

Appendix comparing aspects of gmacs configured to be similar to that of Zheng et al. 2014

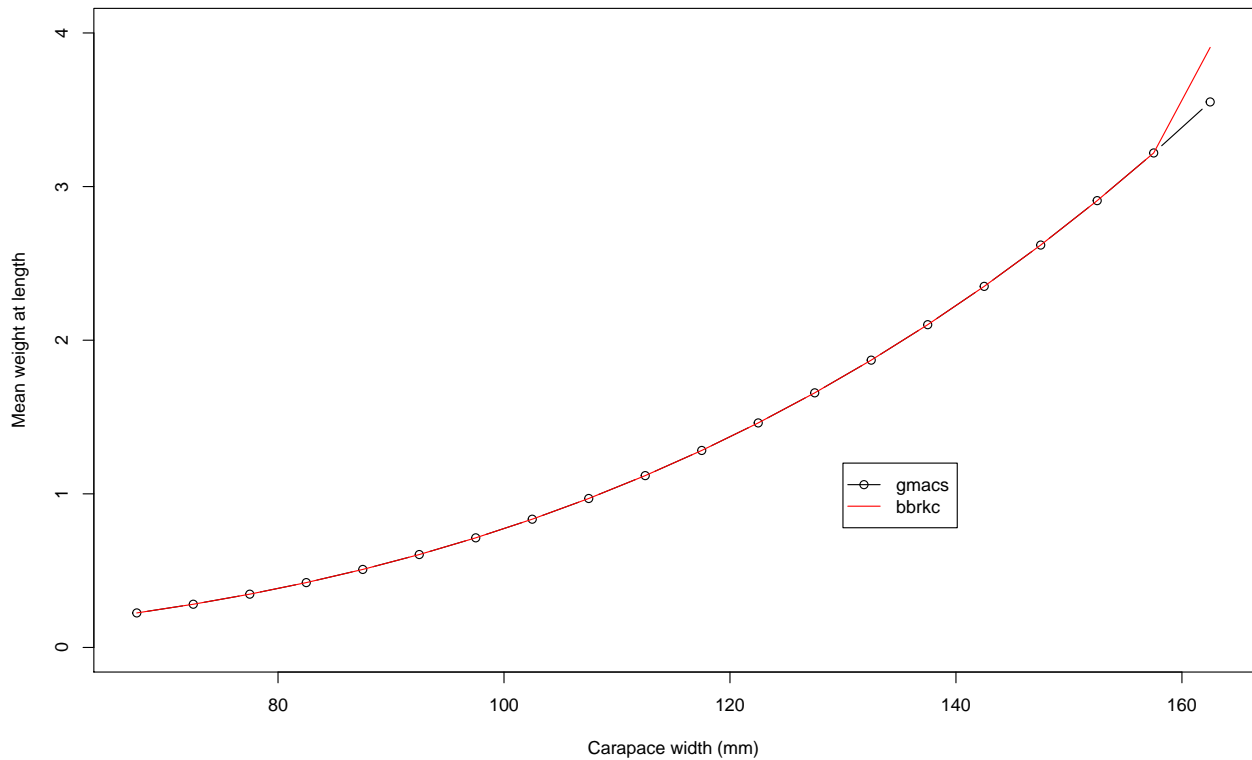
Results culminating from the mid-January 2015 crab modeling workshop

The following summarizes the outcome of some rudimentary comparisons between the existing BBRKC model and an emulated version using the gmacs platform. Since the BBRKC model from Zheng et al. (2014) treats recruits by sex along with sex-specific natural mortality and fishing mortality, results from the male components are compared with results from a gmacs model implementation tuned to male-only data.

Size specific schedules

Mean weight-at-length

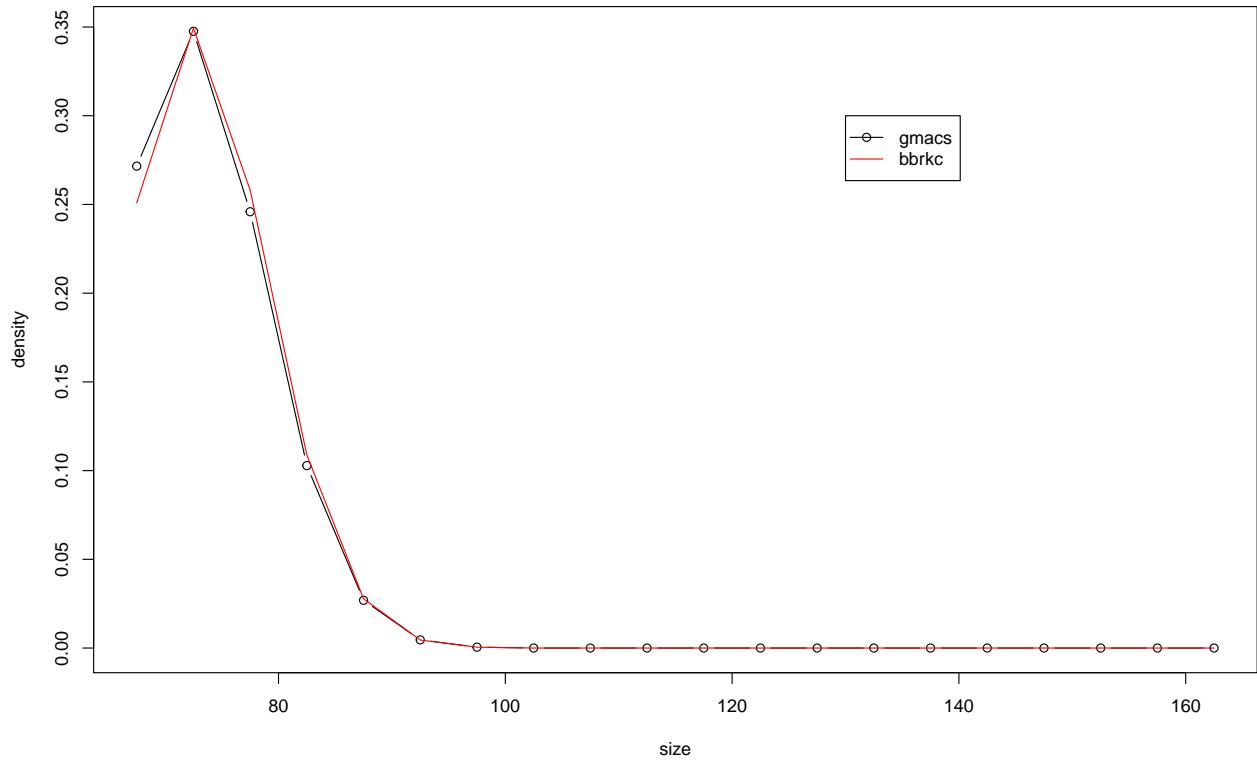
The values used in both models are nearly identical:



