

# Spatiotemporal model-based index development for Bering Sea and Aleutian Islands crab stocks

Update for Crab Plan Team modeling workshop

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## Introduction

The goal of this investigation was to develop spatiotemporal model-based indices of abundance for three Bering Sea and Aleutian Islands (BSAI) crab stocks: Tanner crab (*Chionoecetes bairdi*), Norton Sound red king crab (*Paralithodes camtschaticus*), and St. Matthew Island blue king crab (*Paralithodes platypus*). Research suggests that spatiotemporal model-based indices can be more robust to survey changes than are design-based indices, though the models must be well-specified (Yalcin et al. 2023). Spatiotemporal model-based indices are used in North Pacific Fishery Management Council (NPFMC) groundfish stock assessments for species including Eastern Bering Sea (EBS) walleye pollock (*Gadus chalcogrammus*) and EBS Pacific cod (*Gadus macrocephalus*), both of which use the vector-autoregressive spatial temporal (VAST) approach (Thorson 2019) to produce indices used in the assessments (Ianelli et al. 2024; Barbeaux et al. 2024). Previous BSAI crab stock assessments have presented models using spatiotemporal model-based indices (e.g., Ianelli et al. 2017), although these models were not accepted for harvest specifications (SSC 2017).

We generated biomass and abundance estimates using the R package *sdmTMB* (Anderson et al. 2022), which uses geostatistical time series data to estimate spatial and spatiotemporal generalized linear mixed effects models. This approach allows for index standardization when the set of stations surveyed is not consistent across years: one can generate a spatial grid that covers the area of interest, predict from the model onto that grid, and sum the predicted biomass to obtain an area-weighted biomass index that is independent of sampling locations (Anderson et al. 2022).

All three stock assessments for the crab stocks presented here use data from the National Marine Fisheries Service (NMFS) EBS bottom trawl survey (Stockhausen 2024; Hamazaki 2024; Stern and Palof 2024). The St. Matthew Island blue king crab stock assessment also uses data from the Alaska Department of Fish and Game (ADF&G) St. Matthew Island blue king crab pot survey, while the Norton Sound red king crab stock assessment uses data from the NMFS Northern Bering Sea bottom trawl survey and the ADF&G Norton Sound red king crab trawl survey.

Spatiotemporal model-based index development is expected to confer distinct advantages for each of the three stocks. For the St. Matthew Island blue king crab stock, standardizing the survey indices could allow the assessment to use the existing survey data more rigorously. The NMFS EBS trawl survey is undergoing changes including dropping the high sampling density “corner stations” near St. Matthew Island from 2024 onward (DePhilippo et al. 2023; Stern & Palof 2024); index standardization will allow the assessment to continue using the full time series of data despite changes in the spatial footprint of the survey. For Norton

Sound red king crab, a model-based approach could provide a more consistent way to combine the three existing trawl survey data sets into a single index of abundance.

## Methods

We fit models using the R package *sdmTMB*.

A number of decision points arise when fitting models using *sdmTMB*, including:

- The resolution of the spatial mesh used in fitting the model. A higher number of knots, specified when creating the spatial mesh using the `make_mesh()` function, indicates a higher resolution mesh. Few guidelines exist to aid in selection of an appropriate mesh resolution for a given dataset.
- The spatiotemporal random fields estimation method. The spatiotemporal random fields can be estimated as independent and identically distributed (IID), first-order autoregressive (AR1), a random walk, or fixed at zero.
- The model family. Many options exist, including `tweedie()`, `delta_gamma()`, and `delta_lognormal()`.

For each stock, we present a range of models to show the effects of choices at each of these decision points. After fitting models, we used the following steps for model evaluation:

- Run the `sdmTMB::sanity()` function. Output of this function for a model that passes all sanity checks looks like this:
  - Non-linear minimizer suggests successful convergence
  - Hessian matrix is positive definite
  - No extreme or very small eigenvalues detected
  - No gradients with respect to fixed effects are  $\geq 0.001$
  - No fixed-effect standard errors are NA
  - No standard errors look unreasonably large
  - No sigma parameters are  $< 0.01$
  - No sigma parameters are  $> 100$
  - Range parameter doesn't look unreasonably large
- If a model passed all the sanity checks, we used the R package *DHARMa* (Hartig 2022) to calculate the DHARMa residuals using the function `DHARMa::dharma_residuals()`. Models that did not pass the sanity checks were excluded from further consideration.
- We tested for quantile deviations, under/overdispersion, outliers, and zero inflation using the functions `DHARMa::testQuantiles()`, `DHARMa::testDispersion()`, `DHARMa::testOutliers()`, and `DHARMa::testZeroInflation()`, respectively.
- We evaluated model predictive log-likelihood (the predictive ability of the model for new observations; Anderson *et al.* 2024) using the function `sdmTMB_cv()`. This function measures model predictive log-likelihood by holding out subsets of the data in turn and using each as a test set. These subsets of data are termed “folds” and the number of folds to use can be specified using the `k_folds` argument. To compare models, we ran this function with the same number of folds specified for each model, then extracted the summed log-likelihood value for each model.

## Tanner crab

We utilized abundance and biomass data collected from the NMFS summer bottom trawl survey (1975-2024) to fit Tanner crab models in *sdmTMB*. Sex-size/maturity categories included all males combined, immature females, and mature females, and data were filtered to only include crab with a carapace width greater than or equal to 25mm. As the survey gear and methods were standardized in 1982 (Stauffer 2004), we fit separate models to data before 1982 and data in and after 1982 for each sex-size/maturity category. To evaluate decision points for model formulations, we first fit models to data across entire Eastern Bering Sea survey grid

using a 50-knot, 90-knot, and 120-knot mesh (Figures 2 - 4) using a Tweedie distribution to determine the most effective number of knots. We then used a mesh with the same number of knots to fit male abundance models using a Tweedie, Delta-lognormal, and Delta-gamma distribution and a AR1 versus IID random field. We chose to only evaluate male abundance in order to apply a parsimonious set of model formulations across other sex-maturity categories and biomass. Models were evaluated using diagnostics described above. The best models were then used to predict Tanner crab abundance and biomass on an EBS-wide survey grid (Figure 1), a grid encompassing the EBS area west of 166° (for the Tanner West stock; Figure 19, Appendix), and a grid encompassing the EBS area east of 166° (for the Tanner East stock; Figure 20, Appendix). Each prediction grid was a resolution of 5 km<sup>2</sup>.

### Norton Sound red king crab

We combined data from the NMFS trawl survey (1976-1991), ADF&G trawl survey (1996-2024), and NMFS NBS trawl survey (2010-2023) into a single data set to which we fit models in *sdmTMB*. We filtered the data set to ensure that it included only observations with coordinates falling within the Norton Sound Section of Statistical Area Q. For model fitting, we used spatial meshes at three resolutions: 100 knots, 50 knots, and 30 knots (Figures 18 - 16). We used a prediction grid with resolution of 5 km<sup>2</sup> (Figure 15).

### St. Matthew Island blue king crab

For model fitting, we used spatial meshes at three resolutions: 120 knots, 90 knots, and 50 knots (Figures ?? - ??). We used a prediction grid with a resolution of 4 km<sup>2</sup> (Figure ??).

## Results

### Tanner crab

#### Model diagnostics

#### Predicted abundance

#### Predicted index fits to observations

### Norton Sound red king crab

#### Model diagnostics

The DHARMA residuals diagnostic plots show evidence of quantile deviations for all three NSRKC models (Figures ?? - ??). The models with 100 knots and 50 knots showed evidence of underdispersion, with observed data less dispersed than expected under the fitted models, while the model with 30 knots did not. None of the models showed evidence of outliers or zero inflation.

#### Predicted abundance

Heat maps of predicted NSRKC abundance for the three models are show in figures ?? - ??.

### St. Matthew Island blue king crab

#### Model diagnostics

Examination of DHARMA residuals showed similar patterns for the three SMBKC models (Figures ?? - ??). All three models showed evidence of underdispersion, with observed data less dispersed than expected under the fitted models. None of the models showed evidence of outliers. All three models showed evidence of quantile deviations. The model with 120 knots showed evidence of zero inflation, with the observed data containing more zeros than would be expected under the fitted model, but the models with 50 and 90 knots did not show evidence of zero inflation.

### **Predicted abundance**

Heat maps of predicted SMBKC abundance for the three models are show in figures ?? - ??.

### **Predicted index fits to observations**

The model-predicted indices varied in their fits to the survey biomass observations, with the model fit using a mesh with an intermediate number of knots seeming to fit the survey observations more closely than the models fit to meshes with either higher or lower numbers of knots (Figure ??).

## **Conclusions**

## **Acknowledgements**

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## Tables

Table 1: Tanner crab diagnostic values for abundance models fit with Tweedie or delta gamma families and a spatial resolution of 50, 90, or 120 knots across sex-size maturity categories and model-fitting periods (pre-1982, during or after 1982). Log-likelihood values were estimated using the cross-validation function in sdmTMB with 3 folds. Quantile, dispersion, outlier, and zero-inflation diagnostics were estimated from DHARMA residuals, with values below 0.05 indicating significant metrics. Values are ordered within sex-size maturity category and period by decreasing log-likelihood.

Category	Period	Family	Knots	Log-likelihood	Quantiles	Dispersion	Outliers	Zero-inflation
Immature Female	<1982	Delta-gamma	90	-6371.5	0.0	0.0	0.5	0.5
Immature Female	<1982	Tweedie	90	-6475.4	0.0	0.0	0.0	0.1
Immature Female	<1982	Tweedie	120	-6666.0	0.1	0.0	0.4	0.2
Immature Female	<1982	Delta-gamma	50	-6716.3	0.0	0.2	0.2	0.0
Immature Female	<1982	Tweedie	50	-6850.9	0.1	0.0	0.1	0.1
Immature Female	<1982	Delta-gamma	120	-6907.8	0.0	0.0	0.1	0.1
Immature Female	>=1982	Delta-gamma	50	-53281.6	0.0	0.1	0.0	0.0
Immature Female	>=1982	Tweedie	50	-53380.1	0.0	0.0	0.0	0.0
Immature Female	>=1982	Tweedie	90	-53543.3	0.0	0.0	0.0	0.0
Immature Female	>=1982	Delta-gamma	90	-53553.8	0.0	0.2	0.0	0.0
Immature Female	>=1982	Tweedie	120	-53722.7	0.0	0.0	0.0	0.0
Immature Female	>=1982	Delta-gamma	120	-53852.8	0.0	0.7	0.0	0.0
Male	<1982	Delta-gamma	50	-9256.2	0.4	0.5	0.1	0.4
Male	<1982	Tweedie	90	-9339.9	0.0	0.0	0.0	0.1
Male	<1982	Delta-gamma	90	-9349.7	0.0	0.1	0.5	0.3
Male	<1982	Tweedie	120	-9397.7	0.0	0.0	0.0	0.0
Male	<1982	Delta-gamma	120	-9398.7	0.1	0.5	0.4	0.1
Male	<1982	Tweedie	50	-9540.7	0.0	0.0	0.0	0.0
Male	>=1982	Delta-gamma	50	-76006.3	0.0	0.1	0.0	0.0
Male	>=1982	Tweedie	50	-76072.9	0.0	0.0	0.0	0.0
Male	>=1982	Tweedie	90	-76229.4	0.0	0.0	0.0	0.0
Male	>=1982	Delta-gamma	90	-76277.7	0.0	0.1	0.0	0.0
Male	>=1982	Tweedie	120	-76318.2	0.0	0.0	0.0	0.0
Male	>=1982	Delta-gamma	120	-76509.5	0.0	0.1	0.0	0.0
Mature Female	<1982	Tweedie	90	-6089.8	0.1	0.4	0.1	0.0
Mature Female	<1982	Delta-gamma	90	-6097.3	0.0	0.8	0.5	0.6
Mature Female	<1982	Delta-gamma	50	-6097.4	0.0	0.4	0.0	0.0
Mature Female	<1982	Delta-gamma	120	-6108.3	0.2	0.3	0.1	0.0
Mature Female	<1982	Tweedie	120	-6132.7	0.0	0.0	0.8	0.0
Mature Female	<1982	Tweedie	50	-6189.4	0.1	0.0	0.0	0.0
Mature Female	>=1982	Tweedie	50	-43560.9	0.0	0.0	0.0	0.0
Mature Female	>=1982	Delta-gamma	50	-43625.4	0.0	0.0	0.0	0.0
Mature Female	>=1982	Delta-gamma	90	-43803.8	0.0	0.0	0.0	0.0
Mature Female	>=1982	Delta-gamma	120	-43943.3	0.0	0.0	0.0	0.0
Mature Female	>=1982	Tweedie	90	-43837.0	0.0	0.0	0.0	0.0
Mature Female	>=1982	Tweedie	120	-44059.6	0.0	0.0	0.0	0.0

