A comparison of the status quo stock assessment for eastern Bering Sea snow crab to an assessment developed in GMACS

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Summary

This document presents a completed comparison of the status quo assessment of snow crab in the eastern Bering Sea to the General Model for Assessing Crustacean Stocks (GMACS). The ability of GMACS to replicate the population dynamics of the status quo assessment and a comparison of fits to data sources were presented in May 2020. The CPT judged the replication of the dynamics and the fits to the data by GMACS were sufficient to move forward. The next step in the process was to ensure reference points and calculations of the overfishing level (OFL) are performed appropriately given the new capabilities of GMACS.

This document briefly describes the changes made to the GMACS source code to achieve this comparison and compares the derived quantities used in management produced from the status quo assessment to the same quantities from GMACS. Figures of fits to the data and estimated population processes are presented in this document to facilitate understanding of the differences in calculated management quantities like reference points and the OFL.

There are many differences between GMACS and the status quo model, some of the more fundamental include:

- GMACS currently only uses linear growth models as functional forms (there is a 'free parameter' option too), whereas the status quo model uses a 'kinked' growth curve (only for females now)
- Fishing mortality is appropriately accounted for in GMACS (see May 2020 CPT document and Tanner crab assessment for discussion)
- CVs are used to weight catch sources rather than weights that are not immediately comparable among data sources
- GMACS estimates a single yearly recruitment, then a parameter that divides that recruitment between the sexes. The status quo assessment estimates separate recruitment deviations for sexes.
- GMACS estimates for freely estimated availability curves for both fleets and years of the BSFRF survey selectivity experiment. The status quo assessment uses logistic availability curves for some year/sex/gear combinations.

Changes required to the GMACS source code to produce reference points and the OFL included altering the many projection functions to reflect a terminal molt and a maturity-based natural mortality. Below, the text describing the changes in GMACS needed to fit the snow crab data is retained from the May 2020 CPT document to provide context for the comparison of reference points.

Based on the outcome of this comparison, GMACS appears to appropriately calculate reference points and management quantities. There are differences between the reference points and management quantities produced by the status quo assessment and GMACS, but these differences are expected based on the differences in estimates of parameters associated with processes like recruitment and natural mortality. Given the improvements in GMACS model structure and following the need to standardize assessment methodologies across crab stocks in the Bering Sea, the author recommends adoption of the GMACS platform for use in the assessment and management of snow crab. Data inputs, model structure, and assumptions about population processes should continue to be refined within the GMACS assessment for snow crab, but adopting GMACS for snow crab will ensure that whatever improvements are made can be shared in other stock assessments.

Introduction

The snow crab fishery in the eastern Bering Sea is currently assessed using an integrated size-structured model (referred to within this document as the 'status quo' model). This model was developed following Fournier and Archibald's (1982) methods, with many similarities to Methot (1990), and was implemented using automatic differentiation software developed as a set of libraries under C++ (ADModel Builder). The snow crab assessment is bespoke code aimed at capturing the specific dynamics of the snow crab fishery.

The status quo snow crab population dynamics model tracks the number of crab of sex s, shell condition v, maturity state m, during year y at length l, $N_{s,v,m,y,l}$. A terminal molt is modeled in which crab move from an immature to a mature state, after which no further molting occurs. The mid-points of the size bins tracked in the model span from 27.5 to 132.5mm carapace width, with 5 mm size classes. Parameters estimated within the assessment include those associated with the population processes recruitment, growth, natural mortality, fishing mortality, selectivity (fishery and survey), catchability, and maturity. Weight at length, discard mortality, bycatch mortality, and parameters associated with the variance in growth and proportion of recruitment allocated to size bin are estimated outside of the model or specified. See appendix A for a description of the population dynamics.

In the past, each assessment author for crab stocks in the Bering Sea developed an assessment model to provide management advice, and this has lead to some heterogeneity among assessment methodologies. Recently the General Model for Assessing Crustacean Stocks (GMACS) was developed to promote consistency and comparability among assessments. Several crab assessments have been developed in GMACS and subsequently approved for use in management by the Crab Plan Team. However, GMACS was developed with king crab-like life histories in mind and cannot accommodate species with a life history including a terminal molt.

This document describes the process by which GMACS was modified to accommodate a terminally molting life history and presents a comparison of the model fits and calculated management quantities between the status quo assessment and GMACS.

Methods

Comparing fits to data sources and estimated population processes

Several modifications were needed in the GMACS code to estimate the parameters of the model, including:

- Altering indexing and mirroring of selectivity. Previously, when mirroring was specified, mirrored selectivities were not being counted in an index serving as a pointer to selectivity patterns. This indexing issue was fixed. The order of mirroring and 'embedded' selectivities also had to be reversed, otherwise mirroring overwrote the 'embedded' selectivity.
- Smoothness penalties were added for free selectivity, initial numbers at length, and free molting probability options to improve model stability and 'emphasis factors' were added to control the weights given to these penalties.
- Priors were added for multipliers on immature natural mortality when estimated.
- Calculation of the size composition data was altered so it is now possible to fit to mature length compositions when a terminal molt is specified.
- Calculation of indices of abundance/biomass was altered so that maturity state was represented correctly under a terminal molt.
- Calculation of spawning biomass was amended to correctly capture maturity under a terminal molt.

See appendix B for a description of the GMACS population dynamics model. The GMACS model presented here was not constrained to attempt to reproduce the dynamics of the status quo model. Parameters for processes like growth, probabilities of molting, selectivities and other key parameter determining biological

and fishery-related processes were estimated rather than specified. The comparison of the fits to the data sources will be necessarily qualitative here, as the true underlying population dynamics are unknown and the weighting structures of the models have some dissimilarities. The goal of this document is to identify any data sources that appear to be poorly fit, check the credibility of the estimated population processes, and assess the credibility of the resulting quantities used in management, paying particular attention to how changes in fits and estimates influenced the outcome.

Results

Comparisons of model fits

Survey biomass data

Fits to the survey mature male biomass (MMB) differed somewhat between the status quo model and GMACS, particularly in the transition between survey selectivity eras in the early 1990s, during which GMACS was able to better fit the large biomasses by estimating a smaller survey q during 1982-1989 (Figure 1). GMACS also fit portions of the female mature biomass better than the status quo model, partially due to more variable estimated recruitment (Figure 2). The discrepancy in the last two years of survey data continues to present problems for both models because they do not allow catchability or natural mortality to vary over time, so no model fit the data well.

Growth data

A 'kinked' growth curve (such as that used by the status quo assessment) was not coded into GMACS because the assumptions of a kinked growth curve are not met by the growth increment data available. The central assumption is that a change in the growth increment should exist as animals molt to maturity to reflect the additional energy devoted to reproduction. However, all of the growth increment data available are for immature animals. Further, the molt to maturity takes place over a range of sizes, so a single change point is not biologically representative of the assumed underlying process. In light of these observations, linear growth curves have been attempted in the past with the status quo model, but these models did not converge. Encouragingly, the GMACS model converged with a linear growth curve (Figure 3).

Catch data

Retained catch data were fit by both models well, but GMACS fit the data slightly worse (Figure 4). Female and male discard data were fit much better by GMACS, particularly because of smaller CVs that are likely more reflective of reality than the 'weighting factors' used in the status quo code. Fits to the trawl data were similar between models, but again, GMACS fit the data somewhat better.

Size composition data

Total and retained catch size composition were very similarly fit by both GMACS and the status quo model, however, GMACS generally predicted larger numbers of animals in the largest size bins for the first few years (Figure 5). This phenomenon disappeared in later years with fits to the data that were indiscernible between models. Total catch size composition data were similarly well fit (Figure 6). Trawl size composition data fit similarly between the models, with the same trend of higher estimates or larger crab from GMACS (Figure 7).

Fits to size composition data for the BSFRF survey selectivity experiments produced some notable runs of positive and negative residuals for males in particular (Figure 8). GMACS fit the data in 2010 (which are most important for informing catchability) better than the status quo assessment, but which model best

fit the 2009 data was less clear. Notable differences in fits to NMFS survey size composition data existed (Figure 9, Figure 10, Figure 11 & Figure 12). GMACS fit the immature female size composition data better in many years (e.g. 1984, 1986, 1996, 1997, 2007); GMACS fit the immature males more similarly to the status quo model than the immature females. Fits to mature male size composition data were also very similar between models and the few differences seemed to favor GMACS (e.g. 1984, 1990, 2017-18). Differences between models for fits to mature female size composition data were the smallest for survey size composition data.

Comparison of estimated population processes and derived quantities

Some variation existed among estimated population processes and derived quantities. Estimated MMB at the time of mating varied between models, with GMACS predicting lower MMB in the past two decades than the status quo model (Figure 13). In recent years, the estimates of MMB were very similar between models. Both models estimated lower catchability in era 1 (1982-1988) relative to era 2 (1989-present). The shapes of the NMFS selectivity curves were similar among all models; the largest changes were seen in the catchability coefficient (Figure 14). GMACS estimated a higher catchability coefficient than the status quo model during selectivity era 2, which contributed to the differences in scale of in estimated MMB between the models.

Predicted availability curves for the BSFRF experimental surveys were similar across assessments in years with similar configurations (Figure 15). The status quo assessment historically used a logistic curve for the availability for females in 2009, but this is likely overly restrictive. Both implementations of GMACS estimated a vector of availabilities for both years and sexes of BSFRF data.

In general, the shape of the estimated curve representing the probability of maturing for both sexes were similar, but the magnitude of the probabilities varied, most strongly for females (Figure 16). The GMACS-estimated probability of maturing at smaller sizes was consistently higher for females and this is likely related to the change from a kinked growth curve to a linear growth model. The 'hump' at 32.5 mm carapace width for females is possibly related to the specified curve that determines what fraction of incoming recruitment is placed in which length bin, which has a peak at the same spot as the probability of maturing.

Estimated fishing mortality was very similar between models starting in survey era 2 (post-1988), save the last several years, which were higher for GMACS (Figure 17). GMACS estimated fishing mortality was lower than the status quo during survey era 1. This difference is a result of differences in estimated MMB in the early years of the fishery. Estimated fishery selectivity was dissimilar between models, which is related to how selectivity and fishing mortality are treated in the code (discussed in the May 2020 snow crab document). GMACS estimates of female discard mortality were lower than the status quo, but, when balanced with changes in estimated selectivity, the estimated catches were similar to the status quo (Figure 4).

Patterns in recruitment by sex were similar for both models, but GMACS was more variable than the status quo estimates (Figure 2). Part of this variation likely results from the application of a smoothness penalty to the status quo recruitment deviations, resulting in a smoother time series of recruitment. In general, a period of high recruitment was estimated in which 2 or 3 large male cohorts passed through the population during the 1980s and into the early 1990s. Following that, a period of low recruitment persisted from the early 1990s to 2013. All models indicated a large (relative to the past) recruitment to the survey gear occurred around 2013 for males. Peaks in female recruitment were roughly coincident across models, but the magnitudes could be mismatched. Recruitment entering the model was placed primarily in the first three size bins, the parameters determining the process were fixed in both models.

Estimated natural mortality from GMACS for immature crab was higher than the status quo, in spite of identical priors (Figure 18). Estimated immature natural mortality was higher than mature natural mortality in GMACS, which was not seen in the status quo model. The relationship between immature and mature natural mortality produced using GMACS is more consistent with a 'U-shaped' natural mortality curve with respect to size/age that is posited to be a better reflection of exposure to predation at smaller sizes.

Reference points

In spite of changes in the estimates of parameters determining biological processes, the calculated reference points and associated management quantities were fairly similar (Table 1). Although GMACS fit the point estimate of the terminal year of survey MMB more closely than the status quo model (and was higher than the status quo estimate), the GMACS estimate of MMB at the time of mating was smaller than the status quo. This is a result of a higher estimated catchability coefficient from GMACS that scaled the population size down. Calculated $F_{35\%}$ was higher in GMACS than the status quo assessment, driven by changes in the GMACS estimates of natural mortality, growth, and fishery selectivity relative to the status quo estimates. $B_{35\%}$ was lower in GMACS than the status quo assessment, which is also related to changes in estimated natural mortality and growth.

The status of the stock was similar regardless of the model considered: over-fishing is not currently occurring and the stock is not overfished (Figure 19). The sum of changes in estimated population processes resulted in roughly a 10% change in the calculated OFL (GMACS 55.34 kt vs. status quo 51.63 kt).

Recommendations and future work

The GMACS fits to the data were as good or better than the status quo model in most instances. The over-estimation of the retained size length composition data in the initial model years by GMACS is an exception that should be further examined, but it ultimately does not appear to influence the model appreciably in more recent years. The GMACS estimates of population processes were at least as credible as the status quo model, given what we know about snow crab biology and the fishery (perhaps more so for processes like growth). The resulting changes in reference points and other quantities used in management were readily explained by the observed changes in estimates of parameters determining population processes. Given the improvements in GMACS model structure and following the need to standardize assessment methodologies across platforms, the author recommends adoption of the GMACS platform for the use of assessment and management of snow crab.

Although GMACS appears to be a satisfactory platform with which to assess eastern Bering Sea snow crab, more work exists to address data inputs, model structure, and assumptions about population processes. Future work for snow crab in particular will include reexamining catchability and the functional form of selectivity of the NMFS survey gear. The estimated change in catchability between survey eras is rather large and it is not clear if the changes in survey gear and area surveyed are sufficient to explain these changes. Based on the BSFRF survey selectivities, it is possible that survey selectivity is not logistic, as assumed, and perhaps a more flexible functional form would incorporate the BSFRF data more effectively into the model. Time varying catchability is also a strong potential culprit behind some years of poorly fit survey data (e.g. 2014).

Further work was expected to be accomplished towards organization of the GMACS source code on github and applications to other stocks, but the pandemic has slowed the process. Luckily, funding for a postdoc has been approved and the search will begin mid-September. Some of the duties of this position include:

- Modified GMACS assessment code to accommodate needed variation in life history and population processes
- Unit test, documentation, and a user's manual
- R package for visualization of GMACS output
- Generalized rmarkdown templates for assessment documents
- Peer-reviewed manuscript describing GMACS
- Presentation to the Crab Plan Team
- As time allows, progress on converting other Alaskan crab assessments (e.g. Tanner crab) to GMACS

With this additional effort, GMACS version 2.0 will soon be publicly available and ready for more new users.

