Canaries of the sub-Arctic: the collapse of snow crab in the eastern Bering Sea

Cody Szuwalski (and many others)

May Crab Plan Team update

2022

Still don’t have a great answer

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but I’ve learned some things

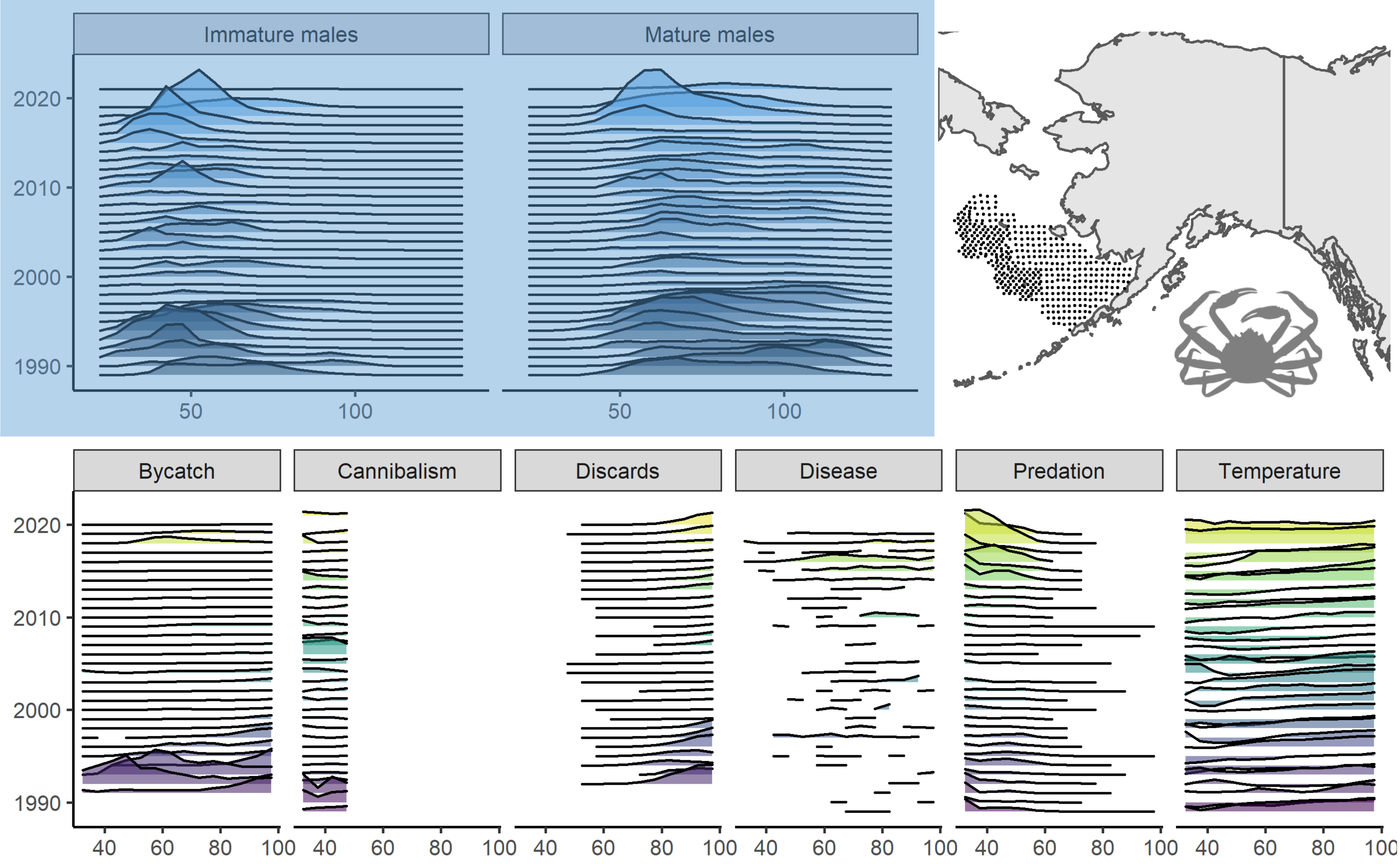
Here’s a reminder of what I did last time…

How have mortality and catchability varied over time?

What drives variability in mortality and catchability?

Estimate maturity and year-specific mortality and catchability

Correlate changes in estimated mortality and catchability with potentially related phenomena



Immature males
Mature males
2020
2010
2000
1990
50
100
50
100
Bycatch
Cannibalism
Discards
Disease
Predation
Temperature
2020
2010
2000
1990
40
60
80
100

Population dynamics model

Goal: explain the observed changes in immature and mature male abundance by estimating recruitment, mortality, and catchability

Details

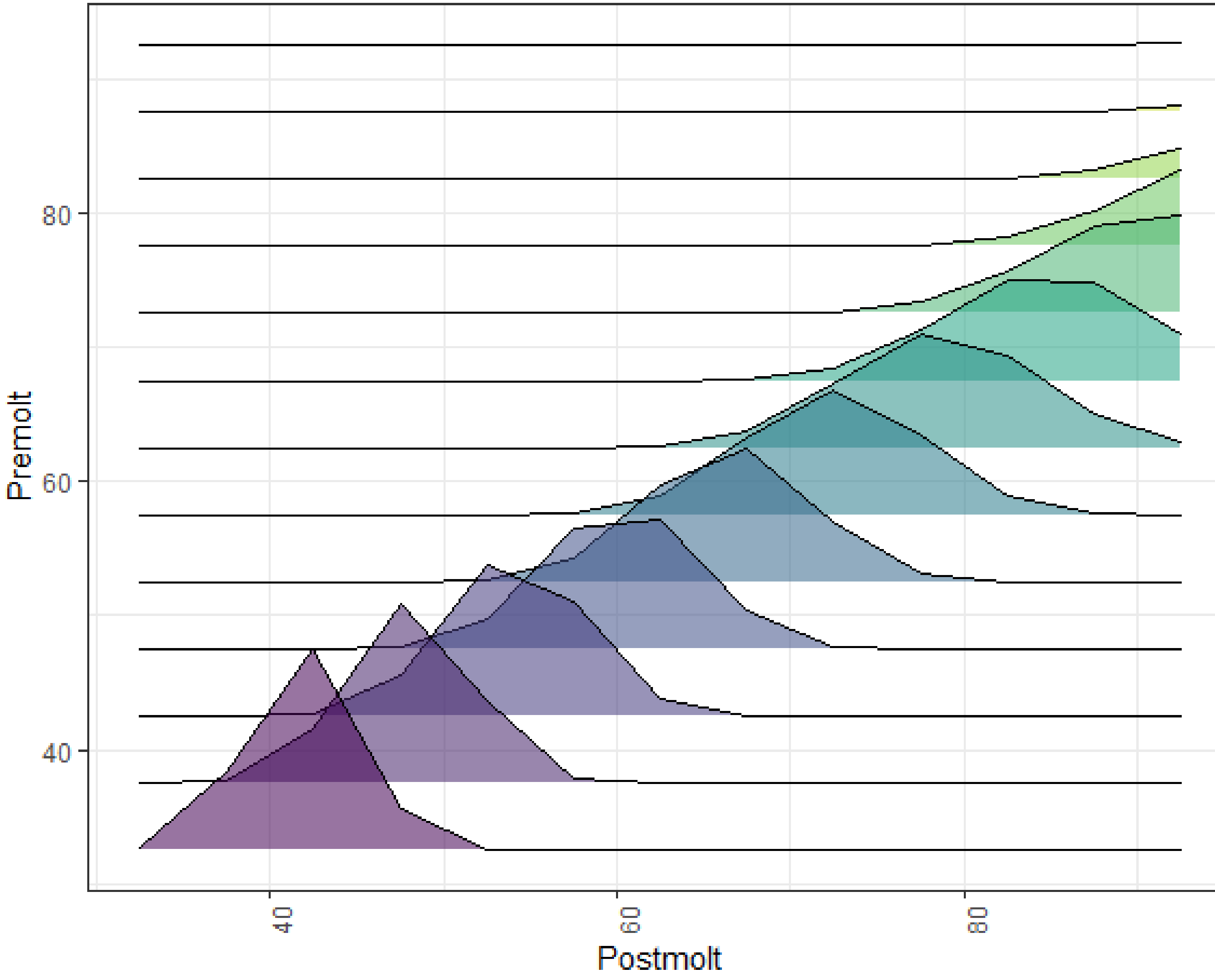
- Spans 1989 to 2021 (survey coverage consistent then)
- Male only
- Sizes 30-95mm carapace width, 5 mm size bins
- Fit to immature and mature indices of abundance (not biomass) + size composition data
- Estimated parameters
  - Initial numbers for immature and mature males
  - Mean mortality for immature and mature males
  - Yearly deviations for mortality and survey catchability by maturity state (why?)
  - Yearly recruitment
  - Proportion of recruitment falling in the first size bins (size bin 2 gets 1-p)
- Input processes
  - Growth
  - Survey selectivity derived from BSFRF data
  - Yearly probability of having undergone terminal molt data
- Rationale discussed

Likelihood	Form	Weighting
Abundance	Lognormal	CV (0.11,0.41)
Size composition	Multinomial	50
Prior on average M	Normal	Mean=0.271, Sigma=0.10
Penalty on M devs	Normal	Sigma = 0.10
Smoothness penalty on M	Second difference	1
Smoothness penalty on q	Second difference	1

Model process	Status quo	Simplified
Time span	1982-2021	1989-2021
Data sources fit	NMFS and BSFRF MMB, FMB, Survey size composition, retained catch, discard, and bycatch	NMFS immature and mature male abundance and size composition
Size range	30-135 mm carapace width	30-95 mm carapace width
Recruitment	First 5 size bins, proportions fixed	First 2 size bins, proportions estimated
Mortality	Natural and fishing mortality split out; 4 natural mortality parameters estimated (sex and maturity state)	Total mortality estimated yearly by maturity state
Growth	Specified based on growth increment data; discretized and renormalized gamma function for variance around mean increment	Specified based on growth increment data; discretized and renormalized normal distribution function for variance around mean increment
Sexes	Male and female	Male
Maturity	Average probability of having undergone terminal molt estimated	Yearly probability of having undergone terminal molt input; average used when data unavailable
Survey catchability	Two eras estimated informed by BSFRF data	Yearly parameter estimated by sex
Survey selectivity	Logistic, two eras	Non-parametric, one era

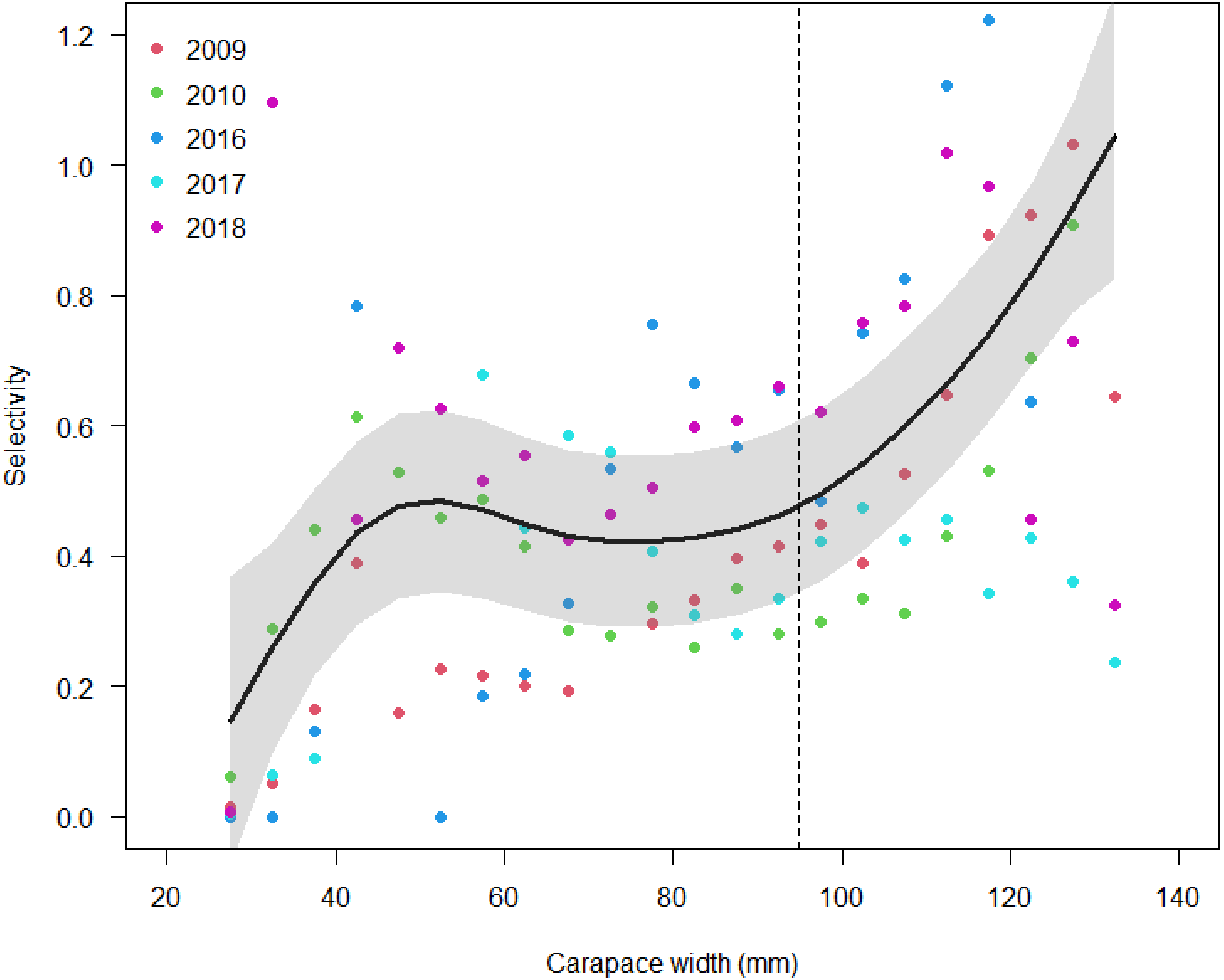
Growth, selectivity, and maturity

- Growth increments based on all available growth data
- Crab can 'outgrow' the model—some of the sums of the rows of the transition matrix equal less than 1.
- Discretized and renormalized normal distributions used for the variance around size increment.