Table 2: Tanner crab diagnostic values for biomass models fit with Tweedie or delta gamma families and a spatial resolution of 50, 90, or 120 knots across sex-size maturity categories and model-fitting periods (pre-1982, during or after 1982). Log-likelihood values were estimated using the cross-validation function in sdmTMB with 3 folds. Quantile, dispersion, outlier, and zero-inflation diagnostics were estimated from DHARMA residuals, with values below 0.05 indicating significant metrics. Values are ordered within sex-size maturity category and period by decreasing log-likelihood.

Category	Period	Family	Knots	Log-likelihood	Quantiles	Dispersion	Outliers	Zero-inflation
Immature Female	<1982	Tweedie	90	-6356.8	0.2	0.0	1.0	0.0
Immature Female	<1982	Delta-gamma	90	-6514.3	0.1	0.3	0.4	0.1
Immature Female	<1982	Delta-gamma	120	-6630.5	0.0	0.1	0.9	0.3
Immature Female	<1982	Tweedie	120	-6823.7	0.1	0.1	0.7	0.8
Immature Female	<1982	Delta-gamma	50	-6874.7	0.0	0.0	0.0	0.0
Immature Female	<1982	Tweedie	50	-7246.5	0.0	0.0	0.2	0.3
Immature Female	>=1982	Tweedie	50	-53292.8	0.0	0.0	0.0	0.0
Immature Female	>=1982	Delta-gamma	50	-53303.1	0.0	0.1	0.0	0.0
Immature Female	>=1982	Tweedie	90	-53587.3	0.0	0.0	0.0	0.0
Immature Female	>=1982	Delta-gamma	120	-53639.8	0.0	1.0	0.0	0.0
Immature Female	>=1982	Tweedie	120	-53652.8	0.0	0.0	0.0	0.0
Immature Female	>=1982	Delta-gamma	90	-53652.9	0.0	0.9	0.0	0.0
Male	<1982	Delta-gamma	50	-9275.5	0.0	0.0	0.0	0.3
Male	<1982	Tweedie	90	-9295.3	0.0	0.0	0.1	0.3
Male	<1982	Tweedie	50	-9309.6	0.0	0.0	0.0	0.1
Male	<1982	Delta-gamma	120	-9343.0	0.0	0.0	0.1	0.7
Male	<1982	Delta-gamma	90	-9349.5	0.0	0.0	0.4	0.0
Male	<1982	Tweedie	120	-9422.2	0.0	0.0	0.5	0.6
Male	>=1982	Delta-gamma	50	-75992.4	0.0	0.0	0.0	0.0
Male	>=1982	Tweedie	50	-76031.1	0.0	0.0	0.0	0.0
Male	>=1982	Delta-gamma	90	-76307.0	0.0	0.0	0.0	0.0
Male	>=1982	Tweedie	120	-76345.7	0.0	0.0	0.0	0.0
Male	>=1982	Delta-gamma	120	-76382.0	0.0	0.0	0.0	0.0
Male	>=1982	Tweedie	90	-76489.4	0.0	0.0	0.0	0.0
Mature Female	<1982	Tweedie	50	-6101.9	0.2	0.0	0.0	0.0
Mature Female	<1982	Delta-gamma	50	-6108.2	0.2	0.1	0.1	0.5
Mature Female	<1982	Delta-gamma	120	-6108.8	0.0	0.4	0.4	0.4
Mature Female	<1982	Delta-gamma	90	-6134.0	0.0	0.3	0.4	0.6
Mature Female	<1982	Tweedie	90	-6135.2	0.2	0.9	0.5	0.0
Mature Female	<1982	Tweedie	120	-6159.8	0.2	0.1	0.0	0.0
Mature Female	>=1982	Tweedie	50	-43735.8	0.0	0.0	0.0	0.0
Mature Female	>=1982	Delta-gamma	90	-43746.8	0.0	0.1	0.0	0.0
Mature Female	>=1982	Tweedie	90	-43818.5	0.0	0.0	0.0	0.0
Mature Female	>=1982	Delta-gamma	50	-43898.4	0.0	0.3	0.0	0.0
Mature Female	>=1982	Delta-gamma	120	-44076.4	0.0	0.0	0.0	0.0
Mature Female	>=1982	Tweedie	120	-44166.4	0.0	0.0	0.0	0.0

## Figures

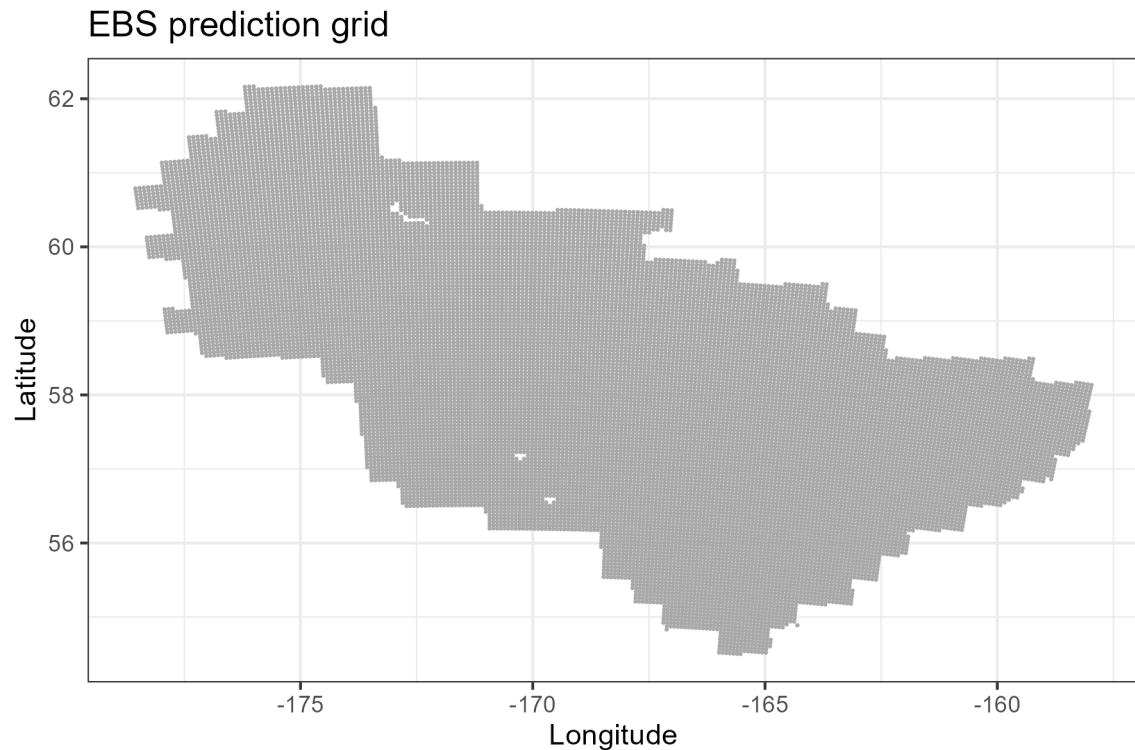
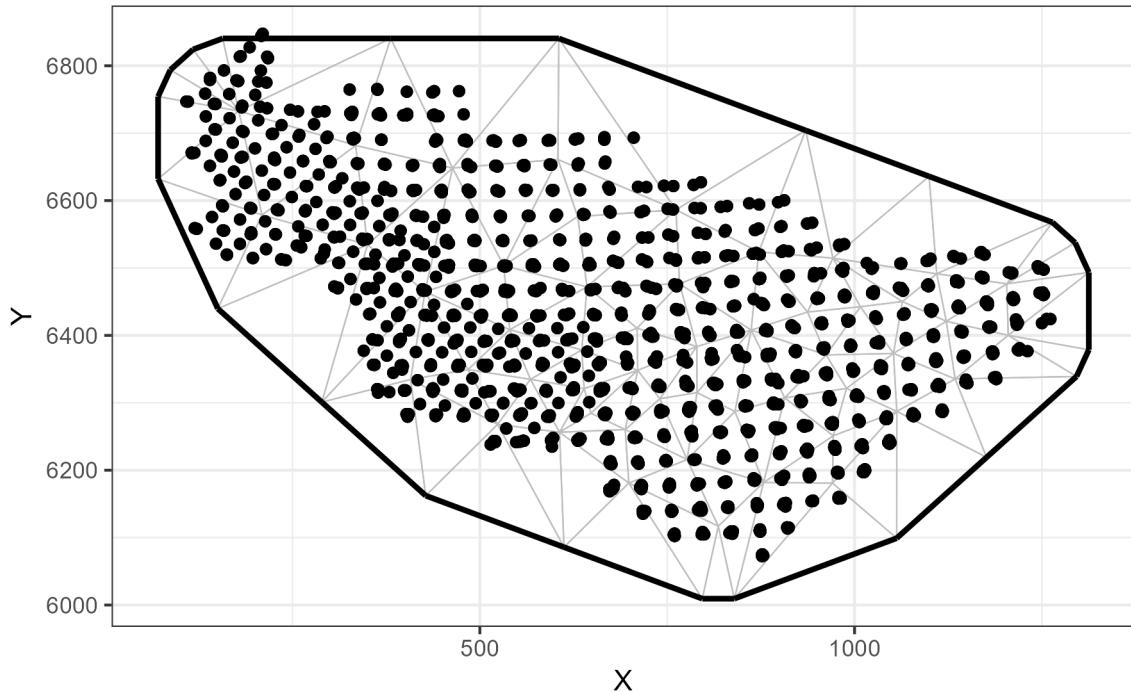


Figure 1: Eastern Bering Sea prediction grid used for Tanner crab spatial abundance and biomass predictions. Spatial resolution is 5km<sup>2</sup> and does not include land.

