

# Spatiotemporal model-based indices for BSAI crab stocks

Update for Crab Plan Team

Emily Ryznar, Jon Richar, and Caitlin Stern  
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# Goals

1. Develop spatiotemporal model-based indices for:
  - Bering Sea Tanner crab
  - Bering Sea snow crab
  - St. Matthew Island blue king crab (see January modeling workshop)
  - Norton Sound red king crab
2. Develop a transparent process for evaluating and selecting models

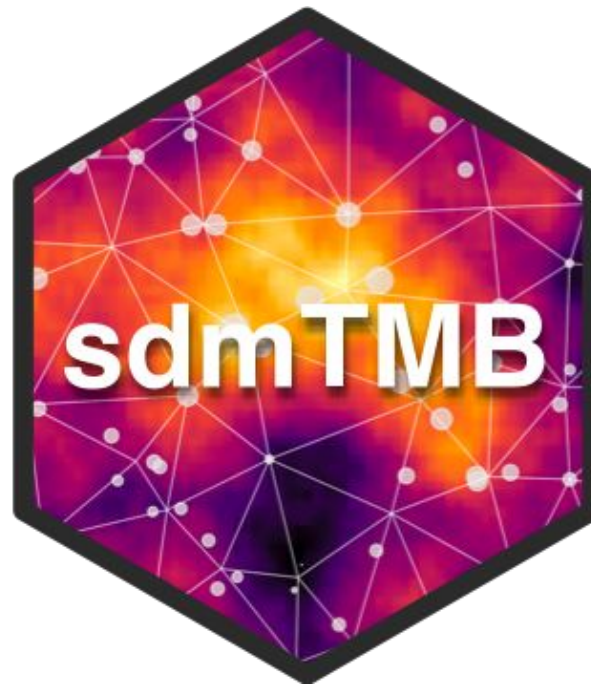


# Approach

Fit models using the *sdmTMB* R package

*sdmTMB* estimates spatial and spatiotemporal generalized linear mixed effects models

Allows for index standardization when the set of stations surveyed is inconsistent across years



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# Comparison with VAST

- VAST models also accomplish index standardization, but are often criticized for:
  - A difficult user interface
  - Slower fitting times
  - Less flexible model specification
- We compared model-indices generated using sdmTMB and VAST (when available) using the best sdmTMB model specification
- The equivalence of VAST and sdmTMB models has been demonstrated in direct comparisons for groundfish stocks:

[https://github.com/afsc-gap-products/model-based-indices/blob/main/species\\_specific\\_code/GOA/sdmTMB\\_VAST\\_index\\_comparison\\_goa.Rmd](https://github.com/afsc-gap-products/model-based-indices/blob/main/species_specific_code/GOA/sdmTMB_VAST_index_comparison_goa.Rmd)



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# Model-fitting decision points

## Resolution of spatial mesh used to fit model

- more knots = higher resolution

## Spatiotemporal random fields estimation

- IID: RF independent from one time step to next
- AR1: RF correlated from one time step to next
- random walk: difference in spatiotemporal deviations from one time step to the next are IID