Initial recruitment size distribution

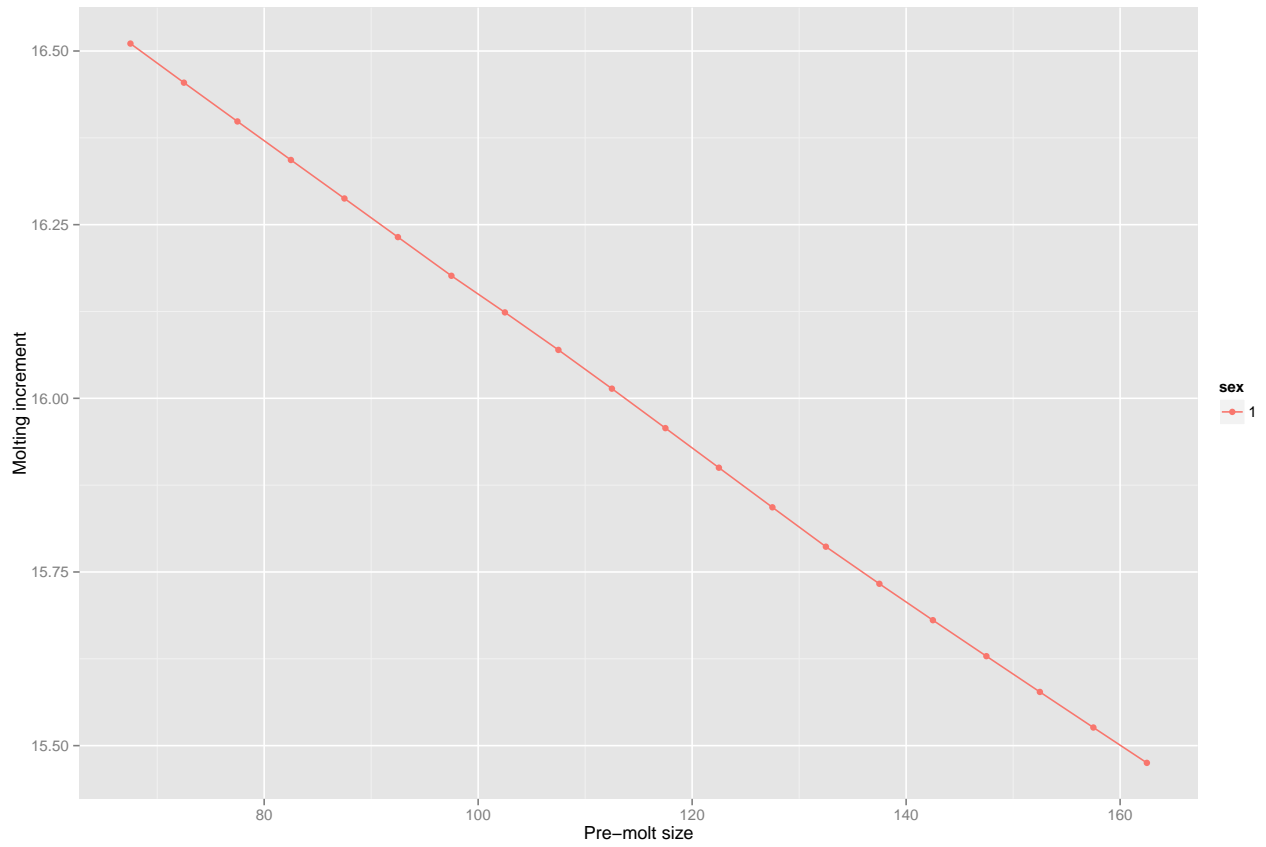
Gmacs was configured to match the Zheng et al. (2014) model closely and this was achieved:

Recruitment size distribution



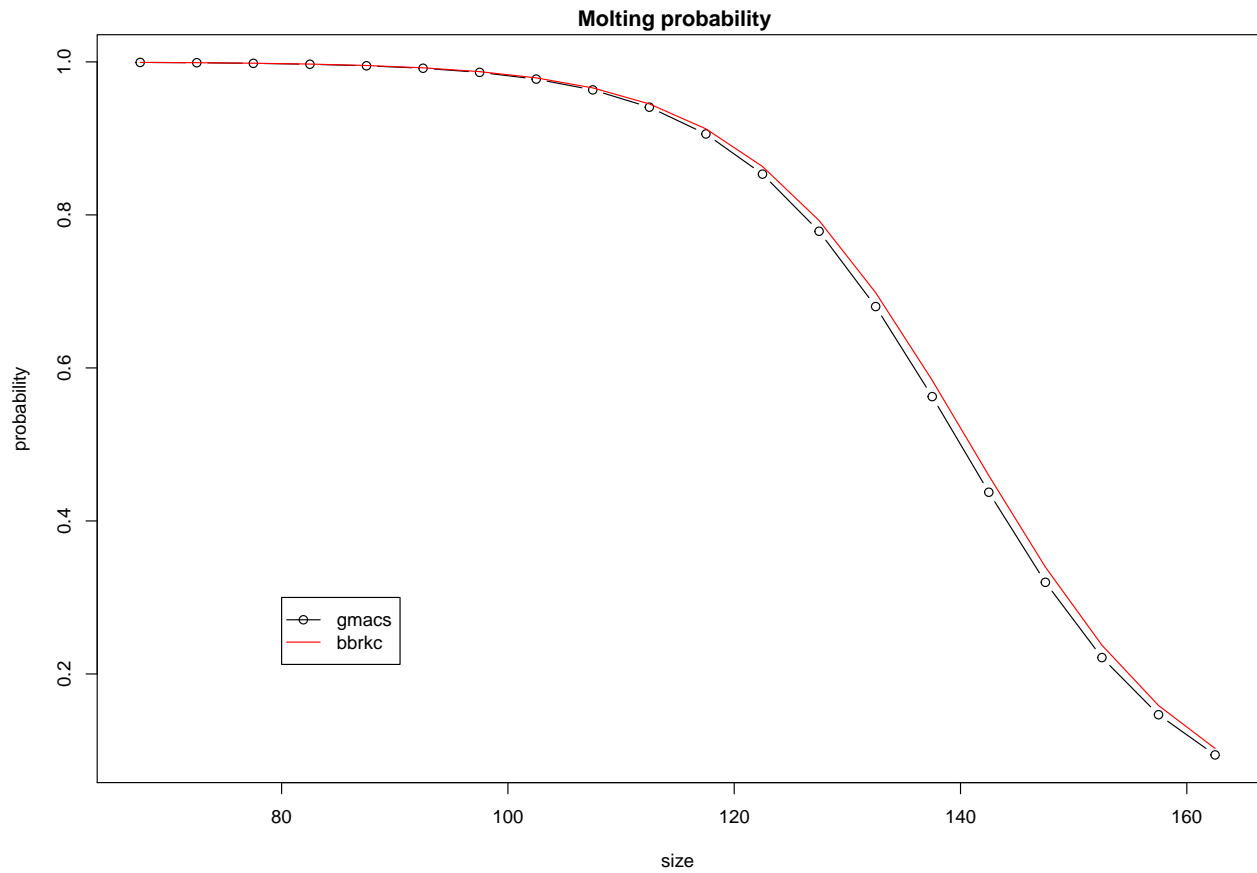
Molting increment width

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 show below.



