

Snow crab: History and status of transition to GMACS

Cody Szuwalski

May 17, 2022

Crab Plan Team meeting

Only one goal for this meeting:
snow crab to GMACS

History of transition

Differences between GMACS and status quo

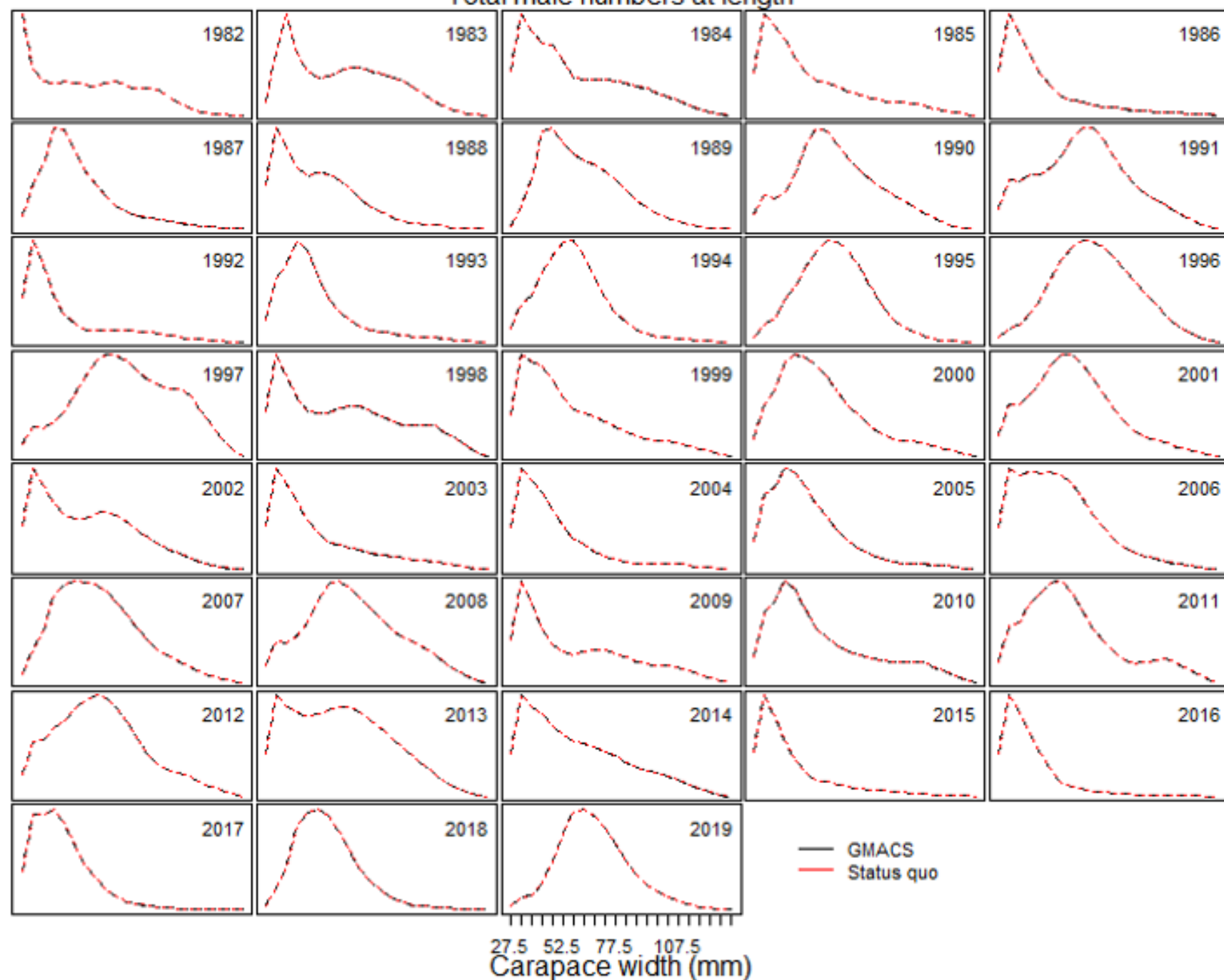
Comparison of most recent GMACS and status quo model

Recommendations

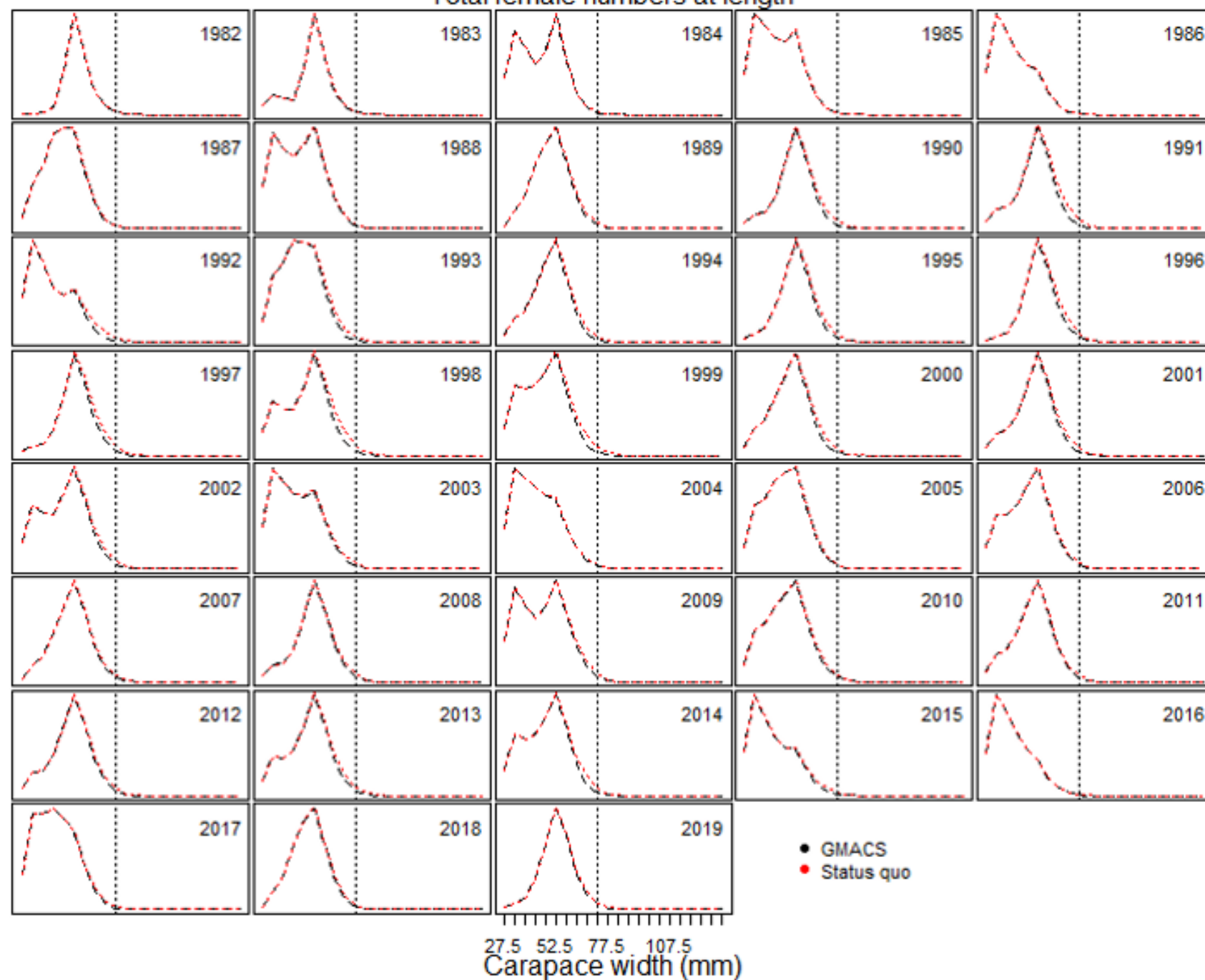
CPT recommended GMACS for use in September of 2020 based on:

- better model fits
- a confirmation that GMACS could reproduce the status quo numbers at size matrix for males with the same input parameters
- improved model structure, assumptions, and stability
- the utility of working towards a common code base for all EBS stocks

Total male numbers at length



Total female numbers at length



SSC rejection

From the SSC report: “The SSC noted that it seems unlikely that the stock is 4x larger than last year’s estimate, while lacking new survey data to support that conclusion.”

The projected biomass for 2020/21 from the author preferred model was 276.7 kt; the estimated biomass from 2019/20 was 167.3 kt (). This was a 65% increase, not ‘4x’. However, the OFL did increase more than 65%, increasing from 54.9 kt to 184.9 kt (a 237% increase). This difference in OFL was a combined result of the largest pseudocohort (i.e. a group of crab of the same size, but not necessarily the same age) ever observed entering the population after a period in which MMB was the lowest on record.

C1 BSAI Crab SAFE Introduction
OCTOBER 2020

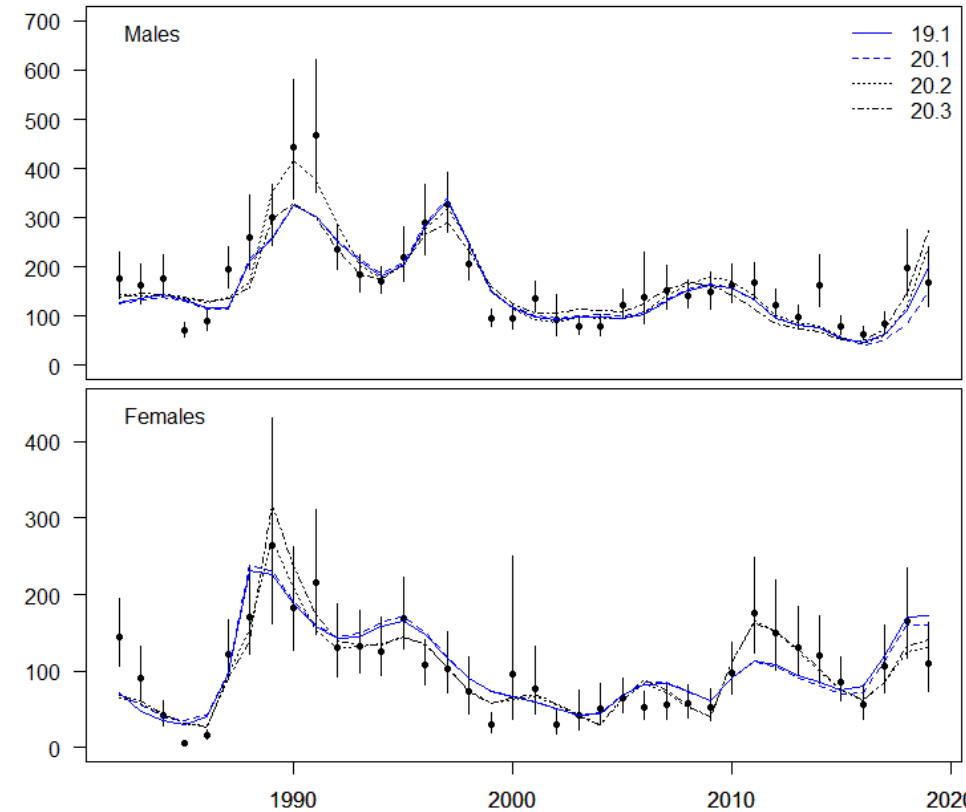
Status and catch specifications (1000 t) for snow crab. Shaded values are new estimates or projections based on the current assessment. Other table entries are based on historical assessments and are not updated except for total and retained catch.

Year	MSST	Biomass (MMB)	TAC	Retained Catch	Total Catch	OFL	ABC
2016/17	75.8	96.1	9.7	9.7	11.0	23.7	21.3
2017/18	71.4	99.6	8.6	8.6	10.5	28.4	22.7
2018/19	63.0	123.1	12.5	12.5	15.4	29.7	23.8
2019/20	56.8	167.3	15.4	15.4	20.8	54.9	43.9
2020/21		276.7				184.9	92.5