Appendix A: Status quo assessment model population dynamics

Numbers of sex s of shell condition v and maturity state m at length l in the initial year of the assessment, $N_{s,v,m,y=1,l}$, were calculated from an estimated vector of numbers at length l by sex s and maturity state m for males, $\lambda_{s,m,l}$ and numbers at length l by sex s and shell condition v for females (i.e. 2 vectors for each sex were estimated). Estimated vectors of initial numbers at length by maturity for females were calculated by splitting the estimated vectors at length by the observed proportion mature in the first year of the survey.

$$N_{s,v,m,y=1,l} = \begin{cases} \Omega_{s,l}^{obs}\lambda_{s,1,l} & \text{if v = new; m = mat, s = fem} \\ 1 - \Omega_{s,l}^{obs}\lambda_{s,1,l} & \text{if v = new; m = imat, s = fem} \\ \lambda_{s,2,l} & \text{if v = old; m = mat, s = fem} \\ 0 & \text{if v = old; m = imat} \end{cases} \tag{1}$$

Initial numbers at length for males were all assumed to be new shell.

$$N_{s,v,m,y=1,l} = \begin{cases} \lambda_{s,1,l} & \text{if v = new; m = mat, s = male} \\ \lambda_{s,2,l} & \text{if v = new; m = imat, s = male} \\ 0 & \text{if v = old; m = mat, s = male} \\ 0 & \text{if v = old; m = imat, s = male} \end{cases} \tag{2}$$

The dynamics after the initial year were described by:

$$N_{s,v,m,y+1,l} = \begin{cases} \Omega_{s,l}\kappa_{s,l'}Q_{s,imat,y,l'}X_{s,l',l} & \text{if v = new; m = mat} \\ 1 - \Omega_{s,l}\kappa_{s,l'}Q_{s,imat,y,l'}X_{s,l',l} + Rec_y^{\epsilon}Pr_l & \text{if v = new; m = imat} \\ Q_{s,mat,y,l'} & \text{if v = old; m = mat} \\ (1 - \kappa_{s,l'})Q_{s,imat,y,l'} & \text{if v = old; m = imat} \end{cases} \tag{3}$$

Where $\Omega_{s,l}$ was the probability of maturing at length l for sex s (a freely estimated vector for both males and females constrained by penalties on smoothness), $\kappa_{s,l'}$ was the probability of molting for an immature crab of sex s at length l' (set to 1 for all immature crab), and $X_{s,l,l'}$ was the size transition matrix describing the probability of transitioning from size l' to size l for sex s. $Q_{s,m,y,l'}$ was the number of crab of sex s, maturity state m, and length l' surviving natural and fishing mortality during year y:

$$Q_{s,m,y,l} = \sum_{v} N_{s,v,m,y,l}e^{Z_{s,v,m,y,l}} \tag{4}$$

Where $N_{s,v,m,y,l}$ represented the numbers, N, of sex s during year y of shell condition v and maturity state m at length l. $Z_{s,v,m,y,l}$ represented the total mortality experienced by the population and consisted of the sum of instantaneous rates of natural mortality by sex and maturity state, $M_{s,m}$, and fishing mortality, $F_{s,f,y,l}$ from each fishery. Each fishing mortality was subject to selectivity by length l, which varied between sexes s and fisheries f (and by year y if specified) . $M_{s,m}$ was specified in the model and a multiplier $\gamma_{natM,m}$ was estimated subject to constraints (see this formulation effectively specified a mean and standard deviation for a prior distribution for M).

$$Z_{s,v,m,y,l} = \gamma_{natM,m}M_{s,m} + \sum_f S_{s,f,y,l}F_{s,f,y,l} \tag{5}$$

Selectivities in the directed and bycatch fisheries were estimated logistic functions of size. Different selectivity parameters were estimated for females and males in the directed fisheries ($S_{fem,dir,l}$ and $S_{male,dir,l}$, respectively), a single selectivity for both sexes was estimated for bycatch in the groundfish trawl fishery ($S_{trawl,l}$), and a retention selectivity was estimated for the directed fishery for males ($R_{dir,l}$; all females were discarded).

$$S_{male,dir,l} = \frac{1}{1 + e^{-S_{slope,m,d}(L_l - S_{50,m,d})}}) \tag{6}$$

$$S_{fem,dir,l} = \frac{1}{1 + e^{-S_{slope,f,d}(L_l - S_{50,f,d})}}) \tag{7}$$

$$S_{trawl,l} = \frac{1}{1 + e^{-S_{slope,t}(L_l - S_{50,t})}}) \tag{8}$$

$$R_{dir,l} = \frac{1}{1 + e^{-S_{slope,m,d}(L_l - S_{50,m,d})}}) \tag{9}$$

Where $S_{slope,s,f}$ was the slope of the logistic curve for sex s in fishery f and $S_{50,s,f}$ was the length at 50% selection for sex s in fishery f. Catches for all fisheries were modeled as pulse fisheries in which all catch was removed instantaneously (i.e. no natural mortality occurred during the fishery). Catch in fishery f during year y was calculated as the fraction of the total fishing mortality, $F_{s,f,y,l}$, applied to a given sex s in a fishery f times the biomass removed by all fisheries for that sex.

$$C_{male,dir,y} = \sum_l \sum_v \sum_m w_{male,l} \frac{R_l F_{male,dir,y,l}}{F_{male,dir,y,l} + F_{trawl,y,l}} N_{male,v,m,y,l} e^{-\delta_y M_{s,m}} \left(1 - e^{-(F_{male,dir,y,l} + F_{trawl,y,l})}\right) \tag{10}$$

$$C_{male,tot,y} = \sum_l \sum_v \sum_m w_{male,l} \frac{F_{male,dir,y,l}}{F_{male,dir,y,l} + F_{trawl,y,l}} N_{male,v,m,y,l} e^{-\delta_y M_{s,m}} \left(1 - e^{-(F_{male,dir,y,l} + F_{trawl,y,l})}\right) \tag{11}$$

$$C_{fem,dir,y} = \sum_l \sum_v \sum_m w_{fem,l} \frac{F_{fem,dir,y,l}}{F_{fem,dir,y,l} + F_{trawl,y,l}} N_{fem,v,m,y,l} e^{-\delta_y M_{s,m}} \left(1 - e^{-(F_{fem,dir,y,l} + F_{trawl,y,l})}\right) \tag{12}$$

$$C_{m+f,trawl,y} = \sum_s \sum_l \sum_v \sum_m w_{s,l} N_{s,v,m,y,l} e^{-\delta_y M_{s,m}} \left(1 - e^{-(F_{trawl,y,l})}\right) \tag{13}$$

Where δ_y was the mid point of the fishery (all fisheries were assumed to occur concurrently and the midpoint was based on the directed fishery, which accounts for the vast majority of the fishing mortality) and $w_{s,l}$ was the weight at length l for sex s. Trawl data and discard data were entered into the model with an assumed mortality of 80% and 30%, respectively. Fully-selected fishing mortality parameters for fishery f were estimated as a logged average over a given time period (F_{avg}^{log}) with yearly deviations around that mean ($F_{dev,y}^{log}$).

$$F_{f,y} = e^{(F_{avg,f}^{log} + F_{dev,f,y}^{log})} \tag{14}$$

Selectivity for the survey was estimated for 2 eras in the base model: 1982-1988 and 1989-present. Selectivity was assumed to be logistic and separate parameters representing the length at which selection probability

equal 50% and 95% ($s_{50,s,e}$ and $s_{95,s,e}$, respectively) were estimated for males and females in the third era (1989-present). Separate catchability coefficients ($q_{s,e}$) were estimated for males and females in all eras.

$$S_{surv,s,l,e} = \frac{q_{s,e}}{1 + e^{-log(19)\frac{L_l - s50,s,e}{s95,s,e - s50,s,e}})}$$ (15)

Survey selectivity was informed by experimental surveys during the years 2009 and 2010. A portion of the NMFS summer survey tows were accompanied by an industry vessel using nephrops trawls with an assumed selectivity of 1 for all size classes. To represent the proportion of the population covered by the experiment, a vector was freely estimated for males, S_y^{free} (subject to a scaling parameter), and a logistic curve was estimated for females.

$$S_{ind,s,l,y} = \begin{cases} \frac{q_{ind,s,y}}{1 + e^{-log(19)\frac{L_l - s50,s,y}{s95,s,y - s50,s,y}})} & \text{if s = female} \\ q_{ind,s,y}S_y^{free} & \text{if s = male} \end{cases}$$ (16)

Based on this logic, after identifying the fraction of the crab at length covered by the experimental surveys, the length frequencies of the NMFS data collected simultaneously with the experimental trawls can be calculated by multiplying the numbers at length 'available' to the experimental trawls by the overall survey selectivity, $S_{surv,s,l,y}$. The predicted numbers at length for the NMFS and industry data from the selectivity experiment were calculated by multiplying the respective selectivities by the survey numbers at length.

$$S_{nmfs,s,l,y} = S_{ind,s,l,y}S_{surv,s,l,y}$$ (17)

Mature male and female biomass (MMB and FMB, respectively) were fitted in the objective function and were the product of mature numbers at length during year y and the weight at length, $w_{s,l}$:

$$MMB_y = \sum_{l,v} w_{male,l}N_{male,v,mat,y,l}$$ (18)

$$FMB_y = \sum_{l,v} w_{fem,l}N_{fem,v,mat,y,l}$$ (19)

$$w_{s,l} = \alpha_{wt,s}L_l^{\beta_{wt,s}}$$ (20)

Mature biomass can be calculated for different time through out the year, in which case the numbers at length are decremented by the estimated natural mortality. Parameters $\alpha_{wt,s}$ and $\beta_{wt,s}$ were estimated outside of the assessment model and specified in the control file.

Molting and growth occur before the survey. Immature crab were assumed to molt every year with an estimated probability of molting to maturity based on length l (in all the scenarios presented here, the probability of molting was 1 for all immature animals). For crab that do molt, the growth increment within the size-transition matrix, $X_{s,l,l'}$, was based on a piece-wise linear relationship between predicted pre- and post-molt length, ($\hat{L}_{s,l}^{pred}$ and $\hat{L}_{s,l}^{post}$, respectively) and the variability around that relationship was characterized by a discretized and renormalized gamma function, $Y_{s,l,l'}$.

$$X_{s,l,l'} = \frac{Y_{s,l,l'}}{\sum_{l'} Y_{s,l,l'}}$$ (21)

$$Y_{s,l,l'} = (\Delta_{l,l'})^{\frac{\hat{L}_{s,l} - (\bar{L}_l - 2.5)}{\beta_s}}$$ (22)

$$\hat{L}_{s,l}^{post,1} = \alpha_s + \beta_{s,1}L_l$$ (23)

$$\hat{L}^{post,2}_{s,l} = \alpha_s + \delta_s(\beta_{s,1} - \beta_{s,2}) + \beta_{s,2}L_l \tag{24}$$

$$\hat{L}^{post}_{s,l} = \hat{L}^{post,1}_{s,l}(1 - \Phi(\frac{L_l - \delta_{a,x}}{stgr})) + \hat{L}^{post,2}_{s,l}(\Phi(\frac{L_l - \delta_{a,x}}{stgr})) \tag{25}$$

$$\Delta_{l,l'} = \bar{L}_{l'} + 2.5 - L_l \tag{26}$$

$\hat{L}^{post,1}_{s,l}$ and $\hat{L}^{post,2}_{s,l}$ were predicted post-molt lengths from each piece of the piece-wise relationship, and $\Phi()$ was a cumulative normal distribution in which $\delta_{a,x}$ was an estimated change point. The model in which linear growth was estimated removed equations 26 and 27 from the model.

An average recruitment for the assessment period (1982-present) and yearly deviations around this average were estimated within the assessment for models in which only a single vector of recruitment deviations was estimated. The sex ratio of recruitment was assumed to be 50/50 male to female. Each year's estimated recruitment was allocated to length bins based on a discretized and renormalized gamma function with parameters specified in the control file.

$$Rec_y = e^{(Rec_{avg} + Rec_{dev,y})} \tag{27}$$

$$Pr_l = \frac{(\Delta_{1,l})^{\alpha_{rec}/\beta_{rec}} e^{-\Delta_{1,l'}/\beta_{rec}}}{\sum_{l'}(\Delta_{1,l'})^{\alpha_{rec}/\beta_{rec}} e^{(-\Delta_{1,l'}/\beta_{rec})}} \tag{28}$$

For models in which separate vectors of recruitment deviations were estimated for males and females, a separate average recruitment was also estimated (in log space). Each vector of deviations was also subject to a smoothing penalty, but were not linked directly in any way (e.g. priors on the ratio of estimated male to female average recruitment).

Three general types of likelihood components were used to fit to the available data. Multinomial likelihoods were used for size composition data, log-normal likelihoods were used for indices of abundance data, and normal likelihoods were used for catch data, growth data, priors, and penalties. Multinomial likelihoods were implemented in the form:

$$L_x = \lambda_x \sum_y N^{eff}_{x,y} \sum_l p^{obs}_{x,y,l} ln(\hat{p}_{x,y,l}/p^{obs}_{x,y,l}) \tag{29}$$

L_x was the likelihood associated with data component x, where λ_x represented an optional additional weighting factor for the likelihood, $N^{eff}_{x,y}$ was the effective sample sizes for the likelihood, $p^{obs}_{x,y,l}$ was the observed proportion in size bin l during year y for data component x, and $\hat{p}_{x,y,l}$ was the predicted proportion in size bin l during year y for data component x.

Log normal likelihoods were implemented in the form:

$$L_x = \lambda_x \sum_y \frac{(ln(\hat{I}_{x,y}) - ln(I_{x,y}))^2}{2(ln(CV^2_{x,y} + 1))} \tag{30}$$

L_x was the contribution to the objective function of data component x, λ_x was any additional weighting applied to the component, $\hat{I}_{x,y}$ was the predicted value of quantity I from data component x during year y, $I_{x,y}$ was the observed value of quantity I from data component x during year y and $CV_{x,y}$ was the coefficient of variation for data component x during year y.

Normal likelihoods were implemented in the form:

$$L_x = \lambda_x \sum_y (\hat{I}_{x,y} - I_{x,y})^2 \qquad (31)$$

L_x was the contribution to the objective function of data component x, λ_x was represents the weight applied to the data component (and can be translated to a standard deviation), $\hat{I}_{x,y}$ was the predicted value of quantity I from data component x during year y, $I_{x,y}$ was the observed value of quantity I from data component x during year y.

Smoothing penalties were also placed on some estimated vectors of parameters in the form of normal likelihoods on the second differences of the vector.