## Observation model family

- Tweedie, delta-gamma, delta-lognormal



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```
m.smbkc.rw.tw.90kn <- sdmTMB(  
  data = bkc_kgkm_utm,  
  formula = kg.km ~ 0 + year_f,  
  spatial = "on",  
  time = "SURVEY_YEAR",  
  mesh = BK_spde_90kn,  
  spatiotemporal = "rw",  
  extra_time = c(2020),  
  silent = FALSE,  
  anisotropy = TRUE,  
  family = tweedie(link = "log"))
```



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# Model diagnostics: sanity checks

`sdmTMB::sanity()`

- ✓ 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



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# Model diagnostics: DHARMa residuals

- Calculated residuals using the *DHARMa* R package
- Tested for quantile deviations, over- or underdispersion, outliers, and zero-inflation using *DHARMa*
- Plotted *DHARMa* residuals spatially to evaluate potential spatiotemporal autocorrelation



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# Model diagnostics: predictive skill

- Used cross validation to estimate log-likelihood values across models
  - Larger log-likelihood, better predictive skill

**The shadow model: how and why small choices in spatially explicit species distribution models affect predictions**

Christian J. C. Commander<sup>1,2</sup>, Lewis A. K. Barnett<sup>3</sup>, Eric J. Ward<sup>4</sup>,  
Sean C. Anderson<sup>5</sup> and Timothy E. Essington<sup>2</sup>

- Evaluated model spatial predictions over time
- Plotted model-predicted indices against observed values



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Tanner crab





# Specific methods for Tanner crab

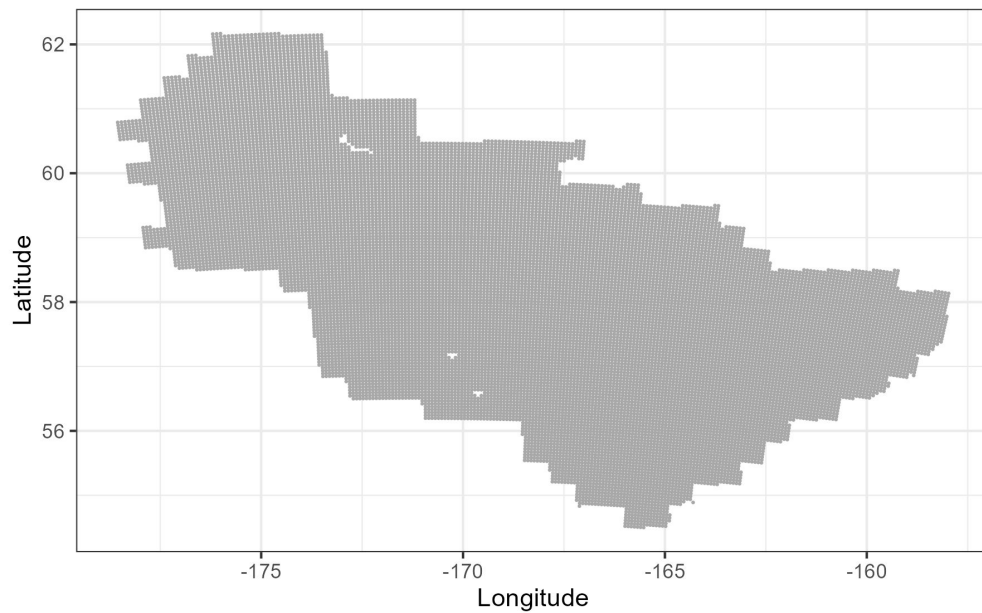
- Fit models for abundance and biomass
- Fit models for all males, mature females, immature females
- Fit separate models for survey data  $<1982$  and  $\geq 1982$  due to gear change
- Fit EBS-wide models, predict Tanners east and west of  $166^\circ$
- Model family: delta-gamma, Tweedie, delta-lognormal