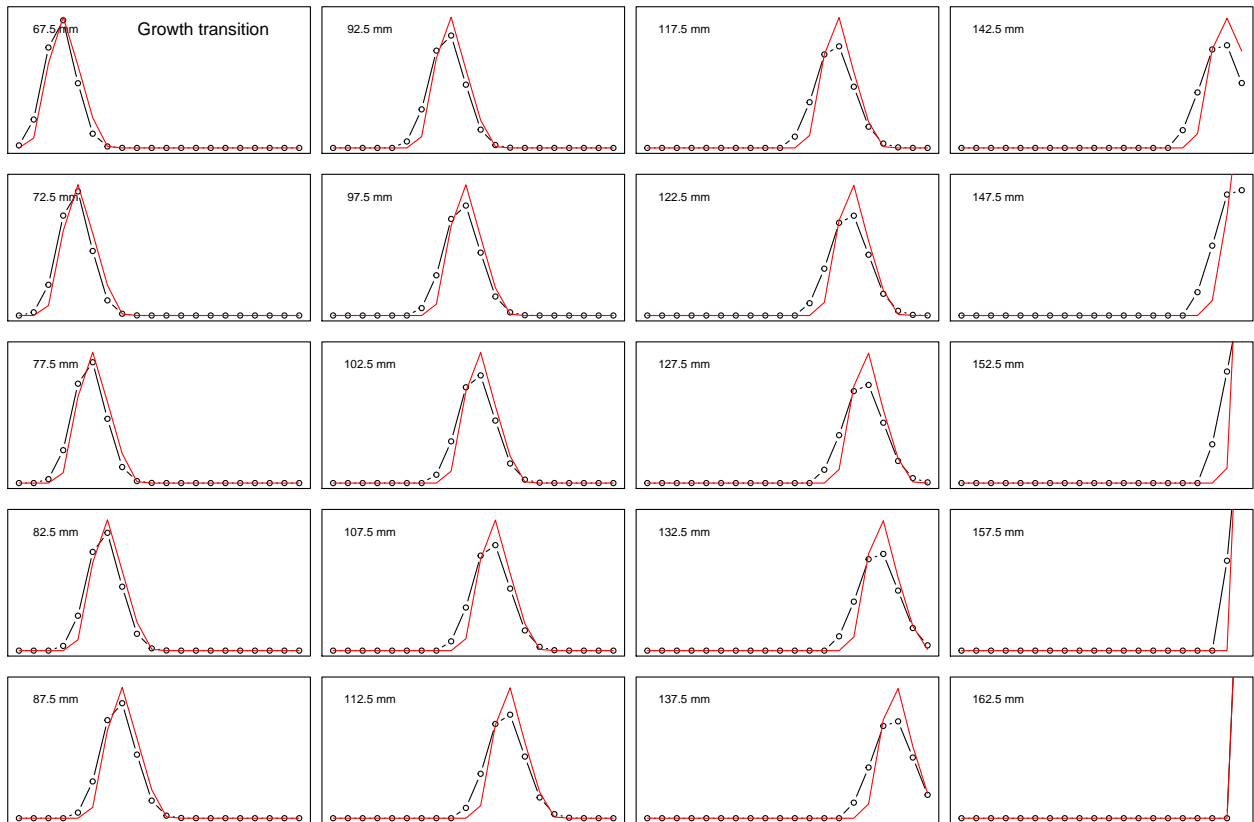
Molting probability

Fixed parameters in gmacs were easily set to represent that assumed from Zheng et al. (2014).

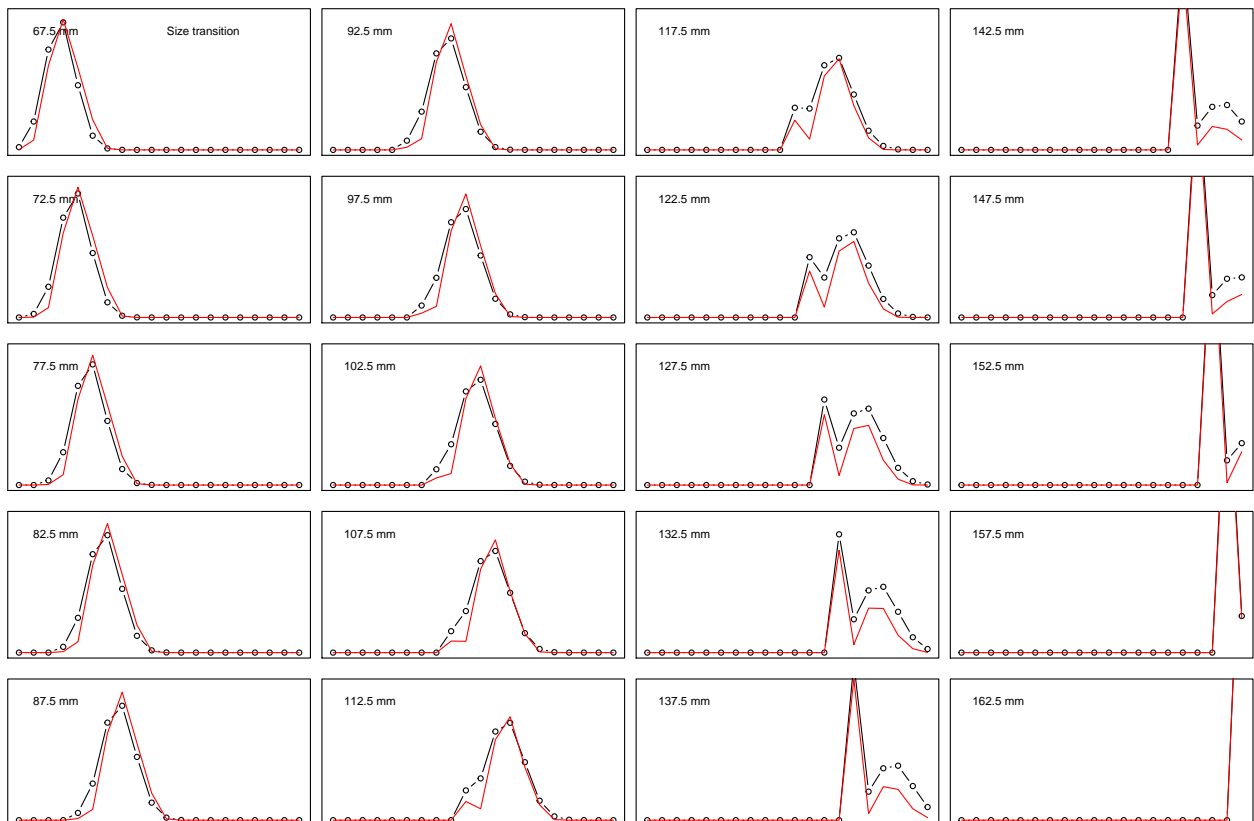


Transition processes

The first set of figures is the growth probabilities (for all crabs that molt)

