



Bristol Bay red king crab

Proposed models for 2023

May 2023

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ADF&G

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Summary

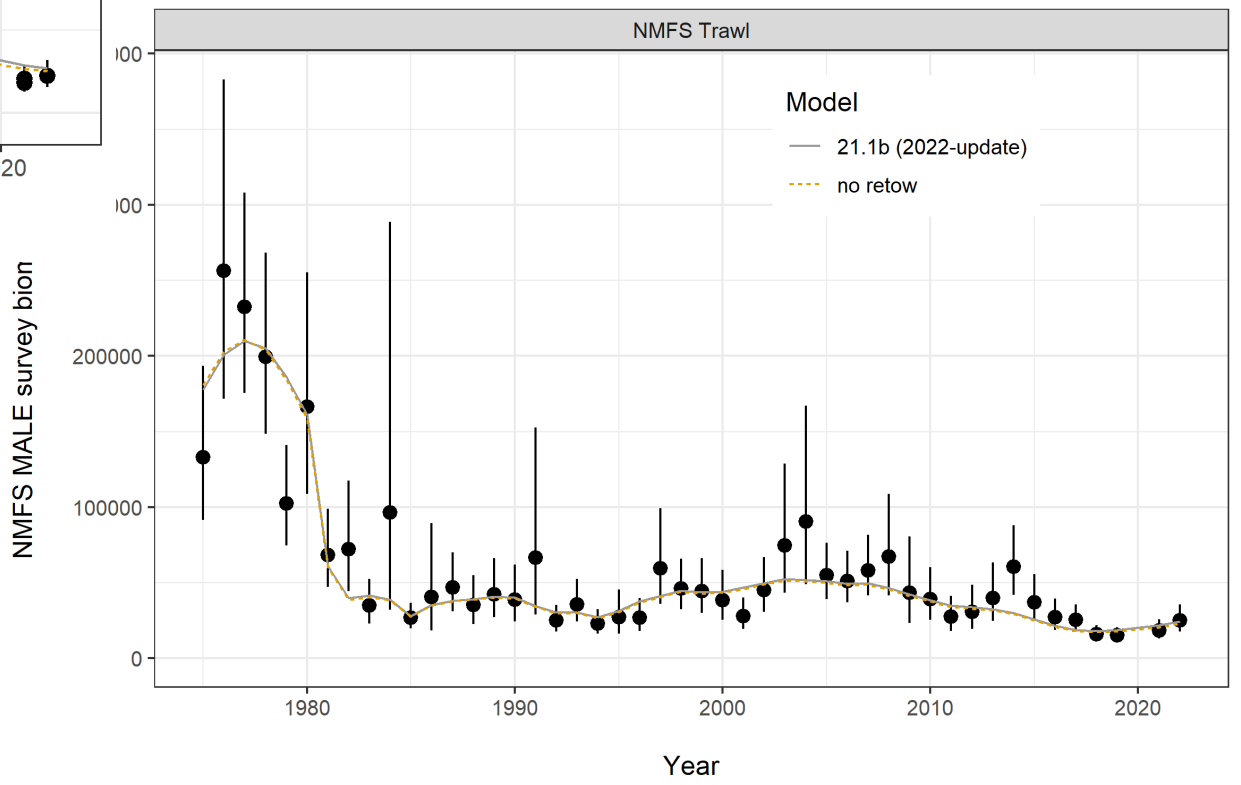
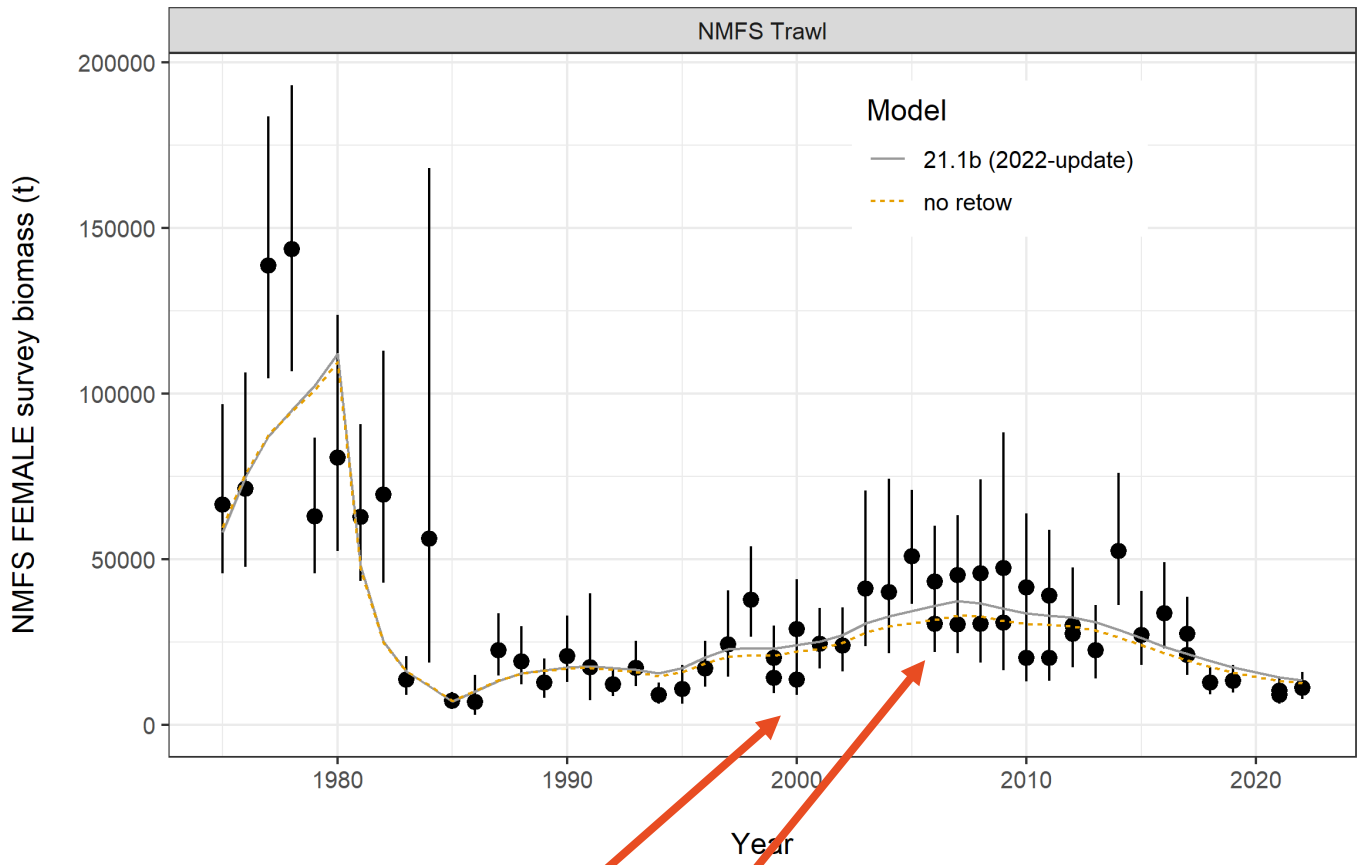
- Stable model in GMACS since 2018
- Directed fishery was closed in 2021/22 and 2022/23 season due to low mature female abundance.
- Low recruitment in recent years (last 8-12 years), projected decline in biomass without a large recruitment event
- Model explorations around a few themes:
 - GMACS updates
 - Start year for model (1975 vs 1985)
 - Natural mortality
 - Q for NMFS trawl survey
 - Sensitivity to female resample data (re-tow data)

CPT / SSC comments

- Stock structure template for Bering Sea red king crab – draft May 2023
- Natural mortality – scale and whether it should be estimated or not
- Q for both surveys
 - Explore how to estimate them and potentially with linked in some fashion
- Retrospective patterns
 - High priority on source of these
 - Decreases some with estimated M – models in 23.0a, 23.0b, 23.0
- Re-tow / resampling for females and the utility of this data
 - Model 23.2
- Other comment themes not yet addressed: initial conditions, VAST, re-do M likelihood profile

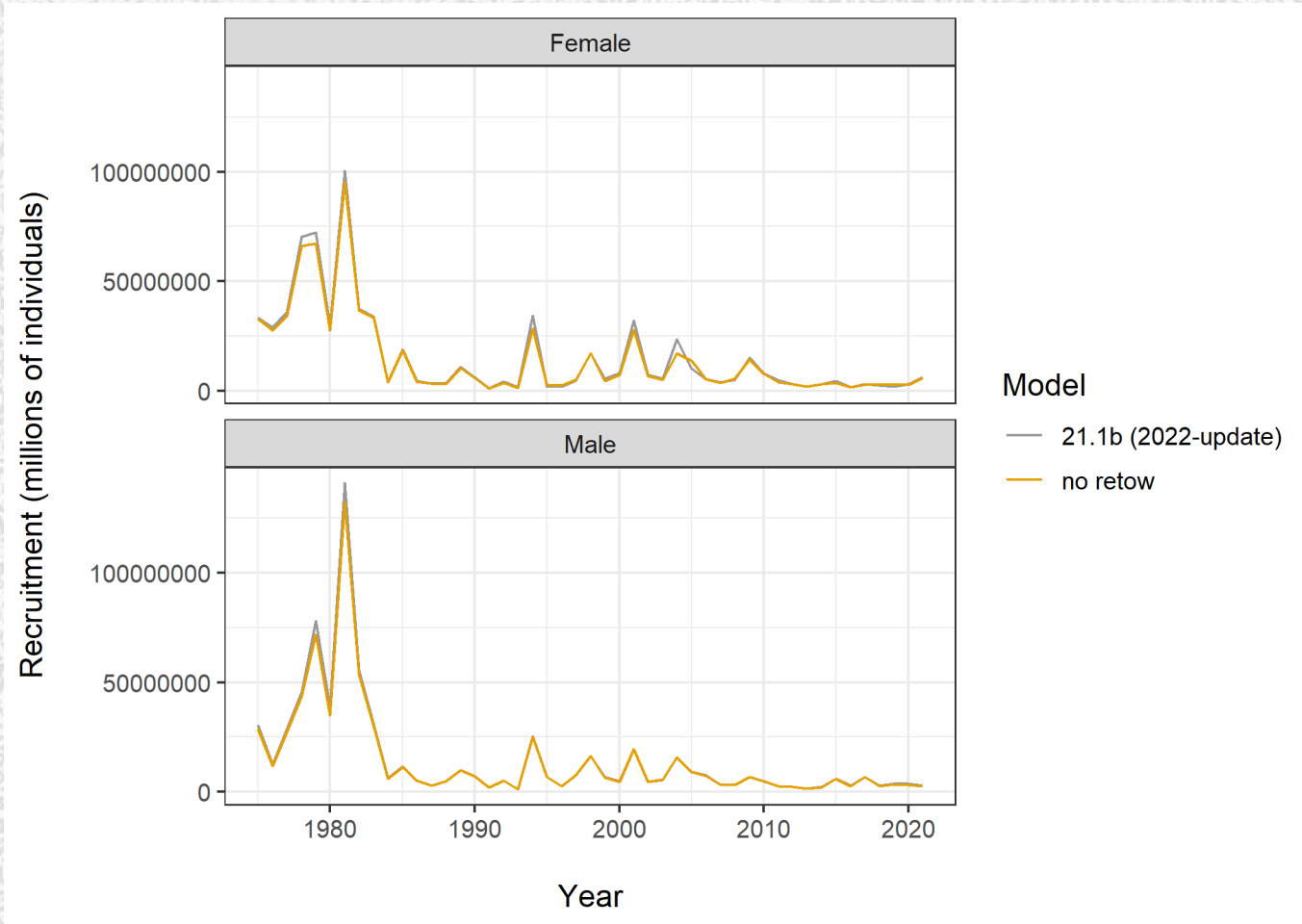
Female re-tow / resampling exploration

- Historic rationale:
 - Characterize the reproductive status of BBRKC mature females given temperature-driven delays in the molt/mate cycle
 - Accurately assess the relative abundance of BBRKC mature females given that females may be outside the surveyed area when the cycle is delayed
- Current rationale clarifications:
 - Improve accurate of size composition data post-molt for females
 - Abundance estimate of mature females (same as previous)
- Resampling occurred in 1999, 2000, 2006 to 2012, 2017, 2021
 - All except 2021 had at least 25% of mature females that did NOT complete the molt-mate cycle
- Model 23.2
 - Remove “re-tow” data from the base model by estimating the base model (21.1b) with only leg 1 survey data – both biomass and size compositions.

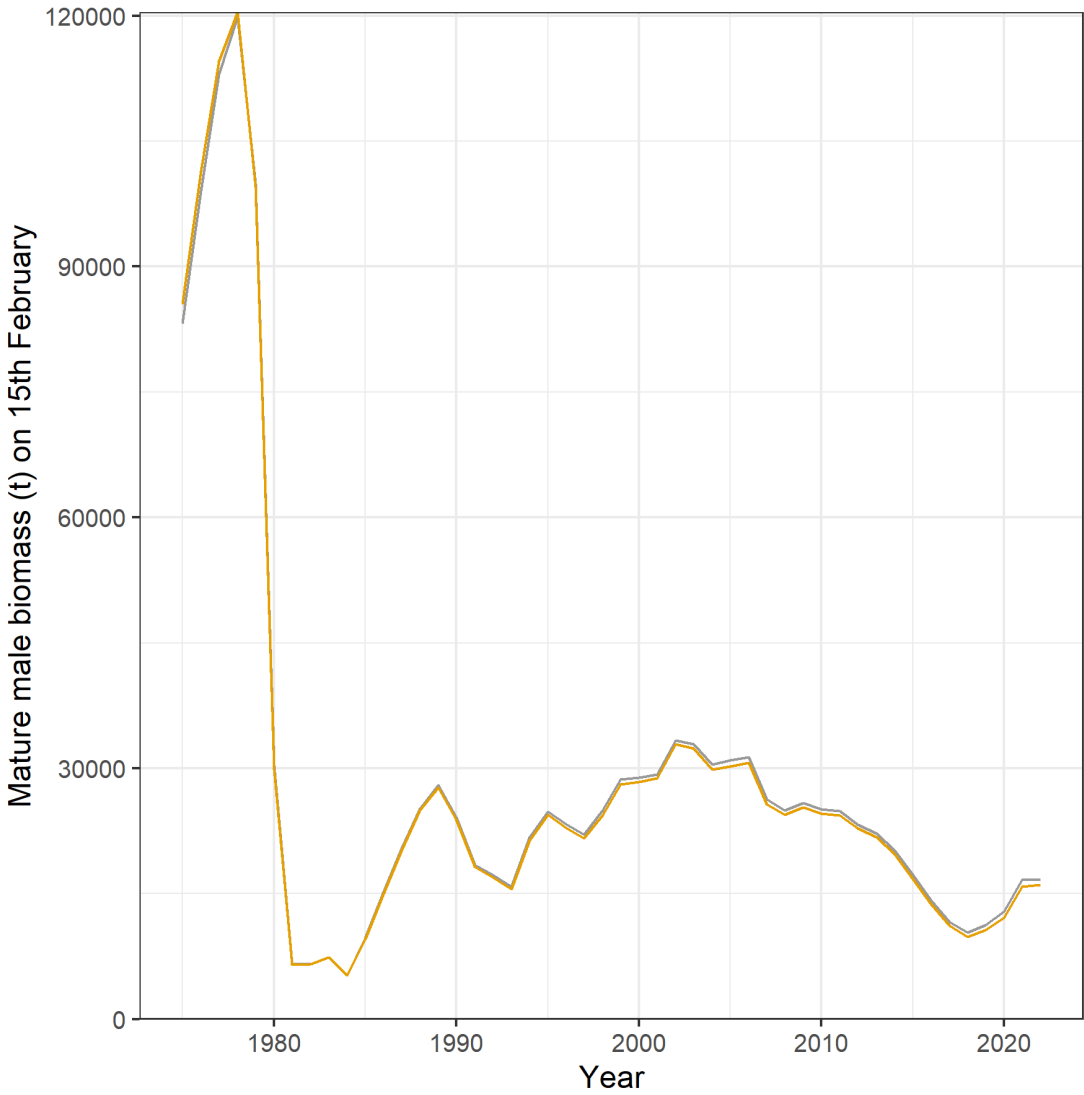


1999, 2000, 2006 to 2012, 2017, 2021

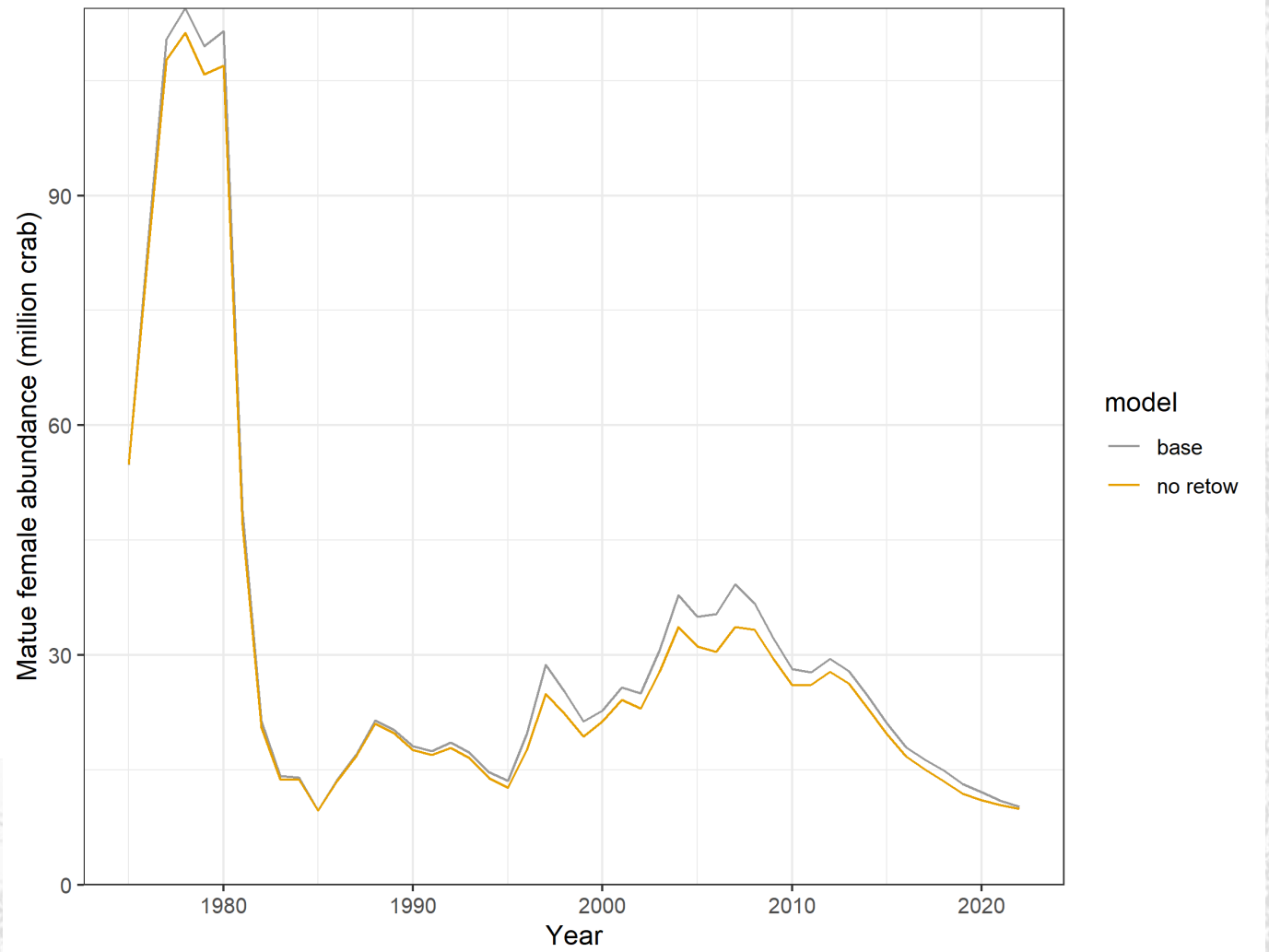
Recruitment – model 23.2



Model scenarios



Female Abundance with and without retow data



Model 23.2: Female re-tow

- Continuation of re-tow for females vital in years where large number of females are delayed in the molt-mate cycle
- Sampling females at the same point in their annual cycle is vital to the assumptions of the population dynamics and therefore the population model
- Did not address the current 10% threshold here or the influence on the State of Alaska harvest strategy

2023 Model explorations

21.1b: the base model from September 2022.

