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 document presents the development and application of two Gmacs models and compares these to the current assessment model for the Bristol Bay Red King Crab (BBRKC) stock. The example assessments are intended to match closely with a model scenario presented to the Fall 2014 BSAI Crab Plan Team Meeting by Zheng and Siddeek (2014).

An important component of the Gmacs framework is the provision of software for understanding the outputs produced by the Gmacs model. This includes 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. This document serves as an example of how Gmacs outputs can be directly incorporated into text in an automated way (for example, this document is compiled by simply typing "make" at the command line in the "gmacs/docs/bbrkc" directory).

The Gmacs-BBRKC model presented here is intended to provide an example of what 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 Center for Independent Experts (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.

- Explicit **Prior specification** now provided 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 reviewers 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
- Specifying q as a model parameter rather than a derived variable

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, sexually 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 (OneSex) in addition to the split two-sex Gmacs configuration (TwoSex). 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	1975	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 the catchability coefficient (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). We feel that the way that q is currently specified in the model (i.e. q is integrated out) is inadequate as it allows the model to explore unrealistic parameter space. We intend to provide an option to specify q as a parameter of the model.
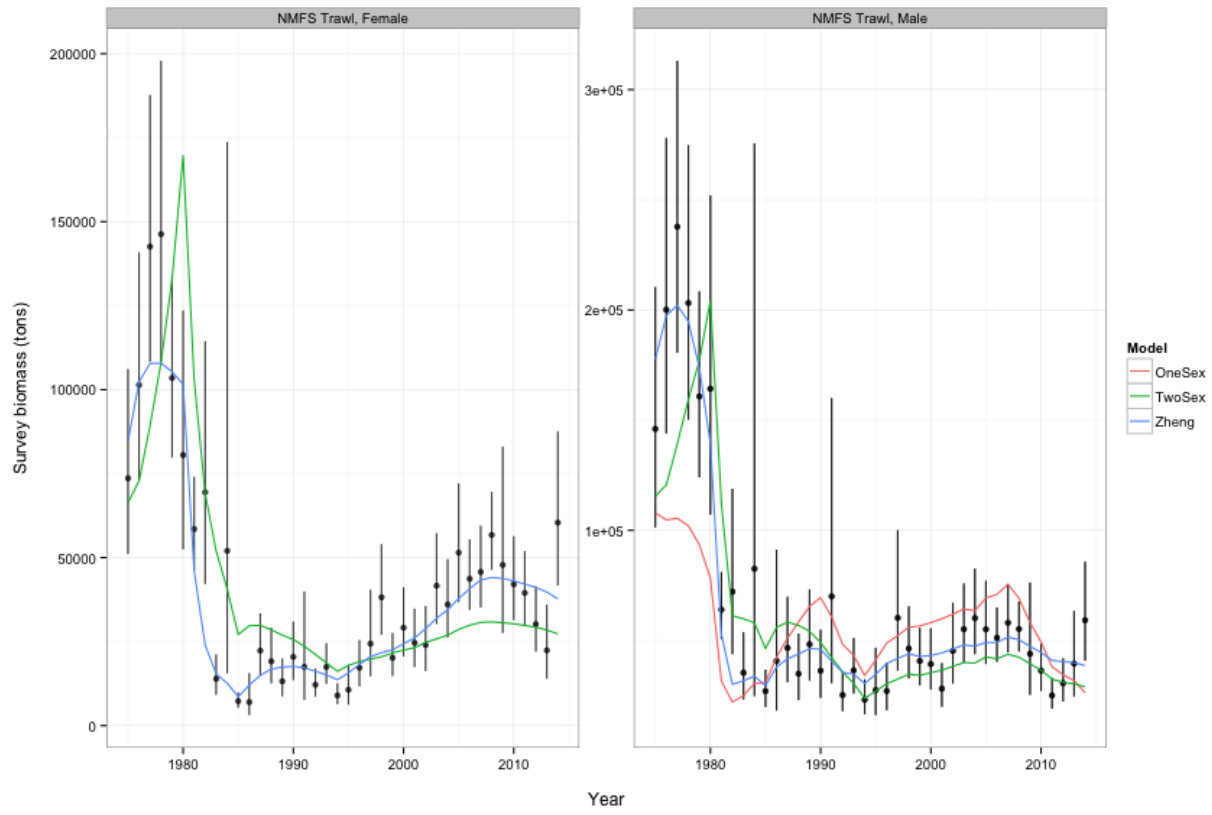
Figure 1: Model fits to sex-specific NMFS trawl survey biomass (tons) from 1975 to 2014. The error bars represent plus and minus 2 standard deviations.

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 mean fishing mortality in the directed pot fishery and the trawl bycatch fishery is 0.2 and 0.05, respectively. The mean fishing mortality in the two surveys is zero.

The observed and predicted catches by gear type in each of the Gmacs models are summarized (Figure 2). Data for discard fisheries were read in with 100% mortality (as clarified in Table 1 of Zheng and Siddeek (2014)).
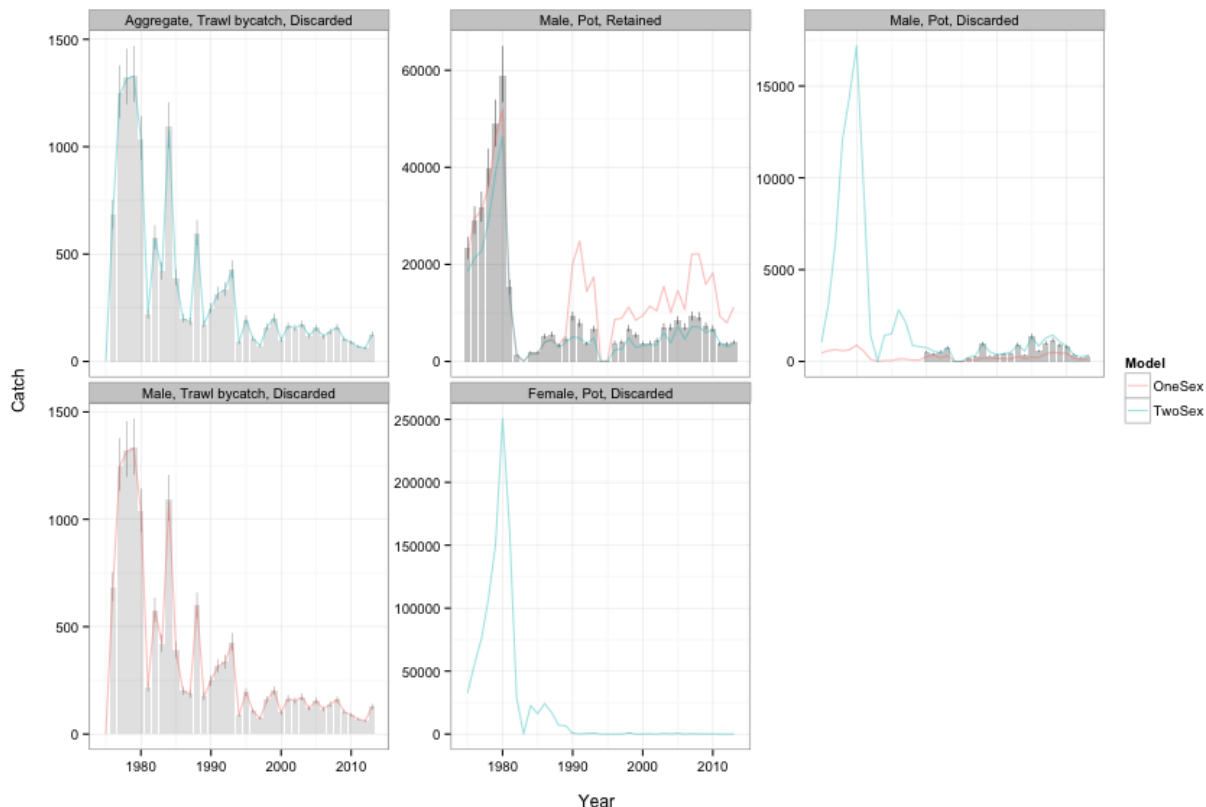
Figure 2: Observed and predicted catch (tons) by gear type for the two Gmacs models. The OneSex model includes catch data from 1953 to 2013. The TwoSex model includes catch data from 1975 to 2013.

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 12).

