

Gmacs Example Stock Assessment

The Gmacs development team

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Introduction

Gmacs is a generalized size-structured stock assessment modeling framework for molting crustacean species. Gmacs can make use of a wide variety of data, including fishery- and survey-based size-composition data, and fishery-dependent and -independent indices of abundance. Gmacs is coded using AD Model Builder.

Crab stocks of Alaska are managed by the North Pacific Fisheries Management Council ([NPFMC](#)). Some stocks are assessed with integrated size-structured assessment models of the form described in Punt, Huang, and Maunder (2013). Currently, each stock is assessed using a stock-specific assessment model (e.g. Zheng and Siddeek (2014)). The Gmacs project aims to provide software that will allow each stock to be assessed independently but using a single modeling framework.

Gmacs is used here to develop an assessment model for the Bristol Bay Red King Crab (BBRKC) stock. The example assessment is intended to match closely with a model scenario presented to the Fall 2014 BSAI Crab Plan Team Meeting by Zheng and Siddeek (2014). The following summarizes the outcome of some comparisons between the existing BBRKC stock assessment model (Zheng and Siddeek 2014) and an emulated version using the Gmacs platform.

An important component of the Gmacs framework is the provision of software for plotting Gmacs model outputs. In what follows, we demonstrate the use of the `gmr` package to process the output of the Gmacs-BBRKC model and produce plots that can be used in assessment reports.

Together, the Gmacs-BBRKC model and this report serve as the first example of what should follow for other crab stocks: that is, direct model comparisons to (1) test the efficacy of Gmacs, and (2) determine whether Gmacs can be used in practice to closely match the outputs of existing ADFG stock assessment models.

New features

New features added to Gmacs since the CIE review include:

- Improved control over selectivity specification including: sex-specific parameter specification (allowing sex-specific retention as well); lower and upper bound specification for each selectivity parameter; priors for each selectivity parameter; provision for additional selectivity types (i.e. coefficient selectivity and double normal).
- Improved control over fitting of size composition data including: the ability to aggregate size compositions (e.g. male and female size compositions from the same fishery) and fit them simultaneously within the multivariate distribution of choice; output files that are read into R for automated plotting of the observed and expected size compositions.
- Prior specification for all model parameters.
- Option to provide a vector of weight at size rather than parameters

Coming soon

New features that will be coming soon include:

- Double normal and coefficient selectivity types
- Dirichlet size composition option
- Additional time-varying options for molt, growth and maturity
- Allowing additional variances to be estimated for abundance indices
- Fully Bayesian MCMC functionality
- A new series of MCMC diagnostic plots including plots of MCMC traces, histograms with priors overlaid, correlation plots, data and posterior predictive distributions
- Please feel free to make suggestions

Summary of analytical approach

To reduce annual measurement errors associated with abundance estimates derived from the area-swept method, the ADFG developed a length-based analysis (LBA) in 1994 that incorporates multiple years of data and multiple data sources in the estimation procedure (Zheng et al. 1995a). Annual abundance estimates of the BBRKC stock from the LBA have been used to manage the directed crab fishery and to set crab bycatch limits in the groundfish fisheries since 1995. An alternative LBA (research model) was developed in 2004 to include small size groups for federal overfishing limits. The crab abundance declined sharply during the early 1980s. The LBA estimated natural mortality for different periods of years, whereas the research model estimated additional mortality beyond a basic constant natural mortality during 1976-1993.

The original LBA model was described in detail by Zheng et al. (1995a, 1995b) and Zheng and Kruse (2002). The model combines multiple sources of survey, catch, and bycatch data using a maximum likelihood approach to estimate abundance, recruitment, catchabilities, catches, and bycatch of the commercial pot fisheries and groundfish trawl fisheries.

Critical assumptions of the model include:

- The base natural mortality is constant over shell condition and size and was estimated assuming a maximum age of 25 and applying the 1% rule (Zheng 2005).
- Survey and fisheries selectivities are a function of size and were constant over shell condition. Selectivities are a function of sex except for trawl bycatch selectivities, which are the same for both sexes. Two different survey selectivities were estimated: (1) 1975-1981 and (2) 1982-2013 based on modifications to the trawl gear used in the assessment survey.
- Growth is a function of size and did not change over time for males. For females, three growth increments per molt as a function of size were estimated based on sizes at maturity (1975-1982, 1983-1993, and 1994-2013). Once mature, female red king crabs grow with a much smaller growth increment per molt.
- Molting probabilities are an inverse logistic function of size for males. Females molt annually.
- Annual fishing seasons for the directed fishery are short.
- Survey catchability (q) was estimated to be 0.896, based on a trawl experiment by Weinberg et al. (2004) with a standard deviation of 0.025. Survey catchability was assumed to be constant over time. Some scenarios estimate q in the model.
- Males mature at sizes = 120 mm CL. For convenience, female abundance was summarized at sizes = 90 mm CL as an index of mature females. For summer trawl survey data, shell ages of newshell crabs were 12 months or less, and shell ages of oldshell and very oldshell crabs were more than 12 months.
- Measurement errors were assumed to be normally distributed for size compositions and log-normally distributed for biomasses.

Gmacs

The data and model specifications used in the Gmacs-BBRKC model are very similar to those used in the ‘4nb’ scenario developed by Zheng and Siddeek (2014), herein referred to as the BBRKC model. The BBRKC model from Zheng and Siddeek (2014) treats recruits by sex along with sex-specific natural mortality and fishing mortality. Here we provide results from two different Gmacs models (1) a two-sex model and (2) a single sex model in which the male components are compared with results from a Gmacs model implementation tuned to male-only data.

Comparison tables of two different model approaches could be done by

Specification	Parameter	ADFG Value	Gmacs OneSex	Gmacs TwoSex
Start year	$t = 0$	1975	1953	1975
End year	$t = T$	2014	2014	2014
No. sexes	s	2	1	2
No. shell condition	ν	2	2	2
No. maturity classes	m	2	1	1
No. size-classes	ℓ	20	20	20
No. Fleets	k	5	2	5

Life History Trait	Parameter	ADFG Value	Gmacs Value	Comments
Natural Mortality	M	Fixed	Fixed	M is fixed in both models

Comparison of model results

The following plots summarize plots made using `gmr` based on output from Zheng and Siddeek (2014) and Gmacs. Two Gmacs models are provided, the OneSex model and the TwoSex model.

Fit to survey abundance indices

The model fit to survey biomass for males was XXX in the Zheng and Siddeek (2014) model (at least visually) than for either of the current implementations of Gmacs (Figure 1).

Estimated retained catch and discards

There are four fisheries defined in each of the models: the directed pot fishery, the groundfish trawl bycatch, the NMFS trawl surveys, and the BSFRF surveys. Each fishery has a mean fishing mortality with annual deviations.

The observed and predicted catches by gear type are summarized in (Figure 2). Data for discard fisheries were read in with 100% mortality (as clarified in Table 1 of Zheng and Siddeek (2014)).

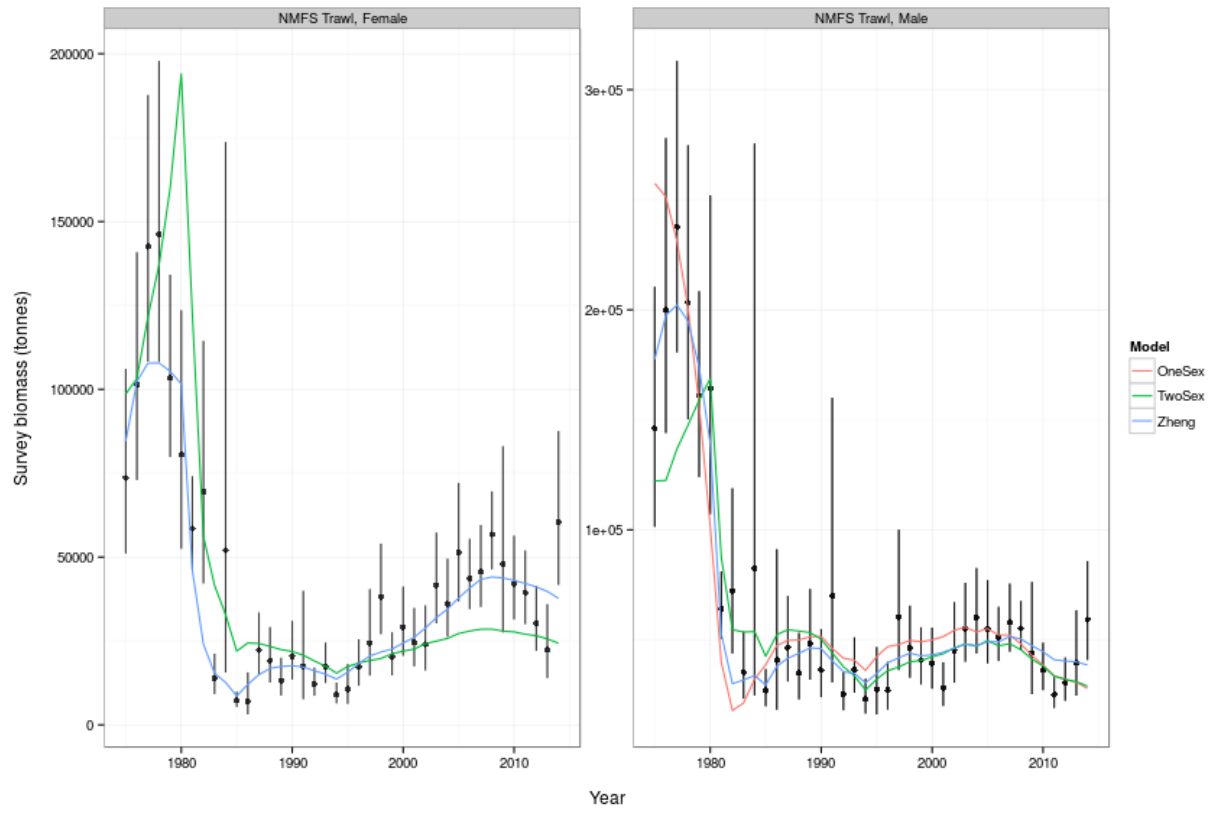


Figure 1: Model fits to sex-specific NMFS trawl survey biomass (tonnes) from 1975 to 2014. The error bars represent plus and minus 2 standard deviations.