21.1b(update): model 21.1b + using the **recently updated version of GMACS** (version).

22.0: model 21.1b (update) + starting in 1985.

23.0: model 21.1b (update) + fixing $M = 0.257$ for males (Then et al. 2015).

23.0a: model 21.1b (update) + +estimating a constant M for males.

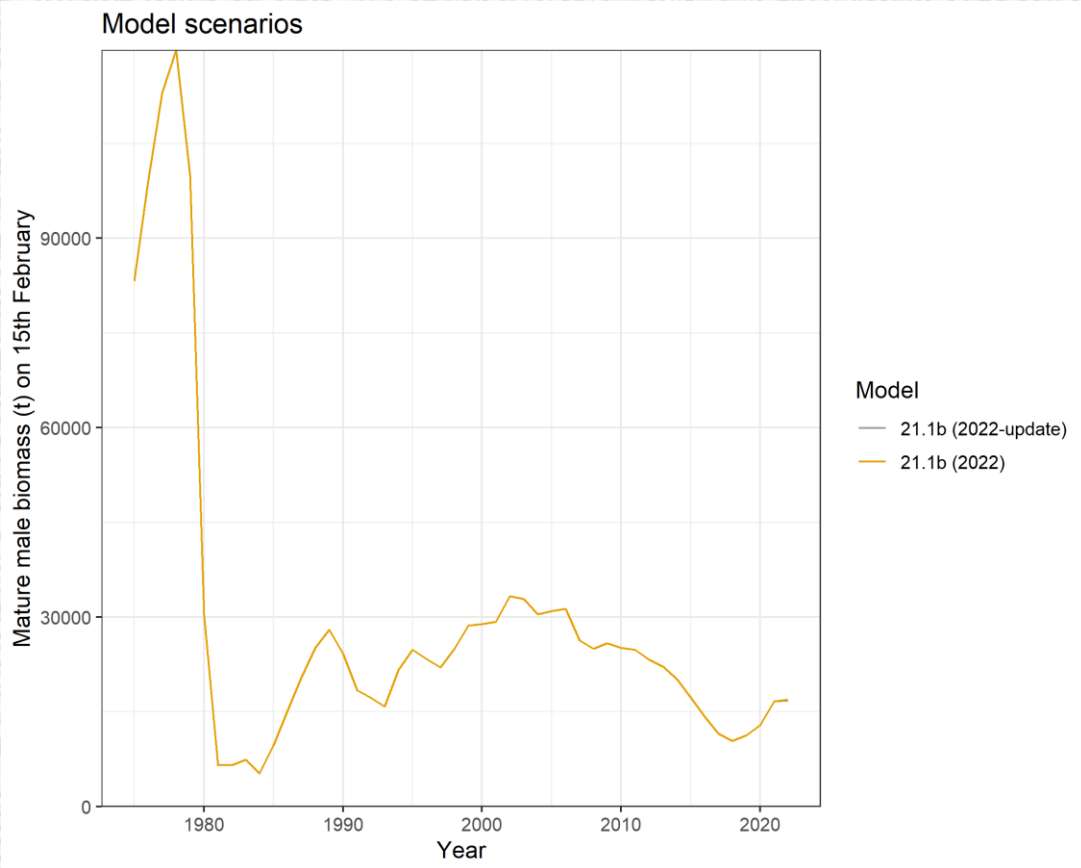
23.0b: model 21.1b (update) + fixing $M = 0.31$ for males from previous likelihood profile work
(2020 & 2021)

23.1a: model 21.1b (update) + increased CV for Q prior for NMFS trawl.

23.3: model 23.1a + 23.0a (increased CV on Q estimating M)

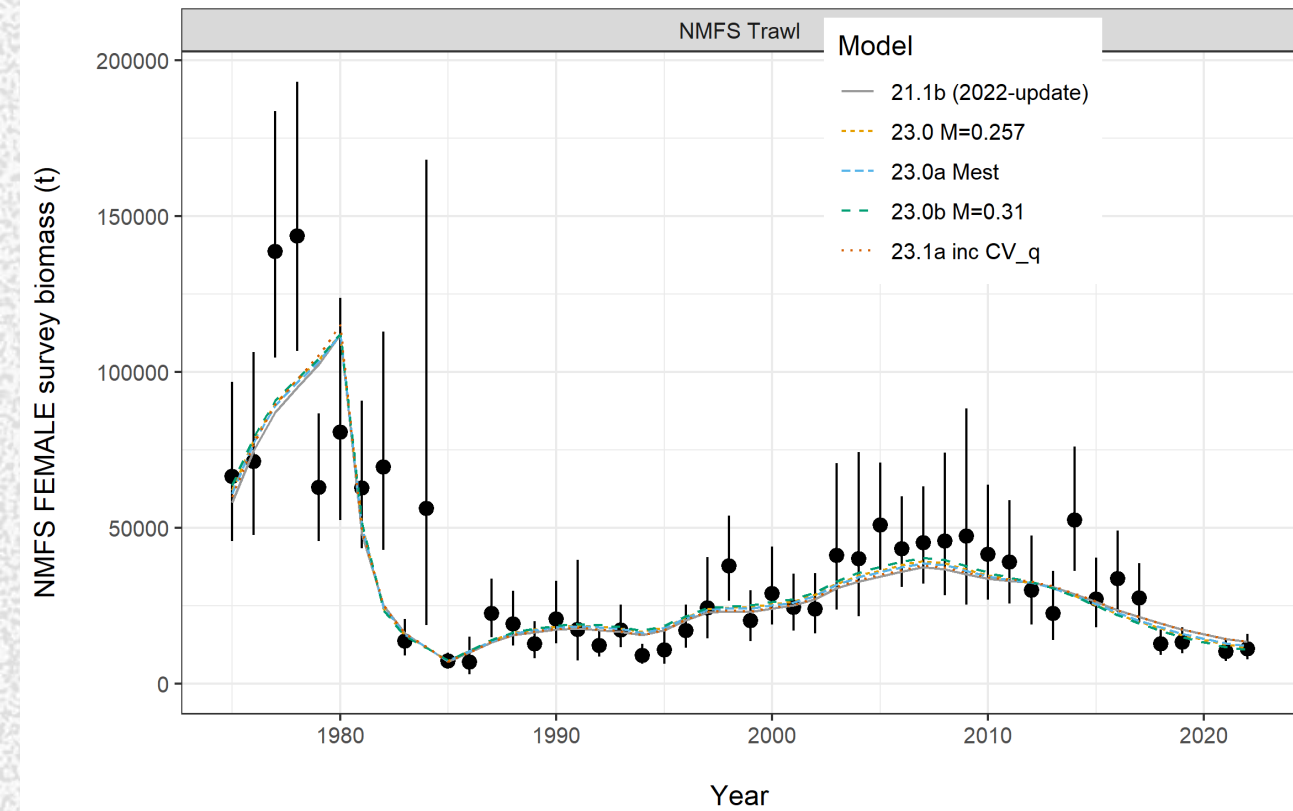
23.2: model 21.1b (update) – removing “retow” data for females in years they were resampled

GMACS updates

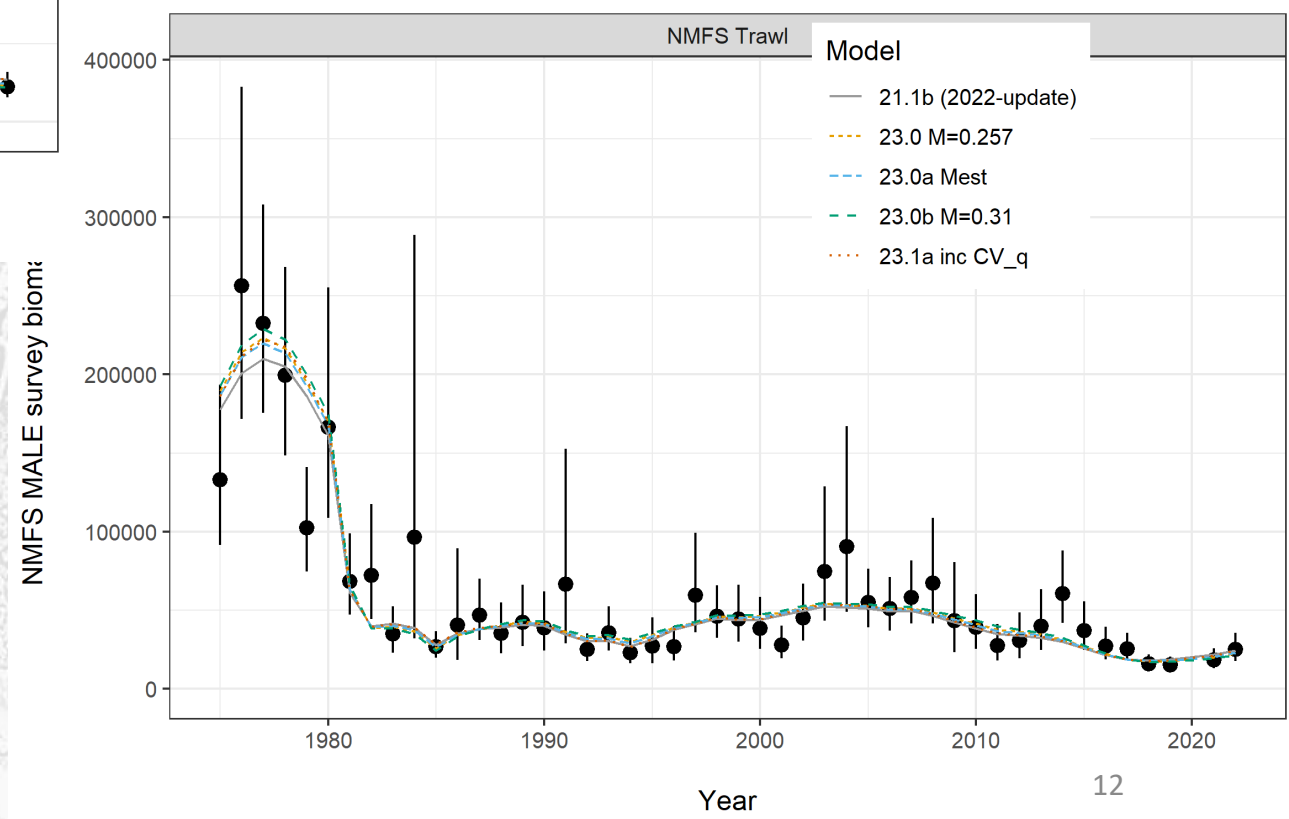


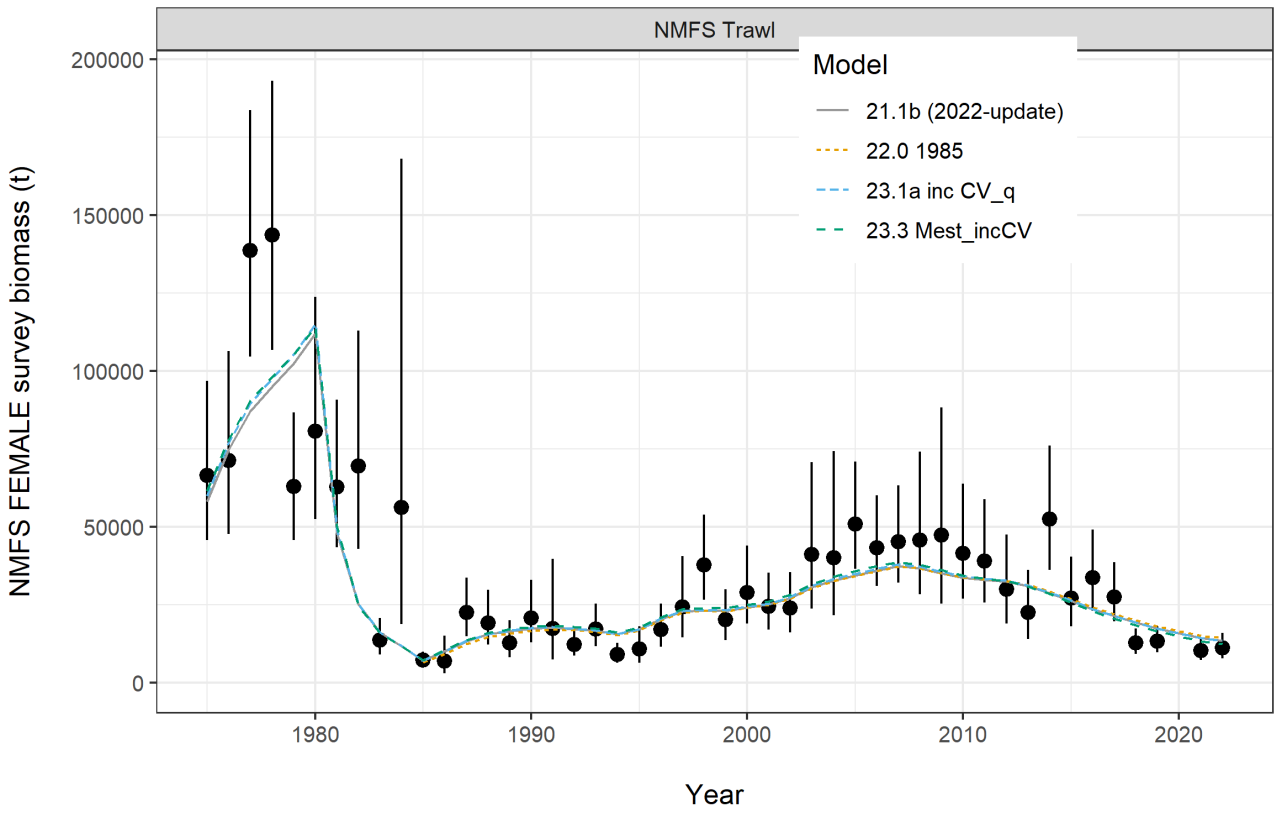
- Likelihoods identical (2 decimal places)
- Small differences in projected specifications – likely due to projection iterations

| Model | Current MMB | $B_{35\%}$ | MMB / B_{MSY} | $F_{35\%}$ | F_{OFL} | OFL |
|---------------|-------------|------------|-----------------|------------|-----------|------|
| 21.1b (2022) | 16.95 | 24.03 | 0.71 | 0.30 | 0.20 | 3.04 |
| 21.1b(update) | 16.76 | 22.25 | 0.75 | 0.30 | 0.22 | 3.21 |