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.*
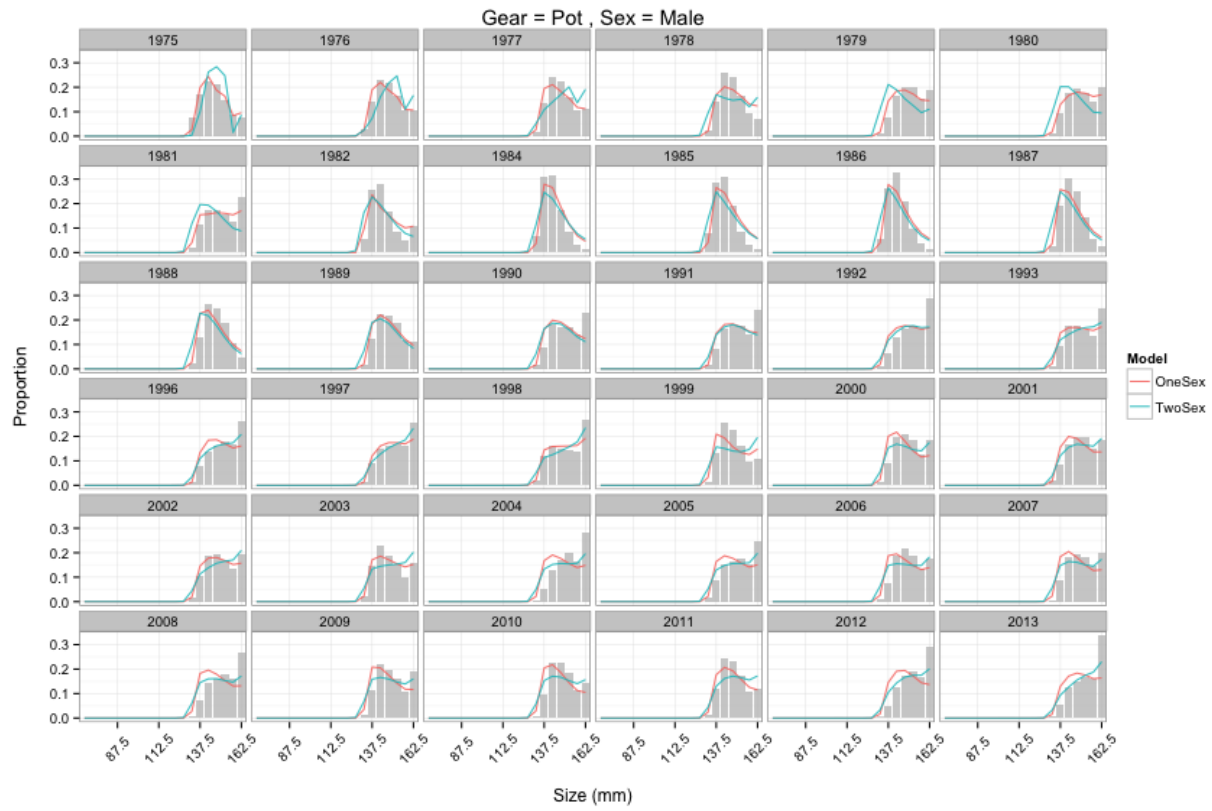
Figure 3: Observed and model estimated size-frequencies of male BBRKC by year retained in the directed pot fishery.
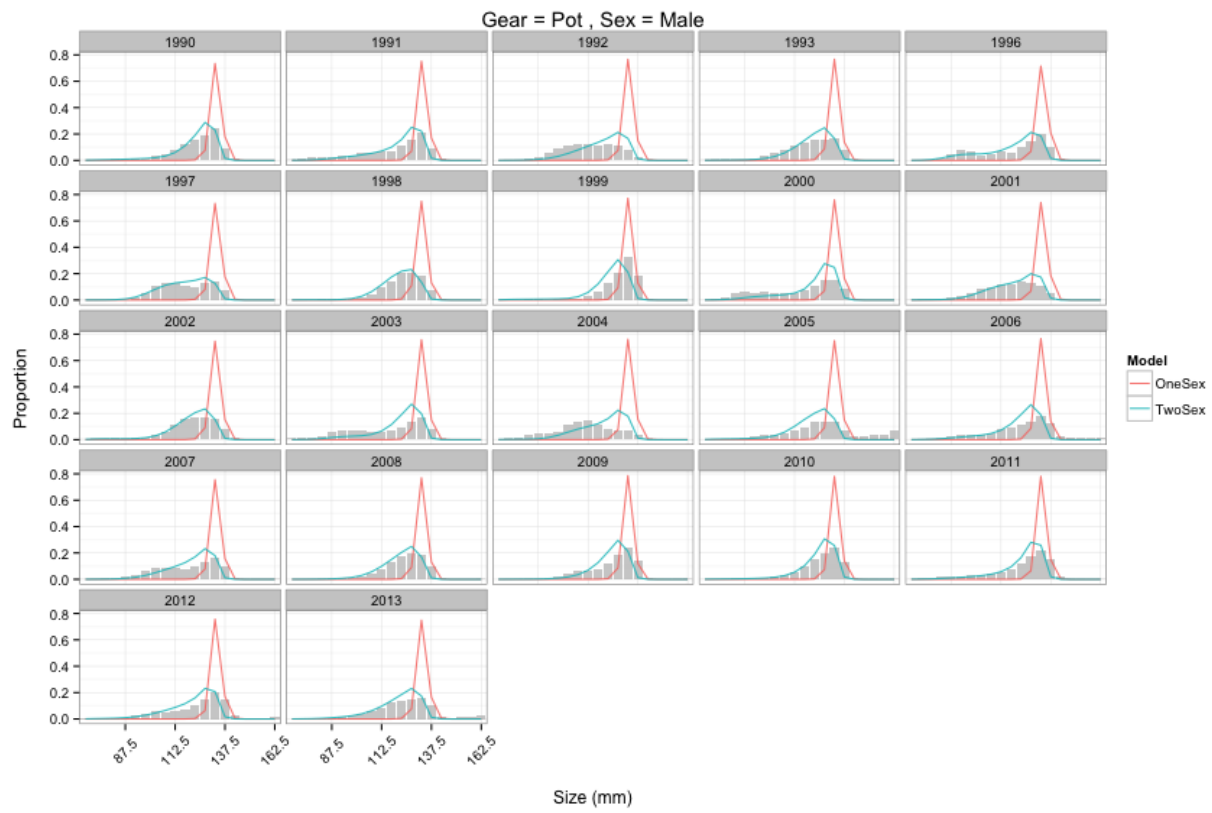
Figure 4: Observed and model estimated size-frequencies of discarded male BBRKC by year in the directed pot fishery.
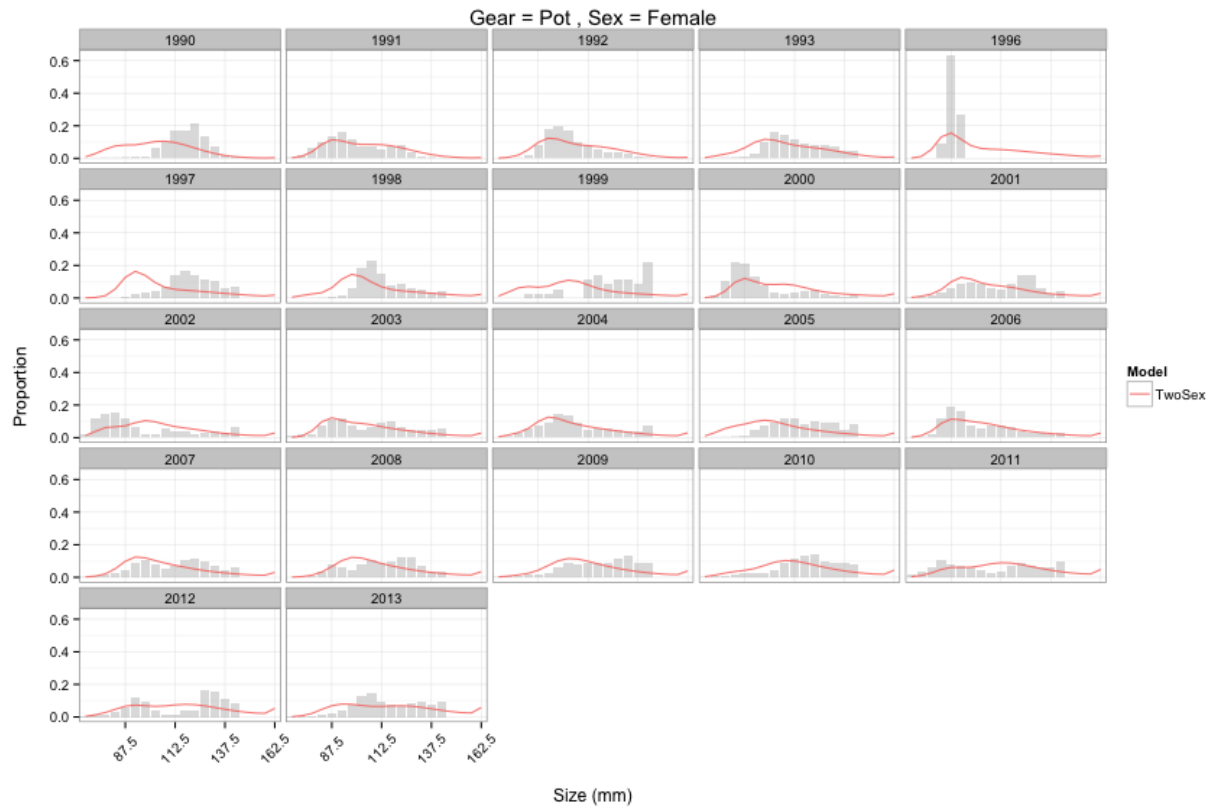
Figure 5: Observed and model estimated size-frequencies of discarded female BBRKC by year in the directed pot fishery.
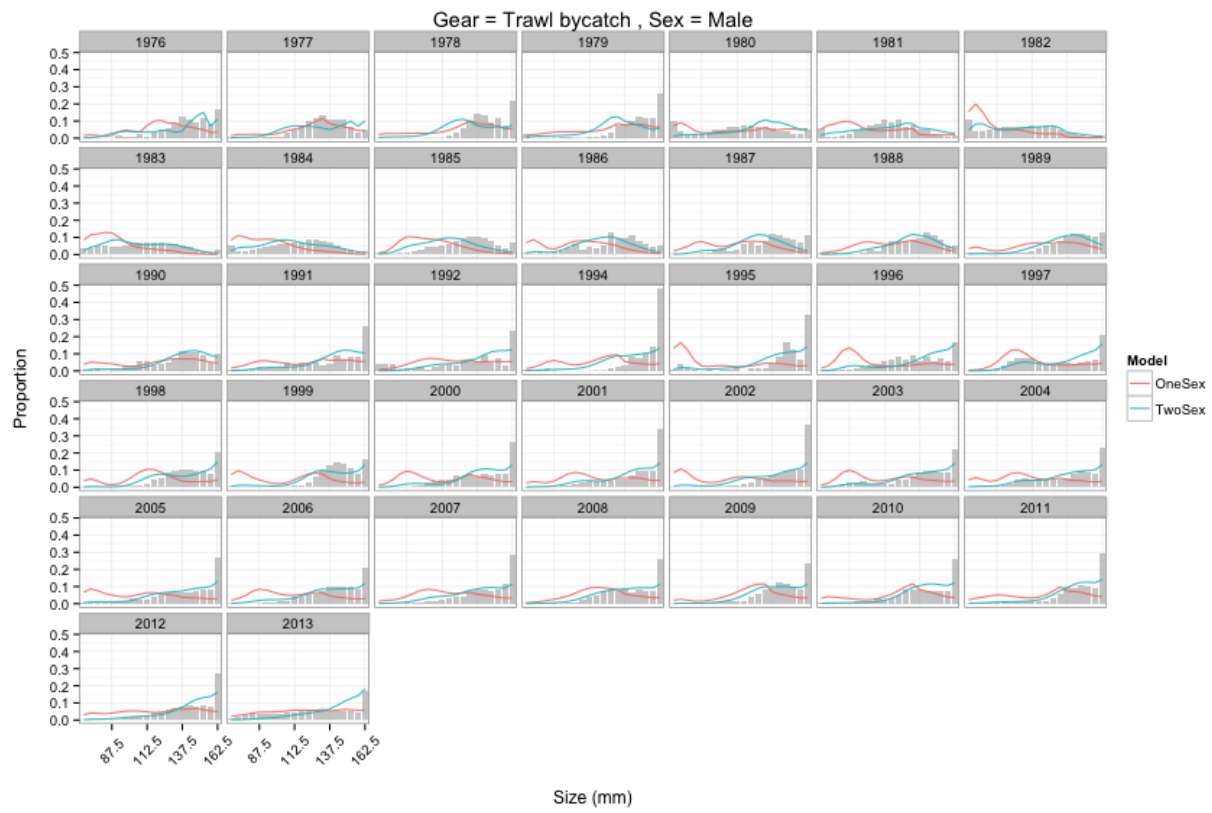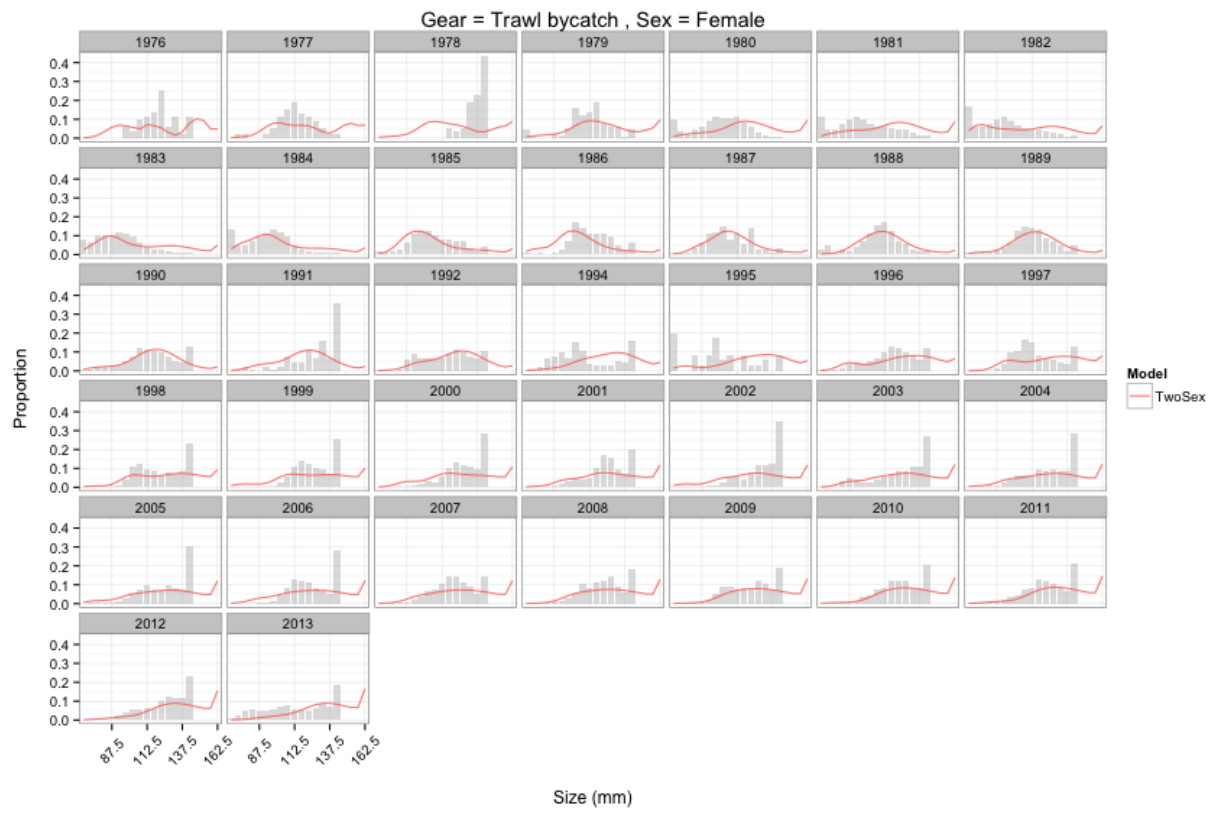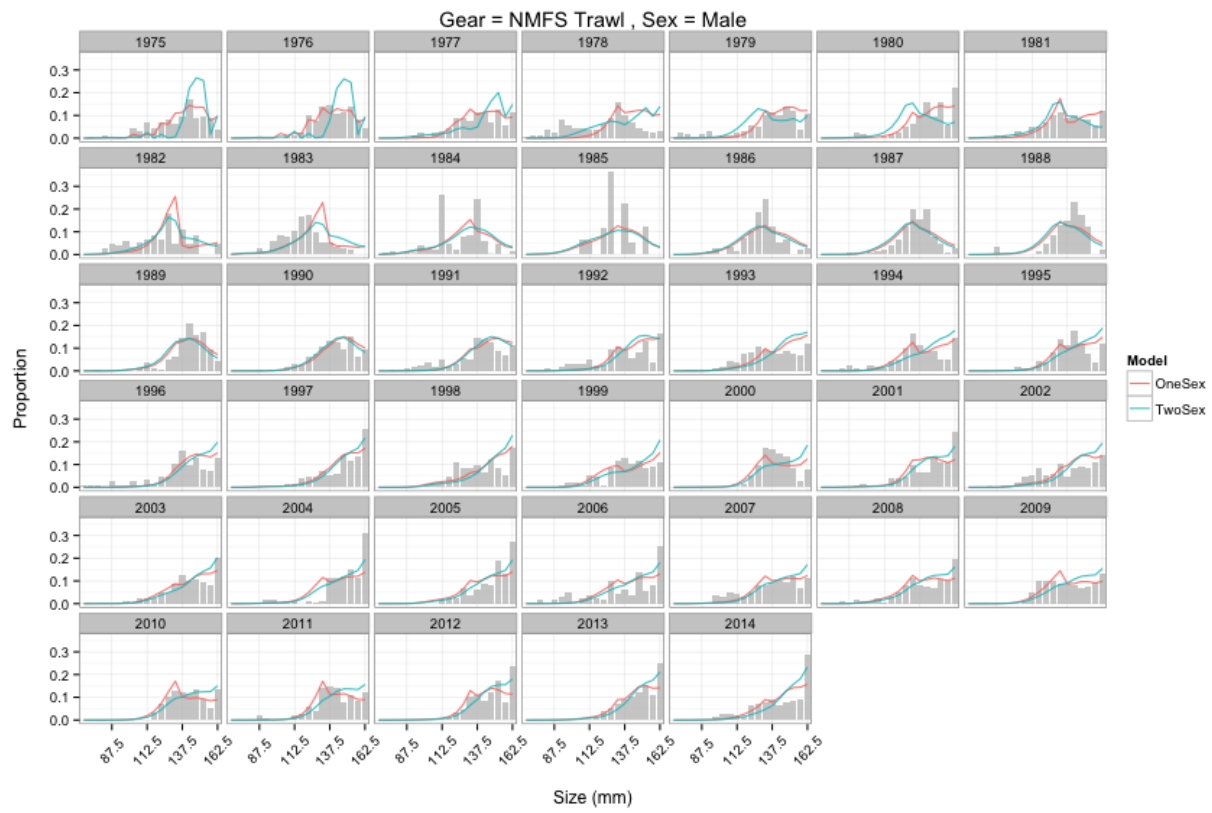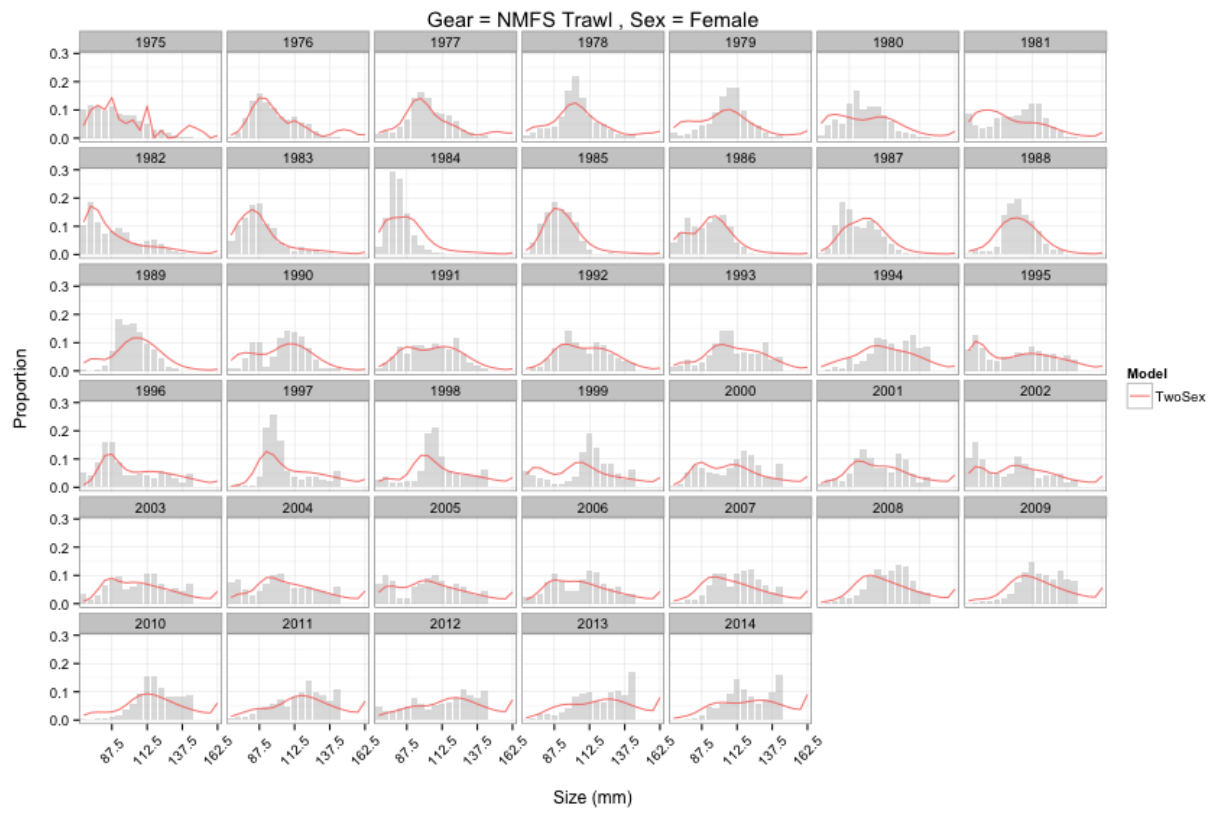
Figure 6: Observed and model estimated size-frequencies of male BBRKC by year in the groundfish trawl bycatch fisheries.

