2025 PIBKC Assessment Considerations

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1 Introduction

The next full assessment for the Pribilof Islands blue king crab (PIBKC) stock will be reviewed by the Crab Plan Team (CPT) in September 2025 and the NPFMC's (North Pacific Fishery Management Council) Science and Statistical Committee (SSC) in October 2025. The stock has been on a two-year cycle for assessment and the last full assessment was conducted in September 2023 (Stockhausen 2023). Following the September 2025 assessment, the stock will begin a four-year assessment cycle and the next full assessment will be conducted in 2029.

This report primarily addresses a number of issues related to data from the NMFS EBS bottom trawl survey for PIBKC that have arisen since the last assessment. First, AFSC's Shellfish Assessment Program (SAP) has developed an R package, "crabpack", as a replacement to AKFIN Answers (https://akfin.psmfc.org) for obtaining crab-related survey data in a standard format. SAP requested that assessment authors test the package and compare results of data pulls using the package with data pulled using the authors' previous methods. Second, as part of the effort to "modernize" the NMFS EBS bottom trawl survey to improve efficiency, the high-density "corner" stations in the NMFS EBS survey grid near the Pribilof Islands and St. Matthew Island were dropped for the 2024 survey and will not be sampled in future surveys. Assessment authors were asked to consider the impact of this change on their assessment. Finally, the 2023 and 2024 surveys found no mature male blue king crab in the Pribilof Islands sampling strata. While this is principally a consequence of applying relatively low sampling effort to a stock at low (but non-zero) abundance, the "hard zeros" introduced in the time series of mature male biomass for PIBKC can be problematic for the subsequent assessment. Several approaches to dealing with this issue are considered here.

This report is organized into the following sections: Responses to previous CPT and SSC Comments (Section 2), "New" Data and Analyses (Section 3), Summary (Section 4), and Acknowledgments (Section 5).

2 Responses to SSC and CPT Comments

2.1 Remarks pertinent to this assessment

2.1.1 CPT Comments Sept 2023-Sept 2024

None

2.1.2 SSC Comments Oct 2023-Oct 2024

None

2.1.3 CPT comments May 2023:

CPT comment

The CPT agreed (following the author's recommendation) with the change to use the **rema** R package for the assessment.

Author response

The *rema* R package, which underwent a favorable Center for Independent Experts (CIE) review during 2023, has been used to fit the random walk model to design-based estimates of MMB at the time of the survey.

2.1.4 SSC comments June 2023:

SSC Comment

The SSC concurs with the author and CPT recommended application of the **rema** R package for this Tier 4 assessment.

Author response

See Section 2.1.3.

SSC Comment

The SSC also looks forward to the SAFE section on rebuilding in September as the rebuilding plan nears its second decade.

Author response

The revised (2014) rebuilding plan does not have a target rebuild date and NMFS cannot predict when or if rebuilding will occur (NPFMC 2021). There is no new and unexpected information that would significantly alter the rebuilding expectations. The recent trajectory of the time series of MMB-at-survey time provides no evidence of an increasing trend. Further, survey size compositions provide no evidence for recent recruitment to the stock. The failure of the EBS shelf survey to catch any mature males this year does not raise the level of concern for this stock above what it has been in the recent past; the survey does not target blue king crab and the result is consistent with sampling a population at low (but non-zero) abundance. The causes of the continued low abundance and failure to recover are not well understood, but are thought to be predominantly due to environmental changes that inhibit recruitment. In April 2022, the last time a determination of overfished status was made was made, the Regional Administrator determined that PIBKC was "not making inadequate progress" towards rebuilding.

3 "New" Data and Analyses

3.1 Crabpack comparisons

The ASFC's Shellfish Assessment Program has introduced `crabpack`, a new R package (R Core Team 2022) to access NMFS EBS crab survey data and subsequently estimate annual abundance, biomass, and size compositions by year for several population categories (e.g., sex, maturity state). The tcsamSurveyData R package has been used previously with survey haul data files downloaded from AKFIN Answers to provide similar information for the PIBKC stock assessment (e.g., Stockhausen 2023). Here, the two approaches are compared for the Pribilof District abundance, biomass, and size compositions for NMFS EBS crab survey data for PIBKC from 1975 to 2023.

3.1.1 Survey abundance estimates

Estimates of Pribilof District abundance from the NMFS bottom trawl survey for male and female PIBKC by population state are compared by year in Figure 1 for calculations made in the 2023 assessment (Stockhausen 2023) and with the `crabpack` R package. Absolute differences and percent differences between the two methods are shown, respectively, in Figures 2 and 3. The percent differences are also shown in Table 1 to two decimal places. The figures and table show excellent agreement between the two methods in all survey years except 1979, when estimates from the two methods differ substantially ($> 10\%$). The estimates from the assessment are larger than those from `crabpack` in 1979. The differences in the two methods may reflect differences in the stratum areas used to expand mean CPUE (numbers/area) within a stratum to stratum abundance or in the actual hauls included in the calculation (`crabpack` appears to include hauls at corner stations that were only conducted in 1979, while these were excluded in the standardized time series used in the assessment).

3.1.2 Survey biomass estimates

Estimates of EBS-wide biomass from the NMFS bottom trawl survey for male and female PIBKC by maturity state are compared by year in Figure 4 for calculations made in the 2023 assessment (Stockhausen 2023) and with the `crabpack` R package. Absolute differences and percent differences between the two methods are shown, respectively, in Figures 5 and 6. The percent differences are also shown in Table 2 to two decimal places.

As with abundance, the figures and table demonstrate excellent agreement between the two methods in all survey years prior to 2016 except 1979, when estimates from the two methods differ substantially ($> 10\%$). Unlike the abundance estimates, the two methods also exhibit small differences (< 5 %) in 2016 and subsequent years. The estimates from the assessment for 2016 and later are larger than those from `crabpack` in all years. The post-2015 differences between the two methods may reflect differences in the size used to calculate the weight of individual crab: the assessment uses carapace width to the first decimal place while `crabpack` apparently uses the carapace width to 1-mm.

3.2 No corner stations

As part of the effort to "modernize" the NMFS EBS bottom trawl survey to improve efficiency, the high-density "corner" stations in the NMFS EBS survey grid near the Pribilof Islands and St. Matthew Island (Figure 7) were dropped for the 2024 survey and will not be sampled in future surveys. Assessment authors were asked to consider the impact of this change on their assessment. This section compares the estimates of mature male biomass (MMB) and other population components derived from previous surveys with corner stations with those obtained by dropping the corner stations in order to obtain a retrospective idea of the importance of the corner stations to estimates of the PIBKC MMB time series.

3.2.1 Survey biomass estimates

Estimates of biomass from the NMFS EBS bottom trawl survey for different components of the PIBKC stock are compared by year in Figure 8 for calculations made including or excluding the corner stations. Absolute differences and percent differences between the sets of survey stations are shown, respectively, in Figures 9 and 10. The percent differences are also shown in Table 3. Figures 11 and 12 provide more detailed coparisons between the two sets of survey stations for mature male biomass (MMB) only.

Estimates of PIBKC MMB were generally higher when the corner stations were included: 25 years versus 17 years when excluding the corner stations resulted in a higher estimate. Since 2013, including the corner stations resulted in higher (or equal) estimates in all years except 2023 and 2024 when no mature males were caught anywhere.

3.3 Sampling-based zeros substitutions

Mature male abundance and biomass of Pribilof Islands blue king crab in the annual NMFS EBS bottom trawl survey has declined substantially since the survey was initiated in 1975 (Figure 13), including zero catches at 86 and 70 survey stations in, respectively, the 2023 and 2024 surveys. At low abundance, abundance appears to scale exponentially with the number of hauls at which mature males were caught (Figure 14). The existence of zeros in the corresponding time series for design-based estimates of mature male biomass within the Pribilof Islands survey strata (Figure 15) poses methodological difficulties for time series modeling approaches like `rema` (Sullivan 2022) that model variability on the log scale. `rema` provides three options for dealing with zeros in an observed time series: 1) treat the zeros as missing data; 2) substitute a small, but arbitrary, value for the zeros; or 3) assume an error distribution based on the Tweedie distribution. For the latter two options (2, 3), an associated error CV (coefficient of variation) must also be specified. Lognormal error distributions are assumed under the first two options (1,2). Using the Tweedie distribution (option 3) has the advantage that it can synthetically fit zeros in the data, but at the cost of estimating an extra parameter (related to the variance) and issues with convergence when optimizing the model (finding the maximum likelihood) may occur.

Survey sampling is conducted across a grid of stations, with one trawl haul conducted at each station, and estimates of area-level abundance (or biomass) are scaled up from the average numbers (or biomass) caught in each haul to the area of the survey stratum. Because a typical area swept during a trawl haul is 0.012 square nautical miles (sq. nmi.) and the total stratum area for PIBKC is 28,070 sq. nmi, a single tow covers only about 0.00004% of the stratum area and 86 tows (the typical number conducted before 2024) covers only 0.0037%. The smallest non-zero value for estimated abundance, which occurred in 2008, is 18,256 mature males or 0.65 mature males/sq. nmi. (the result of 1 mature male caught in 1 haul, out of 86 conducted). Given the nature of the survey sampling, it is thus highly unlikely that mature male biomass was actually 0 in either 2023 or 2024 and that these values were the result of the type of sampling variability expected at low, but non-zero, densities. As such, the question for modeling the time series becomes what might be reasonable values to substitute for the zeros.

The approach proposed here calculates a density, d, consistent with a selected probability p of non-detection (i.e., catching zero crab) in K independent hauls, based on the assumption that crab are randomly-distributed across the survey stratum and hauls represent independent samples. Under the assumption that crab are randomly-distributed across the stratum, the number of crab, N, caught in a haul swept with area A_s is a Poisson-distributed random variable with:

$$Pr(N = n|\lambda) = \frac{\lambda^n e^{-\lambda}}{n!}$$

where $\lambda = d \cdot A_s$. The probability of non-detection (no crab are caught) in K independent hauls is just:

$$Pr(N = 0|\text{K hauls}) = \prod_K e^{-\lambda} = e^{-K \cdot \lambda} \tag{1}$$

Setting $p = Pr(N = 0|\text{K hauls})$ and rearranging to solve for the density, d, one obtains:

$$d = -\frac{ln(p)}{K \cdot A_s} \tag{2}$$

The associated coefficient of variation (CV) can also be derived: for the sum of K independently-distributed Poisson variables, the expected mean is $K \cdot \lambda$, as is the variance, so the CV ($= variance^{1/2}/mean$) is

$$CV = \frac{(K \cdot \lambda)^{1/2}}{(K \cdot \lambda)} = (K \cdot \lambda)^{-1/2} = (K \cdot d \cdot A_s)^{-1/2} = [-ln(p)]^{-1/2}$$

Using the formulae above for mature males in 2024 with $p = 0.5$ (i.e., 50% chance of obtaining no crab while sampling 70 independent survey hauls), $d = 0.8252$ mature males/sq. nmi., total abundance = 23.16 thousand mature males, and $CV = 1.201$. Figure 16 provides a more comprehensive picture of the dependence of density as a function of the probability of non-detection.

The total abundance and biomass corresponding to densities yielding a non-detection probability of 0.5, given the number of survey hauls performed each year, are below the estimated total abundance/biomass (solid black line, Figures 17 and 18) in every year except 2008, when only 1 mature male was caught, and 2023 and 2024 (when, of course, no crabs were caught). Reducing the non-detection probability to 0.2 increases the number of years the estimated survey abundance exceeds the non-detection total abundance by 1 (2022), while it increases the corresponding value for biomass by 2 (2004, 2022). Increasing the non-detection probability to 0.8 results in no years other than 2023 and 2024 in which the estimated survey abundance or biomass is less than the non-detection abundance/biomass.

3.3.1 `rema` results

Five `rema` models were run to compare results from using its standard options for dealing with time series 0's to the proposed distribution-based approach (Table 4). The model that assumed a Tweedie error distribution and used the $p = 0.5$ non-detection criterion may not have converged (the max gradient was 0.0002735 while the variance parameter was estimated essentially at its arithmetic upper bound (estimate = 1.99998, upper bound = 2). In addition, it took seconds for this model to converge as compared with < 1s for the other models.

The results from the five models are compared in Figures 19-26. Results from both the lognormal model that treated the 0's as missing values and the Tweedie model that included the 0's but assigned a large CV to the values were notable in that the estimated values for 2023 and 2024 were the same as the value for 2022, but with increasing uncertainty bounds. Results from the model that assumed a lognormal error distribution and substituted a small constant for the observed 0's stand out from the others both for the lager uncertainty intervals across the time series as well the substantial departure of its estimates in 2022-2024 from the others (particularly noticeable on the log-10 scale, Figures 20 and 22). Of the five, the lognormal error model that used the non-detection criterion exhibited the most satisfactory results: it fit the last non-zero observation better than any of the other models and did not exhibit any really questionable features. MCMC diagnostics for this model appear to be reasonable (Figure 27). One-step ahead (OSA) residuals diagnostics (Figure 28) suggest that the model tends to overestimate the observed values. However, the diagnostics for this model are similar to those for the lognormal model that treats 0's as missing and much better than the lognormal model that substitutes a small constant for the 0's (OSAs are not yet available for Tweedie models).

3.3.2 Discussion

This section presented a novel approach to "fill in" zeros in a survey abundance or biomass time series to facilitate time series modeling, in particular with the `rema` R package (Sullivan 2022), based on substituting abundance/biomass values and CVs determined from a user-selected probability of non-detection in place of the zeros. The utility of this approach was explored using annual survey time series for Pribilof Islands blue king crab mature male abundance and biomass; zeros occurred in these time series in 2023 and 2024. `rema` provides three options for dealing with zeros, two for lognormal error distributions (treat 0's as NAs/ignore as missing; substitute a small value for zeros, and a large value for its CV) and one for a Tweedie error distribution (specify a large CV). In the first case, the predicted value for any zero-value observation is the same as the previous predicted value, while its uncertainty increases–the prediction treats the zero-value observation as if it did not occur. In the second case, a small value is provided, together with a large CV, but the values chosen are rather arbitrary and the resulting predictions are generally very sensitive to the values chosen. Using the Tweedie error distribution, the third case, is intuitively attractive because it allows for zero-value observations whereas the lognormal does not. However, it does require that the user specify a non-zero CV for any zeros and models using the Tweedie distribution have been found to take a very long time to converge, in some cases.

The approach taken here is to recognize that, for populations at low densities relative to the sampling effort, zero-value catches may be the rule rather than the exception–and to use sampling theory to guide the choice of substitute values for the observed non-detection and associated CV. In the simplest case, the sampling of individuals randomly-distributed across a seascape follows a Poisson distribution, which yields a particularly simple form for the probability of obtaining a series of zero-value catches as a function of the density of those individuals (Equation 1). I inverted this relationship to determine the density (Equation 2) that would yield a given probability of non-detection for a given number of survey hauls. For the Poisson distribution, this also allowed me to determine a corresponding CV. For the PIBKC time series, this approach yielded similar estimates for the smoothed time series under both lognormal and Tweedie error distributions, but the Tweedie model took ~50 times longer to run and had either not yet converged or converged to the upper bound for the variance scale parameter. Interestingly, the Tweedie model with the standard `rema` option (fitting the 0's with user-selected large CVs) converged successfully but the estimates for 2023 and 2024 were simply extensions of the 2022 estimates (albeit with increasing uncertainty)–similar to the results for the lognormal model that treated zeros as missing (NA's). The lognormal model that substituted a user-defined small value (and large CV) for the 0's yielded the least satisfactory results, as the estimates were unreasonably small.

Given the results presented here and the relative simplicity and interpretability of the distribution-based approach, I recommend it as the preferred substitution method for time series 0's when fitting `rema` models over the "0's as NAs" and "small constant" methods currently implemented as options for the lognormal error distribution in `rema`. Further I would not recommend using the Tweedie error distribution given its apparent convergence issues.

Sampling distributions other than the Poisson distribution discussed here could also be considered to determine reasonable non-detectable densities and associated CVs from which to derive suitable substitutes for survey index-based zero abundance or biomass estimates. However, for index time series derived from spatially-explicit sampling such as occurs in the NMFS EBS bottom trawl survey, spatiotemporal model-based indices such as those available from a `VAST` or `sdmTMB` (see next section) are probably the most desirable to use.

3.4 `sdmTMB` indices for PIBKC mature male biomass

As noted in the previous section, the NMFS EBS bottom trawl survey captured no mature male PIBKC in 2023 and 2024, introducing problematic zeros into the survey MMB time series that the `rema` model is used to smooth. It was suggested that making assumptions regarding the sampling distribution for mature males was a simple way to develop "reasonable" replacement values for the zeros when using `rema` to obtain the smoothed time series. Although probably better than filling in the zeros with an arbitrary "small" number (as suggested in the `rema` documentation) or simply dropping the zeros from the time series, the suggested method does not avoid requiring possibly arbitrary assumptions regarding the underlying sampling distribution and/or appropriate detection level. One significant drawback to this approach is that it makes the implicit assumption that all sampling locations are statistically interchangeable and independent. In fact, PIBKC mature males have undergone a range contraction over time, as well as a decline in overall abundance/biomass (e.g., Figure 29), indicating that the sampling locations are not interchangeable or independent.

Another, more satisfying, alternative for "filling in the zeros" would be to use a spatiotemporal model such as provided by the `VAST` (Thorson et al. 2015) or `sdmTMB` (Anderson et al. 2024) R packages. Either package provides the ability to statistically model and estimate trends and variability in stock biomass through space and time given spatially-explicit data such as the NMFS EBS bottom trawl survey provides. Here, I investigated the use of `sdmTMB`, a more user-friendly alternative to `VAST`, to estimate a stock biomass time series for PIBKC mature males in the context of survey sampling results that captured no crab in multiple years.

3.4.1 Methods

`sdmTMB` is an R package that fits spatiotemporal Generalized Linear Mixed Effects Models (GLMMs) using Template Model Builder (TMB), R-INLA, and Gaussian Markov random fields. One common application is to create species distribution models (SDMs) from species abundance data collected across space and through time, although its principal advantage here is that it can also estimate stock-level time series by integrating estimated spatially-explicit patterns of abundance or biomass across space. A simple way to think about an `sdmTMB` model is that it provides a way to interpolate survey observations across space and time, taking into account both population variability across space and time as well as variability inherent to the sampling process itself.

Here, four `sdmTMB` models (Table 5) were fit to the spatially-explicit annual survey CPUE data (biomass/unit area) for PIBKC mature males (Figure 29) using a spatial mesh defined by the sampling locations in Universal Transverse Mercator (UTM) coordinates and a cutoff of 5 km (30). Two of the four models, "m3" and "m3-ar" were two-stage "delta-gamma" mixture models that used a binomial family with a log-link to model presence/absence of mature males in a survey haul (the delta model) and a gamma family with a log-link to model non-zero CPUE given that mature males were caught in the given survey haul (the gamma model). Both models included the survey haul depth as a possible covariate, with the possible effects on presence/absence or non-zero CPUE estimated as a smoothly-varying function of ln(depth). Spatiotemporal residuals were modeled as a random walk process in "m3"; in "m3-ar", they were modeled as a first-order autoregressive process. Additionally, the spatial correlation was allowed to be anisotropic and Restricted Maximum Likelihood (REML) was used to fit both models. The remaining two models, "tw" and "tw-ar", were similar to their respective "m3" counterparts except that models used the Tweedie distribution (Tweedie 1984) with a log-link as the statistical basis for the fit rather than a delta-gamma model. The Tweedie distribution is a compound Poisson-gamma distribution that incorporates a single linear predictor (rather than two in the case of a delta-gamma model) but estimates a parameter that reflects the degree of mixing between the underlying Poisson and gamma distributions. (Thorson et al. 2021) recommend using the Tweedie distribution for spatiotemporal models by default, particularly when it is not possible to compare with scale from design-based estimators (although comparison is possible in this case).

3.4.2 Results

Standard model results are presented in Tables 6-9. AIC values for the four models are compared in Table 10 and residual diagnostics using simulated residuals and the DHARMa R package (Hartig 2022) are presented in Figures 31-34. The trends in mature male biomass estimated by the four models were all rather similar. They also generally agreed with the design-based estimates (Figures 35 and 36), with the design-based values falling within the confidence intervals of the model-based indices except at the start of the time series when the design-based indices suggest extreme variability across the first five years. None of the four models exhibited poor residual characteristics Of the four models, the "tw-ar" had the smallest (marginal) AIC and REML score, while both "ar" models had lower AIC and REML scores than their corresponding "non-ar" models. Although the use of AIC as a criterion for selection among models with random effects remains an area of active investigation for statisticians, its use here suggests that the "tw-ar" model should be preferred over the other models.

Compared with the `rema` models from the previous section (3.3), the "tw-ar" model-derived index exhibits greater interannual temporal variability than the `rema` models. This is not unexpected given that the `rema` models are fitting to spatially-aggregated data using the design-based estimates whereas the `sdmTMB` model is capturing both the spatial and temporal variability in the haul-level data. Interestingly, the confidence intervals for the "tw-ar" index are much smaller than those of the `rema` models at the start of the time series but are larger at the end, reflecting the spatial contraction of the stock over time. At the end of the time series, where the design-based estimates are "hard" zeros, the "tw-ar" estimates are substantially lower (proportionally, but non-zero) than the `rema` estimates based on more *ad hoc* assumptions. Although the `rema` estimates fall within the `sdmTMB` model's the confidence bounds, the reverse is not true.

3.4.3 Recommendations

The `sdmTMB` models provide a more statistically sound basis for "filling in the zeros" in the NMFS EBS bottom trawl survey data for mature male PIBKC biomass than do the `rema` models considered in the previous section (3.3). One rationale for using a `rema`-based model is that it generally takes less time to run a model, although convergence issues leading to long run times have been known to occur. With the spatial mesh used here (Figure 30), run times were on the order of an hour or so, which does not seem prohibitive. Finer meshes would be expected to require longer processing times, but time constraints on the author precluded identifying an "optimal" mesh that balances processing time with stability of estimates for this report. In addition, only simple model selection and diagnostic criteria were included in this report. If the CPT recommends, and the SSC requests, that an `sdmTMB` model be used determine the mature male biomass time series used in the 2025 PIBKC stock assessment, recommendations for suitable diagnostics would be appreciated.

4 Summary

I look forward to accessing the NMFS EBS bottom trawl survey data for crab using `crabpack` for the 2025 assessments. However, I recommend

- using the full-precision carapace length measurements with the current length-weight regressions to calculate biomass from NMFS EBS survey abundance and size data and
- dropping the "extra" corner stations not included in the standard 375 stations from the 1979 NMFS EBS survey

With regard to inclusion of historical data from the (now discontinued) corner stations in time series for future assessments, I recommend that these data continue to be included in estimates of abundance/biomass and size compositions. It is worthwhile to consider whether using a spatially-explicit, model-based approach like `sdmTMB` to derive indices of abundance/biomass that takes into account changes in spatial relationships in both the data and the sampling regimes, is better suited to minimize potential biases across the time series and better capture changes in uncertainty.

With regard to "filling in the zeros" in the PIBKC design-based time series for MMB, I look forward to discussions with the CPT and SSC regarding the potential tradeoffs between the relative simplicity of the `rema` approaches and more statistically-defensible approaches like spatially-explicit model-based approach like `sdmTMB`. My recommendation is that `sdmTMB` be adopted as the modeling platform in the 2025 stock assessment to provide this index.

5 Acknowledgments

I would like to acknowledge and thank Shannon Hennessey (AFSC) for developing `crabpack`, Cole Monnahan (AFSC) and Jane Sullivan (AFSC) for comments on the sampling-based approach to filling in time series zeros, Cole for help with interpreting `sdmTMB` results, and Sandra Lowe (AFSC) for providing an internal review of this document.

