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 (Fournier et al. 2012).

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 flexible modeling framework.

This application is developed to compare with the current 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 and incorporating model outputs directly into documentation. 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.

The Gmacs-BBRKC model presented here is intended to be an example comparison which may follow for application to other crab stocks. We provide some direct model comparisons to illustrate the efficacy of Gmacs and show how alternative models can be specified (but please see Wiki for up to date details of model specification and estimation).

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; improvements to output files that are read into R for automated plotting of the observed and expected size compositions.
- **Prior specification explicit** now for all model parameters.

- Option to provide a **vector of weight at size** rather than parameters.
- Diagnostic “gradient.dat” at run completion has been added to help isolate parameters that are resulting in poor estimation properties.
- A reference list `Gmacs.bib` containing references important to crab modeling and length-structured models in general.

These new features have greatly improved the flexibility of the Gmacs modeling framework.

In development

Some other features requested by the NPFMC Crab Plan Team (CPT) and CIE reviews that are presently under development include:

- Double-normal and non-parametric selectivity types
- Additional time-varying options for molt, growth and maturity
- Dirichlet size composition option for likelihoods
- 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 overlayed, correlation plots, data and posterior predictive distributions
- Adding diagnostics of likelihood fitting properties

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. *Note: in the current assessment the survey selectivity asymptotes at 0.94 which may affect interpretation of the survey catchability*
- Growth is a function of size and is constant 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. *Note: this feature for dimorphic time-varying growth is currently unavailable in Gmacs*
- Molting probabilities are an inverse logistic function of size for males. Females molt annually.

- Annual fishing seasons for the directed fishery are short. *Note: Gmacs uses the Baranov catch equation though options for developing pulse sequential forms are in development*
- 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 model configurations

The data and model specifications used in the Gmacs-BBRKC model were patterned after those in the '4nb' scenario developed by Zheng and Siddeek (2014), herein referred to as the BBRKC model. The BBRKC model treats recruits independently by sex along with sex-specific natural mortality (M) and fishing mortality (F). Presently, the split-sex options in Gmacs only allows the assumption that the sex ratio at recruitment is 50:50. After recruiting, sexual dimorphic growth and mortality along with fishery effects can play a role in changes in sex ratio over time. In an attempt to provide a comparison with the male- component of the BBRKC model, we drafted one Gmacs configuration as a "male- only" or single sex model in addition to the split two-sex Gmacs configuration. Also for illustration purposes, the period and extent of data for the single-sex model was extended back to 1953. A full comparison of the approaches are shown in the following table:

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 conditions	ν	2	2	2
No. maturity classes	m	2	1	1
No. size-classes	ℓ	20	20	20
No. Fleets	k	5	2	5

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 presented, the OneSex model and the TwoSex model.

Fit to survey abundance indices

In both the OneSex and TwoSex models priors were placed on q for the NMFS and BSFRF trawl surveys. A normal prior for the NMFS trawl survey was used with $\mu = 0.843136$ (i.e. 0.896×0.941 which is the maximum selectivity of the NMFS survey in Jies model) and $\sigma = 0.01$. A normal prior is also used for the BSFRF trawl survey with $\mu = 1$ and $\sigma = 0.03$.

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

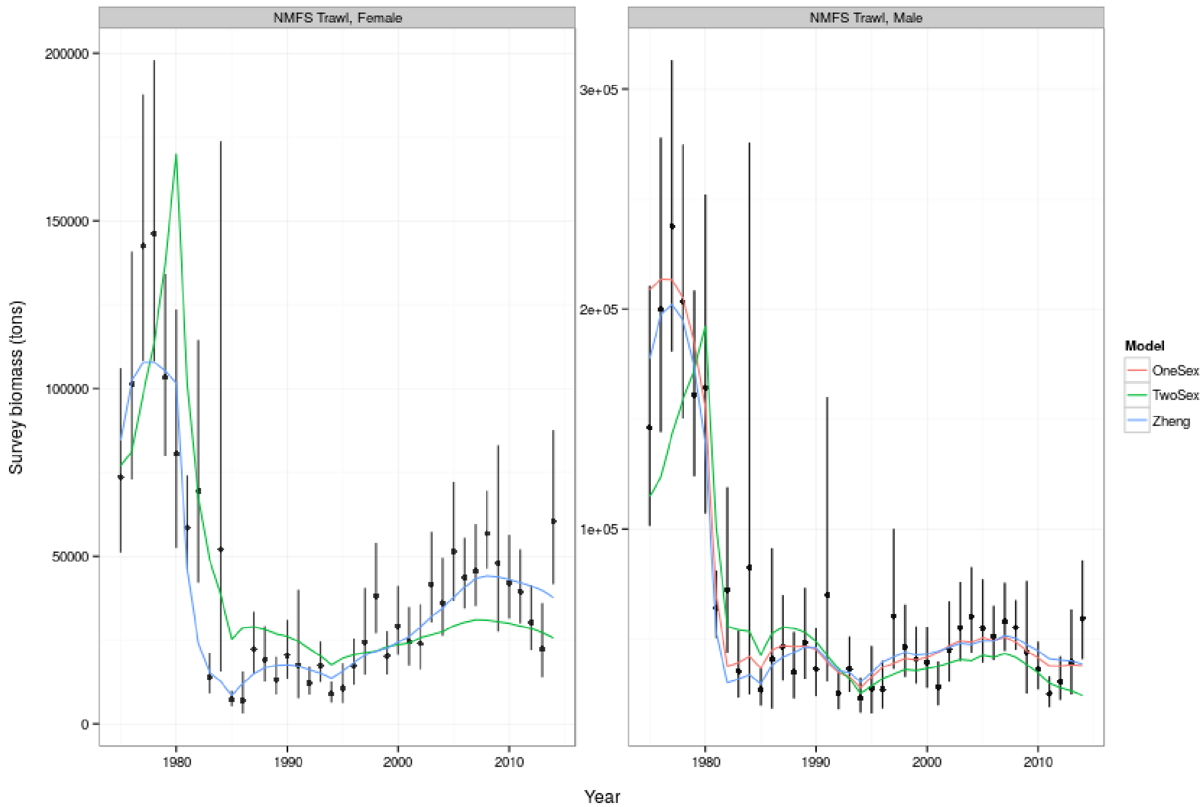

Figure 1: Model fits to sex-specific NMFS trawl survey biomass (tons) from 1975 to 2014. The error bars represent plus and minus 2 standard deviations.

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)).

Fit to size composition data

The fit of the Gmacs models to the BBRKC size composition data are shown 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), the NMFS trawl survey for newshell males (Figure 8), oldshell males (Figure 9) and females (Figure 10), and the BSFRF survey (Figure 11).

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 together with old shell males and females. The plots shown below have been normalized for display purposes. *In future plotting versions the scales will be retained as an option.*

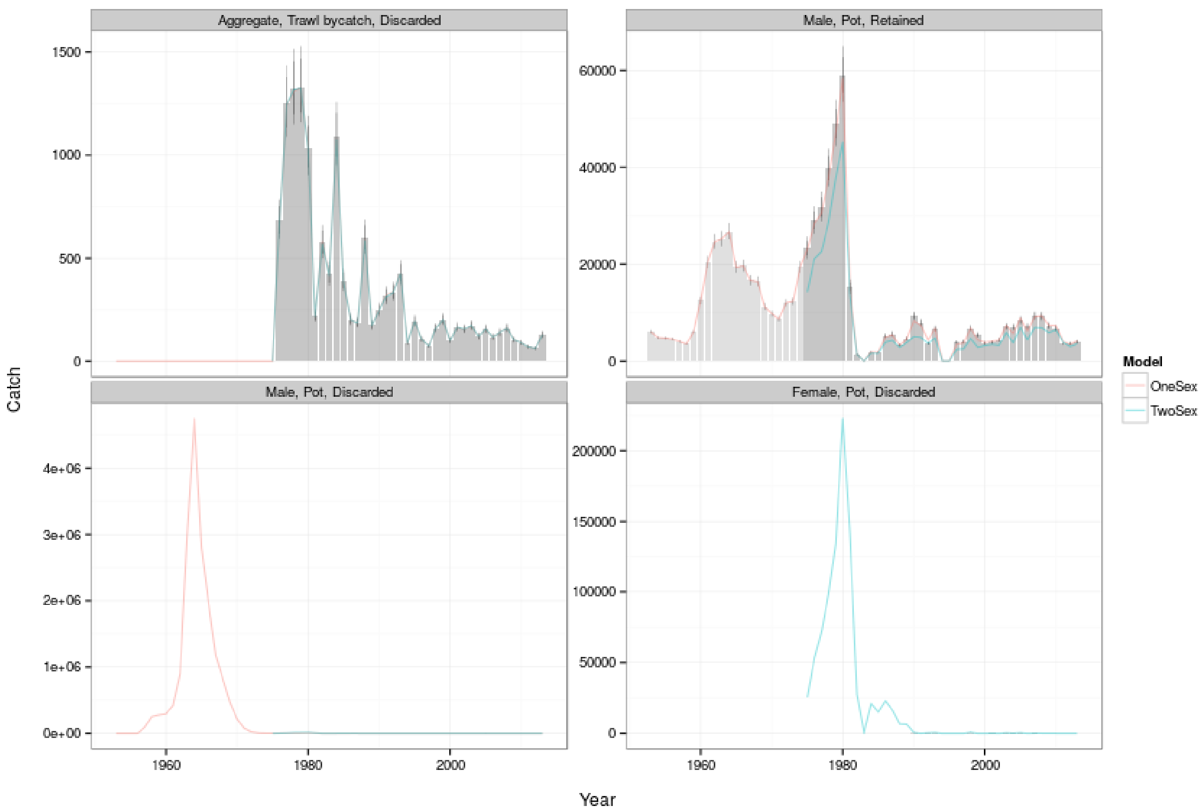

Figure 2: Observed and predicted catch (tons) by gear type for the two Gmacs models. The OneSex model includes catch data from 1953 to 2013. The TwoSex model includes catch data from 1975 to 2013.