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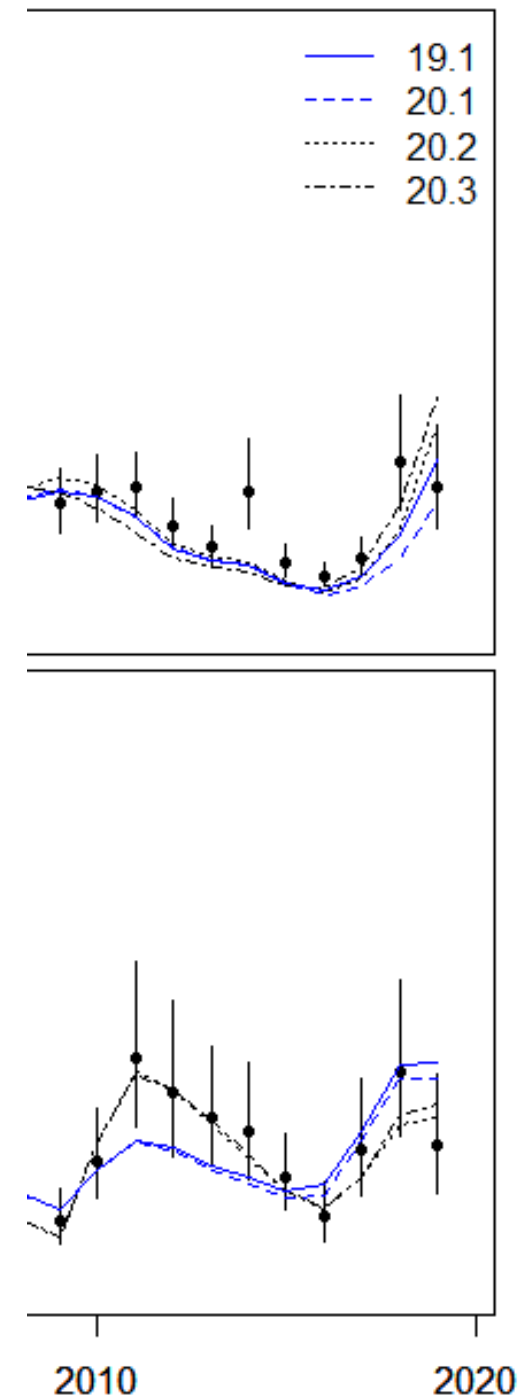
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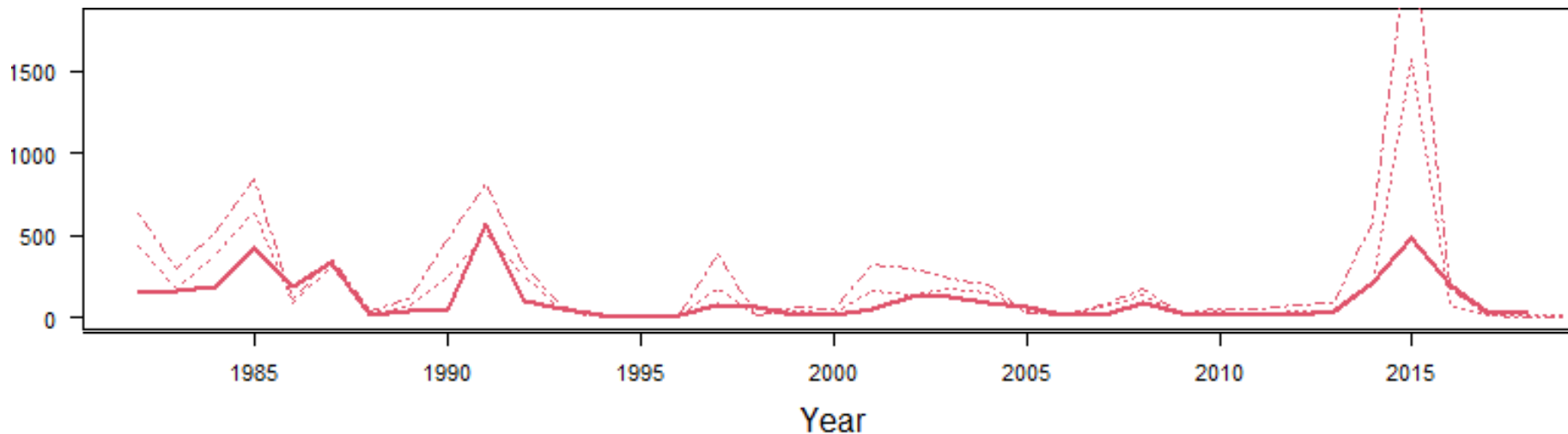
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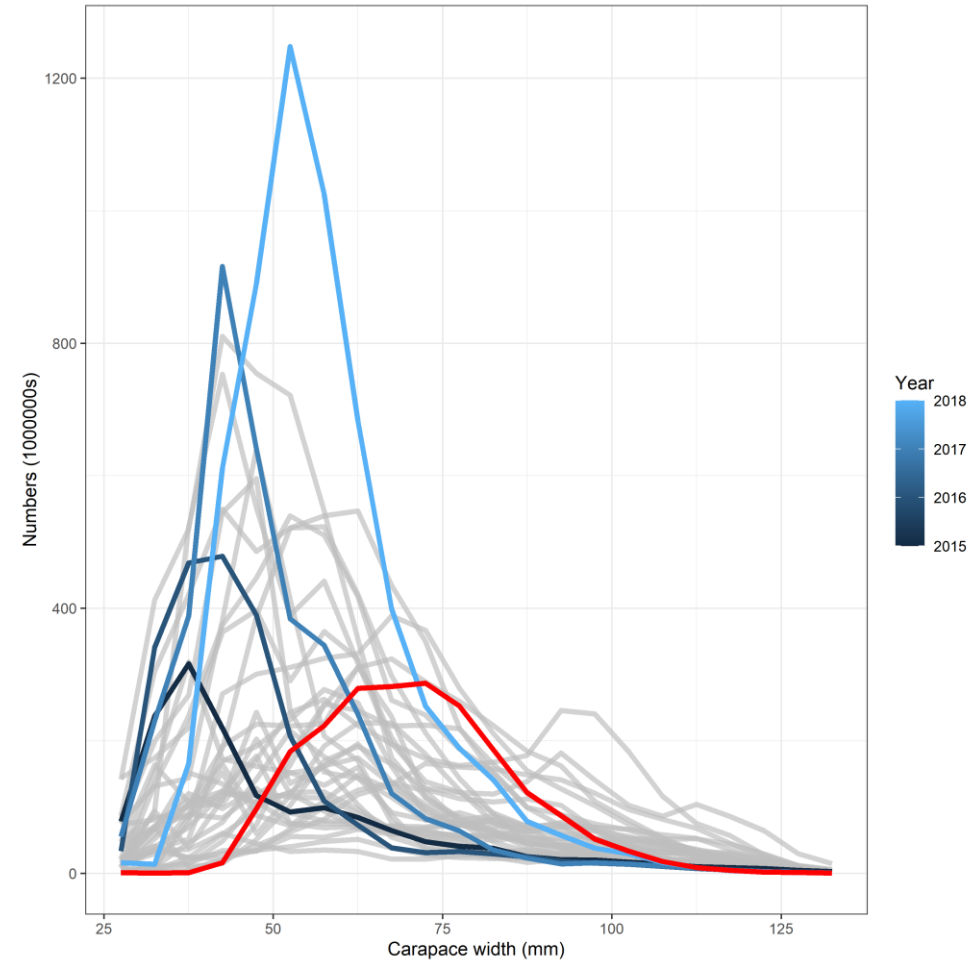
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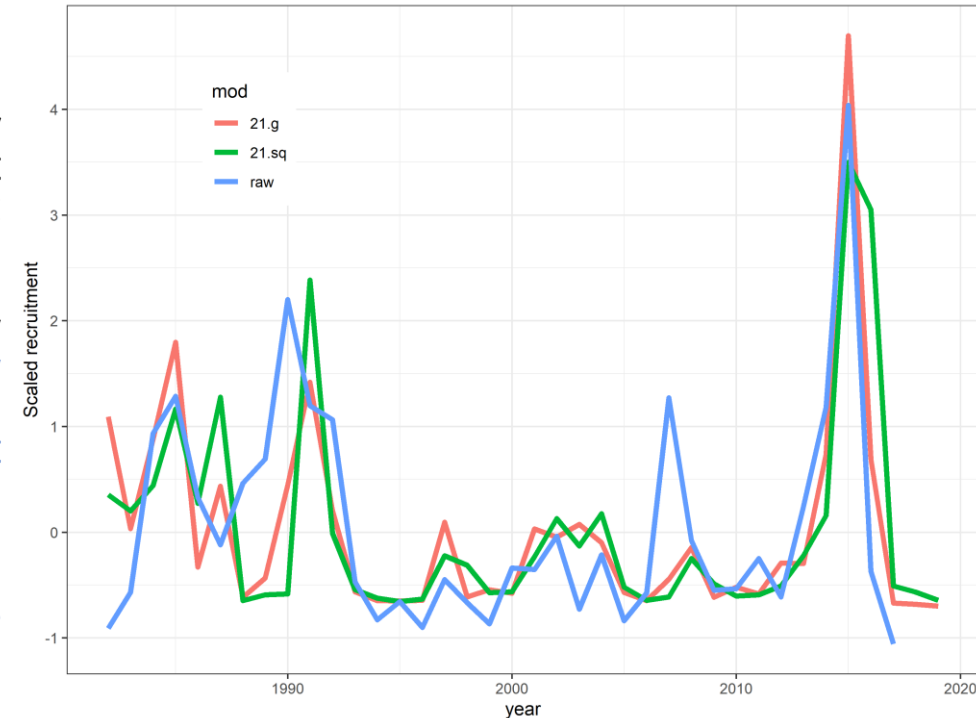
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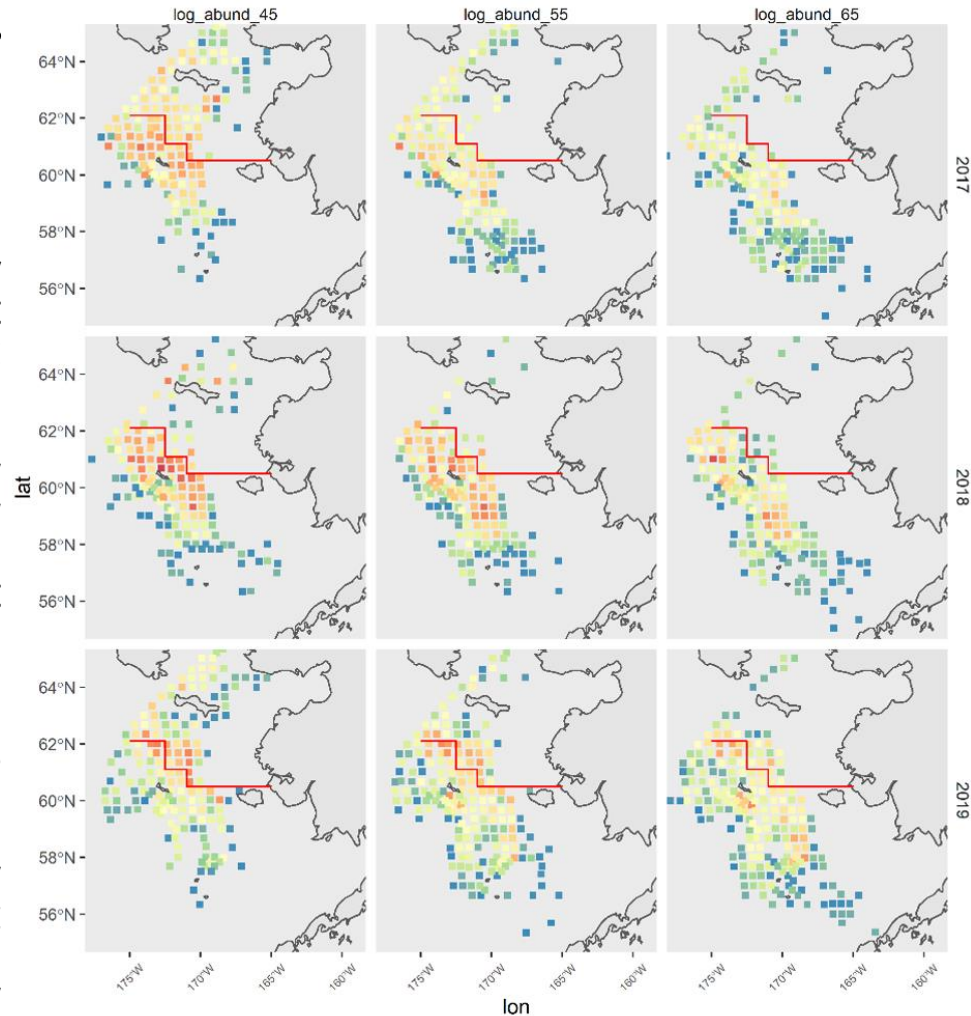
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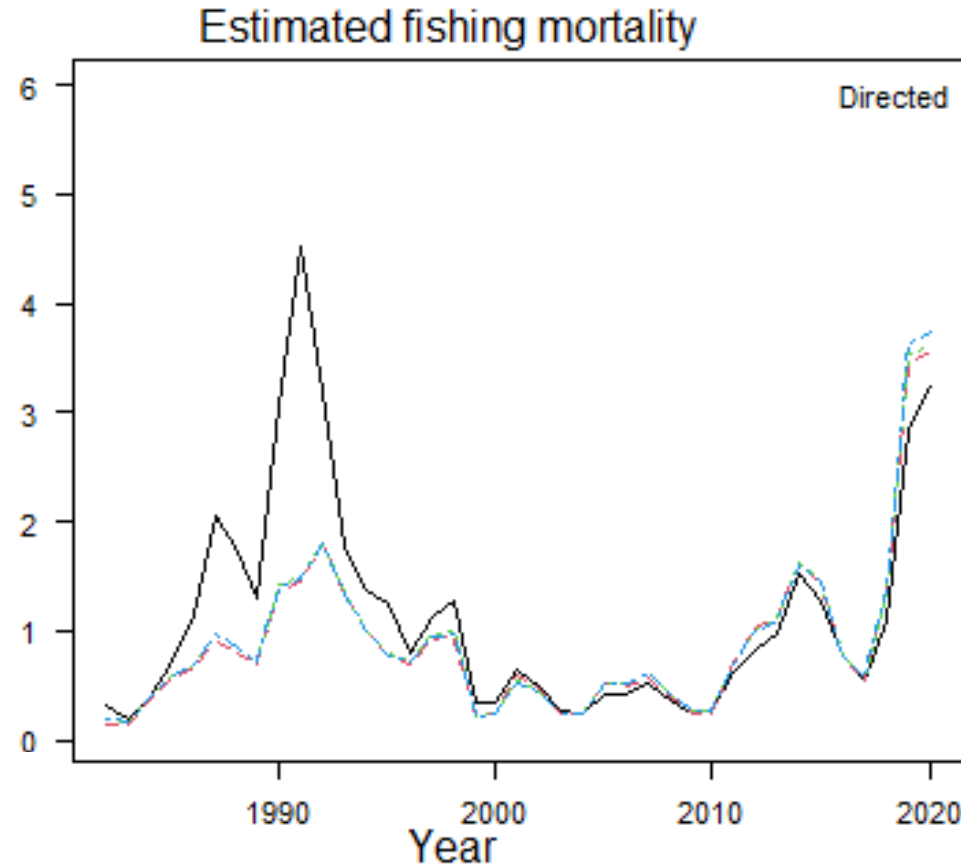
SSC rejection

From the SSC report: “...there is still a very large positive retrospective pattern which is puzzling...”

Retrospective patterns exist in both the status quo model and in GMACS (see the 2019 SAFE in which the status quo model had a Mohn's rho of 0.48-0.54). Retrospective patterns can result from unmodelled variation in population processes like natural mortality or from incomplete data sets (e.g. missing catch data). So, given the same data and population dynamics model, two different models (like the status quo and GMACS) would be expected to produce similar retrospective patterns. They would not, however, be expected to produce identical retrospective patterns. Difference in likelihood formats and weighting of data sets (as exist between the status quo model and GMACS, discussed more below) would influence the relative sizes of retrospective patterns.

SSC rejection

From the SSC report: “Another feature of the author-preferred GMACS model is extremely high fully-selected fishing mortality in some years...”



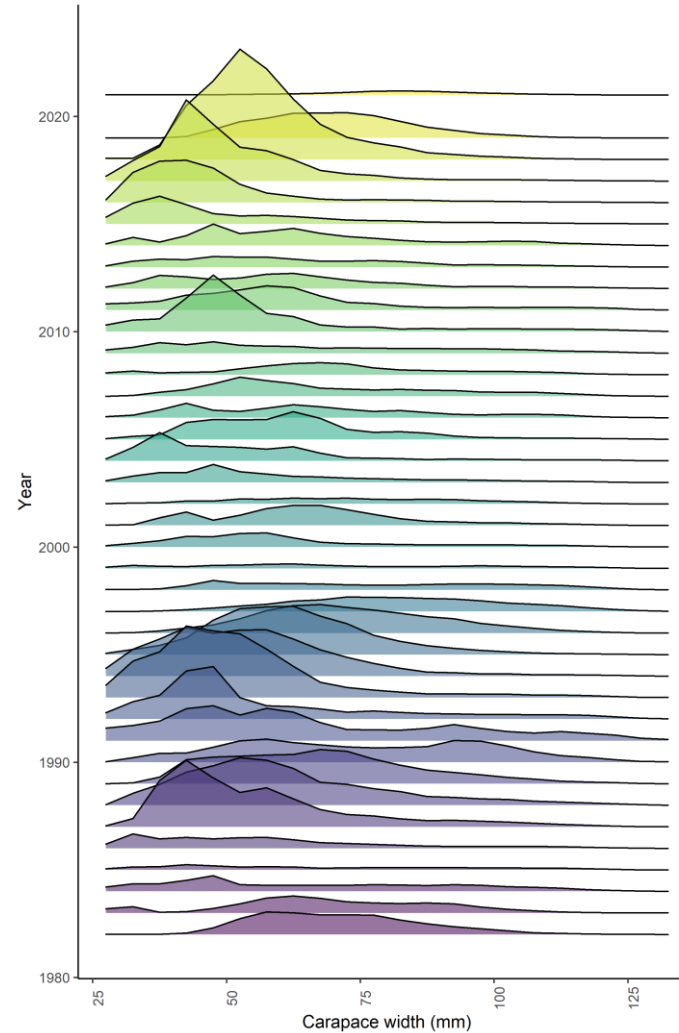
This is actually a feature of the status quo model. GMACS estimates more reasonable (though still high) fishing mortalities in the early period of the assessment.

The problems identified by the SSC were:

1. Important 'features' of GMACS that addressed failings of the status quo model (e.g. the estimated recruitment),
2. Misidentified problems (e.g. high fishing mortality for GMACS),
3. Shared problems of GMACS and the status quo (e.g. retrospective patterns).

What has happened since 2020?

- Large survey decline
- Overfished declaration
- Time-variation in M added into the status quo assessment



Size group	2021 biomass (kt)	Previous low (kt)	Overfished declaration (1999)
>101 mm	12.4	20.7 (2016)	52.0
>24 mm	73.5	99.8 (1985)	111.5
>77 mm	60.1	51.7 (2016)	87.1
>94 mm	24.4	29.4 (2016)	67.4

GMACS vs. status quo model

- Population dynamics
 - Identical except fishing mortality
- Likelihoods
 - Number
 - Format
- Weightings
 - Weights vs. coefficients of variation or standard deviations
- Convergence

Likelihood	Description	in.GMACS.	Same.form.	SQ.weight	Translated.CV	GMACS.wt
Smoothness for recruitment	norm2(devs)		No	1	0.71	1
Constraint on initial numbers of small old shell males	square(exp(numbers))	No		0.000001	707.1	
Retained fishery length comp	Multinomial			100	NA	100
Total fishery length comp	Multinomial			100	NA	100
Female length comp	Multinomial			100	NA	100
Survey length comp	fit to by sex and maturity state			100	NA	100
Trawl length comp	Multinomial			100	NA	100
2009 BSFRF length comp	Multinomial			100	NA	100
2009 NMFS length comp	Multinomial			100	NA	100
Prior on natural mortality	square(multiplier -1)/input_variance		No	0.0154	NA	0.0154
Prior and smoothness on maturity	norm2(second_diff(prob_molt))		No	50	0.1	60
Growth data (male)	sum of squares, no CV		No	1	0.71	0.03
Growth data (female)	sum of squares, no CV		No	1	0.71	0.03
2009 BSFRF mature biomass	log normal, no constants			cv	NA	cv
2009 NMFS mature biomass	log normal, no constants			cv	NA	cv
Fishery CPUE	normal with input 'cv'	No		5	0.32	
Retained catch	normal with input weight, no constants		No	1000	0.02	0.04
Total catch	normal with input weight, no constants		No	20	0.16	0.07
Trawl catch	normal with input weight, no constants		No	1000	0.02	0.1
Female discards	normal with input weight, no constants		No	30000	0	0.07
Survey mature biomass	lognormal with input cv			cv	NA	cv
Penalties on directed F	norm2(F-1.15)	No		10	0.22	
Penalties on trawl F	norm2(F)	No		2	0.5	
Penalties on all but last year of directed F	norm2(F)	No		0.1	2.24	
2010 BSFRF mature biomass	lognormal with input cv			cv	NA	cv
2010 NMFS mature biomass	lognormal with input cv			cv	NA	cv
First year survey length comp additional weight	Multinomial, adds if molt_prob>0.99	No		100	NA	
2010 BSFRF length comp	Multinomial			100	NA	100
2010 NMFS length comp	Multinomial			100	NA	100
Smoothness of selectivity experiment	normal with input SD, if used	No		1	0.71	
Smoothness of female discards	norm2 on first differences of predicted discard	No		10	0.22	

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Likelihoods and weightings

- Extra likelihood components in the status quo
- Lognormal vs. normal for catches and growth data
- Prior on natural mortality
- Differences in relative weightings of the catches

Differences in GMACS are improvements at best
lateral moves at worst

Convergence

- Cutoff close to 0 to demonstrate a lack of non-convergence.
- The status quo model was accepted in spite of the potential issues with convergence.
- A similarly configured GMACS model (21.g) did not have potential convergence issues.