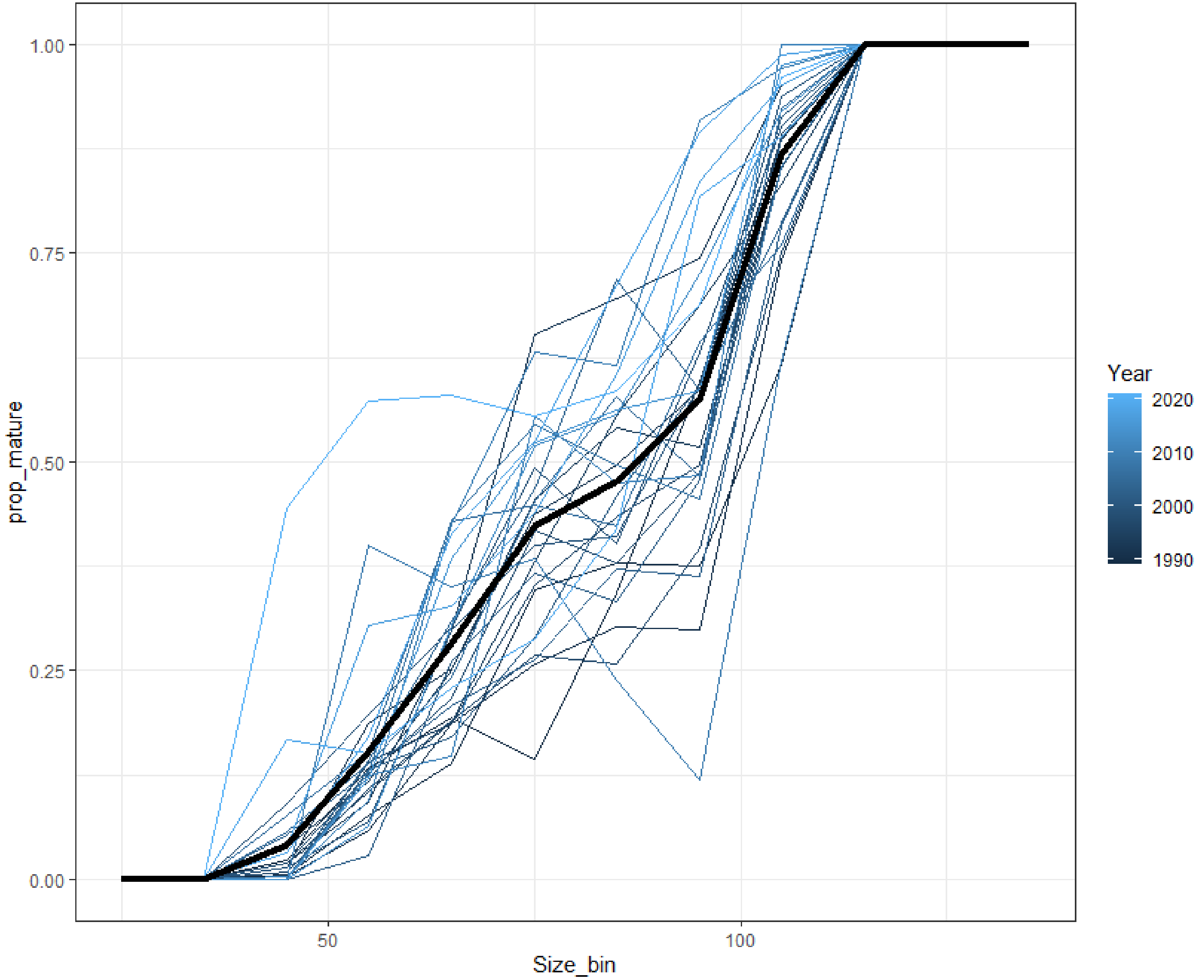
Growth, selectivity, and maturity

- Survey selectivity based on a GAM fit to the BSFRF data at size
- Estimated yearly catchability scales this curve up and down
- Vertical line is the end point of the crab in the model



Growth, selectivity, and maturity

- Chela height measurements used to calculate the proportion of new shell males having undergone terminal molt
- Changes over time
- Status quo assessment estimates the average ogive, but here they are input as data



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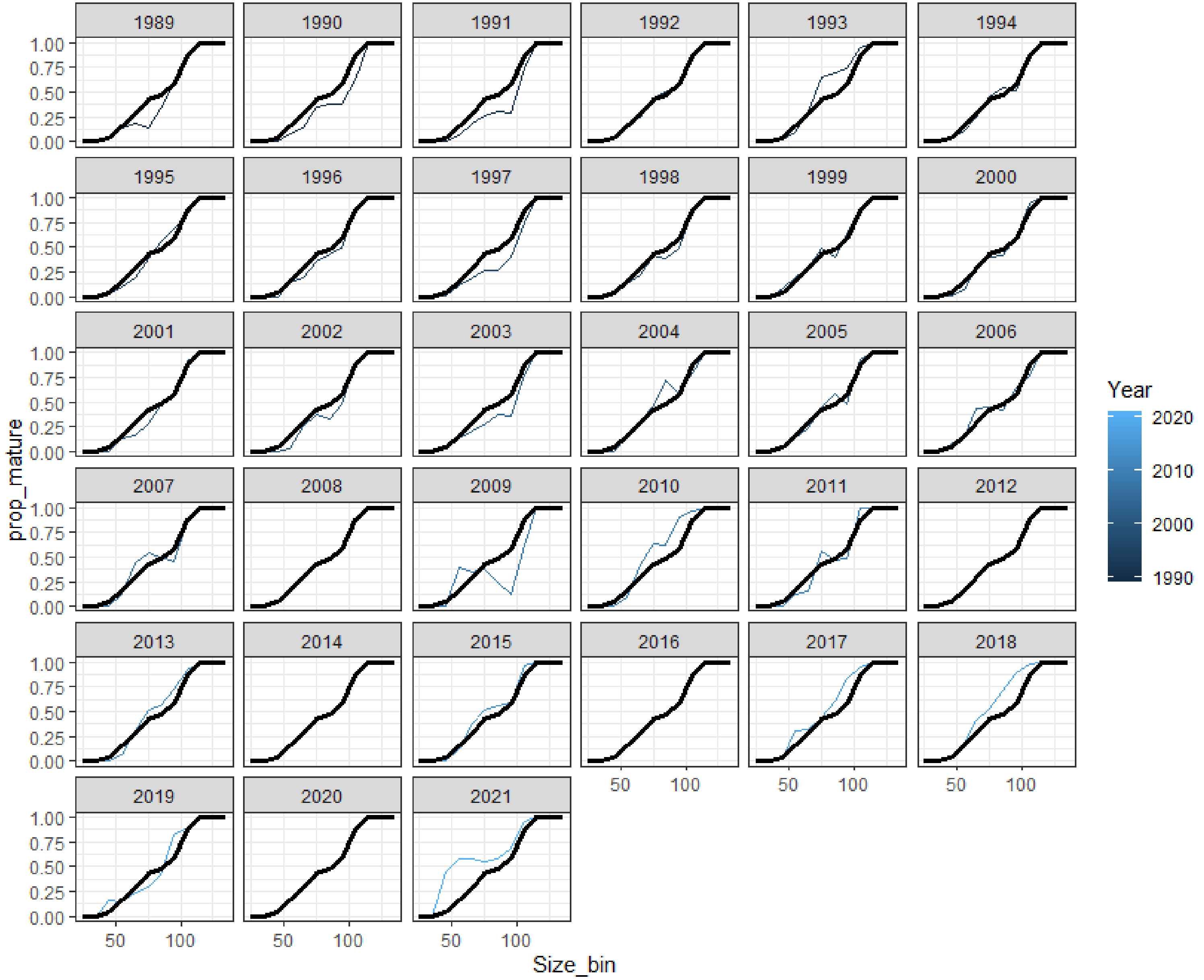


```
for(int year=styr;year<endyr;year++)
 {
 // mortality
 for (int size=1;size<=size_n;size++)
   {temp_imm(size) = imm_n_size_pred(year,size) * exp(-1*0.5*exp( nat_m(year,size)));
     temp_mat(size) = mat_n_size_pred(year,size) * exp(-1*0.5*exp( nat_m_mat(year,size)));}

 // growth
   trans_imm = size_trans * temp_imm;
 // recruitment
    trans_imm(1) += exp(log_recruits(year))*prop_rec(year);
    trans_imm(2) += exp(log_recruits(year))*(1-prop_rec(year));

  // maturity and mortality
 for (int size=1;size<=size_n;size++)
  {imm_n_size_pred(year+1,size) = (trans_imm(size) * (1-prop_term_molt(year,size)))      *  exp(-1*0.5*exp( nat_m(year,size)));
  mat_n_size_pred(year+1,size) = (trans_imm(size) * prop_term_molt(year,size) + temp_mat(size))  *  exp(-1*0.5*exp(nat_m_mat(year,size)));}
 }
```

MORTALITY

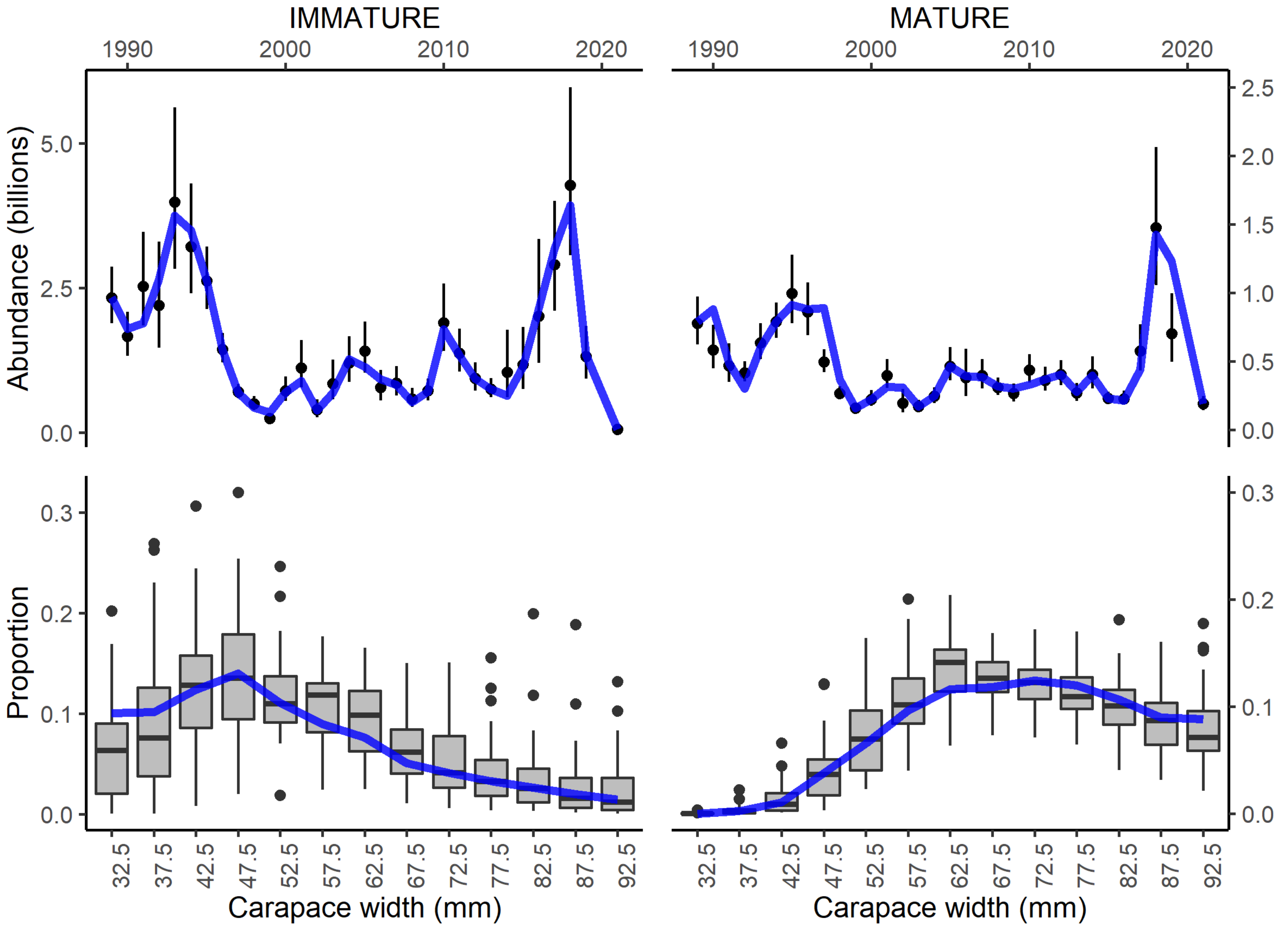
GROWTH

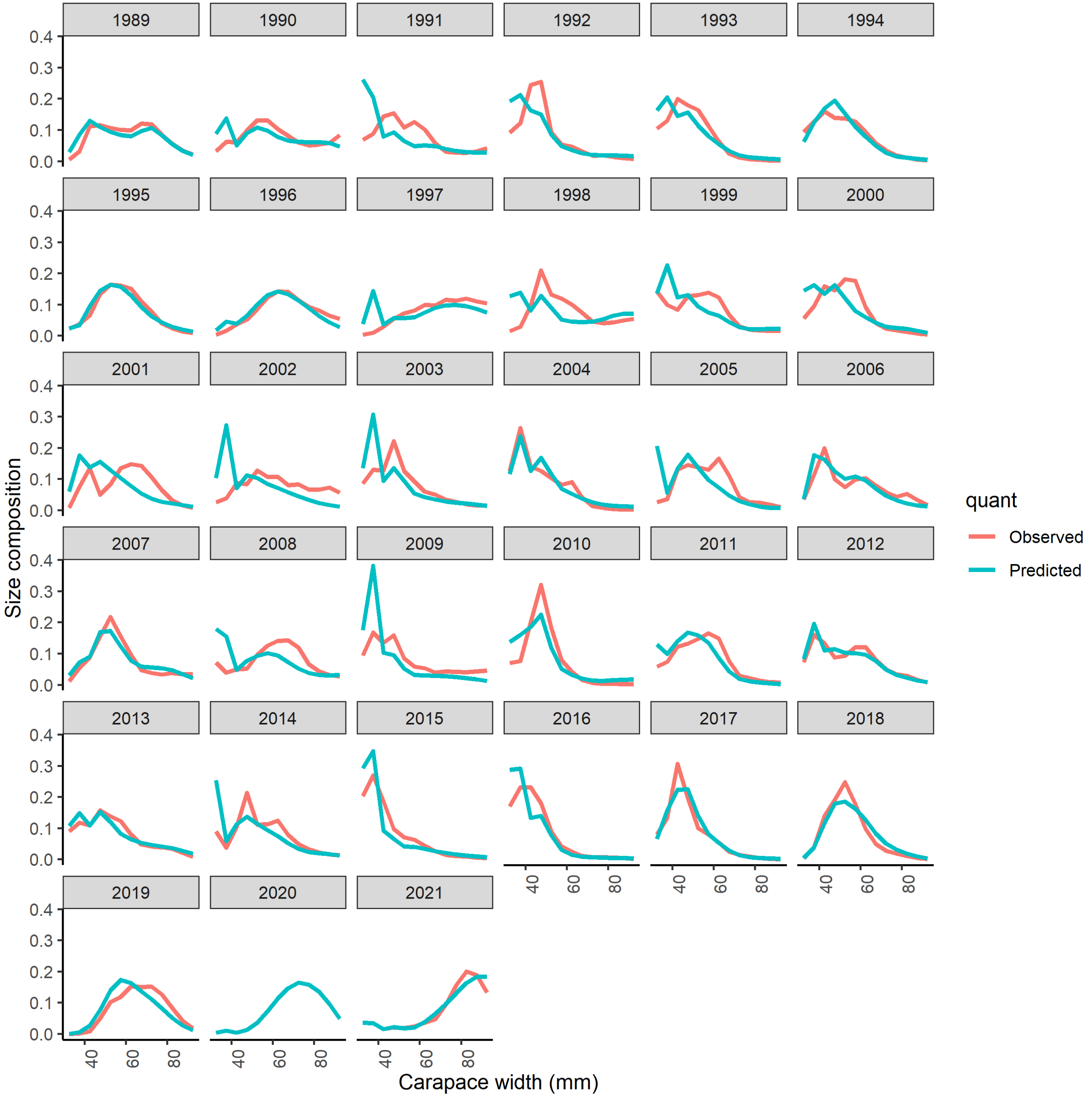
RECRUITMENT

MATURITY

Model fits

- No evidence for non-convergence (max gradient component < -0.009, positive-definite hessian)