Figure 7: Observed and model estimated size-frequencies of female BBRKC by year in the groundfish trawl bycatch fisheries.
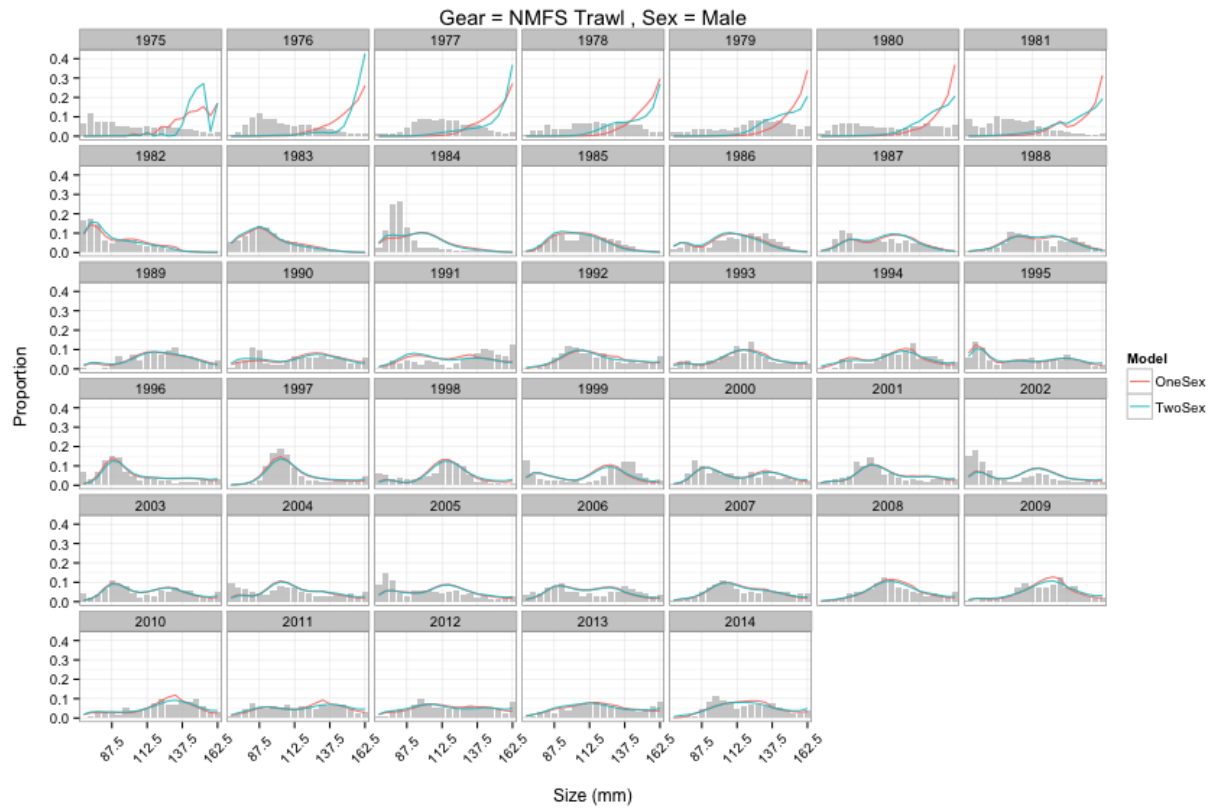
Figure 8: Observed and model estimated size-frequencies of new shell male BBRKC by year in the NMFS trawl survey.