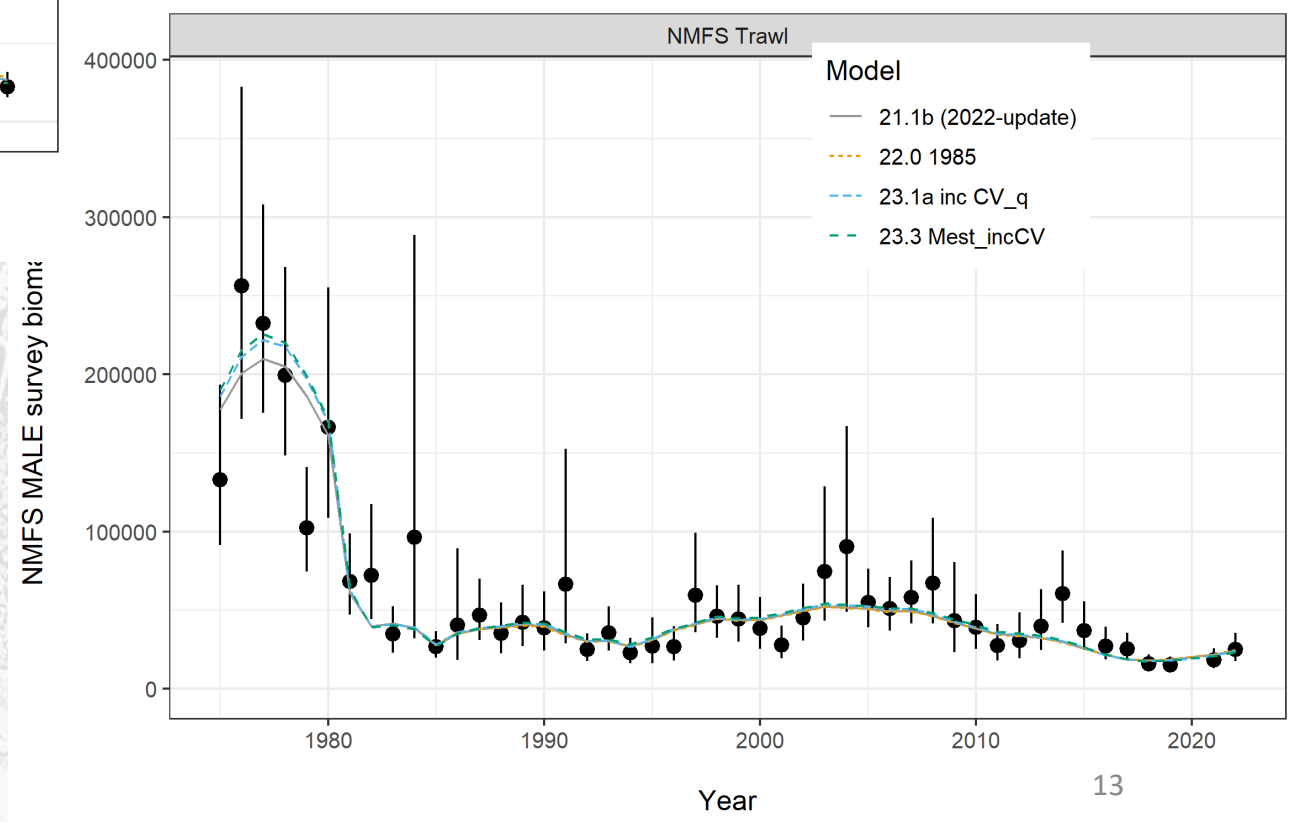


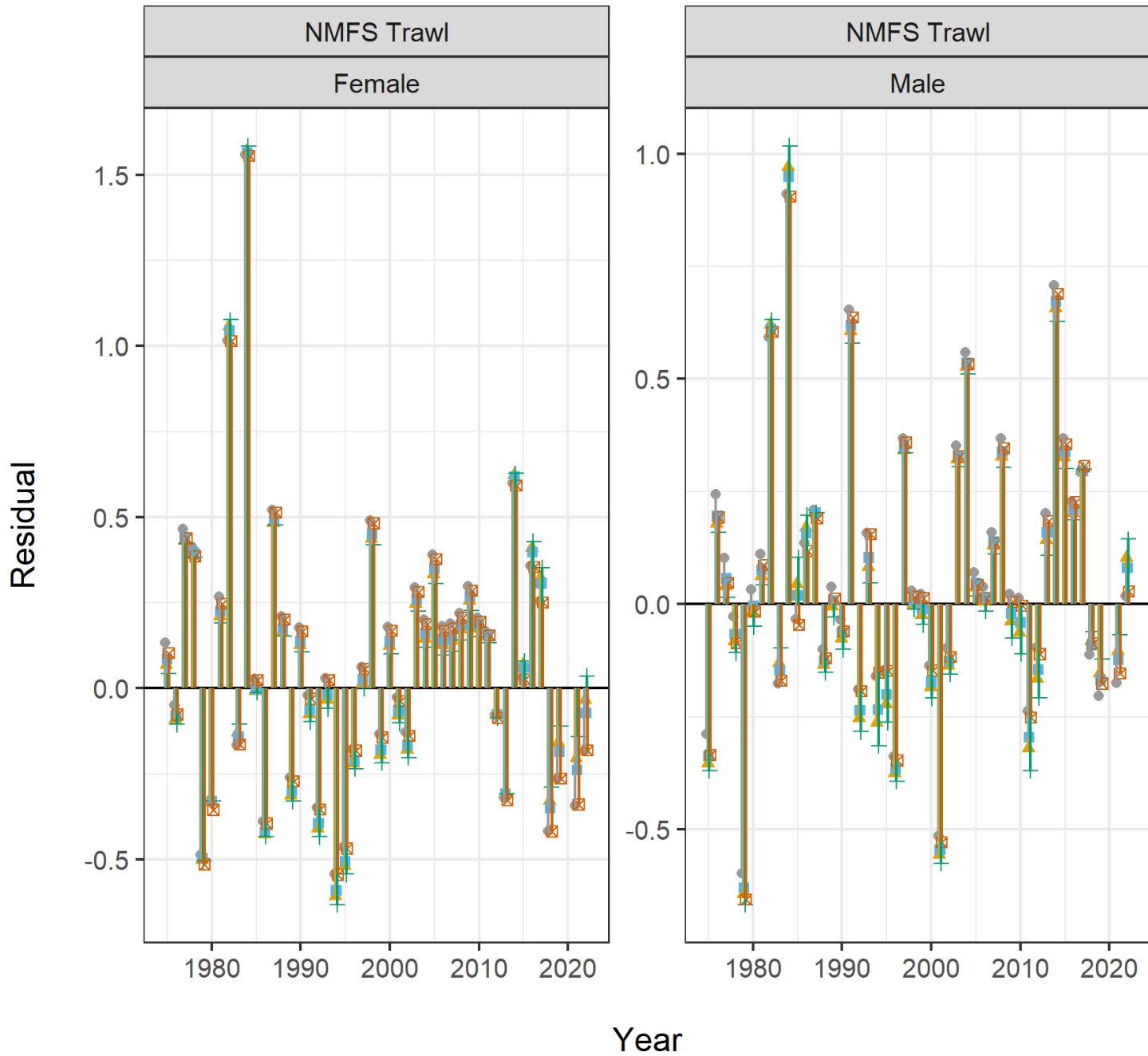
- Model fits to NMFS trawl survey data are similar.



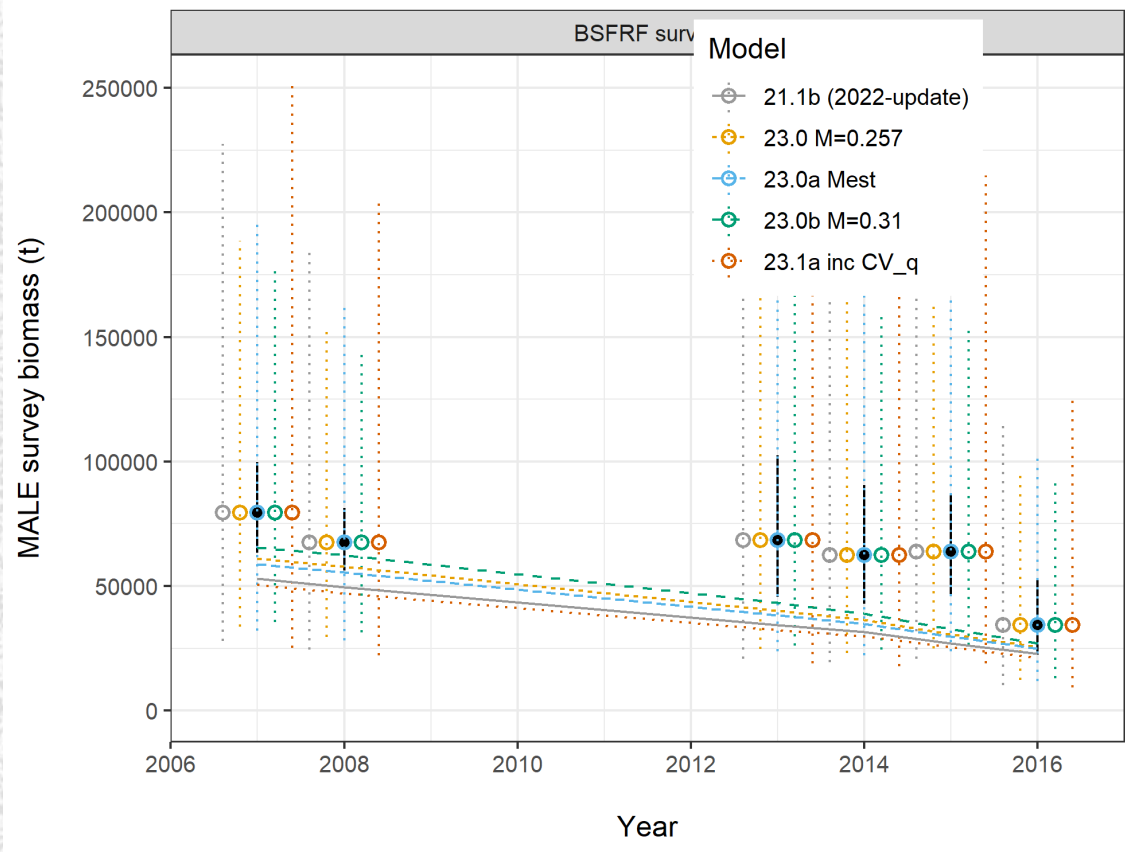


- Model fits to NMFS trawl survey data for models with change in CV on prior for Q.

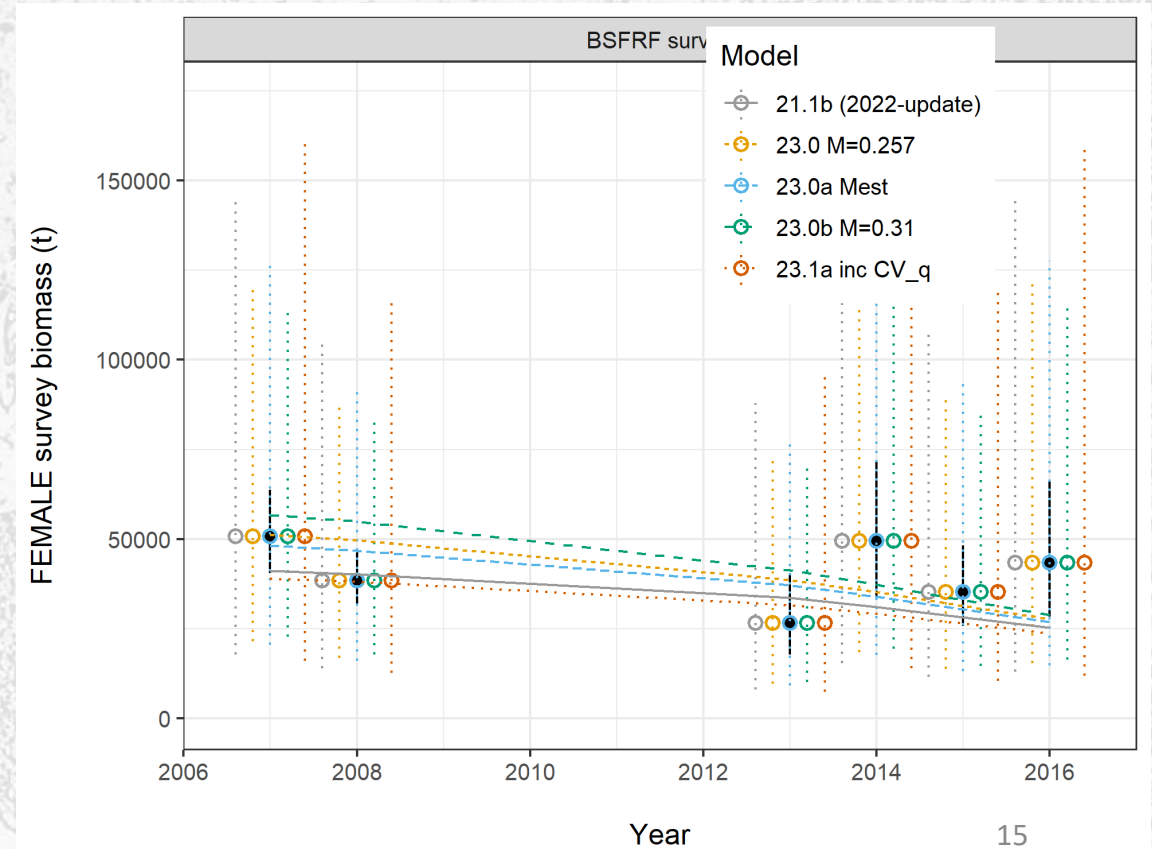




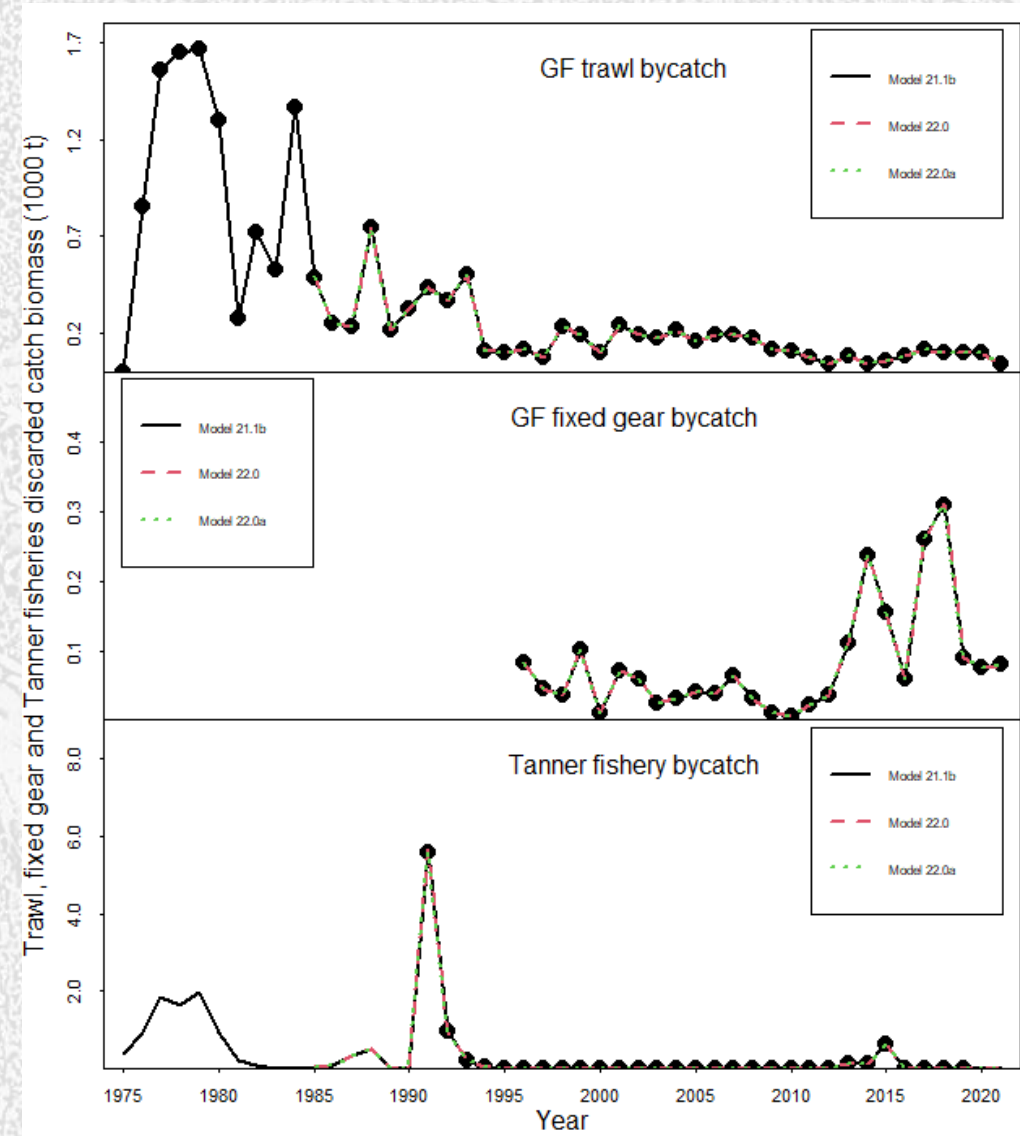
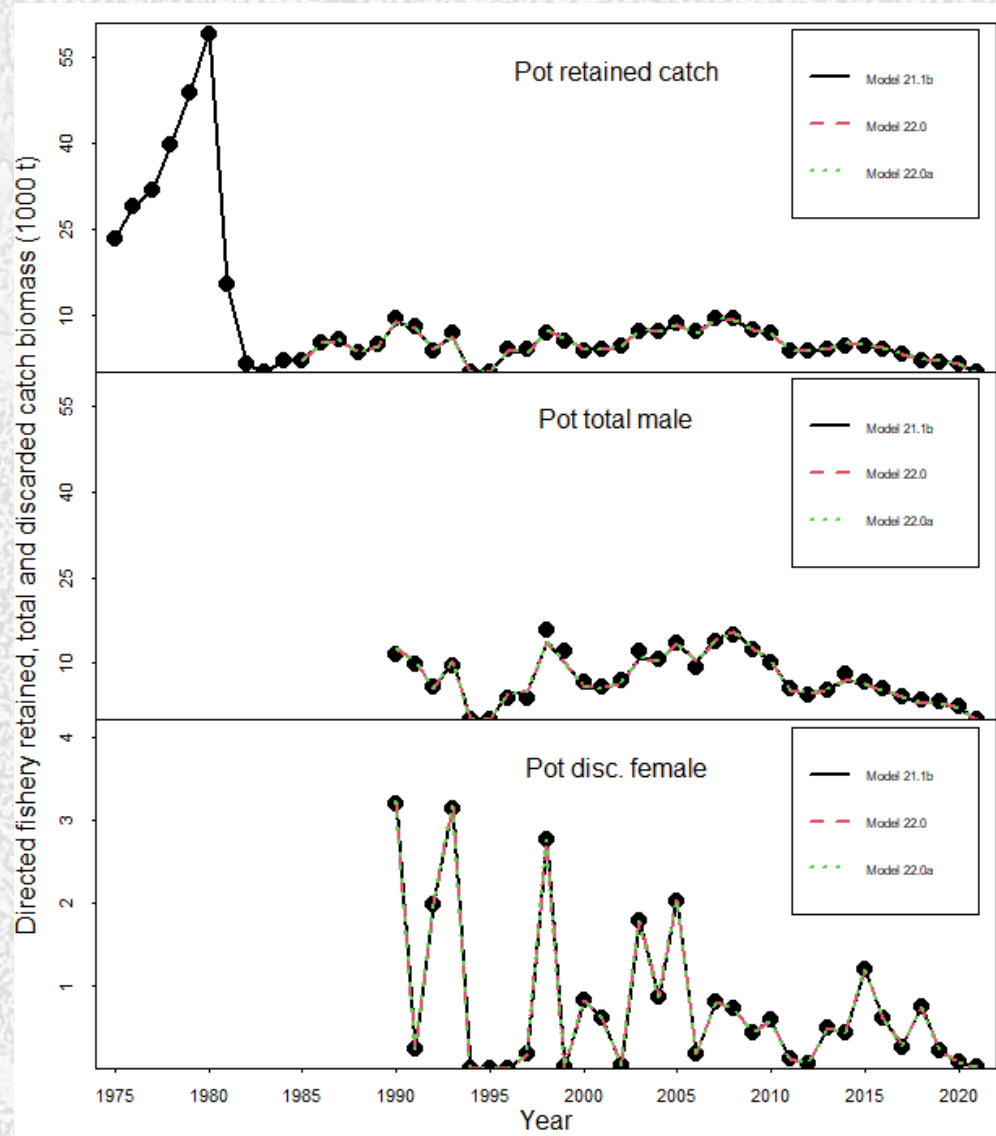
Residuals
of total
NMFS
survey
biomass