<1982 mesh (knots=72)



$\geq$ 1982 mesh (knots=74)

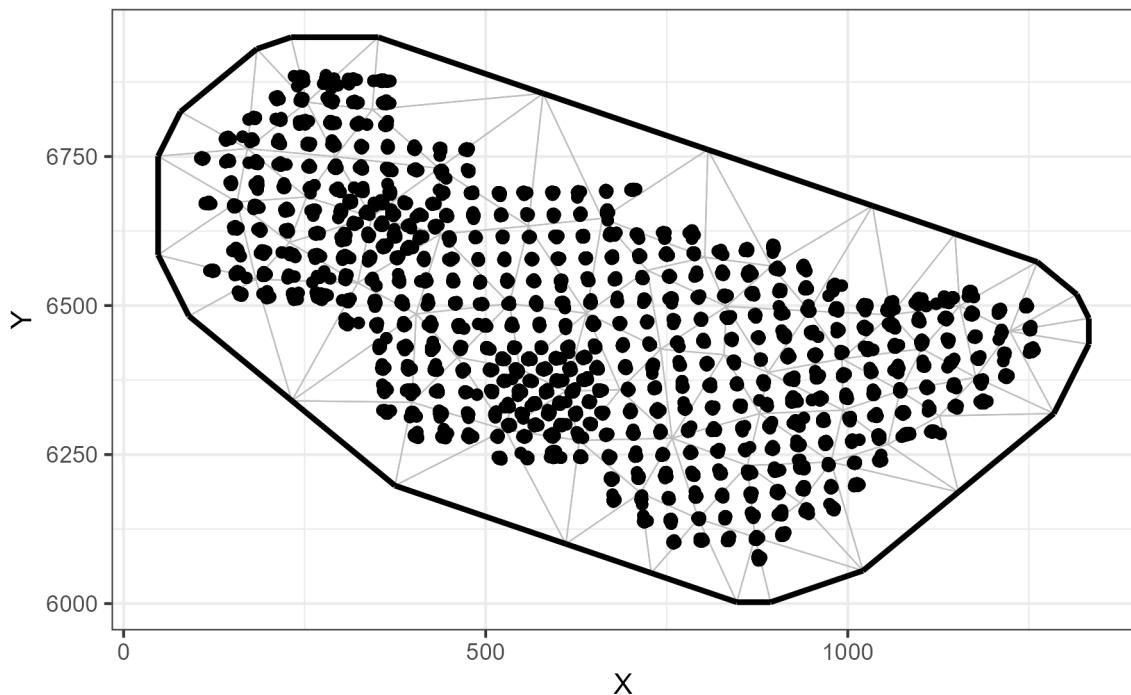
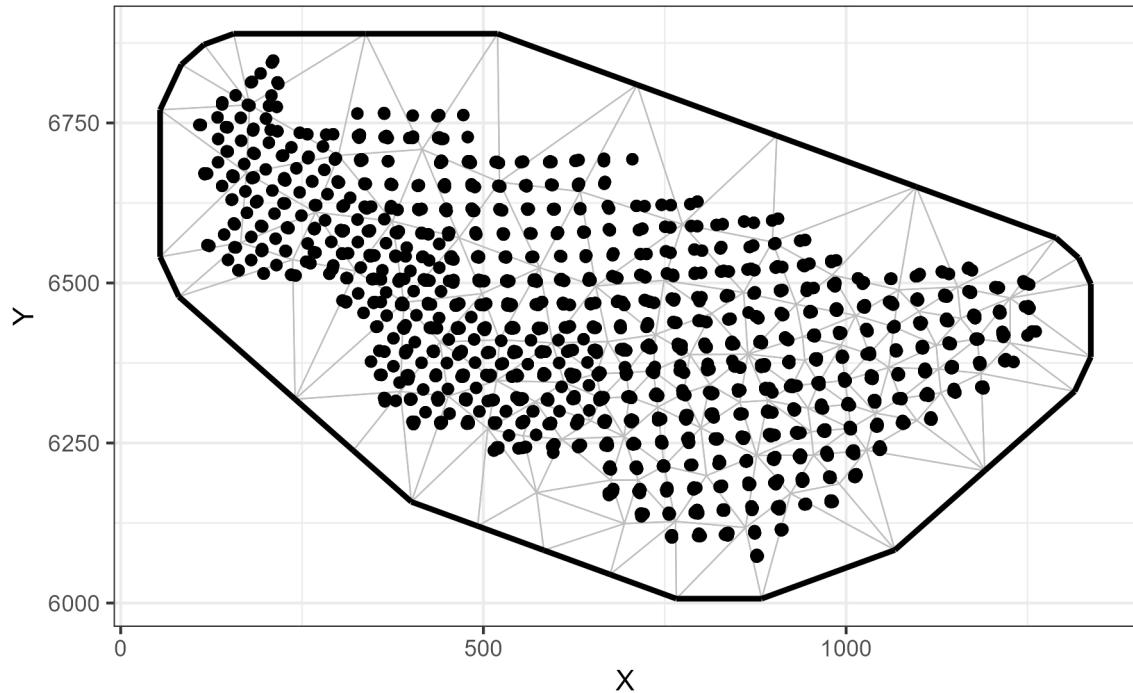


Figure 2: Spatial mesh with 50 knots used for fitting Tanner crab spatial models. Points represent observations and vertices represent knot locations.

<1982 mesh (knots=122)



$\geq 1982$  mesh (knots=122)

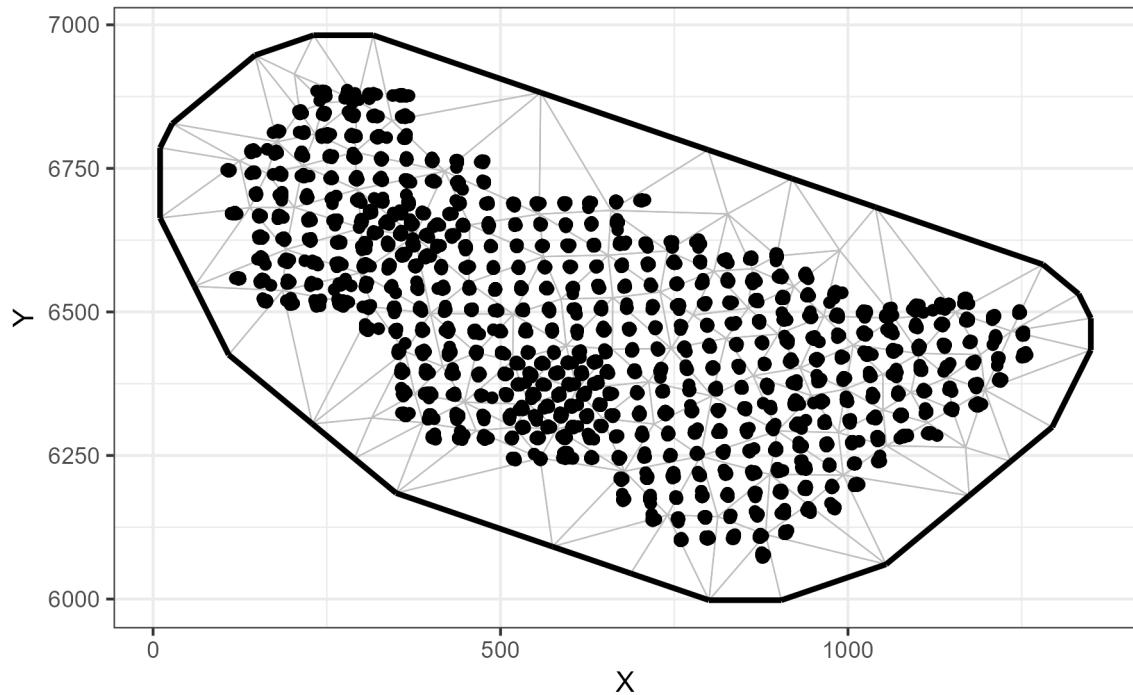


Figure 3: Spatial mesh with 90 knots used for fitting Tanner crab spatial models. Points represent observations and vertices represent knot locations.

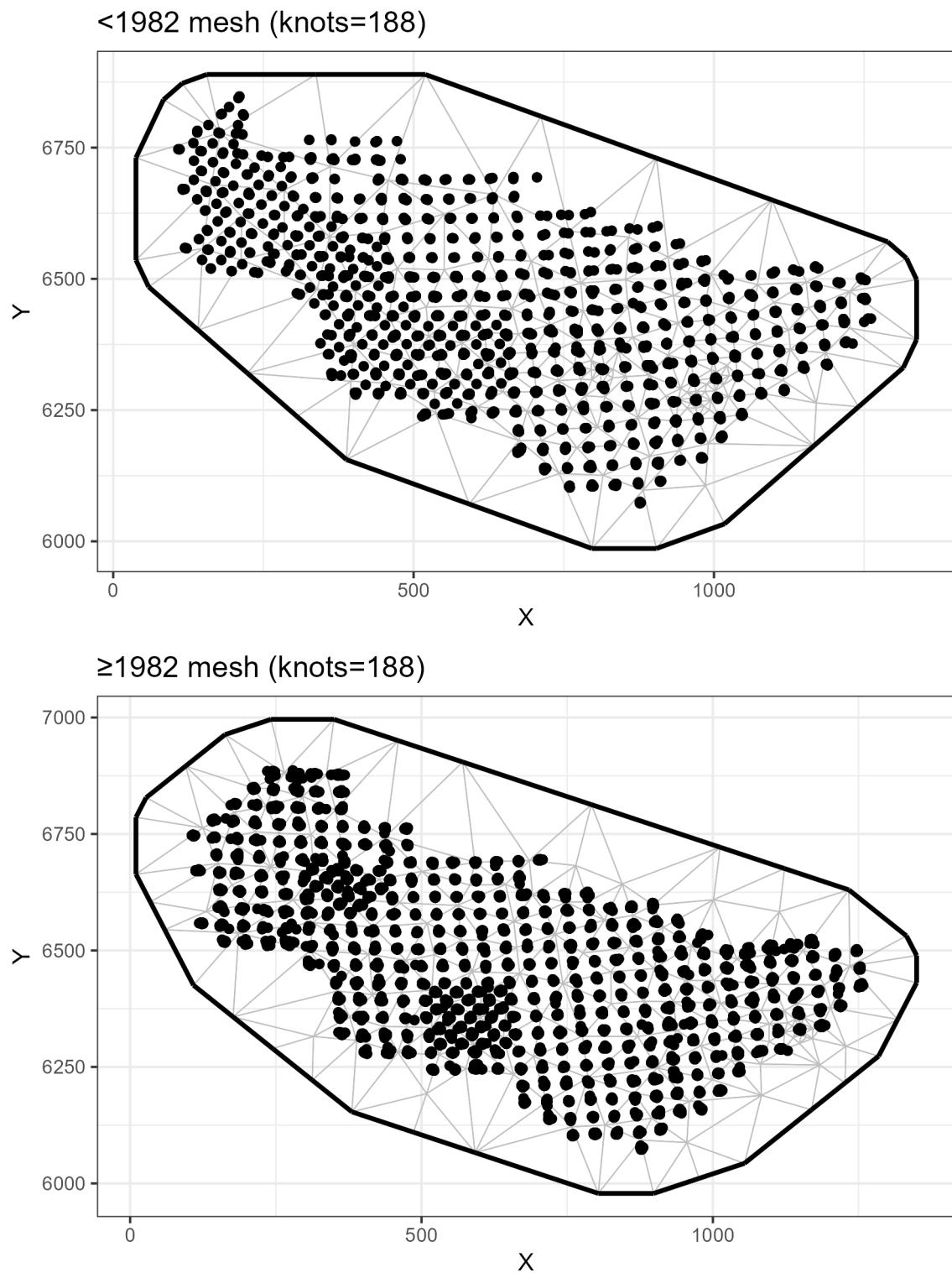


Figure 4: Spatial mesh with 120 knots used for fitting Tanner crab spatial models. Points represent observations and vertices represent knot locations.