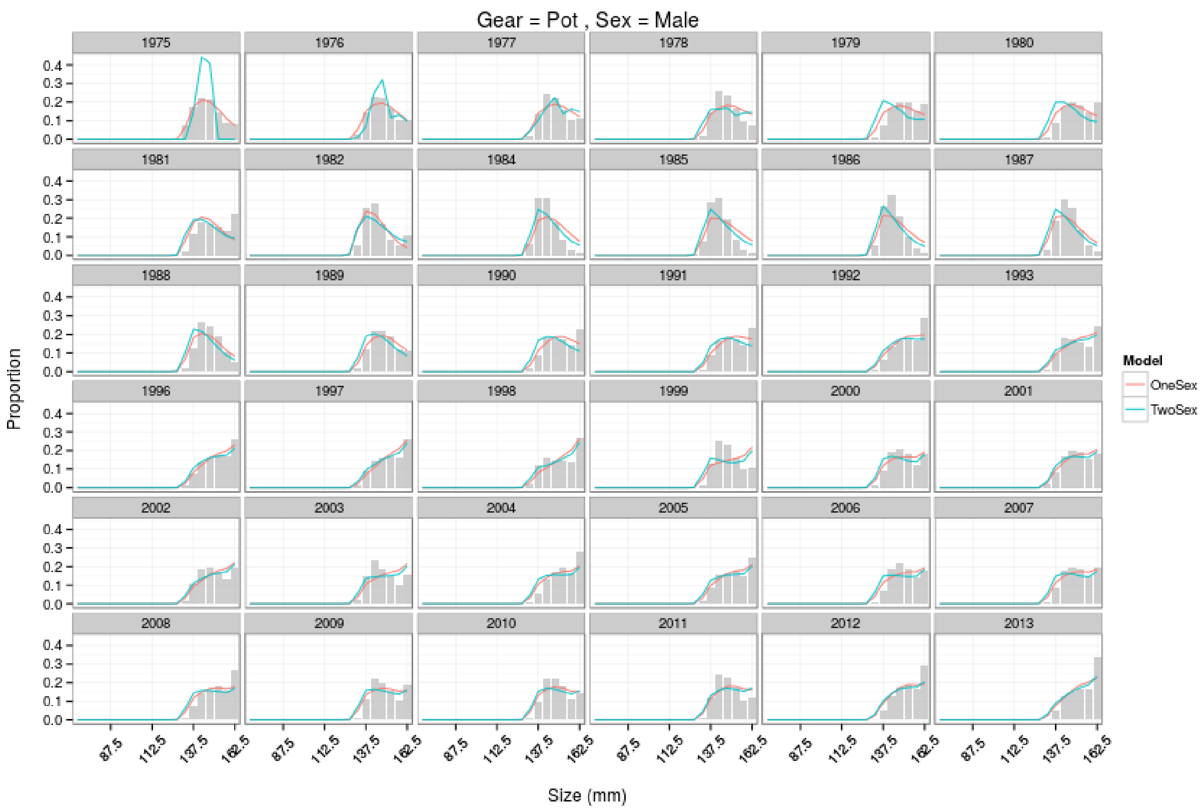

Figure 3: Observed and model estimated size-frequencies of male BBRKC by year retained in the directed pot fishery.

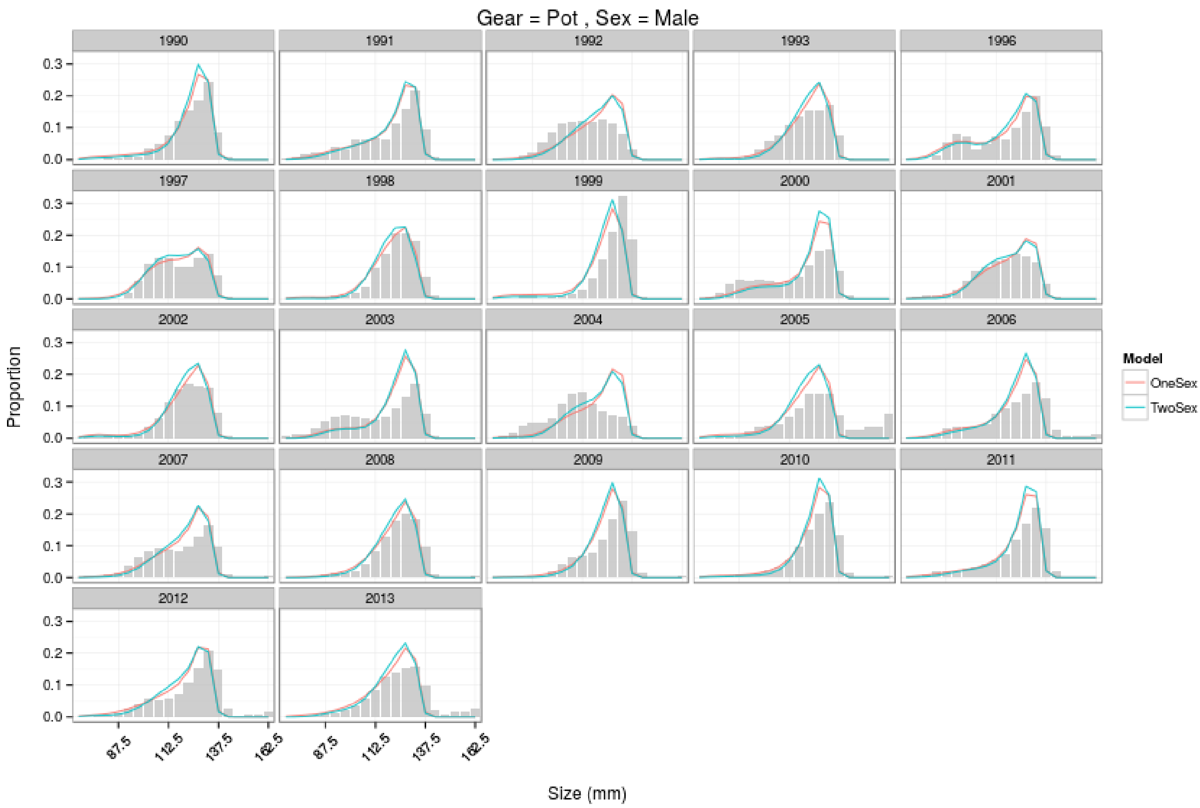

Figure 4: Observed and model estimated size-frequencies of discarded male BBRKC by year in the directed pot fishery.

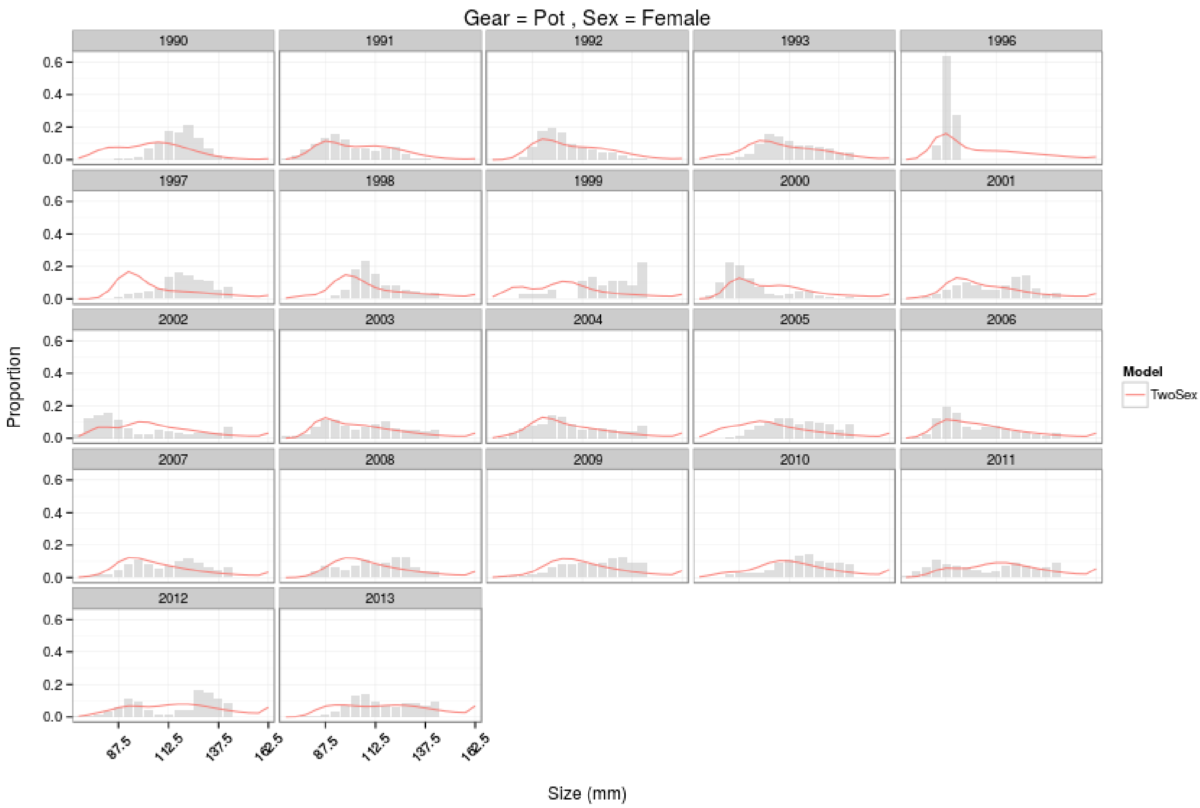

Figure 5: Observed and model estimated size-frequencies of discarded female BBRKC by year in the directed pot fishery.

