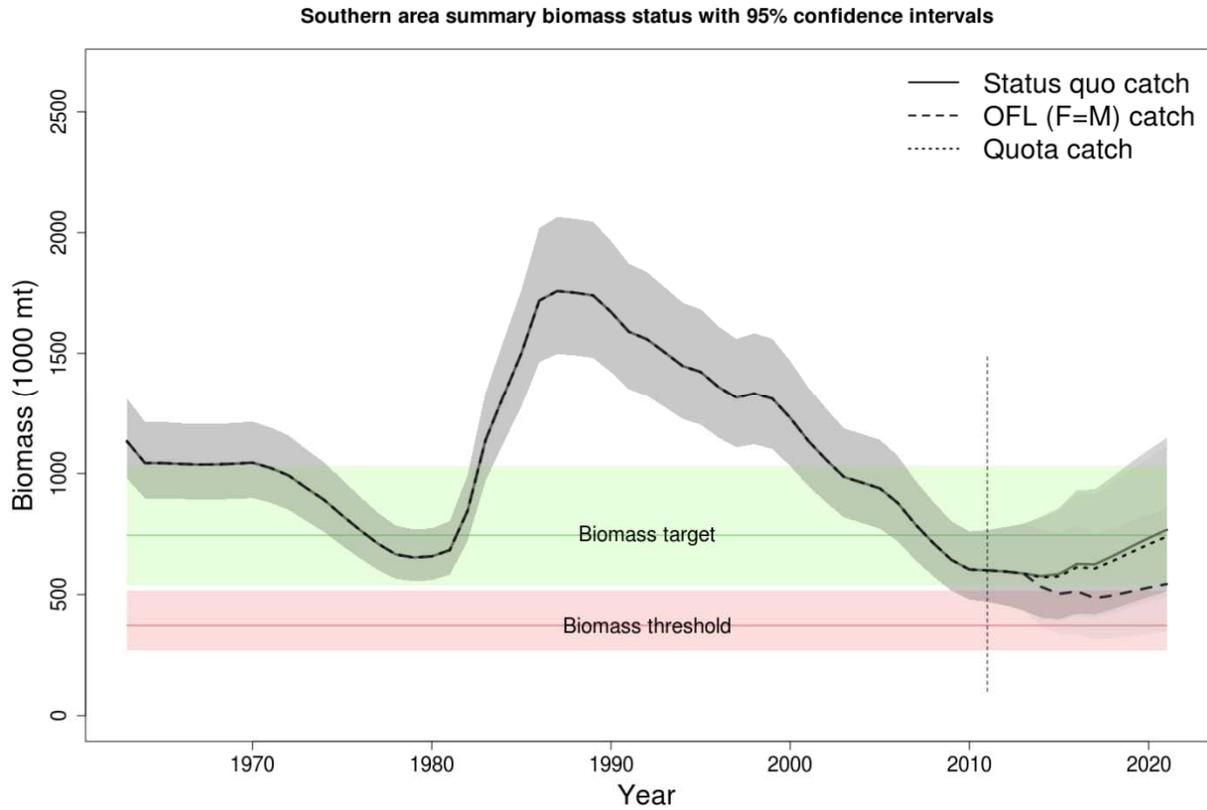


Figure A9.10. Fishing mortality results for projections with the high q (low biomass) scenario in which true southern area biomass was substantially lower than estimated in the basecase model.

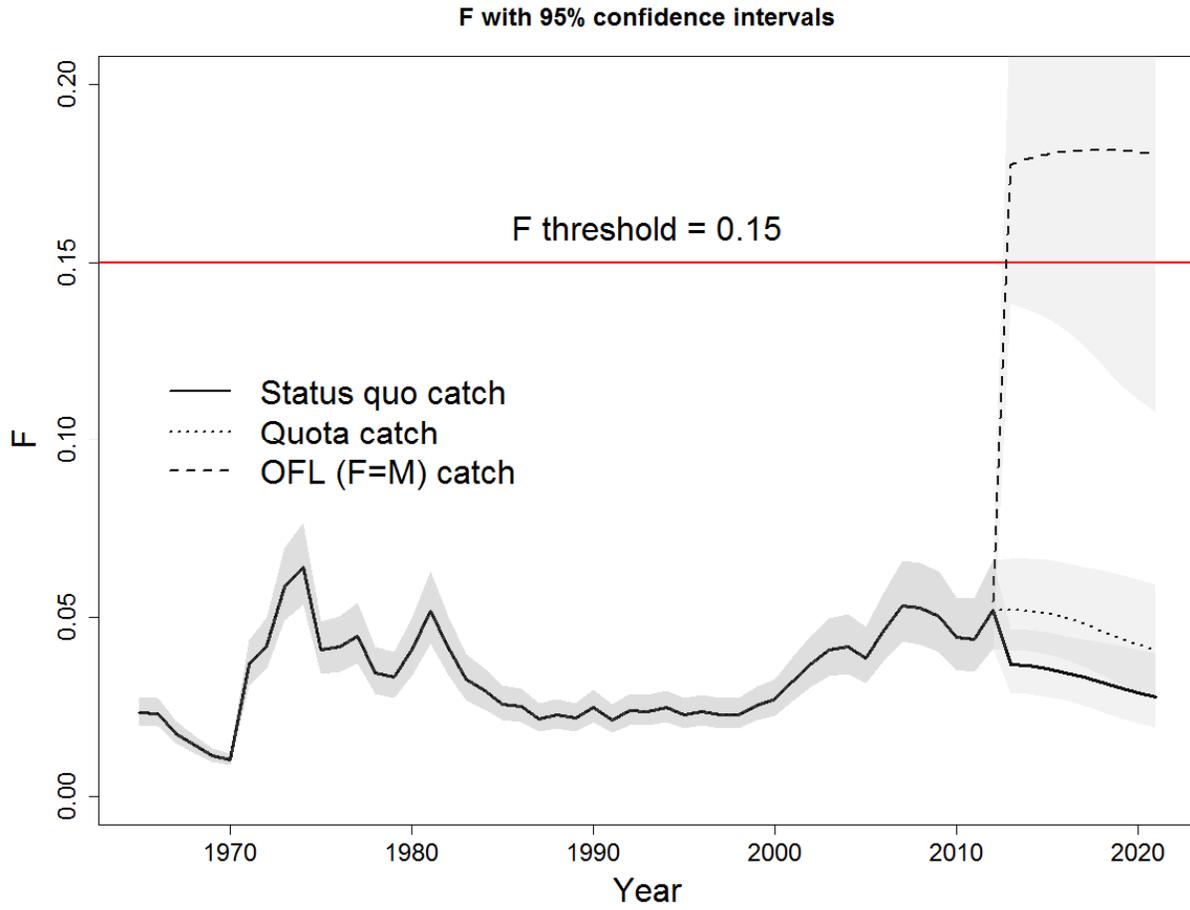


Figure A9.11. Biomass results for projections with the high q (low biomass) scenario in which southern area biomass was substantially lower than estimated in the basecase model. Probabilities are for overfished stock status occurring given the minimum biomass projected between 2013-2017. The biomass reference point is from the basecase model.