Appendix B: GMACS basic population dynamics

The basic dynamics of GMACS account for growth, mortality, maturity state, and shell condition (although most of the equations omit these indices for simplicity):

$$N_{hji} = ((\mathbf{I} - \mathbf{P}_{hji-1}) + \mathbf{X}_{hji-1}\mathbf{P}_{hji-1})\,\mathbf{S}_{hji-1}N_{hji-1} + \widetilde{R}_{hji} \qquad (32)$$

where N_{hji} is the number of animals by size-class of sex h at the start of season j of year i, $\mathbf{P}_{hji}$ is a matrix with diagonals given by vector of molting probabilities for animals of sex h at the start of season j of year i, $\mathbf{S}_{hji}$ is a matrix with diagonals given by the vector of probabilities of surviving for animals of sex h during time-step j of year i (which may be of zero duration):

$$S_{hjil} = exp\left(-Z_{hjil}\right) \qquad (33)$$

$$S_{hjil} = 1 - \frac{Z_{hjil}}{\widetilde{Z}_{hjil}}\left(1 - exp\left(-Z_{hjil}\right)\right) \qquad (34)$$

$\mathbf{X}_{hji}$ is the size-transition matrix (probability of growing from one size-class to each of the other size-classes or remaining in the same size class) for animals of sex h during season j of year i, $\widetilde{R}_{hji}$ is the recruitment (by size-class) to gear g during season j of year i (which will be zero except for one season – the recruitment season), Z_{hjil} is the total mortality for animals of sex h in size- class l during season j of year i, and $\tilde{Z}_{hjil}$ is the probability of encountering the gear for animals of sex h in size-class l during season j of year i. Equation 34 applies when mortality is continuous across a time-step and equation 35 applies when a time-step is instantaneous. Equation 33 can be modified to track old and new shell crab (under the assumption that both old and new shell crab molt), i.e.:

$$N_{hji}^{new} = \mathbf{X}_{hji-1}\mathbf{P}_{hji-1}\mathbf{S}_{hji-1}\left(N_{hji-1}^{new} + N_{hji-1}^{old}\right) + \widetilde{R}_{hji} \qquad (35)$$

$$N_{hji}^{old} = (\mathbf{I} - \mathbf{P}_{hji-1})\,\mathbf{S}_{hji-1}\mathbf{P}_{hji-1}\left(N_{hji-1}^{new} + N_{hji-1}^{old}\right) \qquad (36)$$

Equation 33 can be also be modified to track mature and immature shell crab (under the assumption that immature crab always molt and mature crab never molt and $\mathbf{P}_{hji}$ now represents the probability of moltin gto maturity), i.e.:

$$N_{hji}^{mat} = \mathbf{X}_{hji-1}\mathbf{S}_{hji-1}\mathbf{P}_{hji-1}N_{hji-1}^{imm} + \mathbf{S}_{hji-1}N_{hji-1}^{mat}N_{hji}^{imm} = \mathbf{X}_{hji-1}\mathbf{S}_{hji-1}(\mathbf{I} - \mathbf{P}_{hji-1})N_{hji-1}^{imm} + \mathbf{S}_{hji-1}N_{hji-1}^{mat}$$
$$(37)$$

There are several ways to specify the initial conditions for the model (i.e., the numbers-at- size at the start of the first year, i_1).

- An equilibrium size-structure based on constant recruitment and either no fishing for any of the fleets or (estimated or fixed) fishing mortality by fleet. The average recruitment is an estimated parameter of the model.

- An individual parameter for each size- class, i.e.: $N_{hi_11} = exp(\delta_{hi_1l})$

- An overall total recruitment multiplied by offsets for each size-class, i.e.:

$$N_{hi_11} = \frac{R_{init}exp(\delta_{hi_1l})}{\sum_{h'}\sum_{l'} exp(\delta_{hi_1l'})} \tag{38}$$

Recruitment occurs once during each year. Recruitment by sex and size-class is the product of total recruitment, the split of the total recruitment to sex and the assignment of sex-specific recruitment to size-classes, i.e.:

$$\widetilde{R}_{hjil} = \bar{R}e^{\epsilon_i} \begin{cases} (1+e^{\theta_i})^{-1}p_{hl} & \text{if h = males} \\ \theta_i(1+e^{\theta_i})^{-1}p_{hl} & \text{if h = females} \end{cases} \tag{39}$$

where $\bar{R}$ is median recruitment, θ_i determines the sex ratio of recruitment during year i, and p_{hl} is the proportion of the recruitment (by sex) that recruits to size-class l:

$$p_{hil} = \int_{L_{low}}^{L_{high}} \frac{le^{-l/\beta_h} \frac{(\alpha^h/\beta^h)-1}{\beta_h}}{\Gamma(\alpha_h/\beta h)} dl \tag{40}$$

where α_h and β_h are the parameters that define a gamma function for the distribution of recruits to size-class l. Equation 41 can be restricted to a subset of size-classes, in which case the results from Equation 41 are normalized to sum to 1 over the selected size-classes.

Total mortality is the sum of fishing mortality and natural mortality, i.e.:

$$Z_{hijl} = \rho_{ij}M_{hi}\tilde{M}_l + \sum_f S_{fhijl}(\lambda_{fhijl} + \Omega_{fhijl}(1-\lambda_{fhijl}))F_{fhijl} \tag{41}$$

where ρ_{ij} is the proportion of natural mortality that occurs during season j for year i, M_{hi} is the rate of natural mortality for year i for animals of sex h (applies to animals for which $\tilde{M}_l = 1$), $\tilde{M}_l$ is the relative natural mortality for size-class l, S_{fhijl} is the (capture) selectivity for animals of sex h in size- class l by fleet f during season j of year i, λ_{fhijl} is the probability of retention for animals of sex h in size-class l by fleet f during season j of year i, Ω_{fhijl} is the mortality rate for discards of sex h in size-class l by fleet f during season j of year i, and F_{fhijl} is the fully-selected fishing mortality for animals of sex h by fleet f during season j of year i.

The probability of capture (occurs instantaneously) is given by:

$$\widetilde{Z}_{hijl} = \sum_f S_{fhijl}F_{fhij} \tag{42}$$

Note that Equation 43 is computed under the premise that fishing is instantaneous and hence that there is no natural mortality during season j of year i. The logarithms of the fully-selected fishing mortalities by season are modelled as:

$$ln(F_{fhij}) = ln(F_{fh}) + \epsilon_{fhij} \text{ if h = males} \tag{43}$$

$$ln(F_{fhij}) = ln(F_{fh}) + \theta_f + \epsilon_{fhij} \text{ if h = females} \tag{44}$$

where F_{fh} is the reference fully-selected fishing mortality rate for fleet f, θ_f is the offset between female and male fully-selected fishing mortality for fleet f, and ϵ_{fhij} are the annual deviation of fully-selected fishing mortality for fleet f (by sex). Natural mortality can depend on time according to several functional forms:

- Natural mortality changes over time as a random walk, i.e.:

$$M_{hi} = \begin{cases} M_{hi_1} & \text{if i} = i_1 \\ M_{hi-1}e^{\psi_{hi}} & \text{otherwise} \end{cases} \tag{45}$$

where M_{hi_1} is the rate of natural mortality for sex h for the first year of the model, and ψ_{hi} is the annual change in natural mortality.

- Natural mortality changes over time as a spline function. This option follows Equation 46, except that the number of knots at which ψ_{hi} is estimated is specified.

- Blocked changes. This option follows Equation 46, except that ψ_{hi} changes between 'blocks' of years, during which ψ_{hi} is constant.

- Blocked natural mortality (individual parameters). This option estimates natural mortality as parameters by block, i.e.:

$$M_{hi} = e^{\psi_{hi}} \tag{46}$$

where ψ_{hi} changes in blocks of years.

- Blocked offsets (relative to reference). This option captures the intent of the previous option, except that the parameters are relative to natural mortality in the first year, i.e.:

$$M_{hi} = M_{hi_1}e^{\psi_{hi}} \tag{47}$$

It is possible to 'mirror' the values for the ψ_{hi} parameters (between sexes and between blocks), which allows male and female natural mortality to be the same, and for natural mortality to be the same for discontinuous blocks (based on Equations 47 and 48). The deviations in natural mortality can also be penalized to avoid unrealistic changes in natural mortality to fit 'quirks' in the data.

The model keeps track of (and can be fitted to) landings, discards, total catch by fleet, whose computation depends on whether the fisheries in season t are continuous or instantaneous.

$$C_{fhijl}^{Land} = \begin{cases} \frac{\lambda_{fhijl}S_{fhijl}F_{fhijl}}{Z_{hijl}}N_{fhijl}(1-e^{-\hat{Z}_{hijl}}) & \text{if continuous} \\[2ex] \frac{\lambda_{fhijl}S_{fhijl}F_{fhijl}}{Z_{hijl}}N_{fhijl}(1-e^{-Z_{hijl}}) & \text{if instantaneous} \end{cases} \tag{48}$$

$$C_{fhijl}^{Disc} = \begin{cases} \frac{(1-\lambda_{fhijl})S_{fhijl}F_{fhijl}}{Z_{hijl}}N_{fhijl}(1-e^{-\hat{Z}_{hijl}}) & \text{if continuous} \\[2ex] \frac{(1-\lambda_{fhijl})S_{fhijl}F_{fhijl}}{Z_{hijl}}N_{fhijl}(1-e^{-Z_{hijl}}) & \text{if instantaneous} \end{cases} \tag{49}$$

$$C_{fhijl}^{Tot} = \begin{cases} \frac{S_{fhijl}F_{fhijl}}{Z_{hijl}}N_{fhijl}(1-e^{-\hat{Z}_{hijl}}) & \text{if continuous} \\[2ex] \frac{S_{fhijl}F_{fhijl}}{Z_{hijl}}N_{fhijl}(1-e^{-Z_{hijl}}) & \text{if instantaneous} \end{cases} \tag{50}$$

Landings, discards, and total catches by fleet can be aggregated over sex (e.g., when fitting to removals reported as sex-combined). Equations 49-51 are extended naturally for the case in which the population is represented by shell condition and/or maturity status (given the assumption that fishing mortality, retention and discard mortality depend on sex and time, but not on shell condition nor maturity status). Landings, discards, and total catches by fleet can be reported in numbers (Equations 49-51) or in terms of weight. For example, the landings, discards, and total catches by fleet, season, year, and sex for the total (over size-class) removals are computed as:

$$C_{fhij}^{Land} = \sum_l C_{fhijl}^{Land} w_{hil} \tag{51}$$

$$C_{fhij}^{Disc} = \sum_l C_{fhijl}^{Disc} w_{hil} \tag{52}$$

$$C_{fhij}^{Total} = \sum_l C_{fhijl}^{Total} w_{hil} \tag{53}$$

$$\tag{54}$$

where C_{fhij}^{Land}, C_{fhij}^{Disc}, and C_{fhij}^{Total} are respectively the landings, discards, and total catches in weight by fleet, season, year, and sex for the total (over size-class) removals, and w_{hil} is the weight of an animal of sex h in size-class l during year i.

Many options exist related to selectivity (the probability of encountering the gear) and retention (the probability of being landed given being captured). The options for selectivity are:

- Individual parameters for each size-class (in log-space); normalized to a maximum of 1 over all size-classes (if indicated).
- Individual parameters for a subset of the size-classes (in log-space). Selectivity must be specified for a contiguous range of size-classes starting with the first size-class. Selectivity for any size-classes outside of the specified range is set to that for last size-class for which selectivity is treated as estimable.
- Logistic selectivity. Two variants are available depending of the parametrization:

$$S_l = \frac{1}{1 + exp(\frac{ln19(\bar{L}_l - S_{50})}{S_{95} - S_{50}})} \tag{55}$$

$$S_l = \frac{1}{1 + exp(\frac{(\bar{L}_l - S_{50})}{\sigma_S})} \tag{56}$$

where S_{50} is the size corresponding to 50% selectivity, S_{95} is the size corresponding to 95% selectivity, σ_S is the "standard deviation" of the selectivity curve, and $\bar{L}_l$ is the midpoint of size-class l.

- All size-classes are equally selected.
- Selectivity is zero for all size-classes.

It is possible to assume that selectivity for one fleet is the product of two of the selectivity patterns. This option is used to model cases in which one survey is located within the footprint of another survey. The options to model retention are the same as those for selectivity, except that it is possible to estimate an asymptotic parameter, which allows discard of animals that would be "fully retained" according to the standard options for (capture) selectivity. Selectivity and retention can be defined for blocks of contiguous years. The blocks need not be the same for selectivity and retention, and can also differ between fleets and sexs.

Growth is a key component of any size-structured model. It is modelled in terms of molt probability and the size-transition matrix (the probability of growing from each size-class to each of the other size-classes, constrained to be zero for sizes less than the current size). Note that the size-transition matrix has entries on its diagonal, which represent animals that molt but do not change size-classes

There are four options for modelling the probability of molting as a function of size:

- Pre-specified probability
- Individual parameters for each size-class (in log-space)
- Constant probability
- Logistic probability, i.e.:

$$P_{l,l} = \frac{1}{1 - (1 + exp(\frac{\bar{L}_l - P_{50}}{\sigma_P}))} \tag{57}$$

where P_{50} is the size at which the probability of molting is 0.5 and σ_P is the "standard deviation" of the molt probability function. Molt probability is specified by sex and can change in blocks.