Model	Maximum gradient component	Parameter associated with max gradient
21.sq	0.18	1991 rec dev (f and M also > 0.01)
21.g	0.002	1985 Sex ratio recruitment
21.g.m	0.0004	Log avg recruitment
21.g.m.g	0.0006	2014 sex ratio recruitment

Models

- 21.sq: Accepted model 2021 (status quo)
- 21.g: GMACS formulated similarly to 21.sq
- 21.g.m: 21.g, but with natural mortality fixed to 21.sq estimates
- 21.g.mg: 21.g.m, but with growth fixed to 21.sq estimates

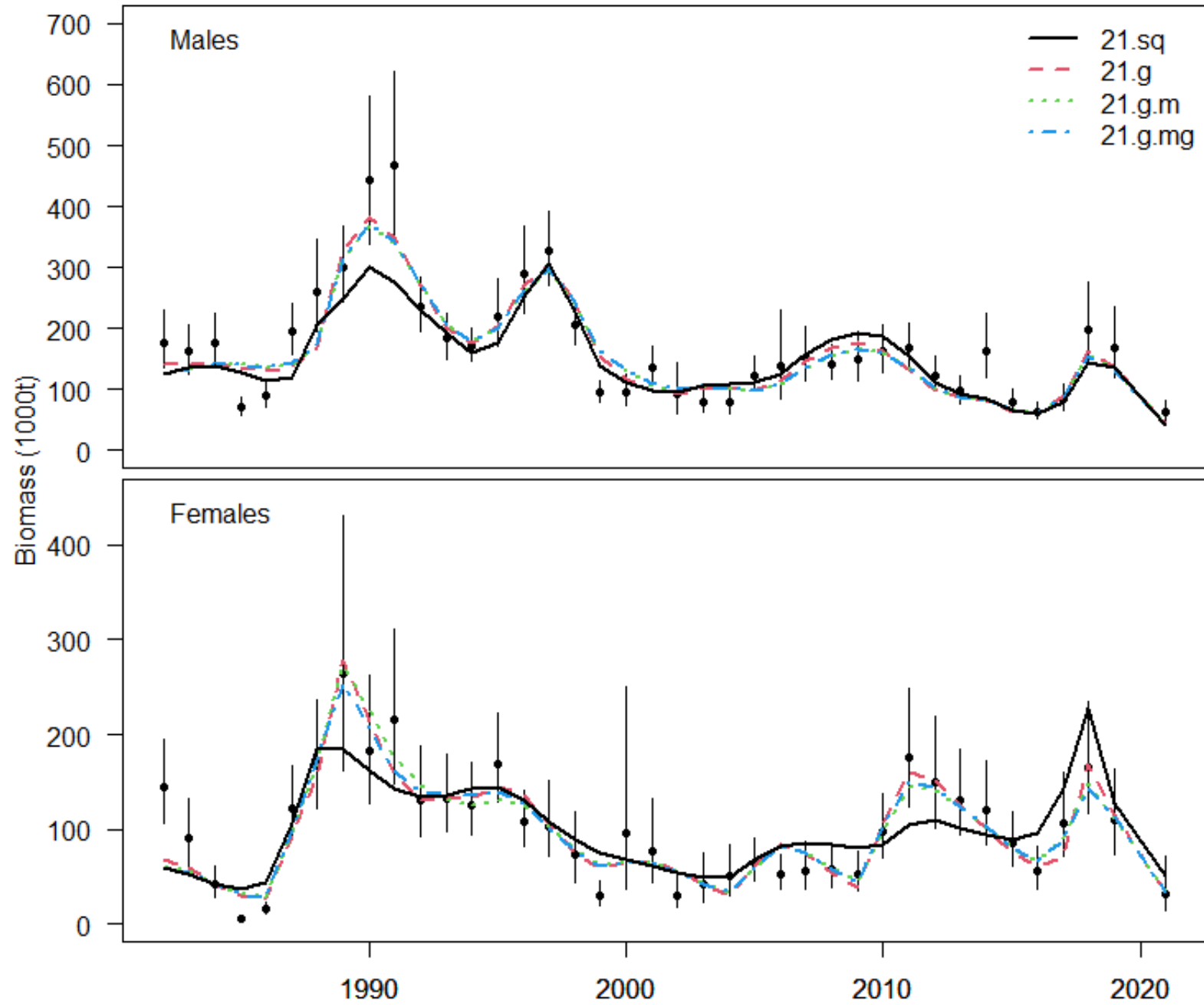
Differences between the status quo and GMACS

- **Linear growth models for males and females are estimated in GMACS**, but the parameters associated with growth are estimated outside of the status quo model and specified because the model will not converge linear growth models
- Availability curves in the status quo were freely estimated vectors of parameters with smoothing components for males, but logistic curves for females. Empirical availability curves were adopted last year. In GMACS, **both sexes have freely estimated vectors of parameters estimated for the availability** of the population to the BSFRF experiments. A better method for incorporating these data will be implemented after the adoption of GMACS.
- The status quo model estimates 3 natural mortality parameters for mature males, mature females and immature crab of both sexes. **GMACS estimates 4 natural mortality parameters** for mature males, mature females, immature males, and immature females.
- The status quo model estimates an average recruitment and yearly deviations for both sexes. GMACS estimates a single average recruitment and yearly deviations, then another time series of sex ratios to divide the recruitment between the sexes.

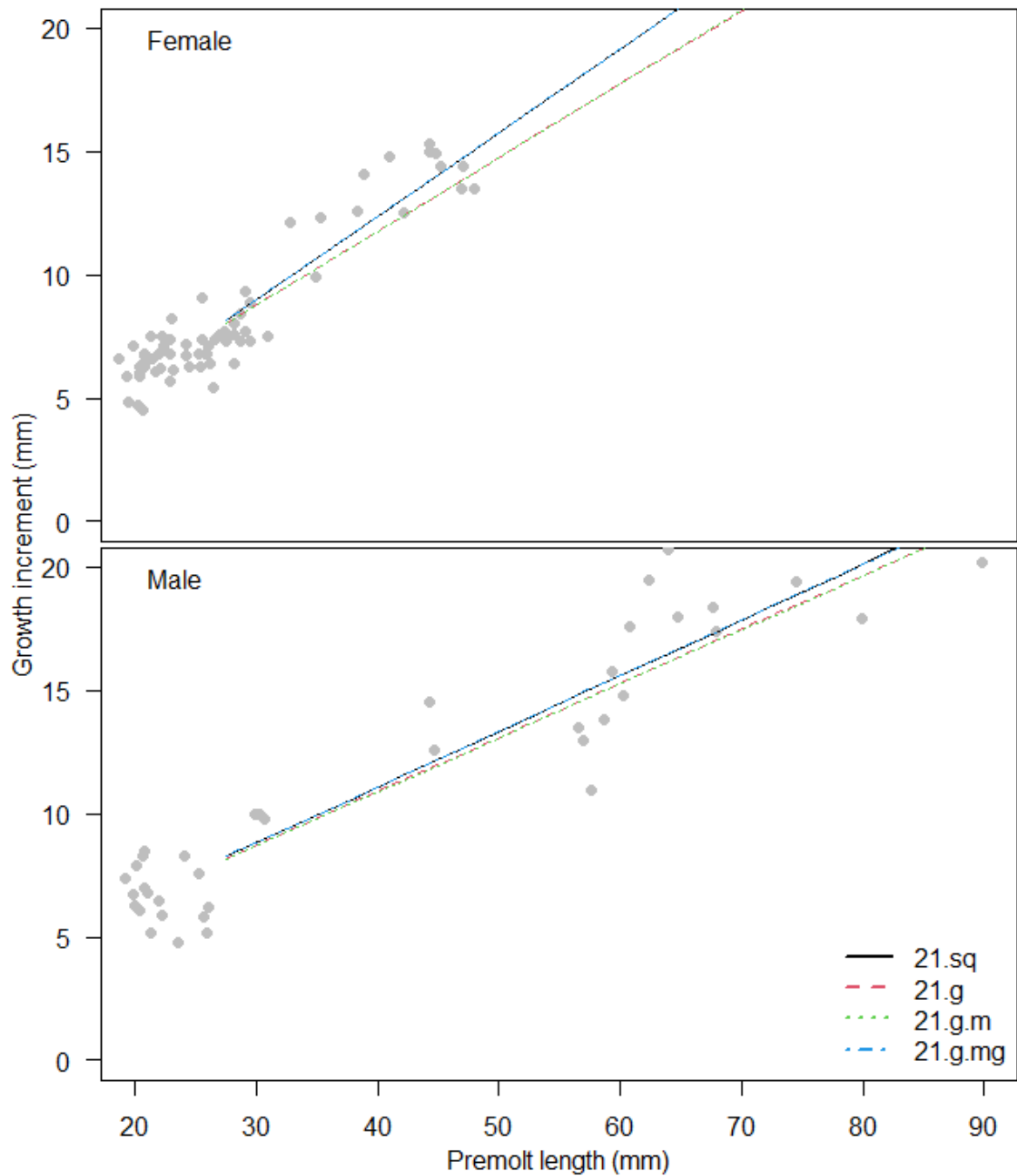
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GMACS fits MMB better in early period, similar in later period

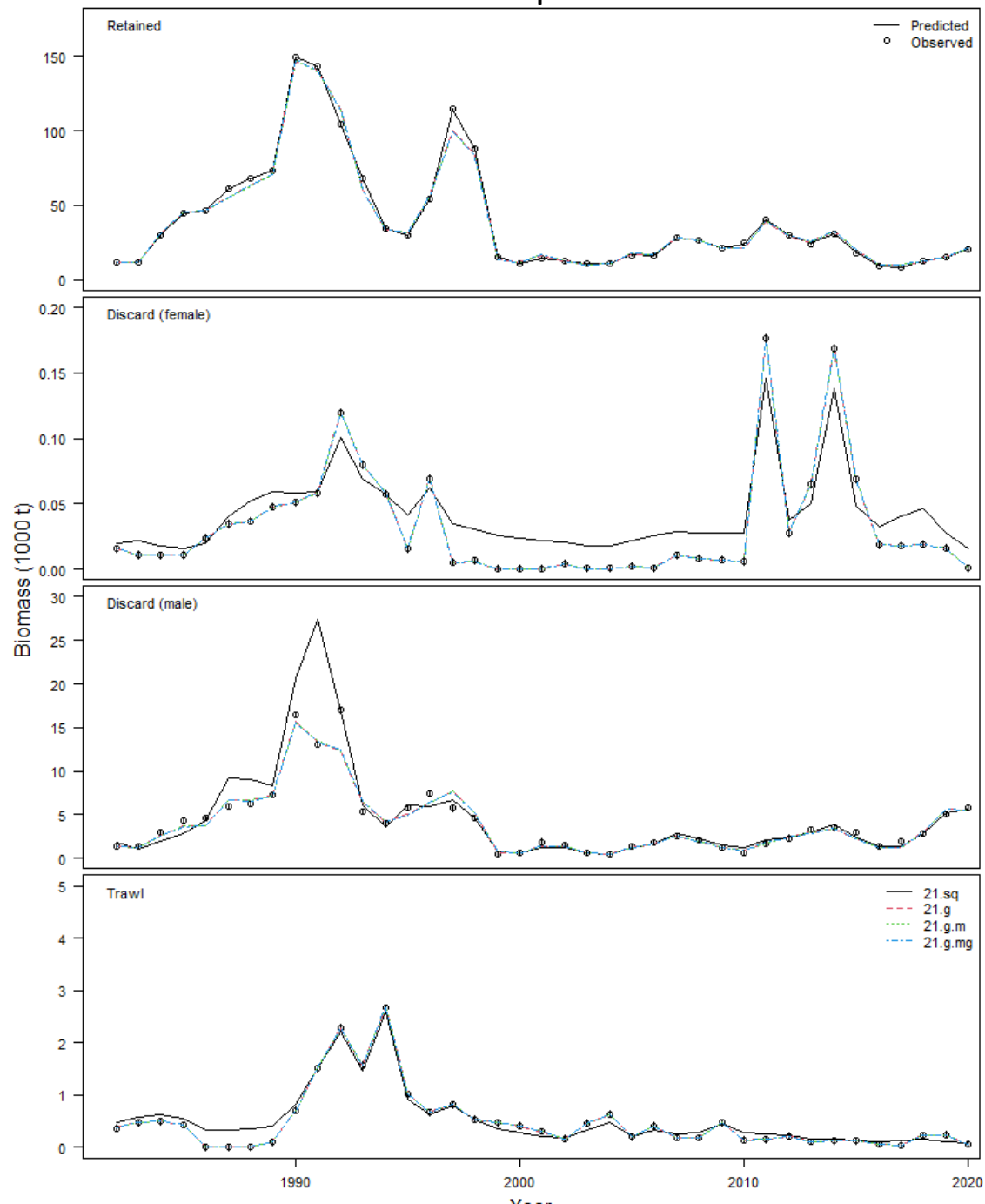
GMACS fits FMB better period



GMACS fits female growth slightly worse; males similarly.

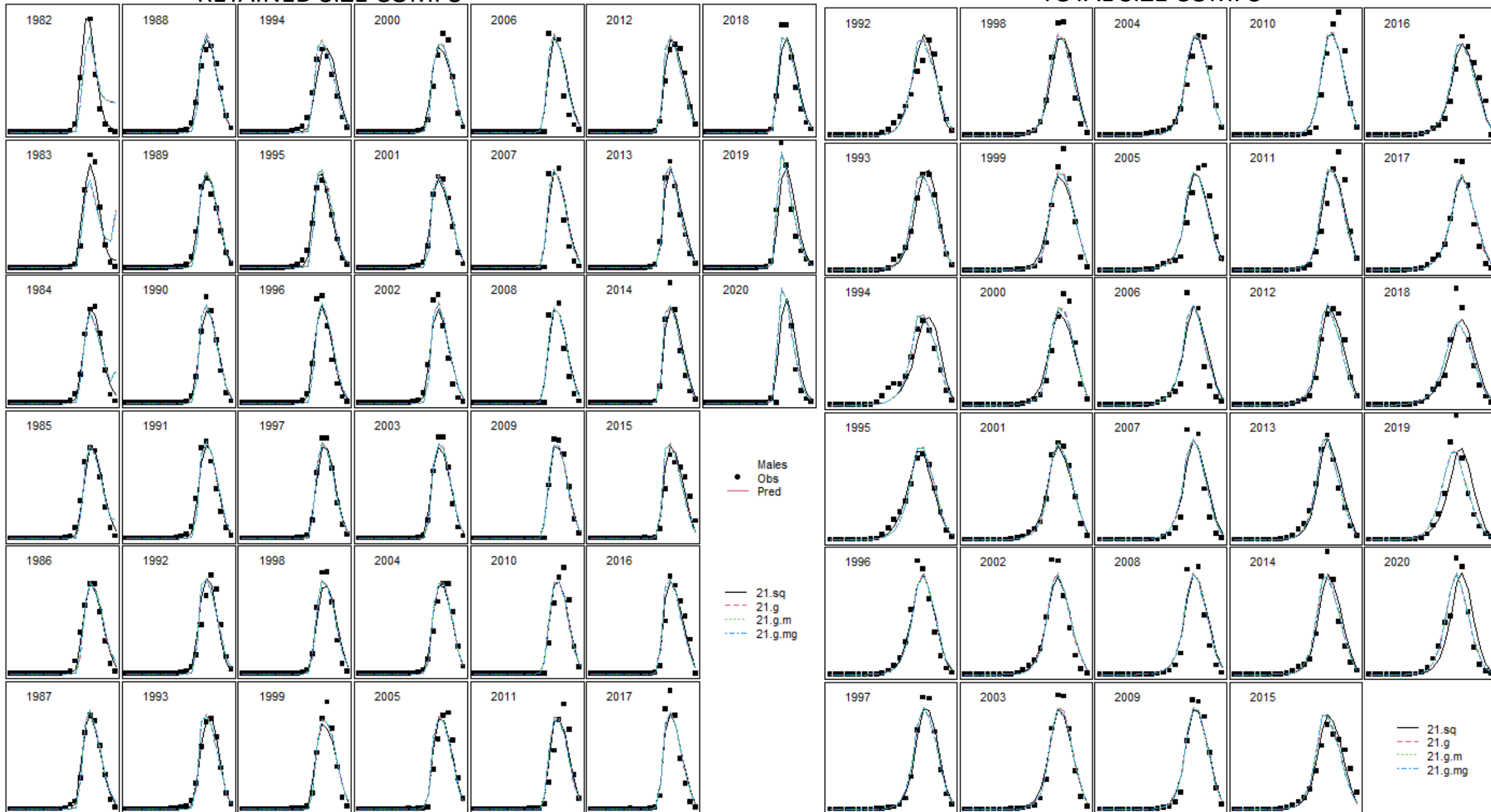


GMACS all catch except retained better.

