Transition from TCSAM02 to GMACS: Results with Parameter Estimation

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1 Introduction

The Tanner crab assessment model is transitioning between the current modeling framework which has been used since 2017, TCSAM02, to GMACS, the modeling framework used in all other Bering Sea crab stock assessments. As part of this transition, the CPT and SSC have requested that results from the two frameworks be compared under identical model scenarios, first for a single iteration of each model and then after optimizing the models. "Identical model scenarios" is understood here to mean model configurations that are "as close as reasonably possible" without altering the GMACS codebase such that continuity for assessments that already use GMACS would be interrupted. In the "Run 1" report (**?**), "exact equivalence" between a Tanner crab model in the two model frameworks was demonstrated by 1) creating a TCSAM02 model that replicates the 2025 assessment model as closely as possible to allow direct comparison with a GMACS model, 2) creating the equivalent model in GMACS, and 3) running both models for a single iteration to demonstrate that the models returned identical results (allowing for small margins of error due to the finite precision of the input files). This report presents the results after optimizing both models to find the parameter estimates that minmize each model's objective function. Although the "Run 1 report demonstrated the exact equivalence of the two models run with exactly equivalent parameter values, the parameter sets for the two models were not expected to be identical after optimization because, although the likelihood components based on data inputs that contributed to the models' objective functions were identical, additional components to the population dynamics and objective functions were model-specific. In particular,

1) selectivity function parameters were estimated on the arithmetic scale in the TCSAM02 model but on the ln-scale in the GMACS model,. This influenced convergence to the minimum objective function values in three ways: * parameter-associated gradients were different between the models, influencing model convergence * prior probabilities placed on parameters were not equivalent
2) natural mortality rates were parameterized differently such that the prior probabilities placed on the parameters were, again, not equivalent
3) two estimates of mean recruitment, corresponding to "spin up" and "normal" time periods, were estimated in the TCSAM02 model whereas only a single estimate for the entire model time period was estimated in the GMACS model. This contributed to very different recruitment time series estimates in the "spin up" period (1948-1973) that led to different initial

population trajectories, although the differences between the models substantially disappered after ~1990.

2 Tanner crab assessment model description

The 2025 Tanner crab assessment (Stockhausen 2025) was based on model configuration "22_03d5" and evaluated using the TCSAM02 modeling framework. The most relevant features of this model configuration include:

- time frame: 1948 - 2025
- biological/population dynamic processes
  - two sexes (males, females), two maturity states (immature, mature), two shell conditions (new shell, old shell)
  - 5 mm size bins from 25 mm CW to 185 mm CW (min and max cutpoint sizes), where the final size bin is an accumulator
  - recruitment
    - ln-scale means and annual deviations are estimated for two time periods
  - natural mortality
    - estimated by sex and maturity state for two time periods
  - molting and growth
    - molting occurs annually for immature crab
    - sex-specific post-molt size are modeled using two-parameter functions of pre-molt size
  - maturation (i.e., terminal molt)
    - sex-specific probability of terminal molt is estimated as a smooth function of size
- fishing mortality
  - based on four fleets: Tanner crab fleet (the directed fishery), snow crab fleet, Bristol Bay red king crab fleet, and groundfish fisheries
  - mortality is 100% for retained catch, 32.1% for discards in the directed fishery and the fisheries that capture Tanner crab as bycatch
  - ln-scale means and sex-specific annual deviations for capture rates are estimated by fleet for years when fleet-related fisheries are open
  - fishery selectivity for total catch is modeled as dome-shaped for males in the snow crab fishery; otherwise it is modeled using sex-specific ascending logistic functions
    - male-specific curves are estimated for three time periods for each of the bycatch fleets, annual deviations to the inflection point are estimated starting in 1991 for males in the directed fishery
  - retention in the directed fishery is modeled as an ascending logistic in two time periods
- survey catchability
  - two surveys are modeled: the annual NMFS EBS bottom trawl survey and the BSFRF side-by-side surveys (2013-2018)

  - fully-selected survey for the NMFS survey is sex-specific and estimated for two time periods; it is 1 for the BSFRF surveys
  - sex-specific survey selectivity is modeled as ascending normal curves of size; it is 1 at all sizes for both sexes for the BSFRF surveys

- data sources used to inform parameter estimation include:
  - annual estimated of fishery retained and total catch biomass and sex-specific size compositions from each of the four fishery fleets from at-sea and dockside observer sampling
  - annual survey biomass and size compositions from the two surveys (when conducted) for males, immature females, and mature females respectively
  - molt increment data from Tanner crab caught in the EBS
  - male maturity ogives estimated from individual chela height/carapace width measurements taken during the NMFS

3 Comparisons of key model quantities

Comparisons of important model quantities are presented in this section. More comprehensive comparisons of model results are provided in Section 5.

3.1 Management reference points

Comparison of management reference points included average recruitment, the OFL, F_{MSY}, F_{OFL}, B_{MSY}, and the biomass projected to the next year under the assumption that the OFL is taken (Table 1, Figure 1). The largest relative difference between the two models is for B_{MSY}, which The GMACS model estimates at ~10% larger than the TCSAM02 model.

3.2 Recruitment and MMB

Estimated recruitment time series differ substantially between the two models in the "spin-up" period from 1948-1973, but are extremely similar afterwards, with estimates for both models falling with the confidence bounds for the other model (Table 2, Figures 2 and 3). Similarly, estimated mature male biomass (MMB) time series differ substantially between the two models in the "spin-up" period from 1948-1973, as well as up to 1985 due to population dynamic lags, but again exhibit extremely similar trends afterwards, although the GMACS estimates tend be at the upper bound of the 90% confidence interval for the TCSAM02 estimates (Table 3, Figures 2 and 3).

3.3 Important processes

Estimated natural mortality (M) by population category differs less than 3% between the GMACS and TCSAM02 models, except for males in the "heightened" (1980-1984) time period of presumed higher-than-normal mortality when the TCSAM02 model estimates it to be 11% larger than that of the GMACS model (Table 4).

Estimated mean growth (post-molt carapace width, CW) as a pre-molt size differs less than 1% between the two models for both males and females (Table 5).

3.4 Data-derived likelihoods

Overall, the GMACS model fit the input data beterr than the TCSAM02 model by ~9 likelihood units (LUs). It fit the size composition data (fisheries and surveys) better than the TCSAM02 model by 35 LUs, but the TCAM02 model fit the survey biomass (20 LUs), catch (2 LUs), and growth (4 LUs) data better (Table 6).

3.5 Penalties and priors

The types of penalties and prior probabilities added to the data-derived likelihoods in the model objective functions differed beteen the GMACS and TCSAM02 models and wre not directly reconcilable without altering GMACS model code, which was not really desirable because of its potential impact on other assessments and a lack of time in which to do the alterations. Consequently, the values for these components are provided in model-specific tables (Tables 7 and 8). The parameterization used to estimate values for natural mortality, M, was different between the two model, but the priors placed on the estimates for this test were designed to be as close as possible given the funcdamental differences in paramterization. That the values in the tables are similar for all three population categories (pDM1 level 1 corresponds to immature crab; pDM1 level 2 corresponds to mature males; pDM1 level 3 corresponds to mature females) indicates that these priors did not have overdue influence on the convergence to the final estimates. The priors applied to the NMFS survey catchabilities (pQ level 2: males 1982+; pQ 1 level 4: females 1982+) were identical, so the difference in values (~11 LUs) indicates different levels of constraintapplied to the convergence of each model.

4 Summary

While the optimized GMACS and TCSAM02 models did not yield identical results, they were generally very similar. Nothing in this comparison should prevent the transition to GMACS as the framework with which to conduct the Tanner crab assessment.

5 Comprehensive model comparisons

More comprehensive comparisons between the GMACS and TCSAM02 models are presented in the following sections. Estimated model processes (e.g., growth, natural mortality, fishery selectivity, etc.) are compared in Section 5.1 using paired figures illustrating the estimates themselves and the differences between between the models. Fits to non-size composition data are compared in Section 5.5.1 while fits to survey size composition data are compared in Section 5.5.2 and fits to fishery size composition data are compared in Section 5.5.3. The likelihoods associated with the fits illustrated in the "Fits" sections are compared in Sections 5.6.1, 5.6.2, and 5.6.3. Non-data-related likelihood penalties and priors were presented in Section 3.5.

5.1 Model processes

5.1.1 Biological processes

Comparisons between results for biological processes incorporated in the models include allometry (sex-specific weight-at-size, Figure 4), size at recruitment (Figure 5), sex/life stage-specific natural mortality rates (Figure 6), sex-specific mean growth (Figure 8), growth transition matrices (Figures 9 and 10), and sex/size-specific probabilities of terminal molt (Figure 11). All differences between the two models are small.

5.1.2 Fishery characteristics

Comparison of fishery characteristics between the model frameworks included size-specific retention and capture/selectivity functions for males (Figures 12-16) and fully-selected capture rates (Figure 17). Differences in the retention curves for the directed fishery were negligible (Figure 12), as were selectivity curves for males after 1990 (Figure 13). However, the estimated directed fishery selectivity in the period before 1990 (i.e., before size composition data was available to inform either model's estimates) from the GMACS model was substantially shifted to smaller sizes relative to that from the TCSAM02 moddel. The estimated bycatch selectivity curves for the snow crab and BBRKC fisheries were very similar from both models (Figure 14 and 15), as were those estimated for the groundfish fisheries, except for the period 1987-1996 when the GMACS-estimated curves for males (in particular) were left-shifted to very small sizes suggesting the groundfish fleets were able to catch males of all sizes with the same efficiency. However, the uncertainty associated with the estimated size-at-50%-selected parameter for this curve was very large. Estimates of fully-selected catchability in the fisheries were remarkably similar between the two models across all of the fisheries, except during the pre-1975 time period for the directed fishery (only retained catch data from the foreign fleets informed the models during this period) and the 1987-1997 period for the groundfish fisheries coinciding with the difference in estimated selectivity (Figure 17).

5.1.3 Survey characteristics

Comparison of survey characteristics between the model frameworks included sex- and size-specific selectivity functions for the NMFS survey (Figure 18) and fully-selected survey catchability (Figure 20). The selectivity curves for females were almost identical for both models for both selectivity time periods (1975-1981; 1982+), while those estimated for males were slightly left-shifted to smaller sizes in the pre-1982 time period. The estimates for fully-selected catchability were als quite similar for females in both time periods and males in the post-1981 time period. The estimated catchability for males in the 1975-1981 time period was higher in the GMACS model than the TSCAM0s2 model, offsetting in large part the differences in estimated male selectivity in this period.

5.2 Predicted population quantities

Comparison of population quantities between the model frameworks included recruitment, cohort progression, aggregated abundance by population category, sex- and stage-specific population size compositions, aggregated biomass by population category, and size-specific male maturity ogives (Figures 21-38). All quantities differed by less than 10^{-4}% between the the two model frameworks. As noted previously, recruitment estimates differ between the two models substatially before 1975 but basically converge afterwards ([Figure 21). The difference in scale of recruitment is over a factor of two prior to 1960 but decreases rapidly and, once informed by data, the patterns in recruitment are very similar. The small differences between estimates for growth and natural mortality illustrated in previous sections have almost no impact on cohort progression (Figures 22 and 23), so any major differences in population trajectories will be due to the differences in estmiated recruitment. Differences in predicted aggregated abundance and abundance-at-size in population sex-by-maturity-state categories decrease from ~100% in the prior to 1965 to ~10% by 1990 (Figures 24-34). Similar differences occur for predicted population biomass by population sex-by-maturity-state category. Differences in predicted maturity ogives are very small, whether on model or observed size bins (Figures 37 and 38).

5.3 Predicted fisheries quantities

Comparison of fishery-related quantities between the model frameworks included fishery-specific capture abundance and biomass, total fishing mortality, and retained catch mortality (Figures 39 and 44). Differences in model estimates for cature abundance in the fisheries were small ($< 2\%$) for bycatch in the groundfish fisheries across all years and after 1990 for all of the crab fisheries, but large relative differences were evident prior to this for the BBRKC fishery and the directed fishery (39). For the directed fishery, the diffrences were due to differences in estimated fully-selected capture rates and poulation abundance (driven by differneces in recruitment)in this period (Figures 39 and 40). For the BBRKC fishery, the fully-selected capture rates were similar; the differences were driven by differences in population sizes through differences in recruitment. Results for capture biomass were similar to those for capture abunadnce (Figures 41 and 42). Differences between the models in total fishing mortality primarily paralleled those for differences in the directed fishery capture abundance and biomass (Figure 43). Differences in estimated retained catch mortality were typically $< 5\%$ before 1980 (when retained catch size composition entered the likelihood) and much smaller afterward (Figure 44).

5.4 Predicted survey quantities

Comparison of survey-related quantities between the model frameworks included sex-specific survey biomass (Figures 45 and 46). Model estimates for NMFS survey biomass followed very similar trends; relative differences were largest (~25% in 1982 for males) and varied in degree before 1985e, but differed less than 5% after 1985 (45). Model estimates for BSFRF survey biomass followed very similar trends as well, with the GMACS estimates ~5-8% larger than the TCSAM02 estimate across most years the survey was conducted.

5.5 Fits to data

5.5.1 Fits to non-size composition data

5.5.1.1 Fits to growth (molt increment) data

The "fits" obtained for growth data using the two model frameworks are compared in Figure 47. They are essentially identical, although differences in estimated post-molt size exhibit a small linear increase with pre-molt size for females.

5.5.1.2 Fits to male maturity ogive data

The "fits" obtained for male maturity ogive data using the two model frameworks are compared in Figure 48. They are essentially identical, with differences in simple (observed - predicted) residuals less than 10^{-3}. However, the GMACS model used the TCSAM02-estimated probability of molt-to-maturity ogive because the ability to estimate it as is done in the TCSAM02 model has not yet been implemented in GMACS. Thus, differences in the predicted ogives are only due to differences in the annual ratios of the predicted abundance of mature new shell males to all new shell males.

5.5.1.3 Fits to survey biomass

The fits obtained to survey biomass data using the two model frameworks are compared in Figures 49-54. Both the data and predicted values are examined, and differences in results between the two model frameworks evaluated based on the differences between the Pearson's residuals, ρ, for each dataset. Because the likelihoods for survey biomass data assume lognormal error distributions, the Pearson's residuals for the model fits were calculated on the ln-scale as well:

$$\rho = \frac{(ln(O) - ln(P))}{\sqrt{ln(1 + cv^2)}} \tag{1}$$

where O is the observed value, P is the predicted value (i.e., from the lefthand plots in Figures 49-54), cv is the coefficient of variation for the observation (all on the arithmetic scale).

As noted previously, the estimates from the two frameworks for NMFS survey biomass are very similar, with relatively small differences between them for males prior to 1985 (1982 exhibiting the largest difference) and only extremely small differences after 1985 (Figure 49). The differences between the esimtated trends for immature and mature females are evan smaller (Figures 50 and 51). However, it must be pointed out that neither model does a great job of fitting either the timing or the magnitude of the peaks and valeys in the observed data.

Similarly, the estimated survey biomass from the two frameworks for BSFRF survey biomass are very similar, and while both fit the data for immature females well (Figure 53), neither does for most of the male or mature female observations (Figures 52 and 54).

5.5.1.4 Fits to fishery catch biomass and abundance

The fits obtained to fishery catch biomass and abundance data using the two model frameworks are compared in Figure 55 for retained catch biomass, Figures 56-59 for total catch biomass, and Figure 60 for total catch abundance in the groundfish fisheries. Both the data and predicted values were examined, and differences in results between the two model frameworks were evaluated based on the differences between the Pearson's residuals, ρ, for each dataset. Because the likelihoods for fishery catch biomass and abundance data assume lognormal error distributions, the Pearson's residuals for the model fits were calculated in the same manner as those for survey biomass (Equation 1).

The results from the two frameworks for fits to the data are essentially identical, with most of the differences between the Pearson's residuals less than 0.1.

5.5.2 Fits to survey size composition data

The equivalence between GMACS and TCSAM02 for fits to survey size composition data are evaluated in this section for the "noInitFs" model scenario. For all survey size compositions, following standard practice, 5% tail compression was performed on both ends of each composition to stabilize model fitting. The resulting size compositions were fit directly by three sex/maturity categories: 1) males, 2) immature females, and 3) mature females. The survey size compositions were fit using these categories to reflect the similar categories used to fit survey biomass data.

Fits to survey size compositions from the NMFS and BSFRF surveys are compared between the model frameworks in Figures 61-72. The relevant observed and predicted size compositions from the two model frameworks are compared by year in the same figure followed by a figure showing the differences between the two frameworks for the associated Pearson's residuals, where Pearson's residuals, r were calculated for a given size composition by size bin in both frameworks using the formula

$$r = \frac{(O - P)}{\sqrt{\frac{(P+\delta)\cdot(1-(P+\delta))}{n}}}$$

where O and P are the observed and predicted values for a size bin, n is the effective sample size for the size composition, and δ is a small value (0.001 here) added to keep the denominator from becoming zero. Pearson's residuals reflect the degree of fit to the data by the predictions and thus the difference between the residuals from the two frameworks reflects on differences in contributions by size bin to differences in the overall likelihood. While it would have been more straightforward to show differences between the frameworks in the likelihoods by size bin, this was not available in the GMACS output.

The figures indicate almost exact agreement between the two frameworks for fits to the survey size composition data, with differences in the Pearson's residuals generally on the order of less than 0.00001.

5.5.3 Fits to fishery size composition data

The equivalence between GMACS and TCSAM02 for fits to fishery size composition data are evaluated in this section for the "noInitFs" model scenario. For all fishery size compositions, following standard practice, 5% tail compression was performed on both ends of each composition to stabilize model fitting. The resulting retained catch size compositions were fit directly while the sex-specific total catch size compositions were fit by appending the female size compositions to the male size composition to form an "extended" size composition that allowed the sex-specific compositions to be fit simultaneously. It was necessary to fit the total catch size compositions in this fashion because the associated catch biomass data was fit in a sex-aggregated fashion.

Fits to fishery size compositions are compared between the model frameworks in Figures 73-90 for retained catch in the directed fishery (males only) and total catch in the directed, snow crab, BBRKC, and groundfish fisheries by sex. For each catch type (retained or total), fishery, and sex, the relevant observed and predicted size compositions from the two model frameworks are compared by year in the same figure followed by a figure showing the differences between the two frameworks for the associated Pearson's residuals, where Pearson's residuals, r were calculated for a given size composition by size bin in both frameworks using the formula

$$r = \frac{(O - P)}{\sqrt{\frac{(P+\delta)\cdot(1-(P+\delta))}{n}}}$$

where O and P are the observed and predicted values for a size bin, n is the effective sample size for the size composition, and δ is a small value (0.001 here) added to keep the denominator from becoming zero. Pearson's residuals reflect the degree of fit to the data by the predictions and thus the difference between the residuals from the two frameworks reflects on differences in contributions by size bin to differences in the overall likelihood. While it would have been more straightforward to show differences between the frameworks in the likelihoods by size bin, this was not available in the GMACS output.

Overall, the figures indicate almost exact agreement between the two frameworks for fits to the fishery size composition data, with differences in the Pearson's residuals generally on the order of less than 0.00001. Notable exceptions occur, however, for fits to female total catch size compositions in the snow crab fishery in 2024 (Figures 81 and 82) and in the BBRKC fishery in 1998 and 2018 (Figures 85 and 86). While notable in terms of the other fits, these differences are still quite small. The source of these differences are the slightly different criteria used in the two frameworks to determine the size bins included in the compression of size composition "tails"; generally, the results are obviously identical.

5.6 Data likelihoods

5.6.1 Non-size composition data likelihoods

5.6.1.1 growth and male maturity data

Negative log-likelihood scores for fits to growth (pre-molt, post-molt size data) agreed within 2 LUs between the models (Figure 91), with the TCSAM02 model fitting the growth data slightly better thatn the GMACS model. Negative log-likelihood scores fits to the male maturity ogive data differed by less than 0.3 LUs (Figure 92); both models fit the data similarly.

5.6.1.2 fishery and survey time series data

Comparison of likelihood-related quantities for input data components between the model frameworks also included summary likelihoods related to fishery catch biomass and abundance time series data (Figures 93-94) and to survey biomass time series data (Figure 95). Due to differences between the two frameworks in whether constant terms were included in the summary likelihoods, these were **not** directly comparable between the two models for fishery catch data and were not expected to agree (catch biomass: Figure 93; catch abundance: 94).

In contrast, the constant terms were treated identically in the two frameworks when calculating summary likelihoods for the fits to survey biomass and thus these are directly comparable: these exhibited a maximum difference of -10 LUs for male biomass from the NMFS survey Figure 95. The TCSAM02 model exhibited the better fit across both surveys for all population categories except mature female biomass in the NMFS survey, which the GMACS model fit slightly better (< 1 LU).

To assess the fits to the fishery retained and total catch biomass and abundance time series data on a comparable basis, the individual likelihood values were recalculated from model output without the constant terms (Figures 96-98). Differences in negative log-likelihod scores were less than 1 LU across all fleets.

5.6.2 Survey size composition data likelihoods

The equivalence between GMACS and TCSAM02 for likelihood values arising from fits to survey size composition data from the NMFS and BSFRF surveys (Section 5.5.2) are evaluated in this section. In both frameworks, multinomial likelihoods were used to assess the degree of fit to the survey size composition data. The differences between the two frameworks for contributions to the overall model likelihood from fits to the survey size composition data were evaluated by comparing the associated negative log-likelihood values by survey (Figure 99) and by year for each survey (Figures 100 and 101).

Overall, the GMACS model fit the survey size composition data better than the TCSAM02 model by ~14 LUs (summed across all categories and both surveys). It fit the immature female and male categories better for both surveys whereas both models fit the mature female size compositions similarly well.

The differences in negative log-likelohood values between the two models varied annually and by population component and survey, with most differences less than 0.5 LUs. Notable exceptions occurred for fits to the male NMFS size compositions in 1979-1984, where the TCSAM02 model fit the data better for 1979-1981 and the GMACS model fit the data better in 1982 and 1984.

5.6.3 Fishery size composition data likelihoods

The equivalence between GMACS and TCSAM02 for likelihood values arising from fits to fishery size composition data are evaluated in this section for the "noInitFs" model scenario. In both frameworks, multinomial likelihoods were used to assess the degree of fit to the fishery size composition data. The differences between the two frameworks for contributions to the overall model likelihood from fits to the fishery size composition data were evaluated by comparing the associated negative log-likelihood values by fleet (Figure 102) and by year for each fleet for retained (directed fishery only, Figure 103) and total catch size compositions (Figures 104-107).

In summsry, the GMACS model fit the fishery-related size compositions better than the TCSAM02 model across all fleets and catch types (retained vs. total) except for male total catch size compositions in the directed fishery, although the differences were fairly small (1-2 LUs) except for fits to the groundfish bycatch size composition data which the GMACS model fit better by ovr 15 LUs.

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Table 1. Management quantities. Units: biomass units in 1,000's t (OFL, prjB: projected biomass, Bmsy: MMB at MSY), fishing mortality units: year^{-1}, recruitment: millions.

type	tcsam	gmacs	%(tcsam-gmacs)
OFL	51.02	55.50	-8.4079
prjB	75.95	83.01	-8.8816
Bmsy	43.22	47.61	-9.6720
Fmsy	1.47	1.42	3.7309
Fofl	1.47	1.42	3.7309
avgRec	601.25	633.80	-5.2710

Table 2. Comparison of ln-scale estimates (`est`, with 90% confidence intervals `lci` and `uci`) for total recruitment by year. Confidence intervals are 90% based on a normal distribution.

	gmacs			tcsam		
year	est	lci	uci	est	lci	uci
1949	7.65	6.83	8.4631	6.46	2.77	10.15
1950	7.65	6.83	8.4627	6.46	2.96	9.96
1951	7.65	6.83	8.4621	6.46	3.15	9.77
1952	7.65	6.83	8.4614	6.46	3.35	9.58
1953	7.65	6.83	8.4603	6.47	3.56	9.38
1954	7.65	6.83	8.4589	6.48	3.78	9.17
1955	7.65	6.83	8.4571	6.49	4.01	8.96
1956	7.64	6.83	8.4547	6.50	4.25	8.75
1957	7.64	6.83	8.4516	6.52	4.50	8.53
1958	7.64	6.83	8.4478	6.55	4.77	8.32
1959	7.64	6.83	8.4429	6.59	5.06	8.12
1960	7.63	6.83	8.4370	6.64	5.36	7.93
1961	7.63	6.83	8.4304	6.72	5.66	7.78
1962	7.63	6.83	8.4259	6.83	5.94	7.71
1963	7.63	6.84	8.4282	6.98	6.17	7.79
1964	7.65	6.85	8.4465	7.22	6.34	8.09
1965	7.69	6.88	8.4934	7.57	6.60	8.54
1966	7.77	6.95	8.5864	8.03	7.05	9.00
1967	7.92	7.06	8.7719	8.46	7.69	9.23
1968	8.23	7.32	9.1343	8.57	7.95	9.19
1969	8.18	7.40	8.9670	8.09	7.45	8.74
1970	7.70	7.06	8.3471	7.62	7.04	8.19
1971	7.58	7.08	8.0740	7.38	6.89	7.87
1972	7.20	6.72	7.6808	6.87	6.35	7.39
1973	6.85	6.35	7.3570	6.52	5.99	7.05
1974	7.49	7.07	7.9137	6.94	6.34	7.53
1975	7.46	6.90	8.0218	7.44	6.93	7.94
1976	8.34	8.04	8.6304	8.07	7.75	8.39
1977	7.73	7.39	8.0818	7.64	7.26	8.03
1978	6.57	6.02	7.1110	6.47	5.71	7.23
1979	6.09	5.58	6.5963	6.00	5.21	6.78
1980	5.95	5.51	6.3980	5.81	5.14	6.49
1981	6.17	5.81	6.5240	6.05	5.59	6.52
1982	6.18	5.82	6.5400	5.93	5.46	6.40
1983	7.26	7.06	7.4540	7.13	6.91	7.34
1984	7.04	6.79	7.2919	6.86	6.58	7.14
1985	6.97	6.70	7.2363	6.96	6.68	7.23
1986	7.11	6.88	7.3421	7.09	6.85	7.33
1987	6.89	6.65	7.1302	6.74	6.45	7.03

(continued)

year	gmacs_est	gmacs_lci	gmacs_uci	tcsam_est	tcsam_lci	tcsam_uci
1988	6.32	6.02	6.6236	6.37	6.04	6.70
1989	5.70	5.37	6.0230	5.58	5.14	6.01
1990	5.07	4.69	5.4562	4.97	4.42	5.52
1991	4.80	4.44	5.1608	4.64	4.11	5.17
1992	4.84	4.52	5.1659	4.76	4.34	5.19
1993	4.92	4.60	5.2412	4.81	4.38	5.23
1994	5.05	4.73	5.3636	4.92	4.51	5.34
1995	5.46	5.19	5.7281	5.44	5.14	5.74
1996	5.45	5.15	5.7509	5.17	4.76	5.57
1997	6.07	5.87	6.2818	6.11	5.90	6.32
1998	5.43	5.10	5.7581	5.13	4.71	5.55
1999	6.68	6.50	6.8606	6.68	6.50	6.87
2000	5.83	5.47	6.1943	5.54	5.06	6.02
2001	7.01	6.82	7.1940	7.03	6.85	7.22
2002	6.14	5.77	6.5039	5.92	5.45	6.39
2003	7.13	6.94	7.3194	7.12	6.93	7.32
2004	6.45	6.19	6.6998	6.46	6.19	6.73
2005	5.56	5.21	5.9140	5.46	5.01	5.90
2006	5.18	4.77	5.5846	4.92	4.29	5.54
2007	5.55	5.18	5.9157	5.51	5.06	5.96
2008	6.39	6.05	6.7363	6.24	5.82	6.67
2009	7.34	7.16	7.5300	7.38	7.20	7.57
2010	6.41	6.13	6.6917	6.35	6.03	6.68
2011	5.57	5.26	5.8837	5.60	5.25	5.95
2012	4.86	4.49	5.2283	4.45	3.83	5.06
2013	5.27	5.03	5.5169	5.31	5.05	5.57
2014	4.77	4.46	5.0733	4.58	4.18	4.98
2015	4.95	4.66	5.2460	4.78	4.42	5.13
2016	5.53	5.30	5.7624	5.43	5.18	5.68
2017	6.93	6.79	7.0682	6.88	6.73	7.03
2018	6.30	6.09	6.5171	6.28	6.05	6.50
2019	6.52	6.28	6.7592	6.53	6.28	6.77
2020	5.96	5.42	6.5054	5.38	4.41	6.36
2021	7.47	7.25	7.6854	7.46	7.24	7.69
2022	7.65	7.40	7.8930	7.66	7.40	7.91
2023	7.61	7.33	7.8796	7.63	7.35	7.92
2024	6.77	6.31	7.2297	6.84	6.32	7.36
2025	6.39	5.86	6.9253	6.49	5.84	7.13

Table 3. Comparison of ln-scale estimates (`est`, with 90% confidence intervals `lci` and `uci`) for mature male biomas (MMB) by year. Confidence intervals are 90% based on a normal distribution.

	gmacs			tcsam		
year	est	lci	uci	est	lci	uci
1948	-11.51	-11.51	-11.5129	-11.51	-11.51	-11.51
1949	-11.51	-11.51	-11.5129	-11.51	-11.51	-11.51
1950	-2.11	-3.05	-1.1649	-2.99	-6.69	0.72
1951	0.56	-0.24	1.3560	-0.50	-4.16	3.17
1952	2.48	1.75	3.2166	1.37	-2.26	5.01
1953	3.90	3.24	4.5682	2.74	-0.85	6.33
1954	4.82	4.23	5.3993	3.62	0.10	7.14
1955	5.32	4.82	5.8301	4.12	0.70	7.53
1956	5.60	5.14	6.0533	4.38	1.10	7.67
1957	5.76	5.34	6.1844	4.55	1.42	7.67
1958	5.86	5.46	6.2678	4.65	1.69	7.61
1959	5.93	5.54	6.3235	4.72	1.95	7.49
1960	5.98	5.60	6.3612	4.78	2.21	7.34
1961	6.01	5.64	6.3855	4.81	2.47	7.16
1962	6.03	5.67	6.4000	4.85	2.74	6.96
1963	6.05	5.69	6.4072	4.88	3.02	6.74
1964	6.05	5.70	6.4108	4.91	3.33	6.50
1965	6.05	5.70	6.4078	4.94	3.62	6.26
1966	6.05	5.70	6.4011	4.98	3.97	6.00
1967	5.99	5.63	6.3619	4.96	4.20	5.71
1968	5.92	5.53	6.3120	4.96	4.52	5.39
1969	5.81	5.37	6.2434	4.91	4.64	5.17
1970	5.72	5.23	6.2003	4.81	4.46	5.16
1971	5.71	5.23	6.1907	5.26	4.55	5.98
1972	5.80	5.40	6.1953	5.80	5.28	6.31
1973	5.91	5.64	6.1863	6.09	5.79	6.39
1974	5.95	5.77	6.1269	6.14	5.94	6.33
1975	5.90	5.76	6.0279	6.05	5.90	6.21
1976	5.68	5.56	5.8043	5.84	5.69	5.99
1977	5.30	5.17	5.4275	5.54	5.38	5.70
1978	4.98	4.84	5.1183	5.29	5.12	5.46
1979	4.78	4.65	4.9222	5.17	4.99	5.36
1980	4.42	4.22	4.6226	4.98	4.81	5.15
1981	4.51	4.32	4.6919	4.91	4.77	5.06
1982	4.62	4.47	4.7806	4.82	4.67	4.96
1983	4.50	4.34	4.6605	4.54	4.37	4.70
1984	4.18	3.98	4.3763	4.11	3.90	4.32
1985	4.15	3.99	4.3095	4.03	3.86	4.19

(continued)

year	gmacs_est	gmacs_lci	gmacs_uci	tcsam_est	tcsam_lci	tcsam_uci
1986	4.32	4.21	4.4297	4.18	4.07	4.29
1987	4.55	4.47	4.6374	4.40	4.31	4.49
1988	4.79	4.72	4.8679	4.64	4.57	4.72
1989	4.84	4.77	4.9131	4.74	4.67	4.82
1990	4.67	4.59	4.7455	4.70	4.62	4.78
1991	4.65	4.58	4.7240	4.71	4.63	4.78
1992	4.56	4.48	4.6408	4.59	4.51	4.67
1993	4.49	4.41	4.5680	4.48	4.40	4.57
1994	4.35	4.27	4.4377	4.32	4.23	4.41
1995	4.16	4.07	4.2523	4.11	4.01	4.20
1996	3.96	3.87	4.0572	3.89	3.79	3.98
1997	3.80	3.70	3.8942	3.70	3.60	3.80
1998	3.69	3.59	3.7875	3.58	3.48	3.68
1999	3.66	3.57	3.7591	3.55	3.45	3.65
2000	3.71	3.62	3.8058	3.59	3.49	3.69
2001	3.82	3.73	3.9111	3.70	3.60	3.79
2002	3.97	3.88	4.0614	3.86	3.76	3.95
2003	4.15	4.06	4.2384	4.05	3.96	4.14
2004	4.35	4.27	4.4400	4.25	4.16	4.34
2005	4.53	4.45	4.6172	4.44	4.35	4.53
2006	4.69	4.61	4.7786	4.60	4.52	4.69
2007	4.82	4.74	4.9033	4.73	4.65	4.82
2008	4.91	4.83	4.9918	4.82	4.74	4.91
2009	4.90	4.81	4.9813	4.81	4.73	4.90
2010	4.78	4.69	4.8620	4.69	4.60	4.77
2011	4.63	4.55	4.7167	4.53	4.44	4.62
2012	4.60	4.51	4.6777	4.50	4.41	4.58
2013	4.72	4.65	4.7997	4.64	4.56	4.72
2014	4.84	4.76	4.9160	4.76	4.68	4.84
2015	4.79	4.71	4.8699	4.71	4.63	4.79
2016	4.67	4.60	4.7515	4.59	4.51	4.67
2017	4.48	4.40	4.5585	4.38	4.30	4.46
2018	4.28	4.20	4.3626	4.17	4.08	4.26
2019	4.13	4.04	4.2104	4.01	3.92	4.10
2020	4.06	3.98	4.1469	3.94	3.86	4.03
2021	4.21	4.12	4.2890	4.10	4.01	4.18
2022	4.45	4.36	4.5304	4.35	4.26	4.43
2023	4.61	4.52	4.6912	4.51	4.43	4.60
2024	4.70	4.61	4.7847	4.60	4.51	4.69

Table 4. Comparison of estimated natural mortality rates (M) by population class from the GMACS and TCSAM02 models. The 'heightened'period is 1980-1984.

		maturity	shell			
period	sex	state	condition	gmacs	tcsam	%(tcsam-gmacs)
heightened	female	immature	undetermined	0.248	0.251	1.245
heightened	female	mature	undetermined	0.660	0.650	-1.572
heightened	male	immature	undetermined	0.248	0.251	1.245
heightened	male	mature	undetermined	0.660	0.738	11.082
normal	female	immature	undetermined	0.248	0.251	1.245
normal	female	mature	undetermined	0.317	0.319	0.692
normal	male	immature	undetermined	0.248	0.251	1.245
normal	male	mature	undetermined	0.309	0.318	2.688

Table 5. Comparison of estimated sex-specific mean growth (post-molt size, mm CW) as a function of pre-molt size (mm CW) from the GMACS and TCSAM02 models.

sex	pre-molt size (mmCW)	gmacs	tcsam	%(tcsam-gmacs)
female	27	35.847	35.751	-0.269
female	32	41.731	41.621	-0.263
female	37	47.519	47.396	-0.259
female	42	53.224	53.088	-0.255
female	47	58.858	58.710	-0.252
female	52	64.429	64.269	-0.249
female	57	69.944	69.772	-0.246
female	62	75.408	75.225	-0.244
female	67	80.826	80.631	-0.241
female	72	86.201	85.995	-0.239
female	77	91.537	91.320	-0.237
female	82	96.836	96.609	-0.235
female	87	102.102	101.864	-0.233
female	92	107.335	107.087	-0.232
female	97	112.539	112.281	-0.230
female	102	117.715	117.446	-0.229
female	107	122.863	122.585	-0.227
female	112	127.987	127.698	-0.226
female	117	133.086	132.788	-0.224
female	122	138.163	137.855	-0.223
female	127	143.218	142.900	-0.222
female	132	148.251	147.924	-0.221
female	137	153.265	152.929	-0.220
female	142	158.259	157.914	-0.219
female	147	163.235	162.881	-0.217
female	152	168.193	167.830	-0.216
female	157	173.134	172.761	-0.216
female	162	178.058	177.677	-0.215
female	167	182.967	182.576	-0.214
female	172	187.860	187.460	-0.213
female	177	192.737	192.329	-0.212
female	182	197.601	197.184	-0.211
male	27	35.125	35.011	-0.325
male	32	41.668	41.547	-0.292
male	37	48.217	48.090	-0.264
male	42	54.771	54.640	-0.239
male	47	61.329	61.196	-0.217

(continued)

sex	pre-molt size (mmCW)	gmacs	tcsam	%(tcsam-gmacs)
male	52	67.891	67.757	-0.198
male	57	74.457	74.323	-0.180
male	62	81.025	80.893	-0.164
male	67	87.596	87.466	-0.149
male	72	94.171	94.044	-0.135
male	77	100.747	100.625	-0.122
male	82	107.326	107.209	-0.109
male	87	113.907	113.796	-0.098
male	92	120.490	120.385	-0.087
male	97	127.076	126.978	-0.077
male	102	133.663	133.573	-0.067
male	107	140.251	140.170	-0.058
male	112	146.842	146.770	-0.049
male	117	153.434	153.372	-0.041
male	122	160.028	159.976	-0.032
male	127	166.623	166.582	-0.025
male	132	173.219	173.189	-0.017
male	137	179.817	179.799	-0.010
male	142	186.416	186.411	-0.003
male	147	193.017	193.024	0.004
male	152	199.618	199.639	0.010
male	157	206.221	206.255	0.016
male	162	212.825	212.873	0.023
male	167	219.430	219.493	0.028
male	172	226.037	226.114	0.034
male	177	232.644	232.736	0.040
male	182	239.252	239.360	0.045

Table 6. Negative log-likelihood contributions to the objective function by data type.

type	gmacs	tcsam	diff(tcsam-gmacs)
catch data	-170.59	-172.59	-2.0071
index biomass data	293.66	273.83	-19.8238
size comp. data	2,181.97	2,217.18	35.2075
growth data	515.01	511.06	-3.9559
MMO data	428.86	428.89	0.0291

Table 7. GMACS negative log-likelihood values for general penalties and priors on parameters. All penalties were set to 0. M: immature crab: (normal) prior on estimated M for immature crab, M: mature females: (normal) prior on estimated M for mature females, M: mature males: (normal) prior on estimated M for mature males, NMFS survey q: (normal) priors on estimated sex-specific catchability coefficients (i.e., q) for the NMFS survey. See text for details on comparison with TCSAM02 values.

parameter	NLL
M: immature crab	-2.323216
M: mature female	25.057168
M: mature males	20.117711
NMFS survey q, females 1982+	76.877890
NMFS survey q, males 1982+	29.726517

Table 8. TCSAM02 negative log-likelihood values for general penalties and priors on parameters. Smoothness: penalties on second differences and decreaing values in the size dependence of estimated male terminal molt parameters. Recruitment/pDevsLnr: sum of (normal) priors on individual recruitment deviation parameters. Natural mortality/pDM1: (normal) priors on estimated multipliers to base M for immature crab (level 1), mature males (level 2), and mature females (level 3). Surveys/pQ: (normal) priors on estimated survey catchability coefficients (i.e., q) for males (level 1) and females (level 2) in the NMFS survey. See text for details on comparison with GMACS values.

category	type	element	level	NLL
penalties	maturity	smoothness	1	1.2059603
penalties	maturity	smoothness	2	0.5827112
priors	recruitment	pDevsLnR	1	47.6452429
priors	recruitment	pDevsLnR	2	70.0206389
priors	natural mortality	pDM1	1	-0.3946661
priors	natural mortality	pDM1	2	26.8932035
priors	natural mortality	pDM1	3	27.9936332
priors	surveys	pQ	2	24.2589957
priors	surveys	pQ	4	70.6390369

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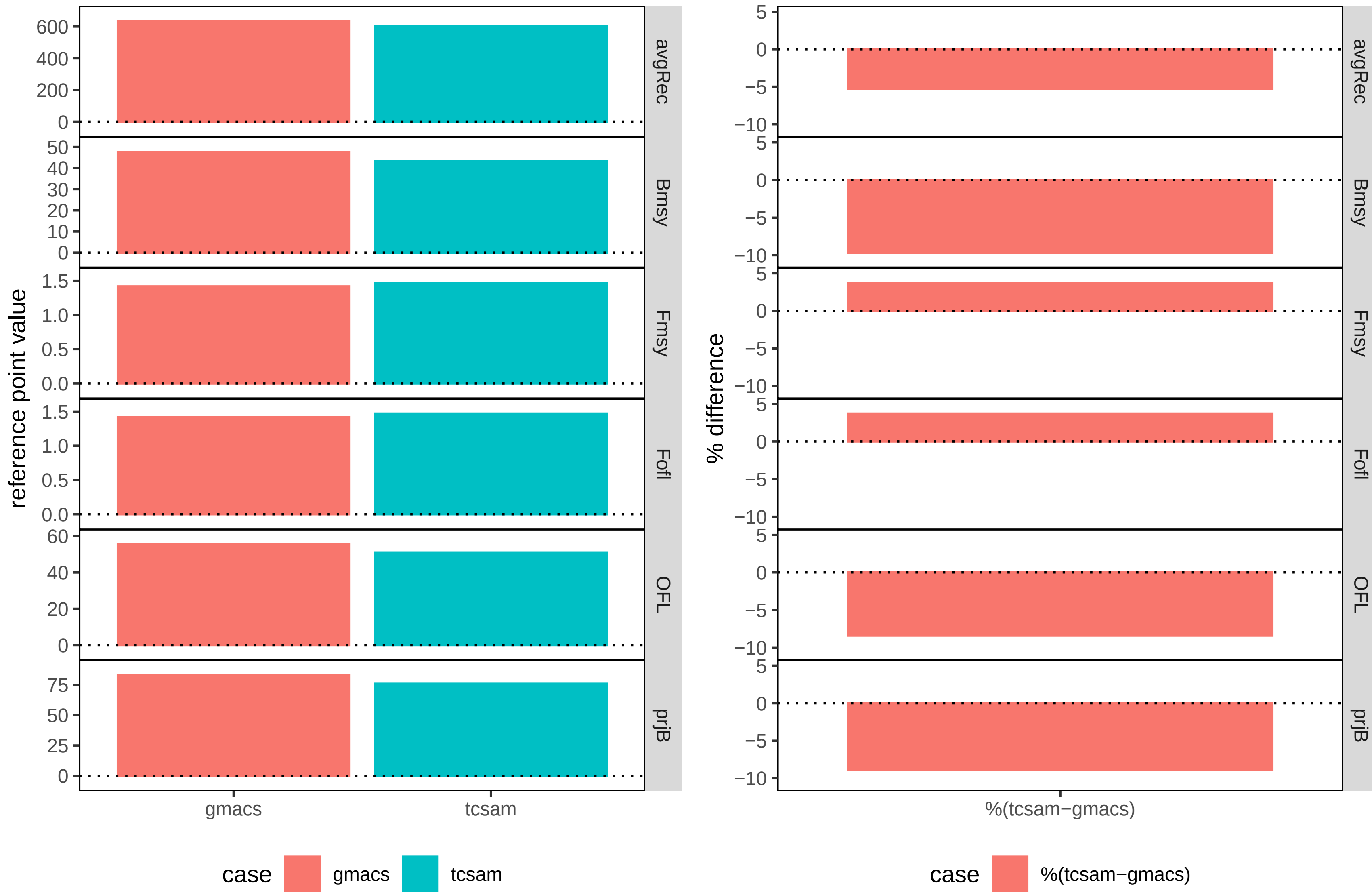


Figure 1. Comparison of management reference point values from the GMACS and TCSAM02 models. Left: values; right: % differences.

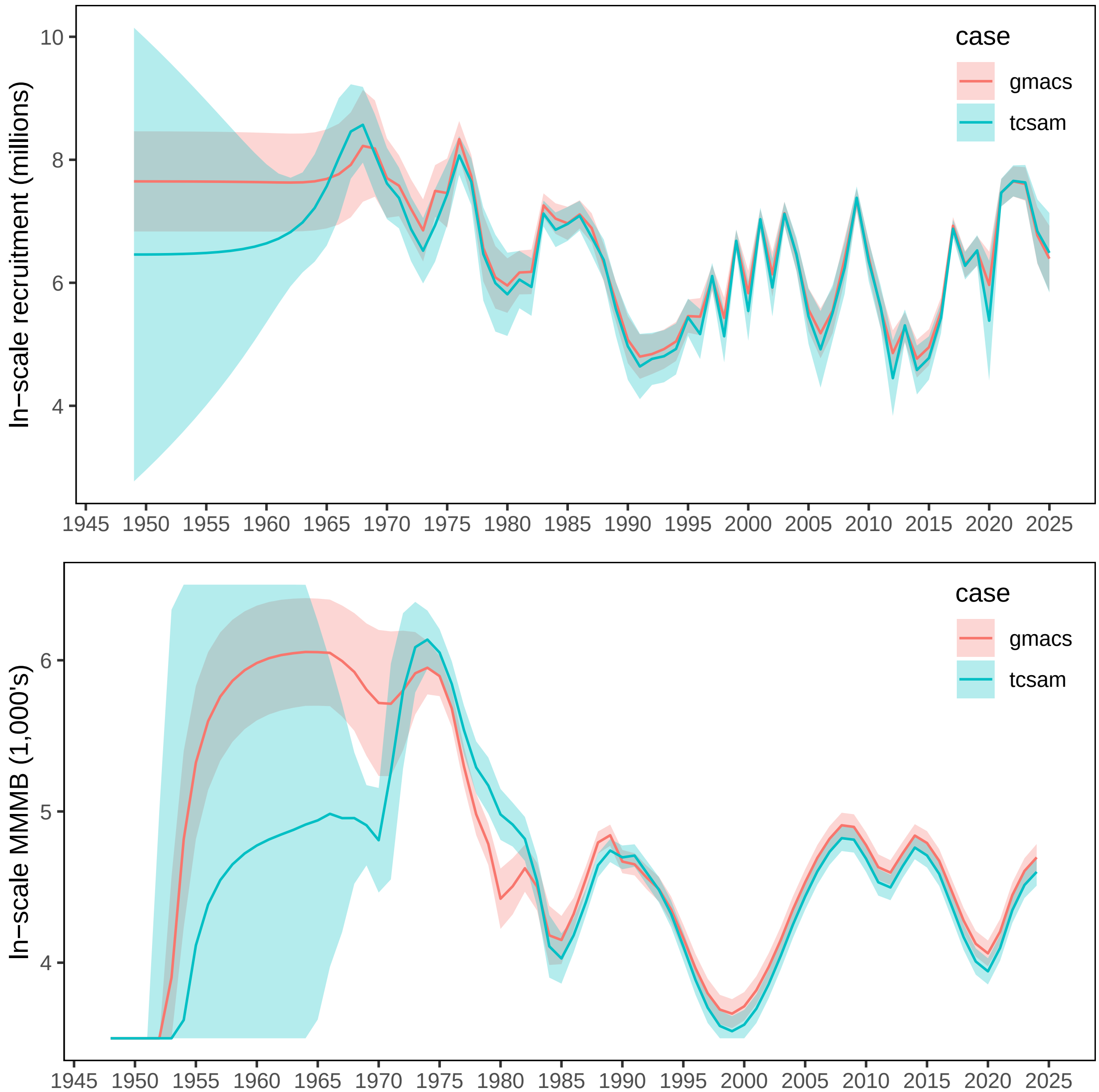


Figure 2. Comparison of estimated ln-scale recuitment and mature male biomass (MMB) from the GMACS and TCSAM02 models. Upper: recruitment (millions); lower: MMB (1,000's). MMB scale excludes initial model spin-up from 1948-1955 to better show later details.

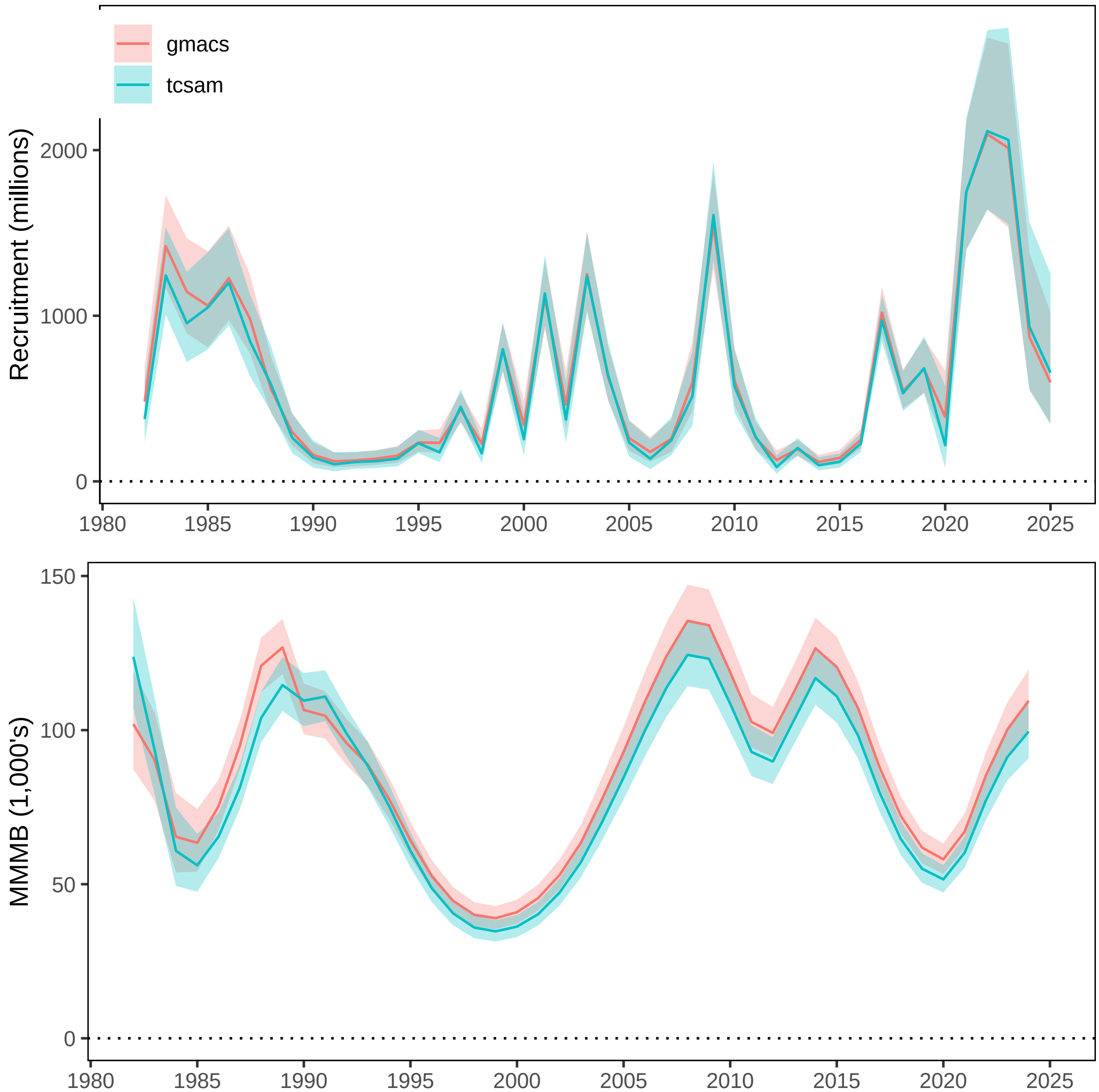


Figure 3. Comparison of estimated (arithmetic scale) recuitment and mature male biomass (MMB) from the GMACS and TCSAM02 models. Upper: recruitment (millions); lower: MMB (1,000's). The time frame starts in 1982 to better show later details.

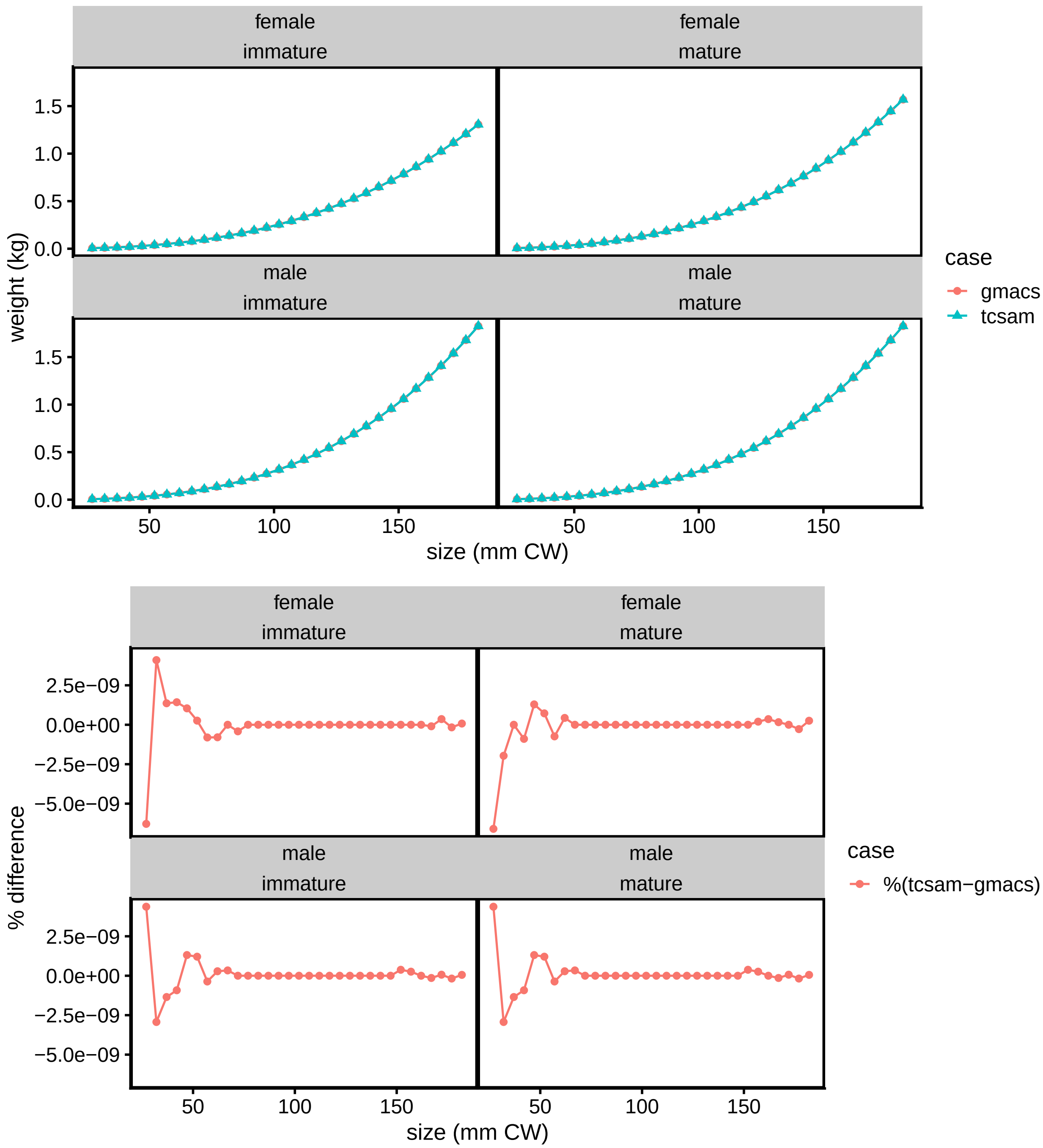


Figure 4. Comparison of weights-at-size used in the GMACS and TCSAM02 models by biological category. Upper: values overlaid; lower: percent differences.

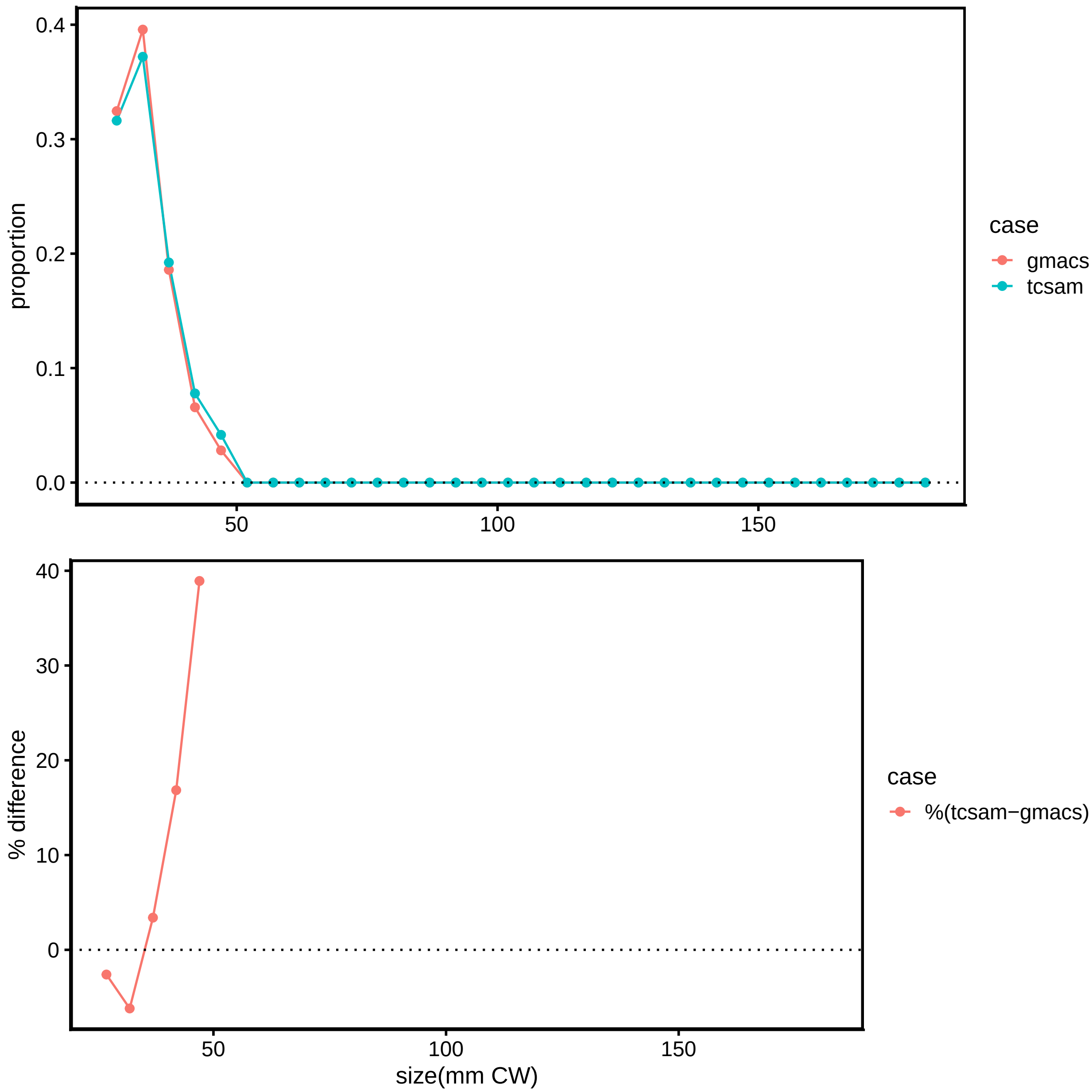


Figure 5. Comparison of size-at-recruitment from the GMACS and TCSAM02 models. Upper: values; lower: percent differences. The size distribution at recruitment is not sex-specific.