The proportion of animals in size-class l that grow to be in size-class l' ($X_{l,l'}$) can either be pre-specified by the user or determined using a parametric form:

- The size-increment is gamma-distributed:

$$X_{l,l'} = \int_{L_{low}}^{L_{high}} \frac{((l - \bar{L}_l)/\tilde{\beta})^{I_l/\tilde{\beta} - 1} e^{-(l - \bar{L}_l)/\tilde{\beta}}}{\Gamma(I_l/\tilde{\beta})} dl \tag{58}$$

- The size after increment is gamma-distributed, i.e.:

$$X_{l,l'} = \int_{L_{low}}^{L_{high}} \frac{(l/\tilde{\beta})^{(\bar{L}_l + I_l)/\tilde{\beta} - 1} e^{-(l/\tilde{\beta})}}{\Gamma((\bar{L}_l + I_l)/\tilde{\beta})} dl \tag{59}$$

- The size-increment is normally-distributed, i.e.:

$$X_{l,l'} = \int_{L_{low}}^{L_{high}} \frac{e^{-(l-\bar{L}_l-I_l)^2/(2\tilde{\beta}^2)}}{\sqrt{2\pi}\tilde{\beta}} dl \quad (60)$$

- There is individual variation in the growth parameters L_∞ and k (equivalent to the parameters of a linear growth increment equation given the assumption of von Bertlanffy growth), i.e.:

$$X_{l,l'} = \int_{L_{low}}^{L_{high}} \int_{L_{low}}^{L_{high}} \int_0^\infty \int_0^\infty \frac{1}{L_{hi,l} - L_{low_l}} \frac{e^{-(ln(L_\infty)-\bar{L_\infty})^2/(2\sigma_{L_\infty}^2)}}{\sqrt{2\pi}\sigma_{L_\infty}^2} \frac{e^{-(ln(k)-\bar{k})^2/(2\sigma_k^2)}}{\sqrt{2\pi}\sigma_{L_k}^2} dL_{L_\infty} dk dl_{l'} dl_l \quad (61)$$

- There is individual variation in the growth parameter L_∞:

$$X_{l,l'} = \int_{L_{low}}^{L_{high}} \int_{L_{low}}^{L_{high}} \int_0^\infty \frac{1}{L_{hi,l} - L_{low_l}} \frac{e^{-(ln(L_\infty)-\bar{L_\infty})^2/(2\sigma_{L_\infty}^2)}}{\sqrt{2\pi}\sigma_{L_\infty}^2} dL_{L_\infty} dl_{l'} dl_l \quad (62)$$

- There is individual variation in the growth parameters k:

$$X_{l,l'} = \int_{L_{low}}^{L_{high}} \int_{L_{low}}^{L_{high}} \int_0^\infty \frac{1}{L_{hi,l} - L_{low_l}} \frac{e^{-(ln(k)-\bar{k})^2/(2\sigma_k^2)}}{\sqrt{2\pi}\sigma_k^2} dk dl_{l'} dl_l \quad (63)$$

The size-transition matrix is specified by sex and can change in blocks.

Table 1: Changes in management quantities for each scenario considered. Reported management quantities are derived from maximum likelihood estimates.

