

Hake Notes

Andrea Odell

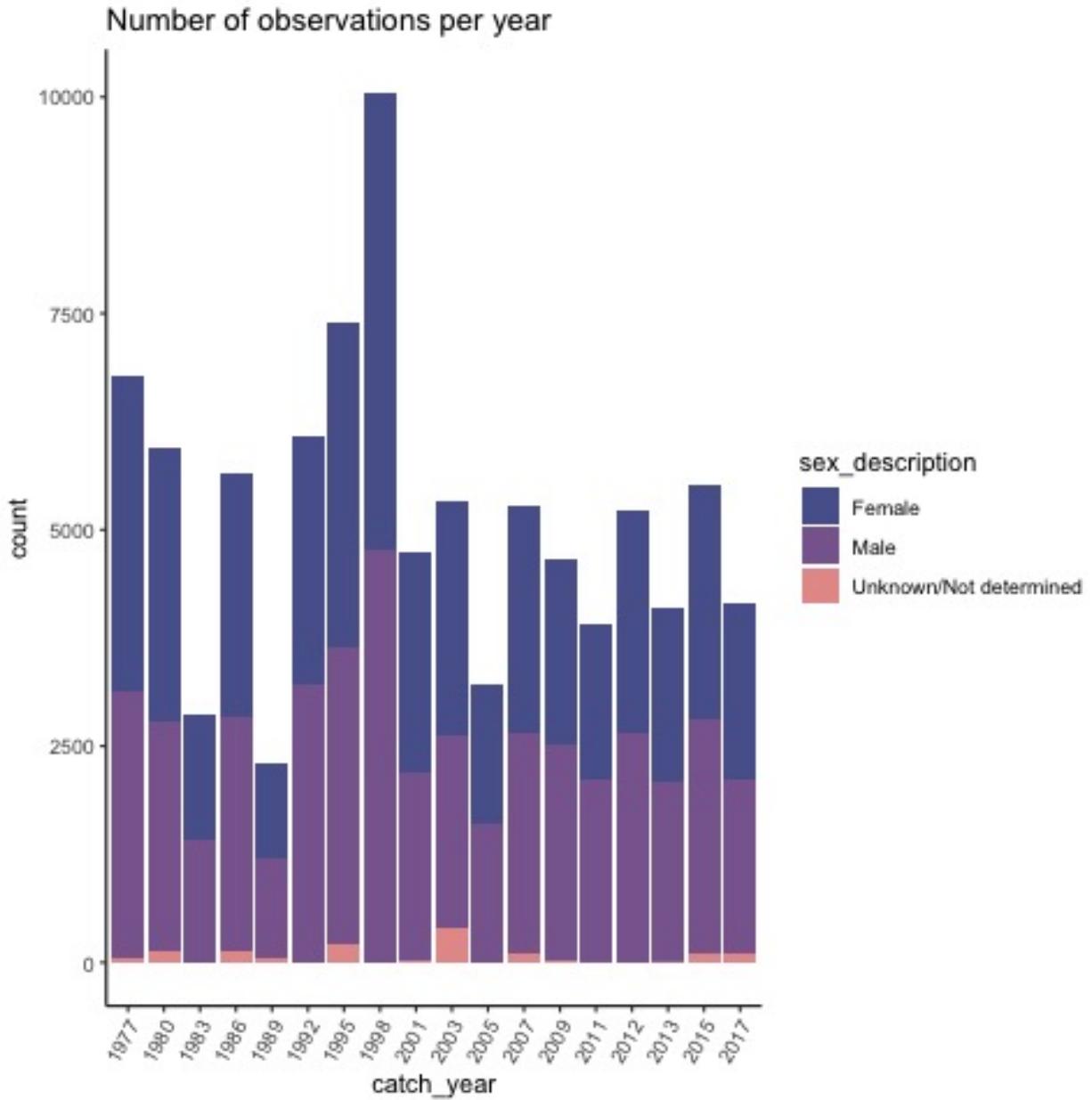
2022-07-04

Contents

June 27 - July 1, 2022	1
July 4-8, 2022	11
July 11-15, 2022	16
July 18-22, 2022	20
July 25-29, 2022	23
Aug 1-5, 2022	27
Aug 8-13, 2022	30
Aug 16-19, 2022	30
Aug 22-29, 2022	39
Sept 12-16, 2022	49
Sept 19-23, 2022	49
Sept 26-30, 2022	53
Oct. 24-28, 2022	62
Nov. 2022 - Jan 2023	63
Feb. 2023 - Jul. 2023	63
August 2023	63
September 2023	72
October 2023	90

June 27 - July 1, 2022

Received acoustic-trawl survey data through NOAA data warehouse - 103,245 observations. Data for 1980 - 2017 are included. I began by creating a new dataset, `hake_df` that included only Pacific Hake observations and relevant information (columns) - 93,186 observations. Date information from the `eq_date` column were used, however, observations with missing years were filled in using information from `hb_date` column. This constituted only observations from year 2017.



There are 46,816 female observations and 44,982 male observations. There seems to be a fairly equivalent number of males vs females.

Looking more closely at growth, particularly the relationship between length and weight, much of the unknown sex descriptions come from smaller sized fish which makes sense. Females and Males seem to follow very similar growth trends, as indicated by fitting separate growth models to each sex and estimated coefficients being fairly similar. Visually, there seems to be a greater abundance of females at those larger sizes.

Because of the similarity between males and females and because males and females are not modeled explicitly in the stock assessment, I went ahead and continued modeling the sexes aggregated together. I did this by first subsetting `hake_df` to observations that had complete length and weight information `fit_hake_df` - 52,382 observations. I log10-transformed the data (this was recommended over natural log transformation), and fit a linear model using `lm()`, a least squares method. The resulting model then became

$$\log_{10}(W) = \log_{10}(a) + b * \log_{10}(L)$$

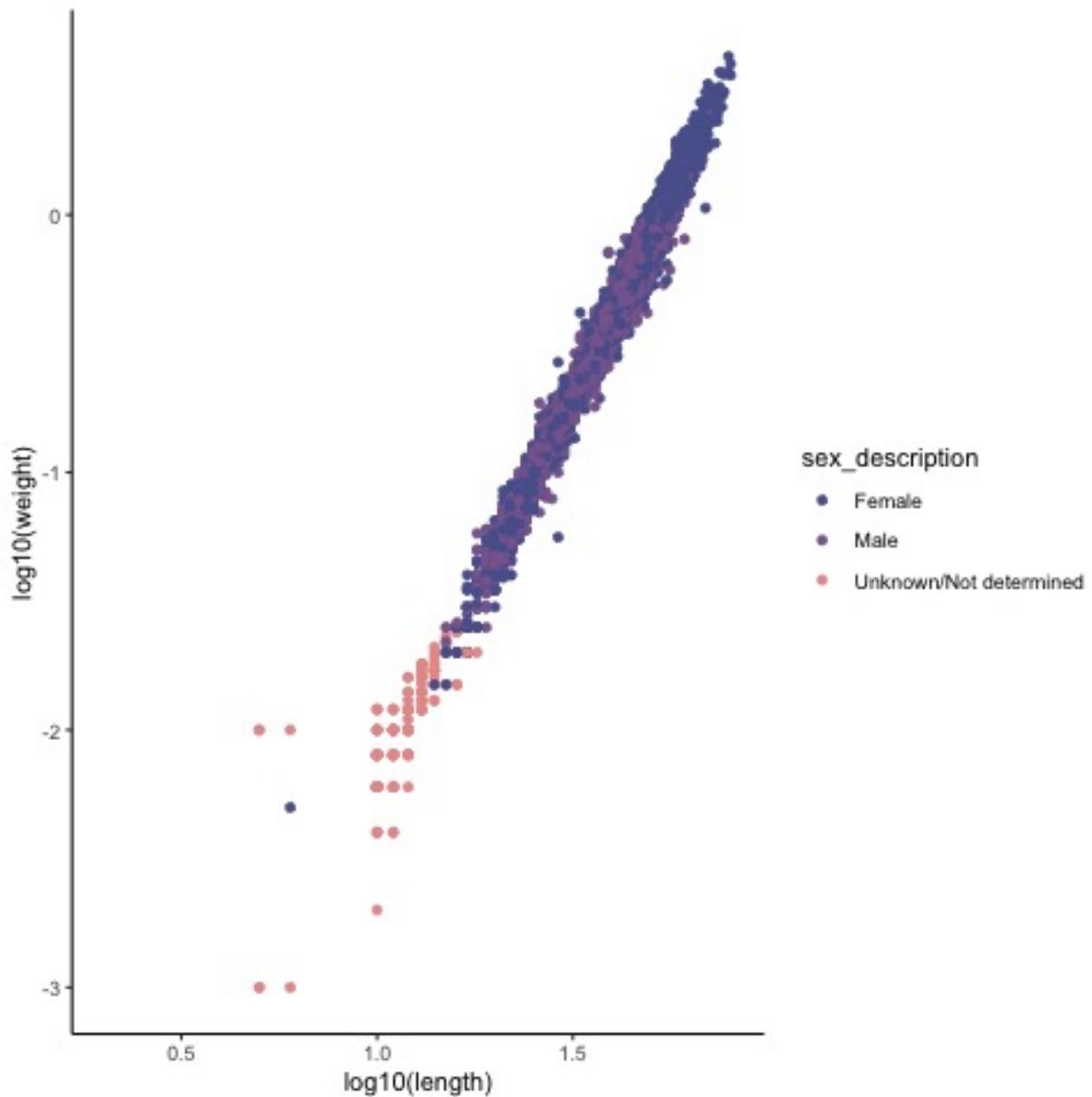
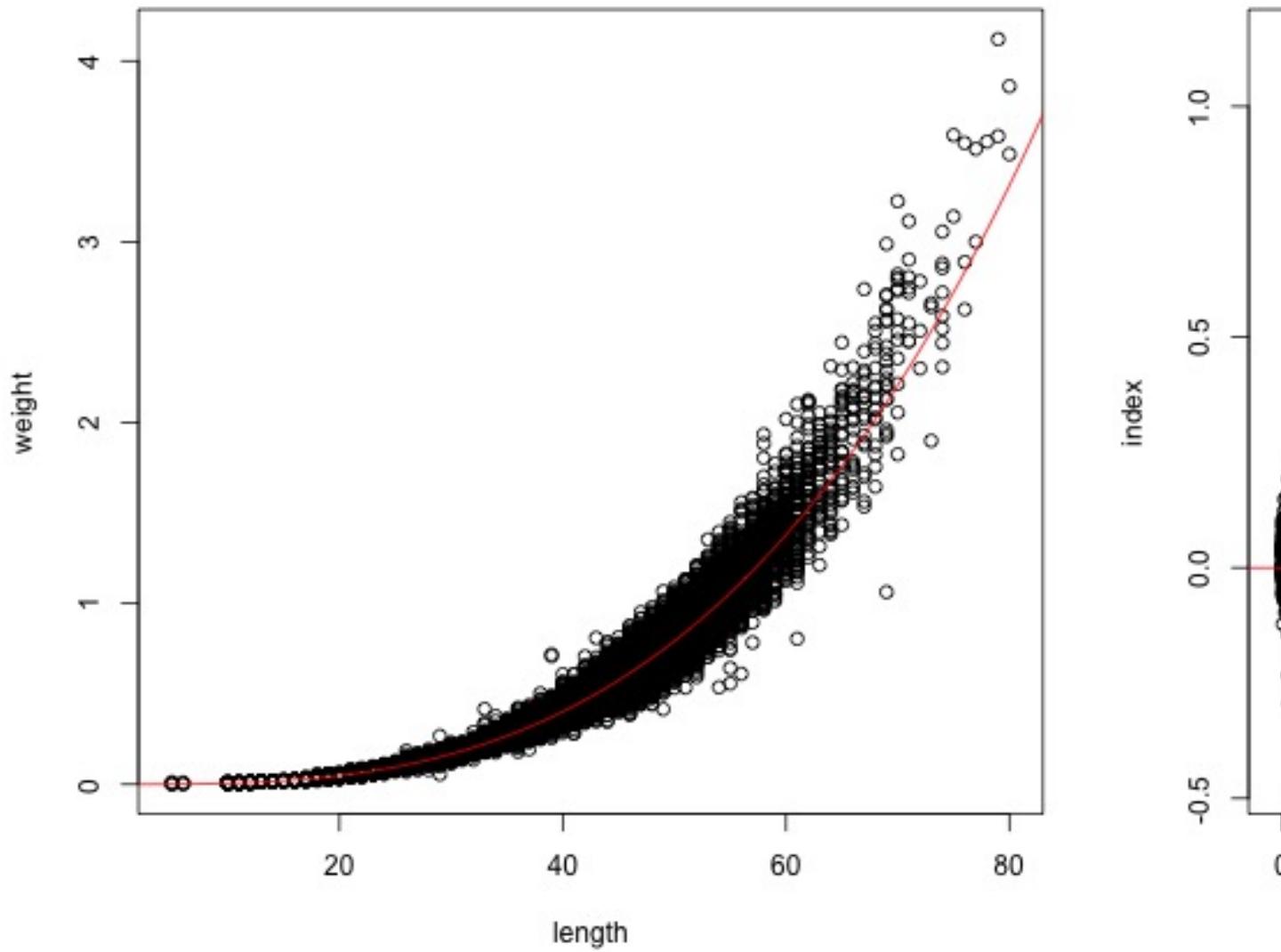


Figure 1: Log10-transformed length weight relationship

Predicted growth over raw data



Above is the fitted model over the raw data and a plot of the residuals. The multiple R-squared value of the fit is 0.9819, which means that 98% of the variability can be explained by the model - which is great!