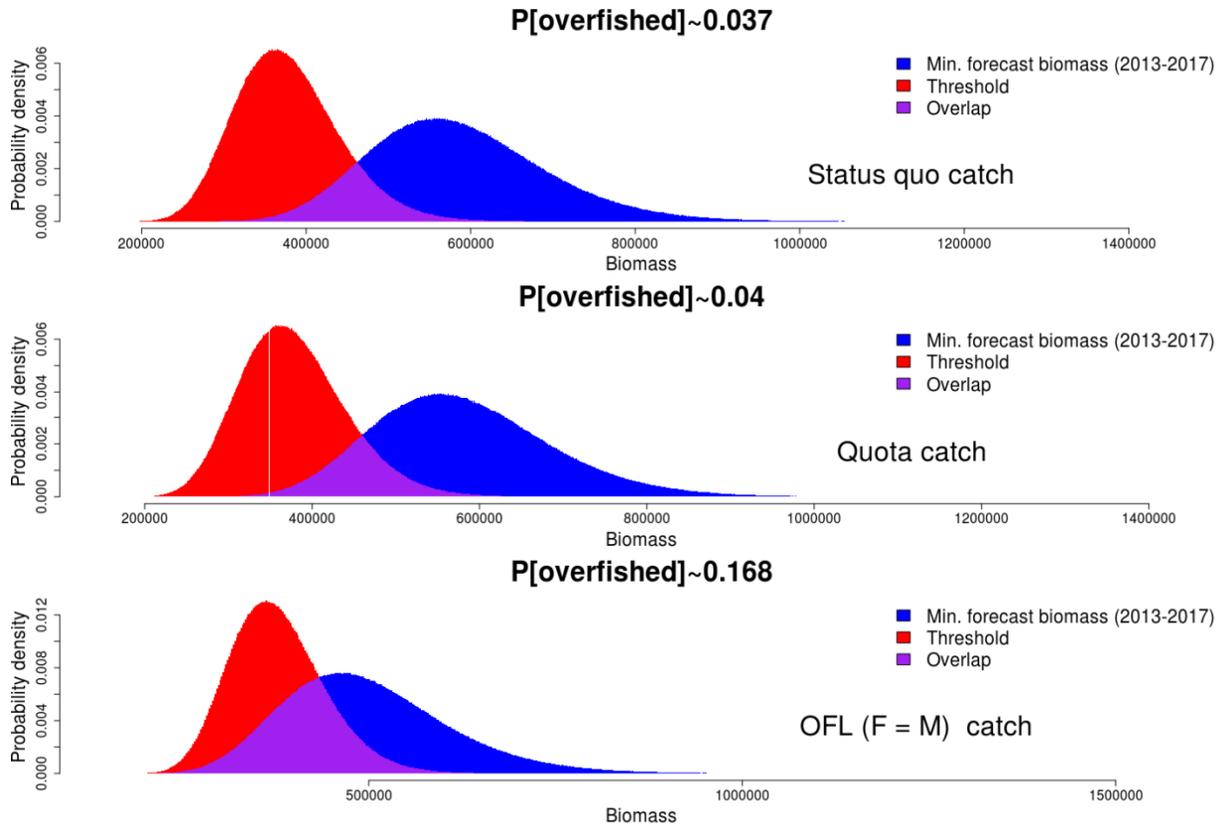


Figure A9.12. Fishing mortality results for projections with the high q (low biomass) scenario in which southern area biomass was substantially lower than estimated in the basecase model. Probabilities are for overfishing occurring given the minimum biomass projected between 2013-2017.