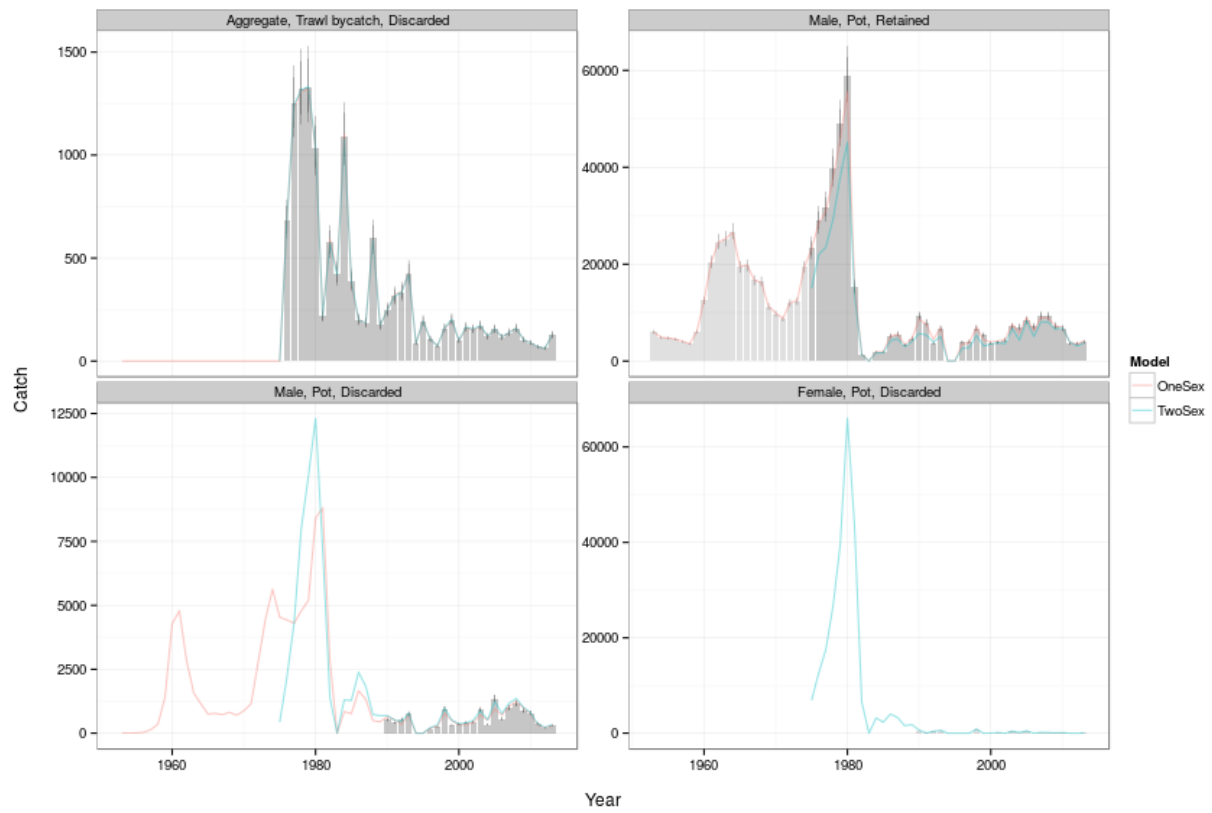


Figure 2: Observed and predicted catch (tonnes) by gear type for the two Gmacs models. The OneSex model includes catch data from 1953 to 2013. The TwoSex model includes catch data from 1975 to 2013.

Fit to size composition data

The fit of the Gmacs models to the BBRKC size composition data are given in the following plots. These include fits to the directed pot fishery for males (Figure 3), male crabs discarded in the directed pot fishery (Figure 4), female crabs discarded in the directed pot fishery (Figure 5), the groundfish trawl bycatch fisheries for males (Figure 6) and females (Figure 7), and the NMFS trawl survey (Figure ??).

All size composition data were fitted using the robust multinomial distribution. In the OneSex model, new shell and old shell males were fitted simultaneously. In the TwoSex model the following size compositions were fitted simultaneously: discarded males and females; trawl bycatch males and females; NMFS trawl survey new shell males, old shell males and females.

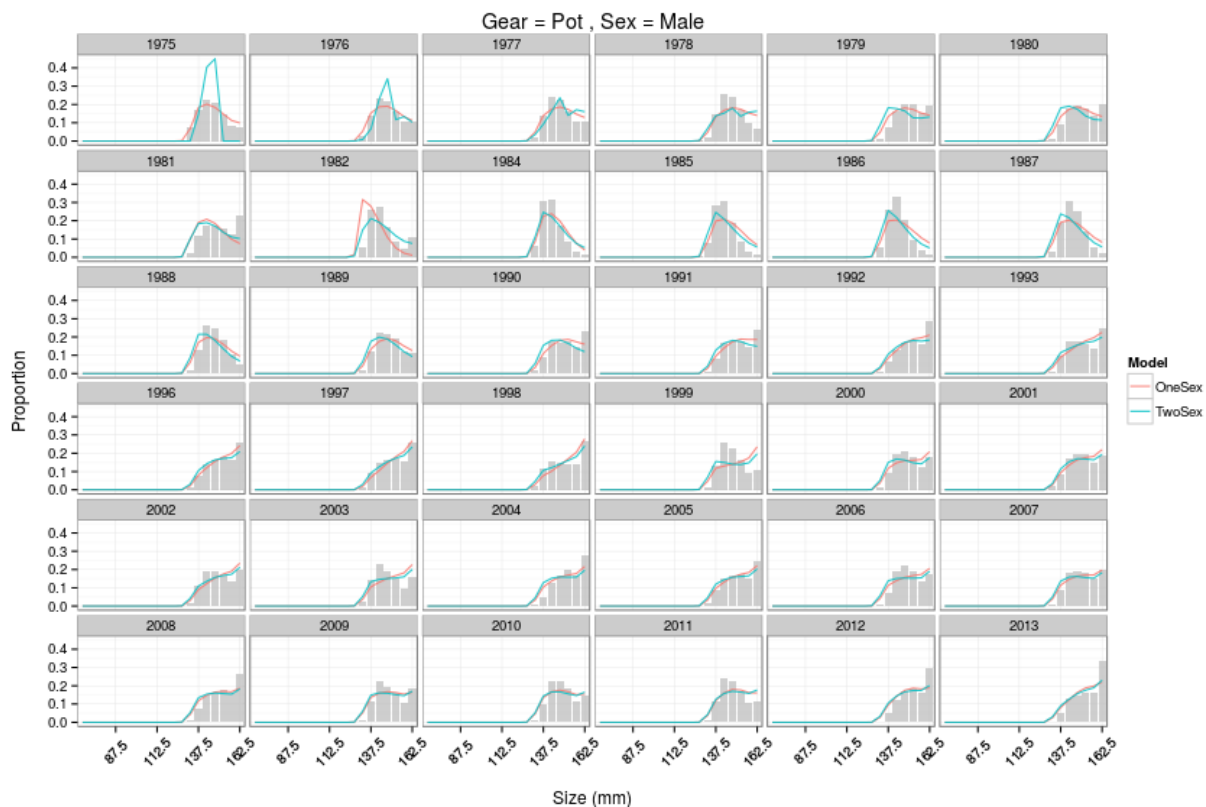


Figure 3: Observed and model estimated size-frequencies of male BBRKC by year retained in the directed pot fishery.

Mean weight-at-size

The mean weight-at-size (w_ℓ) is defined in kg and the carapace length (ℓ , CL) in mm. The mean weight-at-size used in all models is identical because the new option to provide a vector of weights at length is used (Figure 13).

There are differences between immature and mature females hence the unusual shape of the length-weight relationship for females. Given a size, once females mature with eggs, they are heavier than immature females. ADFG uses immature mean weight-at-size for females < 90 mm and mature mean weight-at-size for females > 89 mm. The last four values of mean weight-at-size for females are not used (exceeding the last length group), so the plus group value is simply repeated. In the future, when the immature and mature females are modeled separately, two mean weight-at-size functions should be used. The mean weights for both male and

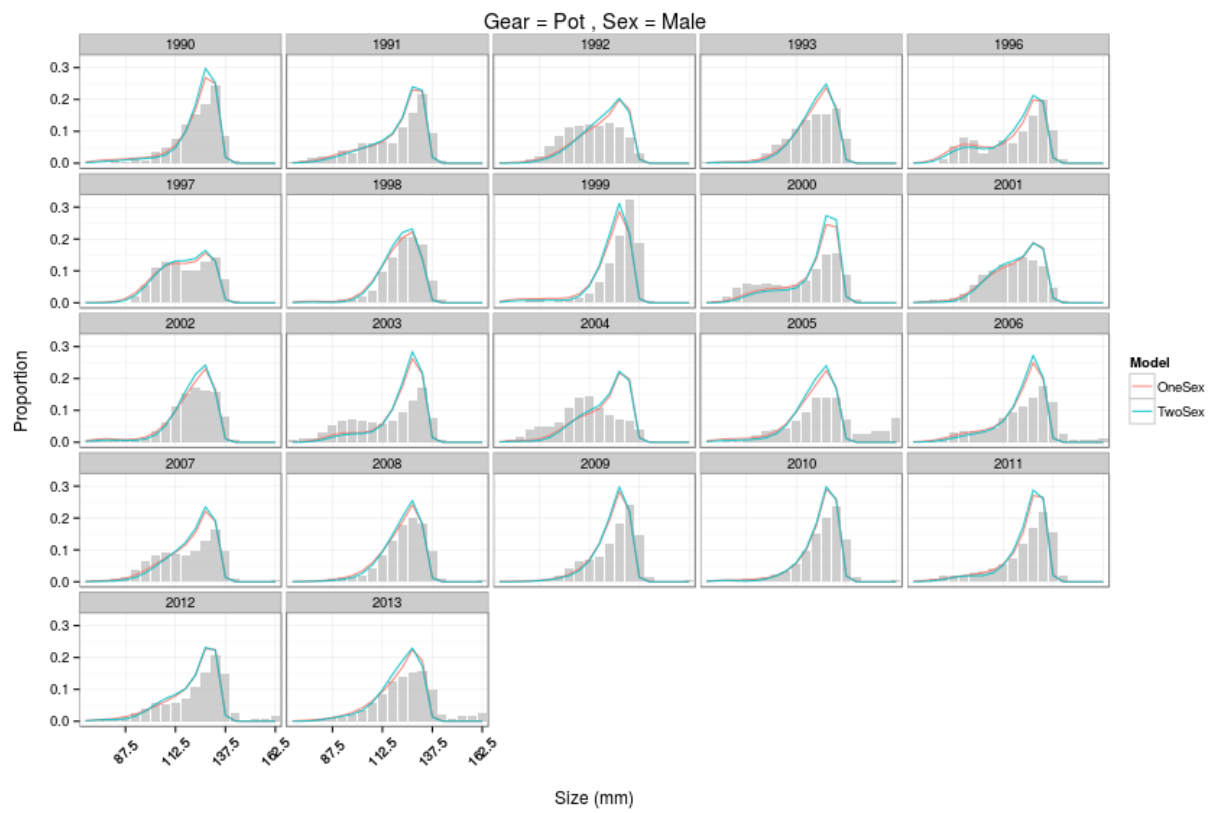


Figure 4: Observed and model estimated size-frequencies of male BBRKC by year discarded in the directed pot fishery.