- Error bars show additional error
- BSFRF survey catchability is assumed to be 1.0
- Similar fits

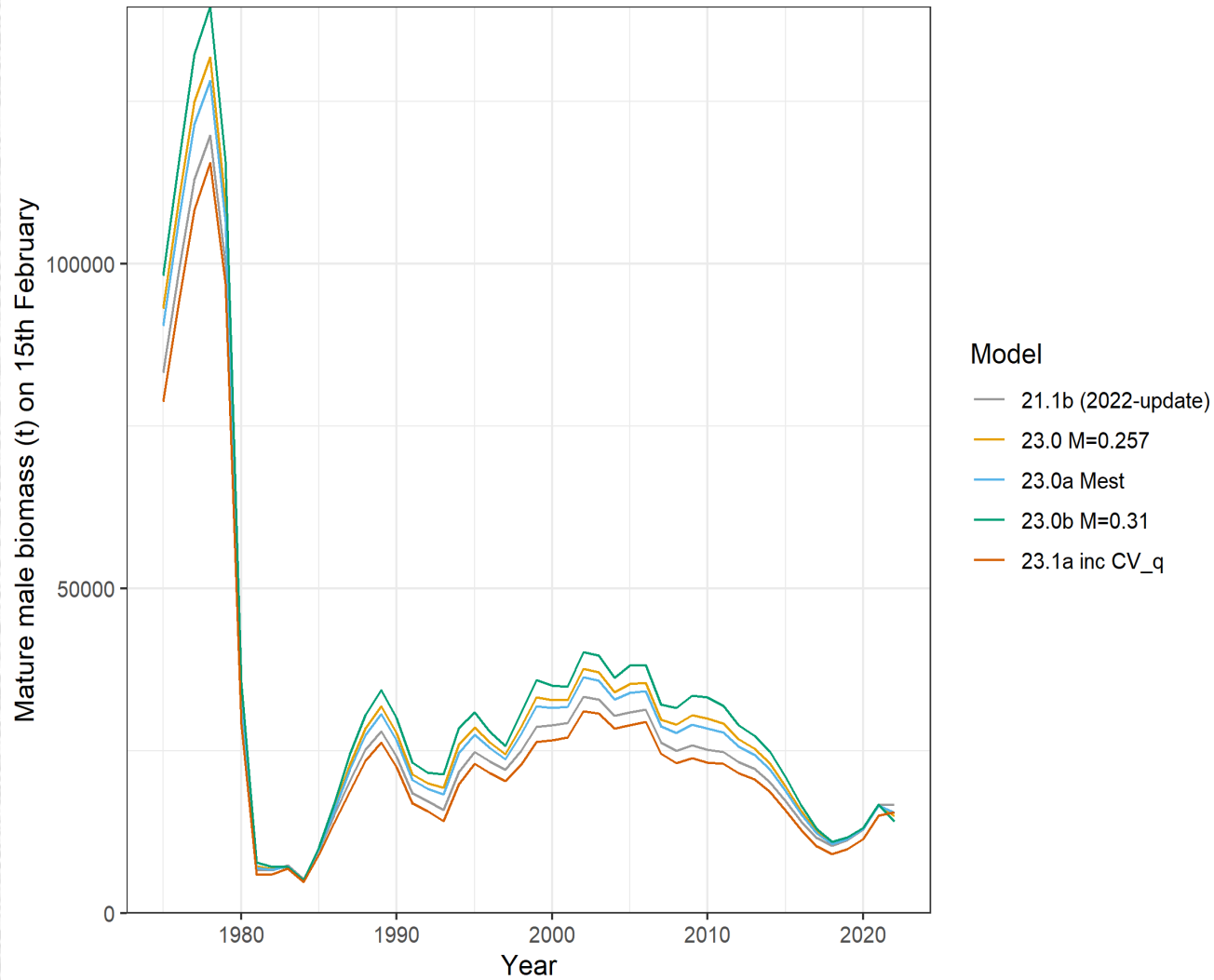


Mortality biomass (equal to catch biomass times handling mortality rate)