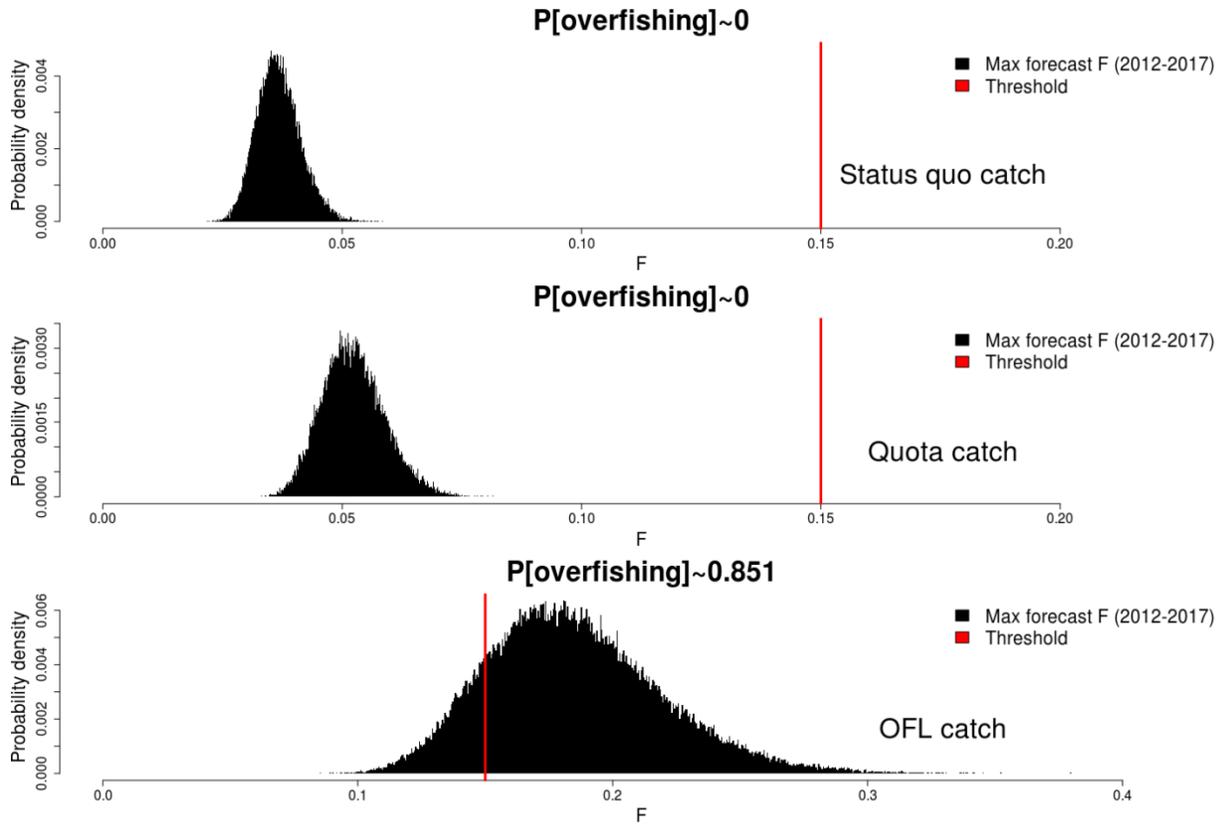


Figure A9.13. Biomass results for projections with the high q (low biomass) scenario in which true southern area biomass was substantially larger than estimated in the basecase model. The biomass reference point is from the basecase model.

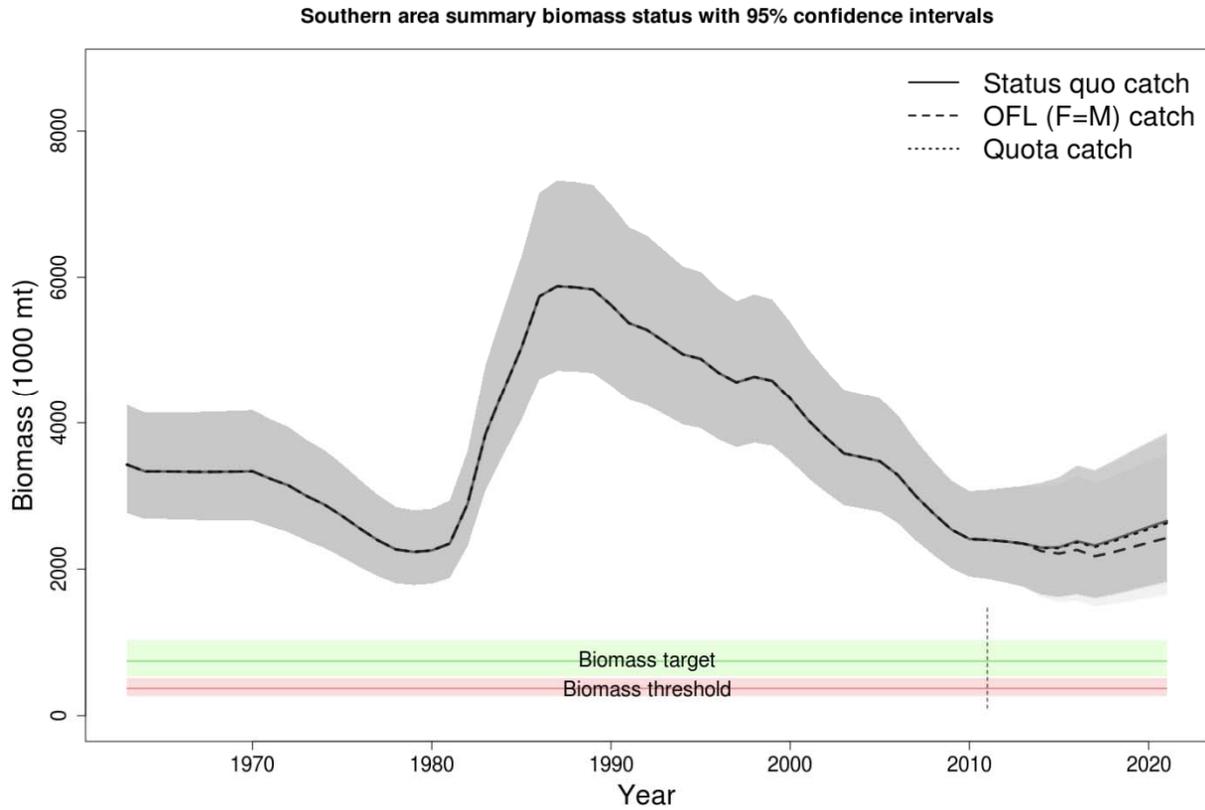


Figure A9.14. Fishing mortality results for projections with the low q (high biomass) scenario in which true southern area biomass was substantially larger than estimated in the basecase model.