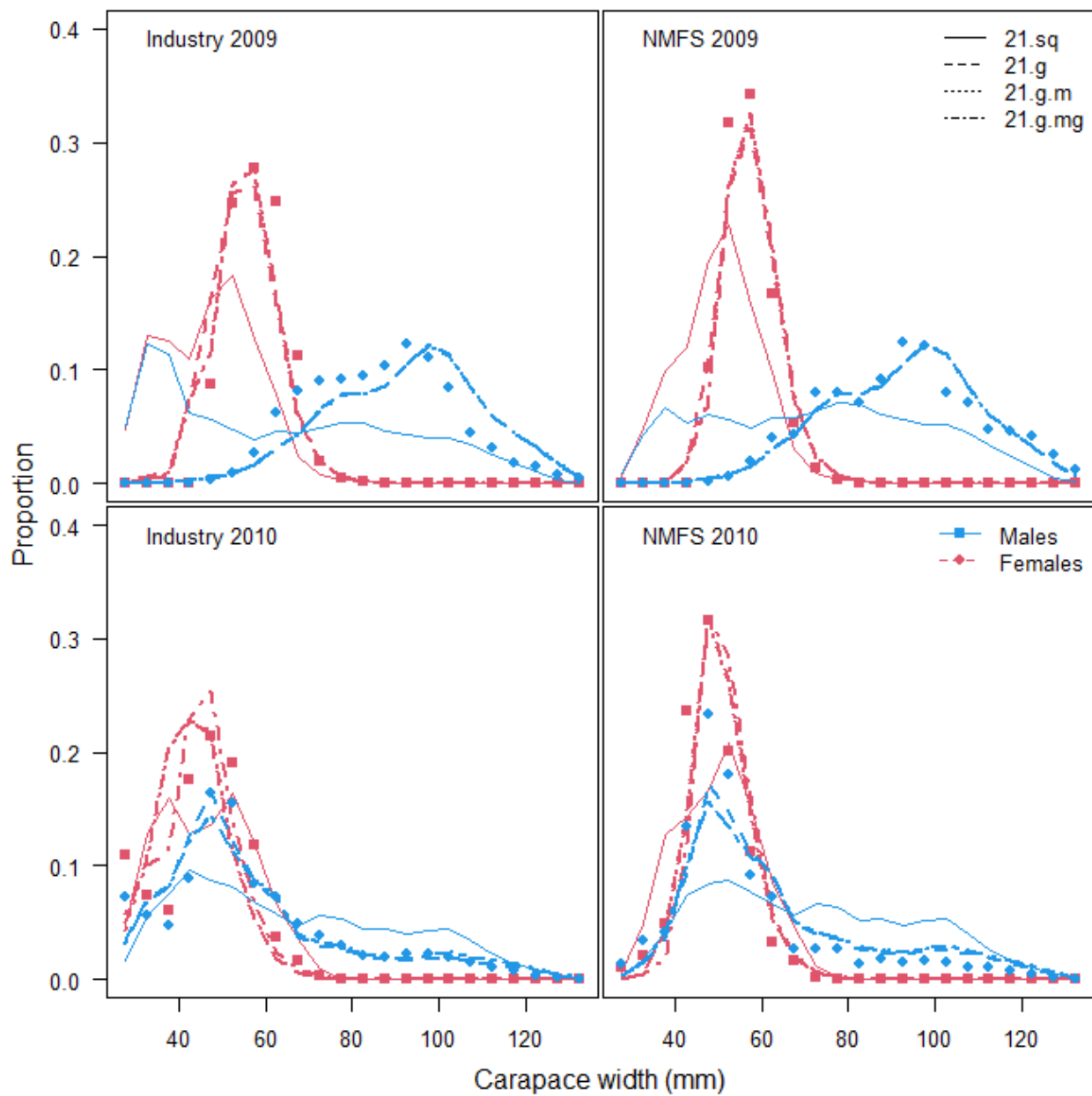
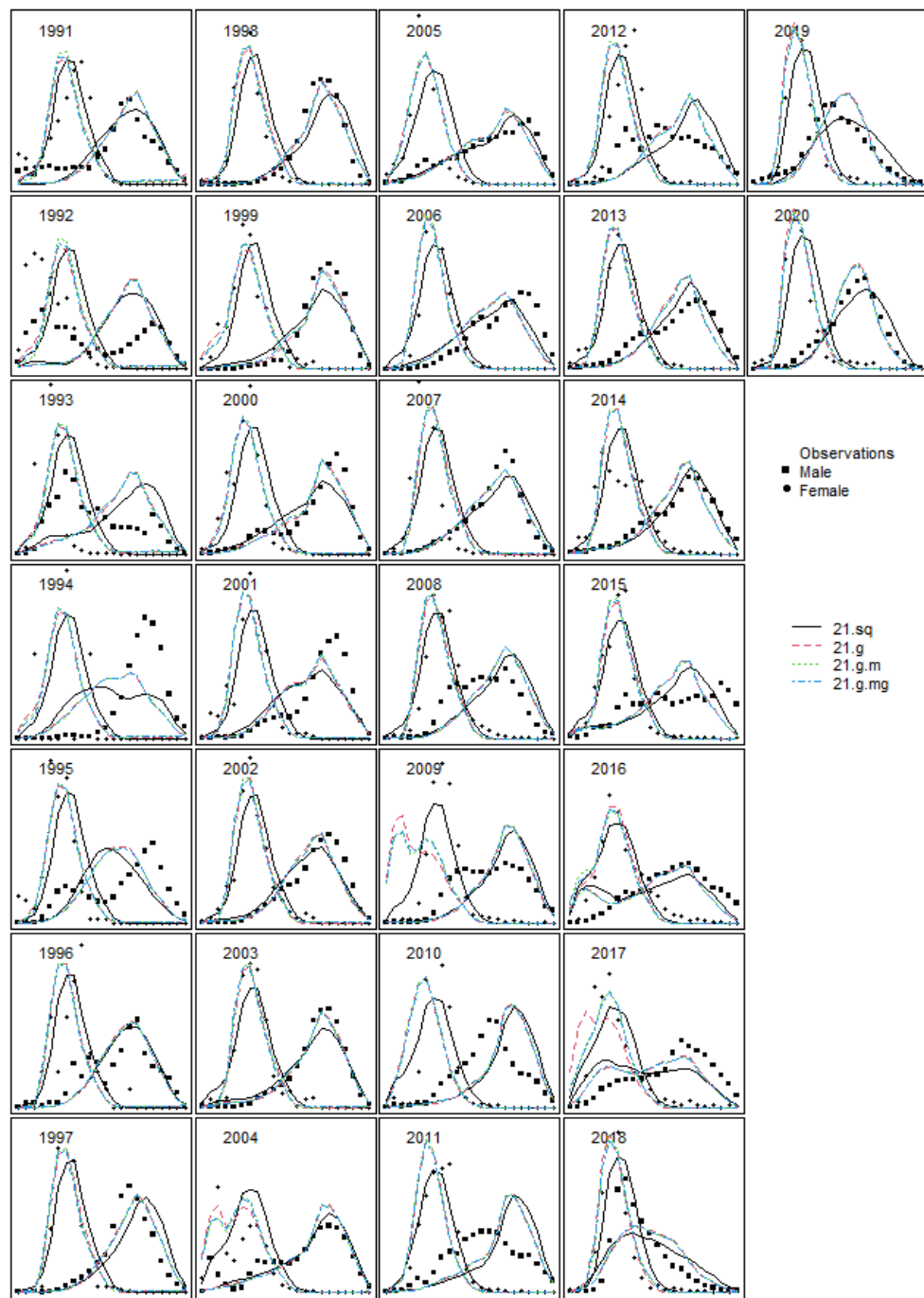


RETAINED SIZE COMPS

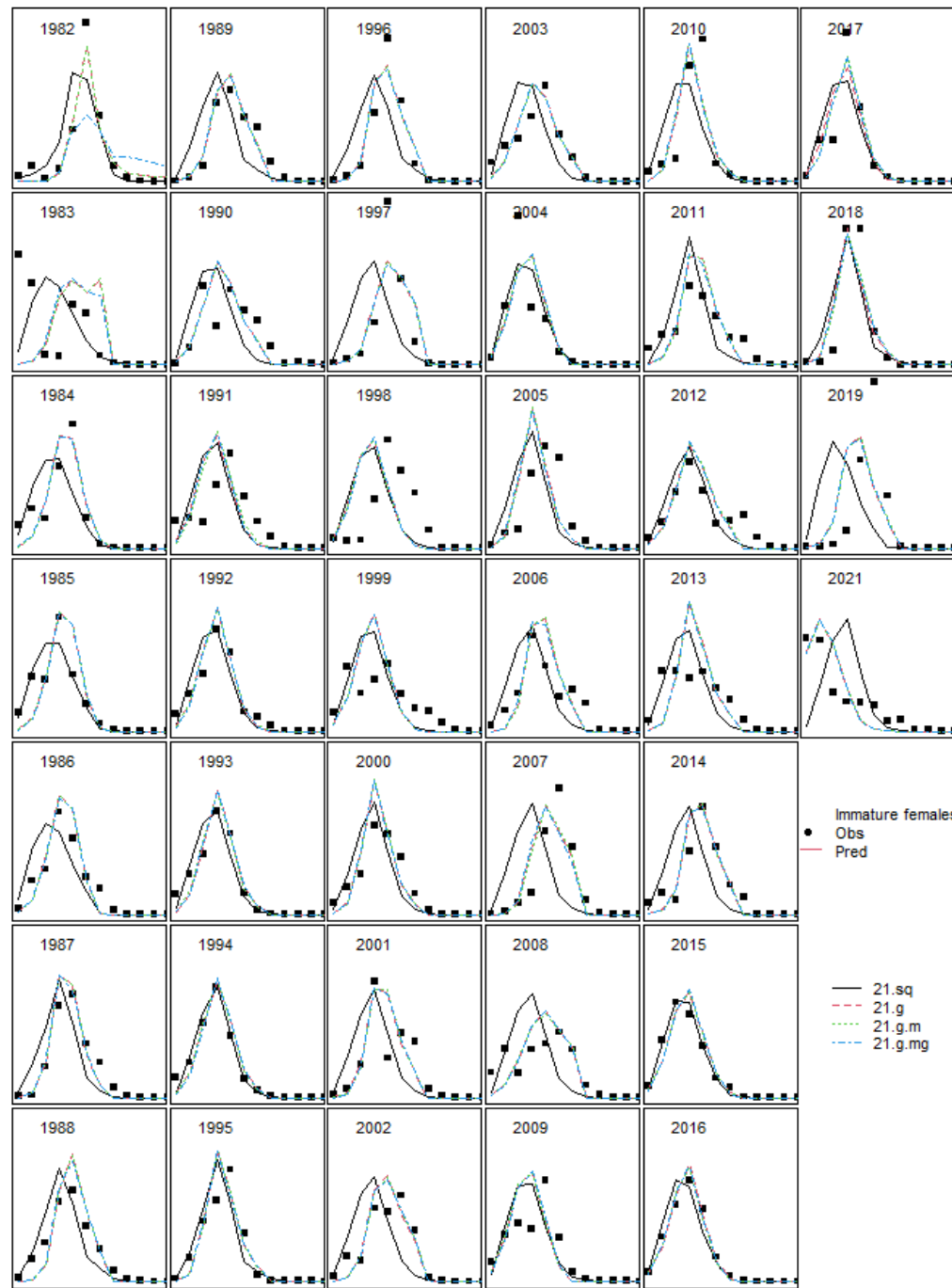
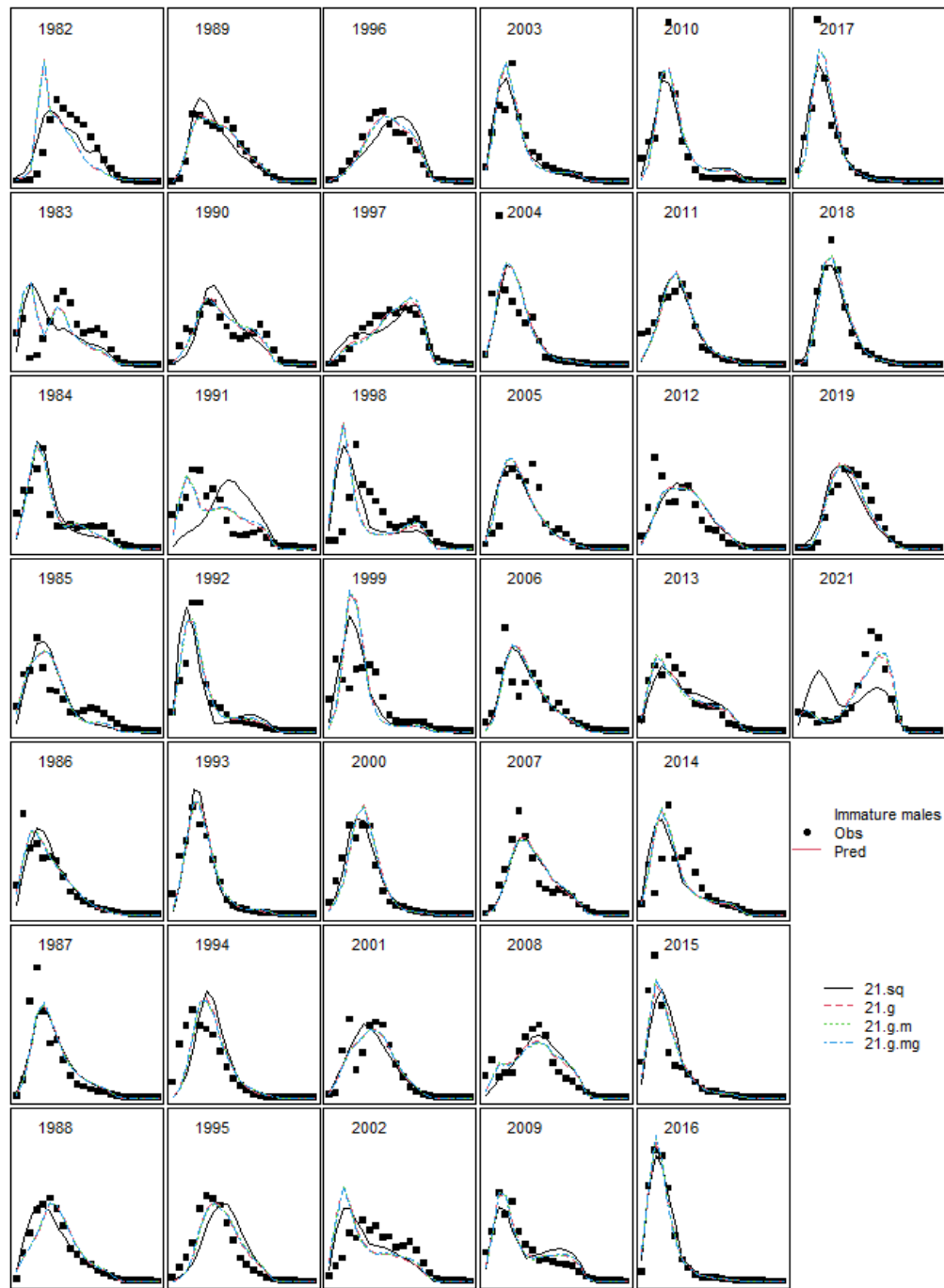
TOTAL SIZE COMPS