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Tables

List of Tables

Table 1. Percent difference, by year, in design-based NMFS survey abundance trends from the 2023 PIBKC assessment and the `crabpack` R package, by population category. NaN: indicates that no crab in the category were caught.

year	immature females	immature males	legal males	mature females	mature males
1975	*NaN*	0.0	0.0	0.0	0.0
1976	0.0	0.0	0.0	0.0	0.0
1977	0.0	0.0	0.0	0.0	0.0
1978	0.0	0.0	0.0	0.0	0.0
1979	54.9	54.9	38.7	54.9	41.2
1980	0.0	0.0	0.0	0.0	0.0
1981	0.0	0.0	0.0	0.0	0.0
1982	0.0	0.0	0.0	0.0	0.0
1983	0.0	0.0	0.0	0.0	0.0
1984	0.0	0.0	0.0	0.0	0.0
1985	0.0	0.0	0.0	0.0	0.0
1986	0.0	0.0	0.0	0.0	0.0
1987	0.0	0.0	0.0	0.0	0.0
1988	0.0	0.0	0.0	0.0	0.0
1989	0.0	0.0	0.0	0.0	0.0
1990	0.0	0.0	0.0	0.0	0.0
1991	0.0	0.0	0.0	0.0	0.0
1992	0.0	0.0	0.0	0.0	0.0
1993	0.0	0.0	0.0	0.0	0.0
1994	0.0	0.0	0.0	0.0	0.0
1995	0.0	0.0	0.0	0.0	0.0
1996	0.0	0.0	0.0	0.0	0.0
1997	0.0	0.0	0.0	0.0	0.0
1998	0.0	0.0	0.0	0.0	0.0
1999	*NaN*	0.0	0.0	0.0	0.0
2000	*NaN*	0.0	0.0	0.0	0.0
2001	0.0	0.0	0.0	0.0	0.0
2002	0.0	*NaN*	0.0	0.0	0.0

(continued)

year	immature females	immature males	legal males	mature females	mature males
2003	0.0	0.0	0.0	0.0	0.0
2004	0.0	0.0	0.0	0.0	0.0
2005	0.0	0.0	0.0	0.0	0.0
2006	0.0	0.0	0.0	0.0	0.0
2007	0.0	0.0	0.0	0.0	0.0
2008	0.0	0.0	0.0	0.0	0.0
2009	0.0	0.0	0.0	0.0	0.0
2010	0.0	0.0	0.0	0.0	0.0
2011	0.0	NaN	0.0	0.0	0.0
2012	0.0	0.0	0.0	0.0	0.0
2013	0.0	0.0	0.0	0.0	0.0
2014	0.0	0.0	0.0	0.0	0.0
2015	NaN	0.0	0.0	0.0	0.0
2016	0.0	0.0	0.0	0.0	0.0
2017	0.0	0.0	0.0	0.0	0.0
2018	0.0	0.0	0.0	0.0	0.0
2019	NaN	0.0	0.0	0.0	0.0
2021	NaN	0.0	0.0	0.0	0.0
2022	NaN	NaN	0.0	0.0	0.0
2023	NaN	0.0	NaN	0.0	NaN
2024	NaN	NaN	NaN	NaN	NaN

Table 2. Percent difference, by year, in design-based NMFS survey biomass trends from the 2023 PIBKC assessment and the `crabpack` R package, by population category. NaN: indicates that no crab in the category were caught.

year	immature females	immature males	legal males	mature females	mature males
1975	NaN	0.0	0.0	0.0	0.0
1976	0.0	0.0	0.0	0.0	0.0
1977	0.0	0.0	0.0	0.0	0.0
1978	0.0	0.0	0.0	0.0	0.0
1979	54.9	54.9	38.6	54.9	40.4
1980	0.0	0.0	0.0	0.0	0.0
1981	0.0	0.0	0.0	0.0	0.0
1982	0.0	0.0	0.0	0.0	0.0
1983	0.0	0.0	0.0	0.0	0.0
1984	0.0	0.0	0.0	0.0	0.0
1985	0.0	0.0	0.0	0.0	0.0
1986	0.0	0.0	0.0	0.0	0.0
1987	0.0	0.0	0.0	0.0	0.0
1988	0.0	0.0	0.0	0.0	0.0
1989	0.0	0.0	0.0	0.0	0.0
1990	0.0	0.0	0.0	0.0	0.0
1991	0.0	0.0	0.0	0.0	0.0
1992	0.0	0.0	0.0	0.0	0.0
1993	0.0	0.0	0.0	0.0	0.0
1994	0.0	0.0	0.0	0.0	0.0
1995	0.0	0.0	0.0	0.0	0.0
1996	0.0	0.0	0.0	0.0	0.0
1997	0.0	0.0	0.0	0.0	0.0
1998	0.0	0.0	0.0	0.0	0.0
1999	NaN	0.0	0.0	0.0	0.0
2000	NaN	0.0	0.0	0.0	0.0
2001	0.0	0.0	0.0	0.0	0.0
2002	0.0	NaN	0.0	0.0	0.0
2003	0.0	0.0	0.0	0.0	0.0
2004	0.0	0.0	0.0	0.0	0.0
2005	0.0	0.0	0.0	0.0	0.0
2006	0.0	0.0	0.0	0.0	0.0
2007	0.0	0.0	0.0	0.0	0.0
2008	0.0	0.0	0.0	0.0	0.0
2009	0.0	0.0	0.0	0.0	0.0
2010	0.0	0.0	0.0	0.0	0.0
2011	0.0	NaN	0.0	0.0	0.0
2012	0.0	0.0	0.0	0.0	0.0
2013	0.0	0.0	0.0	0.0	0.0
2014	0.0	0.0	0.0	0.0	0.0
2015	NaN	0.0	0.0	0.0	0.0
2016	1.3	1.6	0.8	0.8	0.7
2017	1.3	1.4	0.8	0.9	0.7
2018	1.4	1.7	0.9	0.5	0.9
2019	NaN	1.0	1.1	1.1	1.1
2021	NaN	2.2	1.0	0.8	1.0
2022	NaN	NaN	1.3	0.7	1.3
2023	NaN	0.5	NaN	1.1	NaN
2024	NaN	NaN	NaN	NaN	NaN

Table 3. Percent difference, by year, in design-based NMFS survey biomass trends by population category when the corner stations are included ("WCS") and when they are excluded ("NCS"). Note that corner stations were not sampled in 1975-1981 and 2024. Additionally, no survey was conducted in 2020. NaN: indicates that no crab in the category were caught.

year	immature females	immature males	mature females	mature males	sublegal males	legal males	all females	all males
1975	NaN	0.0	0.0	0.0	0.0	0.0	0.0	0.0
1976	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
1977	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
1978	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
1979	87.0	113.2	8.7	4.3	11.8	3.1	13.2	4.7
1980	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
1981	−0.3	27.6	−19.0	20.7	21.5	21.5	−17.7	21.5
1982	48.8	2.6	96.0	12.3	−1.7	14.2	92.7	10.9
1983	173.1	67.3	108.8	37.7	56.0	36.2	110.1	41.7
1984	−45.0	−2.2	−8.9	6.2	36.3	−1.7	−9.1	5.7
1985	45.8	−8.2	−30.2	−18.6	−11.5	−21.1	−29.7	−18.3
1986	51.9	200.0	174.8	16.7	200.0	14.6	173.9	16.9
1987	−47.0	−24.7	48.3	79.0	30.4	74.7	29.7	69.2
1988	105.8	57.0	11.0	72.5	57.0	72.5	29.8	69.8
1989	152.7	174.8	79.8	72.7	174.8	72.7	109.1	126.7
1990	172.3	−6.8	−2.5	−5.0	−10.1	5.6	40.6	−5.7
1991	58.7	17.4	21.9	−15.5	10.0	−22.1	25.9	−8.9
1992	179.3	23.1	−12.2	−1.9	17.5	−6.9	21.7	4.8
1993	54.1	74.6	−20.4	−1.3	31.0	−3.7	−8.5	9.9
1994	−12.0	−1.9	−29.4	−15.8	−10.5	−15.2	−29.2	−13.8
1995	−42.7	−45.5	−20.1	−29.4	−30.2	−31.6	−22.1	−31.2
1996	22.5	−10.0	−0.3	27.4	−0.7	31.4	0.3	21.3
1997	48.2	67.8	−20.2	40.7	50.1	41.3	−17.0	43.3
1998	54.5	52.6	5.7	58.5	29.2	70.3	10.7	57.3
1999	NaN	−36.2	−19.2	−24.5	−7.2	−30.8	−19.2	−25.6
2000	NaN	128.3	−27.2	11.4	19.1	14.4	−27.2	15.3
2001	200.0	−16.4	−32.3	−20.2	10.3	−23.9	−32.3	−20.0
2002	200.0	NaN	−34.5	−6.7	−48.5	−4.0	−34.5	−6.7
2003	173.1	−1.0	−32.2	14.4	88.6	10.0	−30.7	14.0
2004	119.2	87.7	−13.5	−48.5	−15.1	−48.5	3.9	−28.0
2005	−48.5	−43.1	2.0	38.9	−43.1	38.9	−29.9	−9.5
2006	−14.5	114.8	−20.0	31.5	131.4	14.3	−19.7	54.7
2007	88.2	75.9	−48.5	−23.2	15.8	−7.5	−31.9	5.7
2008	−44.5	−43.8	−27.8	−48.5	−43.8	−48.5	−33.7	−44.6
2009	−39.4	−35.4	−44.9	−32.2	−36.0	−24.5	−44.2	−33.3
2010	−13.7	−32.0	−31.0	−34.5	−41.5	−24.9	−27.6	−33.9
2011	−48.5	NaN	50.9	−38.2	−48.5	−36.4	39.4	−38.2
2012	0.0	−48.5	−19.2	−29.4	−48.5	−20.2	−18.6	−33.6
2013	−48.5	−48.5	80.9	90.1	103.3	66.9	64.5	76.2
2014	−48.5	11.5	−5.9	25.2	11.5	25.2	−13.9	21.4
2015	NaN	−11.7	−38.3	12.8	6.1	12.0	−38.3	9.7
2016	−20.0	32.2	1.0	14.5	88.0	−48.5	−1.8	20.5
2017	76.5	200.0	14.4	95.0	200.0	85.0	25.1	107.3
2018	200.0	−12.7	134.2	39.3	−12.7	39.3	140.2	16.2
2019	NaN	9.0	120.6	102.8	9.0	102.8	120.6	60.9
2021	NaN	−48.5	3.5	25.3	36.9	15.7	3.5	21.5
2022	NaN	NaN	−4.8	30.6	NaN	30.6	−4.8	30.6
2023	NaN	200.0	−48.5	NaN	200.0	NaN	−48.5	200.0
2024	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN

Table 4. `rema` models, with timing and maximum gradient as reported for model convergence.

model	error distribution	0's handling	run time (s)	max gradient
LN w/ 0's as NAs	lognormal	0's treated as missing (NA's)	1.5	6.3453e-14
LN w/ small constant	lognormal	small constant (0.01) substituted with large CV	1.4	2.3499e-13
Tweedie w/ CV=1.5	Tweedie	0 included, but with large CV	1.4	3.4102e-11
LN w/ p=0.5	lognormal	Poisson-based; non-detection p = 0.5	1.5	4.9982e-14
Tweedie w/ p=0.5	Tweedie	Poisson-based; non-detection p = 0.5	47.8	2.7346e-04

Table 5. Brief descriptions of the four sdmTMB models. REML is Restricted Maximum Likelihood.

model	distribution type	link(s)	residuals	covariates	anisotropic?	REML?
m3	delta-gamma	log	random walk	log(bottom depth)	true	true
m3-ar	delta-gamma	log	AR(1)	log(bottom depth)	true	true
tw	Tweedie	log	random walk	log(bottom depth)	true	true
tw-ar	Tweedie	log	AR(1)	log(bottom depth)	true	true

Table 6. Summary of results for model 'm3'.

```
###–Results for model m3—-

Spatiotemporal model fit by REML ['sdmTMB']
Formula: wgtCPUE ~ s(log_depth)
Mesh: mesh3 (anisotropic covariance)
Time column: year
Data: dfr
Family: delta_gamma(link1 = 'log', link2 = 'log', type = 'poisson-link')

Delta/hurdle model 1: ————————————————
Family: binomial(link = 'log')
coef.est coef.se
(Intercept) -3.13 1.91
slog_depth 0.07 1.51

Smooth terms:
Std. Dev.
sds(log_depth) 4.88

Matérn anisotropic range (spatial): 192.8 to 322.9 at 156 deg.
Spatial SD: 2.17
Spatiotemporal RW SD: 0.72

Delta/hurdle model 2: ————————————————
Family: Gamma(link = 'log')
coef.est coef.se
(Intercept) -0.21 1.78
slog_depth -0.20 0.14

Smooth terms:
Std. Dev.
sds(log_depth) 0

Dispersion parameter: 2.09
Matérn anisotropic range (spatial): 485.6 to 813.2 at 156 deg.
Spatial SD: 0.88
Spatiotemporal RW SD: 0.09

REML criterion at convergence: 1114.711
```

Table 7. Summary of results for model 'm3-ar'.

```
###–Results for model m3-ar—-

Spatiotemporal model fit by REML ['sdmTMB']
Formula: wgtCPUE ~ s(log_depth)
Mesh: mesh3 (anisotropic covariance)
Time column: year
Data: dfr
Family: delta_gamma(link1 = 'log', link2 = 'log', type = 'poisson-link')

Delta/hurdle model 1: ————————————
Family: binomial(link = 'log')
coef.est coef.se
(Intercept) -5.28 1.19
slog_depth -0.06 1.58

Smooth terms:
Std. Dev.
sds(log_depth) 5.25

Spatiotemporal AR1 correlation (rho): 0.86
Matérn anisotropic range (spatial): 149.4 to 231.3 at 152 deg.
Spatial SD: 1.61
Spatiotemporal marginal AR1 SD: 1.84

Delta/hurdle model 2: ————————————
Family: Gamma(link = 'log')
coef.est coef.se
(Intercept) -1.07 4.40
slog_depth -0.12 0.13

Smooth terms:
Std. Dev.
sds(log_depth) 0

Dispersion parameter: 2.37
Spatiotemporal AR1 correlation (rho): 1.00
Matérn anisotropic range (spatial): 841.4 to 1302.7 at 152 deg.
Spatial SD: 0.00
Spatiotemporal marginal AR1 SD: 1.34

REML criterion at convergence: 1103.904
```

Table 8. Summary of results for model 'tw'.

```
###–Results for model tw—-

Spatiotemporal model fit by REML ['sdmTMB']
Formula: wgtCPUE ~ s(log_depth)
Mesh: mesh3 (anisotropic covariance)
Time column: year
Data: dfr
Family: tweedie(link = 'log')

coef.est coef.se
(Intercept) -4.43 1.64
slog_depth 0.01 1.69

Smooth terms:
Std. Dev.
sds(log_depth) 5.8

Dispersion parameter: 0.47
Tweedie p: 1.17
Matérn anisotropic range (spatial): 148.5 to 195.3 at 136 deg.
Spatial SD: 2.43
Spatiotemporal RW SD: 1.14
REML criterion at convergence: 1123.669
```

Table 9. Summary of results for model 'tw-ar'.

```
###–Results for model tw-ar—-
Spatiotemporal model fit by REML ['sdmTMB']
Formula: wgtCPUE ~ s(log_depth)
Mesh: mesh3 (anisotropic covariance)
Time column: year
Data: dfr
Family: tweedie(link = 'log')

coef.est coef.se
(Intercept) -6.87 0.90
slog_depth -0.08 1.82

Smooth terms:
Std. Dev.
sds(log_depth) 6.31

Dispersion parameter: 0.37
Tweedie p: 1.12
Spatiotemporal AR1 correlation (rho): 0.76
Matérn anisotropic range (spatial): 115.2 to 168.4 at 139 deg.
Spatial SD: 1.54
Spatiotemporal marginal AR1 SD: 2.16
REML criterion at convergence: 1087.056
```

Table 10. AIC scores for the four sdmTMB models.

model	AIC
m3	2259.421
m3-ar	2241.808
tw	2267.339
tw-ar	2196.112

Figures

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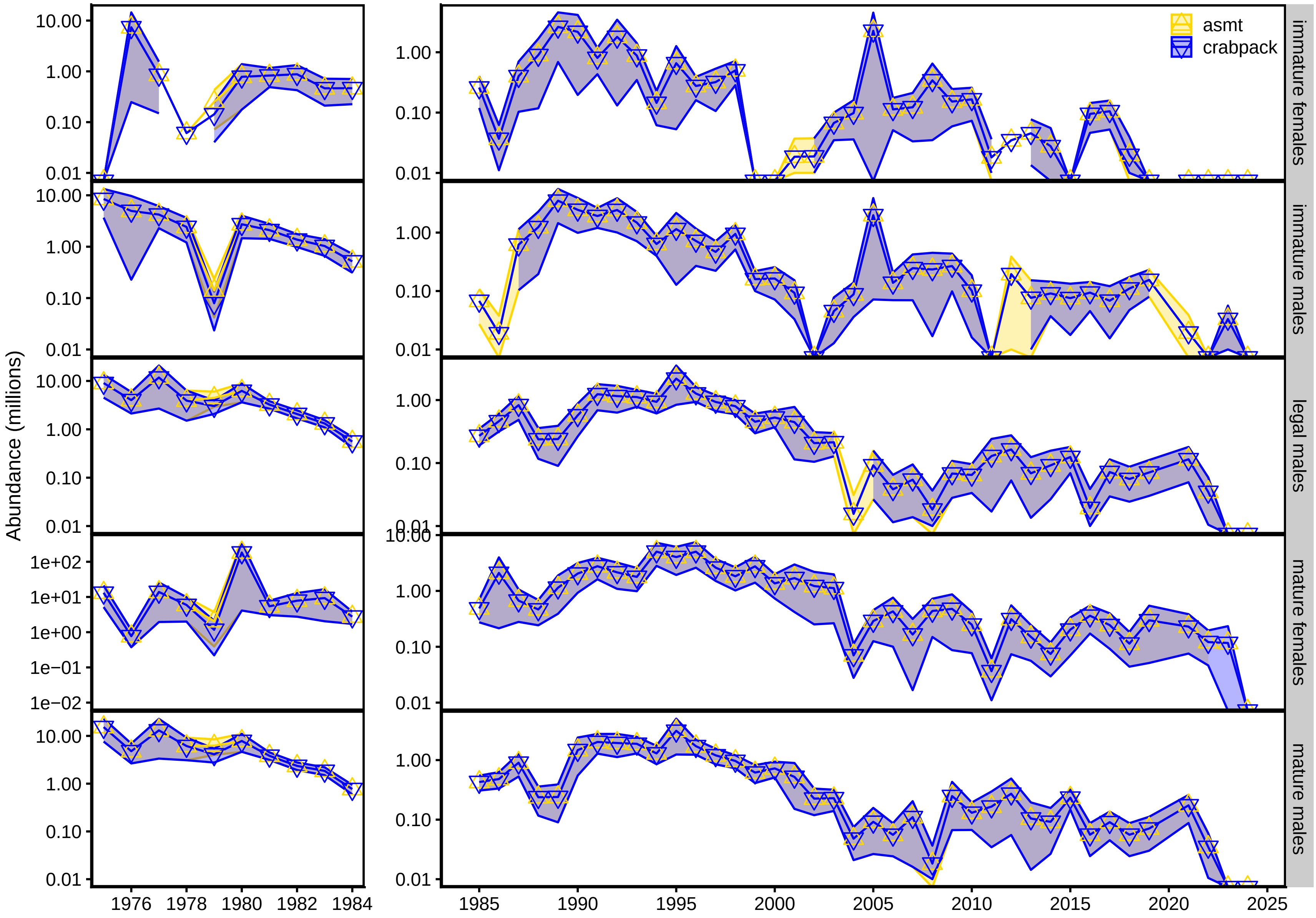

Figure 1. Comparison of annual estimates of design-based area-swept abundance from the NMFS EBS bottom trawl survey by the 2023 PIBKC assessment (*asmt*) and the `crabpack` R package (*crabpack*), by population category.

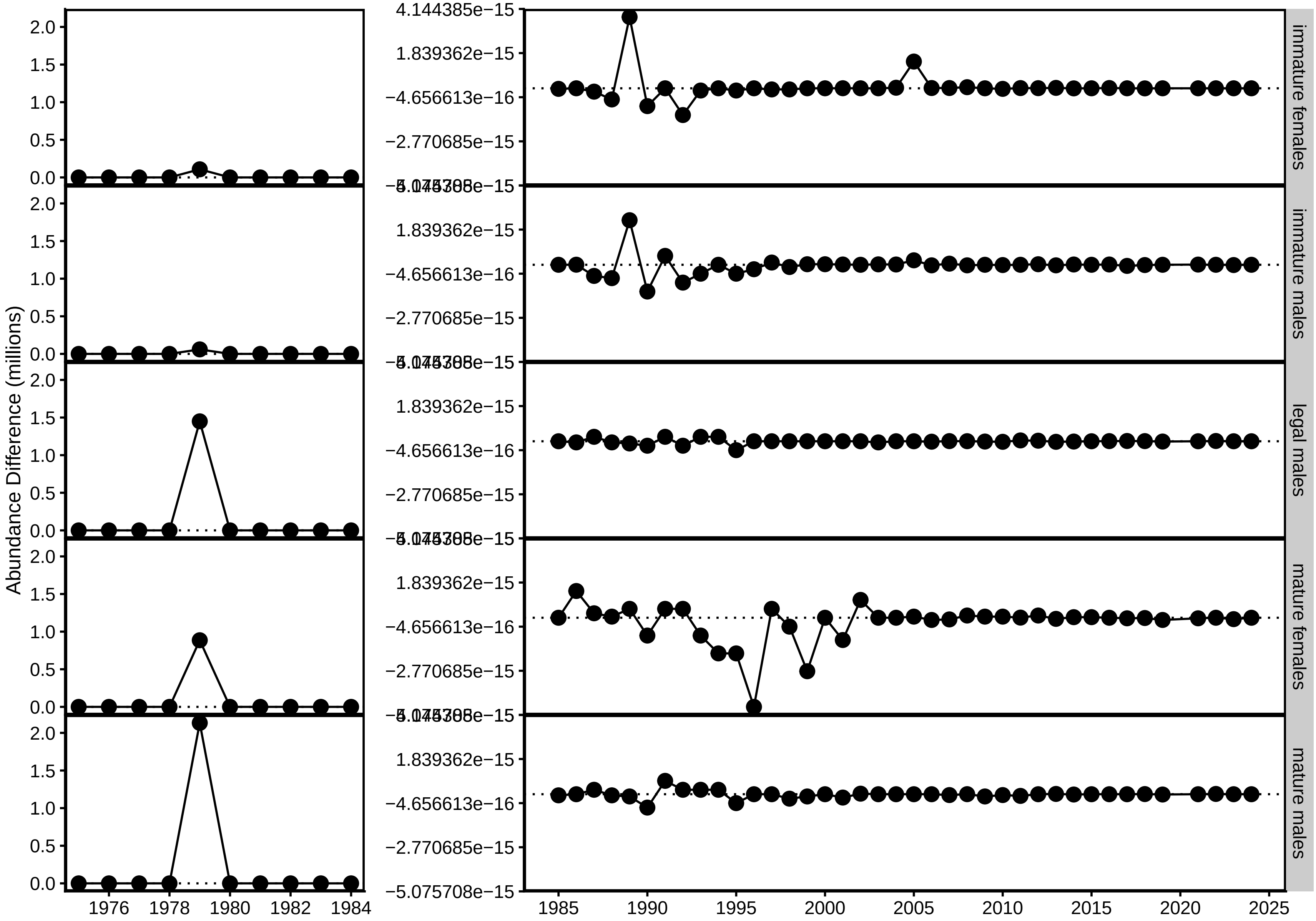

Figure 2. Differences in annual estimates of design-based area-swept abundance from the NMFS EBS bottom trawl survey by the 2023 PIBKC assessment and the `crabpack` R package, by population category.