Model	MMB	B35	F35	FOFL	OFL
Status quo 2019	105.71	123.44	1.78	1.78	51.63
GMACS_2019	90.24	101.58	1.69	1.69	55.34
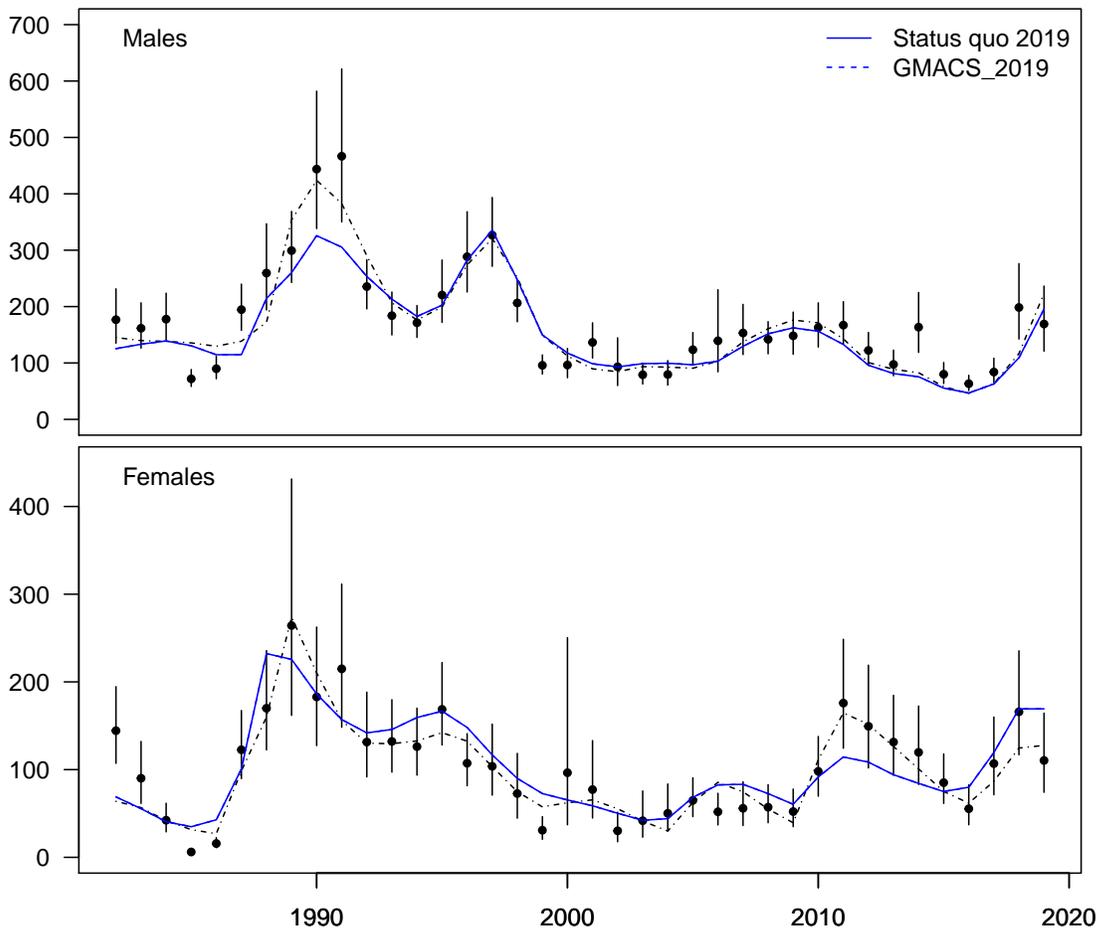
Figure 1: Model fits to the observed mature biomass at survey
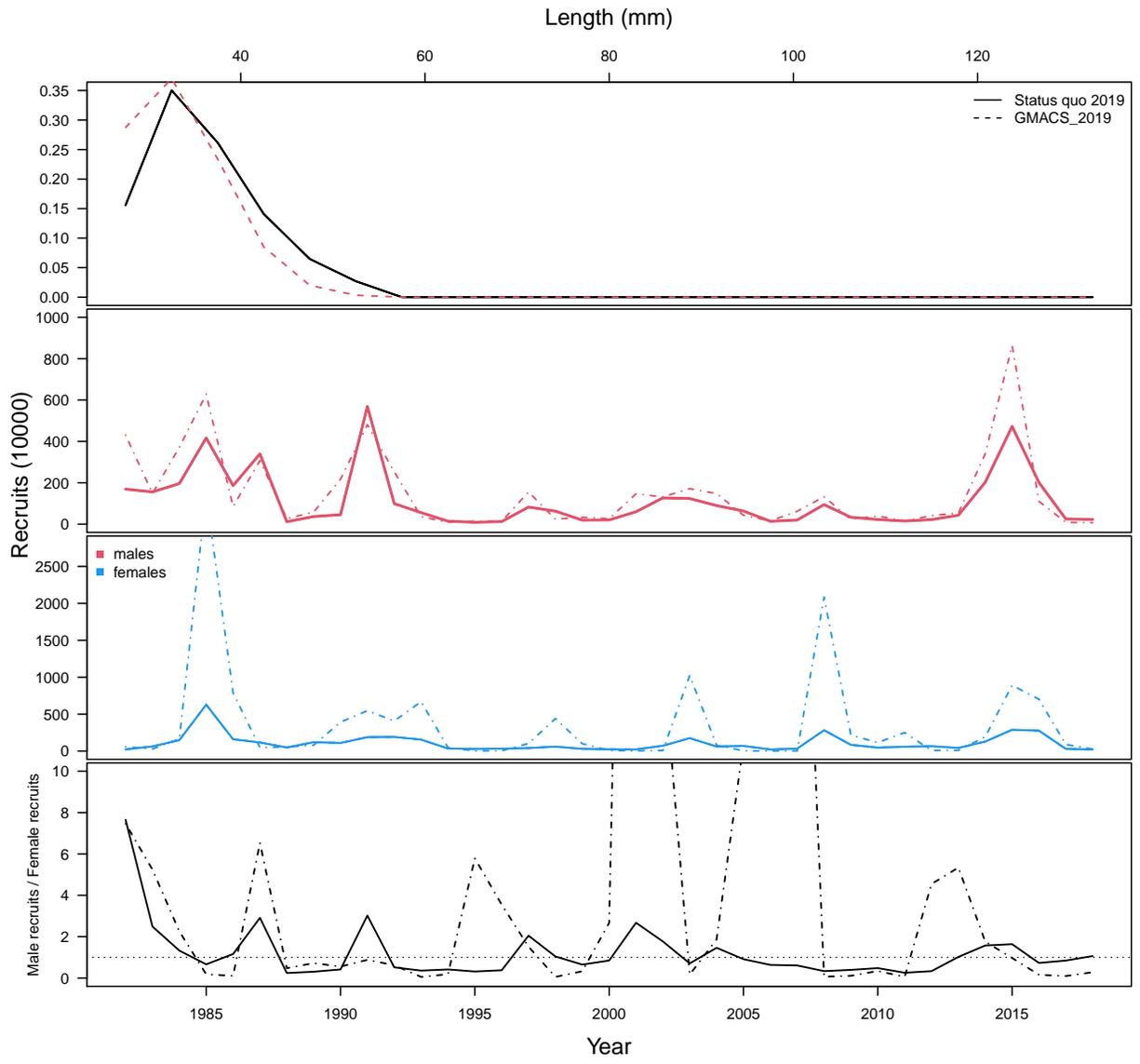
Figure 2: Estimated recruitment and proportions recruiting to length bin.
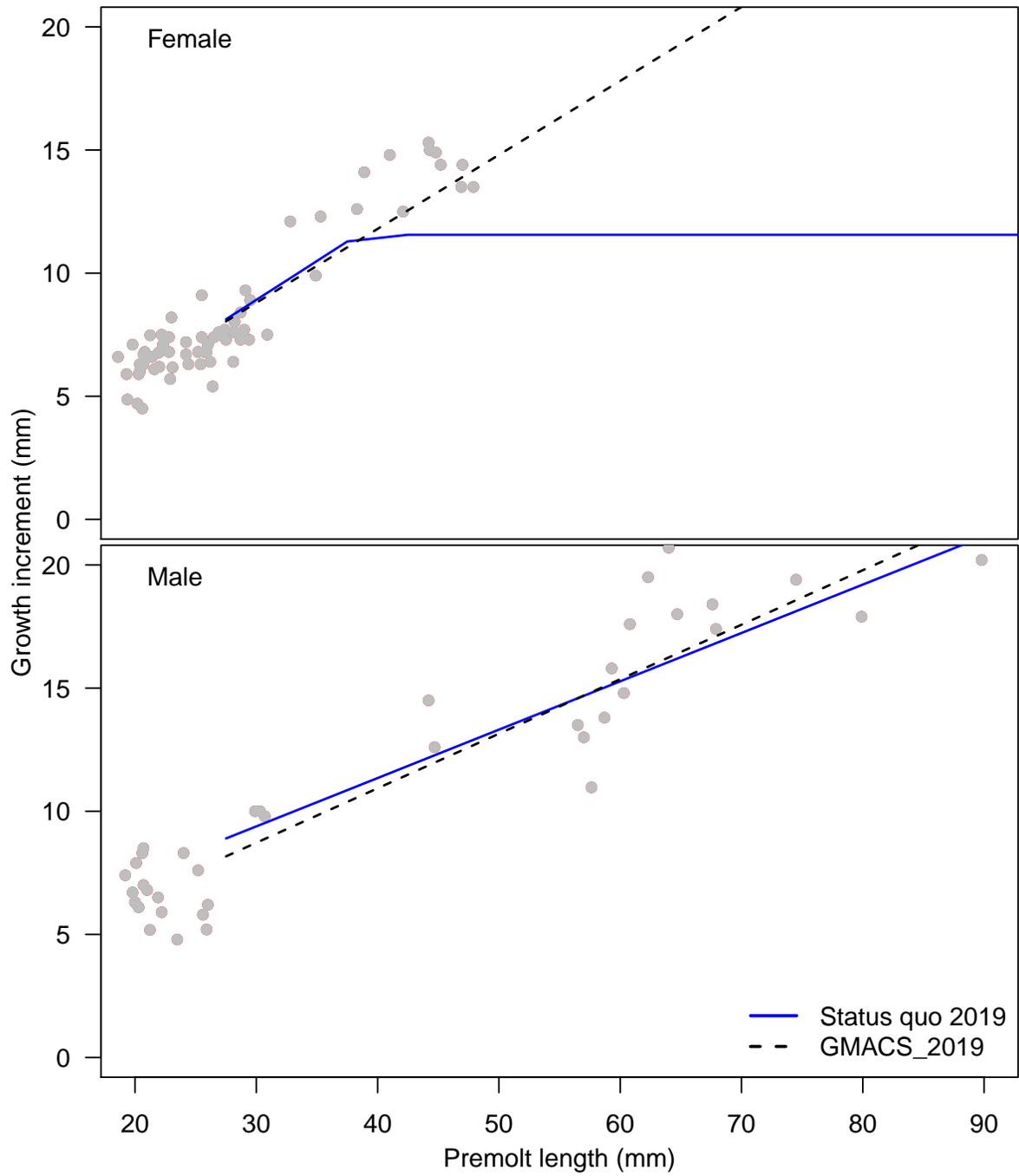
Figure 3: Model fits to the growth data
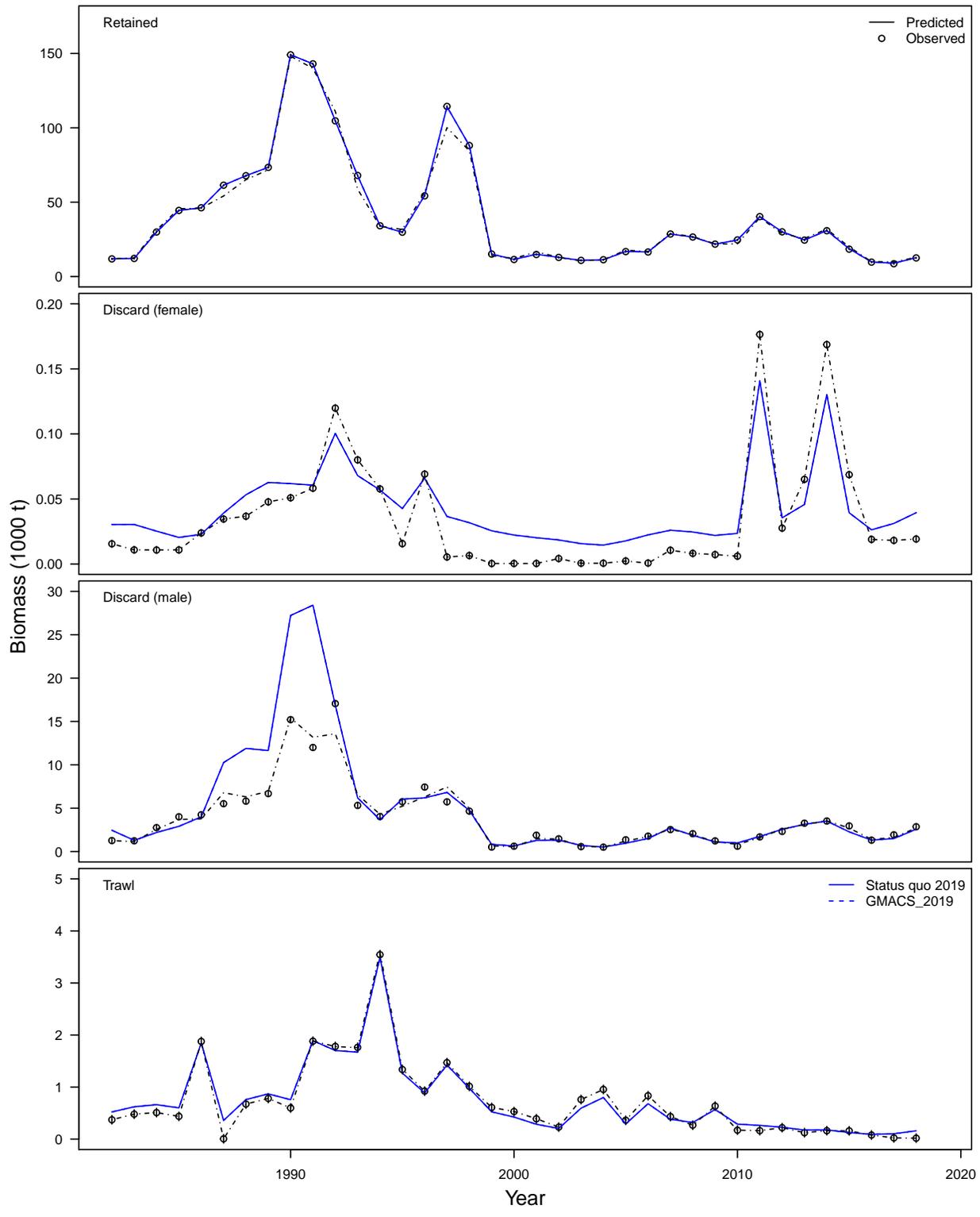
Figure 4: Model fits to catch data
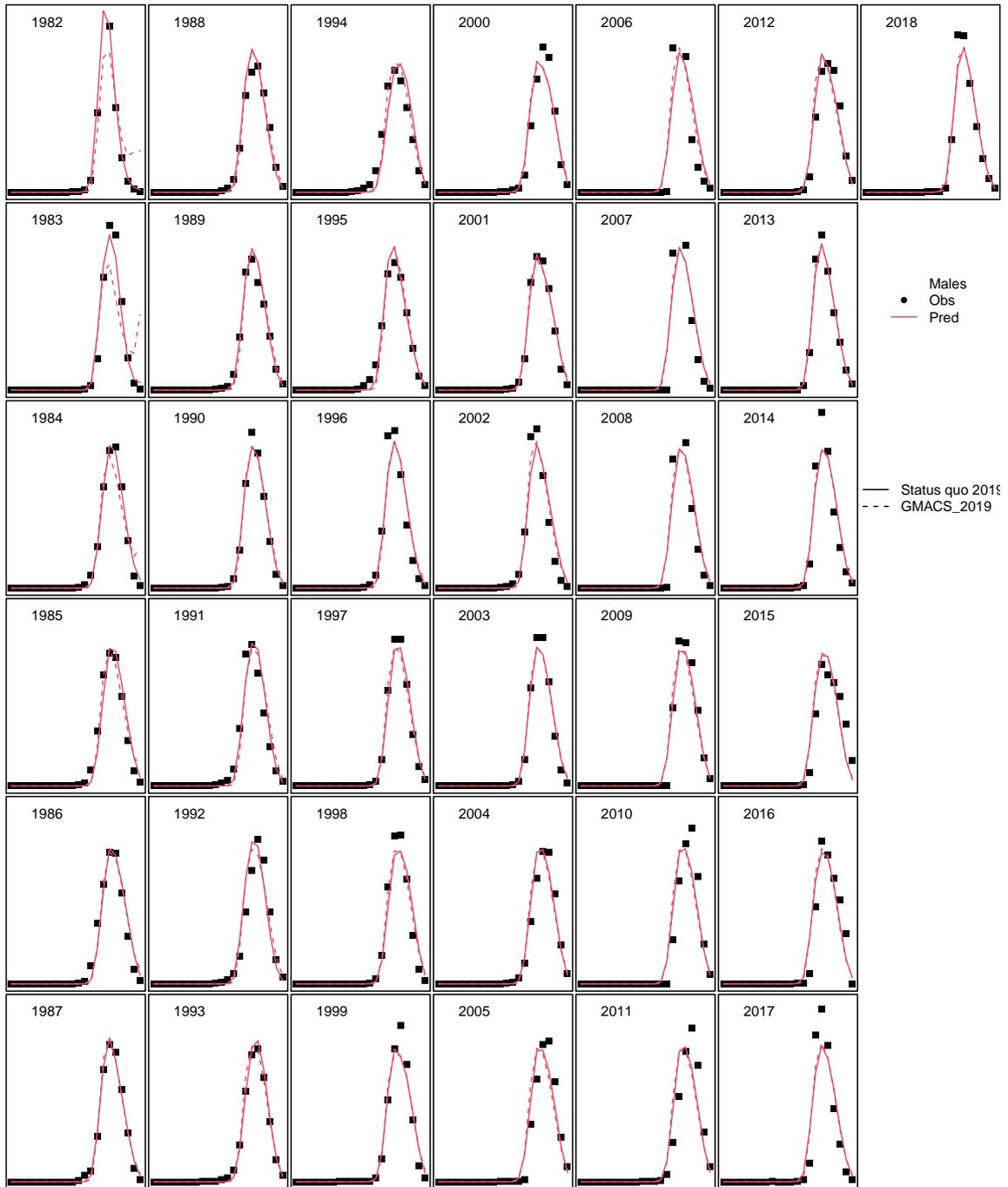
Figure 5: Model fits to retained catch size composition data
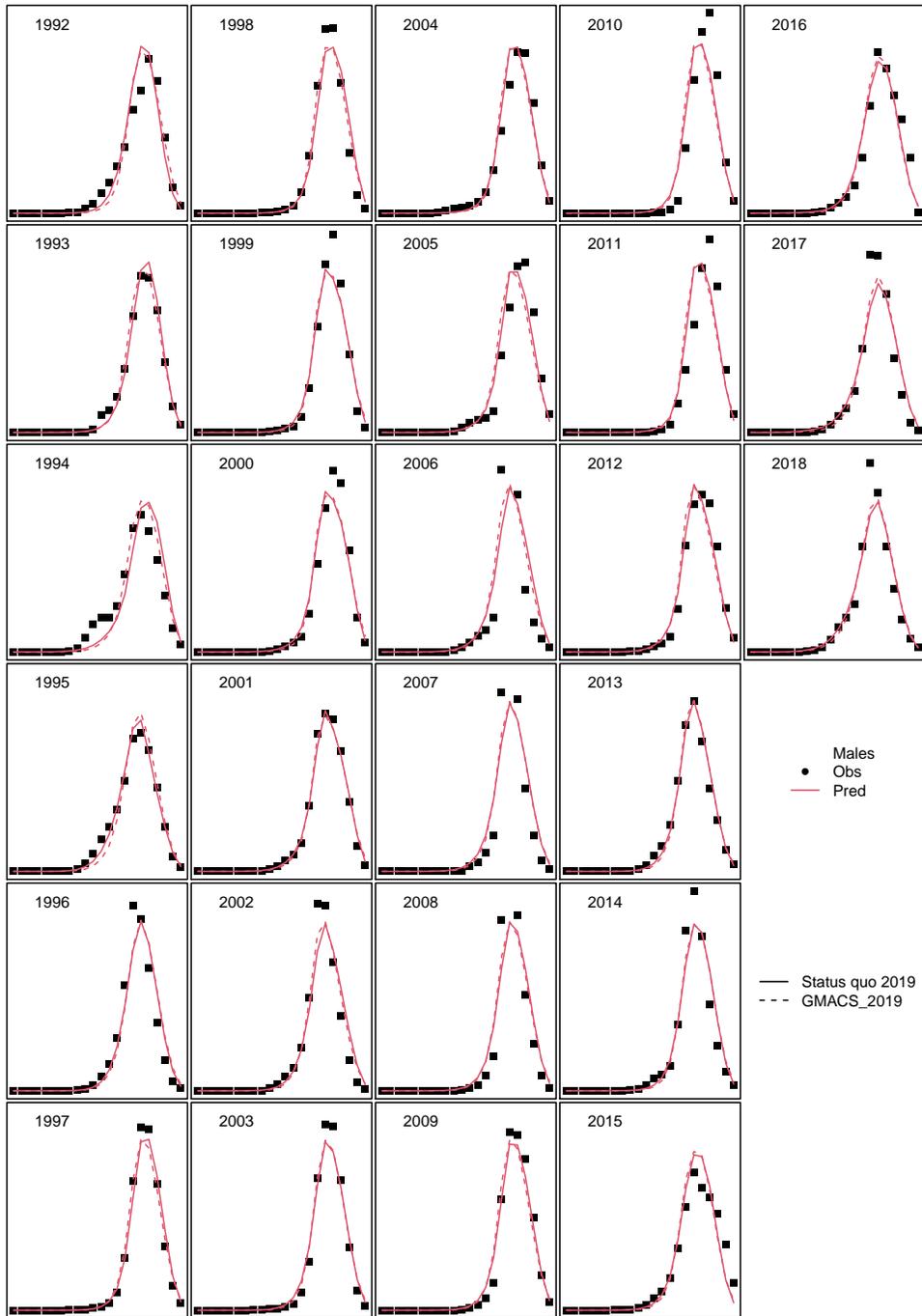
Figure 6: Model fits to total catch size composition data
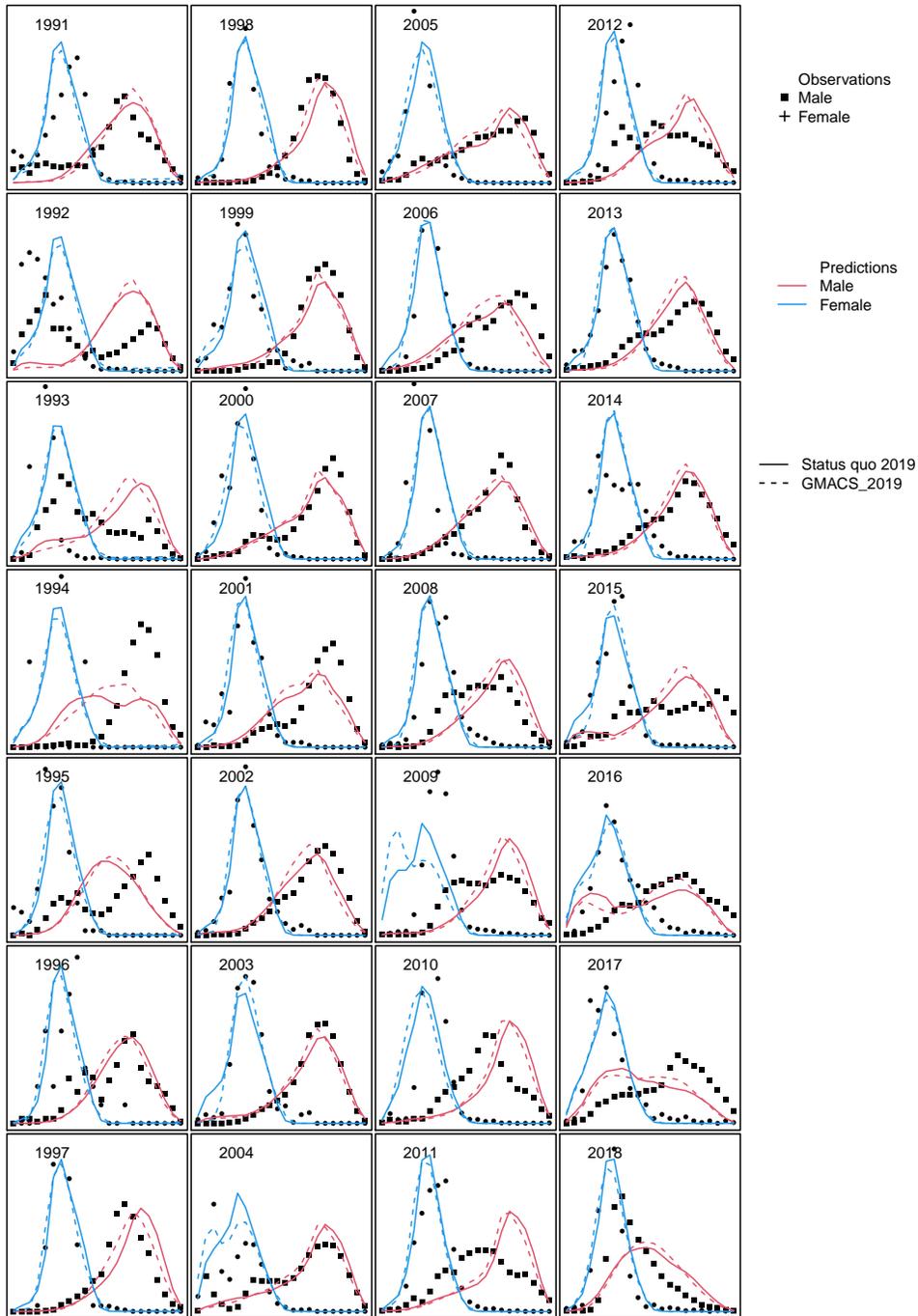
Figure 7: Model fits to trawl catch size composition data
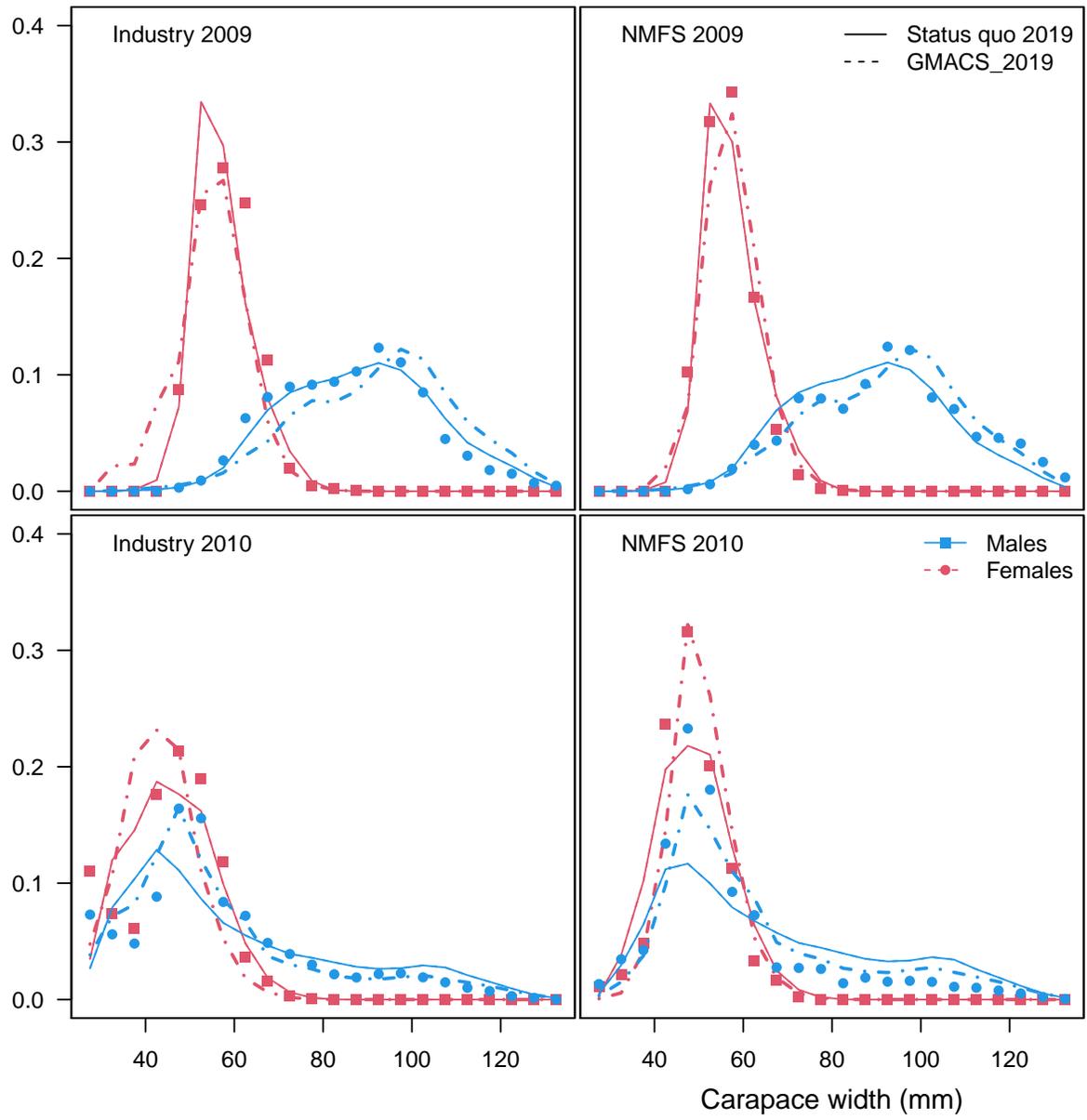
