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 Bristol Bay red king crab (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 mean weight-at-length (w_ℓ) used in both models are nearly identical (Figure 1). The only difference between the two models is in the final length class (160mm) where the mean weight is greater in Zheng's model than in gmacs. This difference is due to. . .

Initial recruitment size distribution

Gmacs was configured to match the Zheng et al. (2014) model closely and this was achieved (Figure 2).

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 (Figure 3).
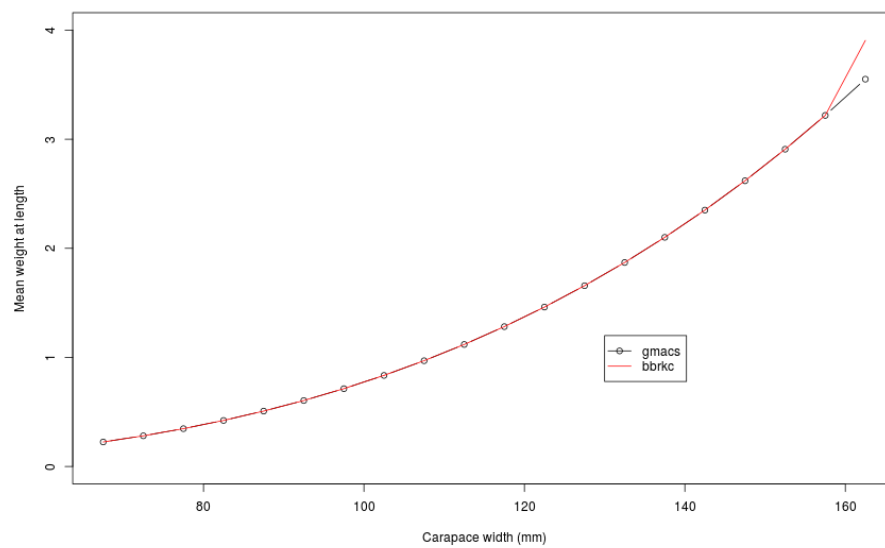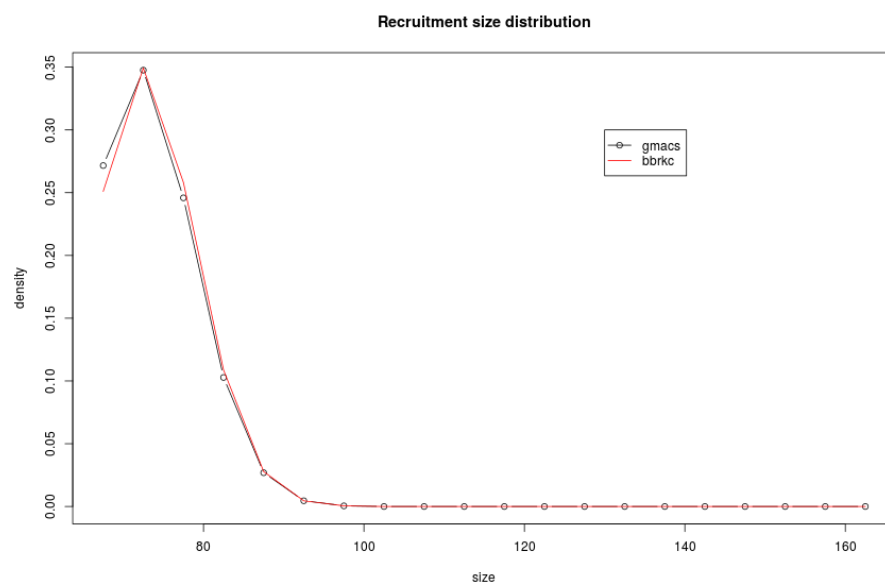
Figure 1: Mean weight-at-length.
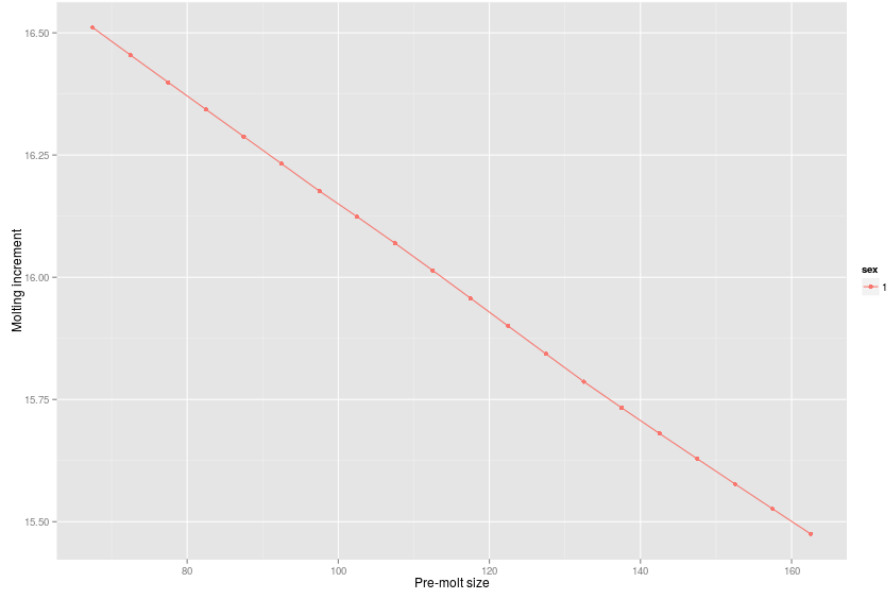