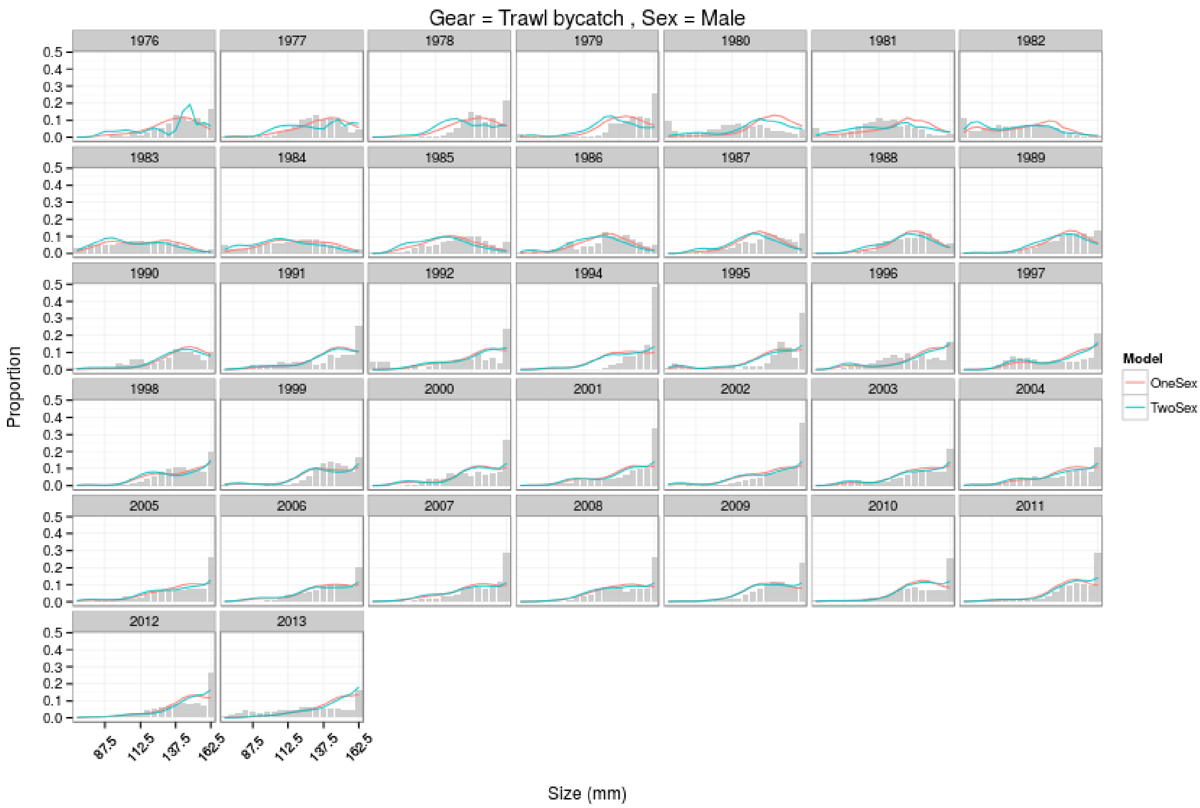

Figure 6: Observed and model estimated size-frequencies of male BBRKC by year in the groundfish trawl bycatch fisheries.

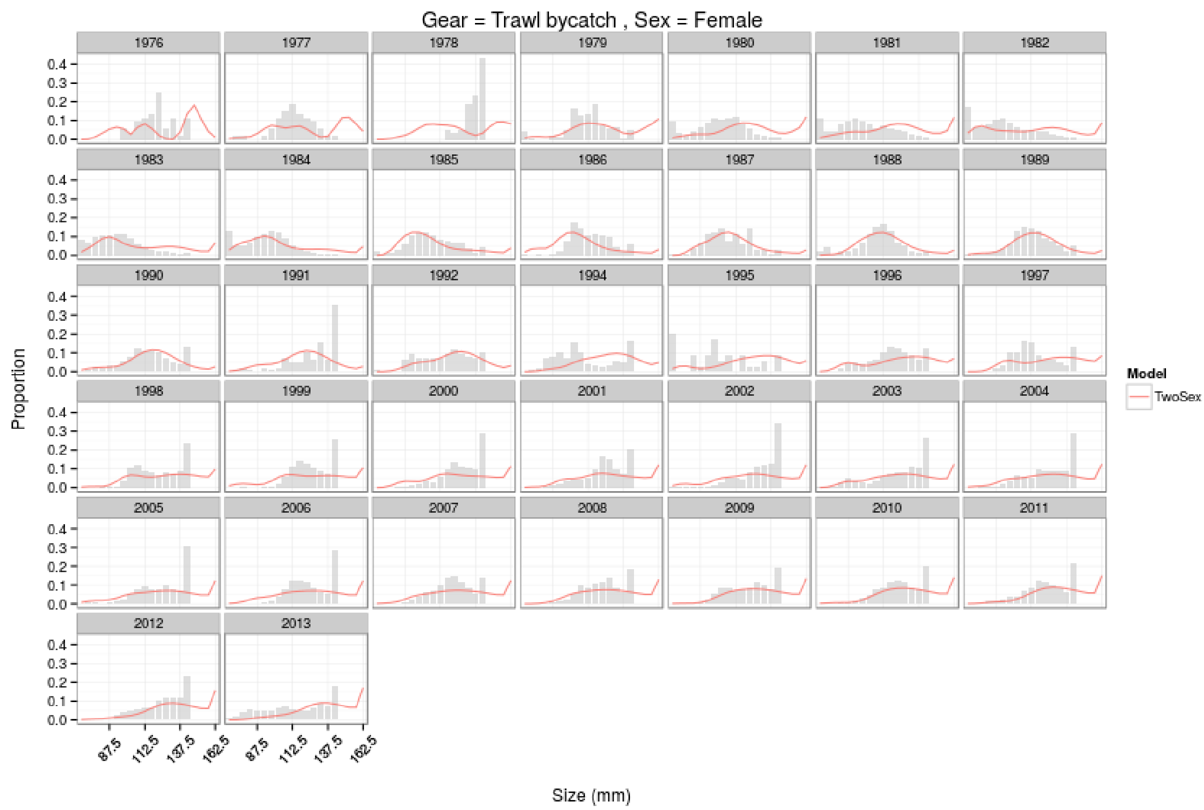

Figure 7: Observed and model estimated size-frequencies of female BBRKC by year in the groundfish trawl bycatch fisheries.

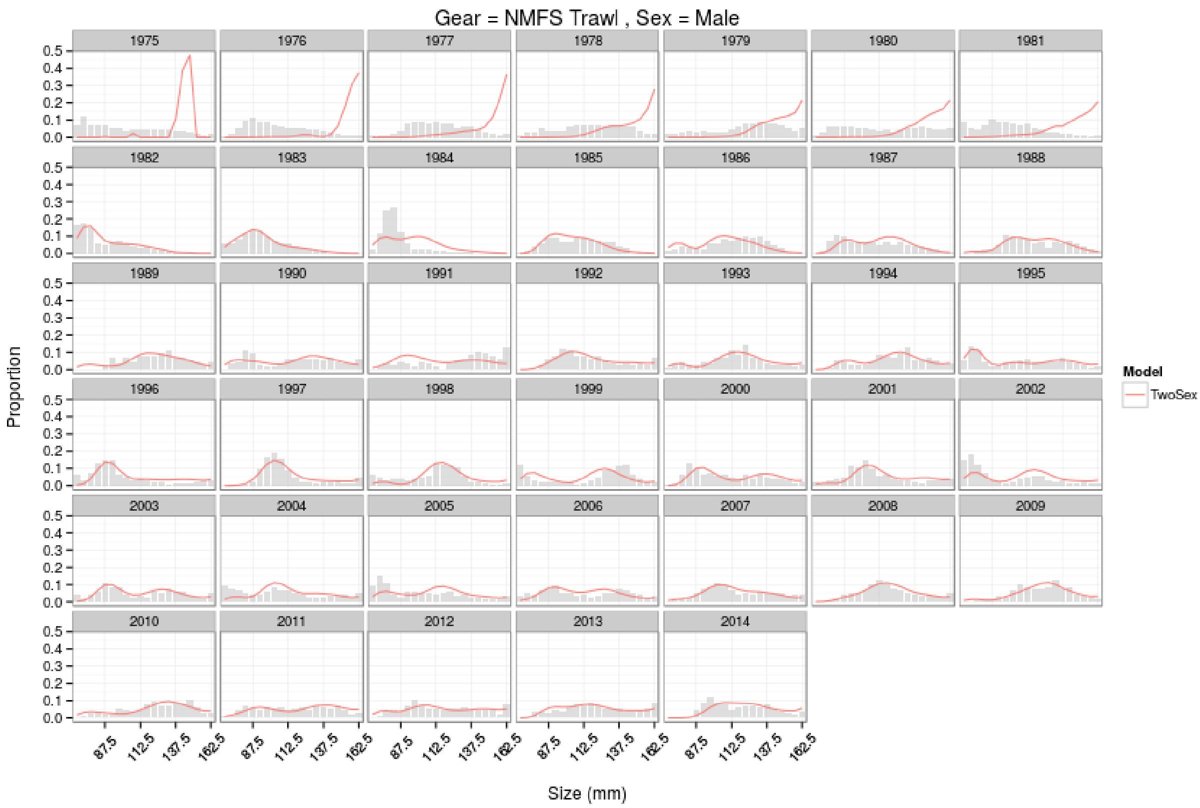

Figure 8: Observed and model estimated size-frequencies of new shell male BBRKC by year in the NMFS trawl survey.