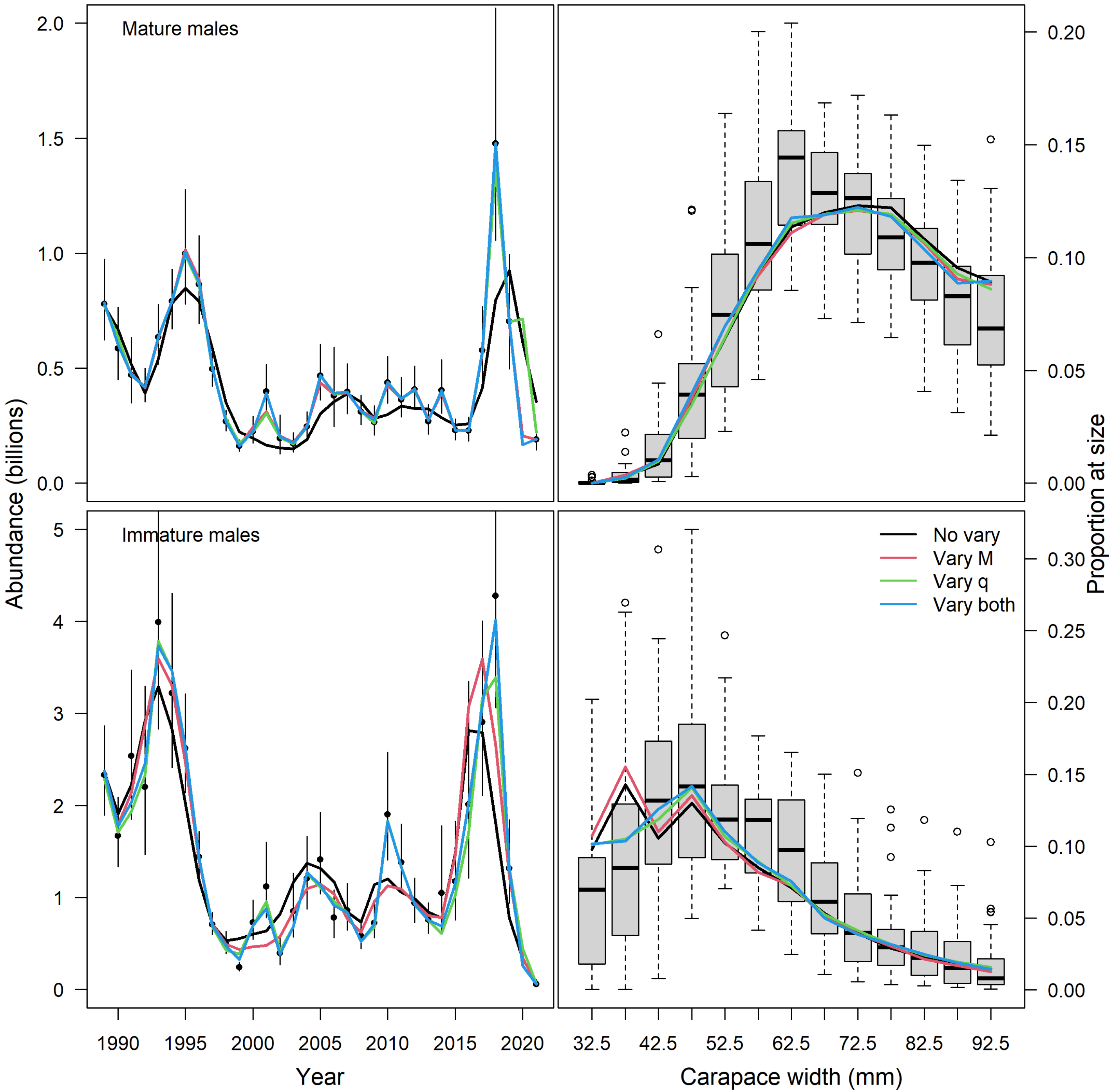


Recruitment occurs in the first two size bins.

Sometimes to fit the size composition in the following year(s), more crab need to be deposited in the first two bins than

This probably could maybe be addressed by fiddling with survey selectivity and the number of bins into which recruits fall.

“Why would you think you can estimate these processes together at all?!”



Recruitment: new small crab

Mortality: changes in abundance are permanent

Catchability: changes are 'reversible'…but also confounded with 'observation error'

This unfortunately makes it difficult to know what cause changes in the terminal year…but preserves the possibility that historical catchability and mortality could be estimated.

To do list

- Sensitivity analyses for assumptions, priors, and penalties (e.g. smaller sigmas for prior on M to see if discrepancy between immature and mature mortality can be shrunk)
- Simulation to see if time-varying q and M can be estimated with these data
- Think about model selection
- Methods for selecting smoothness penalties

- Methods for incorporating variance into the inference model
- Test ‘covariates as fleet’ model

- Do all of this again, but estimating size and year specific m and q…

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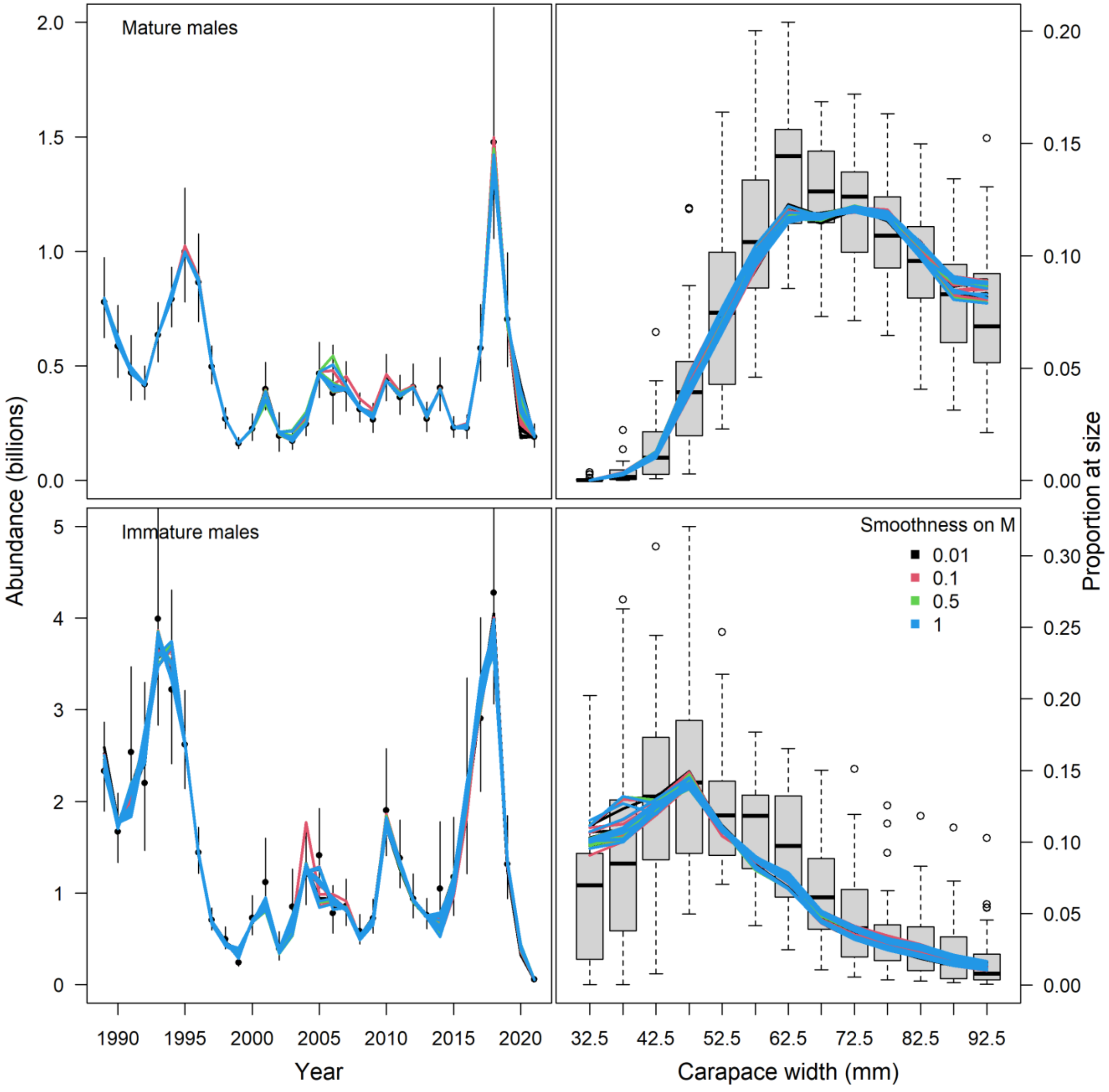
- Methods for incorporating variance into the inference model
- **Test 'covariates as fleet' model**

- ~~Do all of this again, but estimating size and year specific m and q…~~

Sensitivity analysis

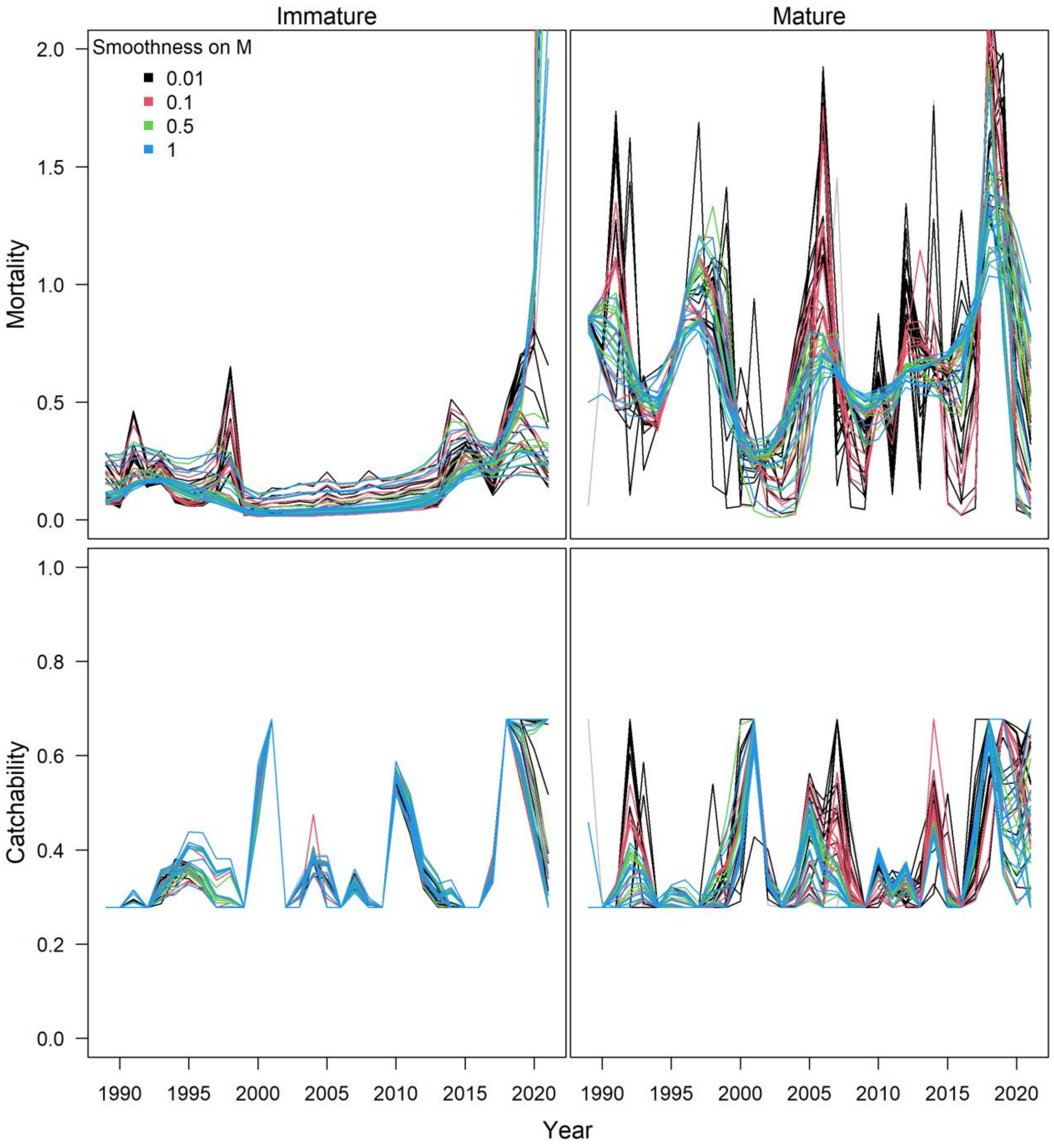
- Fit the model 108 time with different values for poorly known inputs
- Fits were similar regardless of sensitivity

Input parameter	Input values
Size composition weight	25, 50, 100
Prior on average M	0.2, 0.3, 0.45
Sigma on the variability in M	0.01, 0.1, 0.2
Smoothness penalty on M	0.01, 01, 0,5, 1



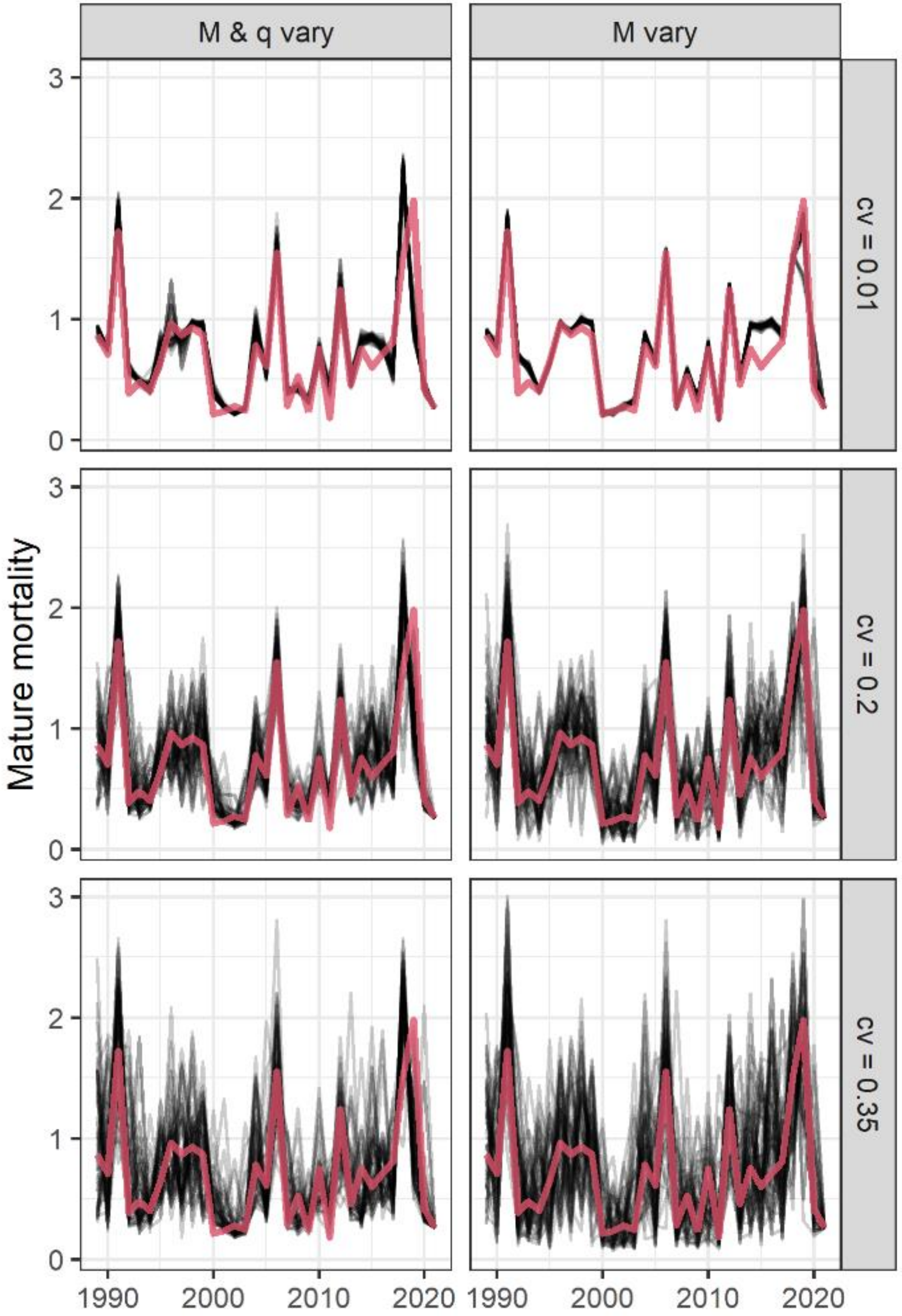
Sensitivity analysis

- Fit the model 108 time with different values for poorly known inputs
- Fits were similar regardless of sensitivity
- Estimated processes, however, varied more widely
- Smoothness on time-variation in M was one of the largest drivers of differences