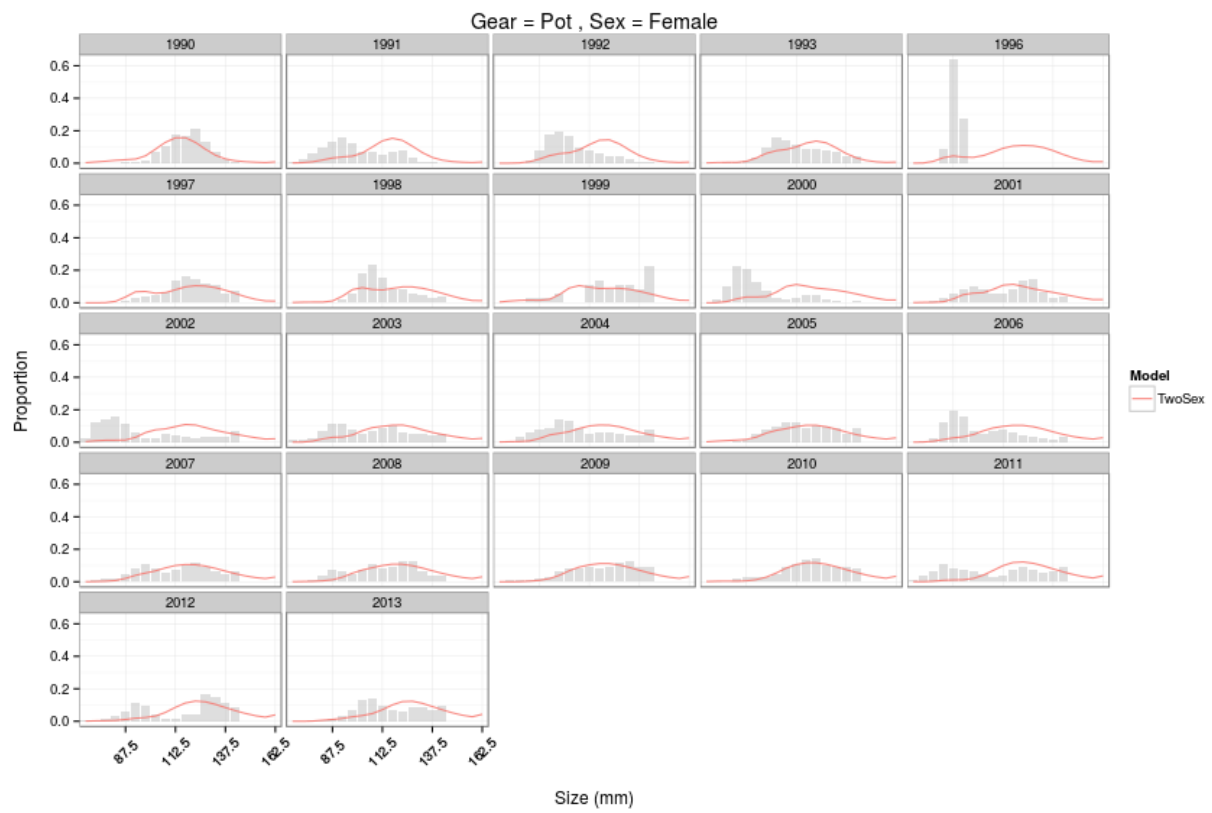


Figure 5: Observed and model estimated size-frequencies of female BBRKC by year discarded in the directed pot fishery.

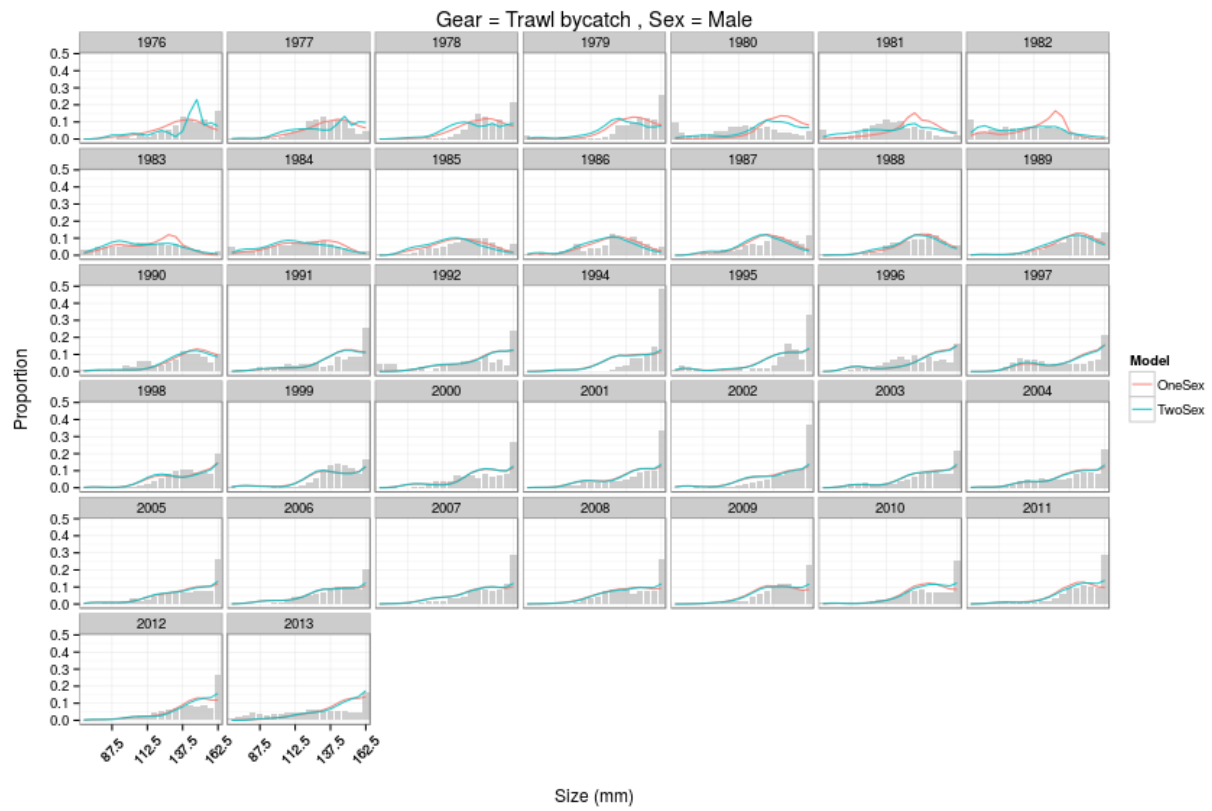


Figure 6: Observed and model estimated size-frequencies of male BBRKC by year in the groundfish trawl bycatch fisheries.

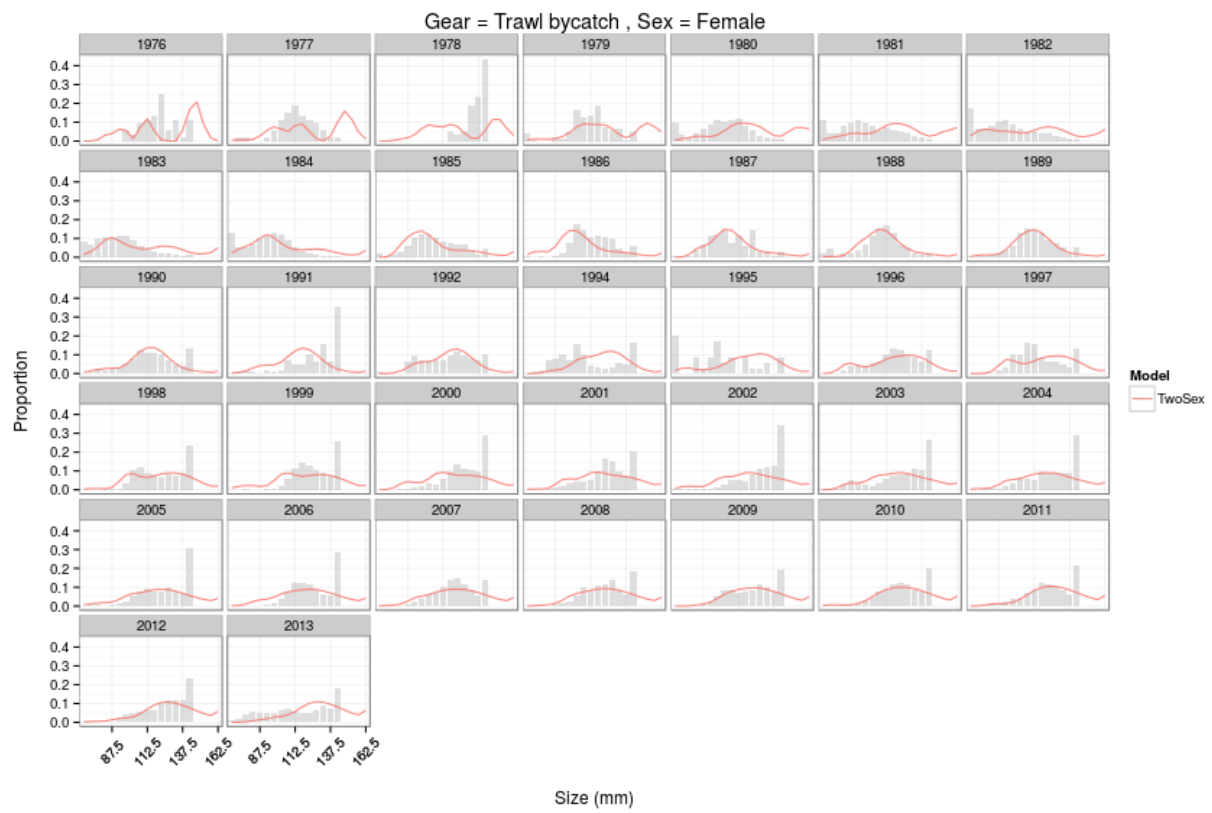


Figure 7: Observed and model estimated size-frequencies of female BBRKC by year in the groundfish trawl bycatch fisheries.

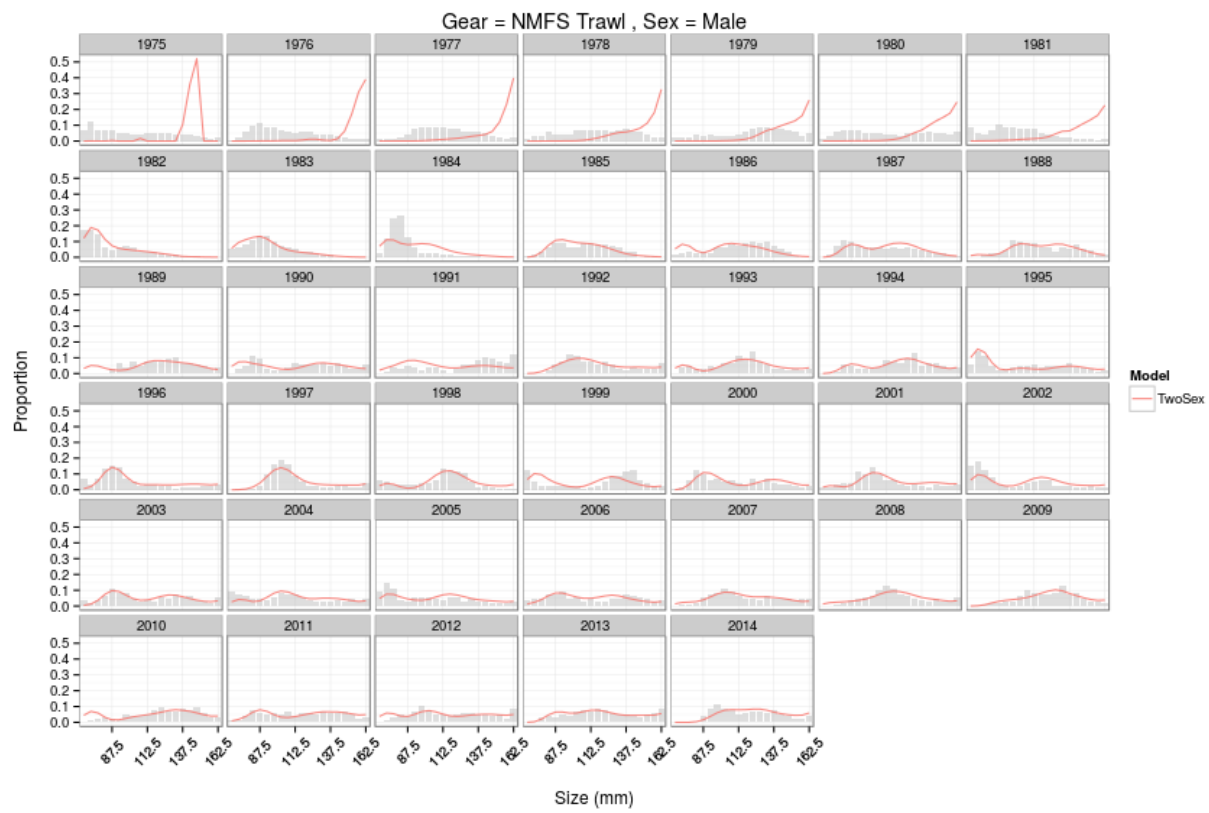


Figure 8: Observed and model estimated size-frequencies of new shell male BBRKC by year in the NMFS trawl fishery.