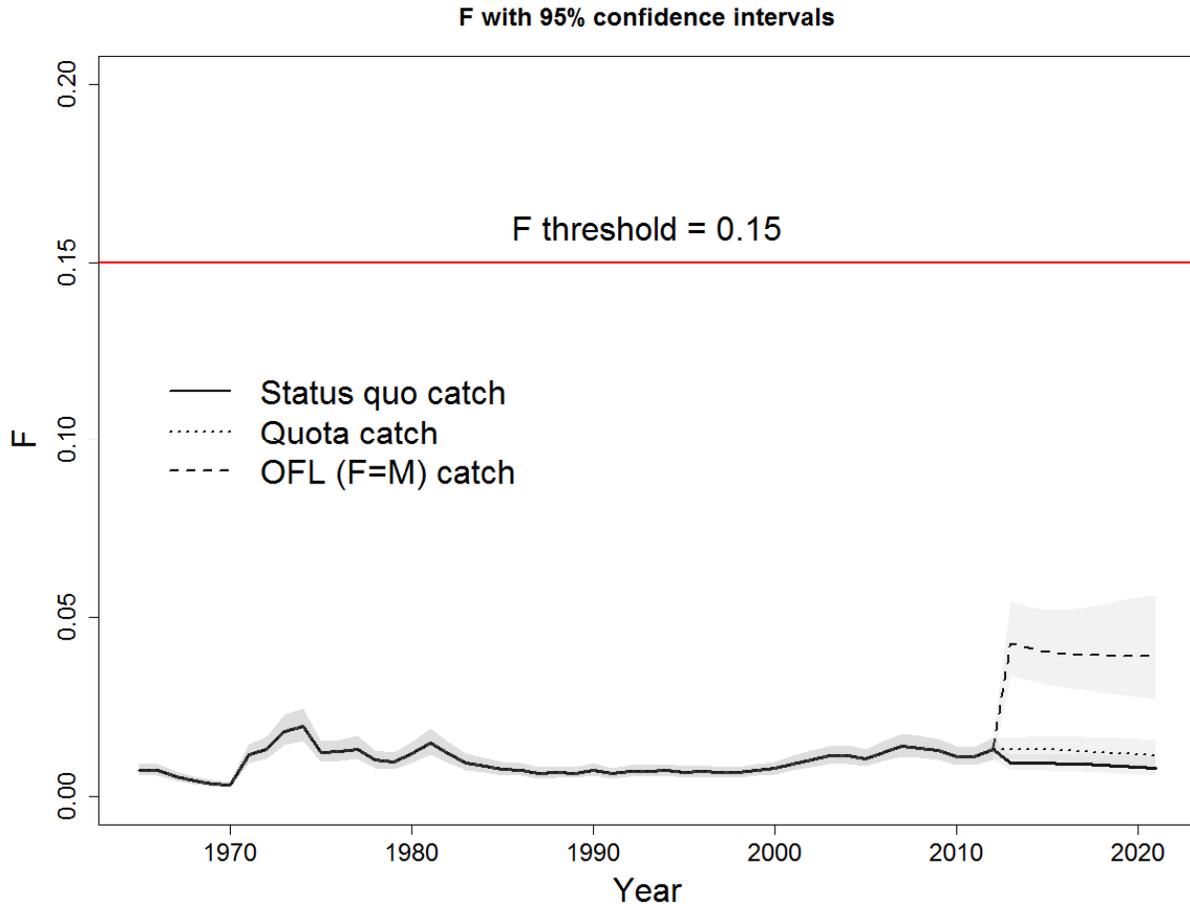


Figure A9.15. Biomass results for projections with the low q (high biomass) scenario in which southern area biomass was substantially larger than estimated in the basecase model. Probabilities are for overfished stock status occurring given the minimum biomass projected between 2013-2017. The biomass reference point is from the basecase model.

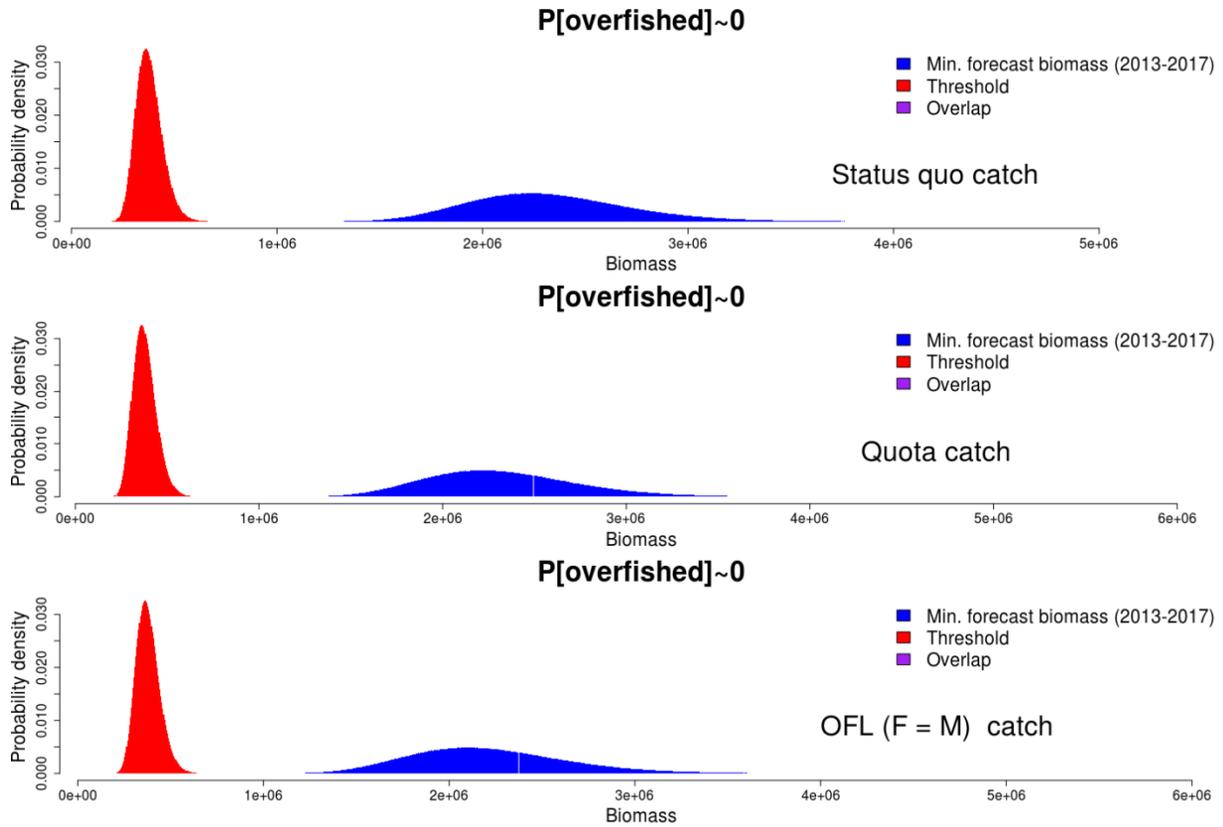


Figure A9.16. Fishing mortality results for projections with the low q (high biomass) scenario in which southern area biomass was substantially larger than estimated in the basecase model. Probabilities are for overfishing occurring given the minimum biomass projected between 2013-2017.