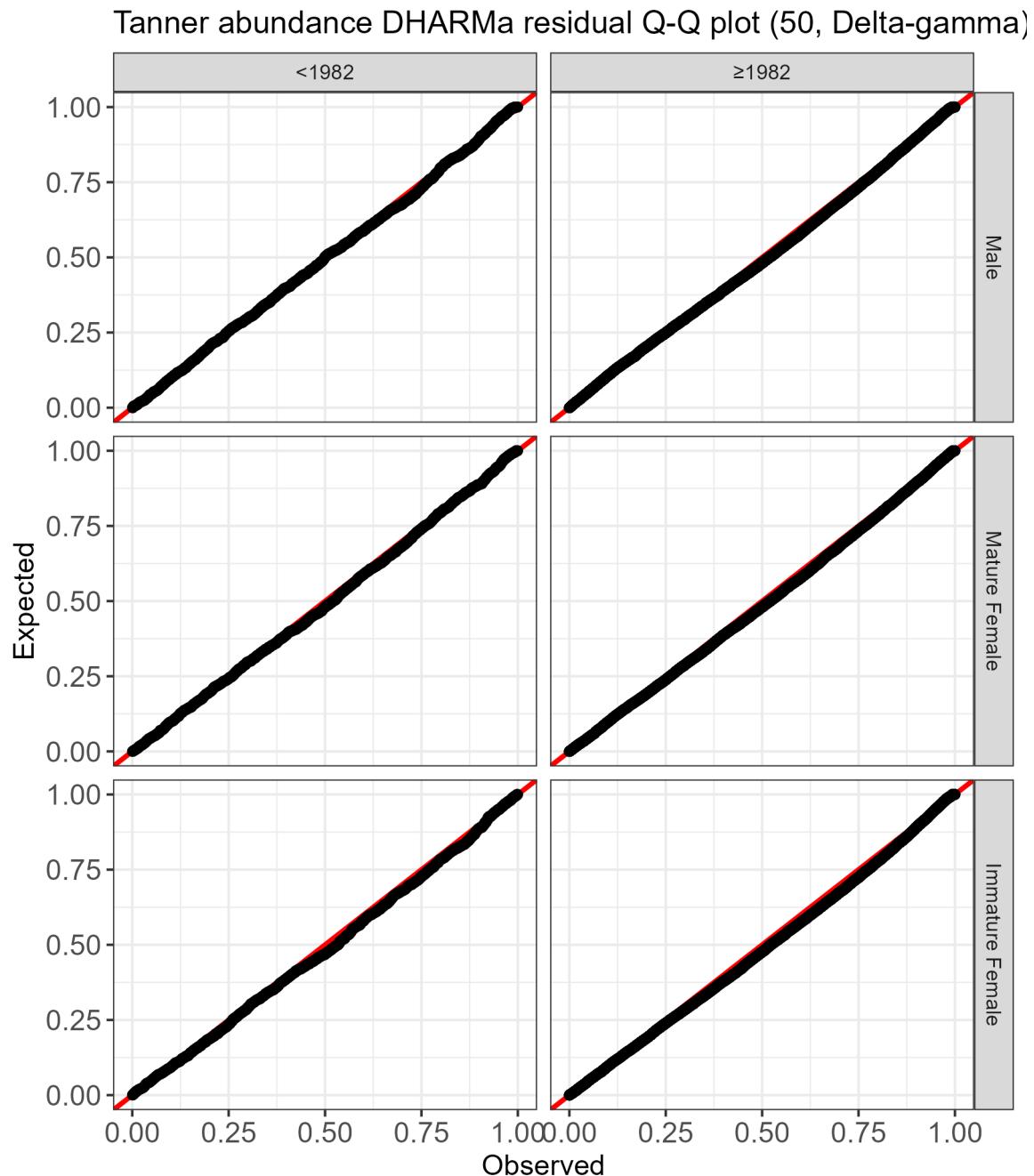


Figure 5: Q-Q plot of DHARMA residuals for abundance models fit with NMFS summer bottom trawl survey data before 1982 (left) and 1982 onward (right) using a delta-gamma model family and 50 knots in the model mesh.

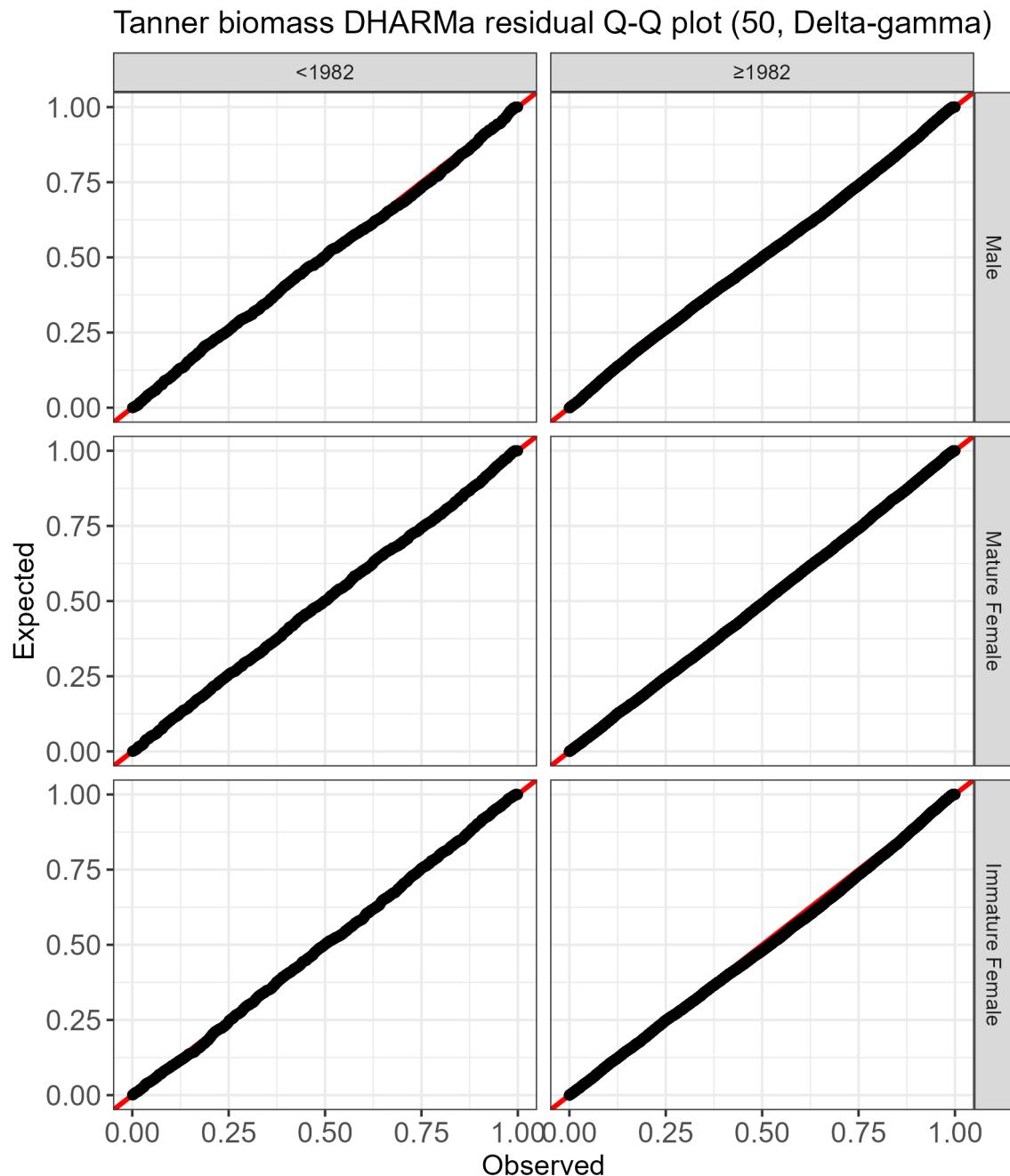


Figure 6: Q-Q plot of DHARMA residuals for biomass models fit with NMFS summer bottom trawl survey data before 1982 (left) and 1982 onward (right) using a delta-gamma model family and 50 knots in the model mesh.

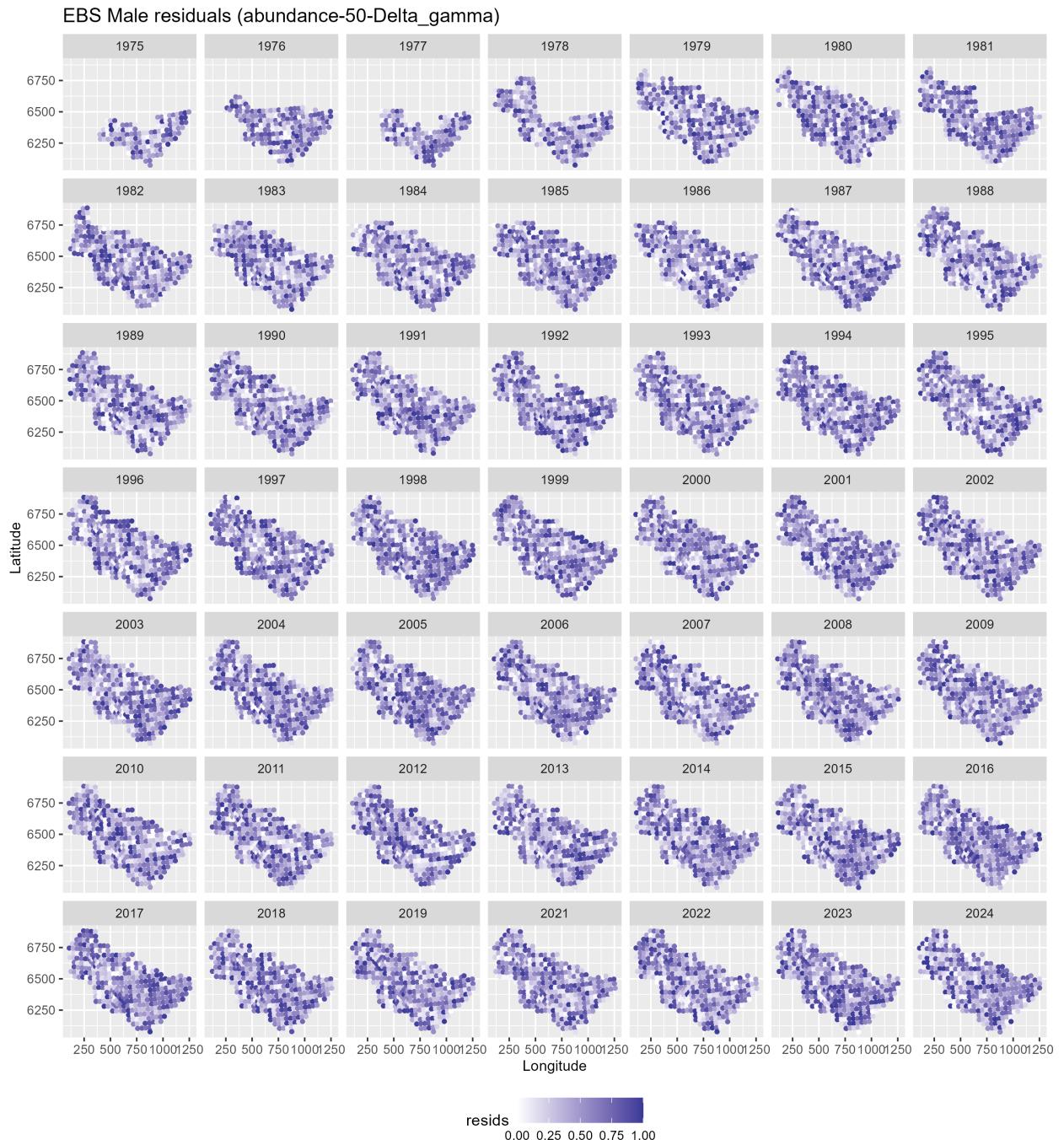


Figure 7: Spatial plot of DHARMA residuals for male abundance models fit using NMFS summer bottom trawl survey data before 1982 and 1982 onward with a 50-knot mesh and delta-gamma model family. Predictions from both of these periods/models are combined in this figure.