Figure 2: Length at recruitment.

Figure 3: Growth increment.

Molting probability

Fixed parameters in gmacs were easily set to represent that assumed from Zheng et al. (2014) (Figure 4).

Transition processes

The first set of figures is the growth probabilities (for all crabs that molt) (Figure 5).

The second set of figures is the combination of growth and molting and represents the size transition (Figure 6).

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) (Figure 7).
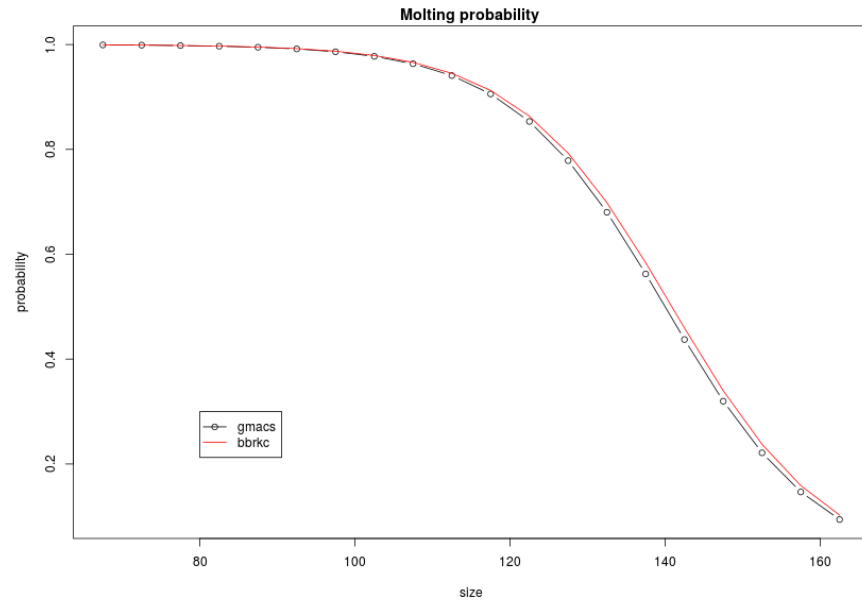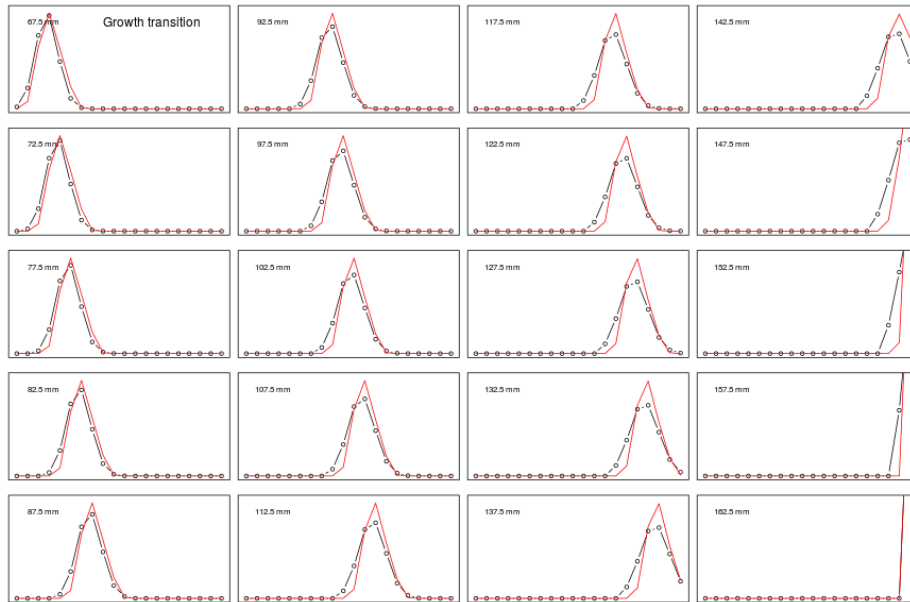
Figure 4: Molting probability.
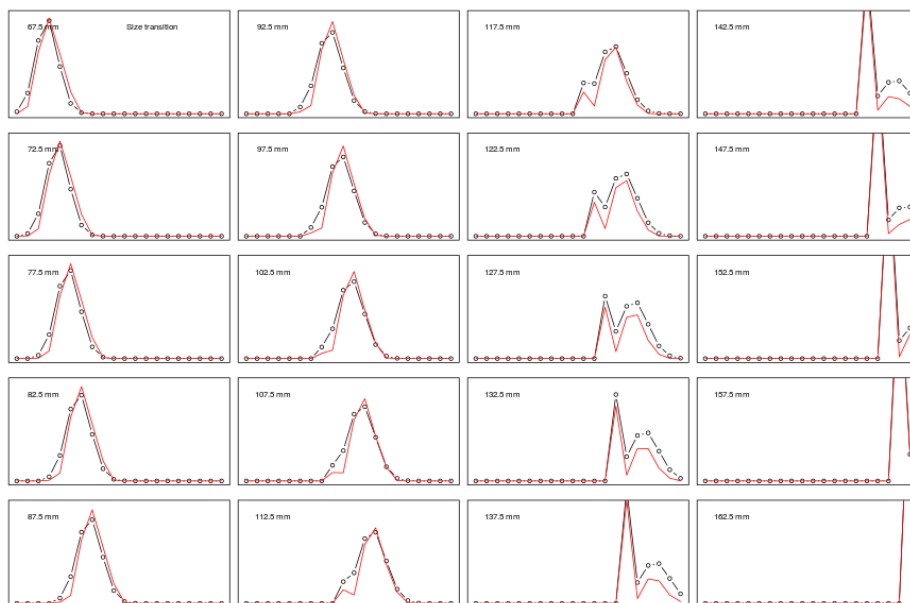

Figure 5: Growth transitions.
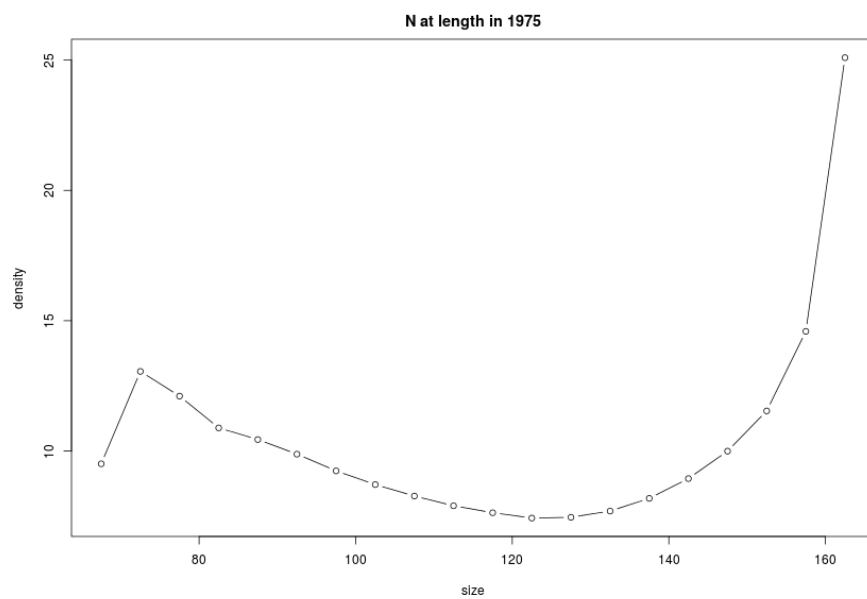
Figure 6: Growth transitions.