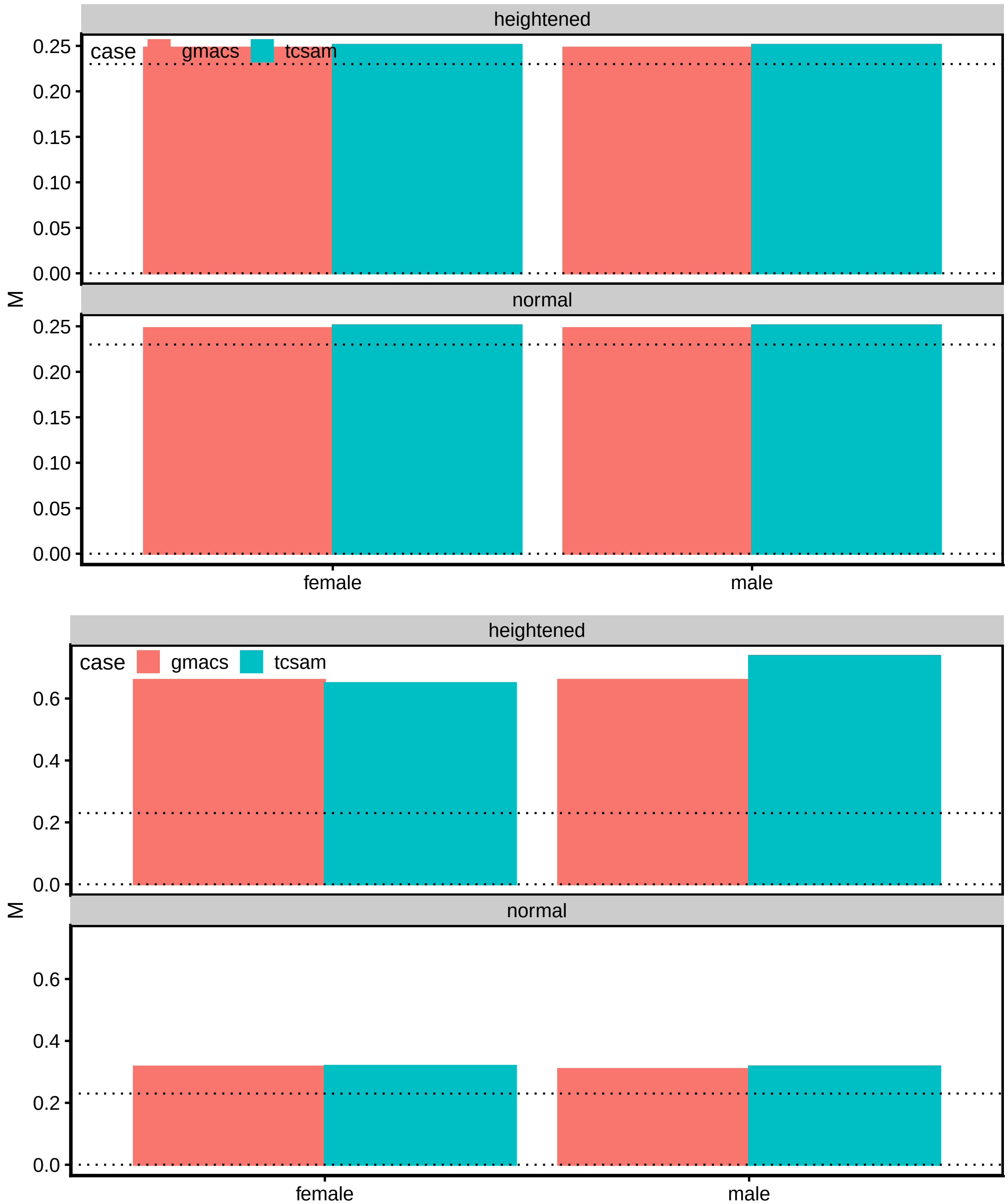


Figure 6. Natural mortality rates (M) used in the GMACS and TCSAM02 models, by biological category. Upper: immature crab; lower: mature crab. “heightened”: 1980-1984 time period; “normal”: remaining time period.

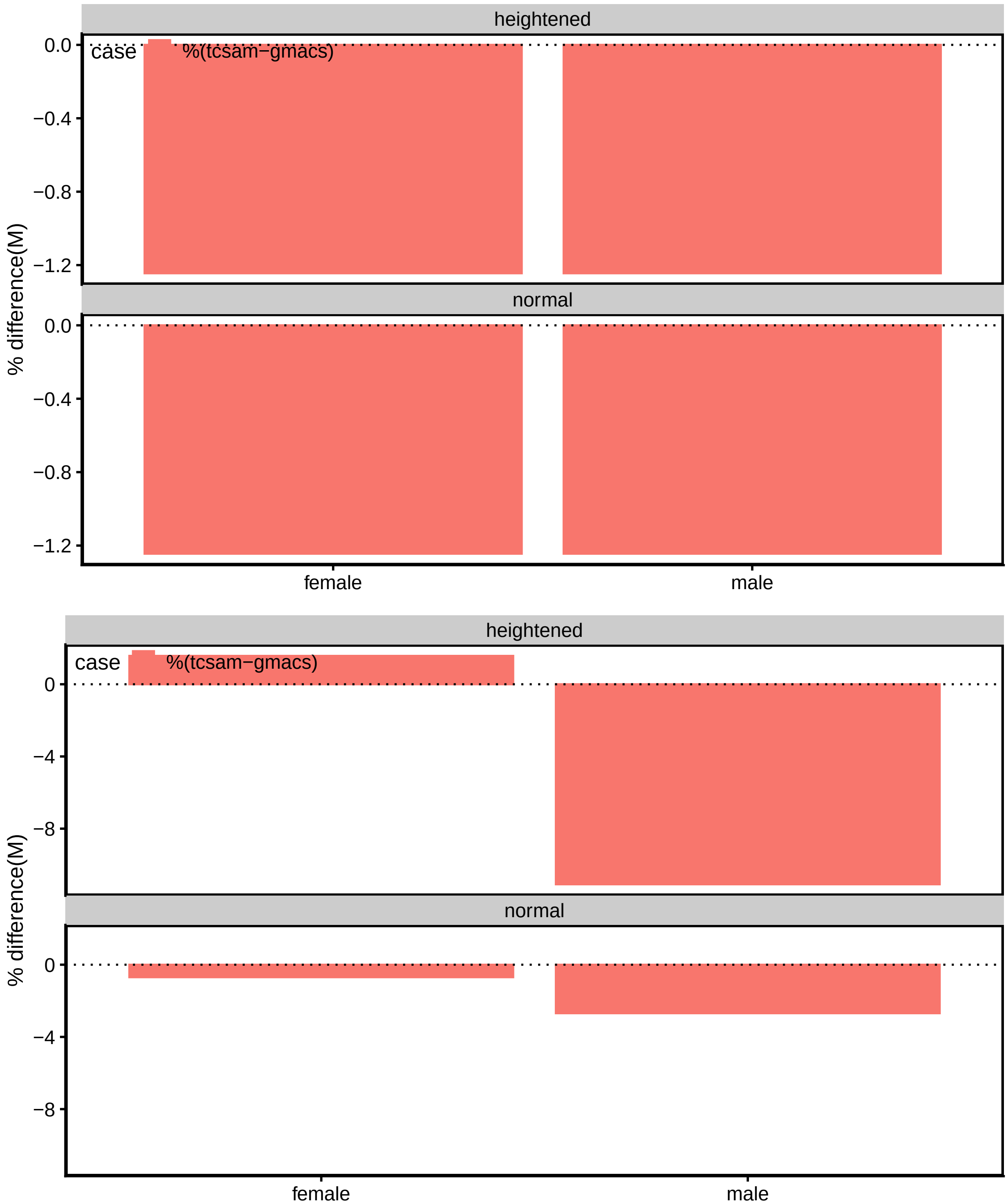


Figure 7. Percent difference in natural mortality rates (M) used in the GMACS and TCSAM02 models, by biological category. Upper: immature crab; lower: mature crab. "heightened": 1980-1984 time period; "normal": remaining time period.

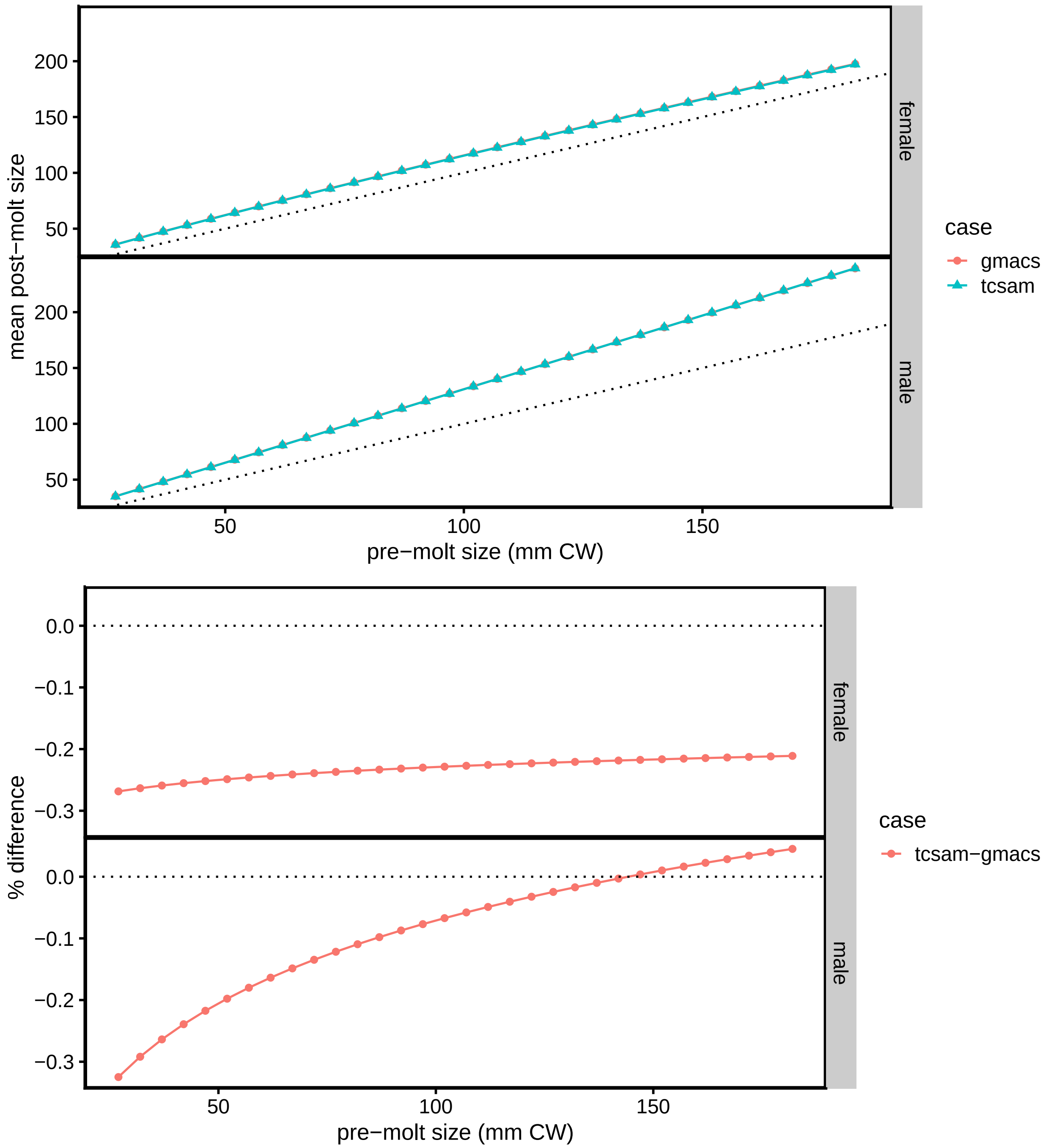


Figure 8. Mean postmolt size, as a function of premolt size, used in the GMACS and TCSAM02 models, by sex. Upper: values; lower: percent difference.

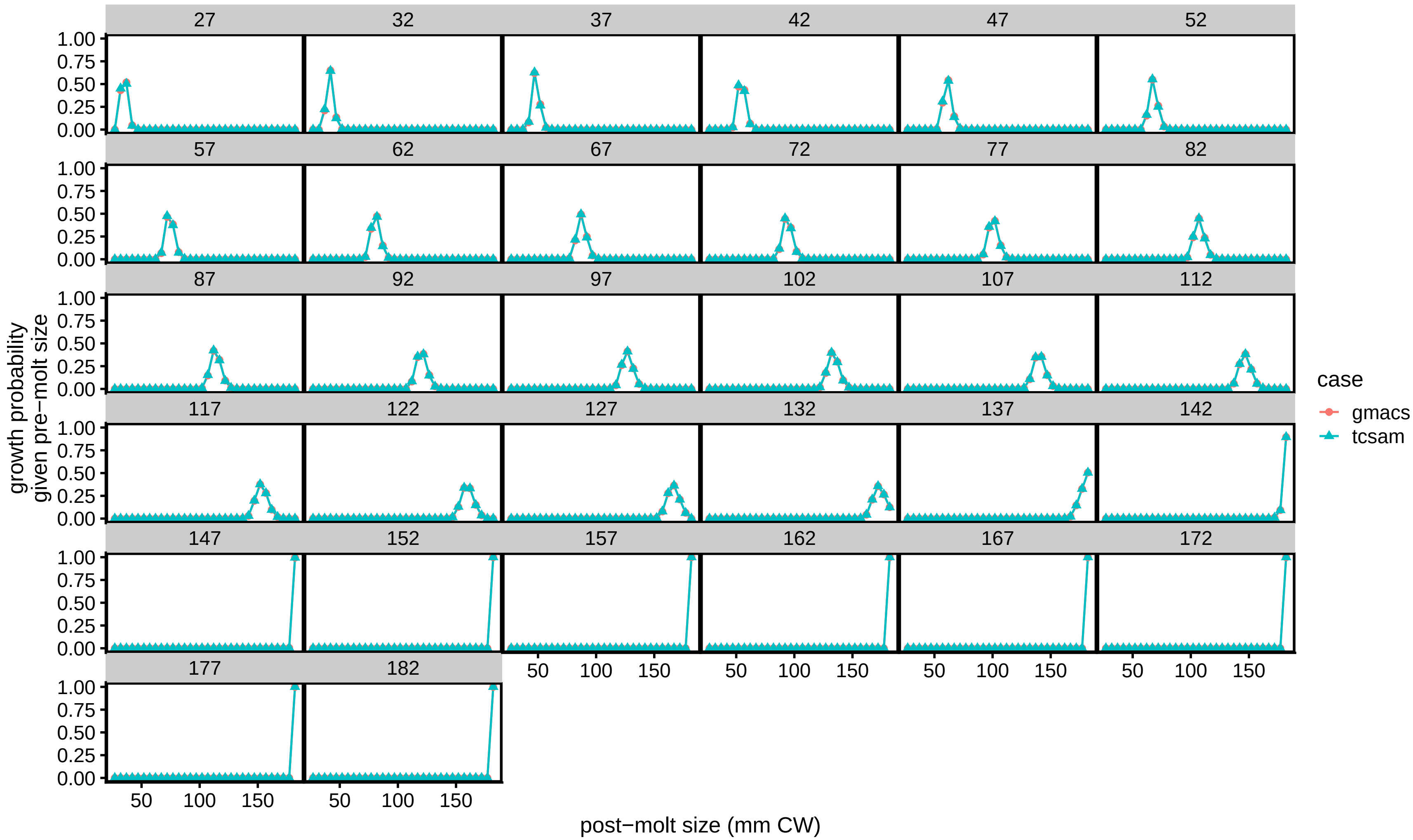


Figure 9. Distribution of postmolt sizes, as a function of premolt size, used in the GMACS and TCSAM02 models for males.

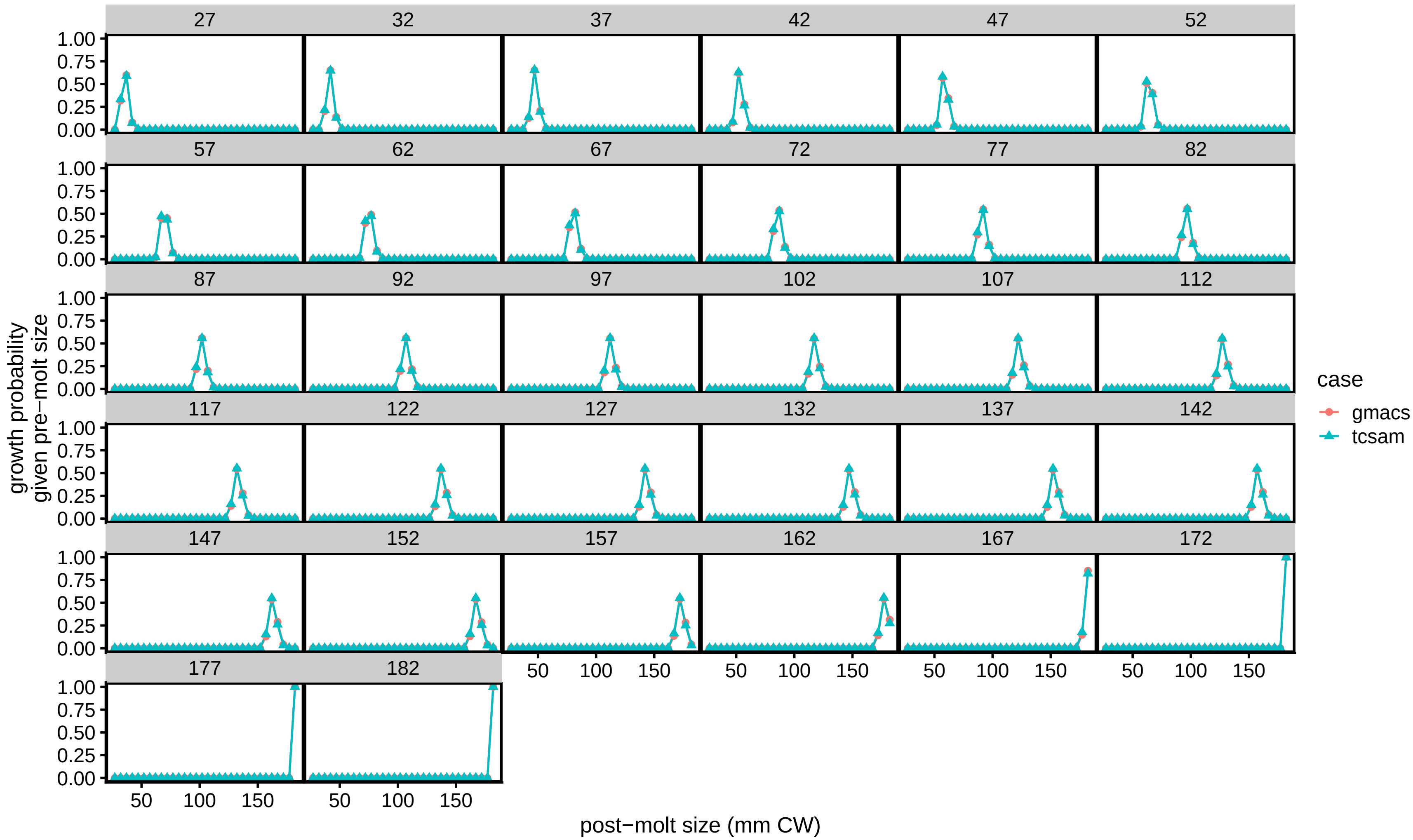


Figure 10. Distribution of postmolt sizes, as a function of premolt size, used in the GMACS and TCSAM02 models for females.

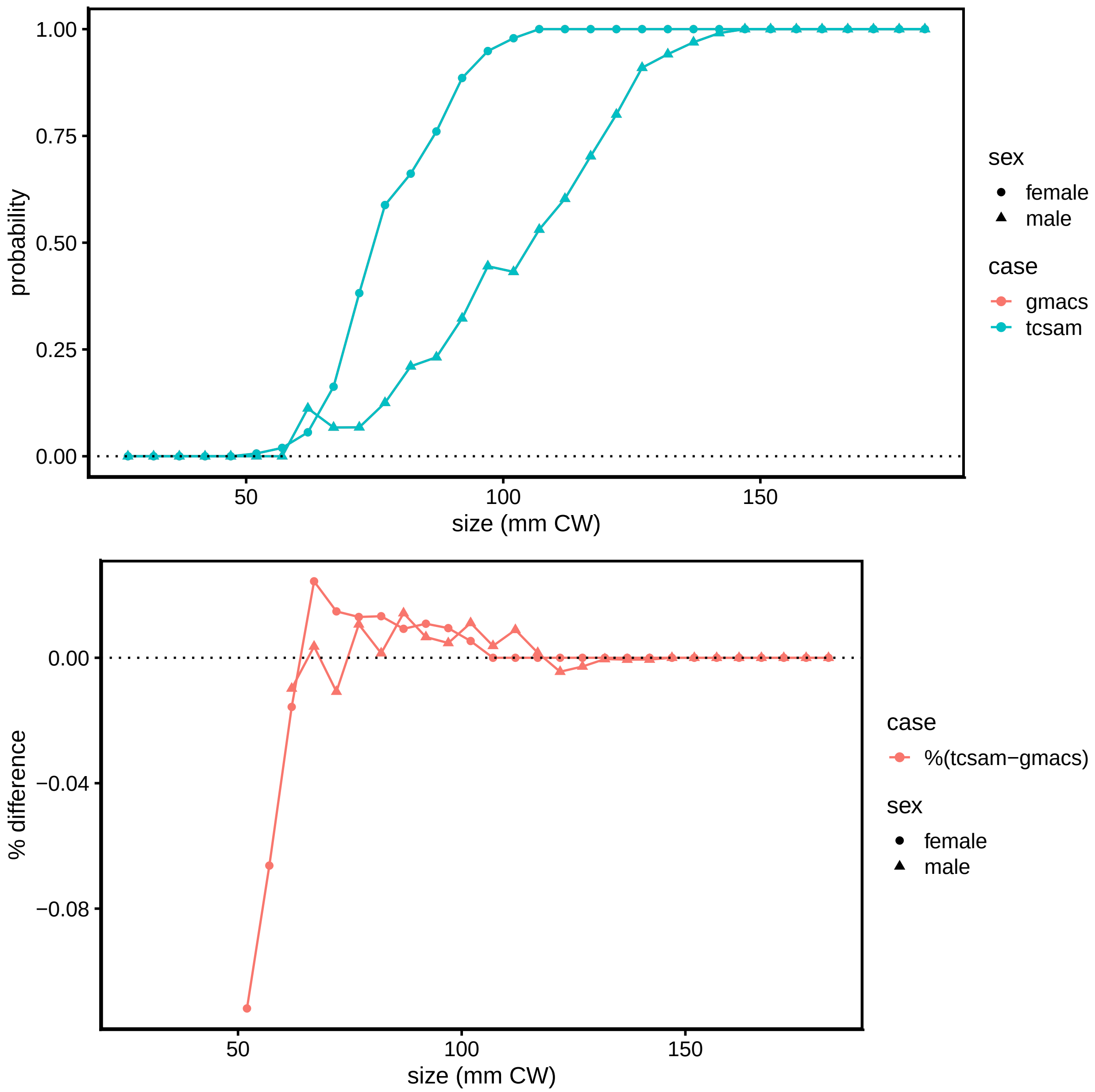


Figure 11. Comparison of the probability of terminal molt used in the GMACS and TCSAM02 models, by sex. Upper: values; lower: percent differences.

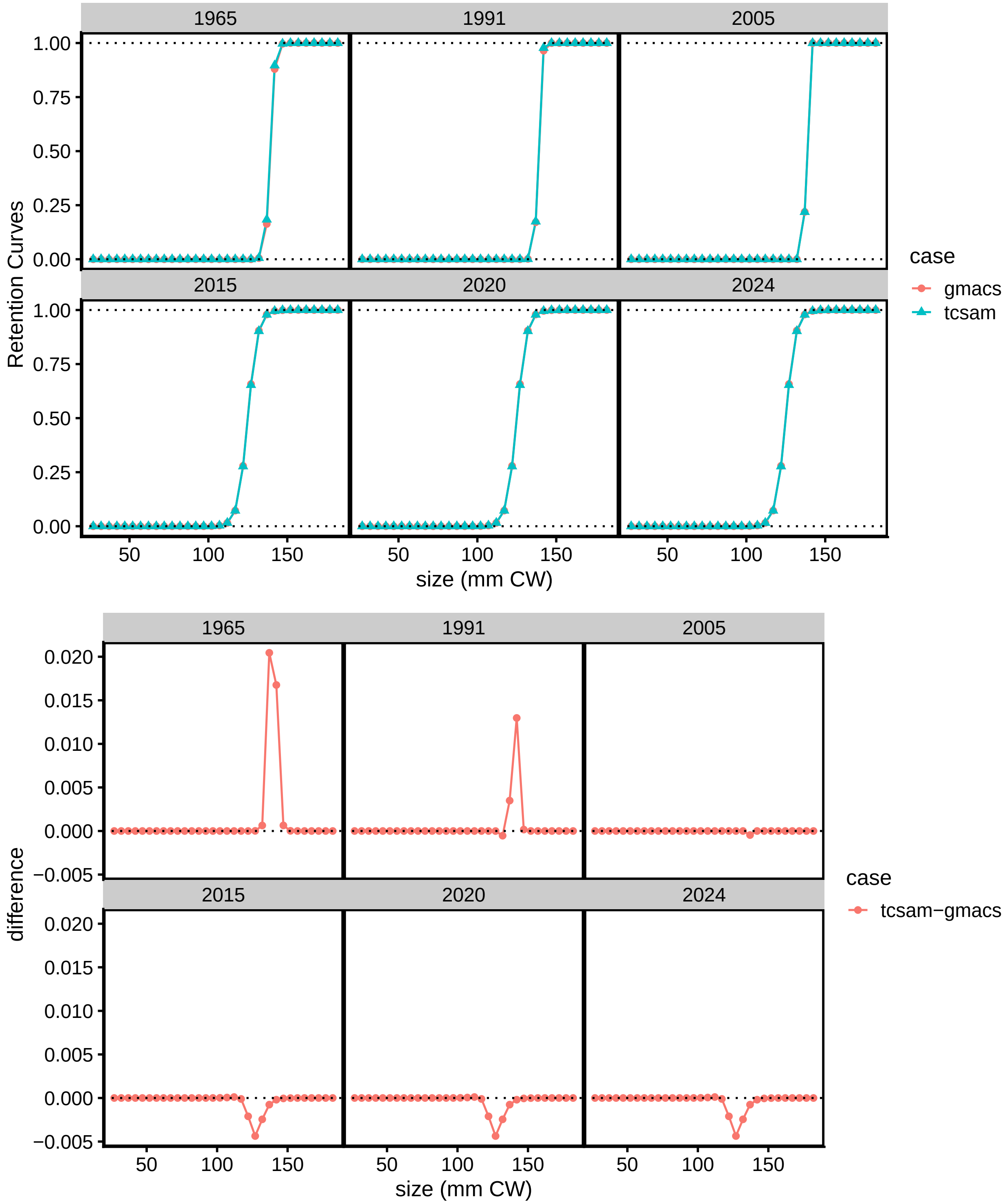


Figure 12. Comparison of the fishery retention curves used in the GMACS and TCSAM02 models. Upper: values for selected years; lower: differences.

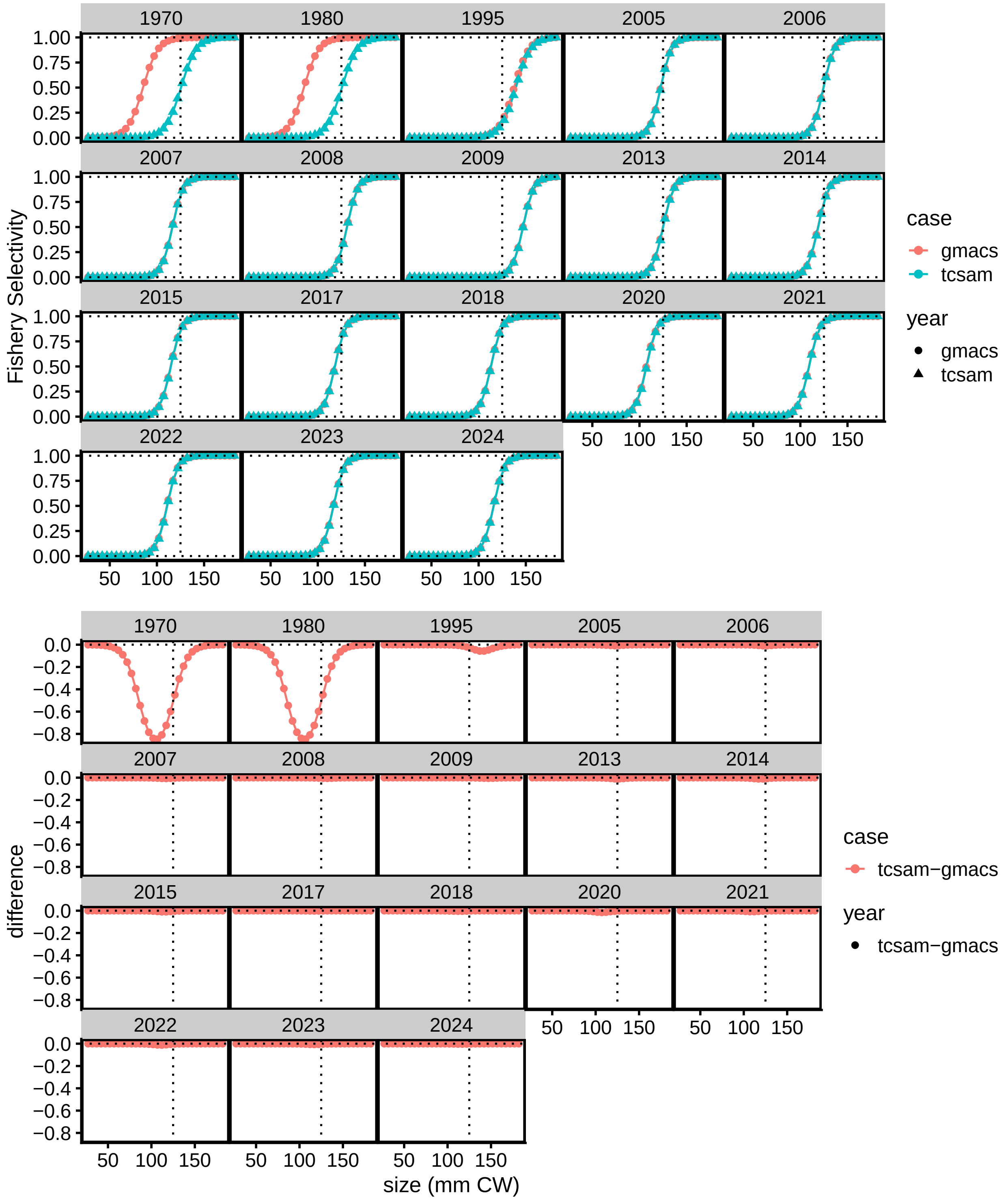


Figure 13. Comparison of the fishery selectivity curves for males in the directed fishery as used in the GMACS and TCSAM02 models. Upper: values for selected years; lower: differences. The dotted line at 125 mm CW provides a reference point to the current industry-preferred size.

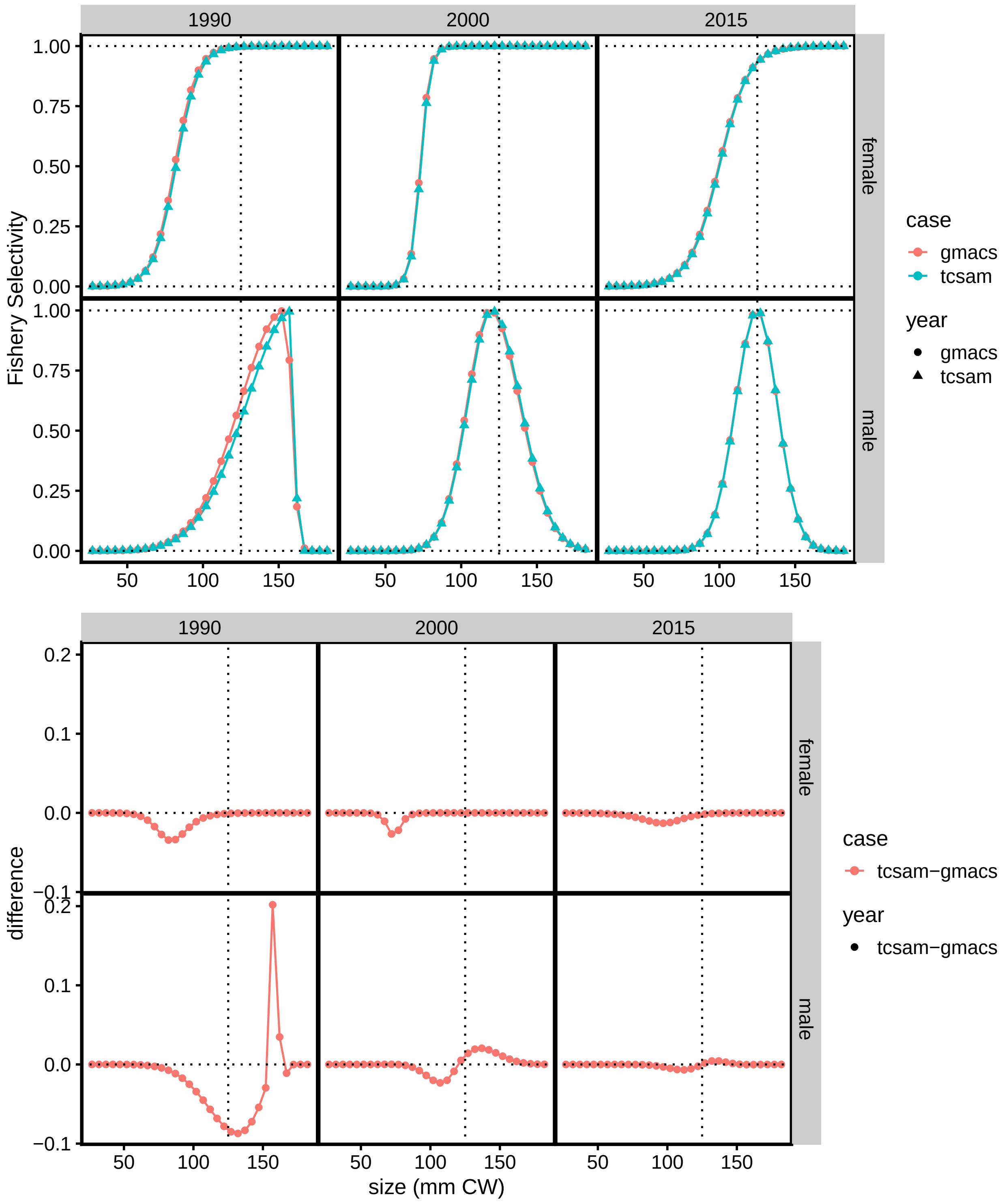


Figure 14. Comparison of the fishery bycatch selectivity curves by sex in the snow crab fishery as used in the GMACS and TCSAM02 models. Upper: values for selected years; lower: differences. The dotted line at 125 mm CW provides a reference point to the current industry-preferred size.

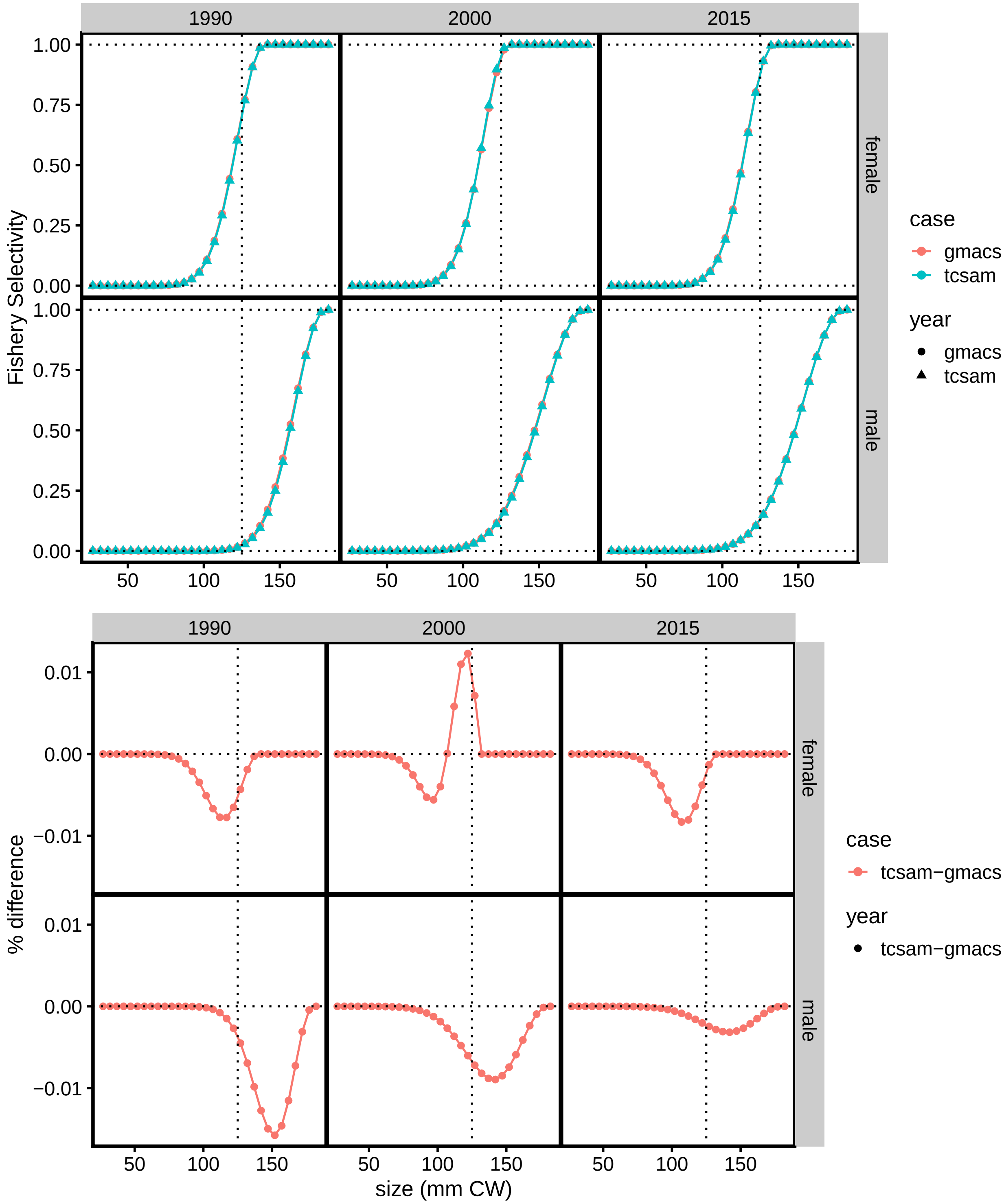
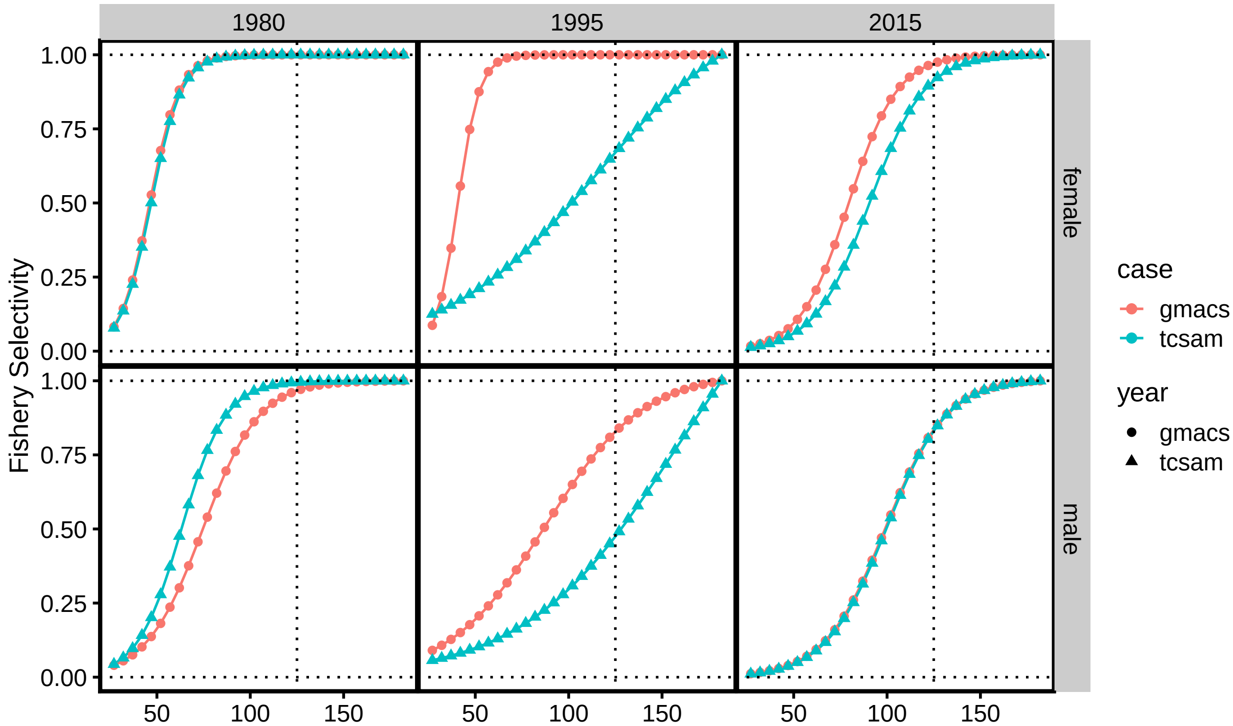


Figure 15. Comparison of the fishery bycatch selectivity curves by sex in the BBRKC fishery as used in the GMACS and TCSAM02 models. Upper: values for selected years; lower: differences. The dotted line at 125 mm CW provides a reference point to the current industry-preferred size.



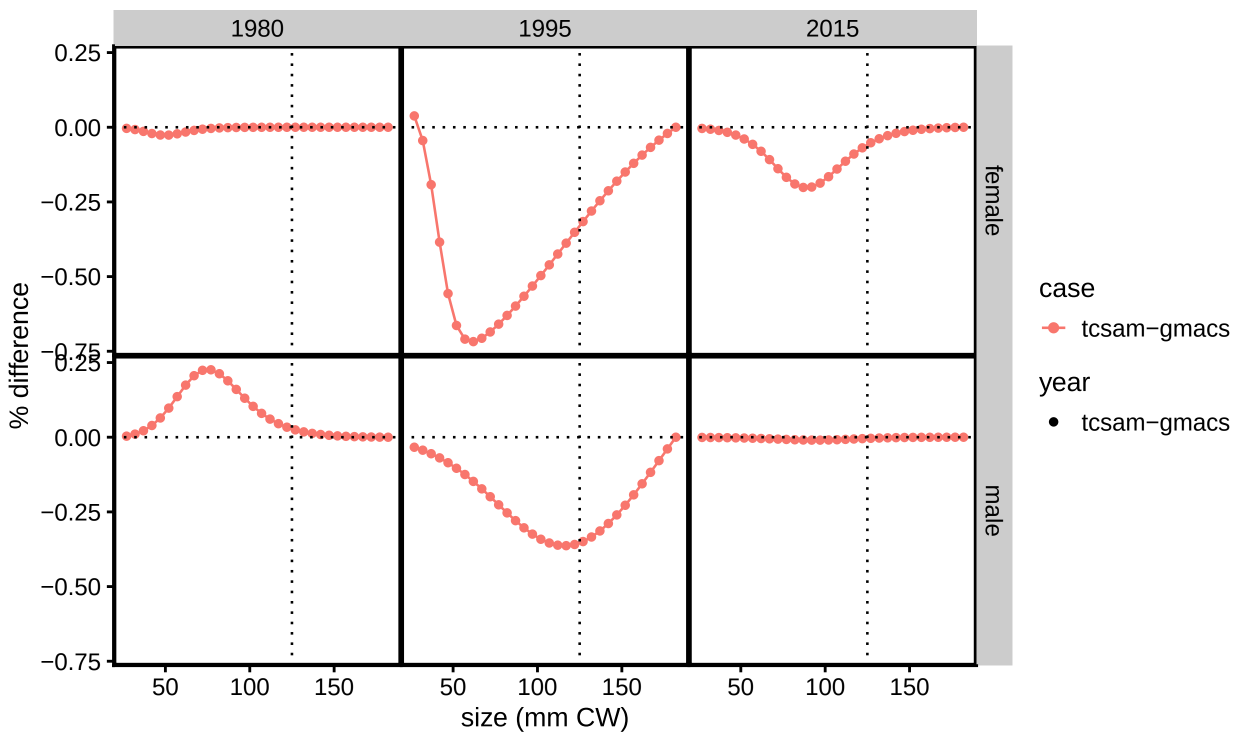


Figure 16. Comparison of the fishery bycatch selectivity curves by sex in the groundfish fisheries as used in the GMACS and TCSAM02 models. Upper: values for selected years; lower: differences. The dotted line at 125 mm CW provides a reference point to the current industry-preferred size.

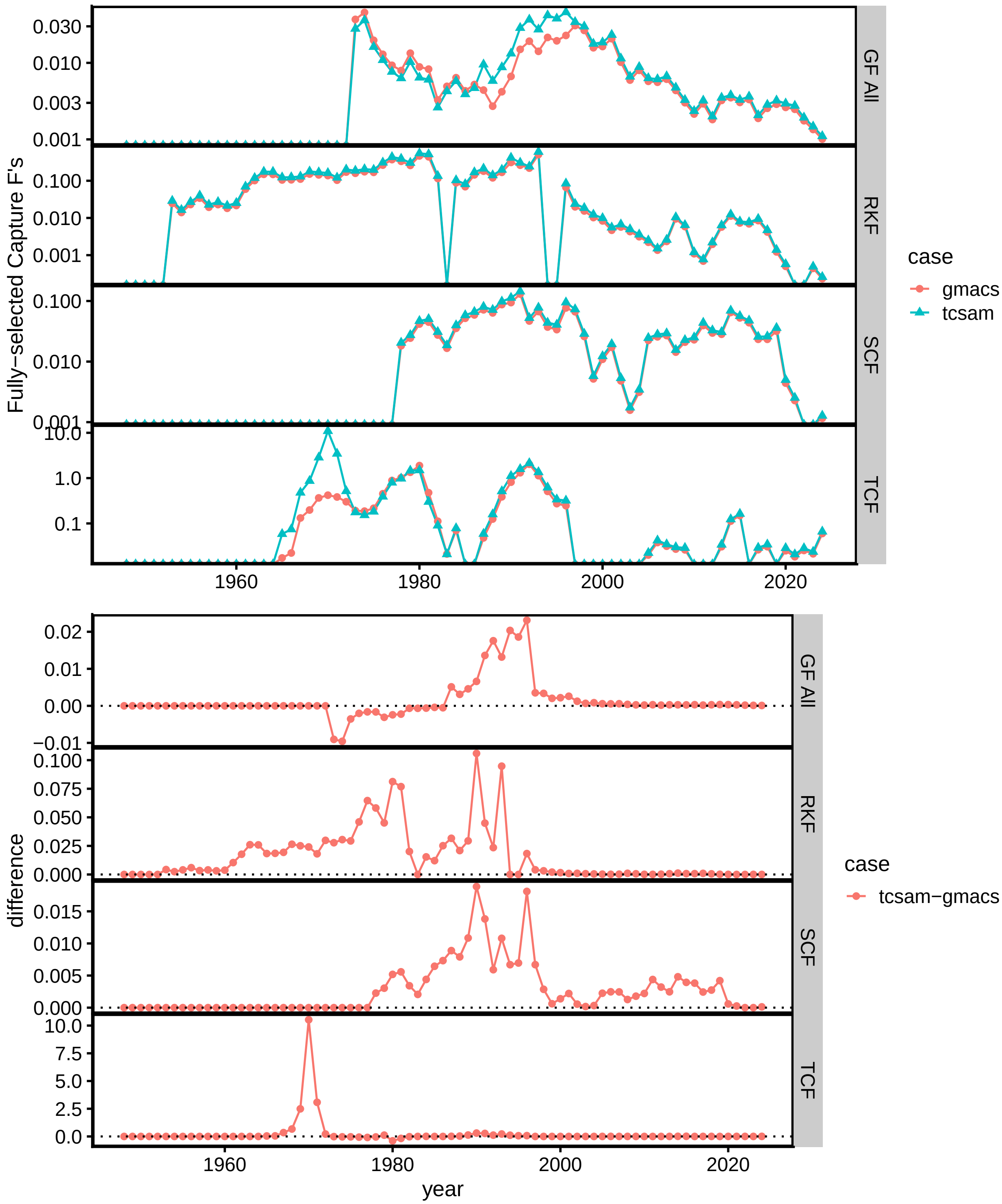


Figure 17. Comparison of the fully-selected fishery capture rates for males in the directed and bycatch fisheries as used in the GMACS and TCSAM02 models. Upper: values on log scale; lower: differences. TCF: directed Tanner crab fishery; SCF: snow crab fishery, RKF: BBRKC fishery; GF All: groundfish fisheries. Capture rates before 1990 in the snow crab and BBRKC fisheries are based on effort extrapolation. Capture rates for females (plots not shown) are propotional to those for males.

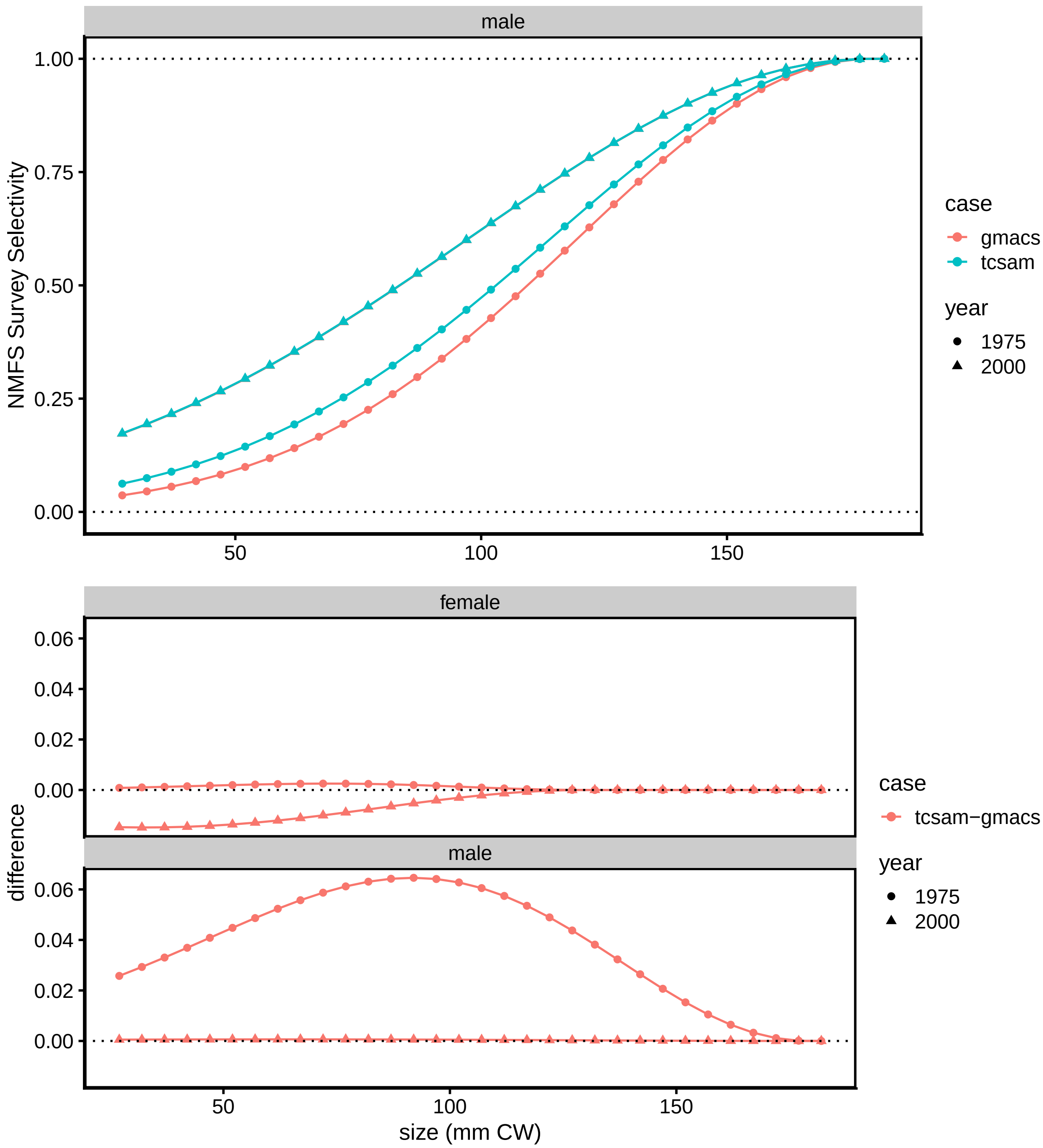


Figure 18. Comparison of the NMFS survey selectivity curves by sex as used in the GMACS and TCSAM02 models. Upper: values for selected years; lower: differences.

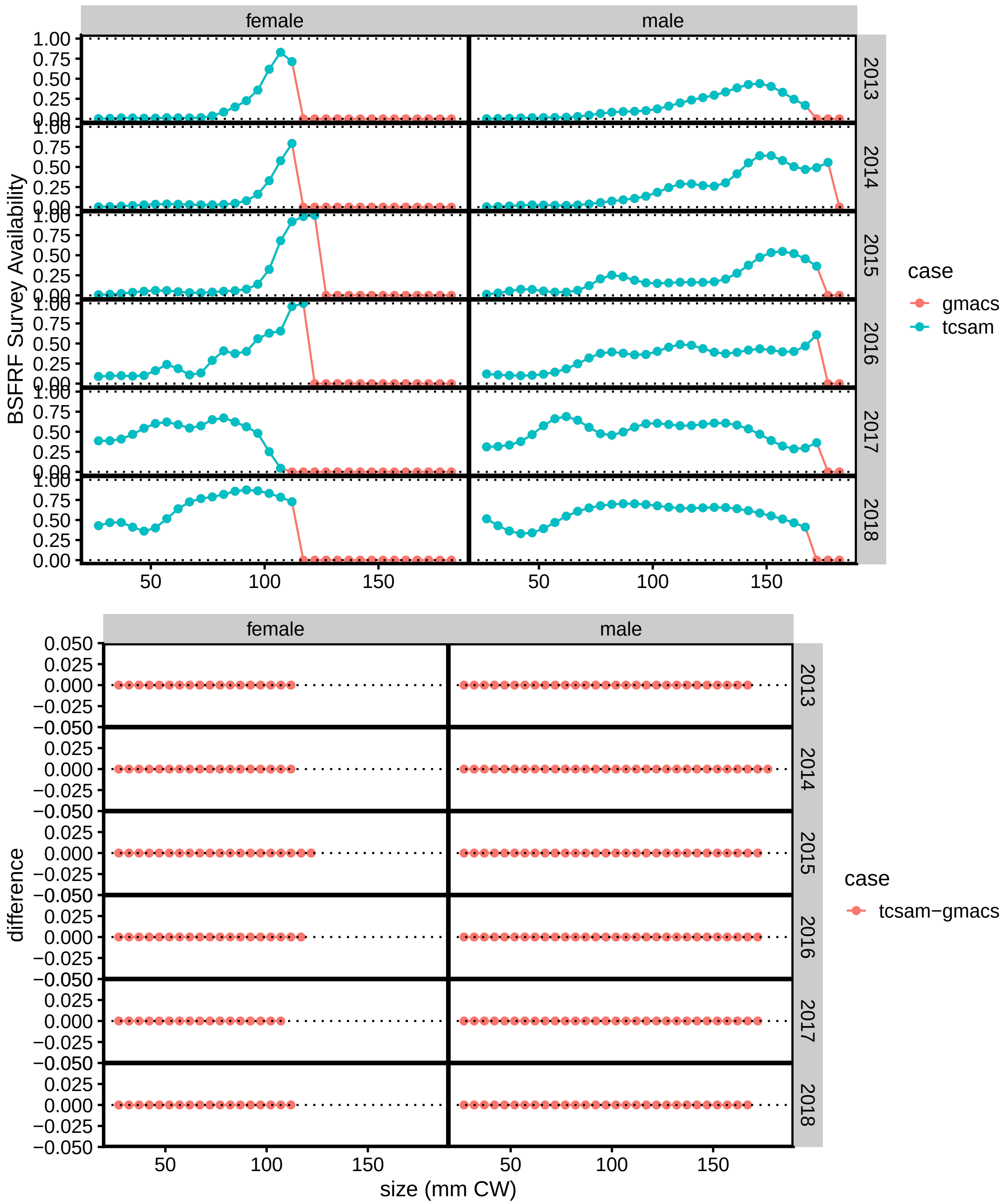


Figure 19. Comparison of the BSFRF survey availability curves by sex as used in the GMACS and TCSAM02 models. Upper: values for selected years; lower: differences.