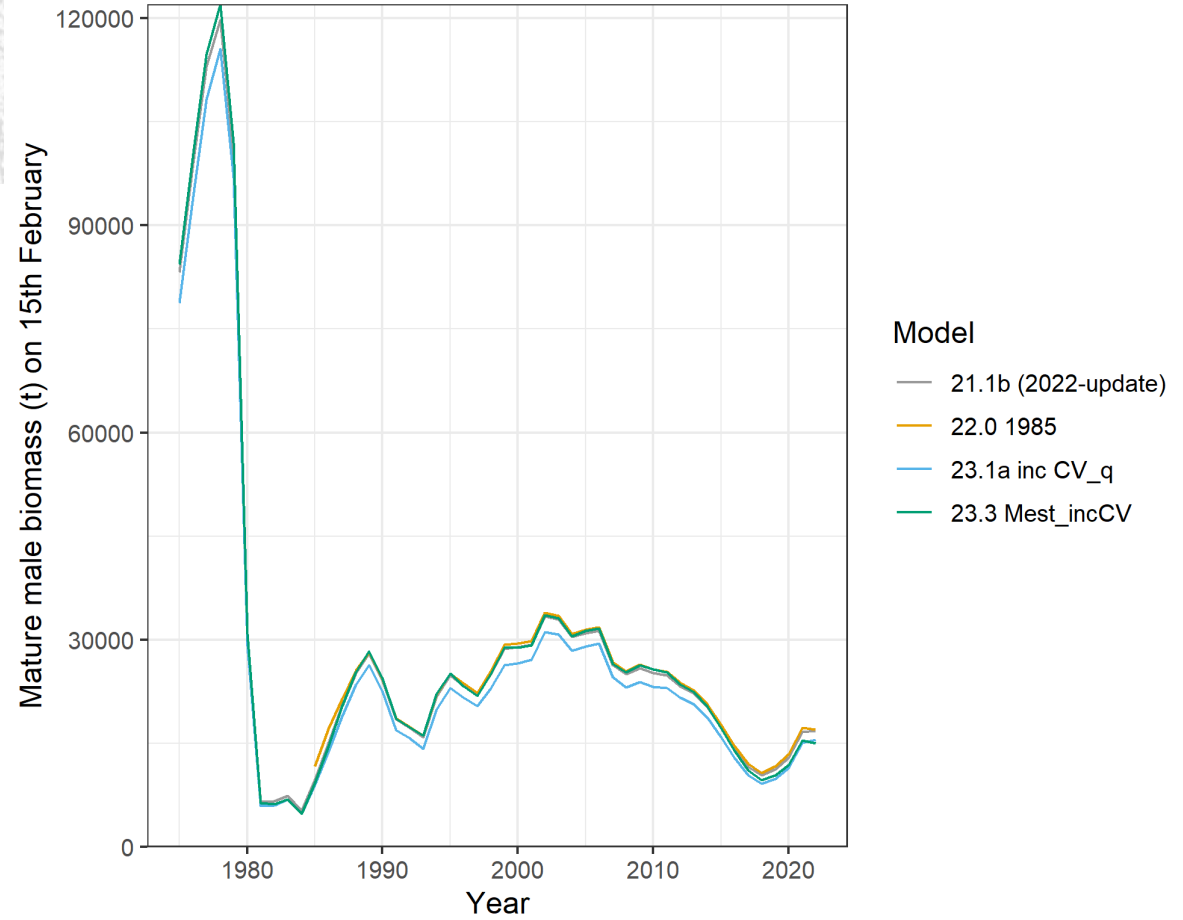


Mature male biomass

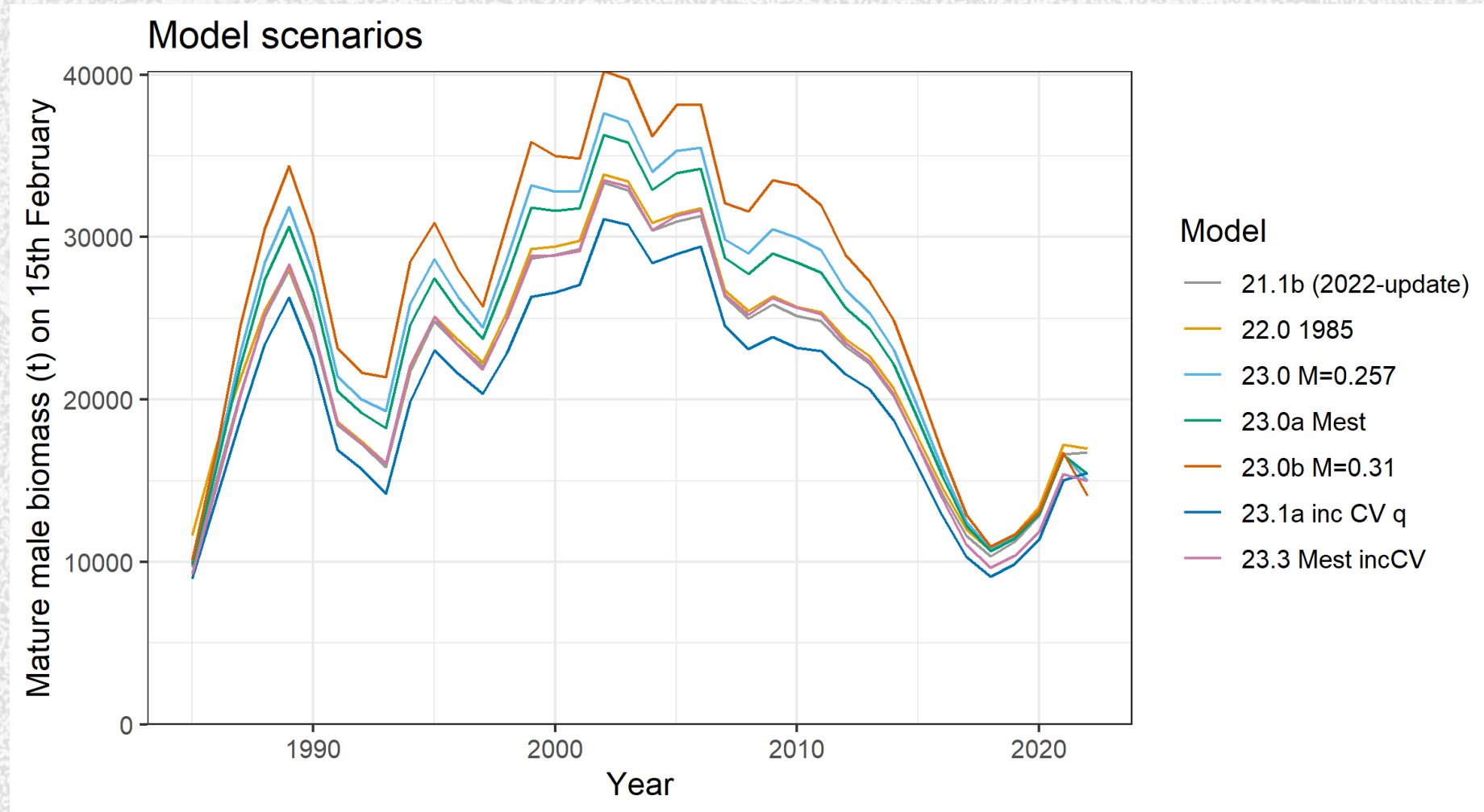
Model scenarios



Model scenarios



Mature male biomass – from 1985 +



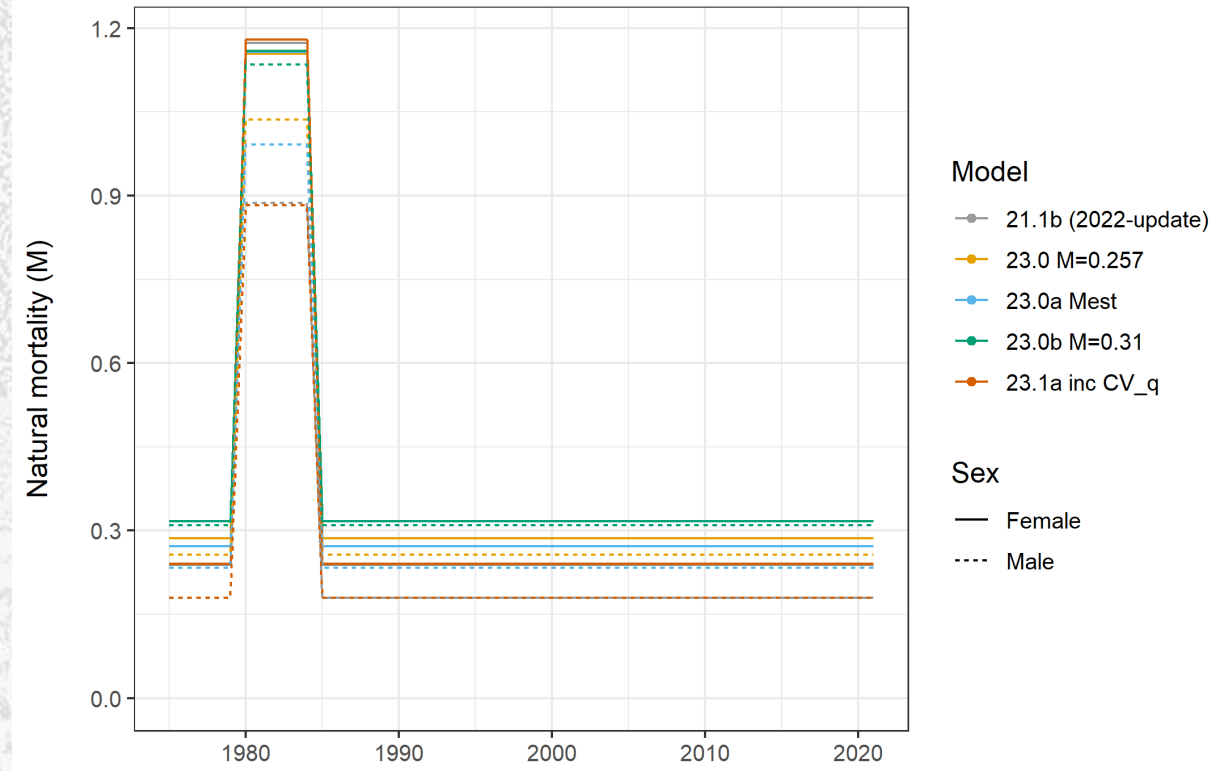
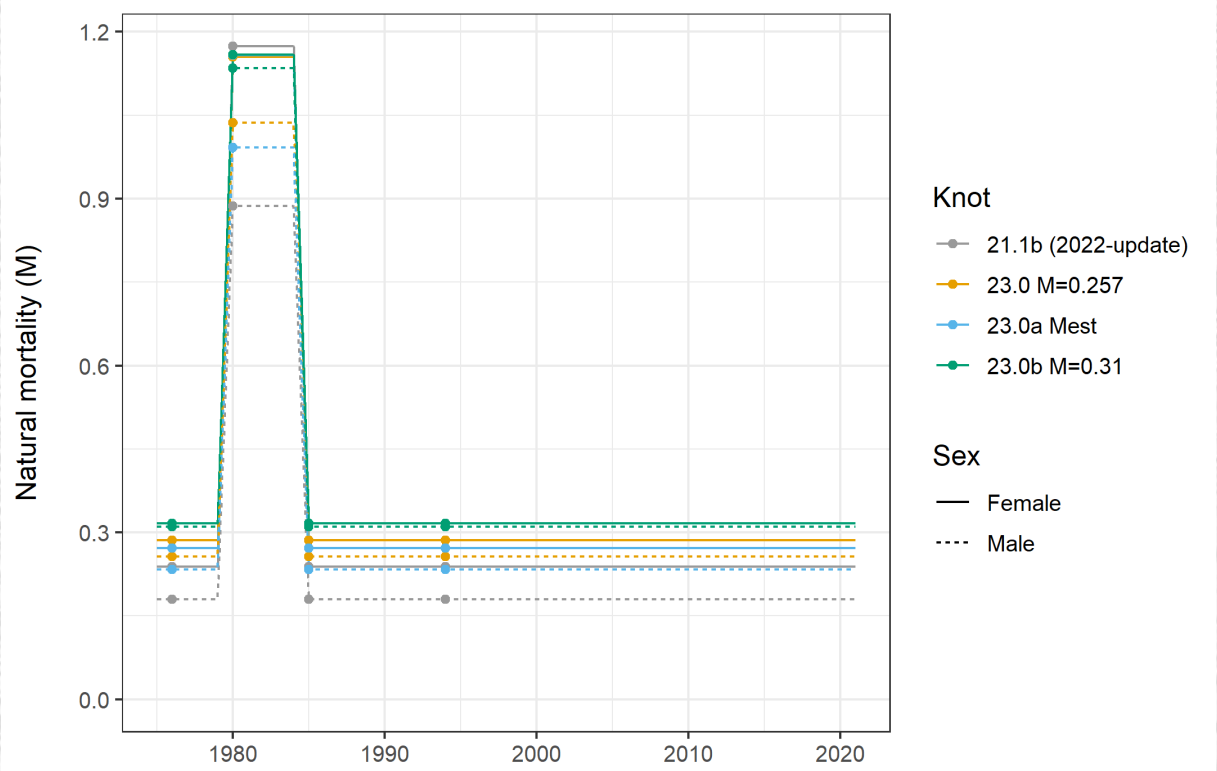
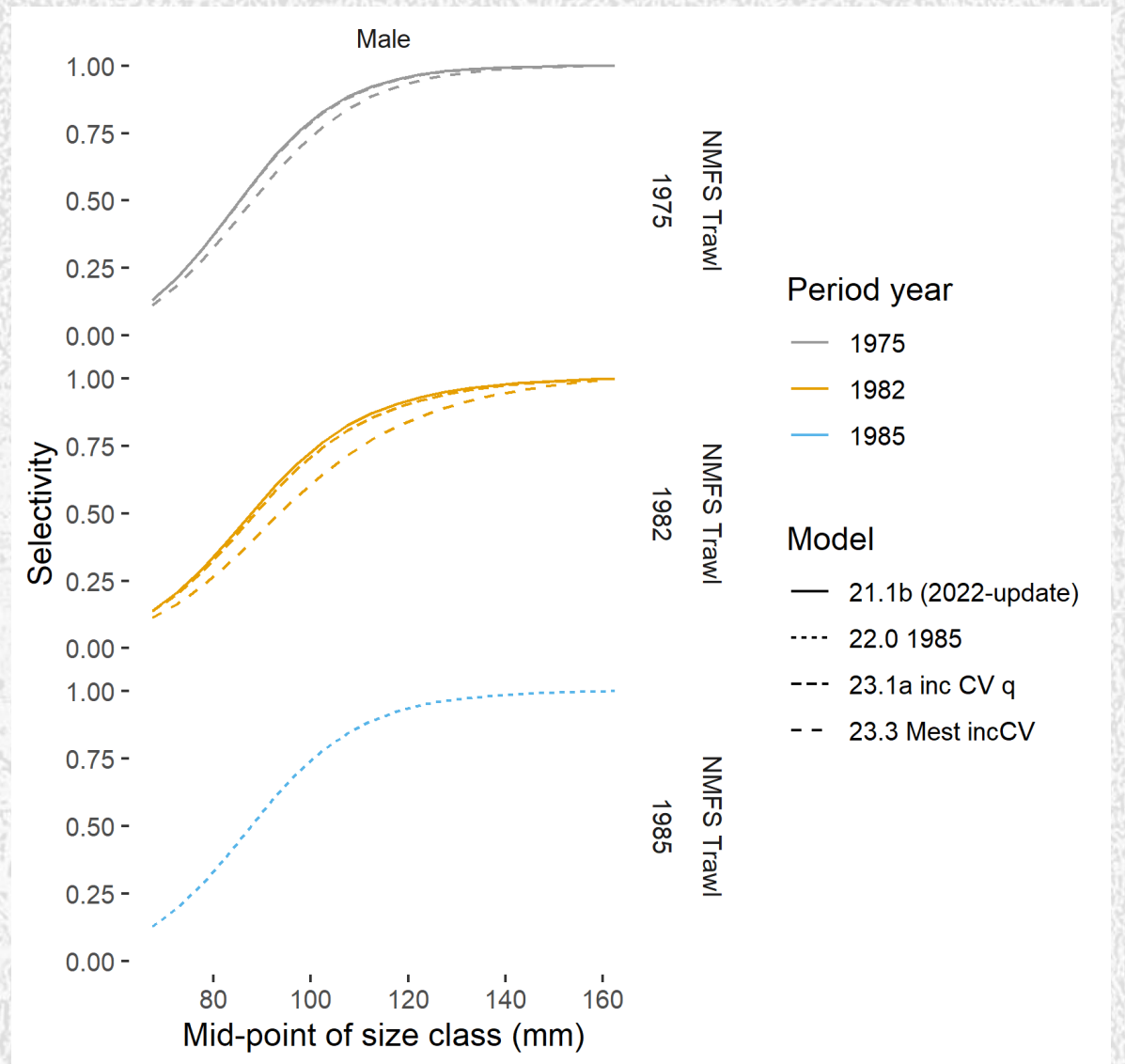
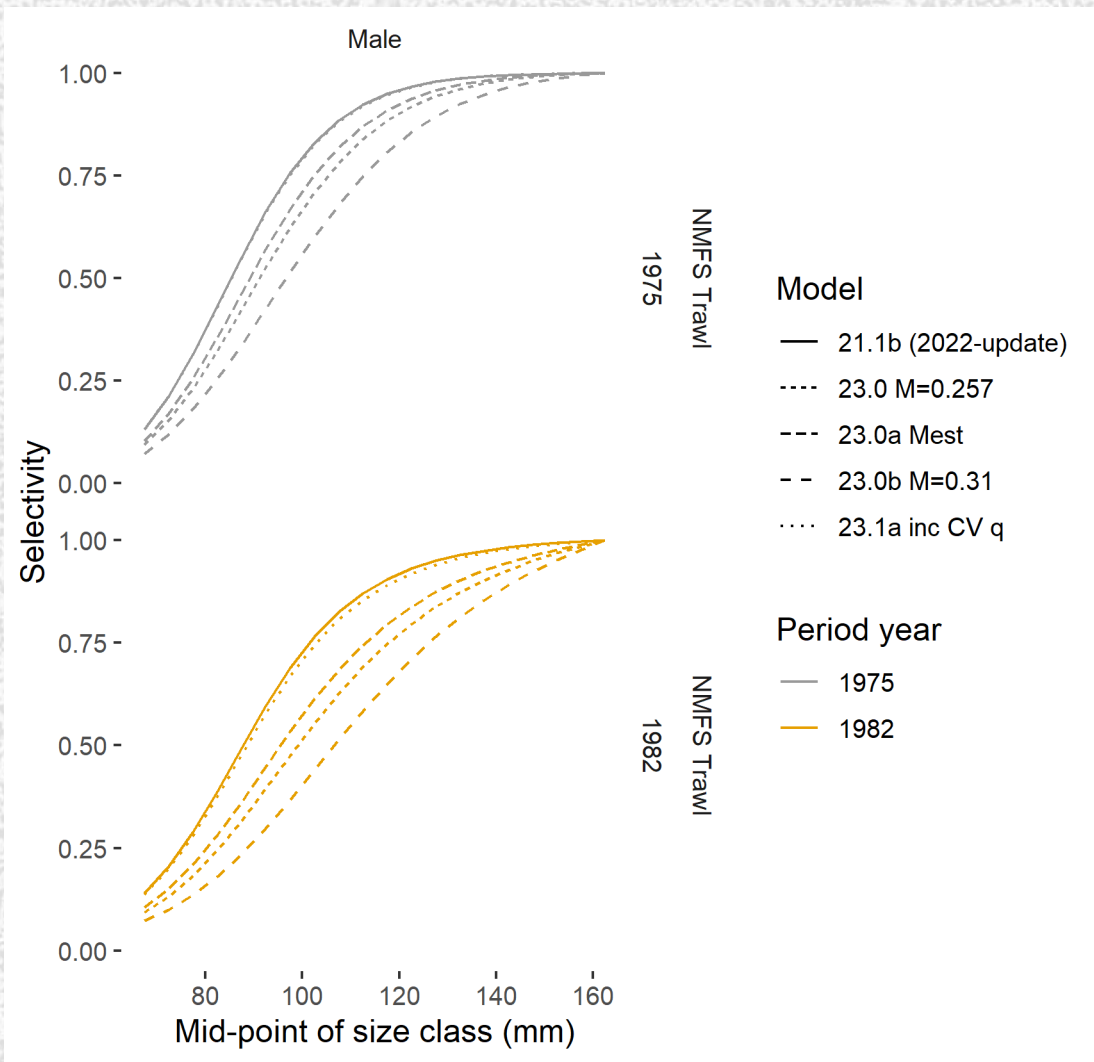
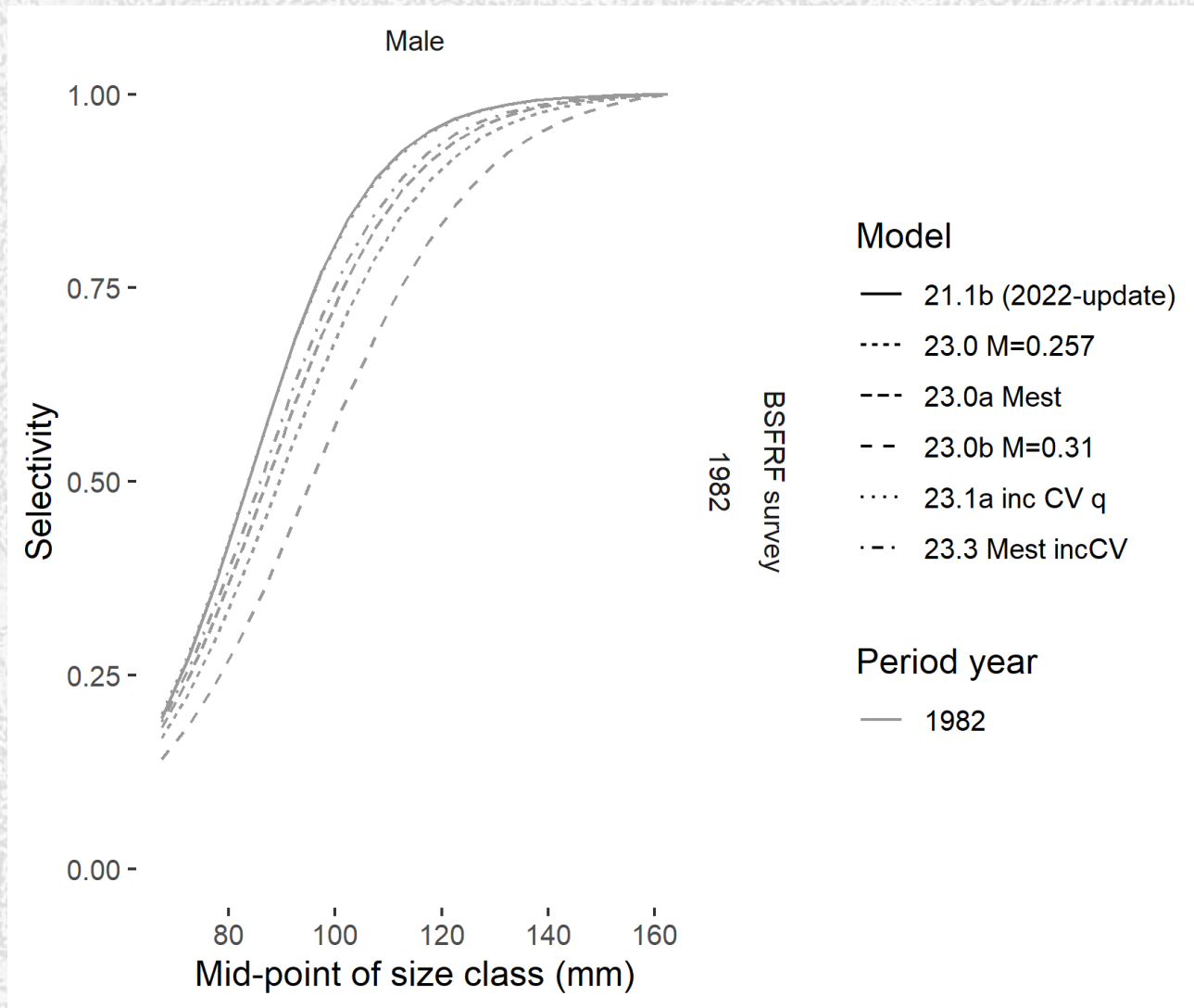


Table 3: Natural mortality estimates for model scenarios during different year blocks.

| Model | Sex | baseM | 1980-84 | 1985-22 |
|---------------------|--------|-------|---------|---------|
| 21.1b (2022-update) | Female | 0.24 | 1.17 | |
| 21.1b (2022-update) | Male | 0.18 | 0.89 | |
| 22.0 1985 | Female | | | 0.23 |
| 22.0 1985 | Male | | | 0.18 |
| 23.0 M=0.257 | Female | 0.29 | 1.15 | |
| 23.0 M=0.257 | Male | 0.26 | 1.04 | |
| 23.0a Mest | Female | 0.27 | 1.16 | |
| 23.0a Mest | Male | 0.23 | 0.99 | |
| 23.0b M=0.31 | Female | 0.32 | 1.16 | |
| 23.0b M=0.31 | Male | 0.31 | 1.13 | |
| 23.1a inc CV q | Female | 0.24 | 1.18 | |
| 23.1a inc CV q | Male | 0.18 | 0.88 | |
| 23.3 Mest incCV | Female | 0.26 | 1.17 | |
| 23.3 Mest incCV | Male | 0.22 | 0.96 | |

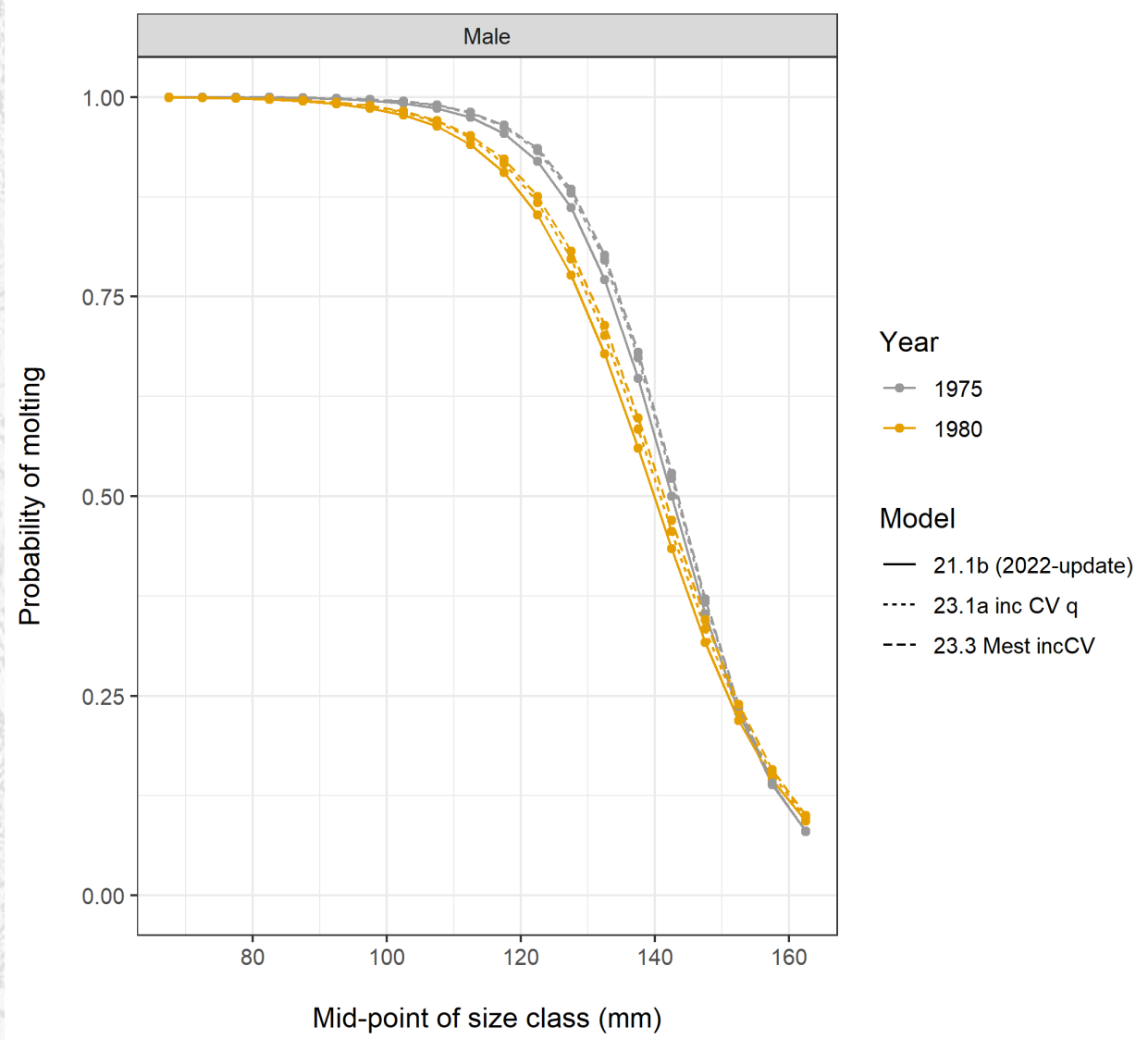
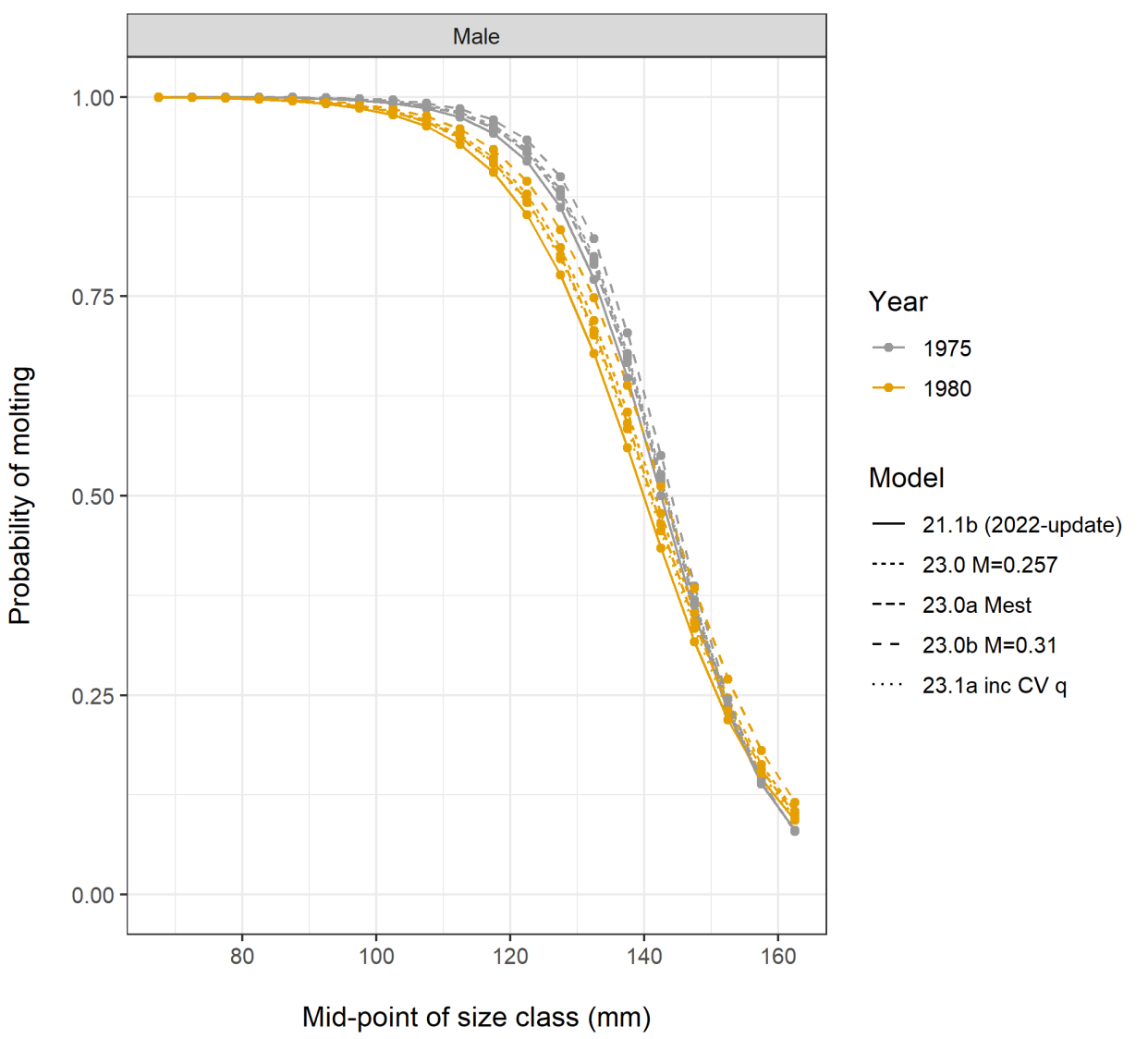