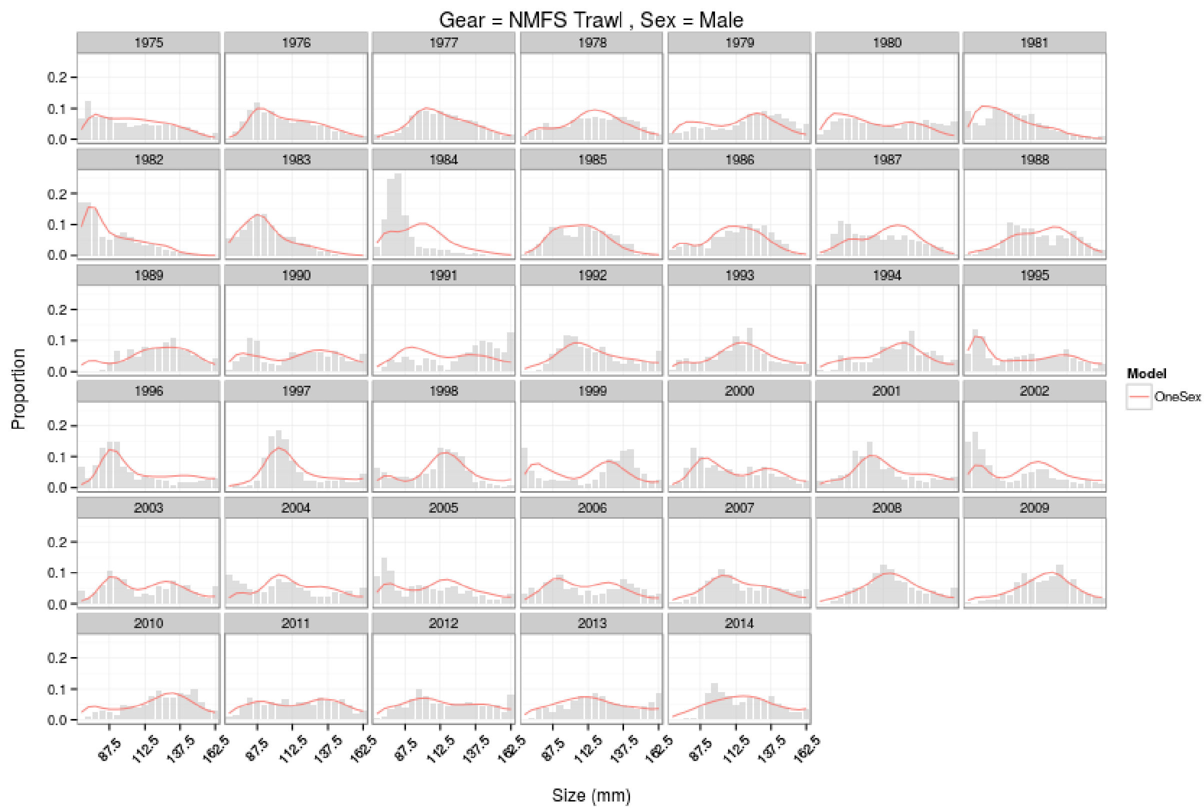

Figure 9: Observed and model estimated size-frequencies of old shell male BBRKC by year in the NMFS trawl survey.

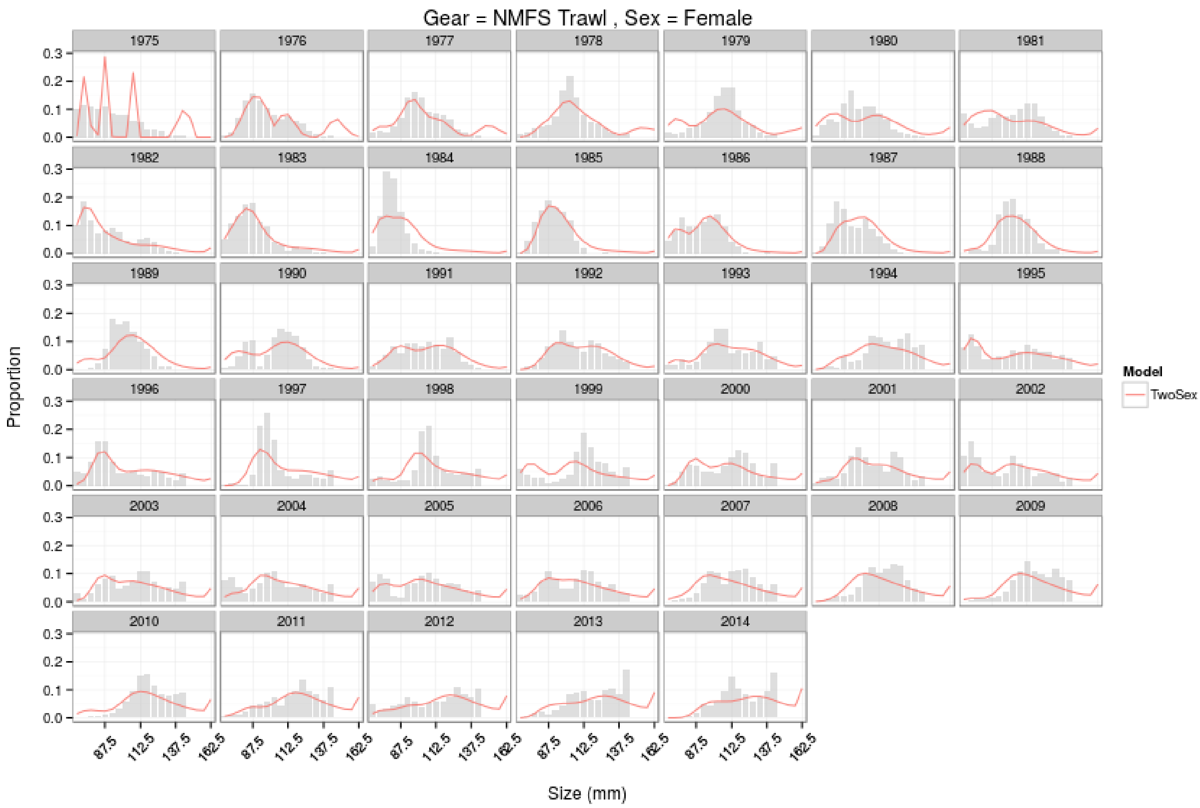

Figure 10: Observed and model estimated size-frequencies of female BBRKC by year in the NMFS trawl survey.

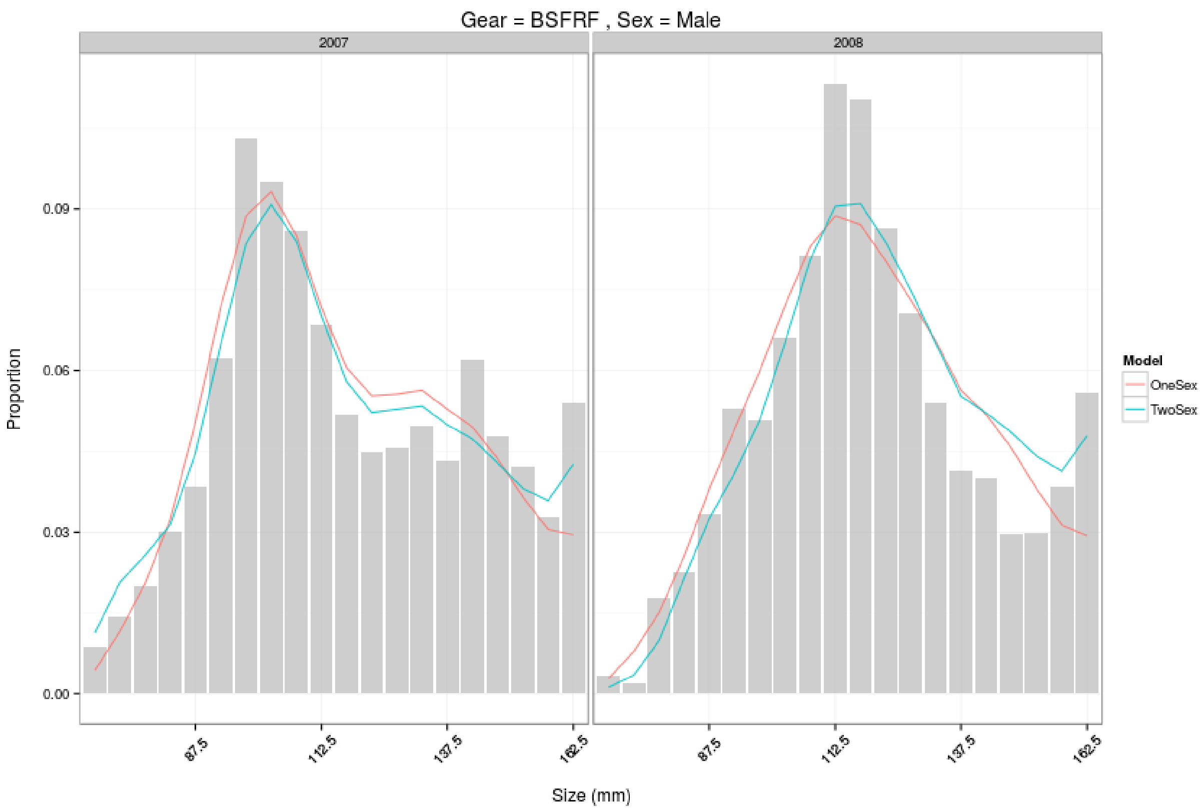

Figure 11: Observed and model estimated size-frequencies of both male and female BBRKC by year in the BSFRF trawl surveys.

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 set to be identical to that of the BBRKC model (Figure 12).

There are differences between immature and mature females hence the unusual shape of the length-weight relationship for females (Zheng and Siddeek 2014). Given a size, once females mature with eggs, they are heavier than immature females. BBRKC 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 effectively excluded (they exceed the last observed length group), so the plus group value is simply repeated. In future versions, when the immature and mature females are modeled separately, two mean weight- at-size functions can be used. The mean weights for both male and female plus length groups are higher than the function values to reflect that there are more crabs larger than the plus group mid sizes. This adjustment is based on the survey length frequency data over time.