- Random field: IID, AR1, random walk



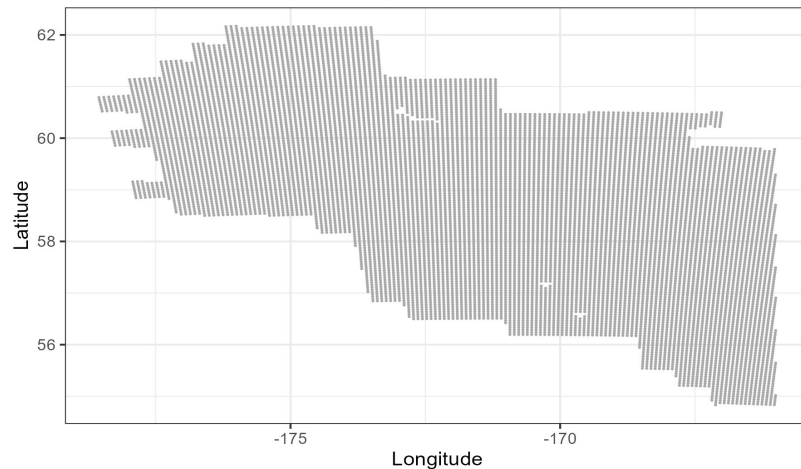
# Prediction grids

- 5 km<sup>2</sup> resolution, no land

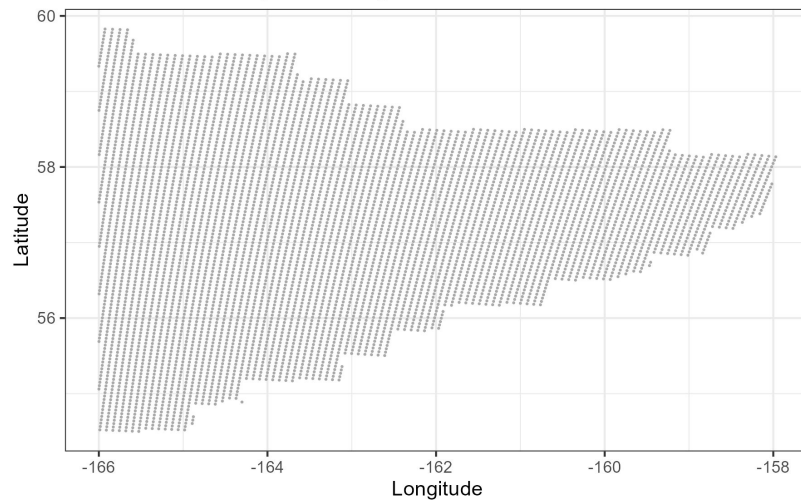
EBS prediction grid



Tanner crab West prediction grid



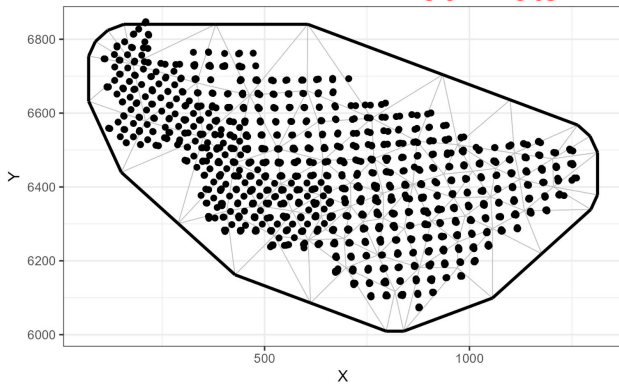
Tanner crab East prediction grid



# Model mesh

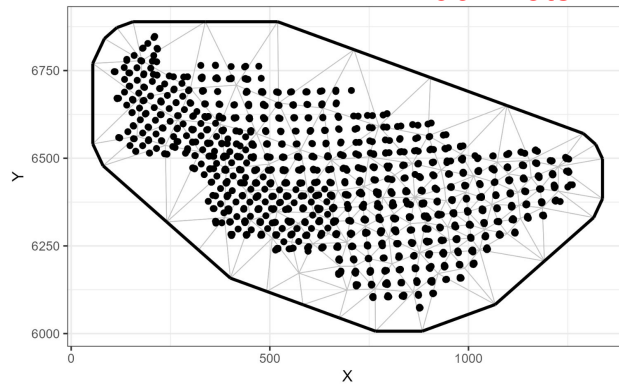
<1982 mesh (knots=72)

50 knots



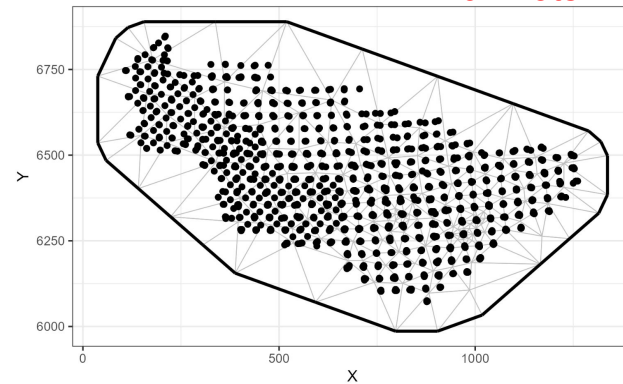
<1982 mesh (knots=122)

90 knots

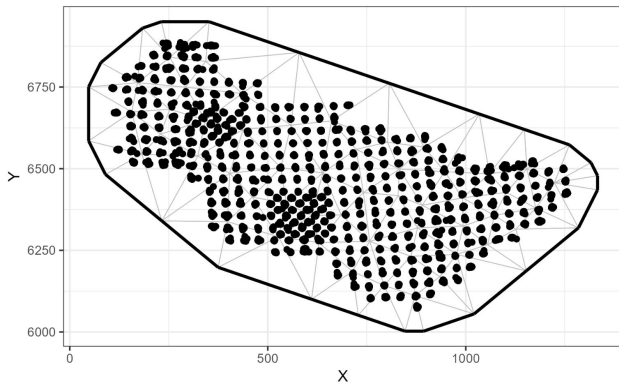


<1982 mesh (knots=188)

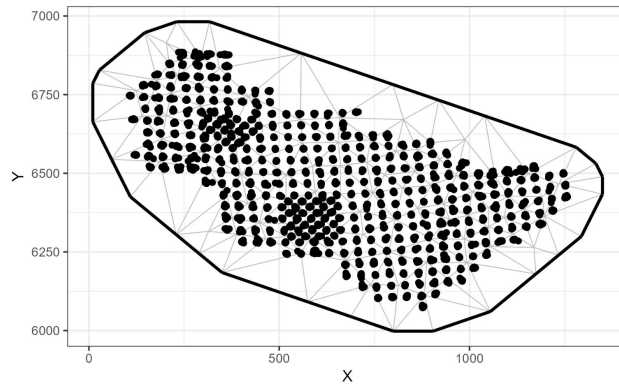
120 knots



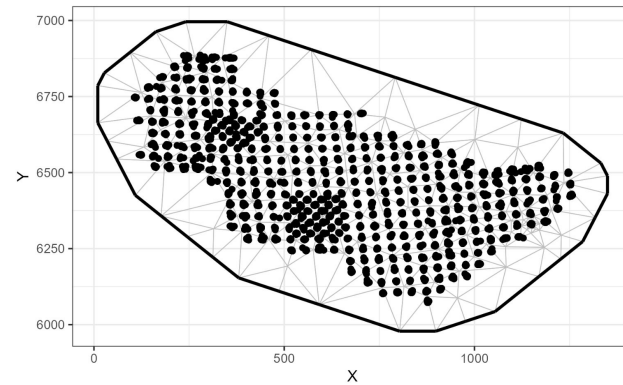
$\geq 1982$  mesh (knots=74)



$\geq 1982$  mesh (knots=122)



$\geq 1982$  mesh (knots=188)



# Overall model diagnostics

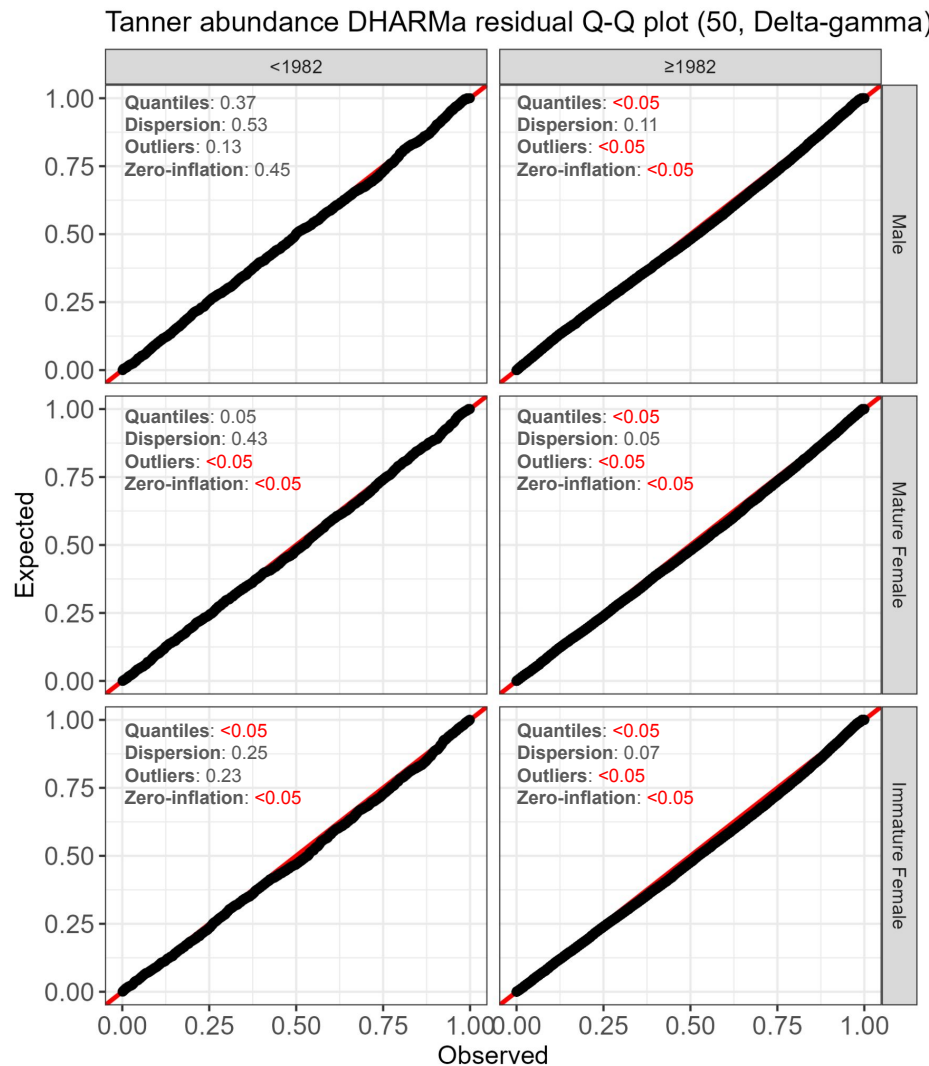
- Best: delta-gamma, 50-knot mesh
- Other model-specifications could be selected by fitting period and sex-maturity category
- Delta-lognormal did not pass model diagnostics, AR1 and random walk did not converge

knots	family	n	loglik	BEST
<int>	<chr>	<int>	<dbl>	<chr>
50	Delta_gamma	6	- <u>194983.</u>	"YES"
50	Tweedie	6	- <u>195595.</u>	""
90	Delta_gamma	6	- <u>195454.</u>	""
90	Tweedie	6	- <u>195515.</u>	""
120	Delta_gamma	6	- <u>196720.</u>	""
120	Tweedie	6	- <u>196297.</u>	""

# Abundance model diagnostics

- No significant residual deviation from 1-1 line
- Statistical evidence of quantile deviation, outliers, and zero-inflation
- True regardless of model family or knot number

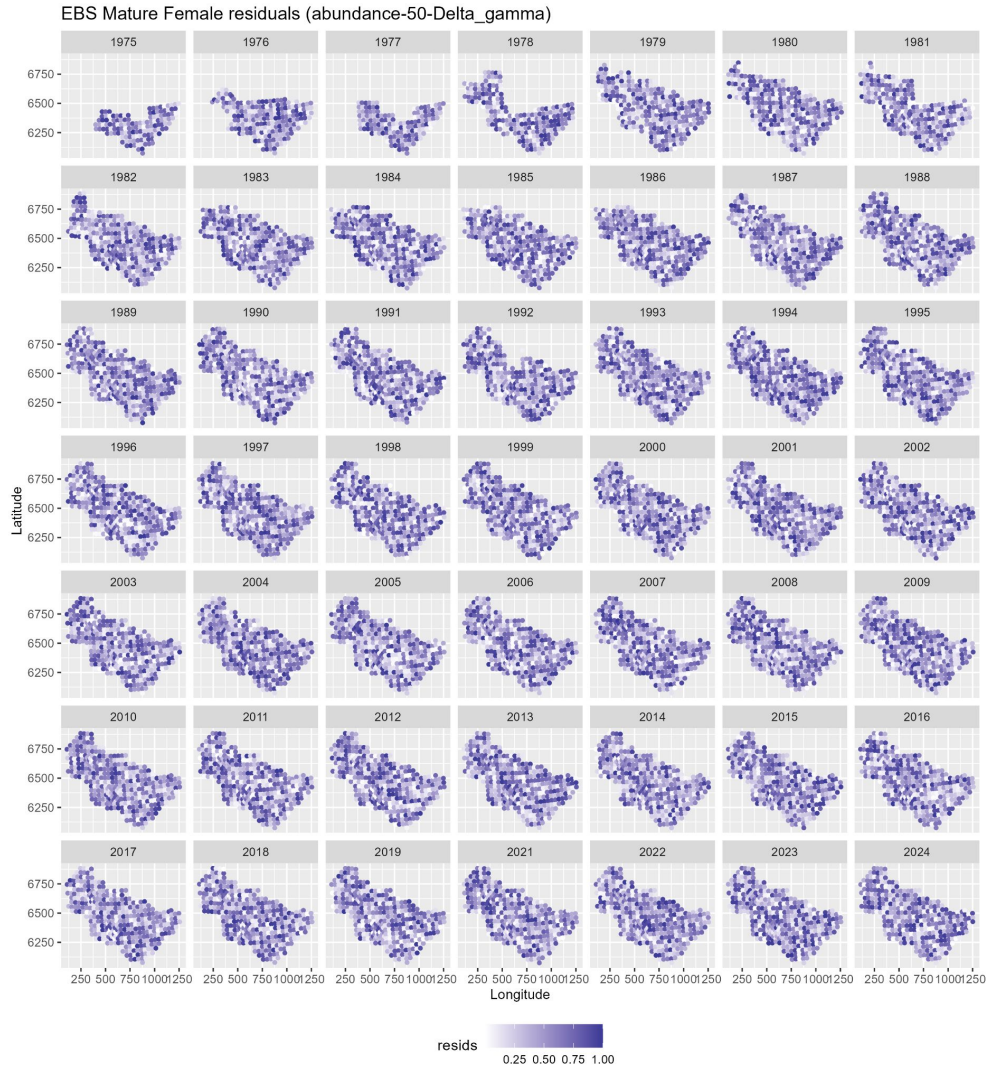
Delta-gamma, 50 knots



# Abundance model diagnostics

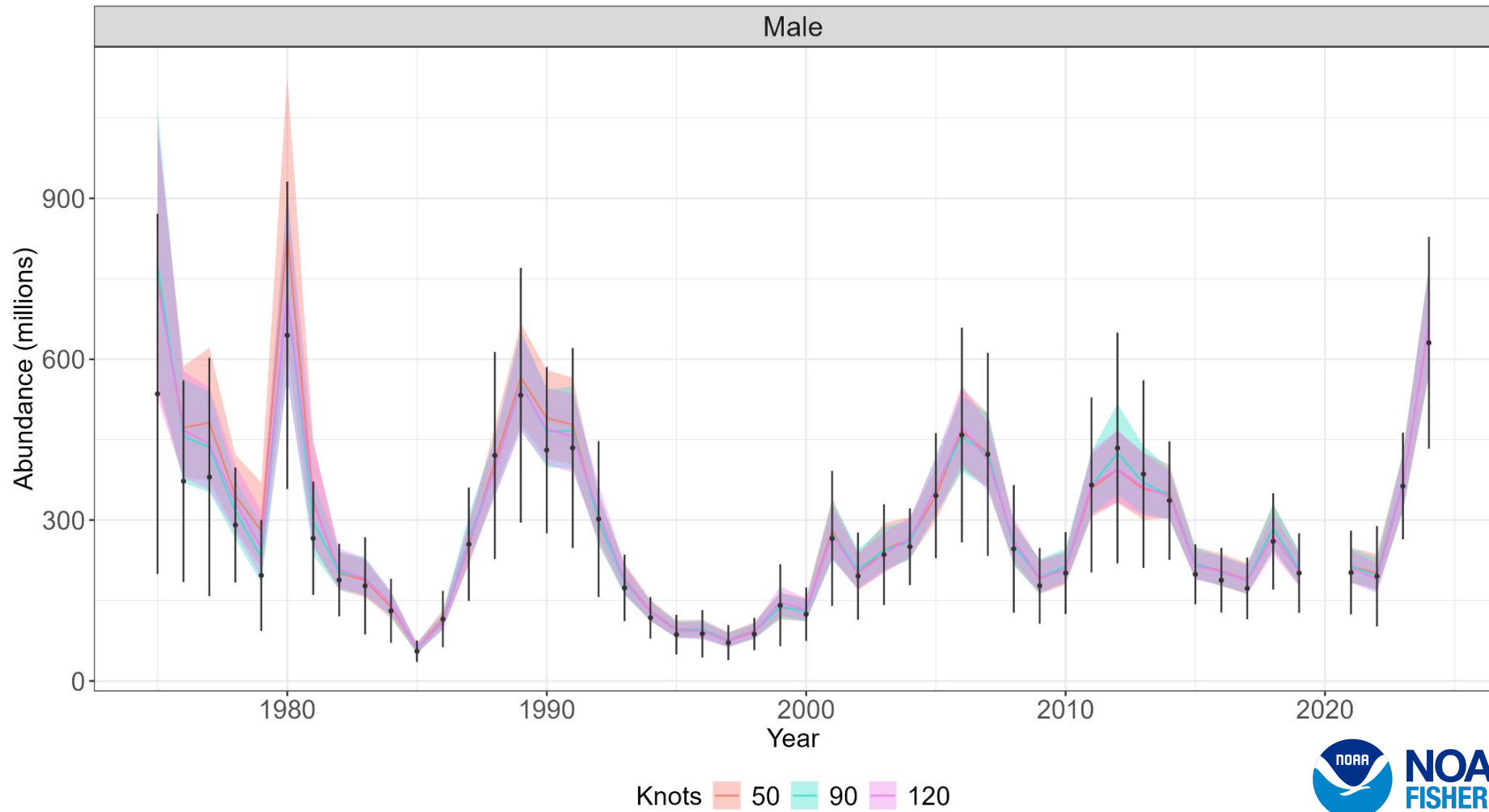
- No evidence of spatiotemporal autocorrelation of DHARMA residuals across categories

Delta-gamma, 50 knots

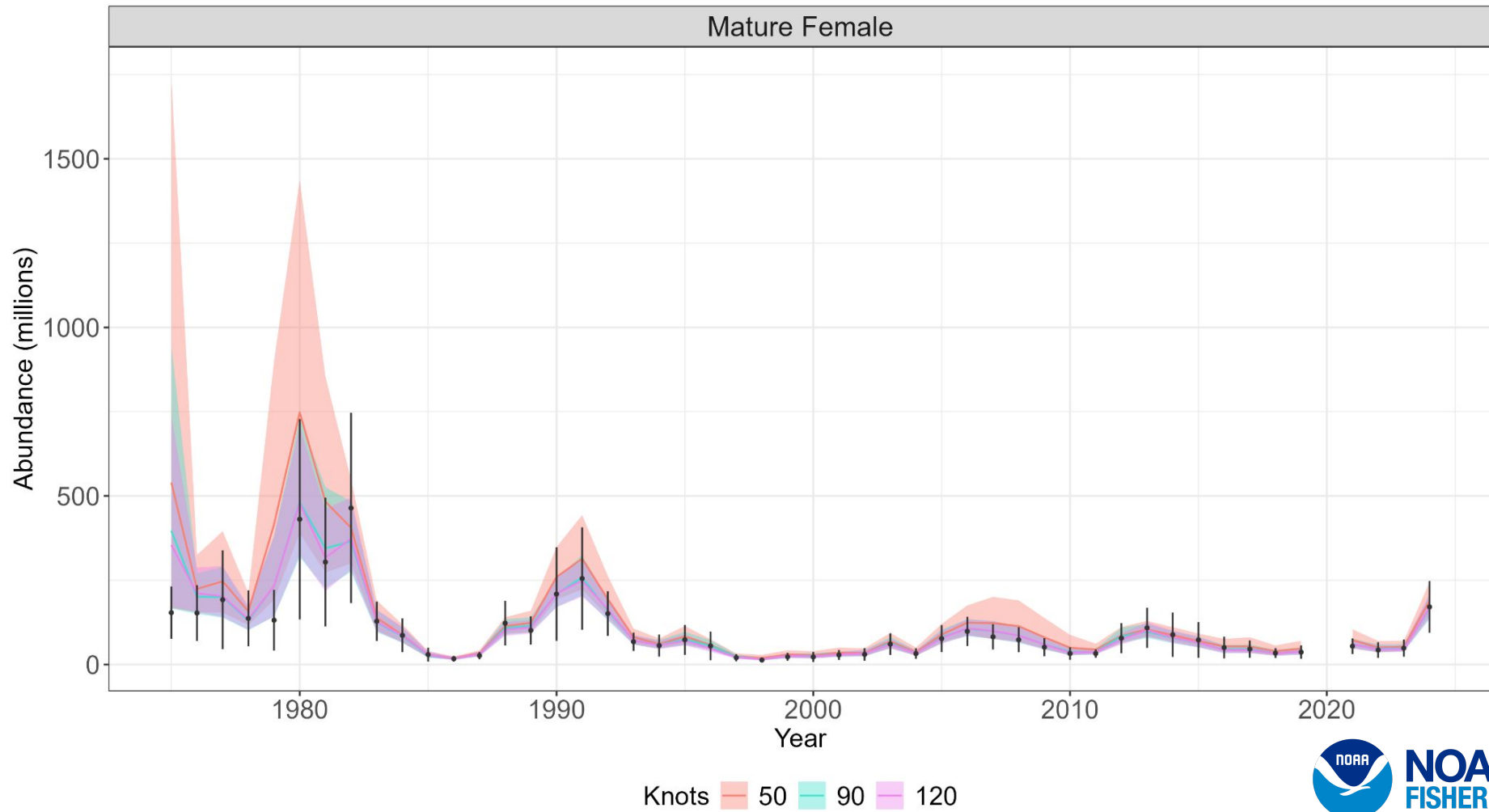




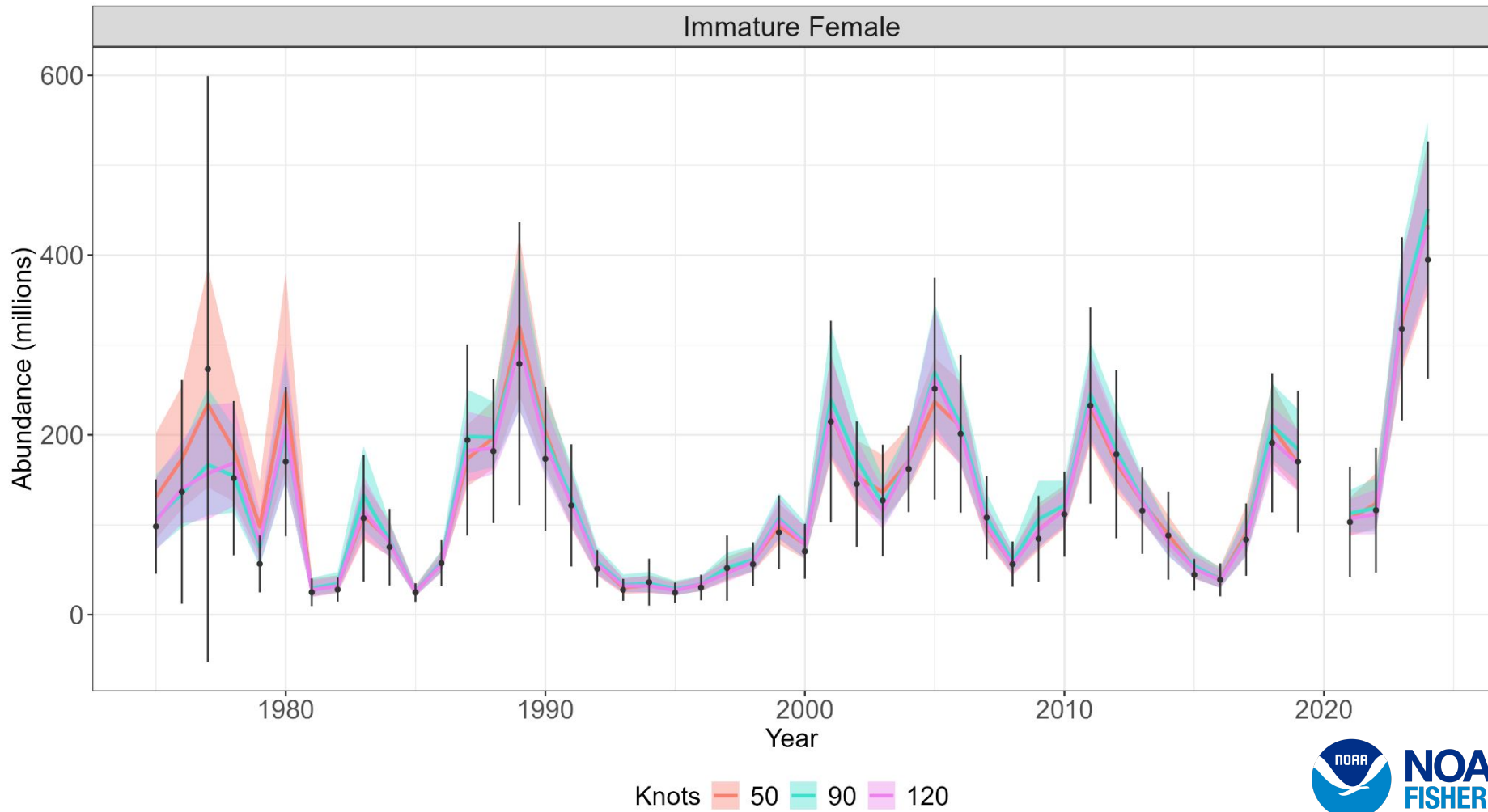
# EBS Tanner estimated abundance



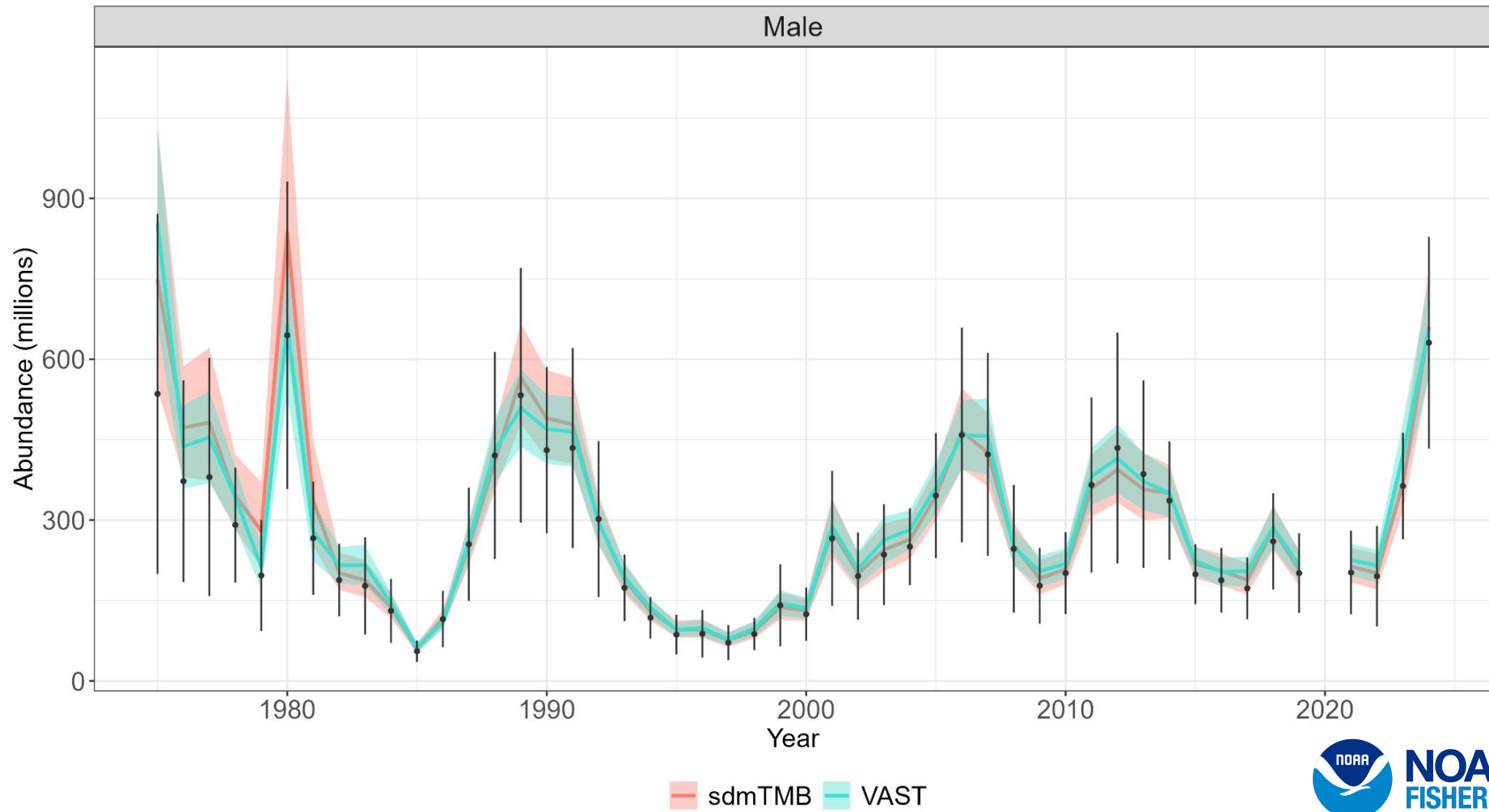
# EBS Tanner estimated abundance



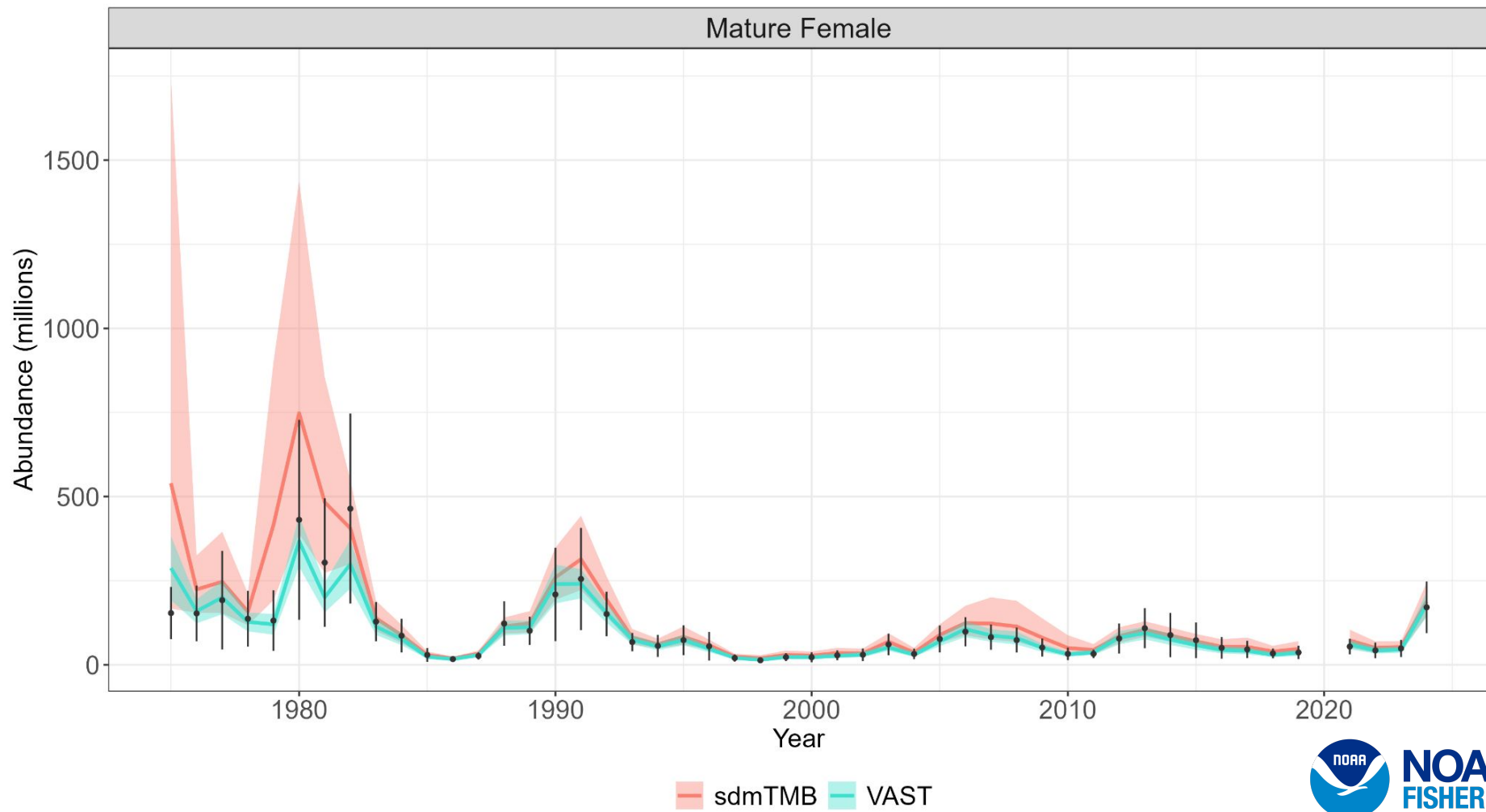