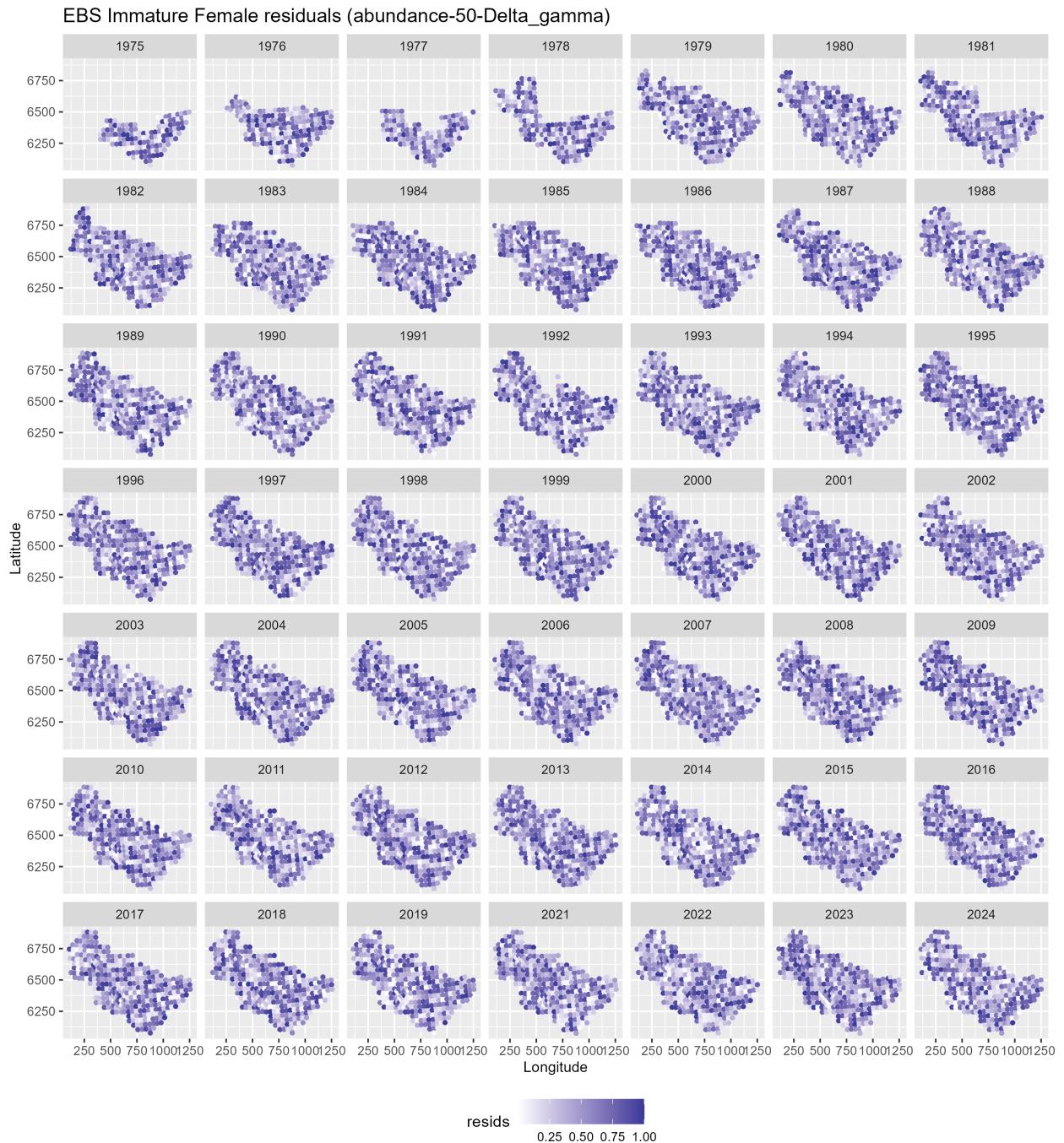


Figure 8: Spatial plot of DHARMA residuals for immature female abundance models fit using NMFS summer bottom trawl survey data before 1982 and 1982 onward with a 50-knot mesh and delta-gamma model family. Predictions from both of these periods/models are combined in this figure.

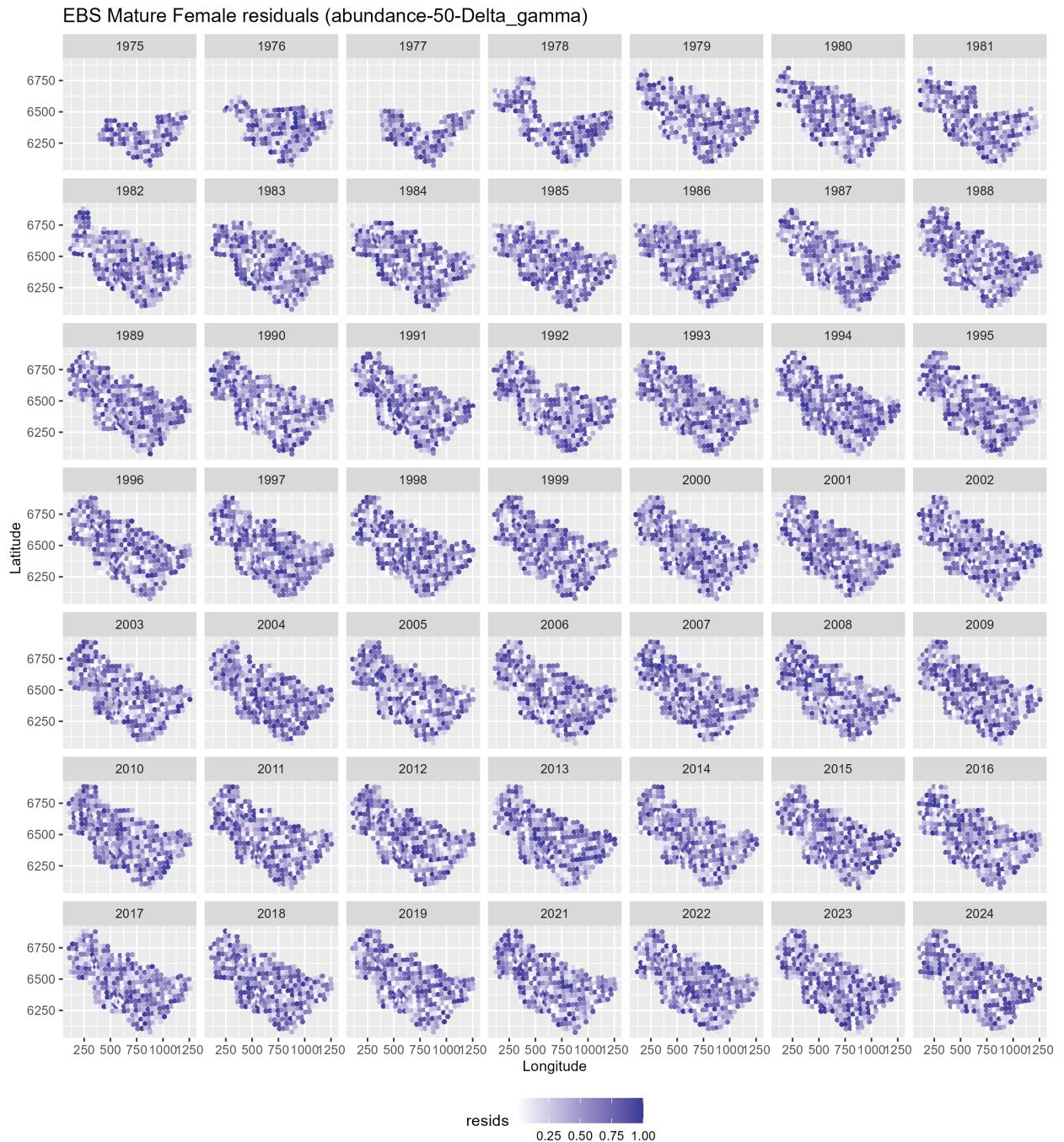


Figure 9: Spatial plot of DHARMA residuals for mature female abundance models fit using NMFS summer bottom trawl survey data before 1982 and 1982 onward with a 50-knot mesh and delta-gamma model family. Predictions from both of these periods/models are combined in this figure.

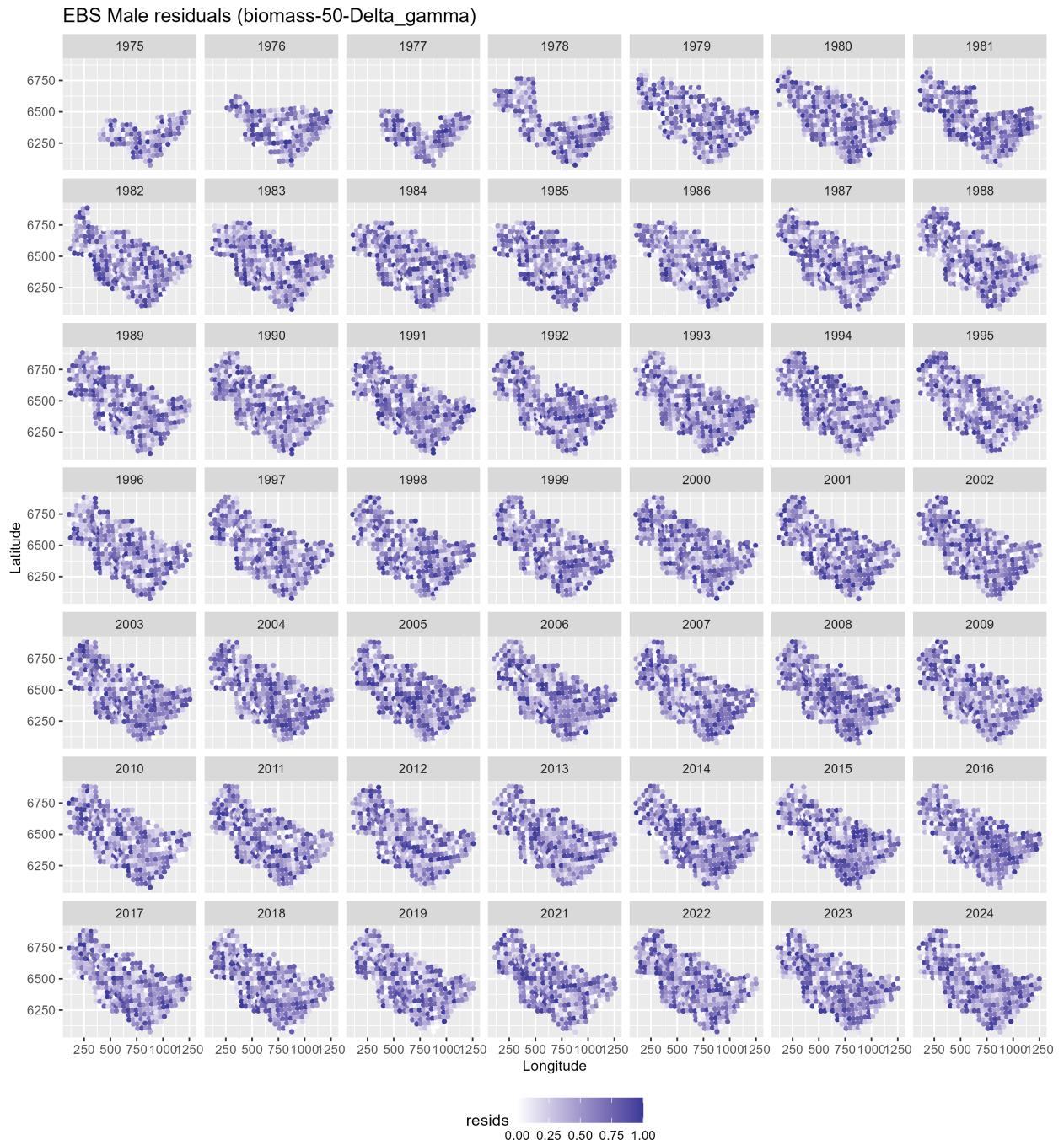


Figure 10: Spatial plot of DHARMA residuals for male biomass models fit using NMFS summer bottom trawl survey data before 1982 and 1982 onward with a 50-knot mesh and delta-gamma model family. Predictions from both of these periods/models are combined in this figure.