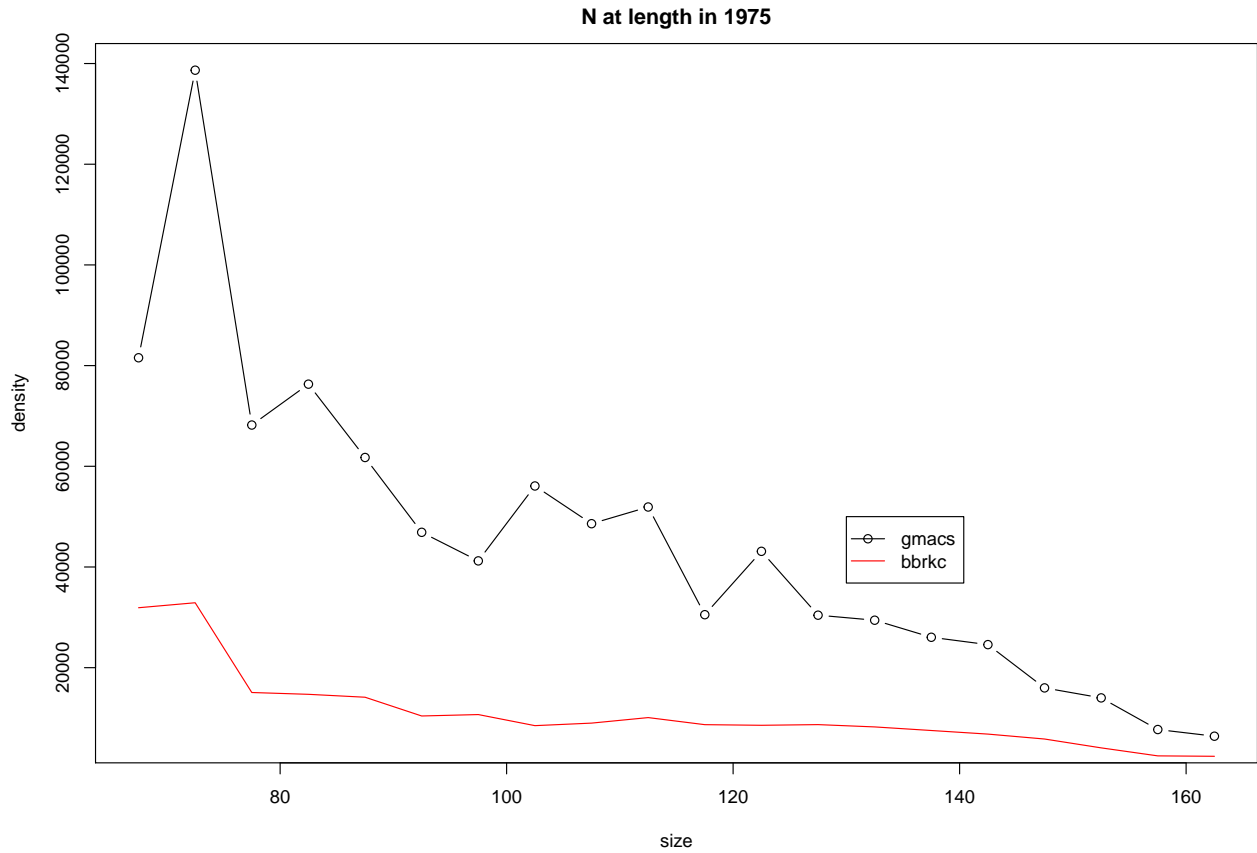


The second set of figures is the combination of growth and molting and represents the size transition:



Numbers at length in 1975

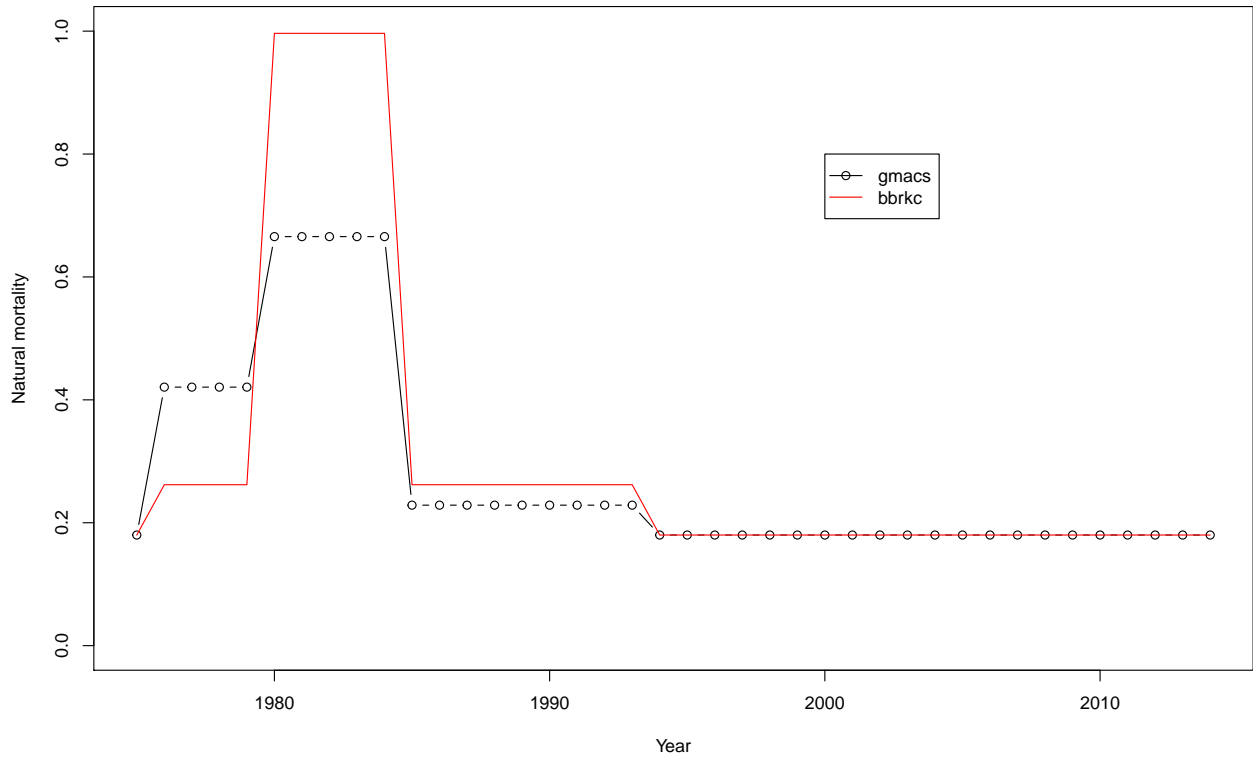
The scale of these results differ significantly and may be related to the interaction with natural mortality estimates and how the initial population-at-lengths were established (the BBRKC model assumes all new-shell).