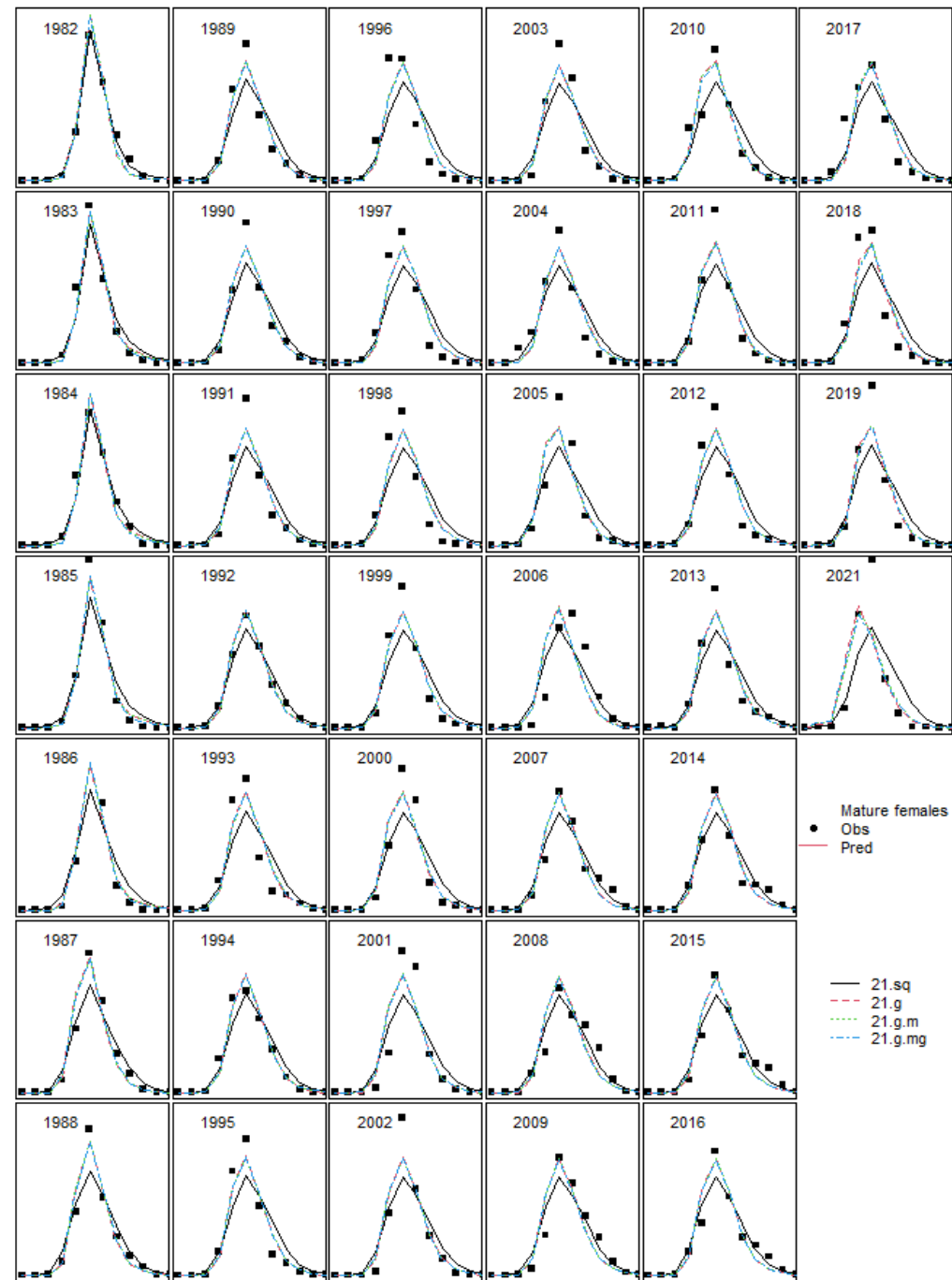
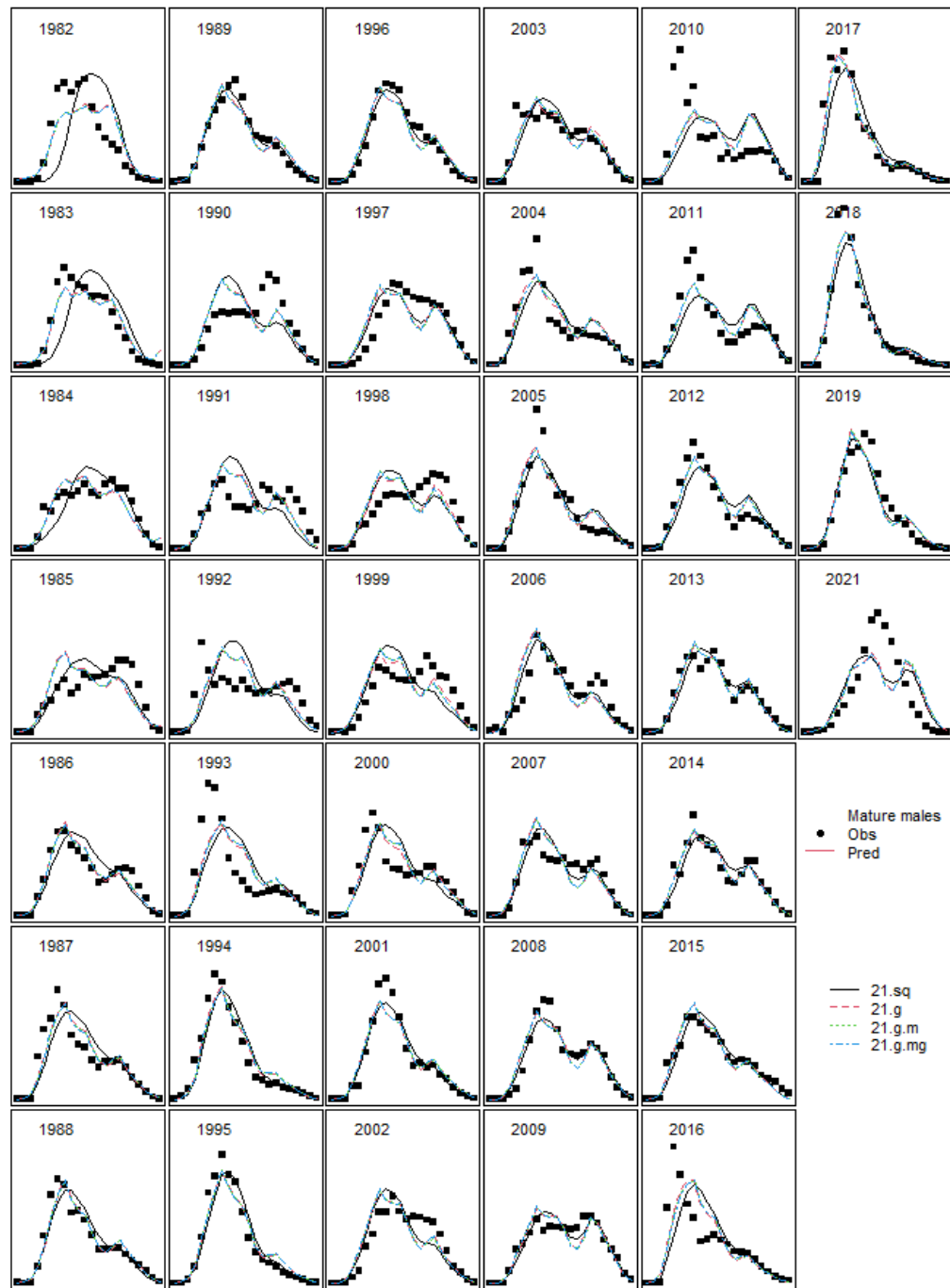
GMACS fits retained catch worse in first two years, but fits retained and total catch for last two years better.



All fits for trawl size comps are not great, GMACS fits BSFRF data better.



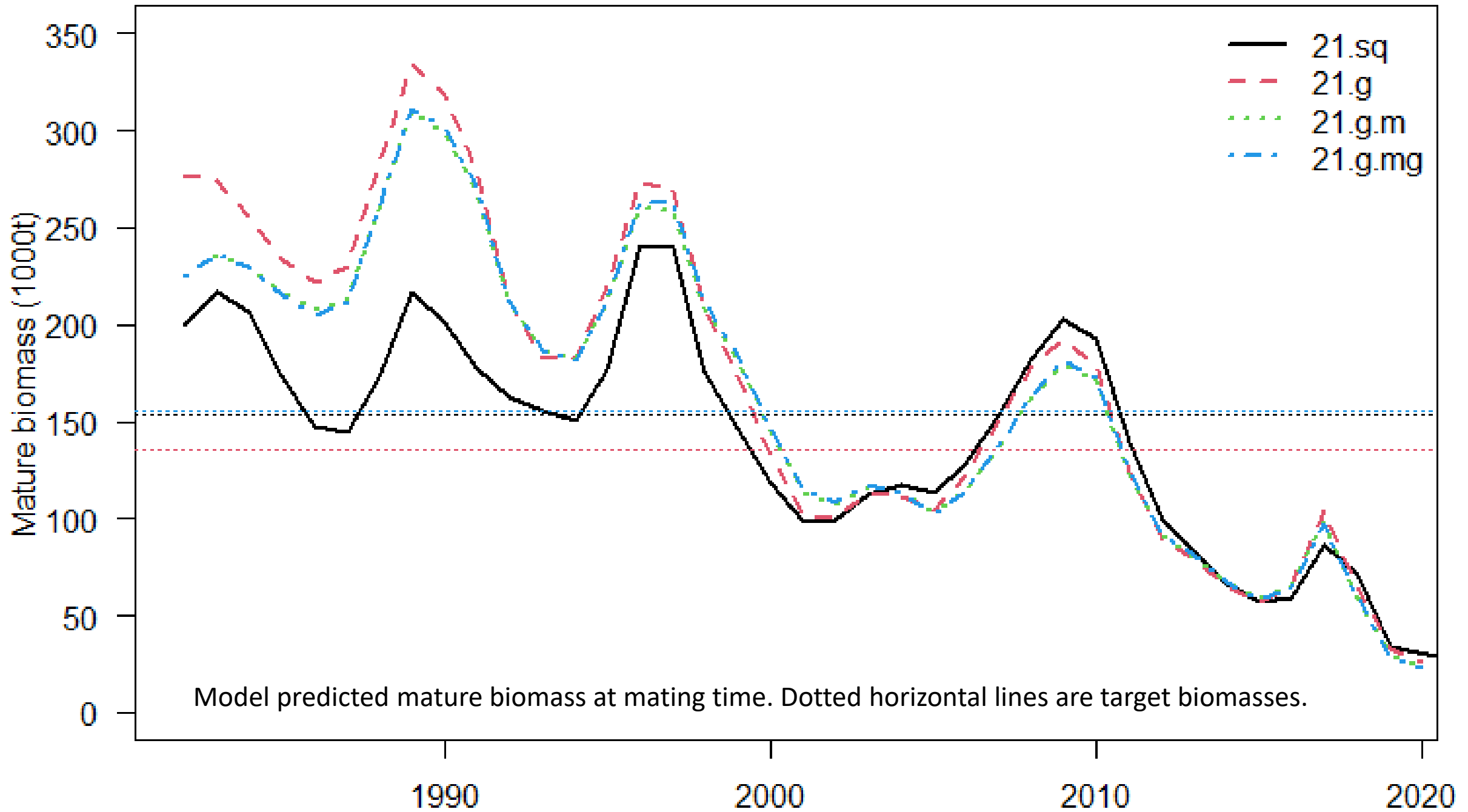
GMACS fits immature males better in the last year, fits immature females better in nearly all years.

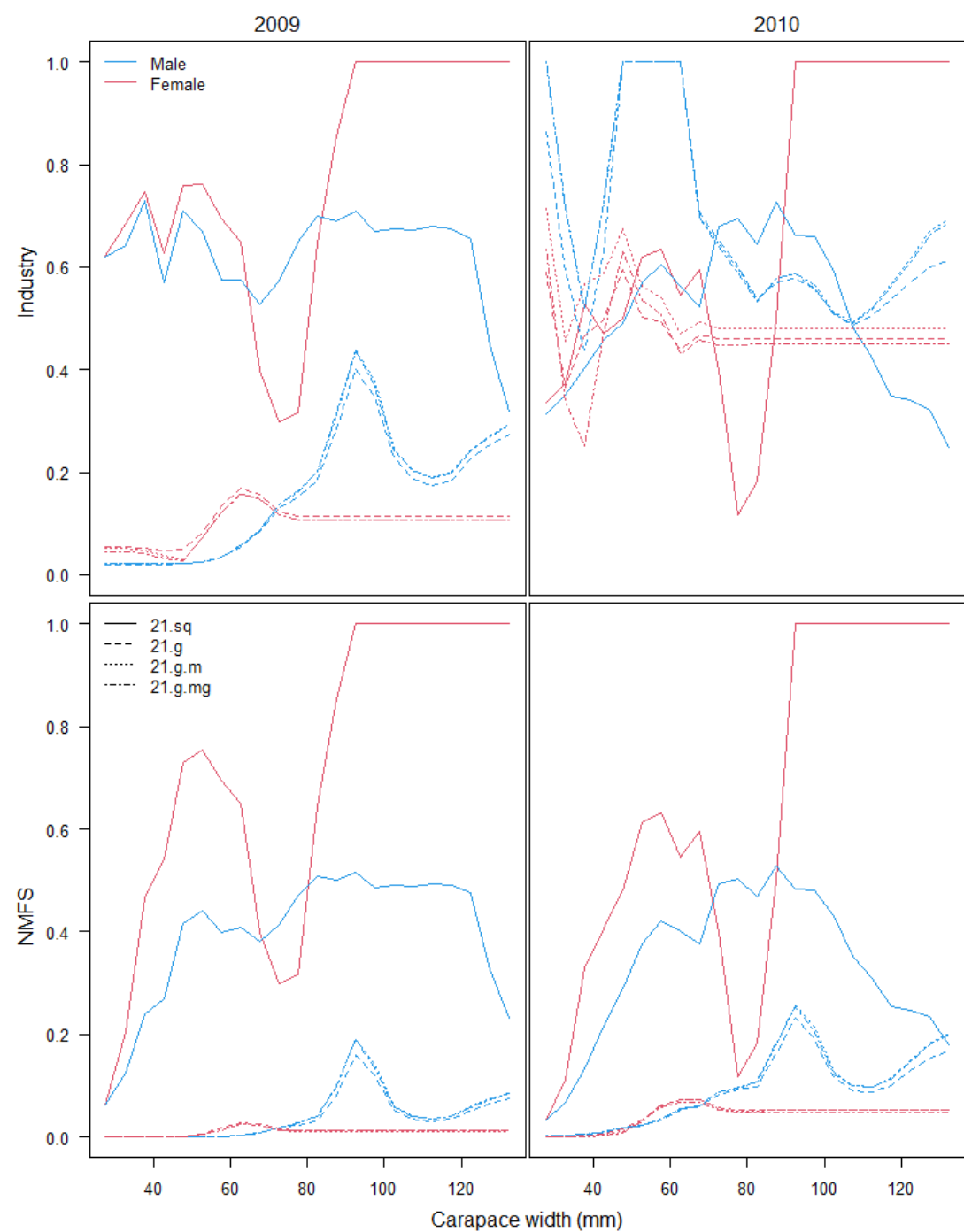
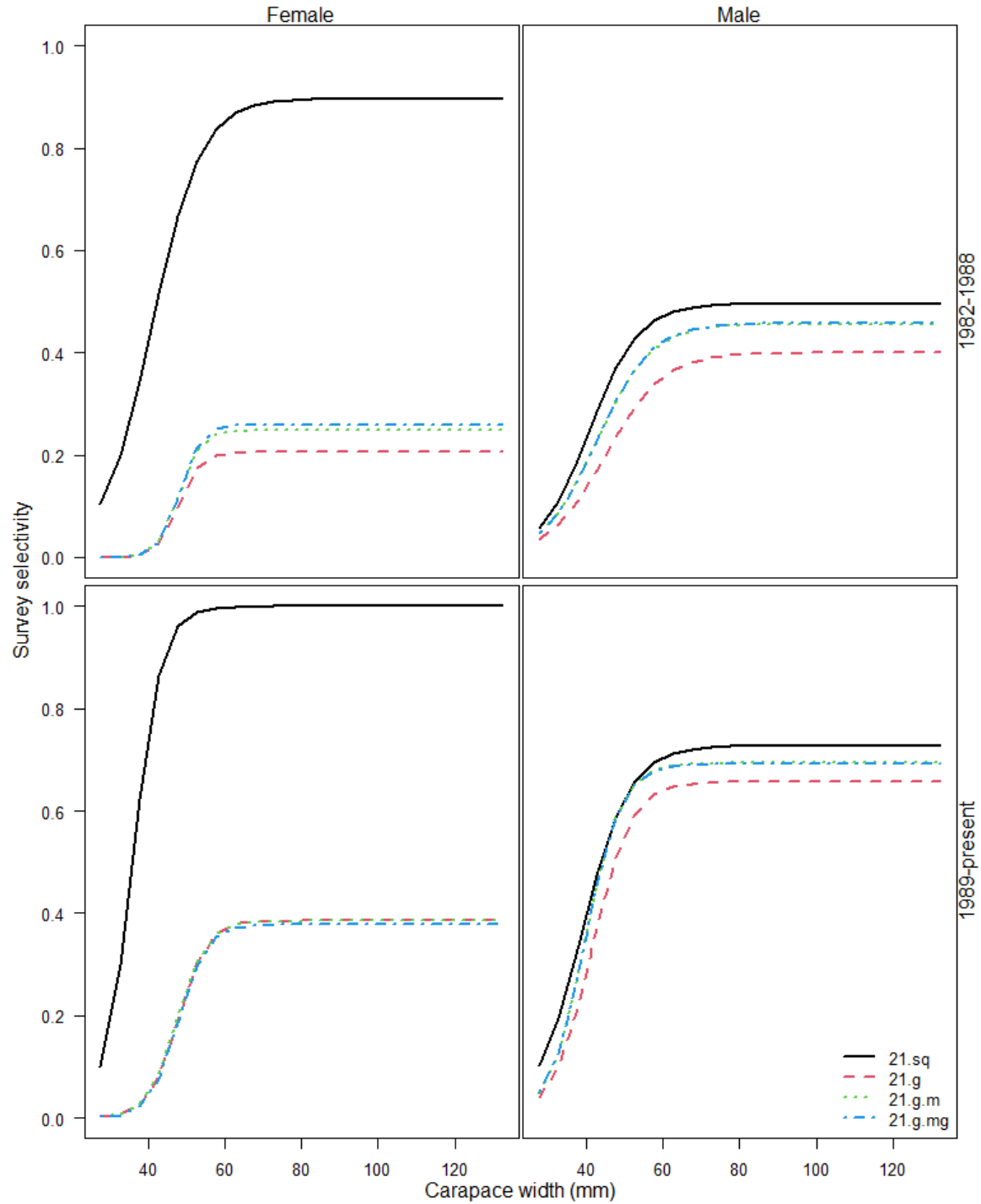