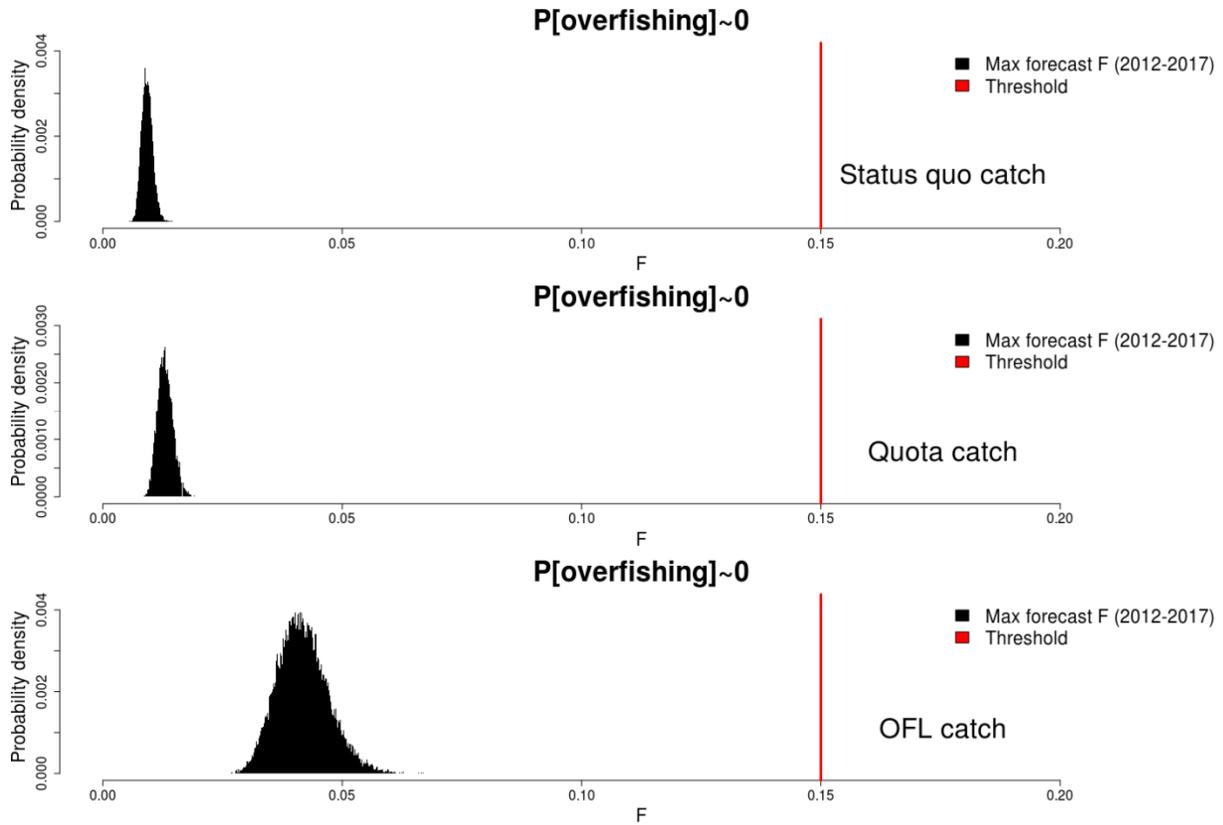


Figure A9.17. Biomass results for projections with the high q (low biomass) scenario in which true northern area biomass was substantially lower than estimated in the basecase model.

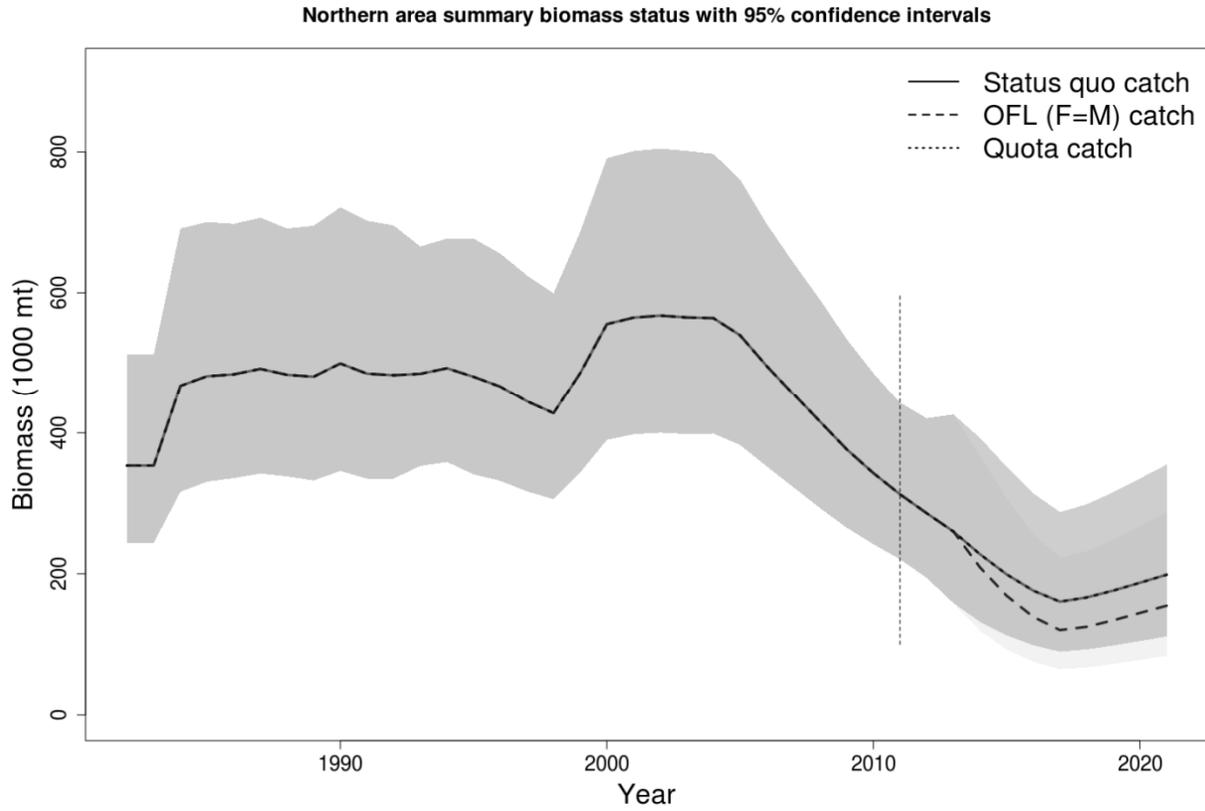


Figure A9.18 Biomass results for projections with the low q (high biomass) scenario in which true whole stock biomass was substantially lower than estimated in the basecase model.