NMFS trawl survey selectivity:
 - largest differences in high M



BSFRF survey
selectivity
- Changes with
increased M on
males

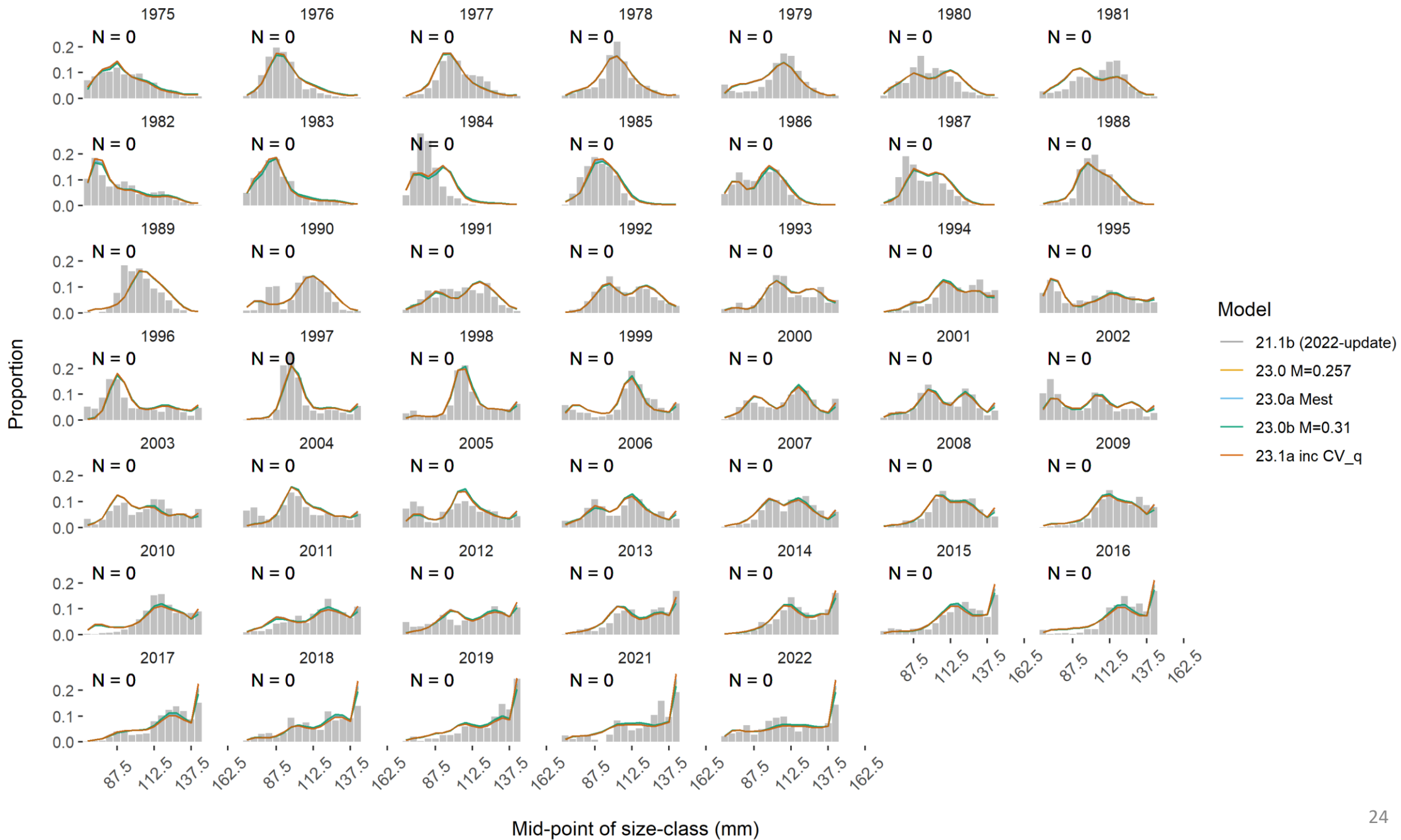
Molting probabilities



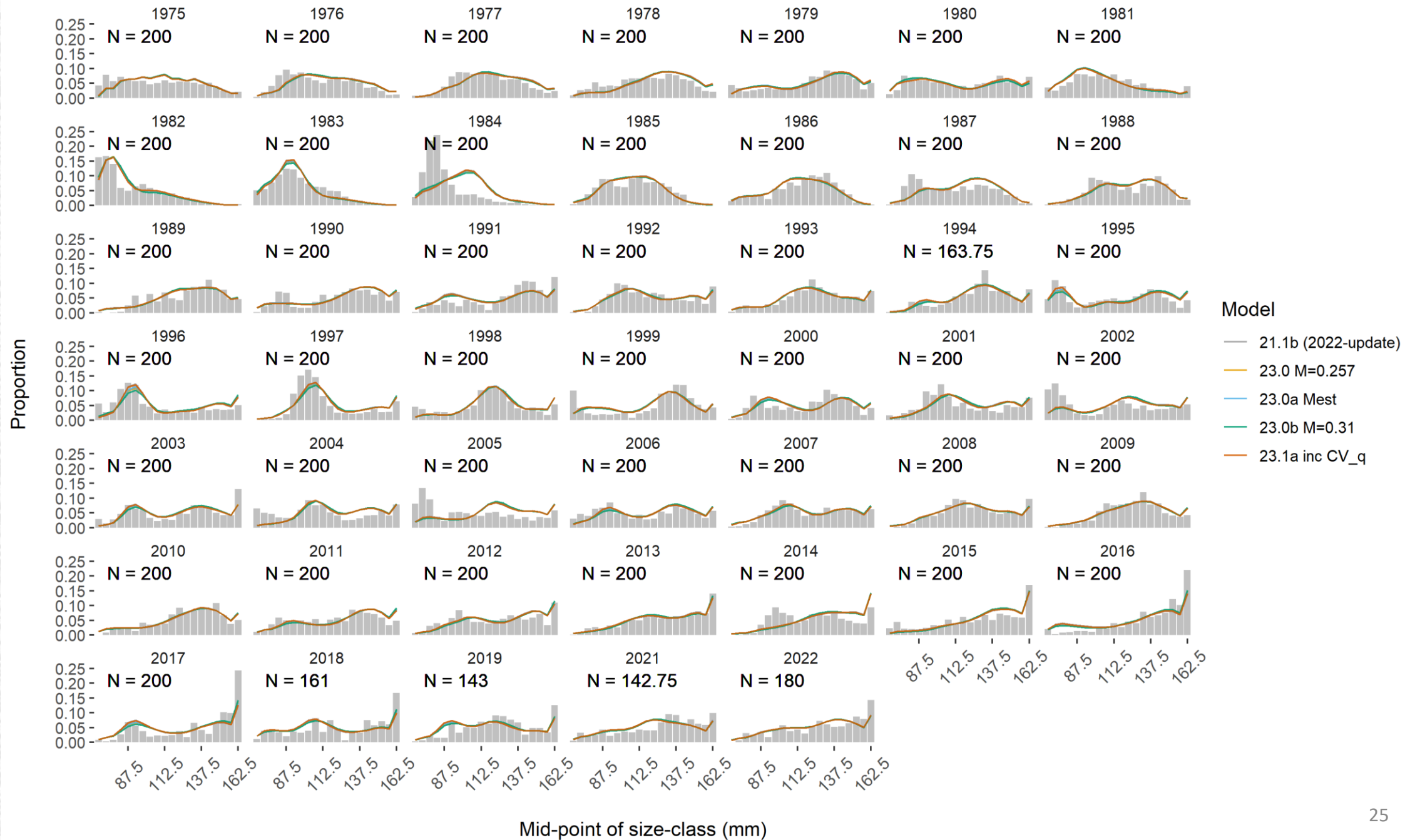
Size composition fit

- Similar for all models
- Models with higher M values fit NMFS size comps slightly better at higher sizes

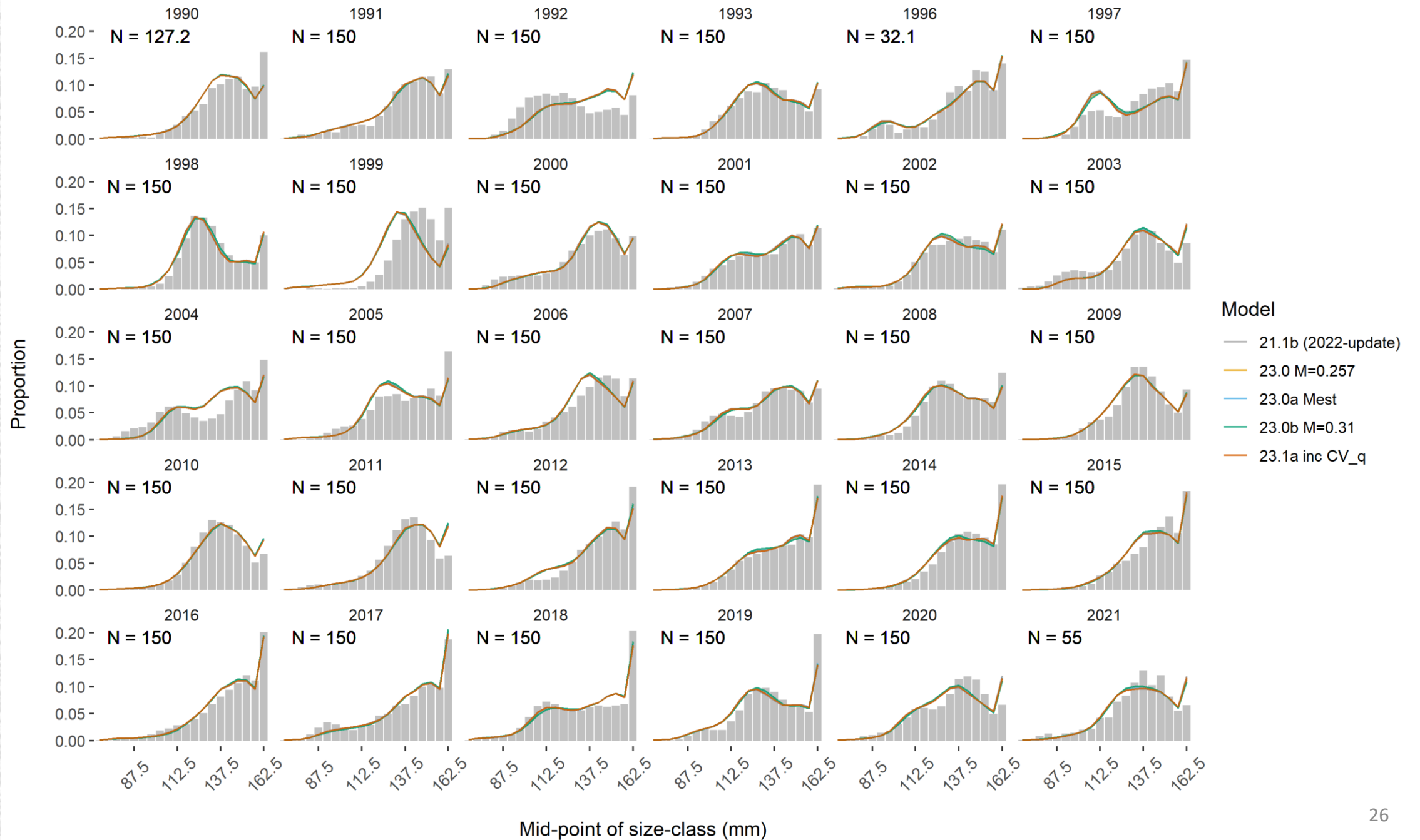
Gear = NMFS Trawl , Sex = Female , Season = 1