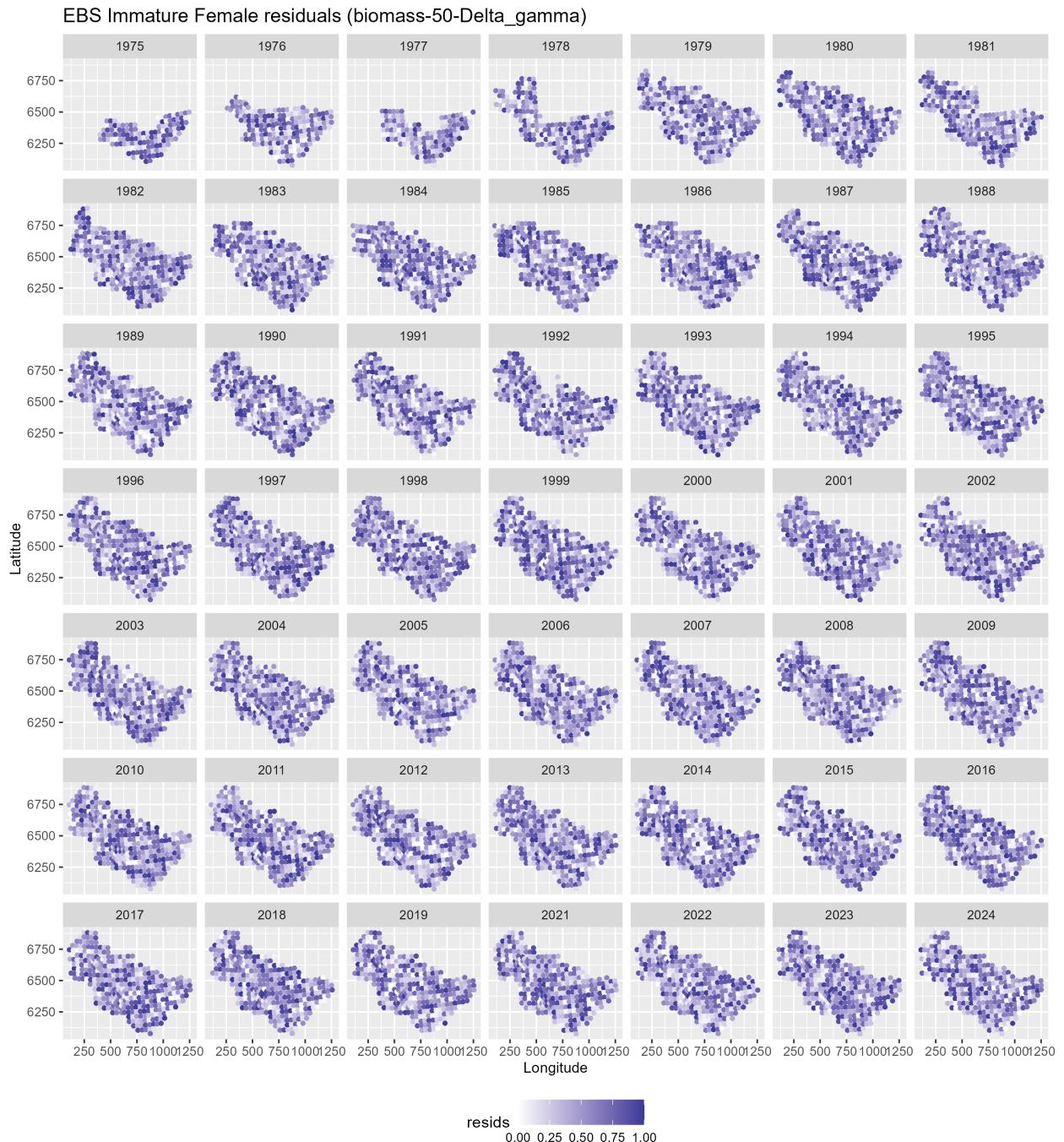


Figure 11: Spatial plot of DHARMA residuals for immature female biomass models fit using NMFS summer bottom trawl survey data before 1982 and 1982 onward with a 50-knot mesh and delta-gamma model family. Predictions from both of these periods/models are combined in this figure.



Figure 12: Spatial plot of DHARMA residuals for mature female biomass models fit using NMFS summer bottom trawl survey data before 1982 and 1982 onward with a 50-knot mesh and delta-gamma model family. Predictions from both of these periods/models are combined in this figure.

## EBS Tanner estimated abundance

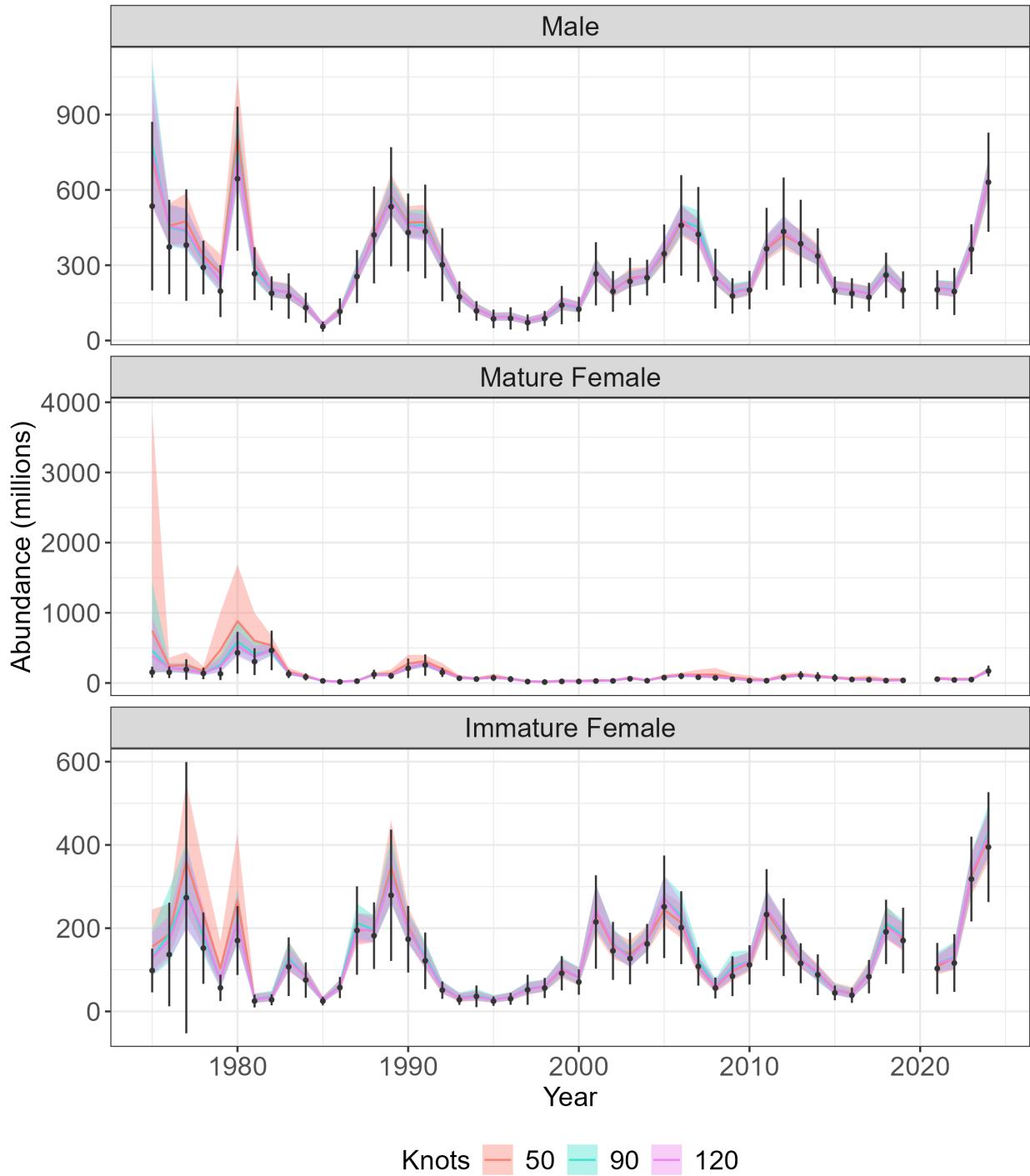


Figure 13: Estimated abundance (millions) for Tanner crab. Colored lines represent abundance ( $\pm 95\%$  CI) estimated by sdmTMB, with orange, blue, and pink denoting models fit with a 50-, 90-, and 120-knot mesh, respectively. Black points represent abundance ( $\pm 95\%$  CI) estimated by the NMFS summer bottom trawl survey.