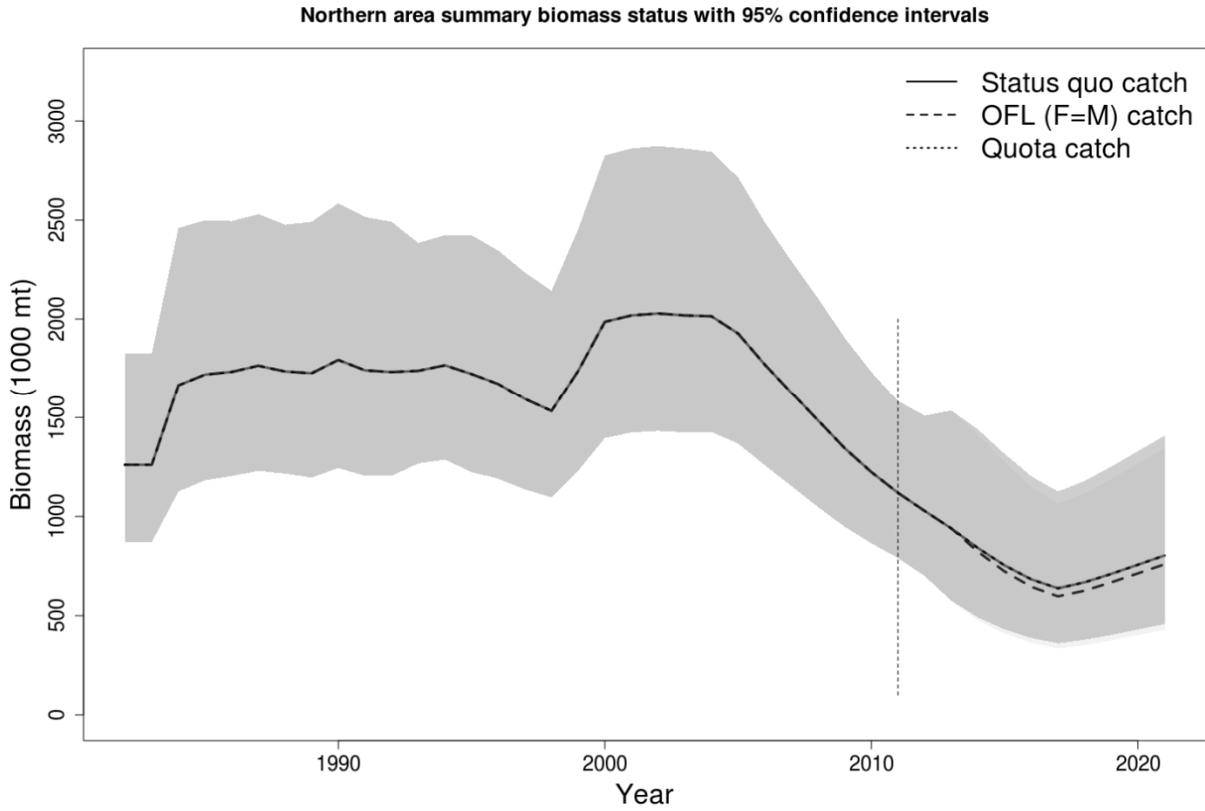


Figure A9.19. Fishing mortality results for projections with the high q (low biomass) scenario in which true northern area biomass was substantially lower than estimated in the basecase model.