GMACS fits mature males similarly, fits mature females better in nearly all years.

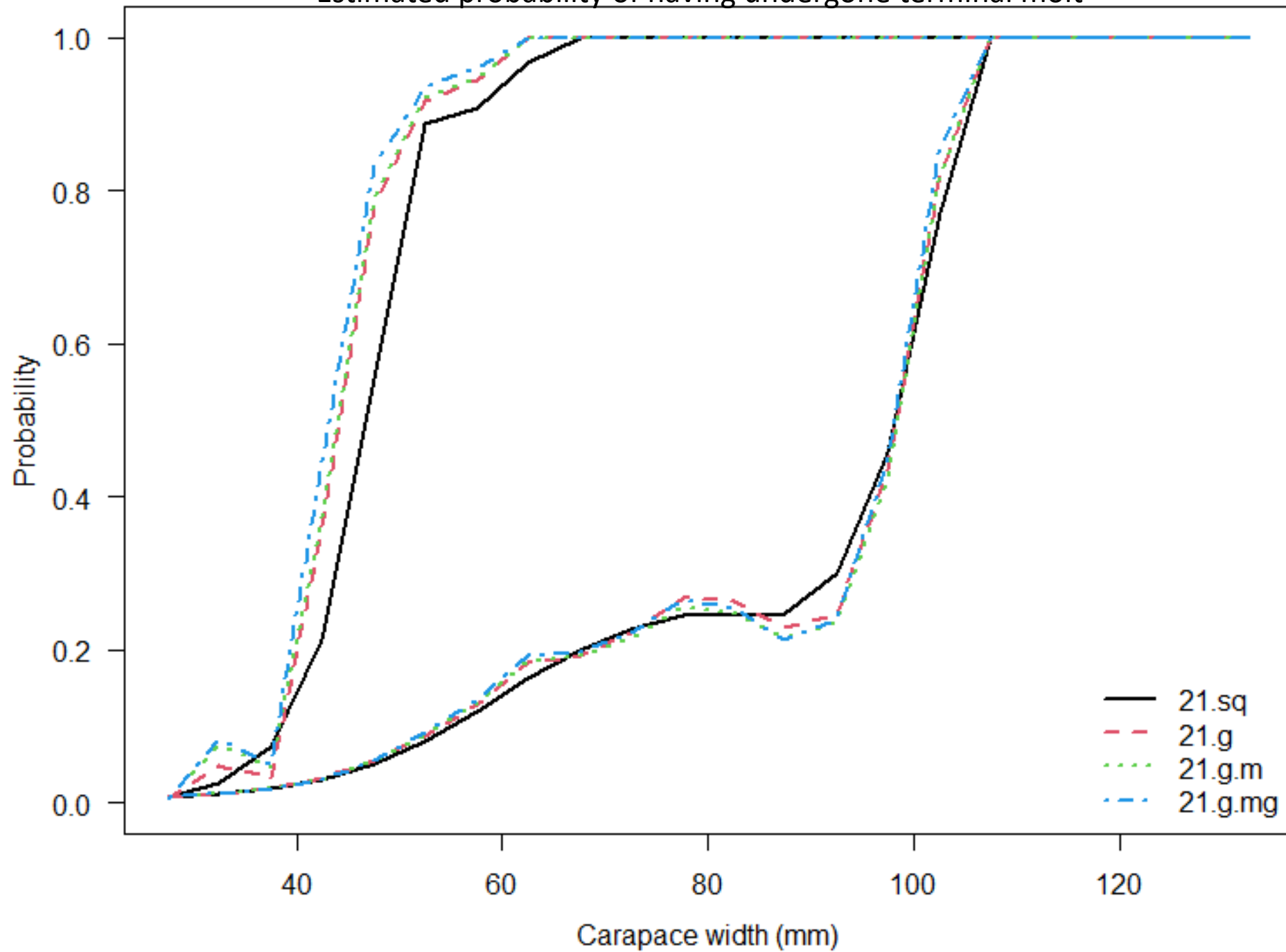
GMACS fits compared to status quo

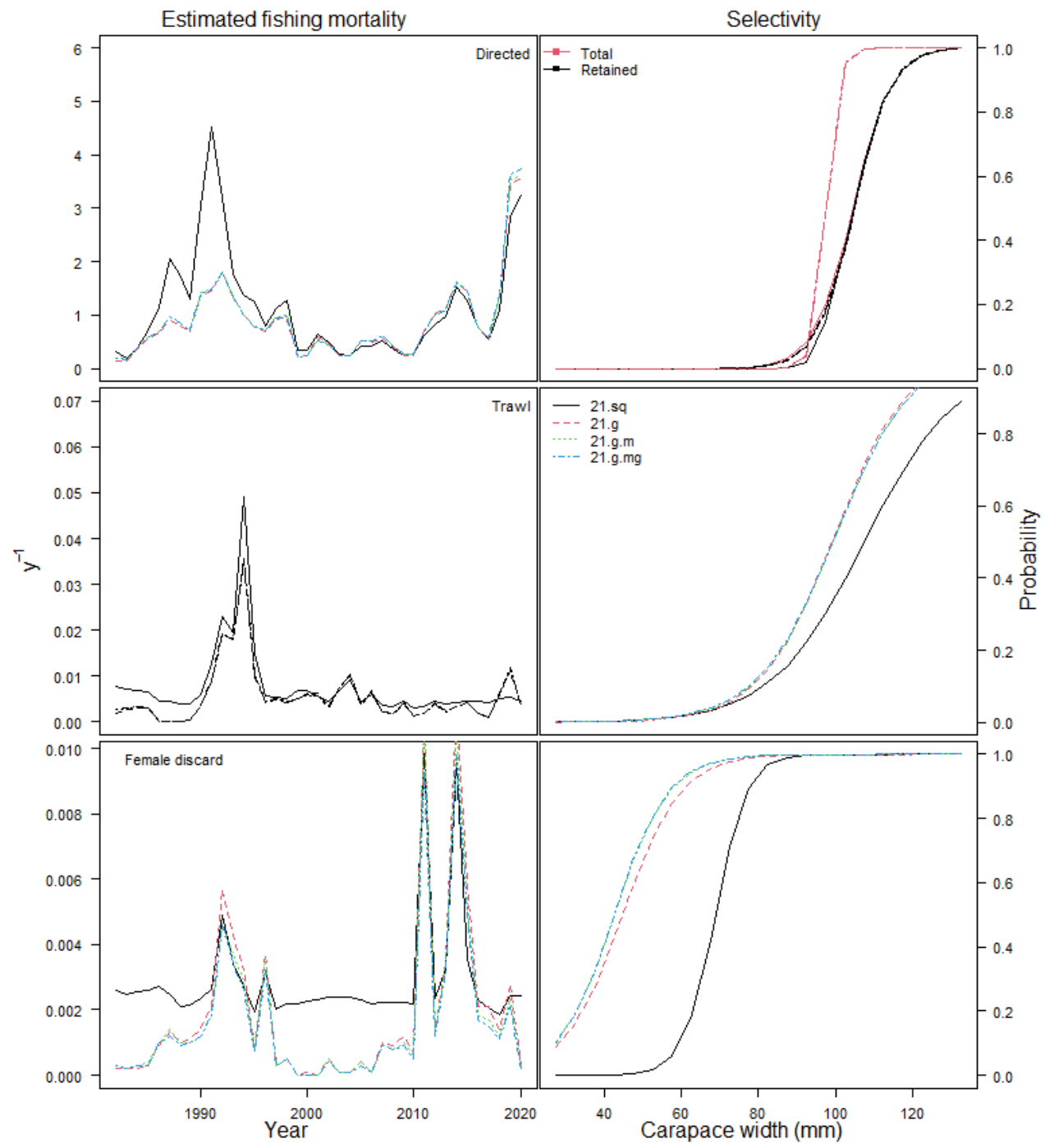
- Mature biomass: better fits in early years, comparable in later
- Growth: slightly worse for GMACS, but it is estimated in the model
- Catches: all but retained catches fit better
- Size comps:
 - Retained catches worse in first two years, same in others
 - Total catches better in last two years, mostly the same in others
 - Trawl just generally poorly fit (needs time-varying)
 - Immature males survey mostly the same, better in final year
 - Immature females survey much better fit
 - Mature males very similar
 - Mature female peaks fit better