Gear = NMFS Trawl , Sex = Male , Season = 1

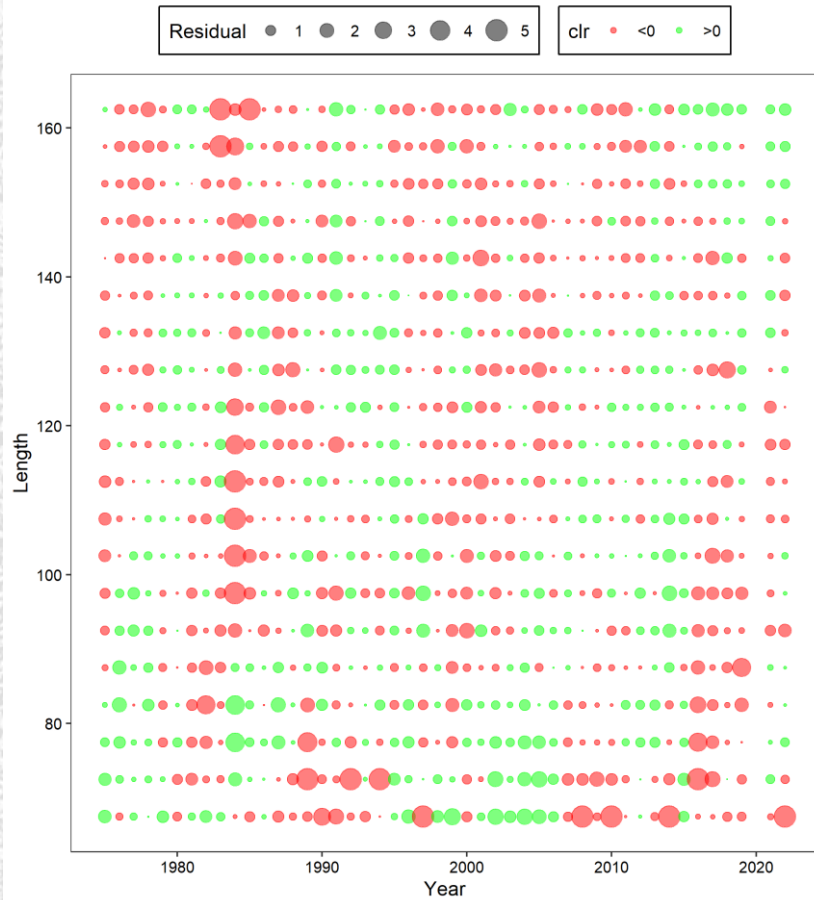


Gear = Pot , Sex = Male , Season = 3

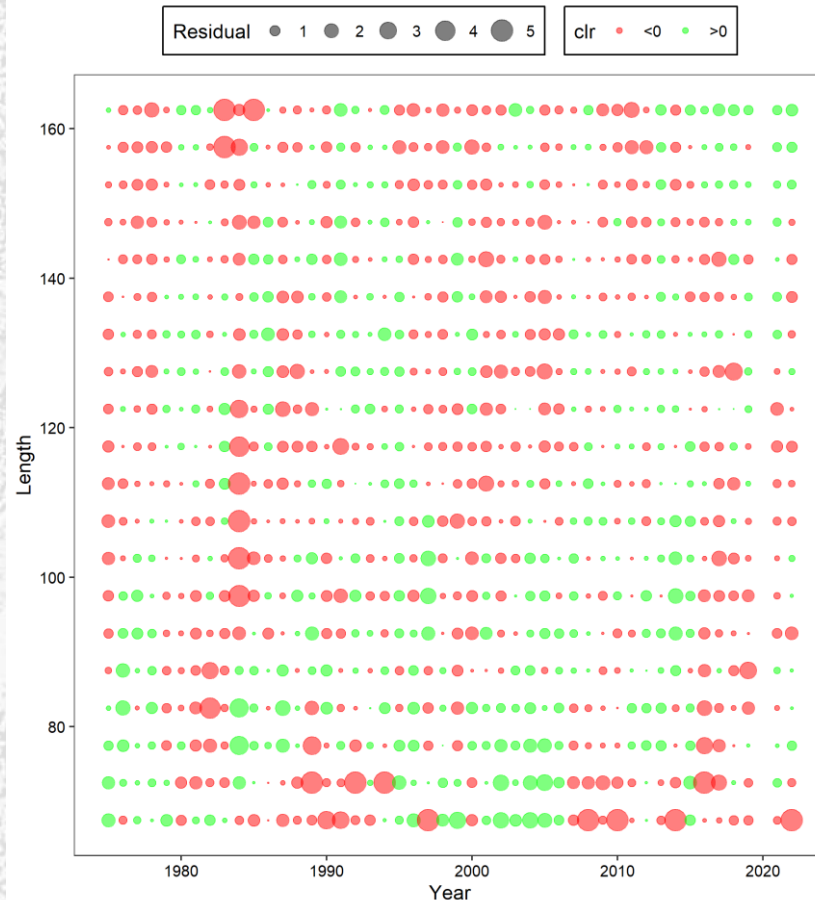


Comparison of residuals for NMFS survey males

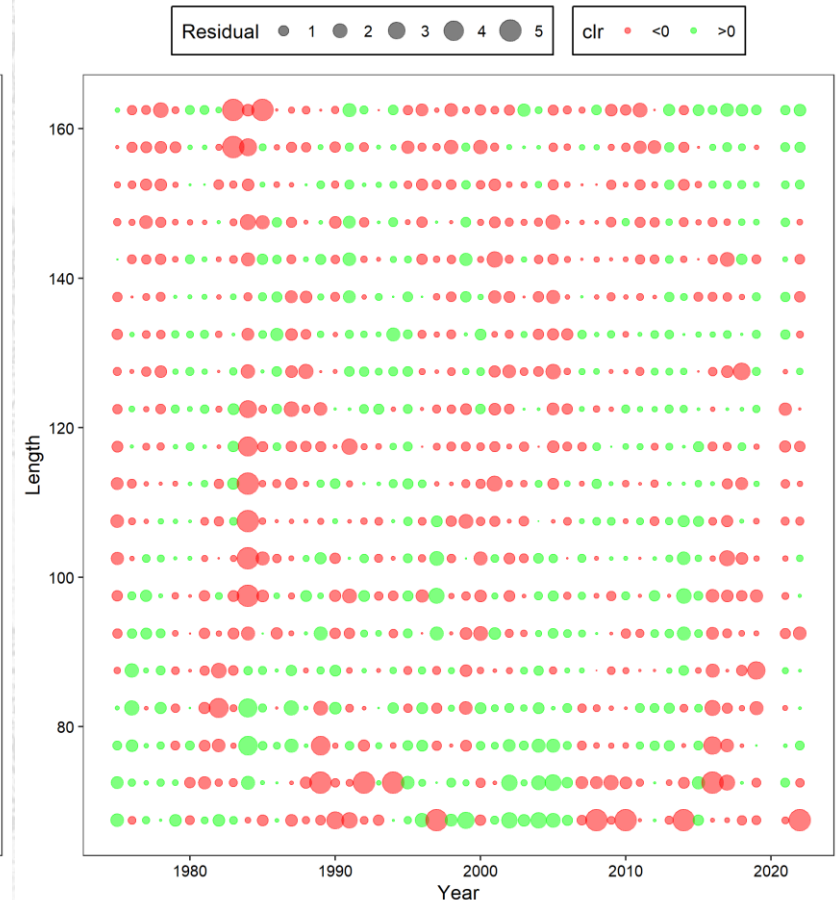
Model 21.1b(update), Survey Males



Model 23.0b, Survey Males

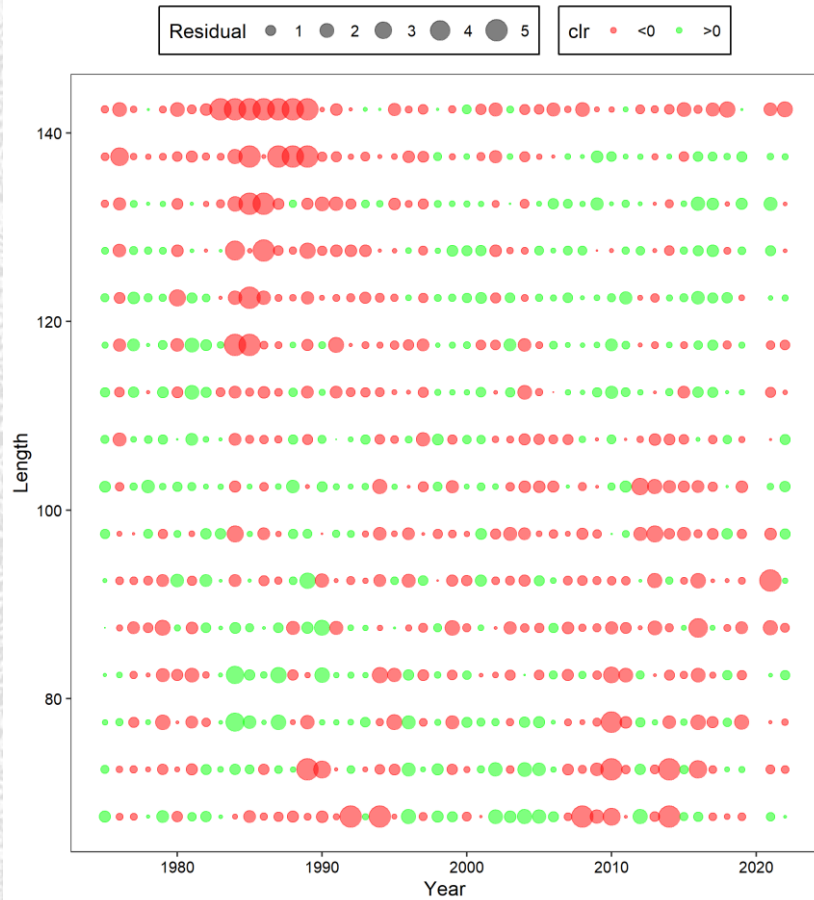


Model 23.3, Survey Males

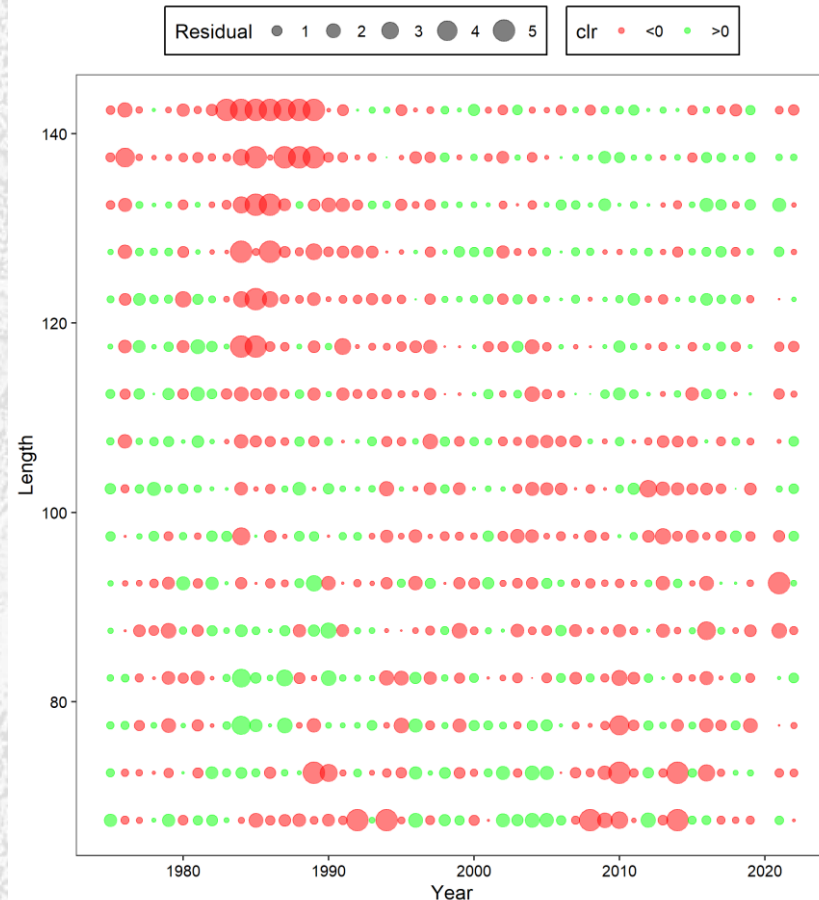


Comparison of residuals for NMFS survey females

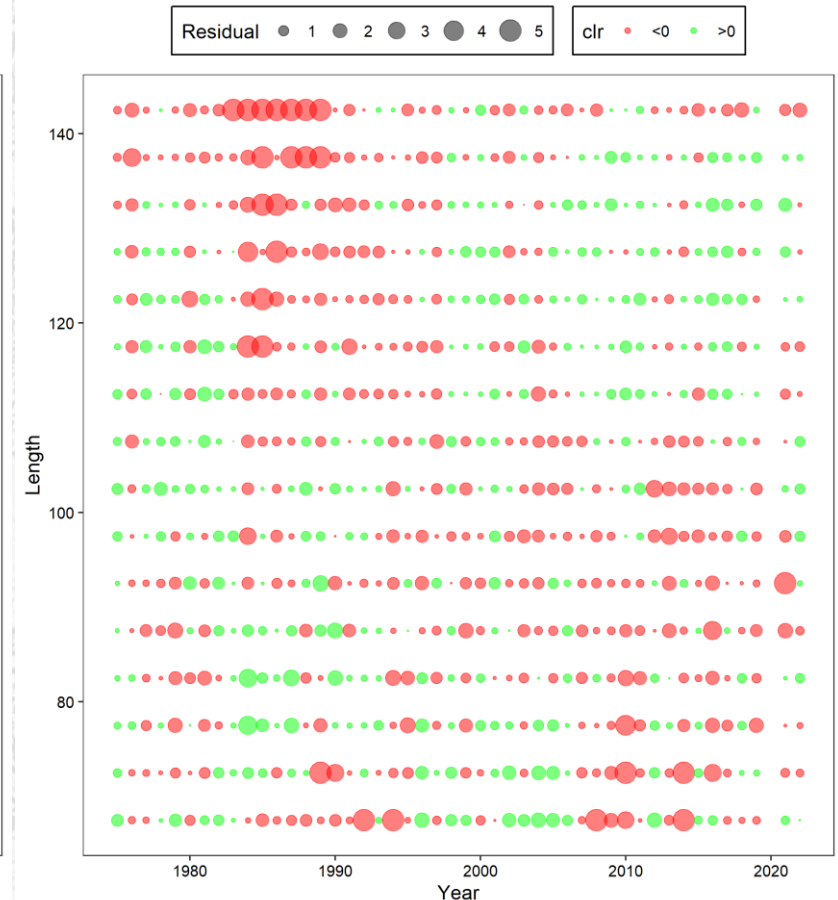
Model 21.1b(update), Survey Females



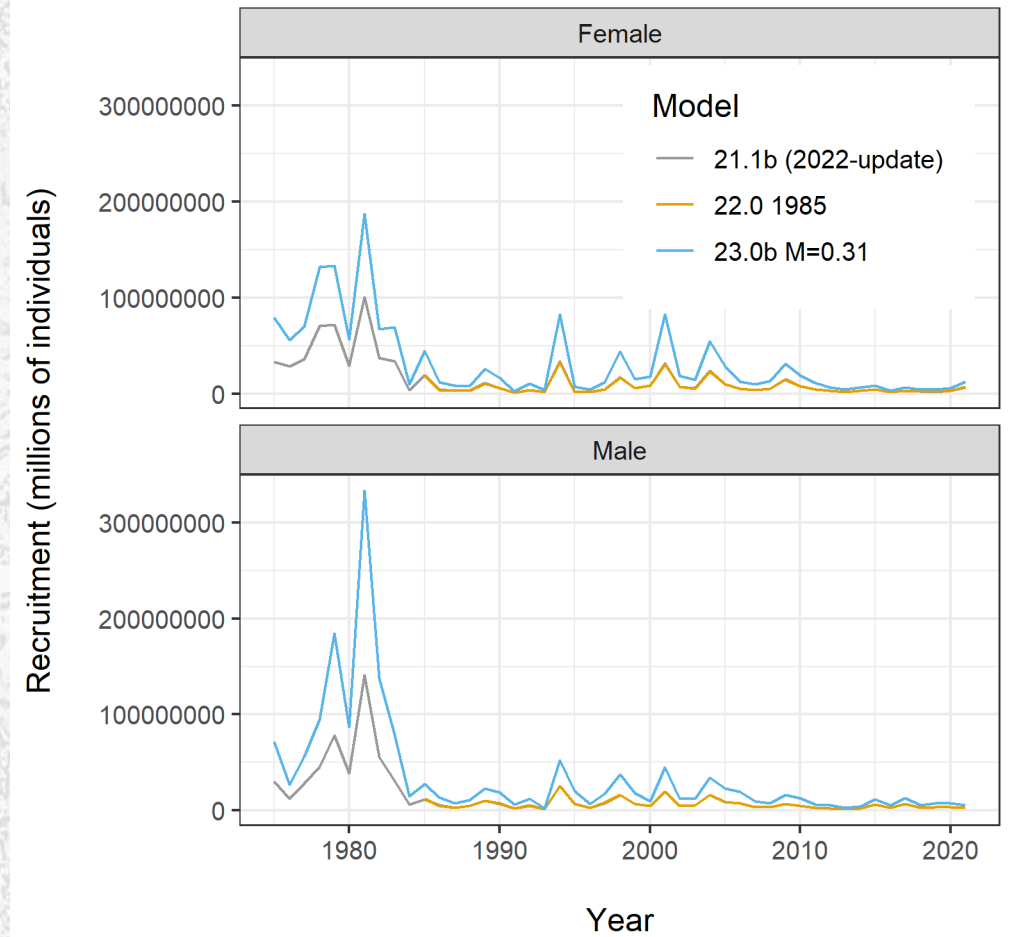
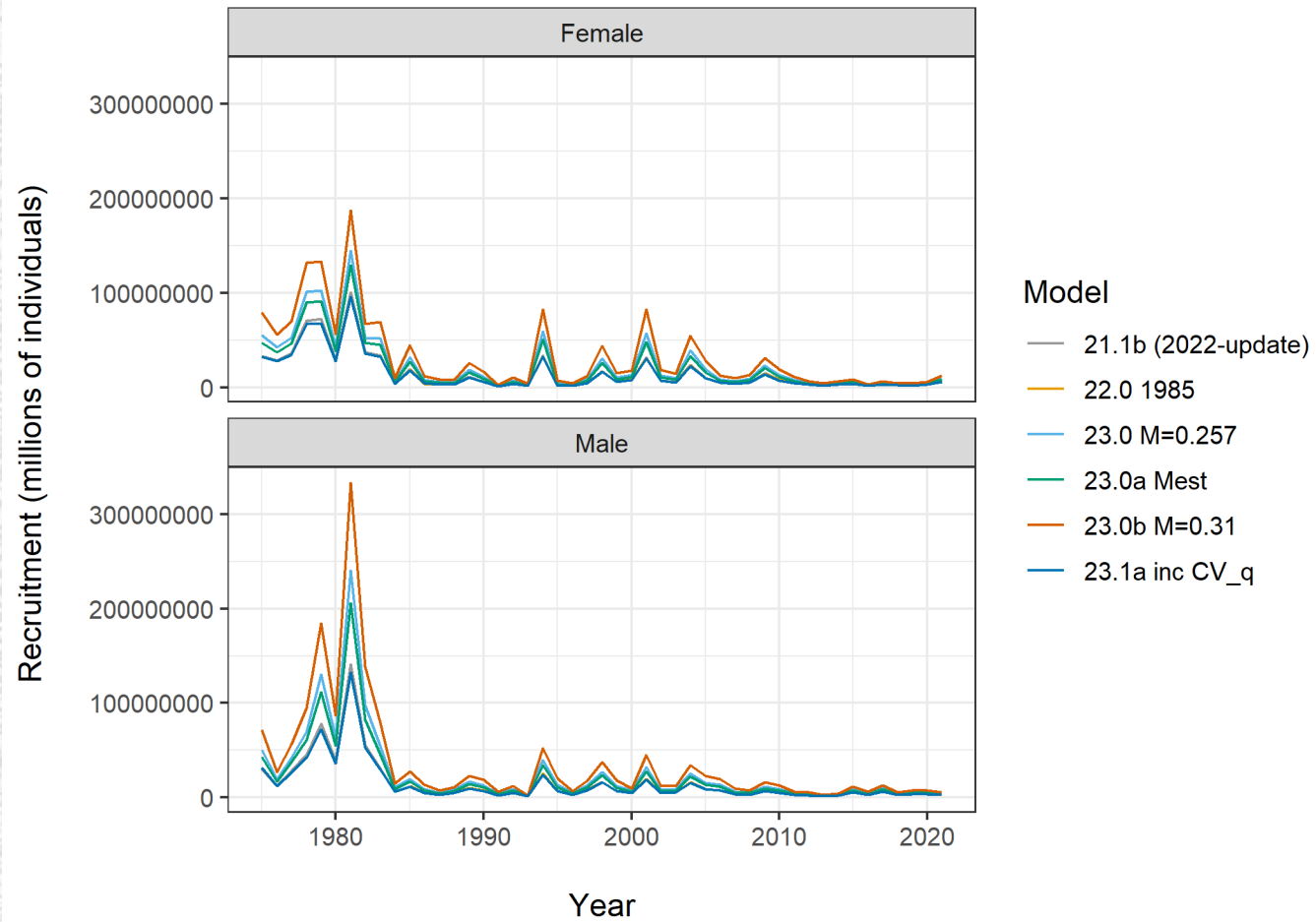
Model 23.0b, Survey Females