Figure 8: Model fits to size composition data from summer survey experiments (2009 & 2010)
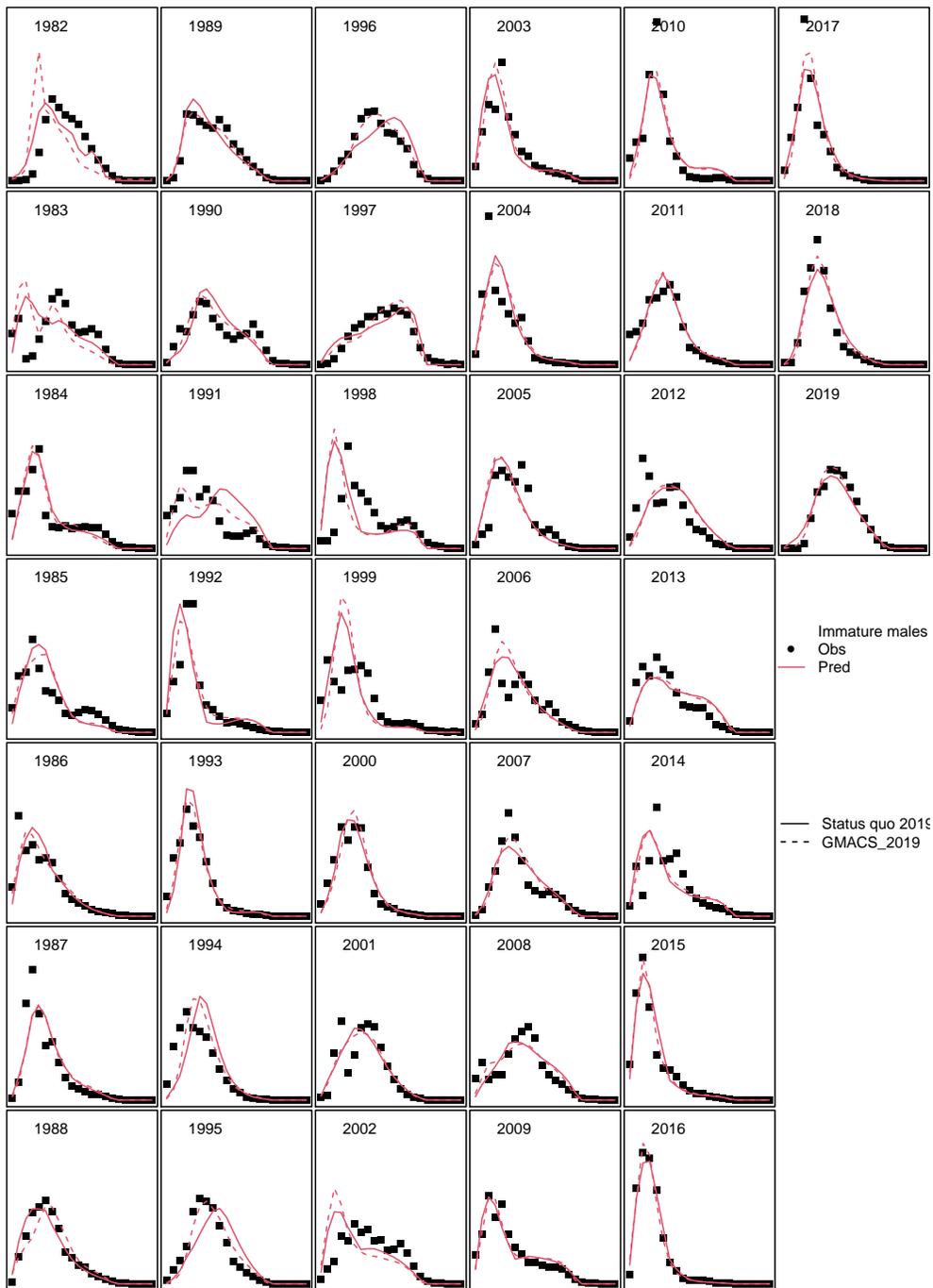
Figure 9: Model fits to immature male survey size composition data. Note that male and female survey selectivity proportions at length in a given year sum to 1. Consequently, the integral of predicted length compositions may appear to be different than the integral of the observed length composition data.
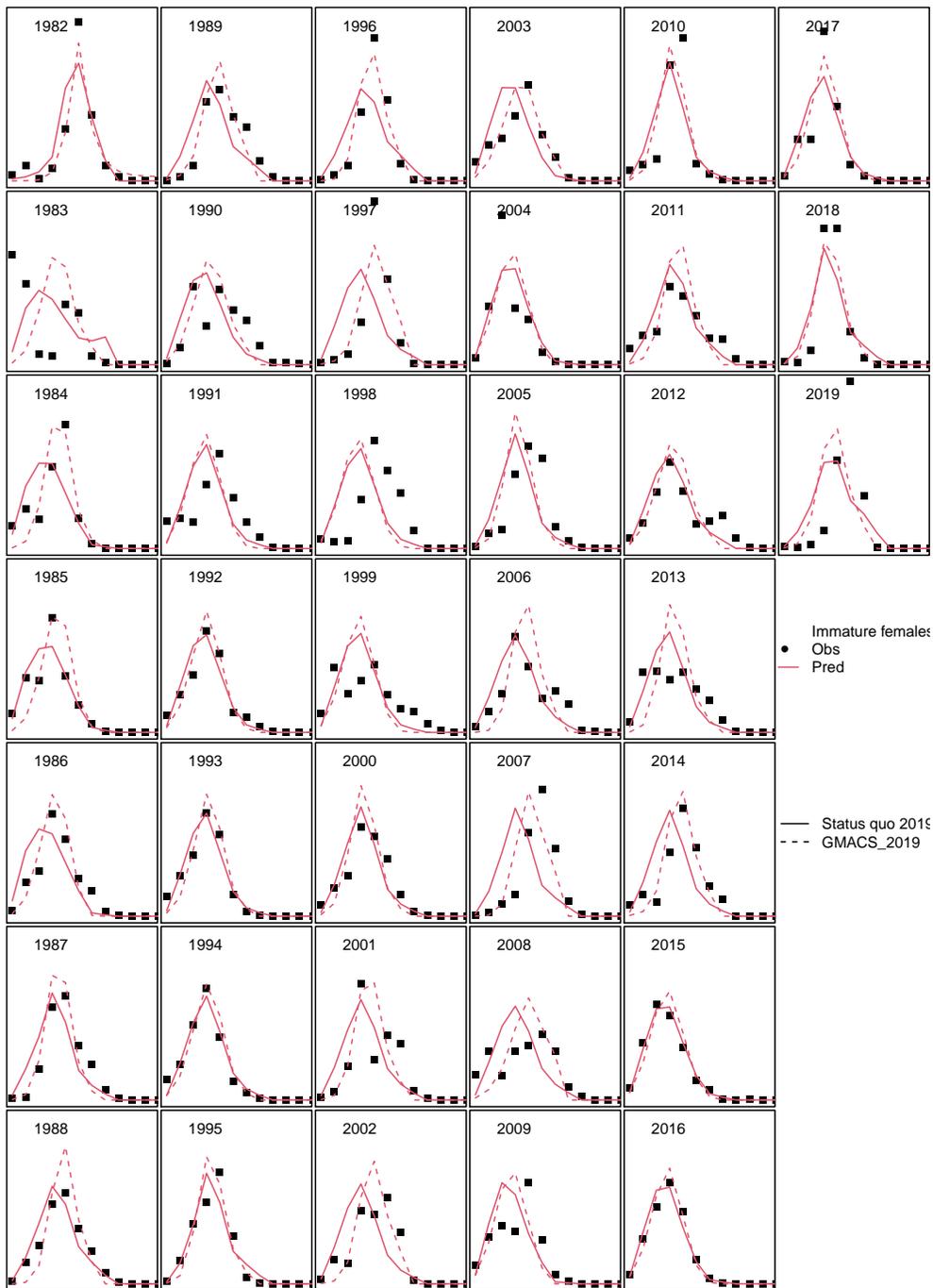
Figure 10: Model fits to immature female survey size composition data. Note that male and female survey selectivity proportions at length in a given year sum to 1. Consequently, the integral of predicted length compositions may appear to be different than the integral of the observed length composition data.