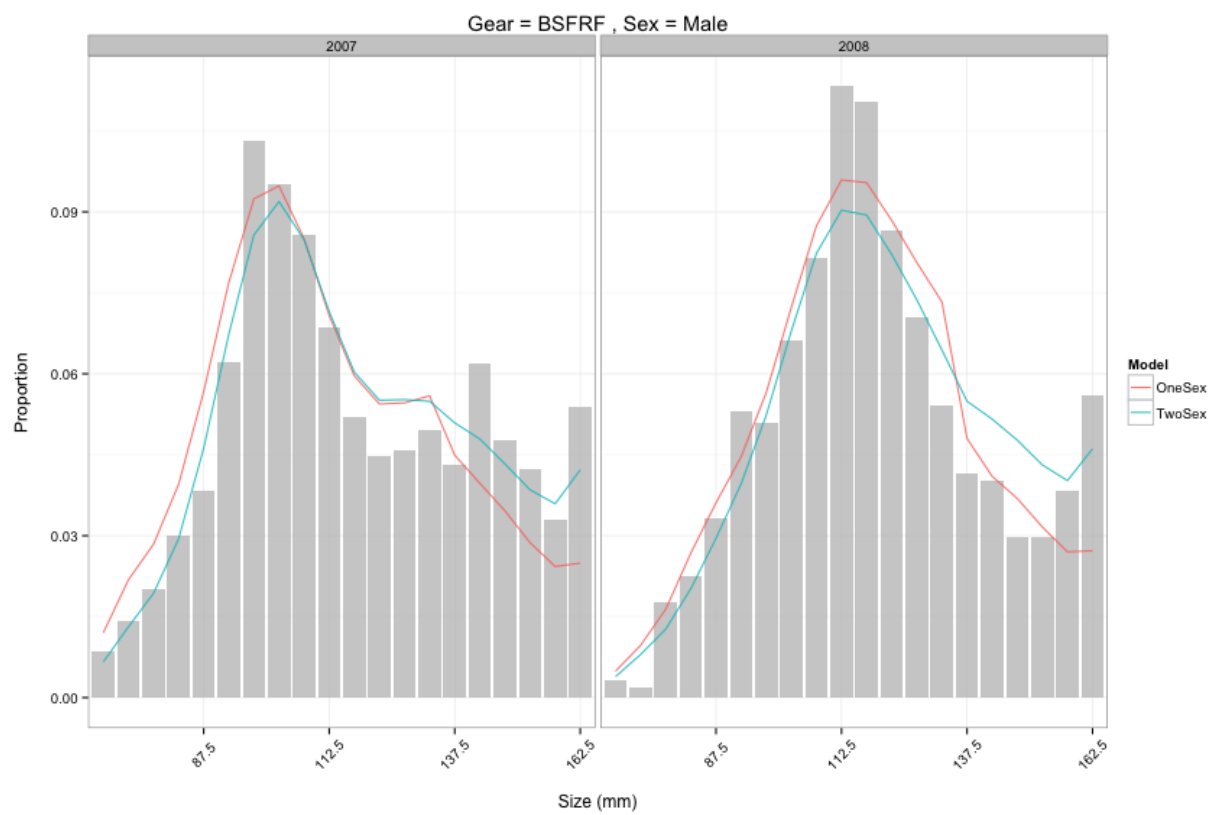Figure 9: Observed and model estimated size-frequencies of old shell male BBRKC by year in the NMFS trawl survey.

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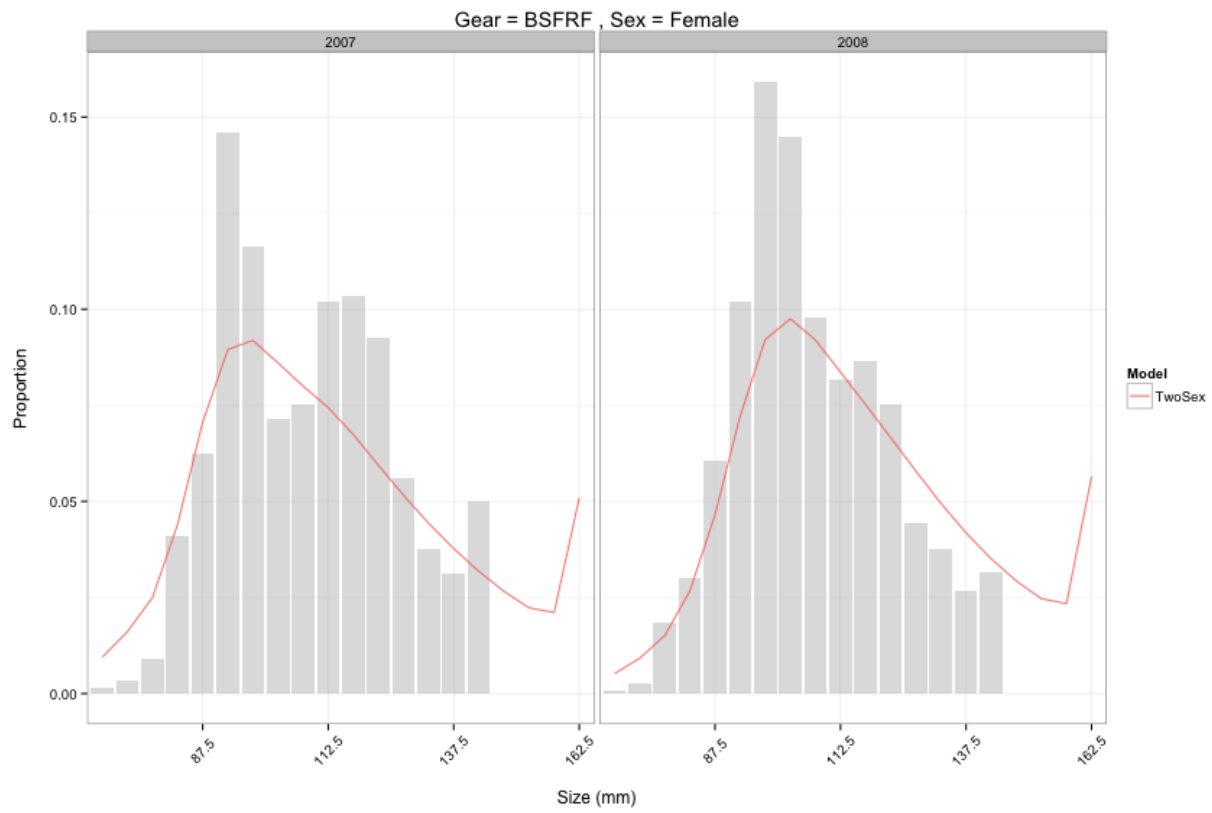
Figure 12: Observed and model estimated size-frequencies of both male and female BBRKC by year in the BSFRF trawl surveys.