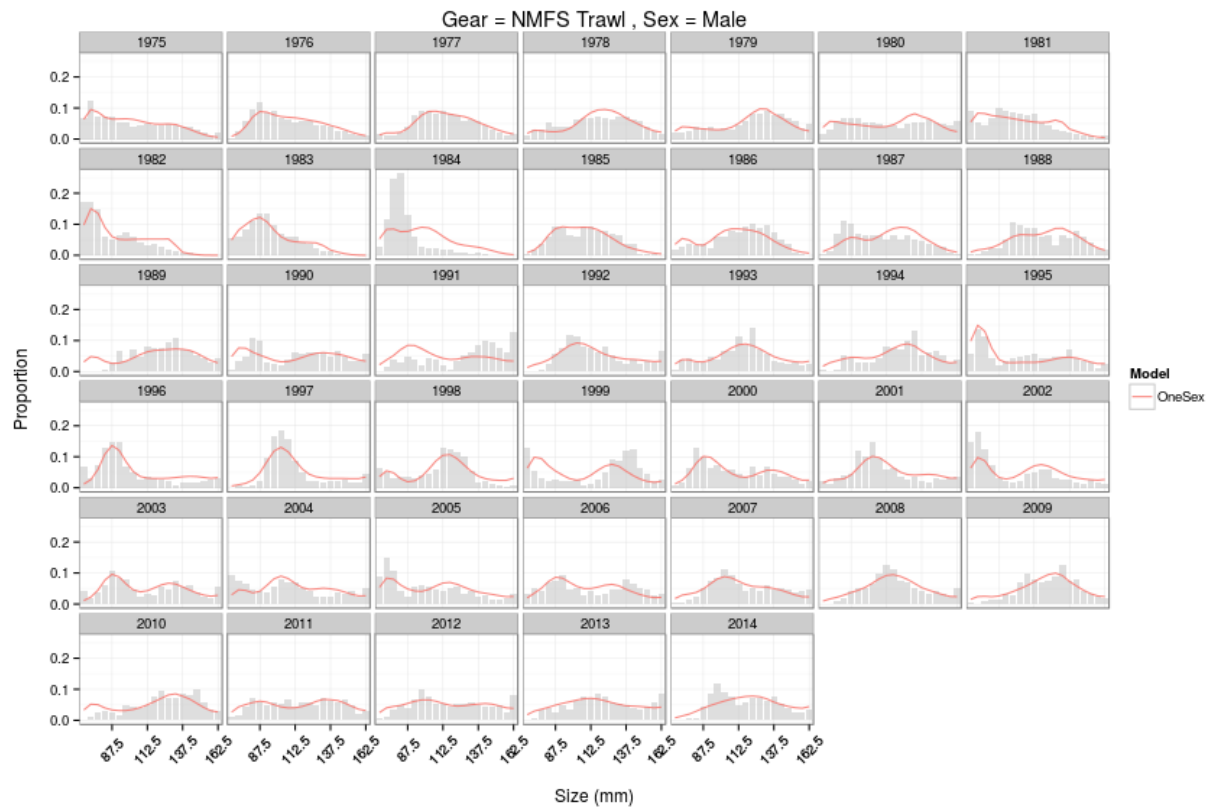


Figure 9: Observed and model estimated size-frequencies of old shell male BBRKC by year in the NMFS trawl fishery.

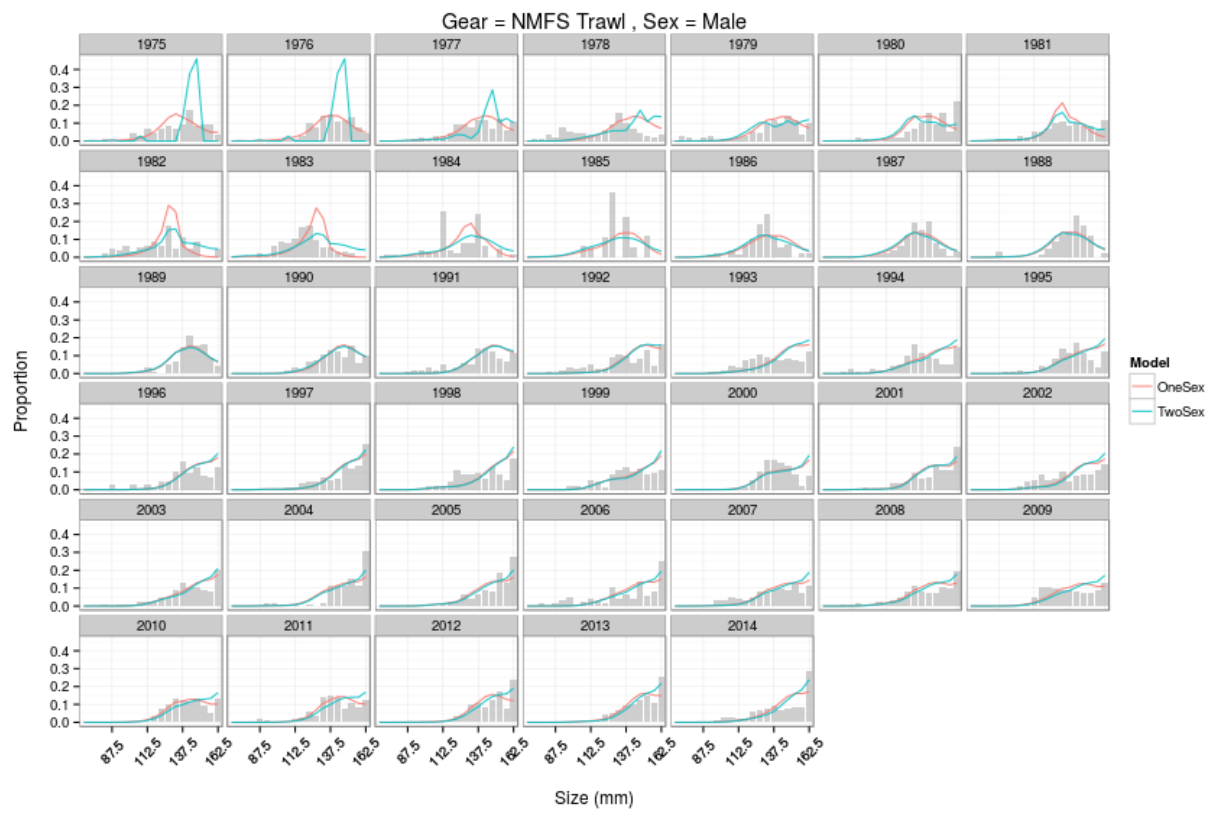


Figure 10: Observed and model estimated size-frequencies of female BBRKC by year in the NMFS trawl fishery.

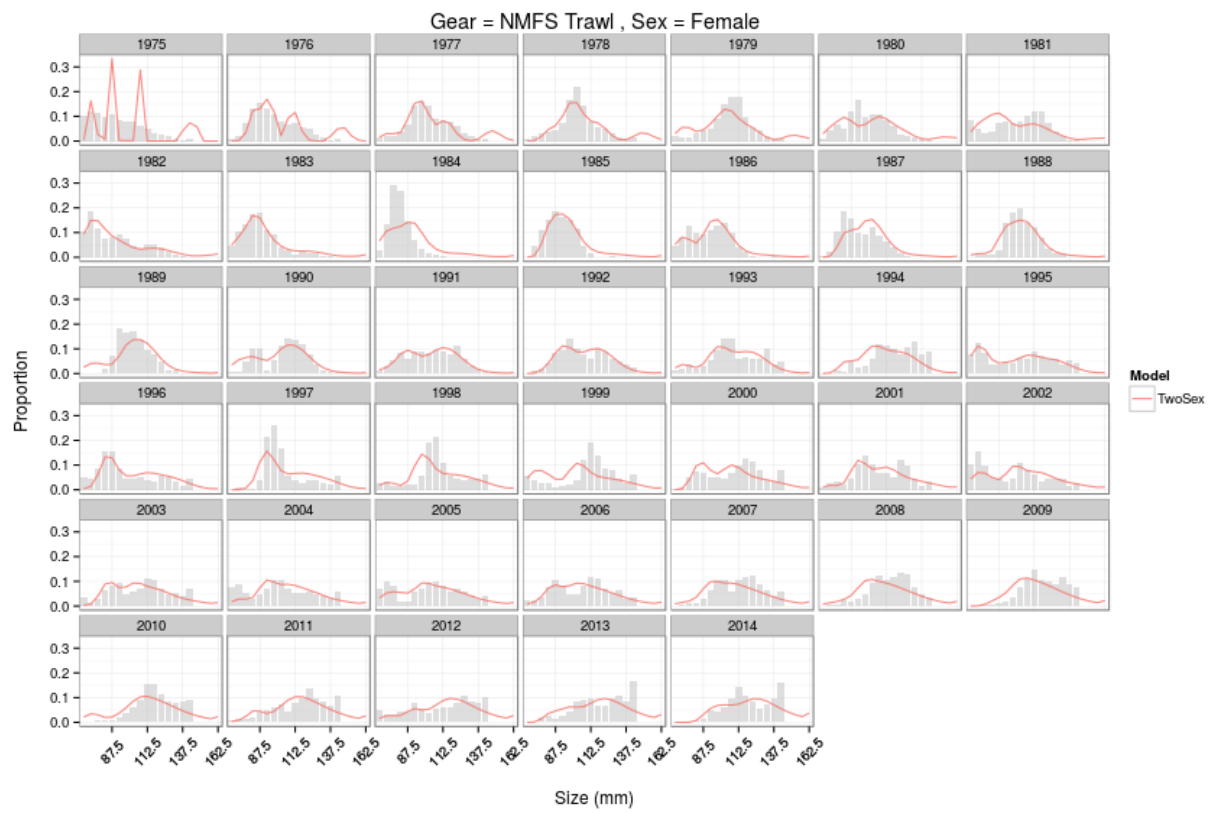


Figure 11: Observed and model estimated size-frequencies of both male and female BBRKC by year in the BSFRF trawl surveys.