From now, I will be referring to residuals as growth anomalies (... makes more sense in my brain). These next few plots will be exploring patterns in growth anomalies as it relates to time, location, and age.

This first graph shows the variability in growth anomalies per year. Immediately, you notice that 1995, 2007, and 2017 have considerable variability in growth anomalies between individuals (i.e. there is a wide distribution of individuals who are both larger and smaller than normal). The distribution in 2007 is largely driven by 3 outliers, where those outliers are small (length) individuals that are much heavier (weight) than normal. I believe this may be due to measurement error. Years 1995 and 2017 are years adjacent to record warm years (marine heatwaves) which may have led to this variability in growth anomalies due to differential responses between fish (spatial or perhaps age?).

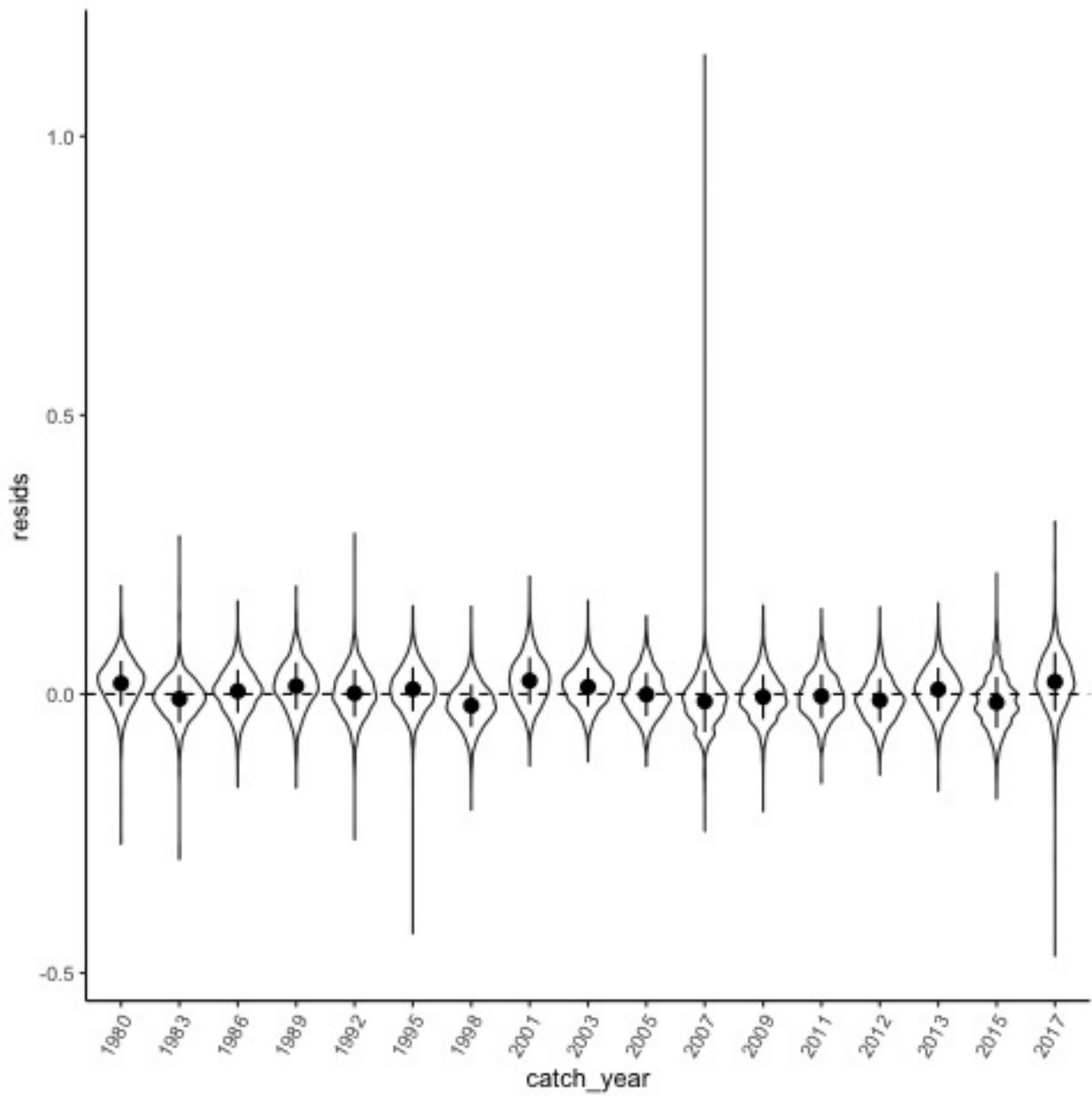


Figure 2: Summary of growth anomalies per year

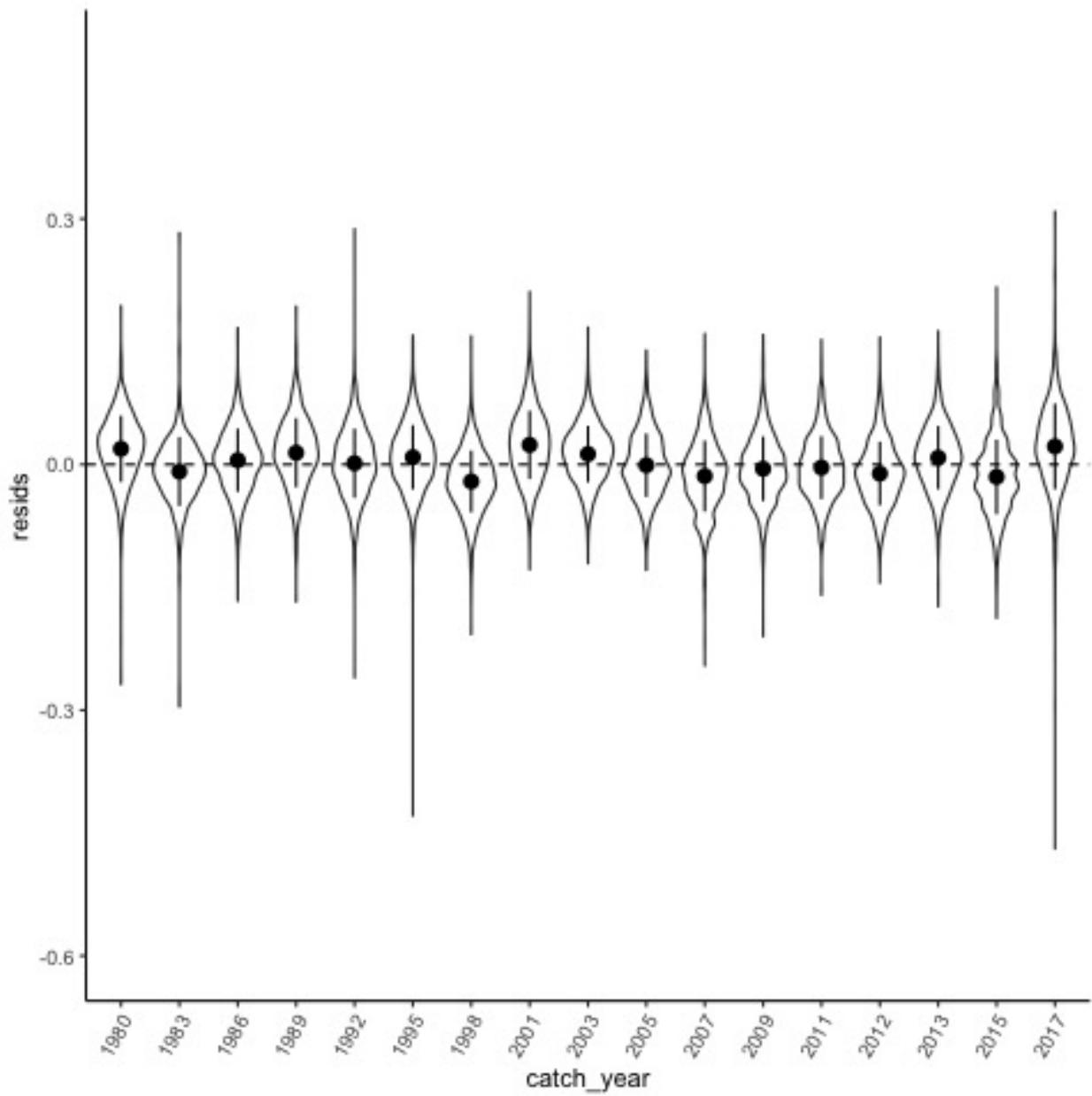


Figure 3: outlier removed

This plot removes the outliers from 2007. You can see that the 3 outliers really drive the distribution - how should we handle these outliers?

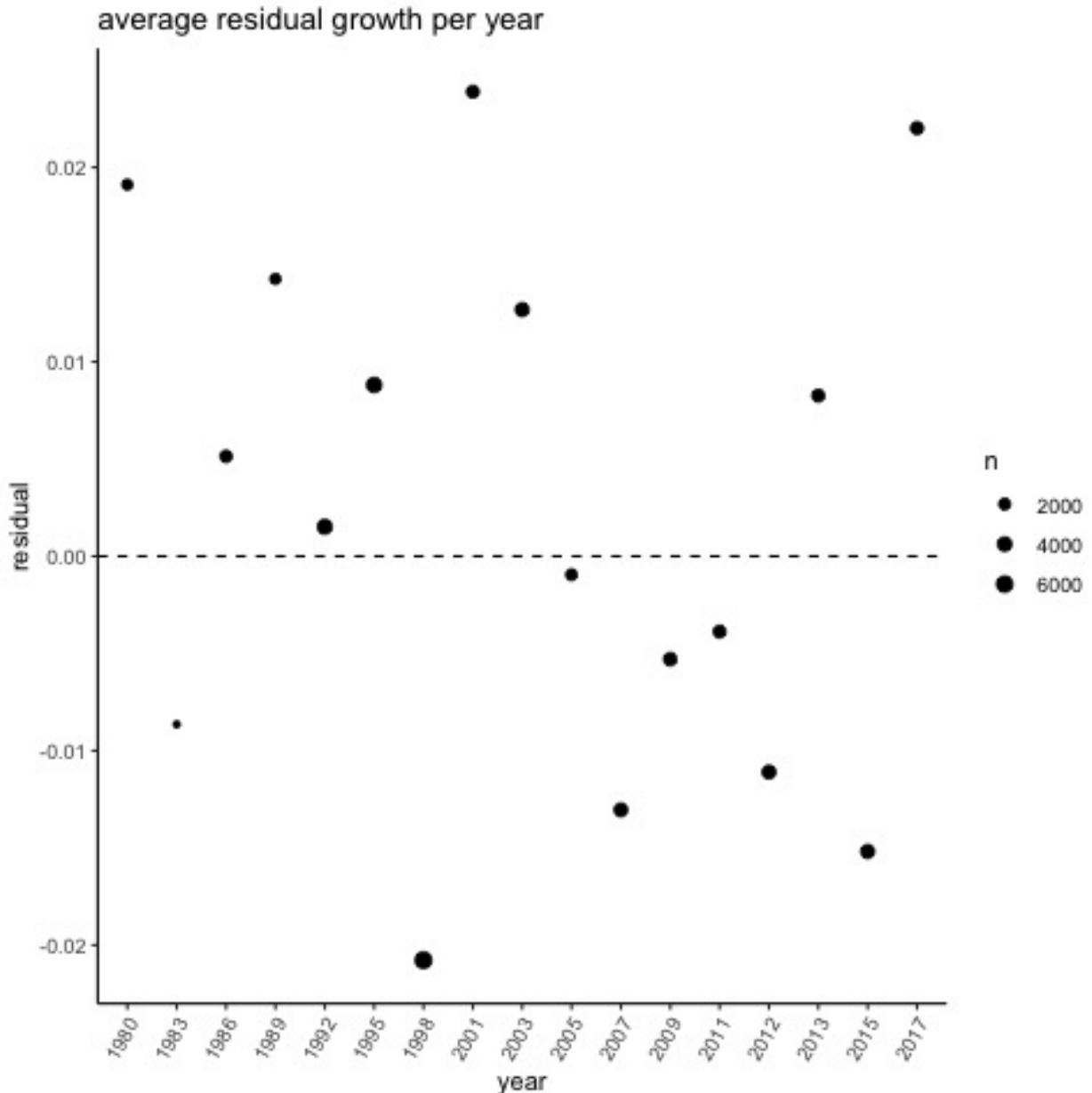


Figure 4: Avg growth anomalies per year

This plot is looking at the average growth anomalies per year without the spread of data. It looks like many of the years prior to 2003 were dominated by larger-than-avg individuals, except the year in which a marine heatwave occurred. Following 2003, many of the years are dominated by smaller-than-avg individuals with the exception of 2013 and 2017.