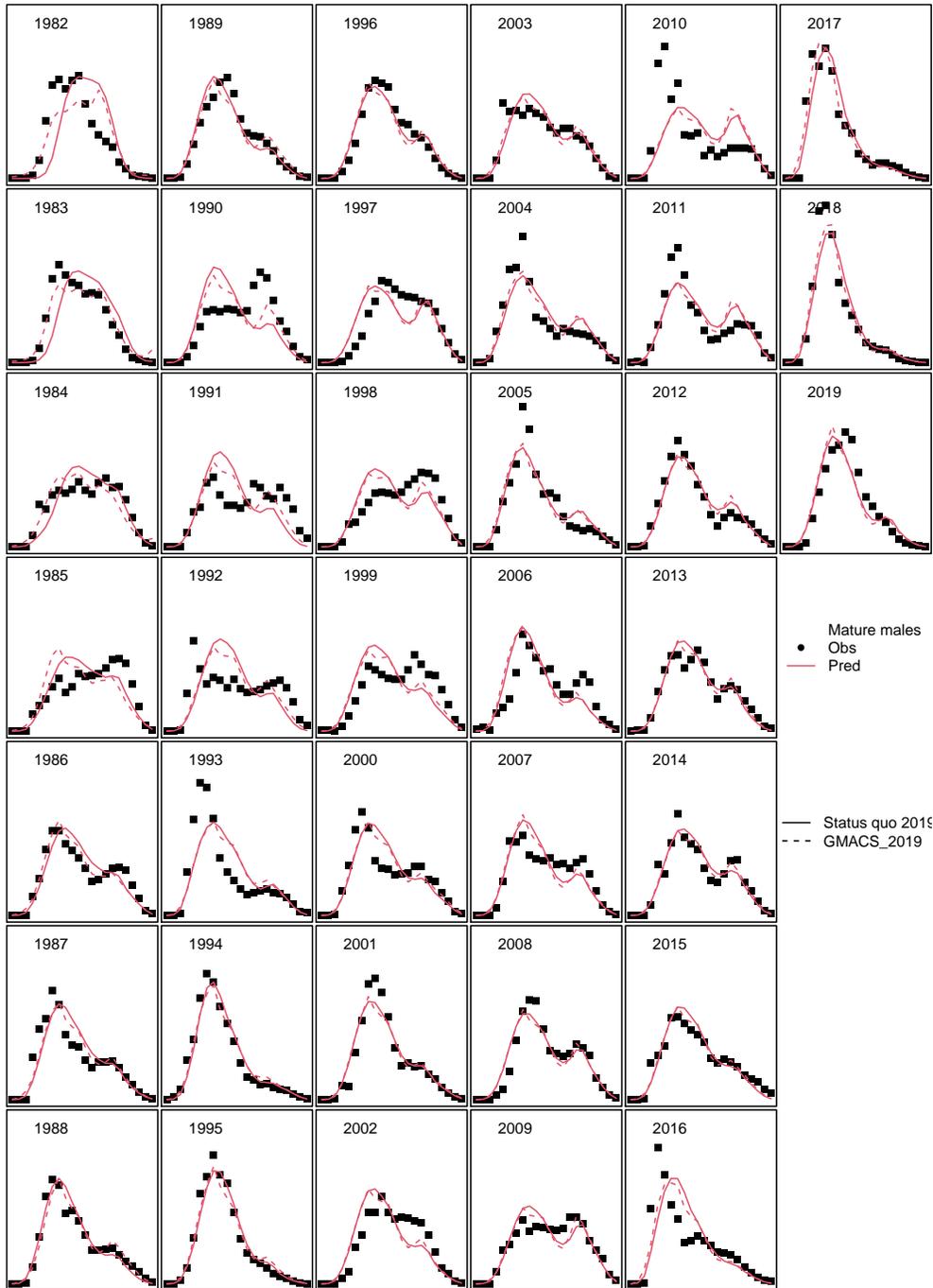
Figure 11: Model fits to mature male survey size composition data. Note that male and female survey selectivity proportions at length in a given year sum to 1. Consequently, the integral of predicted length compositions may appear to be different than the integral of the observed length composition data.
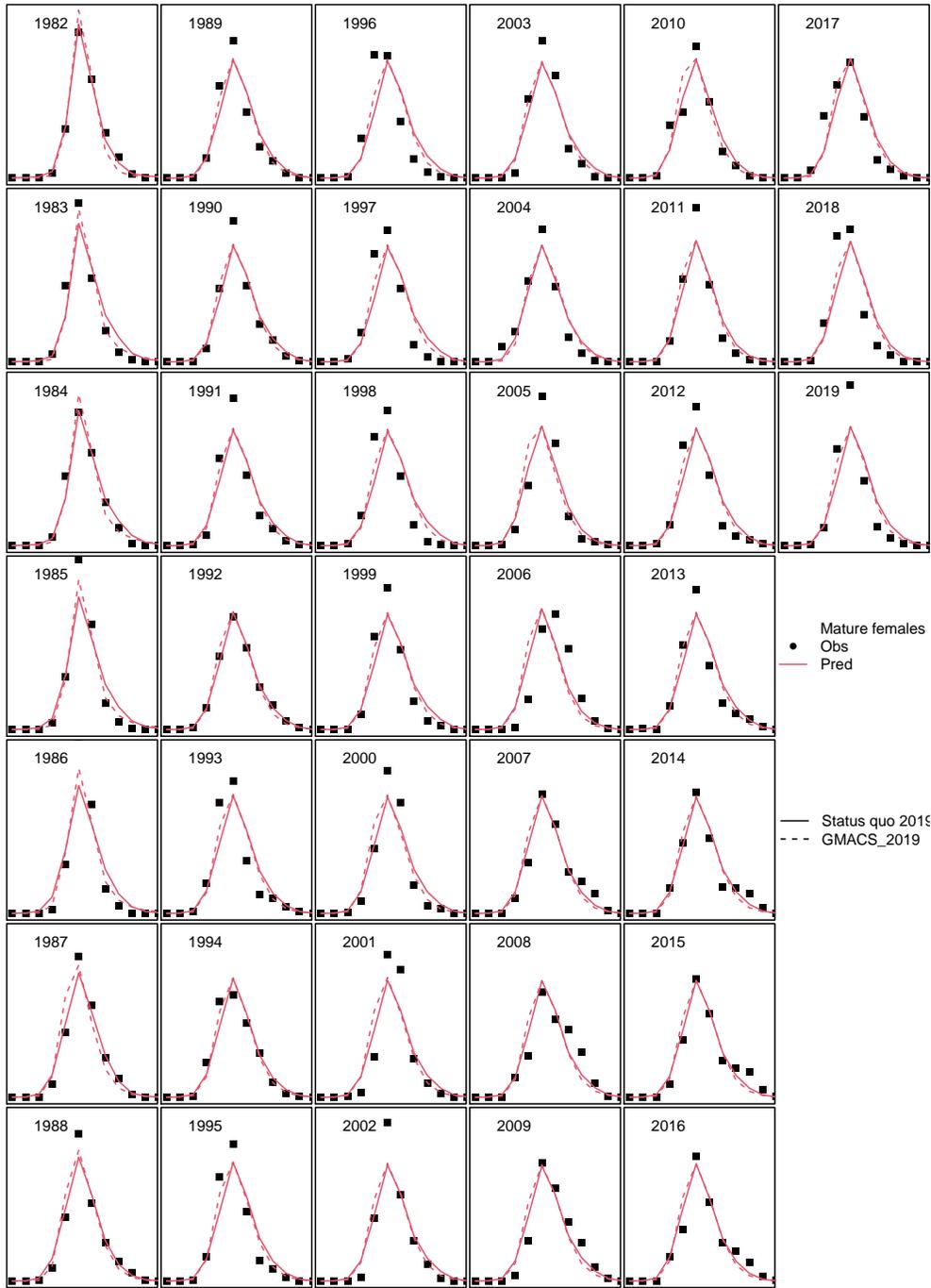
Figure 12: Model fits to mature female survey size composition data. Note that male and female survey selectivity proportions at length in a given year sum to 1. Consequently, the integral of predicted length compositions may appear to be different than the integral of the observed length composition data.
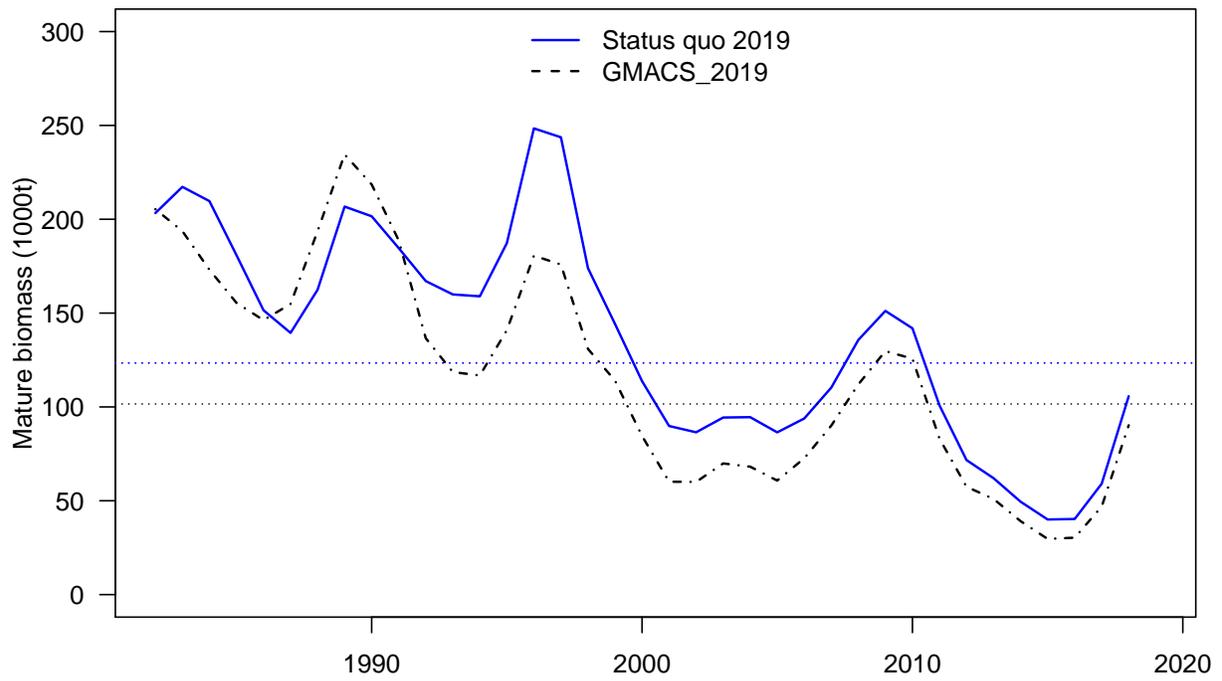
Figure 13: Model predicted mature biomass at mating time. Terminal estimate is on February 15, 2019. Dotted horizontal lines are target biomasses.