Simulation

- Simulated 100 populations for six scenarios
- Operating model was the fitted model M & q vary
- Estimation models
  - Estimate time-varying M & q
  - Estimate time-varying M
- Coefficient of variation on indices of abundance
  - “Perfect info” CV = 0.01
  - “Similar to EBS snow” CV = 0.2
  - “Similar to PIRKC” CV = 0.35
- Mature mortality for only time-varying M better, but both were fairly well estimated



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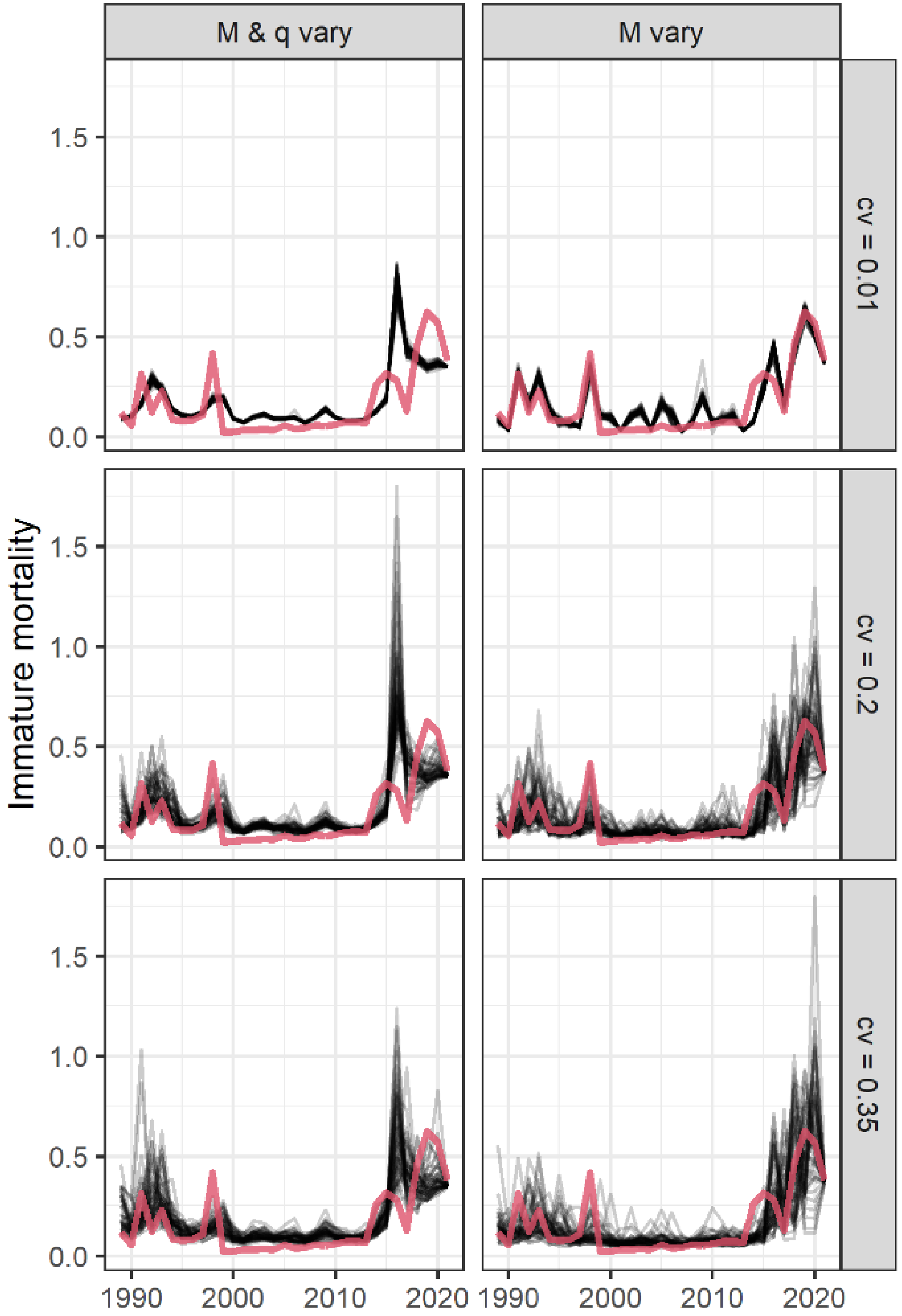

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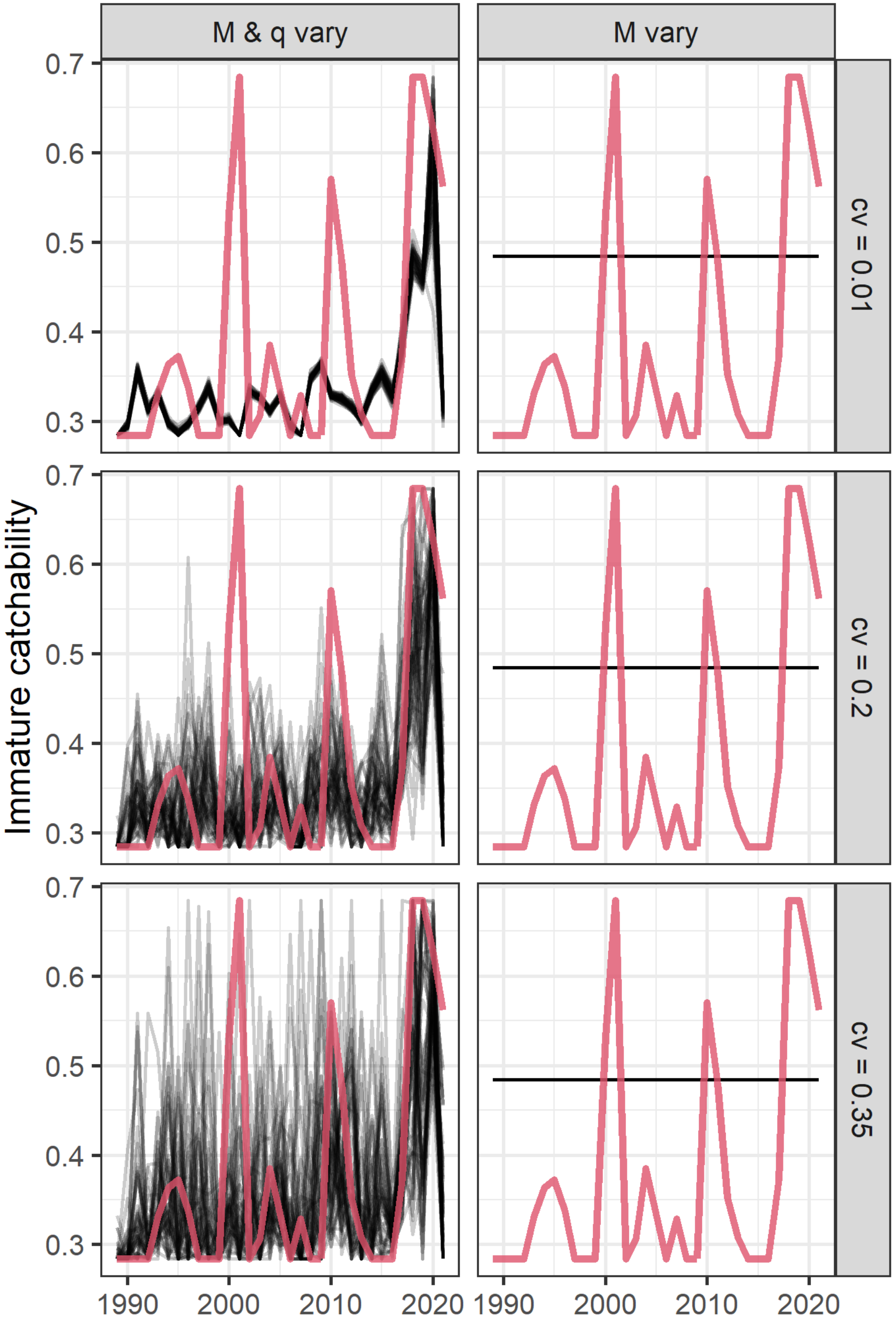

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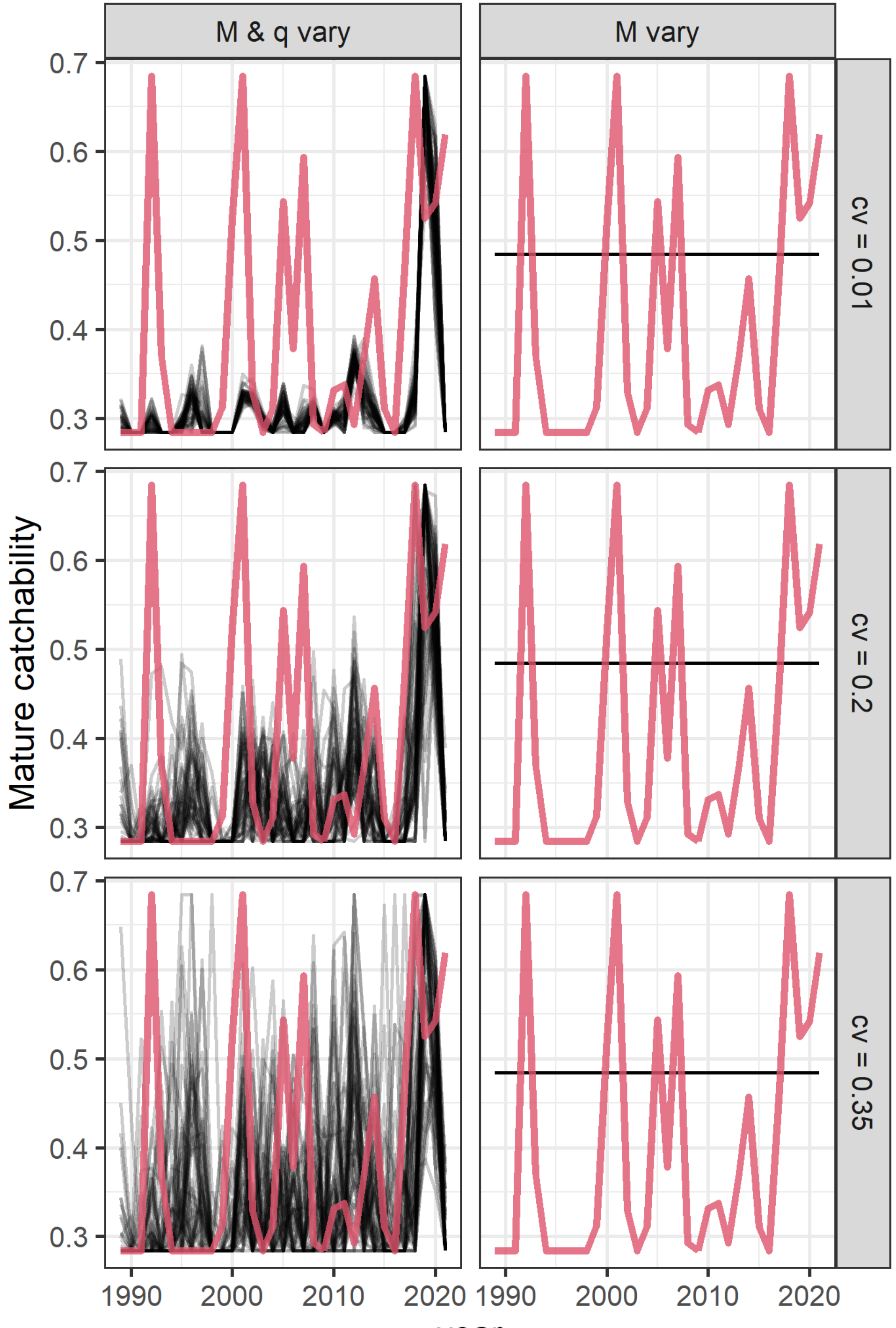

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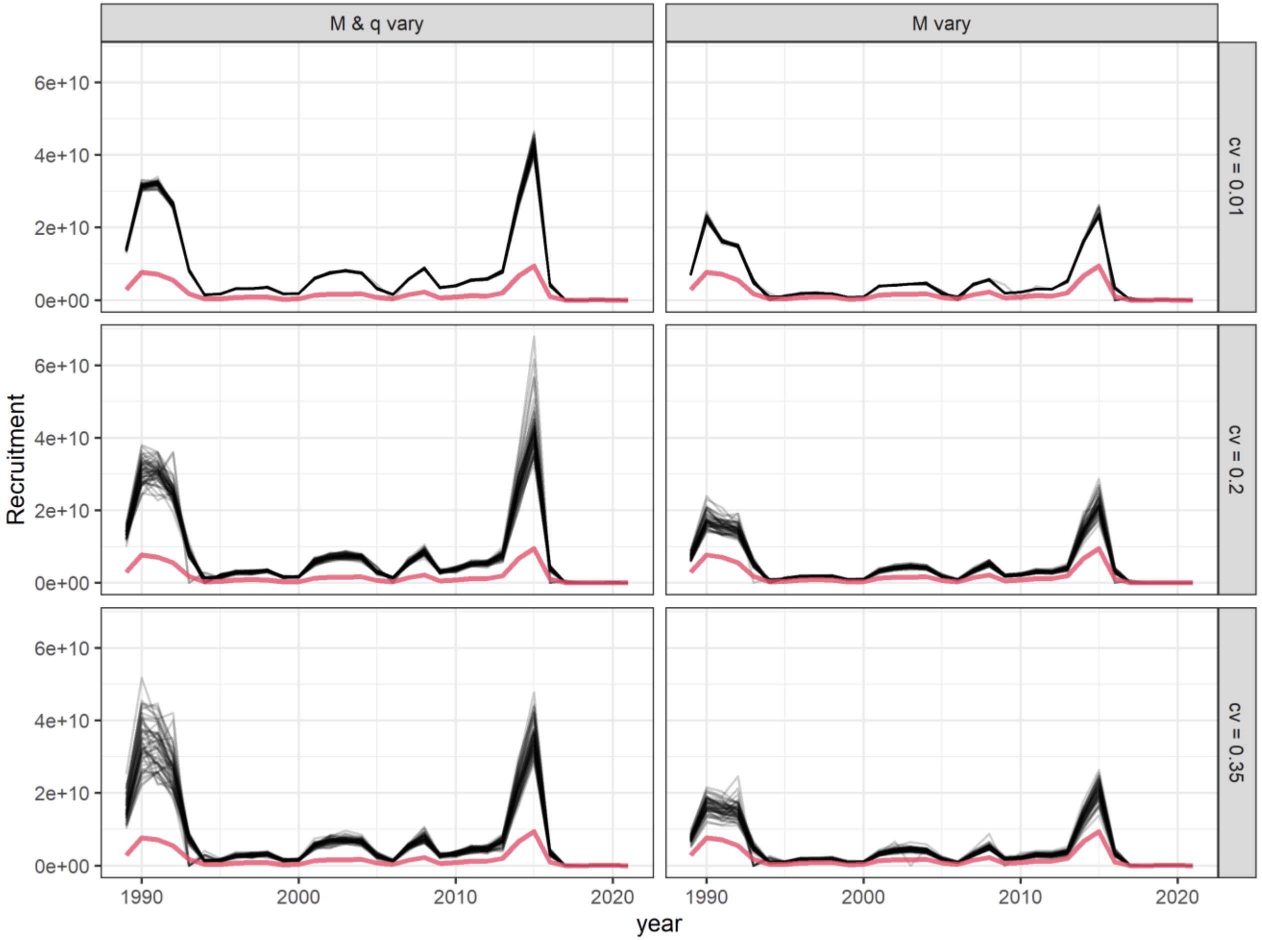
- Immature M for 'M & q' had a large peak in 2016; immature M for 'M vary' more variable during the low period
- Estimating q generally difficult; confounded with observation error
- Scale is hard to estimate appropriately; all models overestimated recruitment, but 'M vary' was closer



Inability to capture scale underscores the use of correlative models instead of inputting the covariates as drivers in the models.