Model 23.3, Survey Females



Recruitment



Highlighted cells show prior density values and total negative likelihood values without prior densities

Table 4: Comparisons of negative log-likelihood values and some parameters for all model scenarios.

| Component | Ref22 | Ref23s | m23.0 | m23.0a | m23.0b | m23.1a | m23.3 |
|------------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Pot-ret-catch | -60.88 | -60.88 | -62.32 | -61.86 | -63.32 | -61.59 | -61.97 |
| Pot-totM-catch | 26.55 | 26.55 | 25.44 | 25.87 | 24.37 | 25.25 | 25.29 |
| Pot-F-discC | -55.70 | -55.70 | -55.72 | -55.71 | -55.72 | -55.69 | -55.71 |
| Trawl-discC | -63.75 | -63.75 | -63.75 | -63.75 | -63.75 | -63.74 | -63.75 |
| Tanner-M-discC | -43.54 | -43.54 | -43.54 | -43.54 | -43.54 | -43.54 | -43.54 |
| Tanner-F-discC | -43.48 | -43.48 | -43.52 | -43.51 | -43.52 | -43.48 | -43.50 |
| Fixed-discC | -36.04 | -36.04 | -36.04 | -36.04 | -36.04 | -36.04 | -36.04 |
| Trawl-suv-bio | -35.47 | -35.47 | -37.38 | -37.66 | -35.69 | -36.47 | -37.70 |
| BSFRF-sur-bio | -2.94 | -2.94 | -5.51 | -4.83 | -6.47 | -1.74 | -3.28 |
| Pot-ret-comp | -3932.20 | -3932.20 | -3941.02 | -3938.84 | -3945.00 | -3933.46 | -3937.79 |
| Pot-totM-comp | -2369.46 | -2369.46 | -2370.57 | -2370.25 | -2371.05 | -2370.45 | -2370.66 |
| Pot-discF-comp | -1449.36 | -1449.36 | -1449.76 | -1449.83 | -1449.45 | -1449.48 | -1449.91 |
| Trawl-disc-comp | -5836.10 | -5836.10 | -5846.22 | -5843.90 | -5849.24 | -5833.97 | -5840.29 |
| Tanner-disc-comp | -1274.28 | -1274.28 | -1277.41 | -1276.99 | -1277.43 | -1274.82 | -1276.69 |
| Fixed-disc-comp | -3393.50 | -3393.50 | -3389.38 | -3390.67 | -3386.48 | -3393.24 | -3391.35 |
| Trawl-sur-comp | -6984.67 | -6984.67 | -6994.36 | -6993.08 | -6993.27 | -6989.36 | -6994.41 |
| BSFRF-sur-comp | -843.53 | -843.53 | -845.00 | -845.16 | -843.83 | -844.36 | -845.40 |
| Recruit-dev | 70.56 | 70.56 | 71.88 | 71.47 | 72.93 | 70.39 | 71.06 |
| Recruit-ini | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Recruit-sex-R | 76.98 | 76.98 | 76.98 | 76.98 | 77.02 | 76.95 | 76.96 |
| $Log_f dev_0$ | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| M-deviation | 43.83 | 43.83 | 39.05 | 40.27 | 36.96 | 43.73 | 41.22 |
| Sex-specific-R | 0.01 | 0.01 | 0.02 | 0.01 | 0.04 | 0.01 | 0.00 |
| Ini-size-struct | | 30.88 | 35.30 | 33.72 | 39.36 | 31.28 | 33.07 |
| PriorDensity | 267.30 | 267.30 | 227.65 | 252.04 | 220.97 | 271.19 | 259.03 |
| Tot-likelihood | -25908.79 | -25908.79 | -25985.17 | -25955.27 | -25992.17 | -25912.63 | -25945.36 |
| Tot-likeli-no-PD | -25641.49 | -25641.49 | -25757.52 | -25703.23 | -25771.20 | -25641.45 | -25686.33 |
| Tot-parameter | 372.00 | 372.00 | 372.00 | 373.00 | 372.00 | 372.00 | 373.00 |
| MMB35 | 24026.11 | 22250.75 | 19136.75 | 19786.44 | 18209.52 | 21655.02 | 19919.11 |
| MMB-terminal | 16952.82 | 16761.49 | 14970.68 | 15431.45 | 14092.35 | 15489.83 | 14971.20 |
| F35 | 0.30 | 0.30 | 0.46 | 0.40 | 0.58 | 0.30 | 0.37 |
| $F_o fl$ | 0.20 | 0.22 | 0.35 | 0.31 | 0.44 | 0.20 | 0.27 |
| OFL | 3035.63 | 3213.98 | 4517.20 | 4132.66 | 5284.13 | 2783.29 | 3492.78 |
| ABC | 2428.50 | 2571.19 | 3613.76 | 3306.13 | 4227.30 | 2226.63 | 2794.22 |
| NMFS Q | 0.97 | 0.97 | 0.93 | 0.94 | 0.91 | 1.05 | 1.01 |

Retrospective patterns

Model 21.1b

Model 22.0

Model 23.0a

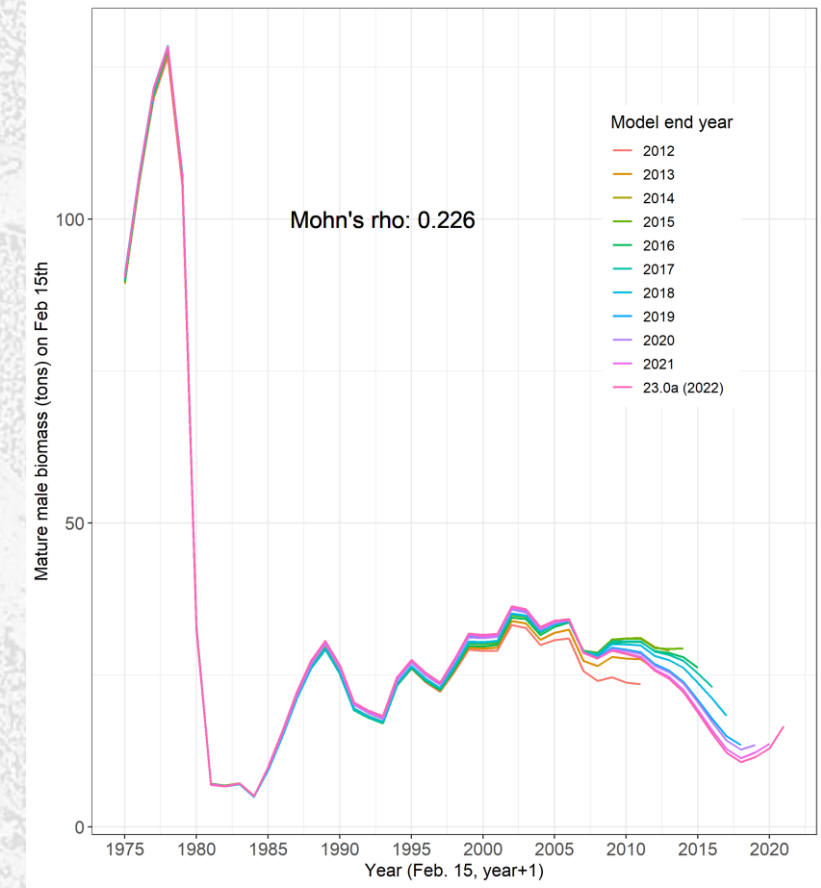
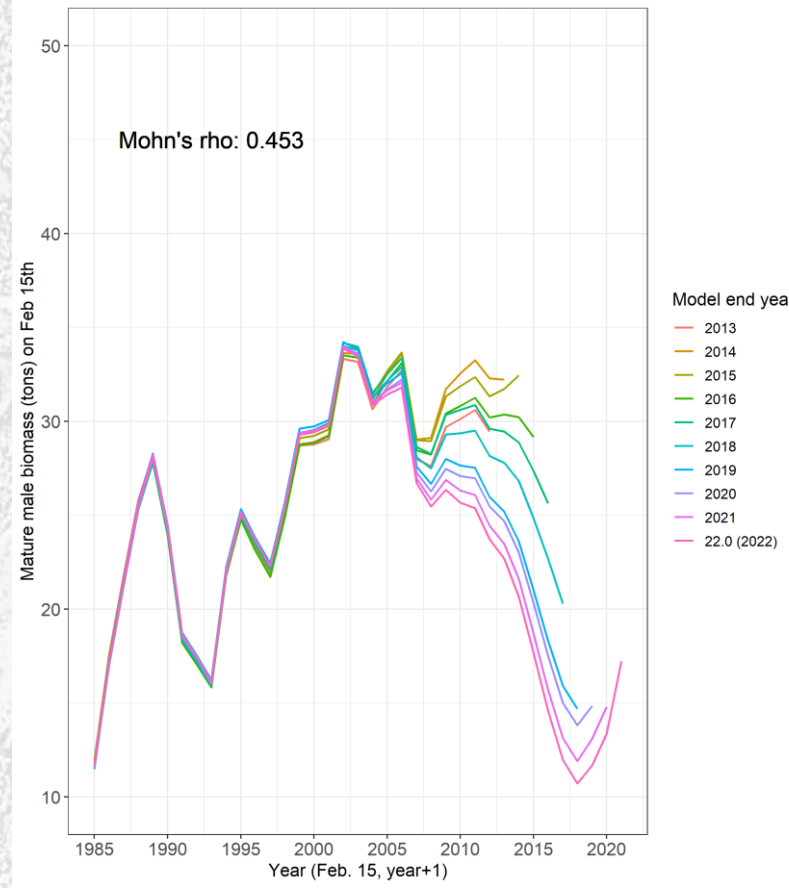
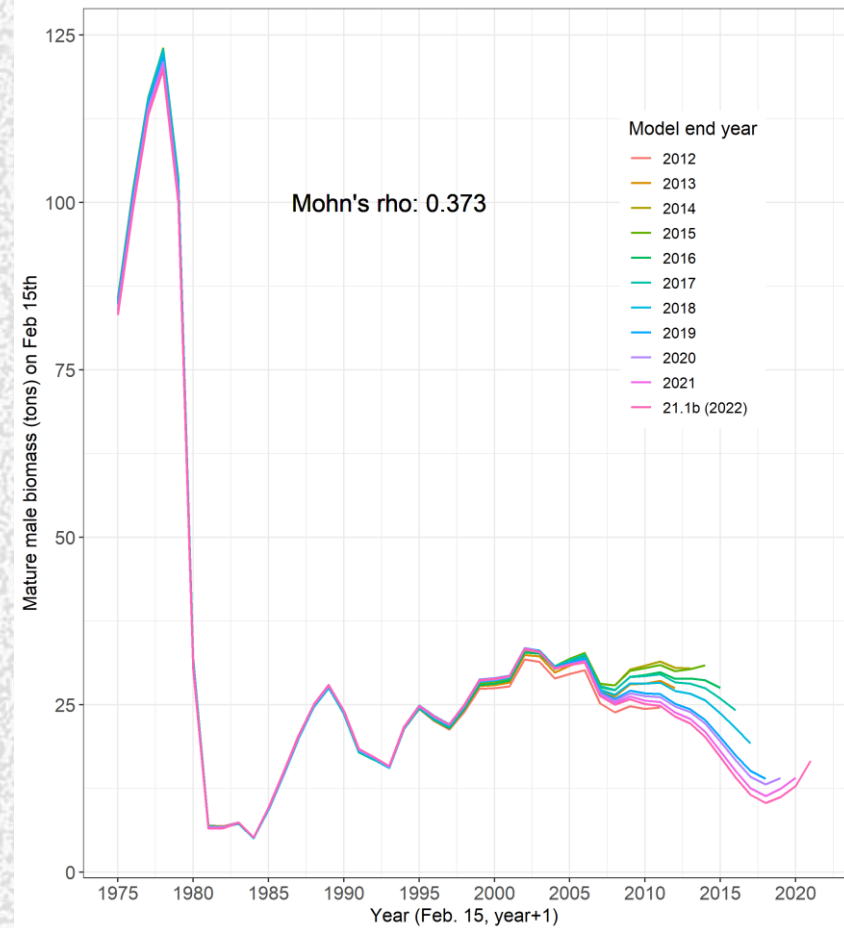


Table 1: Changes in management quantities for each scenario explored. Reported quantities are derived from maximum likelihood estimates. MMB, B35, OFL are reported in 1,000 t. Average recruitment is males and females combined in millions of animals.

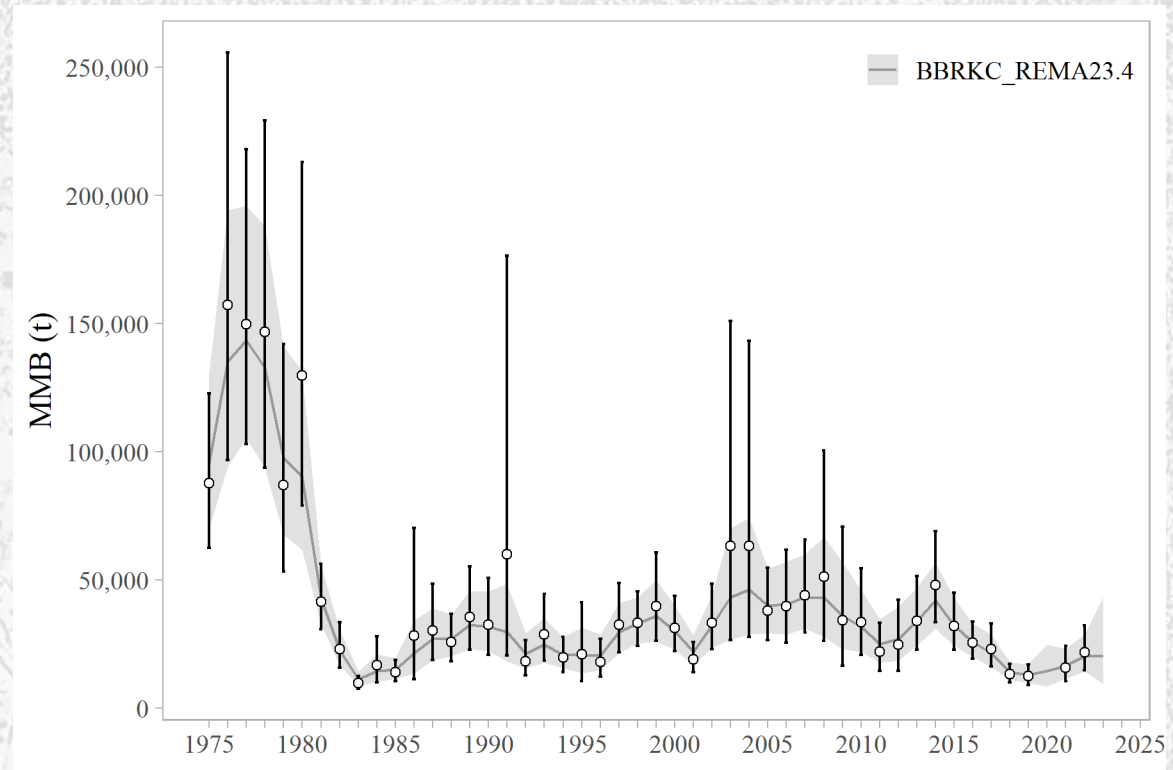
| Model | Current MMB | B35 | MMB/B_{MSY} | F35 | F_{OFL} | OFL | avg rec | maleM |
|---------------------|-------------|-------|---------------|------|-----------|------|---------|-------|
| 21.1b (2022-update) | 16.76 | 22.25 | 0.75 | 0.30 | 0.22 | 3.21 | 15.26 | 0.18 |
| 21.1b (2022) | 16.95 | 24.03 | 0.71 | 0.30 | 0.20 | 3.04 | | 0.18 |
| 22.0 1985 | 16.97 | 20.48 | 0.83 | 0.30 | 0.24 | 3.64 | 13.99 | 0.18 |
| 23.0 M=0.257 | 14.97 | 19.14 | 0.78 | 0.46 | 0.35 | 4.52 | 25.77 | 0.26 |
| 23.0a Mest | 15.43 | 19.79 | 0.78 | 0.40 | 0.31 | 4.13 | 21.97 | 0.23 |
| 23.0b M=0.31 | 14.09 | 18.21 | 0.77 | 0.58 | 0.44 | 5.28 | 36.23 | 0.31 |
| 23.1a inc CV q | 15.49 | 21.66 | 0.72 | 0.30 | 0.20 | 2.78 | 14.68 | 0.18 |
| 23.3 Mest incCV | 14.97 | 19.92 | 0.75 | 0.37 | 0.27 | 3.49 | 18.93 | 0.22 |

Summary and Recommendations

- Model 21.1b represents updated base – updates to GMACS and bycatch data
- Reducing the date time series produces similar results without complicated of M time block (late 70s/ early 80s)
 - Higher retrospective pattern not well understood
- Estimating M results in higher M and higher $F_{35\%}$, confounding issues
- Estimating M results in higher M for males but also reduced retrospective pattern (Mohn's rho reduced from 0.373 to 0.226)
- Recommendations:
 - Base model 21.1b
 - Model 23.0a – estimating M, reduces retrospective pattern, likely more accurate higher M
 - Model 22.0 – appealing but concern over retrospective pattern

Tier 4 simple modeling workgroup option

- Based on the simpler modeling working group discussions
- Mature male biomass (legal size + one growth increment below = mature for BBRKC)
- Average B – calculated using MMB from 1984 to 2021 (matches current Tier 3 assessment $B_{35\%}$ calcs)
- Assume 20% buffer – likely this would be different if we went with a Tier 4 option.



| avgBb (t) | Current B | MMB/ B_{ms} v | M | F_{OFL} | OFL | ABC |
|-----------|-----------|--------------------|------|-----------|---------|---------|
| 28443.11 | 20328.15 | 0.71 | 0.18 | 0.12 | 2499.12 | 1999.30 |

Future work

- Q explorations – modeling workshop topic? More input on potential modeling options
- Initial conditions – explorations on these and suggestions for what to look at
- Sensitivity of model to growth / molting / size increment assumptions
 - Hasn't been revisited in awhile and would be good to explore
- Focus on retrospective pattern