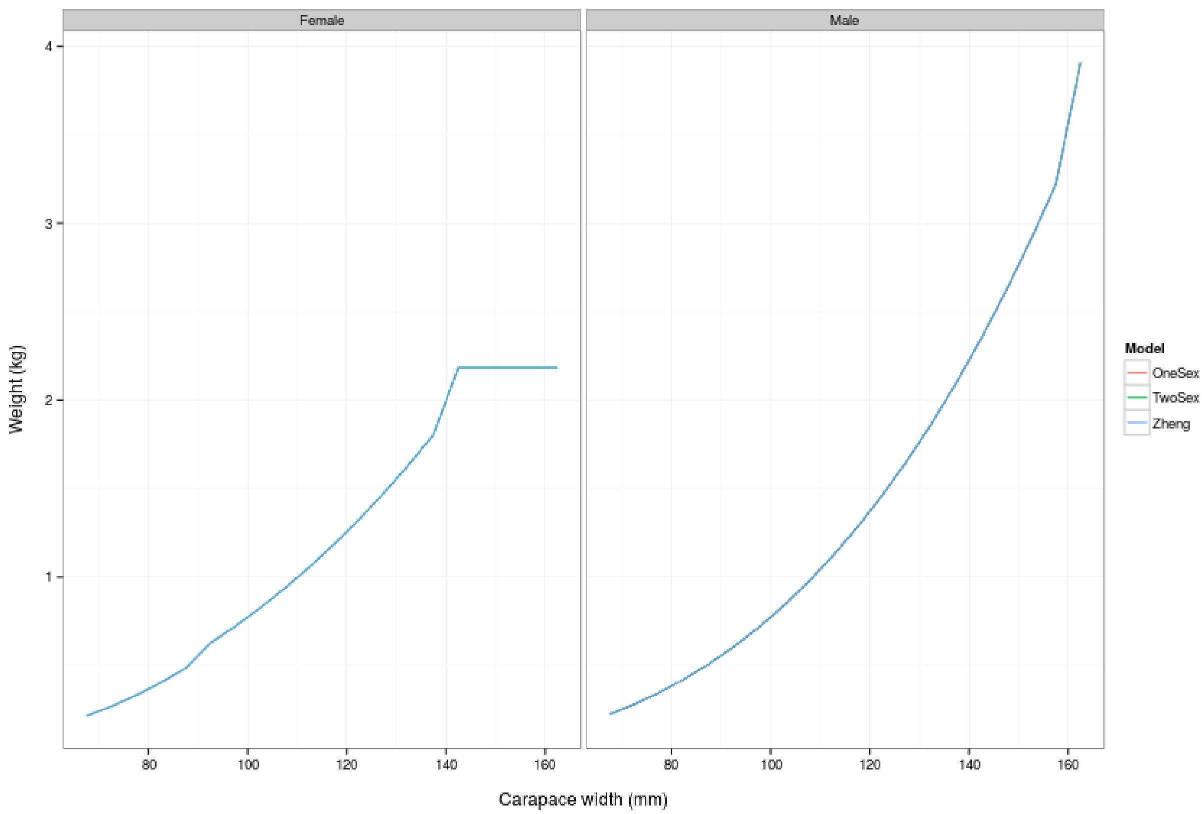

Figure 12: Relationship between carapace width (mm) and weight (kg) by sex in each of the models (provided as a vector of weights at length to Gmacs so lines all overlap).

Initial recruitment size distribution

Gmacs was configured to match the Zheng and Siddeek (2014) model recruitment size distribution closely (Figure 13).

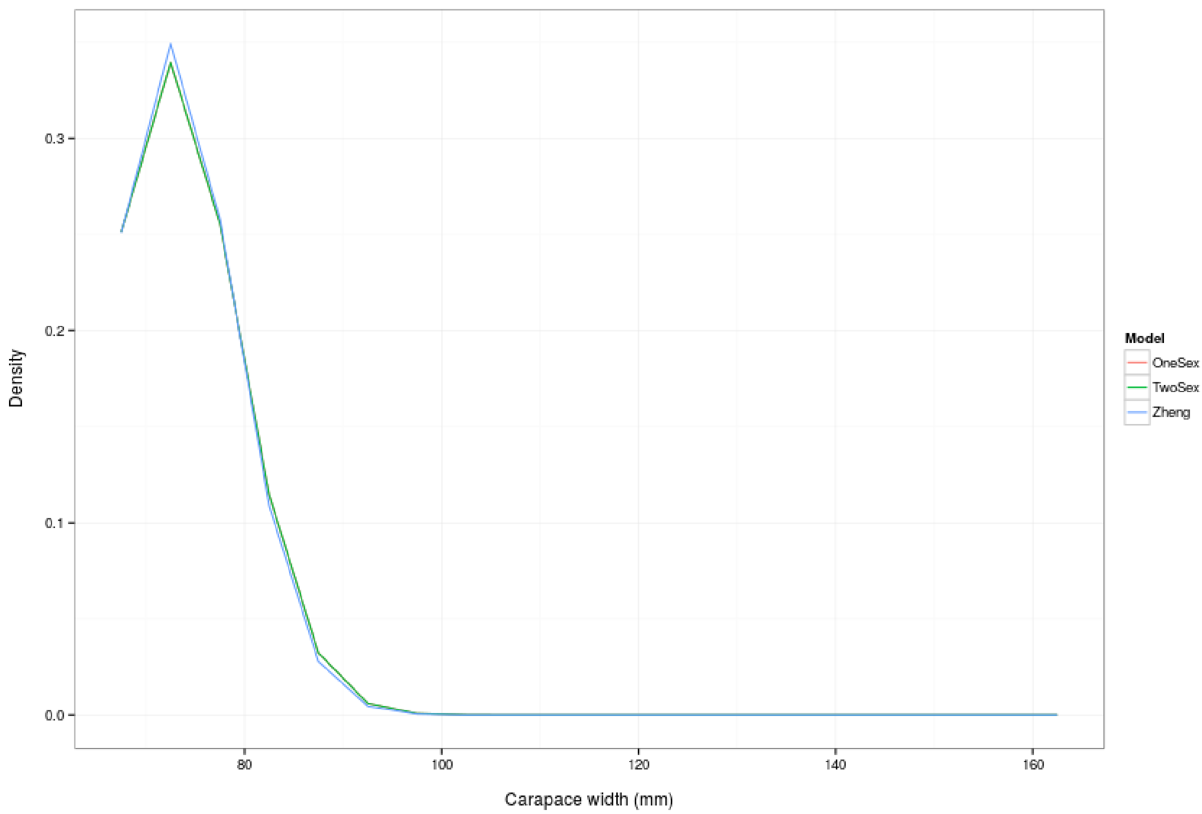

Figure 13: Distribution of carapace width (mm) at recruitment.

Molting increment and probability

In the BBRKC model one functional for for growth increment per molt is used for males and three functions for females (due to changing sizes at maturity).

Options to fit relationship based on data were developed within Gmacs but for the BBRKC system, a size-specific vector was used to determine molt increments as shown below (Figure 14). Fixed parameters in gmacs were set to match assumptions in Zheng and Siddeek (2014) (Figure 15).

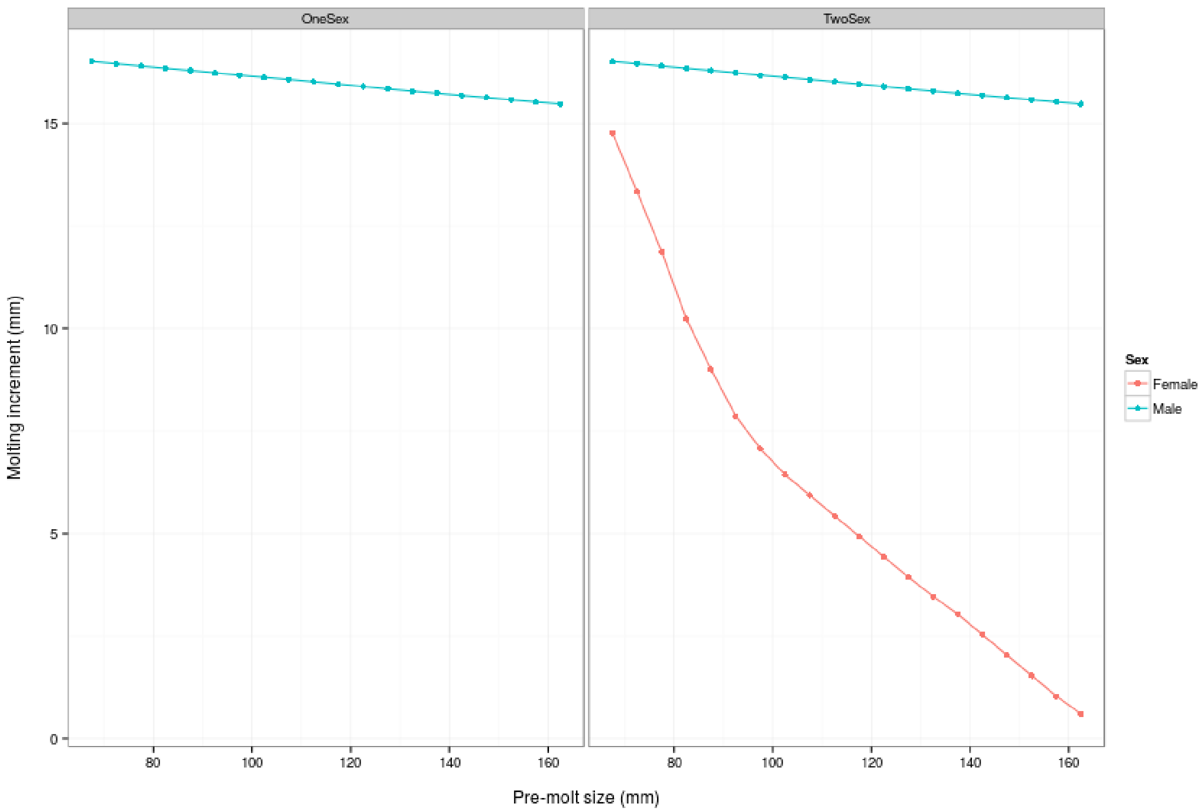

Figure 14: Growth increment (mm) each molt by sex in the OneSex and TwoSex models.