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 13).

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.
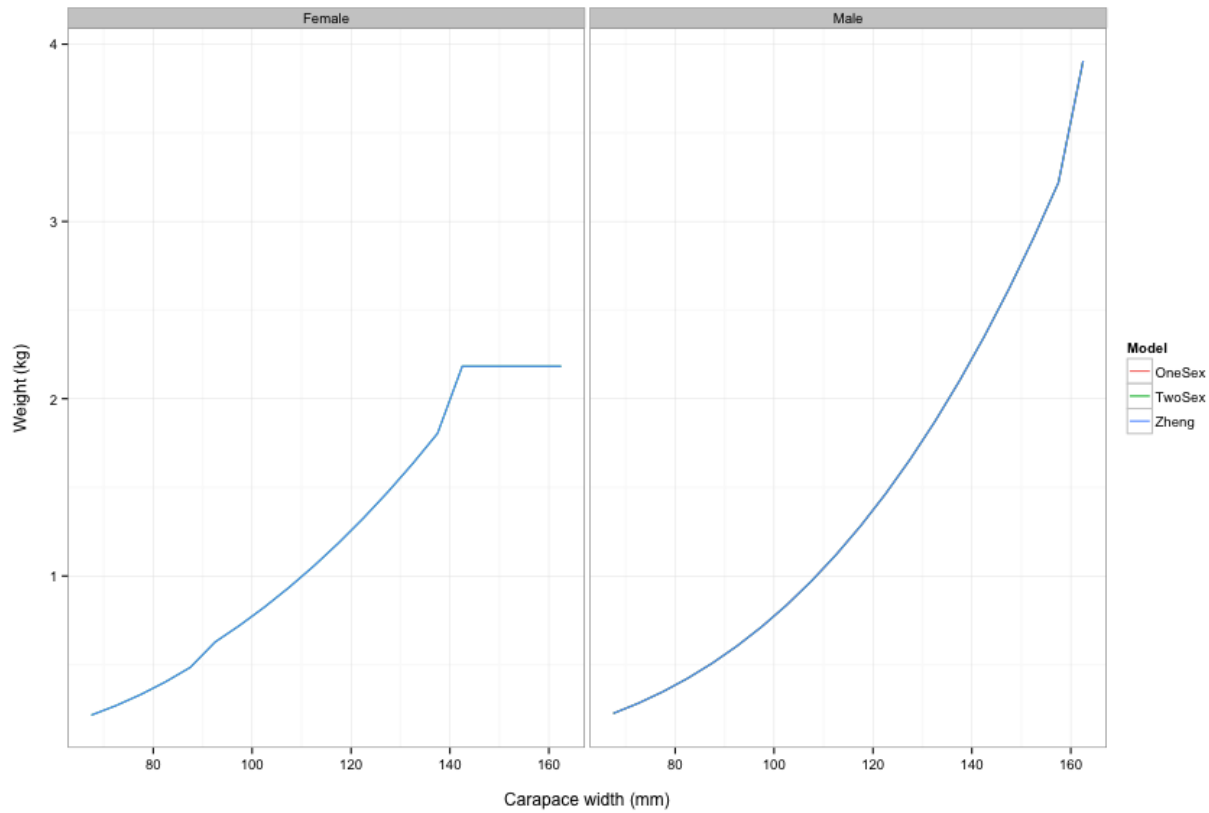

Figure 13: Relationship between carapace width (mm) and weight (kg) by sex in each of the models (provided as a vector of weights at length to Gmacs so lines all overlap).

Initial recruitment size distribution

Gmacs was configured to match the Zheng and Siddeek (2014) model recruitment size distribution closely (Figure 14).
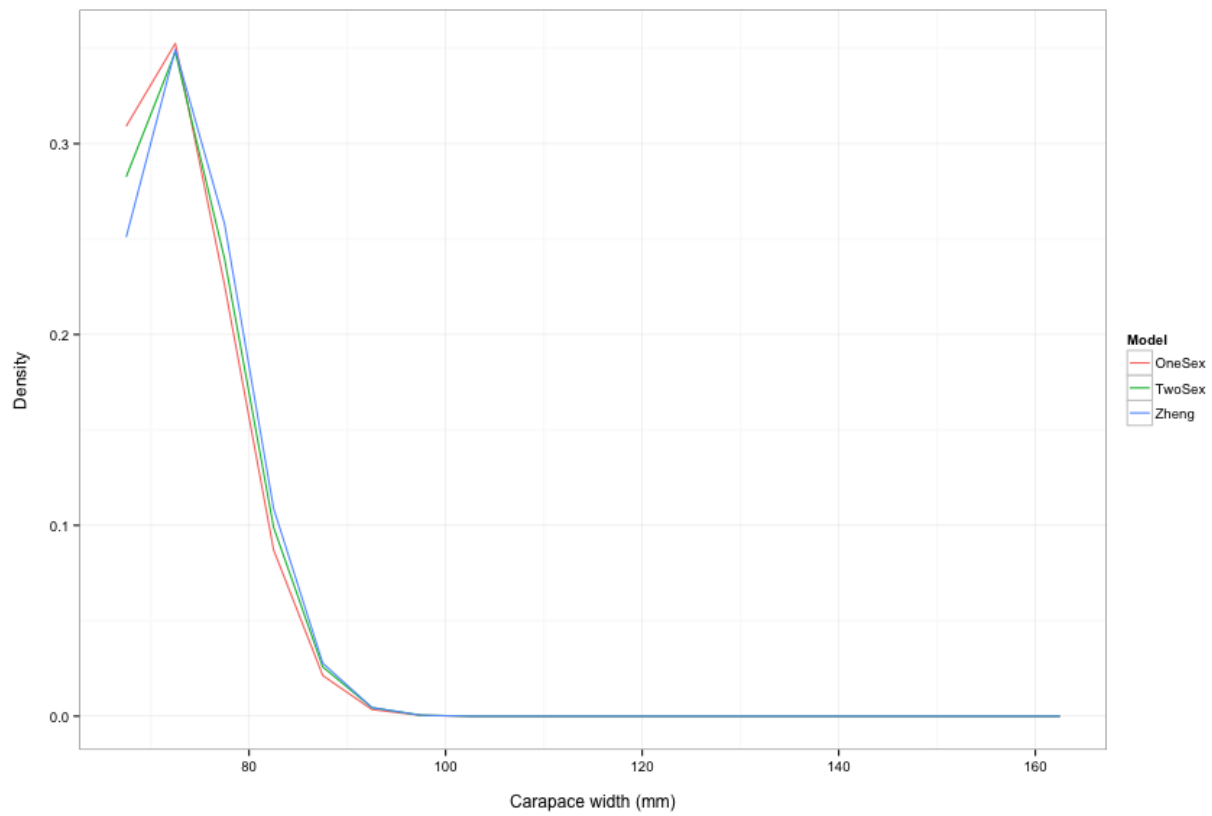
Figure 14: Distribution of carapace width (mm) at recruitment.

Molting increment and probability

In the BBRKC model one function 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 15). Fixed parameters in gmacs were set to match assumptions in Zheng and Siddeek (2014) (Figure 16).
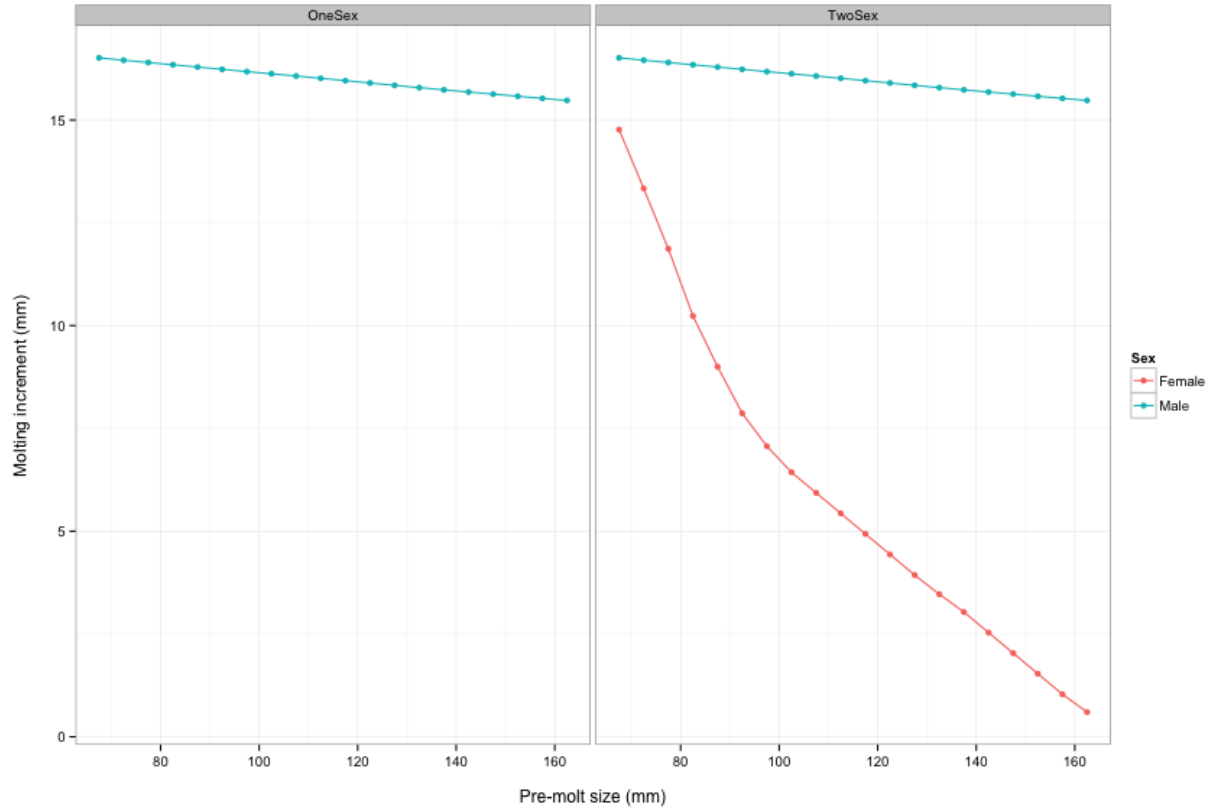

Figure 15: Growth increment (mm) each molt by sex in the OneSex and TwoSex models.