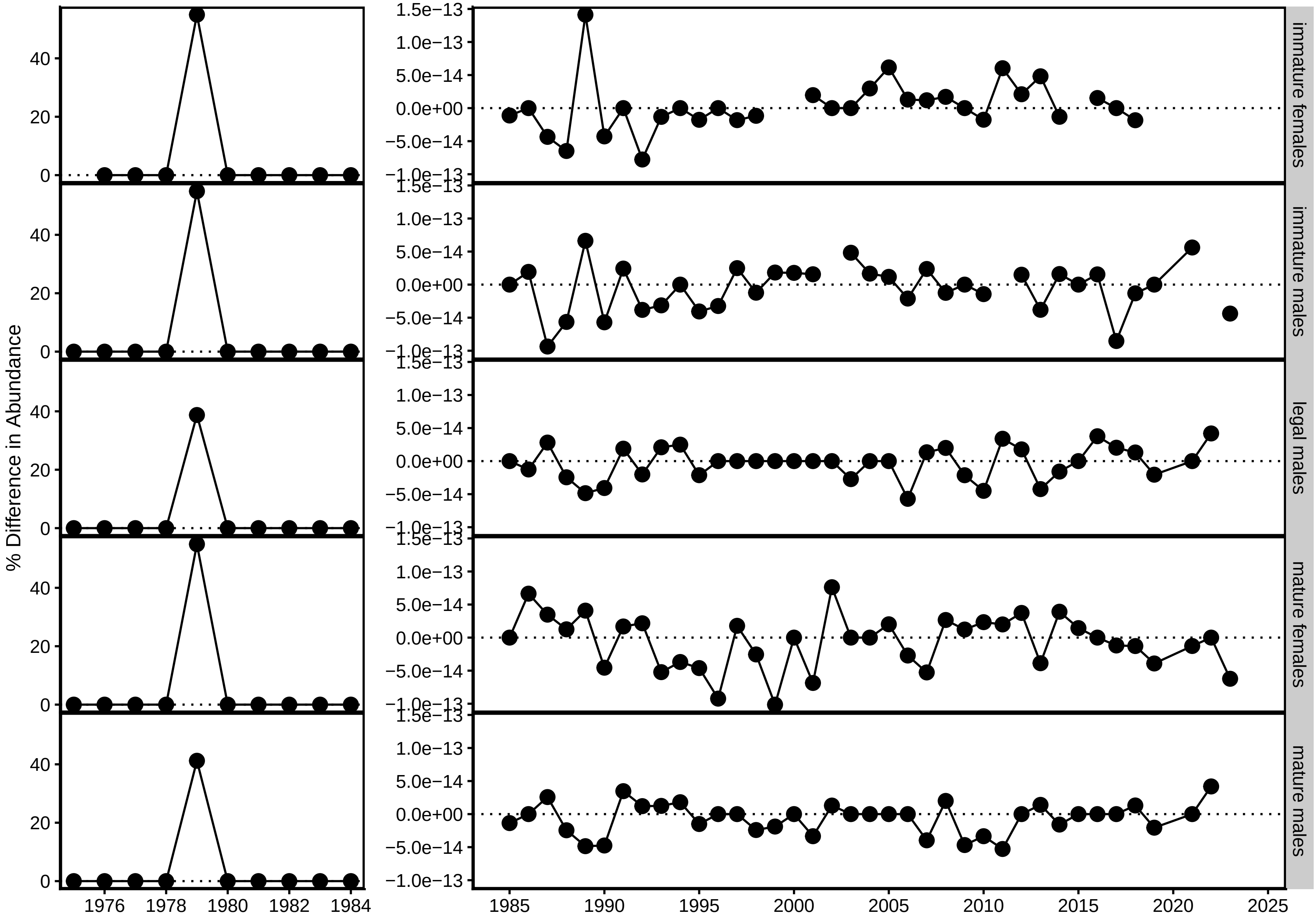

Figure 3. Percent differences in annual estimates of design-based area-swept abundance from the NMFS EBS bottom trawl survey by the 2023 PIBKC assessment and the `crabpack` R package, by population category.

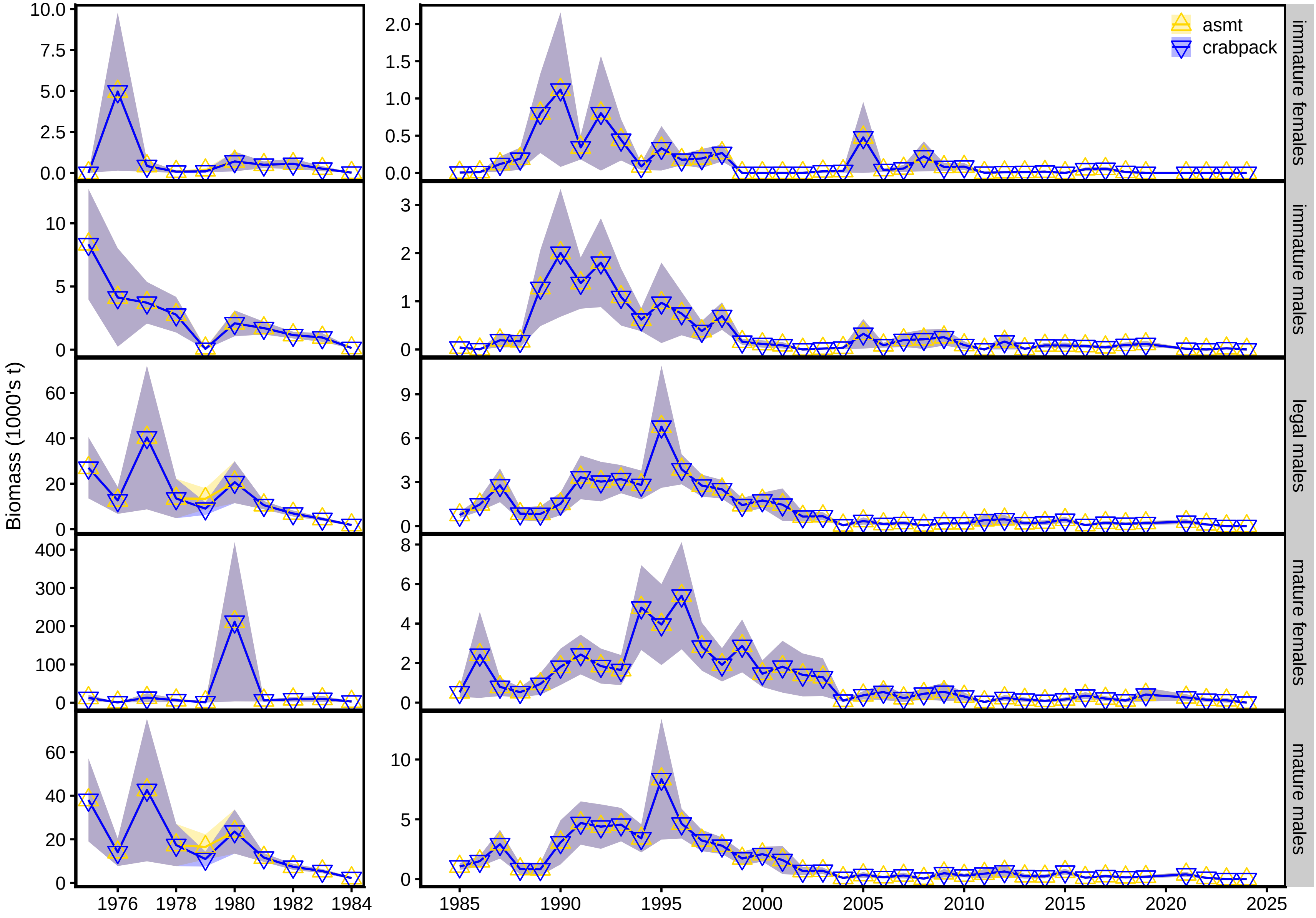

Figure 4. Comparison of annual estimates of design-based area-swept biomass from the NMFS EBS bottom trawl survey by the 2023 PIBKC assessment (*asmt*) and the `crabpack` R package (*crabpack*), by population category.

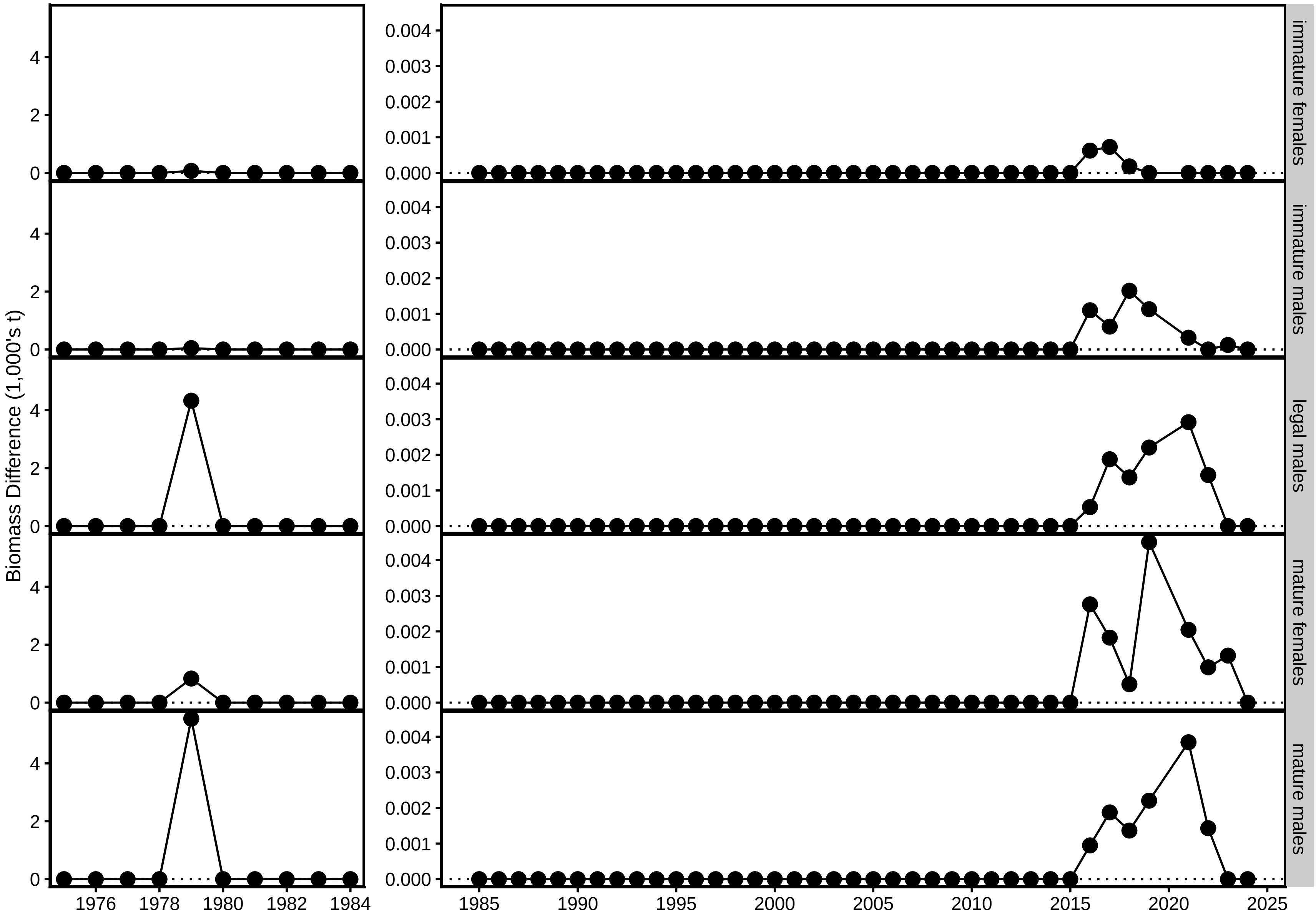

Figure 5. Differences in annual estimates of design-based area-swept biomass from the NMFS EBS bottom trawl survey by the 2023 PIBKC assessment and the `crabpack` R package, by population category.

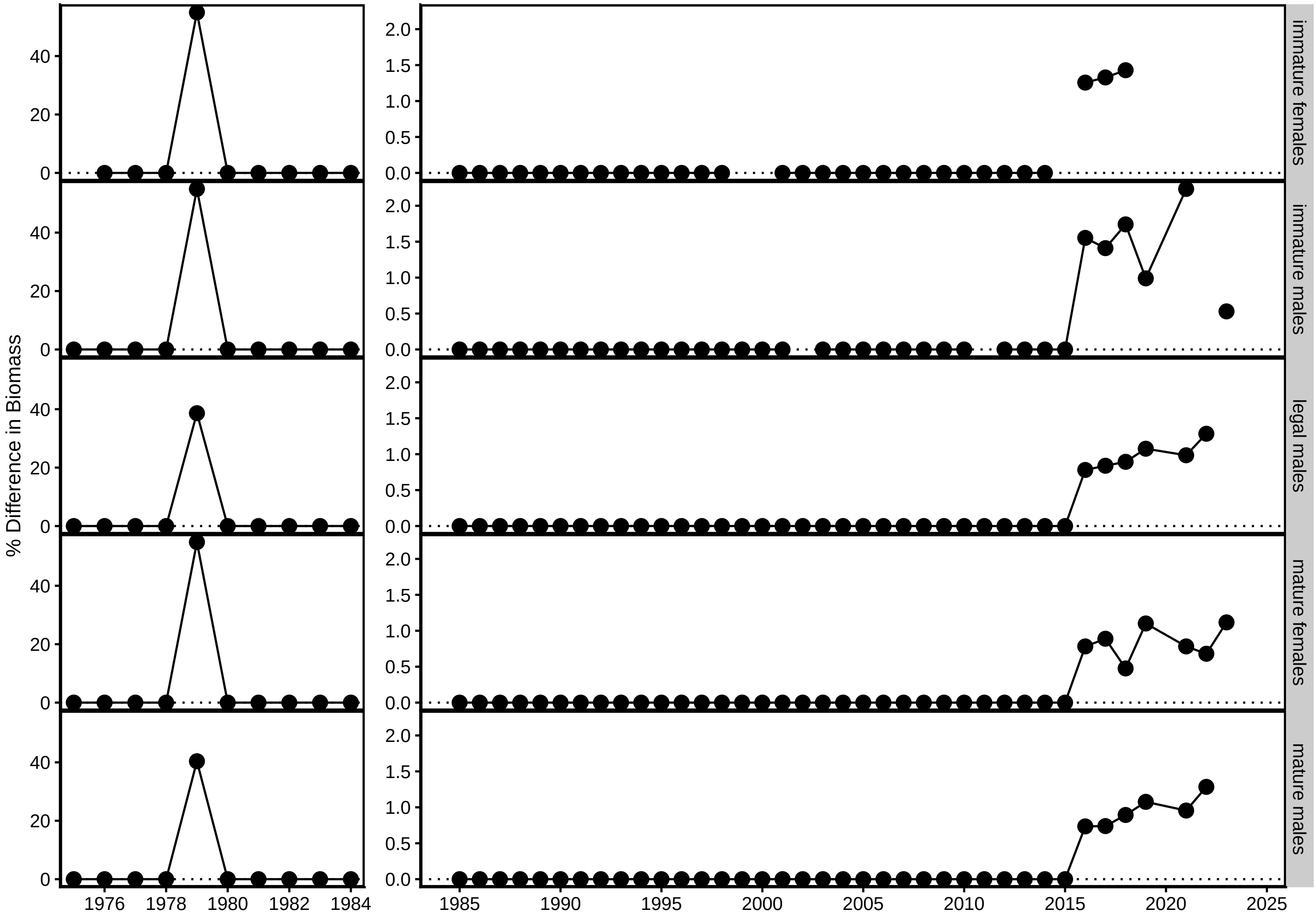

Figure 6. Percent differences in annual estimates of design-based area-swept biomass from the NMFS EBS bottom trawl survey by the 2023 PIBKC assessment and the `crabpack` R package, by population category.

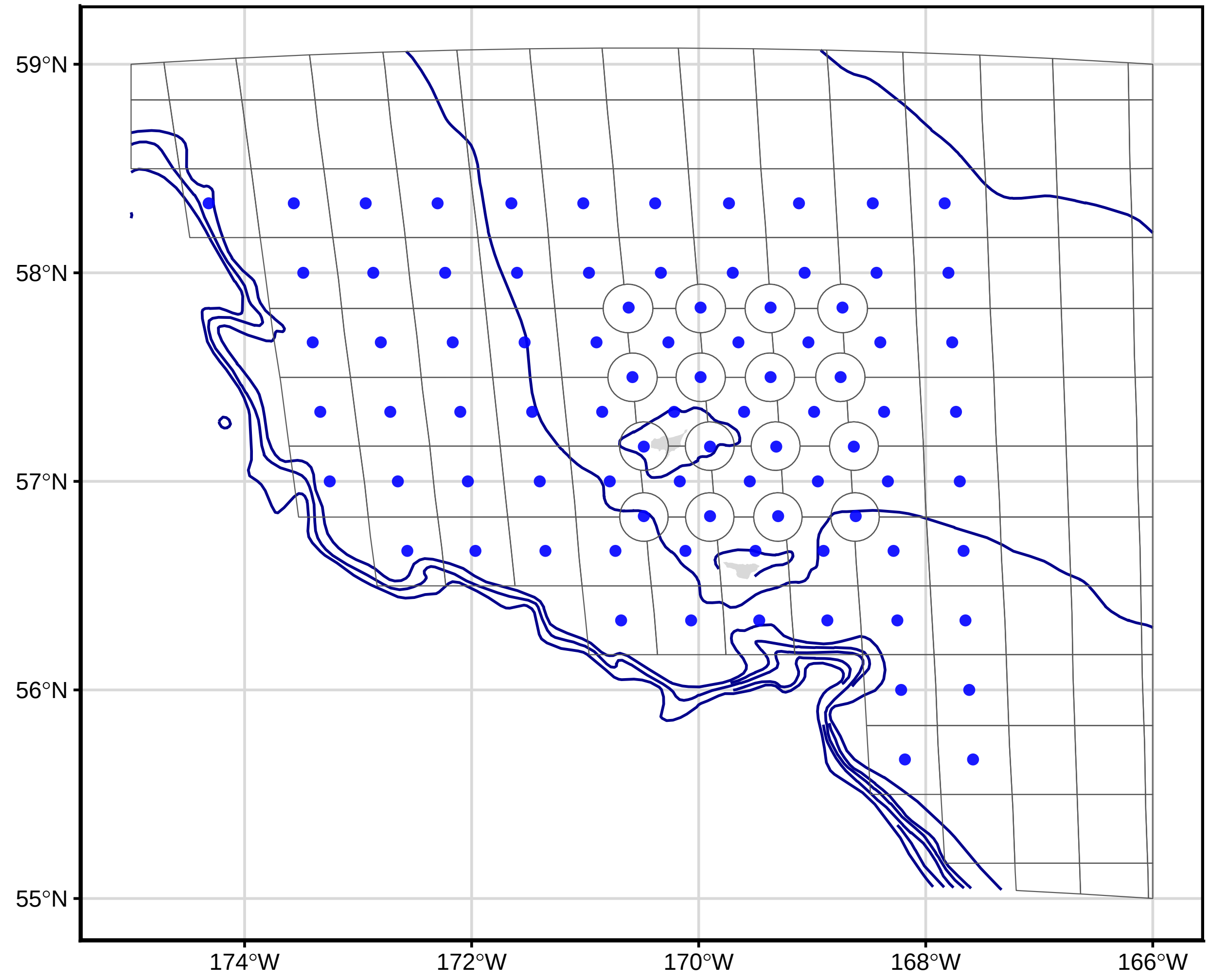

Figure 7. The NMFS EBS Shelf Survey grid cells (thin black lines) and nominal sampling stations (large dots) in the Pribilof District. The "corner" stations in the grid circles (16 stations) were dropped in 2024 and will not be revisited during the survey for the foreseeable future.

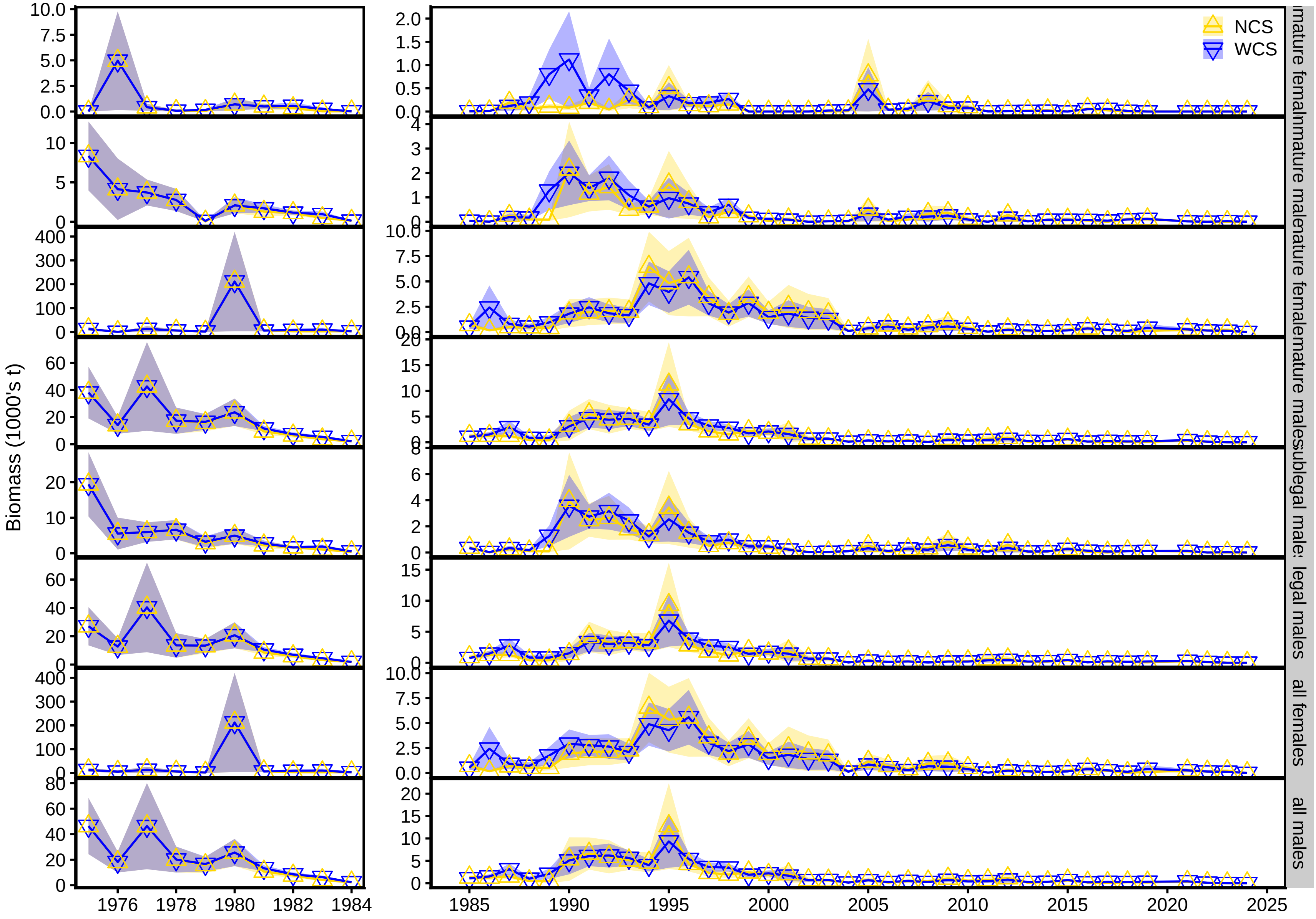

Figure 8. Comparison of annual estimates of design-based area-swept biomass by population category when the corner stations are included (“WCS”) and when they are excluded (“NCS”). Note that corner stations were not sampled in 1975-1981 and 2024. Additionally, no survey was conducted in 2020.