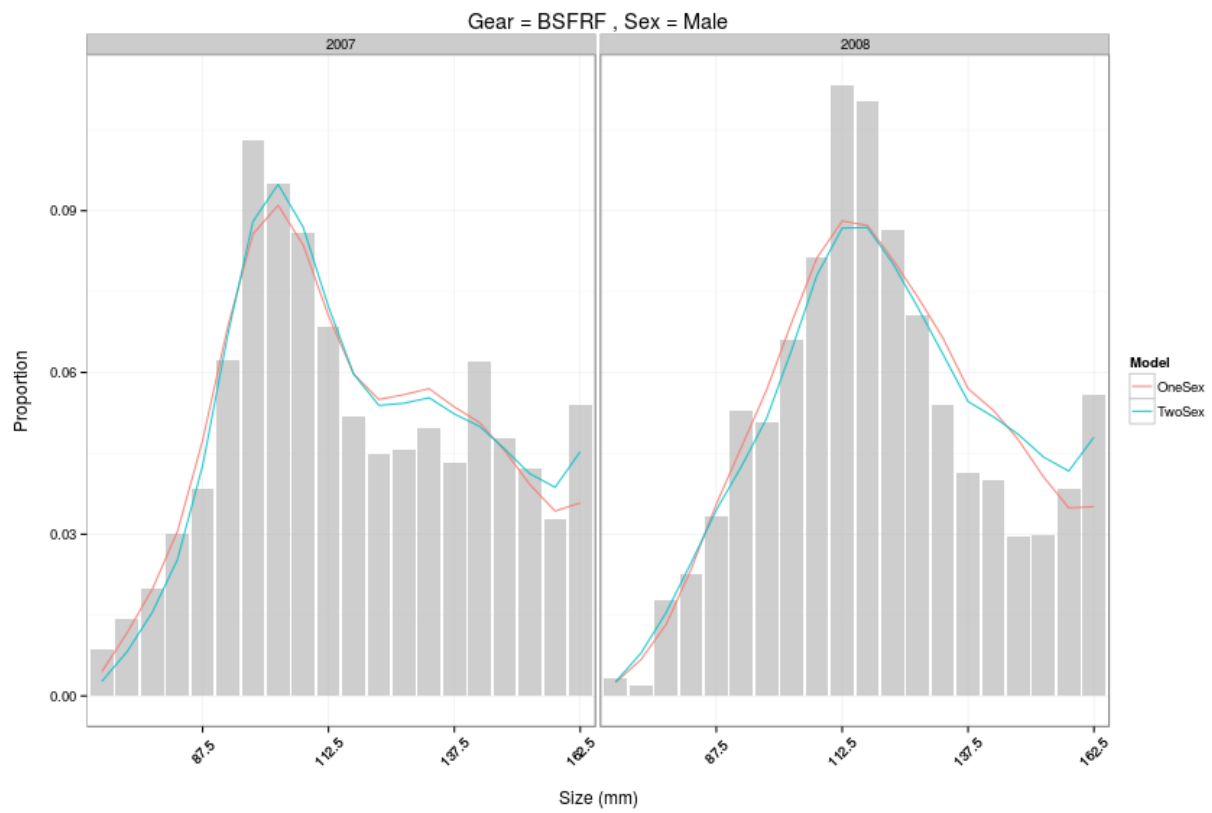


Figure 12: Observed and model estimated size-frequencies of both male and female BBRKC by year in the BSFRF trawl surveys.

female plus length groups are higher than the function values to reflect that there are more crabs larger than the plus group mid sizes. The adjustment is based on the survey length frequency data over time.

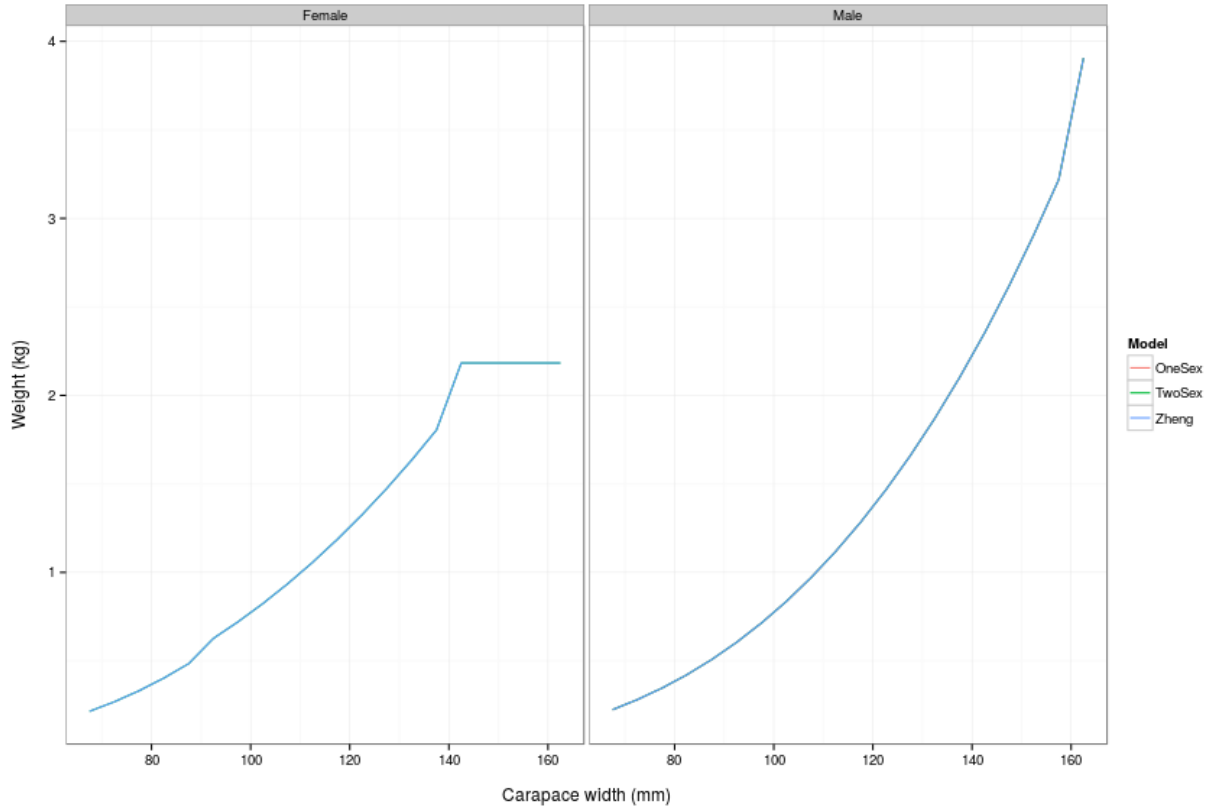


Figure 13: Relationship between carapace width (mm) and weight (kg) by sex in each of the models (provided as a vector of weights at length to Gmacs so lines all overlap).

Initial recruitment size distribution

Gmacs was configured to match the Zheng and Siddeek (2014) model recruitment size distribution closely (Figure 14).

Molting increment and probability

The growth increment per molt is one function for males and three functions for females (due to changing sizes at maturity).

Options to fit relationship based on data was developed but for the BBRKC system, a size-specific vector was used to determine molt increments as shown below (Figure 15). Fixed parameters in gmacs were set to represent that assumed from Zheng and Siddeek (2014) (Figure 16).

In the BBRKC model, females molt annually, so molting probability is always 1 for females. This was replicated in the Gmacs model by fixing the logistic curves parameters to values that result in the molting probability being 1 for females across all modeled length classes. For the males, the BBRKC model has two molting probability curves, one during 1975-78 and another during 1979-present, each with two logistic curve parameters. In the current version of Gmacs, only a single molting probability curve is modeled.

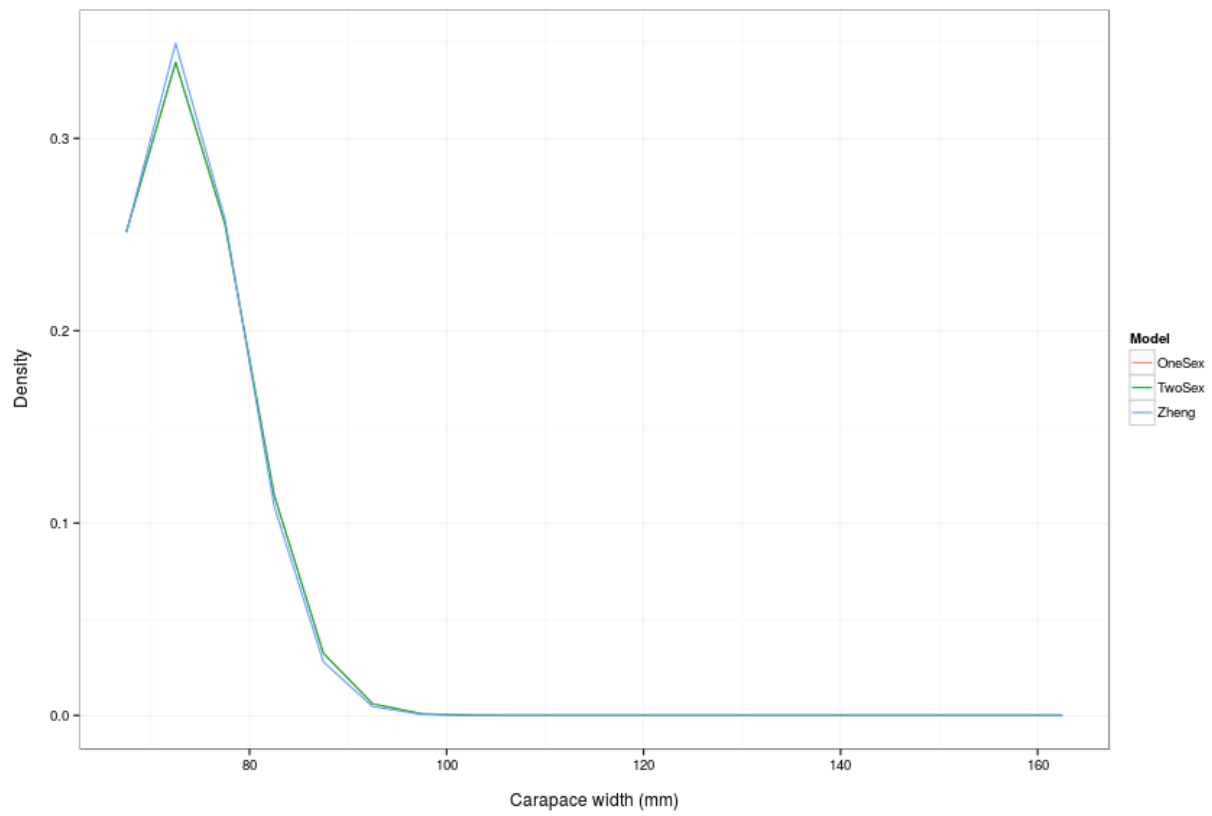


Figure 14: Distribution of carapace width (mm) at recruitment.