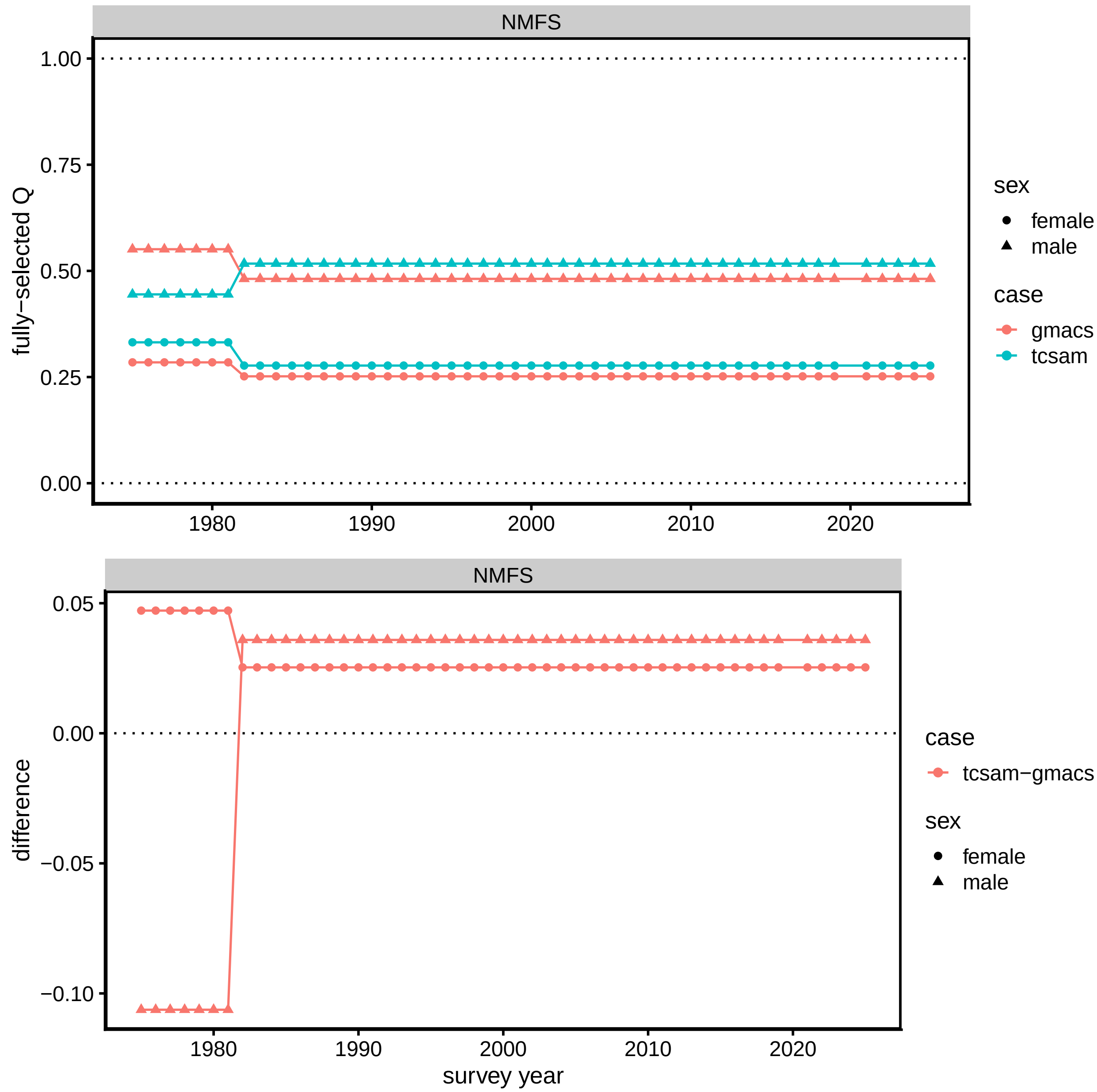


Figure 20. Comparison of fully-selected survey catchability ('q') for the NMFS survey by sex and year as used in the GMACS and TCSAM02 models. Upper: values; lower: differences. Fully-selected q's for the BSFRF surveys are 1 in both models and are not shown.

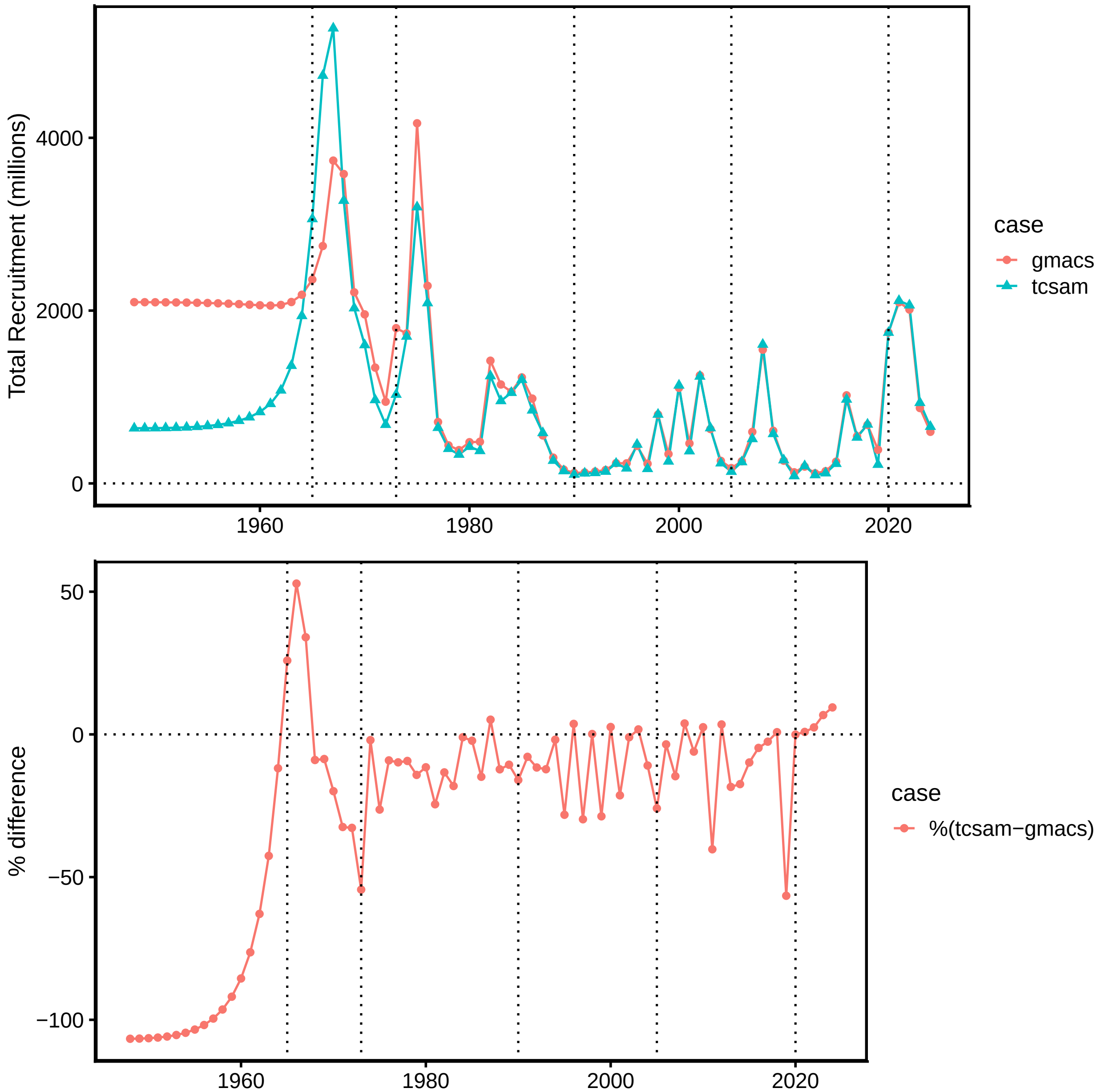


Figure 21. Comparison of recruitment by year from the GMACS and TCSAM02 models. Upper: values; lower: percent differences. The dotted vertical lines various temporal reference points: 1965-start of foreign fleet catch data; 1973-start of groundfish bycatch data; 1990-start of at sea observer estimates of total catch and size compositions in the crab fisheries; 2005-crab rationalization; 2020-no NMFS survey.

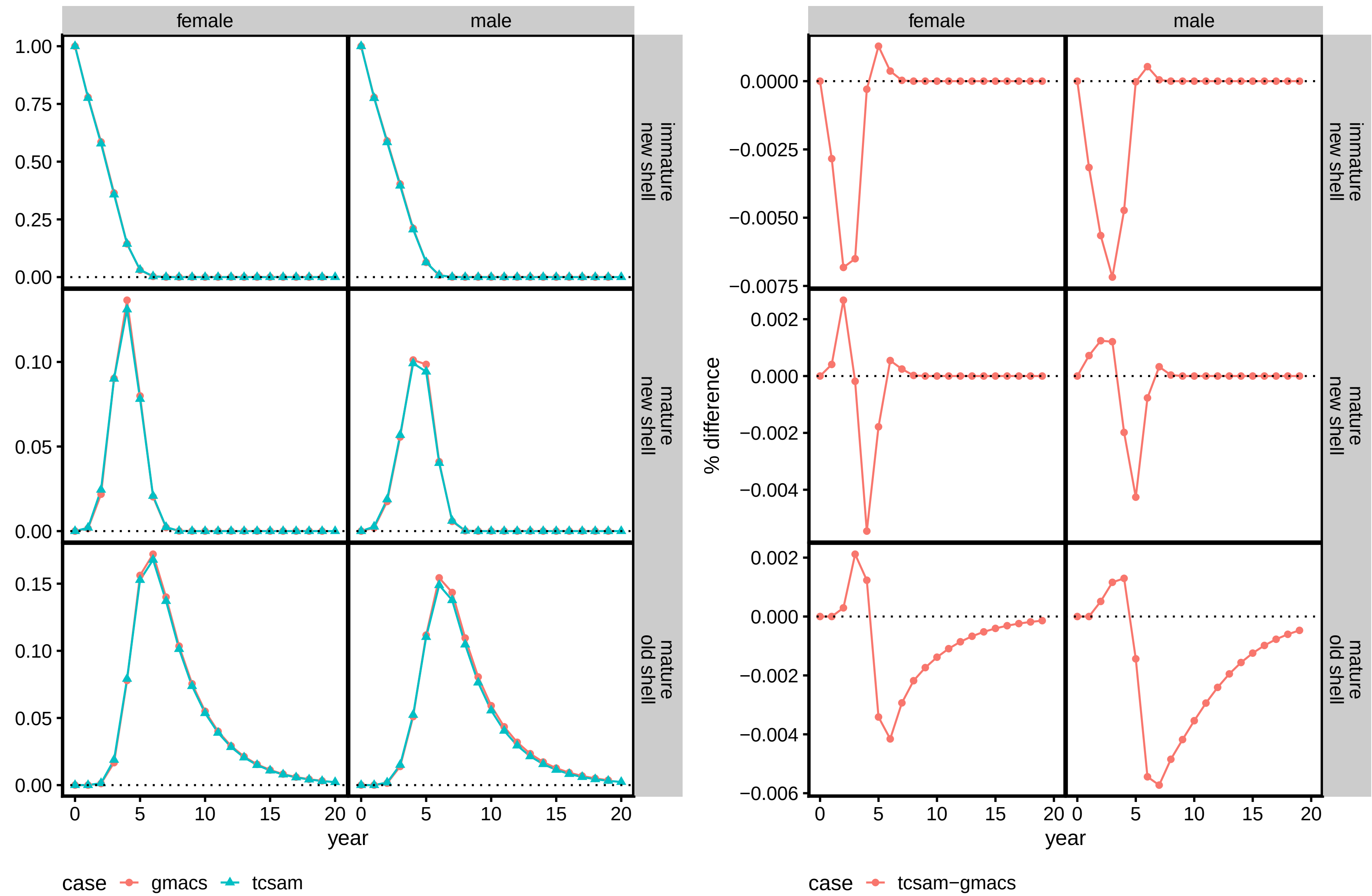


Figure 22. Comparison of the predicted abundance of a single recruitment cohort through time by sex and maturity/shell state using conditions from the final model year for the GMACS and TCSAM02 models. Left: values; right: percent differences.

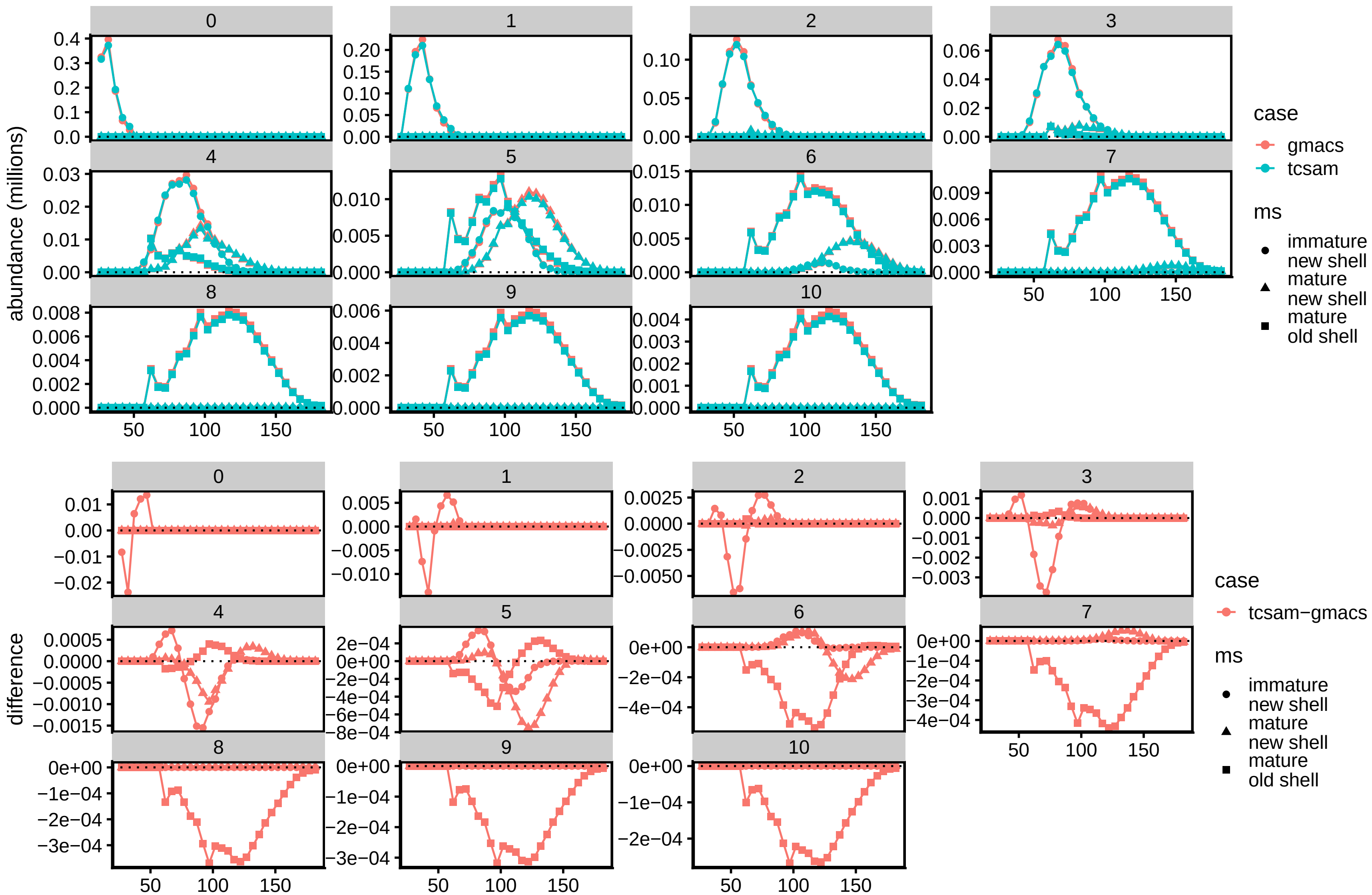


Figure 23. Comparison of the predicted abundance-at-size of a single recruitment cohort through time by sex and maturity/shell condition using conditions from the final model year for the GMACS and TCSAM02 models. Upper: values; lower: differences.

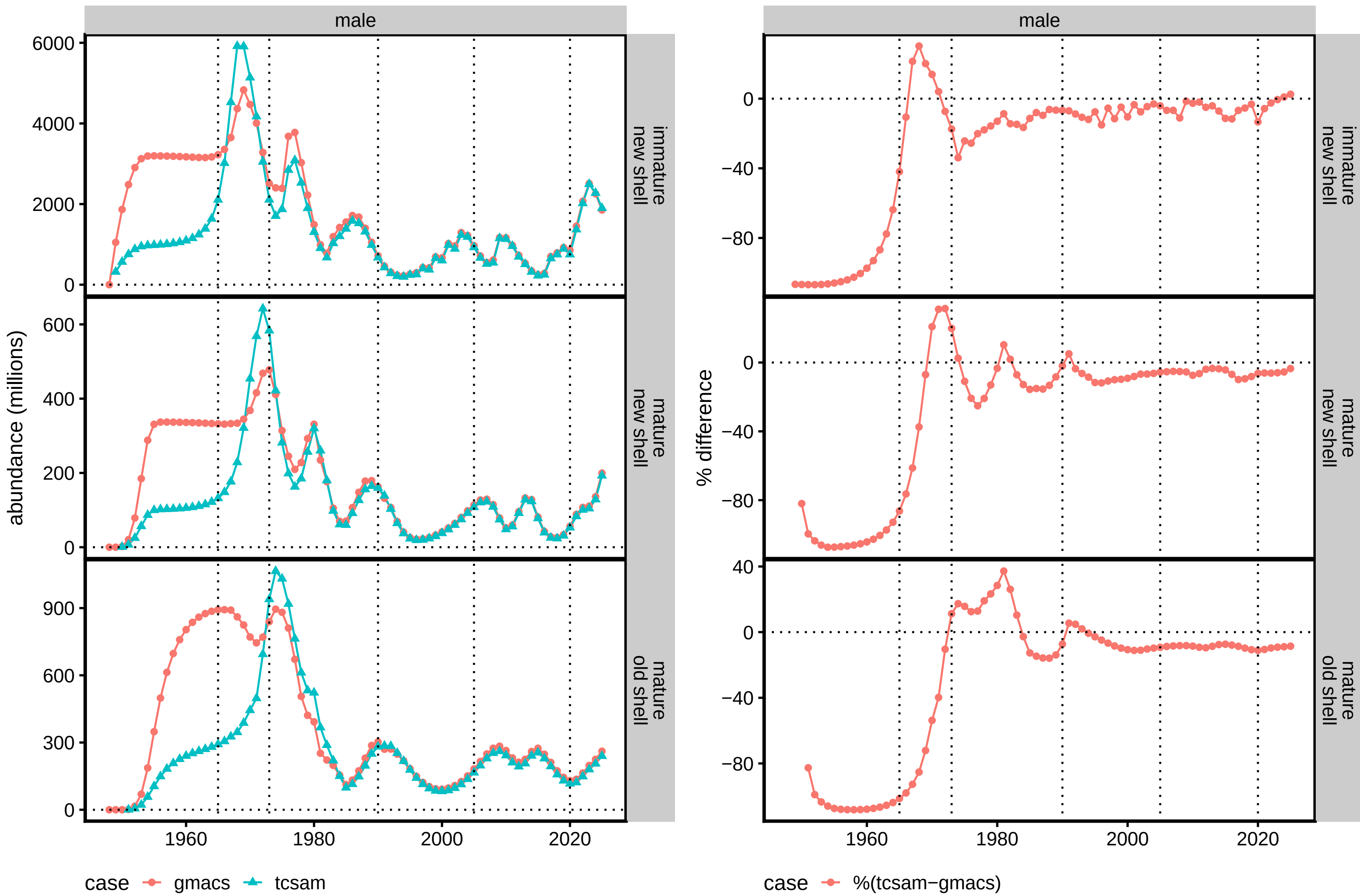


Figure 24. Comparison of the predicted population abundance through time by maturity/shell condition for males from the GMACS and TCSAM02 models. Left: values; right: percent differences. The dotted vertical lines indicate various temporal reference points: 1965-start of foreign fleet catch data; 1973-start of groundfish bycatch data; 1990-start of at sea observer estimates of total catch and size compositions in the crab fisheries; 2005-crab rationalization; 2020-no NMFS survey.

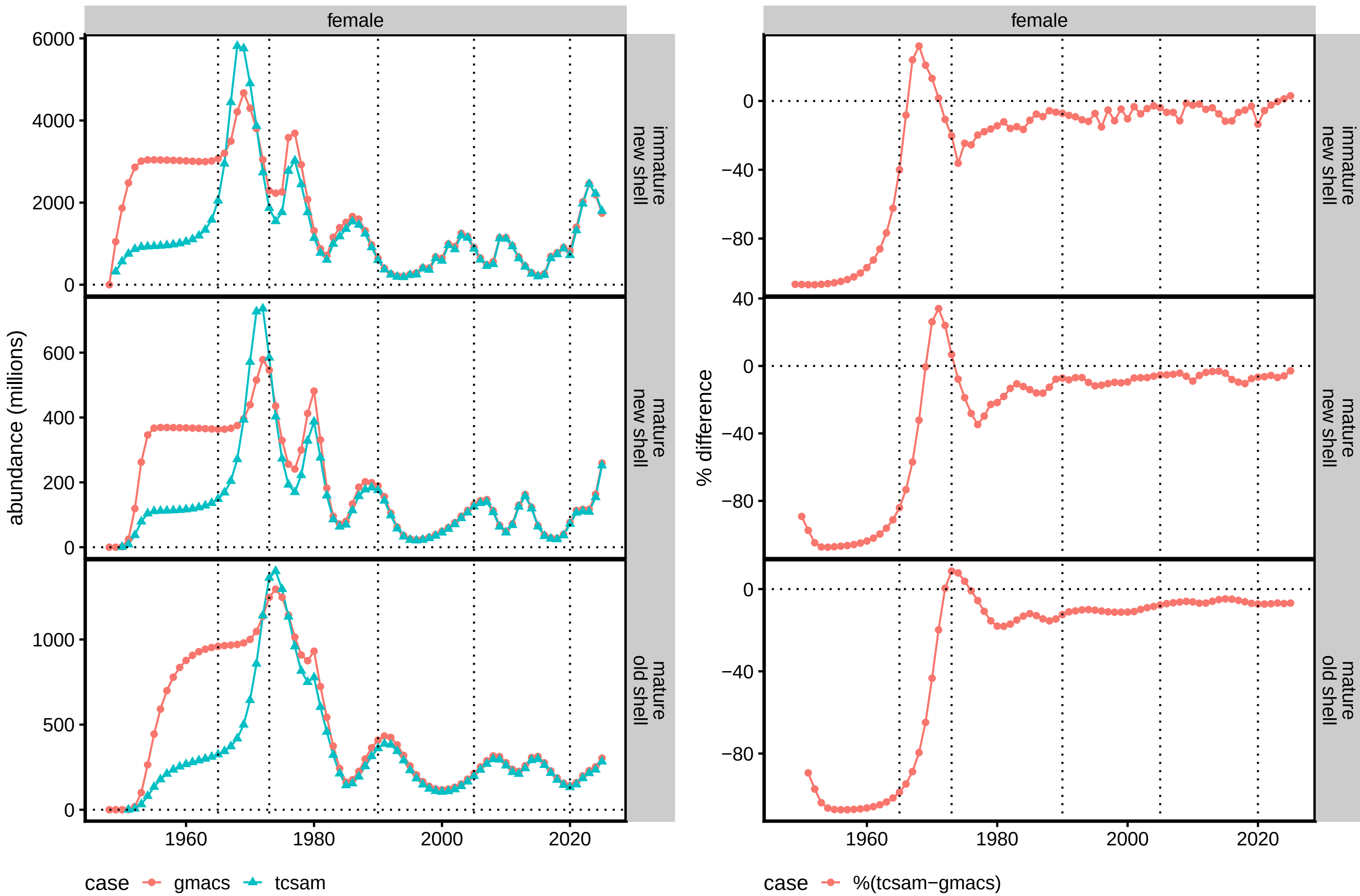


Figure 25. Comparison of the predicted population abundance through time by maturity/shell condition for females from the GMACS and TCSAM02 models. Left: values; right: percent differences. The dotted vertical lines indicate various temporal reference points: 1965-start of foreign fleet catch data; 1973-start of groundfish bycatch data; 1990-start of at sea observer estimates of total catch and size compositions in the crab fisheries; 2005-crab rationalization; 2020-no NMFS survey.

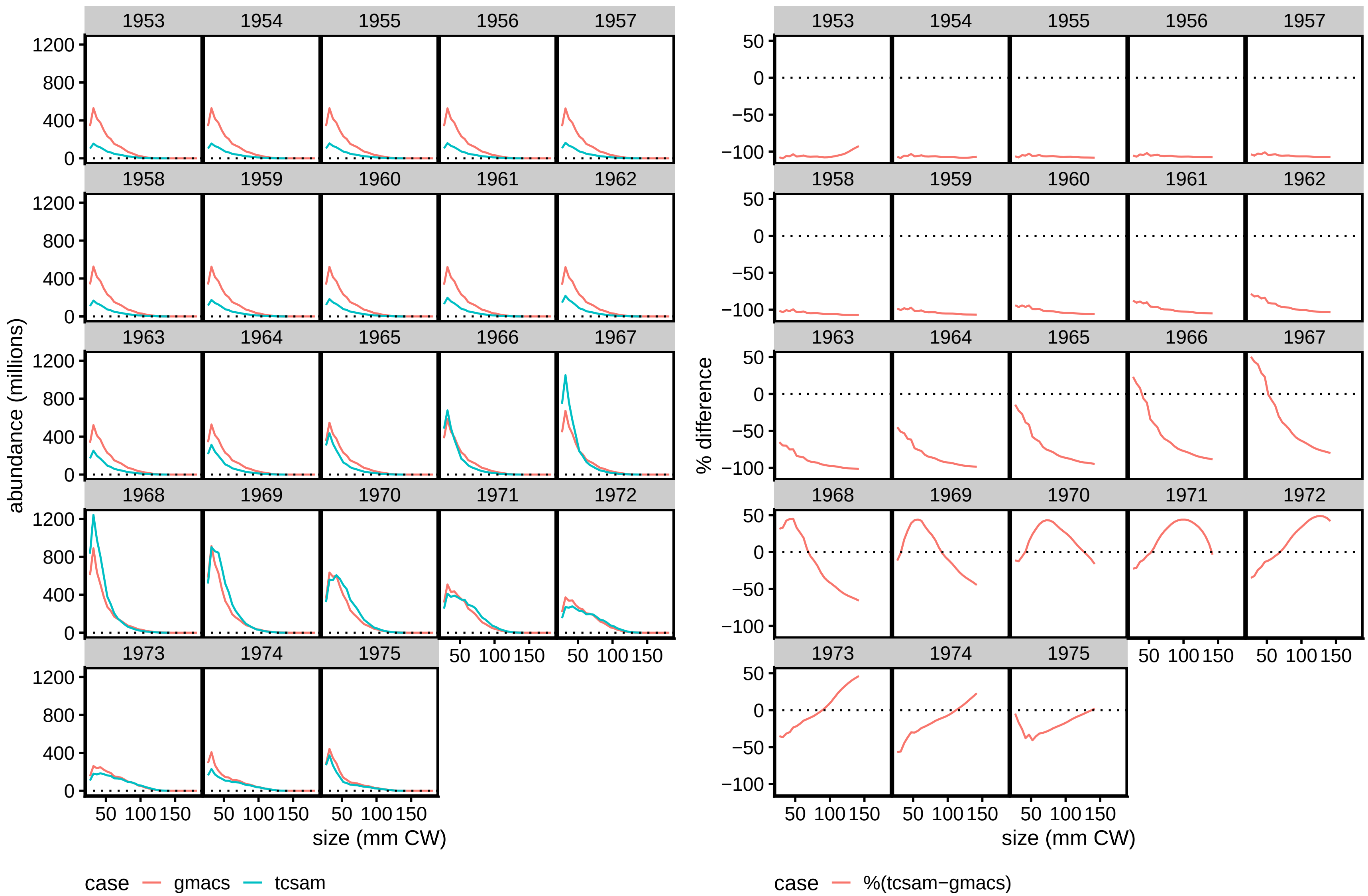


Figure 26. Comparison of the predicted population abundance-at-size through time (1953-1975) for immature, new shell males from the GMACS and TCSAM02 models. Left: values; right: percent differences.

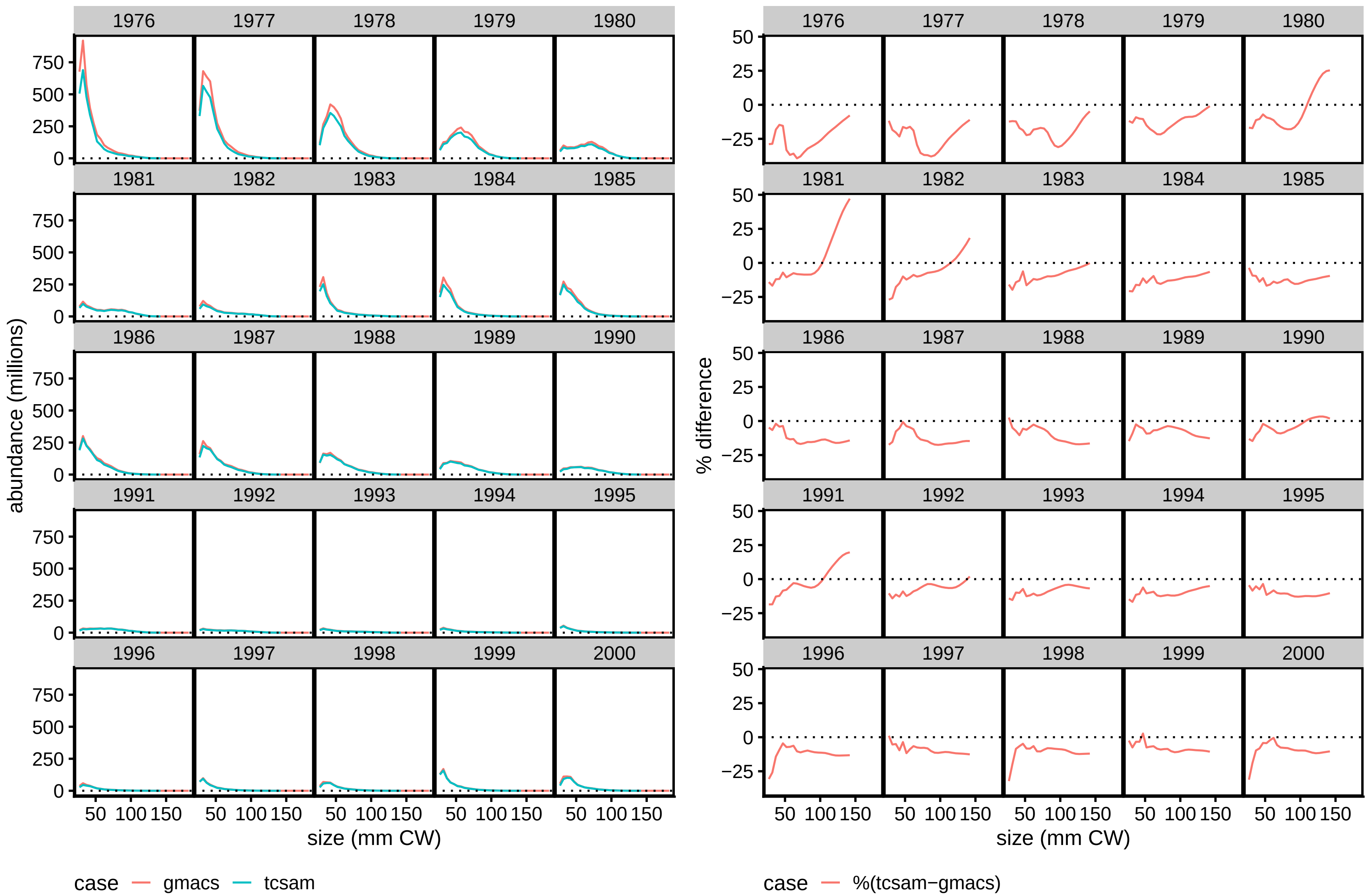


Figure 27. Comparison of the predicted population abundance-at-size through time (1976-2000) for immature, new shell males from the GMACS and TCSAM02 models. Left: values; right: percent differences.

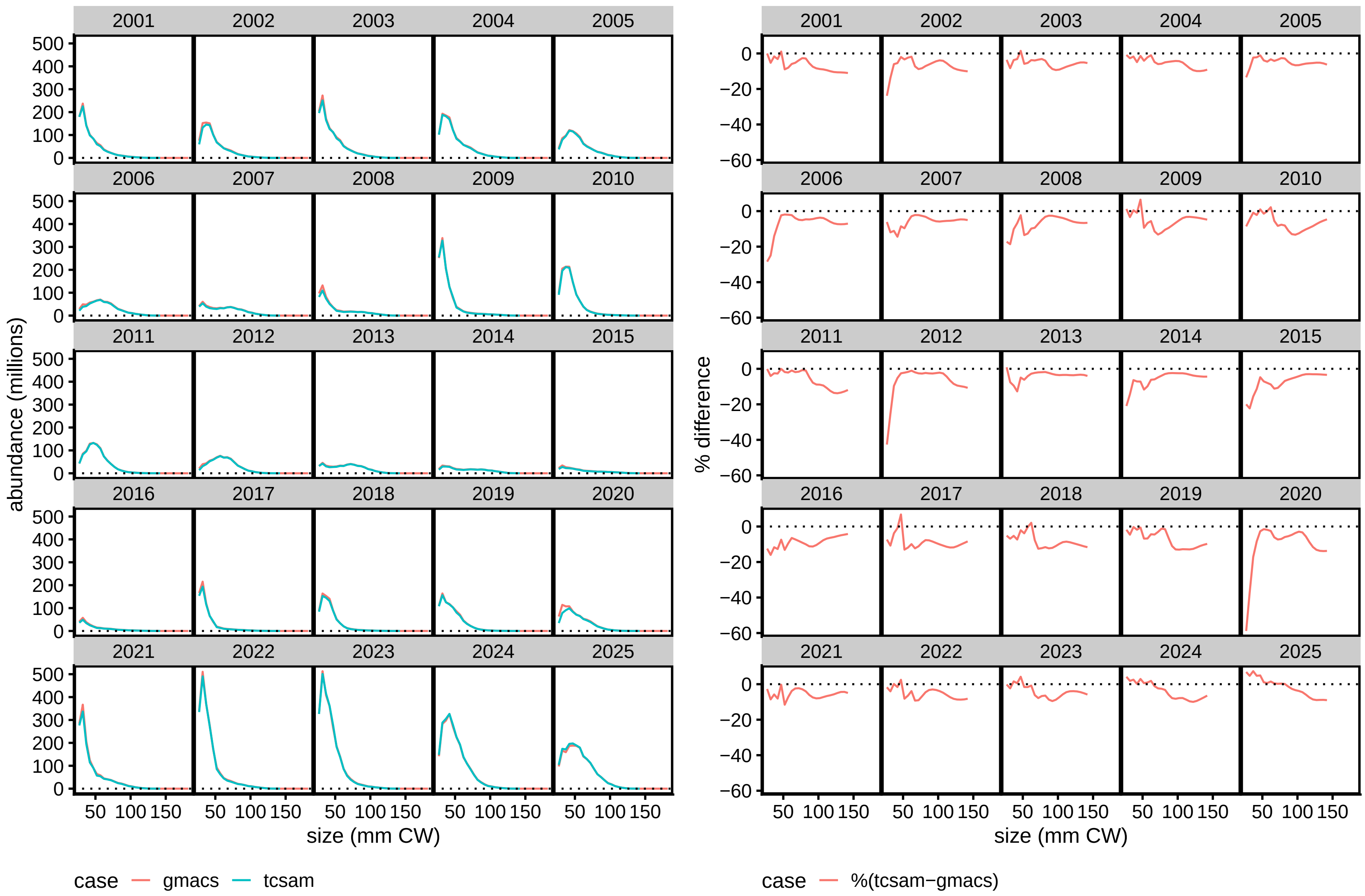


Figure 28. Comparison of the predicted population abundance-at-size through time (2001-2025) for immature, new shell males from the GMACS and TCSAM02 models. Left: values; right: percent differences.

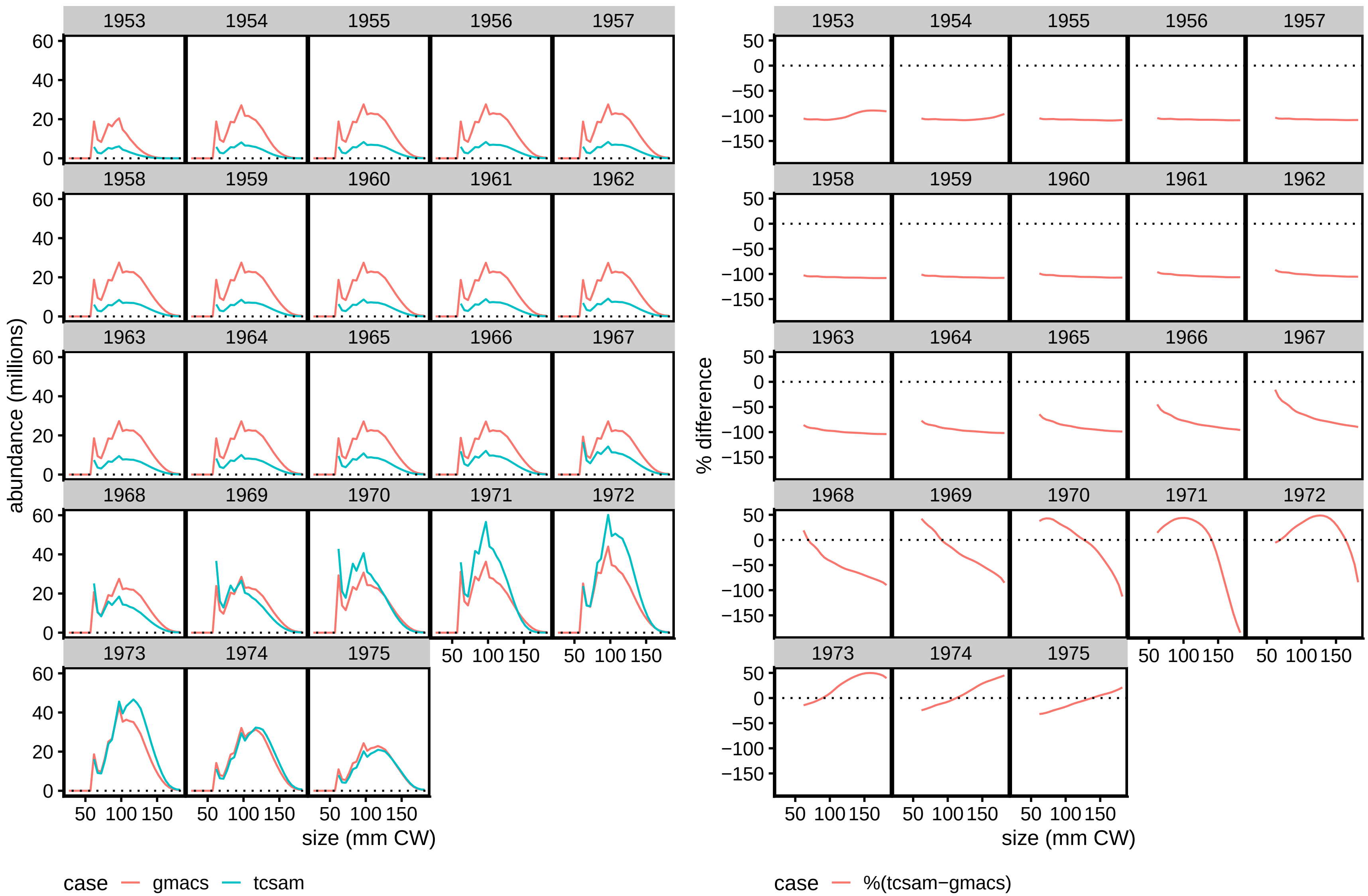


Figure 29. Comparison of the predicted population abundance-at-size through time (1953-1975) for mature, new shell males from the GMACS and TCSAM02 models. Left: values; right: percent differences.

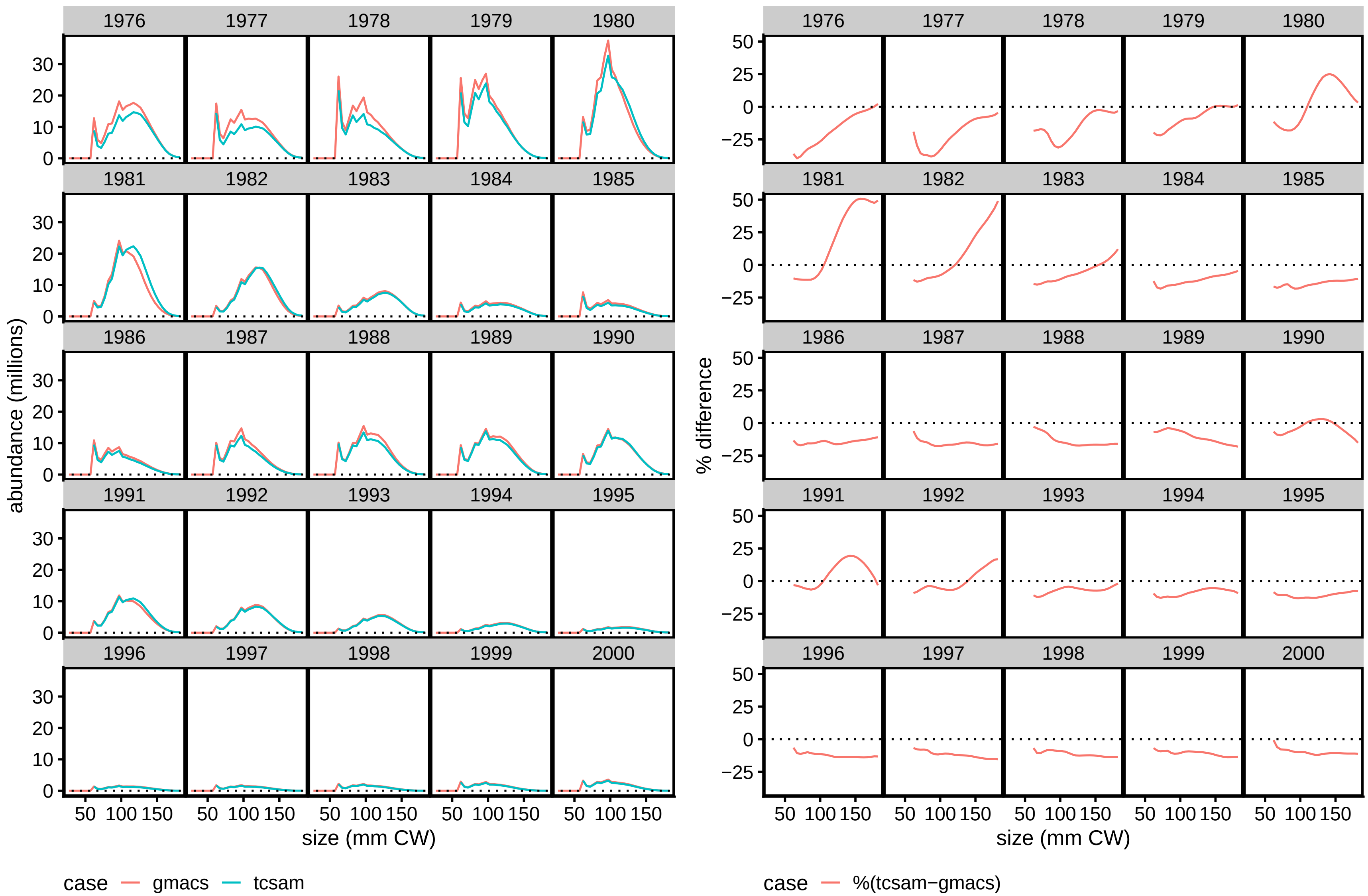


Figure 30. Comparison of the predicted population abundance-at-size through time (1976-2000) for mature, new shell males from the GMACS and TCSAM02 models. Left: values; right: percent differences.

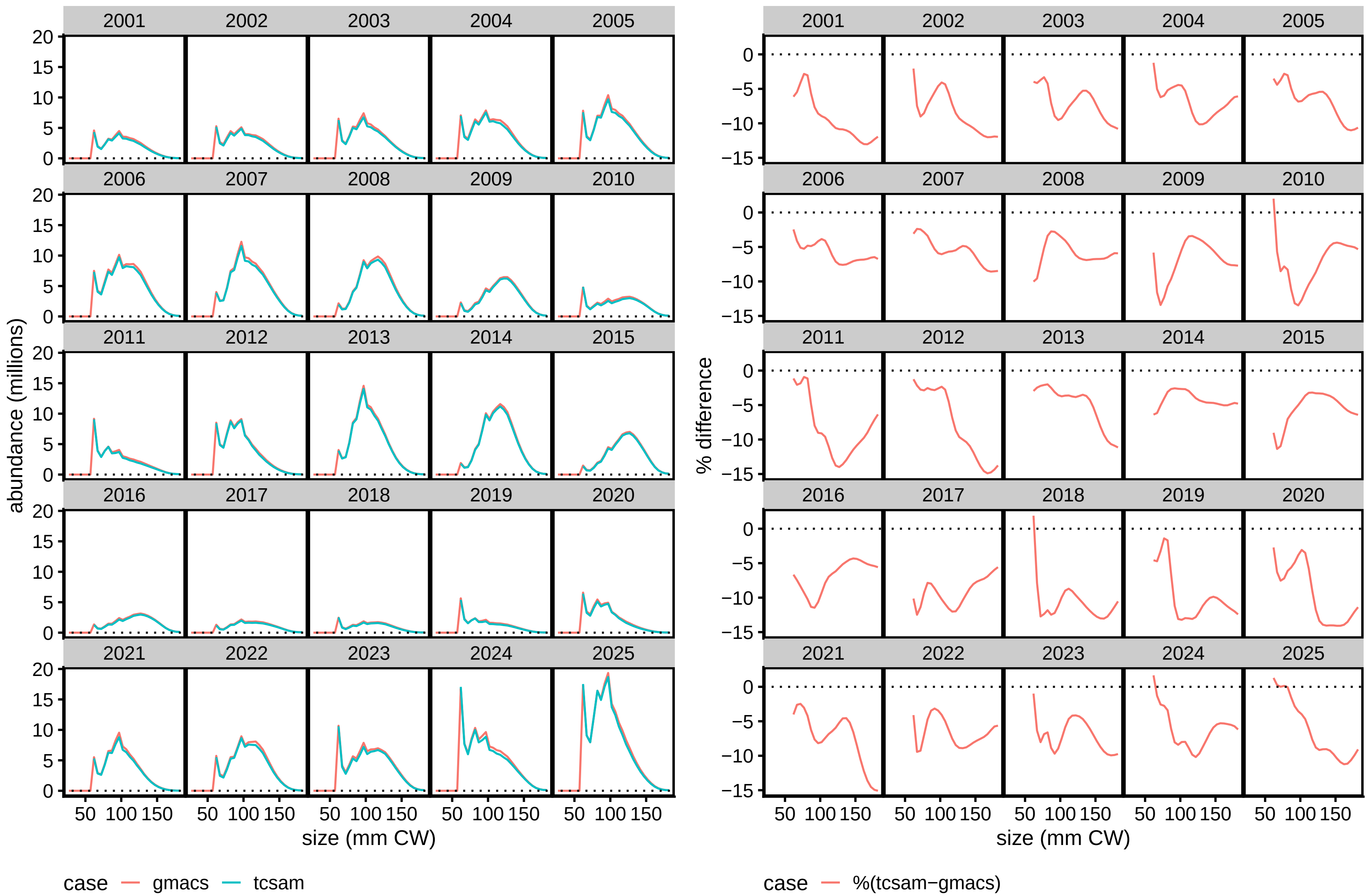


Figure 31. Comparison of the predicted population abundance-at-size through time (2001-2025) for mature, new shell males from the GMACS and TCSAM02 models. Left: values; right: percent differences.

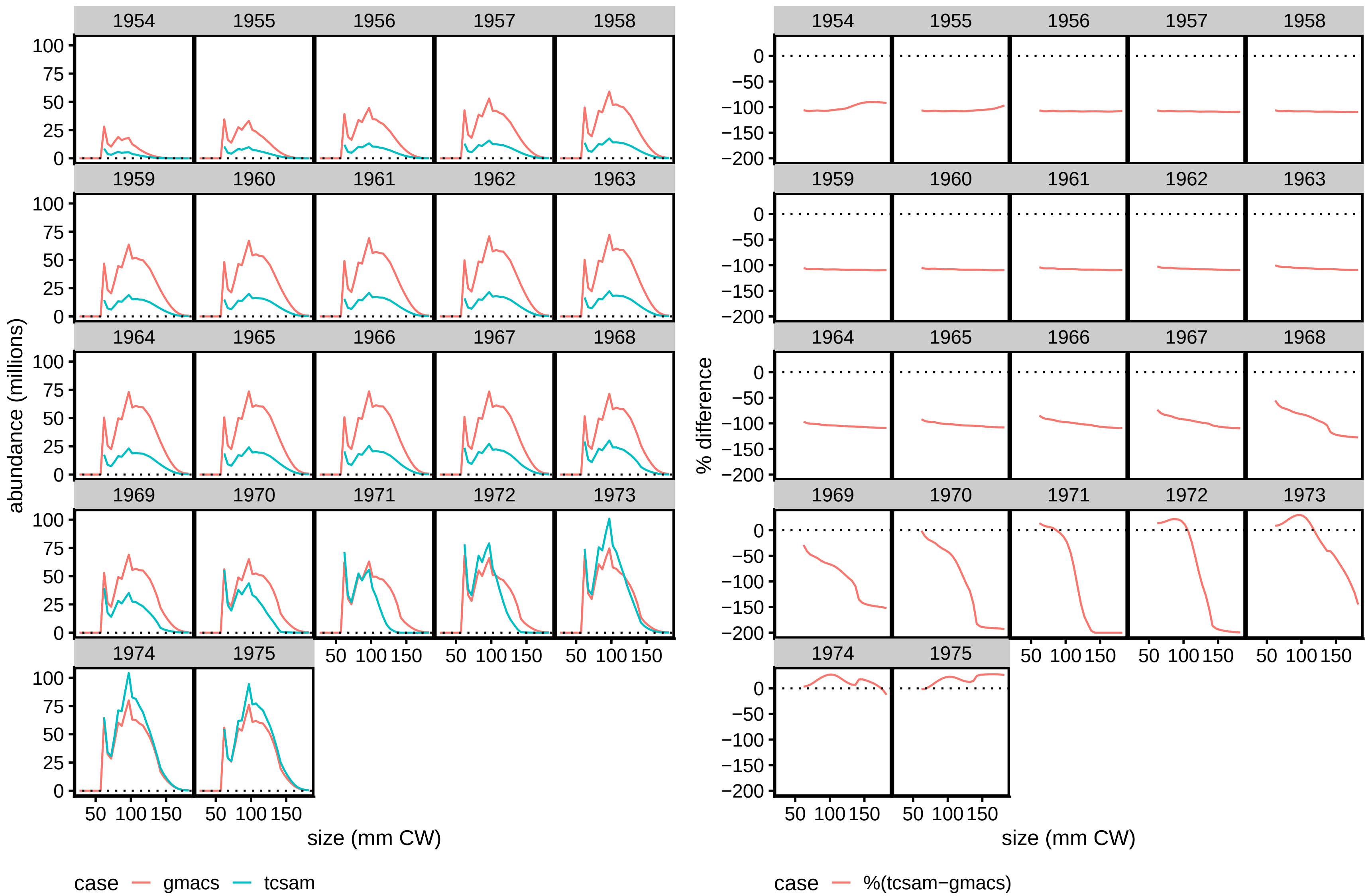


Figure 32. Comparison of the predicted population abundance-at-size through time (1953-1975) for mature, old shell males from the GMACS and TCSAM02 models. Left: values; right: percent differences.

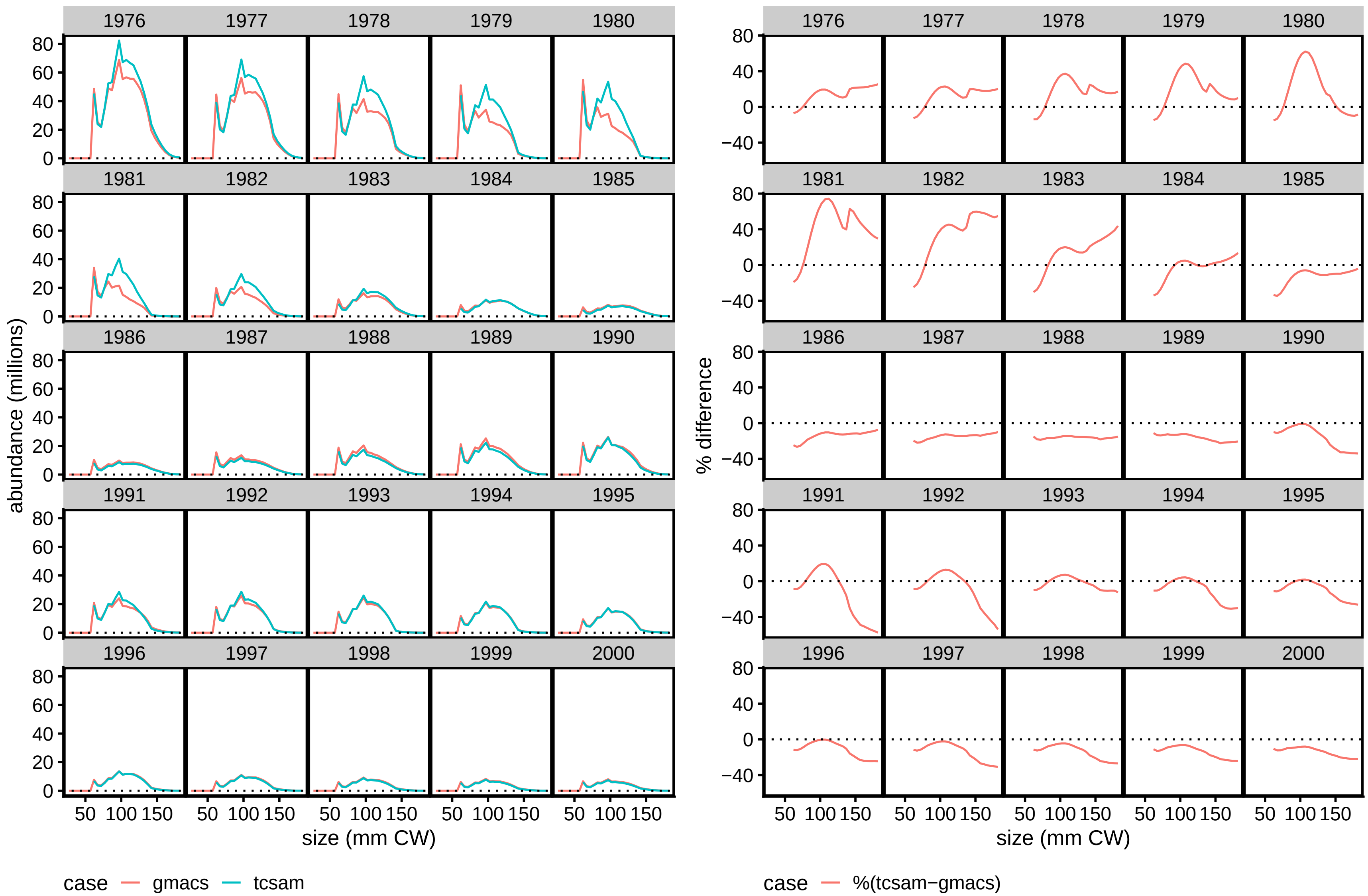


Figure 33. Comparison of the predicted population abundance-at-size through time (1976-2000) for mature, old shell males from the GMACS and TCSAM02 models. Left: values; right: percent differences.