Time series results/comparisons

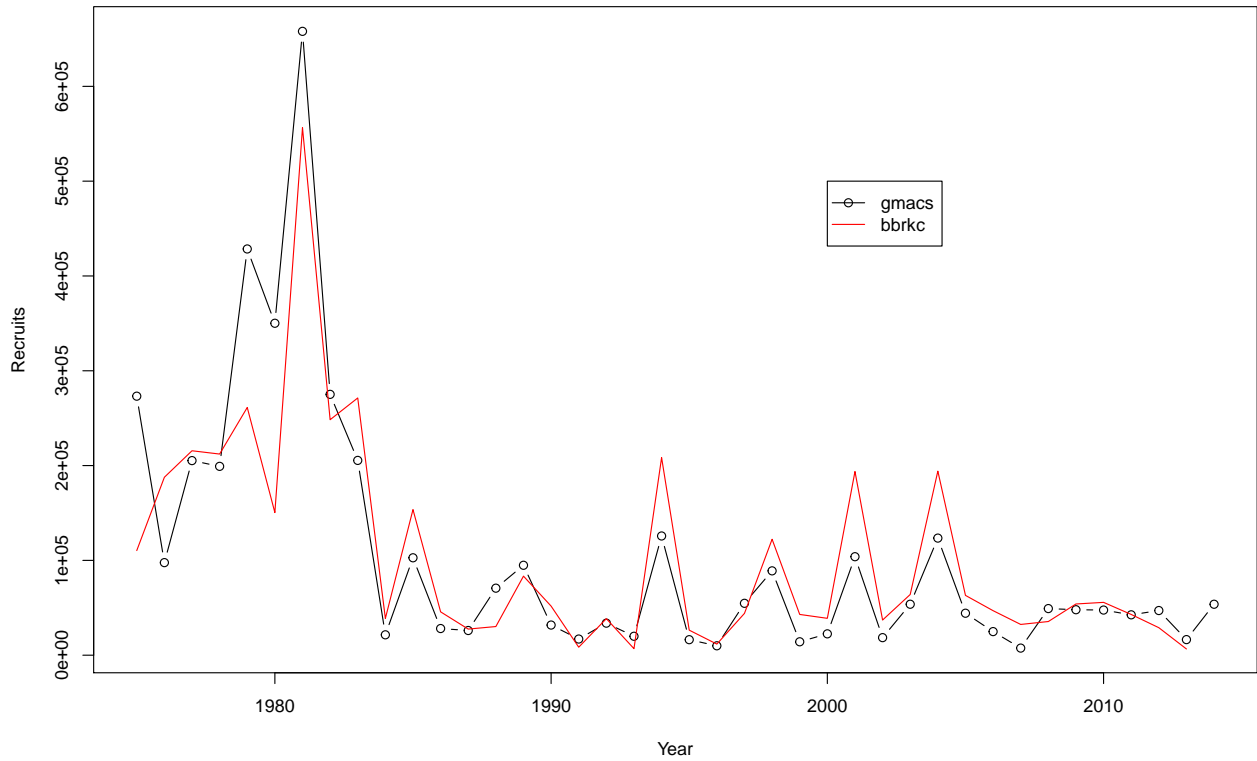
Natural mortality

The figure below illustrates implementation of 4 step changes in M (freely estimated) in gmacs relative to the estimates from Zheng et al. 2014.



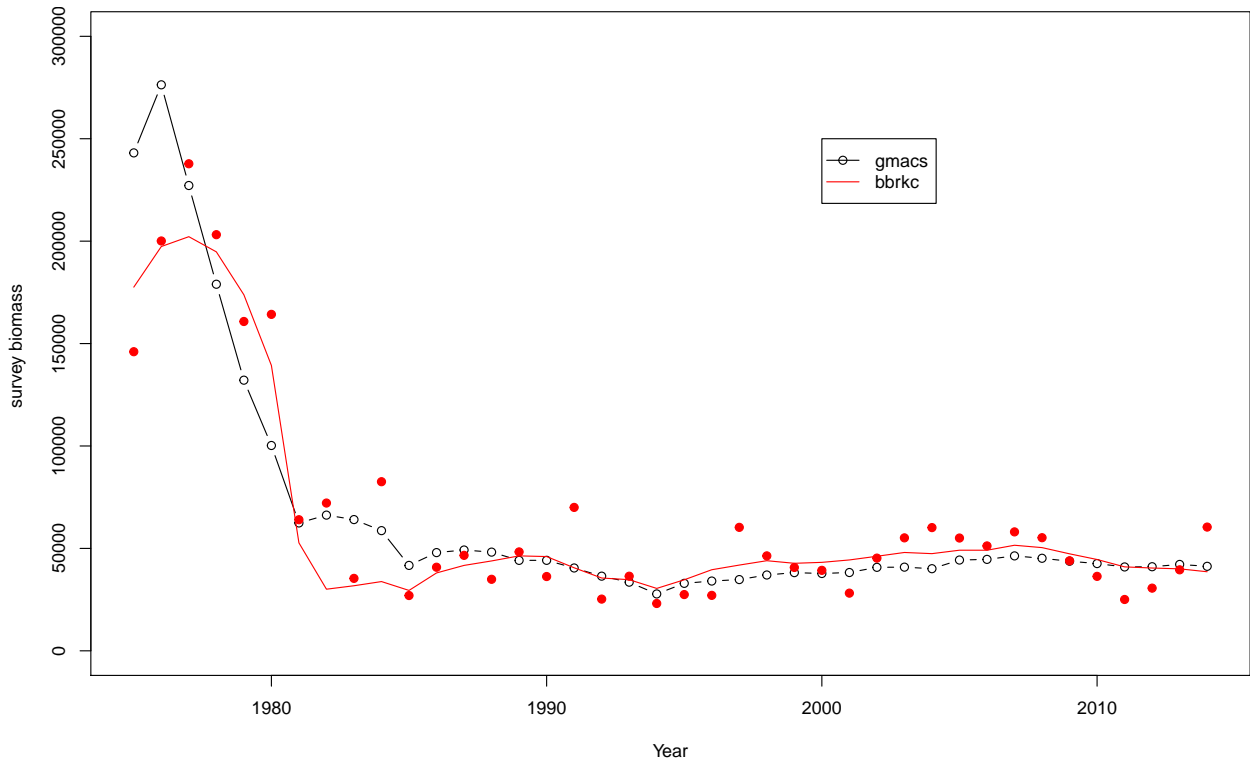
Recruitment

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.



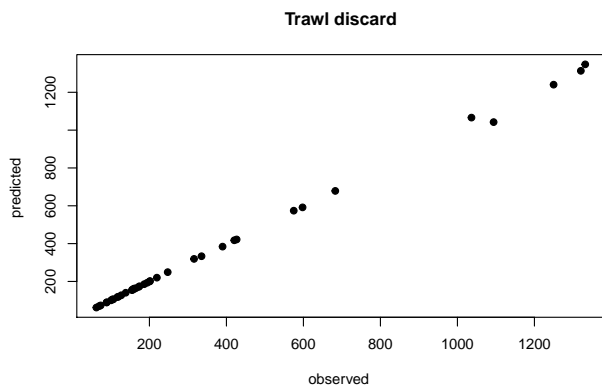
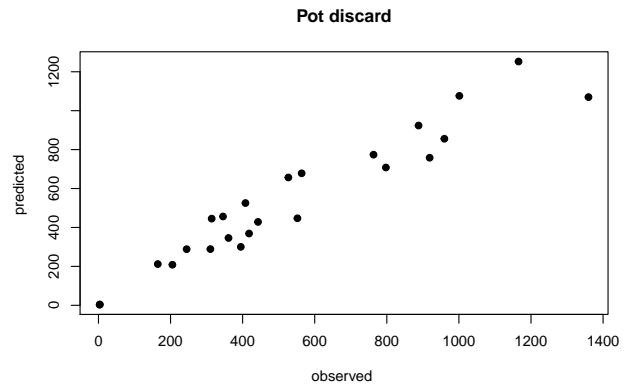
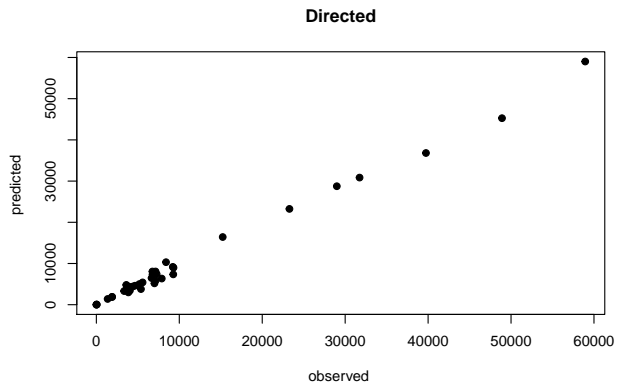
Fit to survey abundance indices