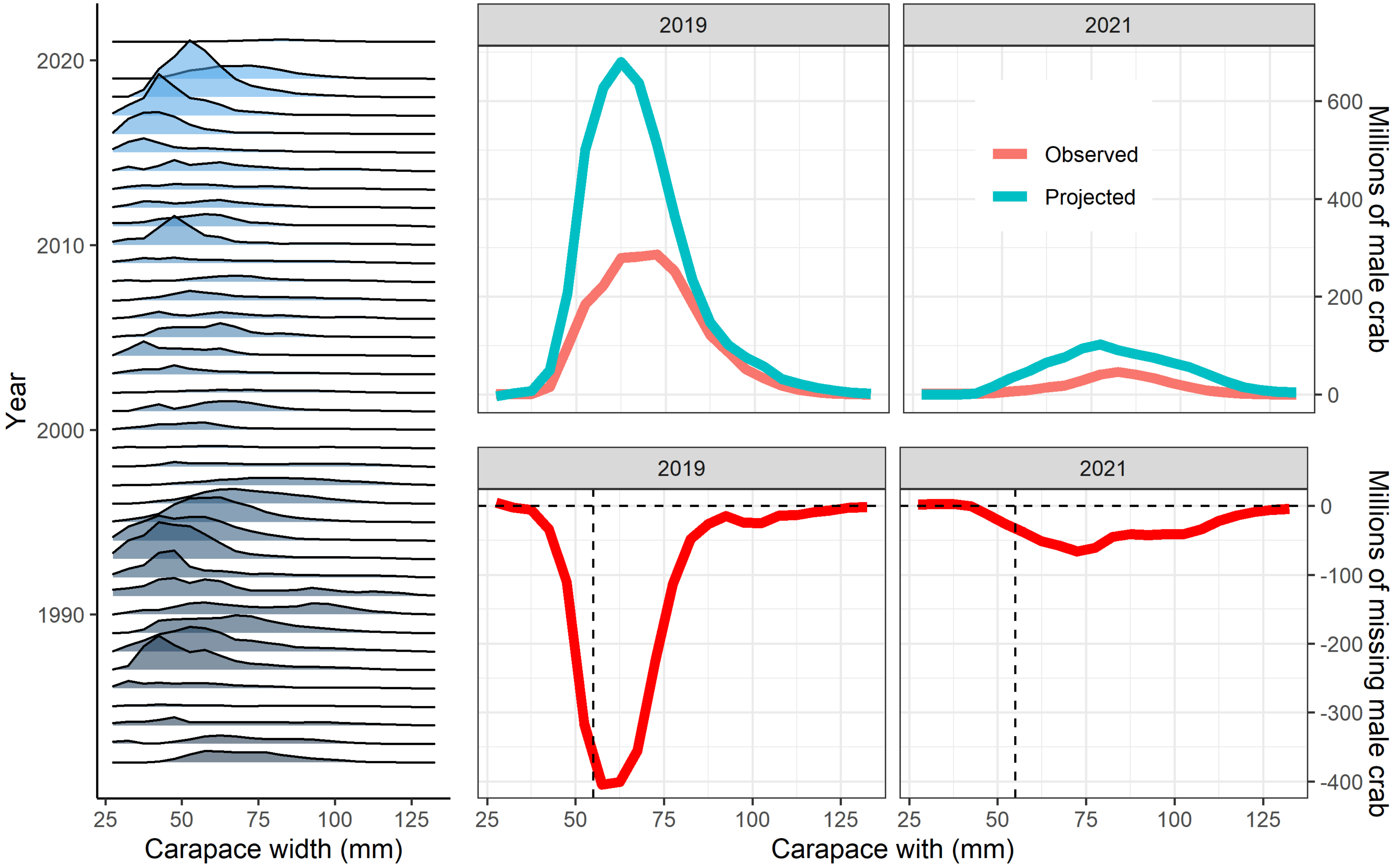
Covariates

- Bycatch & discards were in numbers at size
  - Divided these numbers at size by the predicted numbers at size from the population dynamics model to make it more comparable with the estimated mortality rates
  - Retained catch not included: very little and also highly correlated with discards
- Cannibalism
  - Proportion of the density of small crab overlapping with predator *times*
  - Density of large crab in the overlapping area
- Disease
  - Prevalence (i.e. number of crab visually identified as infected)
- Predation
  - Tons consumed per day
  - Divided this by the biomass (check this) at size predicted at size from the population dynamics model
- Temperature
  - Average temperature occupied by size

What size of crab were missing?

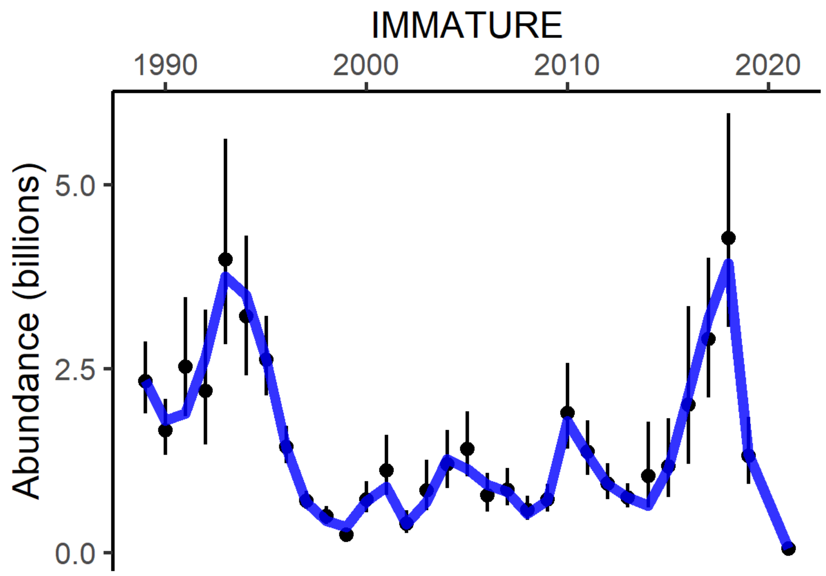
1. Start with 2018 numbers at size
2. Project forward removing catch, implementing growth and average natural mortality
3. Subtract the projected from the observed

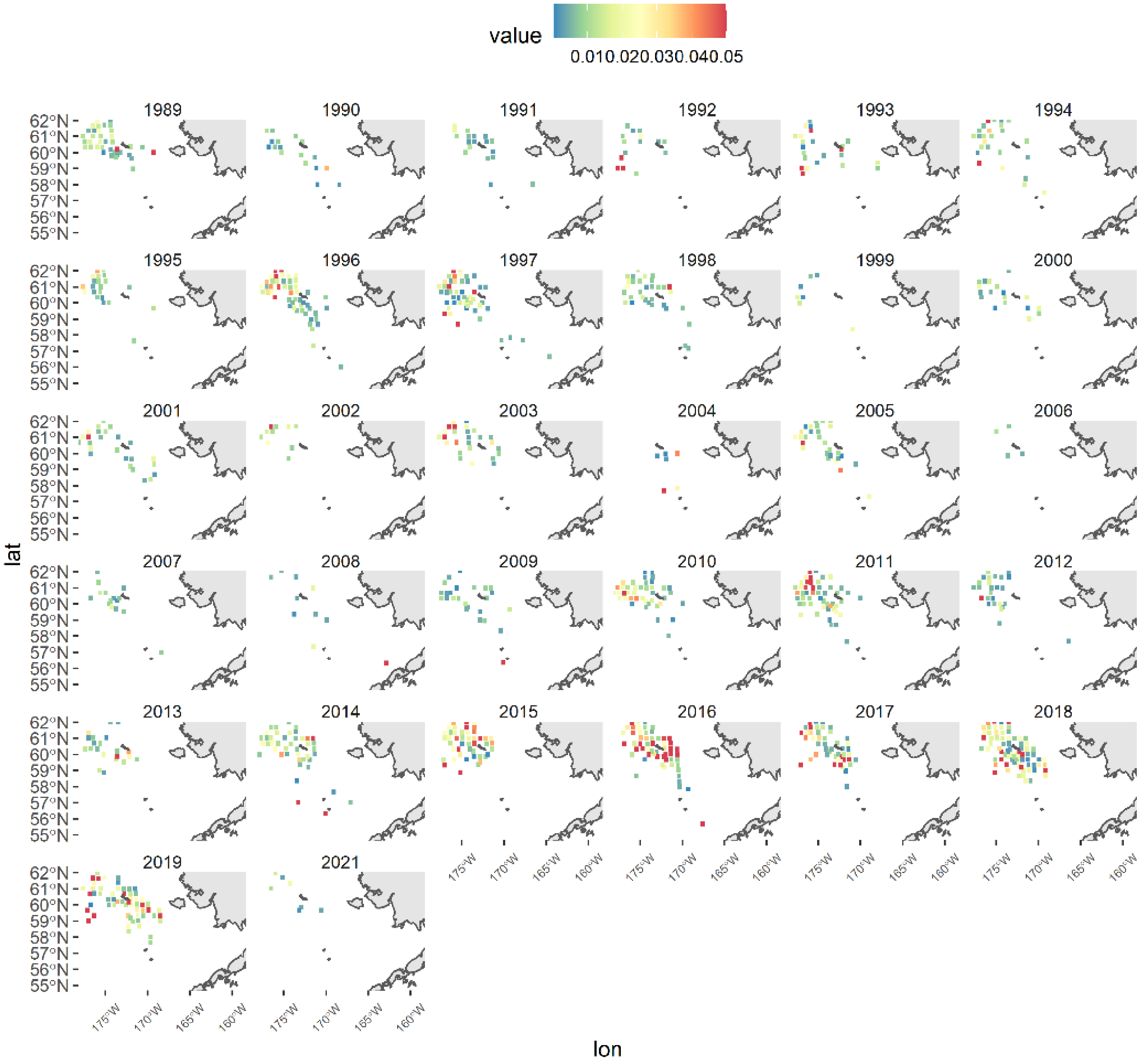
4. Repeat starting with 2019 data and projecting 2 years



Disease prevalence

- Explosion of disease in 2015 and 2016
- Spatial extent of disease was maintained into 2019, but the intensity declined rapidly
- 1996/1997 are the only comparable years, but interestingly those followed a large peak in immature males seen in the 1993-1995 surveys
- The 2015/2016 ‘explosion’ preceded the large immature male survey numbers in 2017-2018