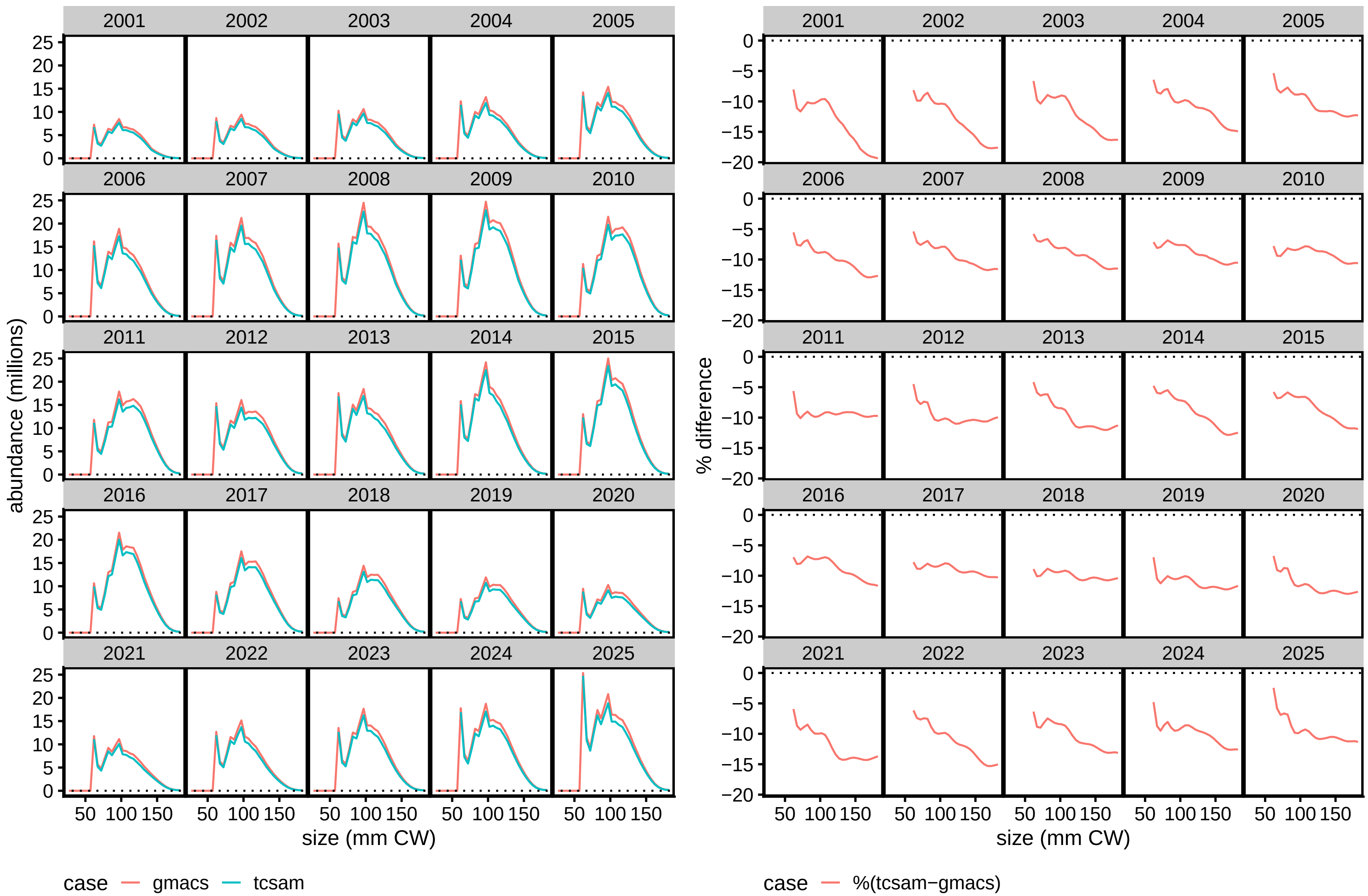


Figure 34. Comparison of the predicted population abundance-at-size through time (2001-2025) for mature, old shell males from the GMACS and TCSAM02 models. Left: values; right: percent differences.

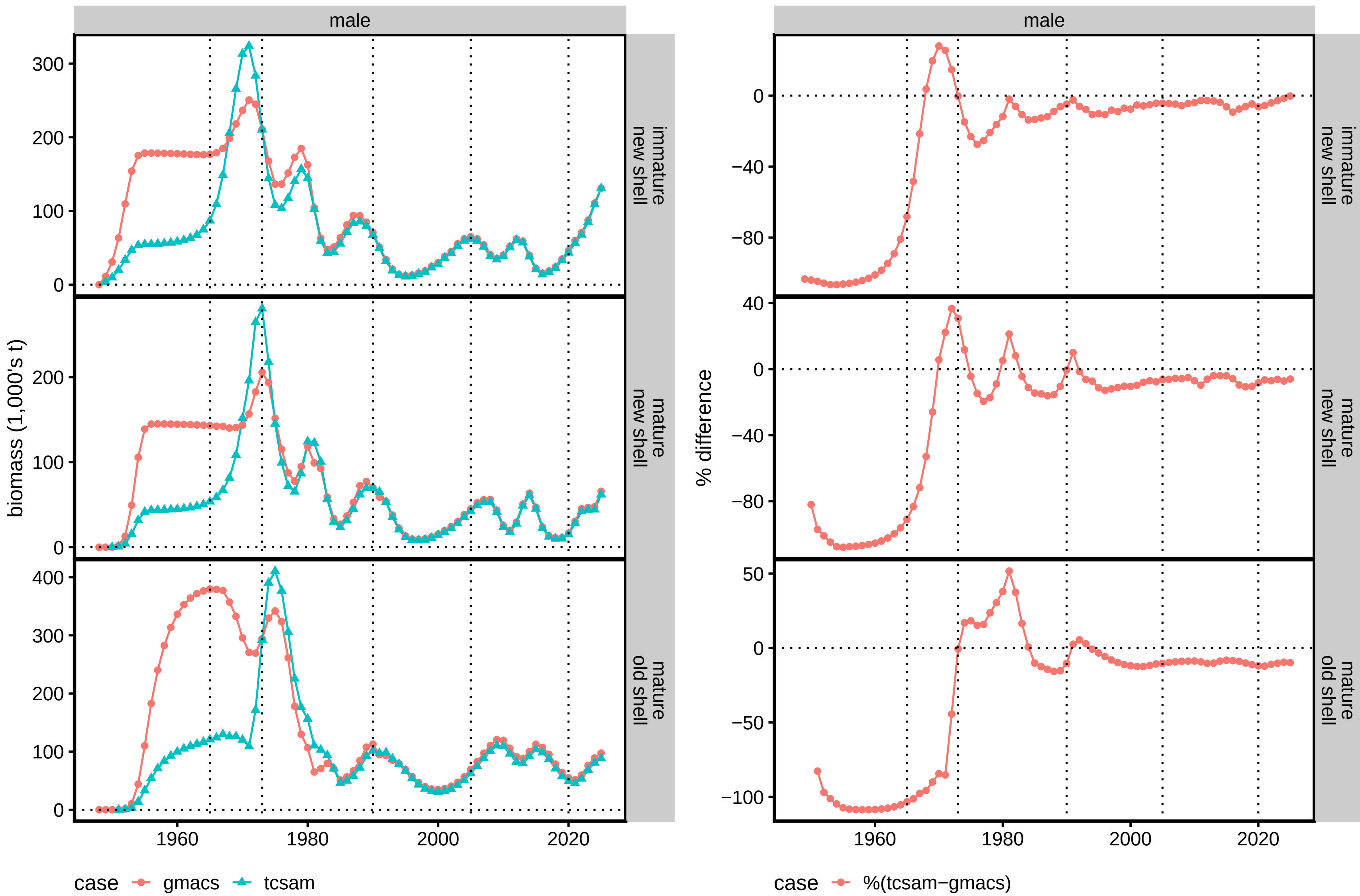


Figure 35. Comparison of the predicted population biomass through time by maturity/shell condition for males from the GMACS and TCSAM02 models. Left: values; right: percent differences. The dotted vertical lines indicate various temporal reference points: 1965-start of foreign fleet catch data; 1973-start of groundfish bycatch data; 1990-start of at sea observer estimates of total catch and size compositions in the crab fisheries; 2005-crab rationalization; 2020-no NMFS survey.

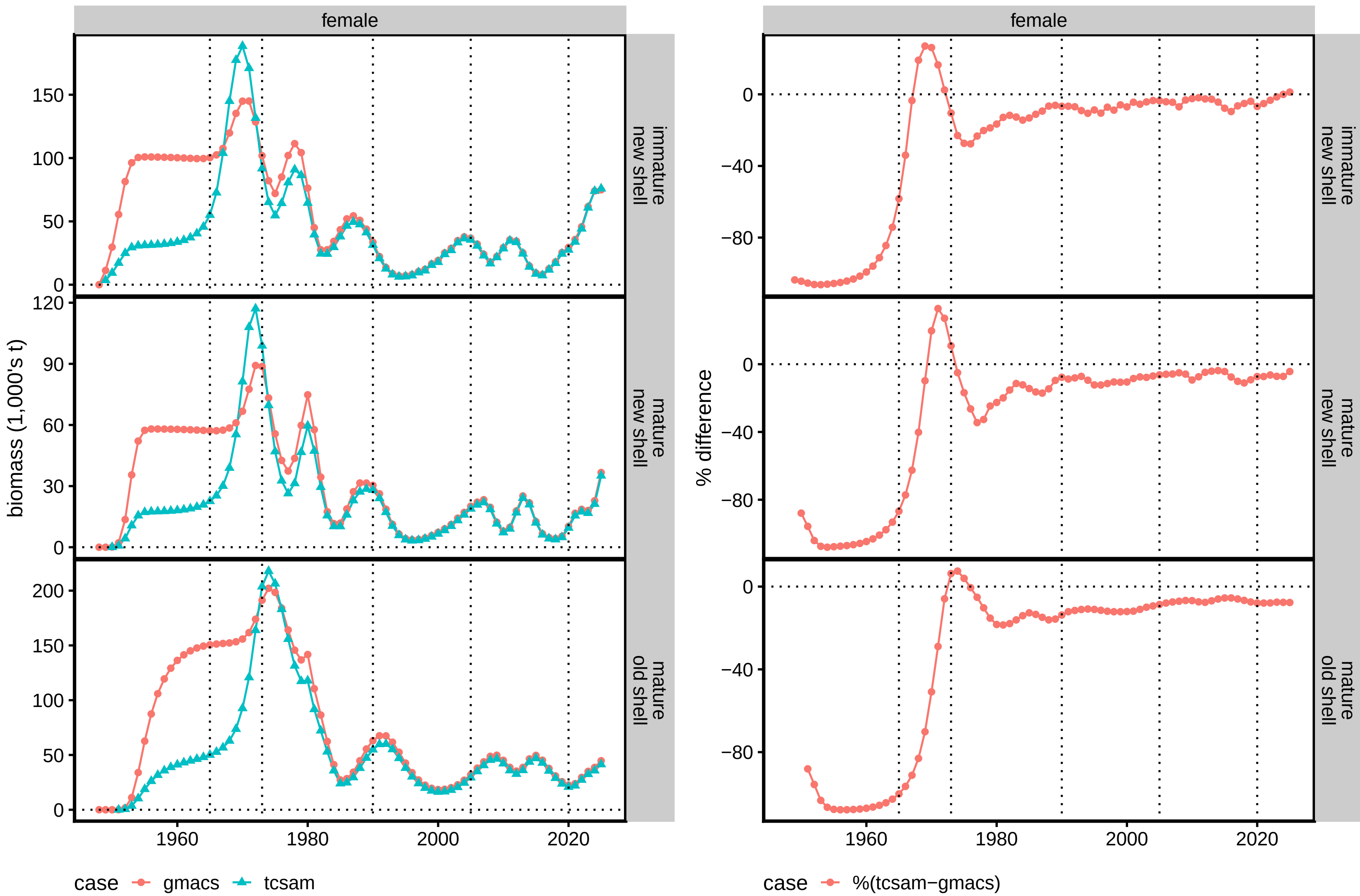


Figure 36. Comparison of the predicted population biomass through time by maturity/shell condition for females from the GMACS and TCSAM02 models. Left: values; right: percent differences. The dotted vertical lines indicate various temporal reference points: 1965-start of foreign fleet catch data; 1973-start of groundfish bycatch data; 1990-start of at sea observer estimates of total catch and size compositions in the crab fisheries; 2005-crab rationalization; 2020-no NMFS survey.

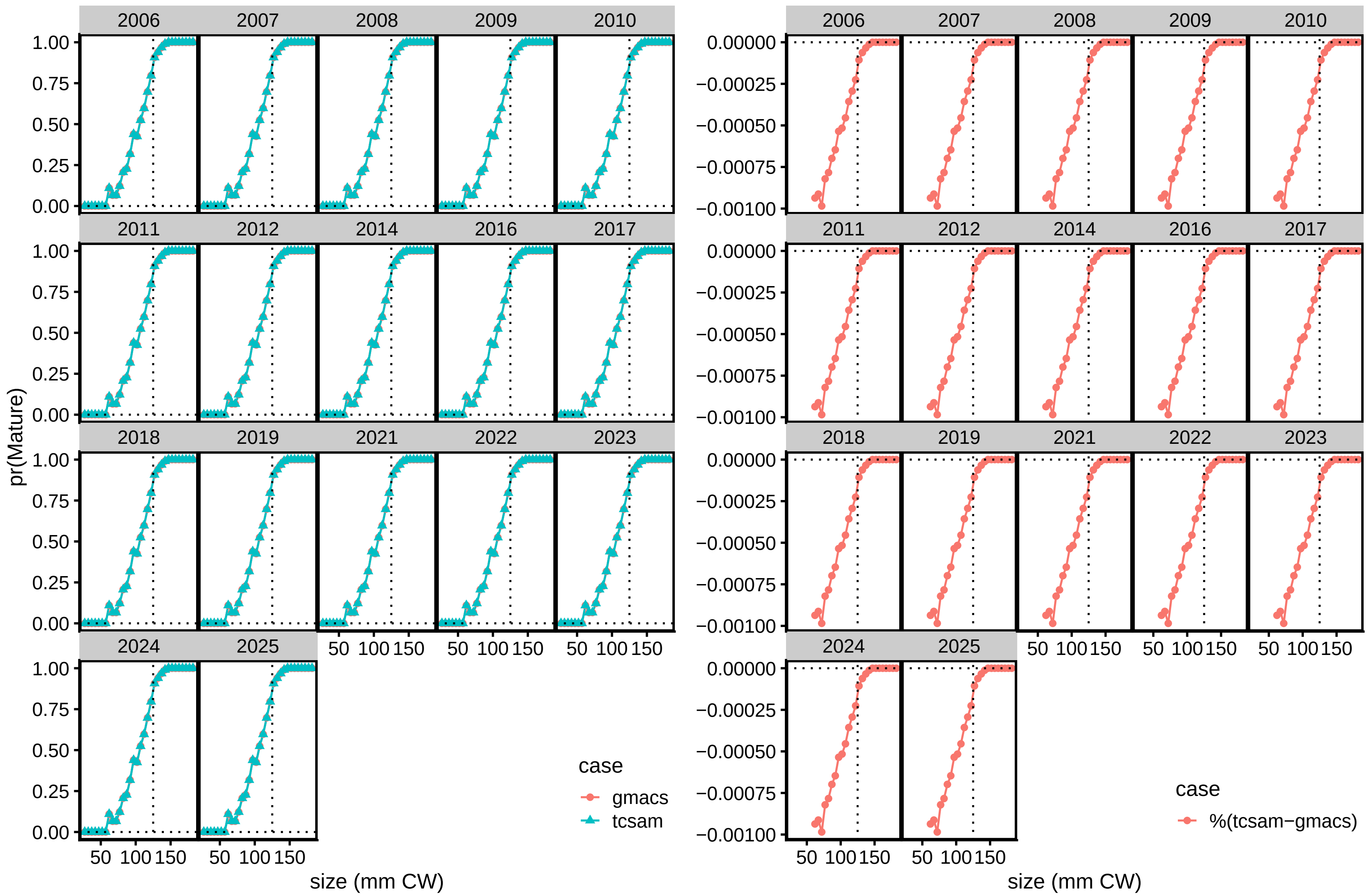


Figure 37. Comparison of the predicted male maturity ogives through time based on predicted NMFS survey abundance-at-size for immature and mature new shell crab from the GMACS and TCSAM02 models using model size bins. Left: values; right: percent differences.

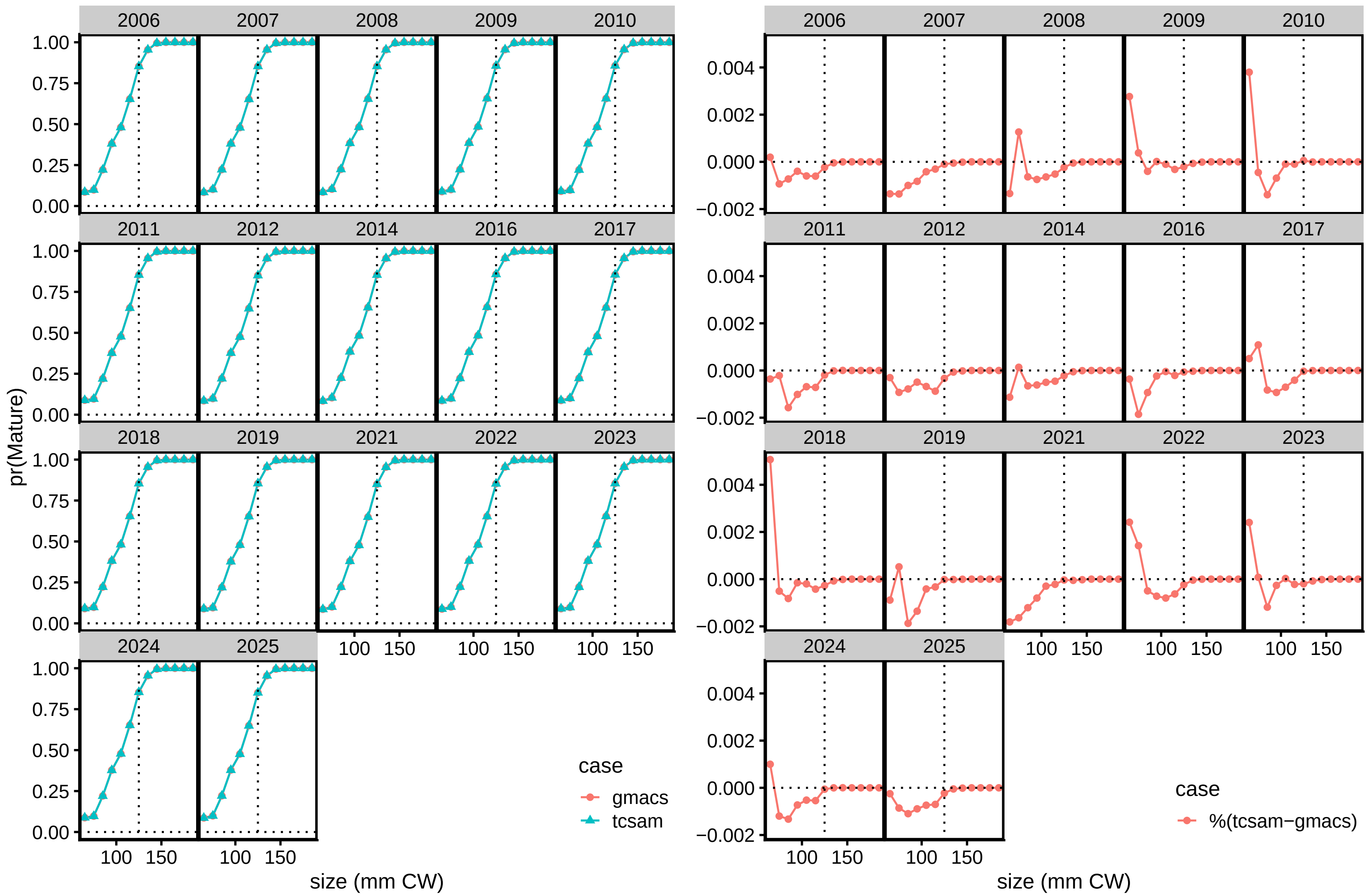


Figure 38. Comparison of the predicted male maturity ogives through time based on predicted NMFS survey abundance-at-size for immature and mature new shell crab from the GMACS and TCSAM02 models, using observed size bins. Left: values; right: percent differences.

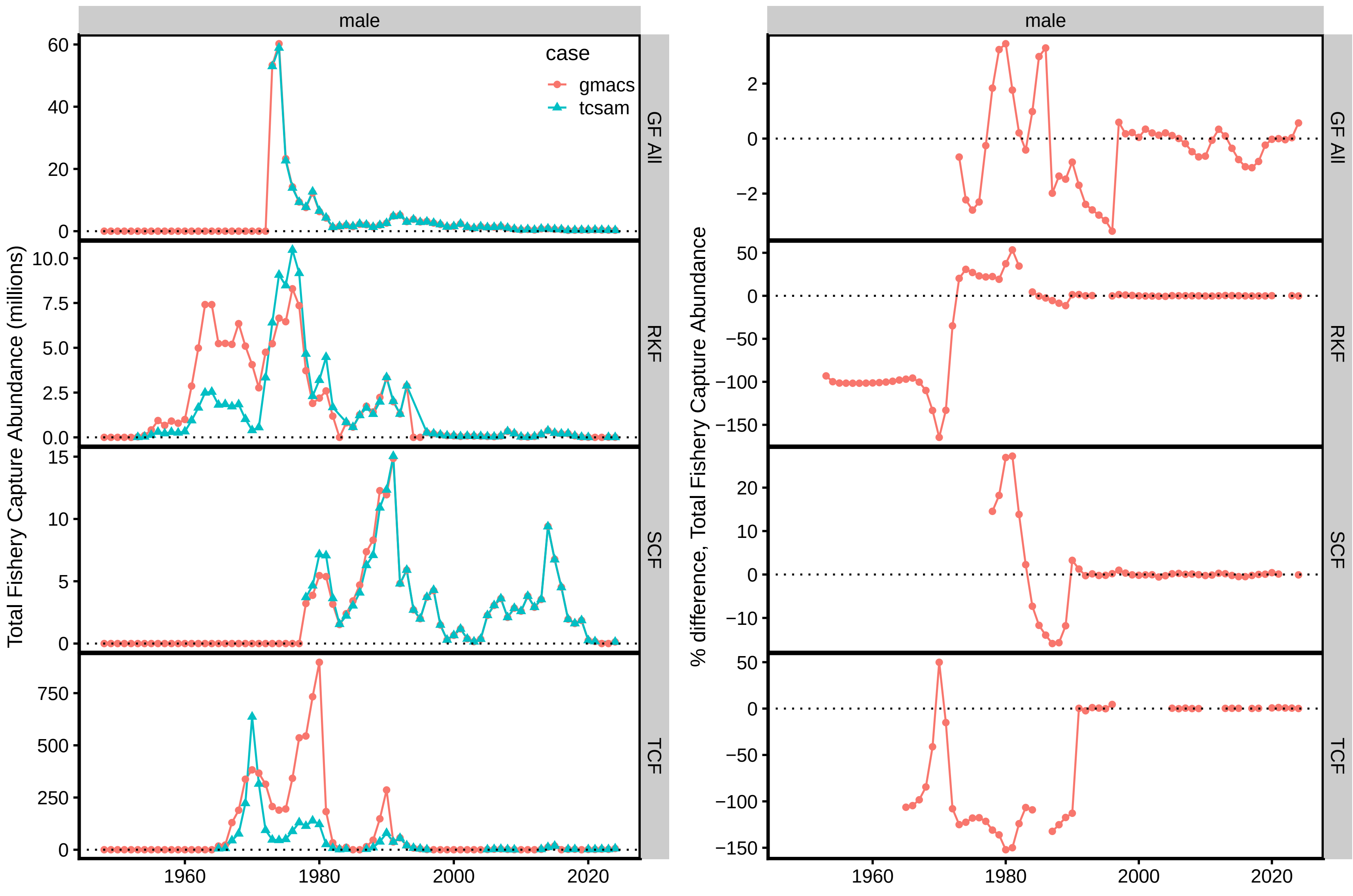


Figure 39. Comparison of the predicted capture abundance by fishery through time for males from the GMACS and TCSAM02 models. Left: values; right: percent differences.

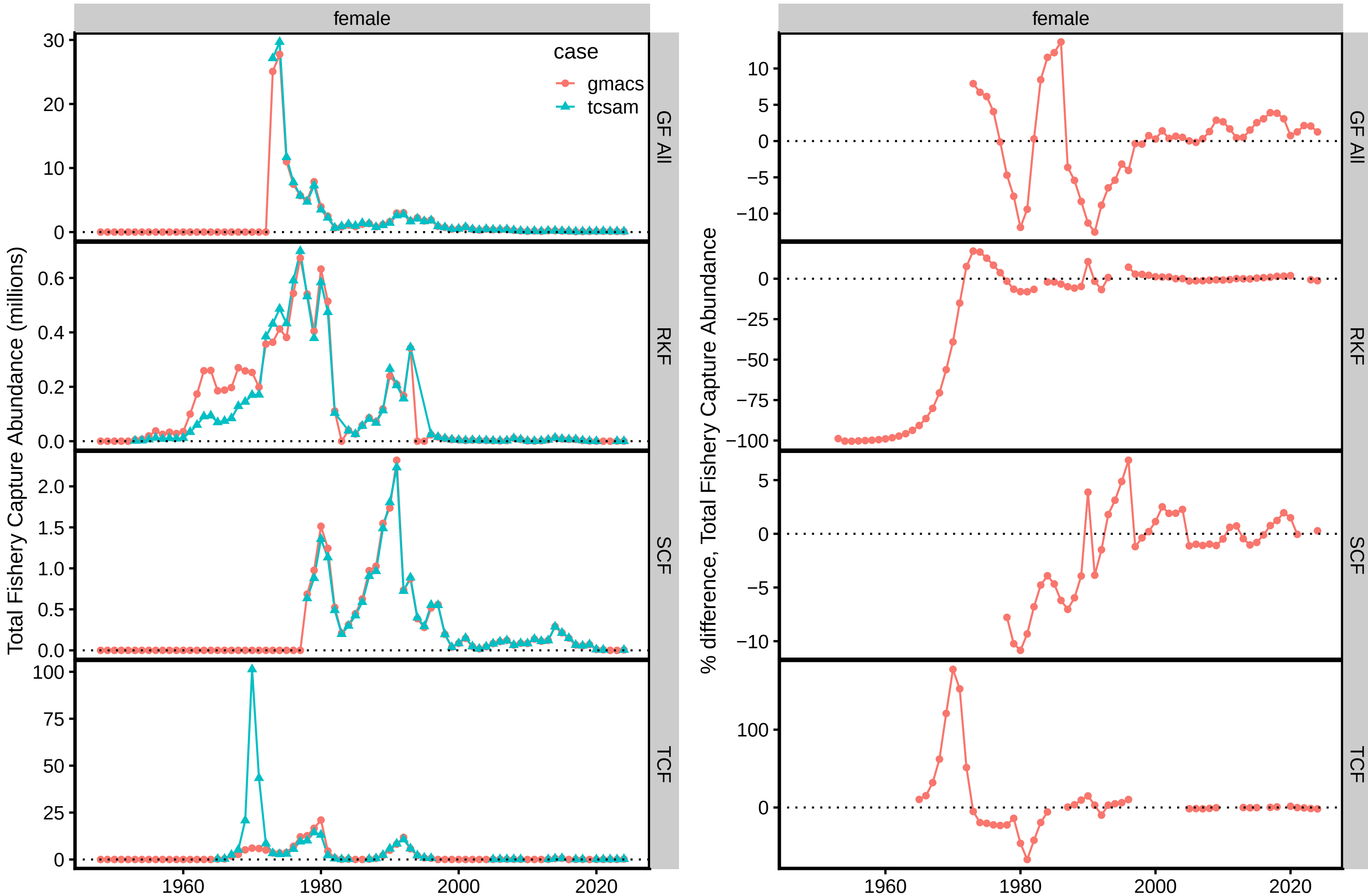


Figure 40. Comparison of the predicted capture abundance by fishery through time for females from the GMACS and TCSAM02 models. Left: values; right: percent differences.

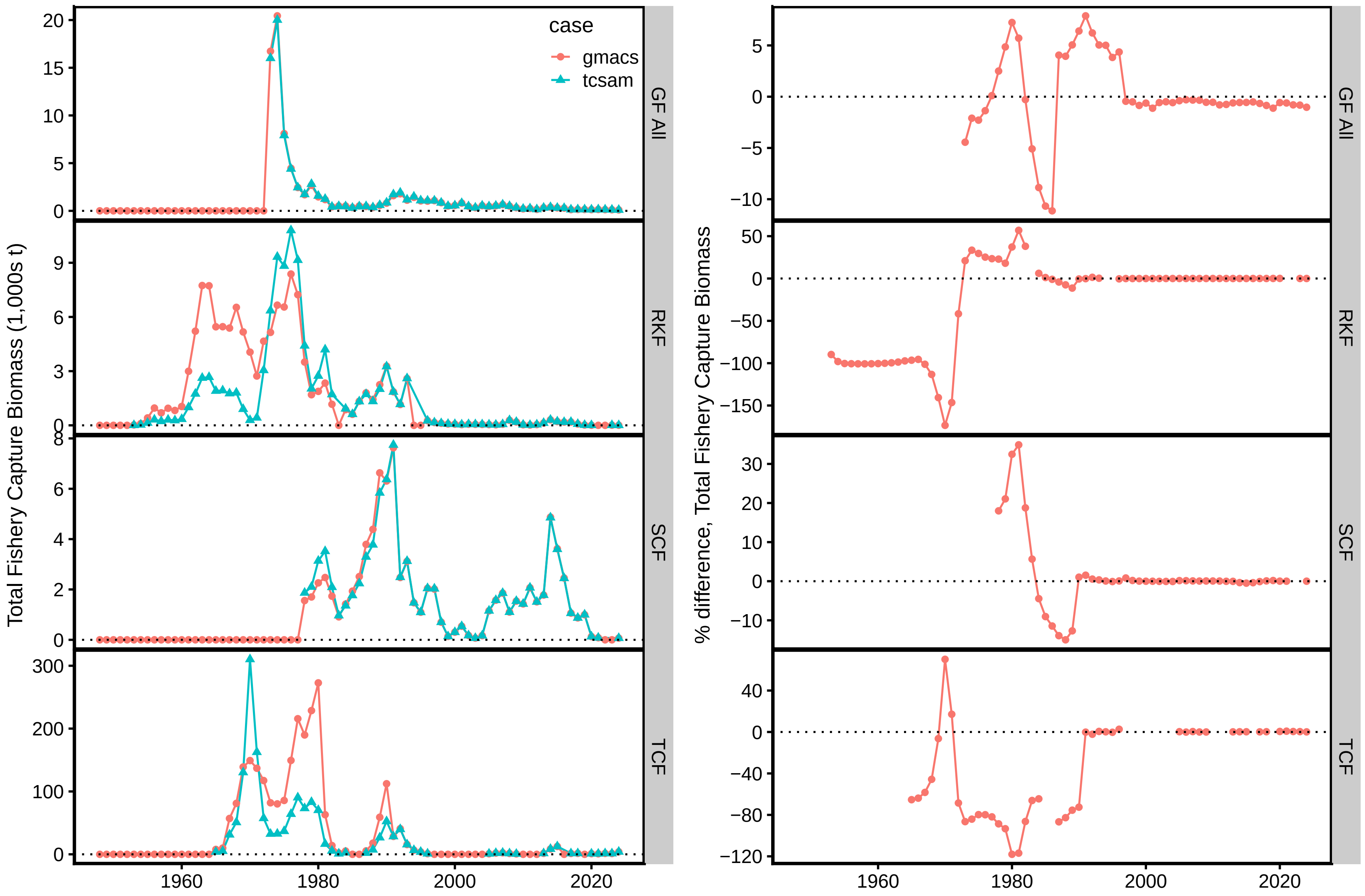


Figure 41. Comparison of the predicted capture biomass by fishery through time for males from the GMACS and TCSAM02 models. Left: values; right: percent differences.

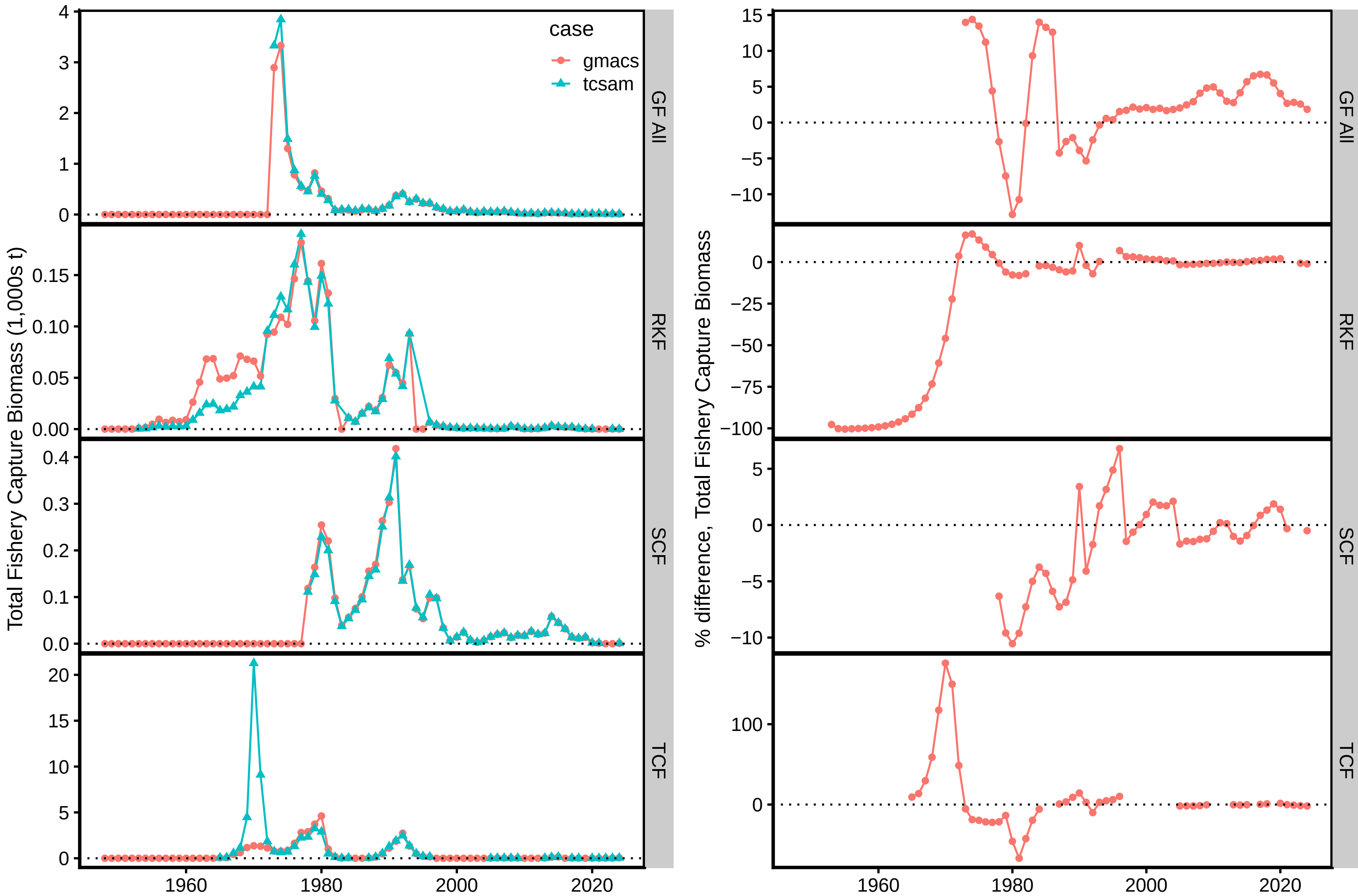


Figure 42. Comparison of the predicted capture biomass by fishery through time for females from the GMACS and TCSAM02 models. Left: values; right: percent differences.

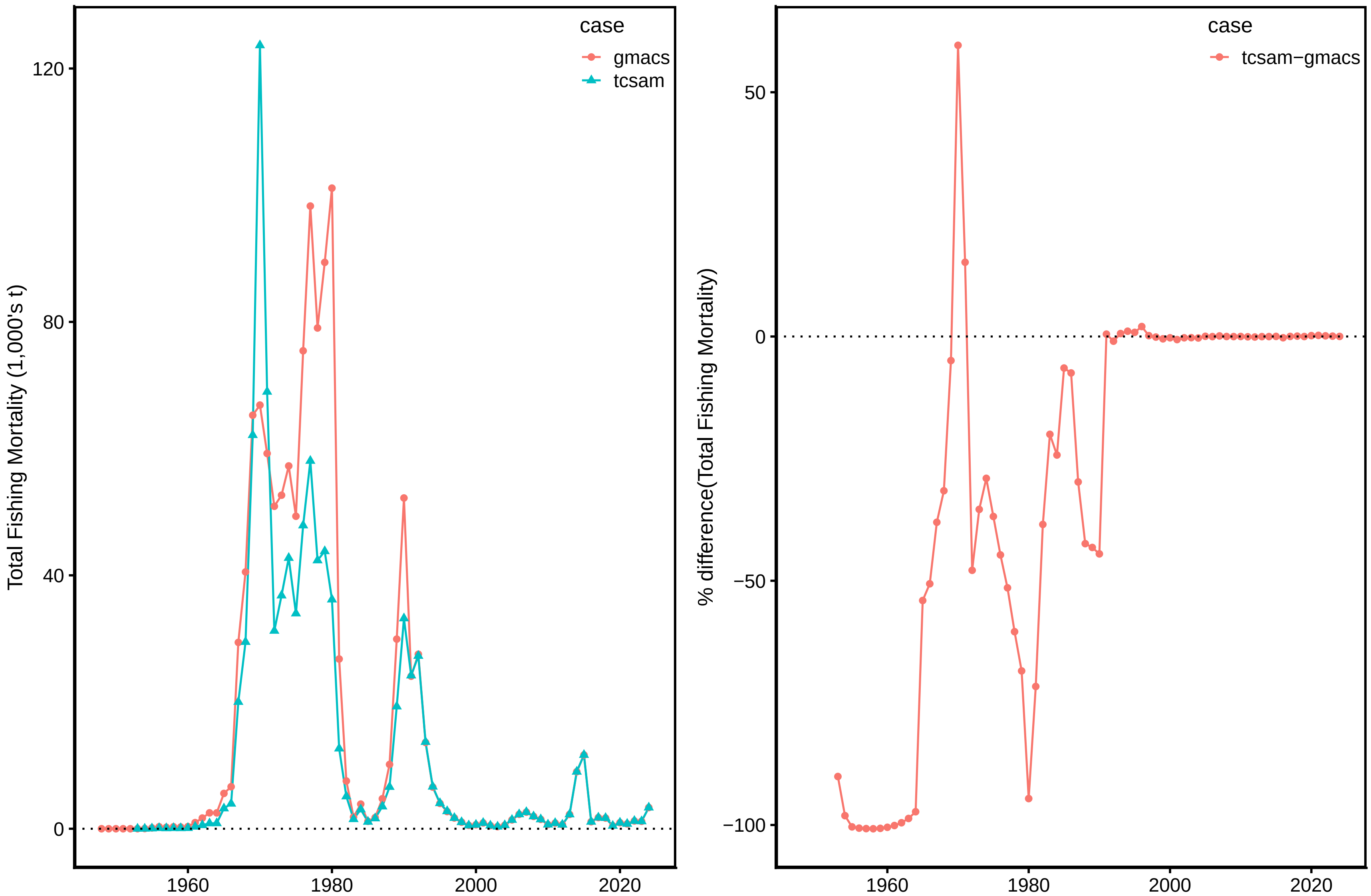


Figure 43. Comparison of the predicted total fishing mortality (biomass) through time from the GMACS and TCSAM02 models. Left: values; right: percent differences.

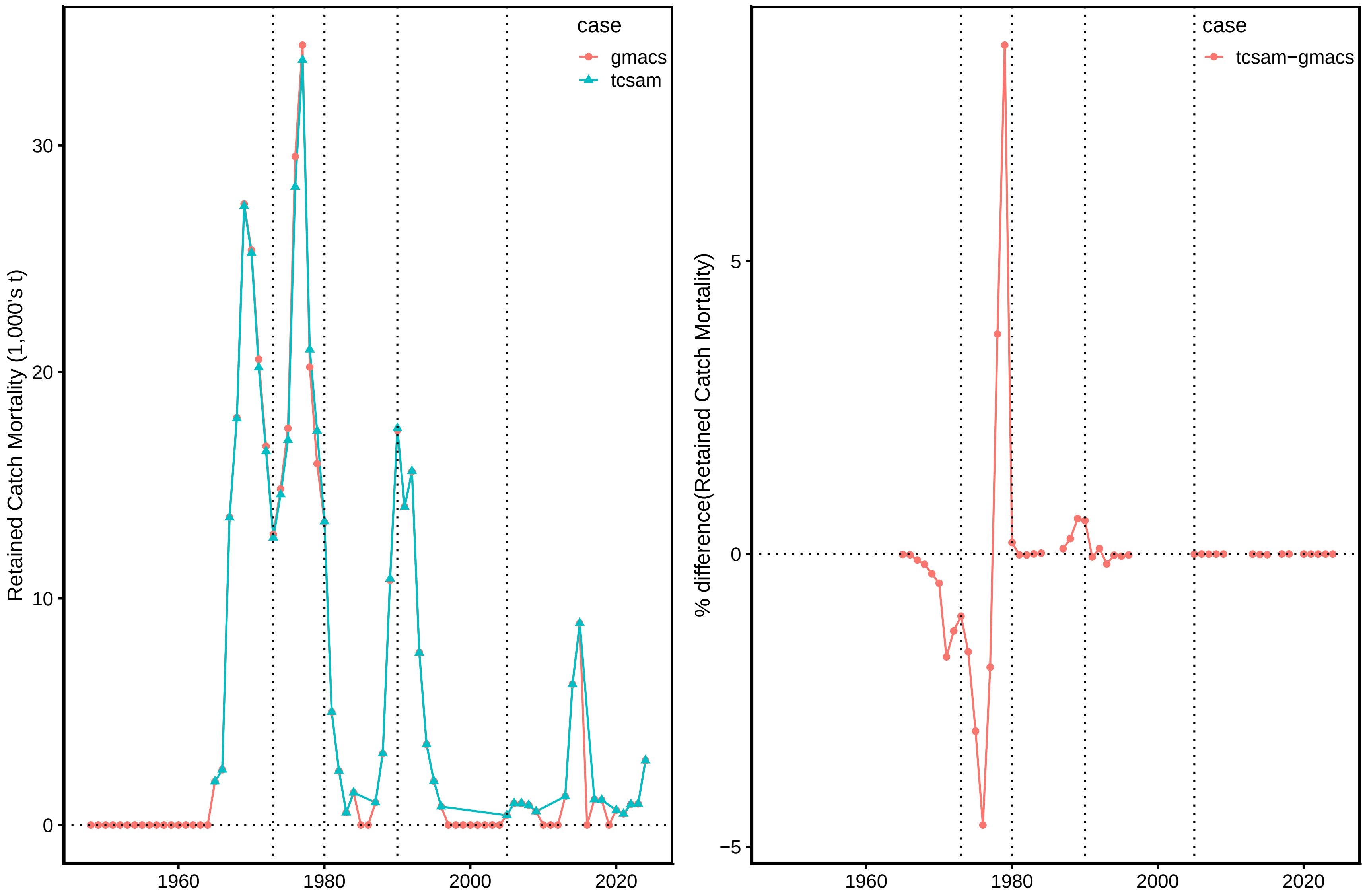


Figure 44. Comparison of the predicted retained catch mortality (biomass) through time from the GMACS and TCSAM02 models. Left: values; right: percent differences. Dotted vertical lines indicate 1973, 1980,1990, and 2005

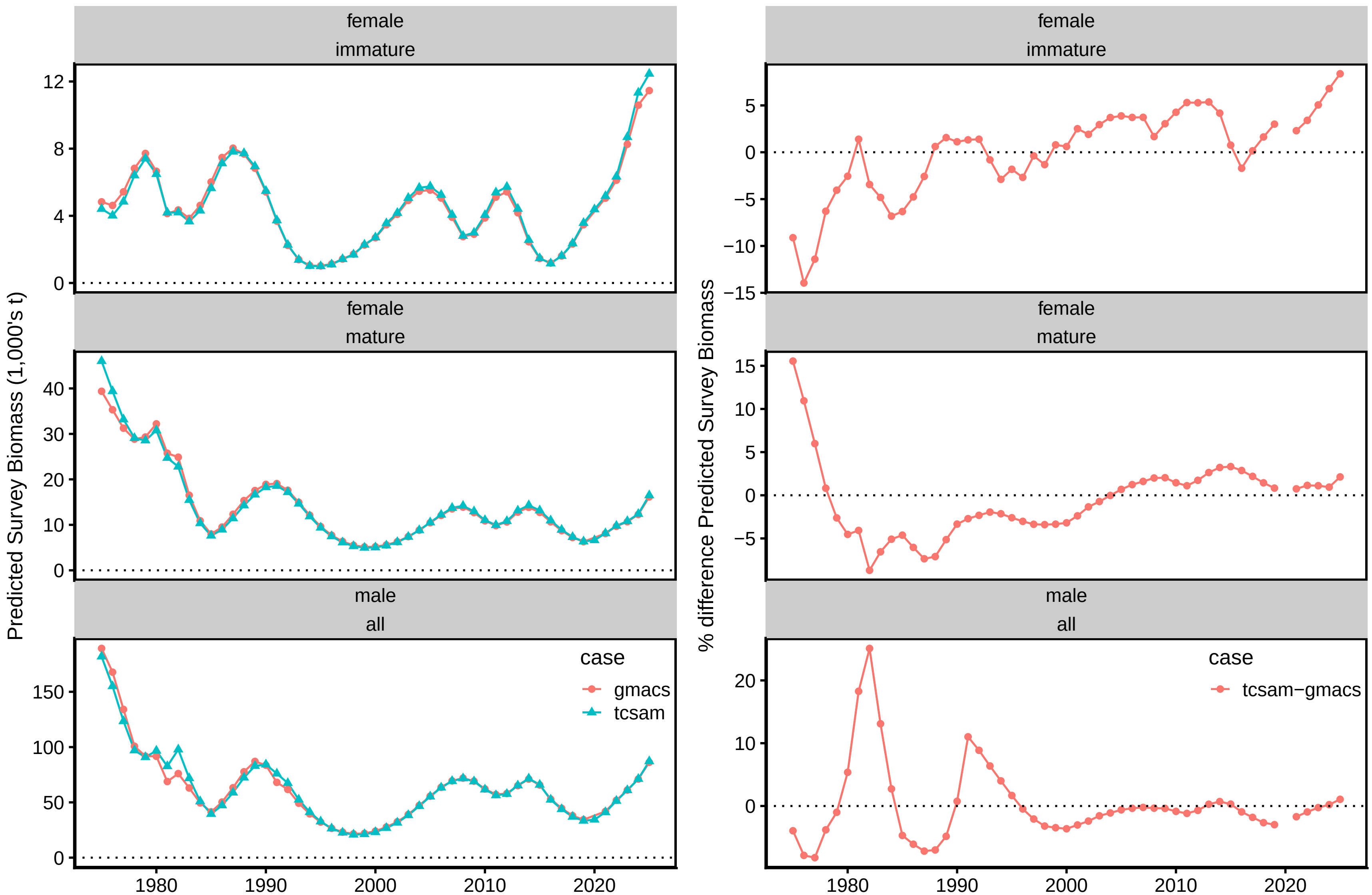


Figure 45. Comparison of the predicted NMFS survey biomass through time from the GMACS and TCSAM02 models. Left: values; right: percent differences.

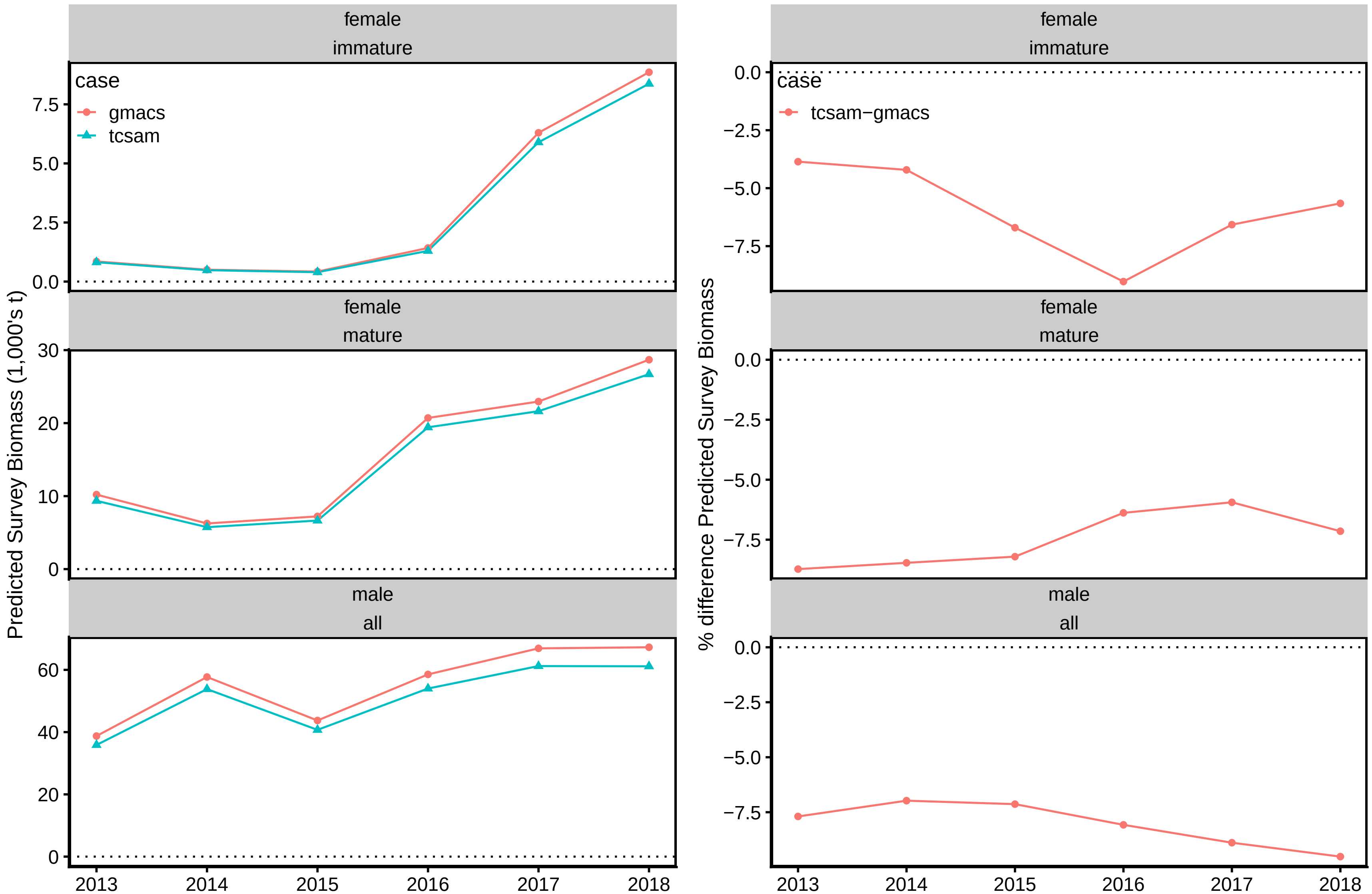


Figure 46. Comparison of the predicted BSFRF survey biomass through time from the GMACS and TCSAM02 models. Left: values; right: percent differences.

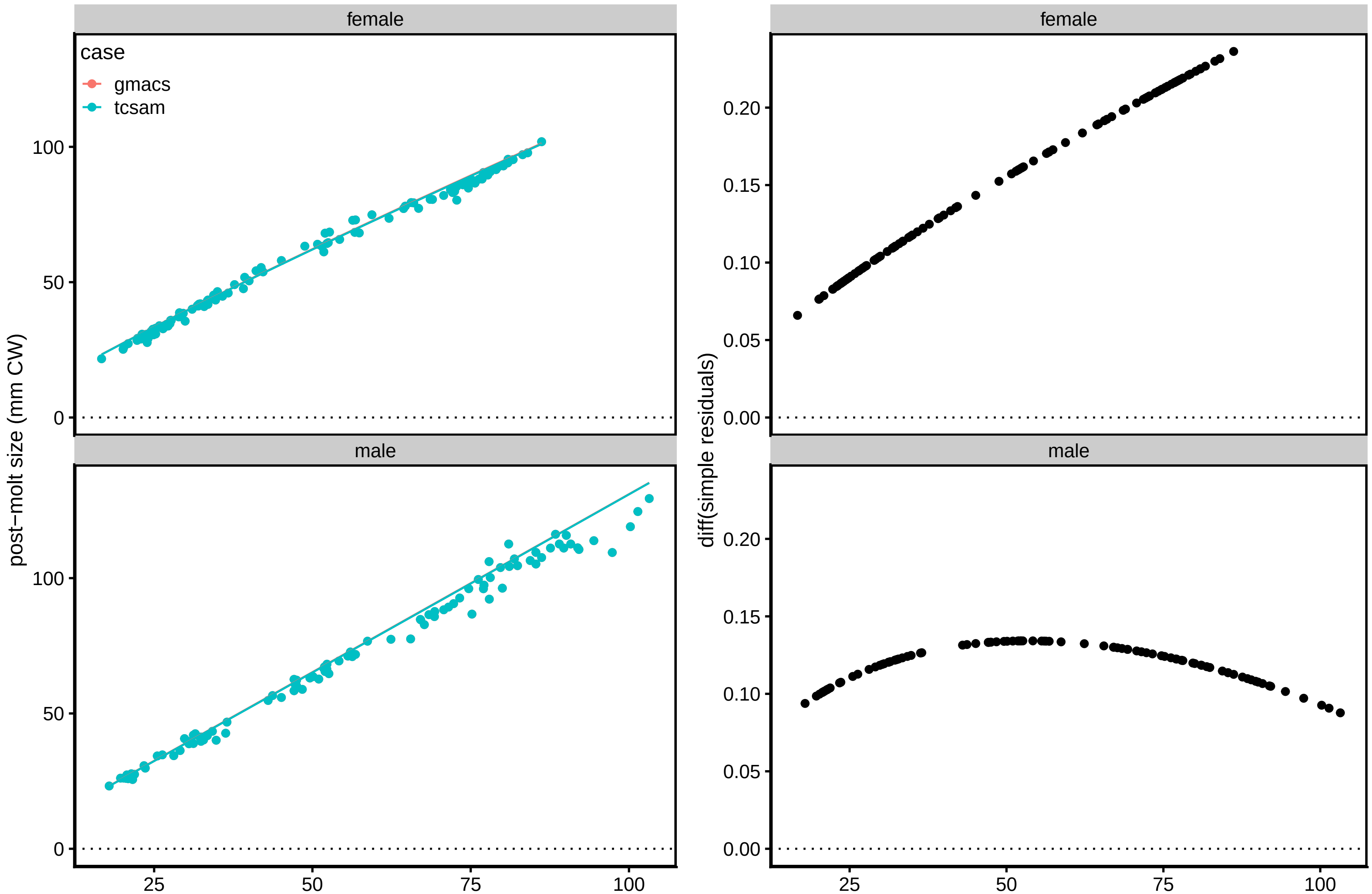


Figure 47. Comparison of fits to molt increment data by sex. Upper: observed–points, predicted–lines; Lower: differences in simple residuals between models.

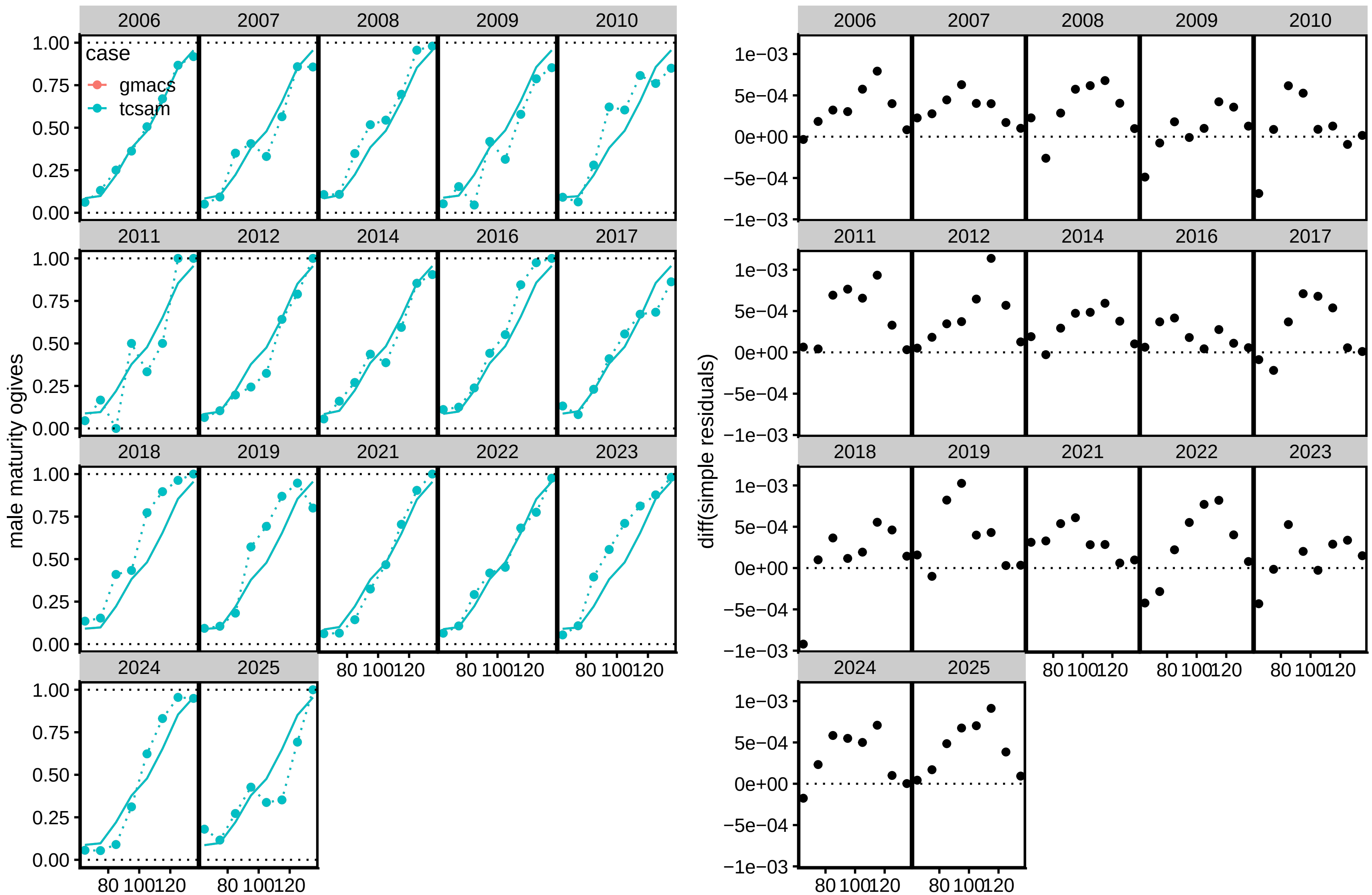


Figure 48. Comparison of fits to male maturity ogives based on chela height/carapace width measurements on males during the NMFS EBS bottom trawl surveys. Right: observed–points and dotted line, predicted–lines; Lower: differences in simple residuals between models.