The model fit to survey biomass (males) was better for the current model (at least visually) than for the current implementation of gmacs:



Estimated retained catch and discards, for whole period

This figure summarizes the observed (horizontal) and predicted (vertical) catches by gear type. Data for discard fisheries were read in with 100% mortality (as clarified in Table 1 of Zheng et al. 2014).

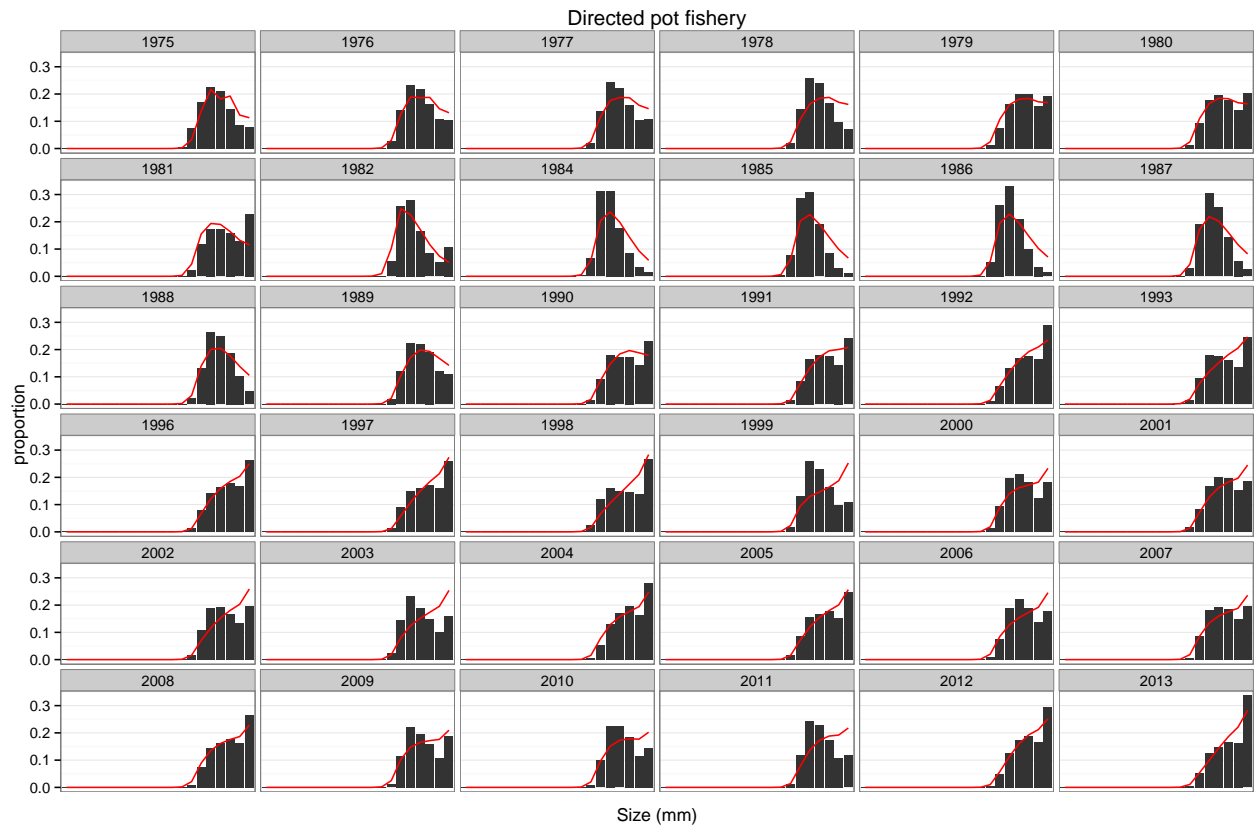


Other diagnostics

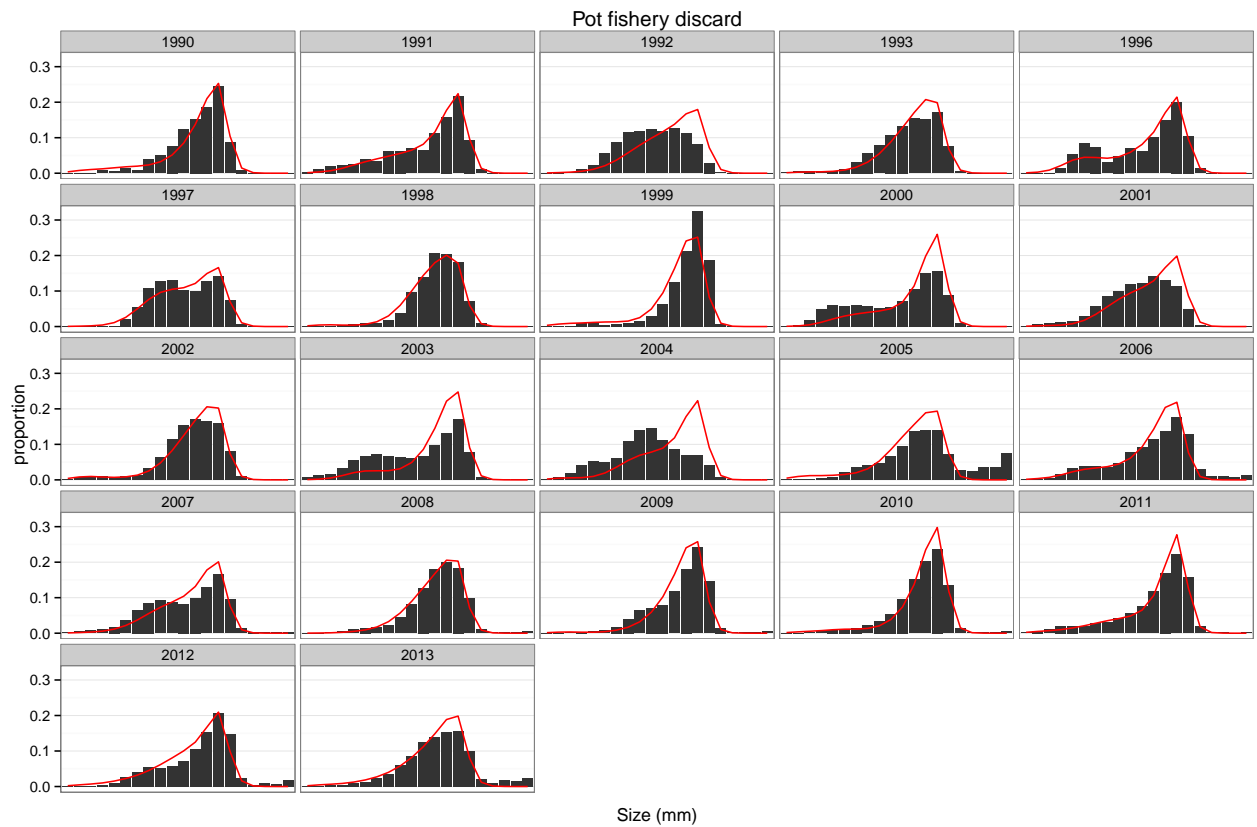
Fit to size frequency data

The subsequent figures provide fits to the male BBRKC data based on gmacs.