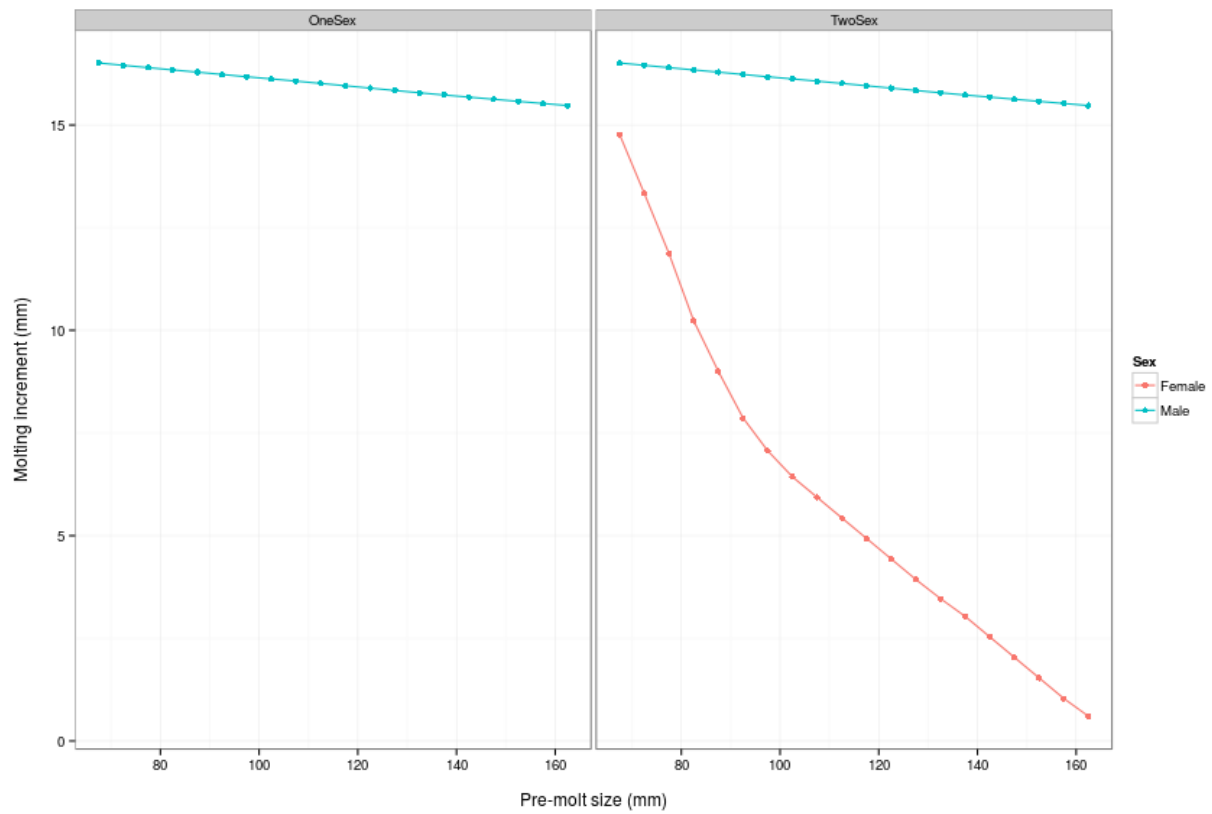


Figure 15: Growth increment (mm) each molt by sex in the OneSex and TwoSex models.

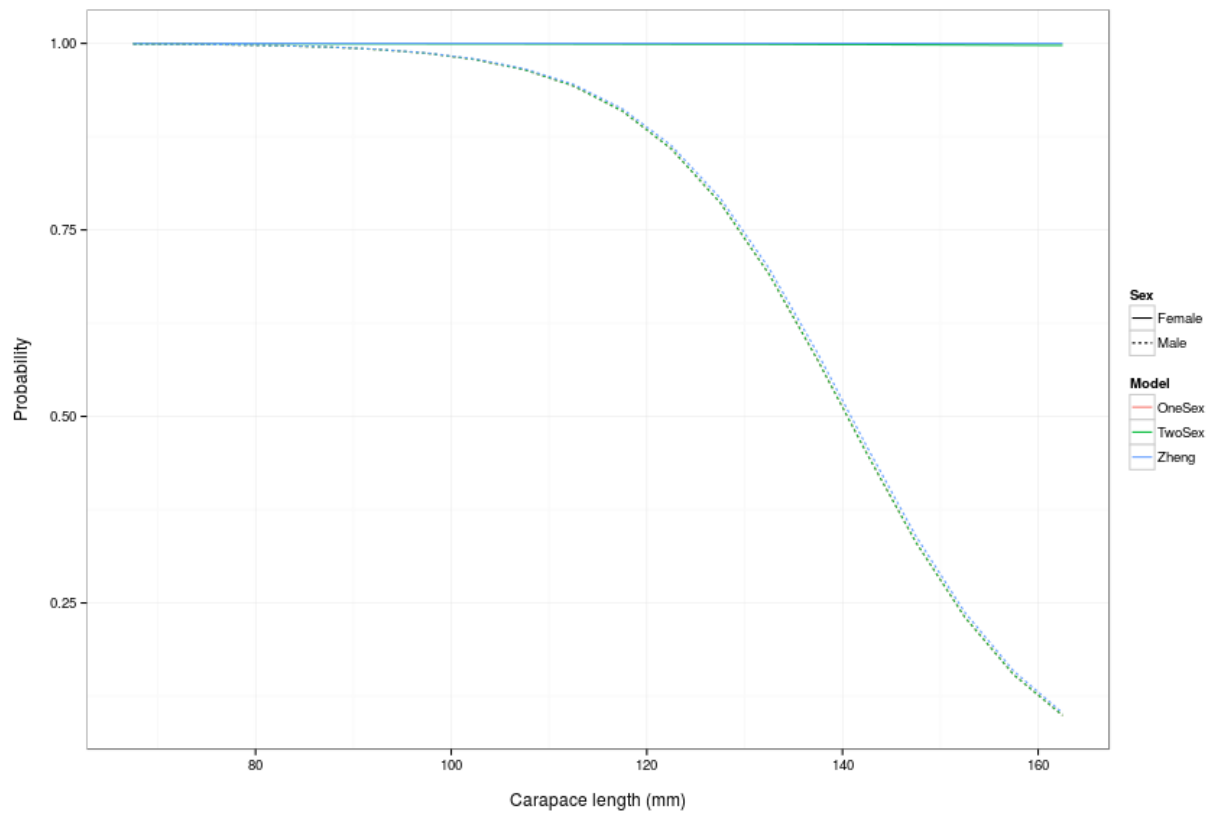


Figure 16: Molting probability for each of the models by sex. The molting probability for females is fixed at 1 as females molt every year.

Transition processes

The first set of figures is the growth probabilities (for all crabs that molt) (Figure 17). The second set of figures is the combination of growth and molting and represents the size transition (Figure 18).

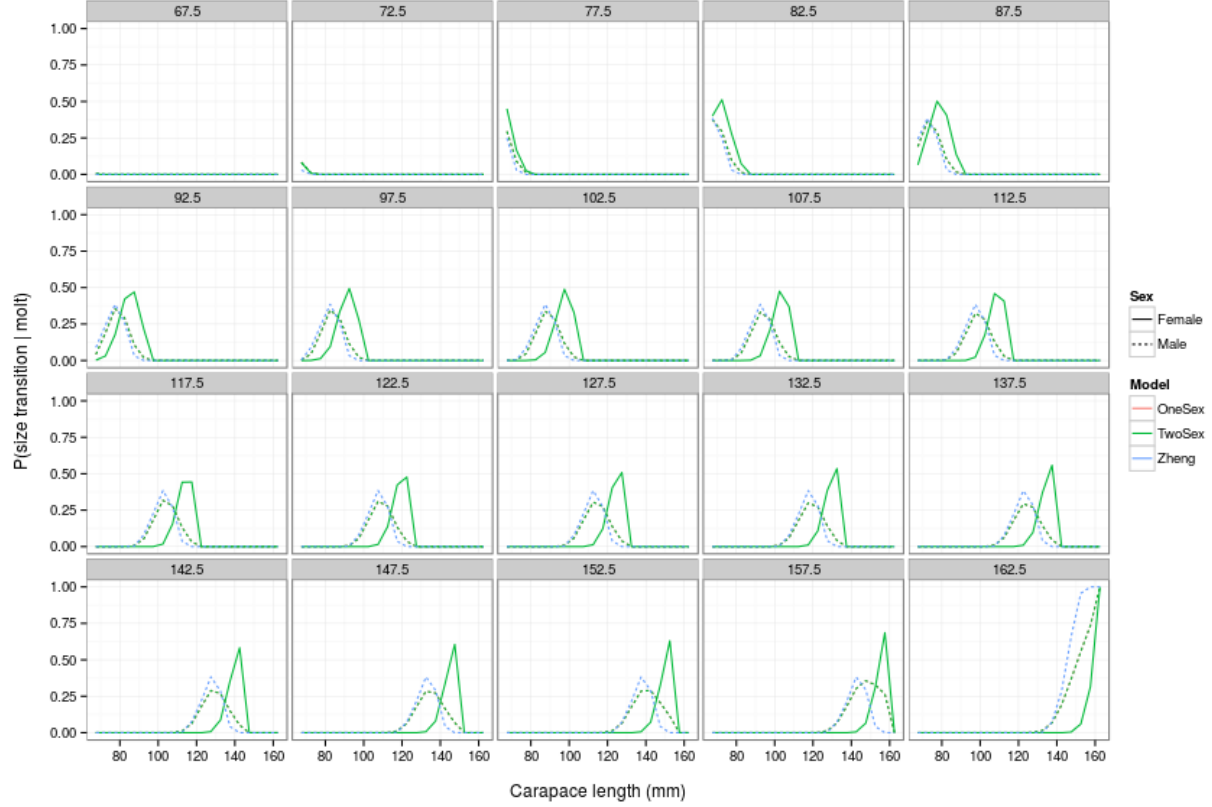


Figure 17: Growth transitions.

Numbers at length in 1975 and 2014

Total abundance and the proportions by length and sex are estimated in 1975 (the models initial year).

The number of crabs in each size class (\mathbf{n}) in the initial year ($t = 1$) and final year ($t = T$) in each model differ substantially (Figure 19). The scale of these results differ significantly and may be related to the interaction with natural mortality estimates and how the initial population-at-lengths were established (the BBRKC model assumes all new-shell).

Selectivity

The selectivity by size (S_ℓ) for each of the fisheries (Figure 20). In the TwoSex model, selectivity in the directed pot fishery is sex-specific. In the remaining fisheries, selectivity is constant by sex. In the NMFS trawl fishery, a different selectivity curve is estimated for the 1975-1981 period and for the 1982-2014 period.