This graph shows how growth anomalies vary along the west coast every year. Values close to 0 (i.e. observed value is close to predicted - no anomaly) are transparent for better visualization of + and - values. Moreover, those 3 outliers in 2007 are included in the graph, but not in the color scale limit, for improved visualization. You can see there is considerable year-to-year variation, where in 1998 and 2015 you see mostly smaller-than-avg fish all along the coast and aligns with the years with marine heatwaves. In some years, there seems to

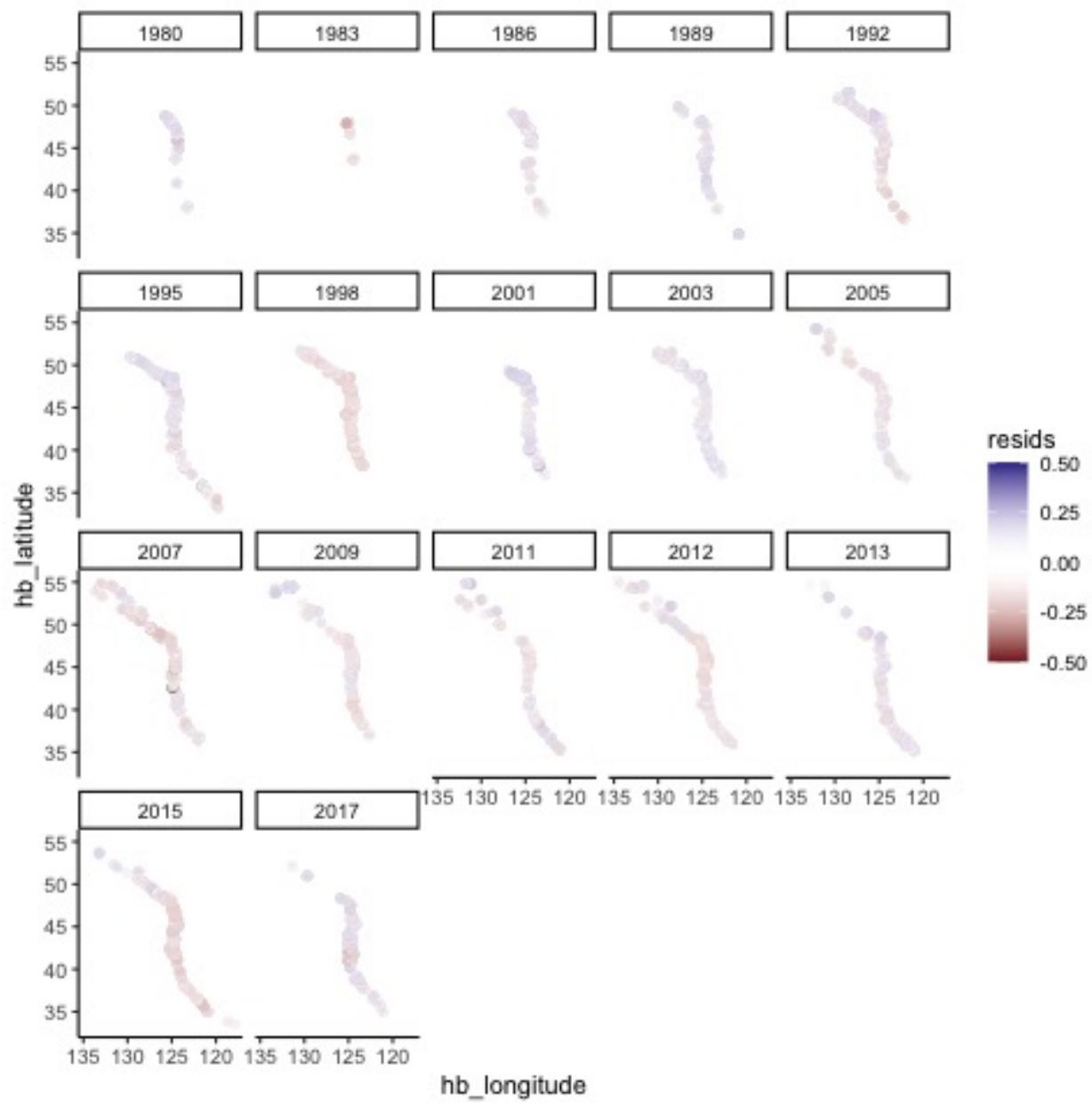


Figure 5: Spatial variation of growth anomalies by year

be a slight stratification, where the northern half of the coast shows larger or smaller-than-avg individuals and southern half vice versa. An issue with this graph is that you can't see individuals who do not exhibit a growth anomaly, which I think would be valuable to see if this occurs in a part of the coast.

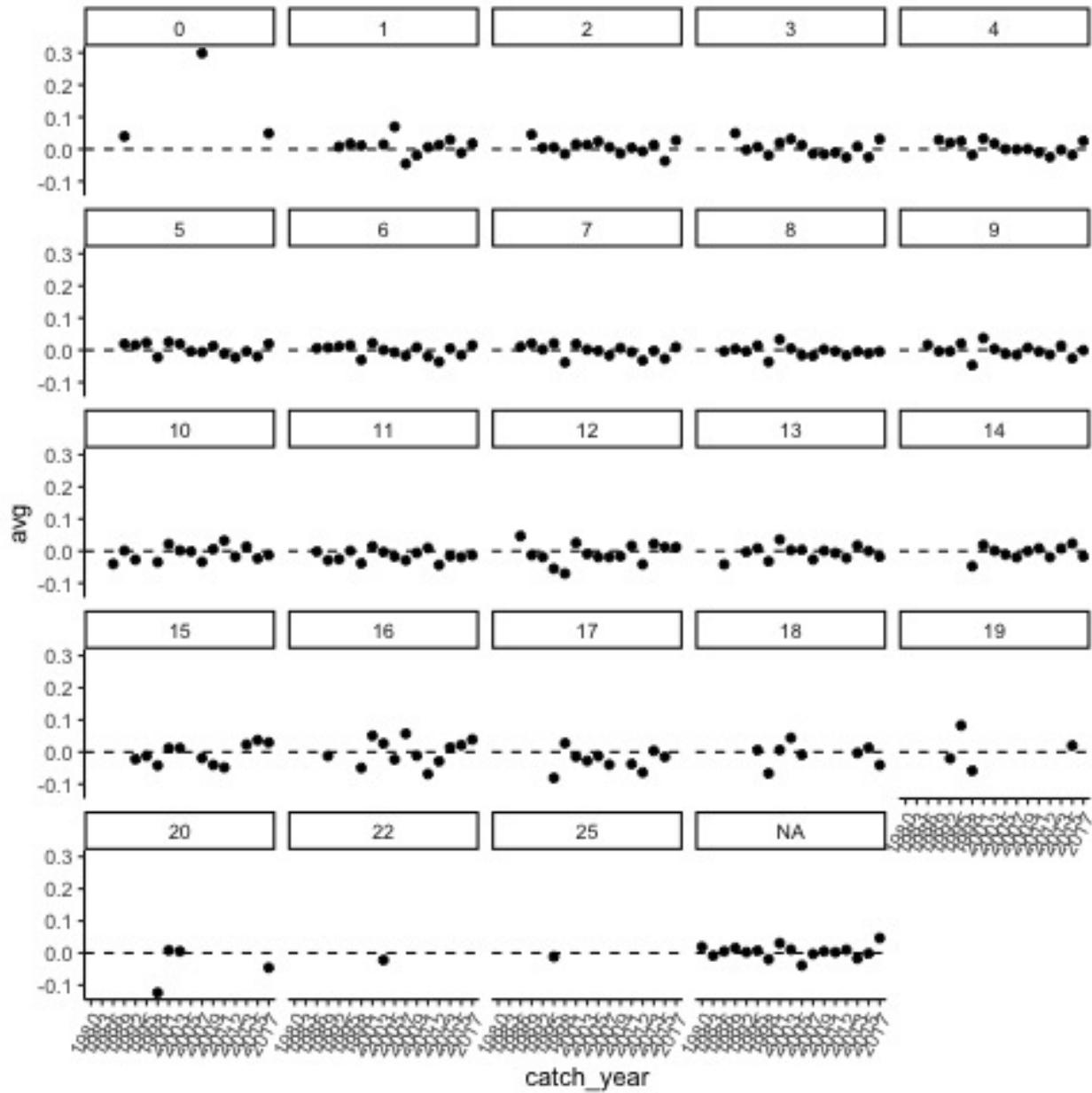


Figure 6: growth anomalies timeseries by age

A time series of average growth anomalies per age group. This essentially reveals how variable growth anomalies are per age - are some ages more vulnerable to variation in growth? are some age classes consistently larger or smaller than average? Either way, this plot is a little hard to decipher.

Summarizing the variability of growth anomalies per age even further, we can see that growth anomalies are most variable at age 0 - likely because there's fewer data and potentially greater measurement error - and that variability in growth anomalies increases slightly with age. However, there are fewer observations at those older age classes. I plan to create a plus group, by concatenating the age classes 15+ as done similarly in the stock assessment.

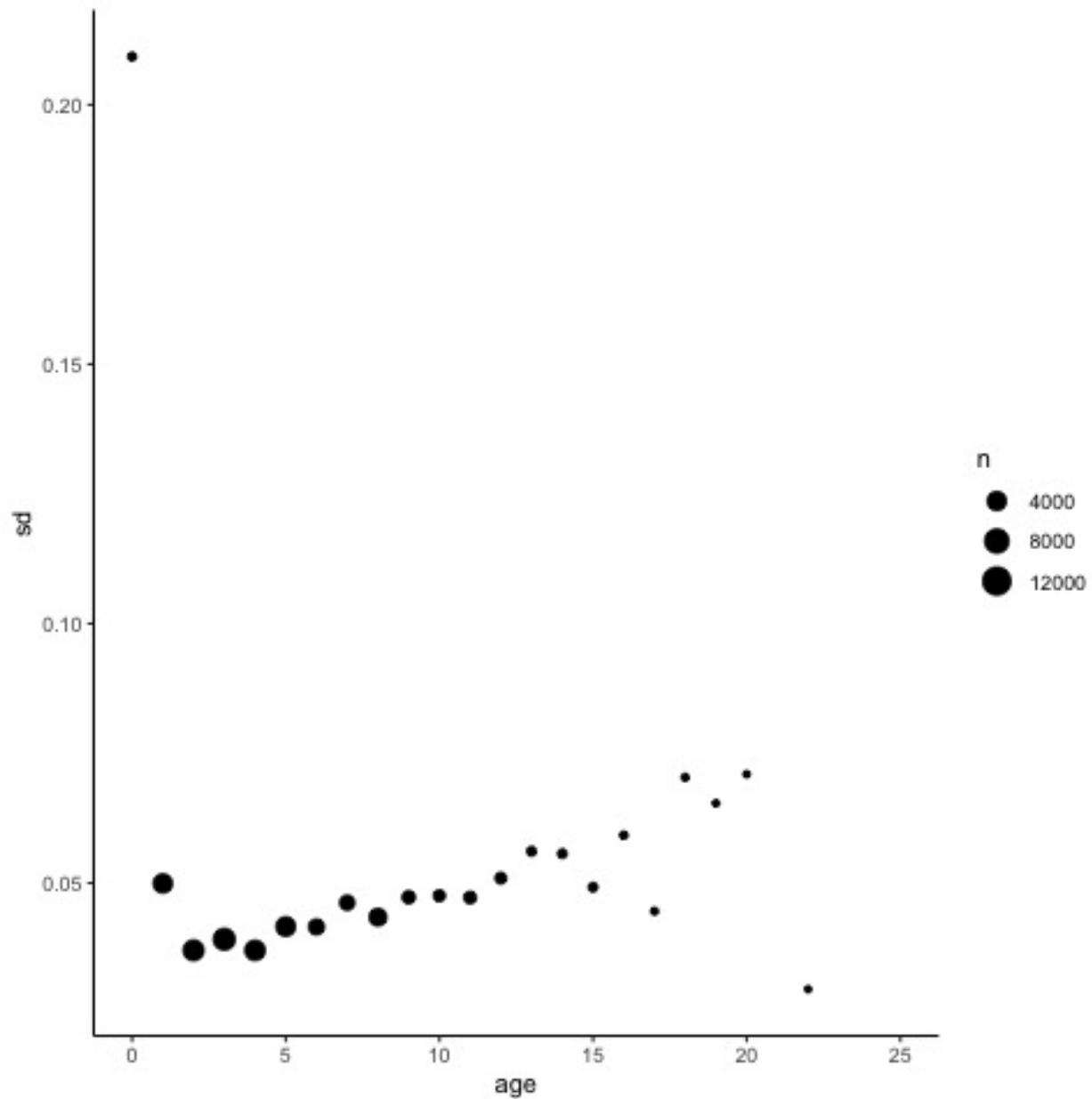


Figure 7: Variability of growth anomaly by age

July 4-8, 2022

Some next steps I plan to take this week is I will fit an age at length model to assign ages that don't have values. I will create a plus group age, grouping all ages 15 and greater. What sort of changes do we see when we make this assumption? I will explore finer temporal resolution to hopefully get an idea of some of the sampling/selectivity bias that might be happening. Another question was whether there was spatial variation in which sex dominates? All of this should then lead to some statistical modeling to determine relative importance of the patterns that I am seeing.