In the BBRKC model, females are specified to molt annually consistent with their biology. This means that molting probability is always 1 for females. This was replicated in the Gmacs model by fixing the logistic curve 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 include the growth probabilities (for all crabs that molt) (Figure 17). The second set of figures is the combination of growth and molting probabilities and represents the size transition (Figure 18).

Numbers at length in the first and last year

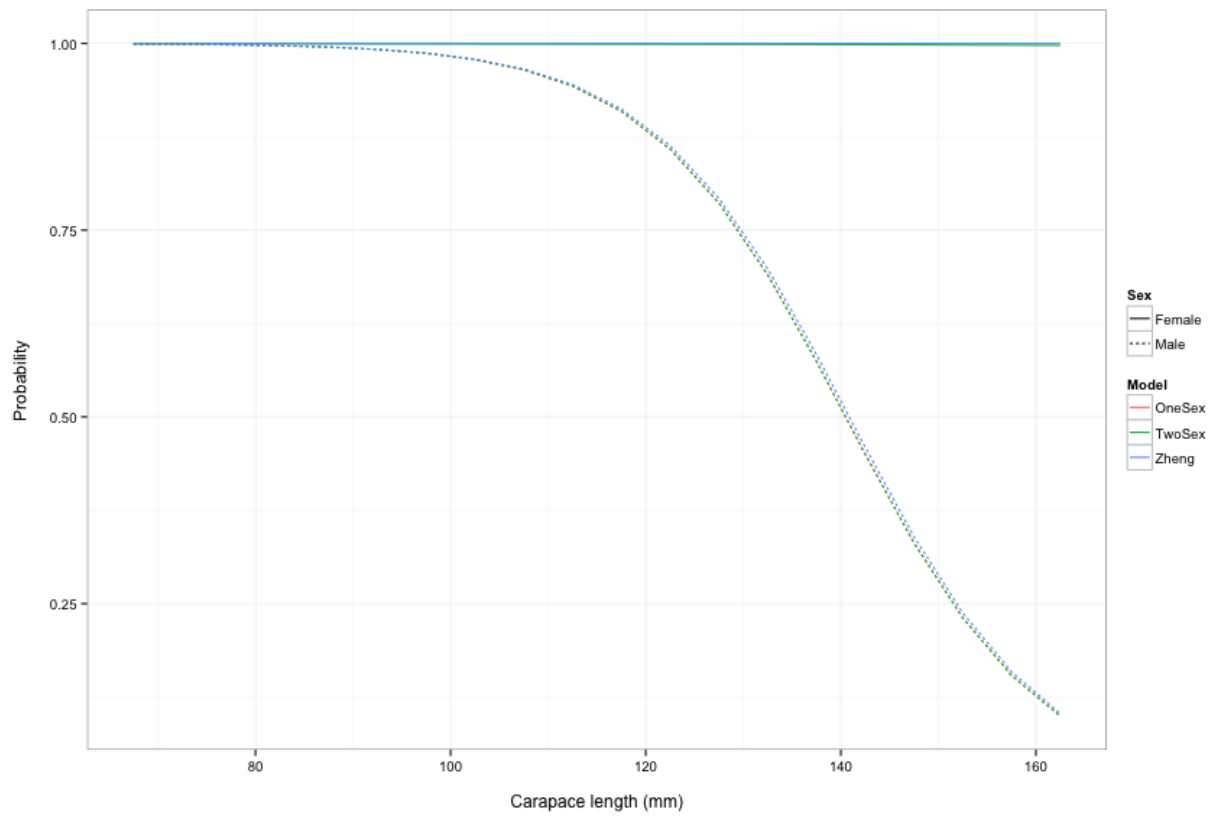Total abundance and the proportions by length and sex are estimated in 1975 (the models initial year).

Figure 16: Molting probability for each of the models by sex. The molting probability for females is fixed at 1 as females molt every year.
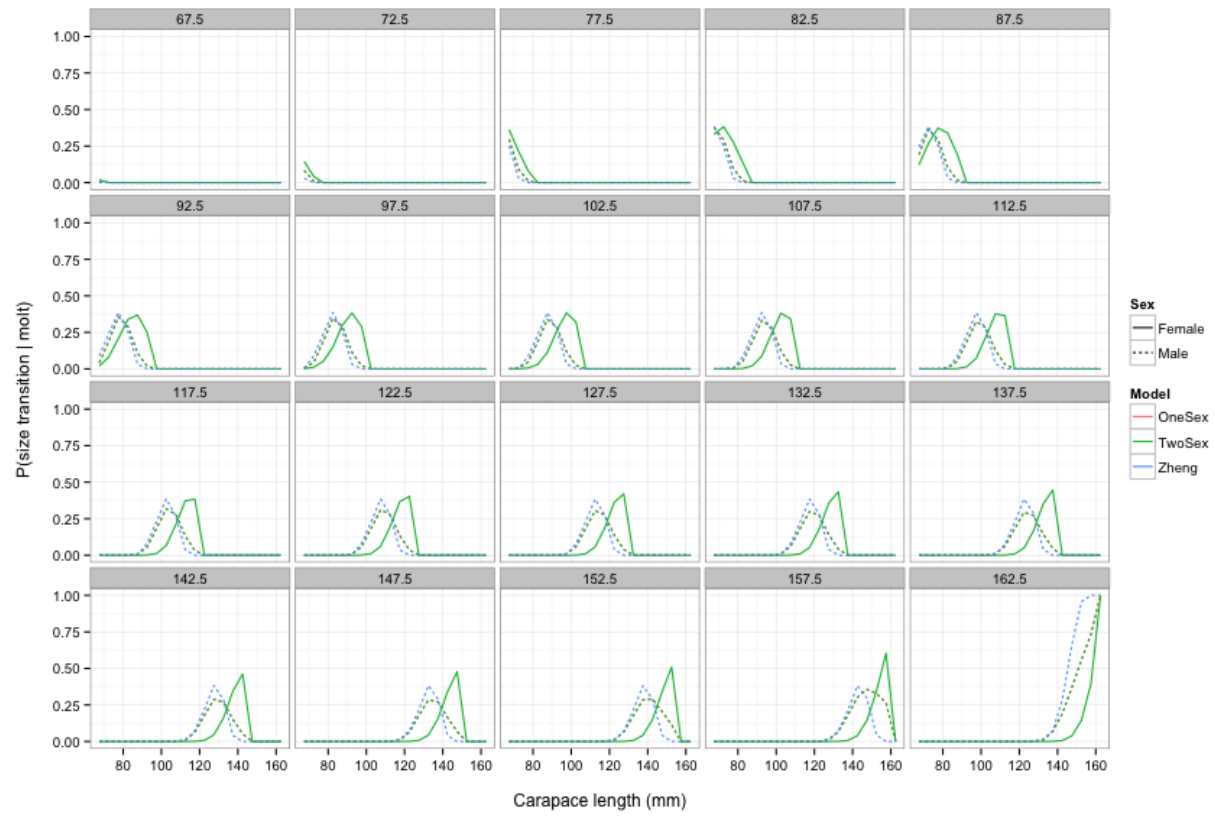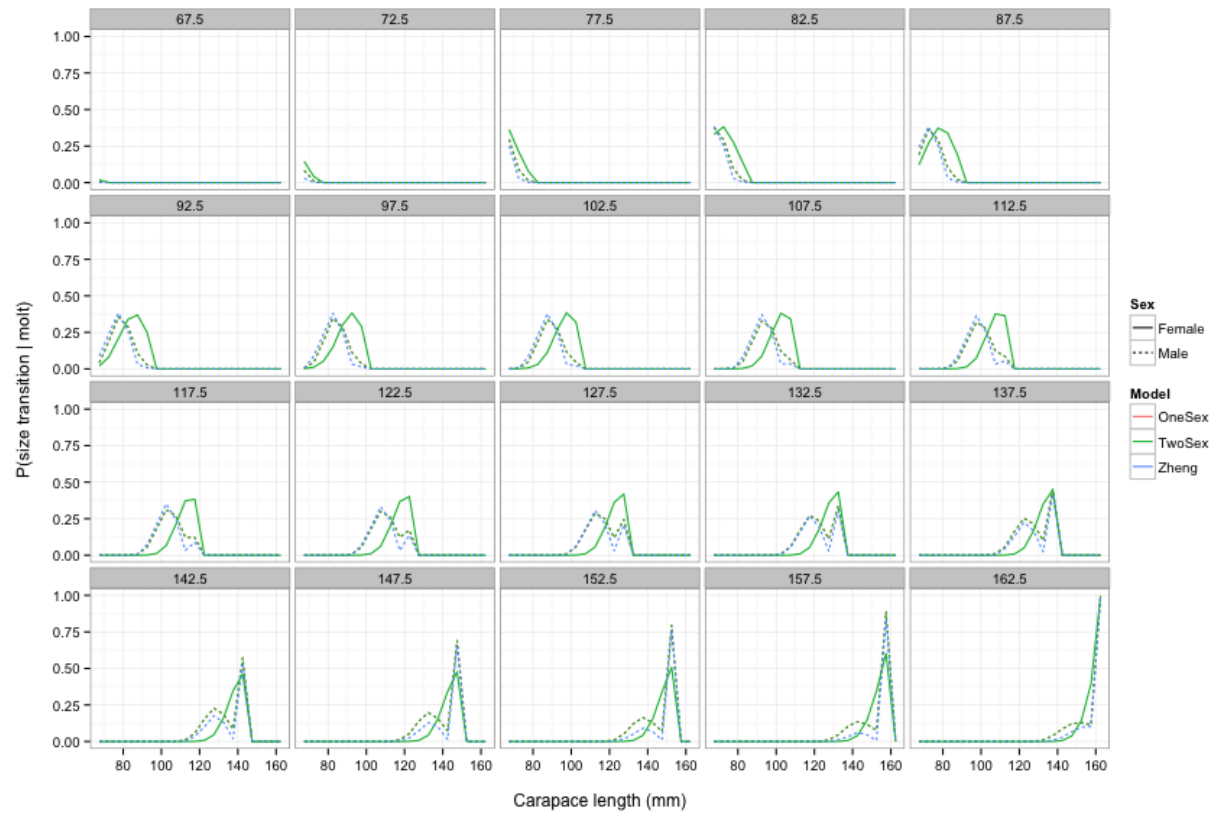
Figure 17: Growth transitions.