## EBS Tanner estimated biomass

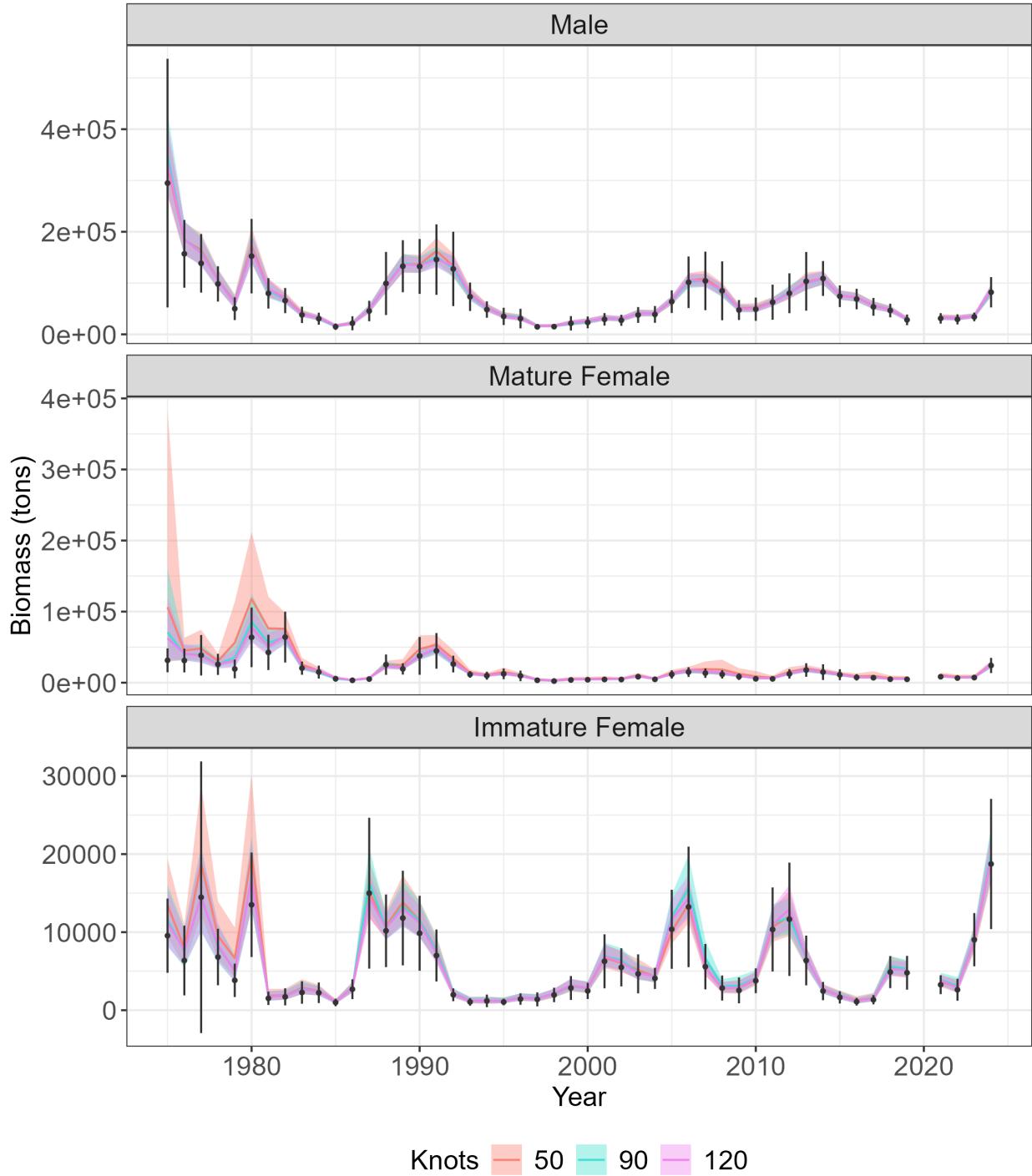


Figure 14: Estimated biomass (tons) for Eastern Bering Sea Tanner crab. Colored lines represent abundance ( $\pm 95\%$  CI) estimated by sdmTMB, with orange, blue, and pink denoting models fit with a 50-, 90-, and 120-knot mesh, respectively. Black points represent biomass ( $\pm 95\%$  CI) estimated by the NMFS summer bottom trawl survey.

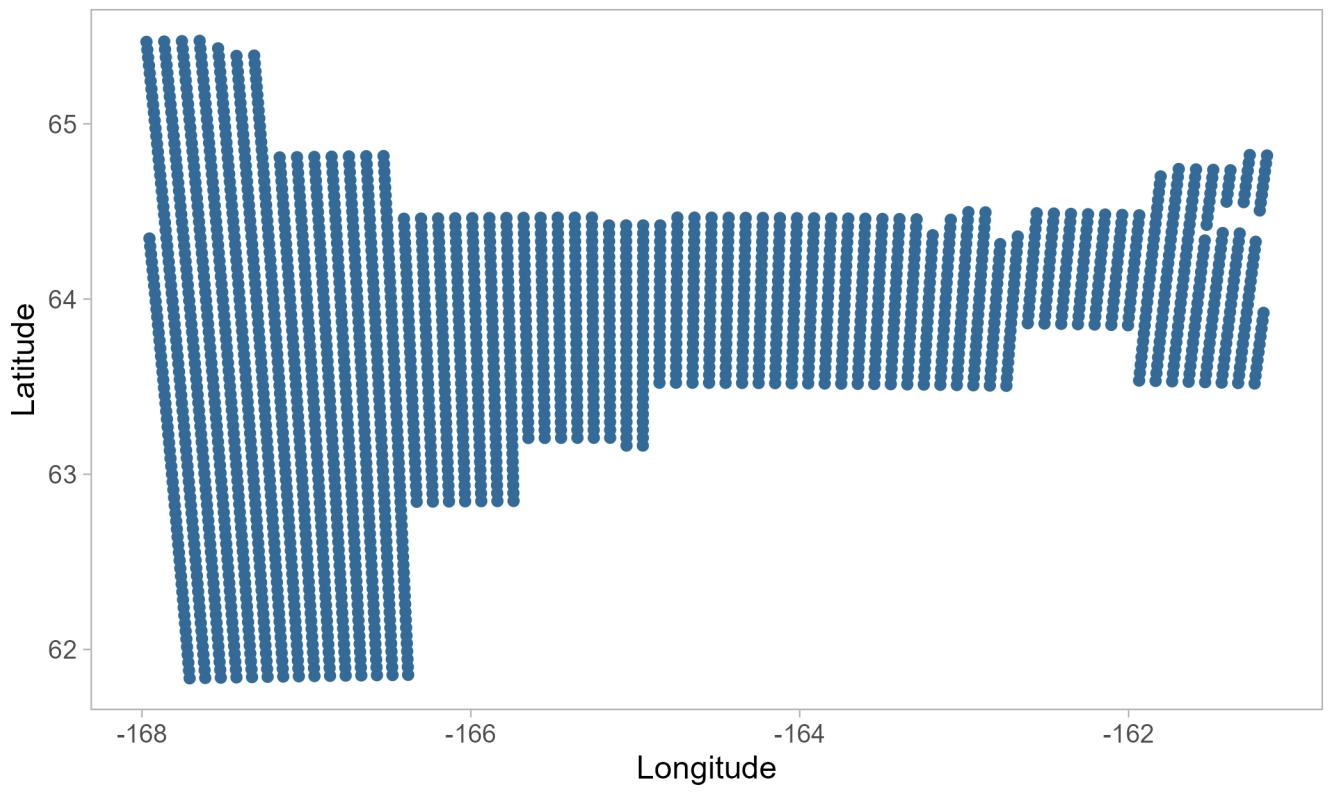


Figure 15: Prediction grid used for Norton Sound red king crab spatial abundance predictions. Spatial resolution is  $5 \text{ km}^2$ .

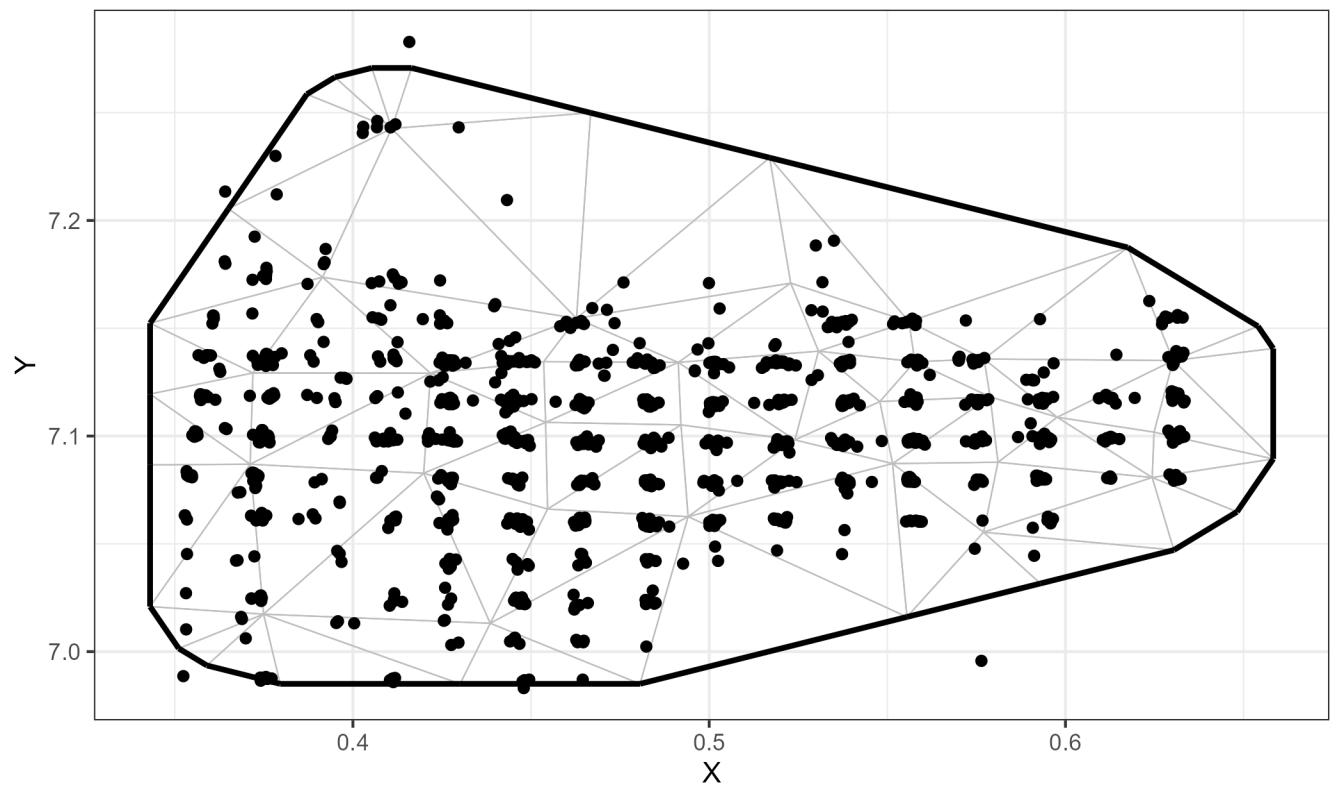


Figure 16: Spatial mesh with 30 knots used for fitting Norton Sound red king crab spatial models. Points represent observations and vertices represent knot locations.