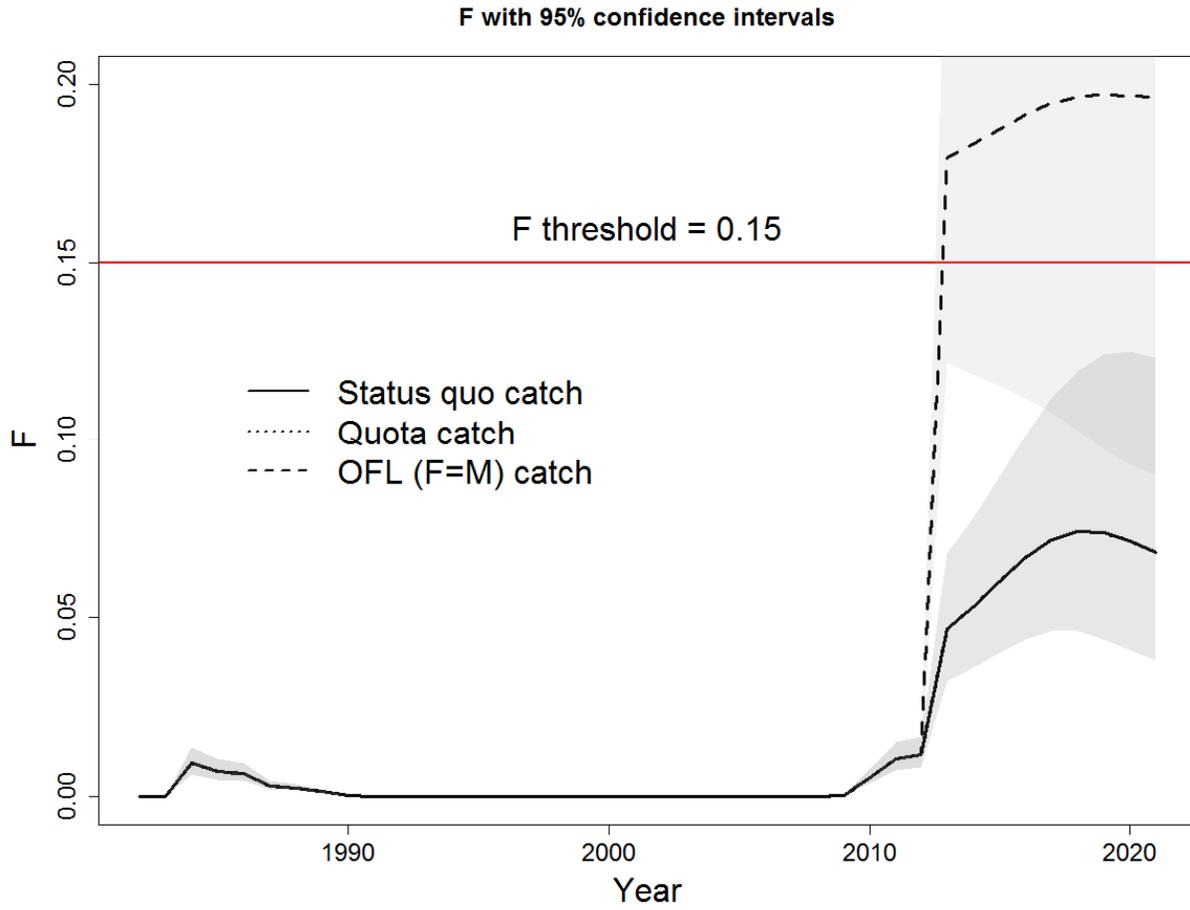


Figure A9.20. Fishing mortality results for projections with the high q (low biomass) scenario in which northern area biomass was substantially lower than estimated in the basecase model. Probabilities are for overfishing occurring given the minimum biomass projected between 2013-2017.

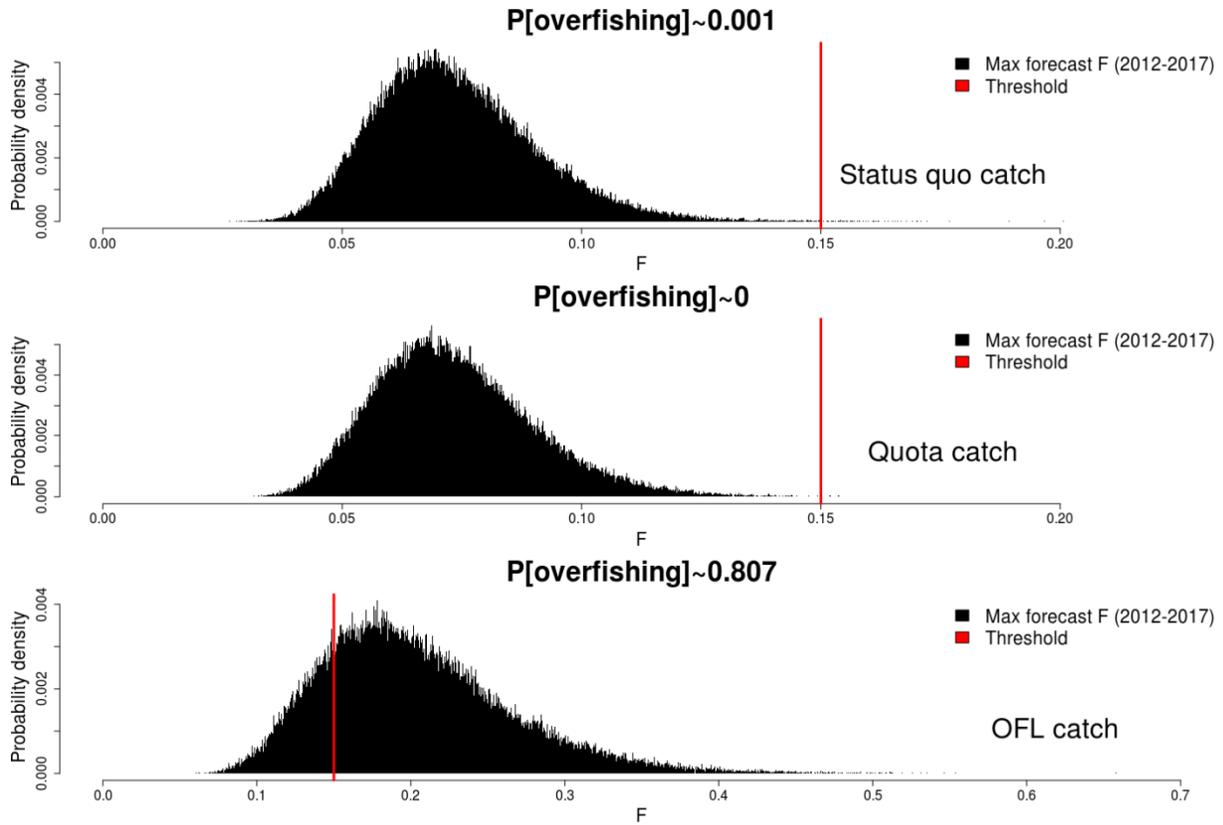


Figure A9.21. Fishing mortality results for projections with the low q (high biomass) scenario in which true northern area biomass was substantially larger than estimated in the basecase model.