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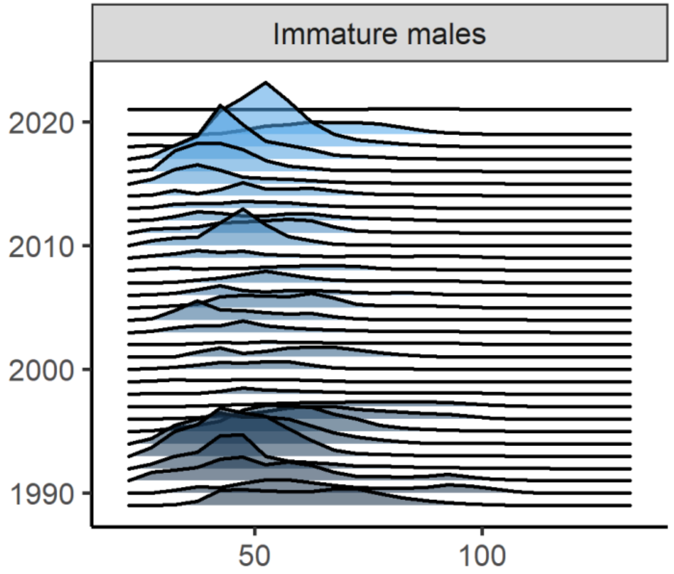
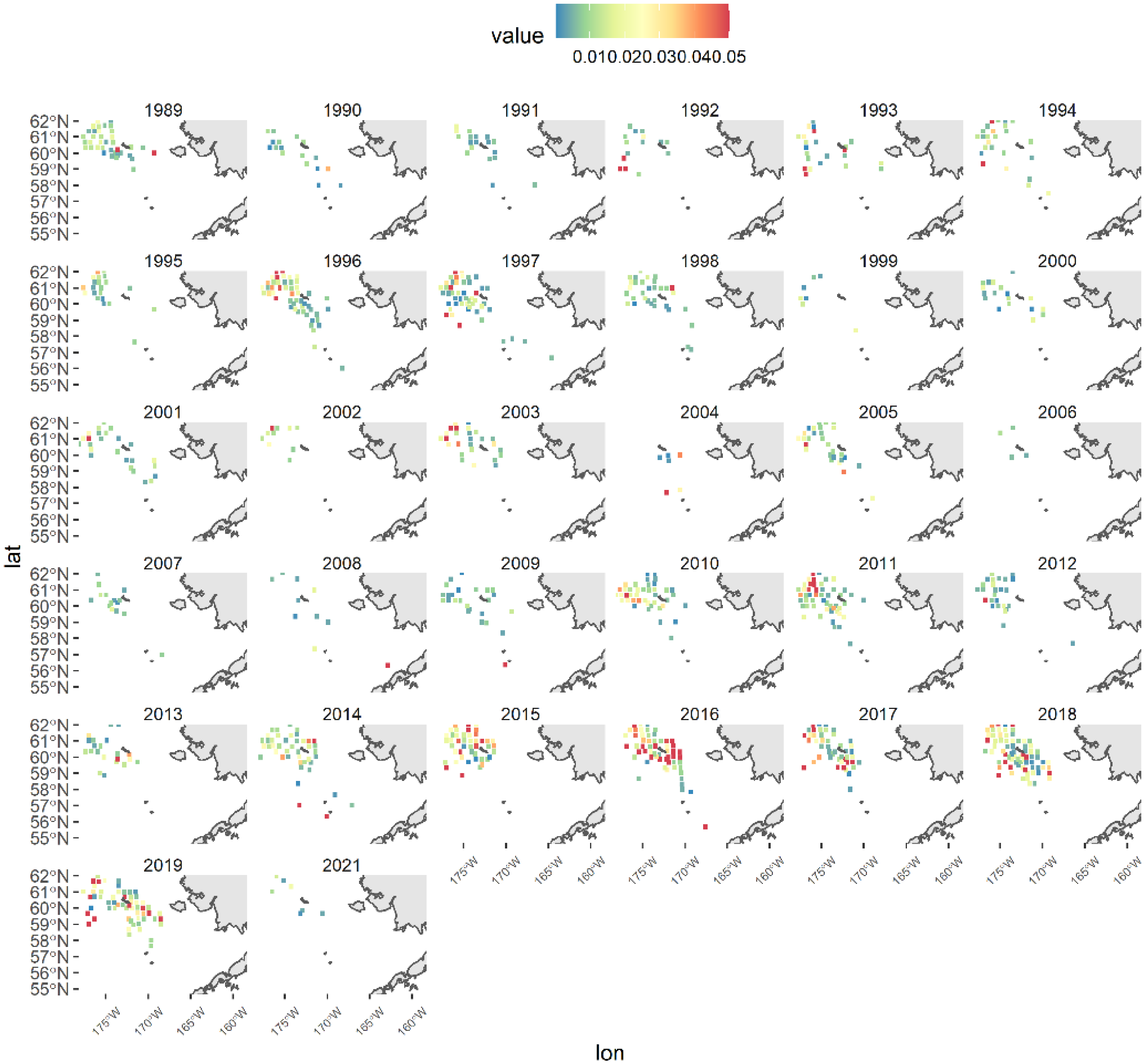
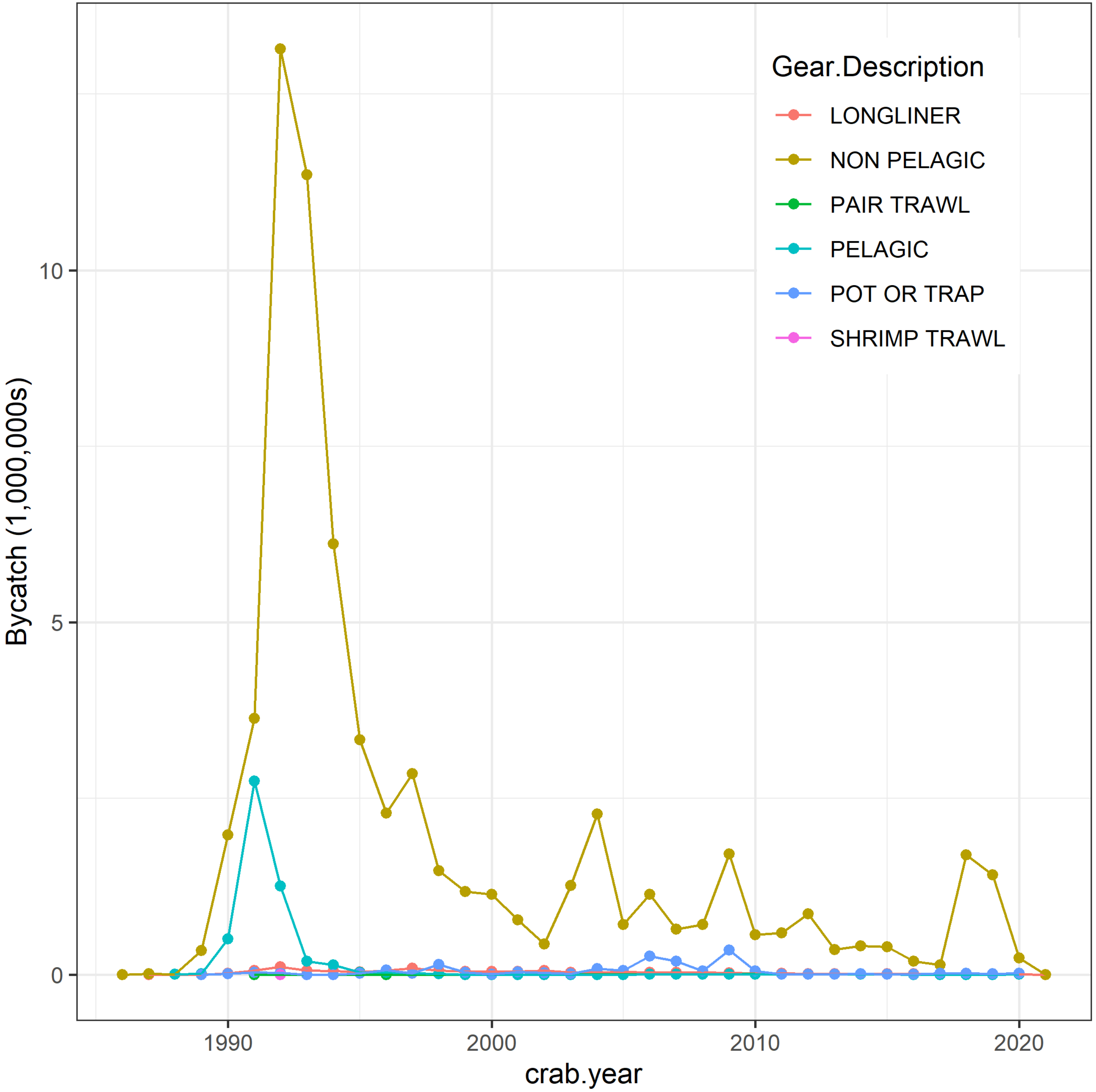




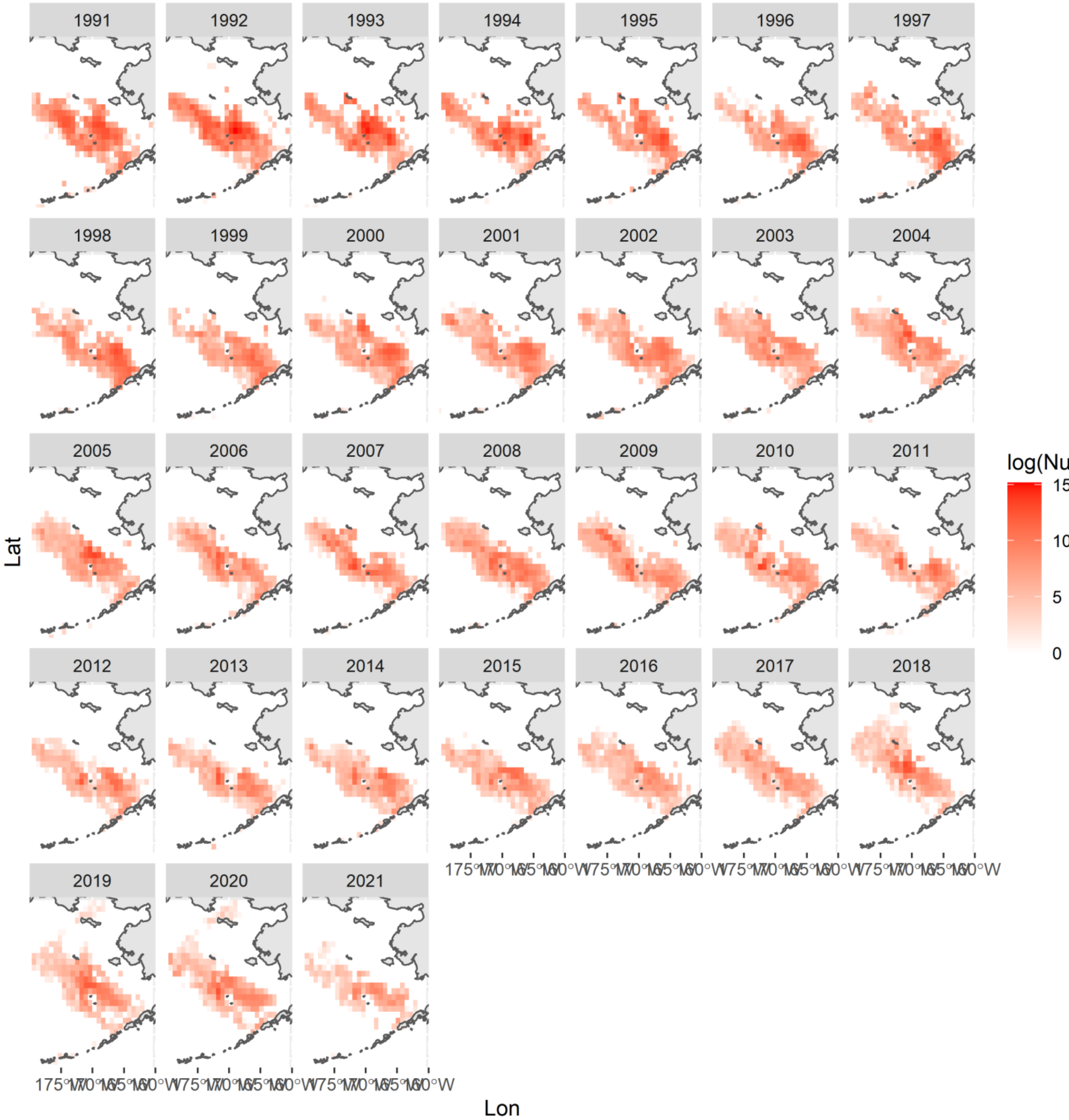
Bycatch

- Declining trend since observer data started



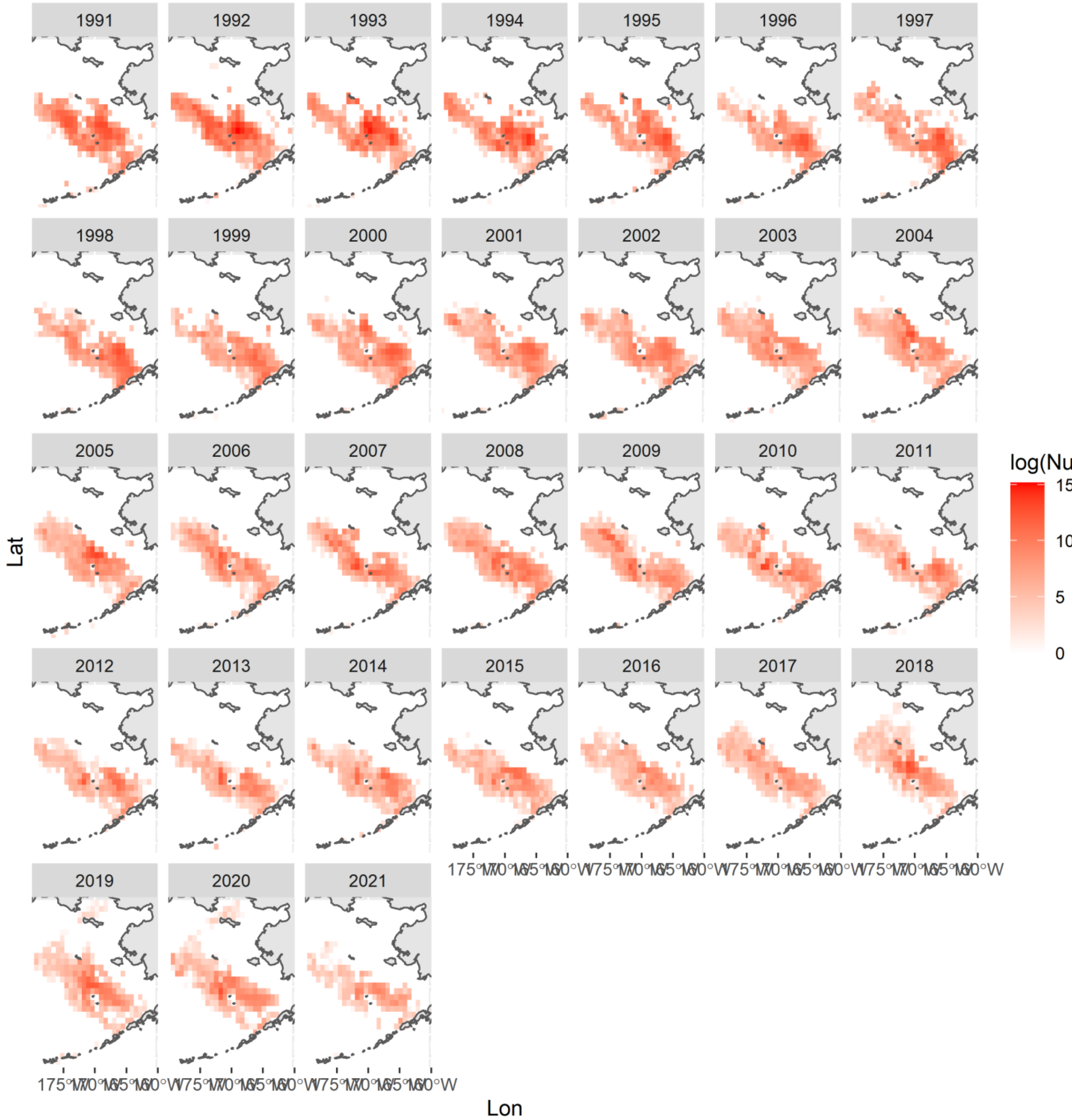
Bycatch

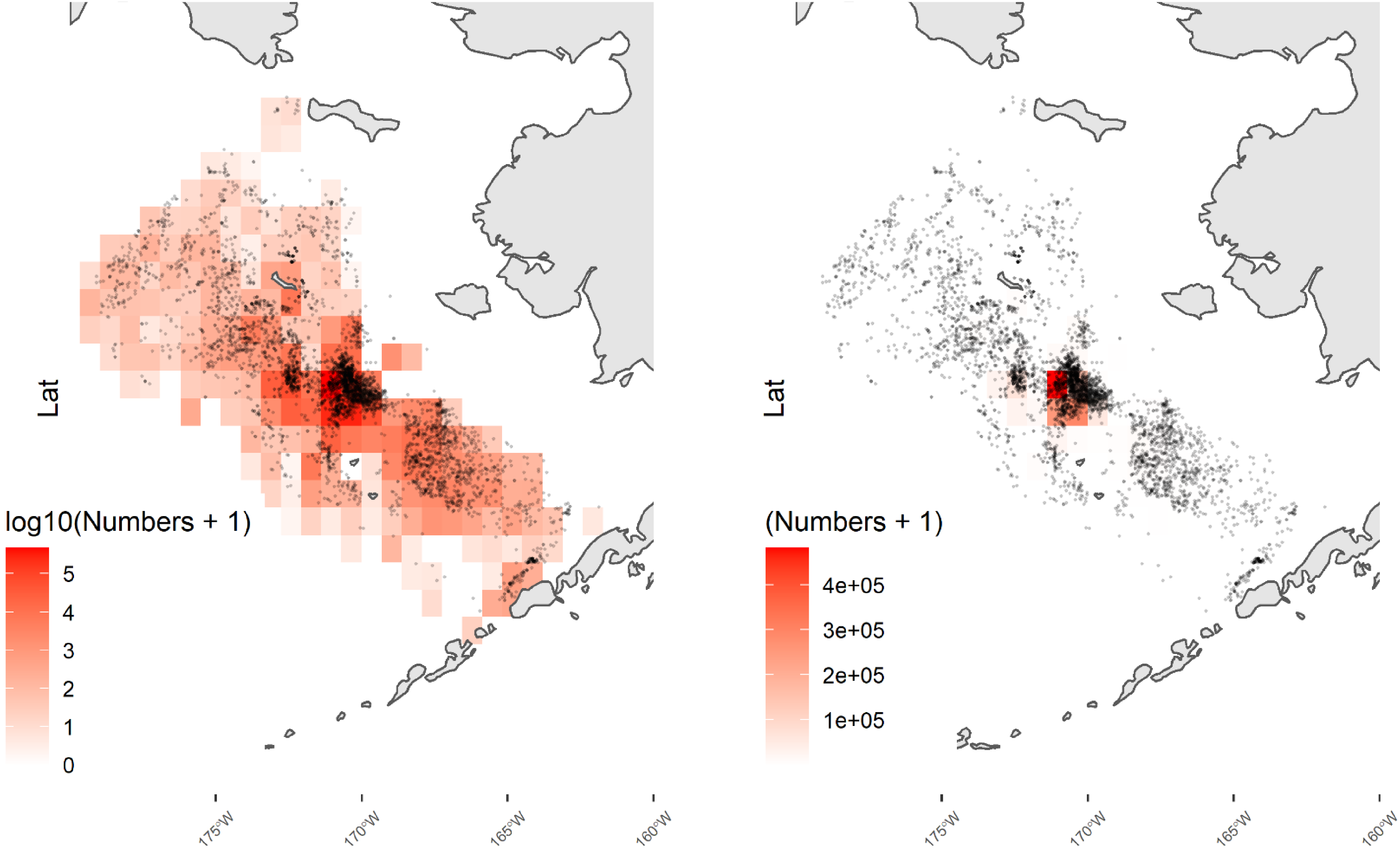
- Declining trend since observer data started
- Spatial extent went farther north in 2018 than any other year