Okay, to start with estimating age using an length-at-age model, I first subsetted the `hake_df` dataframe so that there is only complete cases for age and length columns named `age_hake_df`. Then I added a new column `new_age` which were ages including plus group (ages 15+)

I first fit a Von Bertalanffy model to the whole data (all years combined), then fit a Von Bertalanffy model assuming "two regimes" where I fit the model to years 1980-2003 and 2004-2017, and finally I fit a Von Bertalanffy model to the plus group data. $size \sim L_\infty / (1 + \exp(-K * (age - t_0)))$

I selected the regimes by visually determining years with the most similar average growth anomalies (1980-2003 had larger-than-avg individuals and 2004-2017 had smaller-than-avg).

There was negligible differences in fit and coefficients between the whole data scenario ($RSS = 551852$) and the plus group scenario ($RSS = 551912$). However, when the data was split into regimes the fit of the model improved as indicated by the Residual Sum Squares ($RSS = 324002/200280$).

Overall, the fits didn't look so great - there was a bit of underfitting over the age of 6. The graph below only shows fit for the whole data, however, there were

Because I created a plus group, I wanted to go back and look at some of the data visualizations I did last week to see if there were any big changes.

First, I looked at the variability in growth anomalies per age by plotting the residual standard deviation for each age. The size and color of the points indicate number of observations and whether the residuals are positive on average (i.e. larger-than average), respectively.

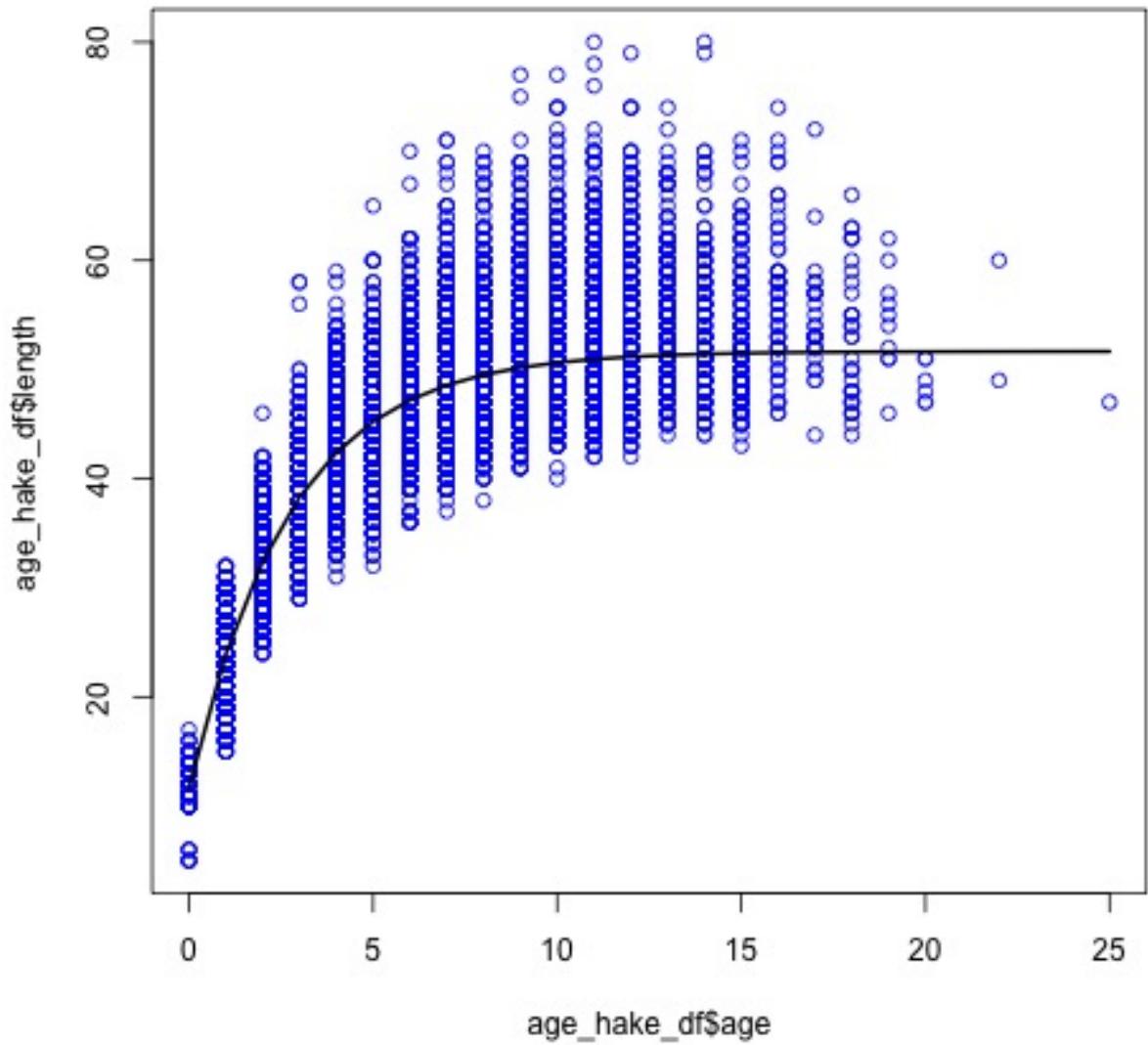
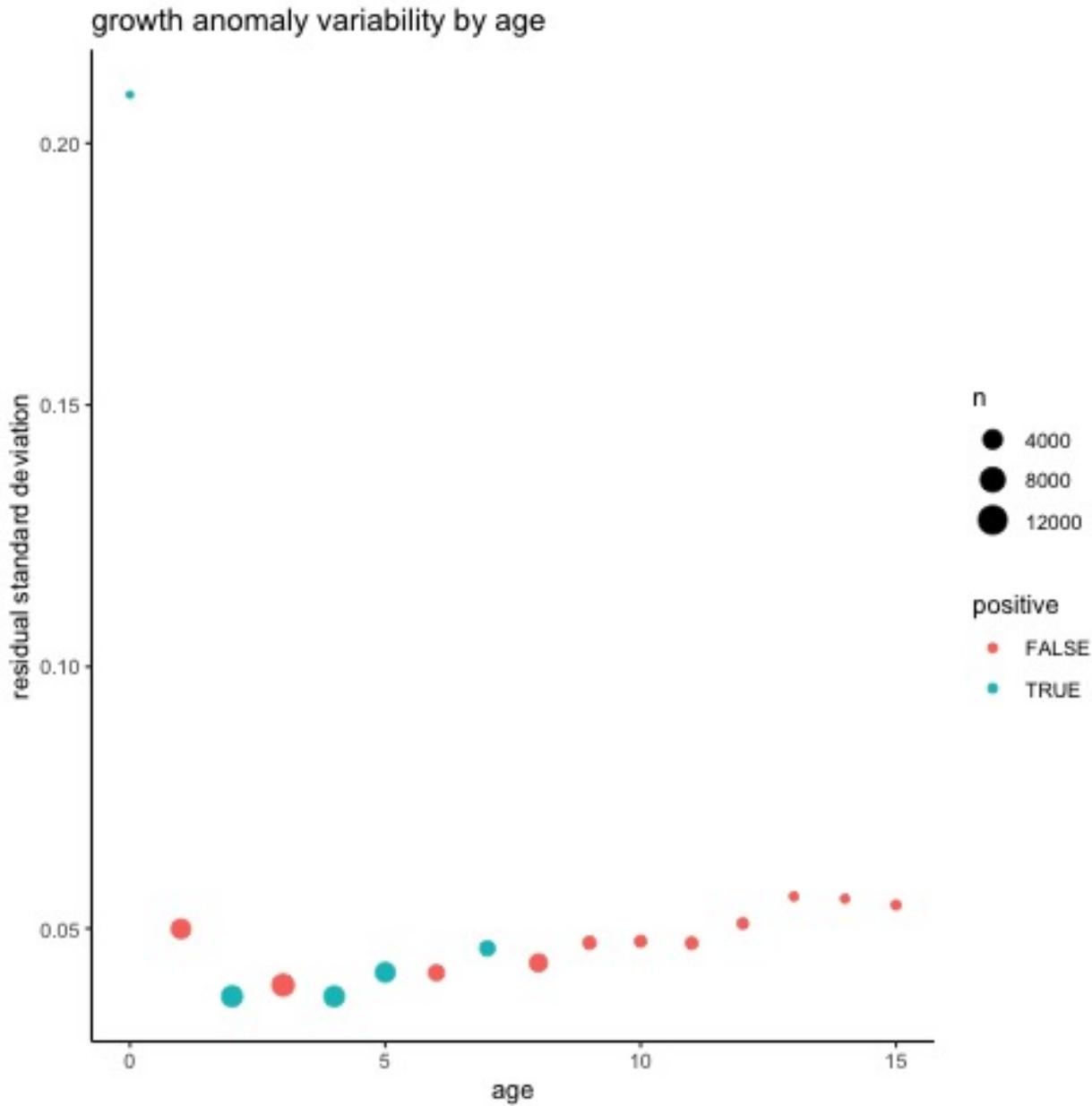
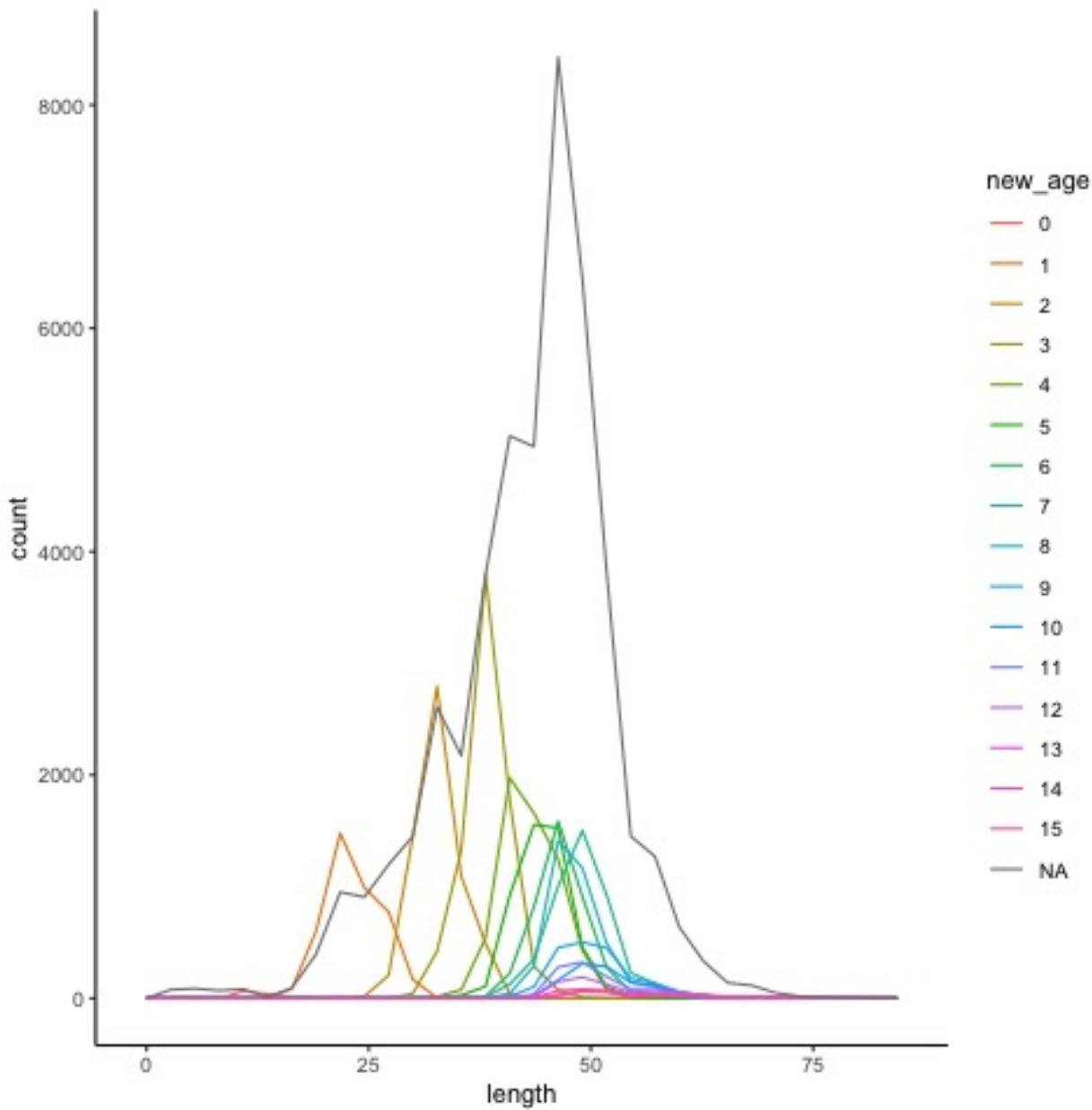


Figure 8: Growth curve to whole data



When estimating ages, it's worth making sure I understand what ages we are estimating. Below is a rough length frequency plot by age, where colors indicate age, and the grey line indicates observations that haven't been assigned an age. A lot of the observations with unassigned ages are larger individuals, and the VB models I have explored so far underestimate the ages of those larger individuals. How should I proceed?



Looks like age 6+ are fairly similar lengths - increased potential for mis-assigning these ages?