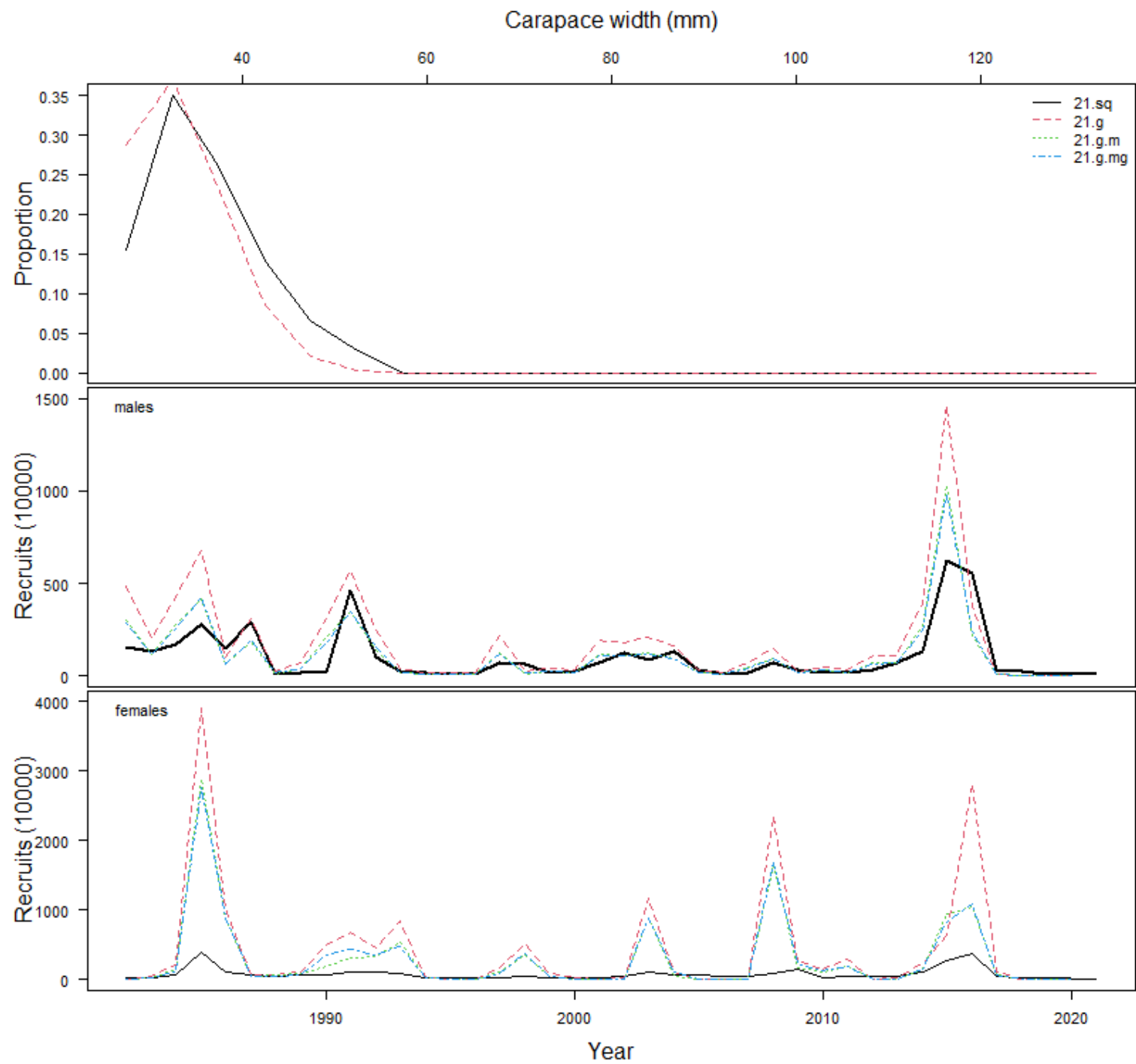




Estimated probability of having undergone terminal molt





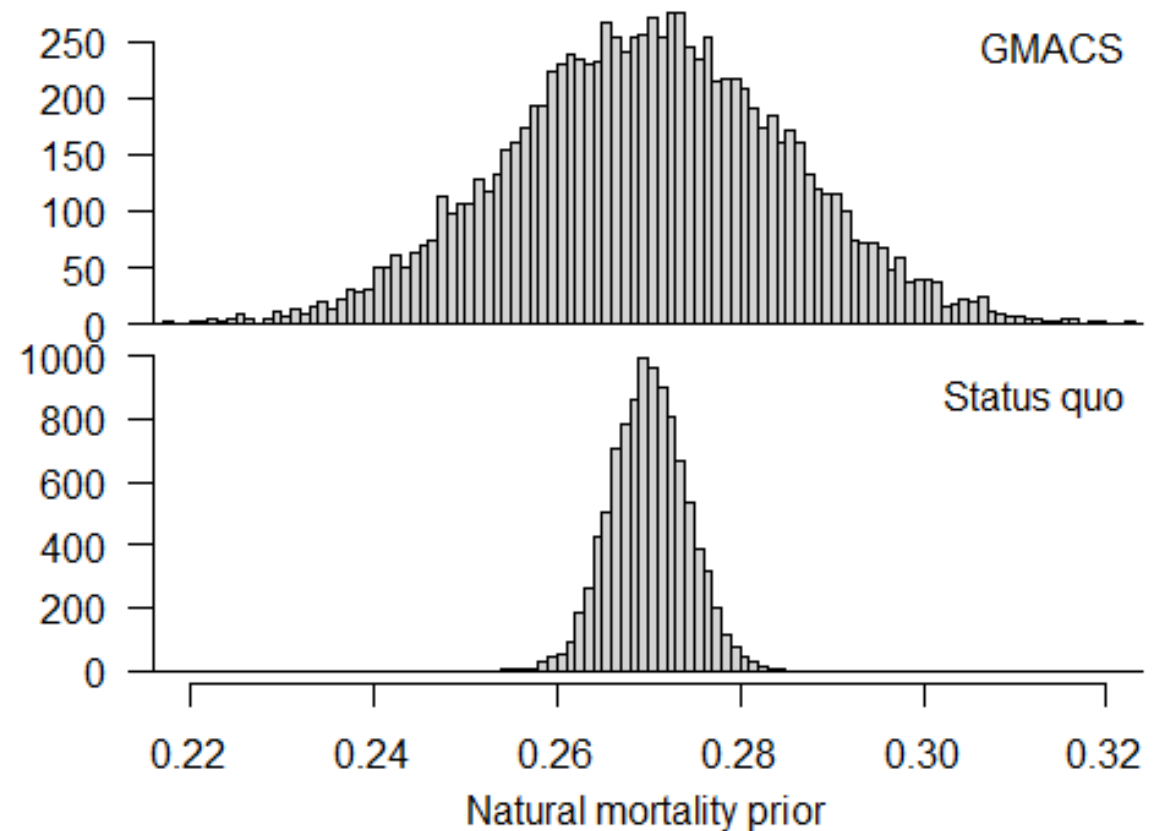


Priors on M

- Status quo:
 - $\text{like_natm} = \text{natm_mult_wght} * \text{square}((\text{Mmult} - 1.0) / \text{natm_mult_var})$
- GMACS:
 - $\text{prior_pdf} = \text{dnorm}(_theta, p1, p2)$

```
gmacs_m <- rnorm(1000, 0.27, 0.0154)
```

```
sq_m <- 0.27 * rnorm(1000, 1, 0.0154)
```



GMACS estimated processes compared to status quo

- MMB more pronounced downward trend
- Much lower female survey catchability; slightly lower male survey catchability. Both more in line with the BSFRF inferred selectivity.
- Higher probability of terminally molted for females; slight differences for males
- Lower fishing mortality in early period, similar in later
- Differences in selectivity as a result of the way fishing mortality is modeled
- Higher recruitment in 2015 for males; higher overall for females
- Higher average natural mortality
- Lower mortality events for immature; larger mortality events for mature

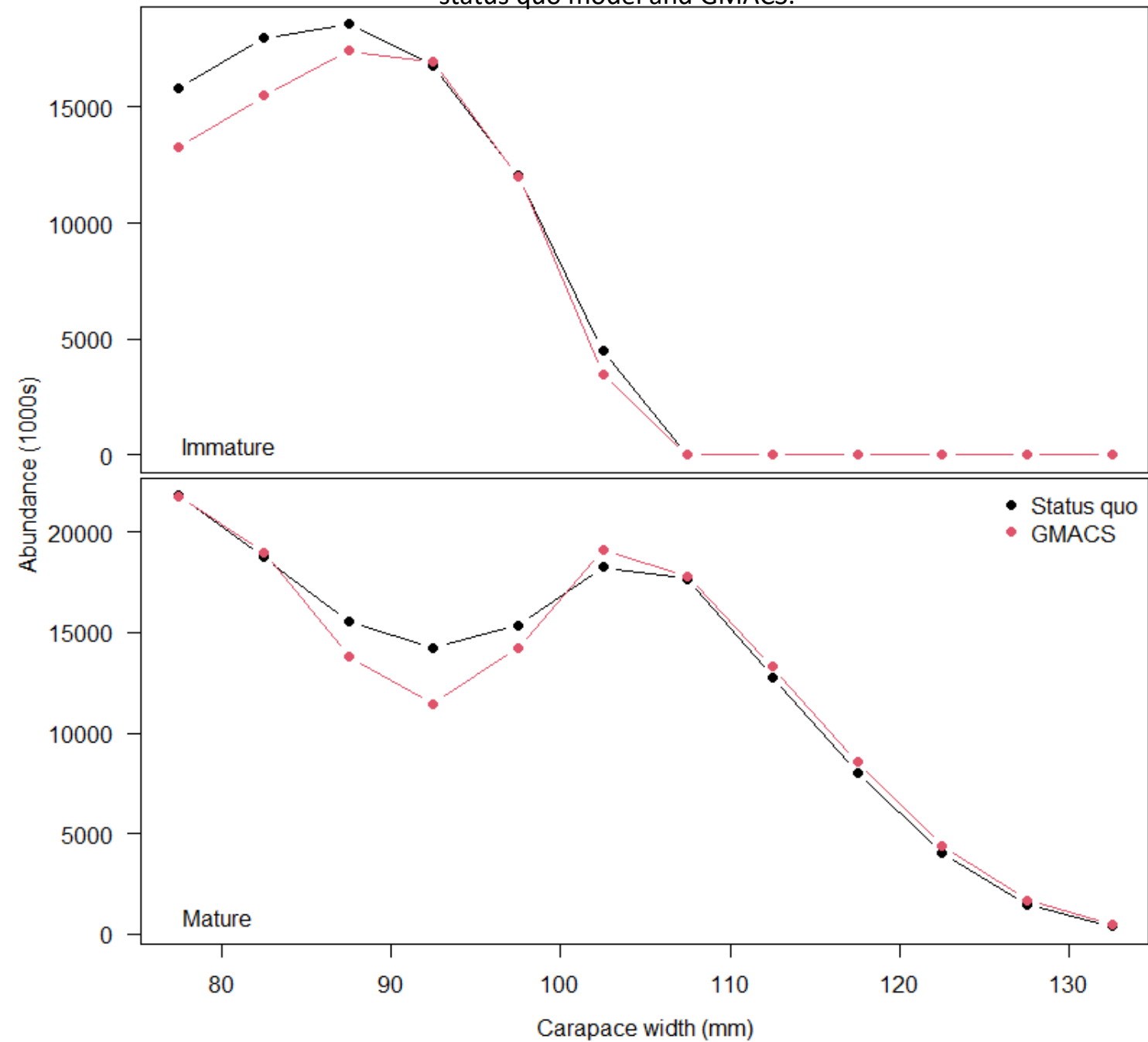
Model	MMB	B35	F35	FOFL	OFL	M	avg_rec
21.sq	26.74	153.42	1.43	0.37	7.5	0.27	106.14
21.g	25.53	135.32	2.31	0.00	0.1	0.36	189.52
21.g.m	23.37	155.94	1.51	0.00	0.1	0.27	119.89
21.g.mg	22.55	155.66	1.52	0.00	0.1	0.27	117.36

Changes in management quantities for each scenario considered. Reported management quantities are derived from maximum likelihood estimates. Reported natural mortality is for mature males and average recruitment is for males.

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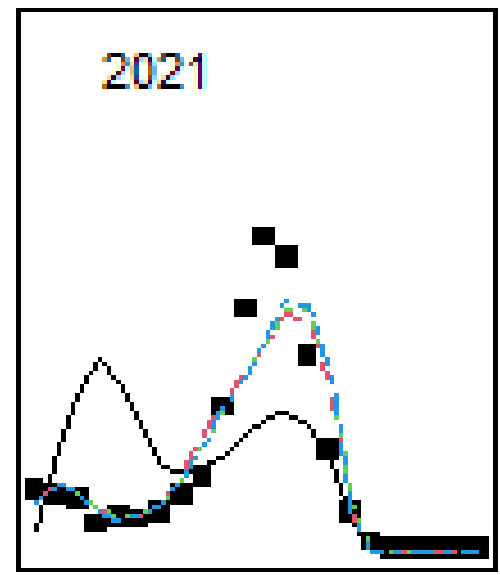
Abundances of immature and mature crab by model in 2021 estimated by the status quo model and GMACS.



Status quo model estimated larger numbers of immature crab poised to molt into commercially preferred size.

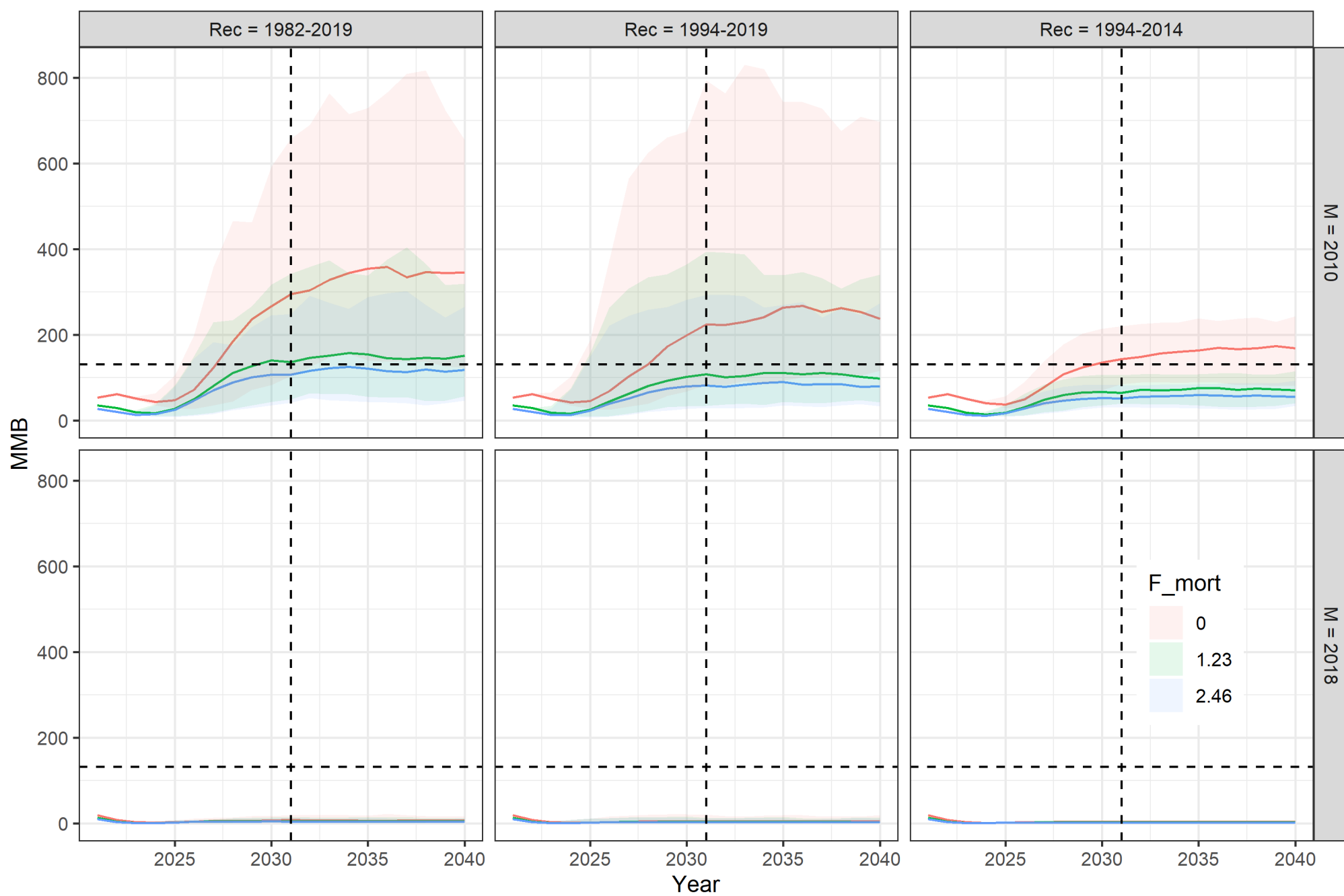
So, when the model was projected forward to the time of the fishery (and ultimately mating to calculate the MMB for comparison to B35%), MMB was higher than in GMACS.

This maintained the population above the threshold for fishery closure.



Rebuilding projections

- Recruitment
 - Status quo: 1982-2019
 - Recent regime: 1994-2019
 - Low recruitment: 1994-201
- Natural mortality
 - Back to average: 0.36 (Mature males; 70% yearly survival)
 - Mortality event on-going: ~2 (Mature males; 13.5% yearly survival)
- Fishing mortality
 - Directed $F = 0$
 - Directed $F = 0.5 F_{35\%}$
 - Directed $F = F_{35\%}$
- All fishing mortality scenarios have bycatch mortality included, but it is generally very small.



T min ranged from 7 years to infinity.