Figure 18: Size transitions.

The number of crabs in each size class (**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).
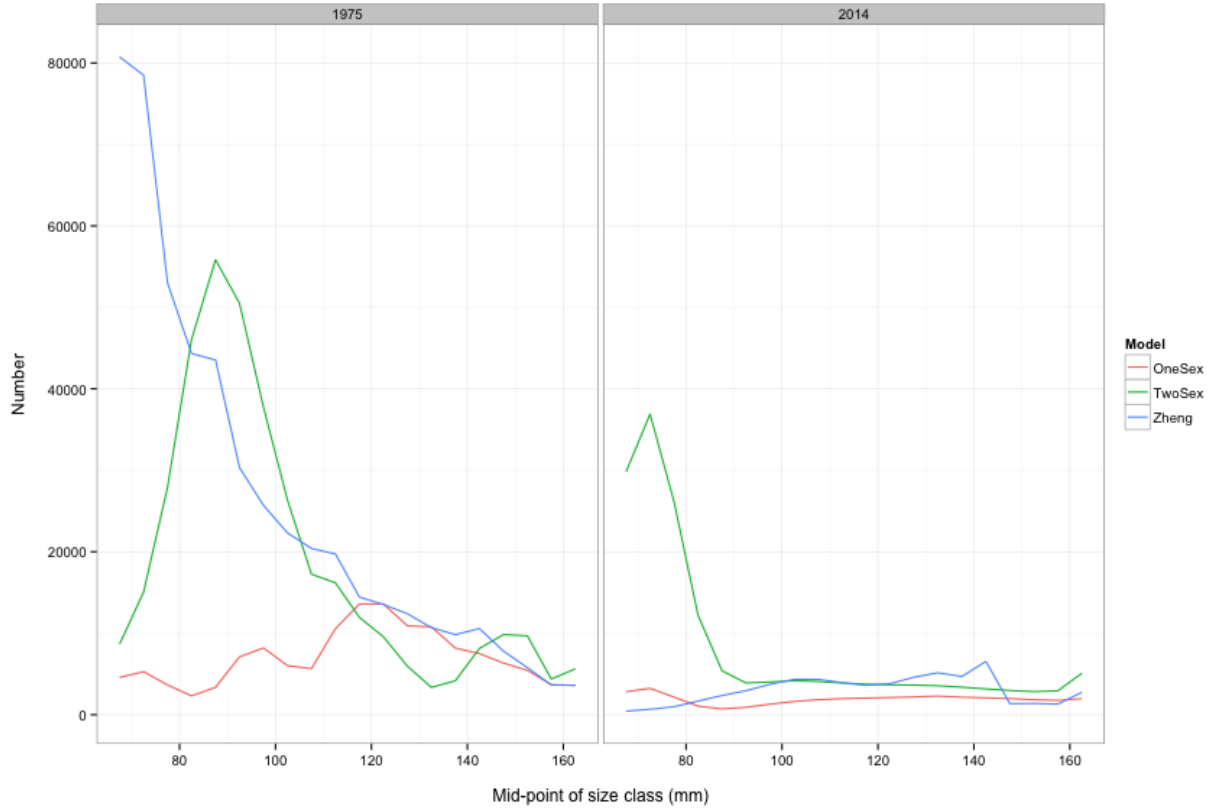

Figure 19: Numbers at length in 1953, 1975 and 2014 in each of the models. The first year of the OneSex model is 1953. The first year of the Zheng and TwoSex models in 1975.

Selectivity

The selectivity by size (S_ℓ) for each of the fisheries are presented below (Figure 20). In the all models, selectivity in the trawl bycatch fishery is constant by sex. In all other fisheries, selectivity is sex-specific. In the NMFS trawl fishery, a different selectivity curve is estimated for the 1975-1981 period and for the 1982-2014 period.

Natural mortality

In both the BBRKC and Gmacs 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 at 1976, 1980, 1985 and 1994. The pattern in time-varying natural mortality is reasonably similar between the three models (Figure 21), however the peak in natural mortality during the early 1980 is not as high in the Gmacs models. *In the Gmacs model, a spline function for natural mortality changes over time is also available as an option.*
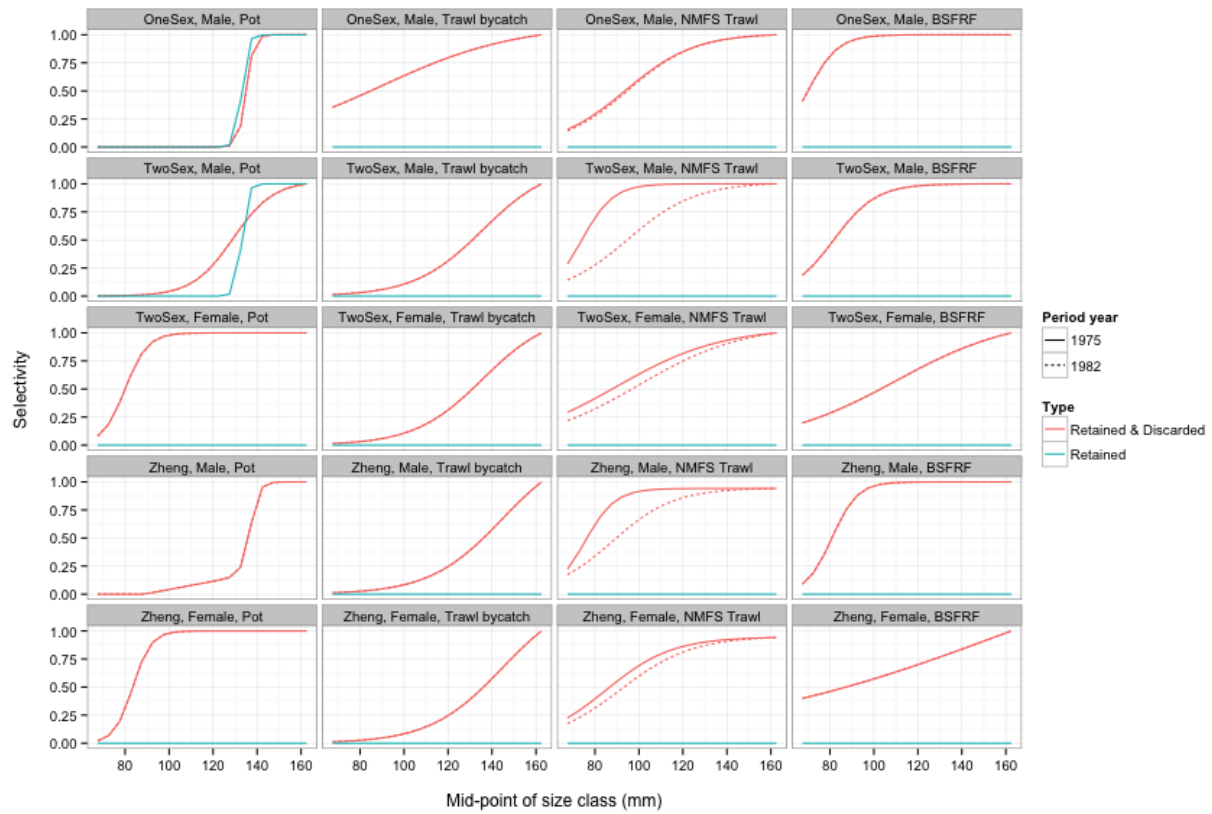
Figure 20: Estimated selectivity at size, sex and fishery in the OneSex, TwoSex and Zheng models. Estimated selectivities are shown for the directed pot fishery, the trawl bycatch fishery, the NMFS trawl survey, and the BSFRF survey.
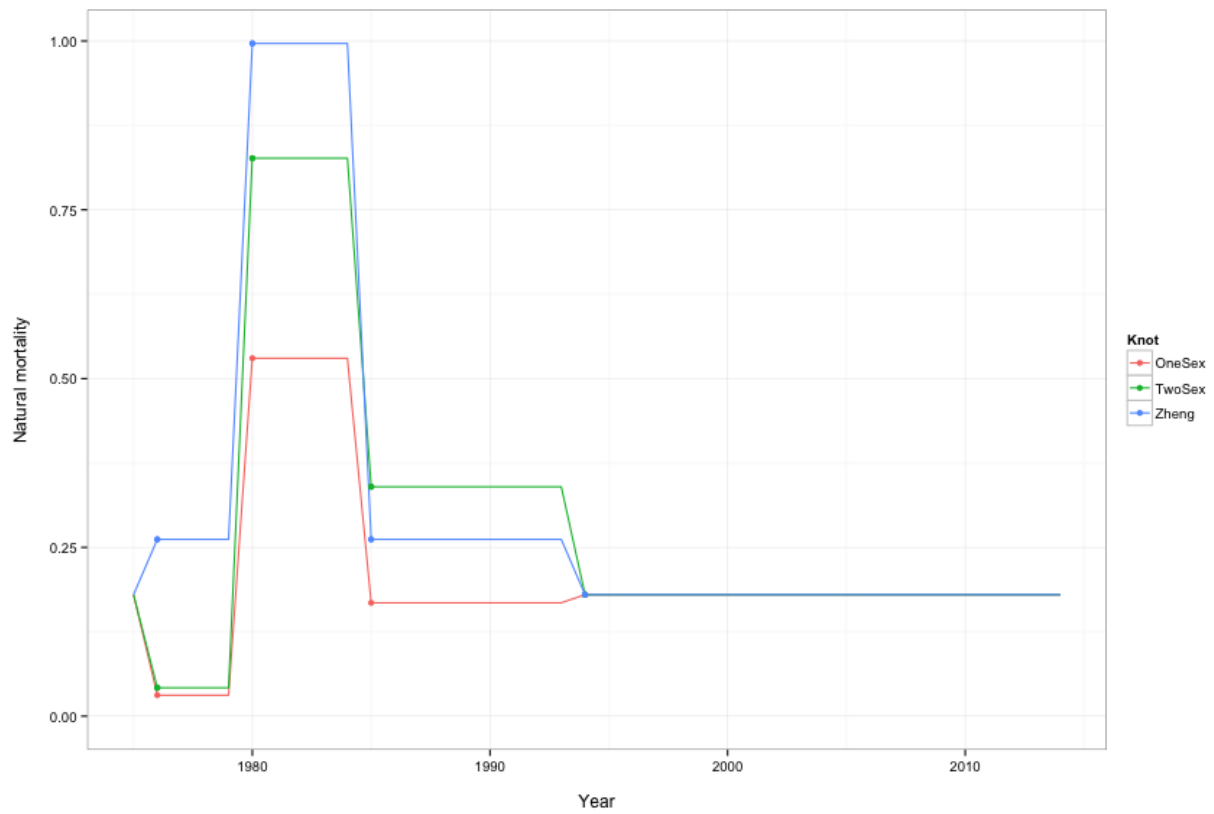
Figure 21: Time-varying natural mortality (M_t). Periods begin at 1976, 1980, 1985 and 1994.