# EBS Tanner estimated abundance



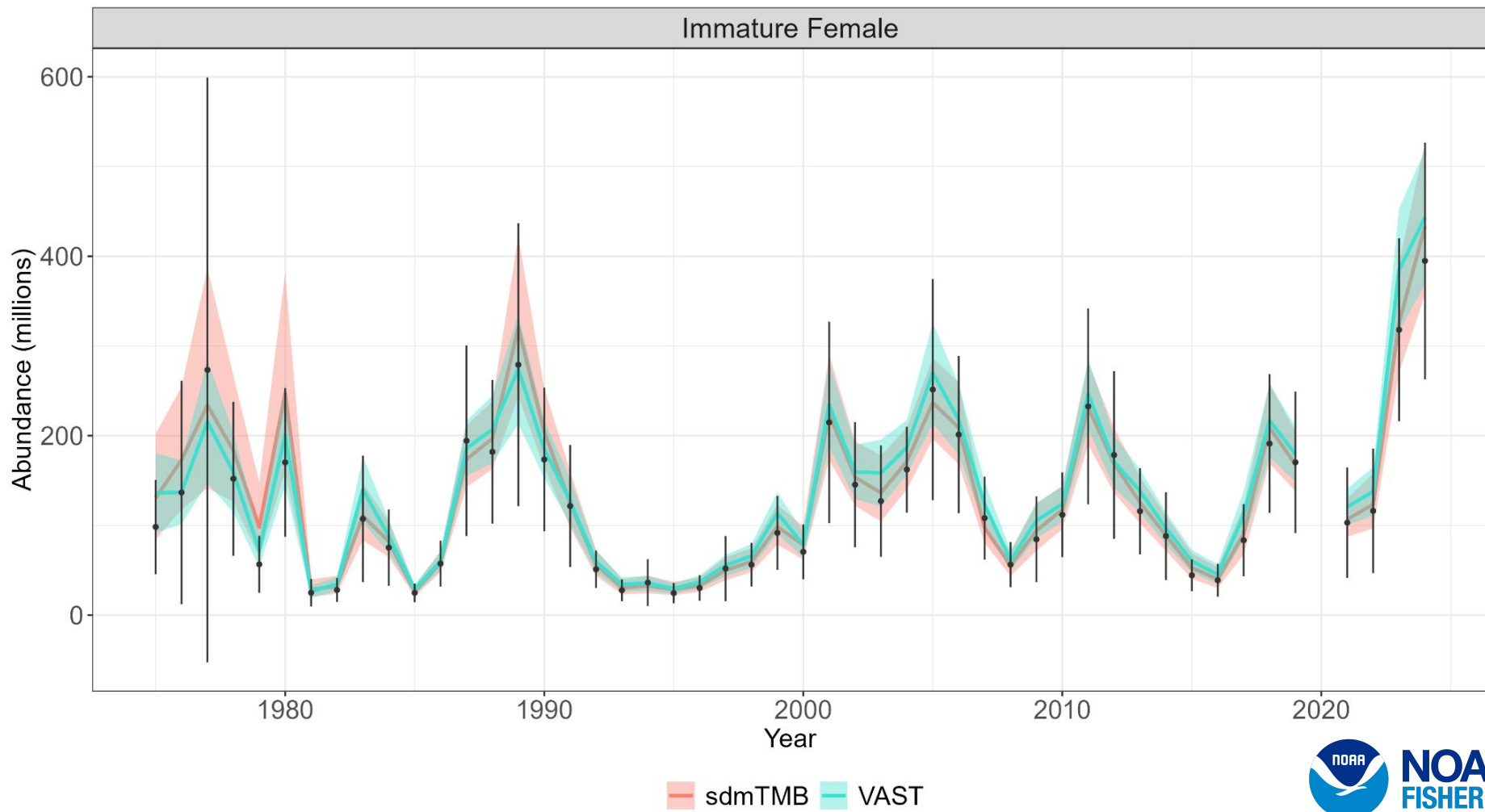
# EBS Tanner estimated abundance



# EBS Tanner estimated abundance



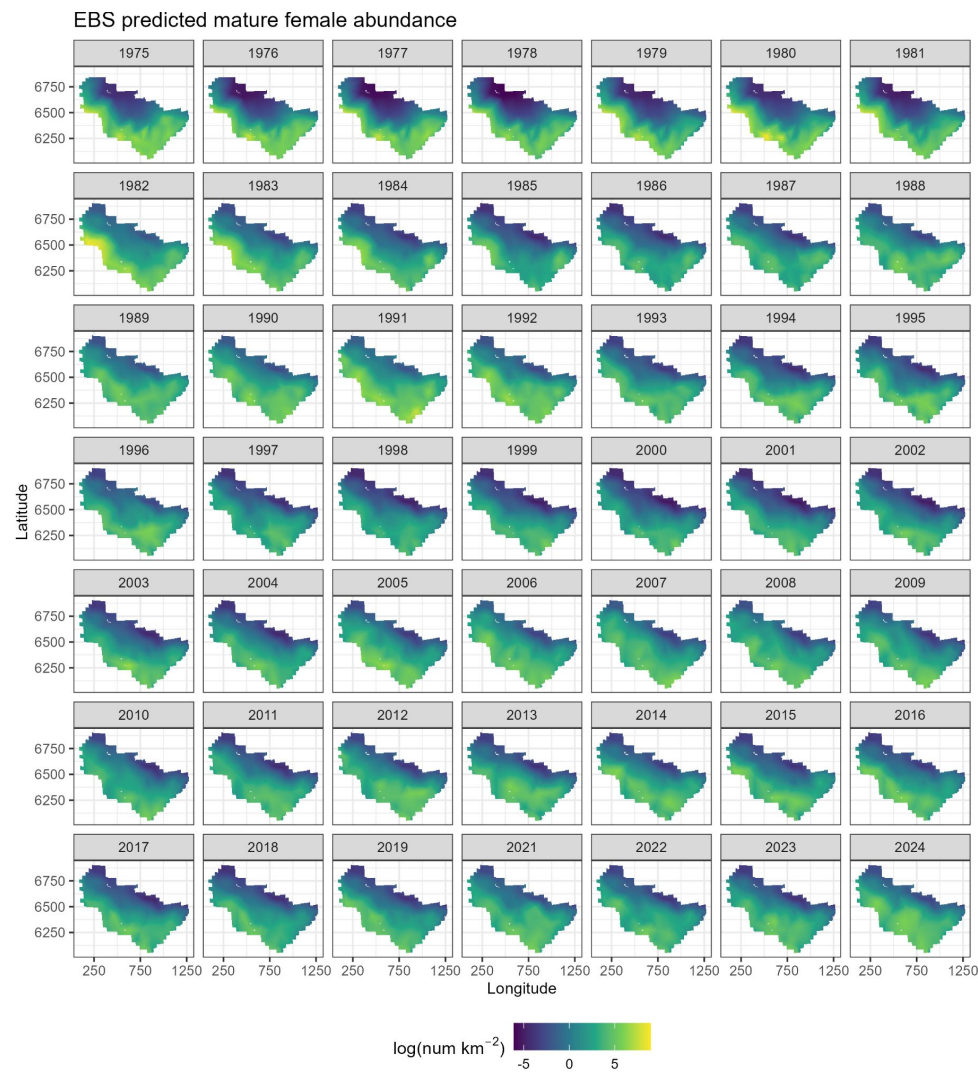
# EBS Tanner estimated abundance



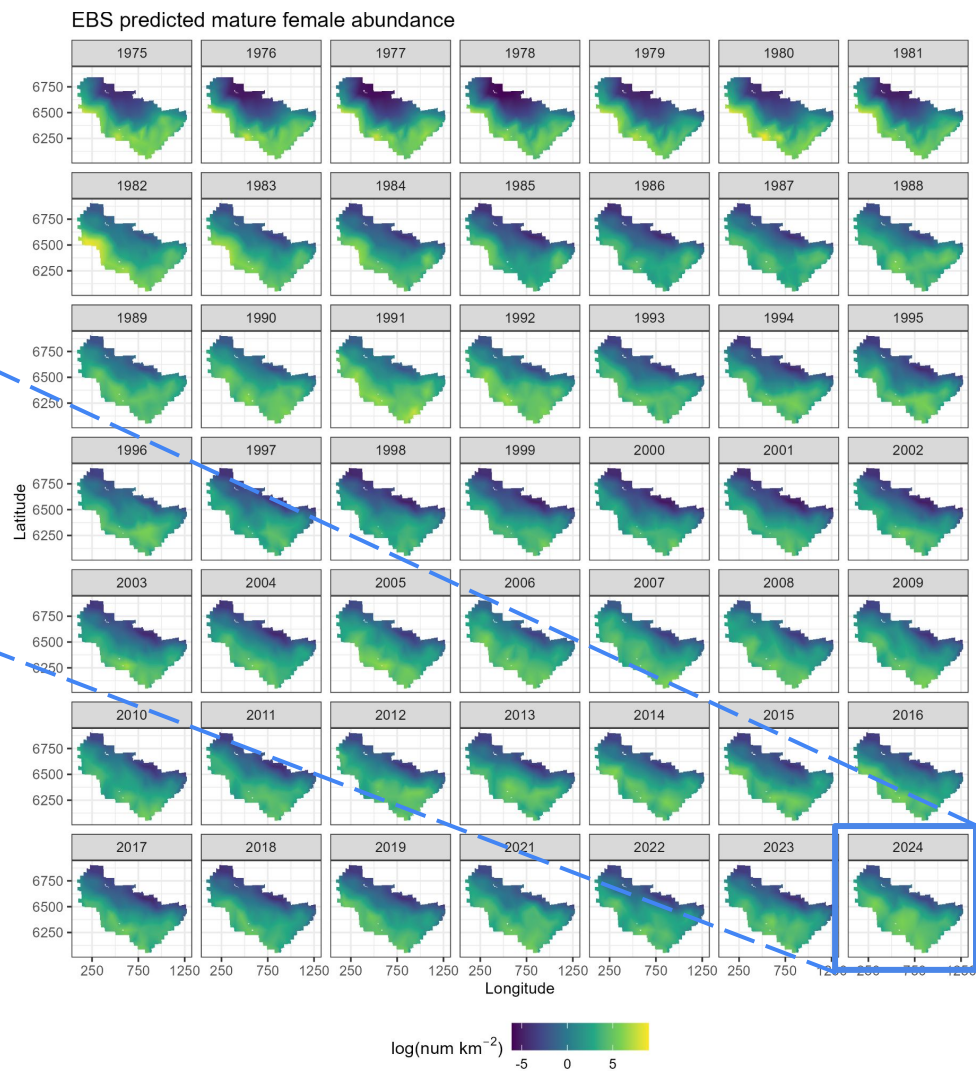
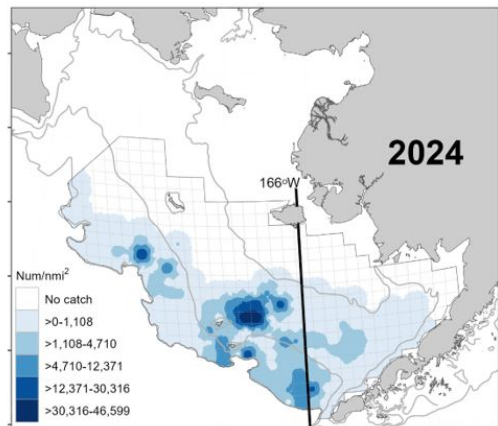
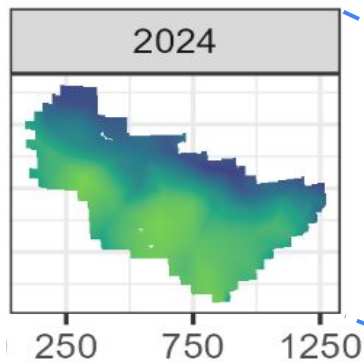


# Predicted abundance

Delta-gamma, 50 knots



# Predicted abundance



# Tanner crab conclusions and next steps

- Delta-gamma using a 50-knot mesh has the best overall predictive skill
- Questions:
  1. Should model frameworks be specific to period and/or sex-maturity category or the same?
  2. How to balance model diagnostics versus visual fits to observations?



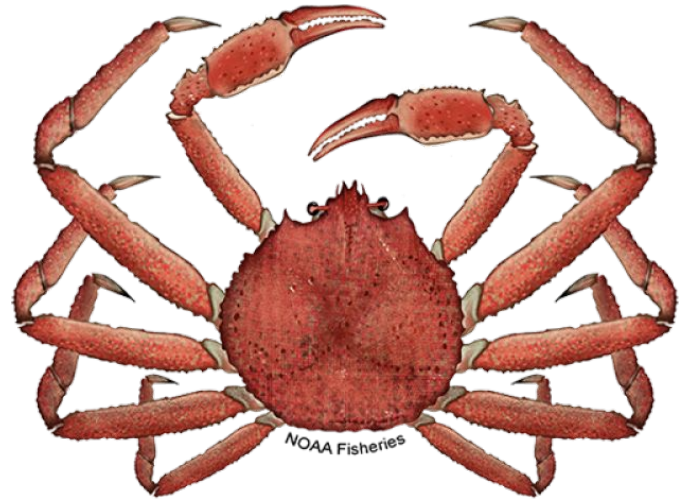


Snow crab



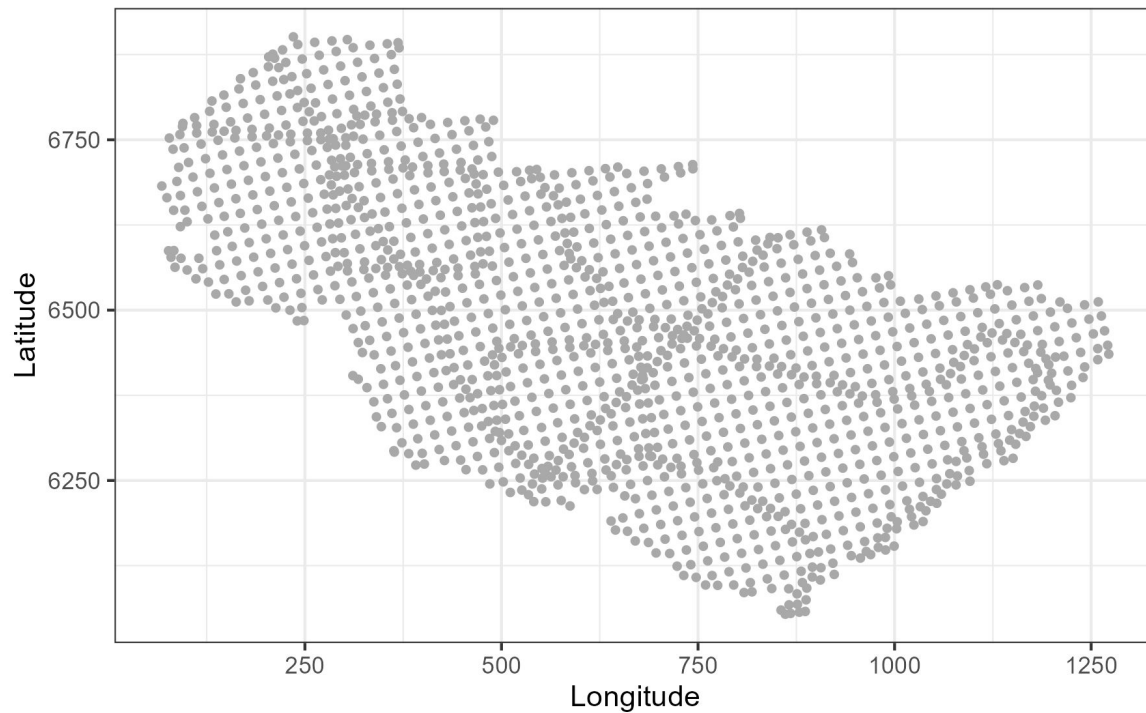
# Specific methods for snow crab

- Only fit biomass models
- Fit models for males  $> 95\text{mm}$  and mature females
- Fit models with EBS-only and EBS-NBS data, predict to EBS, compare
- Model family: delta-gamma and Tweedie
- Random field:
  - IID (EBS-data only)
  - AR1 (EBS-NBS data)



# Prediction grid

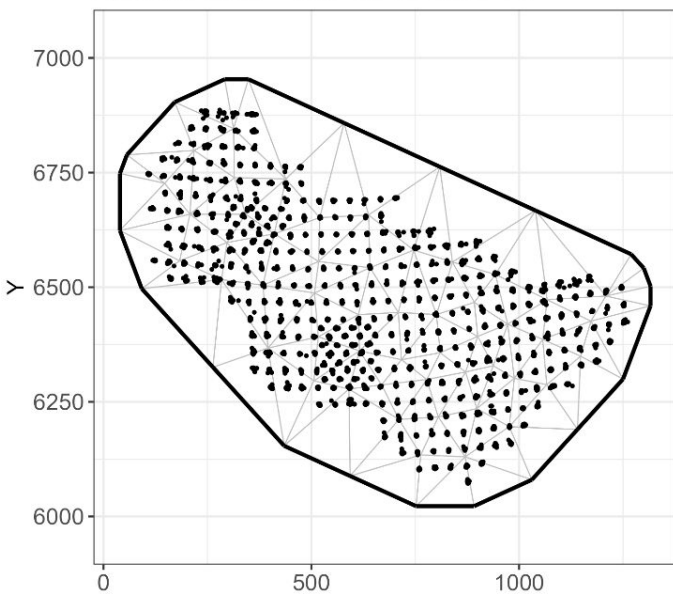
- 41 km<sup>2</sup> resolution, no land



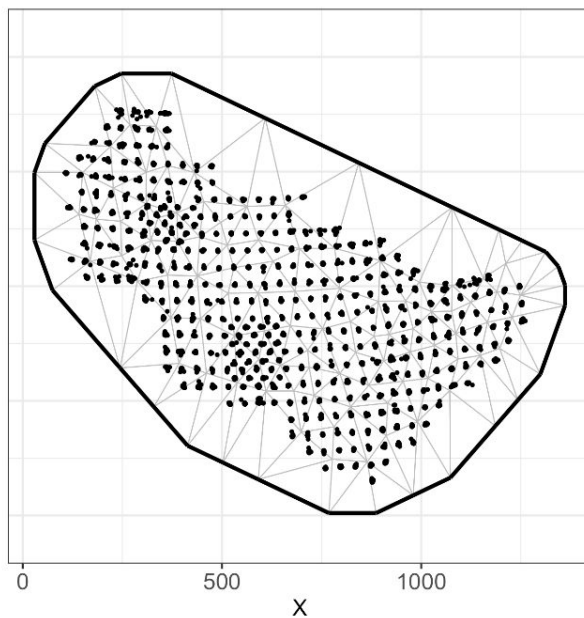


# EBS model mesh

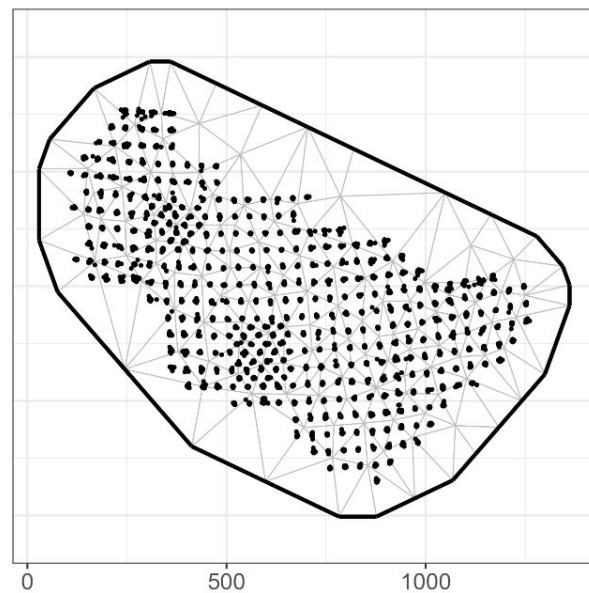
Specified knots = 50, realized knots=72



Specified knots = 90, realized knots=119

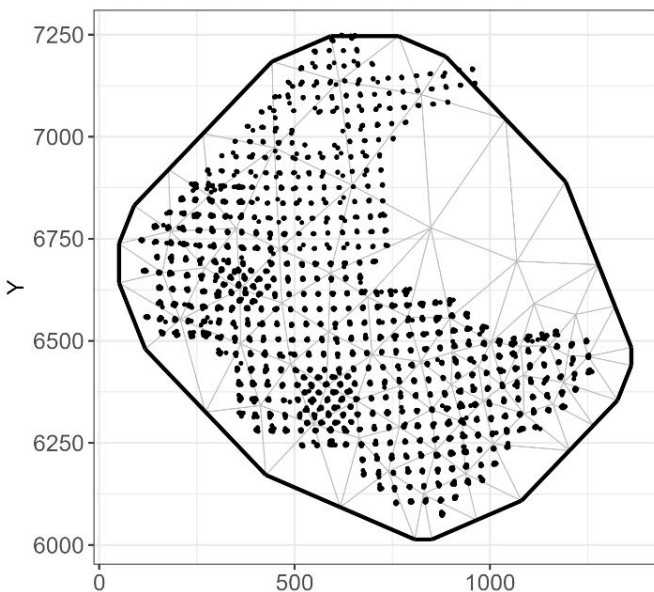


Specified knots = 120, realized knots=155

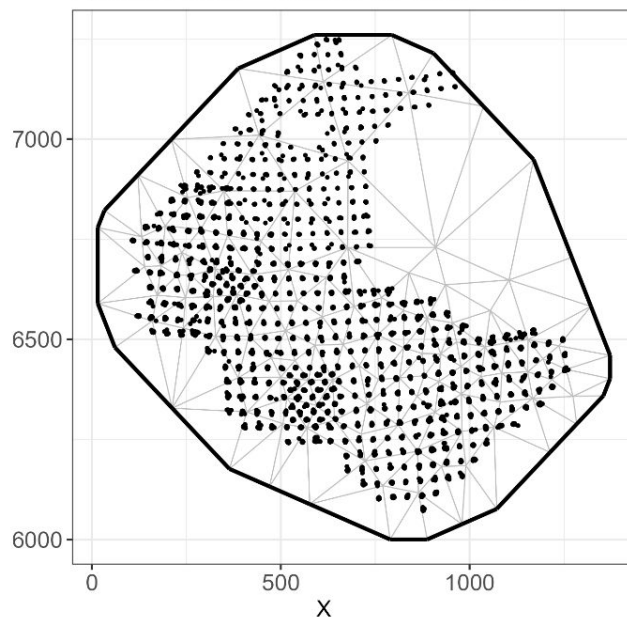


# EBS-NBS model mesh

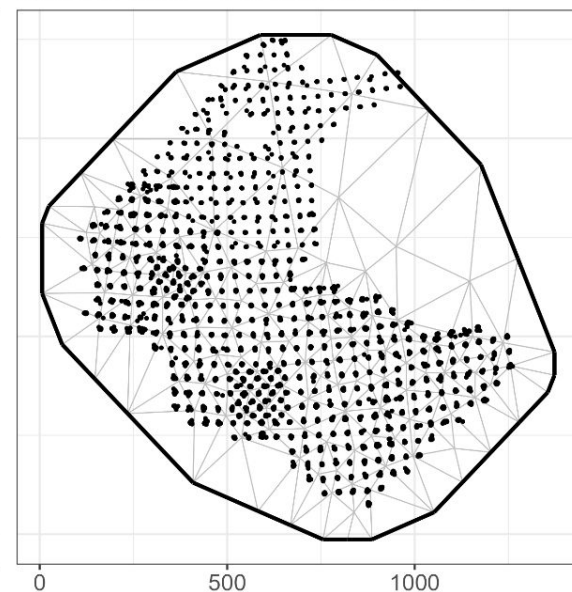
Specified knots = 50, realized knots=80



Specified knots = 90, realized knots=123



Specified knots = 120, realized knots=158



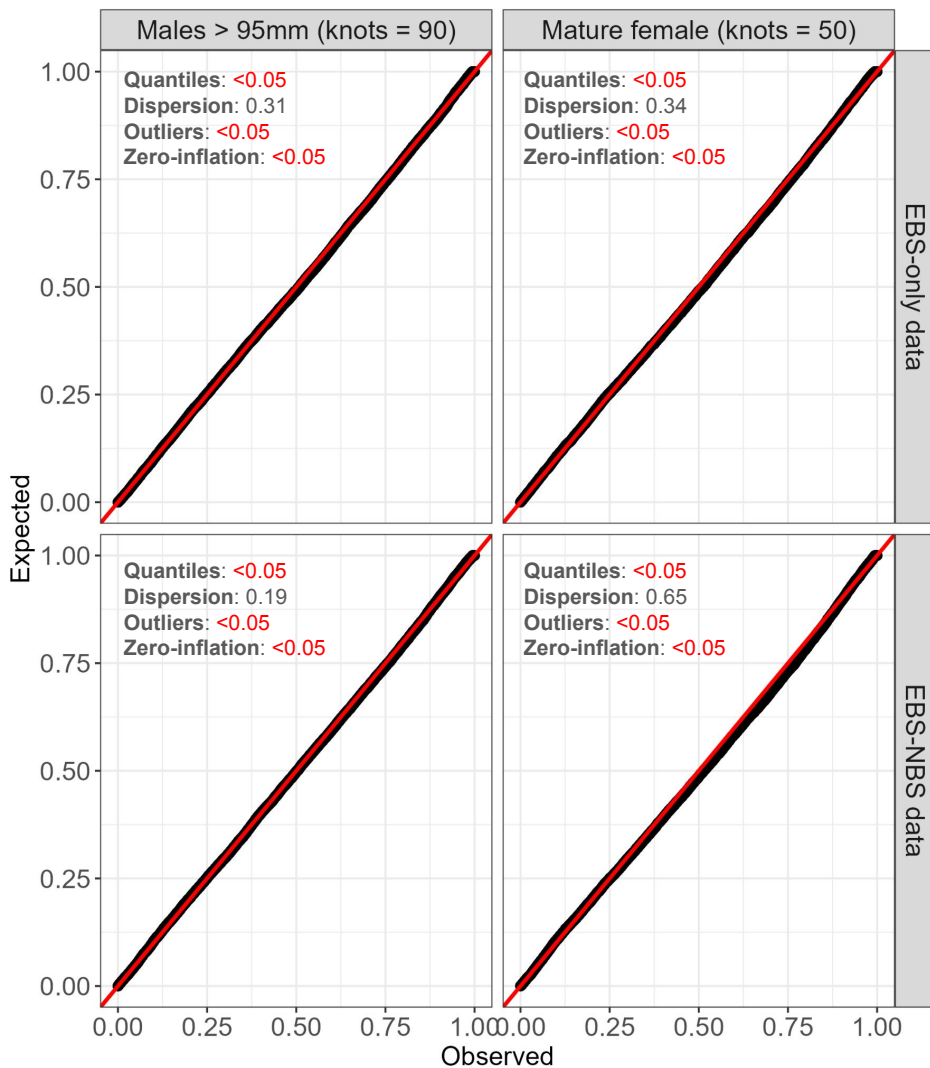
# Overall model diagnostics

- Best: delta-gamma
  - 90-knot mesh for males > 95mm
  - 50-knot mesh for mature females
- IID Tweedie models had difficulty converging