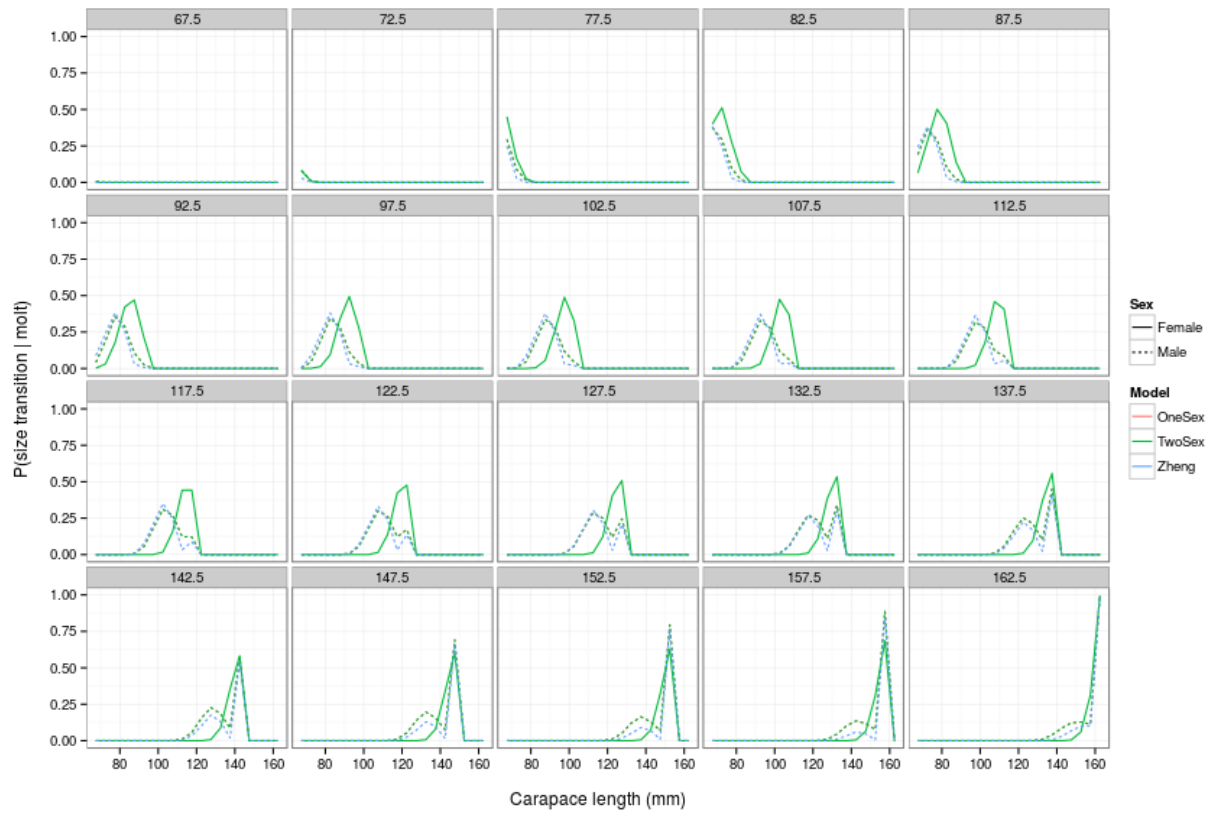


Figure 18: Size transitions.

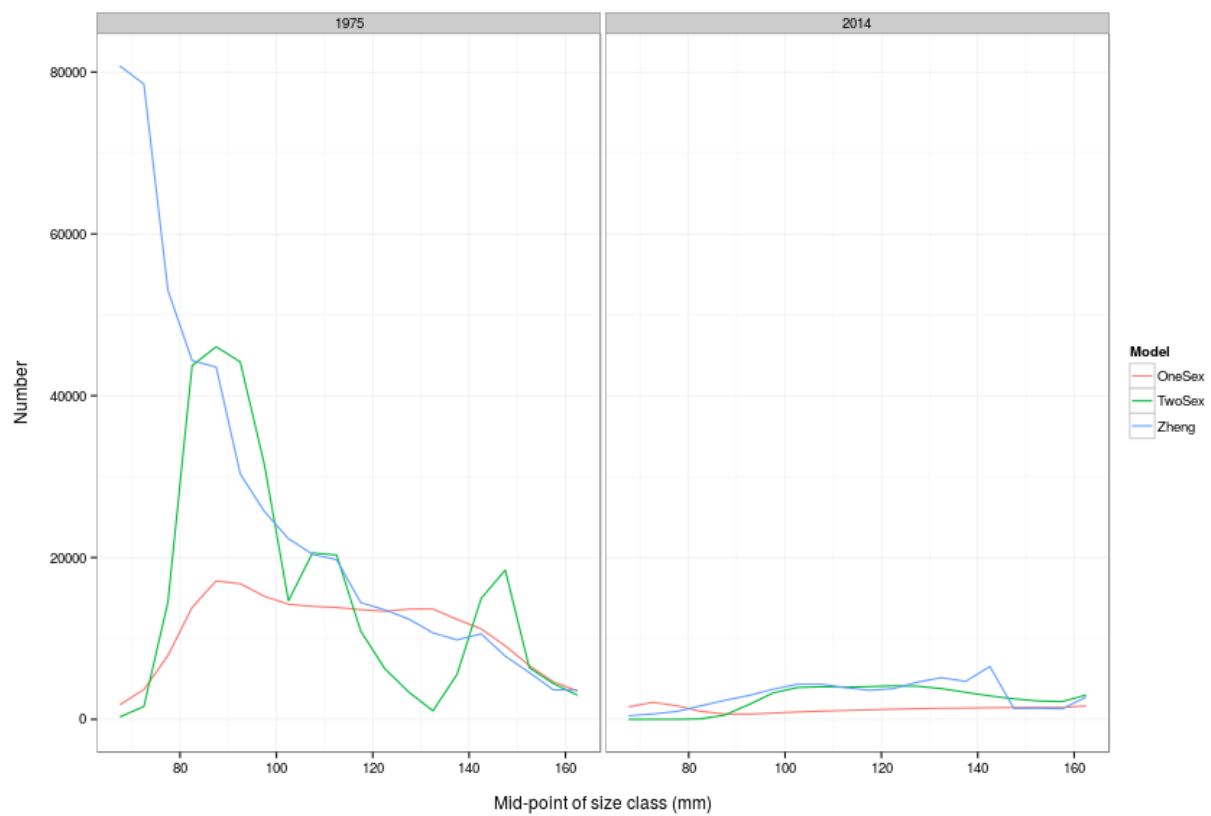


Figure 19: Numbers at length in 1975 and 2014.

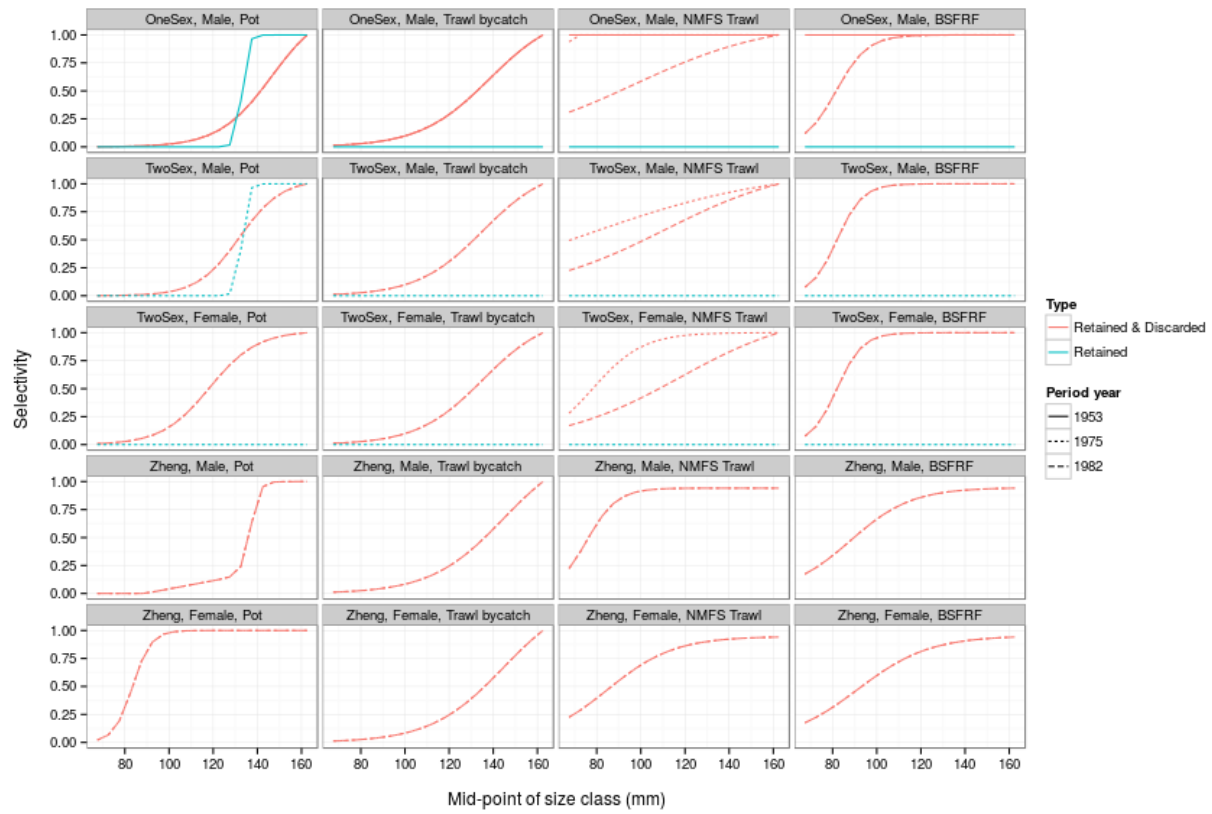


Figure 20: Estimated selectivity at size, sex and fishery in the OneSex, TwoSex and Zheng models. Estimated selectivities are shown for the directed pot fishery, the trawl bycatch fishery, the NMFS trawl survey, and the BSFRF survey.

Natural mortality

The figure below illustrates implementation of four step changes in M_t (freely estimated) in gmacs relative to the estimates from Zheng et al. 2014 (Figure 21). In both the ADFG-BBRKC and Gmacs-BBRKC models, time-varying natural mortality (M_t) is freely estimated with four step changes through time. The years (t) that each of these steps cover are fixed a priori. The pattern in time-varying natural mortality is reasonably similar between the two models (Figure 21), however the peak in natural mortality during the early 1980 is not as high in the Gmacs-BBRKC model.