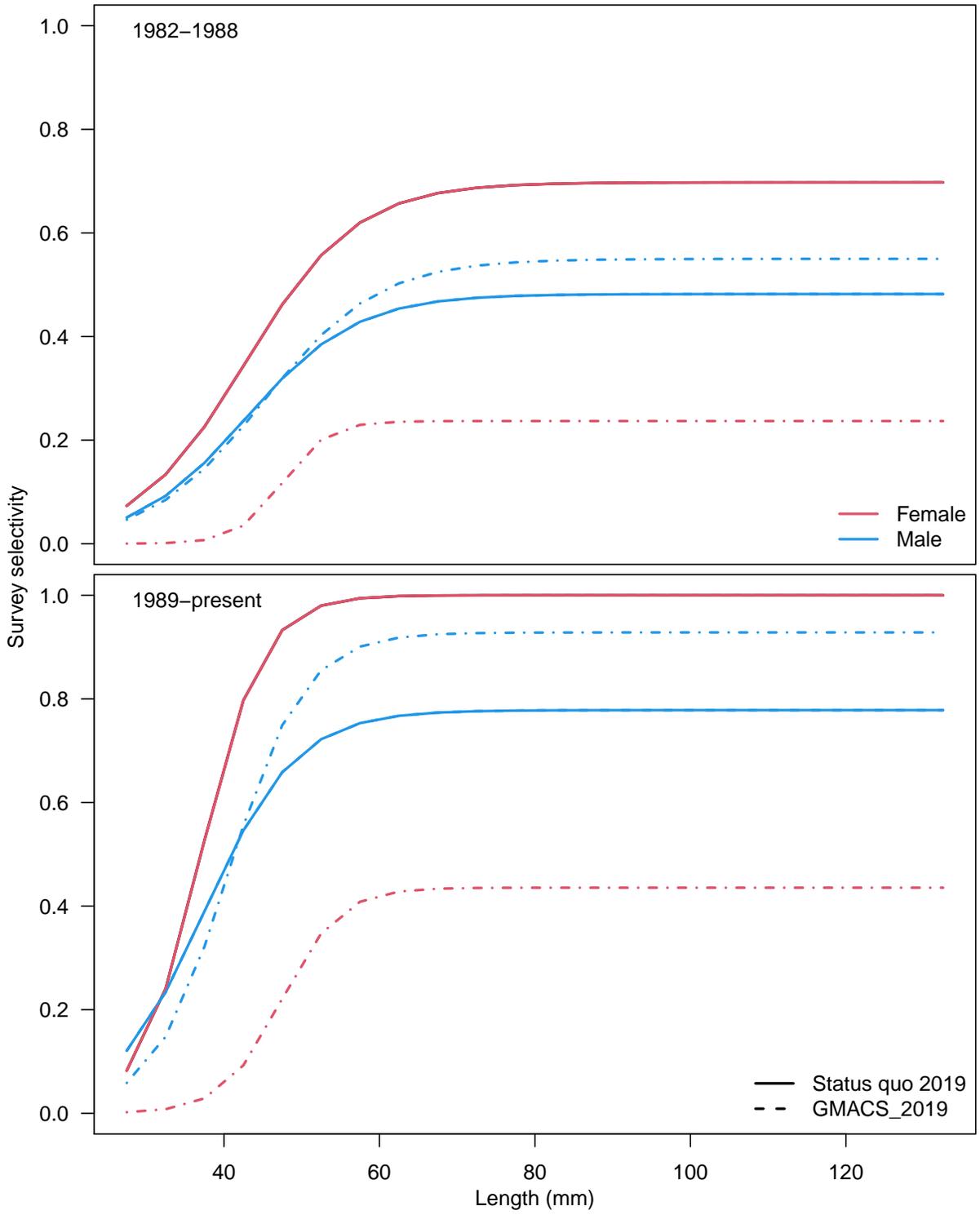
Figure 14: Estimated survey selectivity
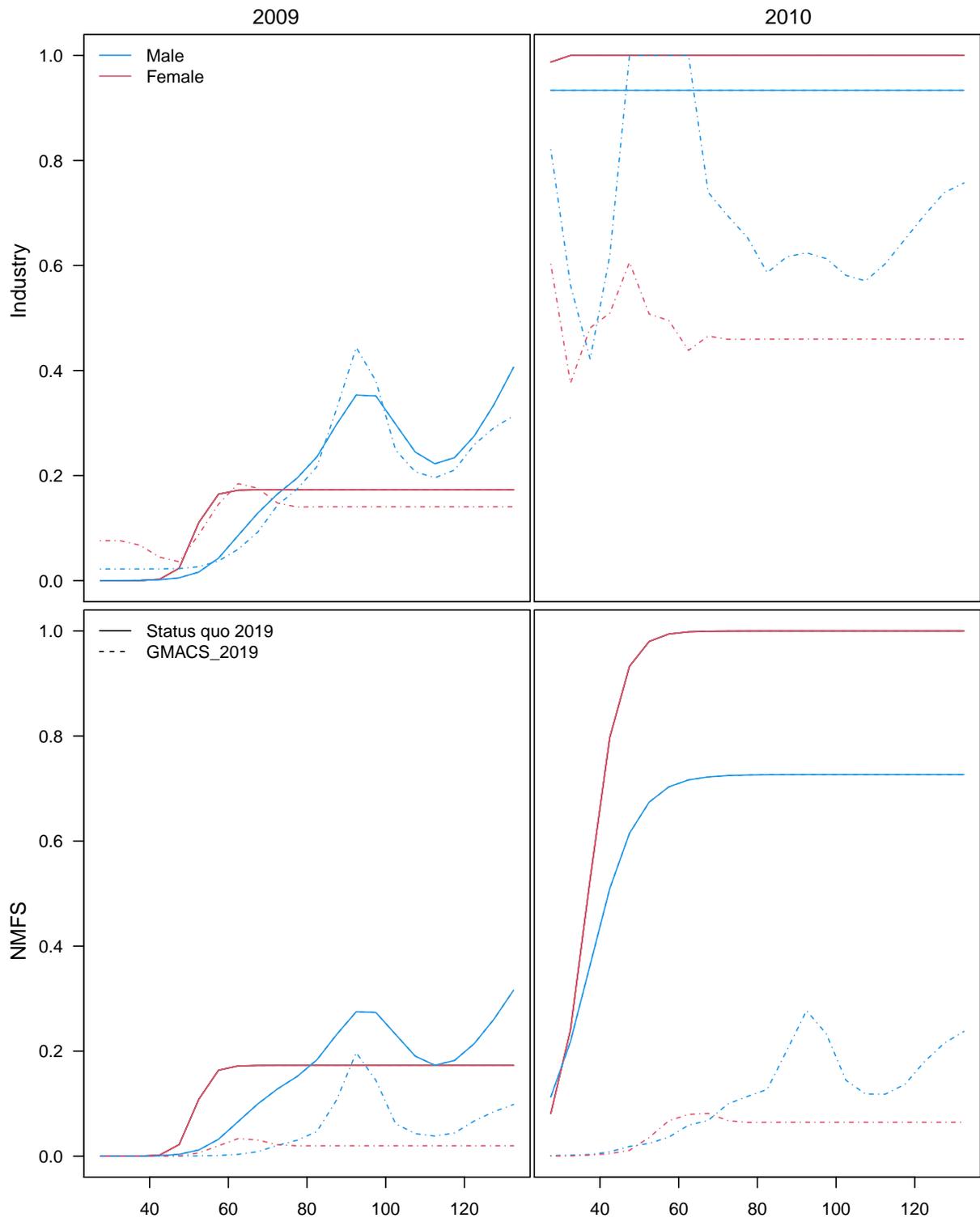
Figure 15: Estimated experimental survey selectivity (availability * survey selectivity)
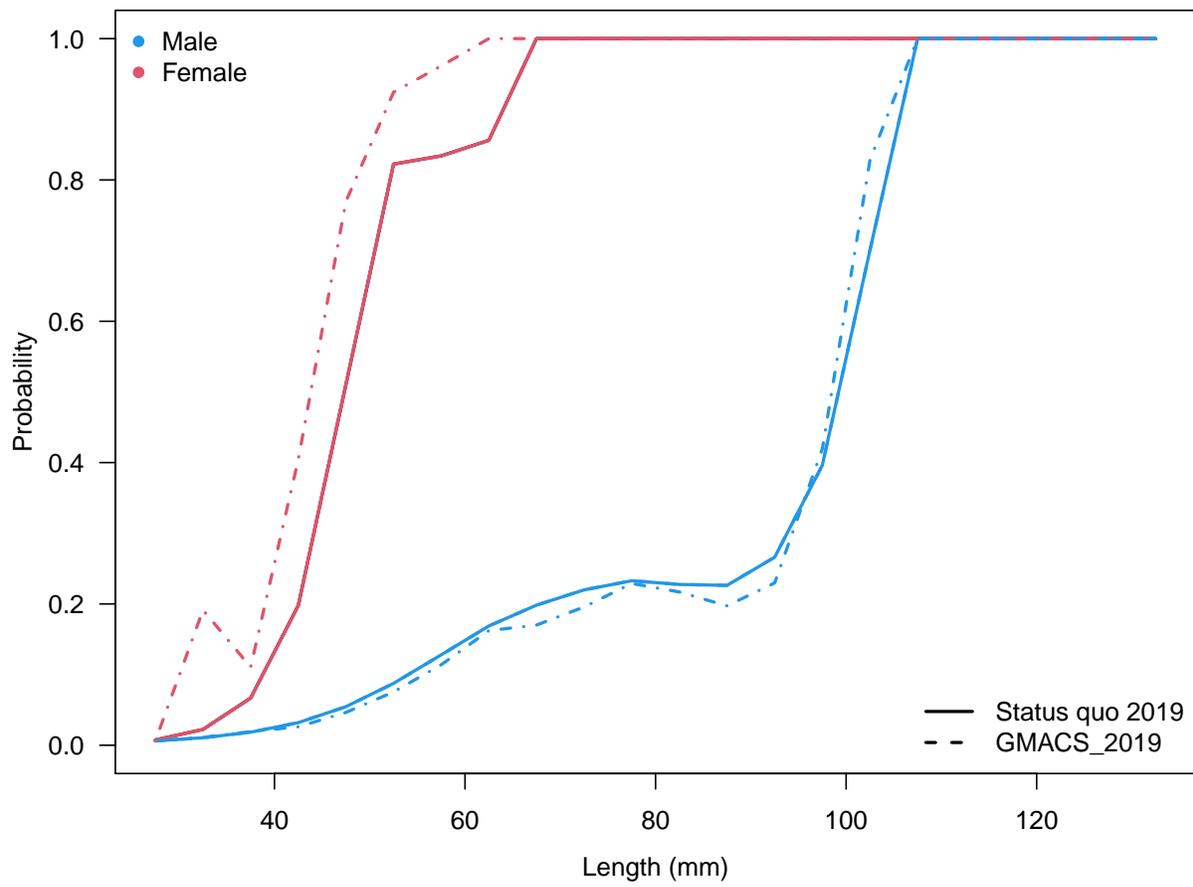
Figure 16: Estimated probability of maturing
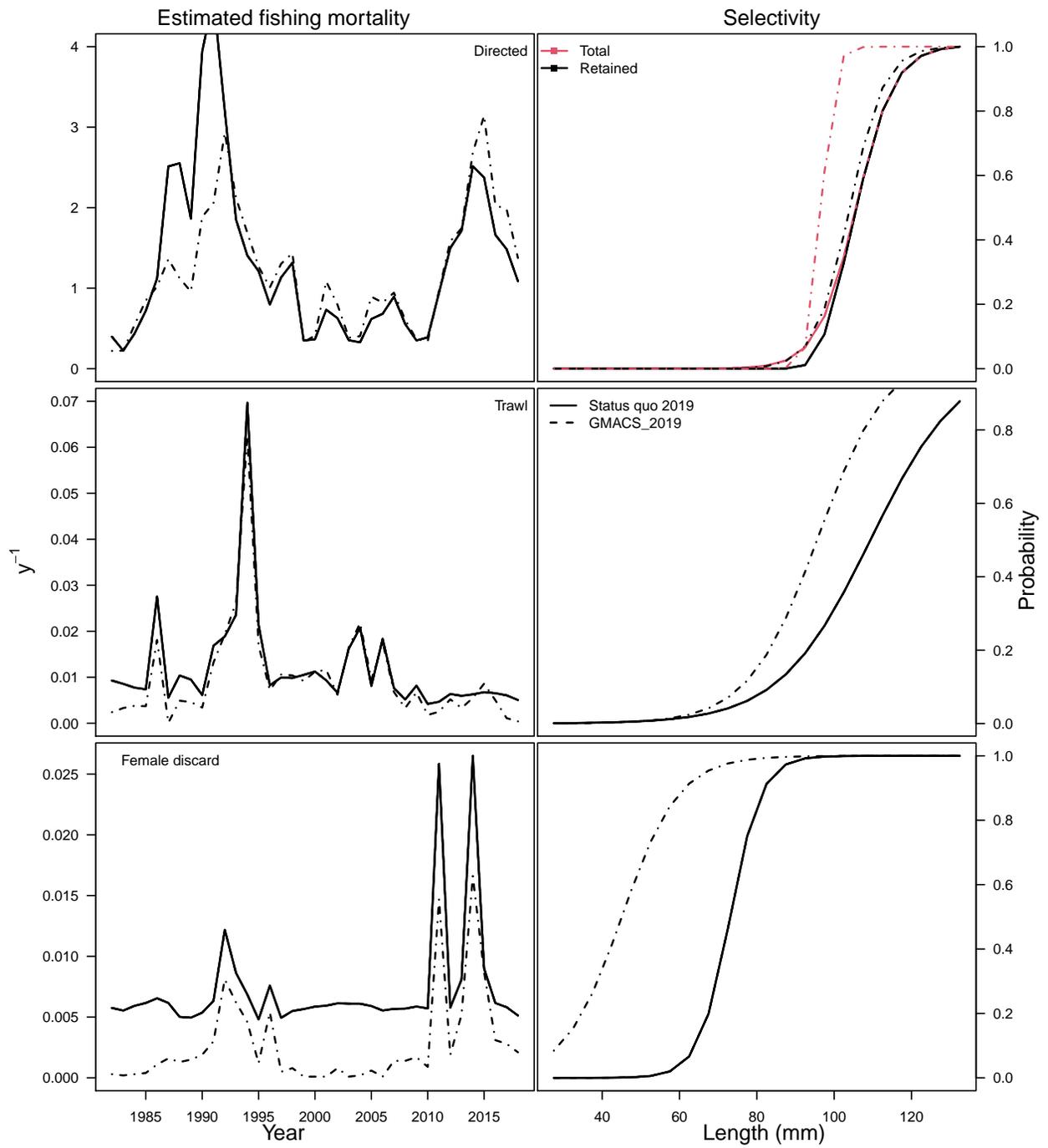
Figure 17: Model predicted fishing mortalities and selectivities for all sources of mortality
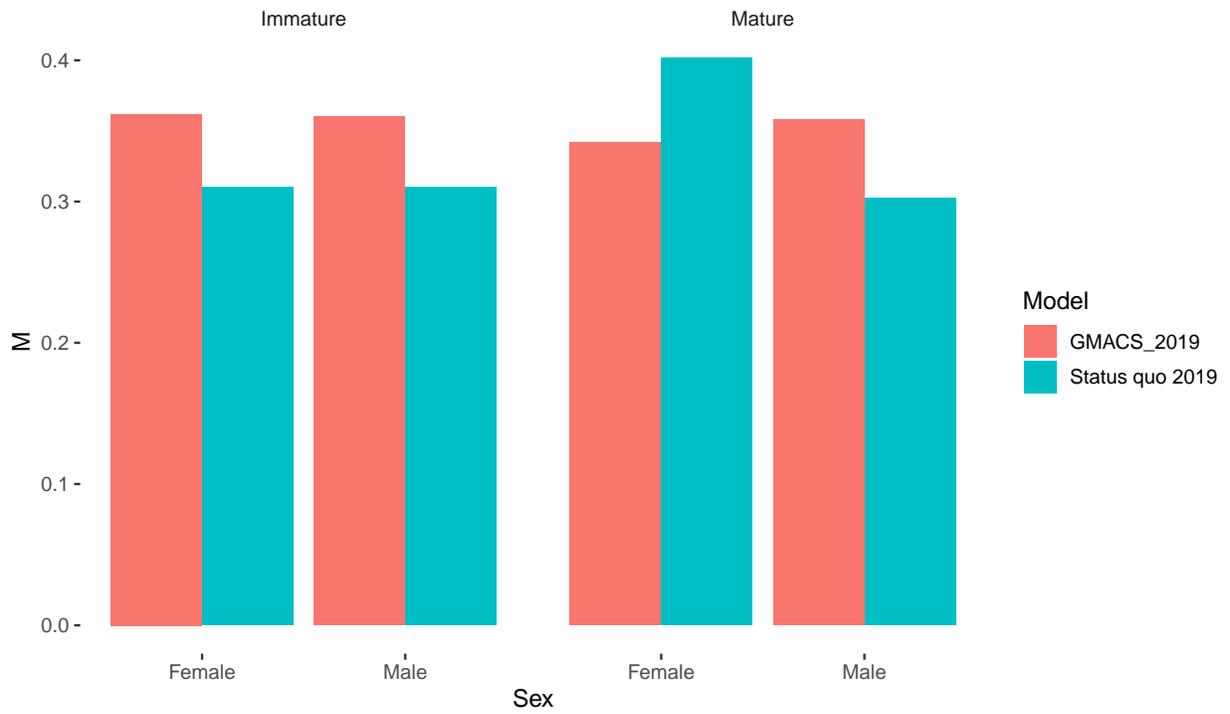
Figure 18: Estimated natural mortality by sex and maturity state.
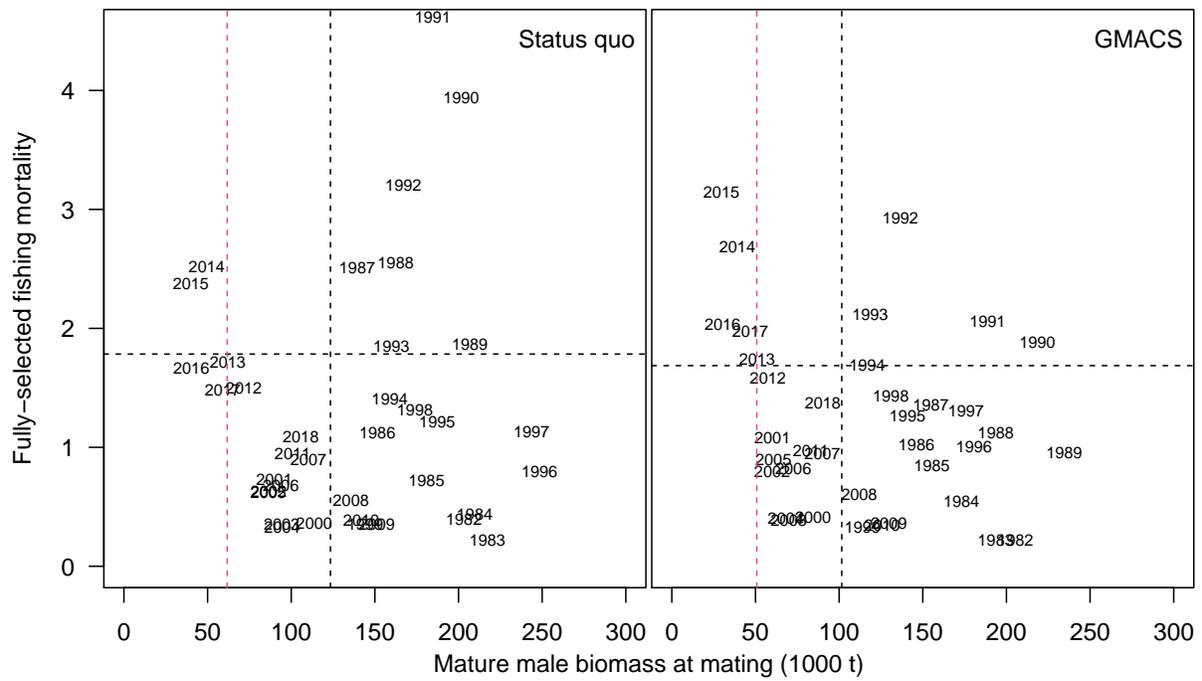
Figure 19: Kobe plot. Vertical dashed black line represents the MLE value for B35; Vertical dashed red line represents the overfished level, horizontal dashed black line represents F35