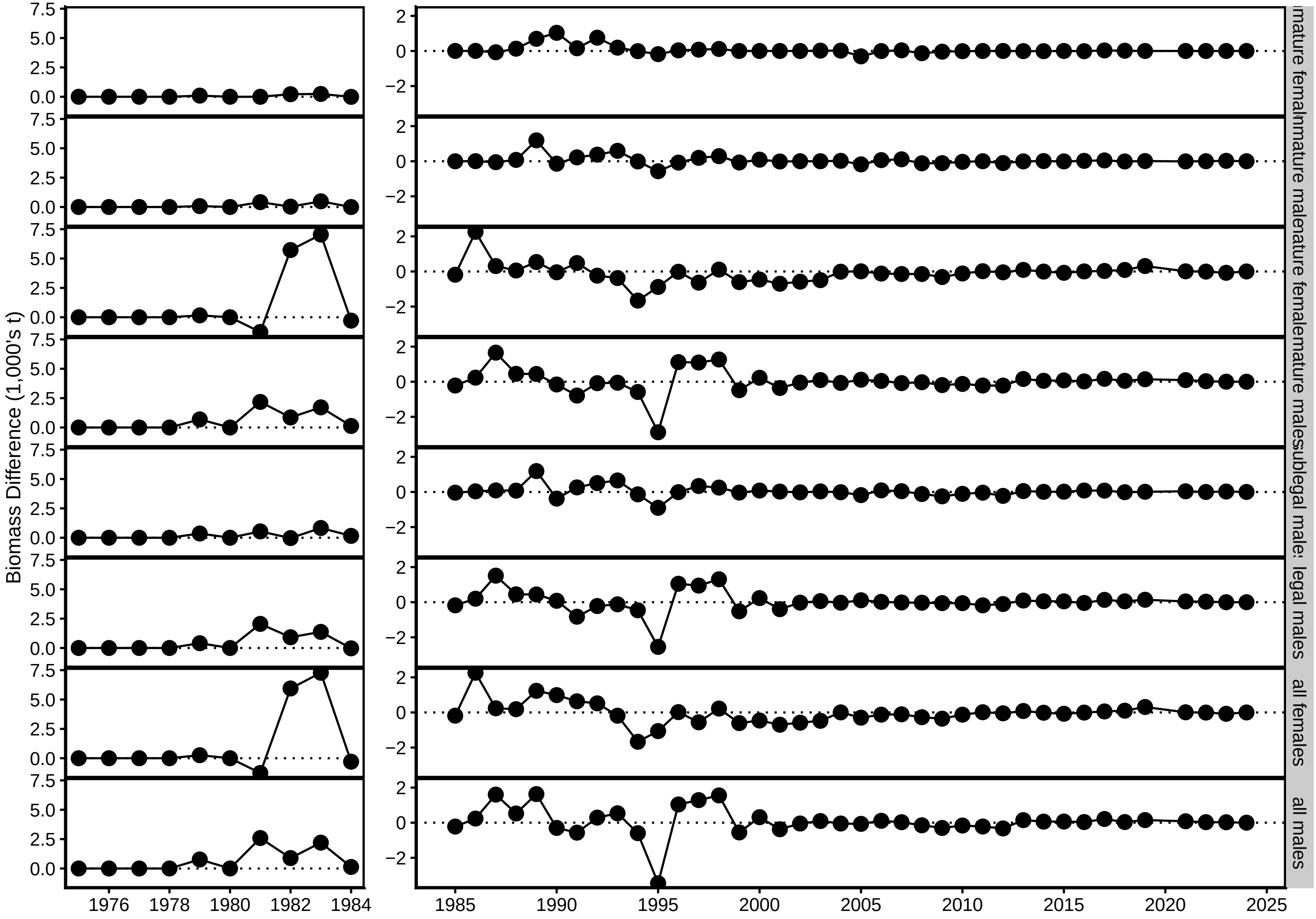

Figure 9. Differences in annual estimates of design-based area-swept biomass by population category when the corner stations are included ("WCS") and when they are excluded ("NCS"). Note that corner stations were not sampled in 1975-1981 and 2024. Additionally, no survey was conducted in 2020.

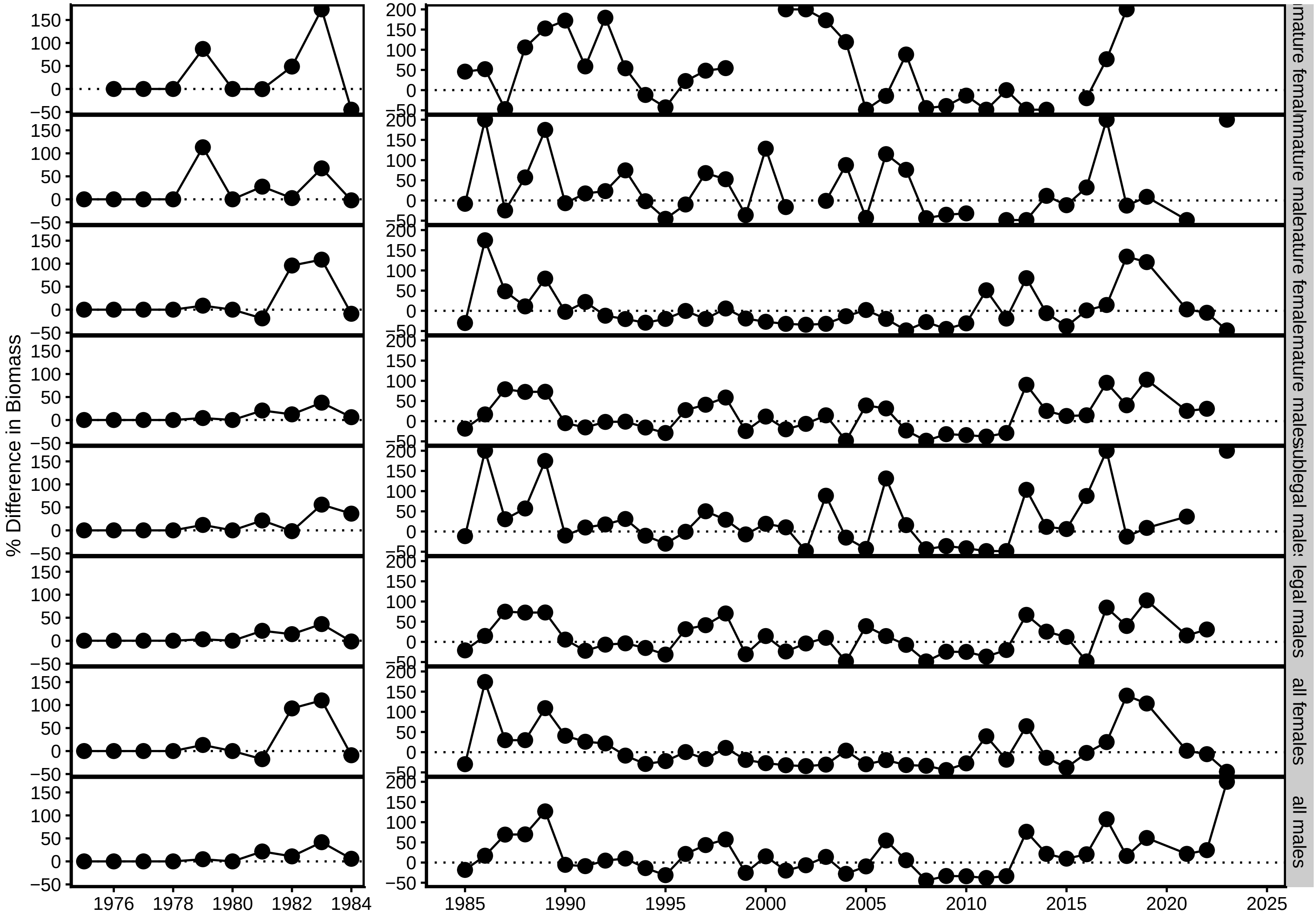

Figure 10. Percent differences in annual estimates of design-based area-swept biomass by population category when the corner stations are included (“WCS”) and when they are excluded (“NCS”).Note that corner stations were not sampled in 1975-1981 and 2024. Additionally, no survey was conducted in 2020.

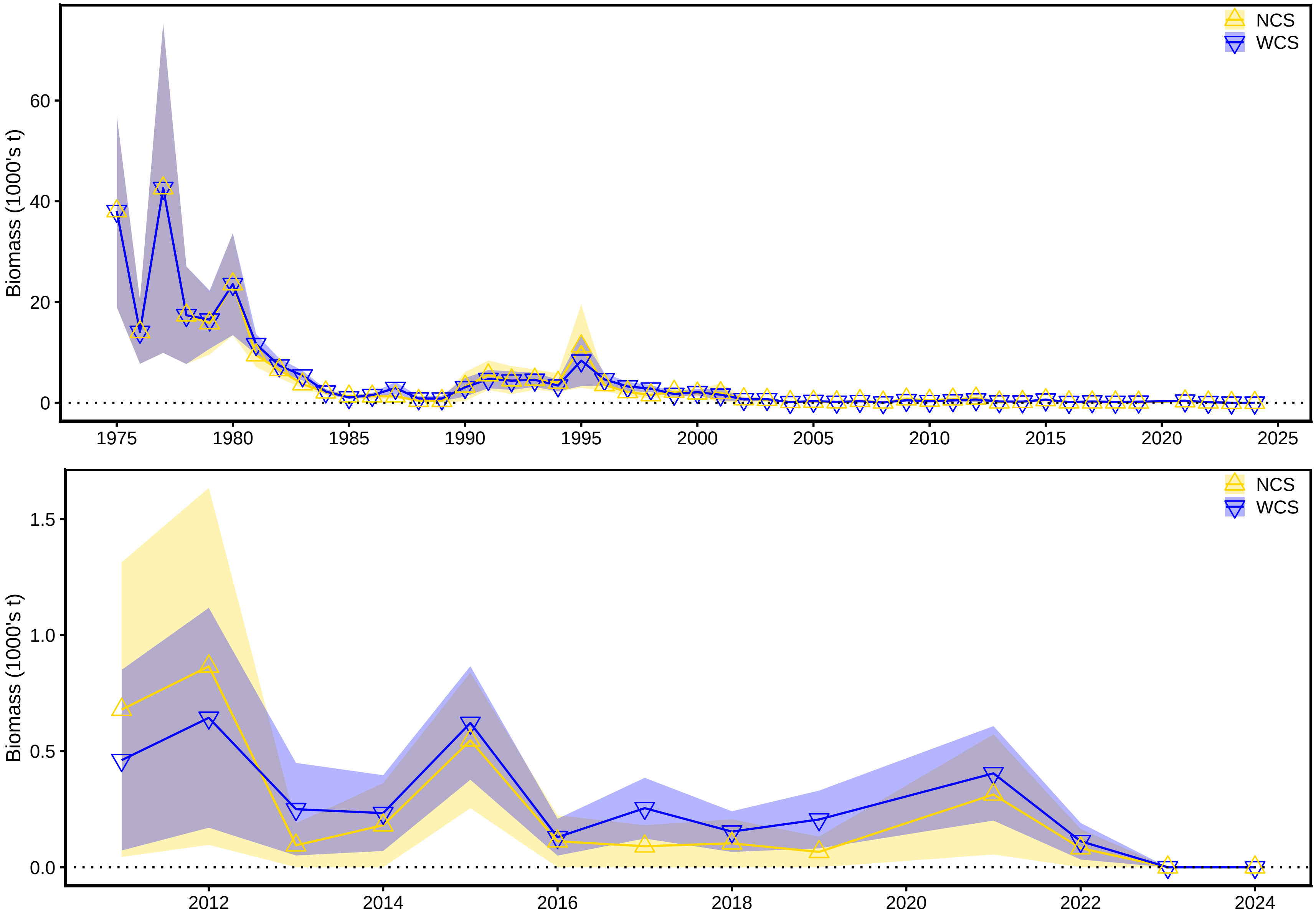

Figure 11. Comparison of time series of PIBKC MMB obtained by including corner stations (“WCS”) and excluding them (“NCS”). Note that corner stations were not sampled in 1975-1981 and 2024. Additionally, no survey was conducted in 2020.

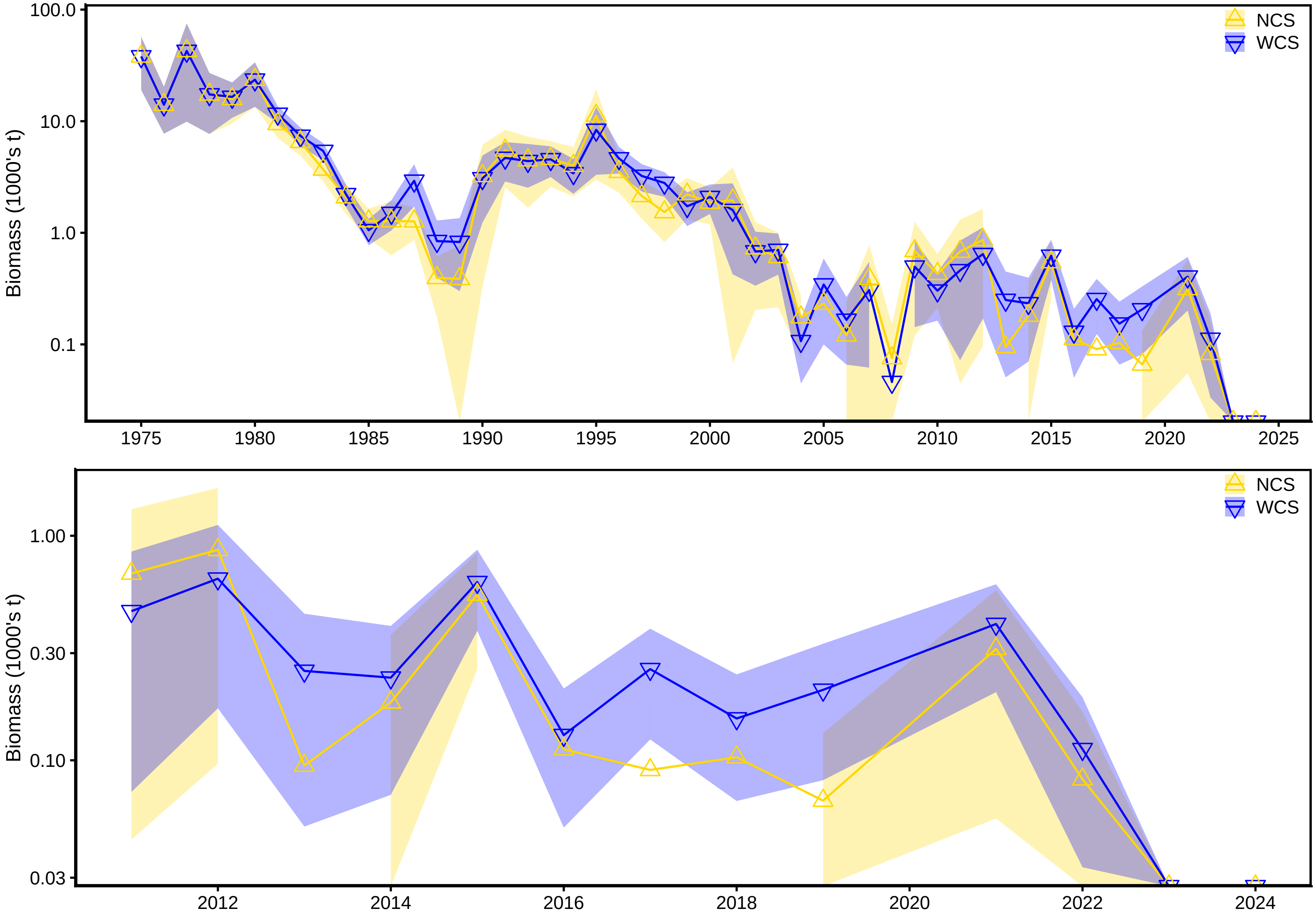

Figure 12. Comparison of time series of PIBKC MMB obtained by including corner stations ("WCS") and excluding them ("NCS"). Note that corner stations were not sampled in 1975-1981 and 2024. Additionally, no survey was conducted in 2020.

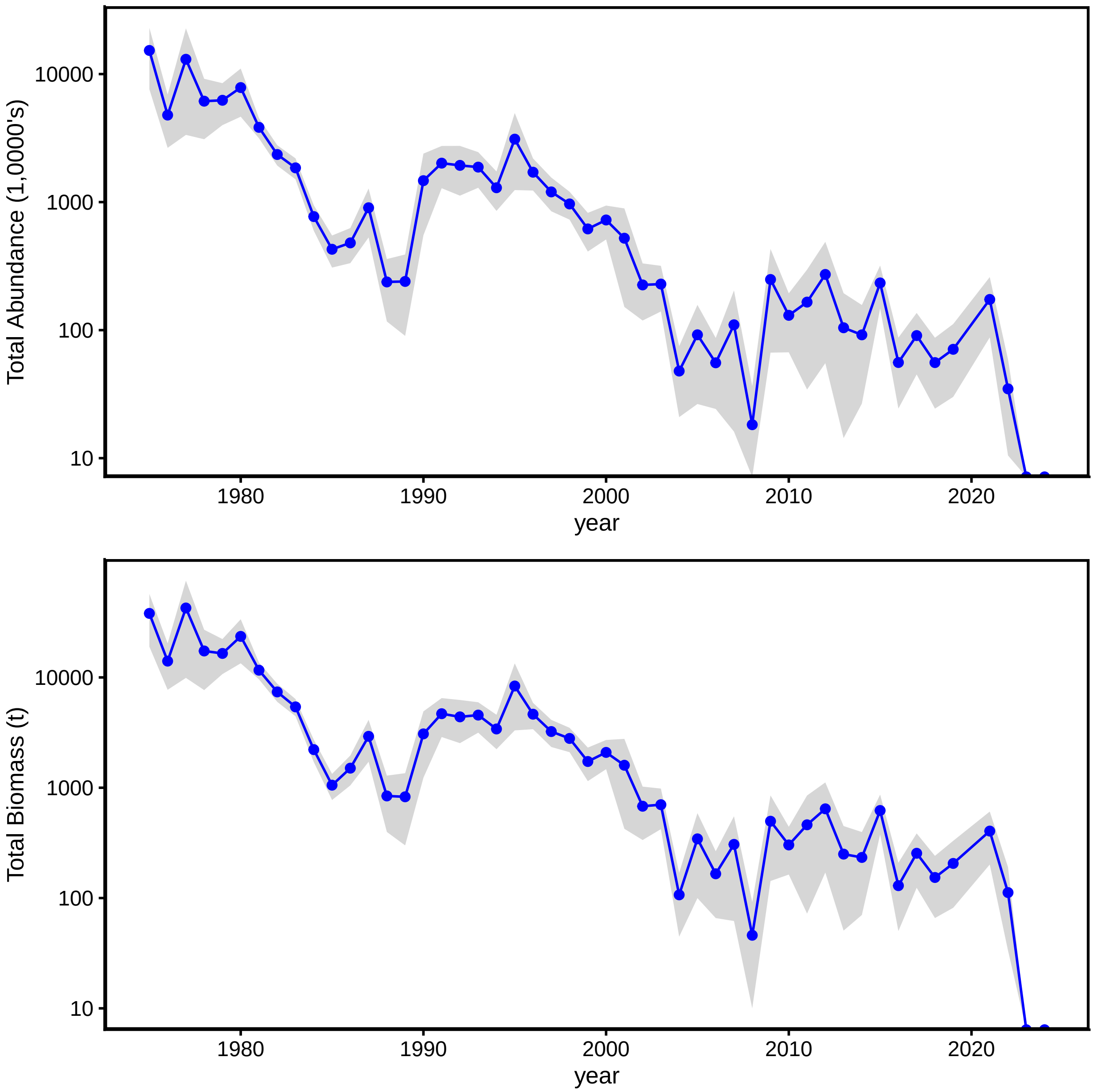

Figure 13. Estimated total survey abundance (upper plot) and biomass (lower plot) for PIBKC mature males. The ribbons indicate +/- 1 standard error.

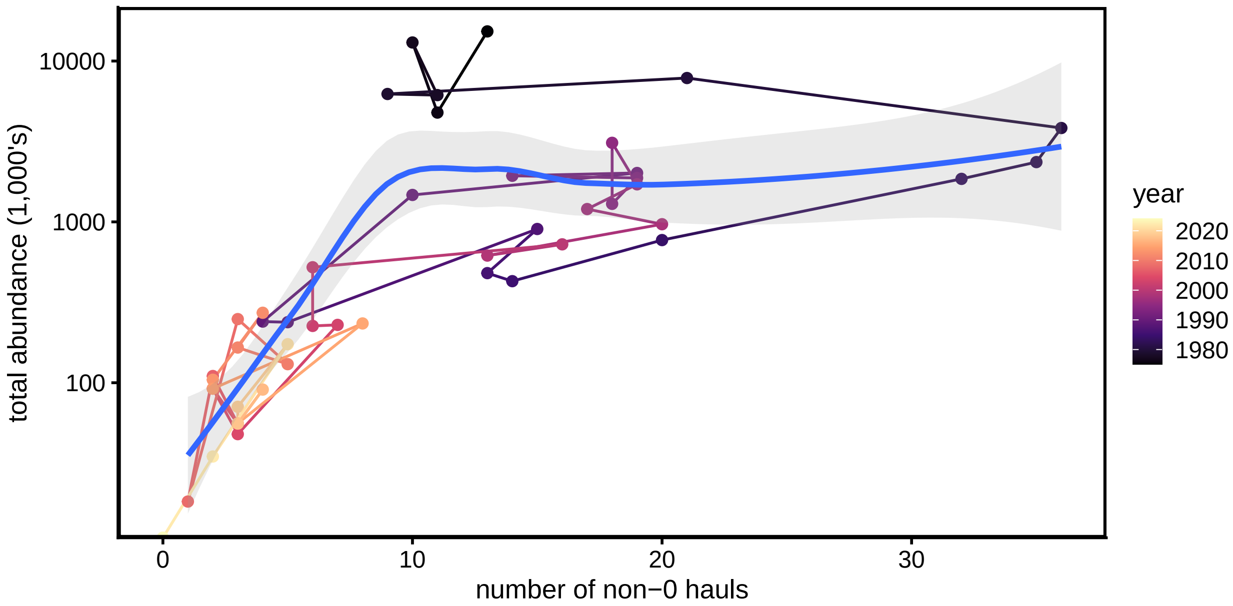

Figure 14. The number of NMFS EBS survey hauls with non-zero catch of mature males, plotted as a function of estimated total abundance.