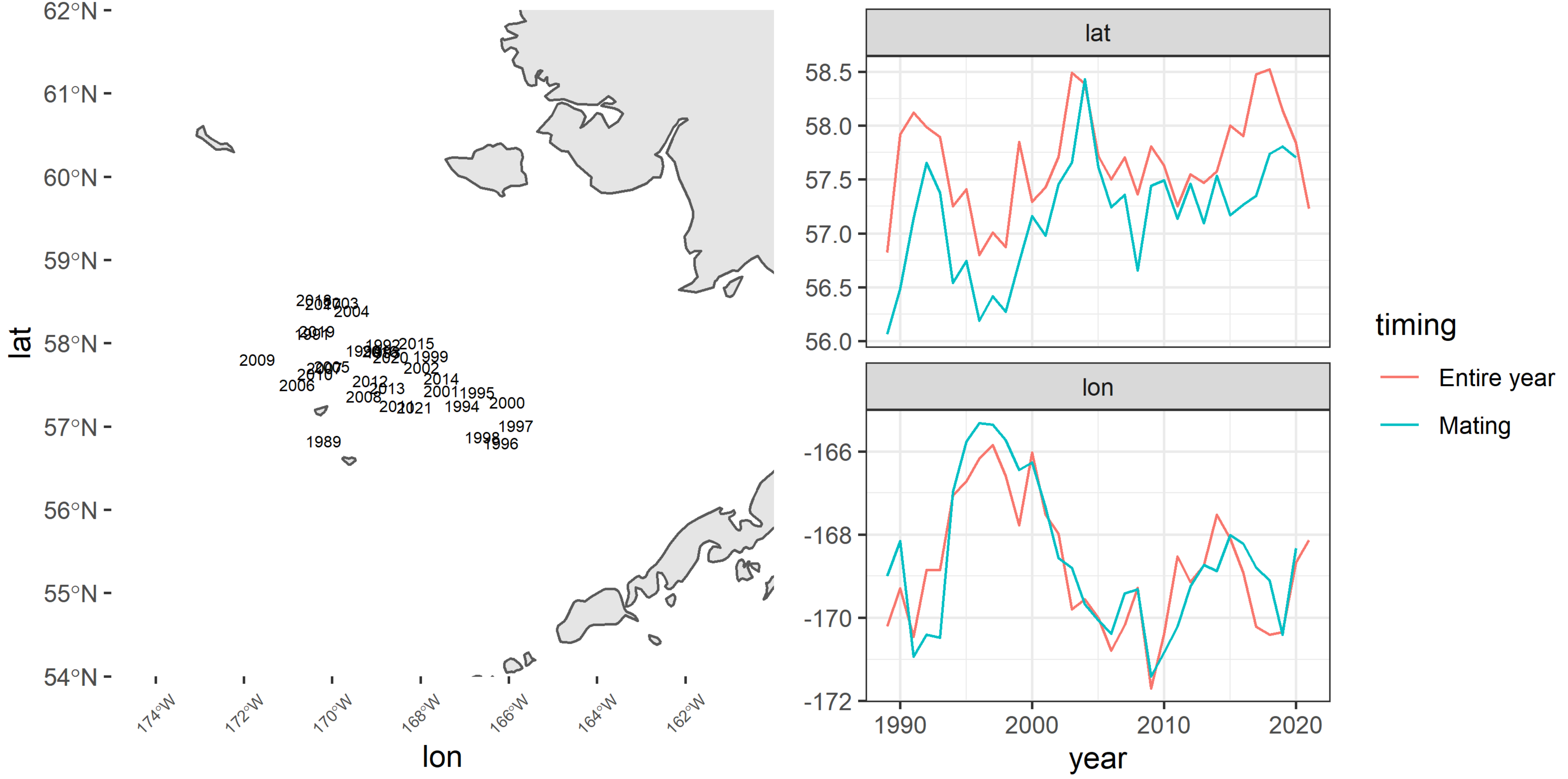


Bycatch

- Declining trend since observer data started
- Spatial extent went farther north in 2018 than any other year
- That said, we need to be careful with logs




Lat
log10(Numbers + 1)
5
4
3
2
1
0
175°W
170°W
165°W
160°W
Lat
(Numbers + 1)
4e+05
3e+05
2e+05
1e+05
175°W
170°W
165°W
160°W


62°N
61°N
60°N
59°N
58°N
57°N
56°N
55°N
54°N
lat
174°W
172°W
170°W
168°W
166°W
164°W
162°W
lon
2009
2006
2004
2012
2013
2008
2015
1999
2002
2014
1995
2000
1994
1997
1996
1989
lat
58.5
58.0
57.5
57.0
56.5
56.0
lon
-166
-168
-170
-172
1990
2000
2010
2020
year
timing
Entire year
Mating

$$\text{Mortality} = s(\text{Temp}) + s(\text{Disease}) + s(\text{Discards}) + s(\text{Bycatch}) + s(\text{Cannibalism}) + s(\text{Predation})$$

$$\text{Catchability} = s(\text{Temp}) + s(\text{Longitude}) + s(\text{Latitude})$$

Model stress testing

Mortality = s(Temp) + s(Disease) + s(Discards) + s(Bycatch) + s(Cannibalism) + s(Predation)

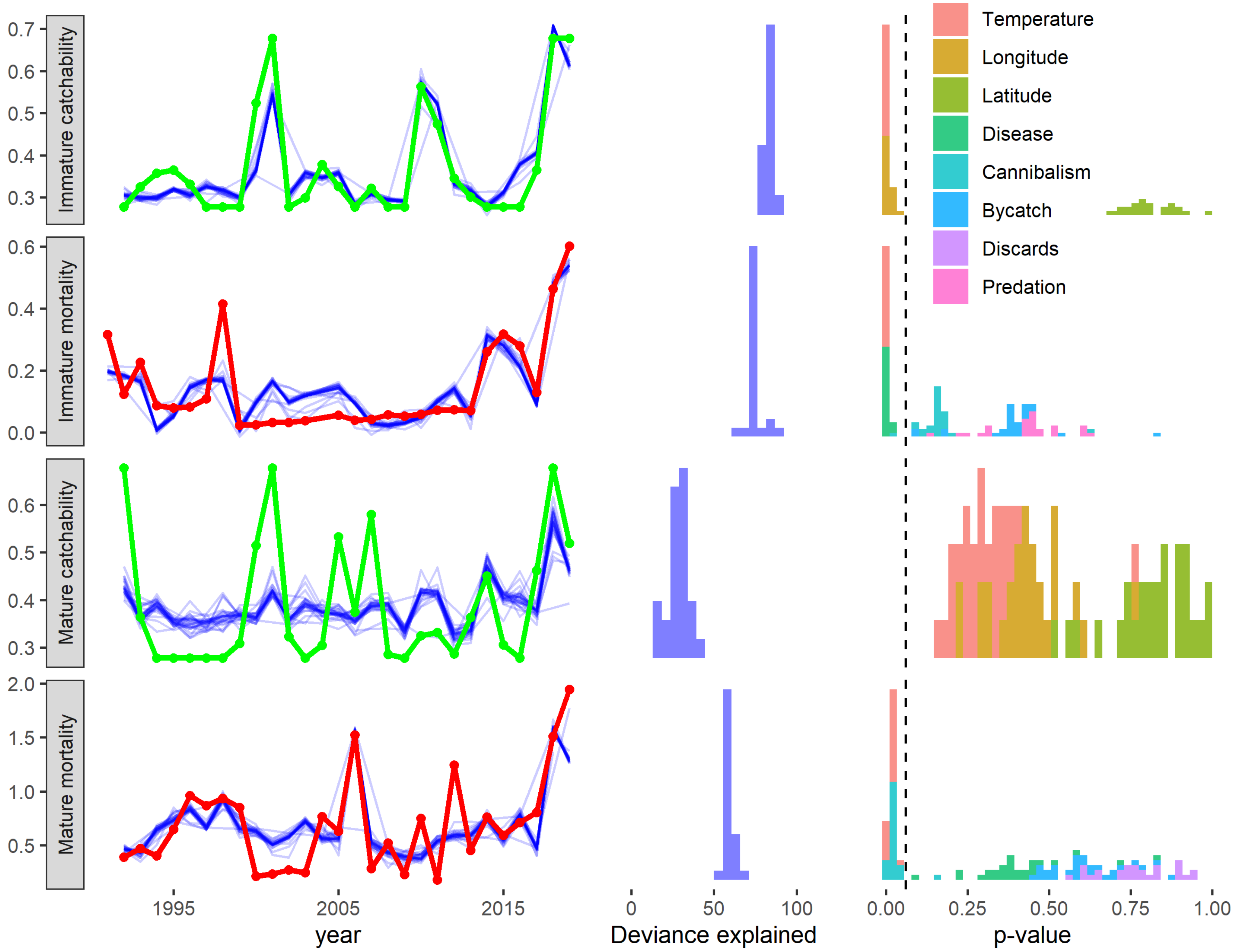
Catchability = s(Temp) + s(Longitude) + s(Latitude)

- Leave one out cross-validation
- Three year out prediction
- Randomization (does the model fit just because of the degrees of freedom given to the GAM?)

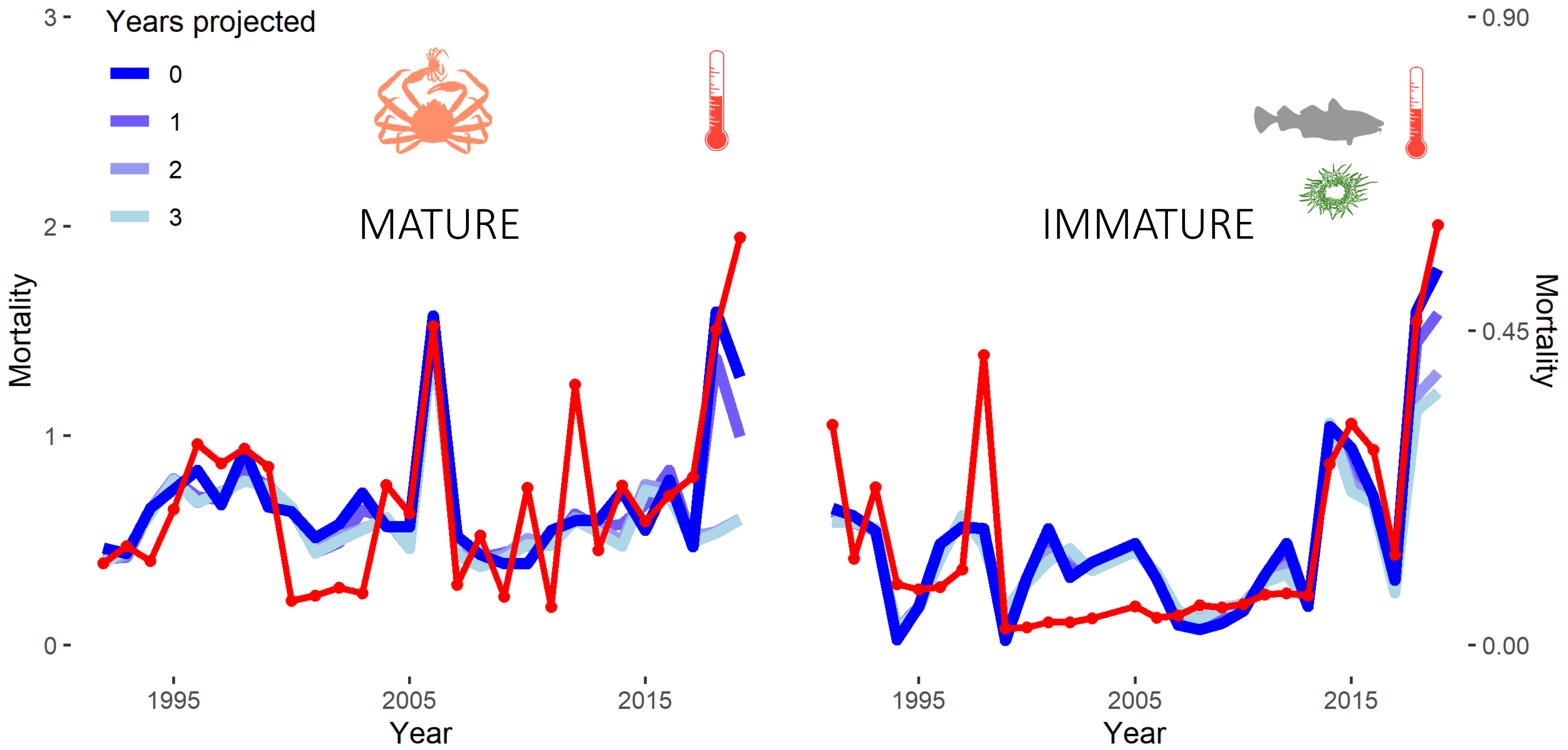
LOOCV

Leave one out cross validation

1. Exclude a year of data
2. Fit the model
3. Record deviance explained
4. Record important variables
5. Repeat for all years of data
6. Check if changes in data availability change inference