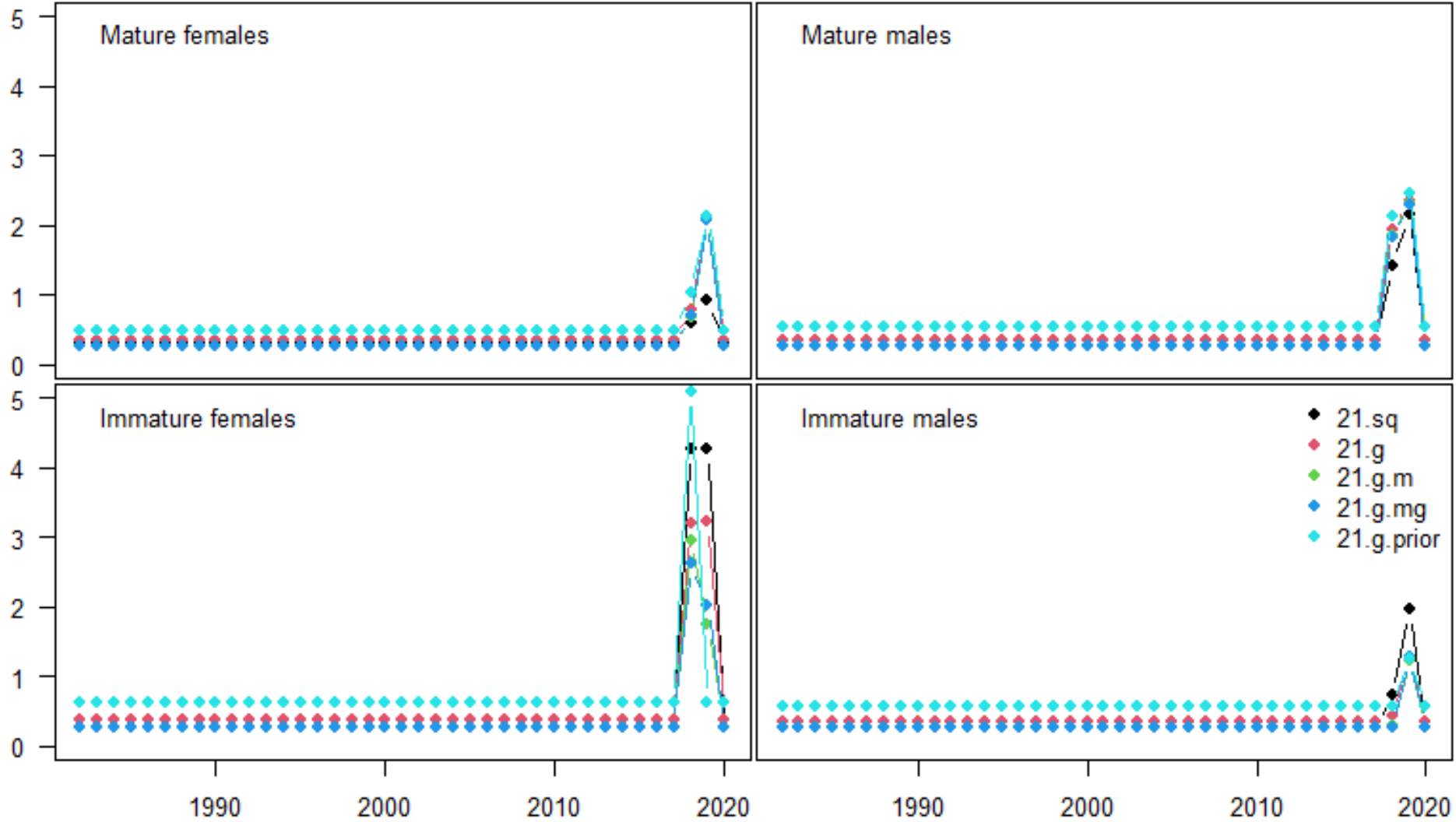
Recommendations

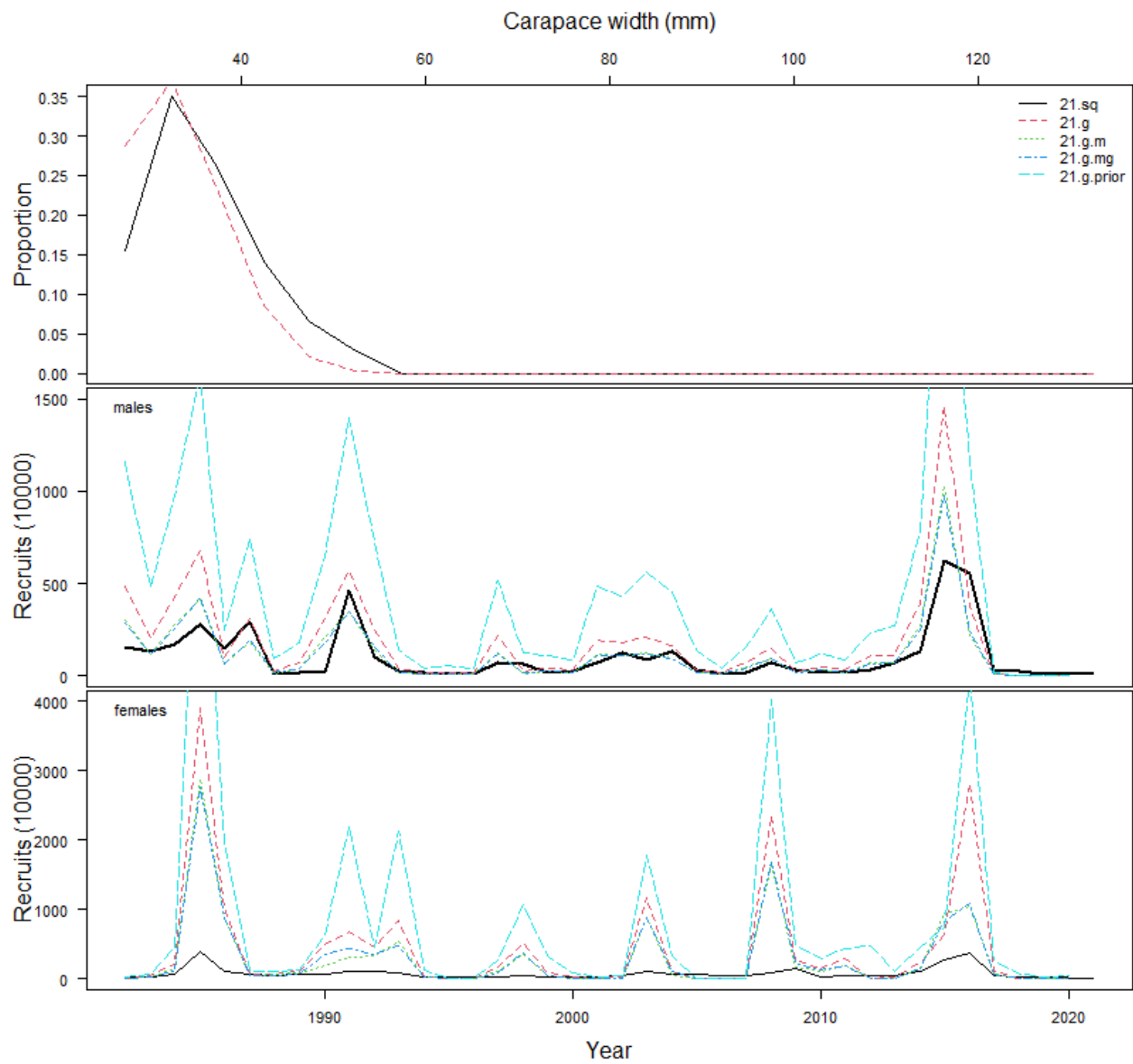
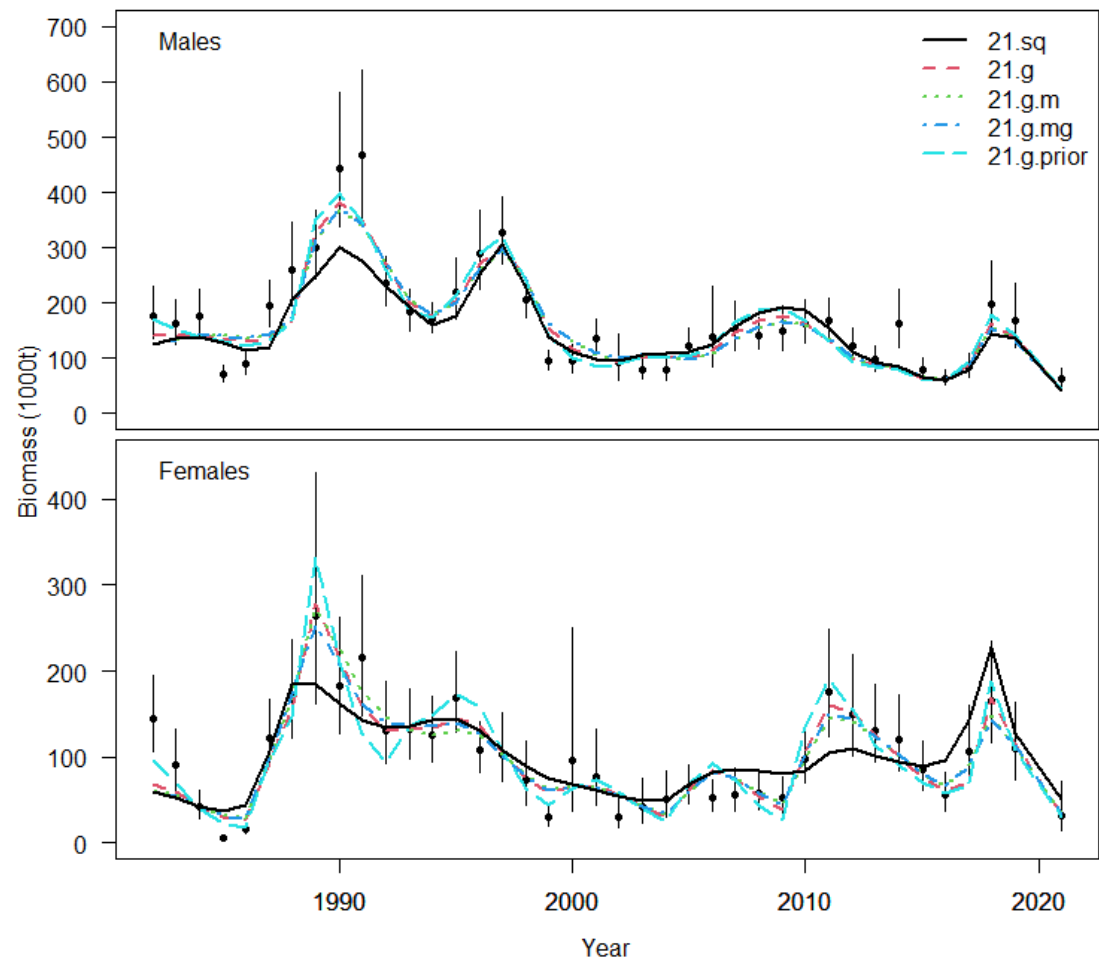
- Use GMACS as is based on:
 - Superior convergence statistics
 - Improved model assumptions
 - Better fits to data sources
 - Improvements in transparency and reproducibility
- Do not pursue further matching exercises
- Spend time working on actual problems instead of trying to match the dynamics of the status quo with GMACS
 - Time-variation in population processes
 - Currency of management and issues with F35%
 - Treatment of maturity and BSFRF data
 - Reference points in a changing environment
 - Spatial issues

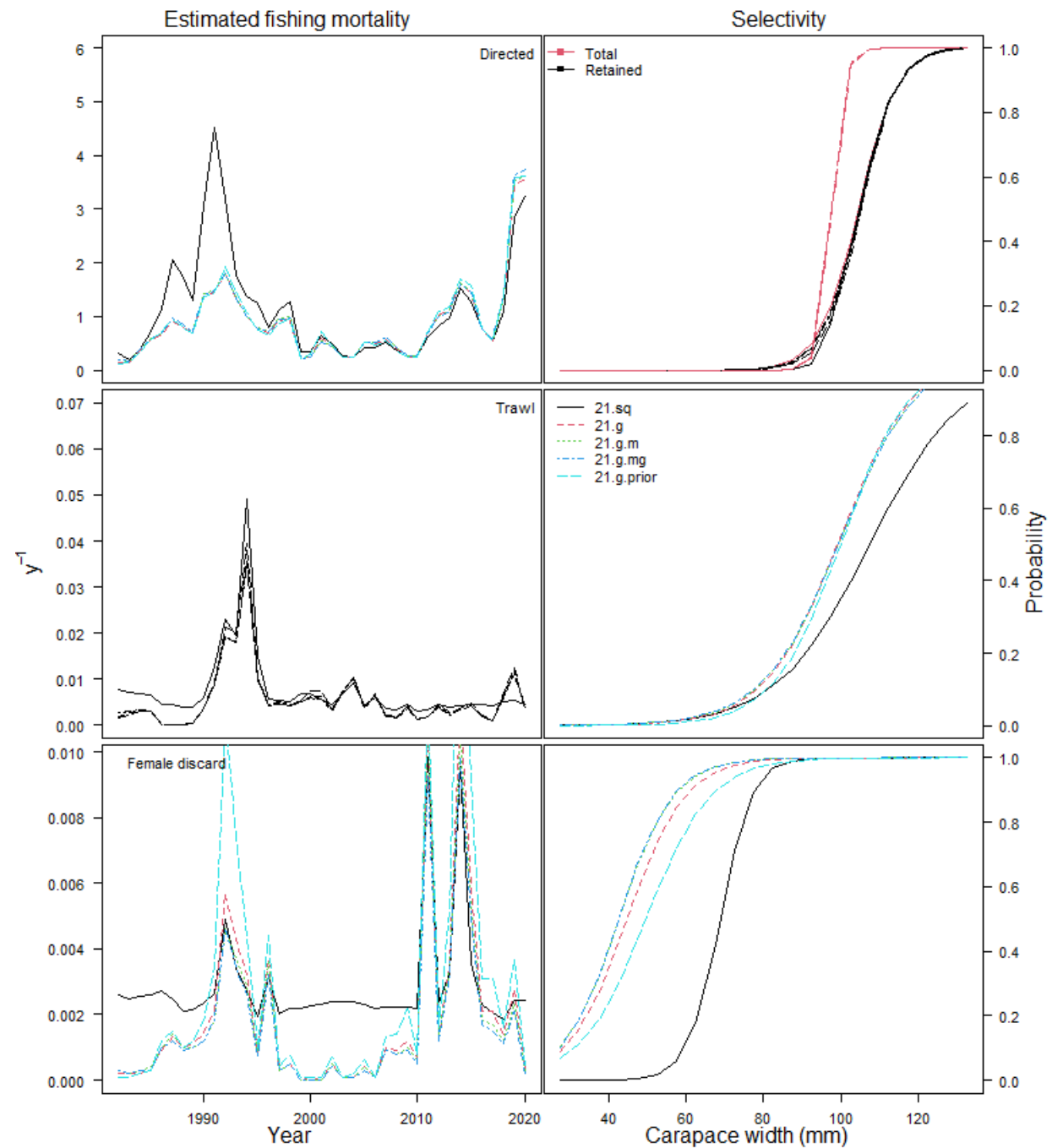
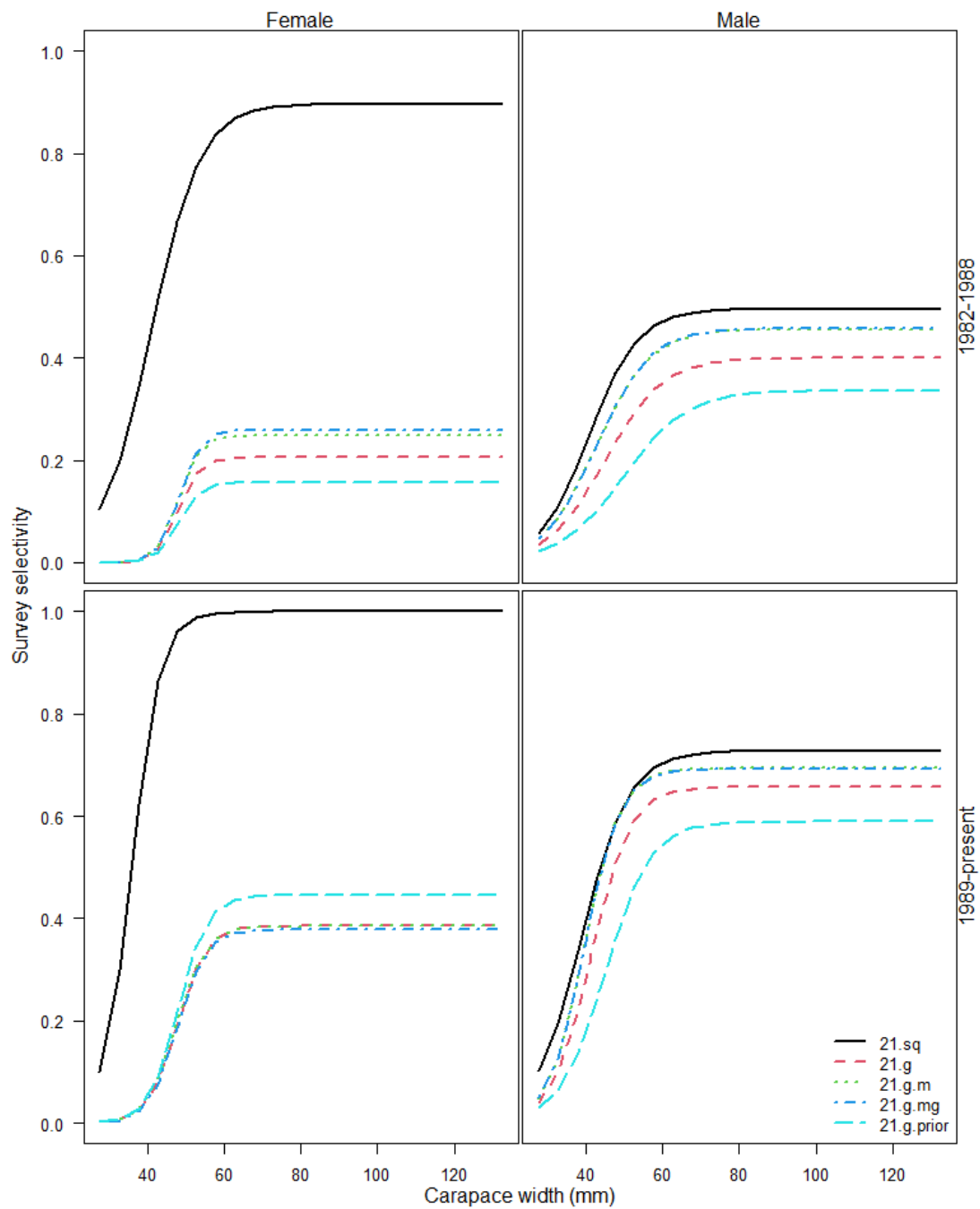
Recommendations

- Models in September:
 - GMACS with current prior on M
 - GMACS with a better defended (and possibly different) prior on M

Change prior on sd for M to 0.5







Model	MMB	B35	F35	FOFL	OFL	M	avg_rec
21.sq	26.74	153.42	1.43	0.37	7.5	0.27	106.14
21.g	25.53	135.32	2.31	0.00	0.1	0.36	189.52
21.g.m	23.37	155.94	1.51	0.00	0.1	0.27	119.89
21.g.mg	22.55	155.66	1.52	0.00	0.1	0.27	117.36
21.g.prior	28.61	114.80	5.86	0.00	0.1	0.54	453.46