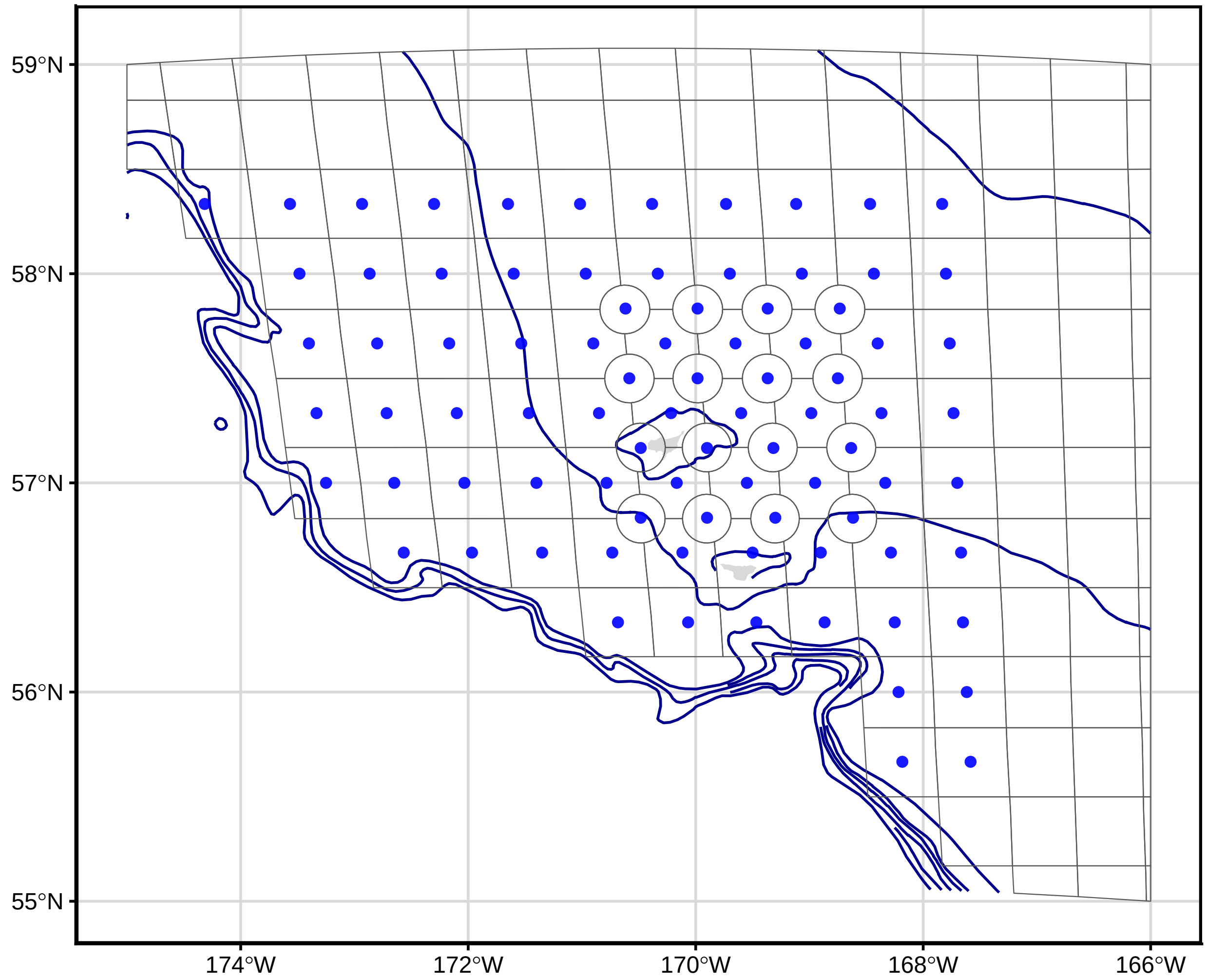

Figure 15. The NMFS EBS Shelf Survey grid cells (thin black lines) and nominal sampling stations (large dots) in the Pribilof District. The "high density" stations in the grid circles (16 stations) were dropped in 2024.

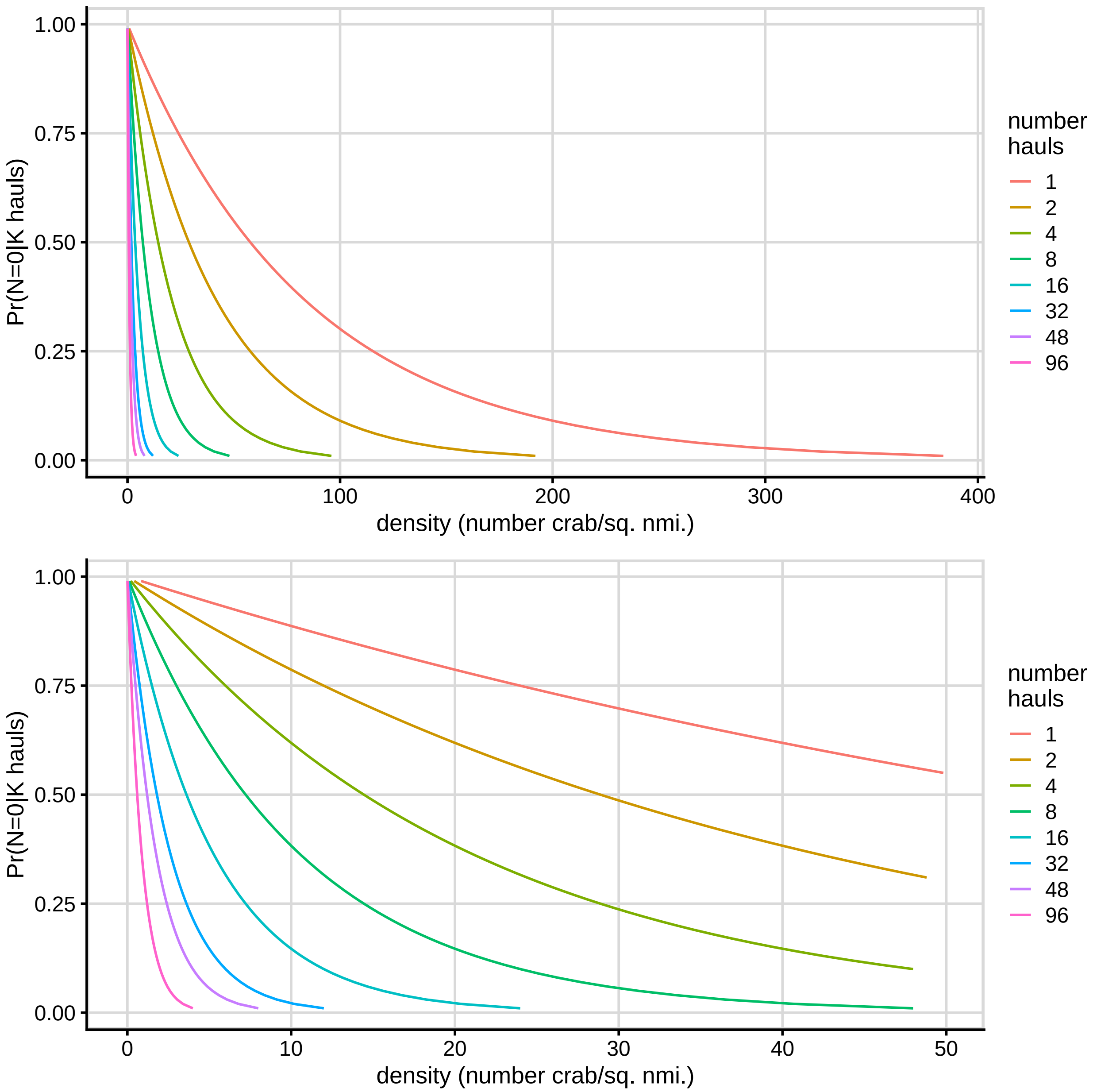

Figure 16. The probability of non-detection (zero catch), by crab density (x-axis) and number of hauls (color scale). Densities (x axis) were calculated as a function of the probability of non-detection (y axis) and the number of hauls, but the plot has been transposed. The lower plot is limited to density < 50 crab/sq. nmi to better show details at low densities.

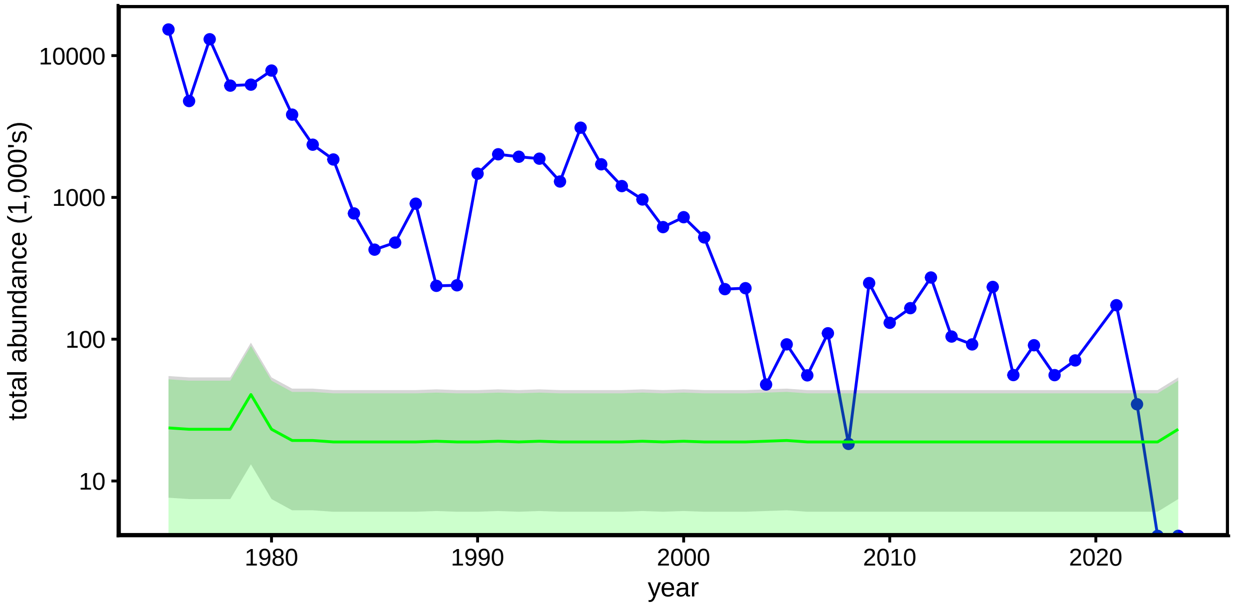

Figure 17. The estimated time series of mature male total abundance from the NMFS survey (blue line and points), with total abundance corresponding to non-detection probabilities of 0.5 (green line) and 0.8 and 0.2 (lower and upper bounds of grey shading), based on the number of hauls conducted for PIBKC each year. The green shading indicates the +/- 1 CV interval for the 0.5 non-detection values.

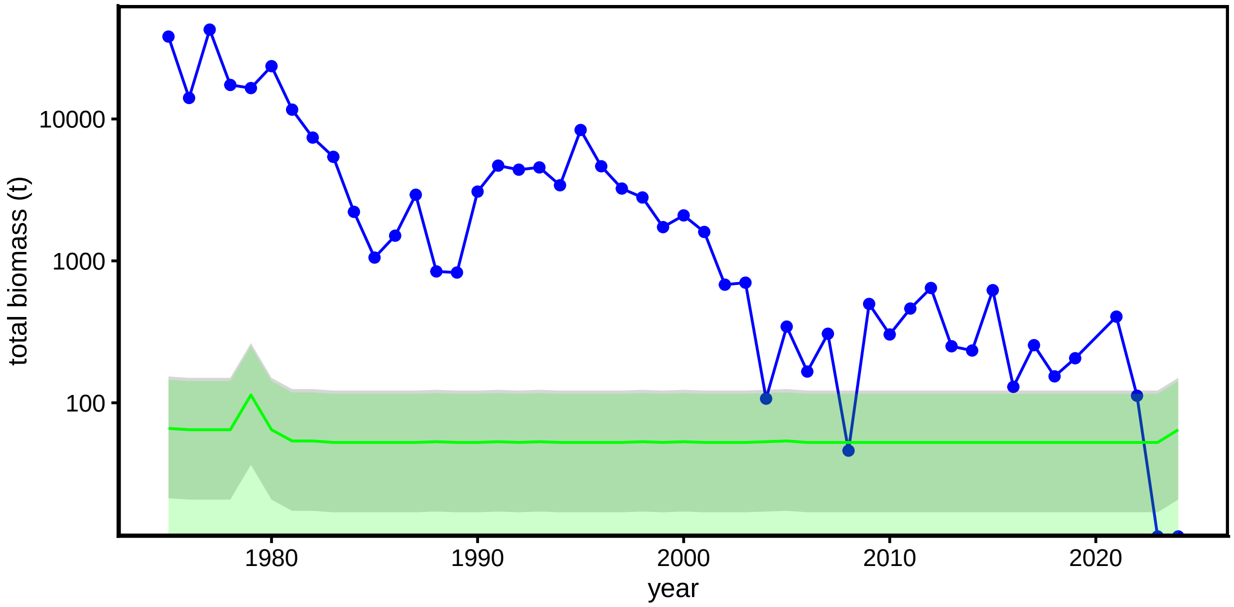

Figure 18. The estimated time series of mature male total biomass from the NMFS survey (blue line and points), with total biomass corresponding to probabilities of zero catch of 0.5 (black line) and 0.8 and 0.2 (lower and upper bounds of grey shading), based on the number of hauls conducted for PIBKC each year.The green shading indicates the +/- 1 CV interval for the 0.5 non-detection values.

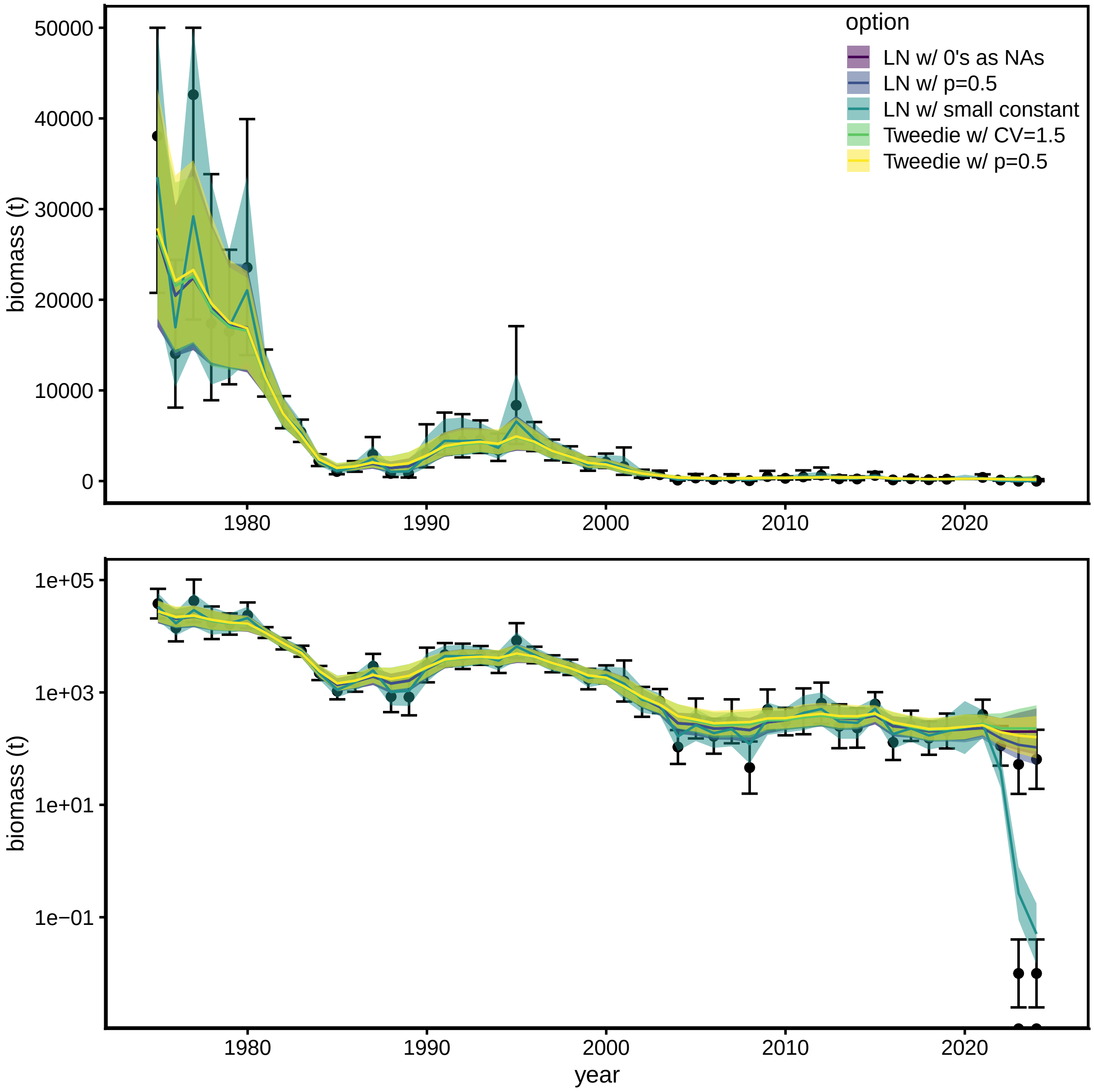

Figure 19. Comparison of the `rema` results from fitting the PIBKC survey biomass time series for mature males using the five error distributions and 0-substitution methods discussed in the text. Full time series results. Upper figure: arithmetic scale; lower figure: log-10 scale.

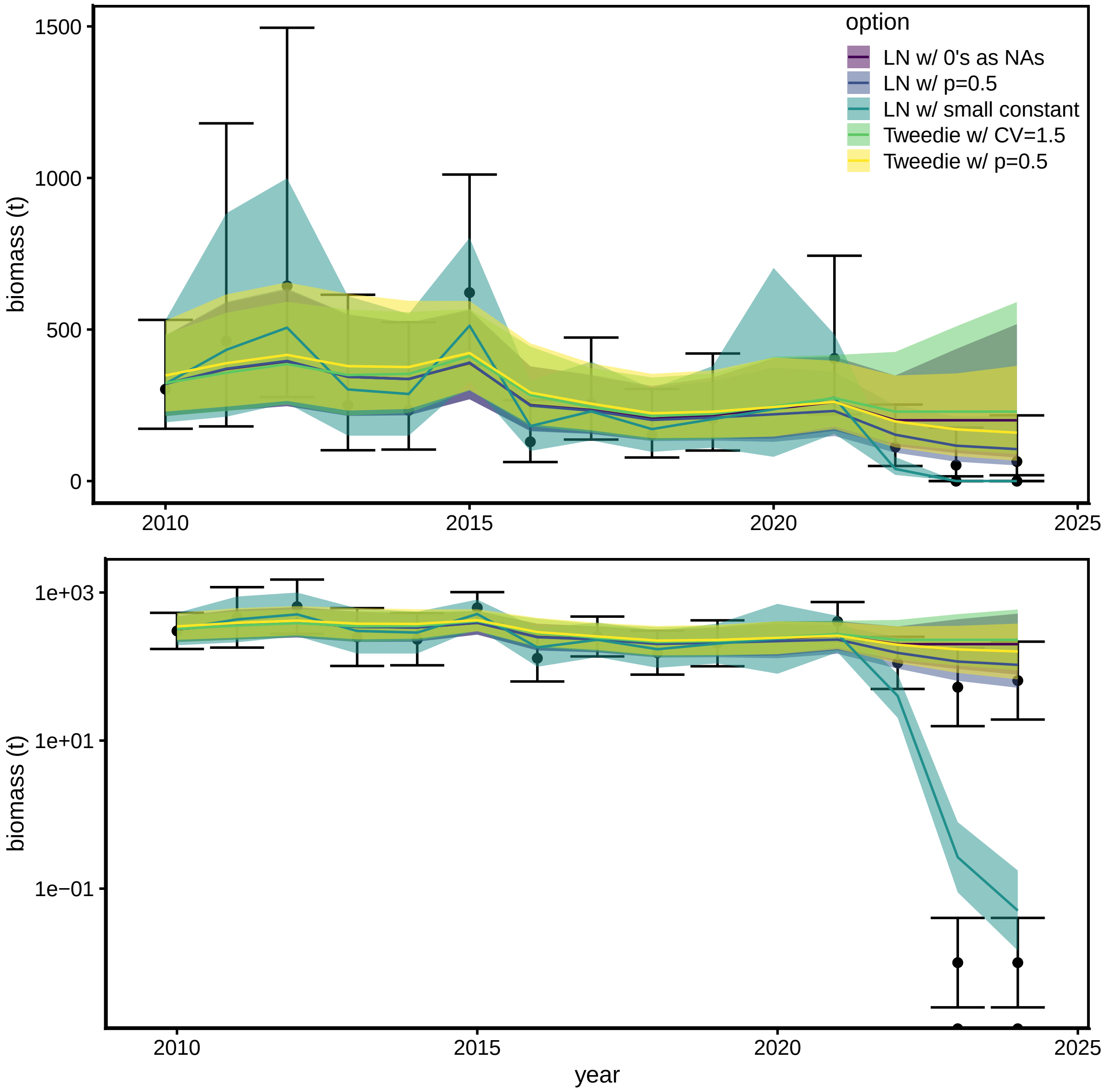

Figure 20. Comparison of the `rema` results from fitting the PIBKC survey biomass time series for mature males using the five error distributions and 0-substitution methods discussed in the text. Only results starting in 2010 to show detail at end of time series. Upper figure: arithmetic scale; lower figure: log-10 scale.

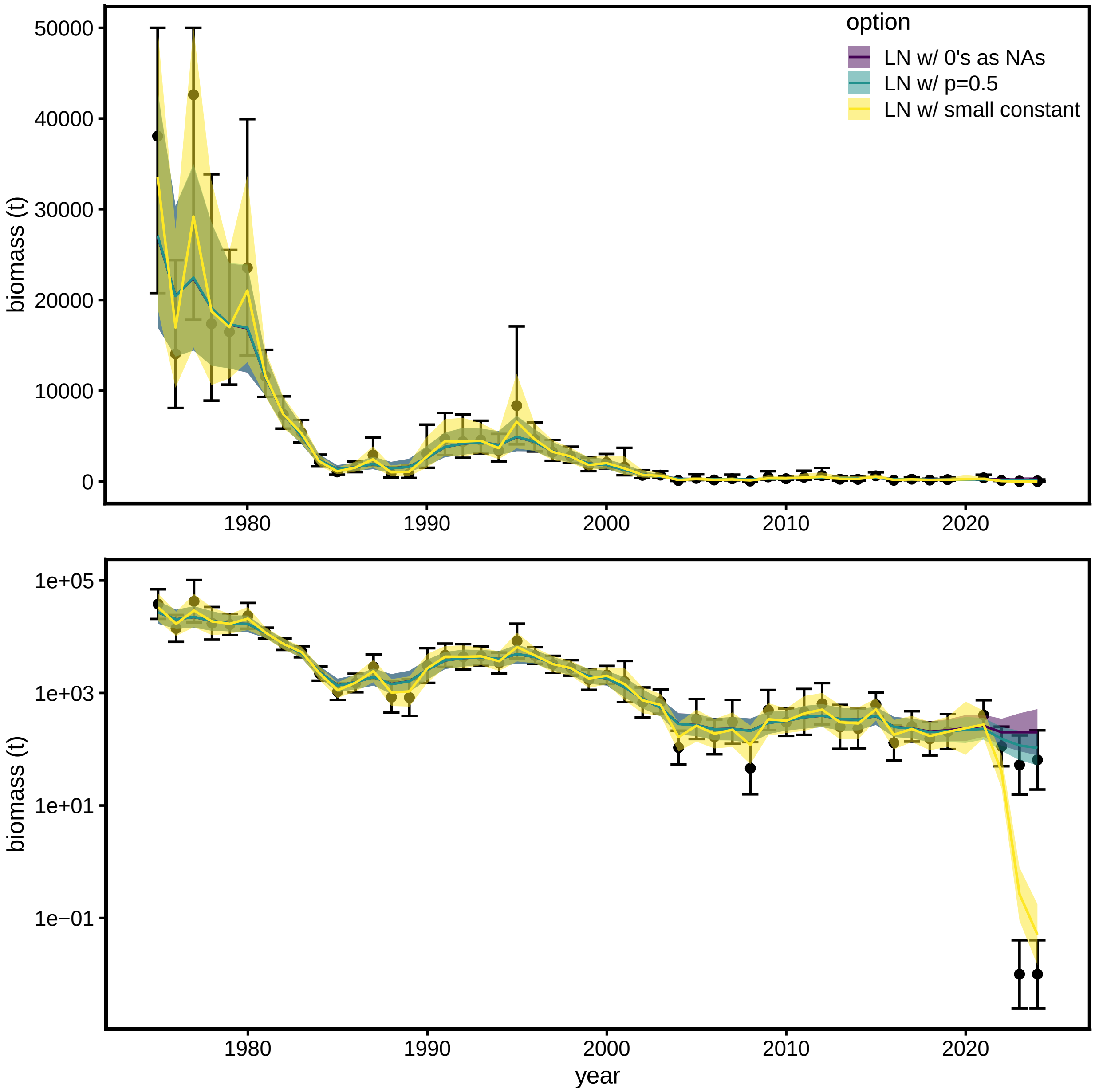

Figure 21. Comparison of the `rema` results from fitting the PIBKC survey biomass time series for mature males using the lognormal error distributions and 0-substitution methods discussed in the text. Full time series results. Upper figure: arithmetic scale; lower figure: log-10 scale.