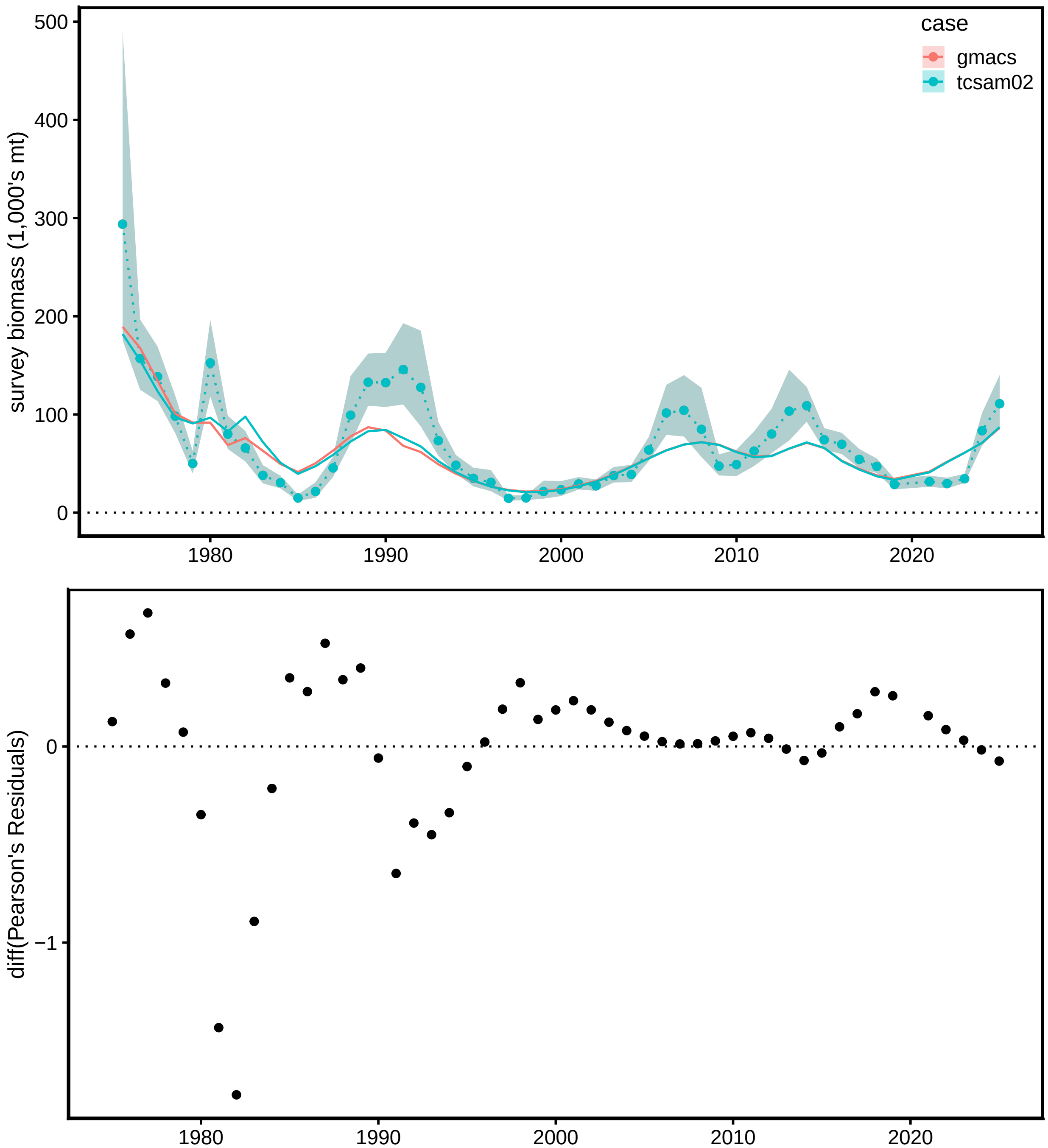


Figure 49. Comparison of fits to male survey biomass in the NMFS surveys. Upper: observed–points, dotted line, and shading (90% lognormal CIs), predicted–lines; Lower: difference in Pearson's residuals between models.

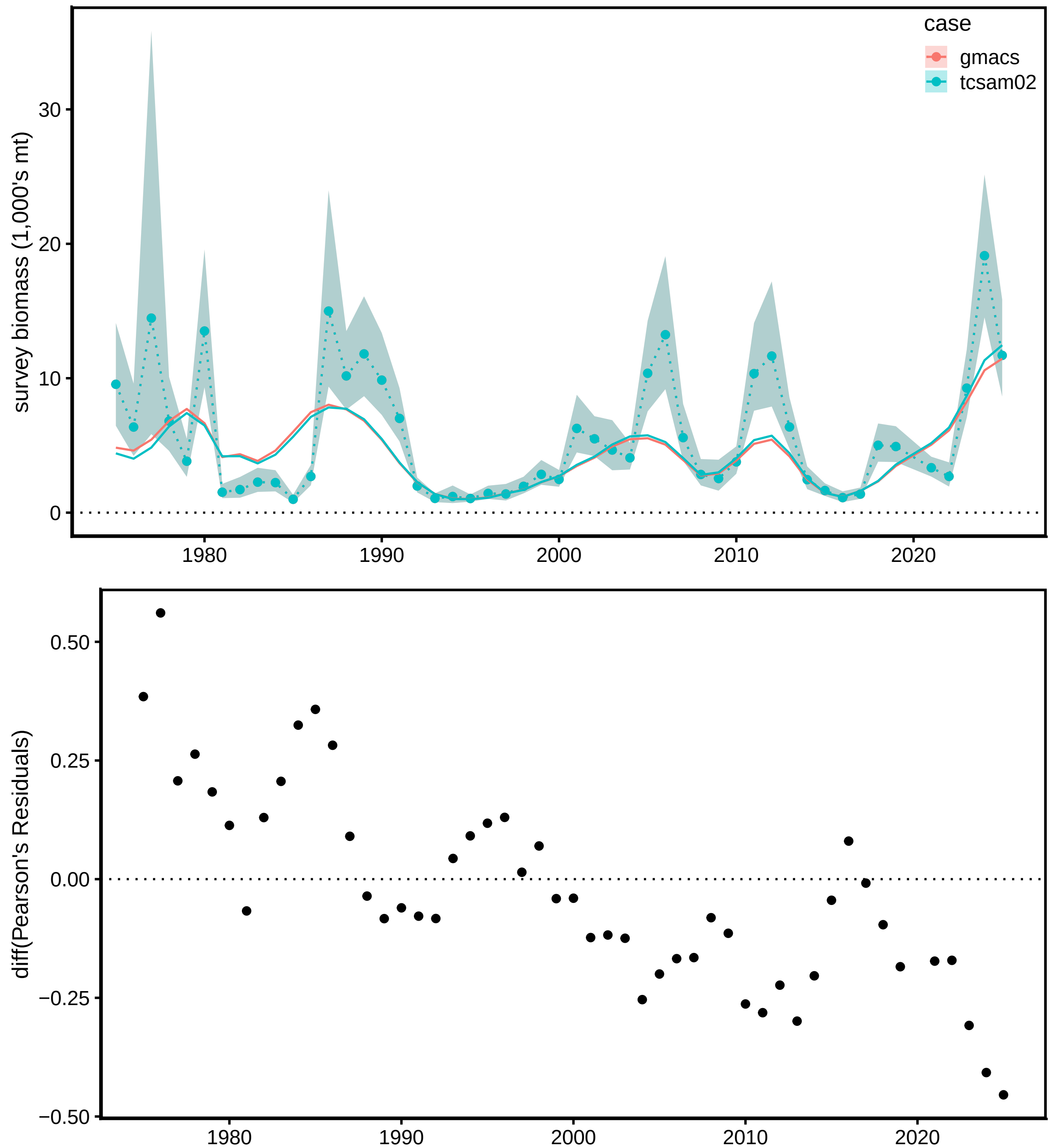


Figure 50. Comparison of fits to immature female survey biomass in the NMFS surveys. Upper: observed–points, dotted line, and shading (90% lognormal CIs), predicted–lines; Lower: difference in Pearson's residuals between models.

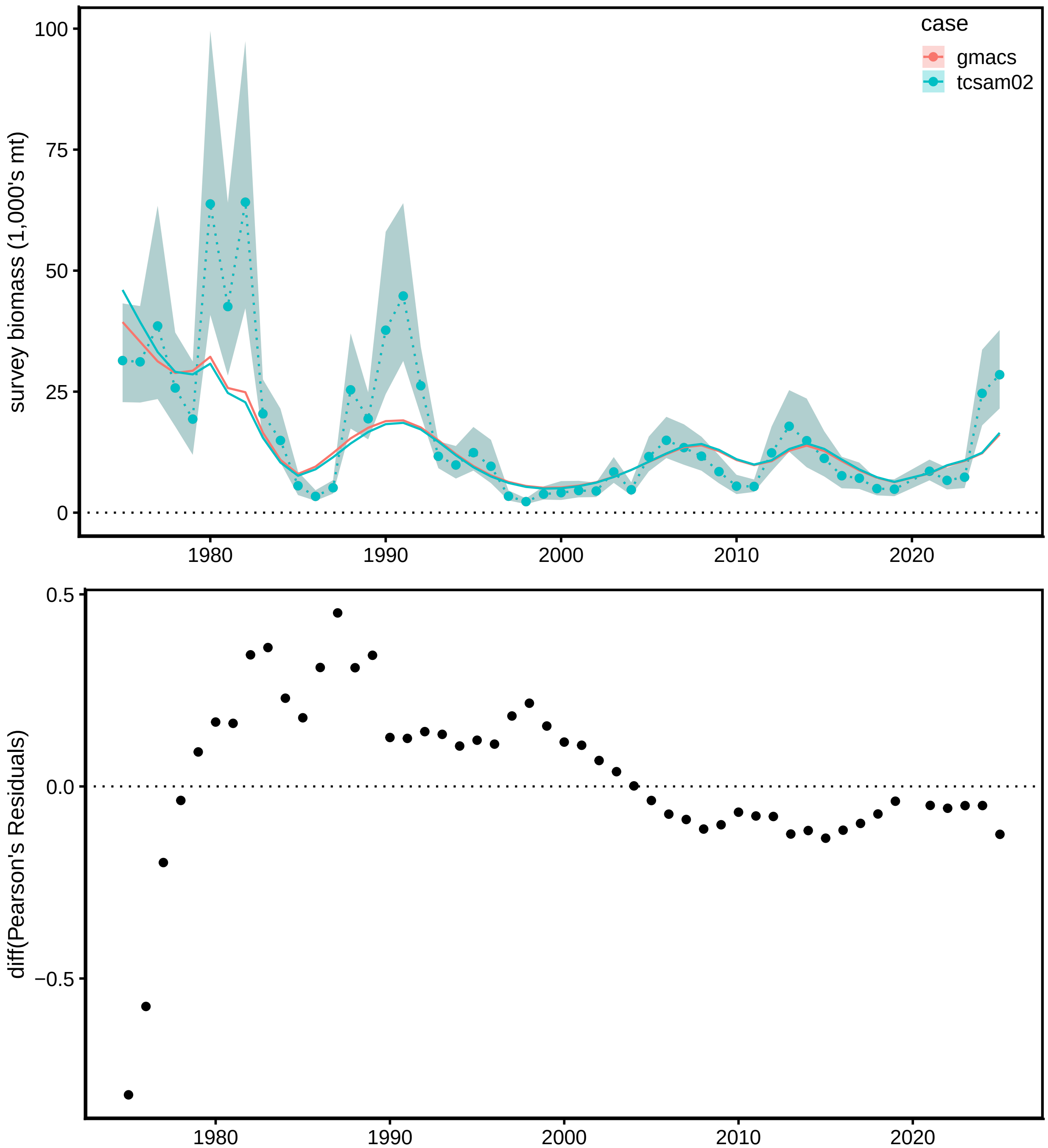


Figure 51. Comparison of fits to mature female survey biomass in the NMFS surveys. Upper: observed–points, dotted line, and shading (90% lognormal CIs), predicted–lines; Lower: difference in Pearson's residuals between models.

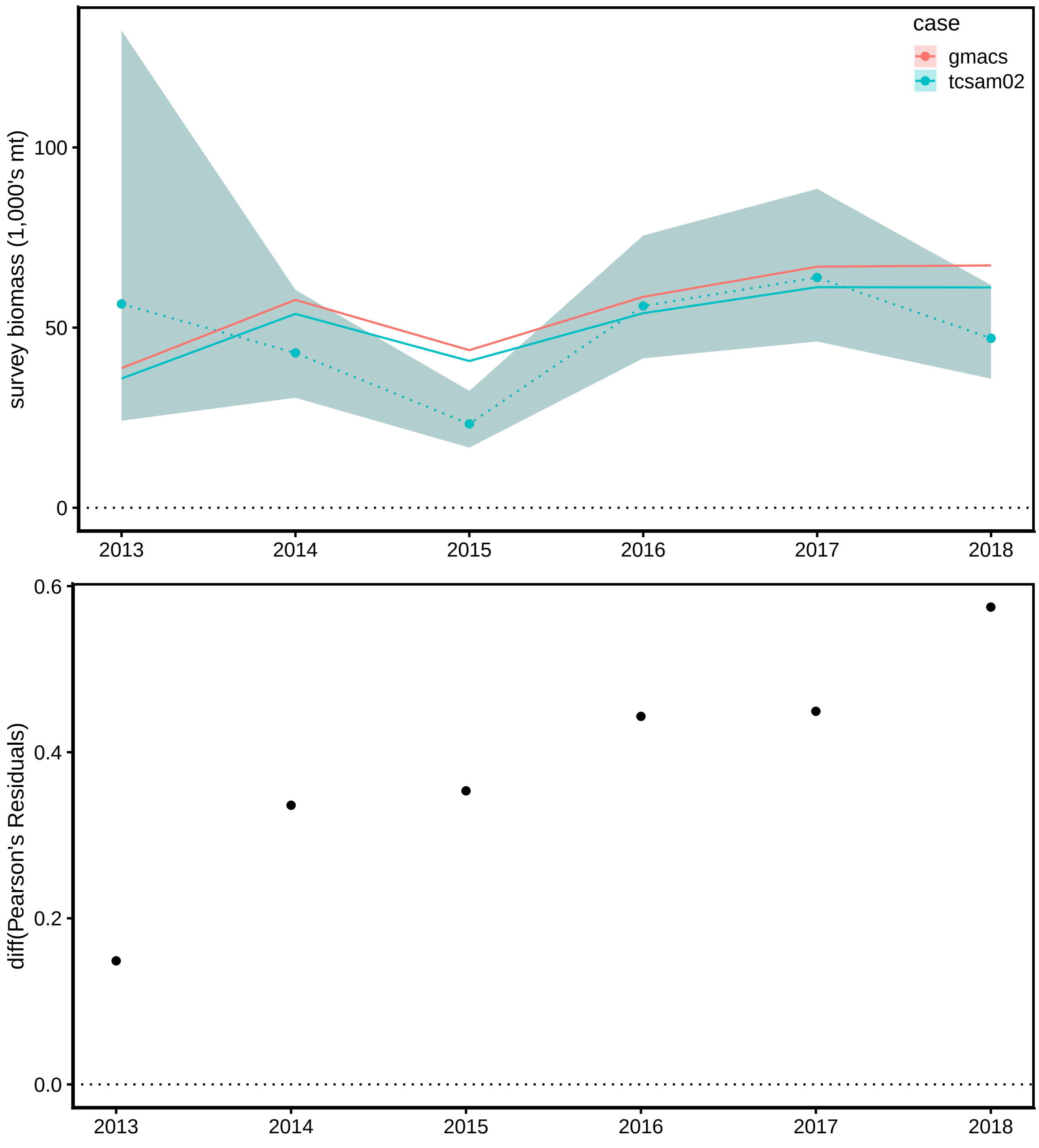


Figure 52. Comparison of fits to male survey biomass in the BSFRF surveys. Upper: observed–points, dotted line, and shading (90% lognormal CIs), predicted–lines; Lower: difference in Pearson's residuals between models.

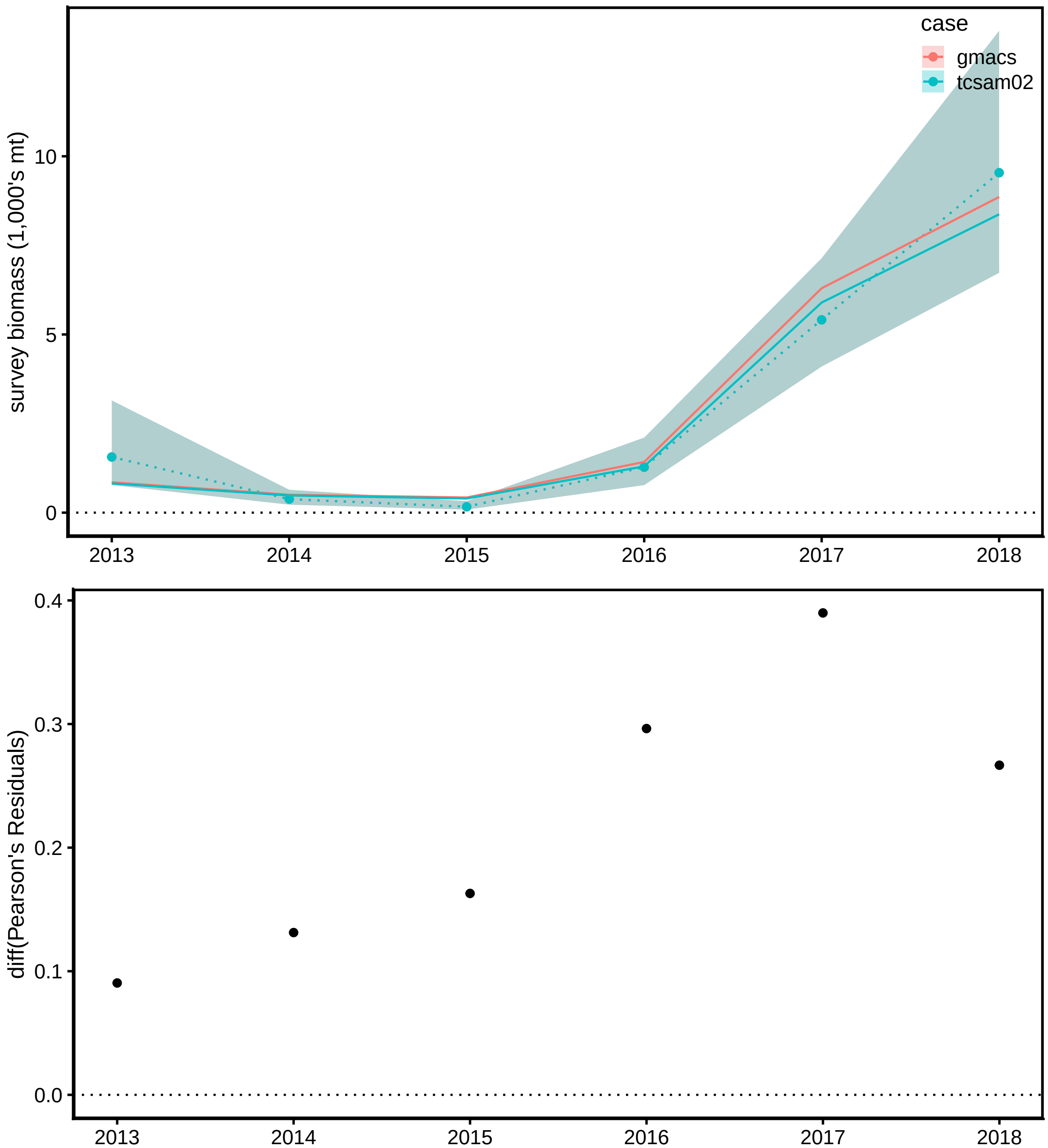


Figure 53. Comparison of fits to immature female survey biomass in the BSFRF surveys. Upper: observed–points, dotted line, and shading (90% lognormal CIs), predicted–lines; Lower: difference in Pearson's residuals between models.

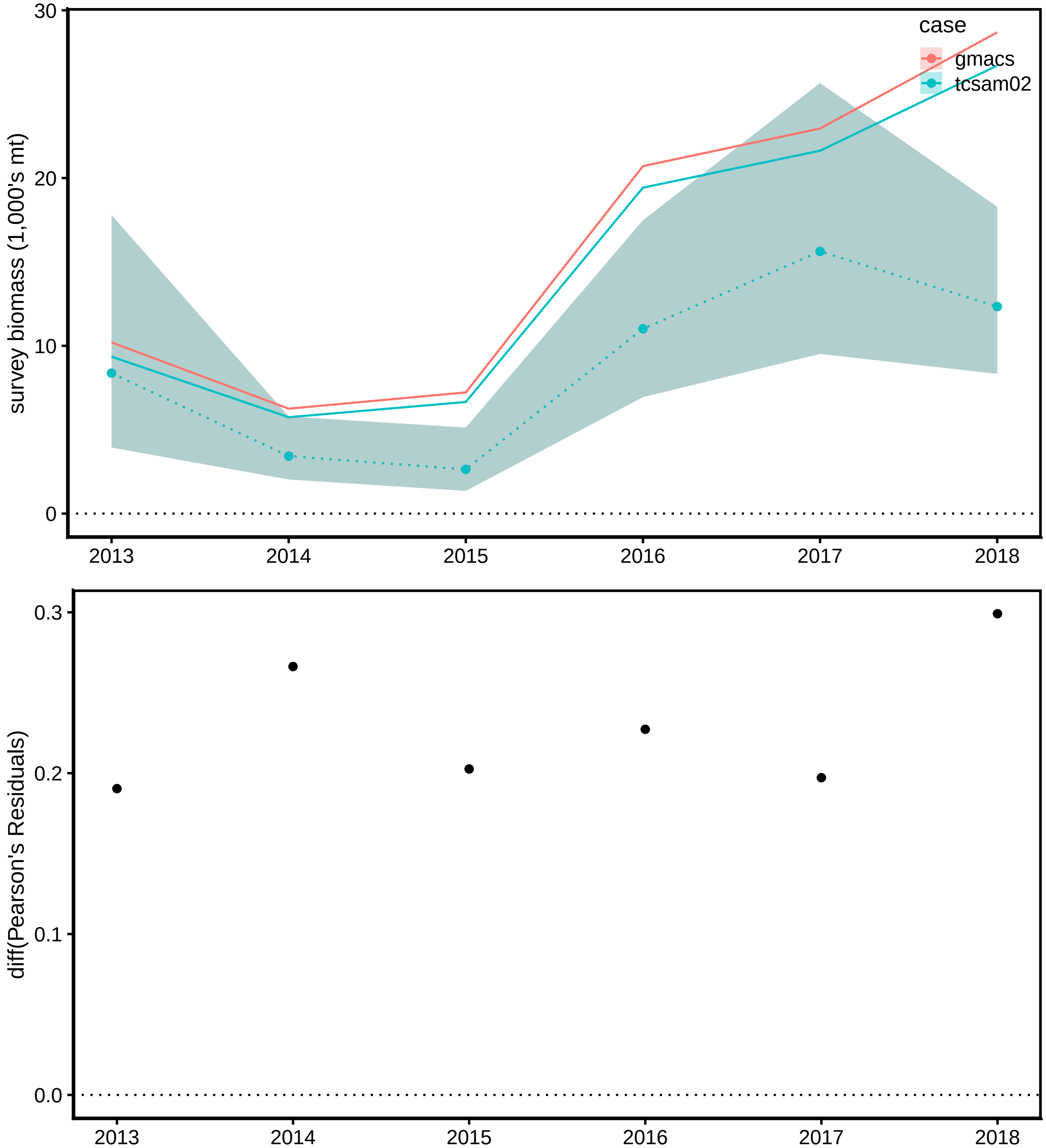


Figure 54. Comparison of fits to mature female survey biomass in the BSFRF surveys. Upper: observed–points, dotted line, and shading (90% lognormal CIs), predicted–lines; Lower: difference in Pearson's residuals between models.

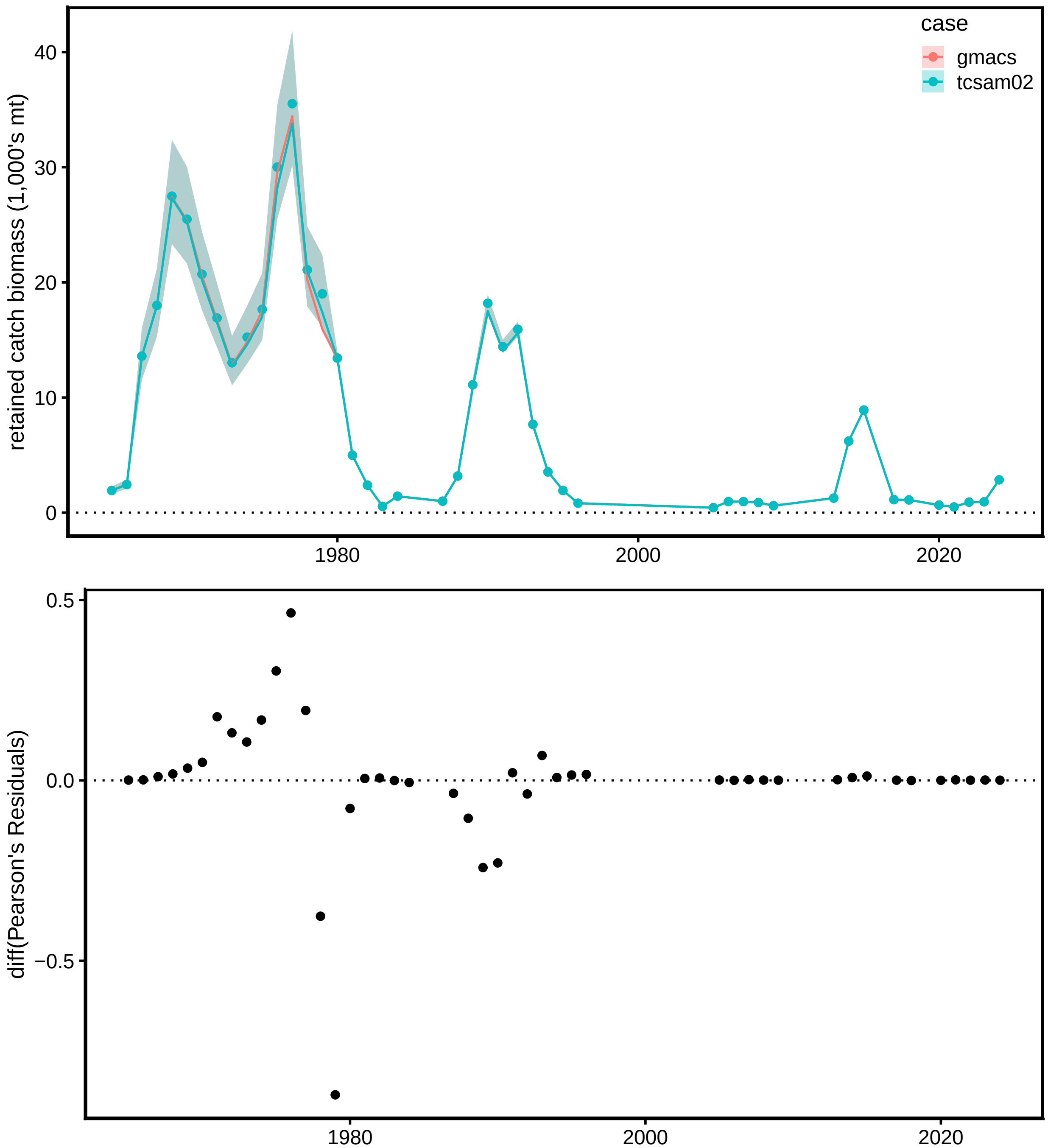


Figure 55. Comparison of fits to retained catch biomass in the directed fishery. Upper: observed–points, dotted line, and shading (90% lognormal CIs), predicted–lines; Lower: difference in Pearson's residuals between models.

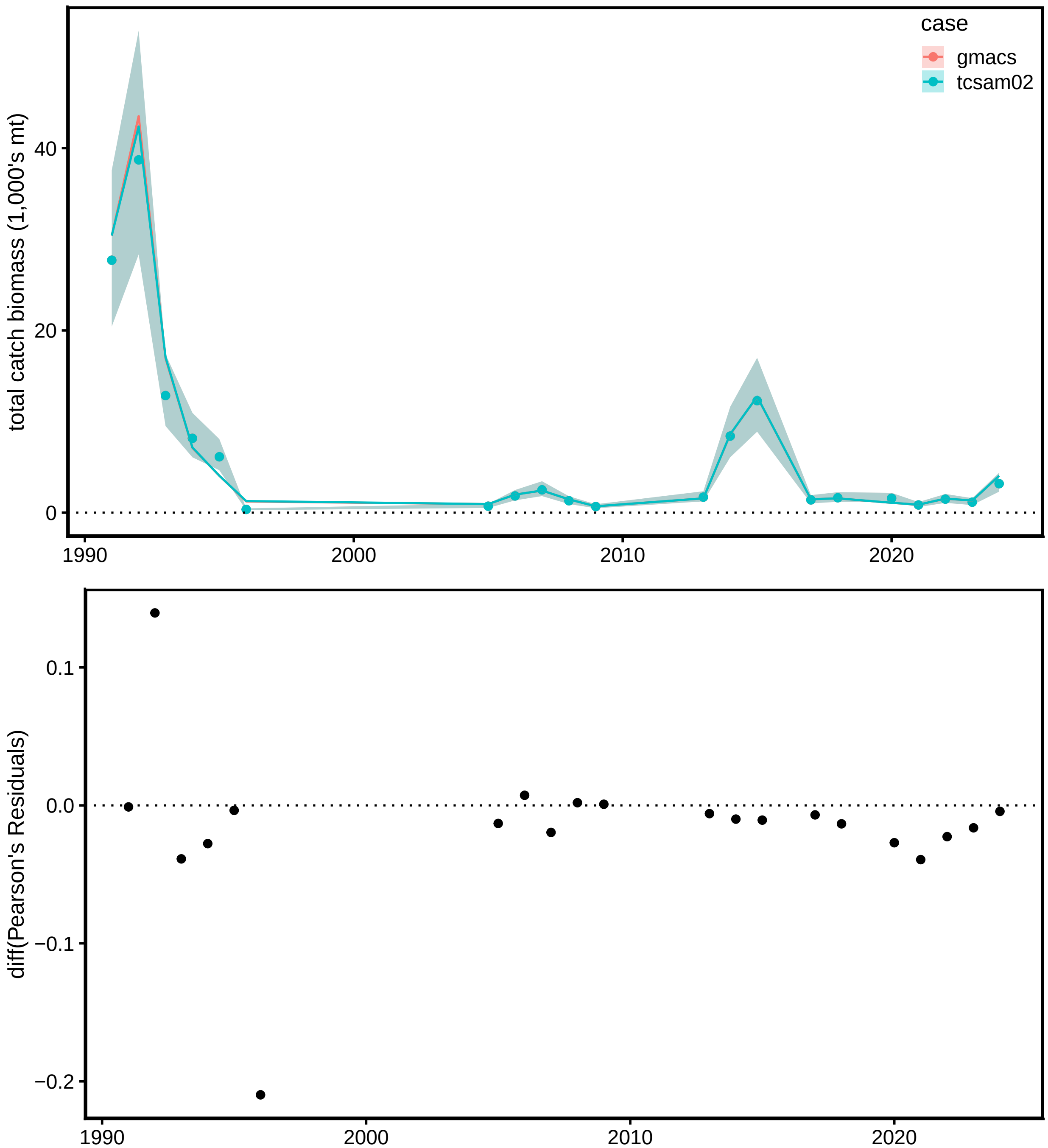


Figure 56. Comparison of fits to total catch biomass in the directed fishery. Upper: observed–points, dotted line, and shading (90% lognormal CIs), predicted–lines; Lower: difference in Pearson's residuals between models.

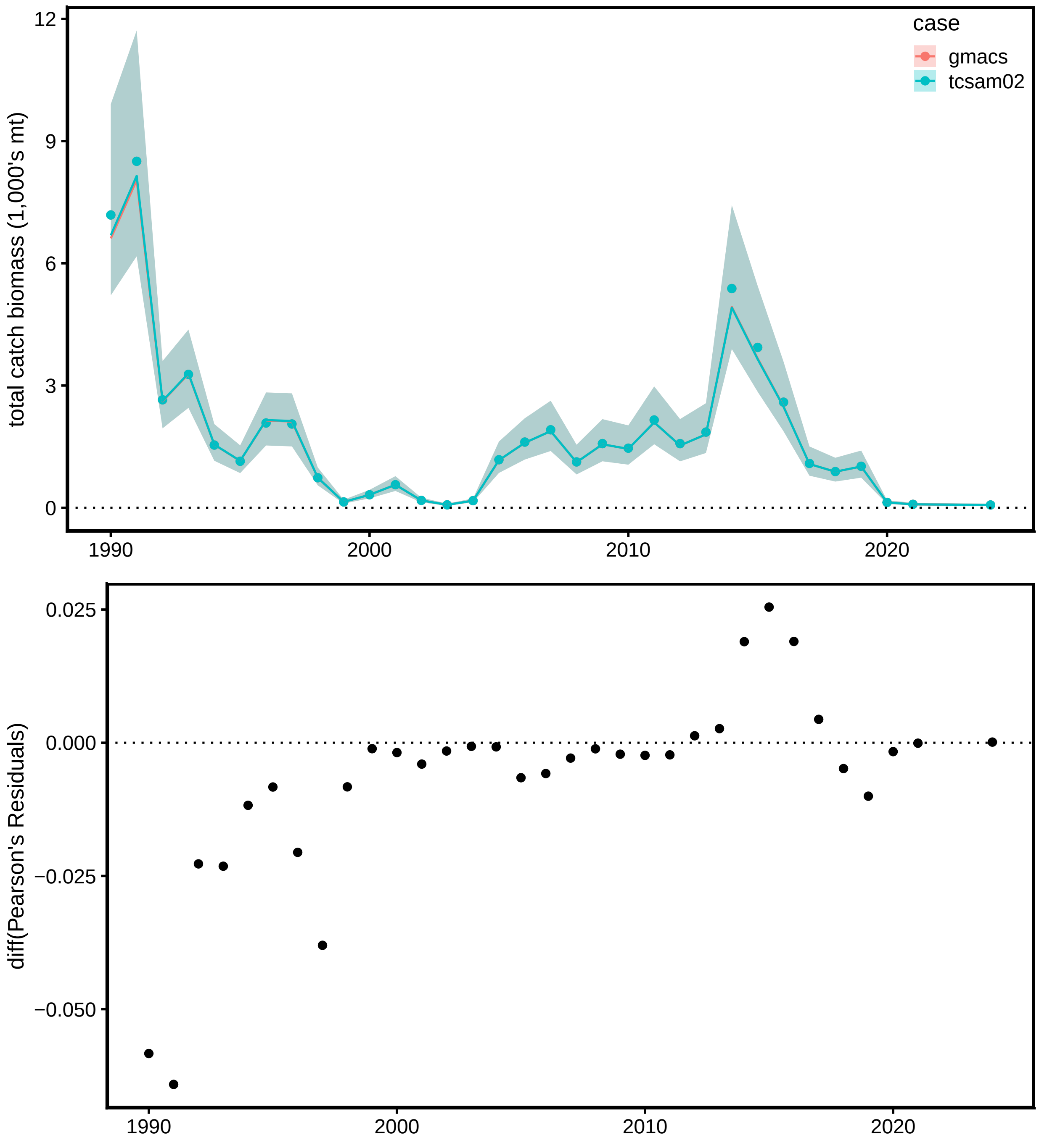


Figure 57. Comparison of fits to total catch biomass in the snow crab fishery. Upper: observed–points, dotted line, and shading (90% lognormal CIs), predicted–lines; Lower: difference in Pearson's residuals between models.

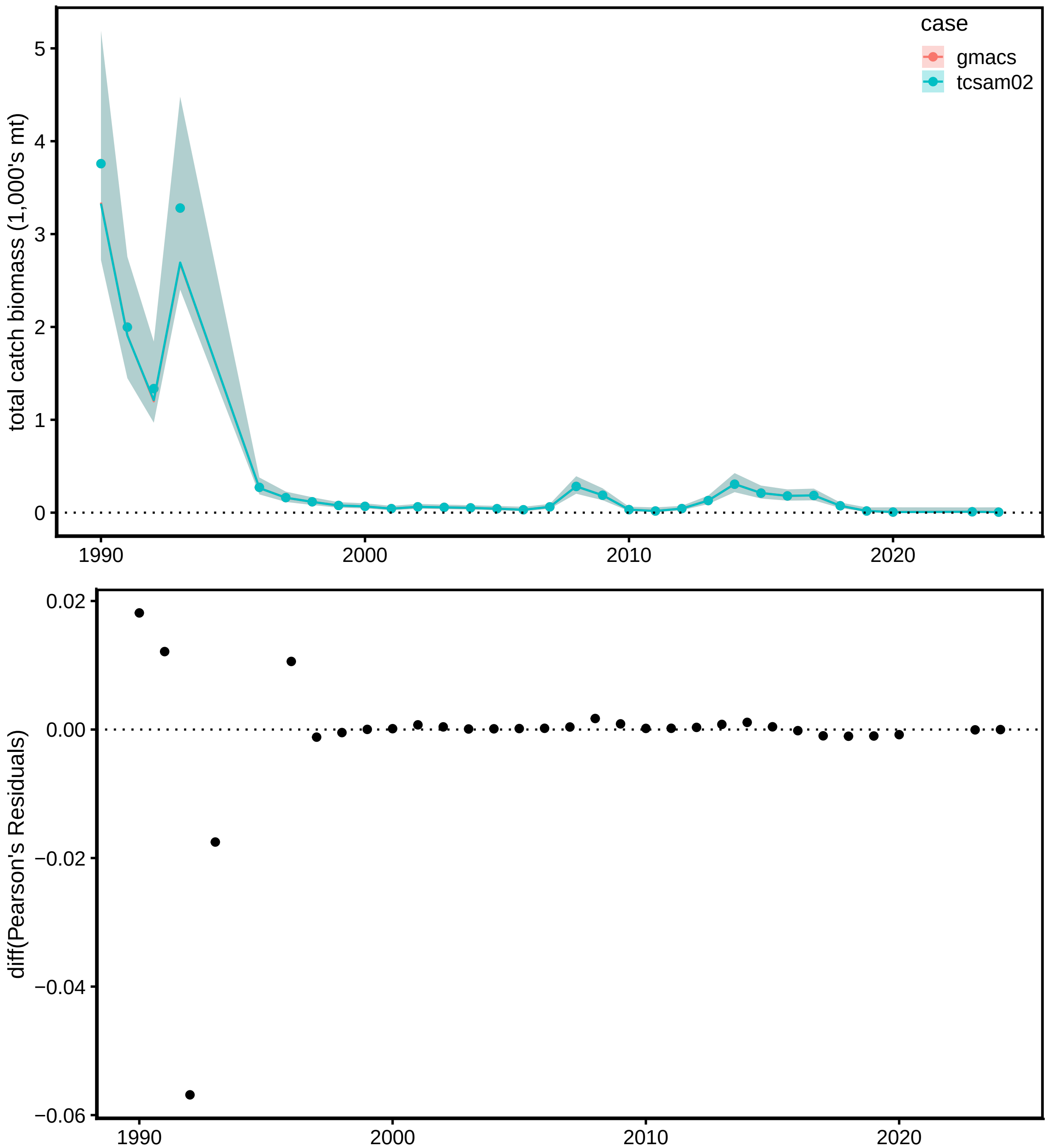


Figure 58. Comparison of fits to total catch biomass in the BBRKC fishery. Upper: observed–points, dotted line, and shading (90% lognormal CIs), predicted–lines; Lower: difference in Pearson's residuals between models.

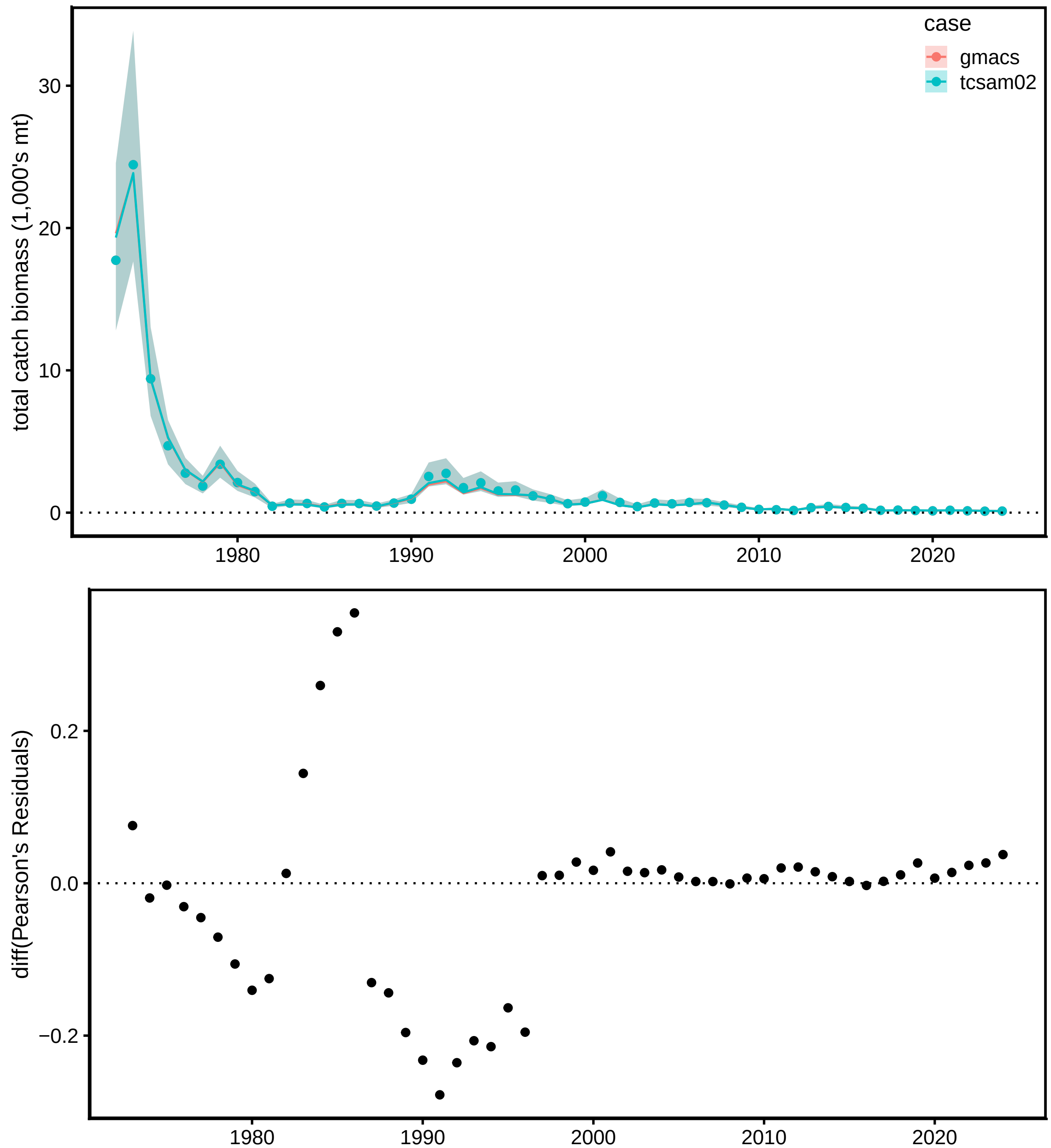


Figure 59. Comparison of fits to total catch biomass in the groundfish fisheries. Upper: observed–points, dotted line, and shading (90% lognormal CIs), predicted–lines; Lower: difference in Pearson's residuals between models.

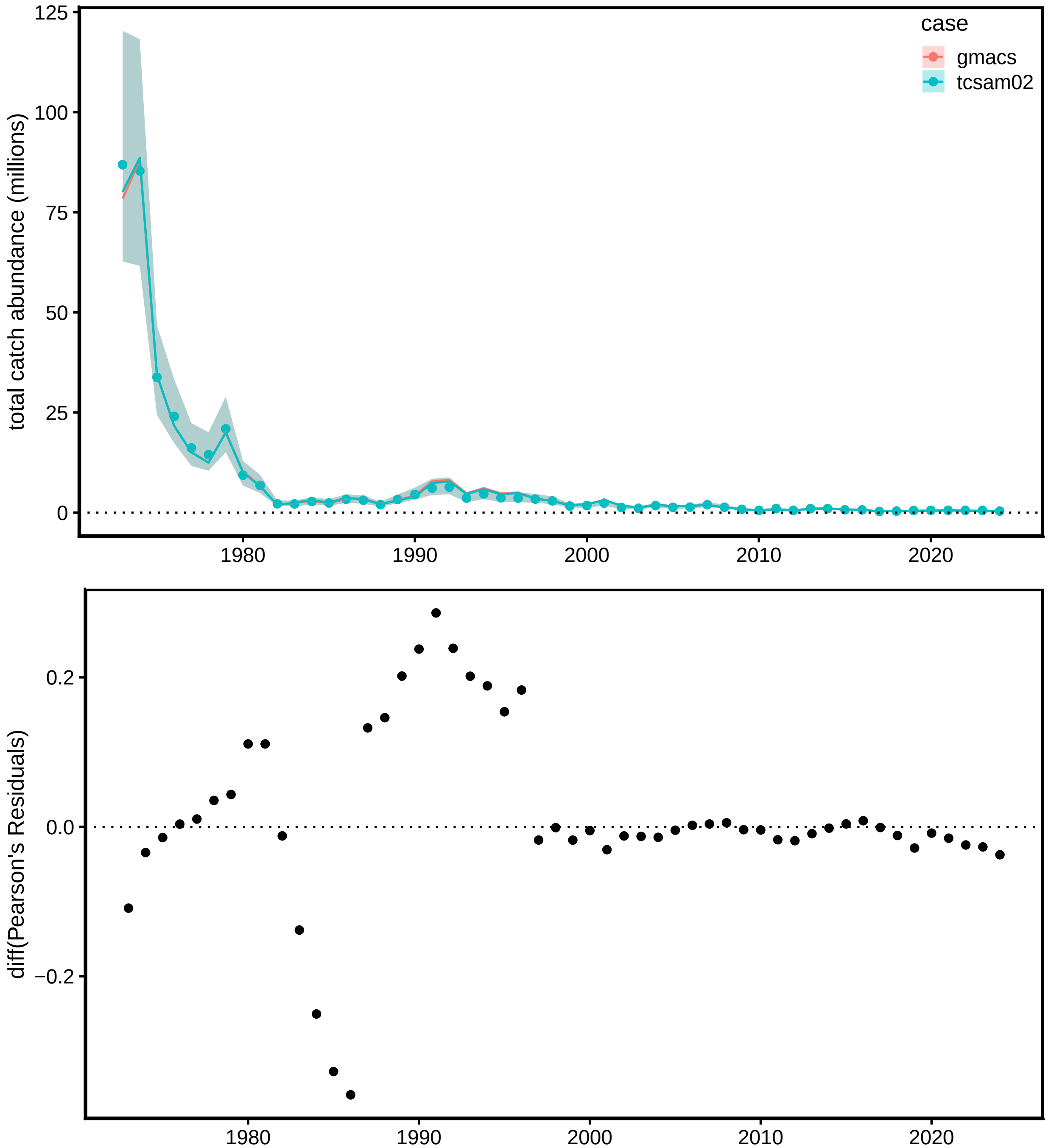


Figure 60. Comparison of fits to total catch abundance in the groundfish fisheries. Upper: observed–points, dotted line, and shading (90% lognormal CIs), predicted–lines; Lower: difference in Pearson's residuals between models.

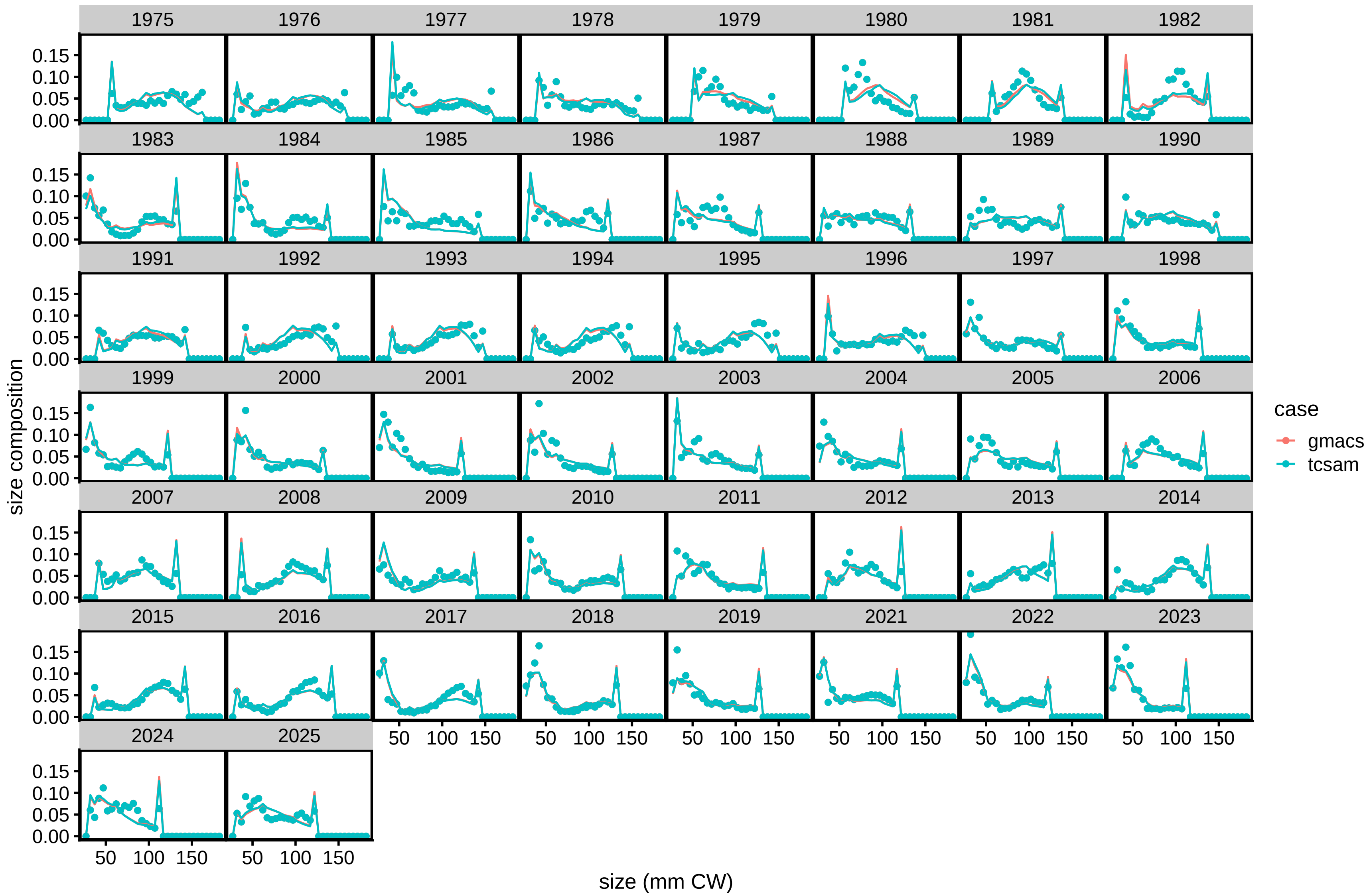


Figure 61. Fits to size composition data from the NMS surveys for males. Points: observed values; lines: predicted values.

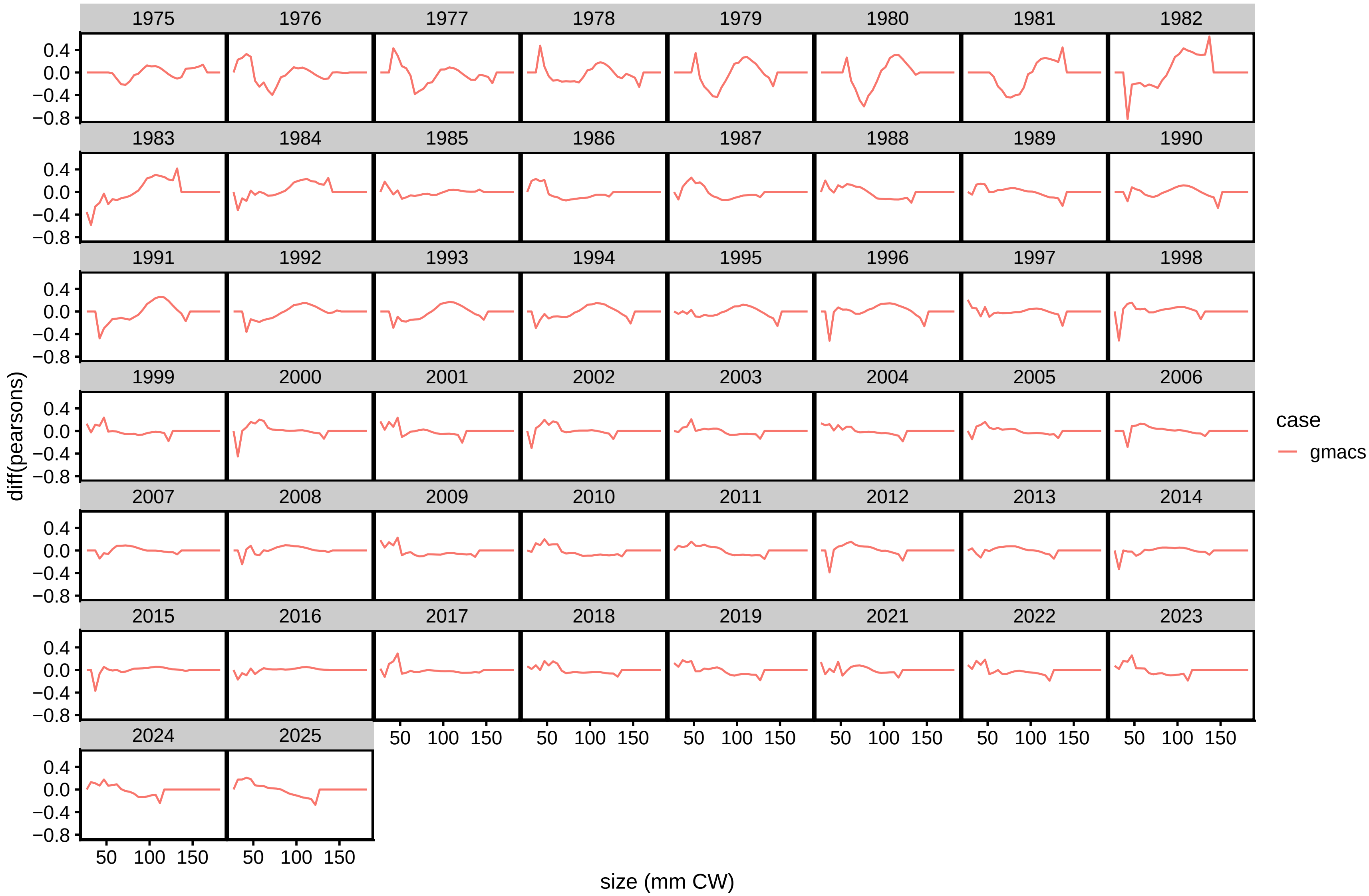


Figure 62. Differences from the TCSAM02 model in Pearson's residuals for fits to size composition data from the NMFS surveys for males.

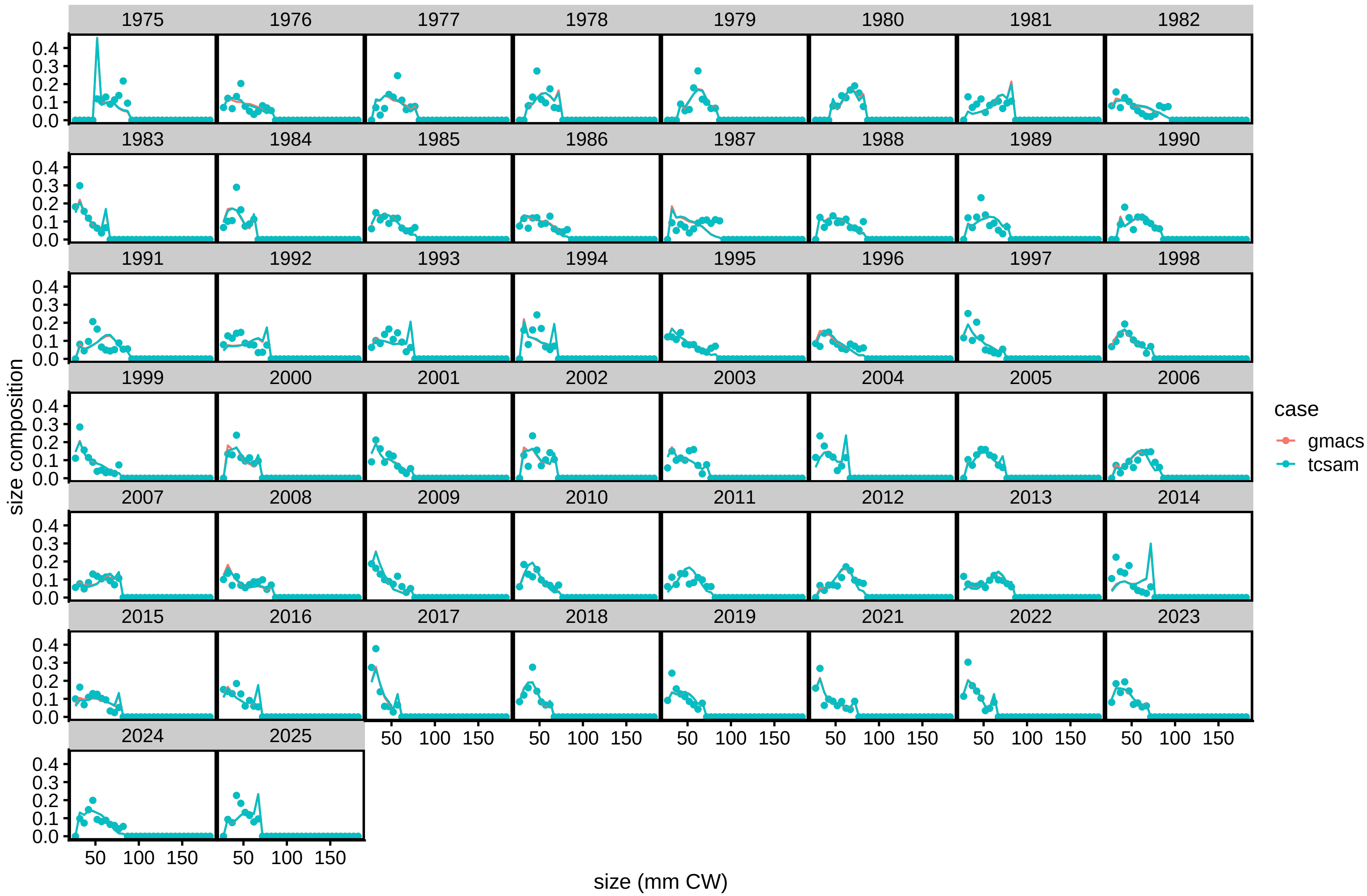


Figure 63. Fits to size composition data from the NMFS surveys for immature females. Points: observed values; lines: predicted values.