- Cross validation could not be completed for some model combinations → used other diagnostics

category <chr>	region <chr>	knots <dbl>	family <chr>	method <chr>	loglik <dbl>	BEST <chr>
Male95	EBS-NBS	90	Delta_gamma	ar1	- <u>61673</u> .	Y
Male95	EBS	90	Delta_gamma	iid	- <u>61745</u> .	Y
Mature female	EBS-NBS	50	Delta_gamma	ar1	- <u>47619</u> .	Y
Mature female	EBS	50	Delta_gamma	iid	- <u>46460</u> .	Y

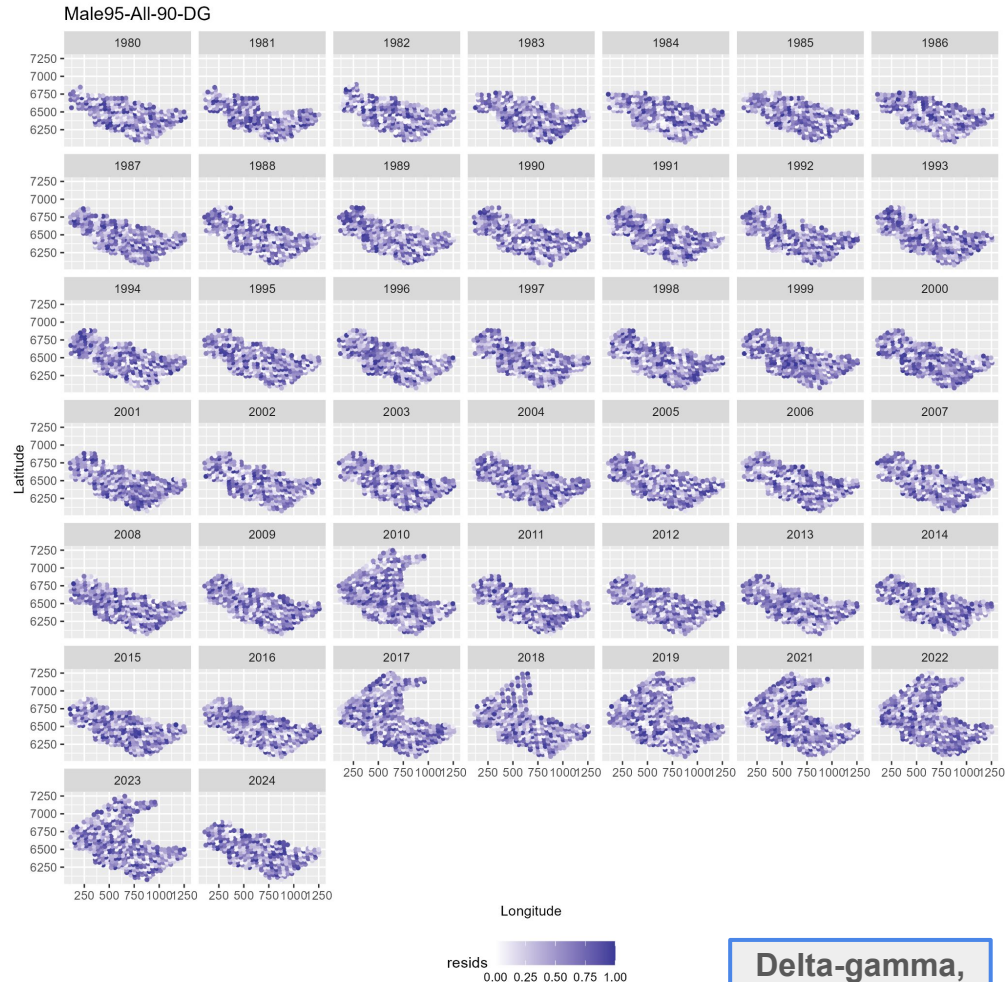
# Biomass model diagnostics

- No significant residual deviation from 1-1 line for delta-gamma models
- Statistical evidence of quantile deviation, outliers, and zero-inflation
- True regardless of model family, knot number, or data region



# Male biomass model diagnostics: EBS-NBS data

- No evidence of spatiotemporal autocorrelation of DHARMA residuals

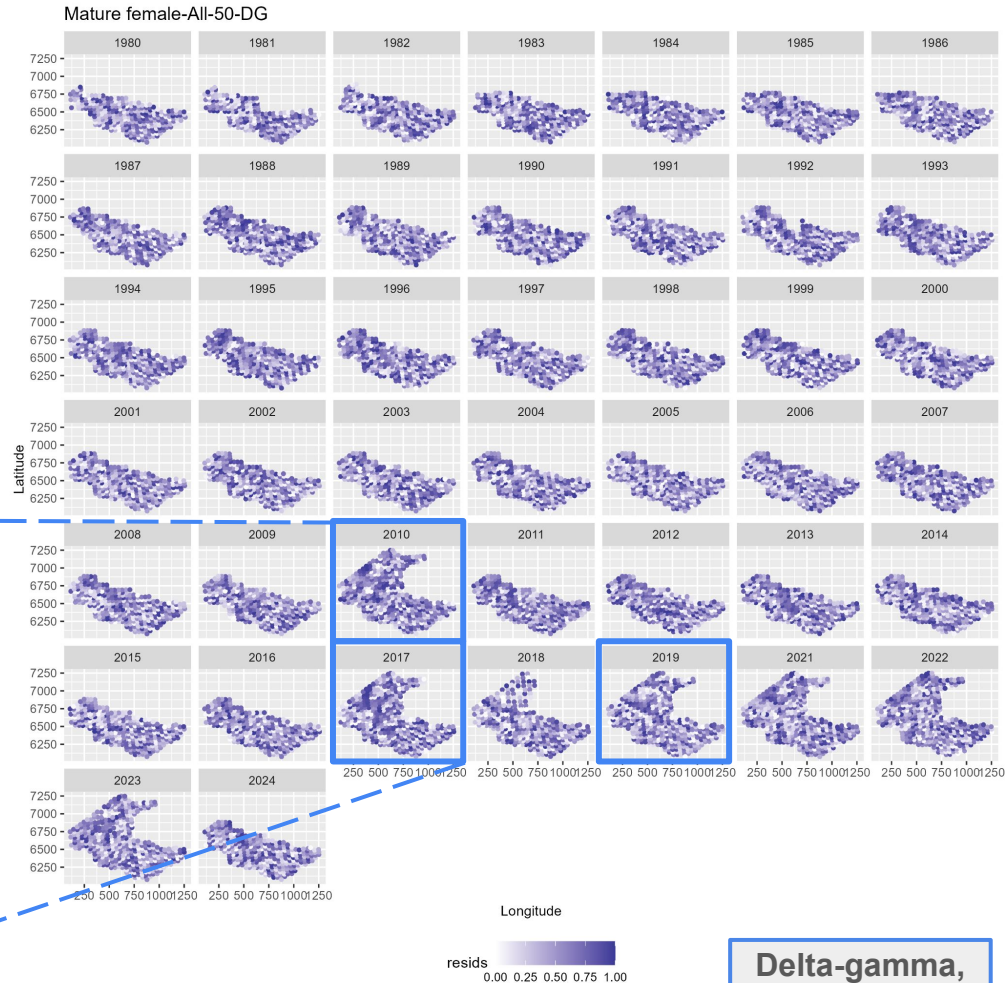
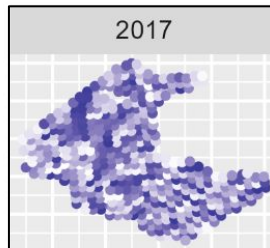
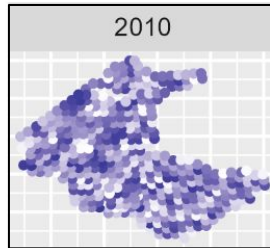


**Delta-gamma,  
90 knots**



# Female biomass model diagnostics: EBS-NBS data

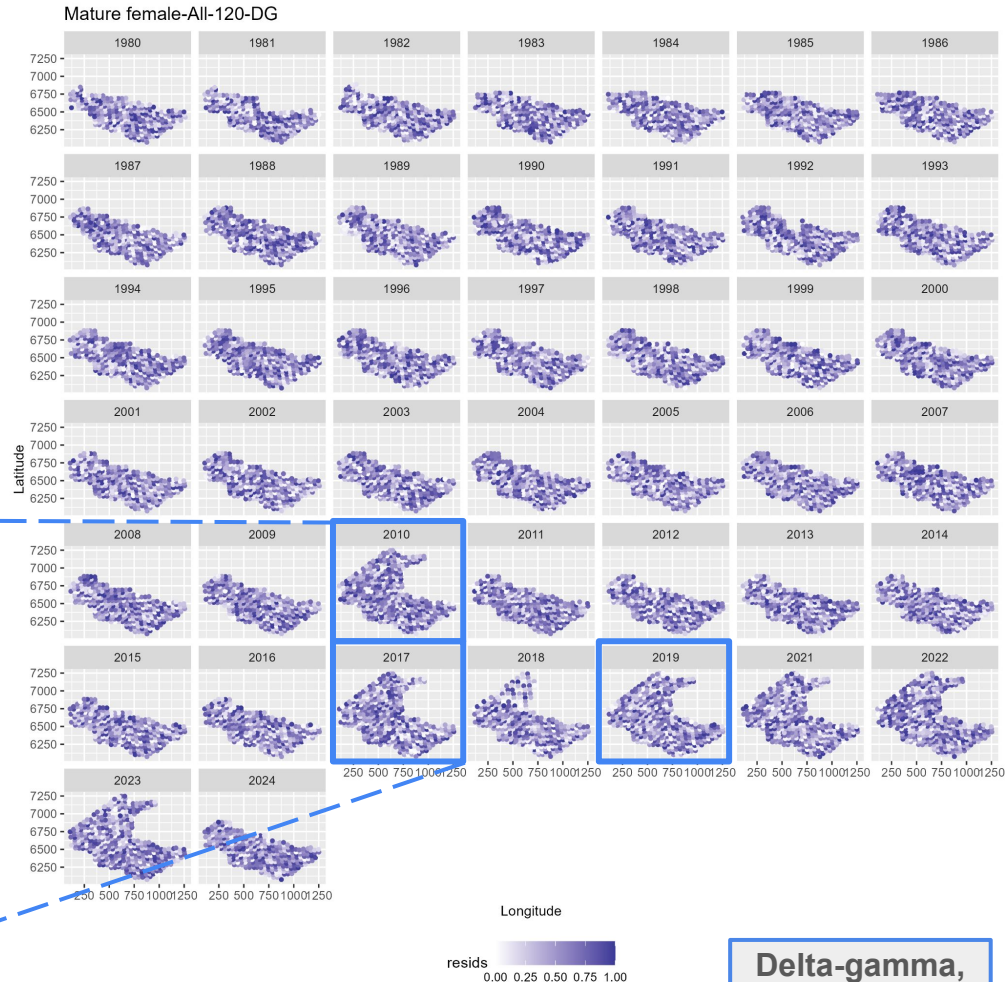
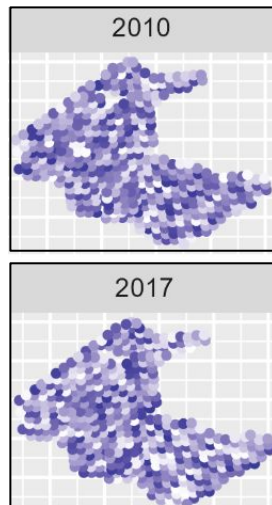
- Some evidence of spatiotemporal autocorrelation of DHARMA residuals





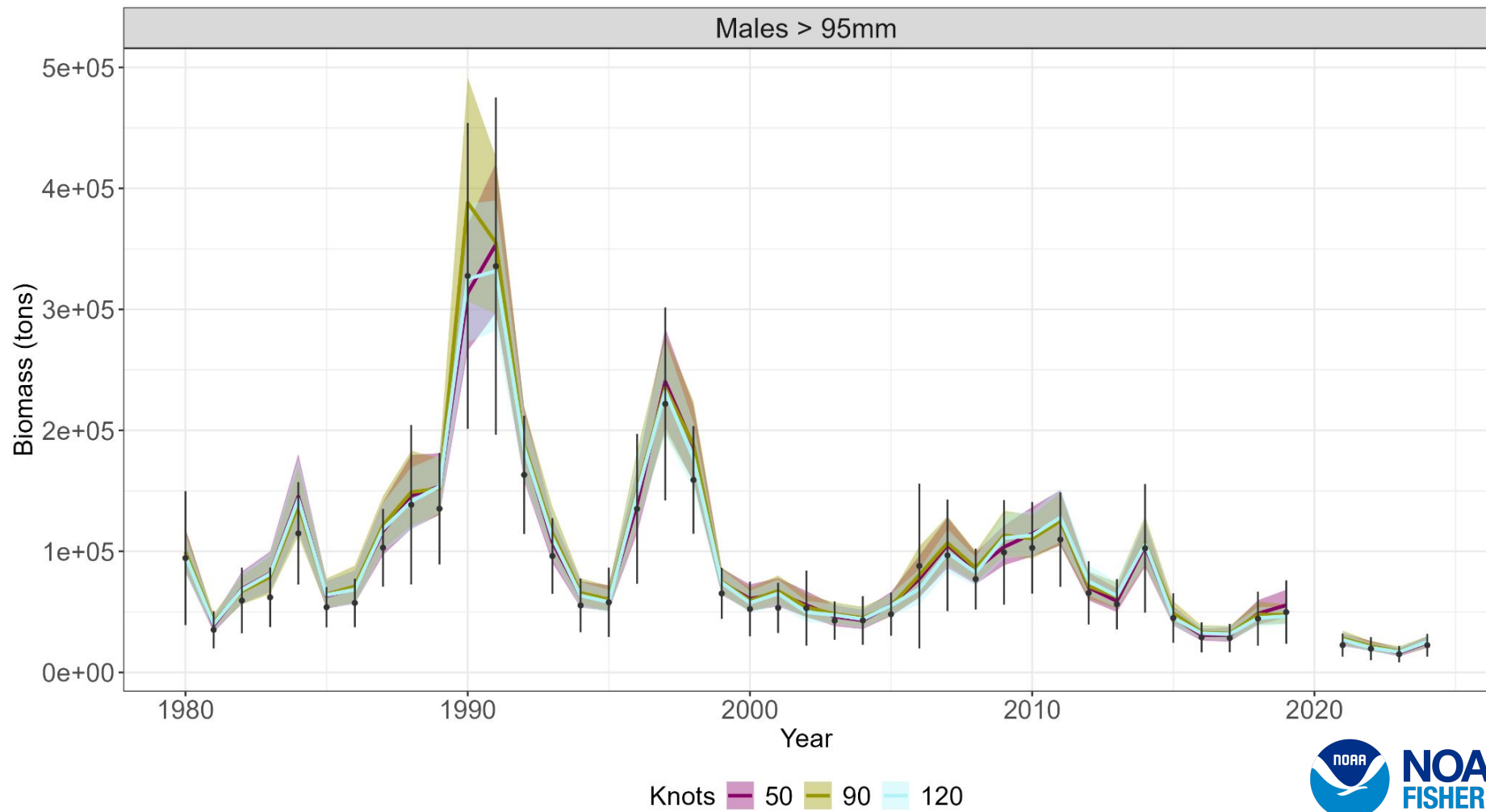
# Female biomass model diagnostics: EBS-NBS data

- Autocorrelation patterns improve with higher resolution mesh

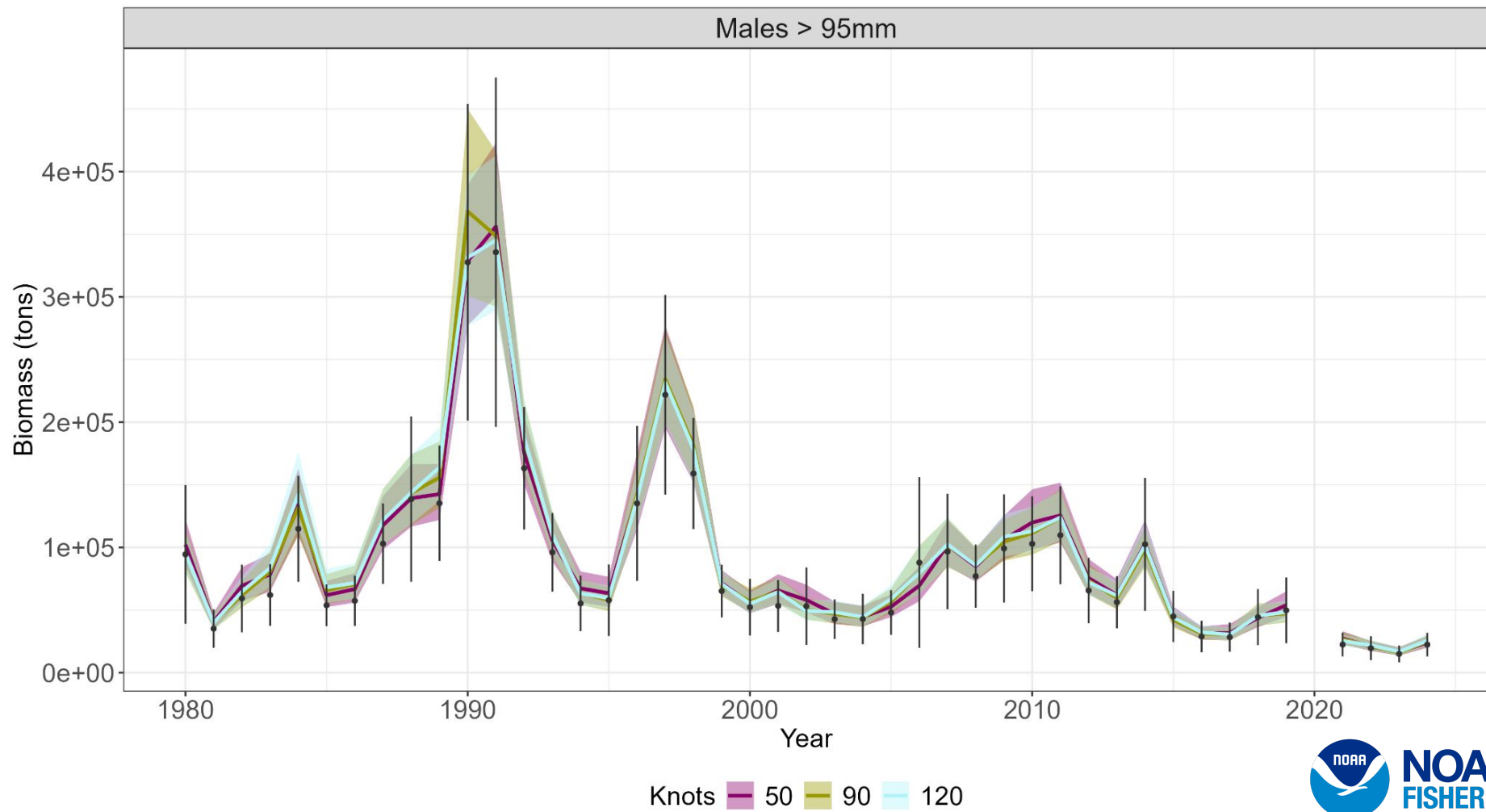


**Delta-gamma,  
120 knots**

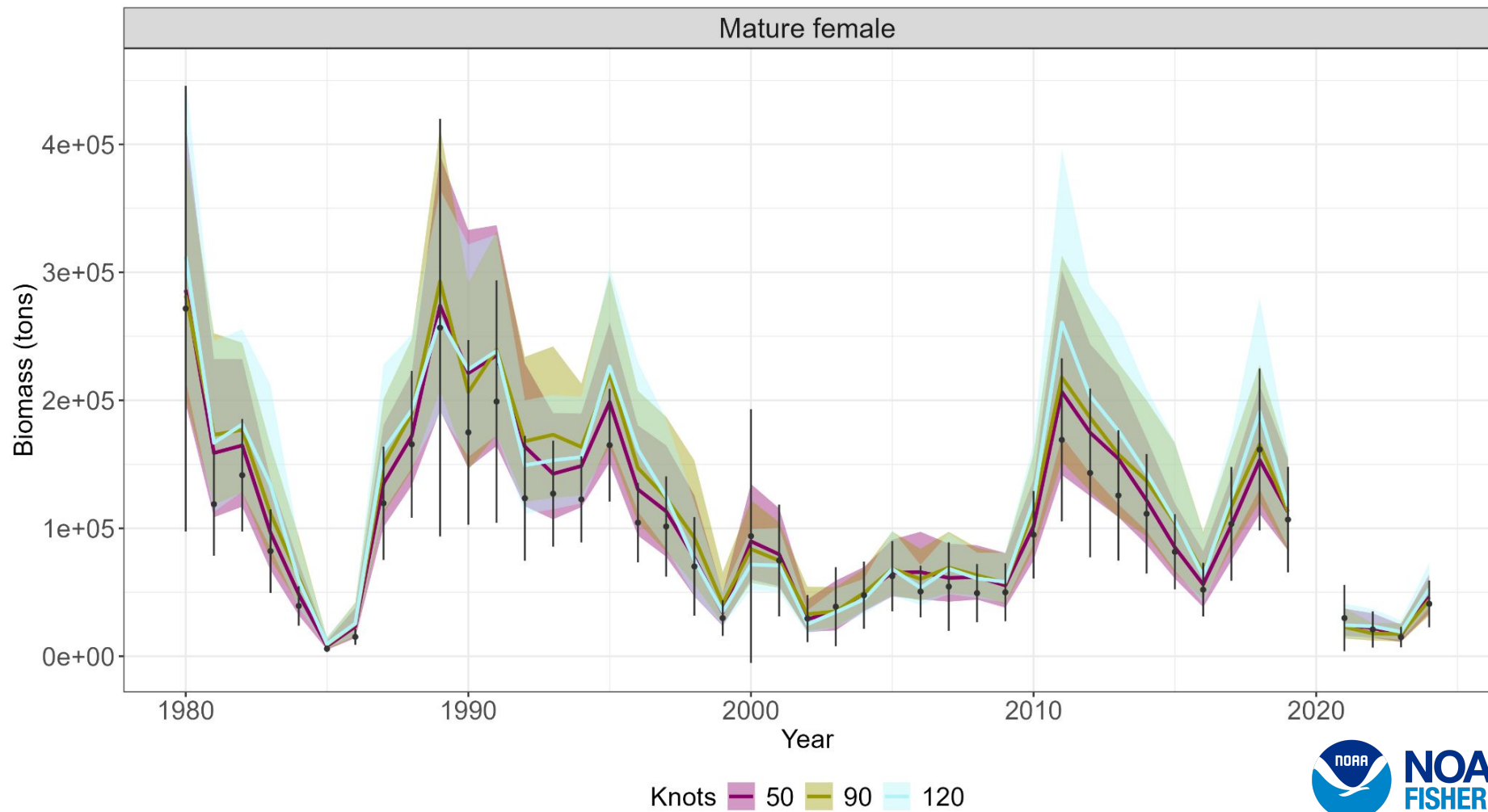
# EBS snow crab estimated biomass (EBS-data only)



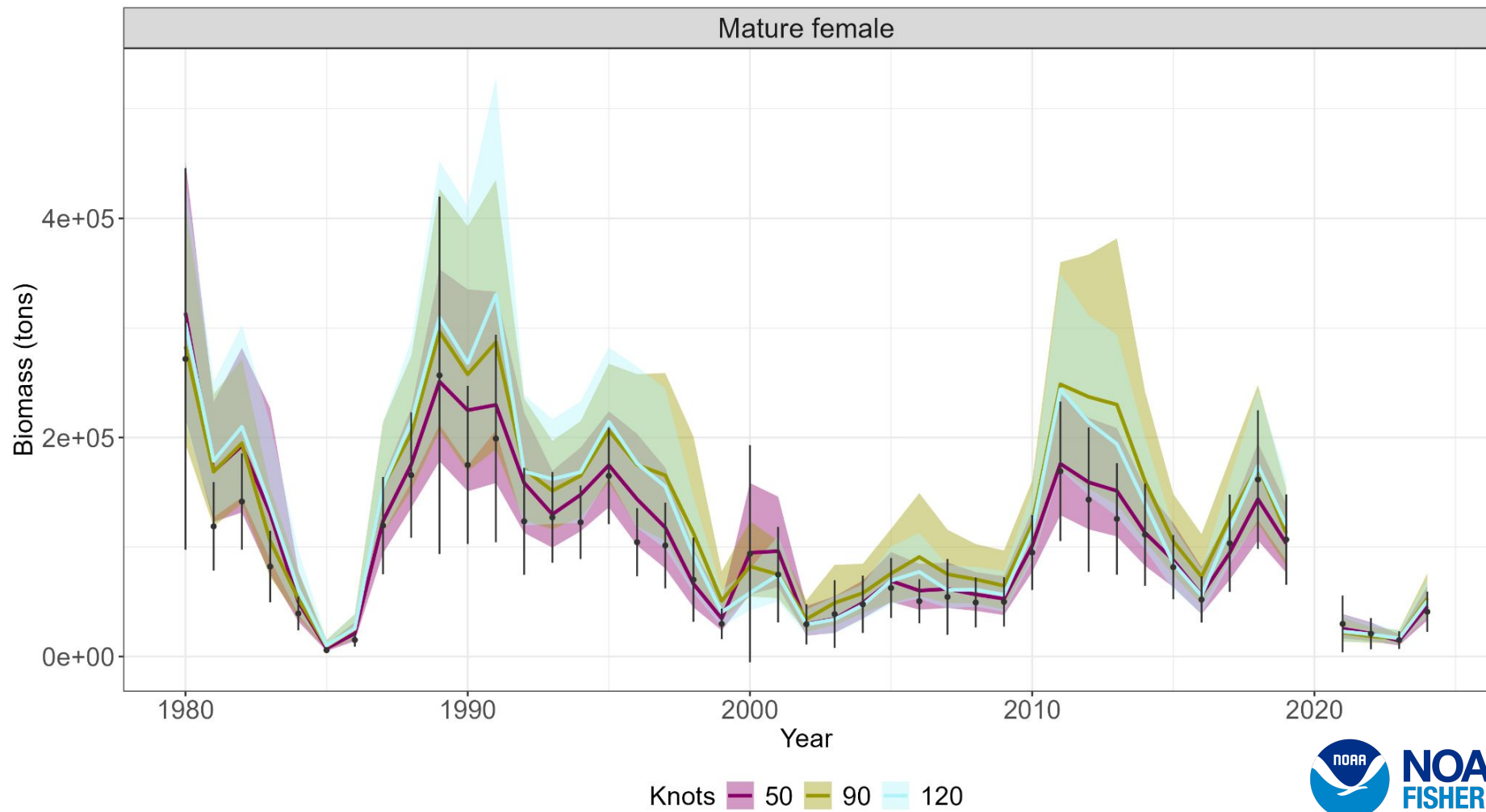
# EBS snow crab estimated biomass (EBS-NBS data)



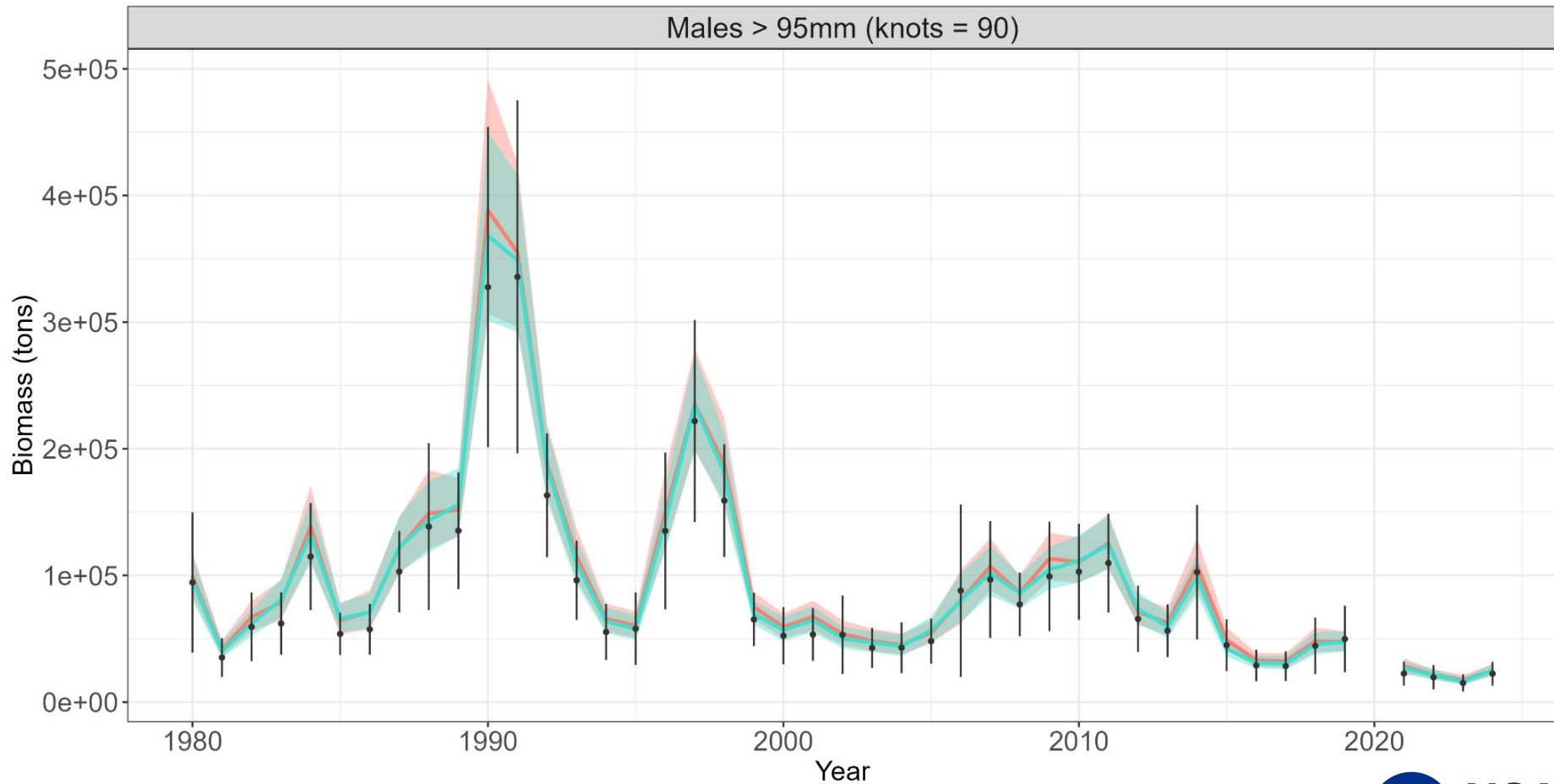
# EBS snow crab estimated biomass (EBS-data only)



# EBS snow crab estimated biomass (EBS-NBS data)

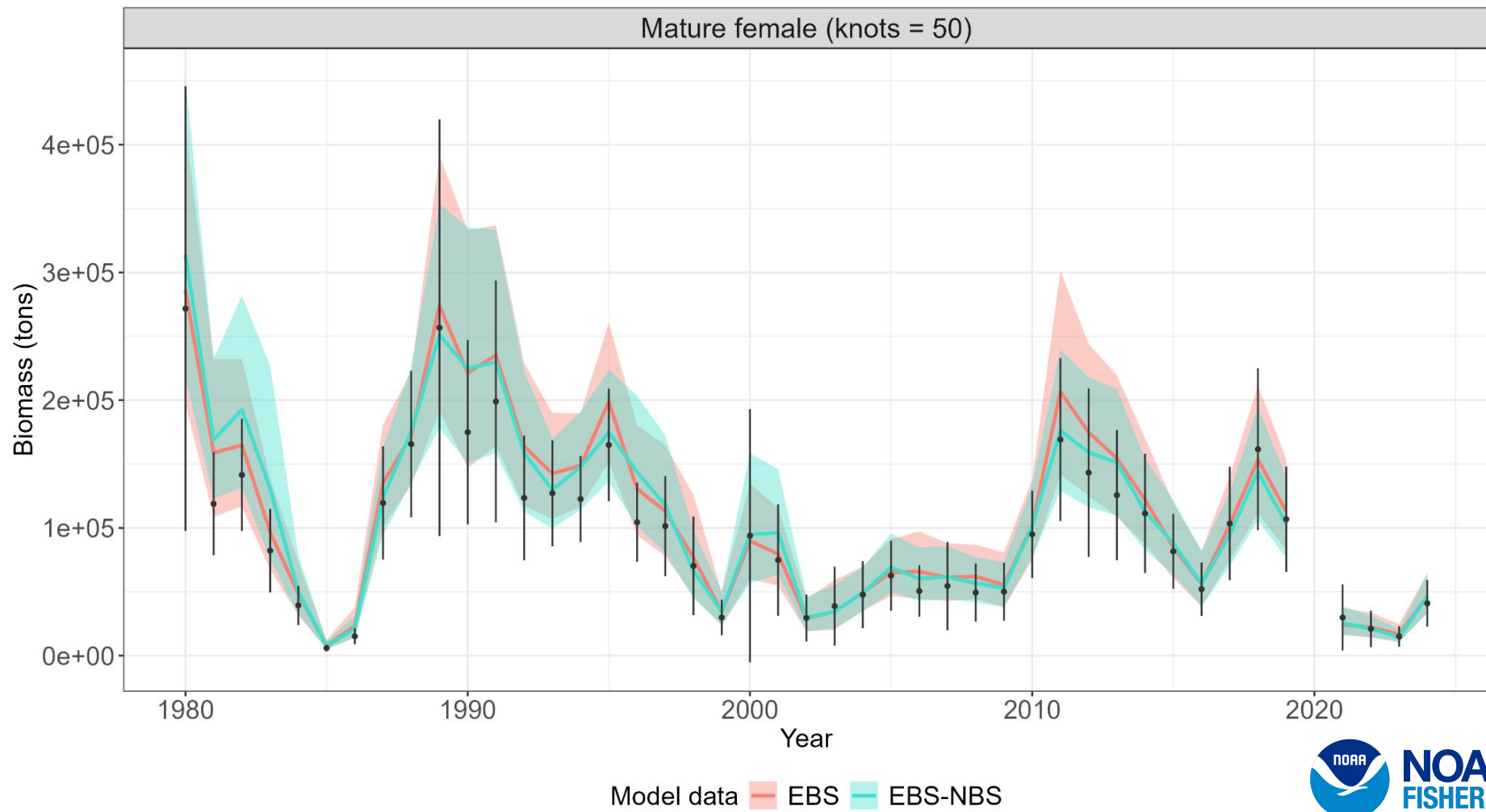


# EBS snow crab estimated biomass

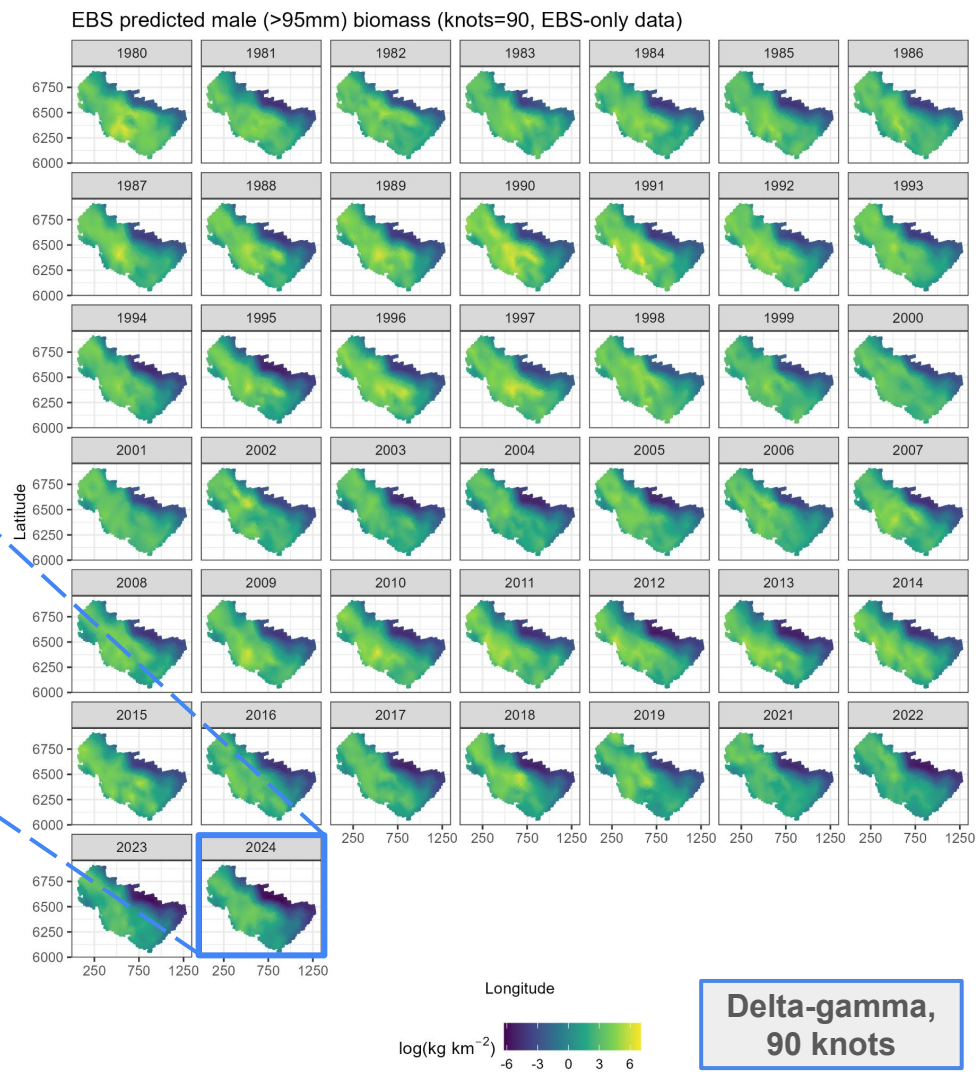
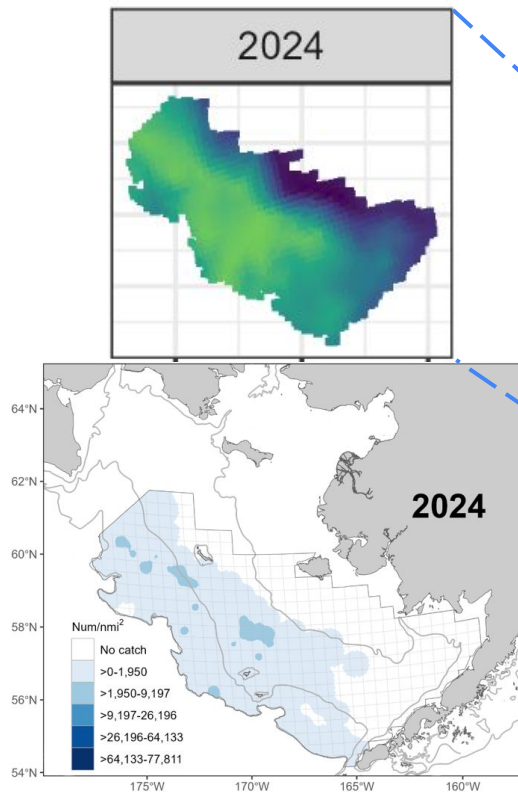




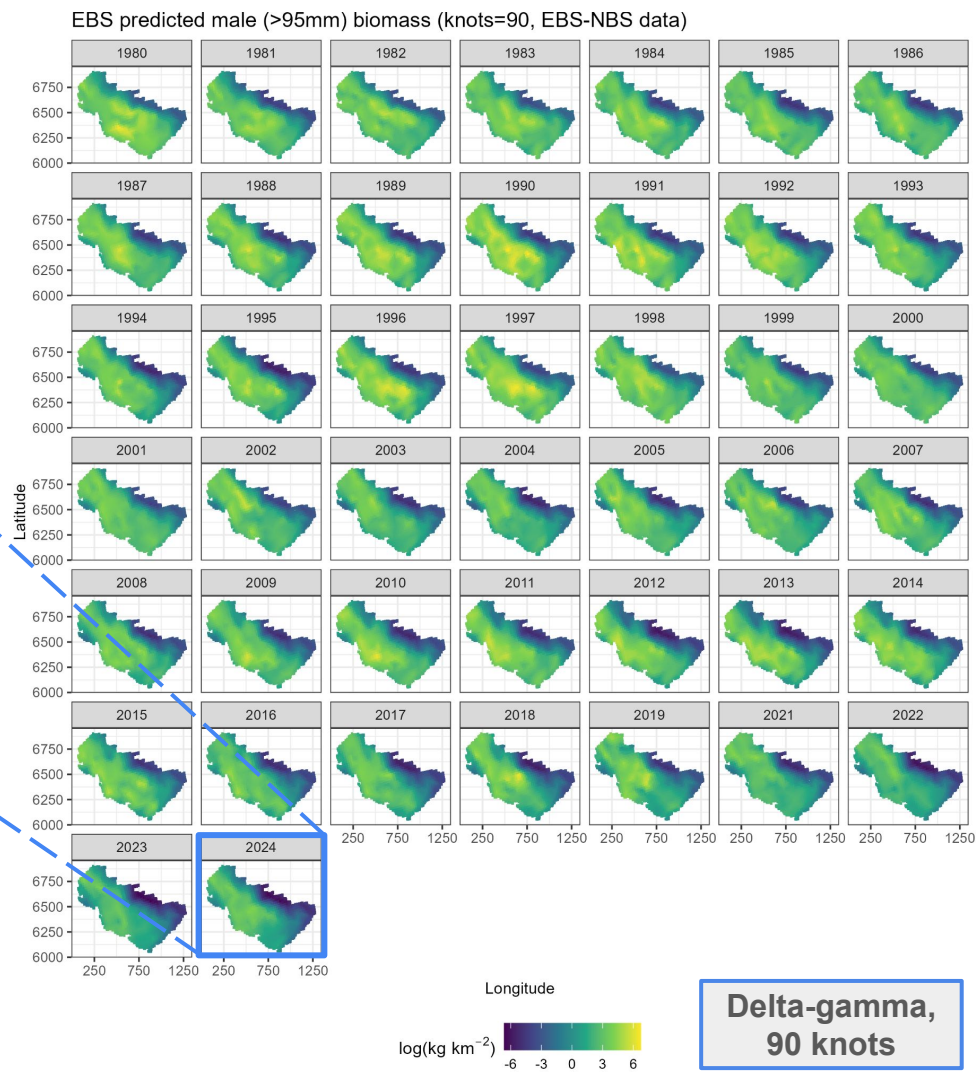
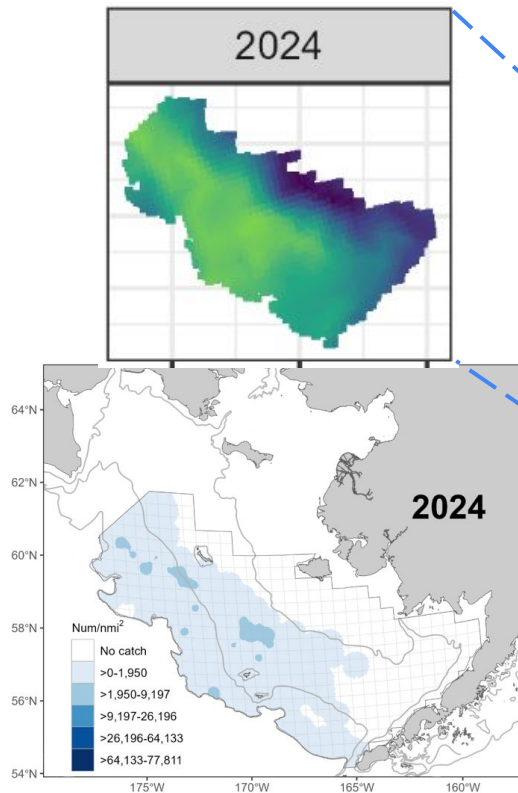
# EBS snow crab estimated biomass



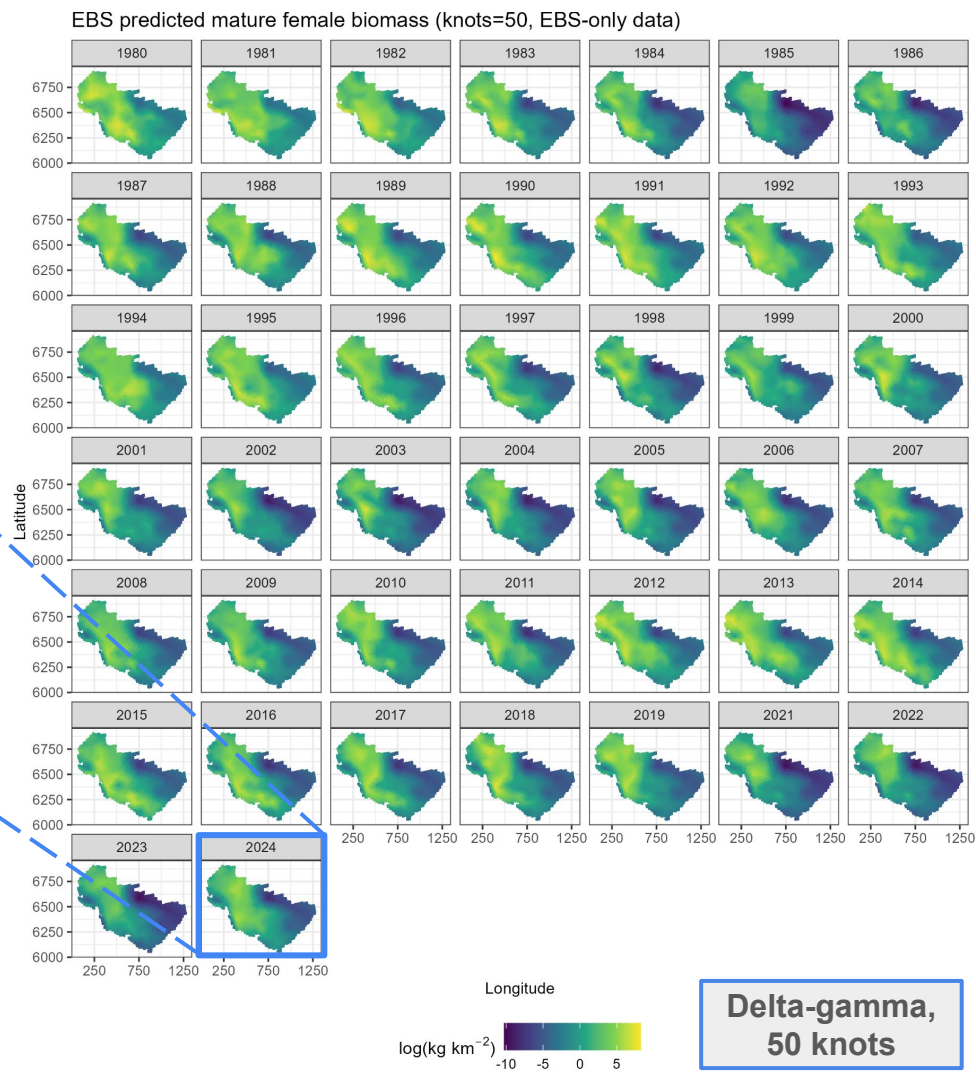