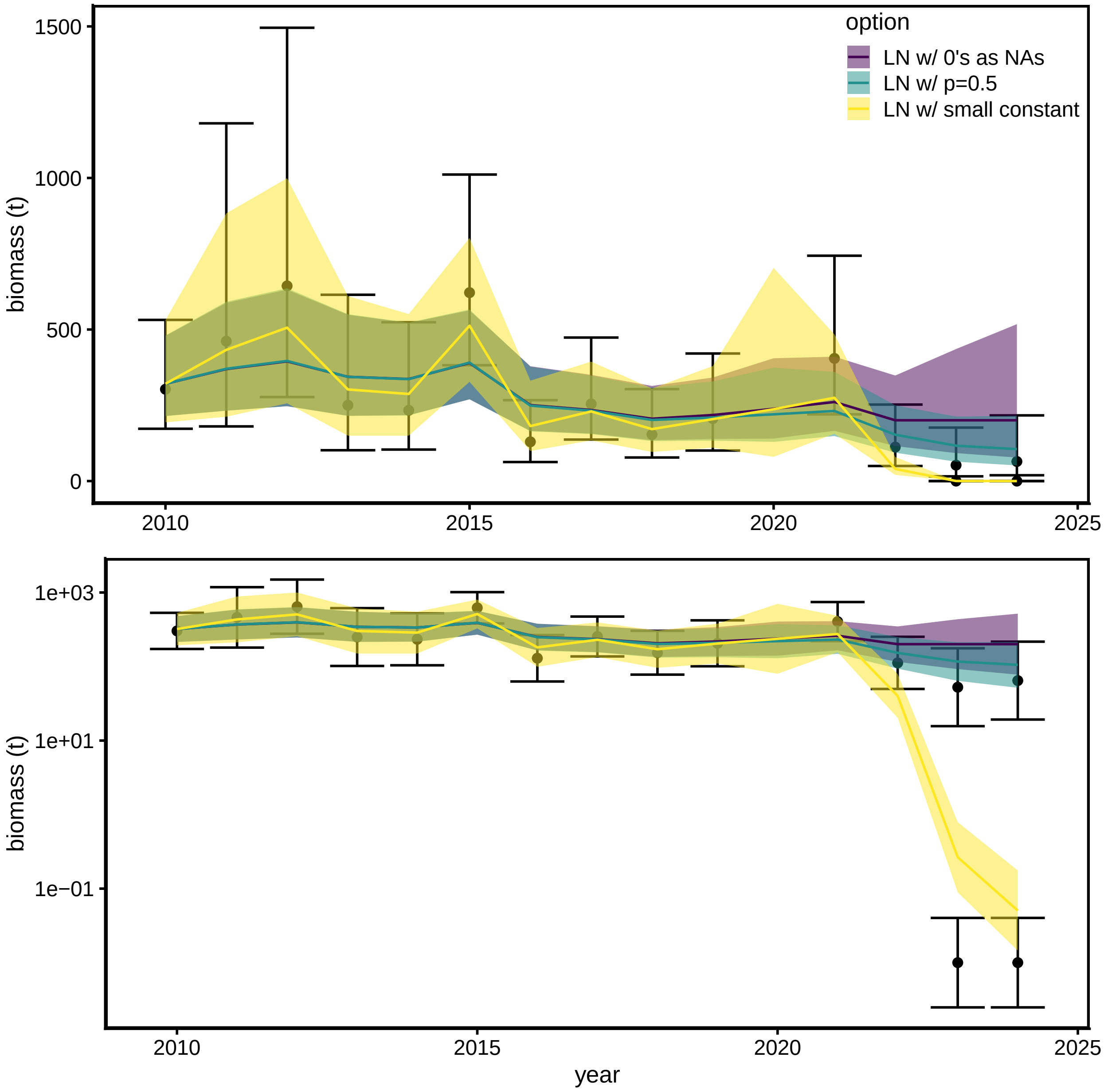

Figure 22. Comparison of the `rema` results from fitting the PIBKC survey biomass time series for mature males using the lognormal error distributions and 0-substitution methods discussed in the text. Only results starting in 2010 to show detail at end of time series. Upper figure: arithmetic scale; lower figure: log-10 scale.

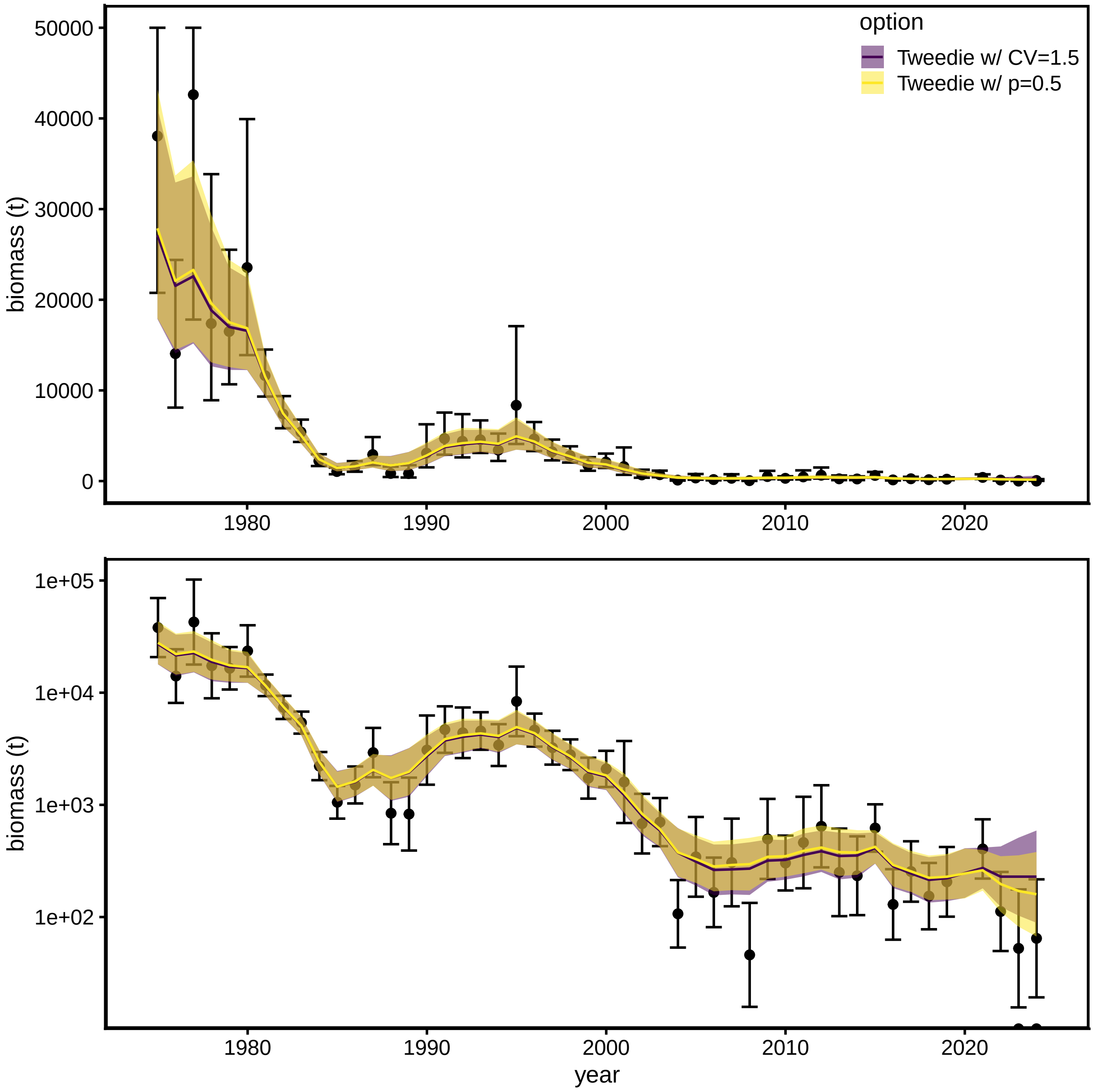

Figure 23. Comparison of the `rema` results from fitting the PIBKC survey biomass time series for mature males using the Tweedie error distributions and 0-substitution methods discussed in the text. Note that the "p=0.5" model was probably not converged. Full time series results. Upper figure: arithmetic scale; lower figure: log-10 scale.

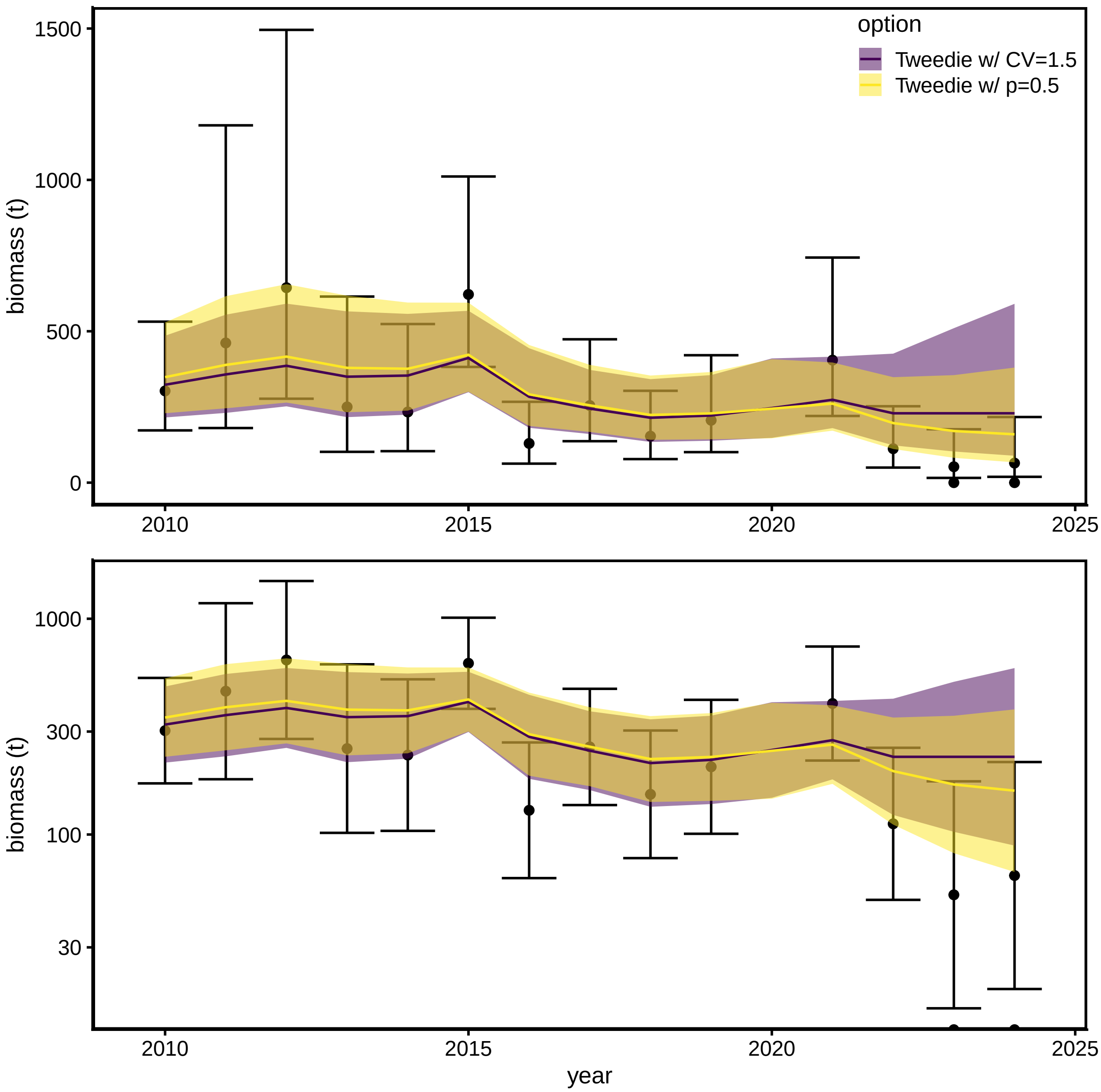

Figure 24. Comparison of the `rema` results from fitting the PIBKC survey biomass time series for mature males using the Tweedie error distributions and 0-substitution methods discussed in the text. Note that the “p=0.5” model was probably not converged. Only results starting in 2010 to show detail at end of time series. Upper figure: arithmetic scale; lower figure: log-10 scale.

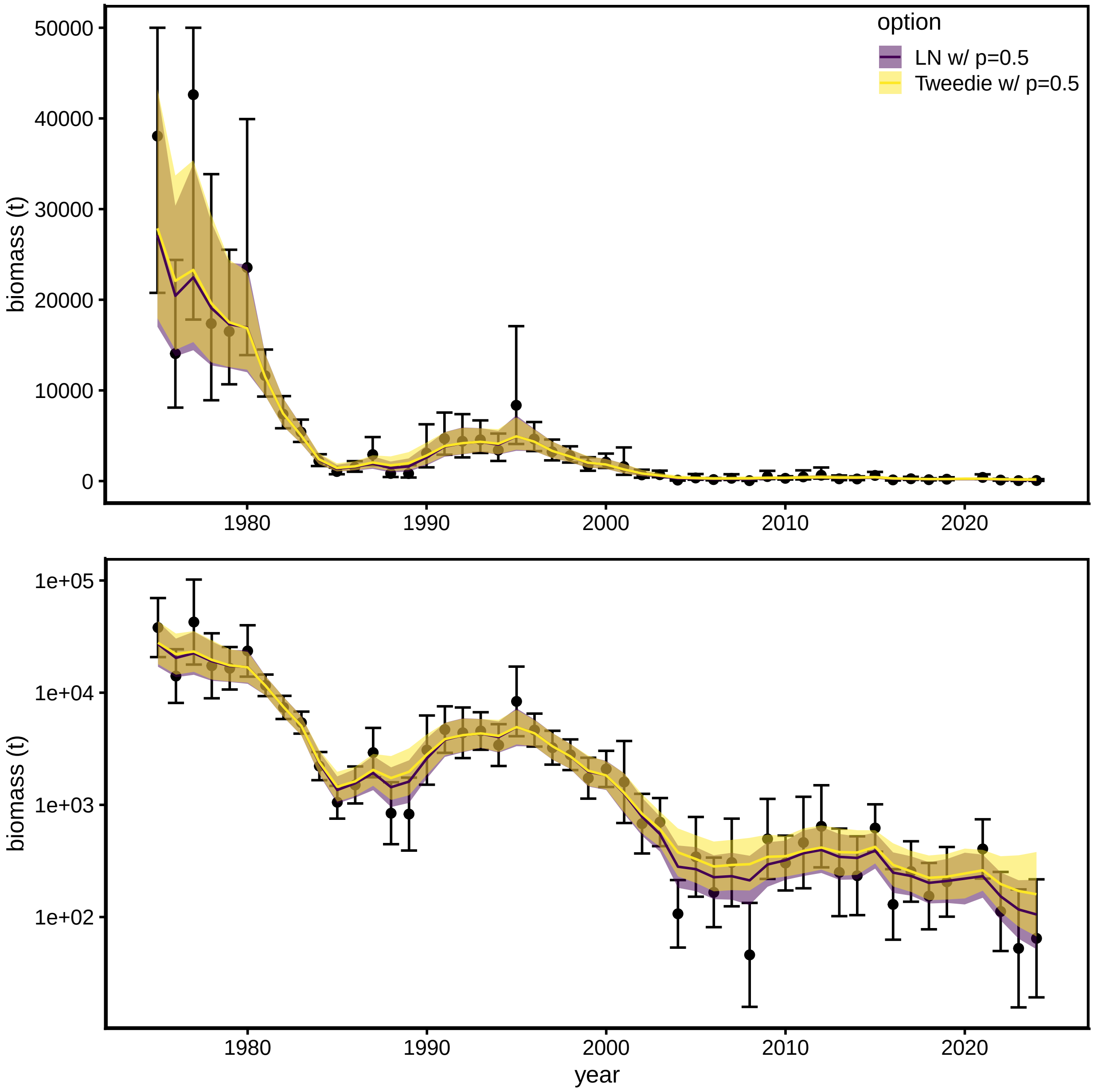

Figure 25. Comparison of the `rema` results from fitting the PIBKC survey biomass time series for mature males using the two error distributions and "p=0.5" substitution method discussed in the text. Note that the Tweedie model was probably not converged. Full time series results. Upper figure: arithmetic scale; lower figure: log-10 scale.

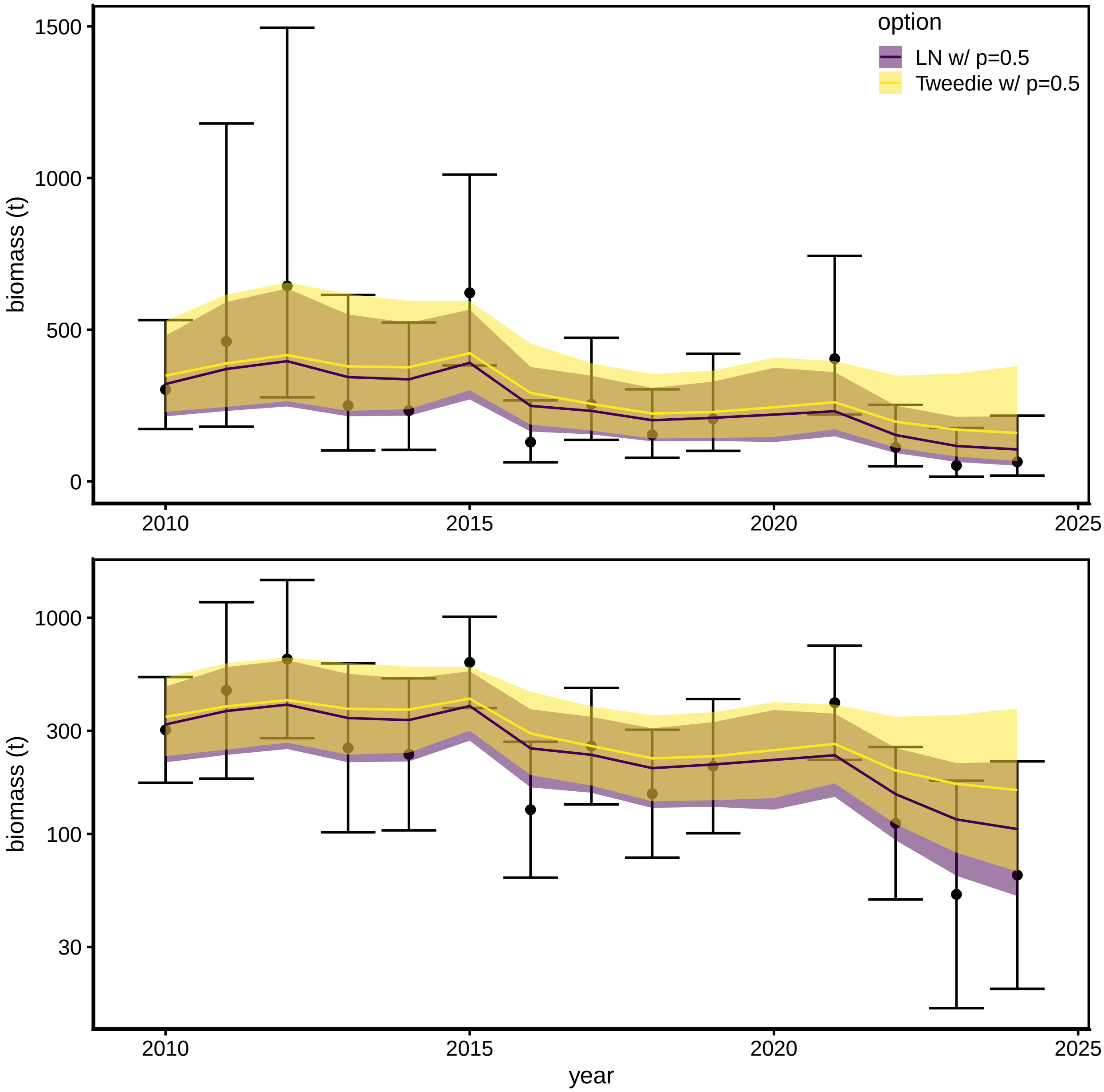

Figure 26. Comparison of the `rema` results from fitting the PIBKC survey biomass time series for mature males using the two error distributions and "p=0.5" substitution method discussed in the text. Note that the Tweedie model was probably not converged. Only results starting in 2010 to show detail at end of time series. Upper figure: arithmetic scale; lower figure: log-10 scale.

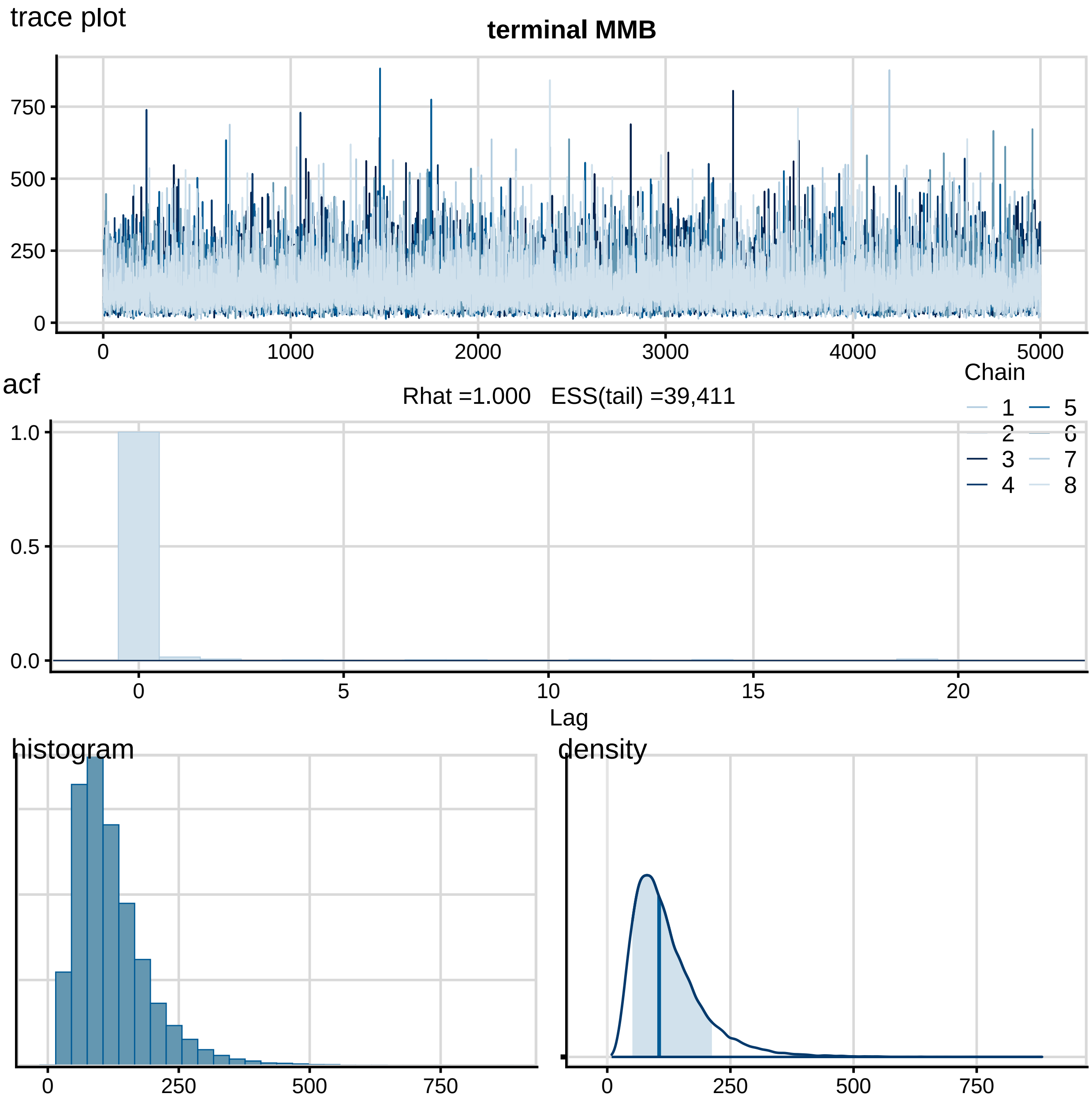

Figure 27. MCMC diagnostics for the “LN w/ p=0.5” model.