Figure 7: Initial numbers.

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 (Figure 8).
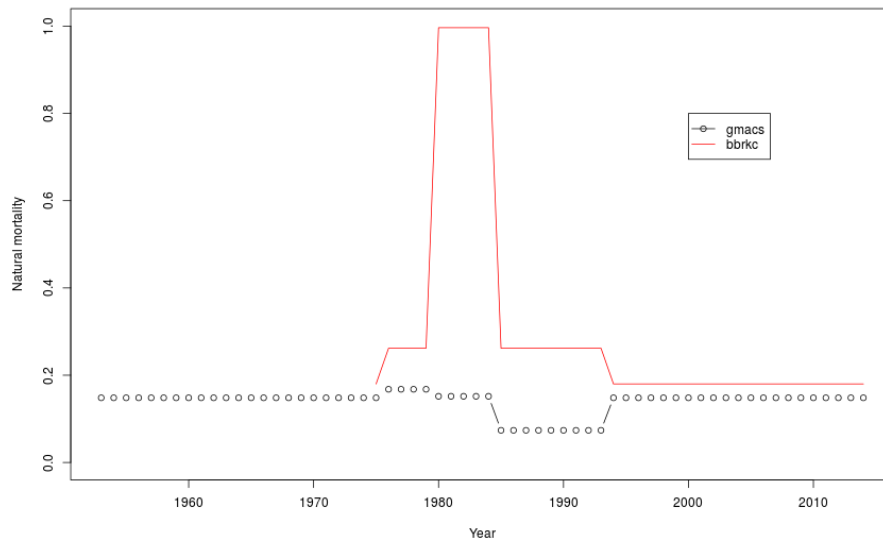

Figure 8: Time-varying natural mortality (M_t).

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 9).

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 (Figure **??**).

```
## Error in xy.coords(x, y, xlabel, ylabel, log): 'x' and 'y' lengths differ
```

```
## Error in plot.xy(xy.coords(x, y), type = type, ...): plot.new has not been called yet
```
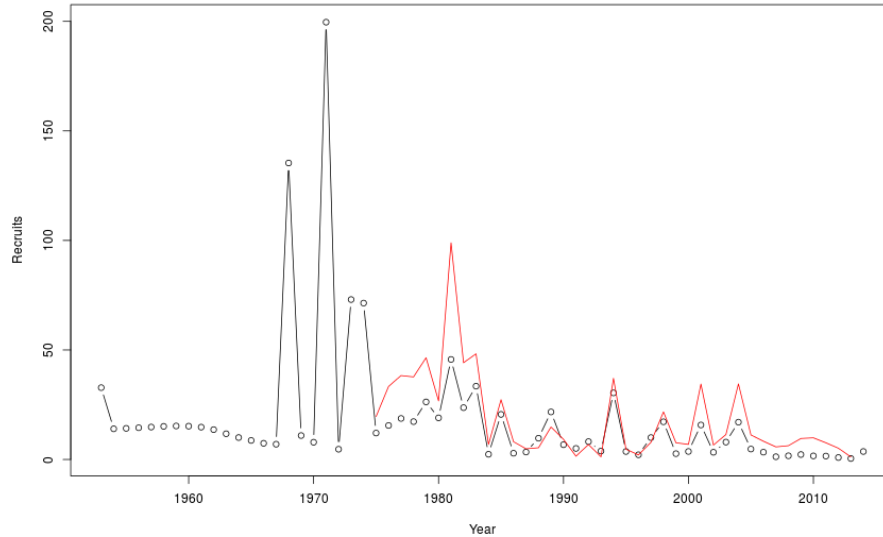
Figure 9: Recruitment (R_t).

```
## Error in plot.xy(xy.coords(x, y), type = type, ...): plot.new has not been called yet

## Error in strwidth(legend, units = "user", cex = cex, font = text.font): plot.new has not
```

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) (Figure 10).