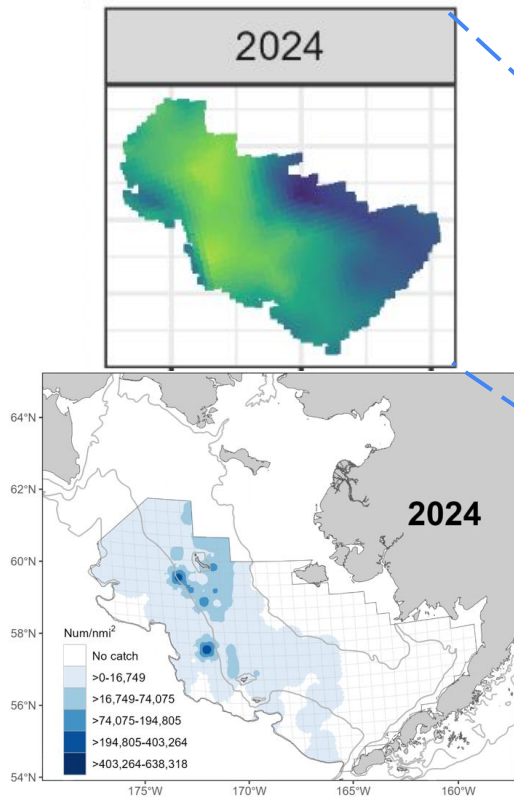
# Predicted male biomass: EBS data



# Predicted male biomass: EBS-NBS data

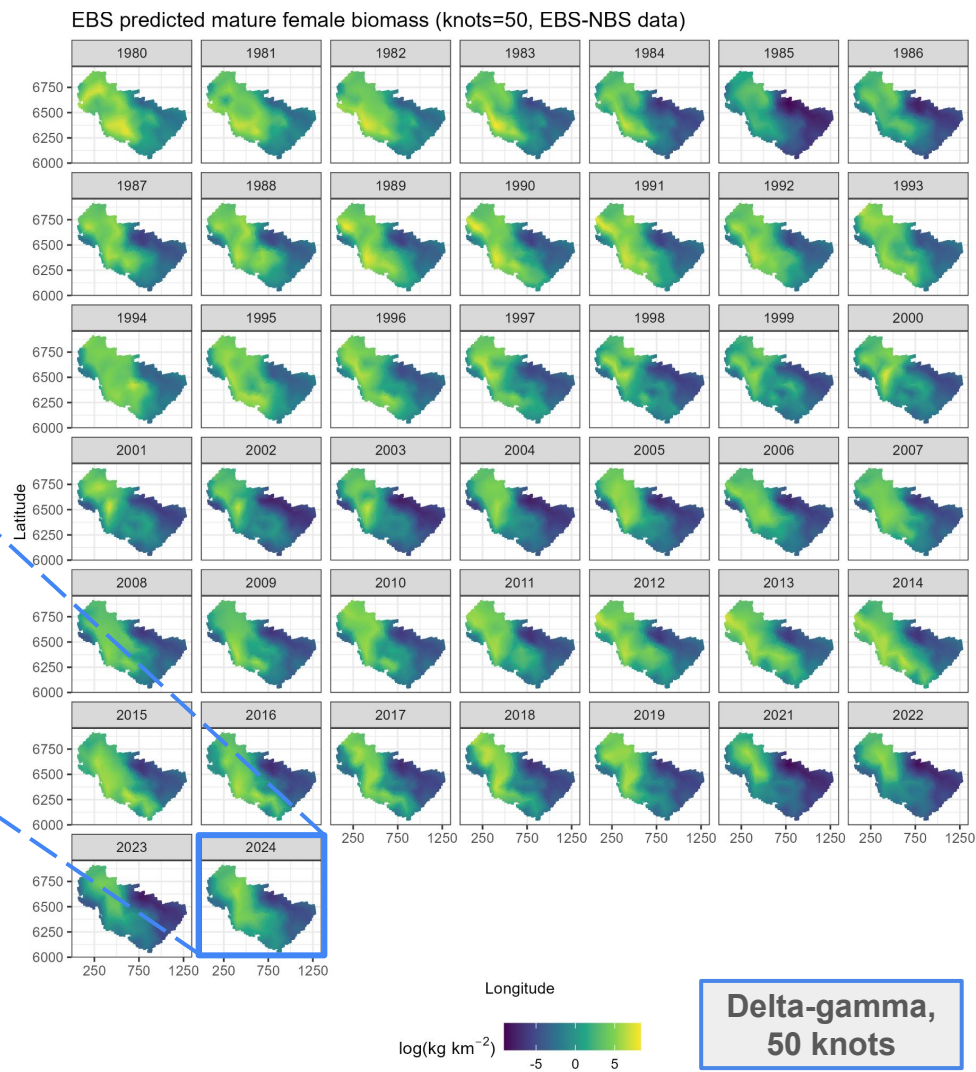
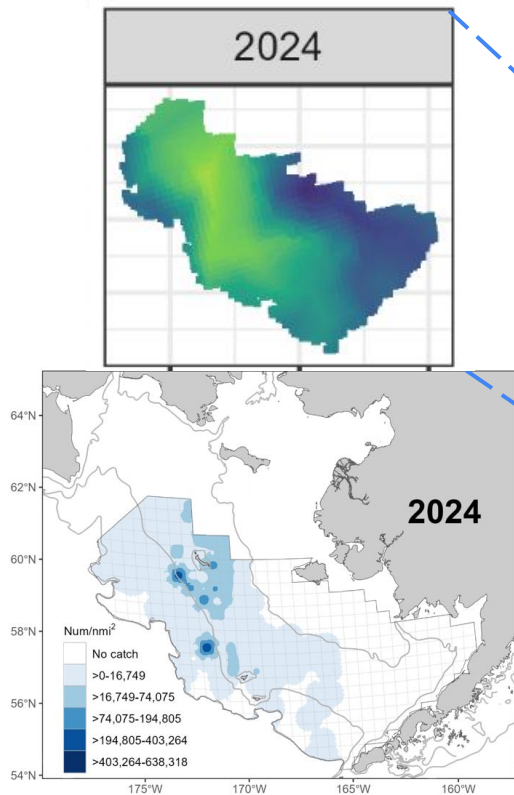


# Predicted female biomass: EBS data



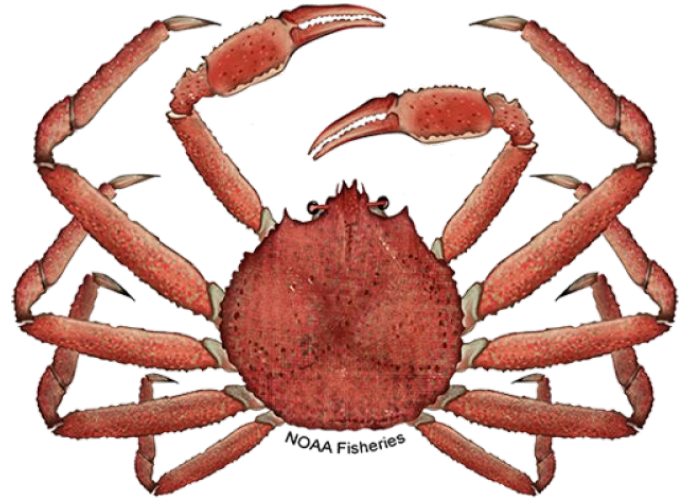


# Predicted female biomass: EBS-NBS data



# Snow crab conclusions and next steps

- Best model framework:
  - Delta-gamma, 90-knot mesh for males > 95mm
  - Delta-gamma, 50-knot mesh for mature females
  - EBS data only? EBS-NBS combined?
- Next steps:
  - Evaluate spatiotemporal autocorrelation with explicit statistics (e.g., global Moran's I clustering analysis)
  - Explore methods for reducing NBS autocorrelation (e.g., mesh size, covariates)





# MODEL-BASED SIZE FREQUENCIES

Jonathan Richar  
NOAA RACE SAP Kodiak  
lab  
[jon.richar@noaa.gov](mailto:jon.richar@noaa.gov)



# INTRODUCTION

- ▶ EBS Tanner crab
- ▶ VAST
- ▶ Ongoing effort
- ▶ Complimentary to model based population estimates
- ▶ Previously, model based estimates used w/design based size frequencies
- ▶ System resources
- ▶ Model fit issues

# PROGRESS

- ▶ It runs! (kind of)
- ▶ Models run in sequence
- ▶ By 5 mm size bin
- ▶ Output compiled
- ▶ Multiple series run exploring different settings



# COMMON SETTINGS

- ▶ ObsModel (2,4)
  - ▶ Delta-gamma model
  - ▶ Poisson-link
  - ▶ Encounter probability set to 1/0
- ▶ 75 or 125 kts (latest series)
  - ▶ Group sample locations for estimation of spatial variables
  - ▶ Spatial/spatiotemporal variation of a knot assumed constant within time steps
  - ▶ Tradeoff: Estimation accuracy vs computation efficiency
- ▶ Beta
  - ▶ Temporal variation in encounter/catch
  - ▶ IID
- ▶ Rho
  - ▶ Specifies temporal structuring of intercepts/spatiotemporal variation
  - ▶ **0 (fixed effect)**

# INDIVIDUALIZED SETTINGS

- ▶ Settings changed (within series)
  - ▶ Omega, Epsilon, anisotropy
    - ▶ Omega: spatial variation
    - ▶ Epsilon: spatio-temporal variation