In terms of the stock assessment, the 2006 assessment modeled growth 3 ways: time-varying K, density dependent growth, and cohort-specific K.

Notes from meeting with Kristin 7/7/22

- The weight/age/year data may not be considered confidential and could request to get that data.
- Interesting to look at spatial and temporal variation (check Maia Kapur's work).
- Potential big-picture questions
 - How can we leverage this information of growth anomalies? Are there cohort effects? Is there an effect on future spawning?
 - Are there bigger recruitment events in years with fatter fish?
 - Do fish that are fatter in the early life stages, stay fatter throughout their life?
 - Ultimately, how can we develop a model that goes into the MSE?
- Next steps:

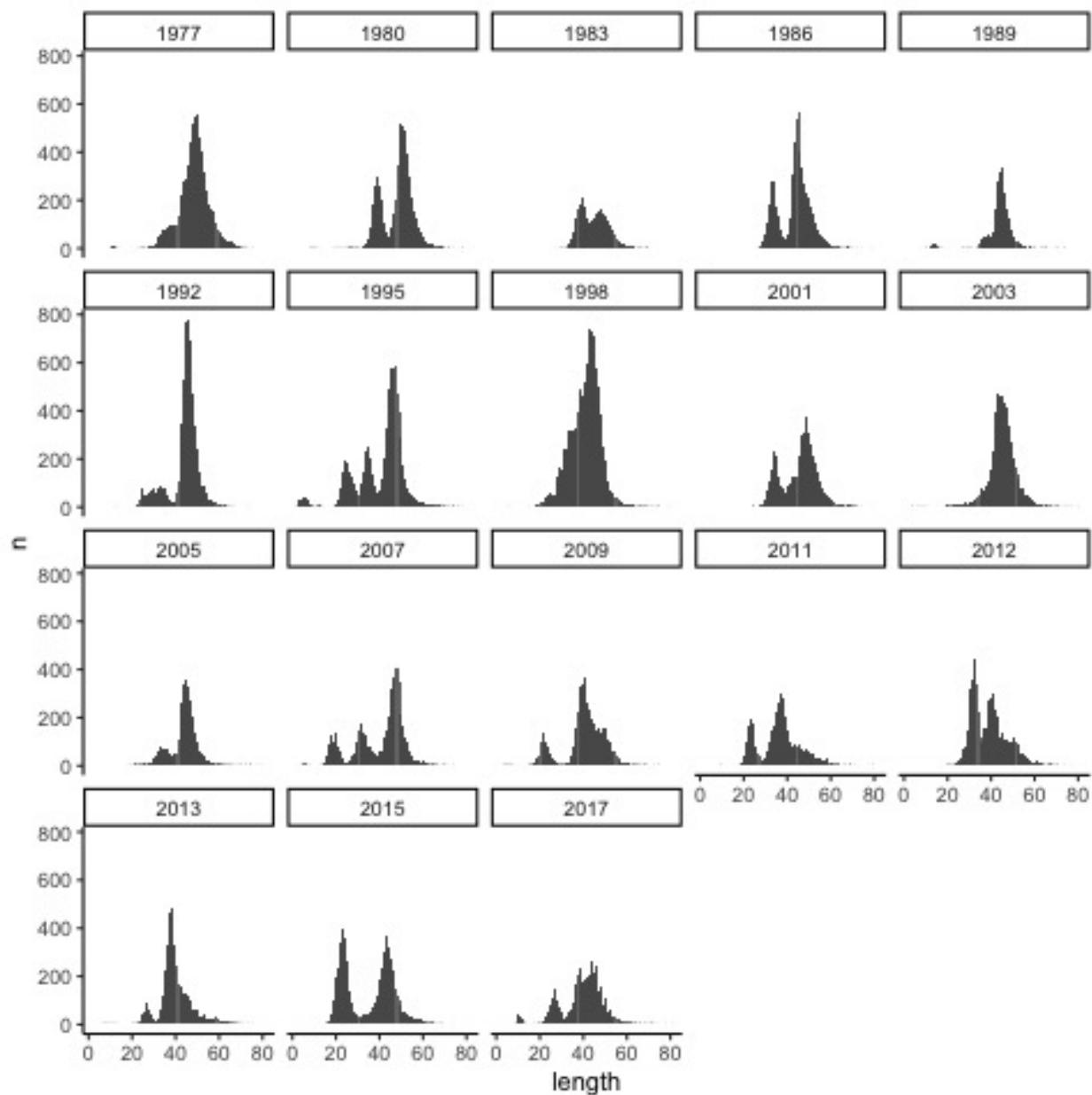
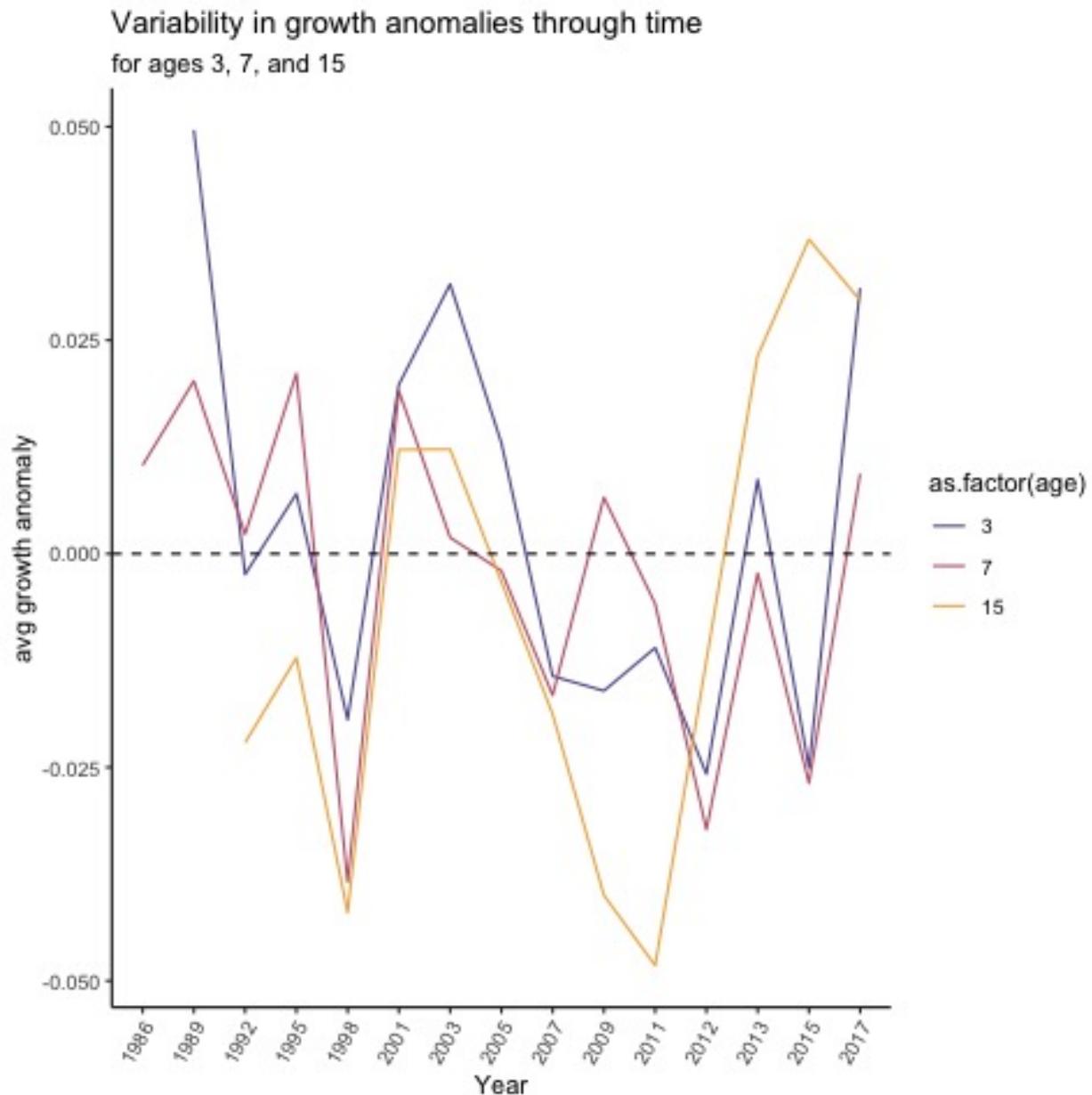


Figure 9: Length frequencies by year

- Still have to explore finer temporal resolution
- hierarchical or mixed growth model with time varying K

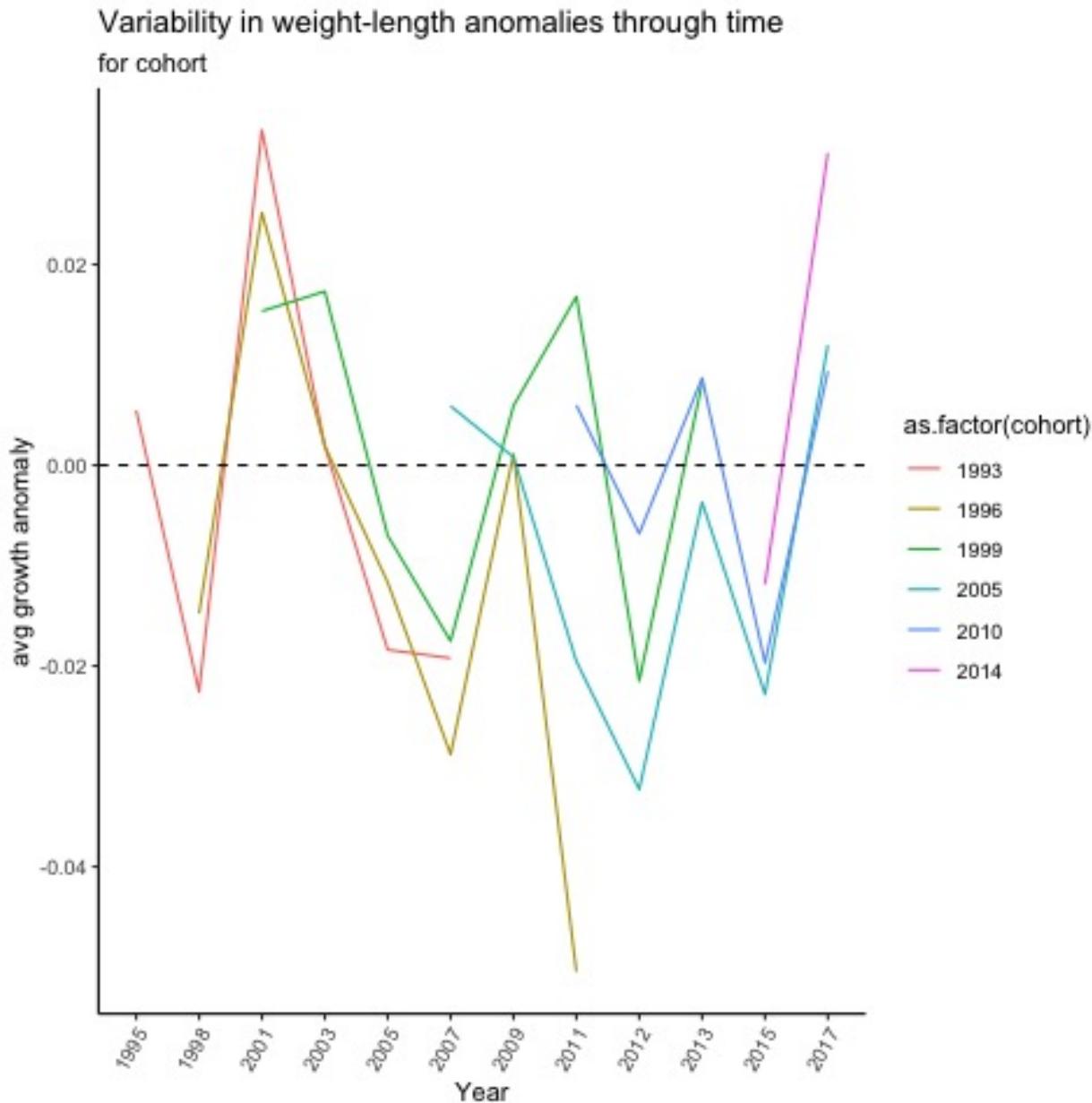
July 11-15, 2022

How do weight-length anomalies vary through time for a specific age?



It looks like fish condition for a younger ages vary much more stochastically compared to the plus group age that has much more low-frequency fluctuations. Potentially because they aren't growing quite as much at this age? Or lag effect with younger ages moving into this plus group?

And similarly, looking at how cohort condition varies through time



Doesn't look like there aren't too many patterns between cohorts.

- **Meeting with Kelli Johnson (7/14/22) on weight at age**
 - weighting process
 - * summarizes the data and then use that to weight things
 - * assumes all fish of the same age have the same weight
 - * only use individuals with ages when working with age composition and weight at age
 - * use individuals with length, weight, and age to groundtruth if needed
 - data_wtage()
 - * needs maturity ogive and catches to get mean weight at age. uses previous years to fill in missing age information
 - * assumes every population process going through SS uses the same weight at age (between different data sources - fishery vs survey vs etc)
 - * sampling date as potential covariates (do we need to take into account sampling month when we do weighting?)