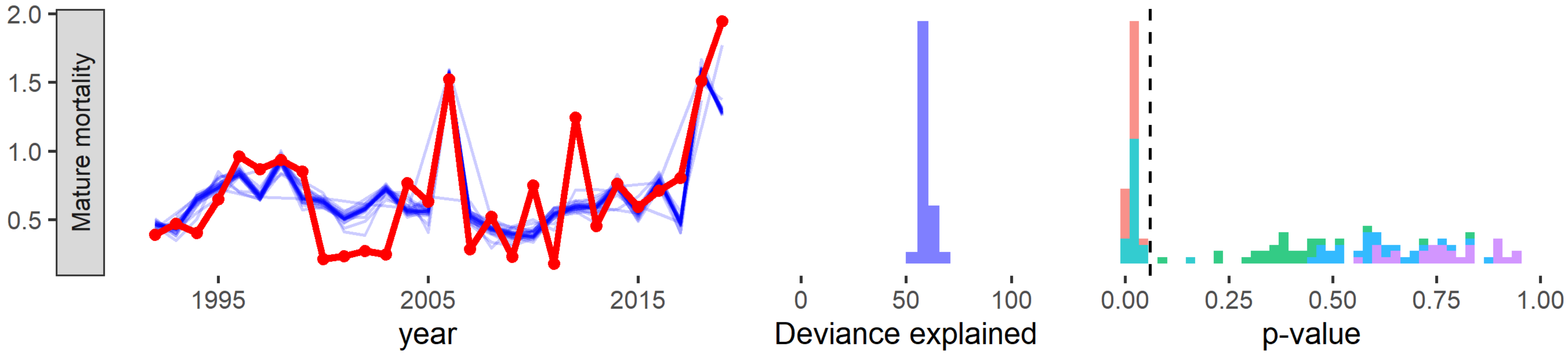


Prediction

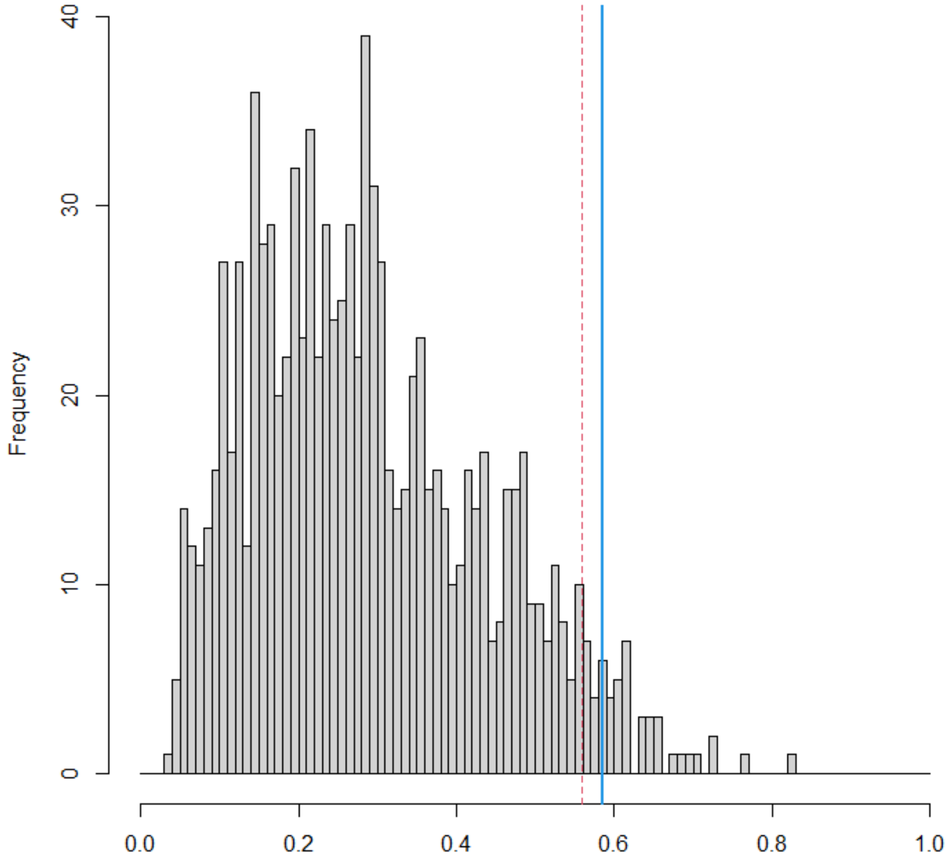


Years projected
0
1
2
3
MATURE
IMMATURE
Mortality
Mortality
Year
Year
3
2
1
0
0.90
0.45
0.00
1995
2005
2015
1995
2005
2015

Randomization



1. Randomize the covariates
2. Fit the model
3. Record deviance explained
4. Do 1-3 1000 times
5. Find the 95th quantile of deviance explained
6. If 'real' model exceeds that, the 'significance' of the model fit is not just a result of the flexibility given to the model by the number of smooths and degrees of freedom

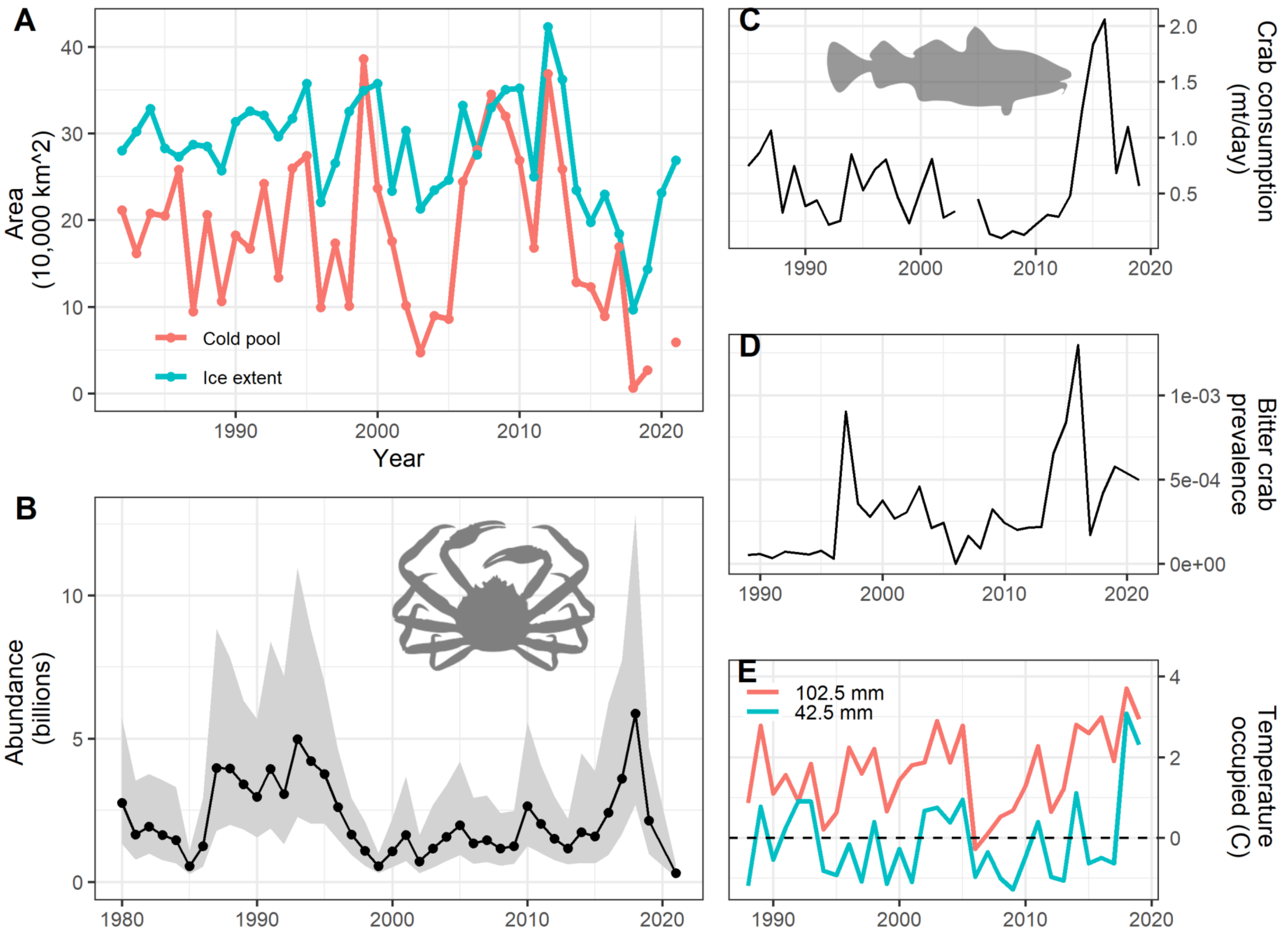


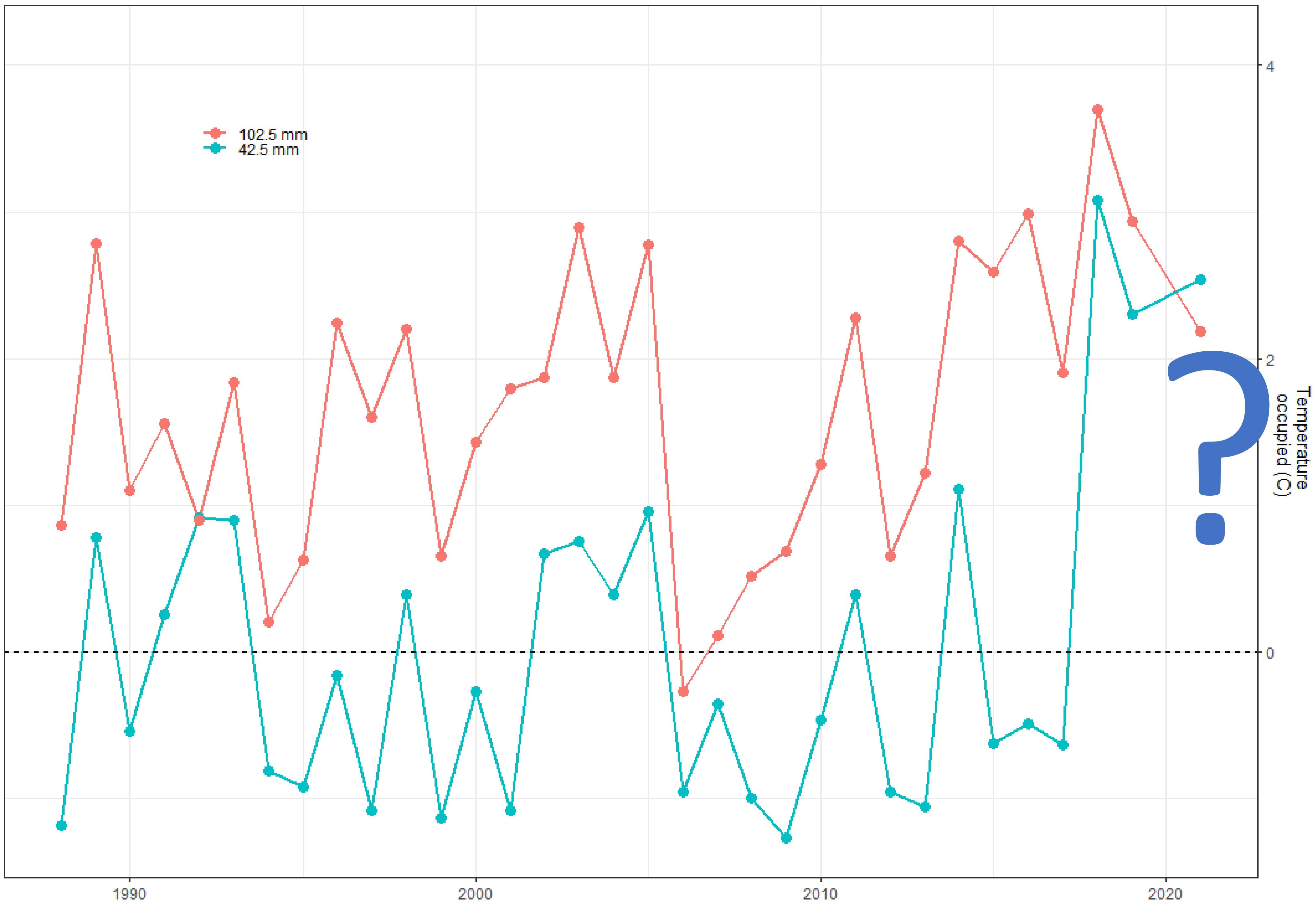
New problems

- Should I use estimates from just M-varying or M & q-varying models?
  - M was better estimated by the just M-varying models, somewhat surprisingly
  - ‘time-varying q’ is another way of saying ‘observation error’

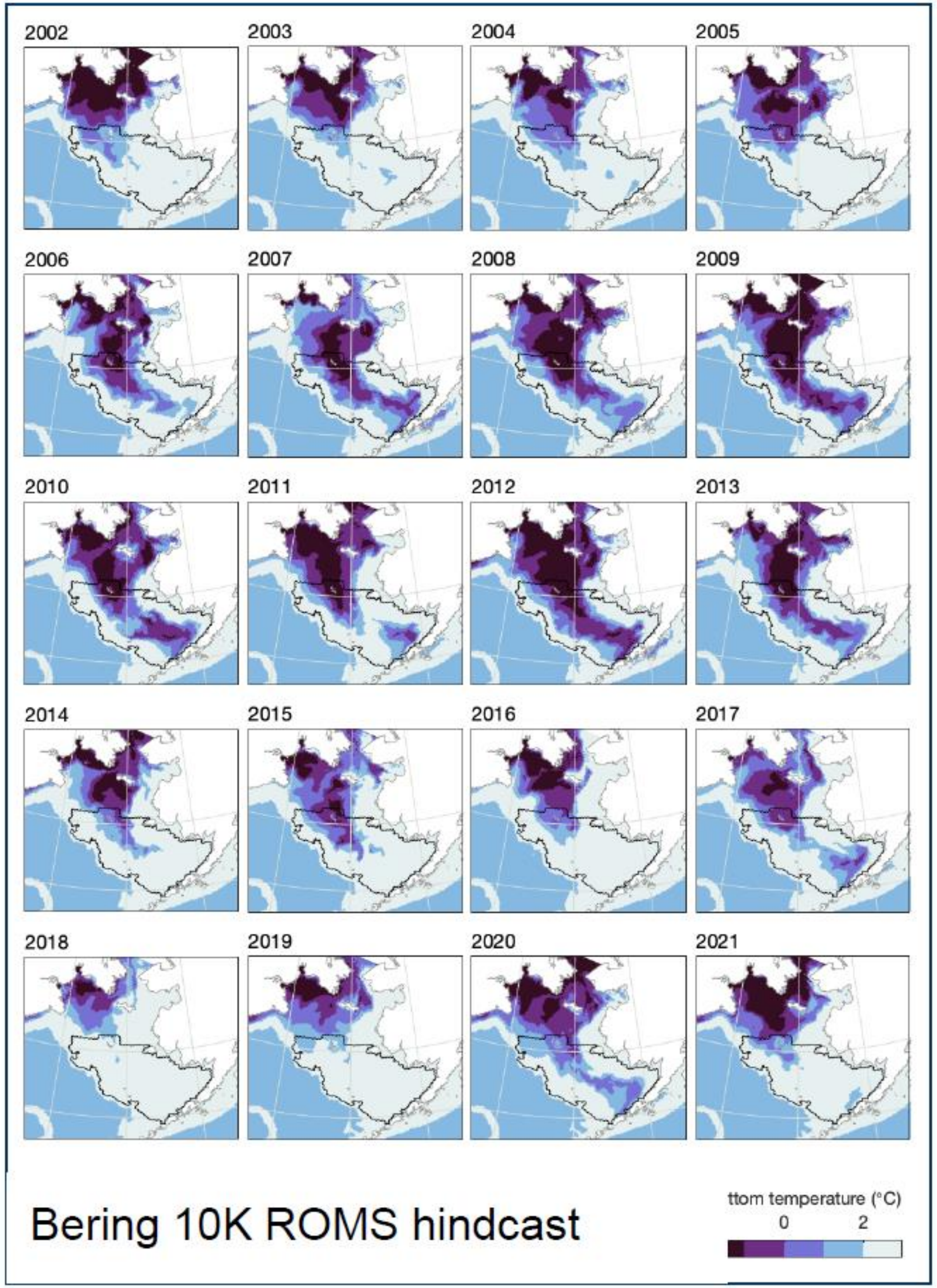
- What values should I use for the sensitivity parameters?
  - Use them all and fit models to all the time series to see what is a consistently important covariate?

What should M be in rebuilding projections?





102.5 mm
42.5 mm
4
2
0
Temperature occupied (C)
1990
2000
2010
2020
?


2002
2003
2004
2005
2006
2007
2008
2009
2010
2011
2012
2013
2014
2015
2016
2017
2018
2019
2020
2021
Bering 10K ROMS hindcast
ttom temperature (°C)
0
2