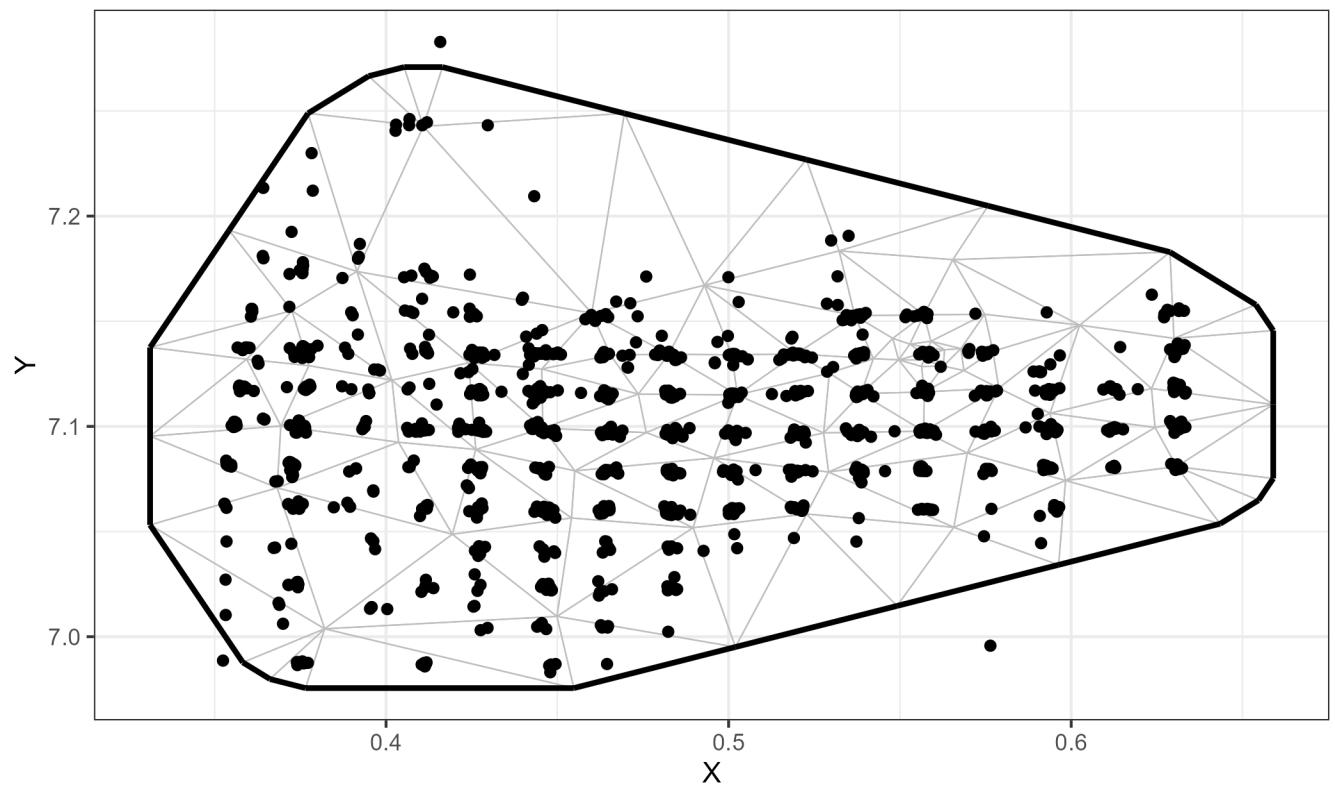


Figure 17: Spatial mesh with 50 knots used for fitting Norton Sound red king crab spatial models. Points represent observations and vertices represent knot locations.

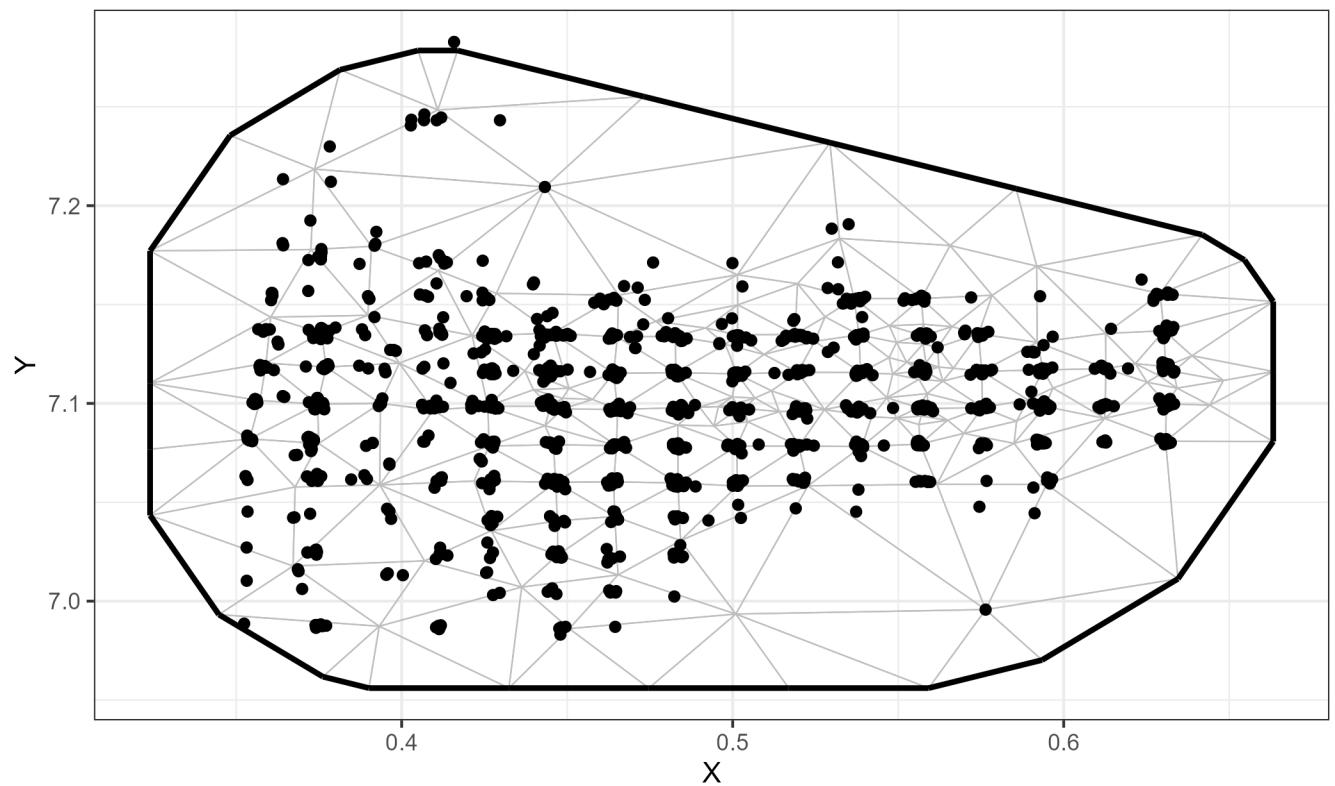


Figure 18: Spatial mesh with 100 knots used for fitting Norton Sound red king crab spatial models. Points represent observations and vertices represent knot locations.

## Appendix

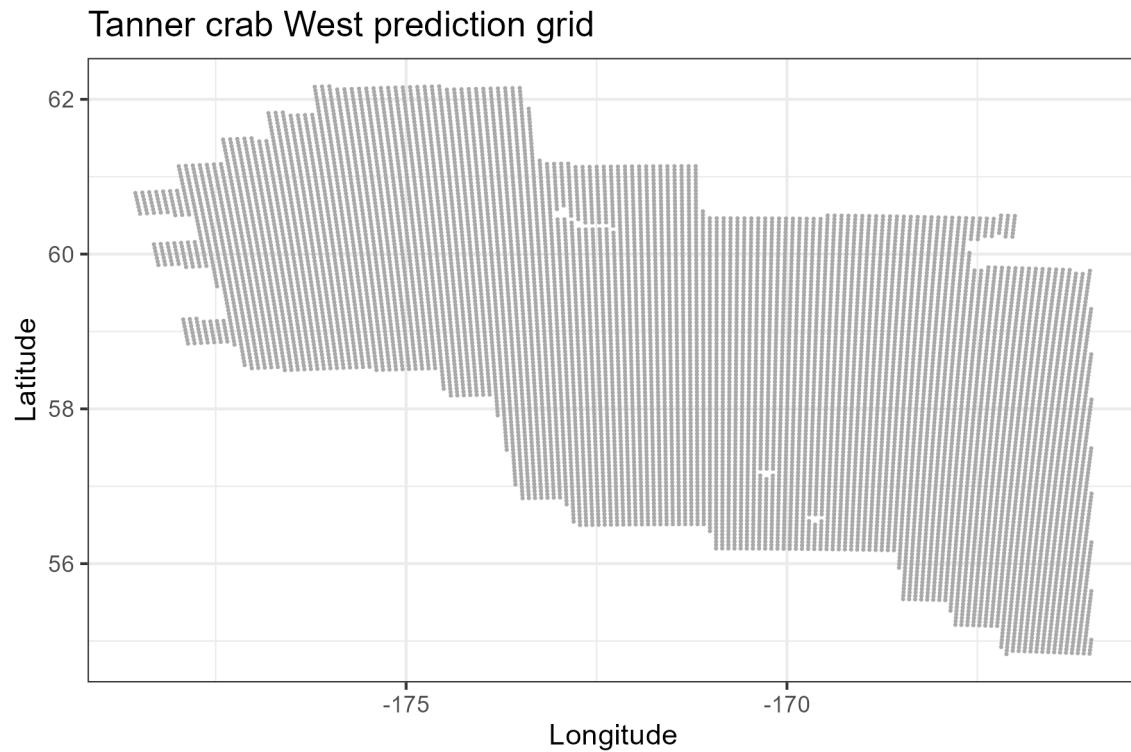


Figure 19: Prediction grid used to predict spatial abundance and biomass for Tanner crab west of  $166^{\circ}$ . Spatial resolution is  $5\text{km}^2$  and does not include land.

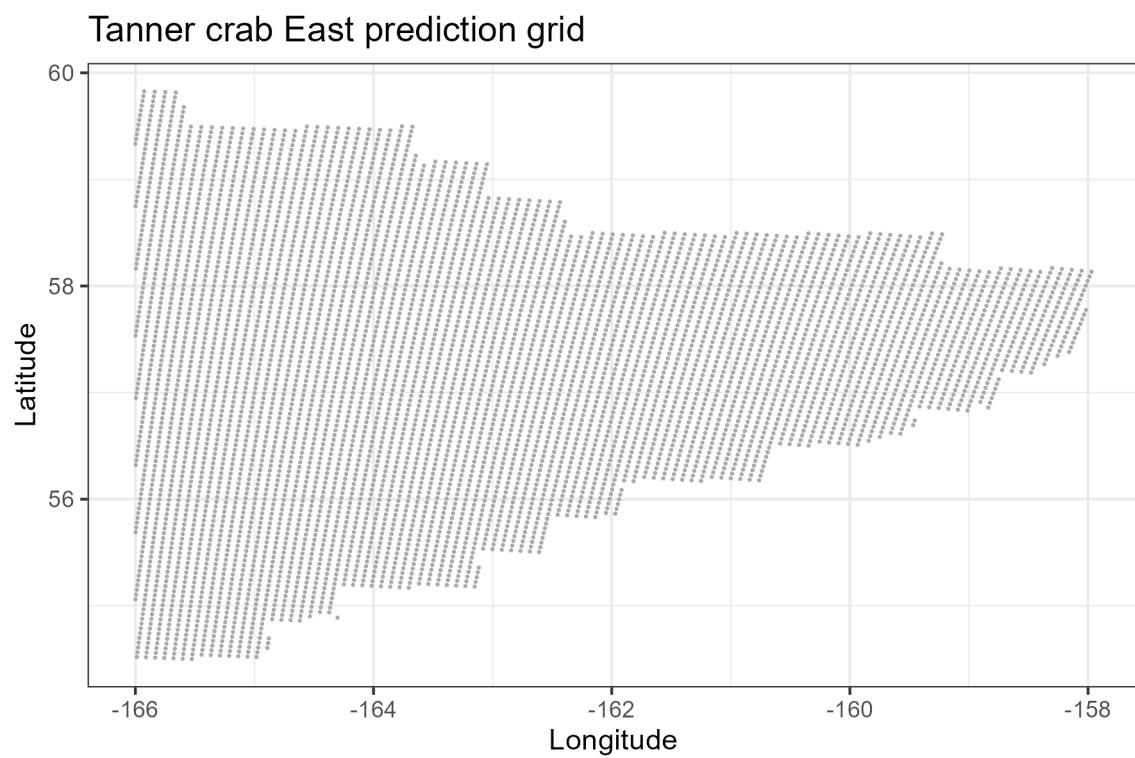


Figure 20: Prediction grid used to predict spatial abundance and biomass for Tanner crab west of  $166^{\circ}$ . Spatial resolution is  $5\text{km}^2$  and does not include land.