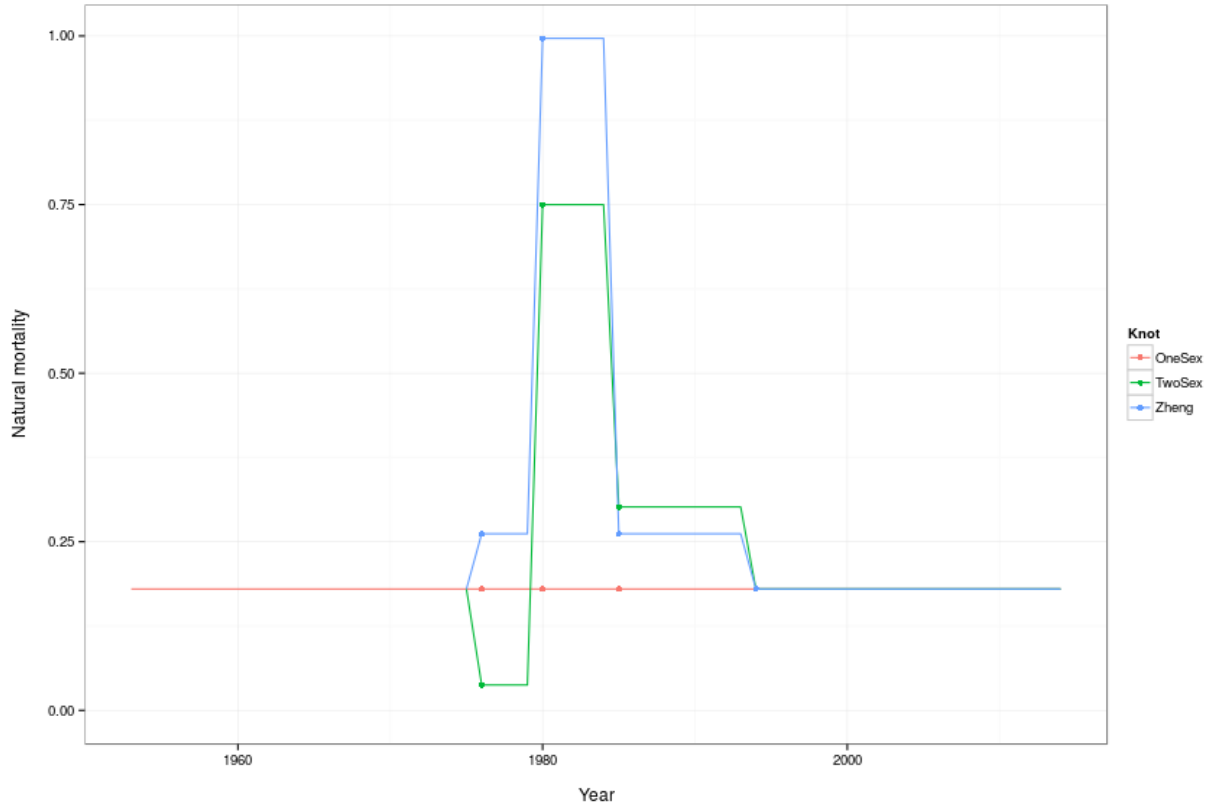


Figure 21: Time-varying natural mortality (M_t). Periods begin at 1976, 1980, 1985 and 1994.

Recruitment

Recruitment patterns are similar, but differences in natural mortality schedules will affect these matches. The figure below plots the values to have the same mean (Figure 22). Patterns in recruitment through time (R_t) estimated in the two models are similar, but differences in natural mortality schedules will affect these matches (Figure 22).

Mature male biomass (MMB)

The spawning stock biomass (tonnes) of mature males, termed the mature male biomass (MMB_t), also differs a lot between the two models (Figure 23). The OneSex model is not plotted here as the uncertainty during the early years is extremely high. The Zheng model is plotted without uncertainty.

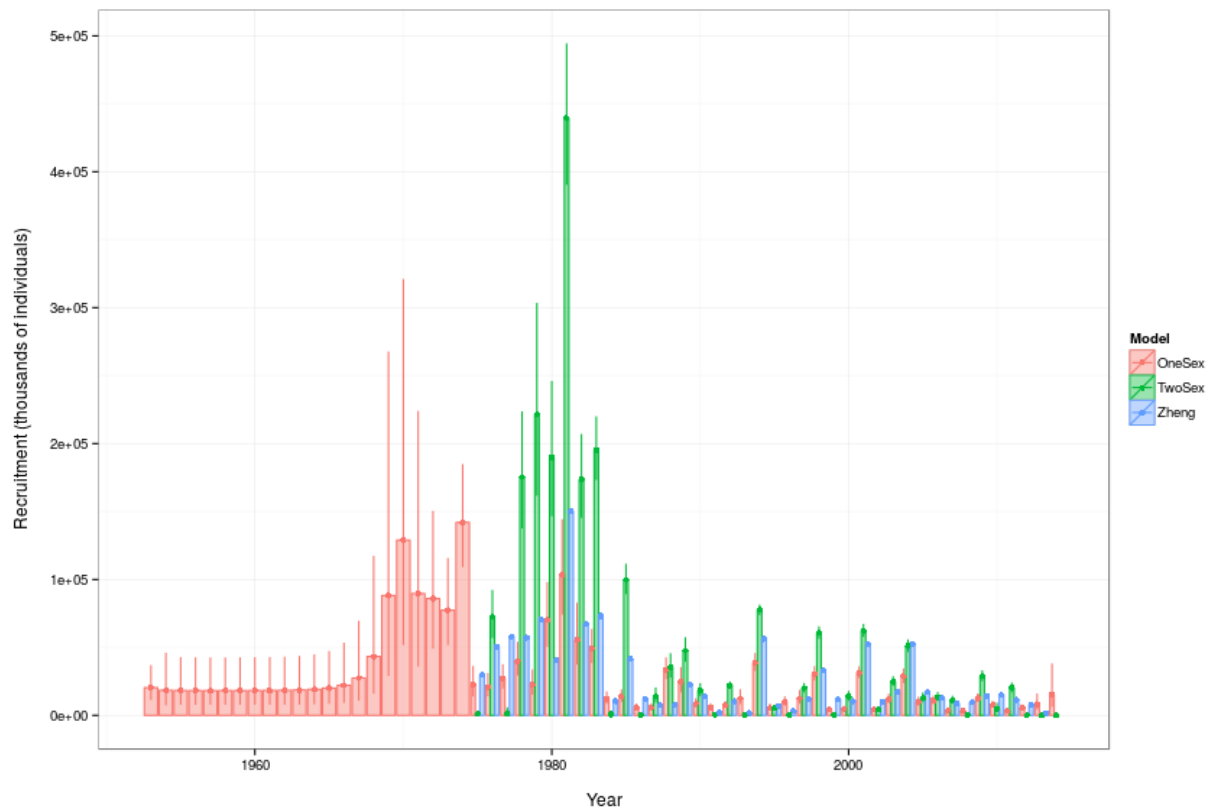


Figure 22: Estimated recruitment time series (R_t).

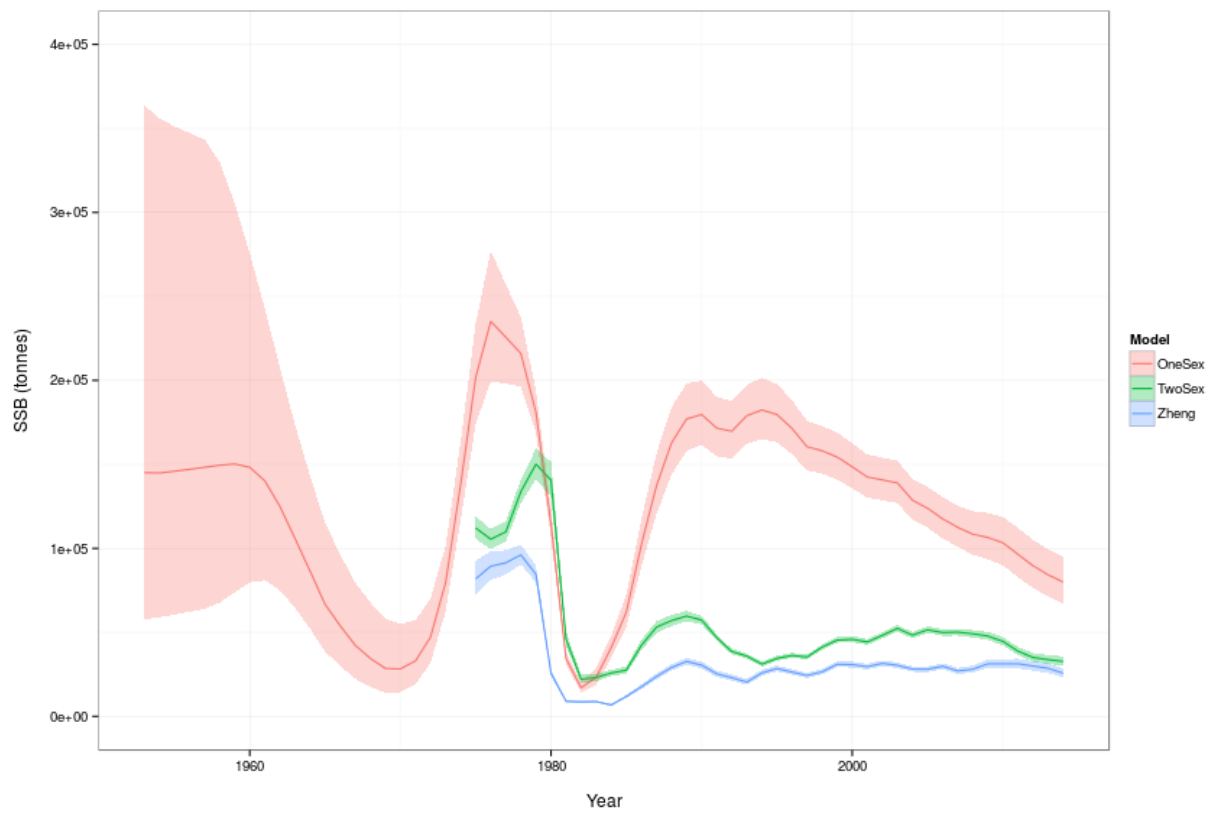


Figure 23: Mature male biomass (MMB) predicted in the two versions of the Gmacs model (OneSex and TwoSex) and the Zheng model.

Comparison of model results

The results of the ADFG-BBRKC model are compared here to the results of the Gmacs-BBRKC model.

Model	FSPR	BSPR	FOFL	OFL	RSPR
Gmacs (one sex)	0.28	32995.95	0.28	3373.93	8160.40
Gmacs (two sex)	0.21	22205.54	0.21	3030.39	16959.09

Gmacs results

We need to be able to produce a table of the comparative likelihoods (by component) of the alternative models. For best practice, just try and do what we do with SS models for SESSF stocks anyway. See the pink link report, and enter a section for each of those, and see if we can emulate a report of that type.

Discussion

Comparisons of actual likelihood function values and year-specific fits using the robust-multinomial would be the next step after selectivity issues are resolved. Subsequent to that, it would be worth exploring aspects of alternative model specifications (e.g., constant natural mortality over time, time-varying selectivity, etc) to evaluate sensitivities.

This discussion will focus on the challenges in developing a Gmacs version of the BBRKC model: those met, and those yet to be met.

References

- Punt, A. E., T. Huang, and M. N. Maunder. 2013. "Review of Integrated Size-Structured Models for Stock Assessment of Hard-to-Age Crustacean and Mollusc Species." *ICES Journal of Marine Science* 70 (1) (January): 16–33. doi:[10.1093/icesjms/fss185](https://doi.org/10.1093/icesjms/fss185). <http://icesjms.oxfordjournals.org/cgi/doi/10.1093/icesjms/fss185>.
- Zheng, J., and M.S.M Siddeek. 2014. "Bristol Bay Red King Crab Stock Assessment in Spring 2014." *Alaska Department of Fish and Game*: 149.