- * could model season (season just means month) but the caveat is that we need to fill in everything, and so that's just more estimating ages
 - * if the estimated ages look the same regardless if we add biological realism then who cares
 - * female only modeled
 - * ignoring this dilutes the potential that surveys/data sources are sampling different fish
 - * may need some way to fill in missing information better based on the results that we (kristin and i) find
 - what if there's a regime shift but we don't account for that
 - are there environmental covariates that may drive changes in weight at age?
 - * SS there's flexibility in how you want to fill in these values
 - * factors influencing weight at age
 - sampling bias
 - cohort effects
 - environmental effects
 - * check how Pollock assessment fills in missing information
 - * Sablefish also has a lot of data to test on
 - * visualize weight at age over the raw data to see if there are strong cohorts coming through
 - * Line 157 in github code - beginning of where they fill in missing values
- Meeting with Kristin
 - random effects
 - * year
 - * cohort
 - * to establish cohort, we can create a cohort ID that is their birth year (cohort ID = current year - age) - We could also look at how growth anomalies relate to the size of the population or cohort to get into some density dependence effects
 - 3 potential ways to model weight at age
 - * random effect just on age
 - * gam (does brms have gams)
 - * boosted regression trees
 - Doesn't give insight into mechanism, so might be difficult to translate into something for MSE
 - For the growth anomaly variability line graph, we could also look at
 - * ages 1 and 2
 - * immature vs mature fish
 - * To think about: age 3 fish have fairly variable growth anomalies and they are also the biggest contributor to recruitment
 - how does this variability affect population dynamics
 - Note: big cohorts happened in 1999 and 2010

I tested out different GAMs using `gam()`, as well as running it in `brms`.

1. Simple GAM with no random effects

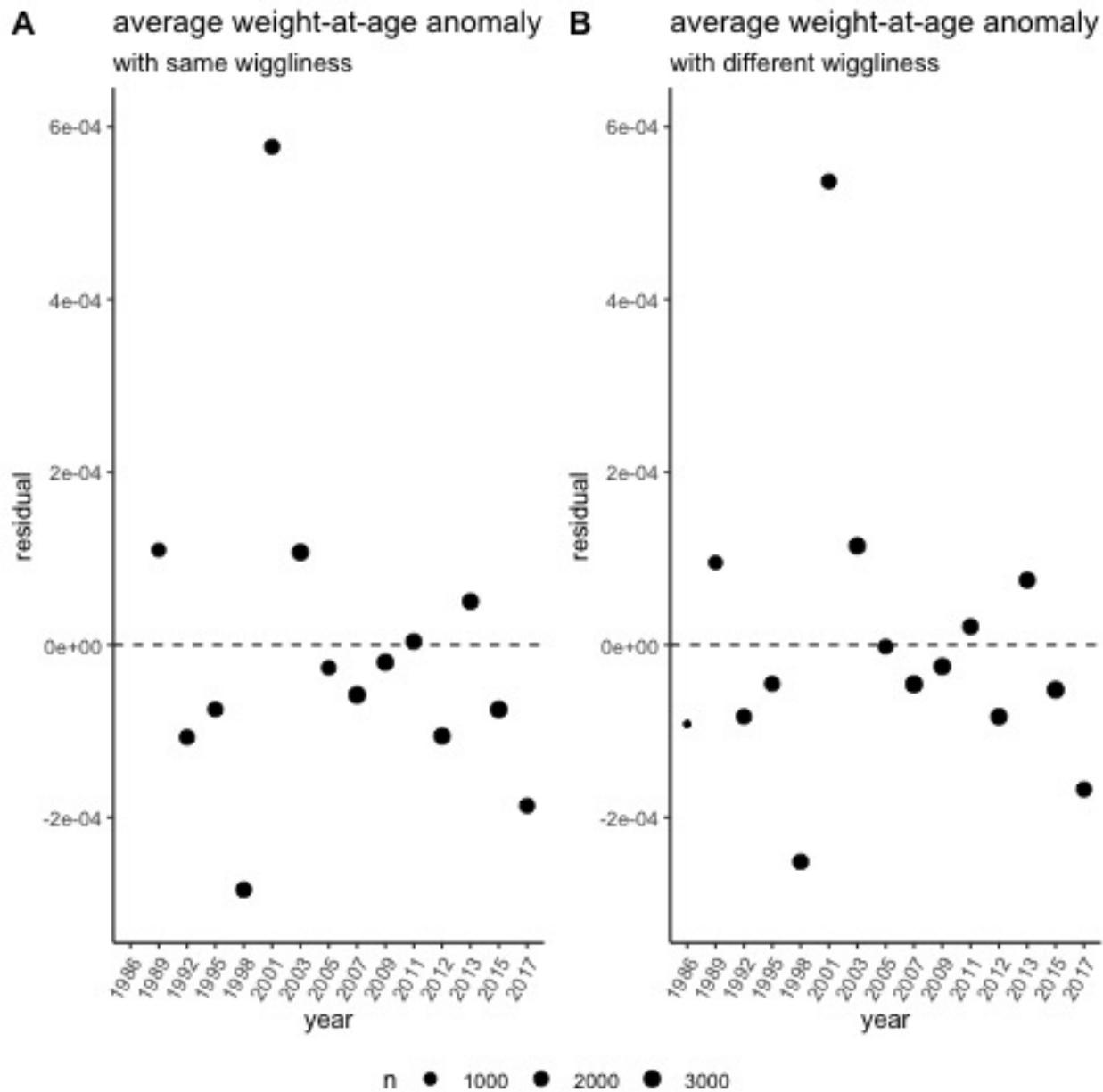
```
gam_out <- gam(weight ~ s(new_age), data = hake_weight_age_df, method = "REML")
```

2. GAM with group-level smoothers with different wigginess for year

```
gamm_out = gam(weight ~ s(new_age, bs="tp") +
  s(new_age, by = catch_year, m = 1, bs="tp") +
  s(catch_year, bs="re"),
  data = hake_weight_age_df, method="REML")
```

3. GAM with group-level smoothers with same wigginess for year

```
gamm_GS_out = gam(weight ~ s(new_age, m = 2) +
  s(new_age, catch_year, bs="fs", m = 2),
  data = hake_weight_age_df, method="REML")
```

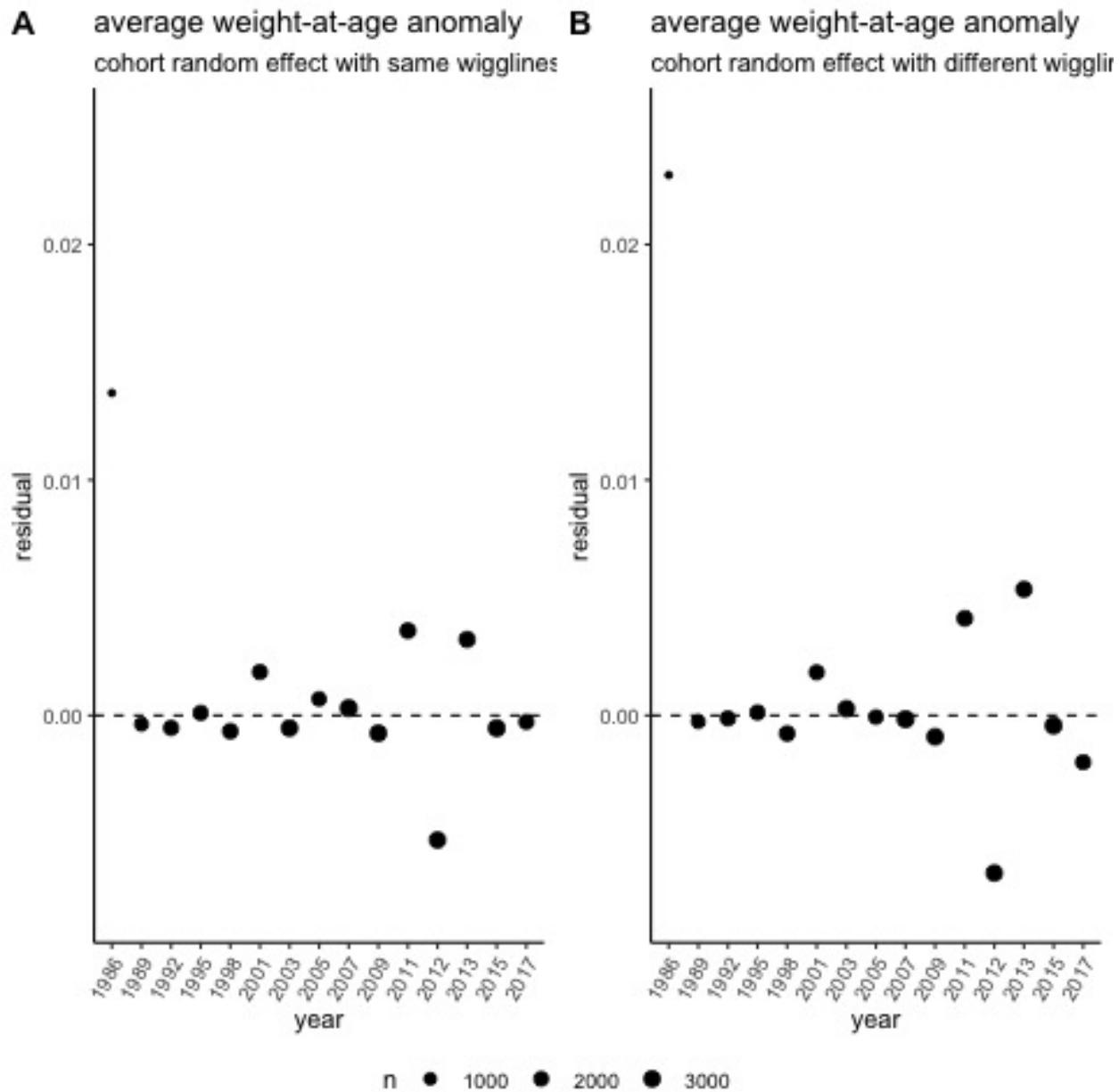


4. GAM with group-level smoothers with different wiggliness for cohort

```
gamm_cohort_out = gam(weight ~ s(new_age, bs="tp") +
                      s(new_age, by = cohort, m = 1, bs="tp") +
                      s(cohort, bs="re"),
                      data = hake_weight_age_df, method="REML")
```

5. GAM with group-level smoothers with same wiggliness for cohort

```
gamm_GS_cohort_out = gam(weight ~ s(new_age, m = 2) +
                           s(new_age, cohort, bs="fs", m = 2),
                           data = hake_weight_age_df, method="REML")
```



July 18-22, 2022

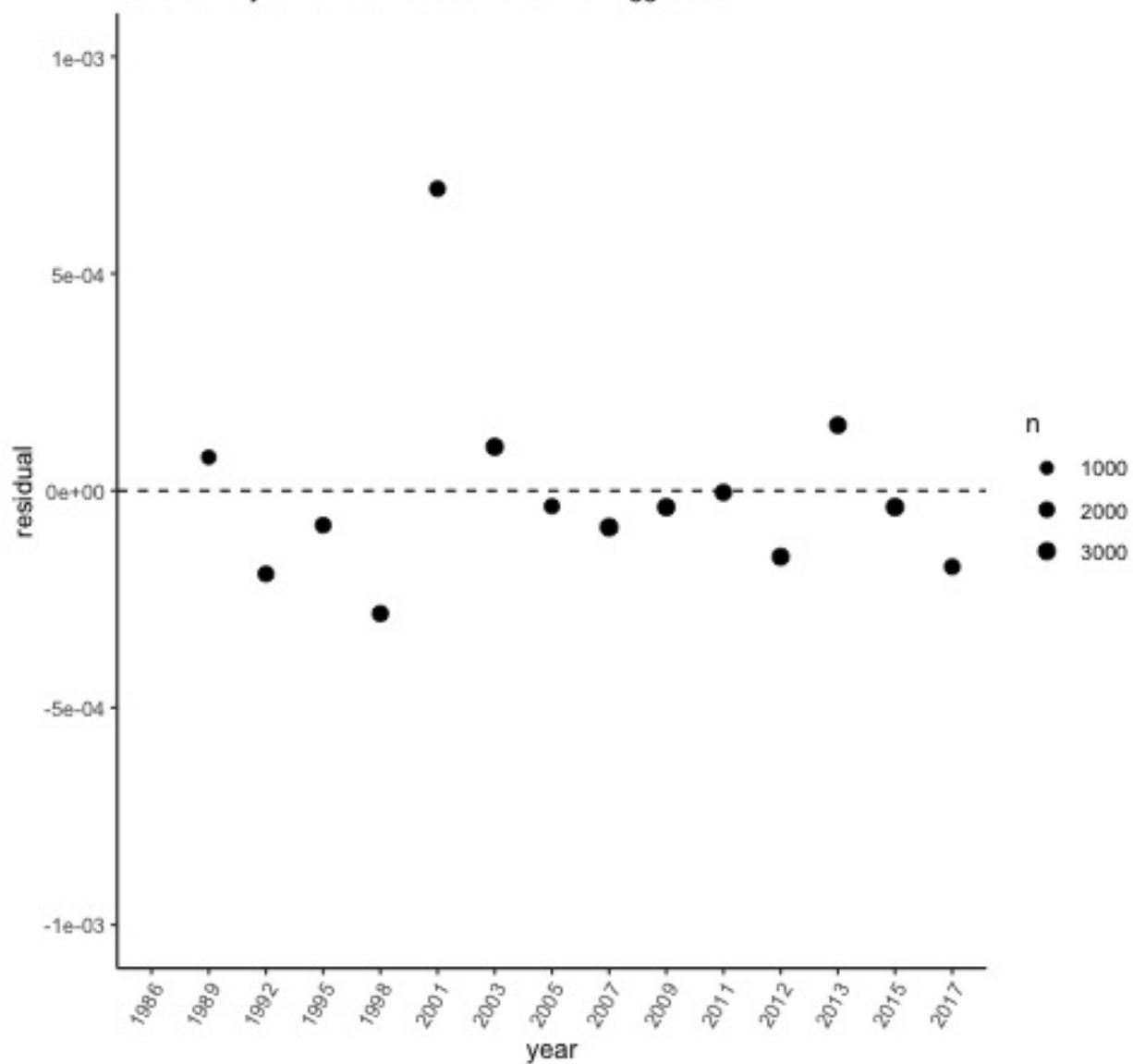
Of all 5 models, `gamm_GS_cohort_out` had the smallest AIC value.