Other diagnostics

Fit to size frequency data

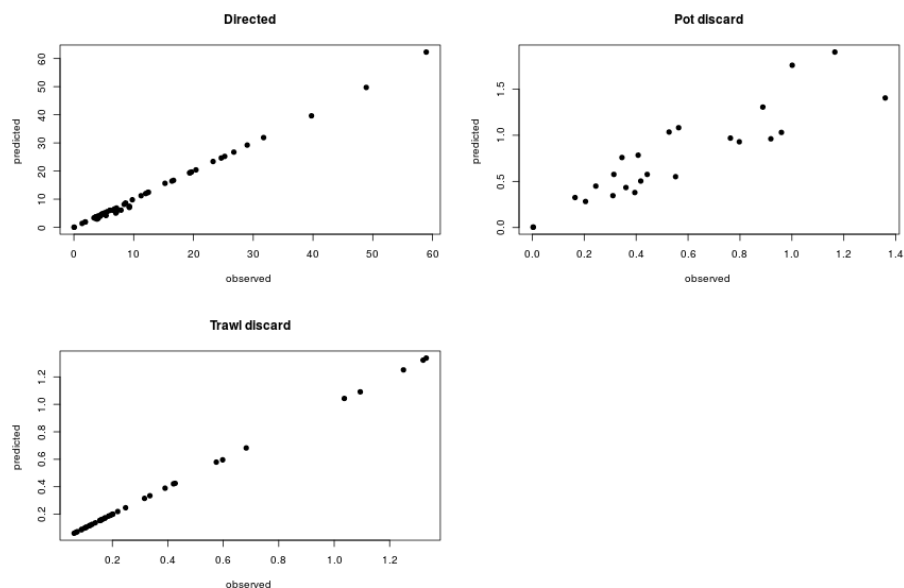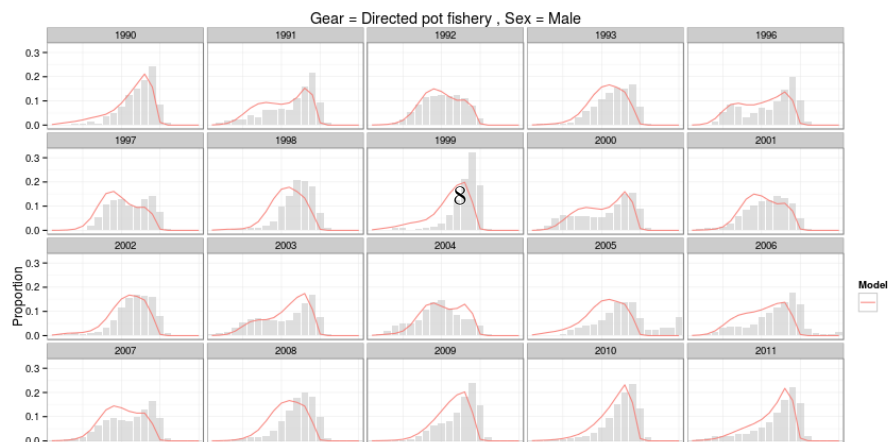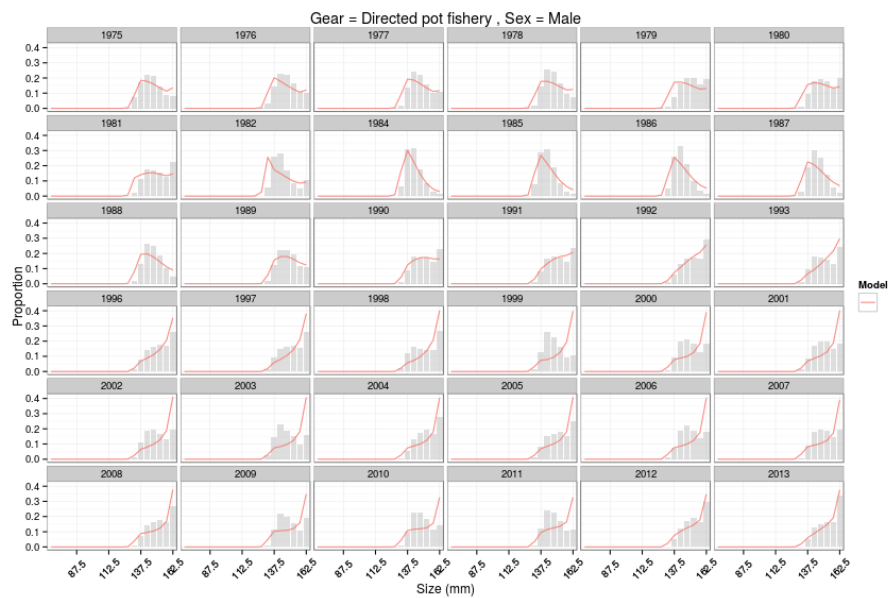