      - ▶ 2 parameters each
        - ▶ 1 for encounter probability
        - ▶ 1 for positive catch rates
    - ▶ Anisotropy: directionality in autocorrelation

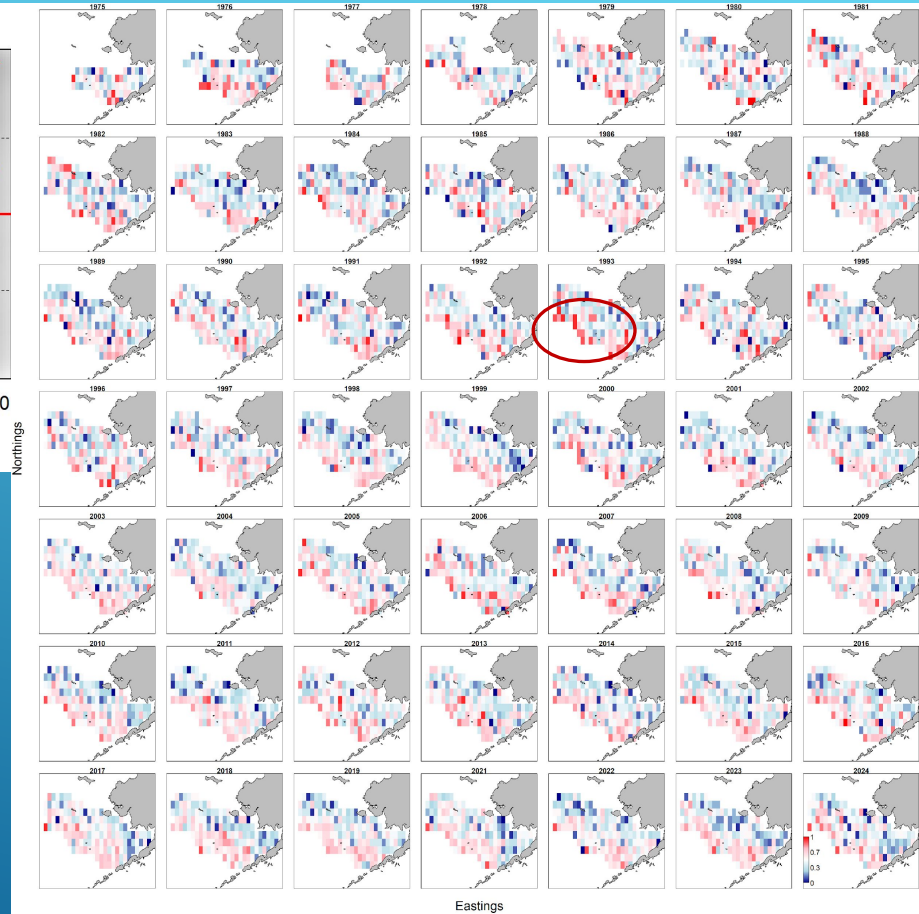
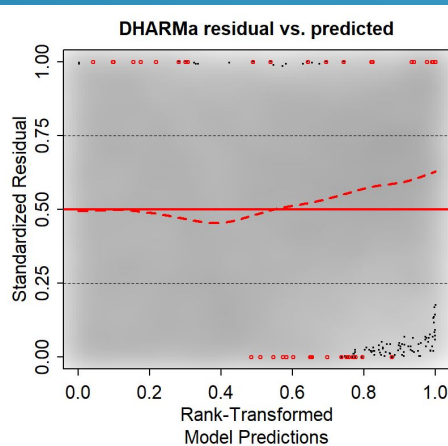
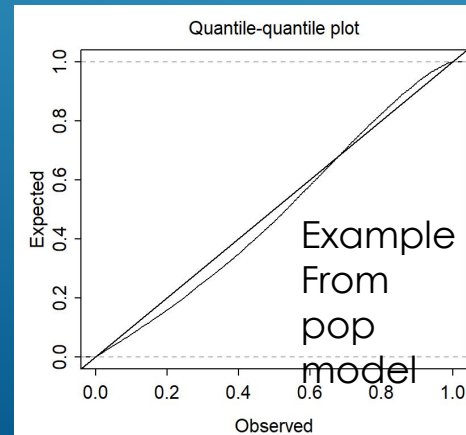
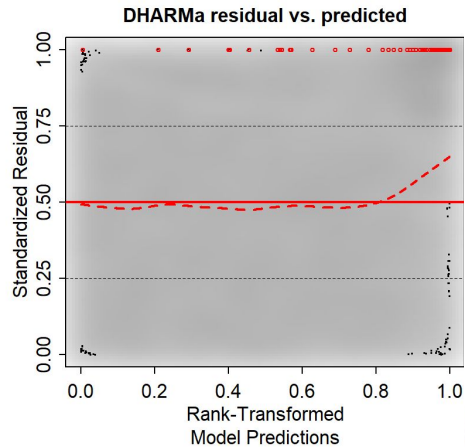
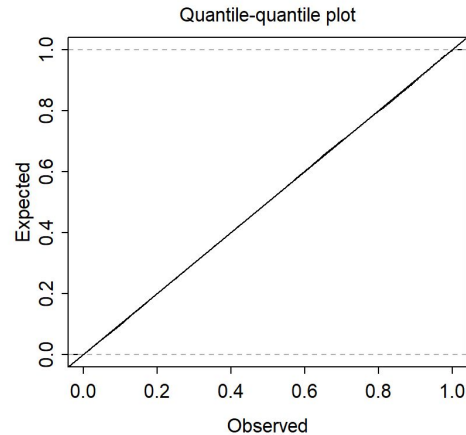
- ▶ Models at size range extremes very simple (limited sample sizes)
  - ▶ Most spatial parameters disabled
  - ▶ Anisotropy disabled
  - ▶ Not sufficient in some cases
- ▶ Central models fully parameterized
- ▶ Run times; 20 min to 4+ hrs
  - ▶ ~80 model runs required to do males, immature females and mature females
  - ▶ Currently running 4<sup>th</sup> series of models
    - ▶ #1: Minimum basic settings common to all models
    - ▶ #2 and 3: More settings/parameters enabled where possible
    - ▶ #4: settings for #3, but more knots
  - ▶ >300 models run



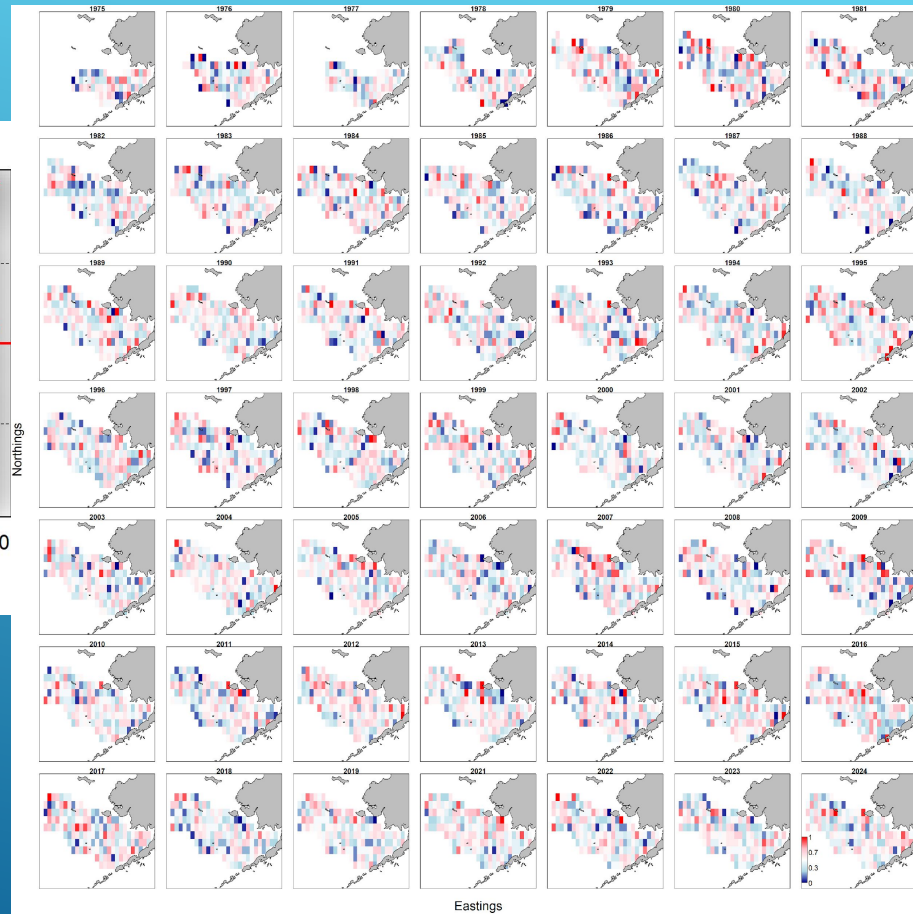
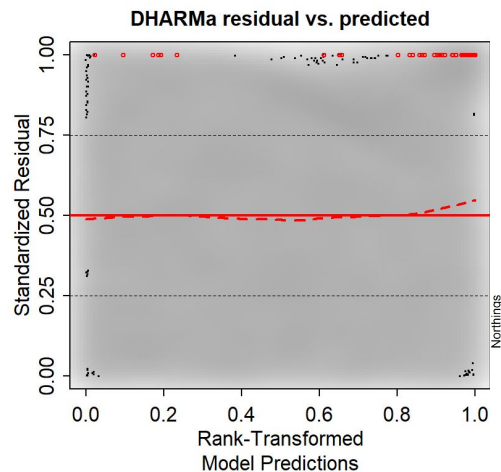
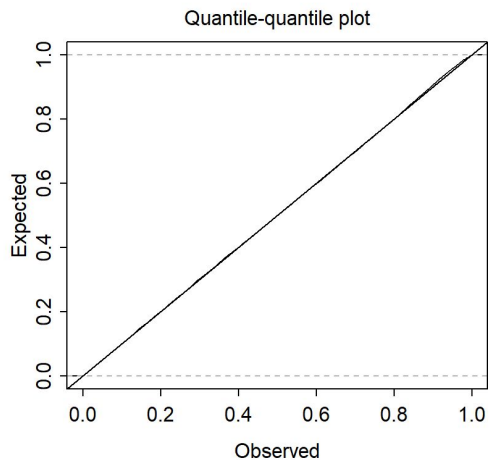
# EXAMPLE DIAGNOSTICS



# MALES 30-35MM

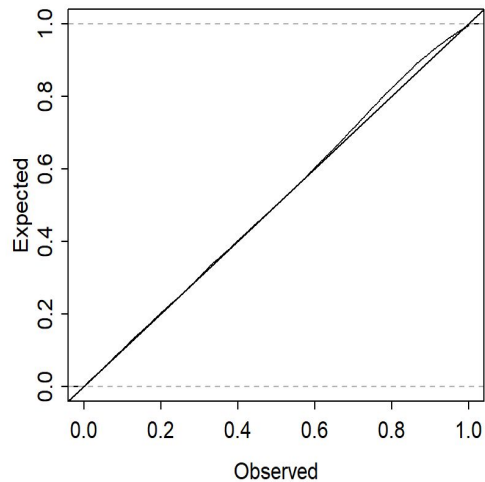


# MALES 50-55MM

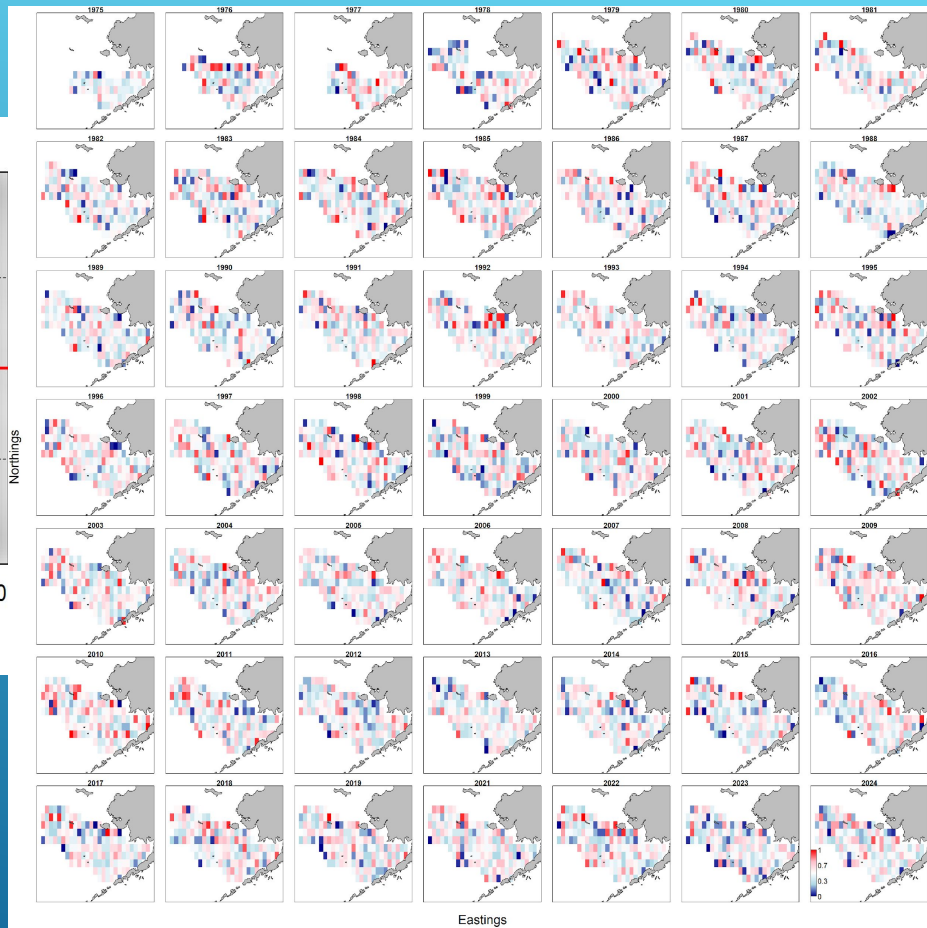
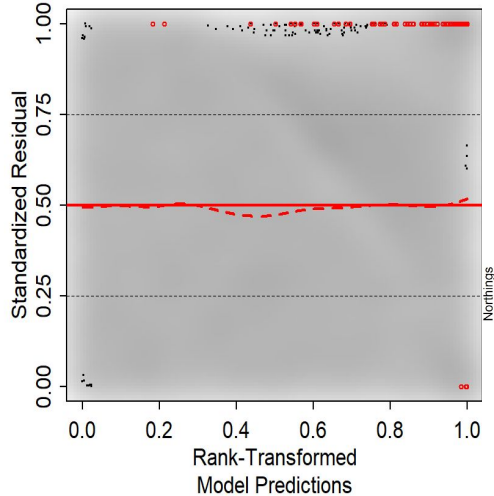


# MALES 100-105 MM

Quantile-quantile plot

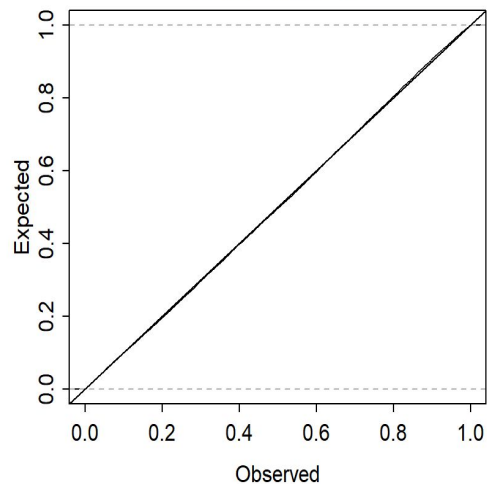


DHARMA residual vs. predicted

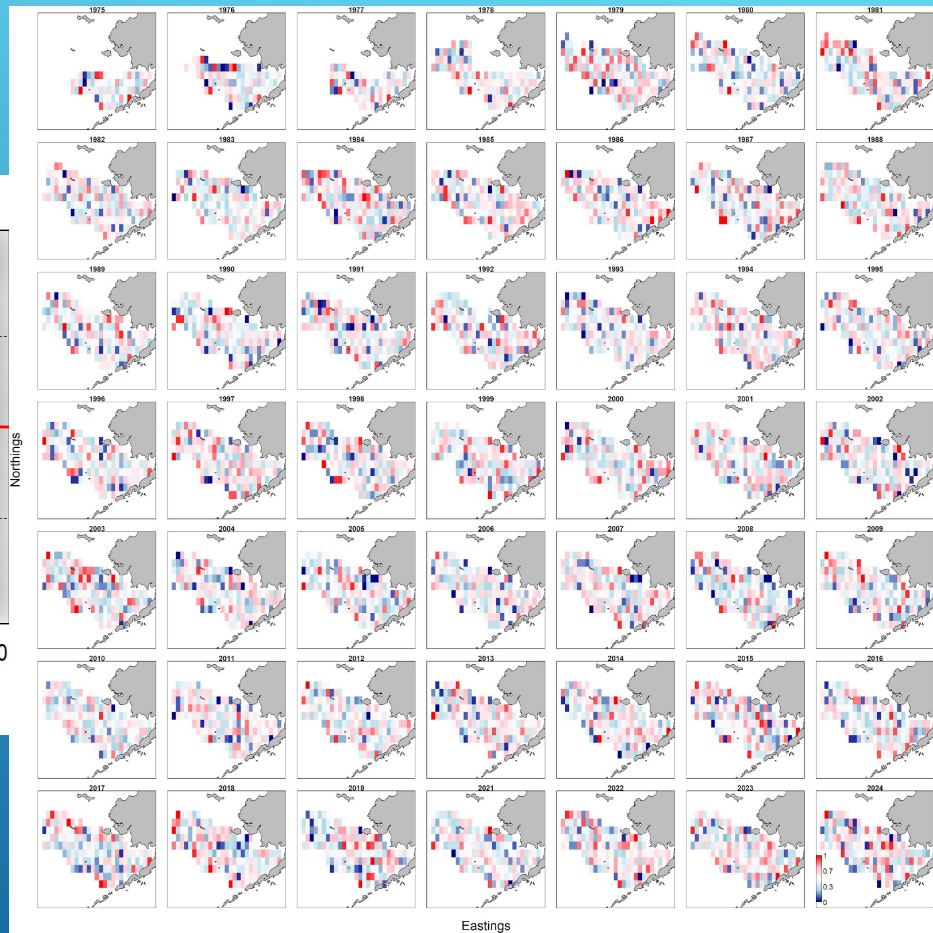
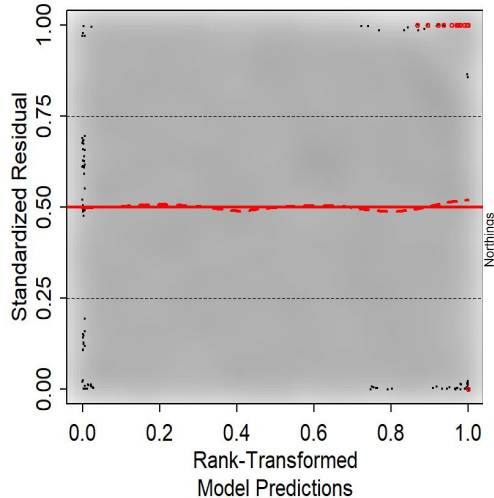


# MALES 150-155MM

Quantile-quantile plot

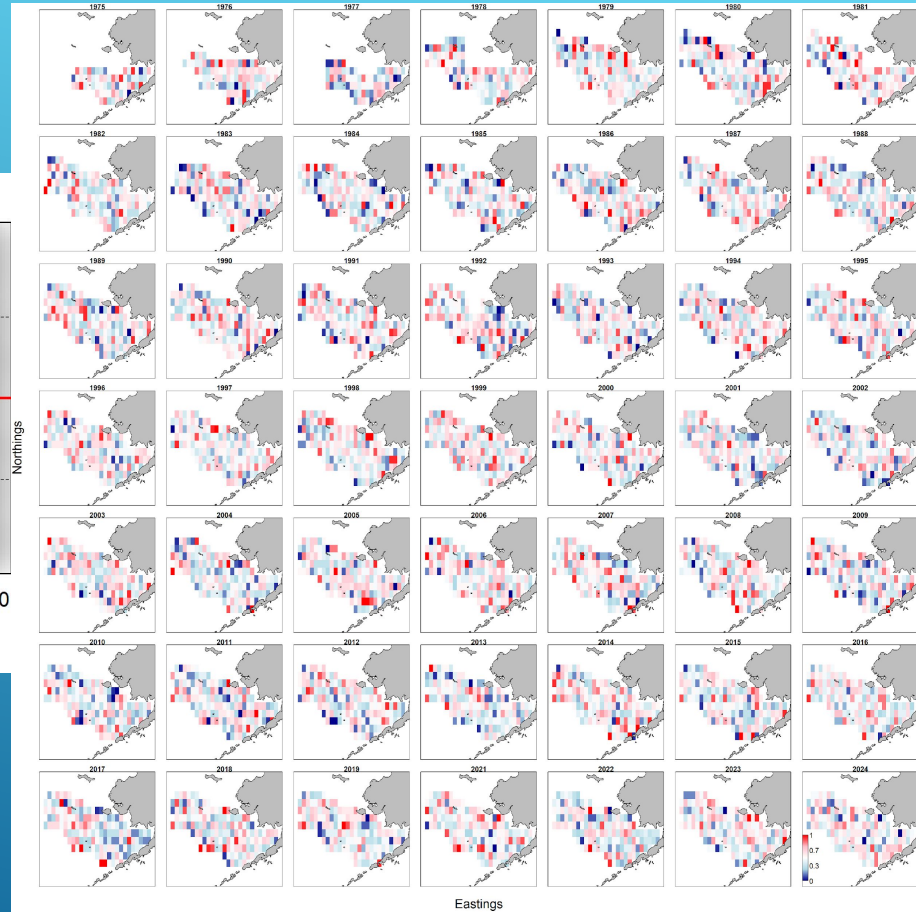
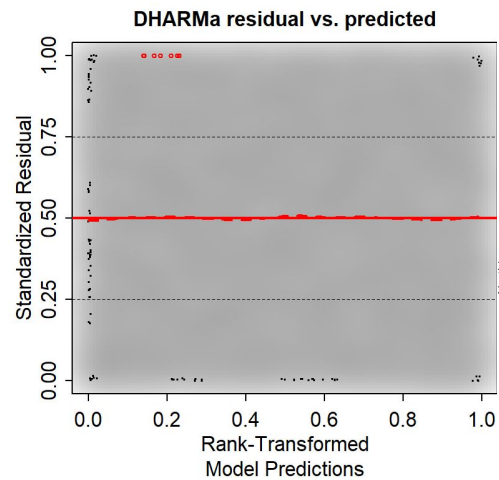
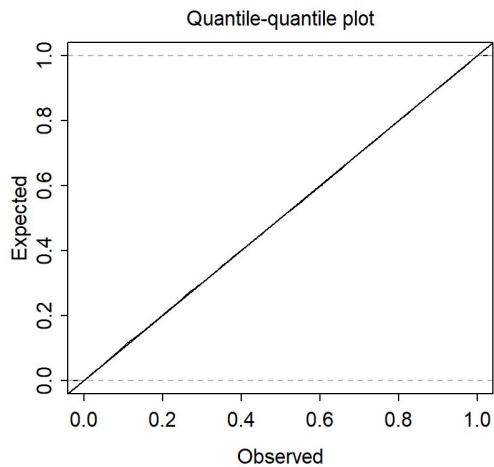


DHARMA residual vs. predicted





# MALES 180+

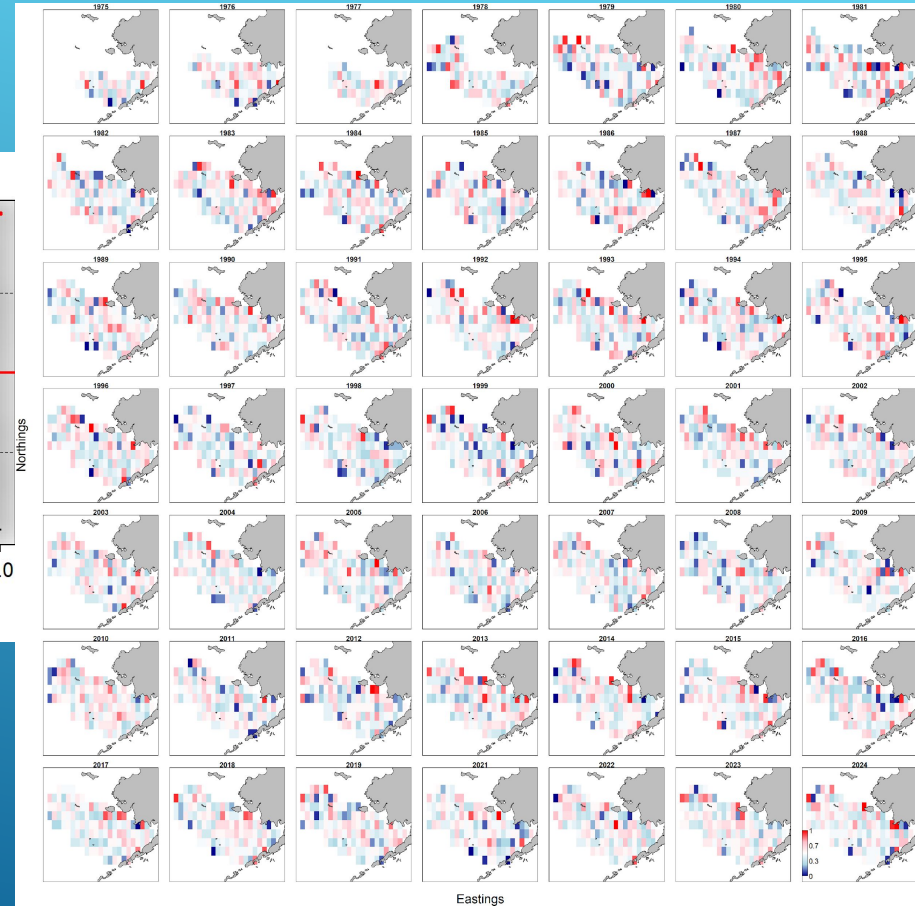
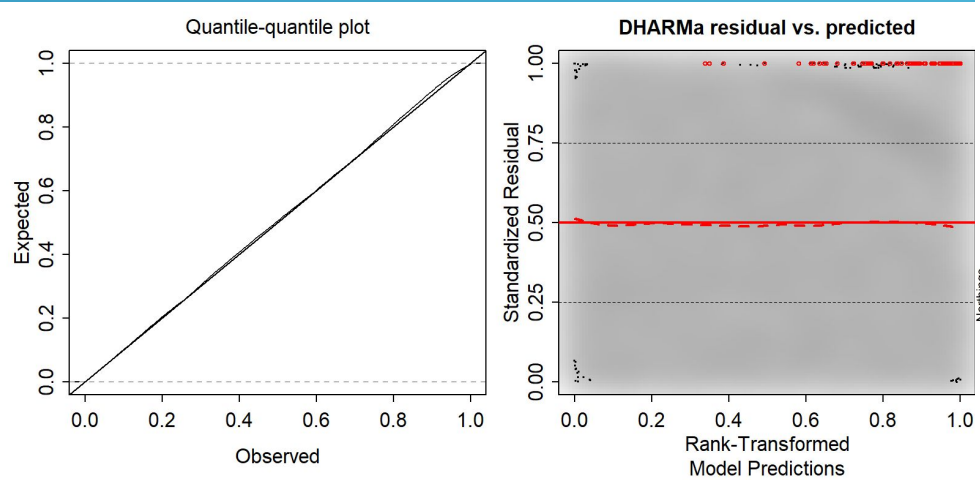




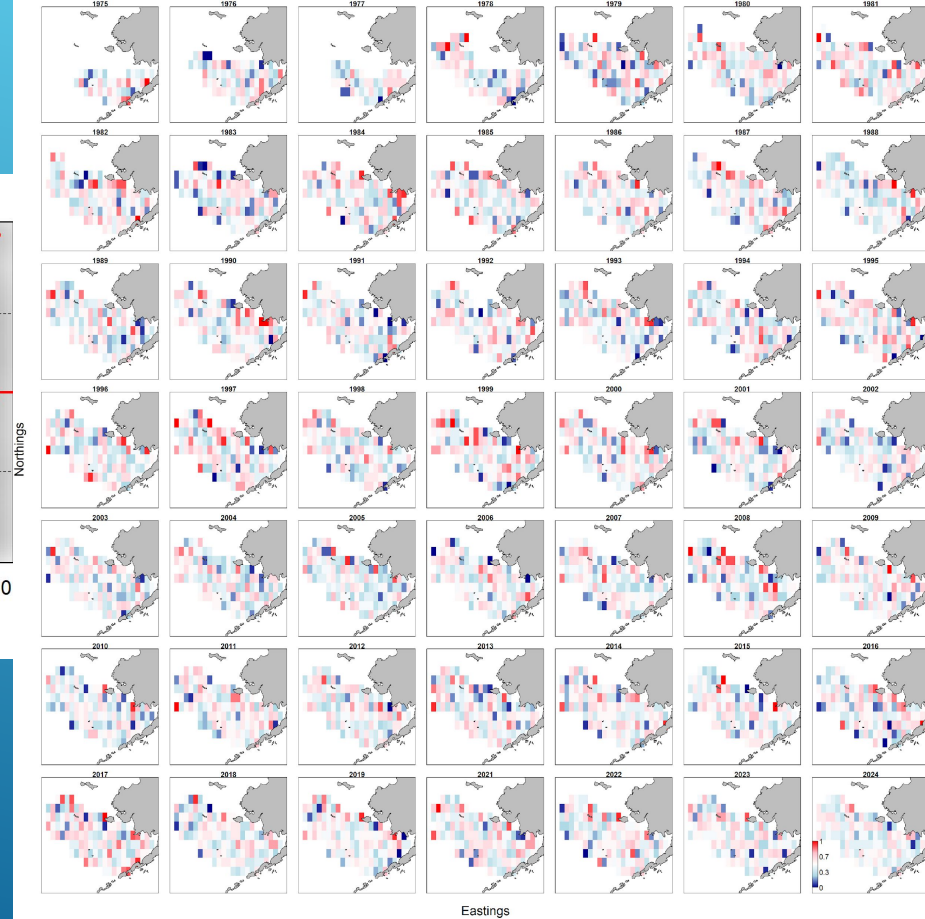
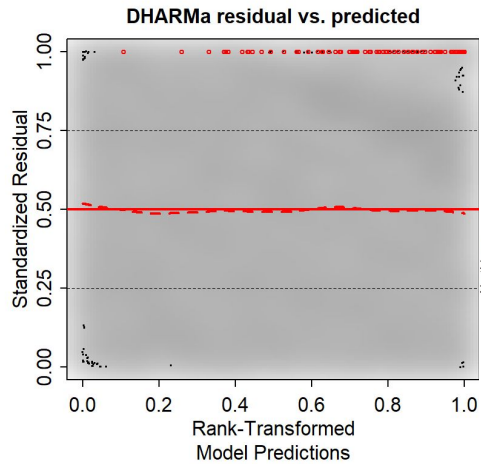
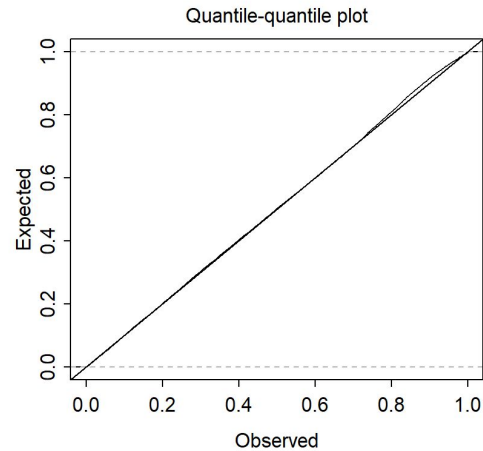
# IMMATURE FEMALES



# IMMATURE FEMALES 25-30 MM

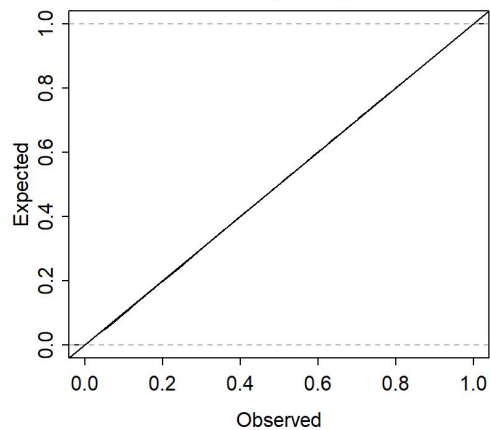