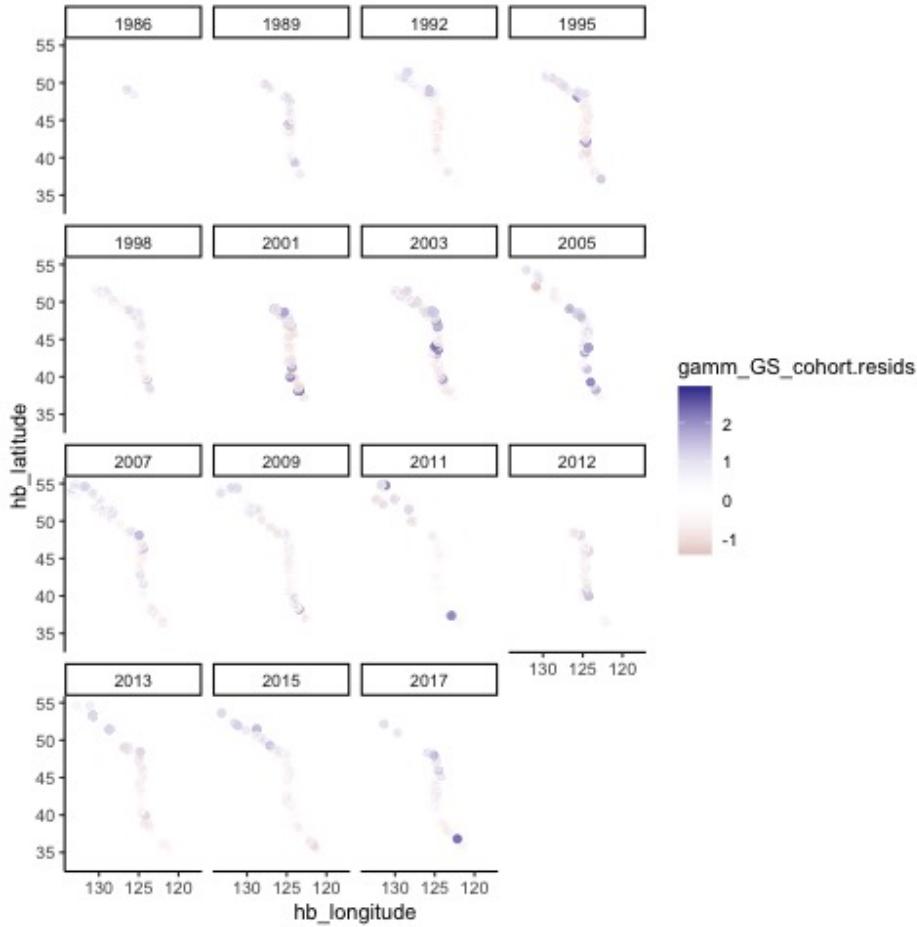
- Notes on weight-length and weight-at-age and how they may relate
 - weight-length relationships are indicative of “body condition”
 - weight-at-age is a rate, so potentially indicative of growth rate

6. GAM with group-level smoothers with same wiggles for cohort and year

```
gamm_GS_year_cohort_out = gam(weight ~ s(new_age, m = 2) +
                               s(new_age, cohort, bs="fs", m = 2) +
                               s(new_age, catch_year, bs="fs", m = 2) ,
                               data = hake_weight_age_df, method="REML")
```

average weight-at-age anomaly
cohort and year random effect with same wiggliness





Looking at how weight-at-age anomalies vary spatially by year, there seems to be a lot more within year, spatial variation compared to between years. This is in stark contrast from visualising the length-weight relationship. This plot only shows for the gam model with cohort RE and same wiggliness (model 5). However, there were no visual differences between the other models that I tried (model 3 and 6).

Okay, I need a recap:

- weight-length relationship
 - greater year-to-year spatial variation
 - plus group has lower freq variability through time vs younger ages are much more stochastic
 - No clear pattern between cohorts when looking at weight-length variability through time
- weight-at-age
 - greater within-year spatial variation
 - Different temporal trends in average growth anomaly depending on model used

Meeting with Kristin

- gams
 - don't put smoothers on random effect
- year-to-year effects are better explained because the residuals are smaller
- write down hypothesis about how weight-at-age should vary with cohorts or years
 - different curve for each cohort
- LOOIC instead of AIC (look at Michael Malick papers 2020)
- Think about what I want to get out of the internship and make sure we're accomplishing that

July 25-29, 2022

Potential questions of interest

- Explore spatio-temporal patterns in growth of Pacific Hake
- Identify potential covariates of growth trends and develop an environmental index
- Quantify the performance of incorporating an environmental index on growth
- Separately, test importance/sensitivity of SS of filling in missing weight-at-age information assuming average vs environmentally driven weight-at-age
- Incorporate into the MSE?

Goals for the rest of the summer

- Solidify motivation and guiding questions
- Identify promising methods/approaches
- Begin writing

This week I did more work on the gam modeling and now have a better grasp on what I am modeling. Last week, the models I was fitting were gam models with “random wigginess” where each cohort and year had their own wigginess/spline action. However, we are more interested in random effects where there is just a shift in the position of the curve (intercept?), but the shape remains the same. With that in mind, I realized we could still use the smoothing function (because smoothing process also involves shrinkage and has a direct link to the shrinkage involved in random effects) and specify `bs = 're'`.

I just tested a Bayesian GAMM with year and year+cohort random effects.

1. Bayesian GAMM with only year RE

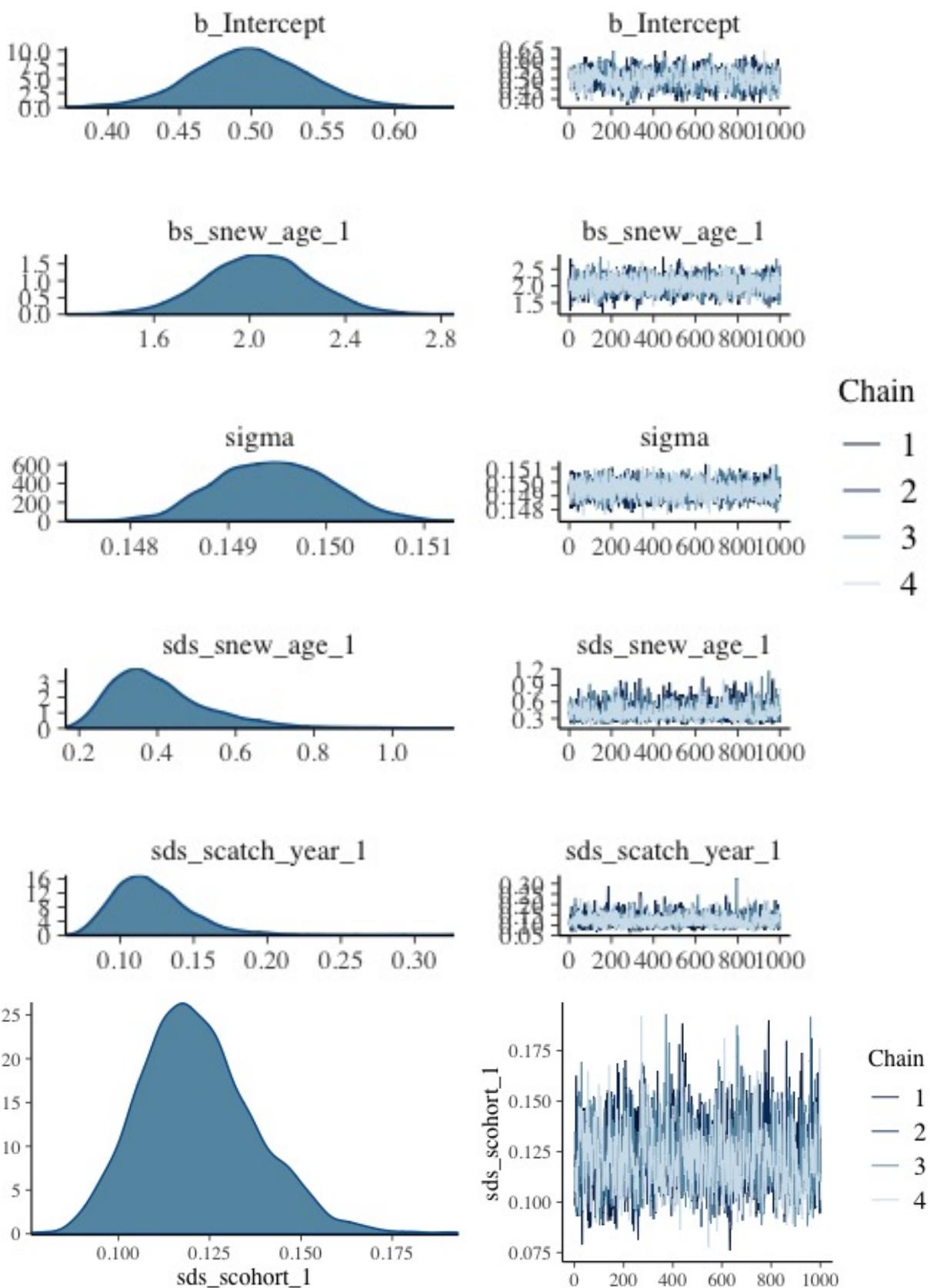
```
gamm_year_brm_out = brm(bf(weight ~ s(new_age) + s(catch_year, bs="re")),
                         data = hake_weight_age_df, family = gaussian(), cores = 4,
                         iter = 2000, warmup = 1000, chains = 4)
```

2. Bayesian GAMM with year and cohort RE

```
gamm_year_cohort_out = brm(bf(weight ~ s(new_age) + s(catch_year, bs="re")
                                + s(cohort, bs="re")), data = hake_weight_age_df, family = gaussian(),
                                cores = 4, iter = 2000, warmup = 1000, chains = 4)
```

Model comparisons: elpd_diff se_diff gamm_year_cohort_out 0.0 0.0 gamm_year_brm_out -1632.4 110.9

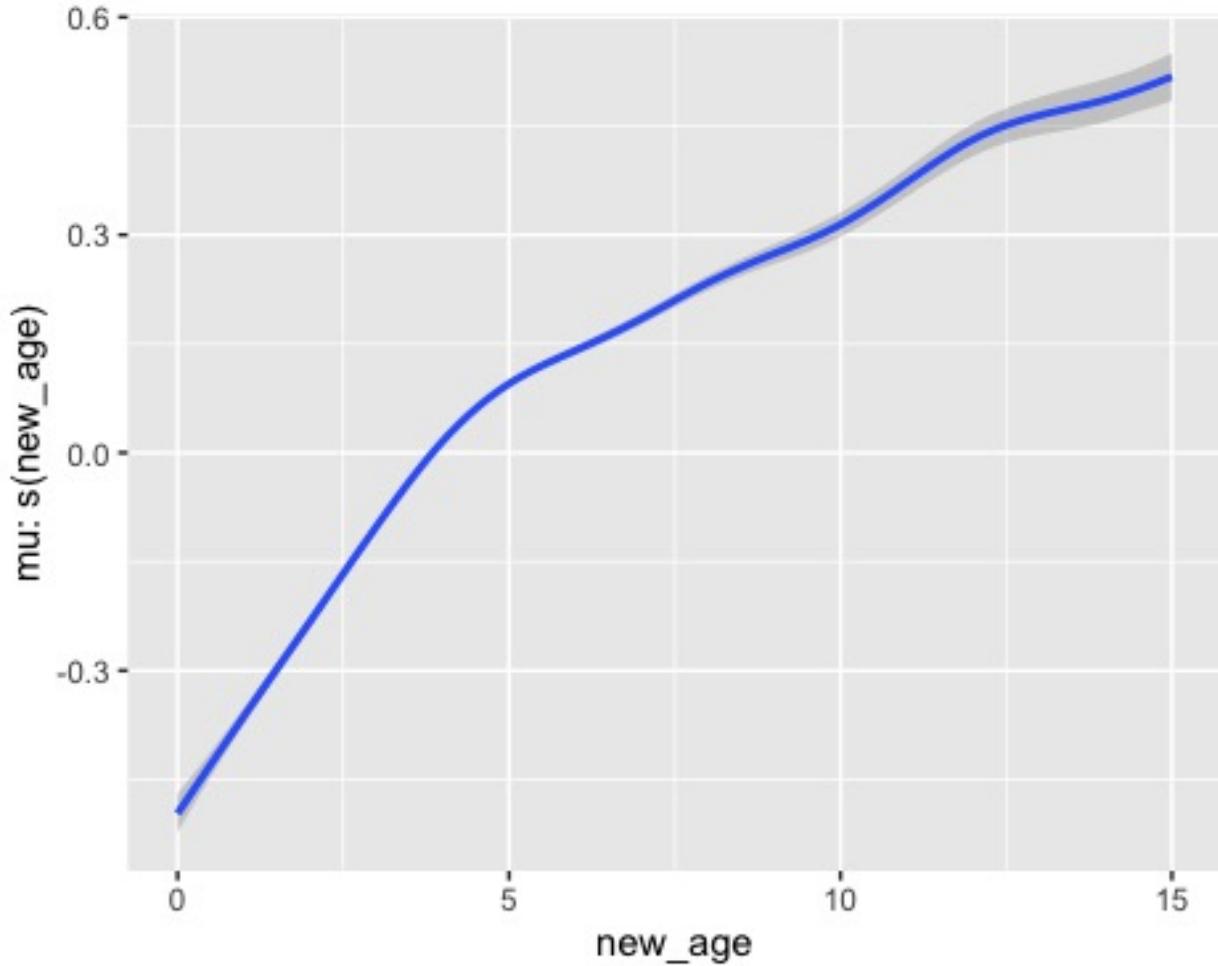
Because the model with year + cohort RE was a better fit to the data, I continue on only looking at that model