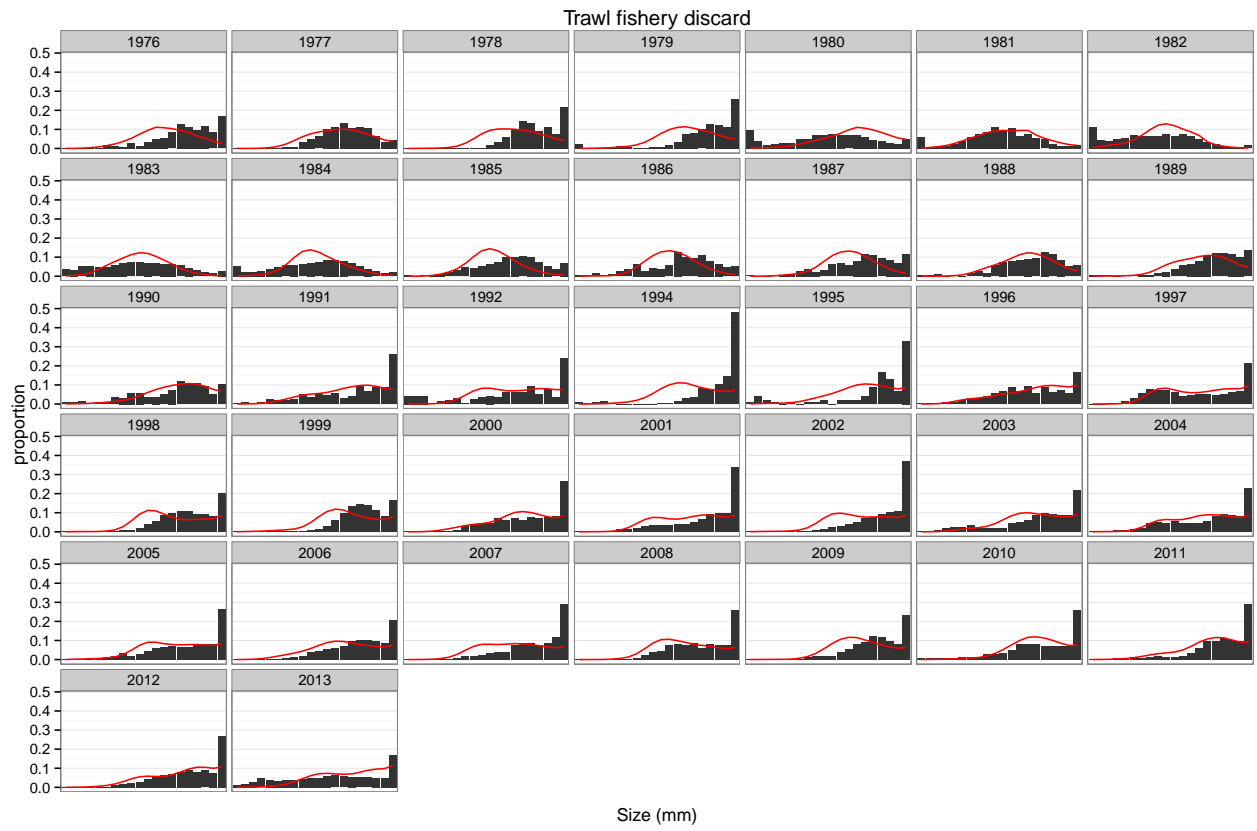
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## [[1]]
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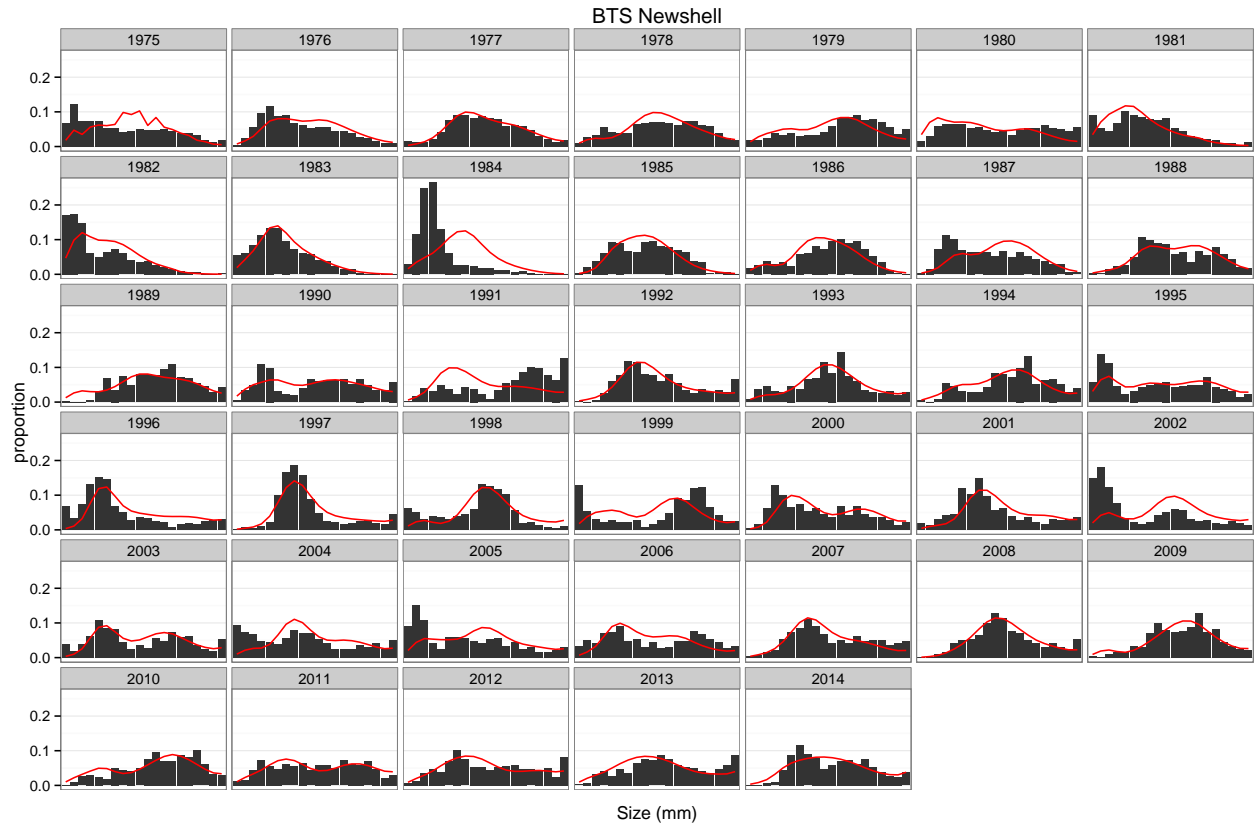
[[1]]