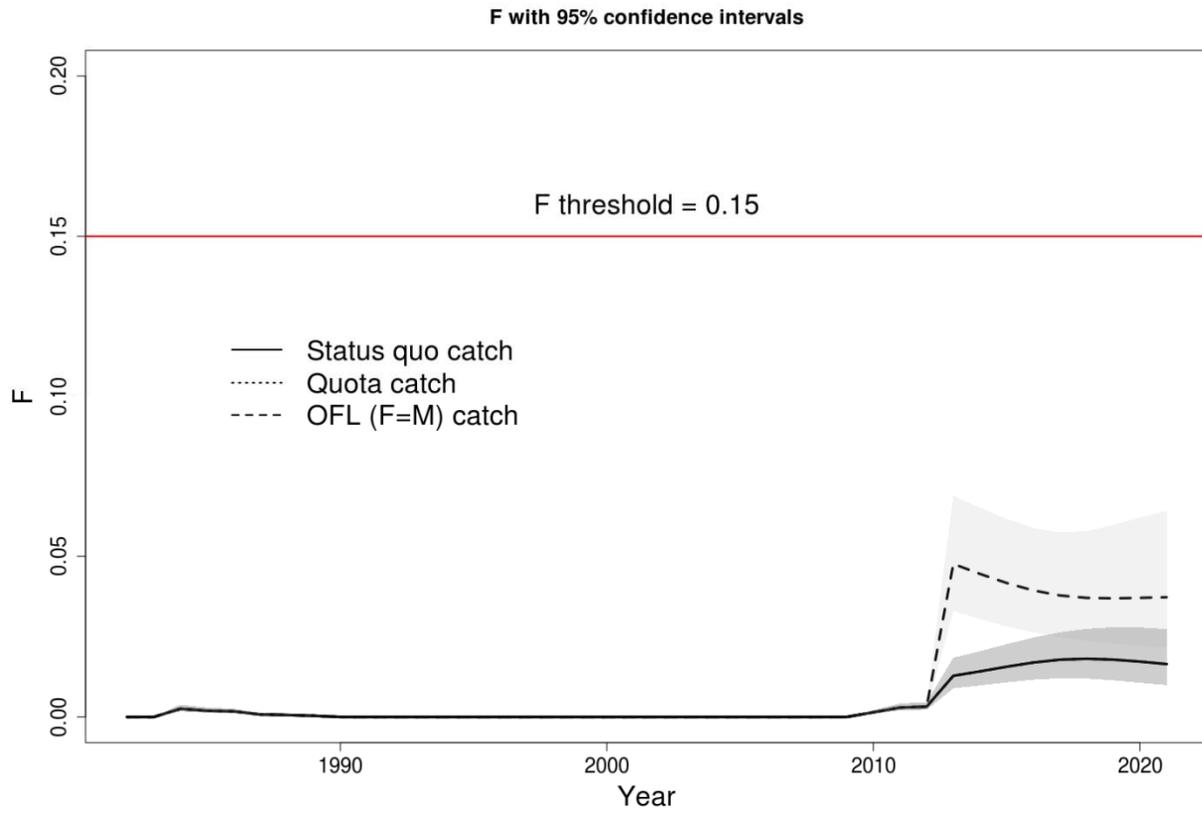
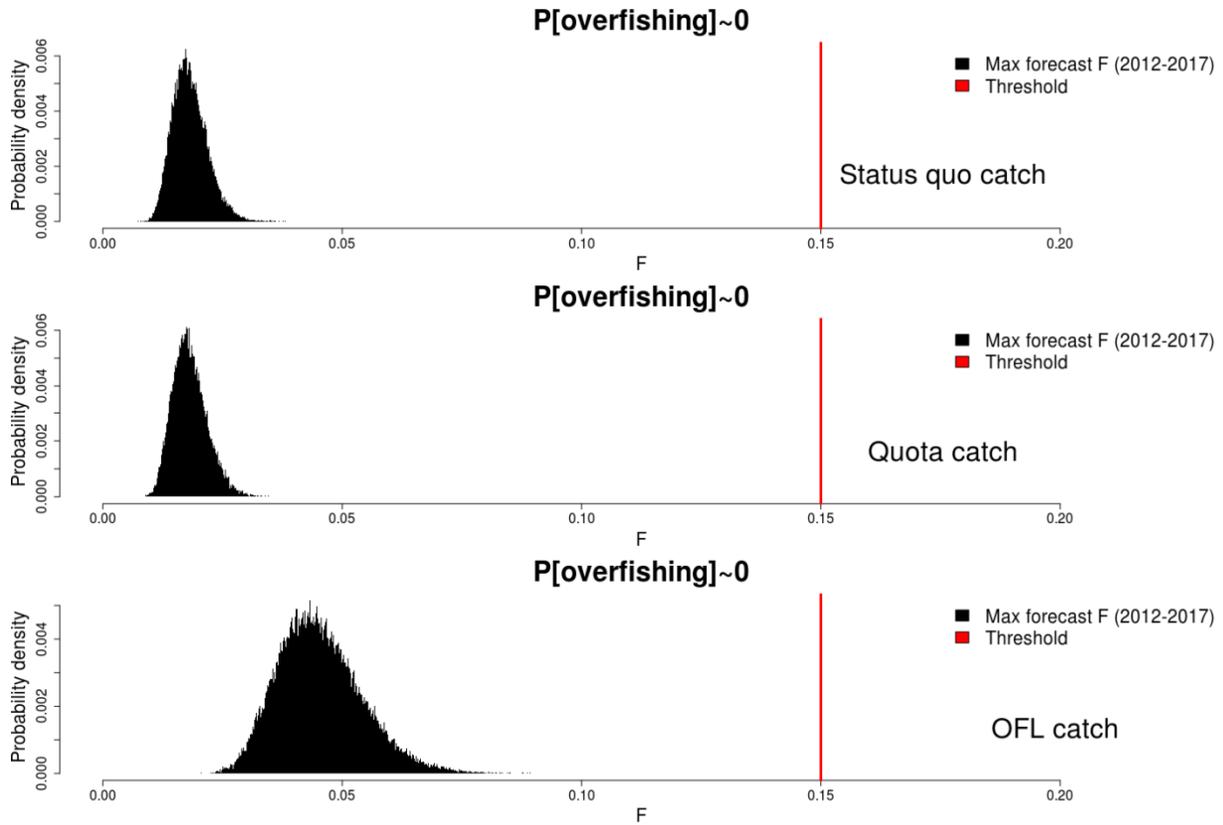


Figure A9.22. Fishing mortality results for projections with the low q (high biomass) scenario in which northern area biomass was substantially larger than estimated in the basecase model. Probabilities are for overfishing occurring given the minimum biomass projected between 2013-2017.



Appendix A10: Invertebrate Subcommittee

Persons who attended Invertebrate Subcommittee meetings and contributed to this report are:

Larry Jacobson (NEFSC, Chair)
Dan Hennen (NEFSC, assessment lead)
Toni Chute (NEFSC)
Chris Legault (NEFSC)
David Wallace (Wallace & Associates, Inc.)
Eric Powell (University of Southern Mississippi)
Daphne Munroe (Rutgers University)
Xinzhong Zhang (Rutgers University)
Fred Serchuk (NEFSC)
Jiashen Tang (NEFSC)
Jon Deroba (NEFSC)
Paul Rago (NEFSC)
Roger Mann (VIMS)
Tom Alspach (Sea Watch International, Inc.)
Tom Hoff (Wallace & Associates, Inc.)
Wendy Gabriel (NEFSC)
Jessica Coakly (MAFMC)
Jose Montanez (MAFMC)
Ed Houde (University of Maryland)
Doug Potts (NERO)
Guy Simmons (Sea Watch International, Inc.)
Bonnie McCray (Rutgers University)
Dvora Hart (NEFSC)
Carolyn Creed (Rutgers University)
Richard McBride (NEFSC)
Jeff Normant (NJ Division of Fish and Wildlife)
Jennifer O’Odwyer (NYSDEC)