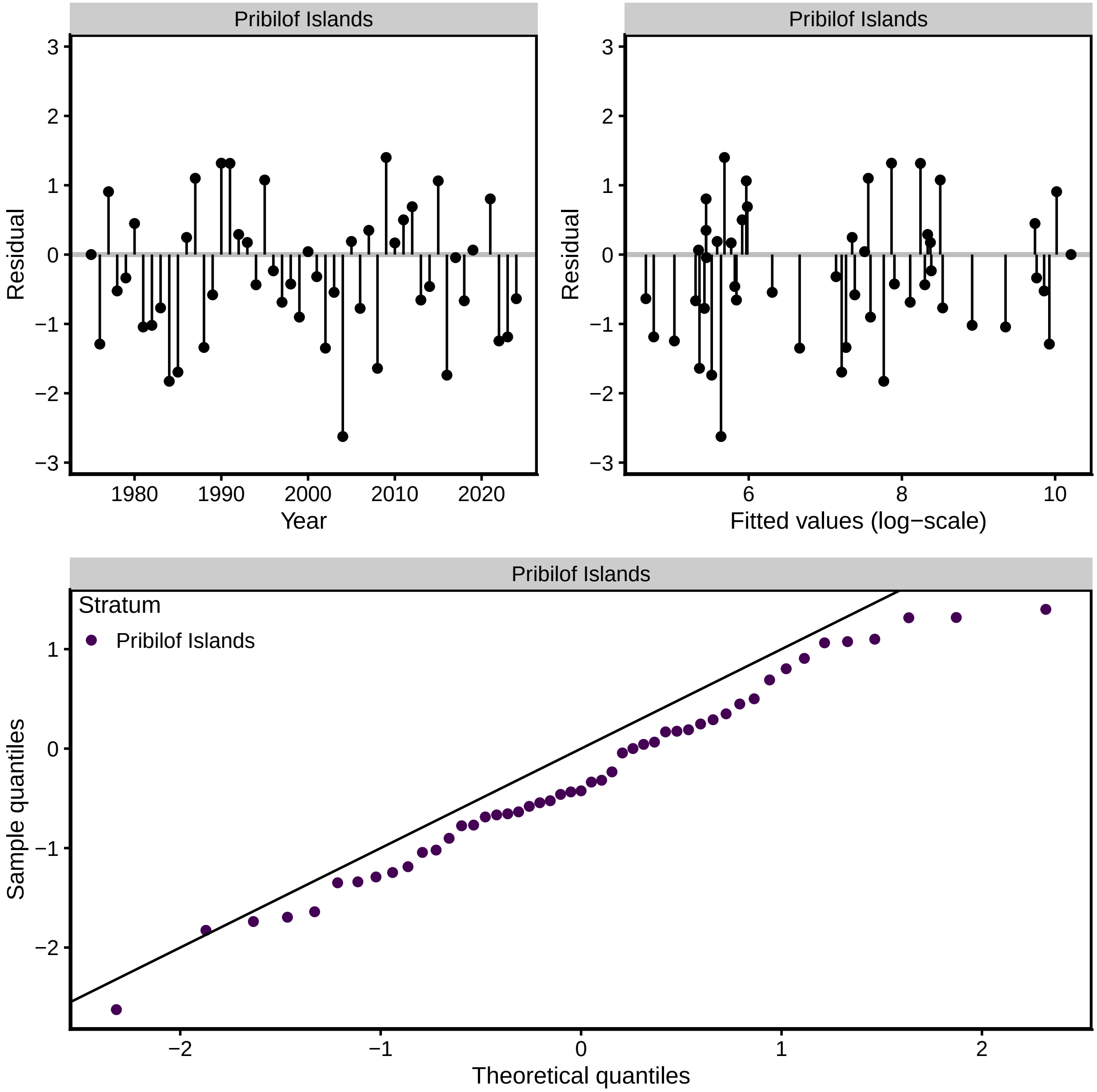

Figure 28. OSA (one-step ahead) diagnostics for the "LN w/ p=0.5" model.

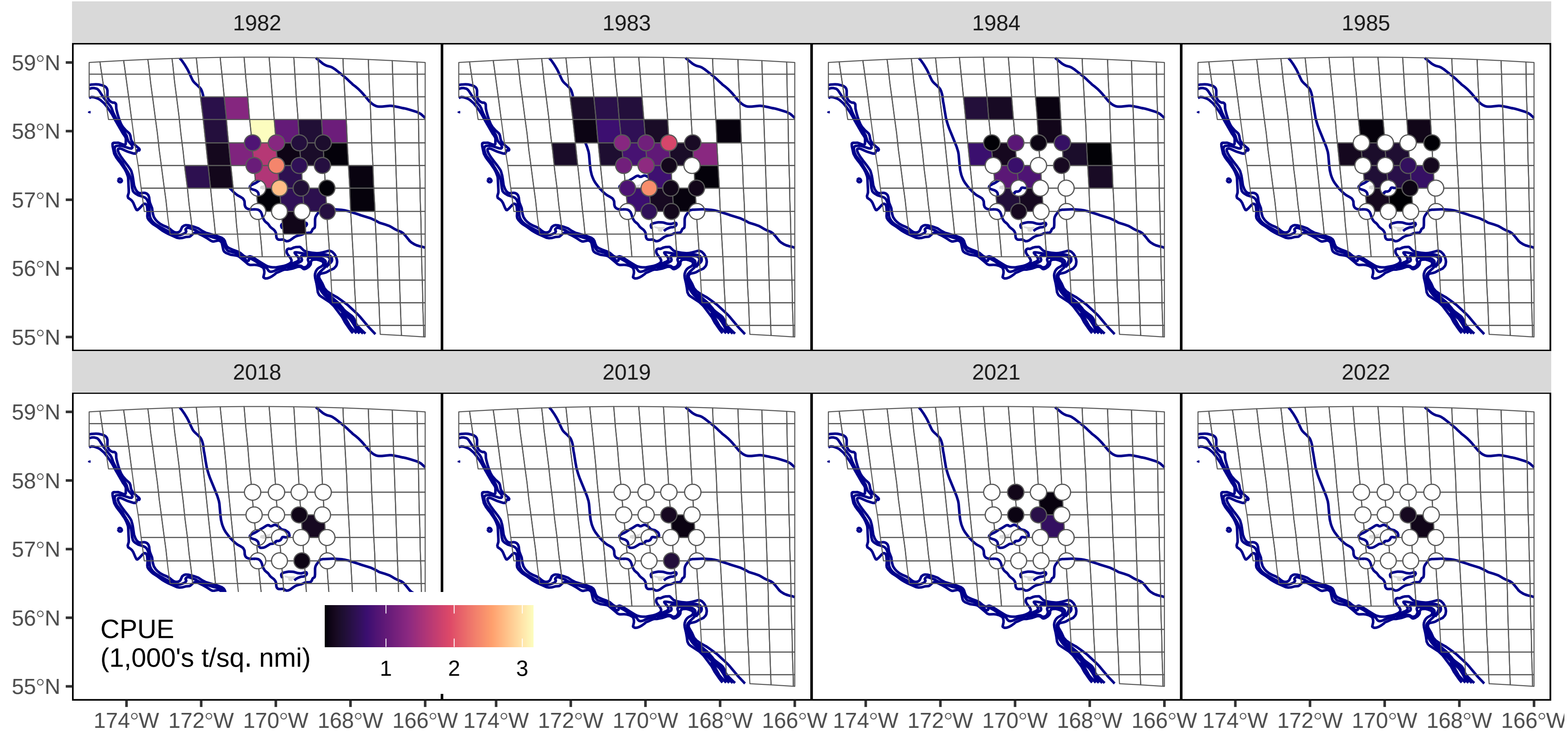

Figure 29. CPUE (1,000's t/sq. nmi.) for mature male PIBKC biomass from the NMFS EBS bottom trawl survey for selected years, illustrating the range contraction and decline in population size over time. The survey has sampled PIBKC annually since 1975 (with the exception of 2020). No mature males were caught in 2023 or 2024.

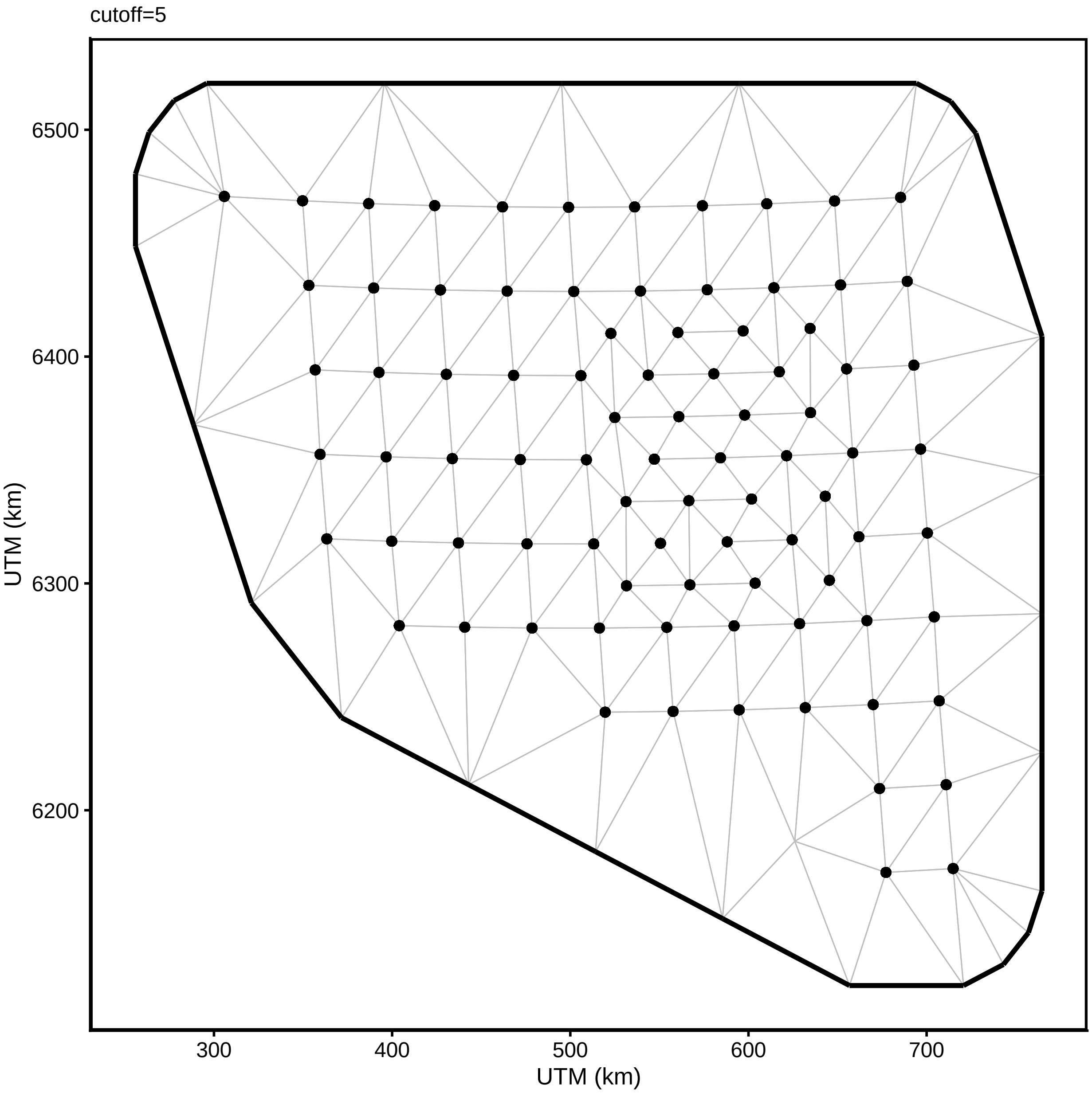

Figure 30. The spatial mesh generated by sdmTMB and used for the sdmTMB models. The points indicate the NMFS EBS bottom trawl survey sampling locations usd to create the mesh.

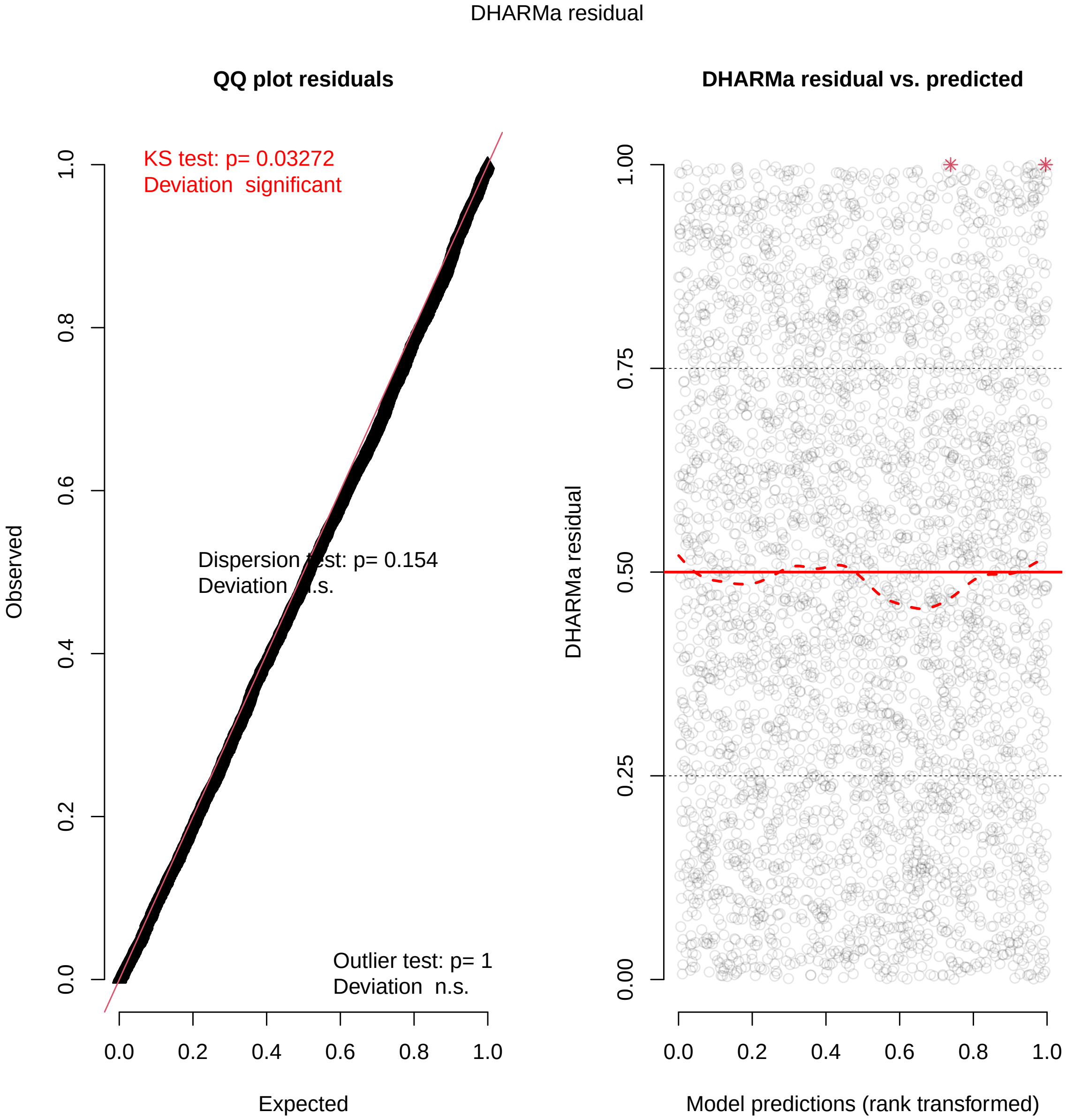

Figure 31. DHAMRa residuals diagnostics plots for 'm3'.

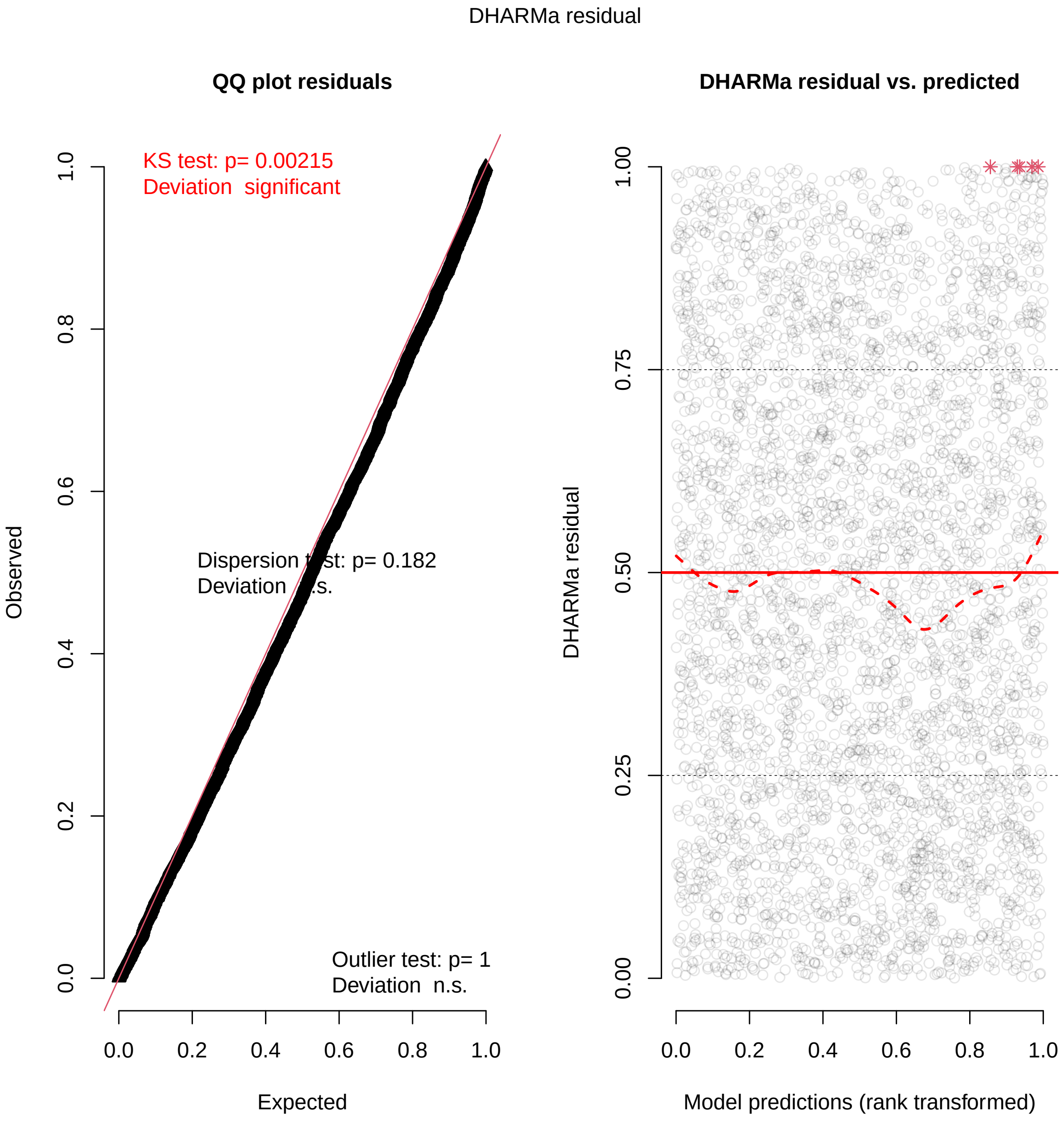

Figure 32. DHAMRa residuals diagnostics plots for 'm3-ar'.

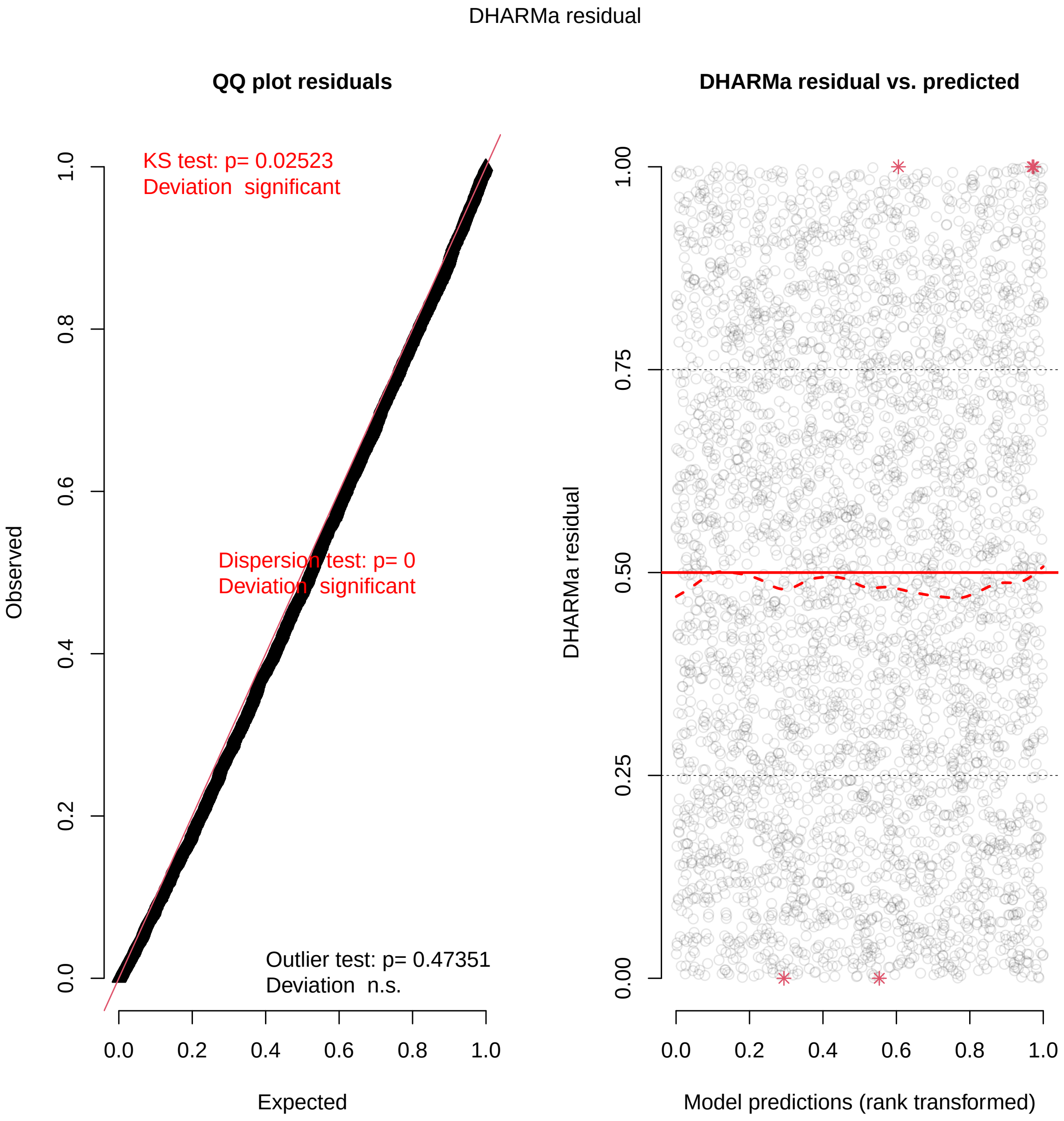

Figure 33. DHAMRa residuals diagnostics plots for 'tw'.