# IMMATURE FEMALES 50-55MM

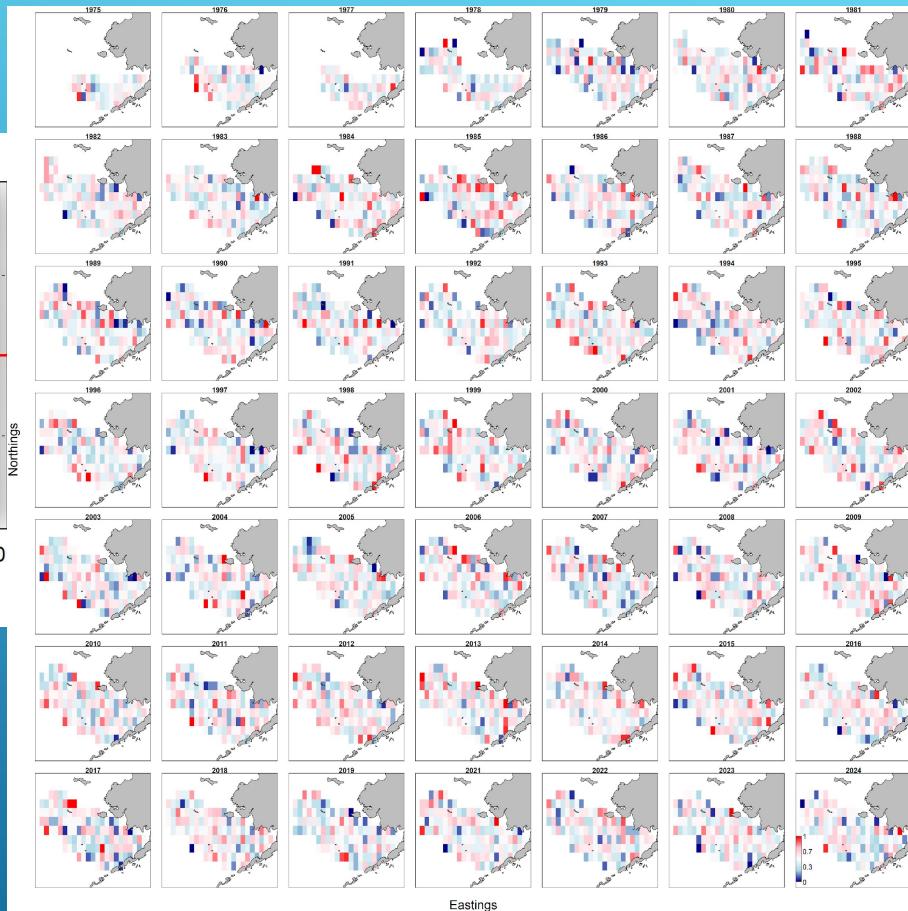
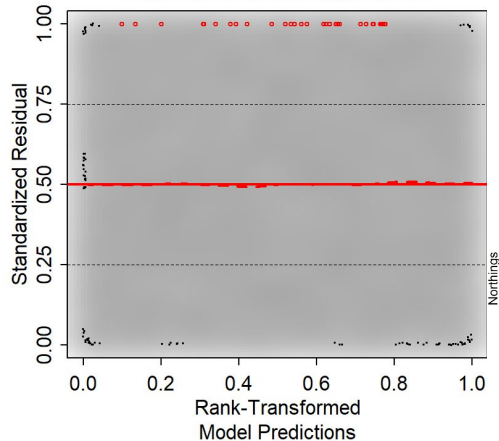


# IMMATURE FEMALES 90-95 MM

Quantile-quantile plot



DHARMa residual vs. predicted

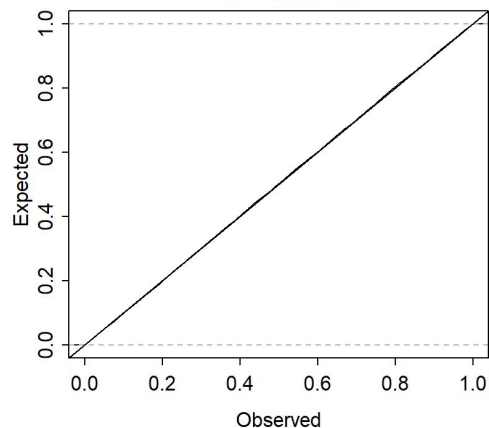


MATURE FEMALES

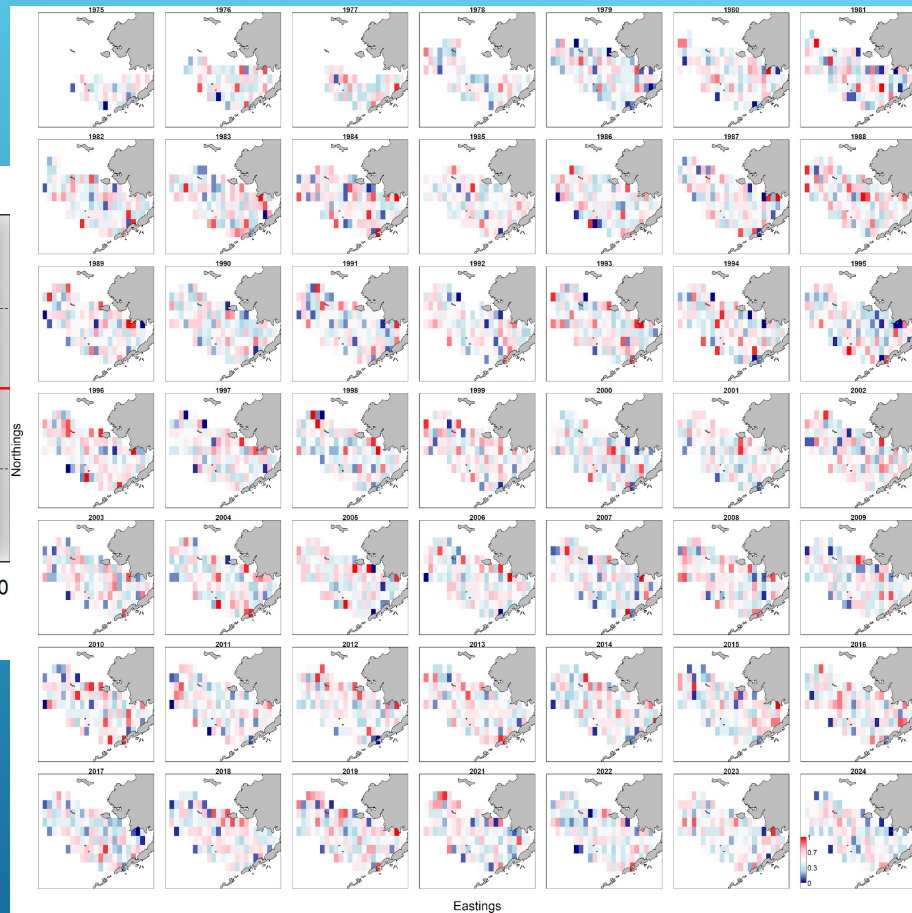
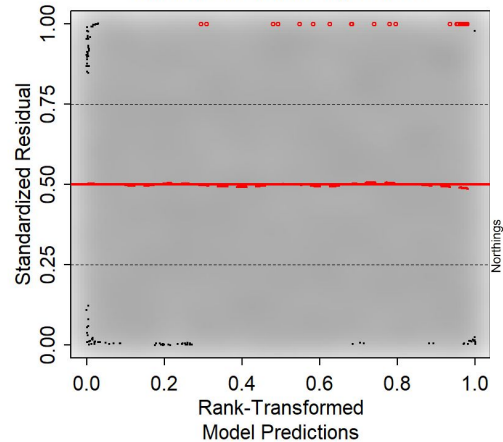


# MATURE FEMALES 60-65 MM

Quantile-quantile plot



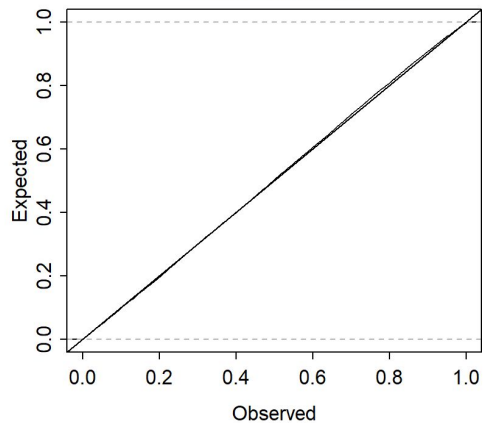
DHARMa residual vs. predicted



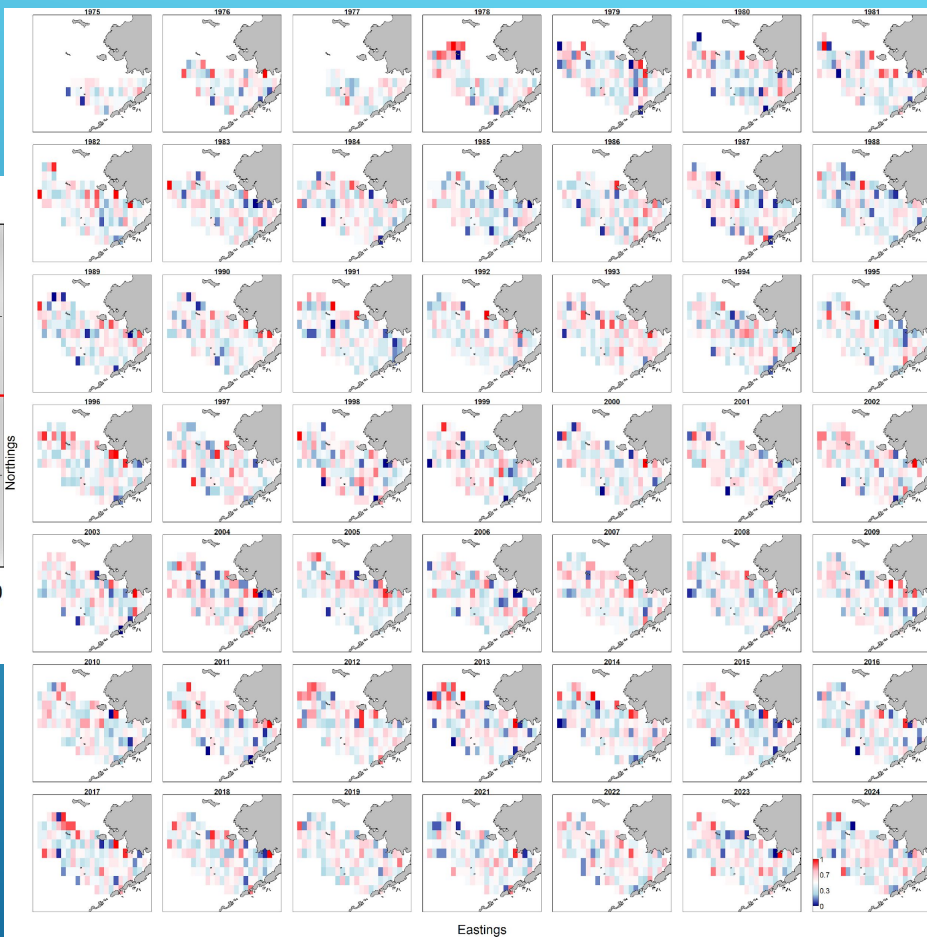
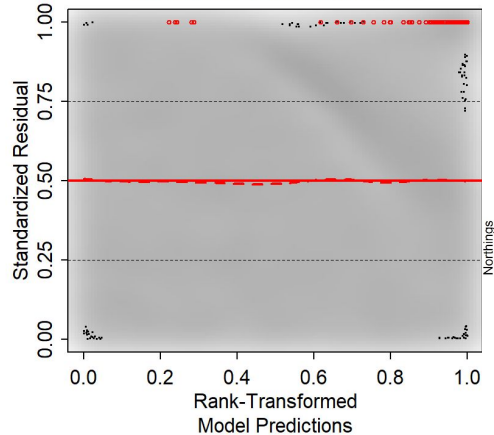


# MATURE FEMALES 85-90 MM

Quantile-quantile plot

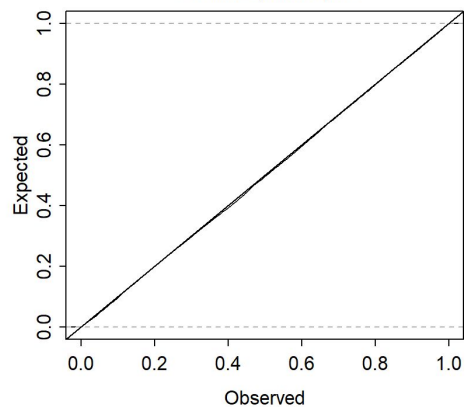


DHARMA residual vs. predicted

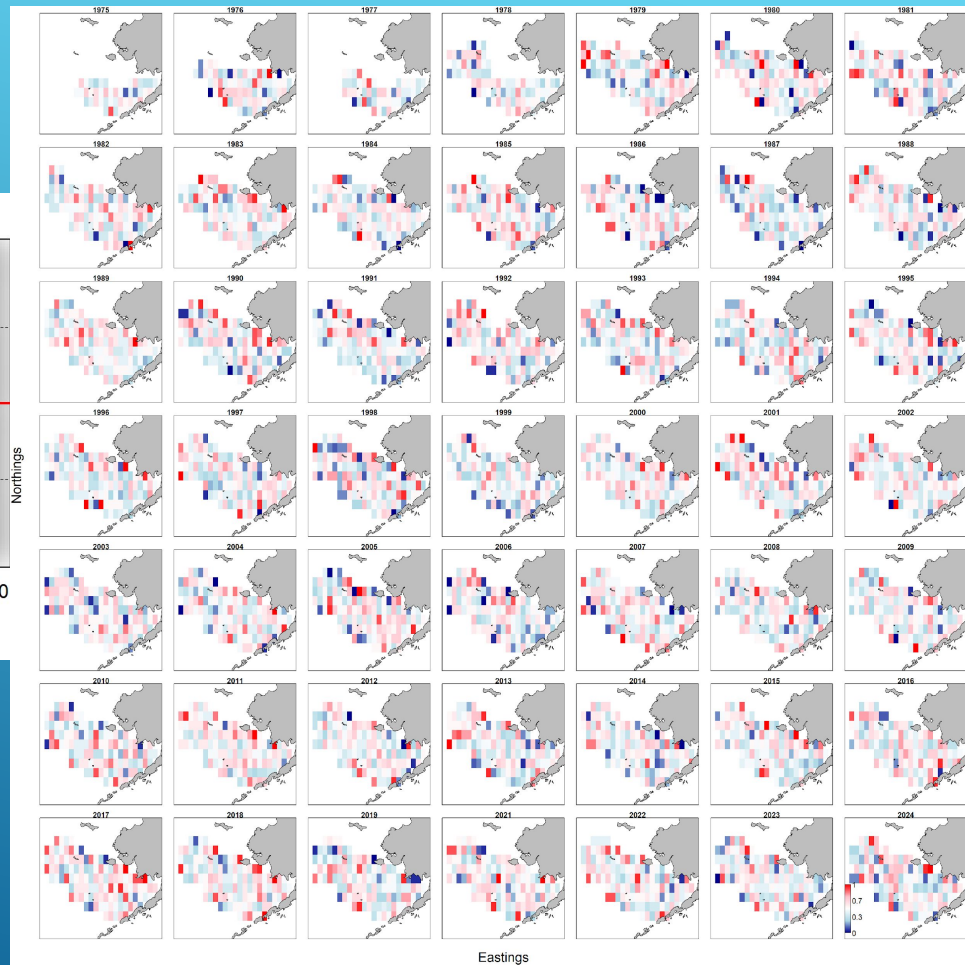
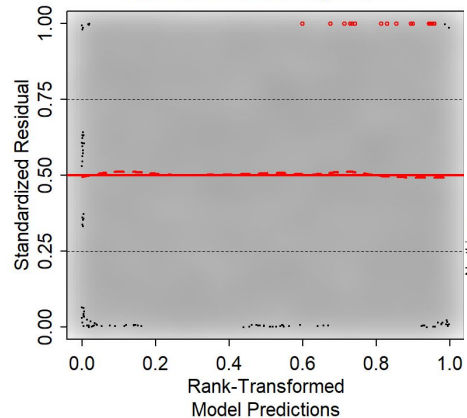


# MATURE FEMALES 110-115 MM

Quantile-quantile plot



DHARMA residual vs. predicted



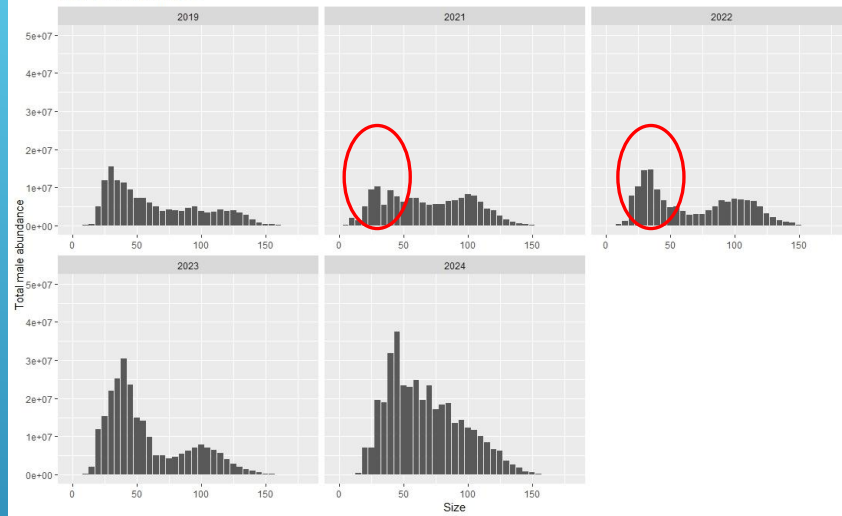
# COMPILED SIZE-FREQUENCIES



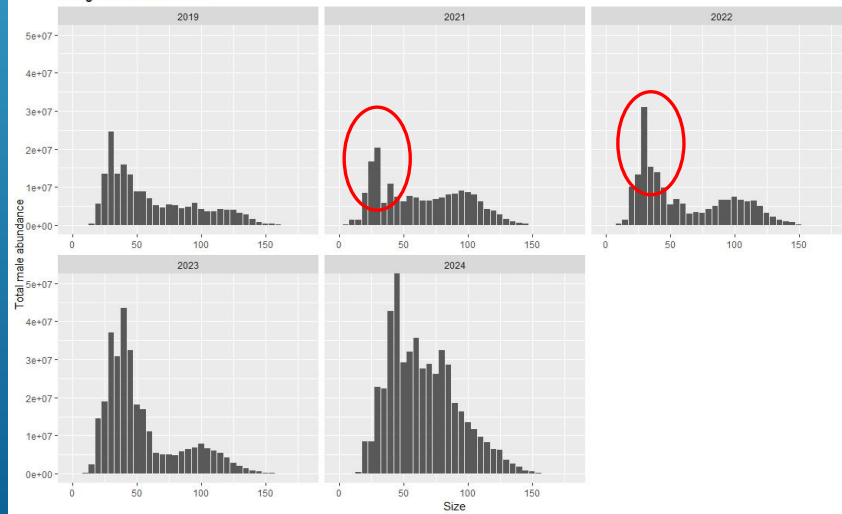
TOTAL MALES

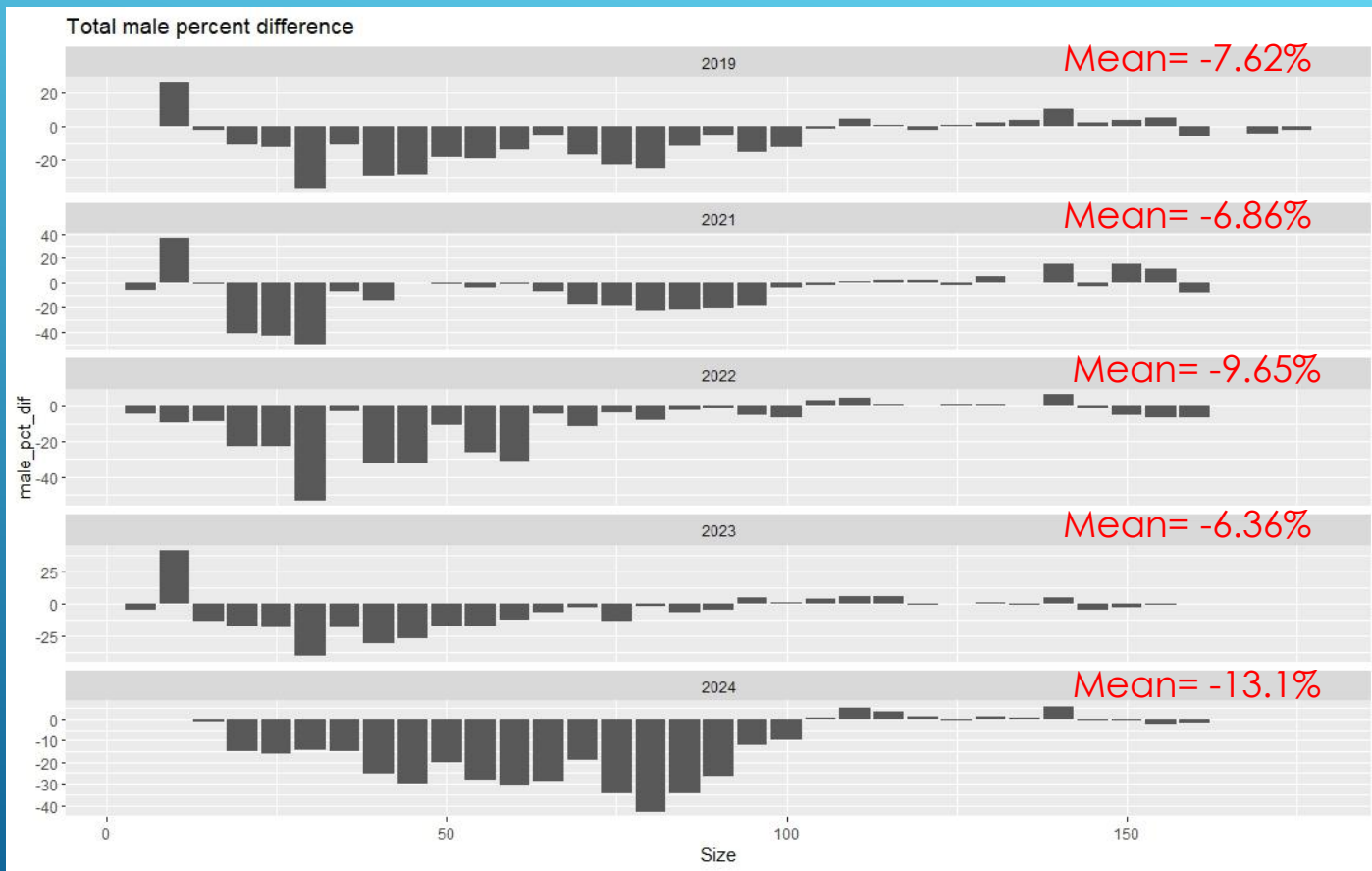


Model-based estimates



Design-based estimates



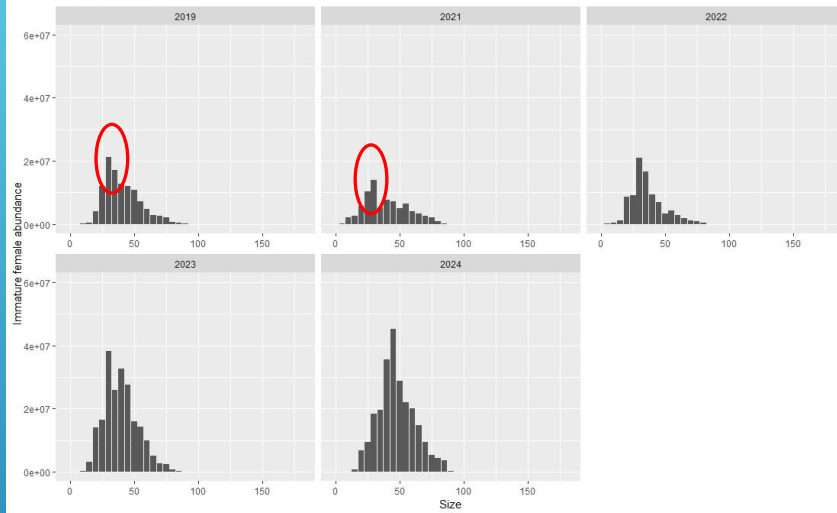




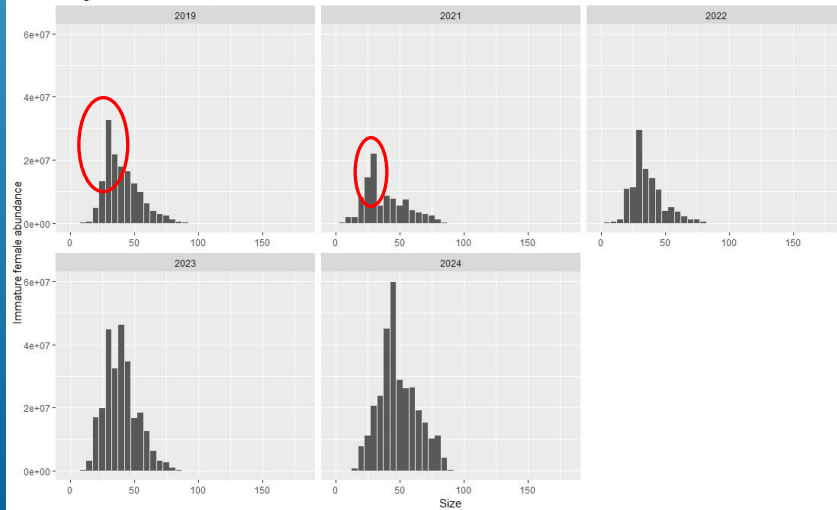
# IMMATURE FEMALES

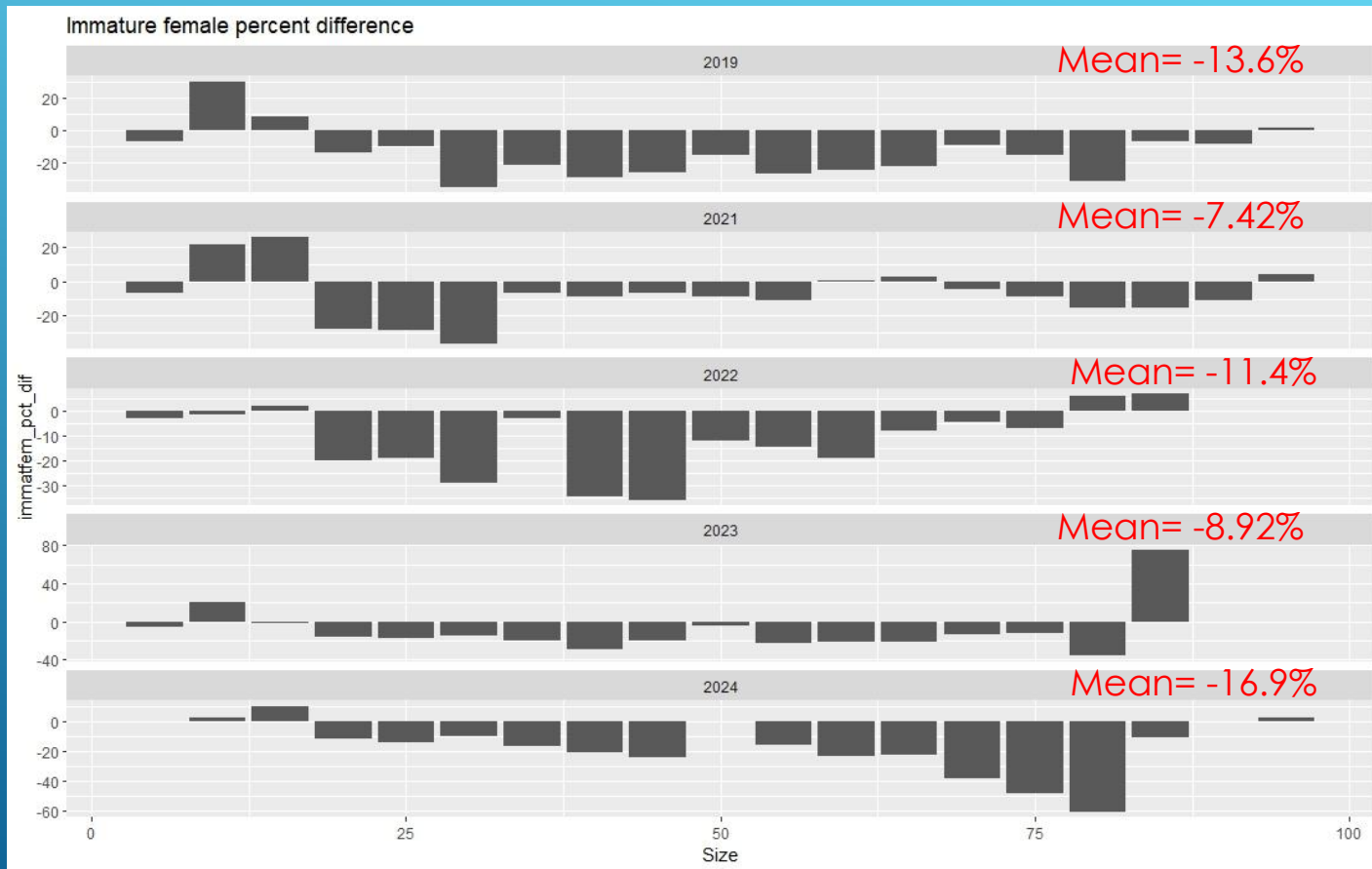


Model-based estimates



Design-based estimates

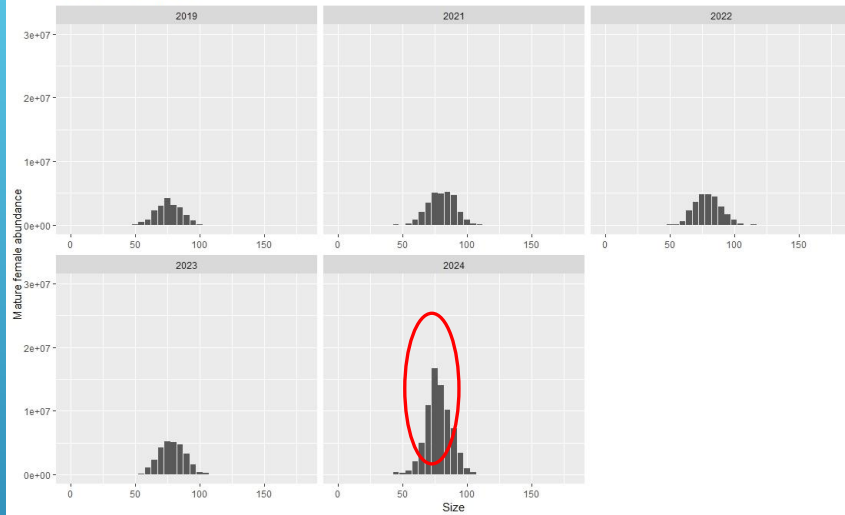




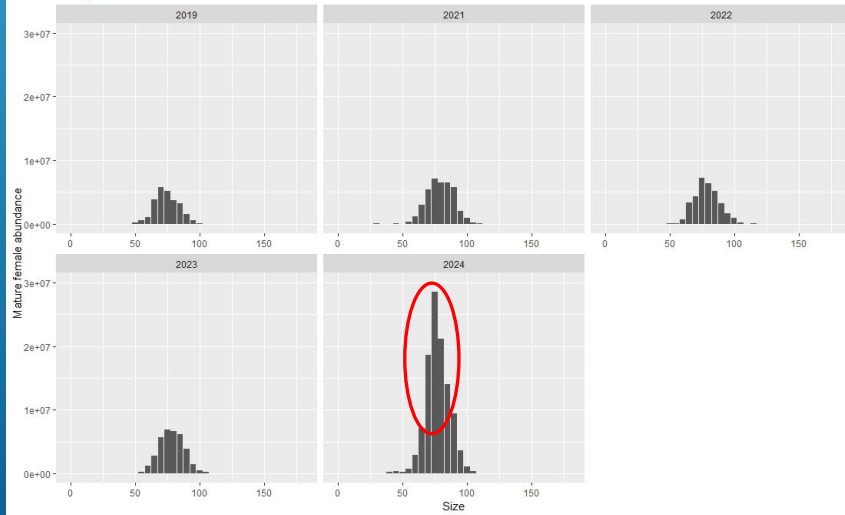
MATURE FEMALES

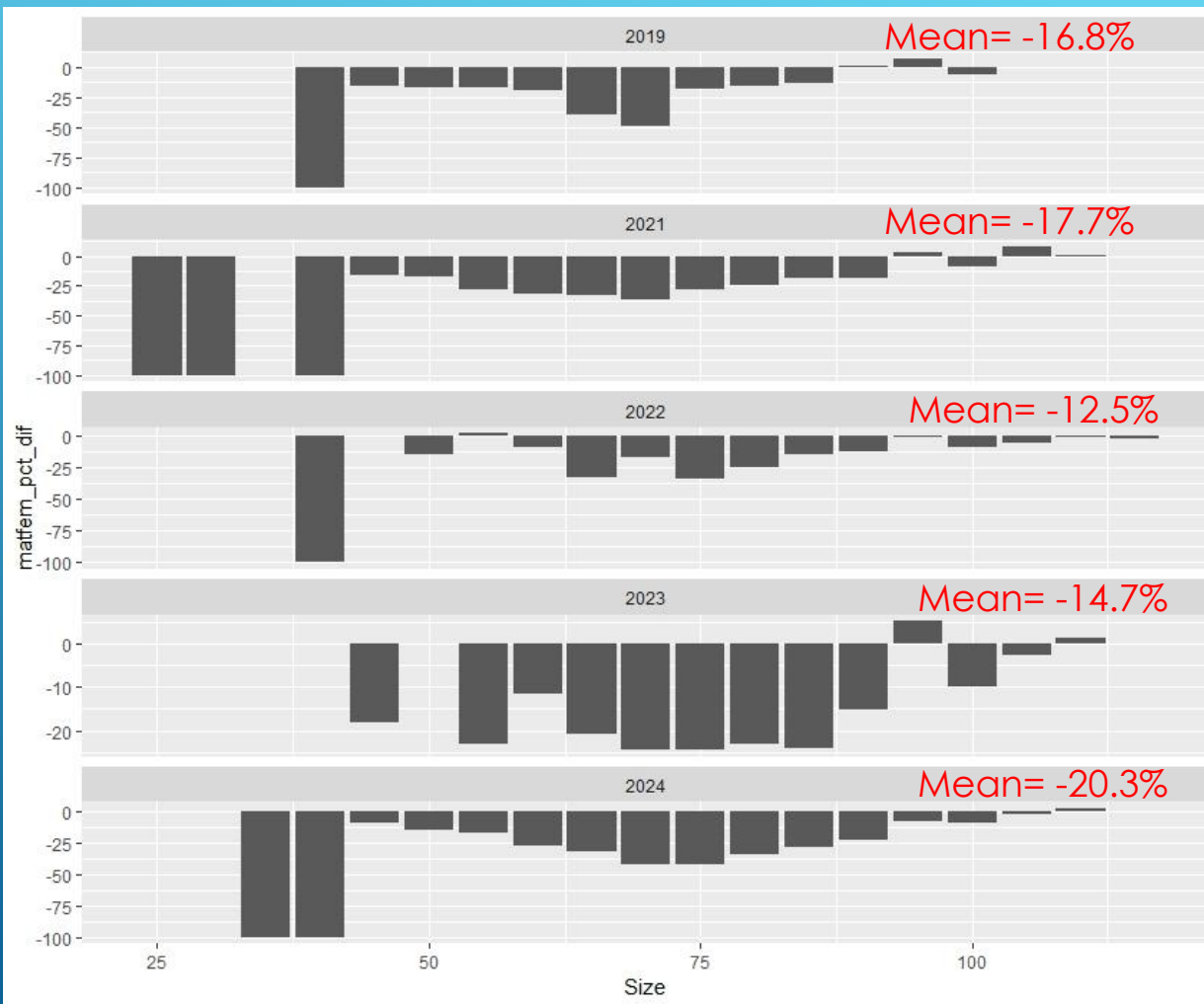


Model-based estimates



Design-based estimates







# SUMMARY

- ▶ Model diagnostics look \*good\*
- ▶ Estimates generally lower than design based
  - ▶ Model specification issue?
  - ▶ Consequence of down weighting significance of large haul-stations?
- ▶ Design-based and model-based size-frequencies \*broadly\* similar, but estimate discrepancies are.....concerning

# FUTURE DIRECTIONS

- ▶ Continue effort to investigate/resolve discrepancies (May-July)
- ▶ Beta/ObsModel/Rho
  - ▶ 125 kts probably ceiling given run times
- ▶ Move to tinyVAST, or given iterative approach, sdmTMB (Fall)