In the BBRKC model, females are specified to molt annually consistent with their biology. This means that molting probability is always 1 for females and 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. Male BBRKC molting patterns differ from females. As such, the BBRKC model was specified to have two molting probability curves, one during 1975-78 and another from 1979 to the present. *For the current version of Gmacs, only a single molting probability curve is allowed.*

Transition processes

The first set of figures is the growth probabilities (for all crabs that molt) (Figure 16). The second set of figures is the combination of growth and molting probabilities and represents the size transition (Figure 17).

Numbers at length in the first and last year

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

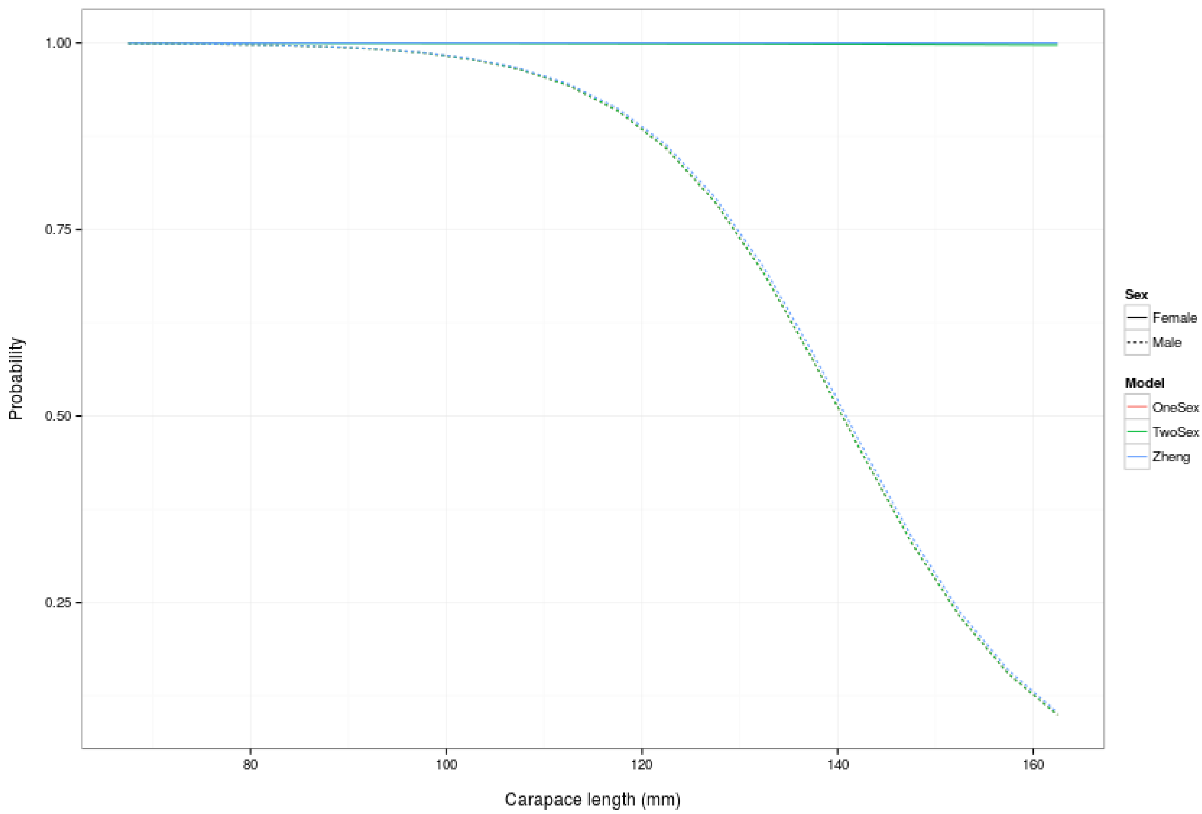

Figure 15: Molting probability for each of the models by sex. The molting probability for females is fixed at 1 as females molt every year.

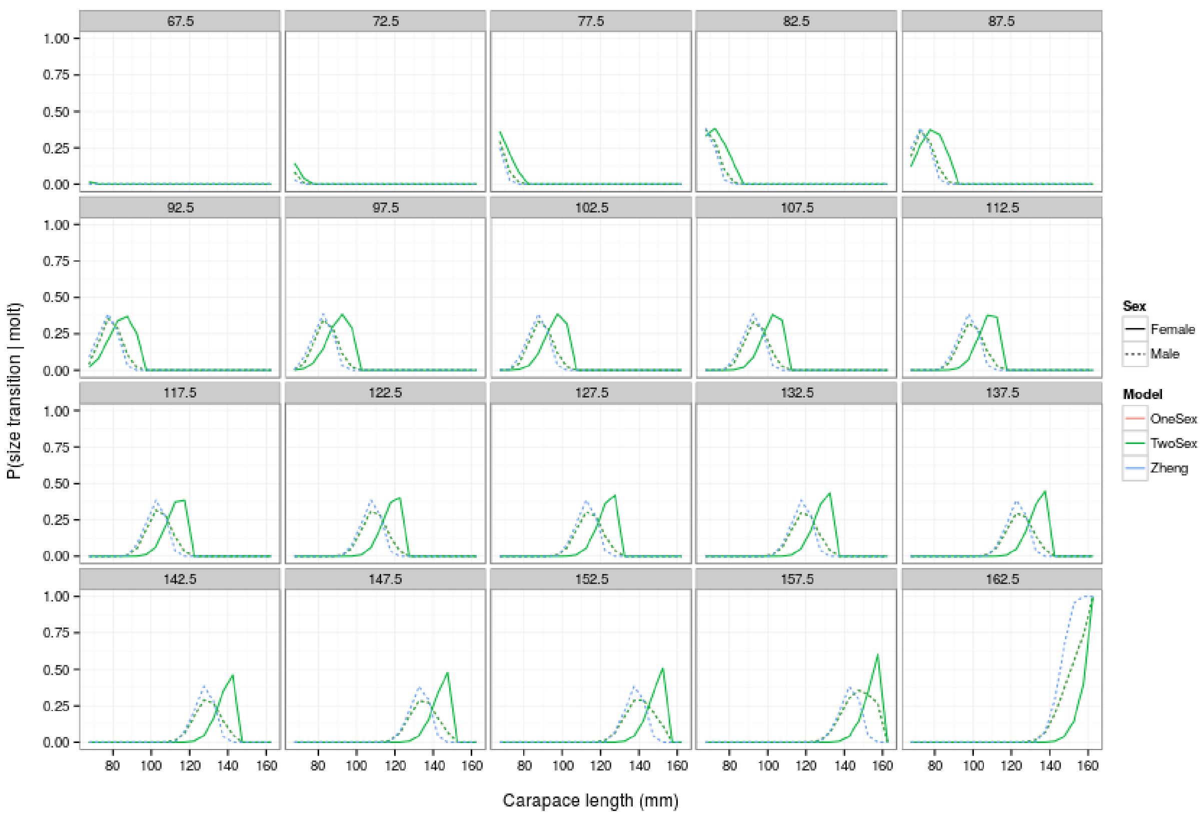

Figure 16: Growth transitions.

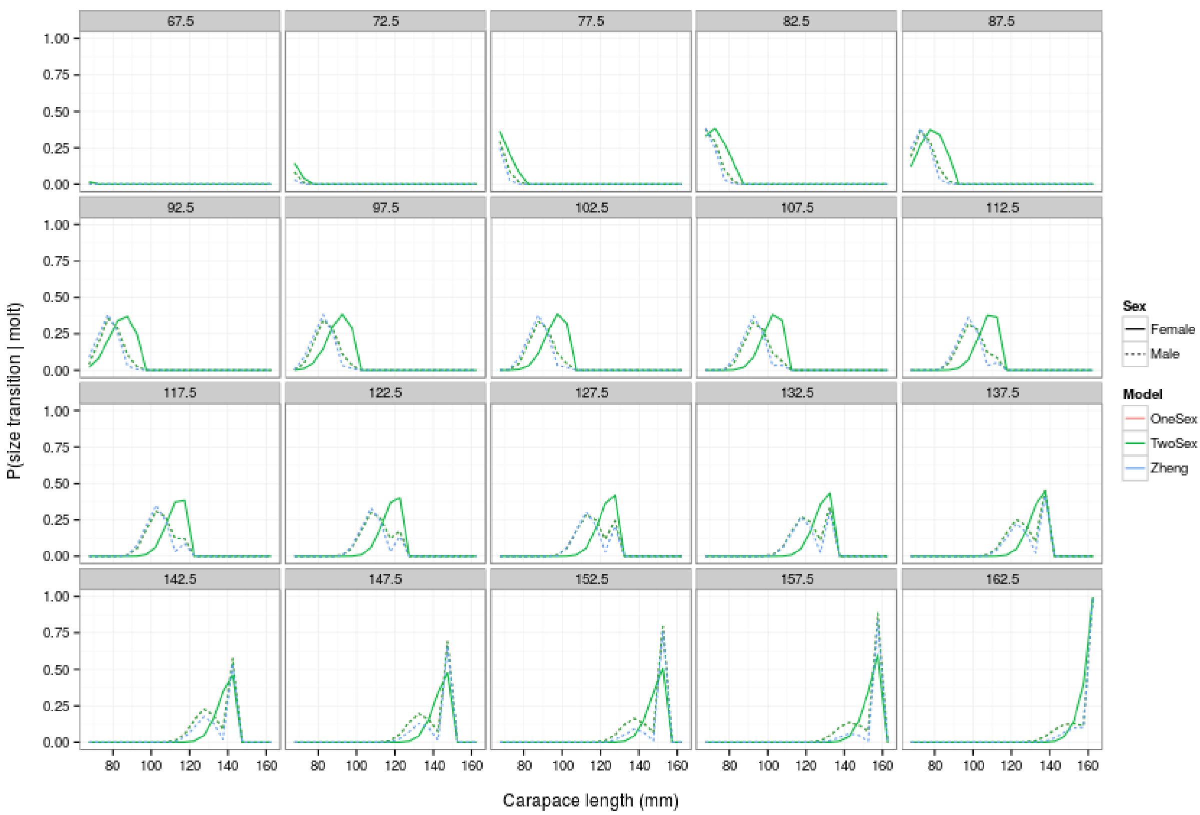

Figure 17: Size transitions.