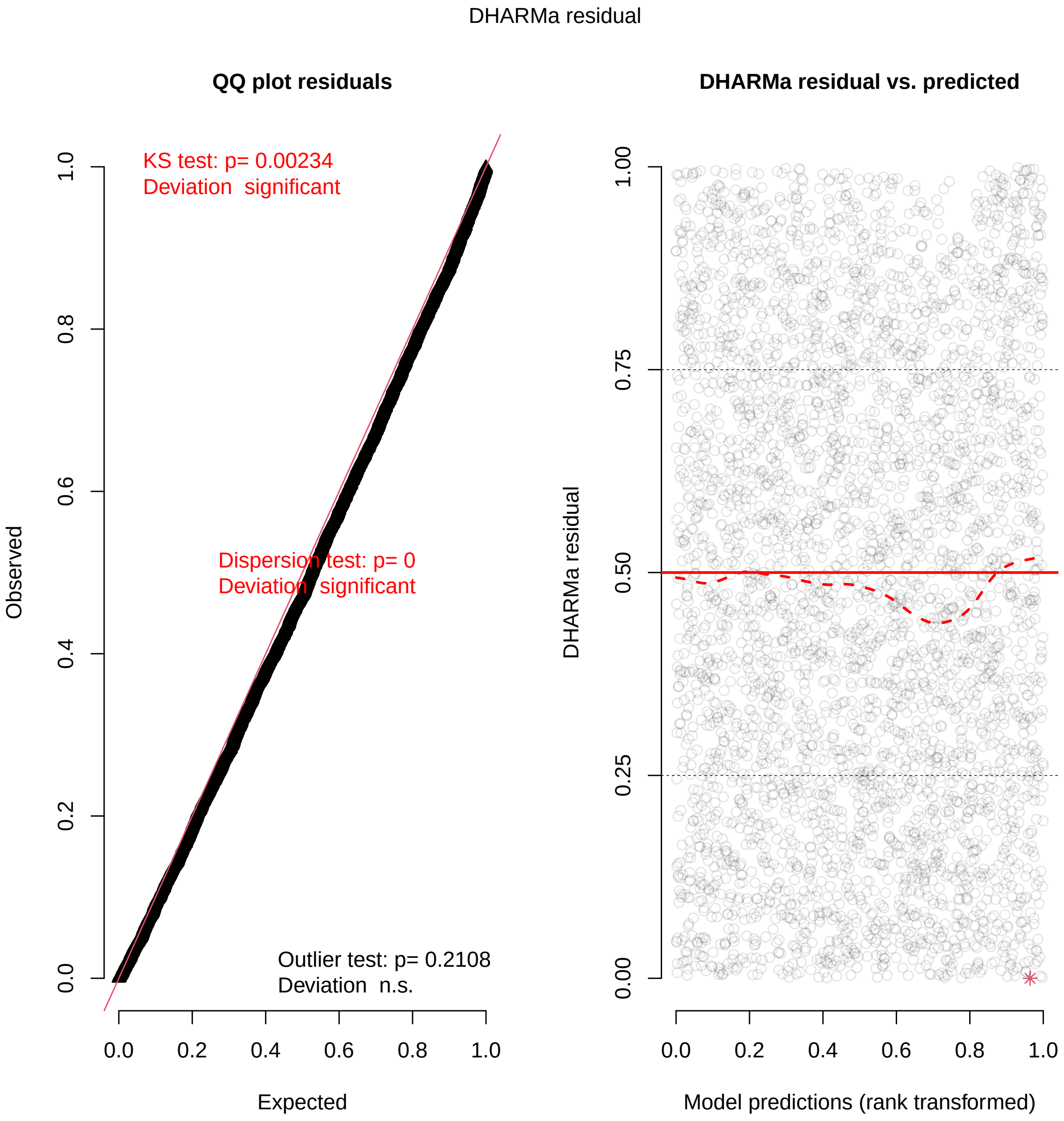

Figure 34. DHAMRa residuals diagnostics plots for 'tw-ar'.

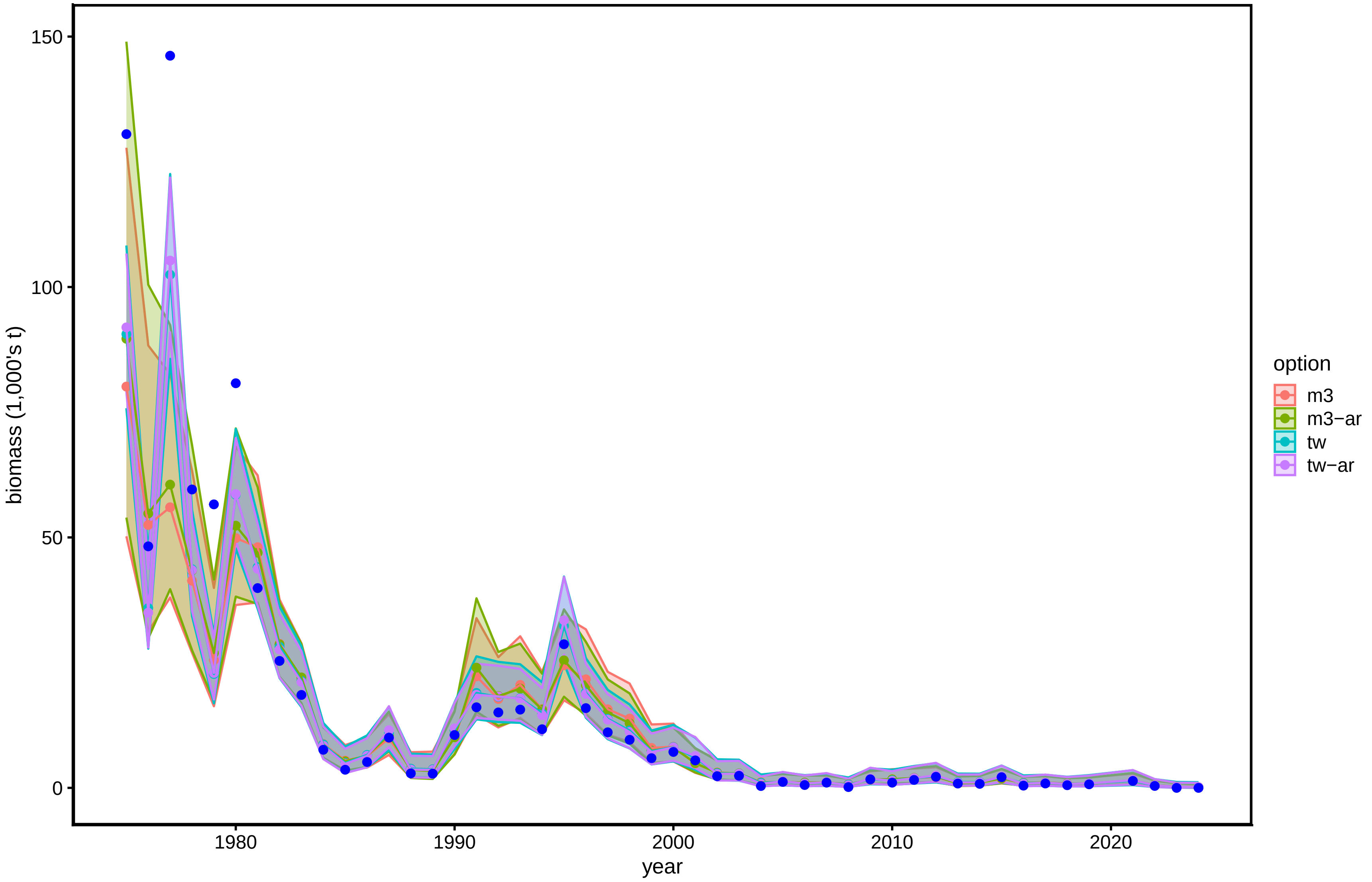

Figure 35. Biomass time series for mature male PIBKC, as estimated by each of the four sdmTMB models. Blue dots indicate the estimates obtained using design-based calculations.

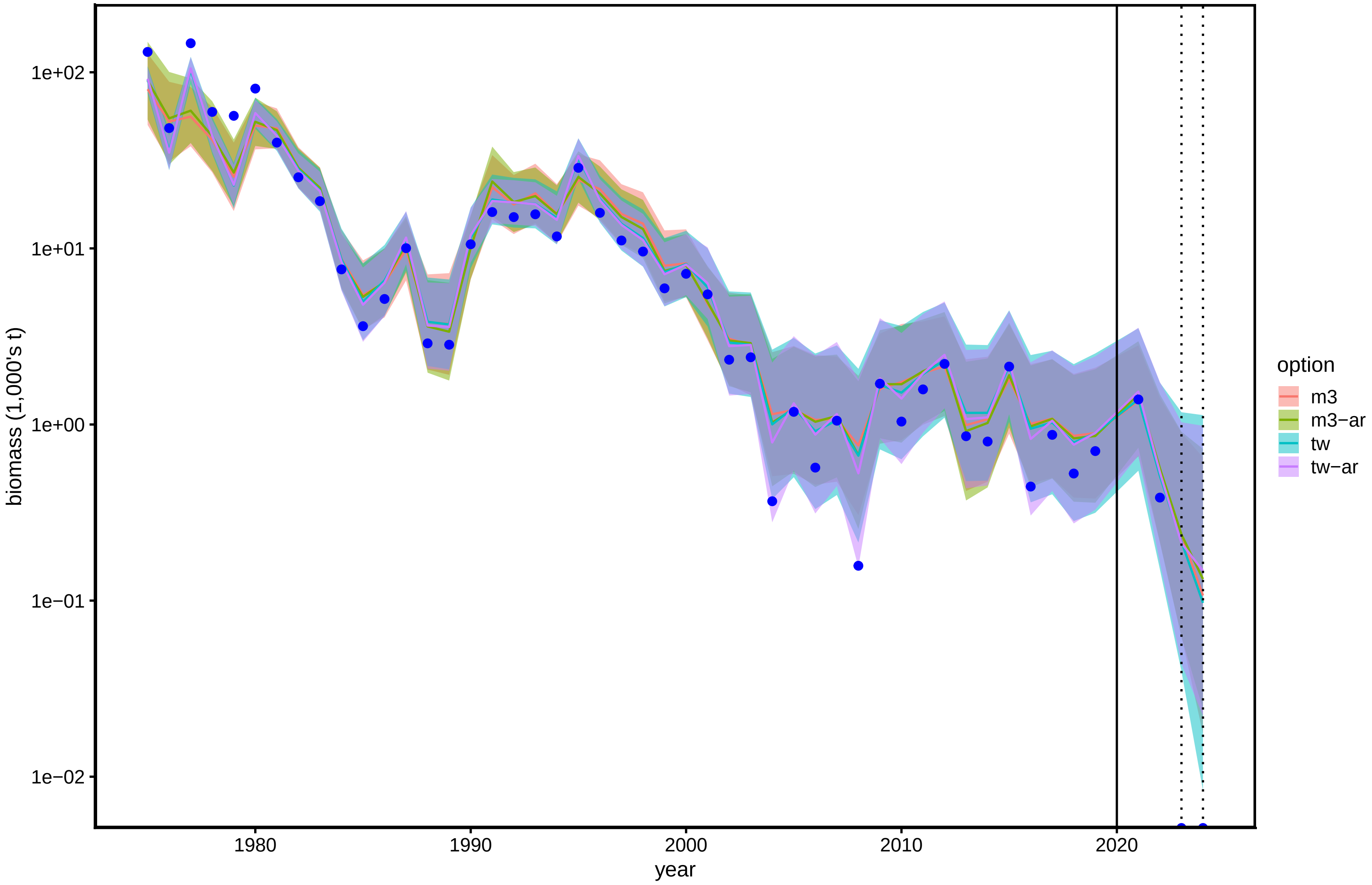

Figure 36. Biomass time series on a log10-scale for mature male PIBKC, as estimated by each of the four sdmTMB models. Blue dots indicate the estimates obtained using design-based calculations.

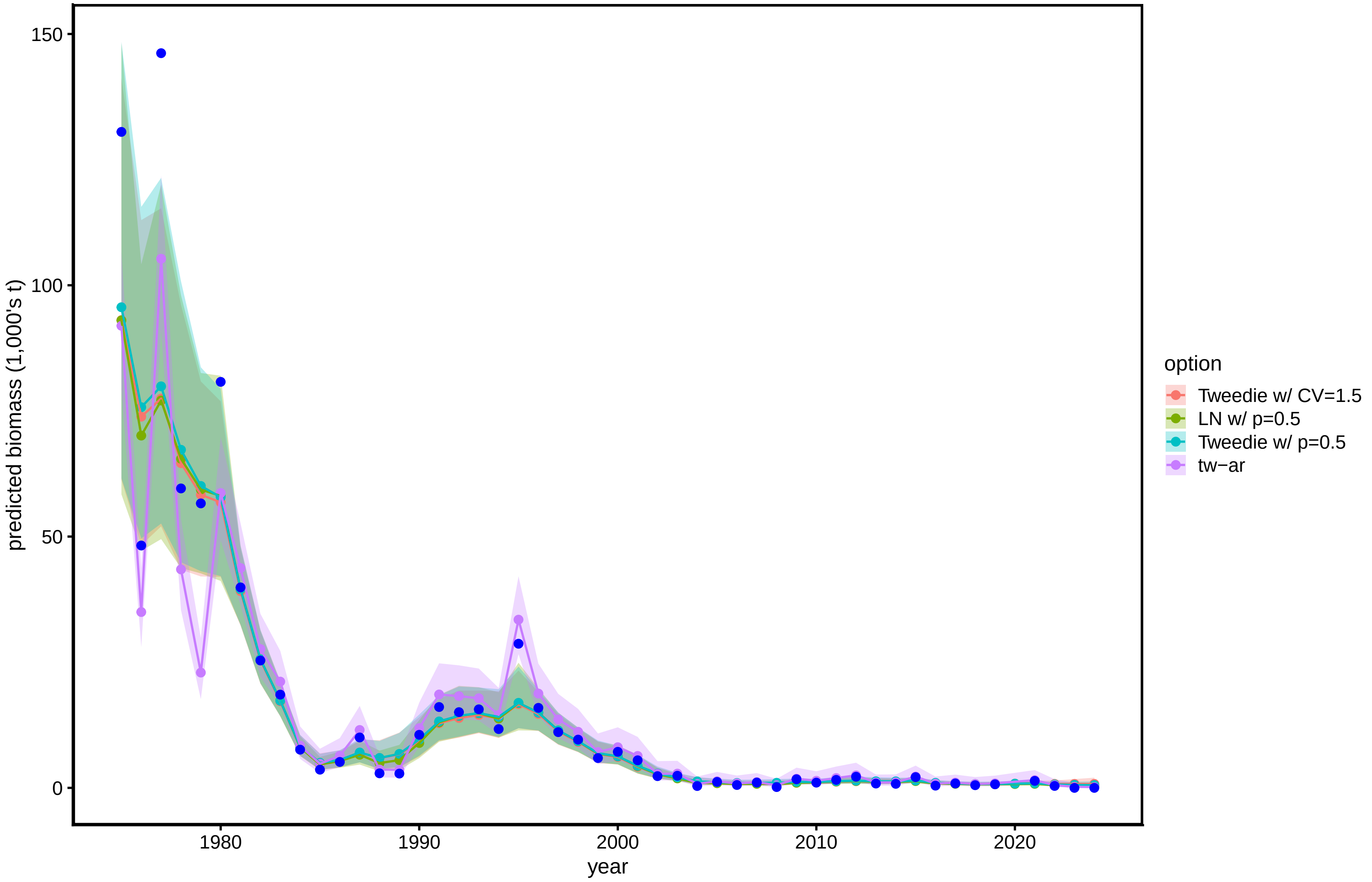

Figure 37. Biomass time series for mature male PIBKC, as estimated using each of the `rema` zeros options and the preferred sdmTMB model, `tw-ar`. Blue dots indicate the estimates obtained using design-based calculations.

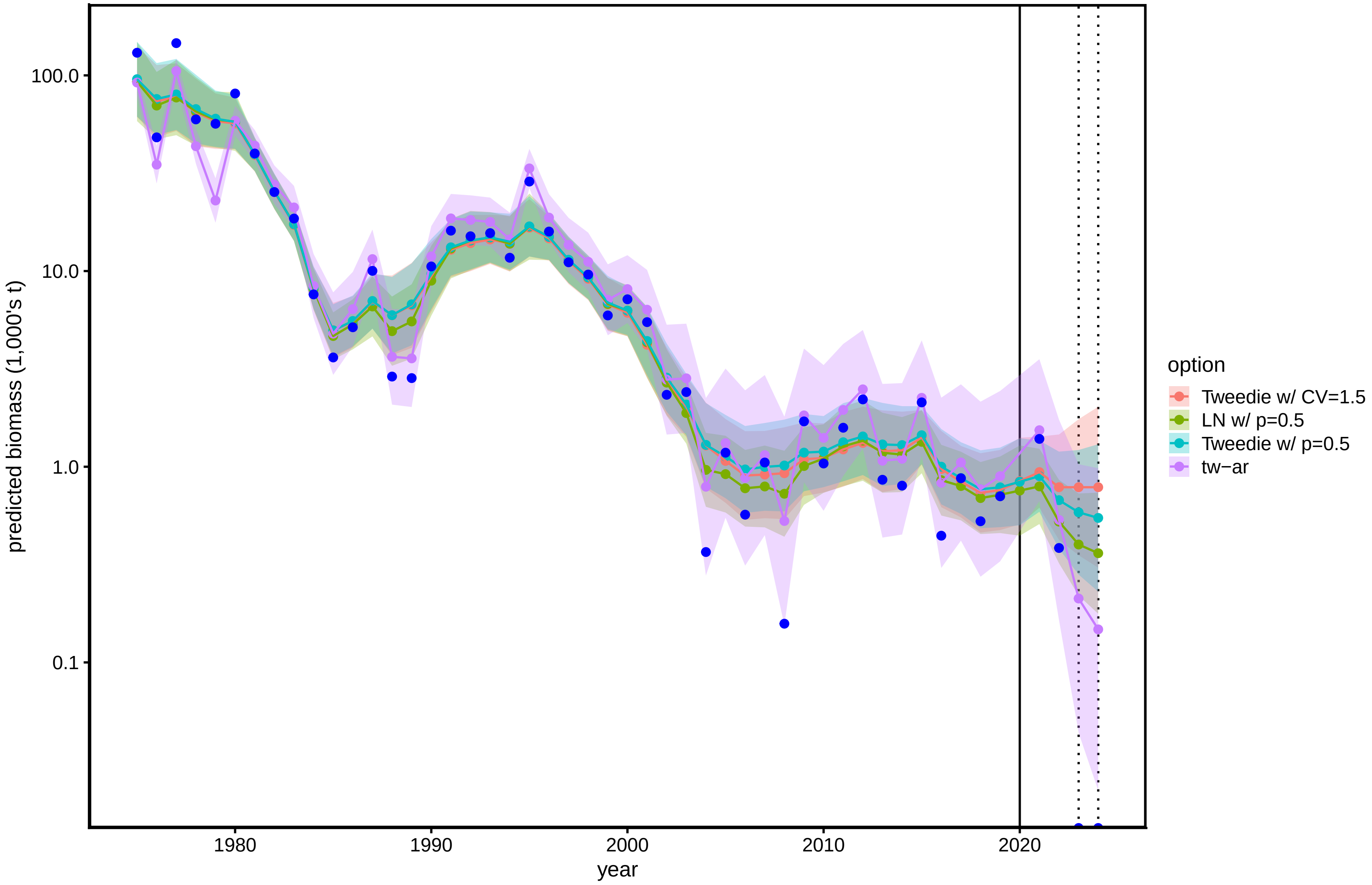

Figure 38. Biomass time series for mature male PIBKC on the log10-scale, as estimated using each of the `rema` zeros options and the preferred sdmTMB model, `tw-ar`. Blue dots indicate the estimates obtained using design-based calculations.

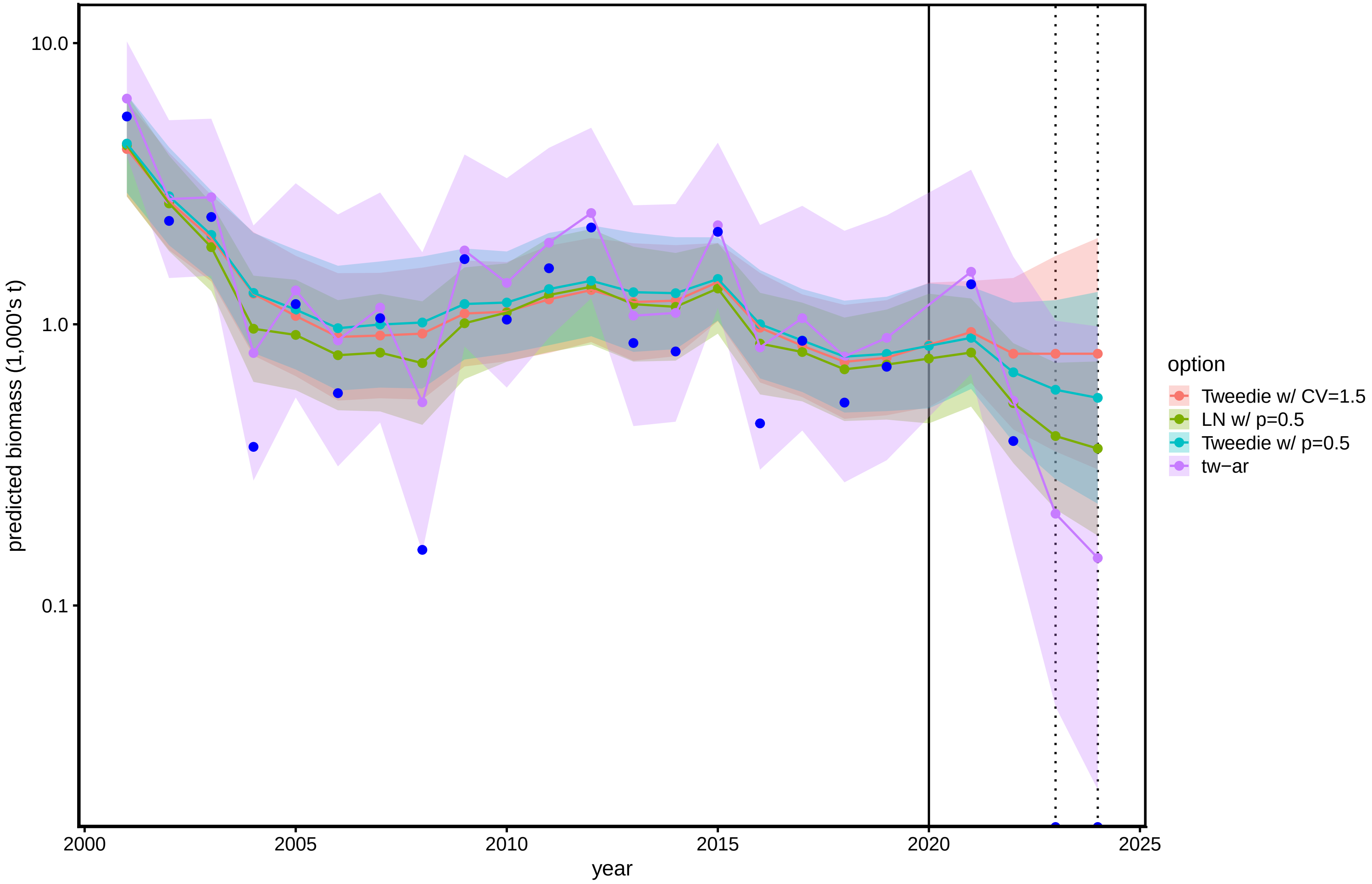

Figure 39. Biomass time series since 2020 for mature male PIBKC on the log10-scale, as estimated using each of the `rema` zeros options and the preferred sdmTMB model, `tw-ar`. Blue dots indicate the estimates obtained using design-based calculations.