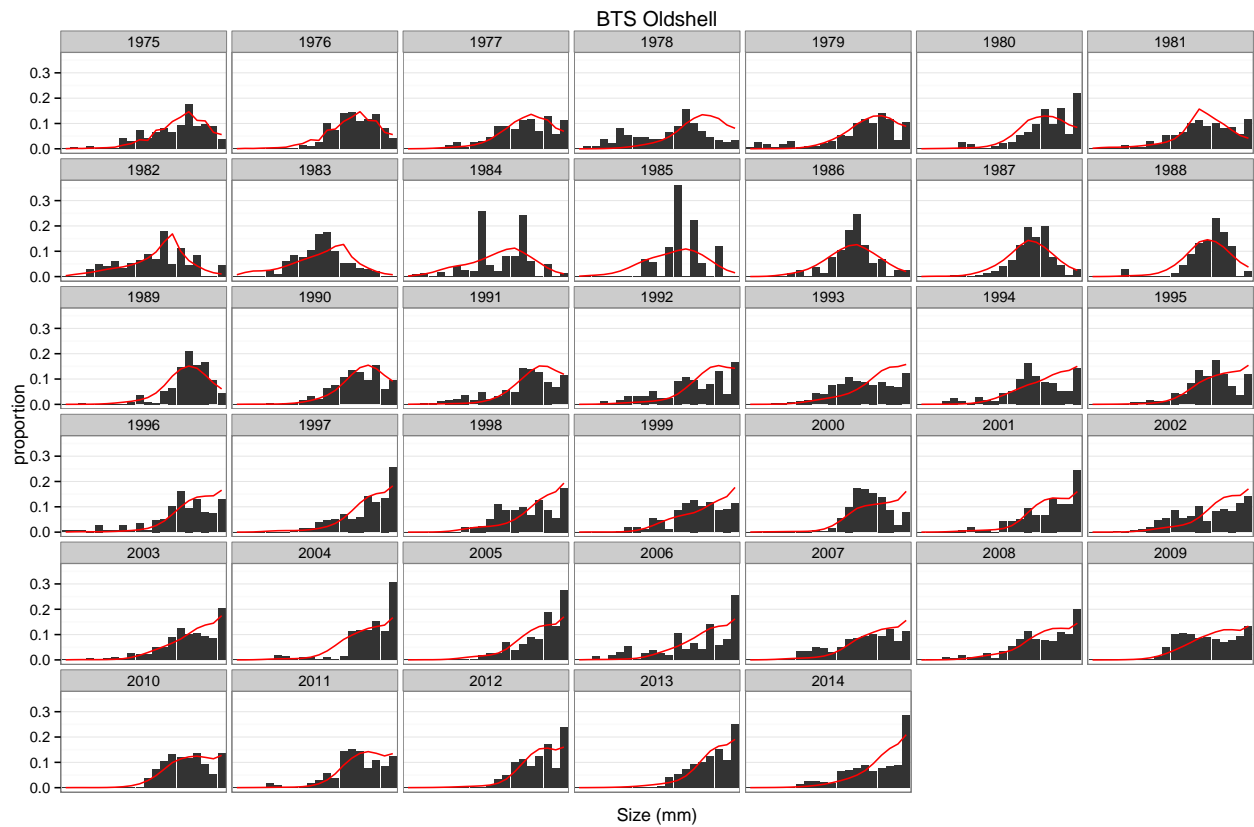
[[1]]



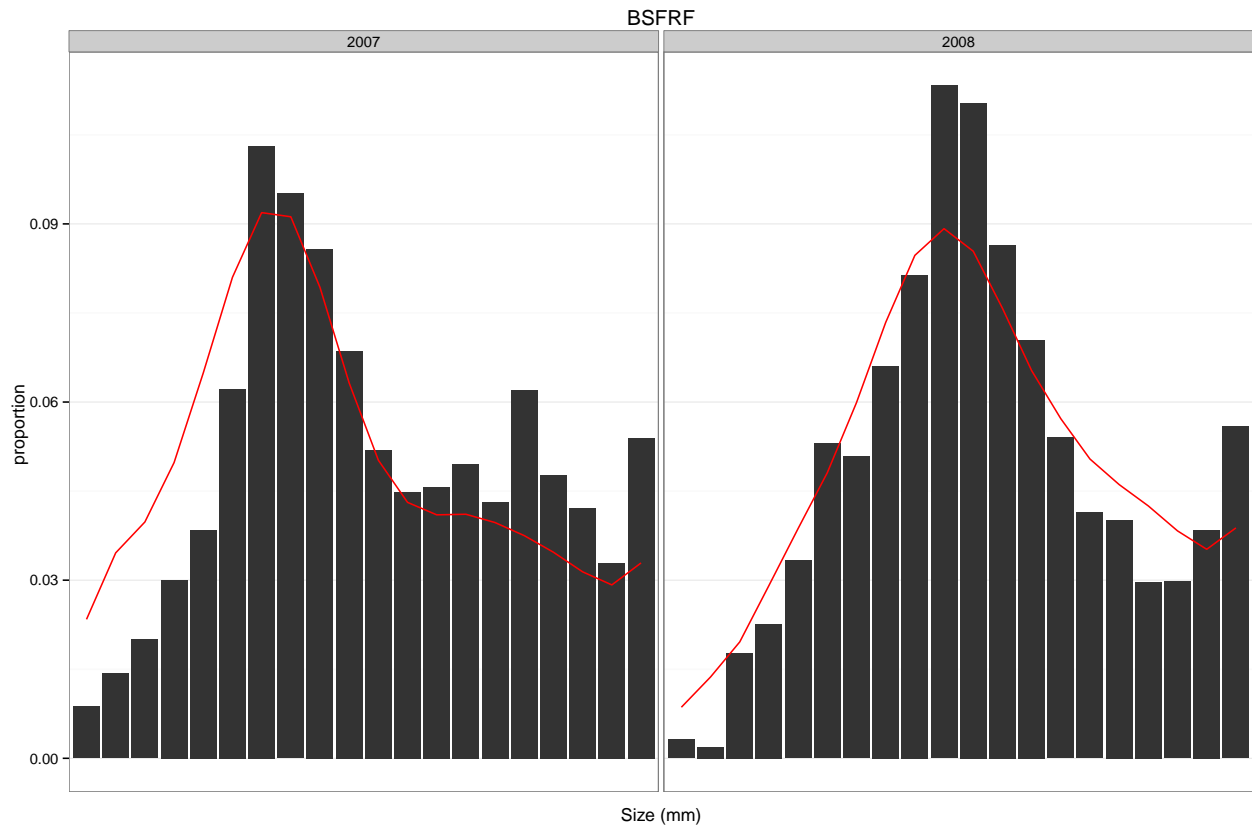
[[1]]



[[1]]



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## [[1]]
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Summary

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.