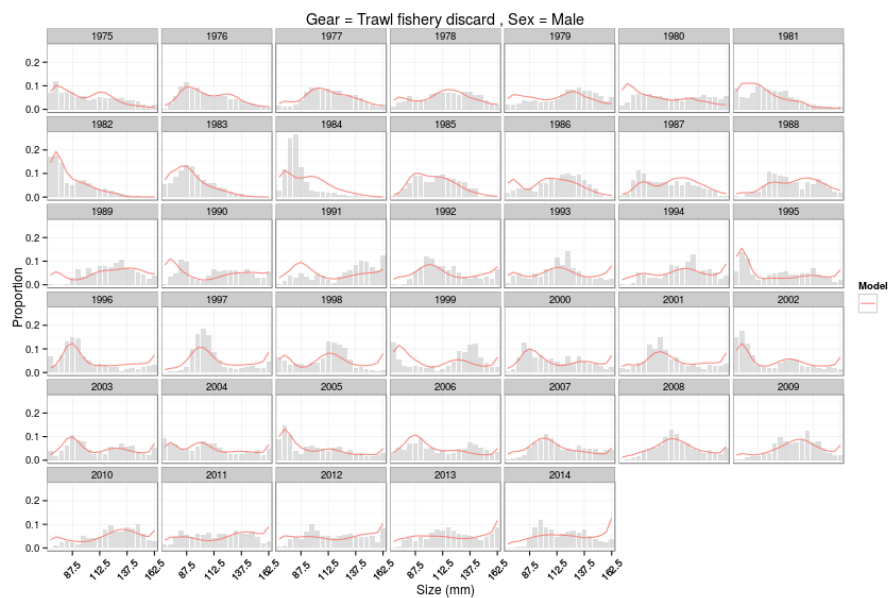The subsequent figures provide fits to the male BBRKC data based on gmacs (Figure ??).