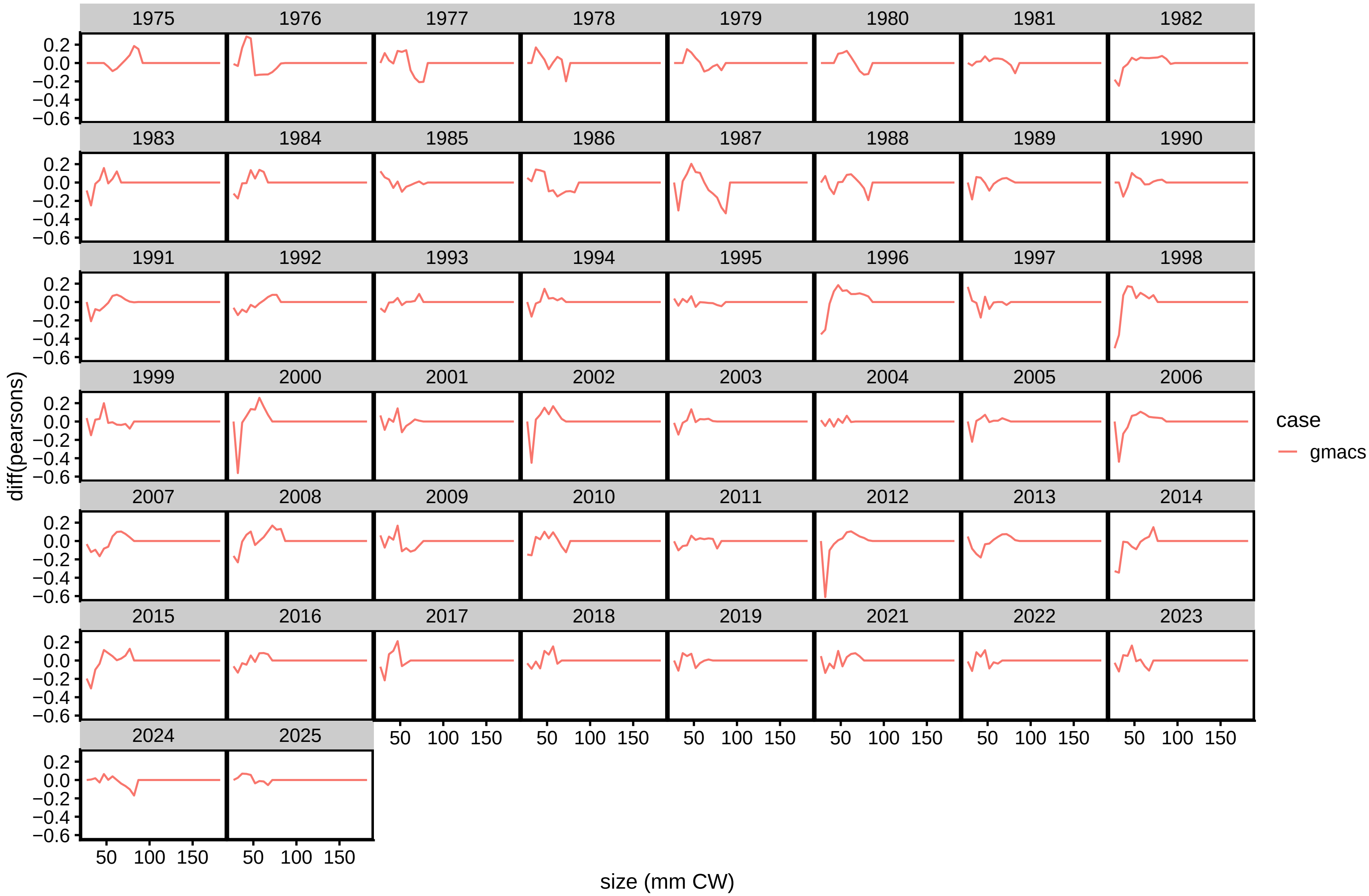


Figure 64. Differences from the TCSAM02 model in Pearson's residuals for fits to size composition data from the NMFS surveys for immature females.

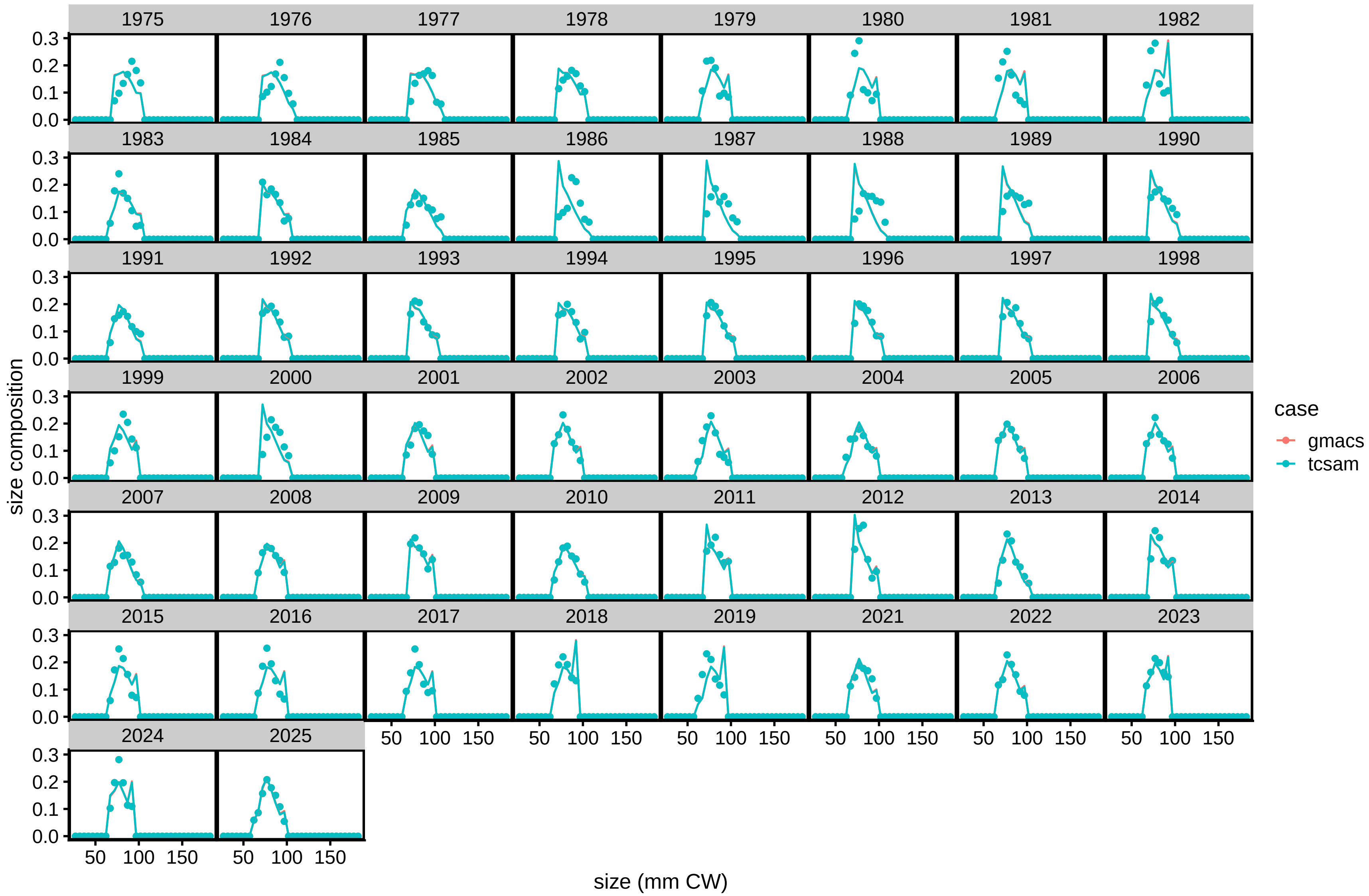


Figure 65. Fits to total catch size composition data from the NMFS surveys for mature females. Points: observed values; lines: predicted values.

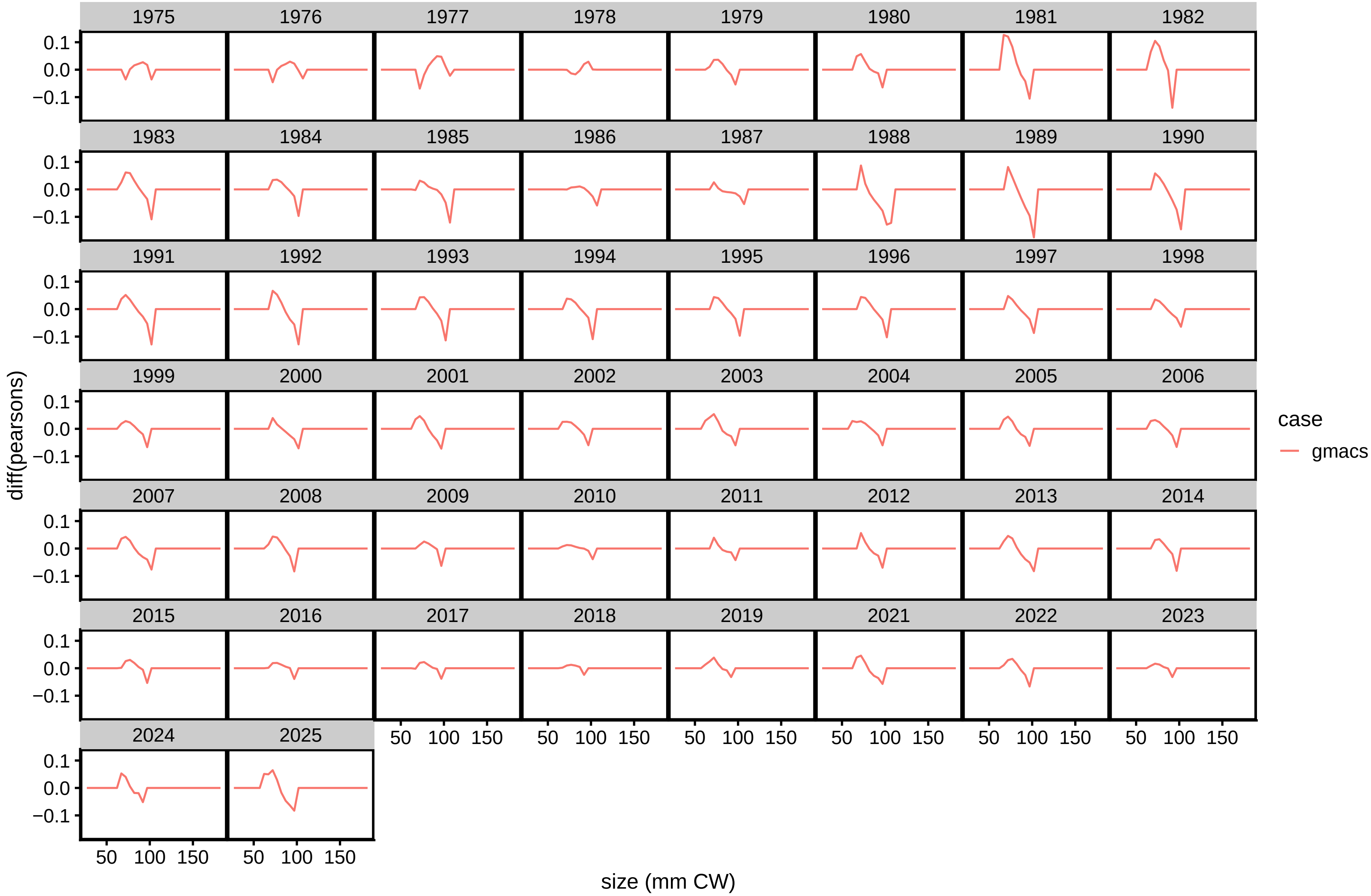


Figure 66. Differences from the TCSAM02 model in Pearson's residuals for fits to size composition data from the NMFS surveys for mature females.

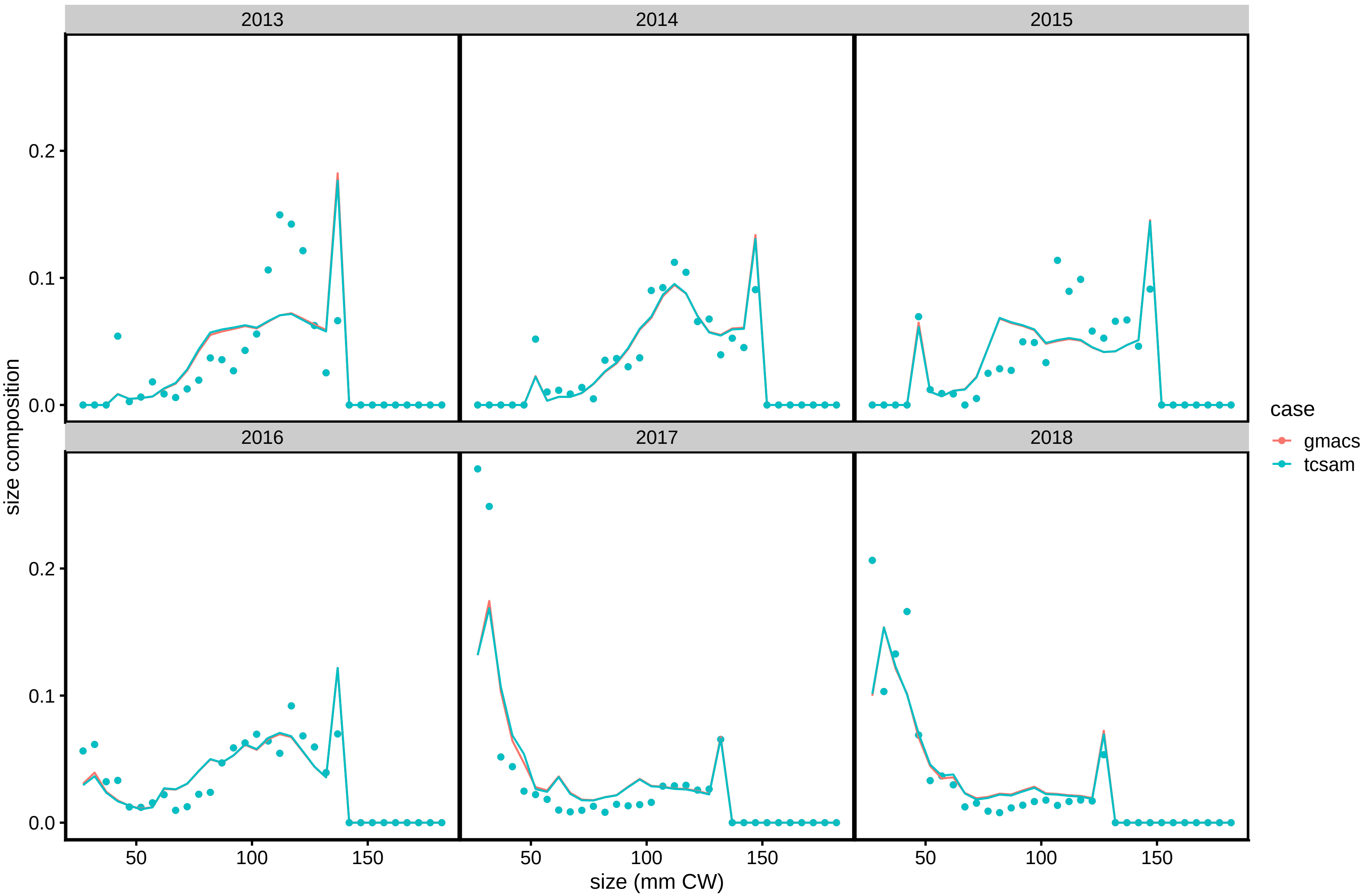


Figure 67. Fits to size composition data from the BSFRF surveys for males. Points: observed values; lines: predicted values.

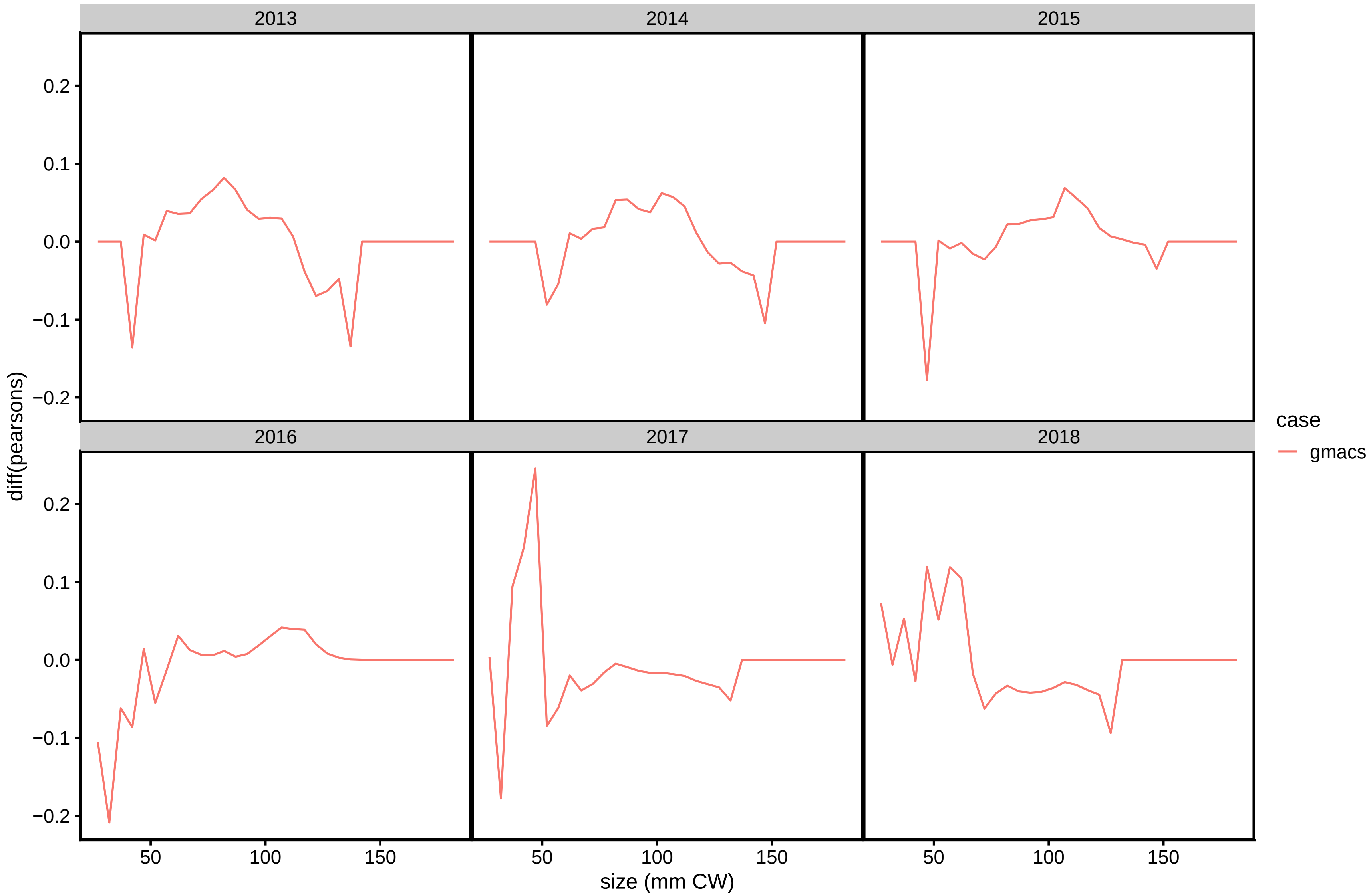


Figure 68. Differences from the TCSAM02 model in Pearson's residuals for fits to size composition data from the BSFRF survey for males.

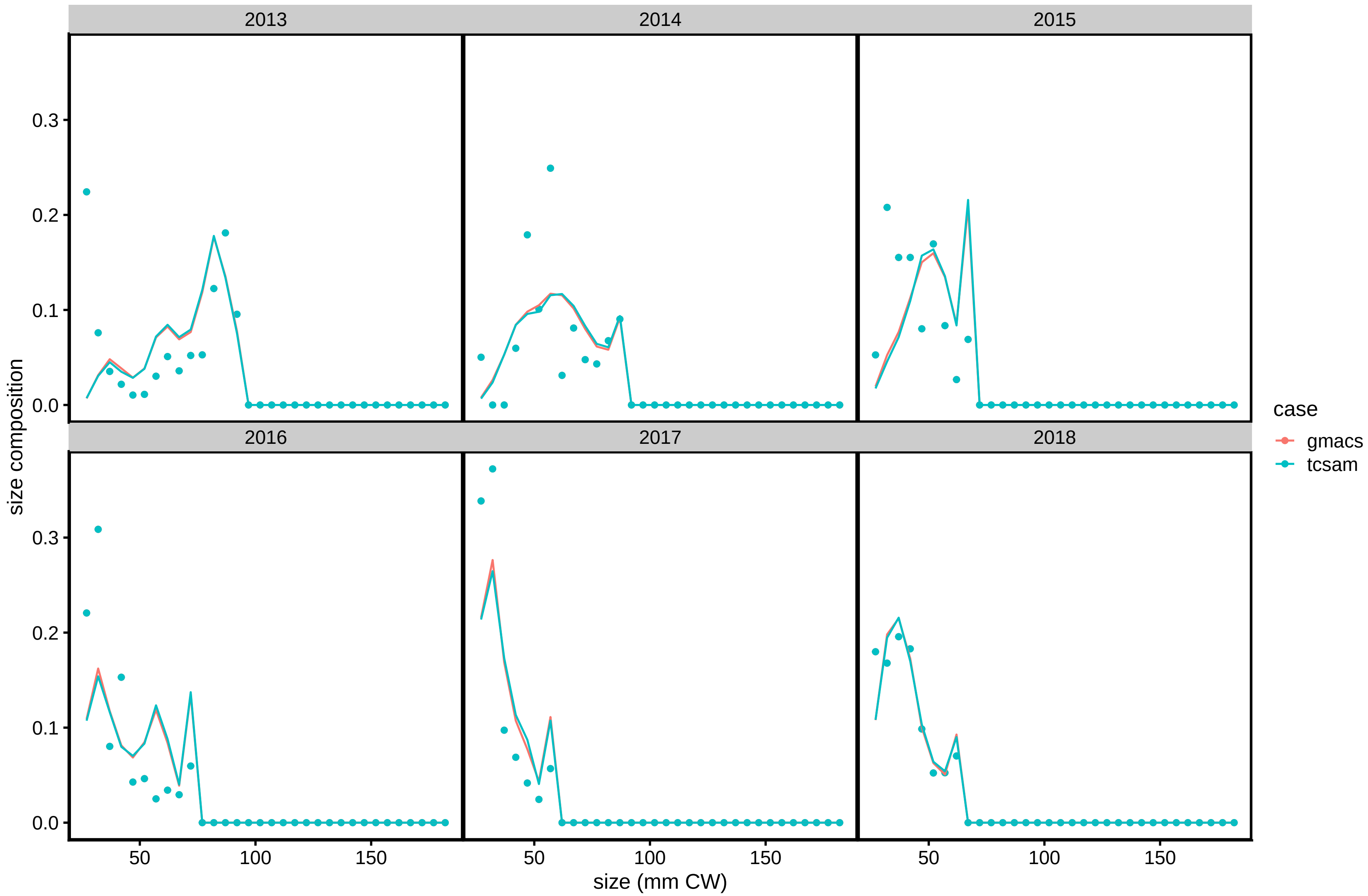


Figure 69. Fits to size composition data from the BSFRF survey for immature females. Points: observed values; lines: predicted values.

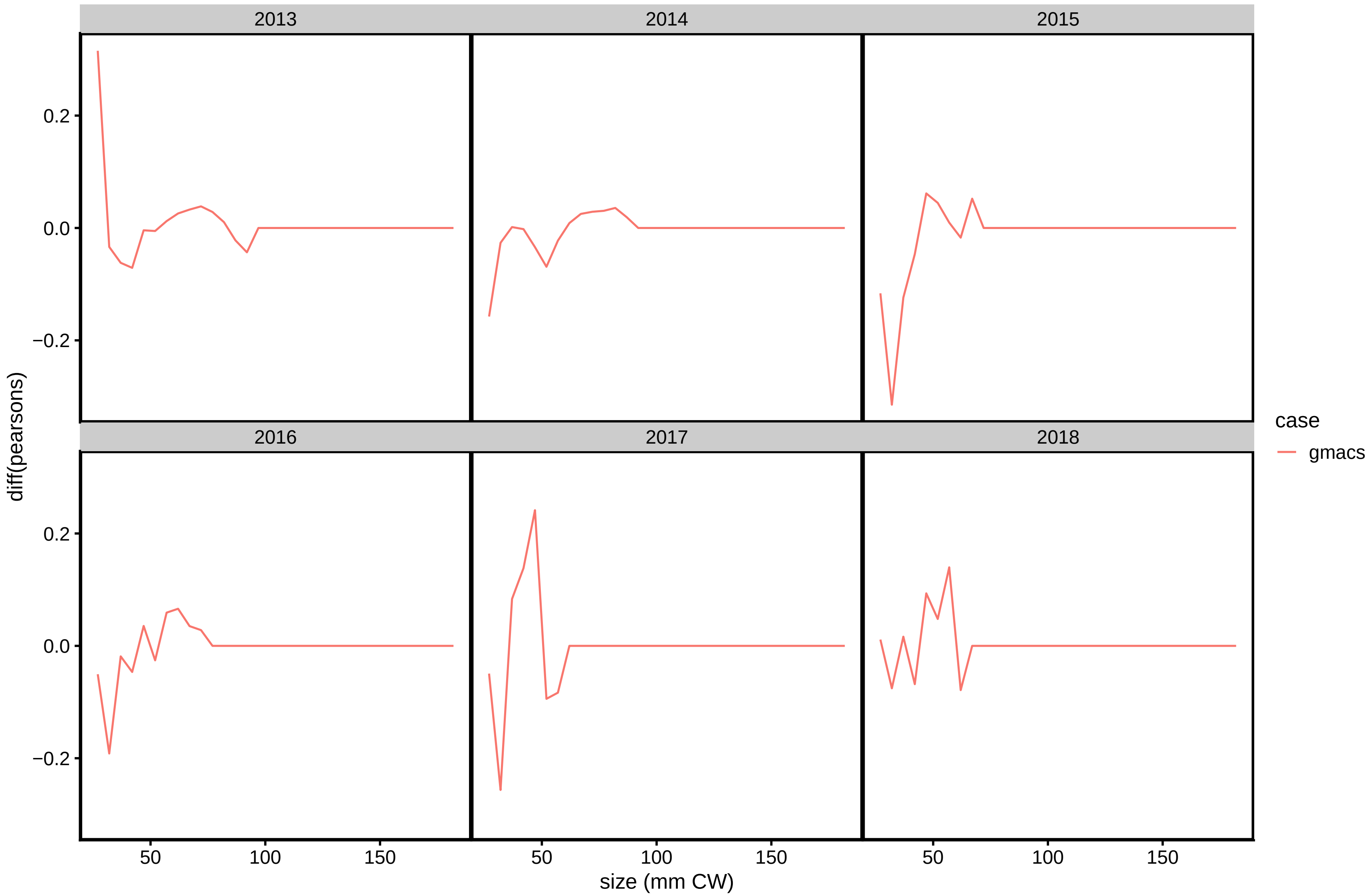


Figure 70. Differences from the TCSAM02 model in Pearson's residuals for fits to size composition data from the BSFRF surveys for immature females.

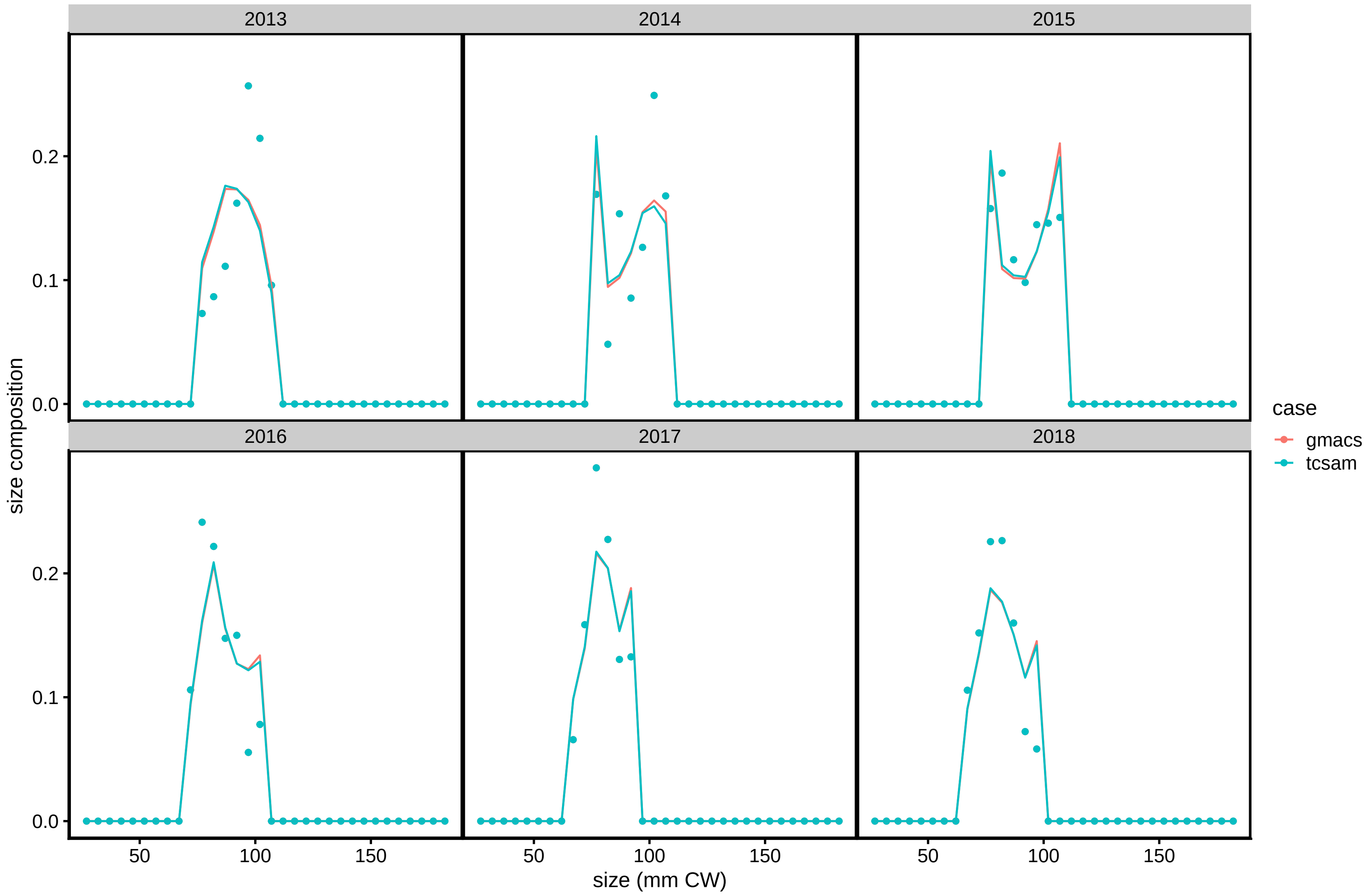


Figure 71. Fits to total catch size composition data from the BSFRF surveys for mature females. Points: observed values; lines: predicted values.

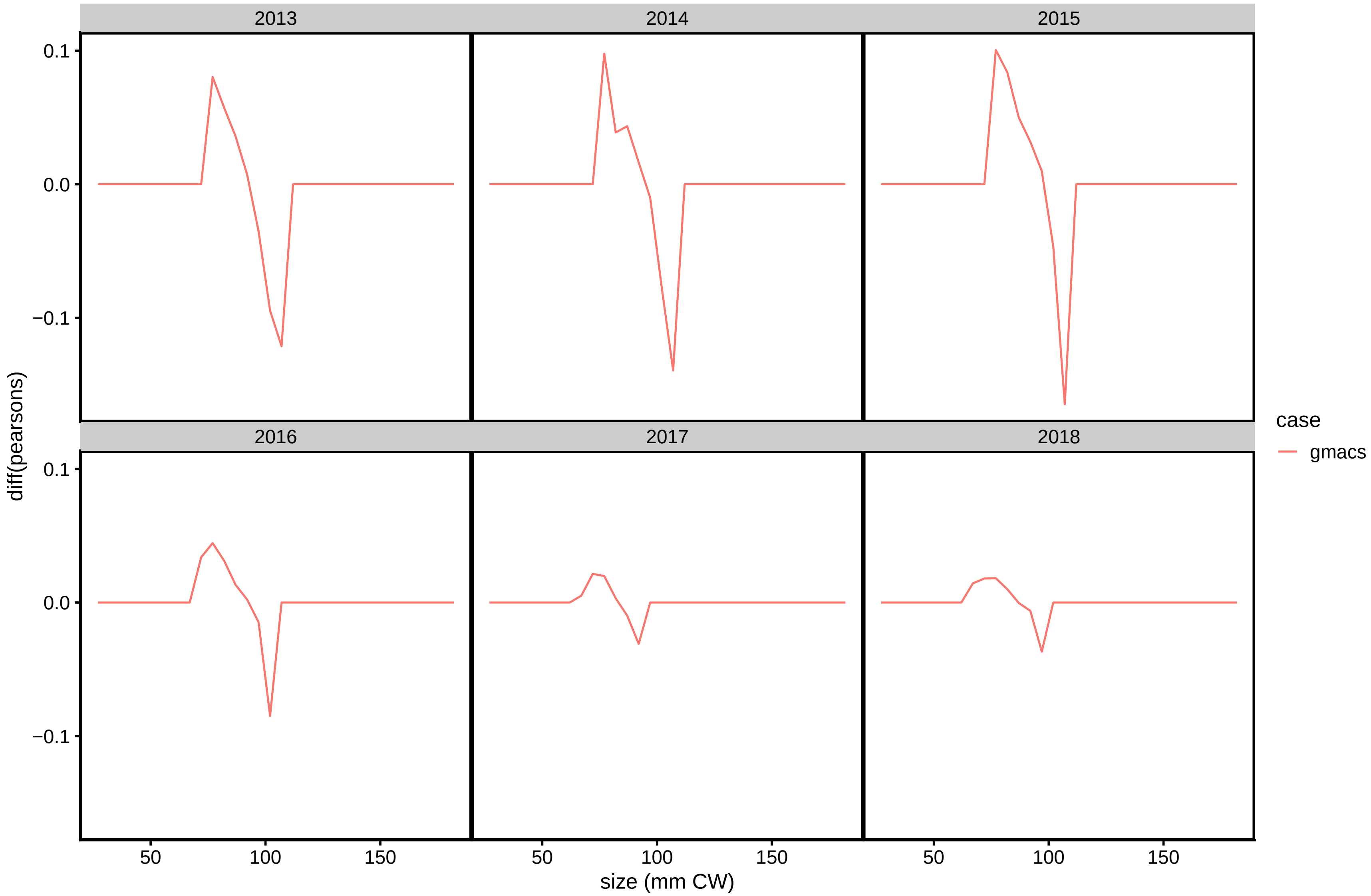


Figure 72. Differences from the TCSAM02 model in Pearson's residuals for fits to size composition data from the BSFRF surveys for mature females.

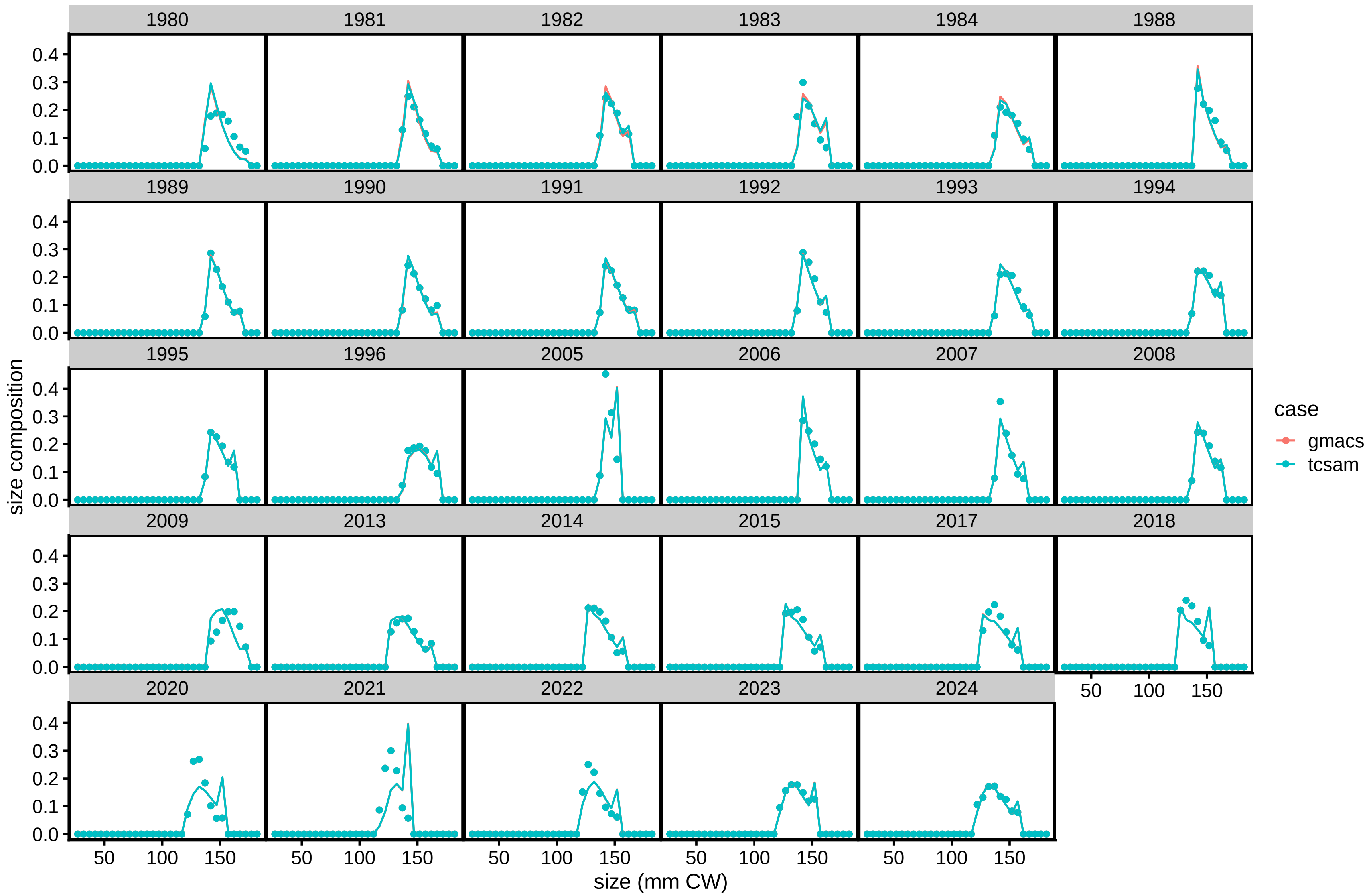


Figure 73. Fits to retained catch size composition data from the directed fishery. Points: observed values; lines: predicted values.

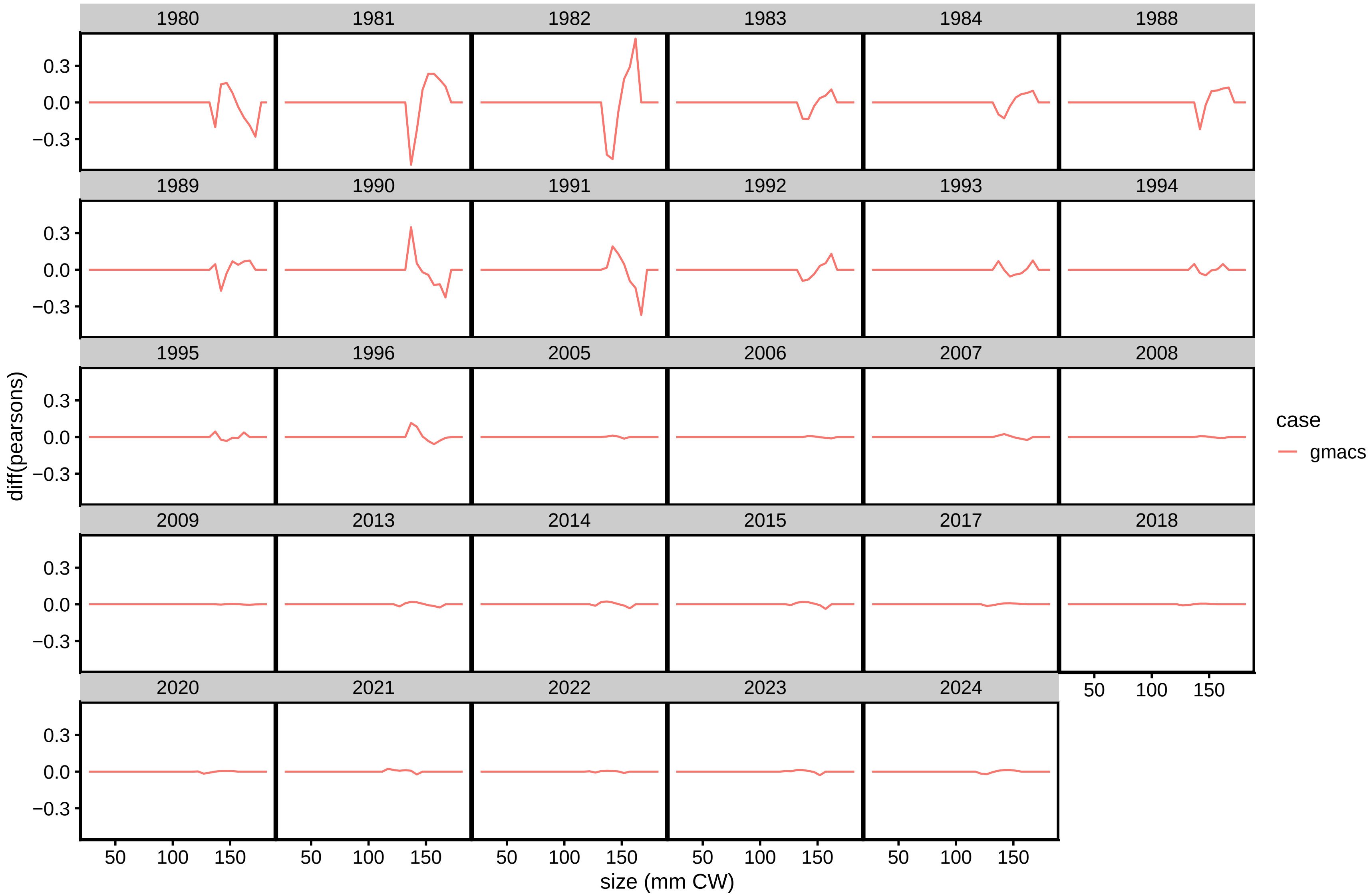


Figure 74. Differences from the TCSAM02 model in Pearson's residuals for fits to retained catch size composition data from the directed fishery.

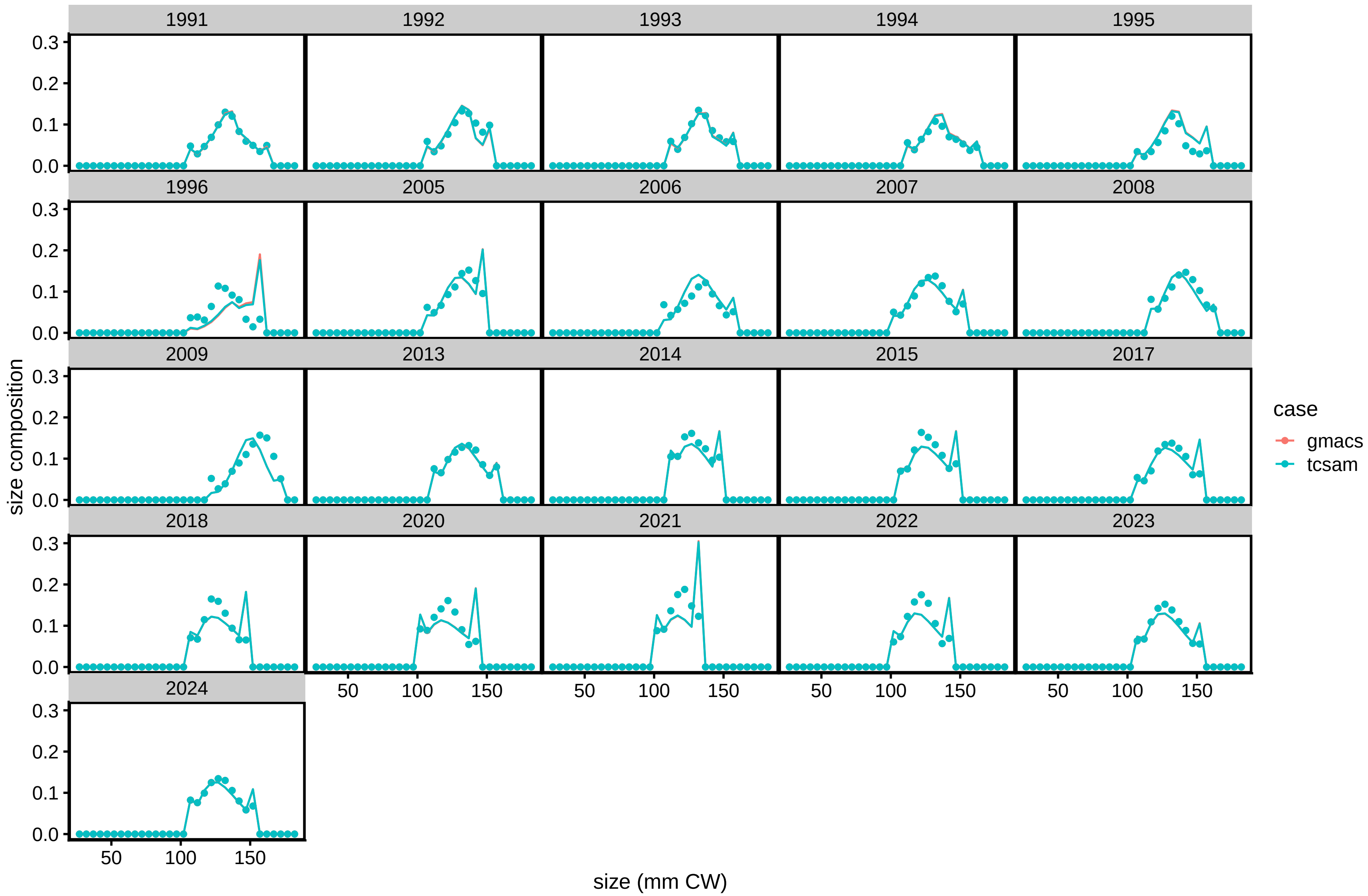


Figure 75. Fits to total catch size composition data from the directed fishery for males. Points: observed values; lines: predicted values.

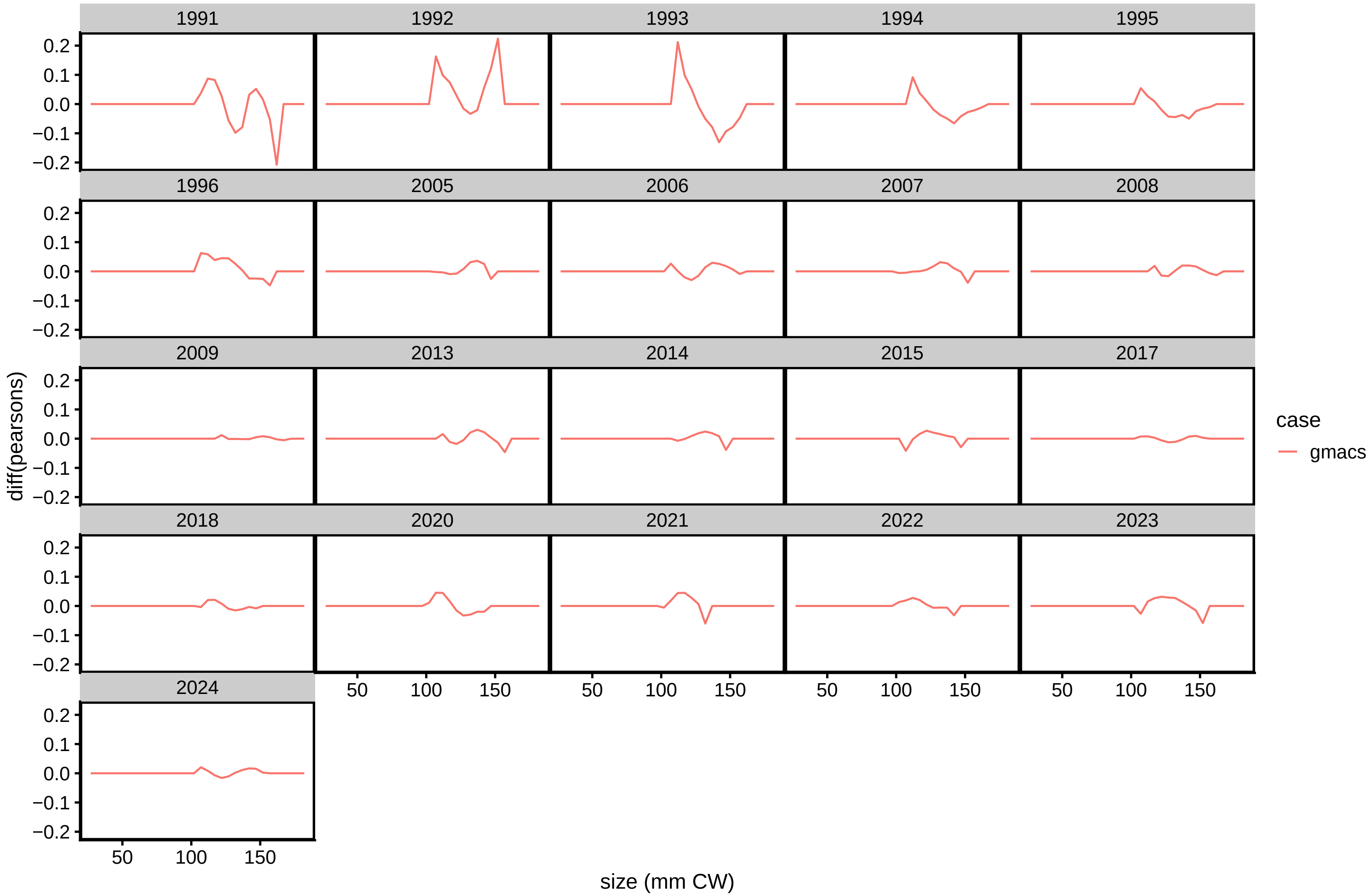


Figure 76. Differences from the TCSAM02 model in Pearson's residuals for fits to total catch size composition data from the directed fishery for males.

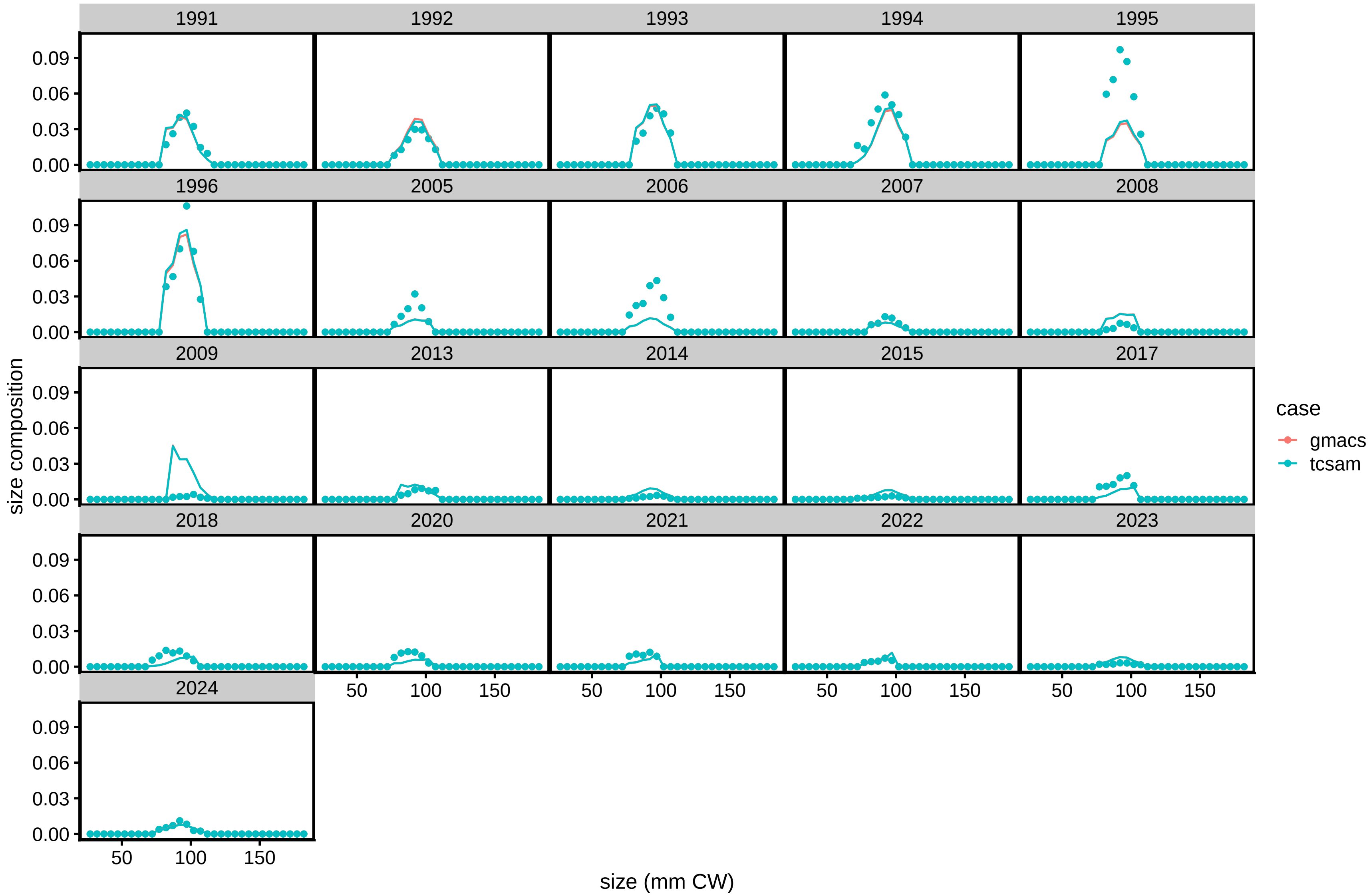


Figure 77. Fits to total catch size composition data from the directed fishery for females. Points: observed values; lines: predicted values.

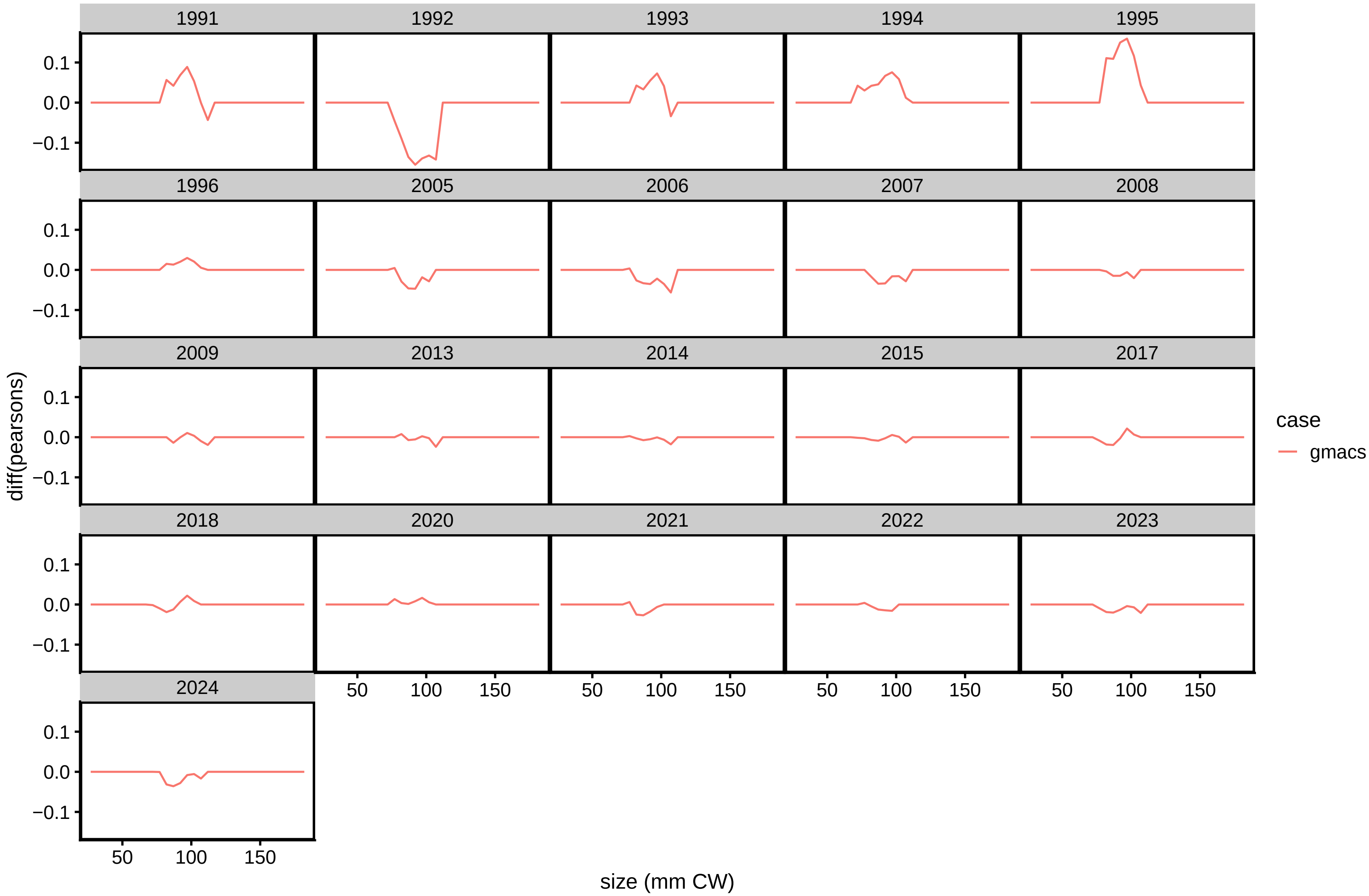


Figure 78. Differences from the TCSAM02 model in Pearson's residuals for fits to total catch size composition data from the directed fishery for females.