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 18). 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).

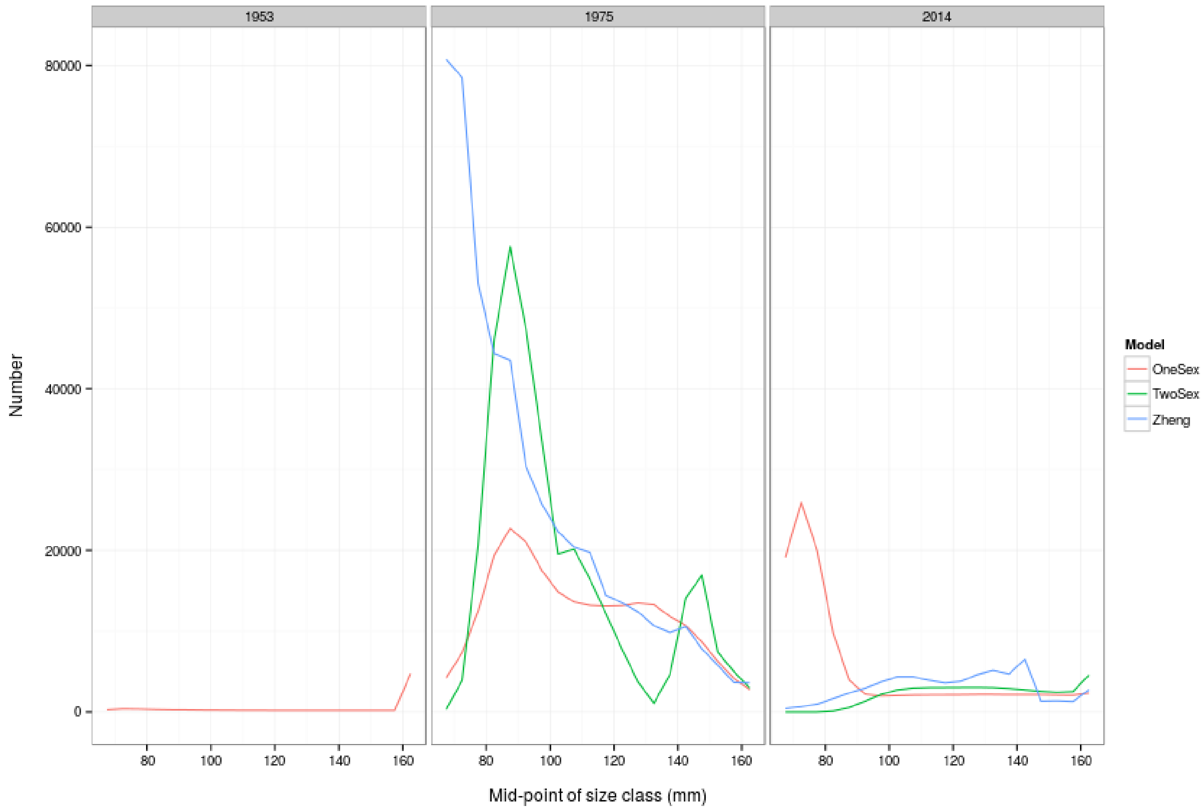

Figure 18: Numbers at length in 1953, 1975 and 2014 in each of the models. The first year of the OneSex model is 1953. The first year of the Zheng and TwoSex models in 1975.

Selectivity

The selectivity by size (S_ℓ) for each of the fisheries (Figure 19). 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.

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 20). 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 20), however the peak in natural mortality during the early 1980 is not as high in the Gmacs-BBRKC model. *In the Gmacs model, a spline function for natural mortality changes over time is an available as an option.*

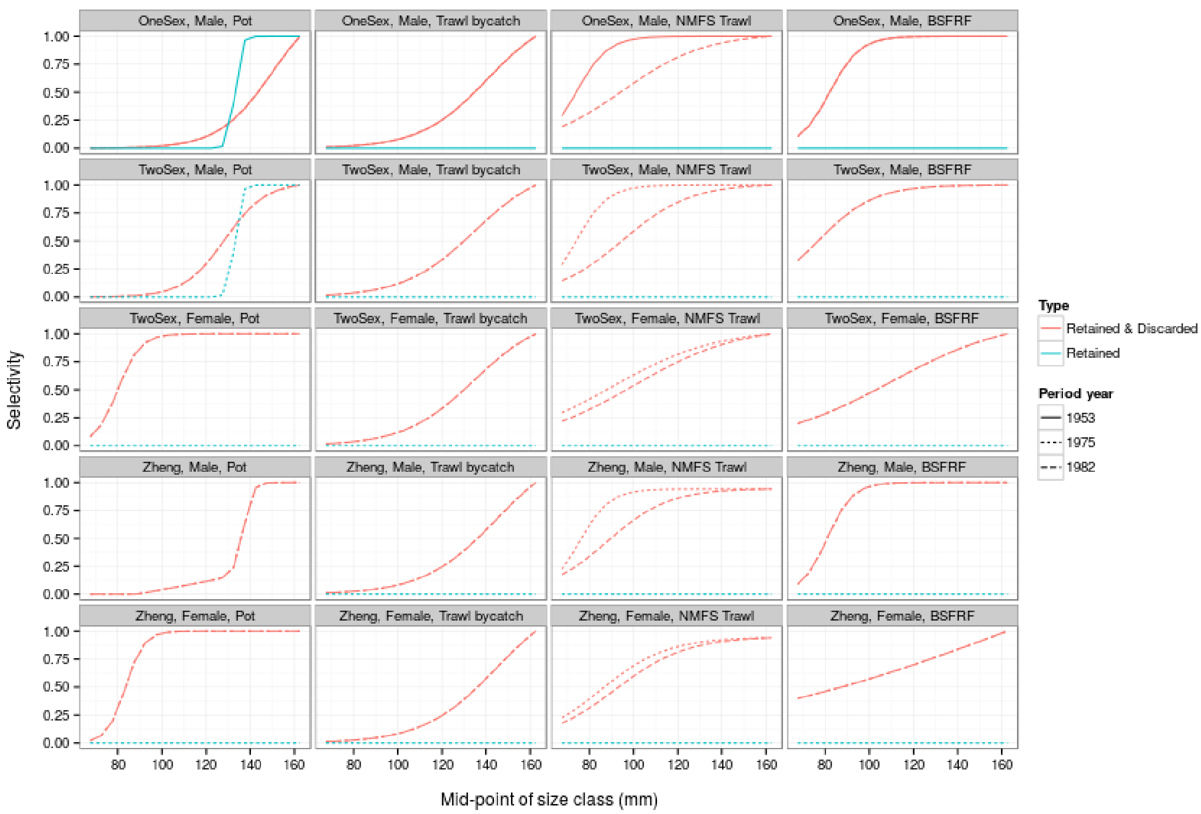

Figure 19: Estimated selectivity at size, sex and fishery in the OneSex, TwoSex and Zheng models. Estimated selectivities are shown for the directed pot fishery, the trawl bycatch fishery, the NMFS trawl survey, and the BSFRF survey.

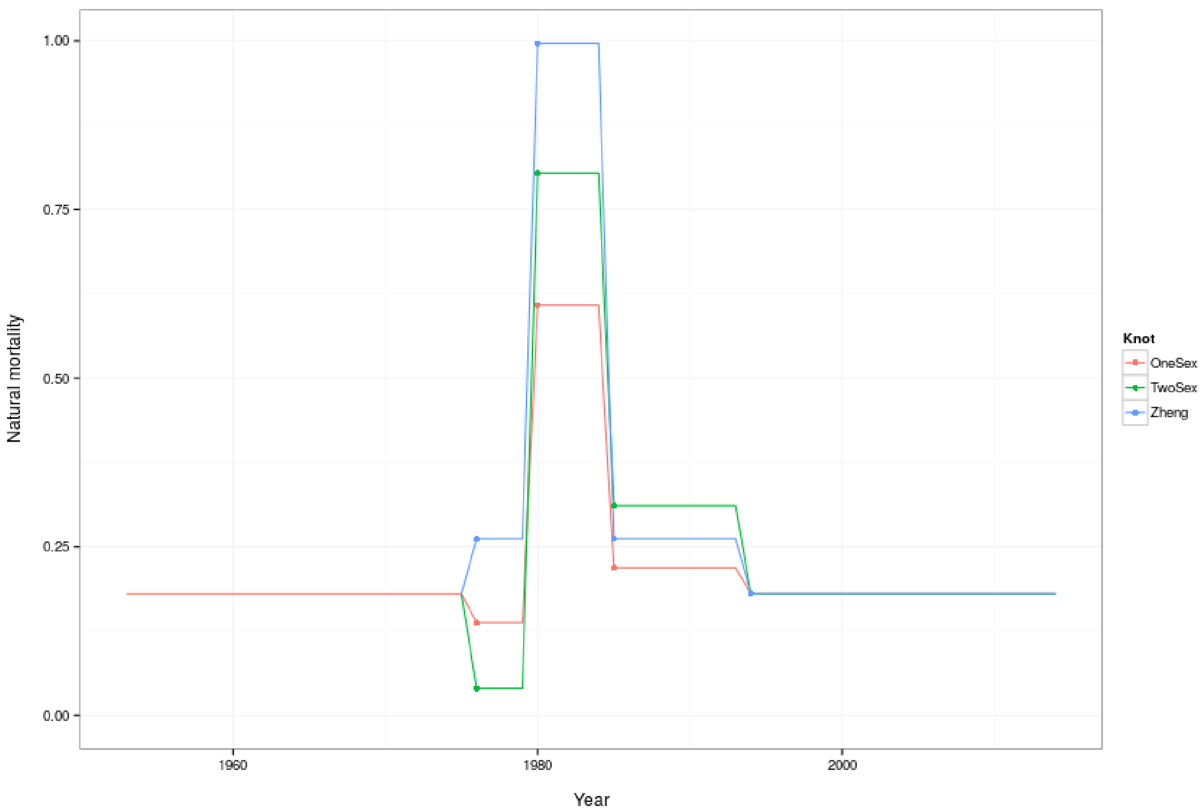

Figure 20: Time-varying natural mortality (M_t). Periods begin at 1976, 1980, 1985 and 1994.