Recruitment

Recruitment (R_t) patterns are similar among models, but differences in natural mortality schedules will affect these matches. It is also important to keep in mind that recruitment in the OneSex model only represents recruitment of males, while in the TwoSex and BBRKC models recruitment is for females and males combined. The figure below shows that the values have roughly the same mean (Figure 22).
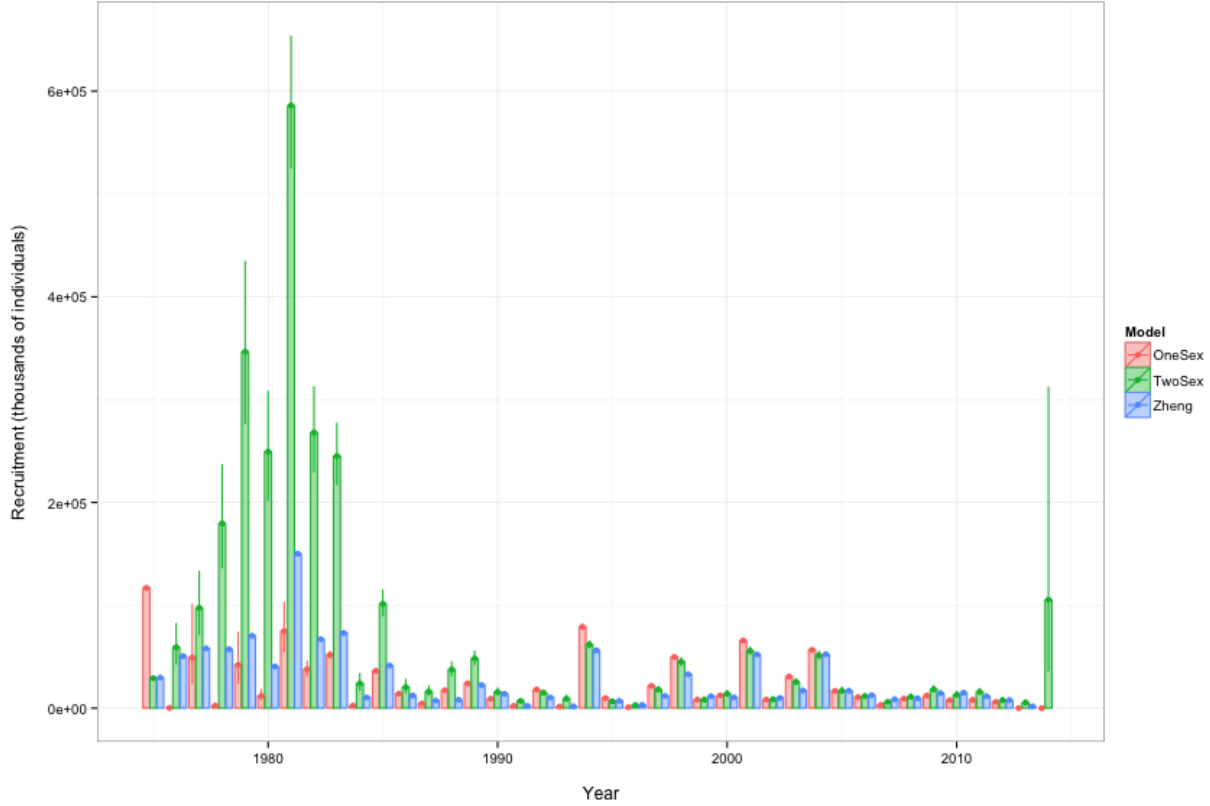

Figure 22: Estimated recruitment time series (R_t) in the OneSex, TwoSex and BBRKC models. Note that recruitment in the OneSex model represents recruitment of males only.

Mature male biomass (MMB)

The spawning stock biomass (tons) of mature males, termed the mature male biomass (MMB_t), varies somewhat between each of the models (Figure 23).

Comparison of likelihoods between models

In the tables below the OneSex and TwoSex model likelihoods (Table 2) and penalties (Table 3) 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).
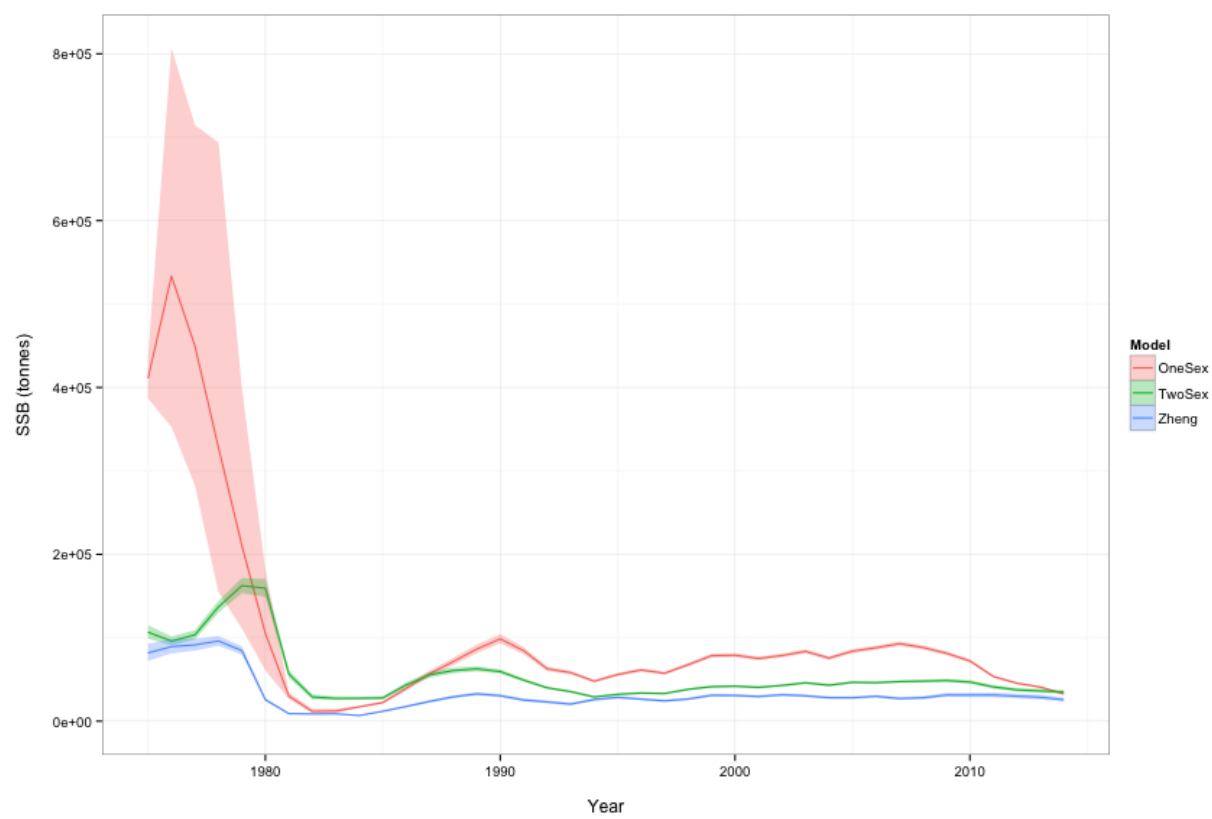
Figure 23: Mature male biomass (MMB) predicted in the two versions of the Gmacs model (OneSex and TwoSex) and the Zheng model.

Table 2: Likelihoods in log-space.

	OneSex	TwoSex
Abundance1	110.70	172.04
Abundance2	-1.41	-1.25
Catch1	3522.11	581.88
Catch2	4432.07	229.31
Catch3	-78.86	-49.78
Catch4		-78.73
Growth increment1	0.00	0.00
Recruitment deviations1	166.76	266.08
Size composition1	590.89	579.06
Size composition2	45005.77	3877.05
Size composition3	6017.39	2336.41
Size composition4	468473.11	31242.93
Size composition5	429.45	247.73

Table 3: Penalties in log-space.

	OneSex	TwoSex
log_fdev	0.00	0.00
mean F	9.47	9.47
M	18.91	12.29
rec_dev	0.00	0.00
rec_ini	0.00	0.00
rec_dev_	73.70	60.60

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.

We feel that the differences between Gmacs and the BBRKC model produced by Zheng and Siddeek (2014) are largely due to the use of the Baranov catch equation in Gmacs amd the way that the initial numbers at length are derived. We intend to change the catch equations and intialization of Gmacs to a method more similar to that used by Zheng and Siddeek (2014).

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): 233–49. doi:10.1080/10556788.2011.597854.

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): 16–33. 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.