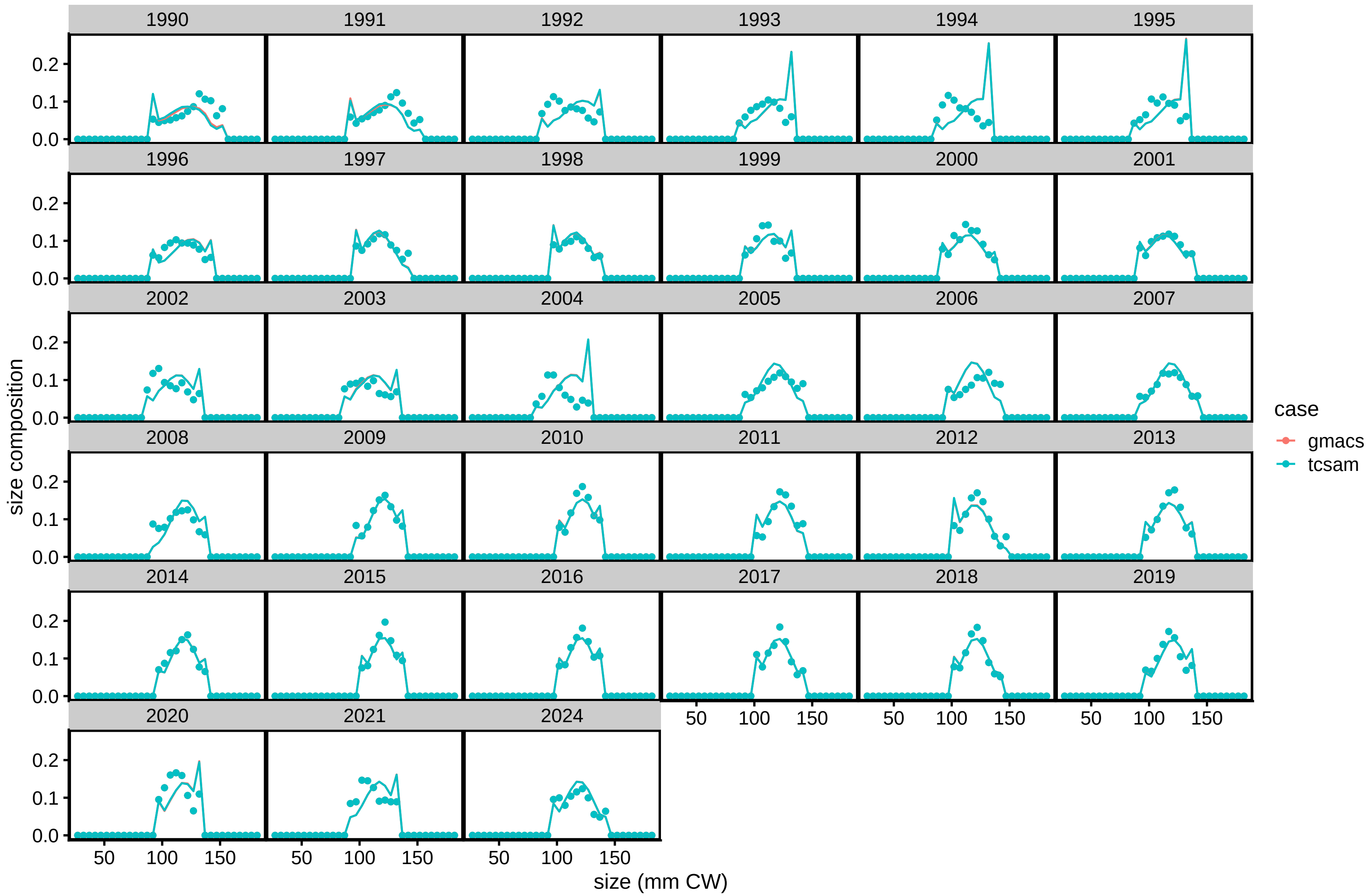


Figure 79. Fits to total catch size composition data from the snow crab fishery for males. Points: observed values; lines: predicted values.

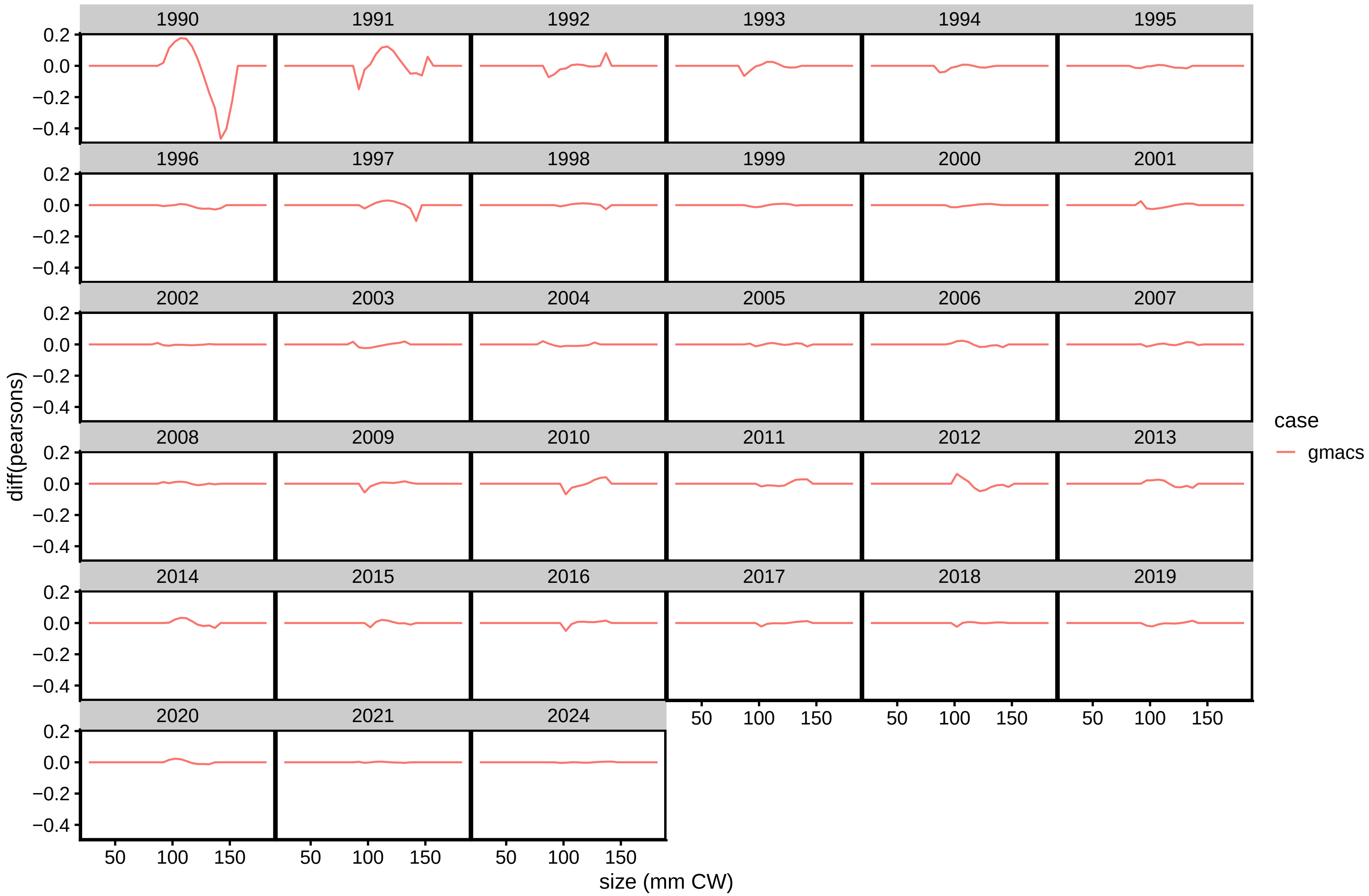


Figure 80. Differences from the TCSAM02 model in Pearson's residuals for fits to total catch size composition data from the snow crab fishery for males.

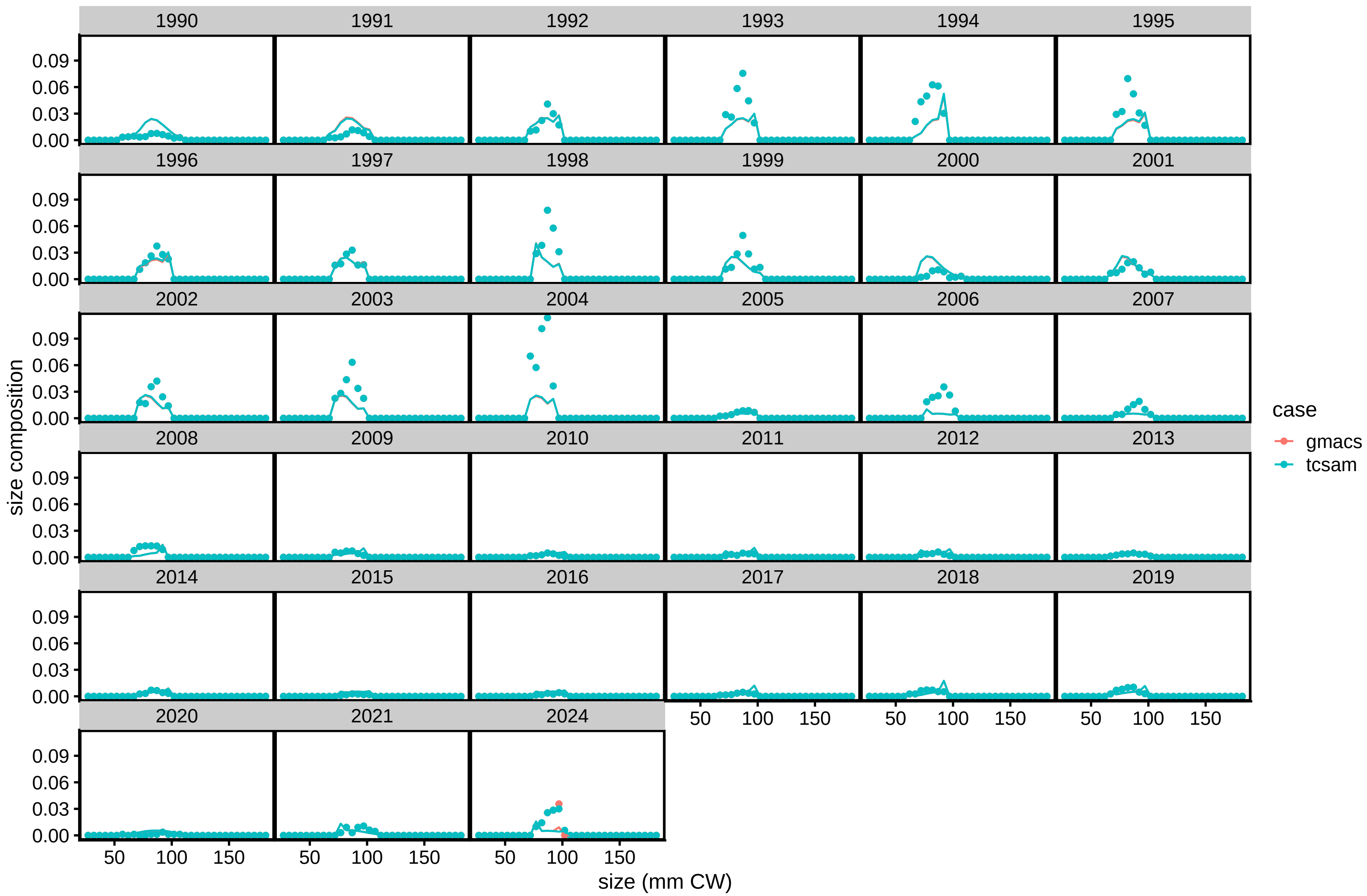


Figure 81. Fits to total catch size composition data from the snow crab fishery for females. Points: observed values; lines: predicted values.

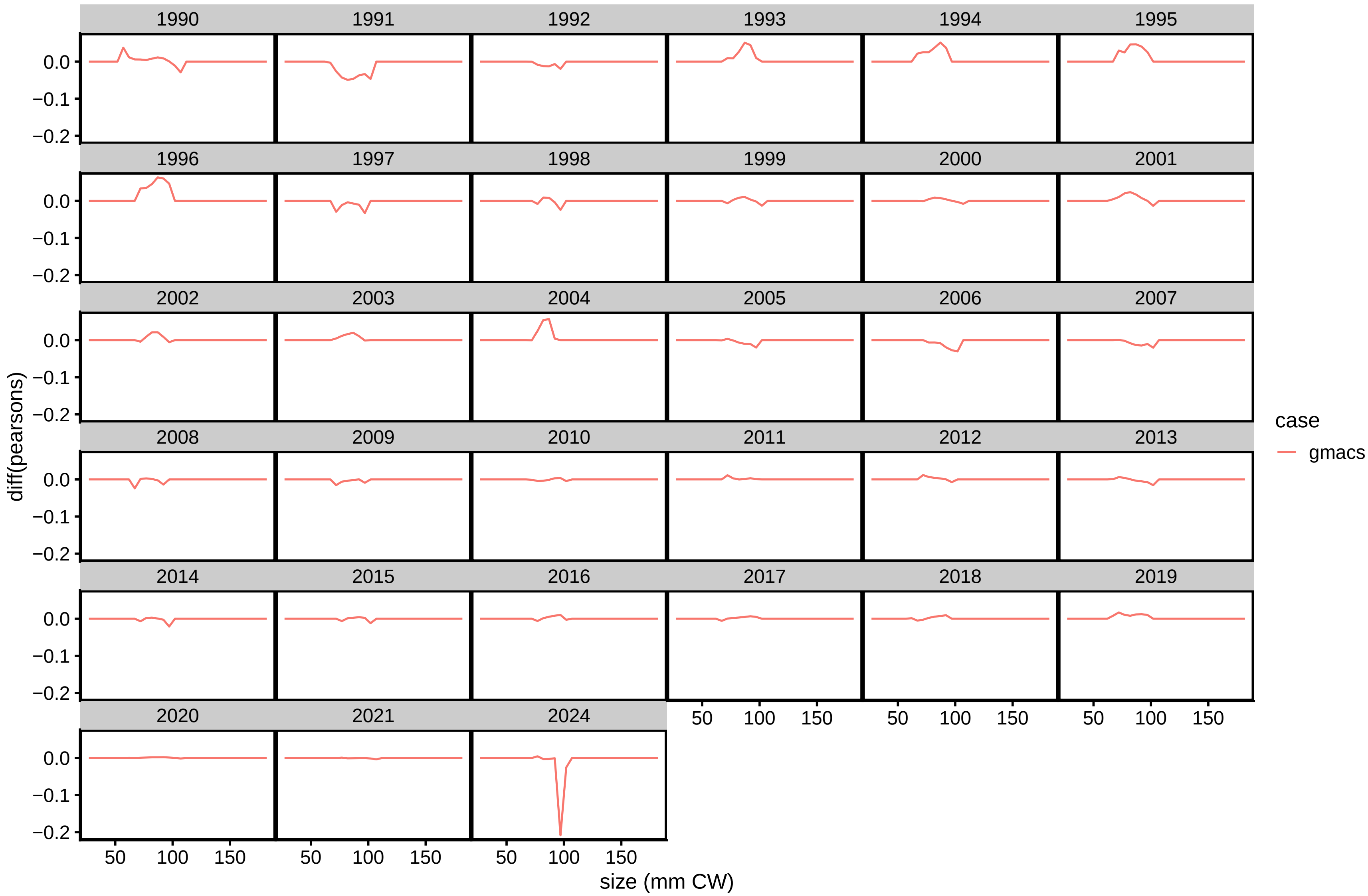


Figure 82. Differences from the TCSAM02 model in Pearson's residuals for fits to total catch size composition data from the snow crab fishery for females.

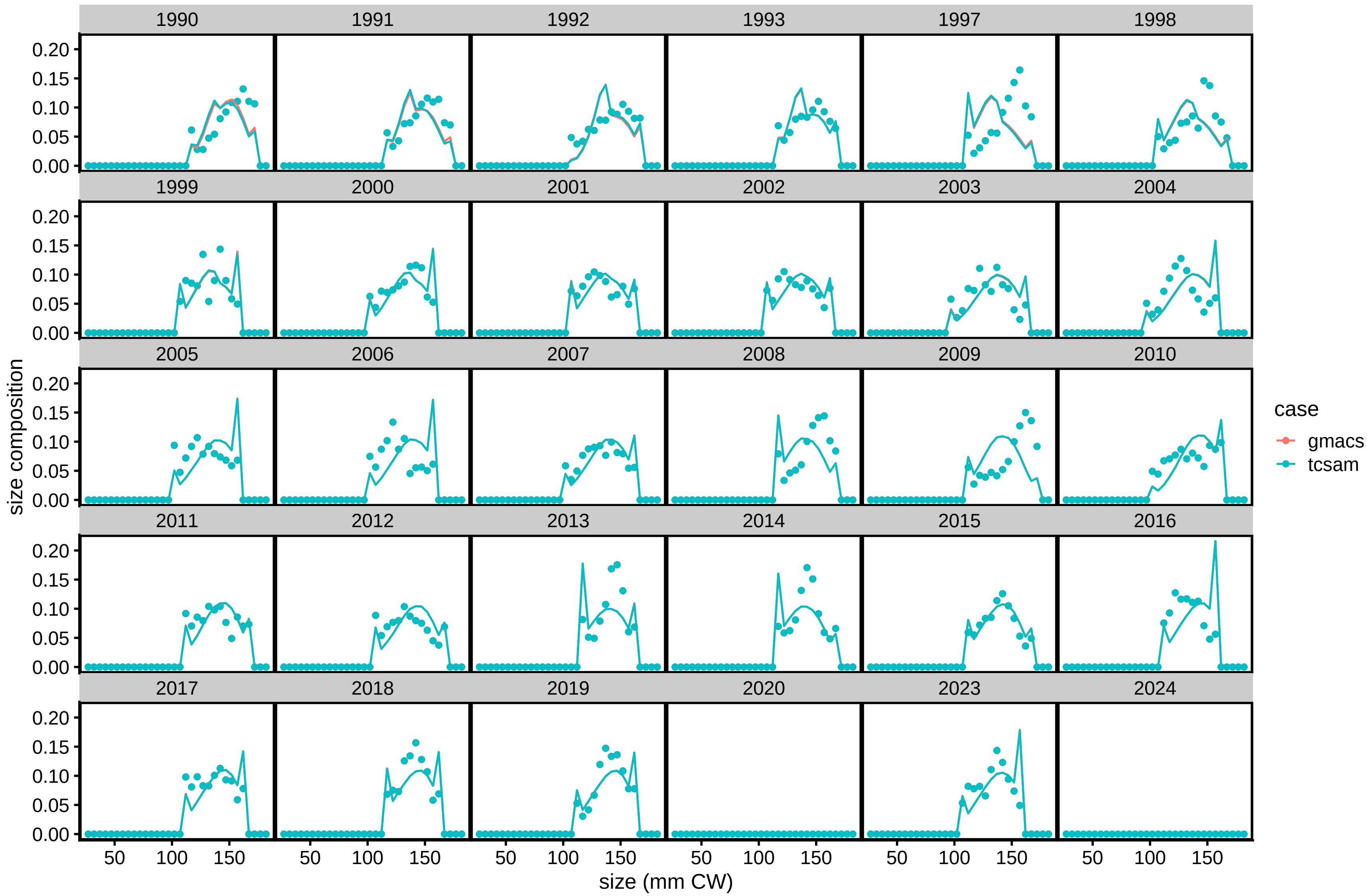


Figure 83. Fits to total catch size composition data from the BBRKC fishery for males. Points: observed values; lines: predicted values.

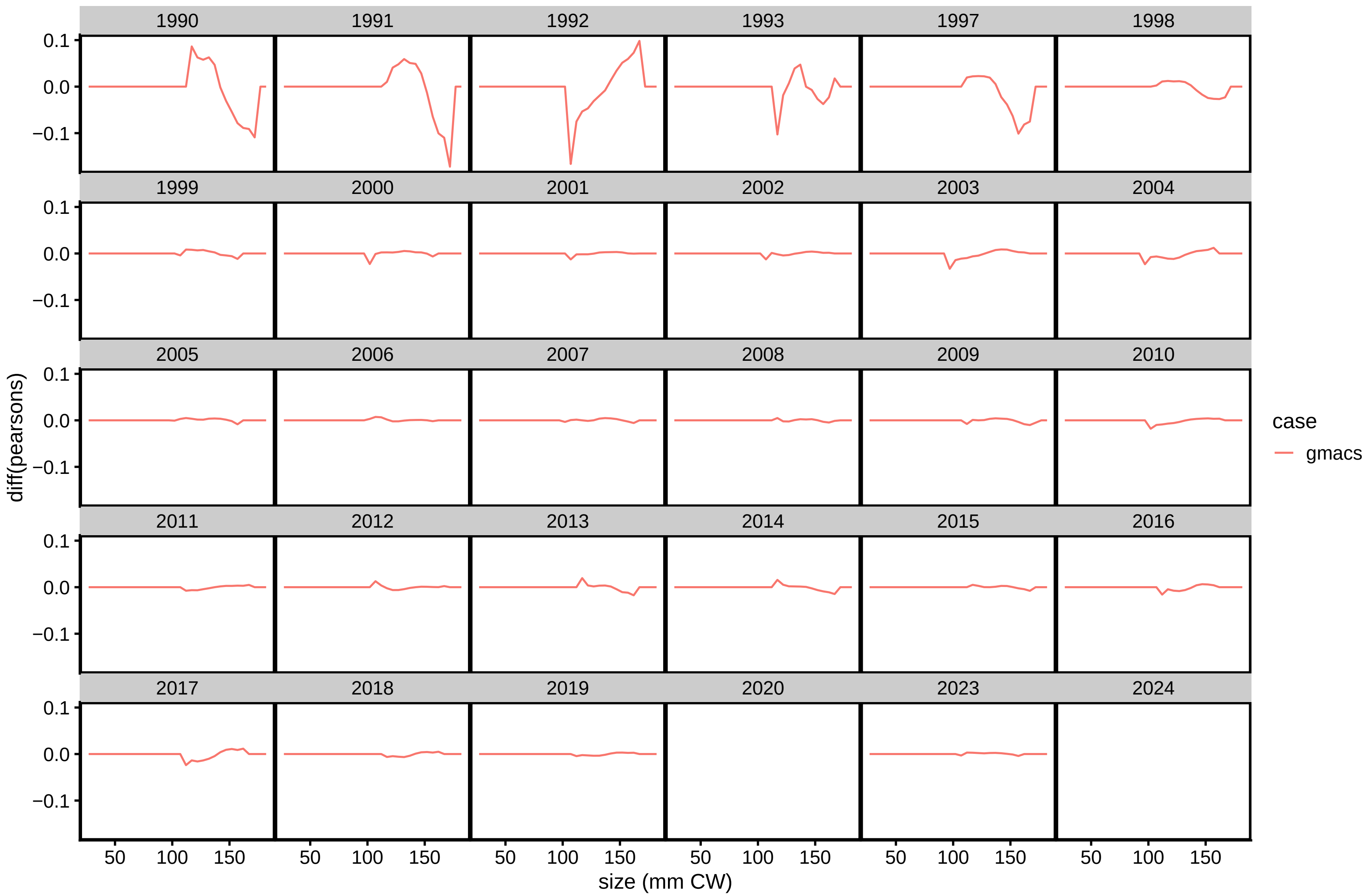


Figure 84. Differences from the TCSAM02 model in Pearson's residuals for fits to total catch size composition data from the BBRKC fishery for males.

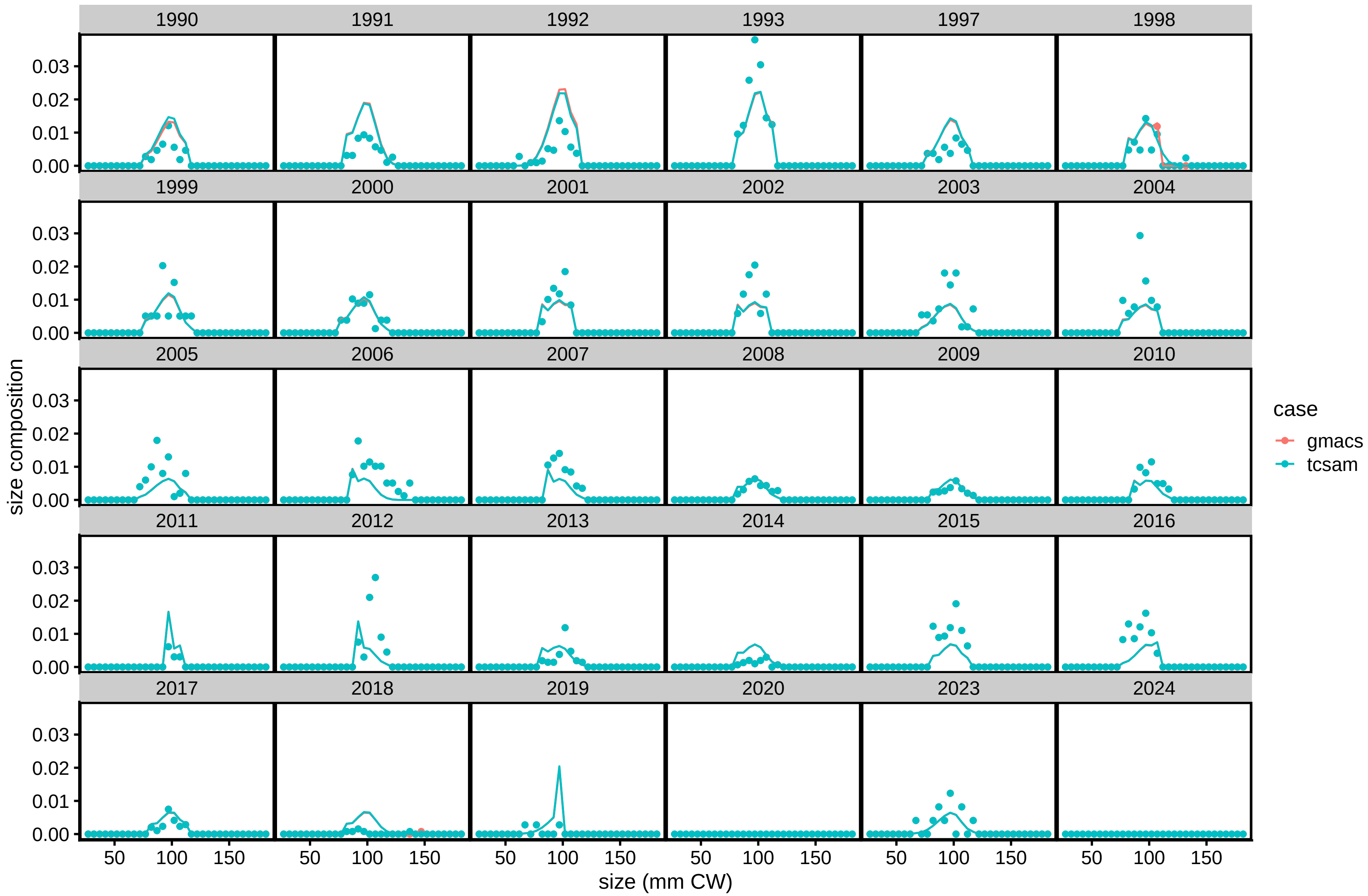


Figure 85. Fits to total catch size composition data from the BBRKC fishery for females. Points: observed values; lines: predicted values.

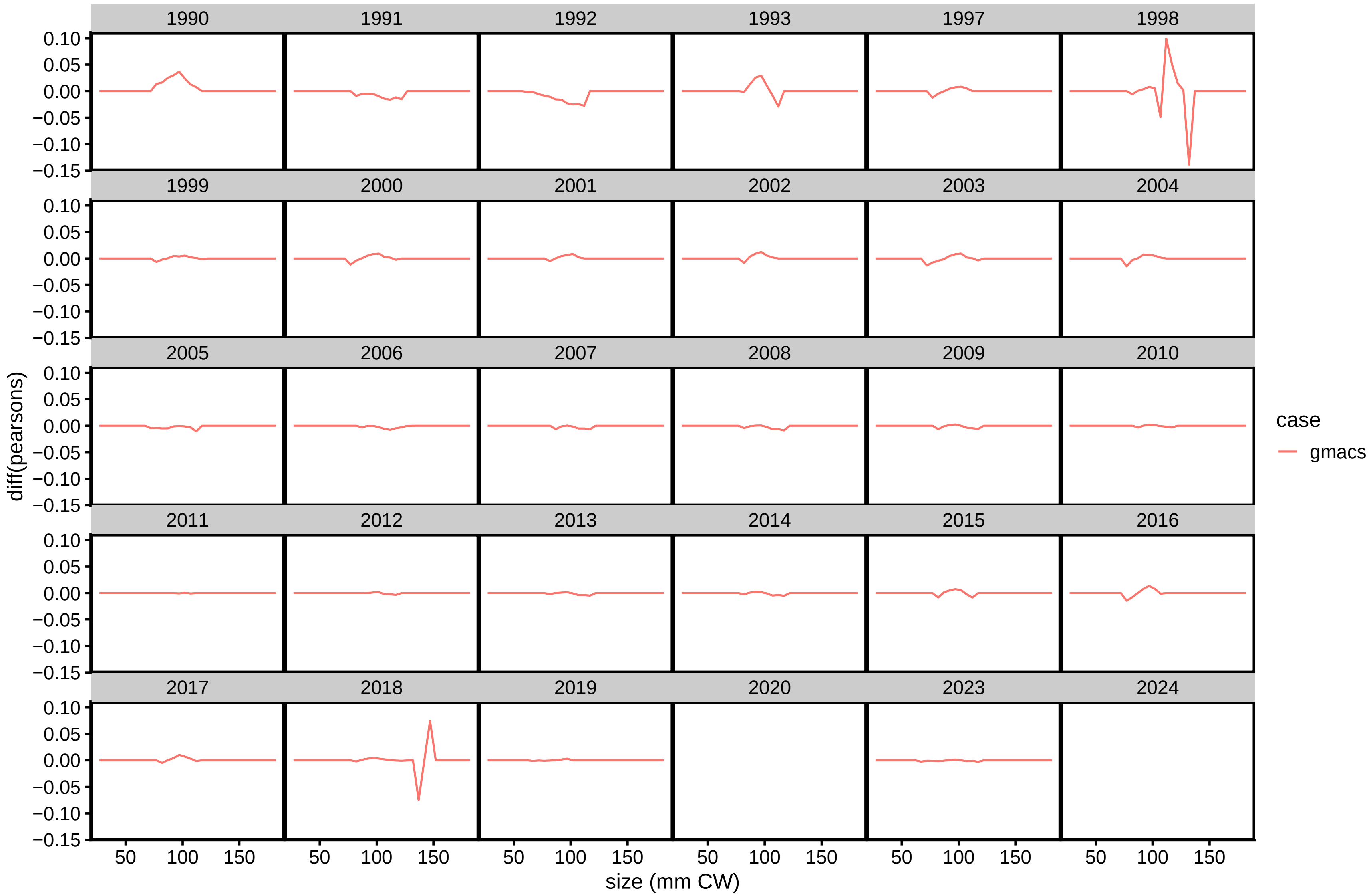


Figure 86. Differences from the TCSAM02 model in Pearson's residuals for fits to total catch size composition data from the BBRKC fishery for females.

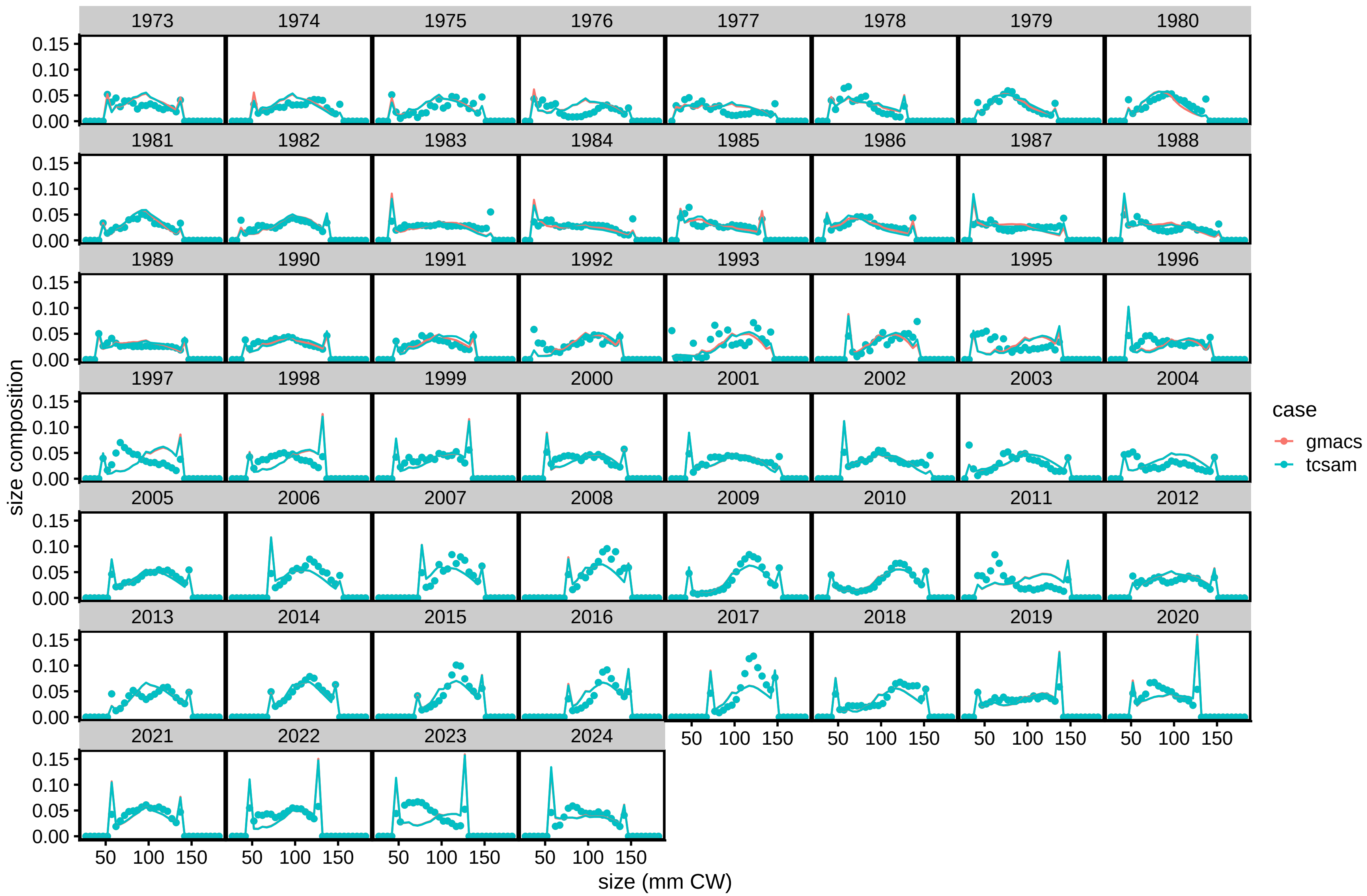


Figure 87. Fits to total catch size composition data from the groundfish fisheries for males. Points: observed values; lines: predicted values.

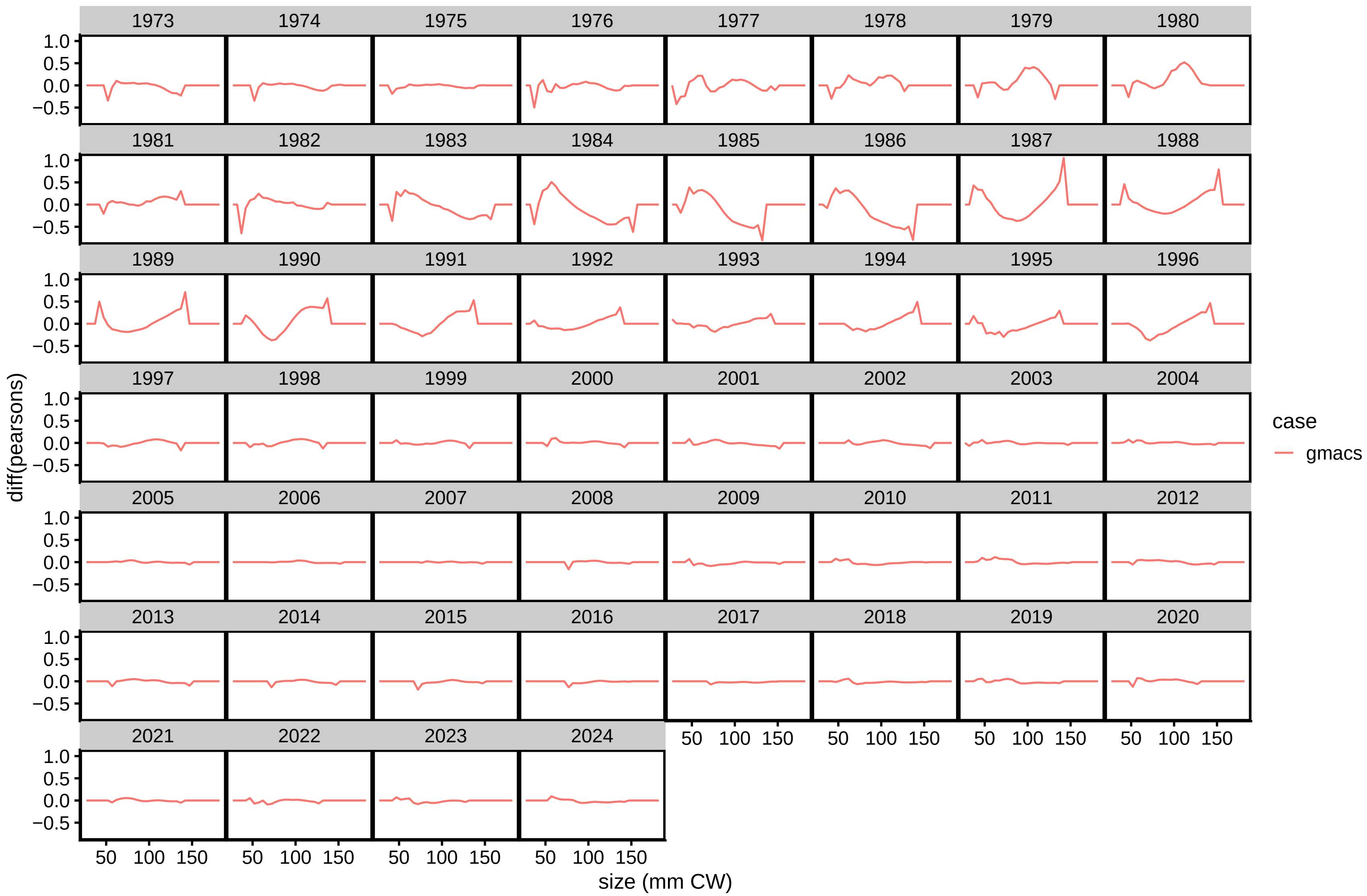


Figure 88. Differences from the TCSAM02 model in Pearson's residuals for fits to total catch size composition data from the groundfish fisheries for males.

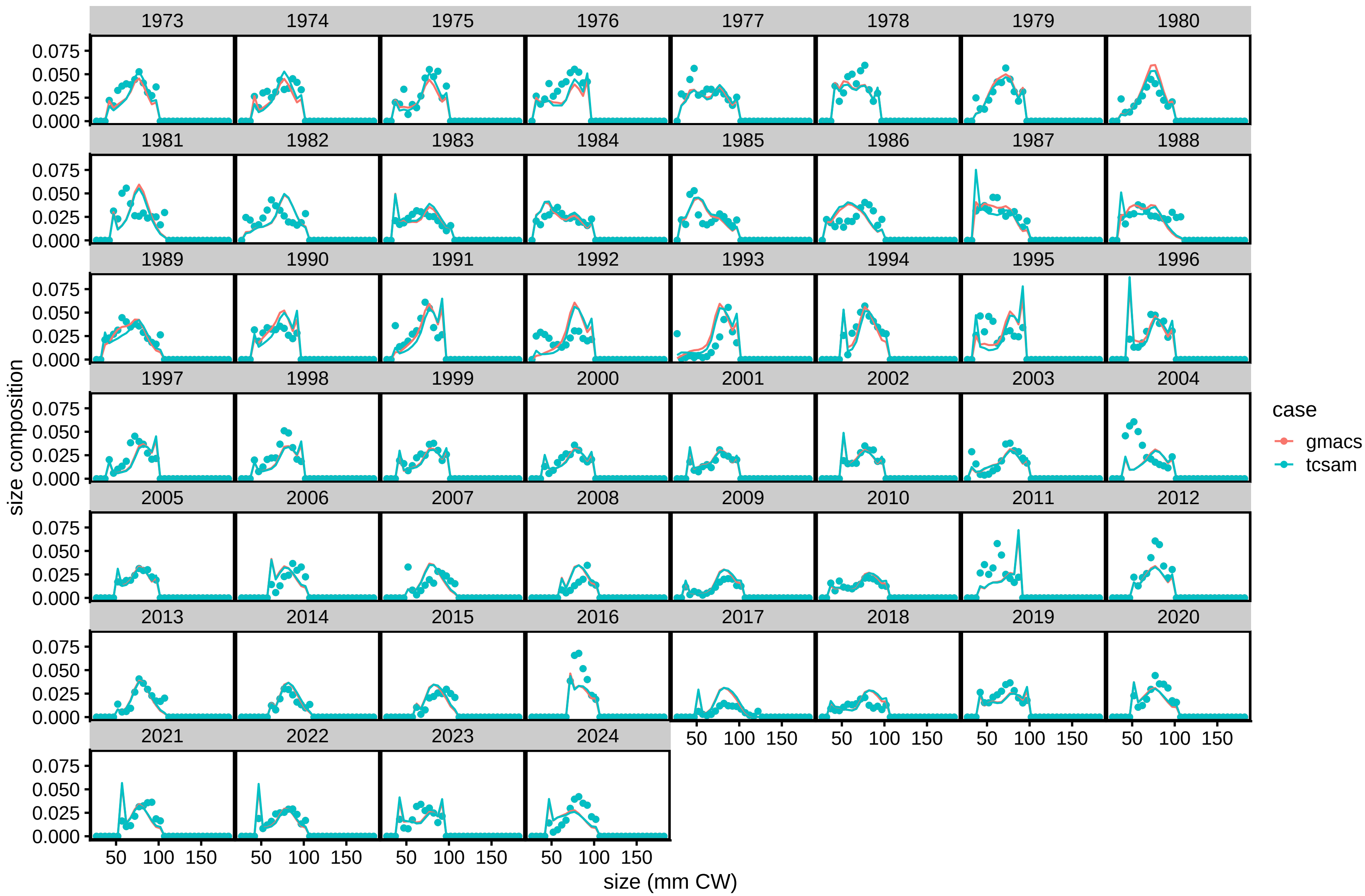


Figure 89. Fits to total catch size composition data from the groundfish fisheries for females. Points: observed values; lines: predicted values.

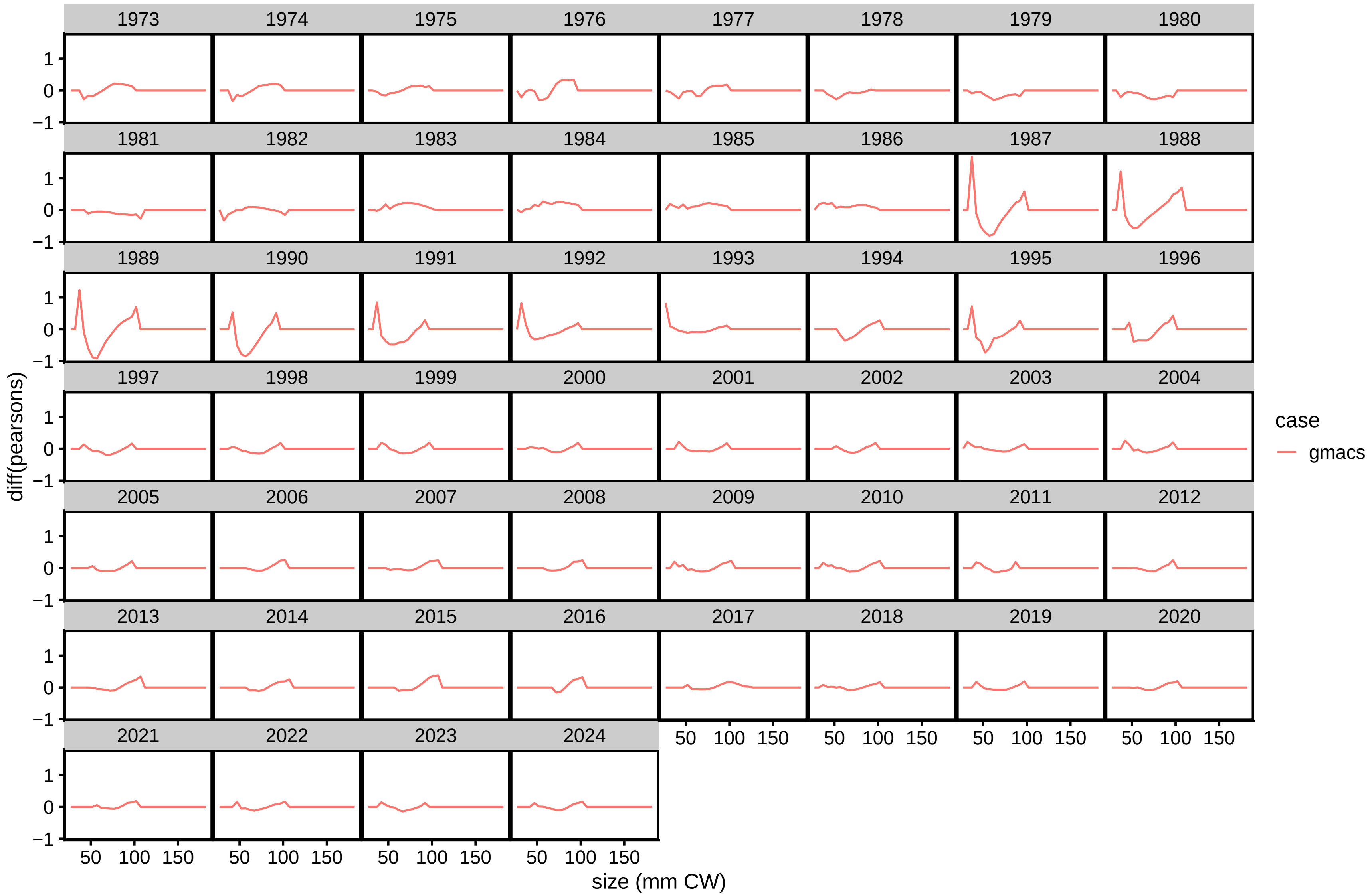


Figure 90. Differences from the TCSAM02 model in Pearson's residuals for fits to total catch size composition data from the groundfish fisheries for females.

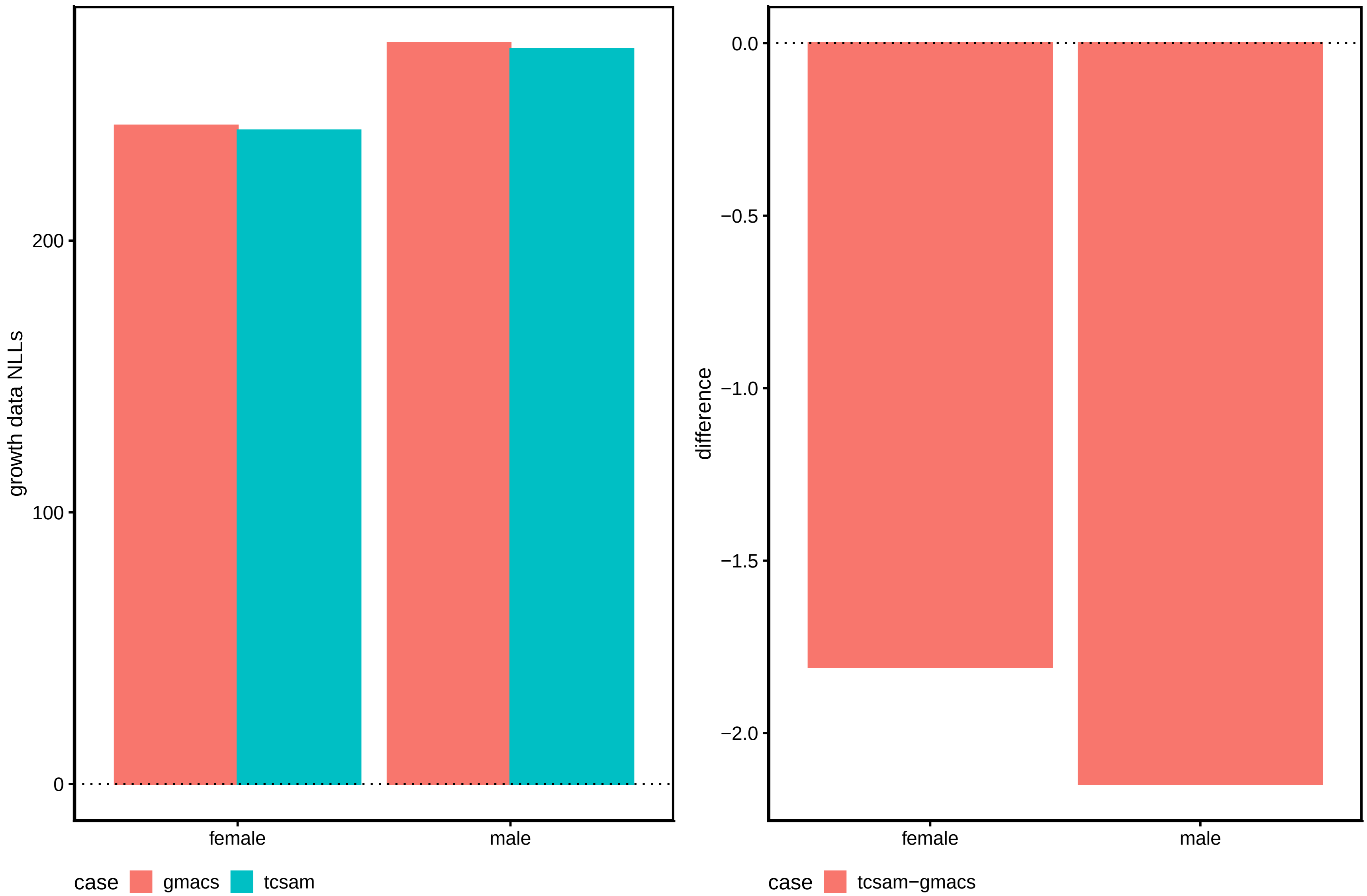


Figure 91. Comparison of summary negative log-likelihood (NLL) values for fits to sex-specific growth data from the GMACS and TCSAM02 models. Left: values; right: differences. These values are comparable between the model frameworks.

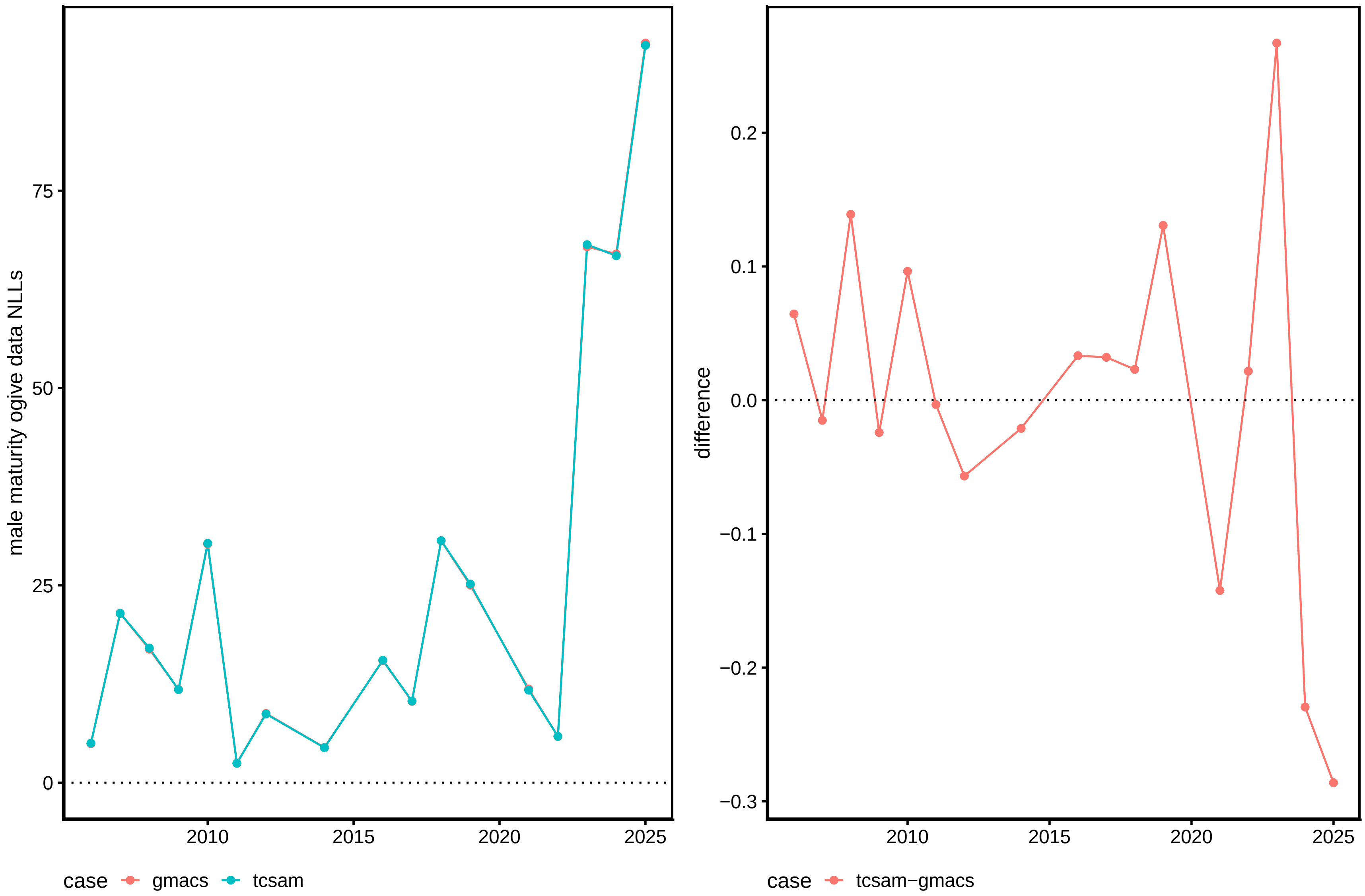


Figure 92. Comparison of summary negative log-likelihood (NLL) values for fits to male maturity ogive data from the GMACS and TCSAM02 models. Left: values; right: differences. These values are comparable between the model frameworks.

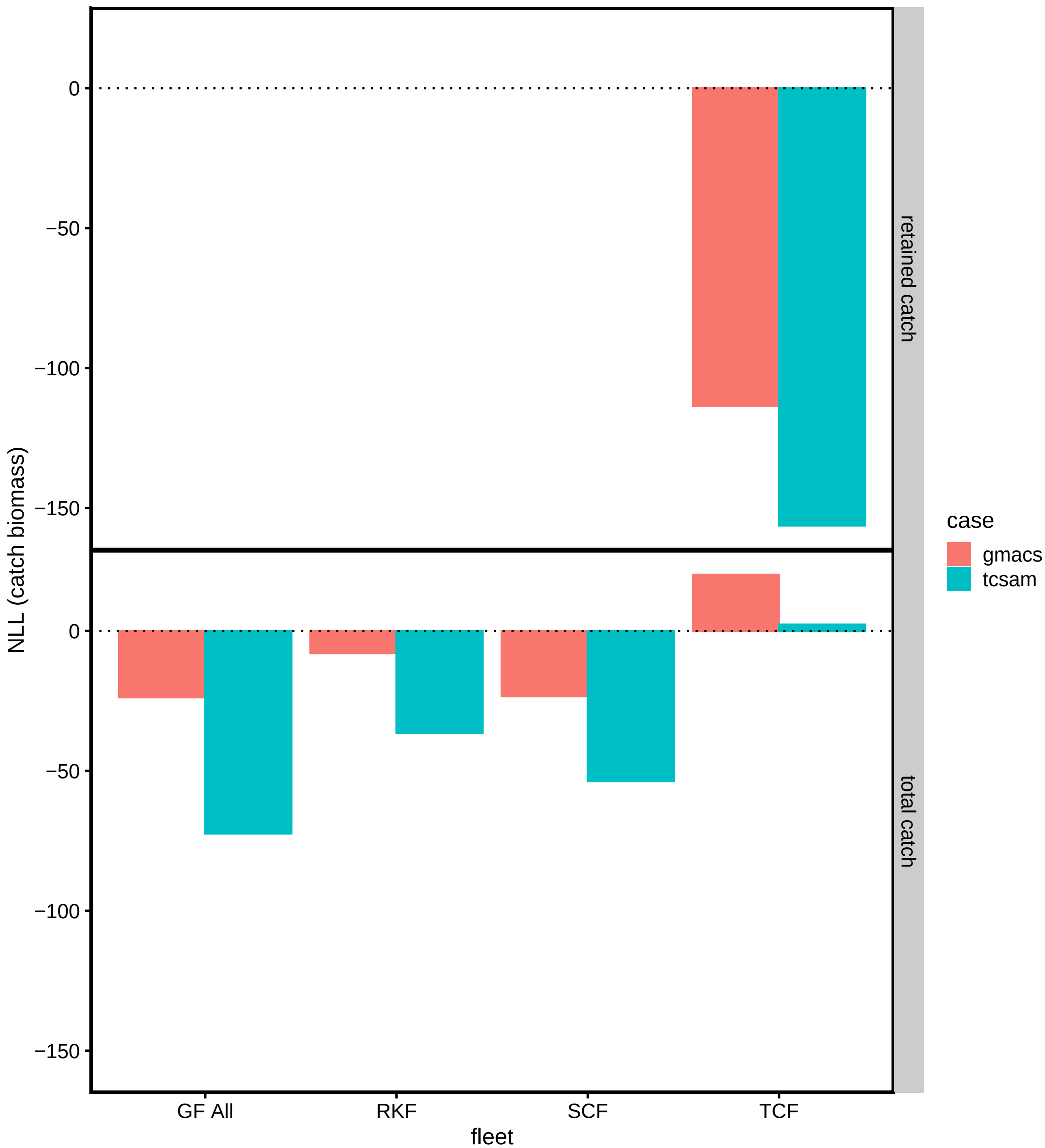


Figure 93. Comparison of summary negative log-likelihood (NLL) values for fishery catch biomass data from the GMACS and TCSAM02 models. Upper: retained catch; Lower: total catch. These values are **not** expected to agree between the models because constant terms in the NLL calculation are handled differently in the two model frameworks.