Figure 10: Fit to catch.

Gear = Pot fishery discard , Sex = Male

Gear = Trawl fishery discard , Sex = Male

Gear = Trawl fishery discard , Sex = Male

Gear = BTS Newshell , Sex = Male
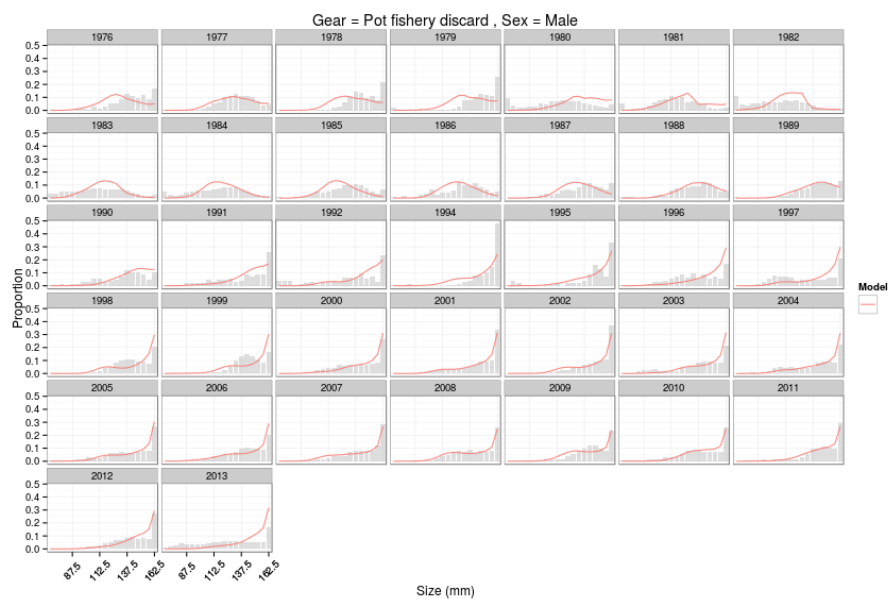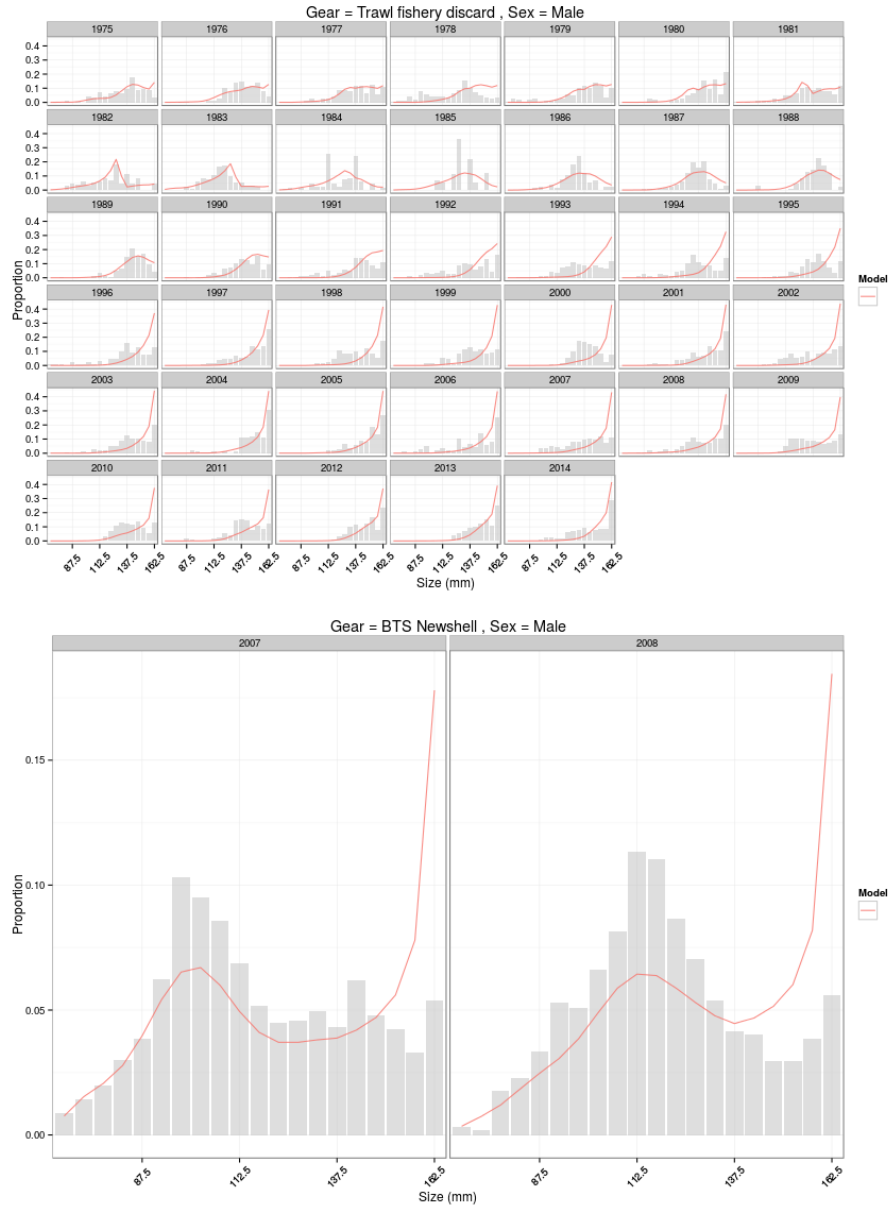
Summary

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

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specifications (e.g., constant natural mortality over time, time-varying selectivity, etc) to evaluate sensitivities.