Recruitment

Recruitment (R_t) patterns are similar among models, but differences in natural mortality schedules will affect these matches. The figure below shows that the values have roughly the same mean (Figure 21).

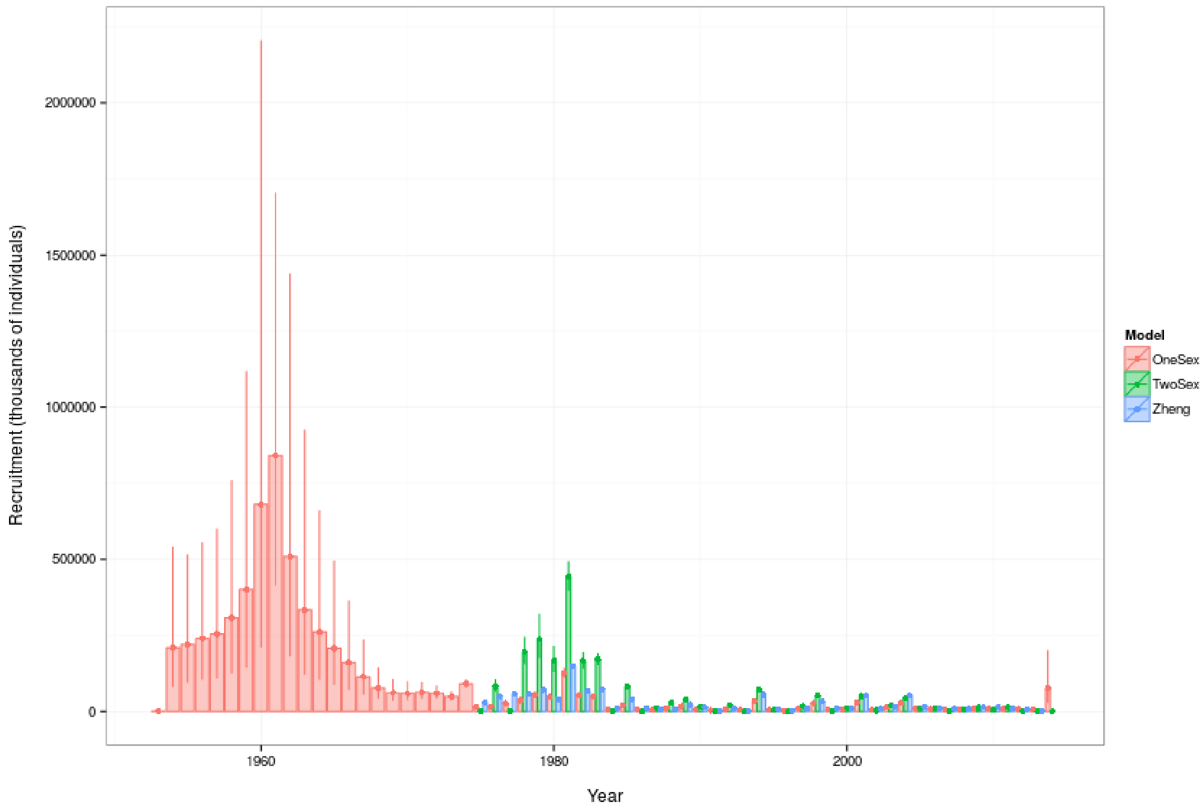

Figure 21: Estimated recruitment time series (R_t).

Mature male biomass (MMB)

The spawning stock biomass (tons) of mature males, termed the mature male biomass (MMB_t), varies some between the models (Figure 22).

Comparison of likelihoods between models

In the tables below the OneSex and TwoSex model likelihoods (Table **??**) and penalties (Table **??**) are compared.

Discussion

Comparisons of likelihood function components are available from the output but more detailed evaluation is needed. Simulation testing is also slated for evaluating alternative model specifications for robustness (e.g., constant natural mortality over time, time-varying selectivity, etc).

The current Gmacs models require that many of the key model parameters be fixed to obtain model fits that look similar to the BBRKC model.

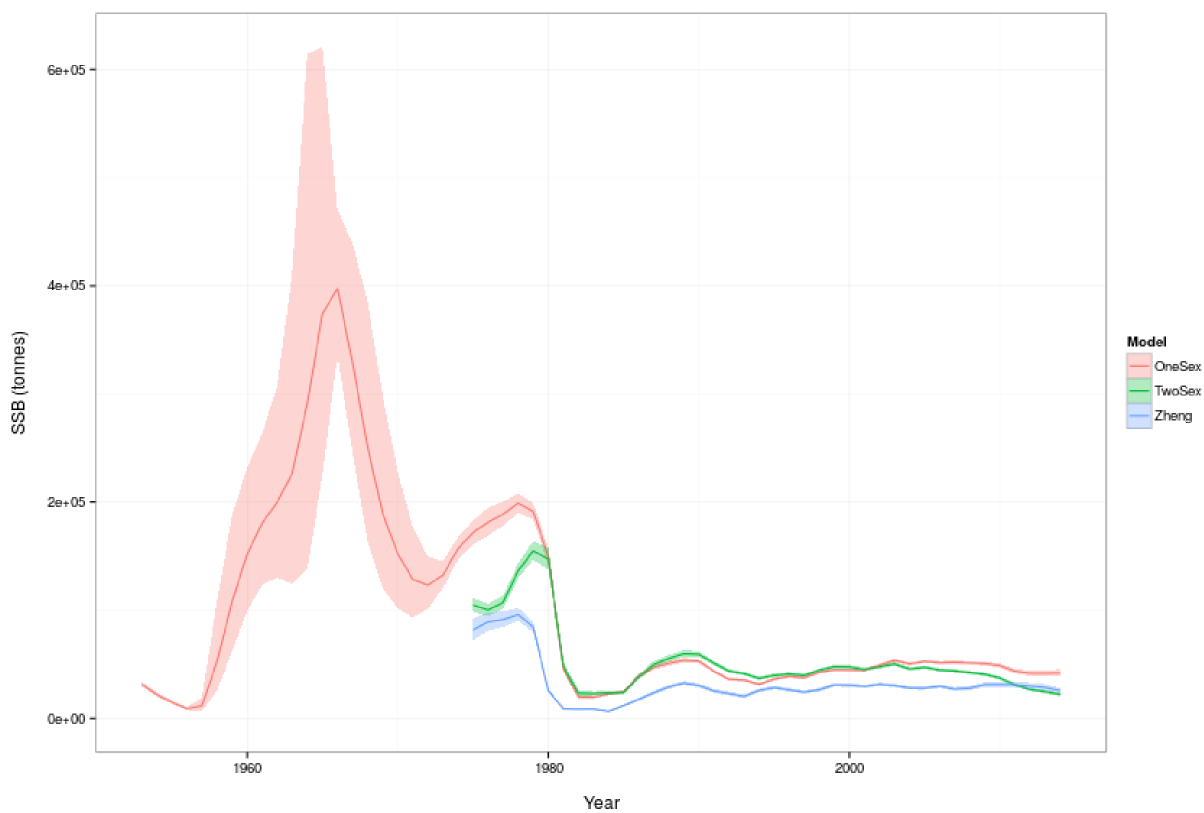

Figure 22: Mature male biomass (MMB) predicted in the two versions of the Gmacs model (OneSex and TwoSex) and the Zheng model.

Table 2: Likelihoods in log-space.

	OneSex	TwoSex
Abundance1	52.74	166.23
Abundance2	-1.31	-1.28
Catch1	-38.95	683.16
Catch2	203.80	221.91
Catch3	-65.63	-49.75
Catch4		-78.62
Growth increment1	0.00	0.00
Recruitment deviations1	242.44	810.67
Size composition1	469.10	820.81
Size composition2	1099.60	3834.18
Size composition3	1019.66	2448.87
Size composition4	2388.65	32232.31
Size composition5	13.84	257.15

Table 3: Penalties in log-space.

	OneSex	TwoSex
log__fdev	0.00	0.00
mean F	9.48	9.47
M	10.53	18.93
rec__dev	0.00	0.00
rec__ini	0.00	0.00
rec__dev__	77.64	212.36

References

Fournier, David a., Hans J. Skaug, Johnoel Ancheta, James Ianelli, Arni Magnusson, Mark N. Maunder, Anders Nielsen, and John Sibert. 2012. "AD Model Builder: Using Automatic Differentiation for Statistical Inference of Highly Parameterized Complex Nonlinear Models." *Optimization Methods and Software* 27 (2) (April): 233–249. doi:10.1080/10556788.2011.597854. http://www.tandfonline.com/doi/abs/10.1080/10556788.2011.597854.

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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.