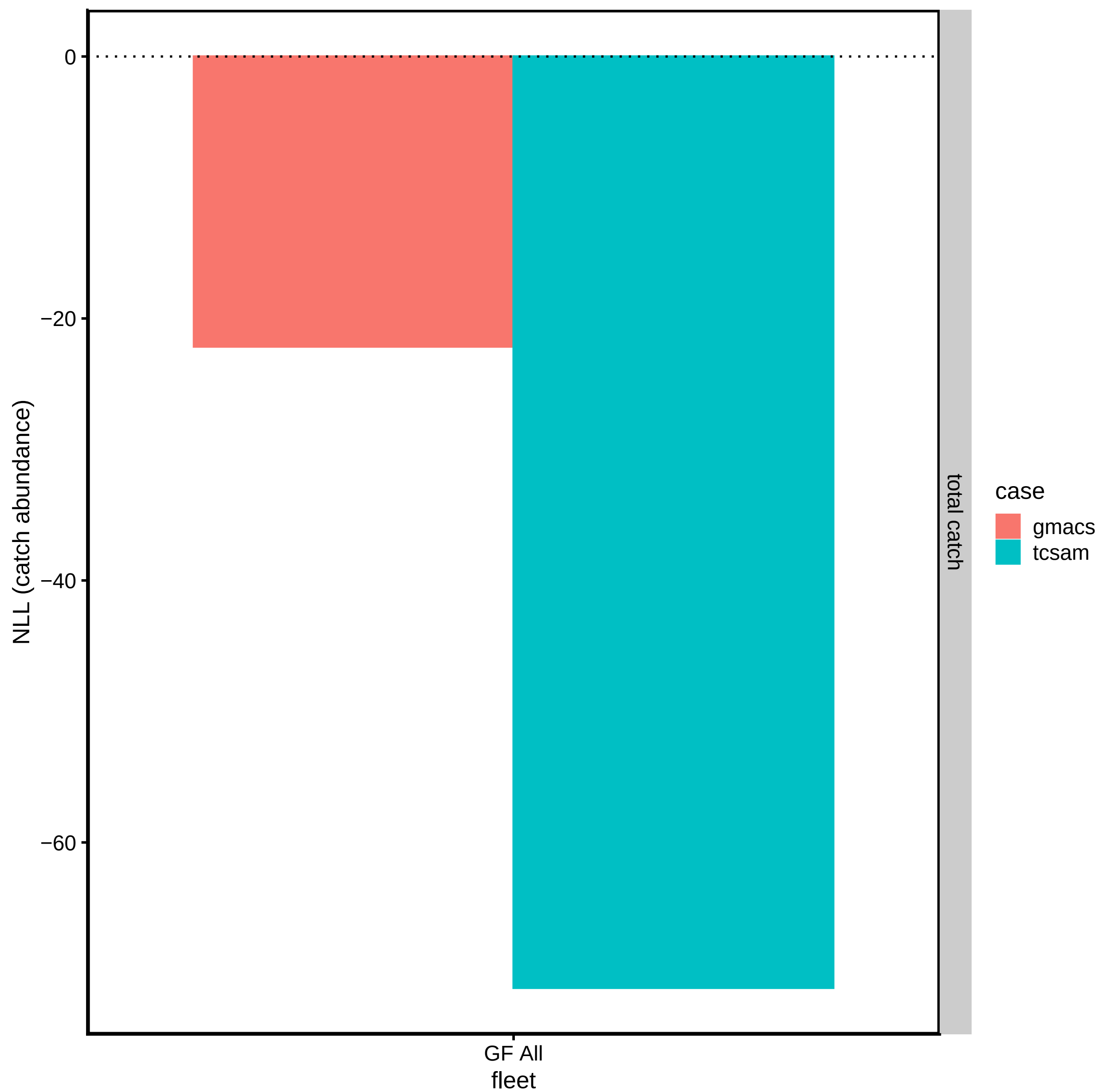


Figure 94. Comparison of summary negative log-likelihood (NLL) values for fishery catch abundance data from the GMACS and TCSAM02 models. Catch abundance is fit only from the groundfish fisheries. These values are **not** expected to agree between the models because constant terms in the NLL calculation are handled differently in the two model frameworks.

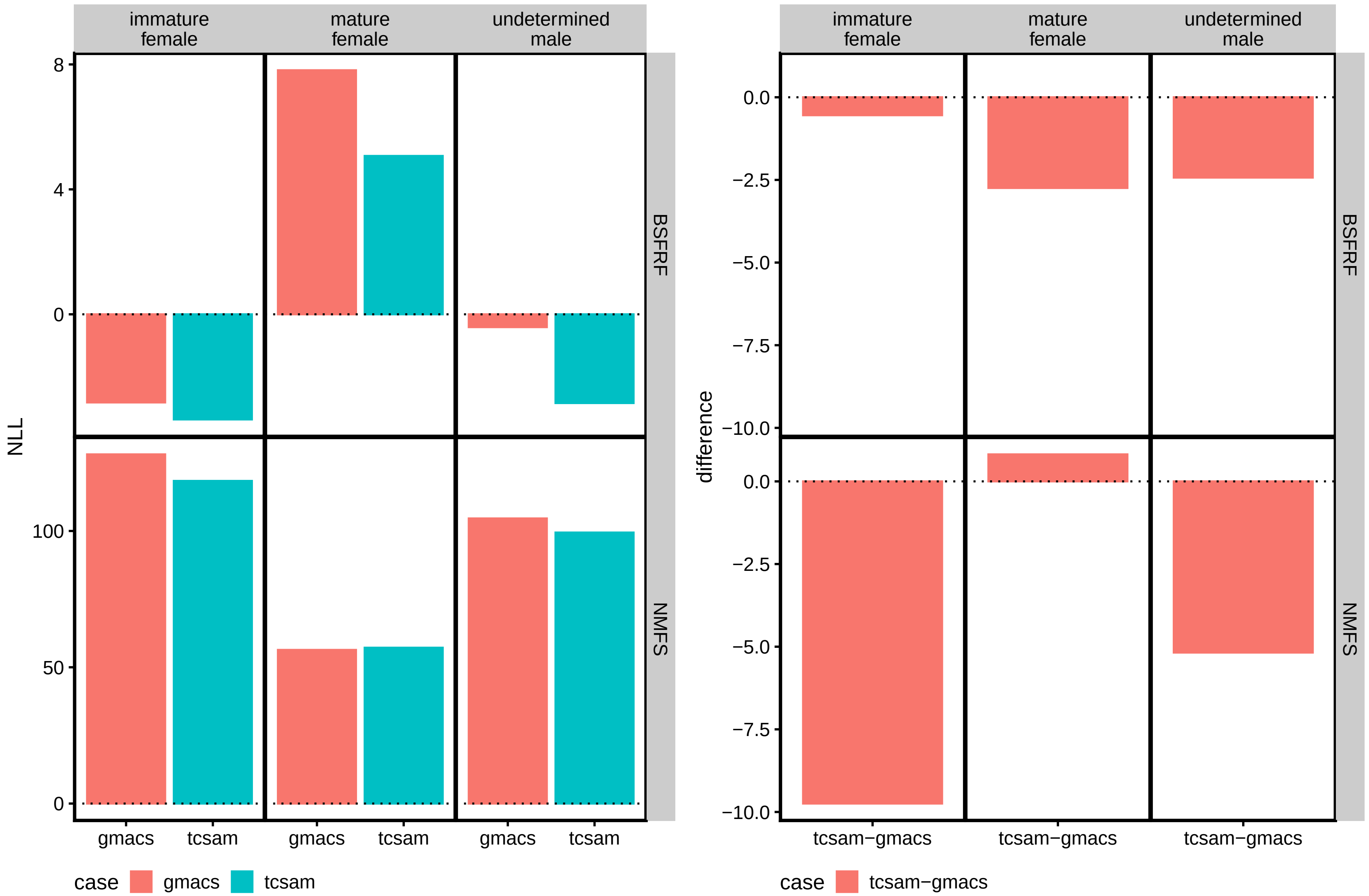


Figure 95. Comparison of summary negative log-likelihood (NLL) values for fits to survey biomass data from the GMACS and TCSAM02 models by fleet and biological category. Left: values; right: differences. These values are comparable.

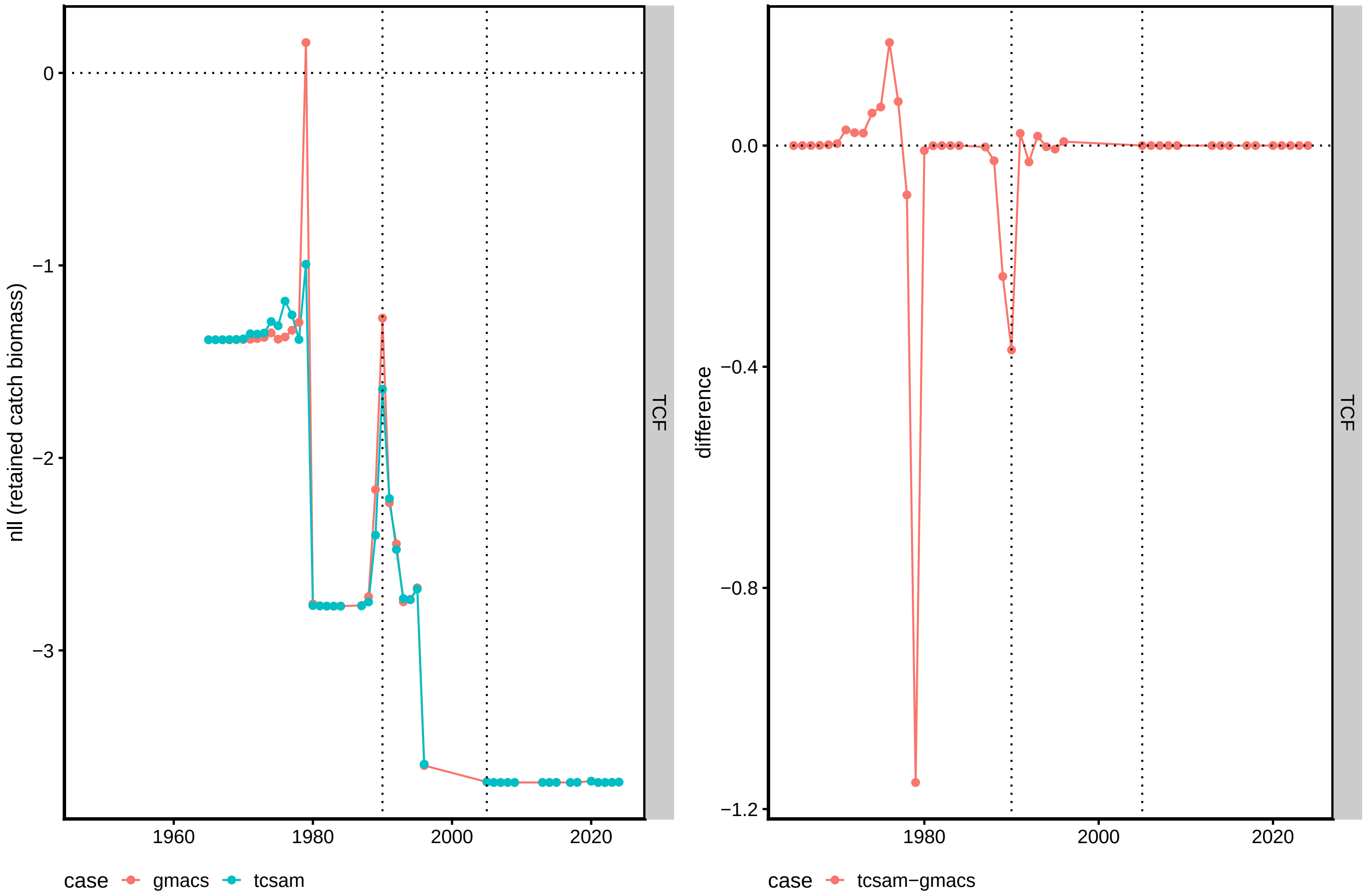


Figure 96. Comparison of summary negative log-likelihood (NLL) values for fits to fishery retained catch biomass data from the GMACS and TCSAM02 models. Left: values; right: differences. TCF: directed Tanner crab fishery. The vertical dotted lines indicate 1990 and 2005. These values are comparable.

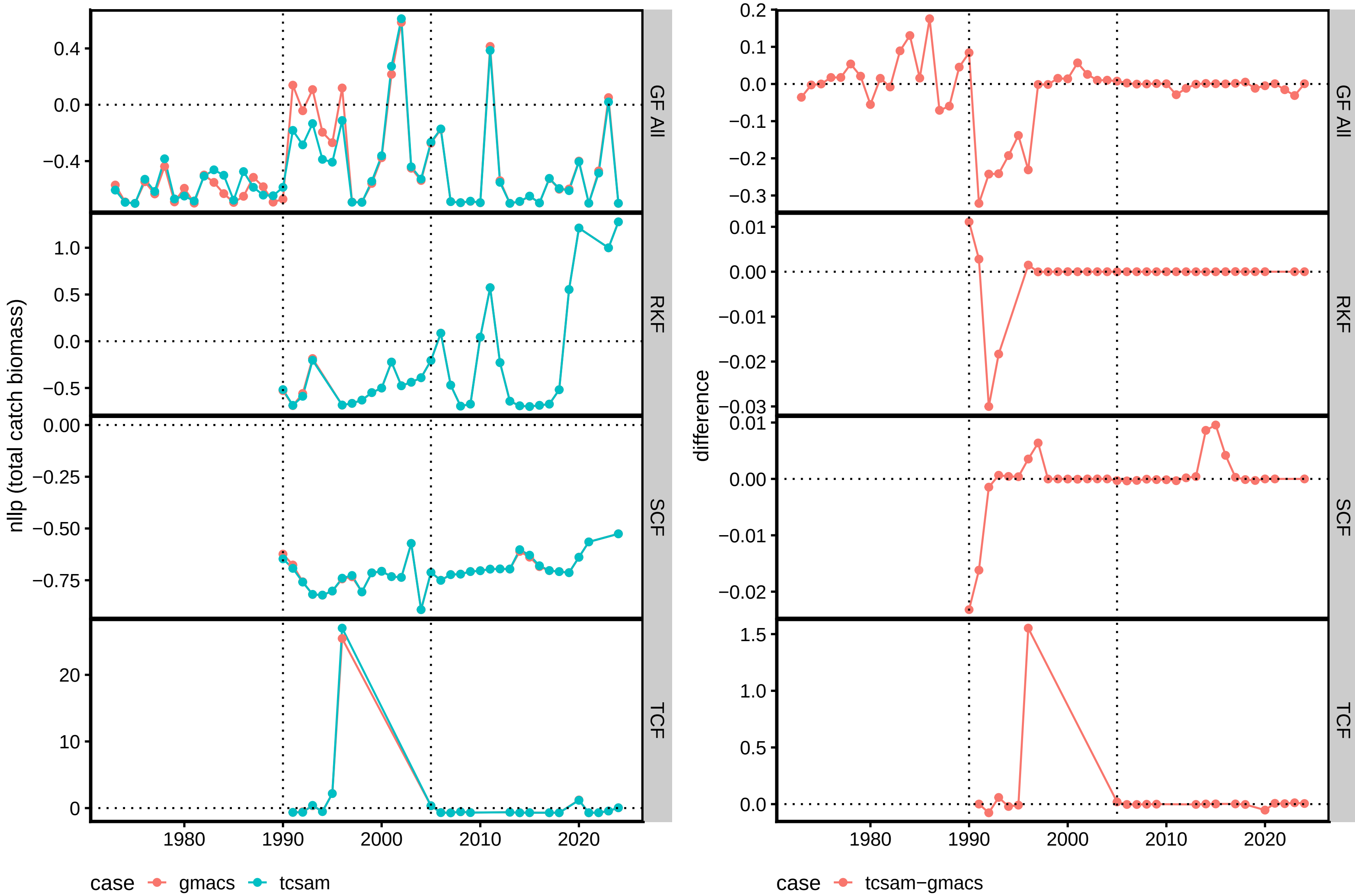


Figure 97. Comparison of summary negative log-likelihood (NLL) values for fits to fishery total catch biomass data from the GMACS and TCSAM02 models by fleet. Left: values; right: differences. TCF: directed Tanner crab fishery; SCF: snow crab fishery; RKF: BBRKC fishery; GF All: groundfish fisheries. The vertical dotted lines indicate 1990 and 2005. These values are comparable.

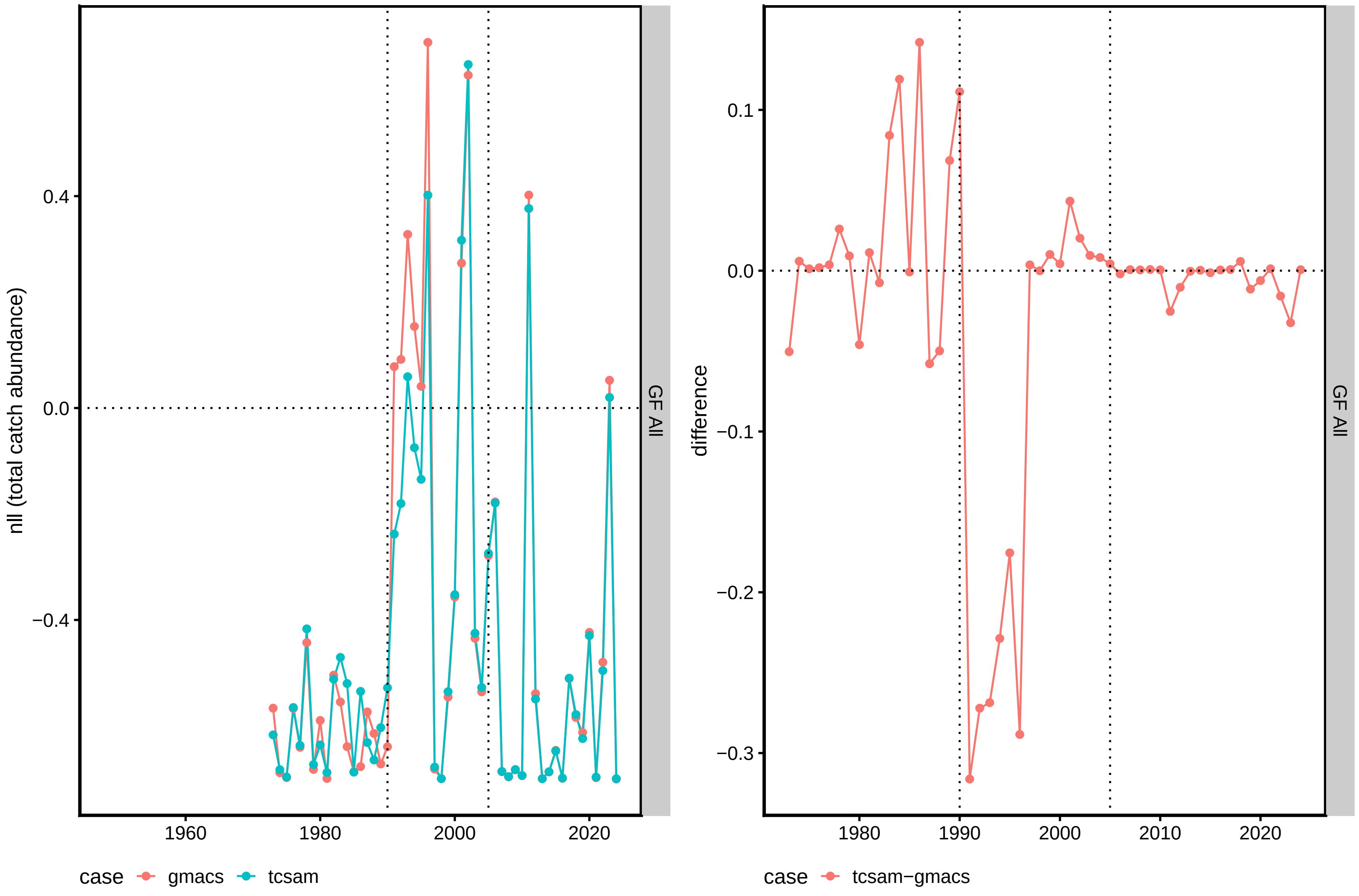


Figure 98. Comparison of summary negative log-likelihood (NLL) values for fits to fishery total catch abundance data from the GMACS and TCSAM02 models by fleet. Left: values; right: differences. Catch abundance data are fit only from the groundfish fisheries. The vertical dotted lines indicate 1990 and 2005. These values are comparable.

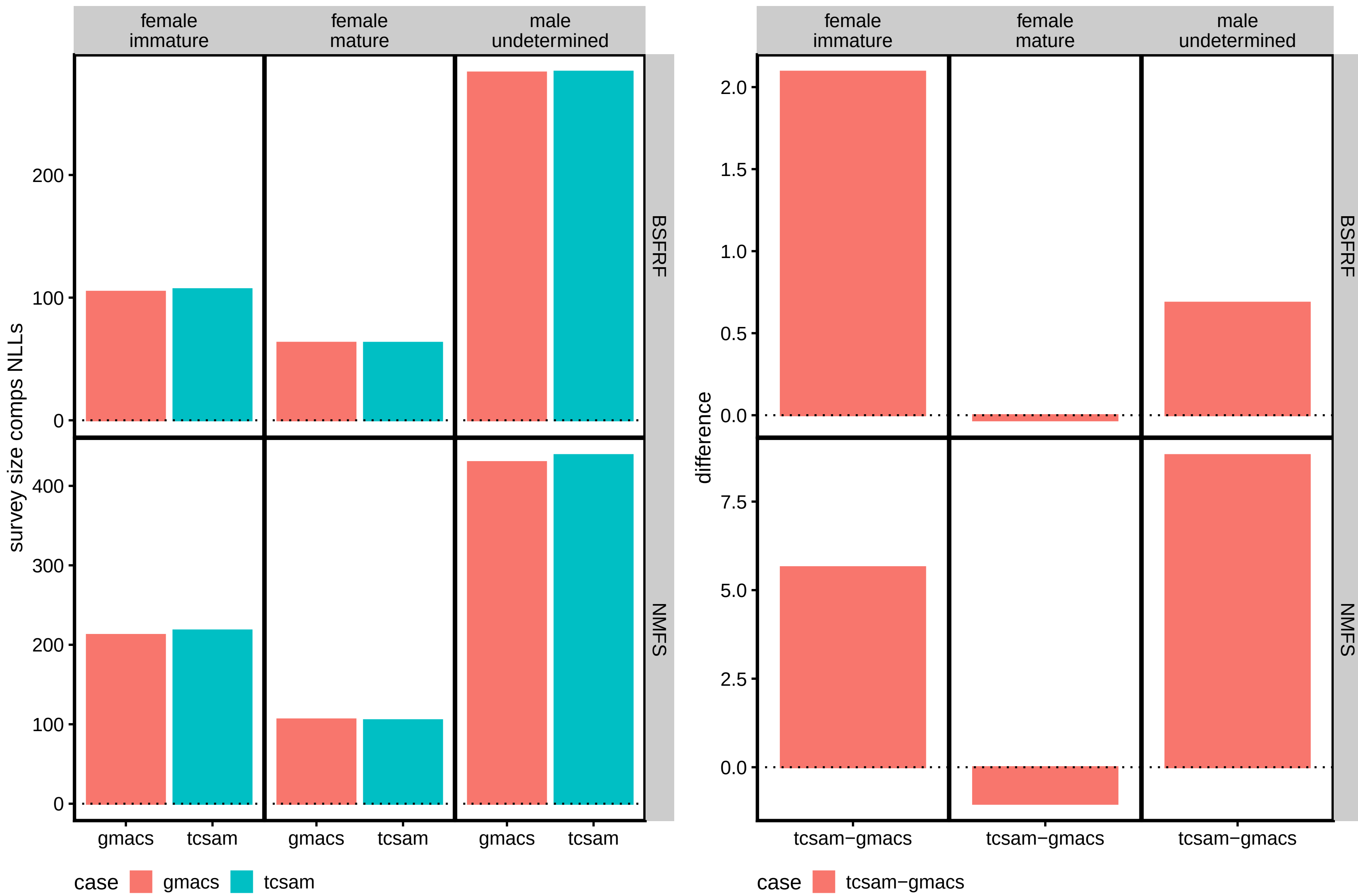


Figure 99. Comparison of negative log-likelihood (NLL) values for fits to survey size composition data from the GMACS and TCSAM02 models by fleet. Left: values; right: differences.

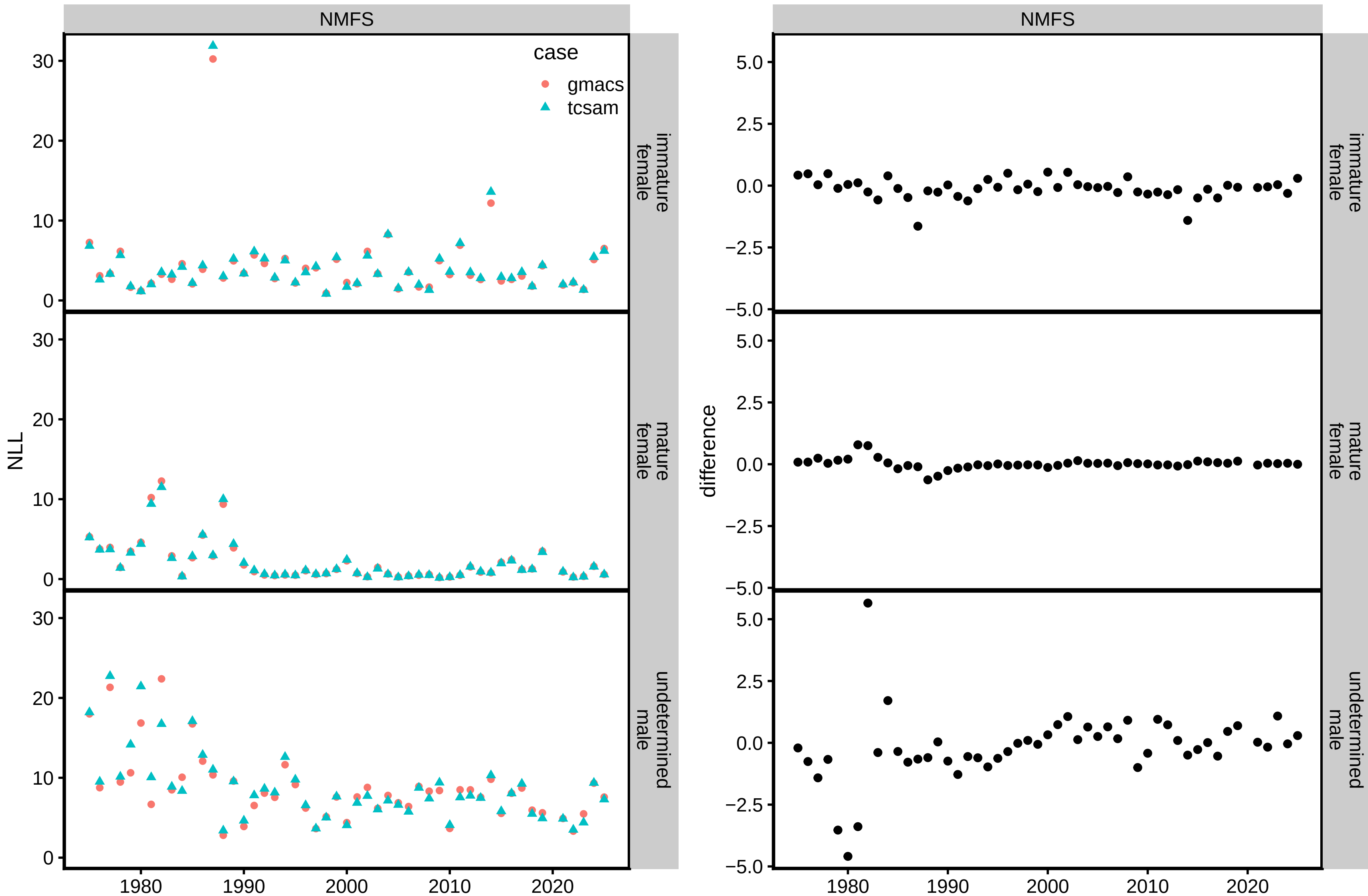


Figure 100. Comparison of negative log-likelihoods by year for Tanner crab size compositions from the NMFS surveys.Lefthand column: values; righthand column: differences from TCSAM02 model values.

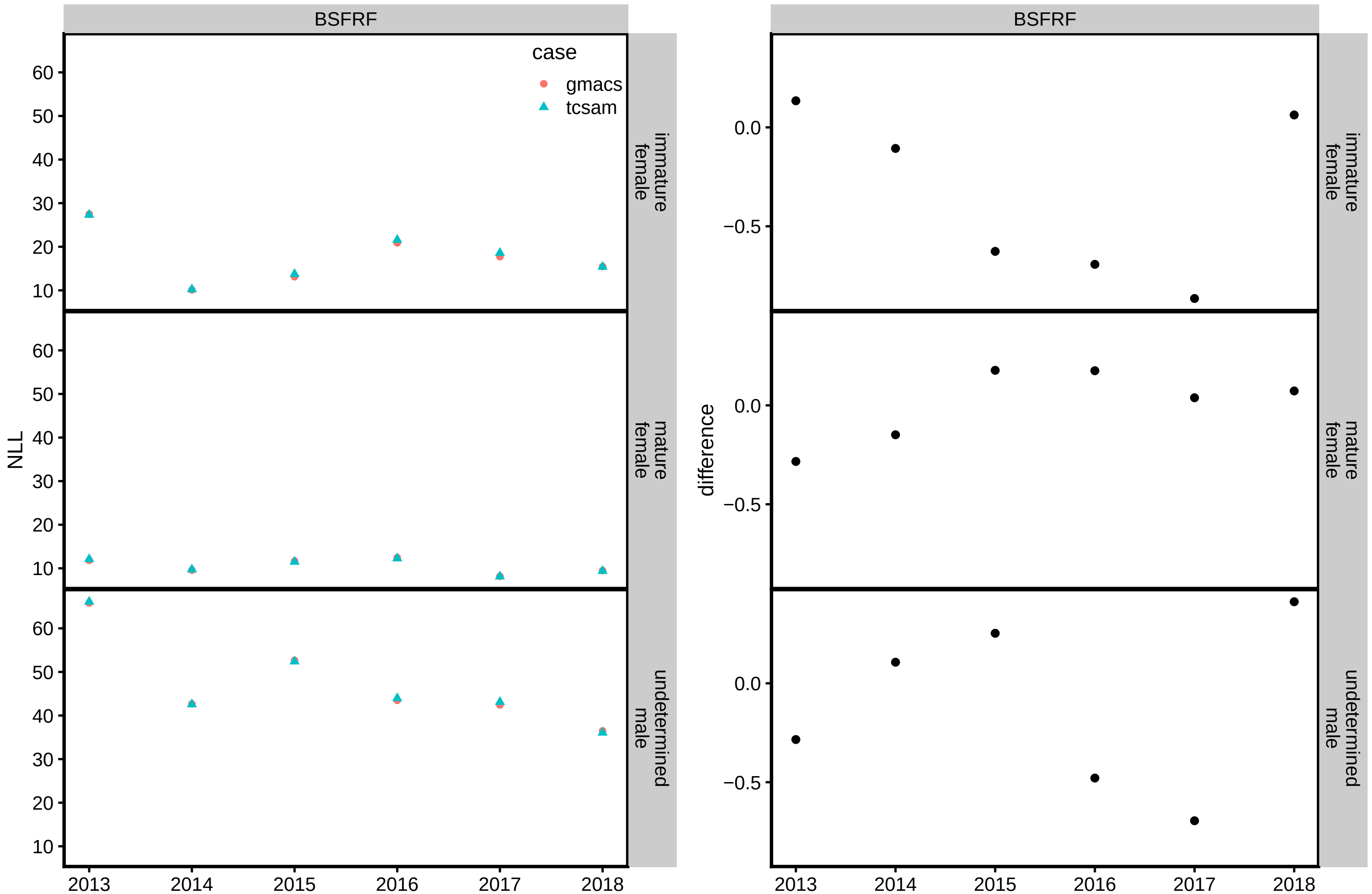


Figure 101. Comparison of negative log-likelihoods by year for Tanner crab size compositions from the BSFRF surveys.Lefthand column: values; righthand column: differences from TCSAM02 model values.

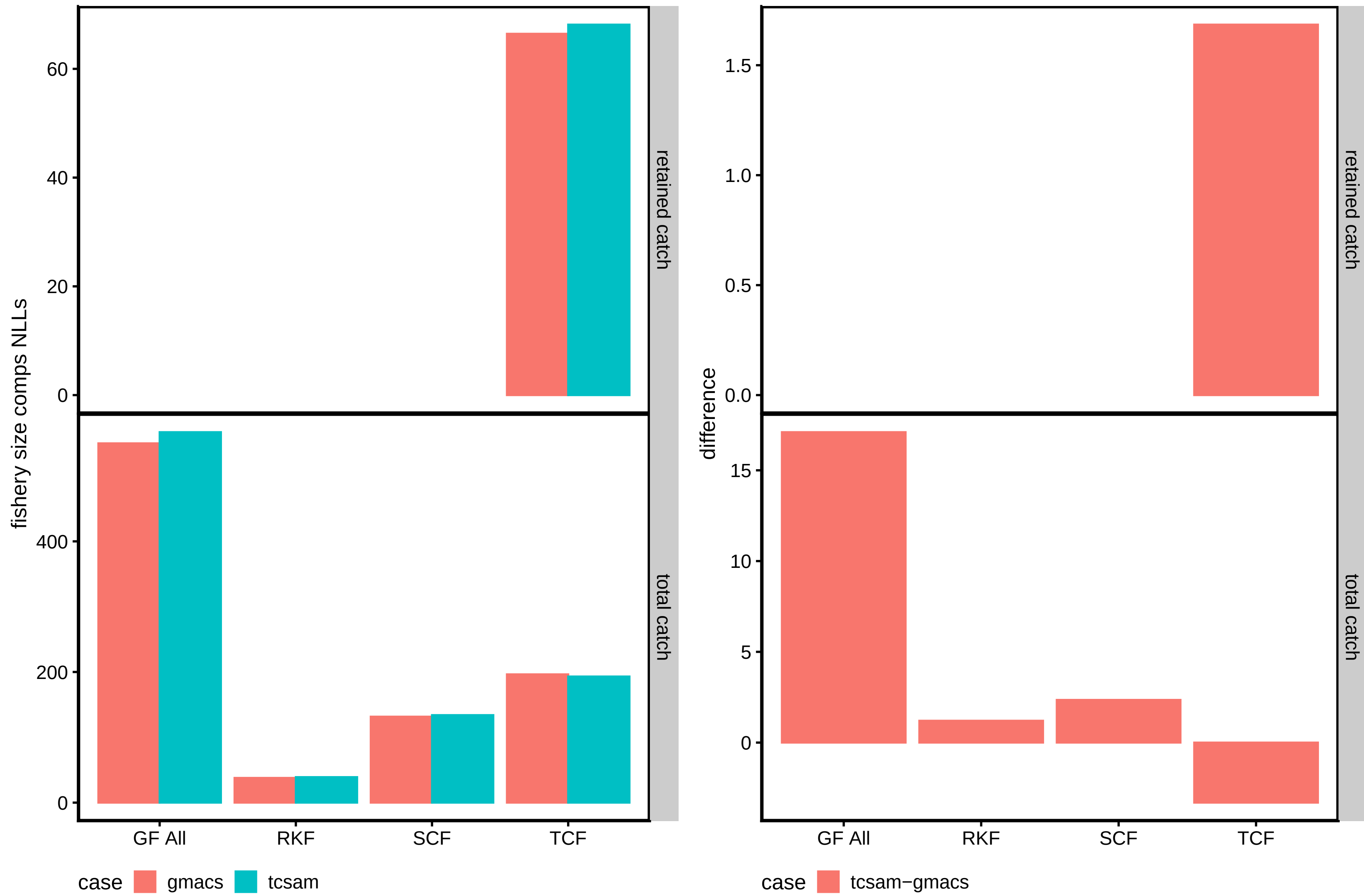


Figure 102. Comparison of negative log-likelihood (NLL) values for fits to fishery size composition data from the GMACS and TCSAM02 models by fleet. Left: values; right: differences.

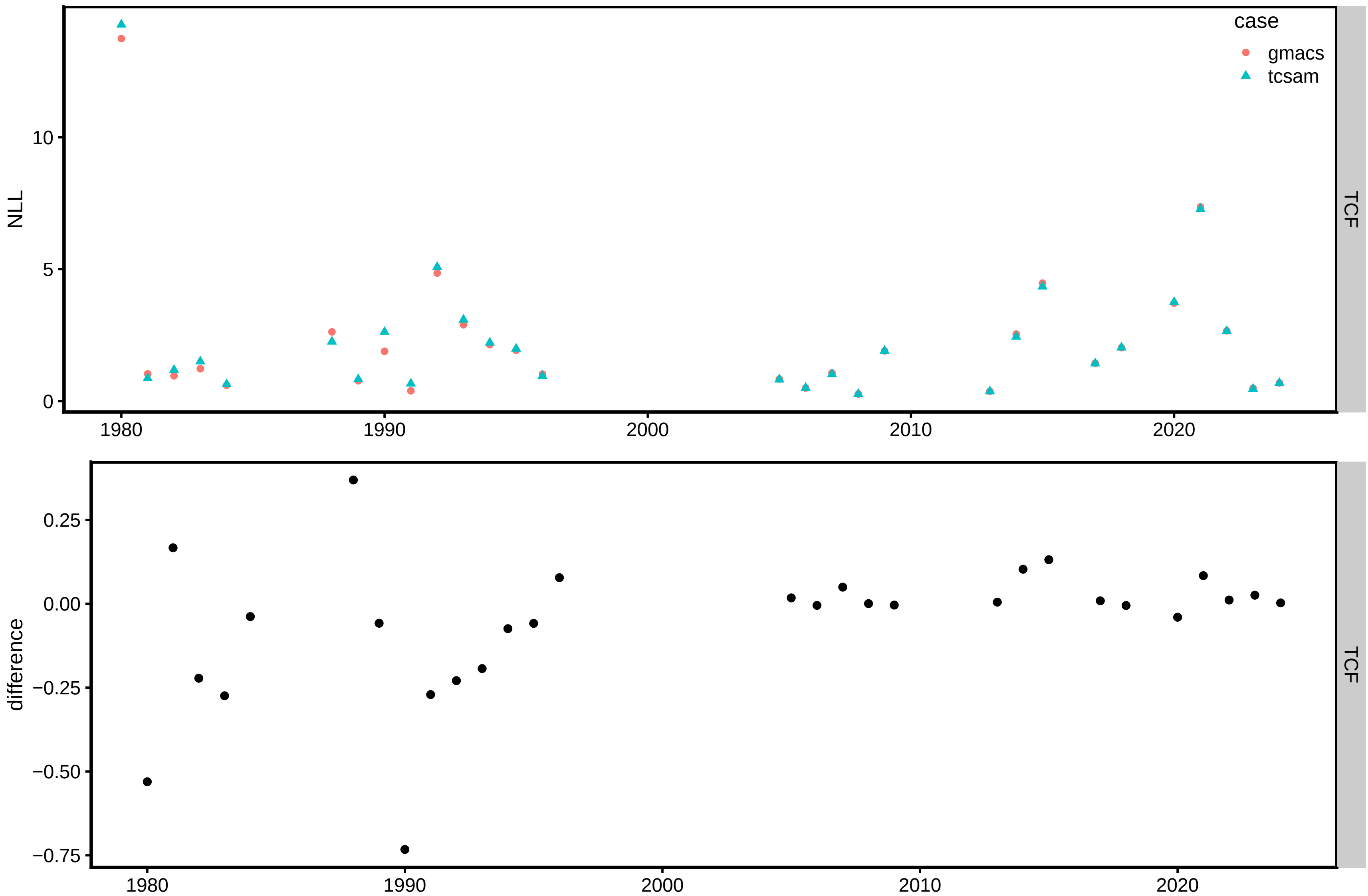


Figure 103. Comparison of negative log-likelihoods by year forTanner crab retained catch size comps in the directed fisheries.Upper plot: values; lower plot: differences from TCSAM02 model values.

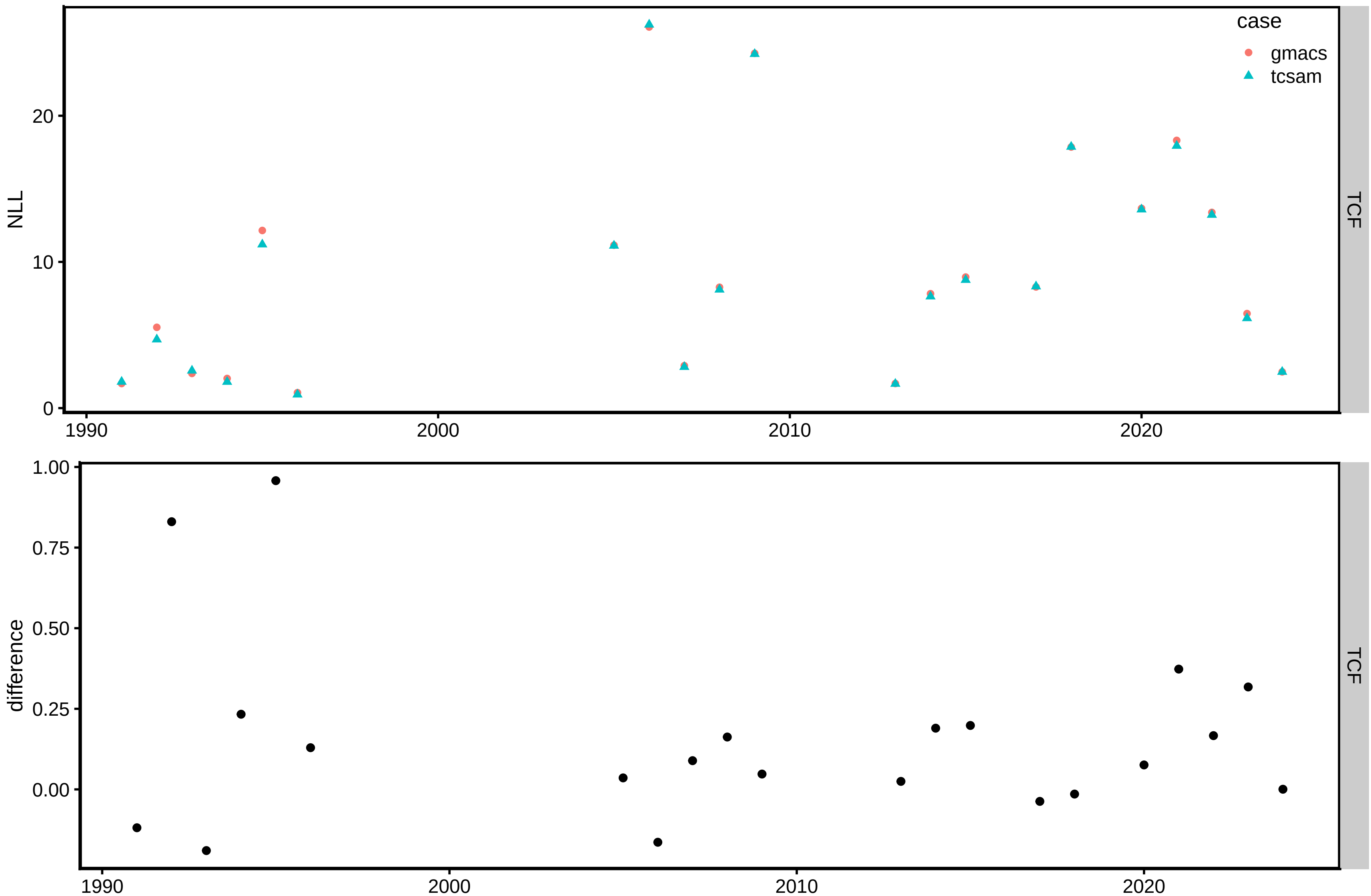


Figure 104. Comparison of negative log-likelihoods by year for Tanner crab total catch size comps in the directed fisheries.Upper plot: values; lower plot: differences from TCSAM02 model values.

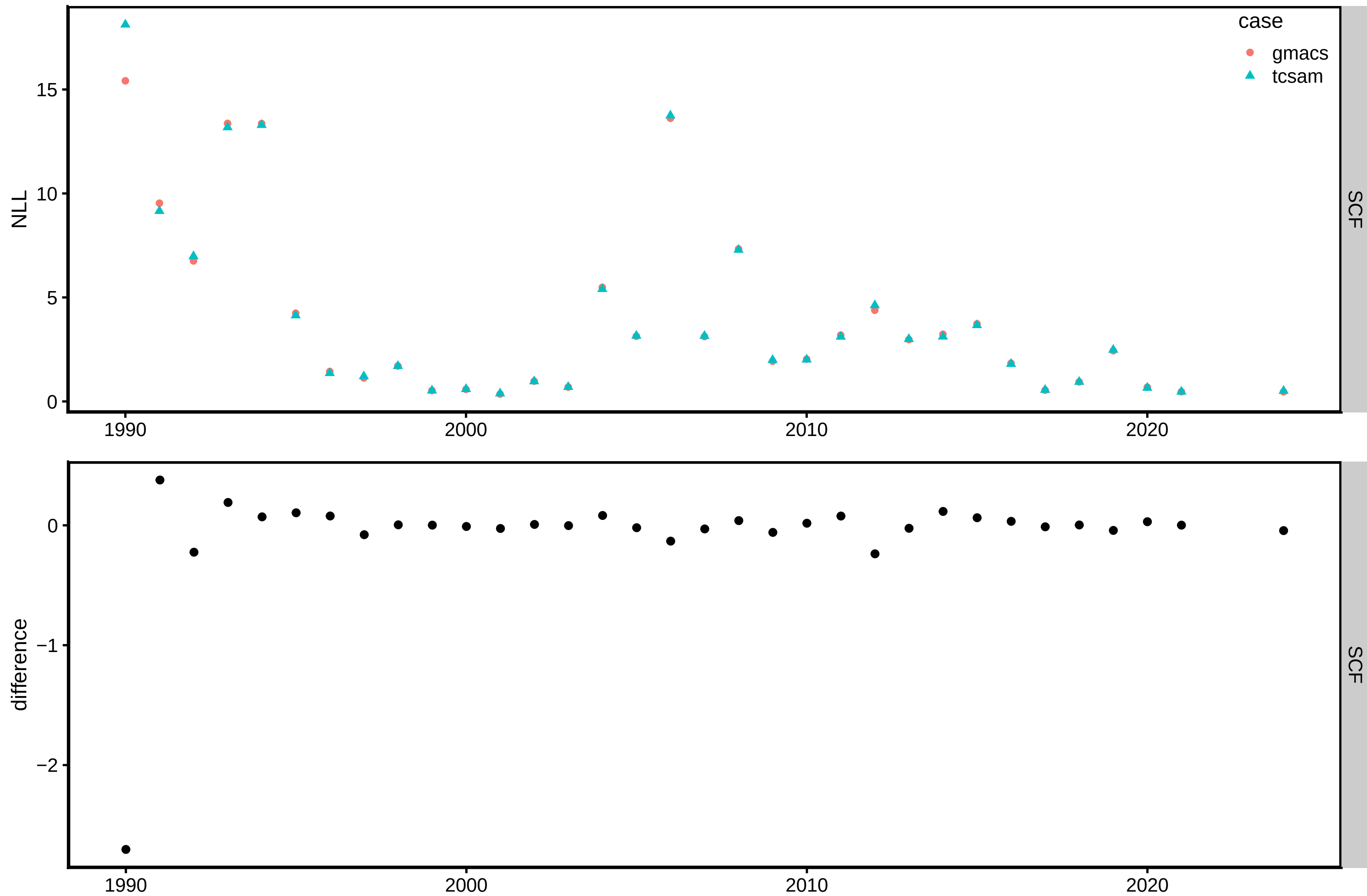


Figure 105. Comparison of negative log-likelihoods by year for Tanner crab total (by)catch size comps in the snow crab fishery.Upper plot: values; lower plot: differences from TCSAM02 model values.

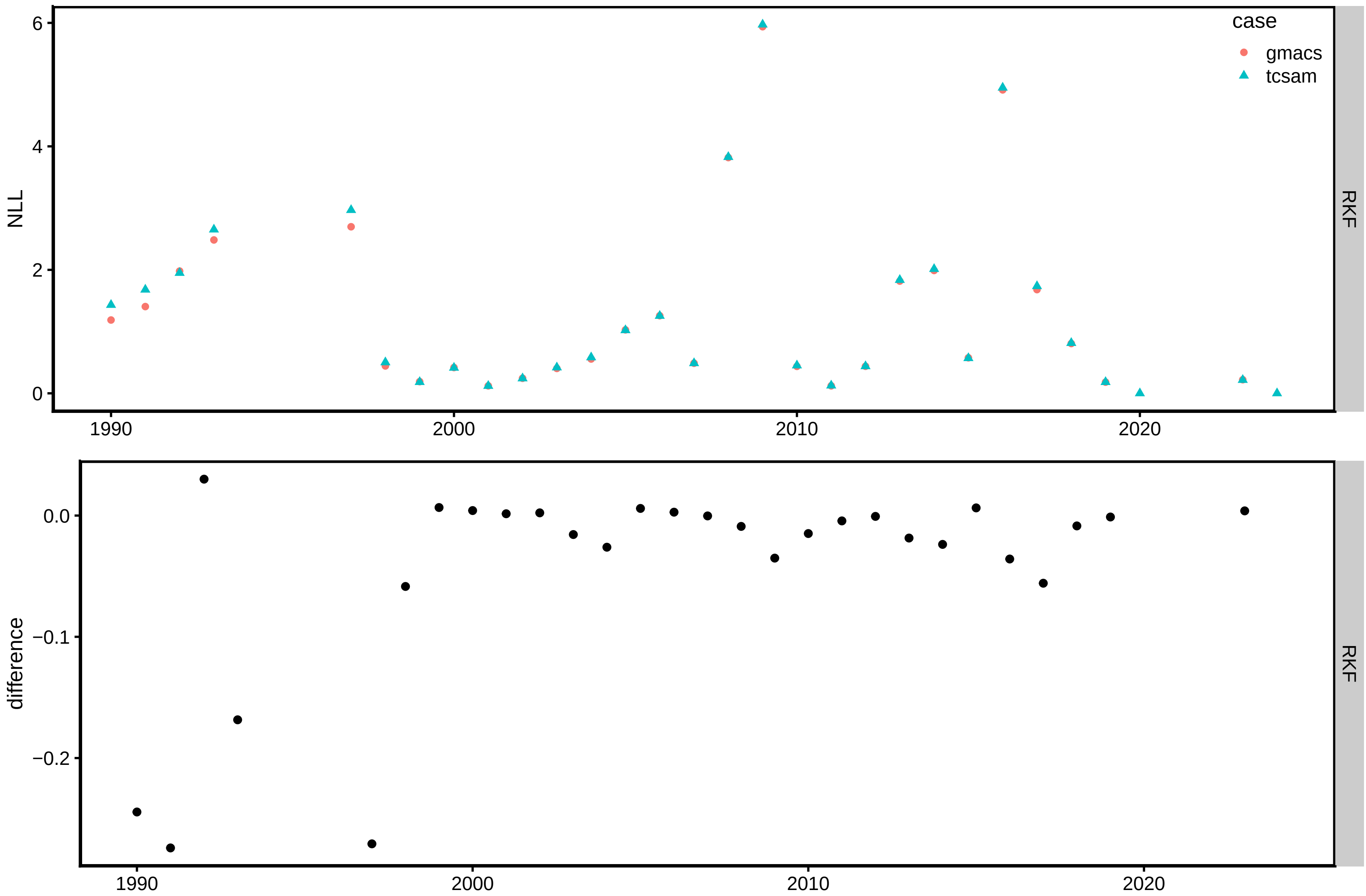


Figure 106. Comparison of negative log-likelihoods by year for Tanner crab total (by)catch size comps in the BBRKC fishery.Upper plot: values; lower plot: differences from TCSAM02 model values.

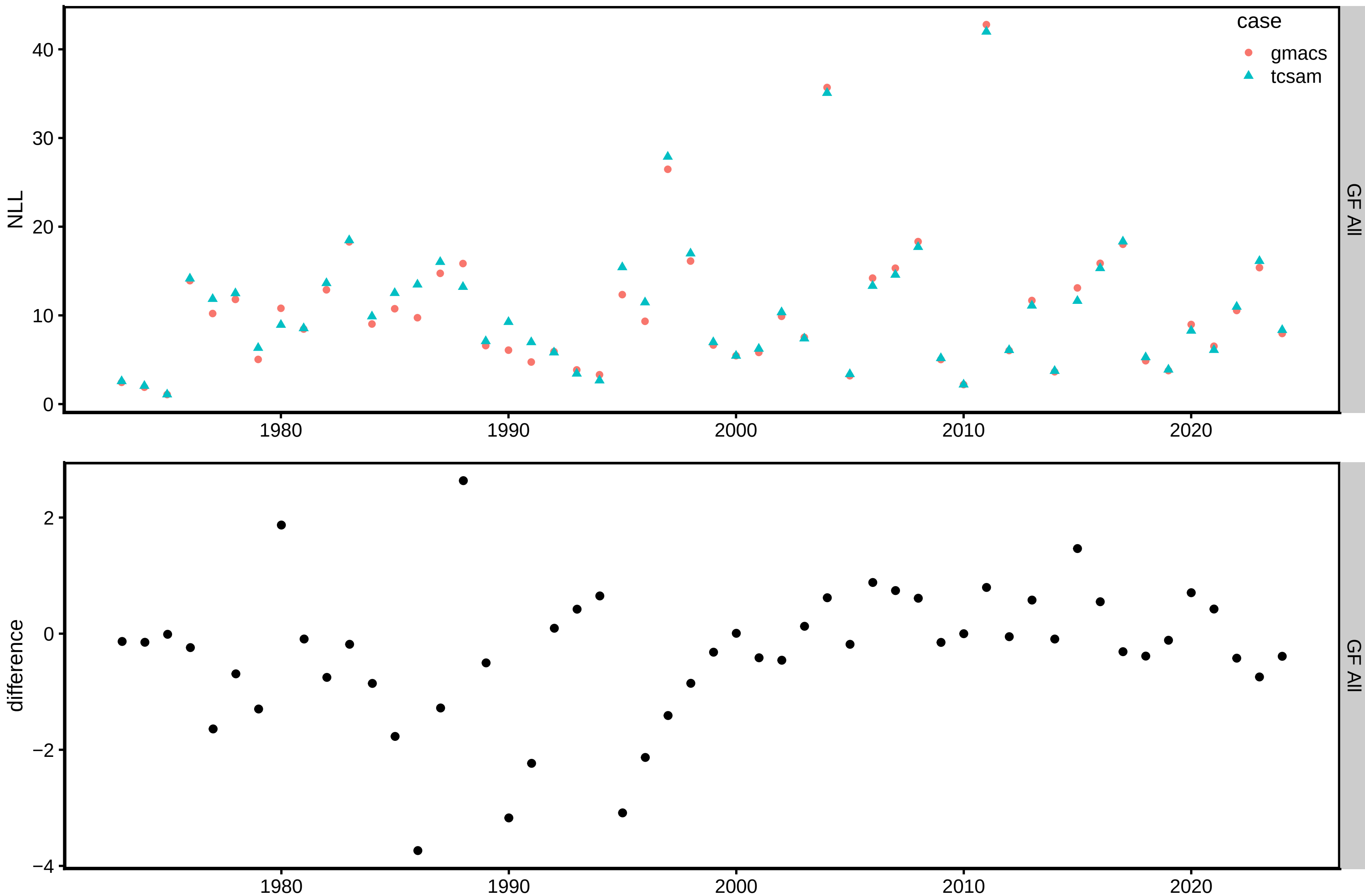


Figure 107. Comparison of negative log-likelihoods by year for Tanner crab total (by)catch size comps in the groundfish fisheries.Upper plot: values; lower plot: differences from TCSAM02 model values.

Stockhausen, W.T. 2025. 2025 Stock Assessment and Fishery Evaluation Report for the Tanner Crab Fisheries of the Bering Sea and Aleutian Islands Regions. *In* Stock Assessment and Fishery Evaluation Report for the KING AND TANNER CRAB FISHERIES of the Bering Sea and Aleutian Islands Regions 2025 Final Crab SAFE. North Pacific Fishery Management Council, Anchorage, AK. Available from https://meetings.npfmc.org/Meeting/Details/3097.