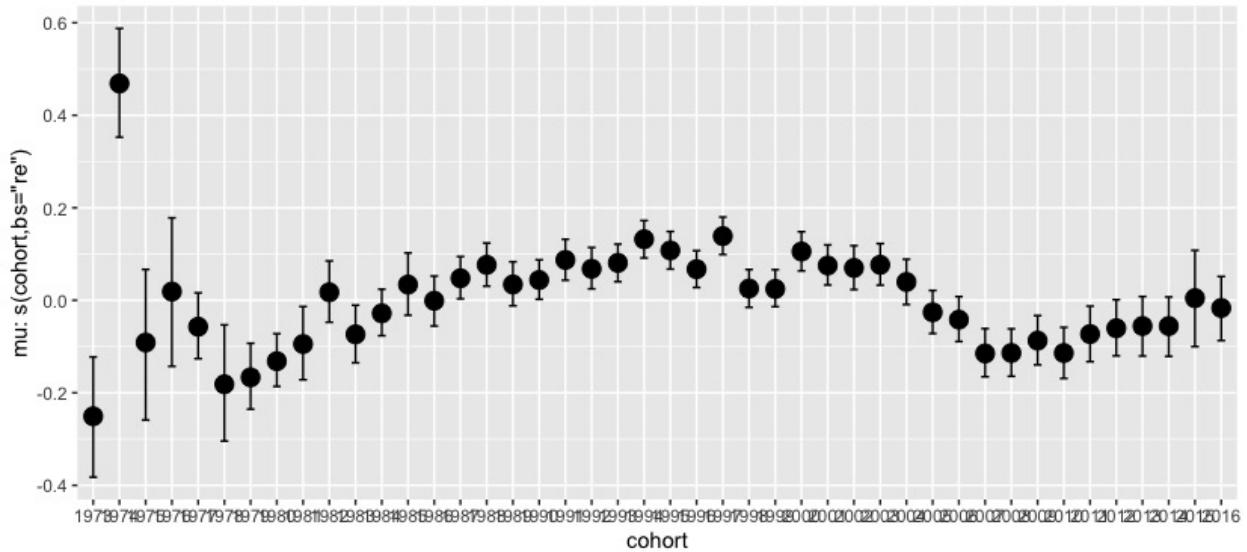
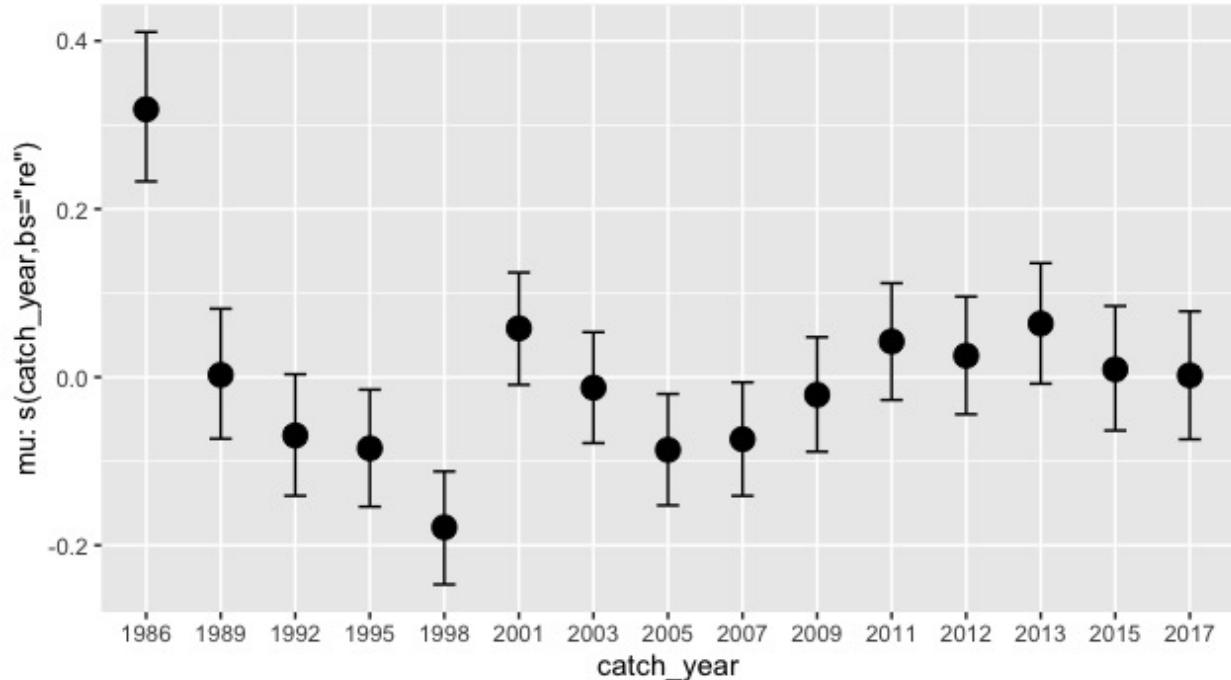


Density and traceplots look good - got the hairy caterpillars

However, the posterior predictive check doesn't look quite as good. This plot shows the observed data (in dark blue) and simulations from the joint posterior predictive distributions (in light blue). The replicated data should align with the observed data, unless there is model misfit or by chance. I used a gaussian distribution, however there is a bit of a right skew and potentially a lognormal or gamma distribution might be a better fit. I really have no clue what might be causing the multi-modes though... thoughts?

Either way, the next few plots will be summaries of the coefficients.





I am still trying to figure out how to graph these myself so that I can customize the graphs, but for now these will do..

Very clear year and cohort effects, some with credible intervals not passing over 0. Does that mean something like how it means in confidence intervals?

Questions

- How to best explore “year” and “cohort” effects - is just specifying random effects okay?
 - are these effects important and how important are they relative to each other?
 - * have a model for each (no RE, just cohort, just year, both)
 - * look at sd for year vs cohort. which has more variability
- where can I get recruitment and biomass information?

Questions for presentation in hake meeting

- potential environmental covariates to explore linked to growth? What is available?
- spatio-temporal methods?
 - sdm-TMB
 - gam with smoothers on lat,long
- thoughts on length-weight vs weight at age?
- Other assessments that use environmental indicators/indices that I can gain inspiration from?
- proposed research questions

Meeting with Kristin

- what makes weight at age different from recruitment? there is no real way to put an environmental driver into stock assessment since it is empirical
 - rather, explore how incorporating an environmental driver affects the matrix of weight at age that does go into the assessment
 - MSE: historical period using same empirical weight at age as estimation model, future assumes average weight at age (not a good assumption)
- Fix assumed distribution in brms (lognormal/gamma)
- does spatial matter? If not, then we can lump data together with fishery data and get a longer time series
 - dig into smaller time-scale
- Next steps
 - model comparison
 - * add smoother on lat,long (start simple model with just weight at age no RE)
 - identifying potential covariates
 - * temperature, upwelling, decadal?
- recruitment and biomass information
 - pacific hake mse github - assessment repository
 - include as a potential driver

Aug 1-5, 2022

Notes from presentation

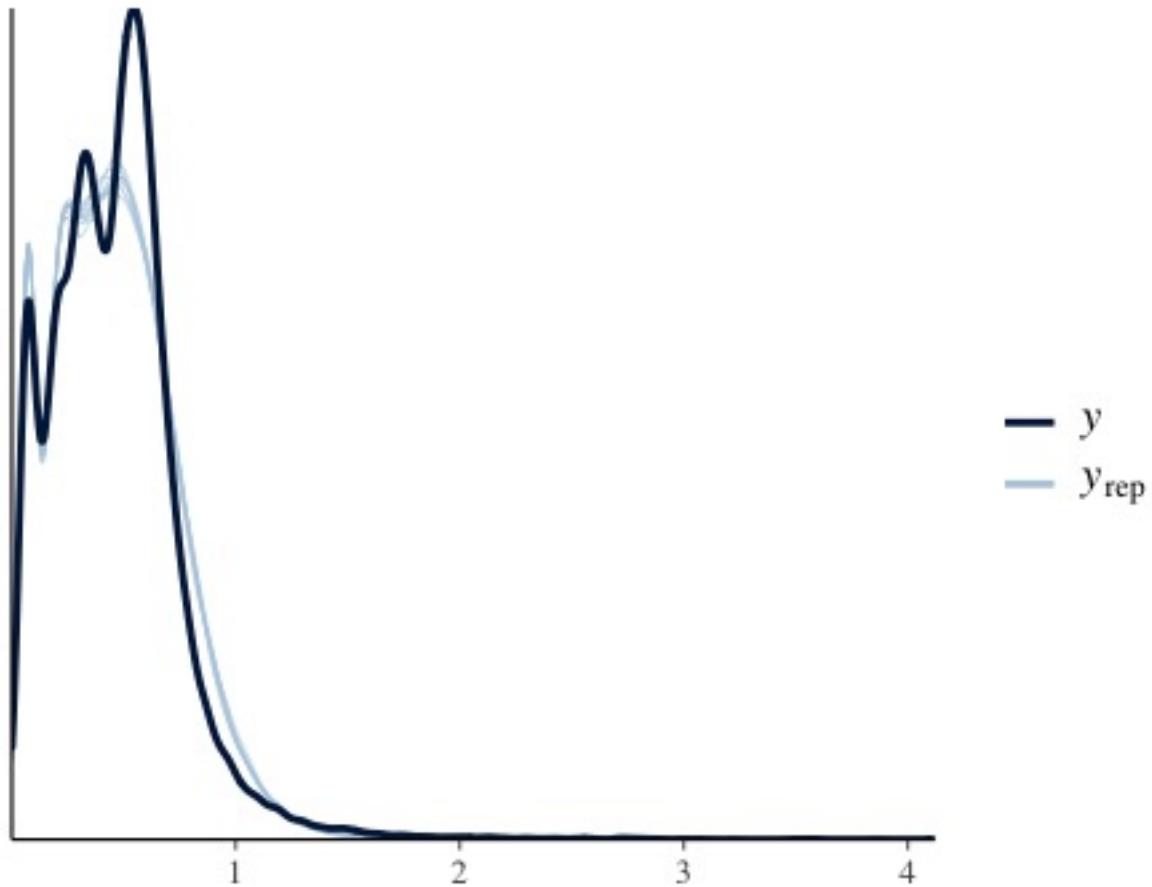
- Kelli: cohort effect of ageing error
 - strong cohorts have more ageing error
 - * can lead to unequal smoothing
 - * smoother would be smoothing out ageing error?
 - * in stock synthesis, treat strong cohorts differently
 - maybe add a cohort effect for large cohorts
 - Kiva doesn't think it's that important (error in variables)
 - Even if I don't include it in the model immediately, it could be a way to explain some of the results
- For gamm with year and cohort random effect, there was agreement on the presence of autocorrelation in the cohort random effect
 - perhaps above average weight at age carrying through
- In terms of temporal trends, previous surveys were a different temporal window. If we could show that there are no differences in short timescale, then that's also good to know
- sdm-TMB - run all the models with and without spatial effects - get started on this (after looking into modes - next point)
- Figure out what those modes are in the observed weight data (pp_check) - are they ages 1,2, and 3?

- Motivations for population dynamics fellowship
 - Lay the groundwork for what we might build into a forecast (so instead of interpolating, we can extrapolate)
 - They want to include an internally estimate weight at age into FIMS, and so this work can directly inform how they do that

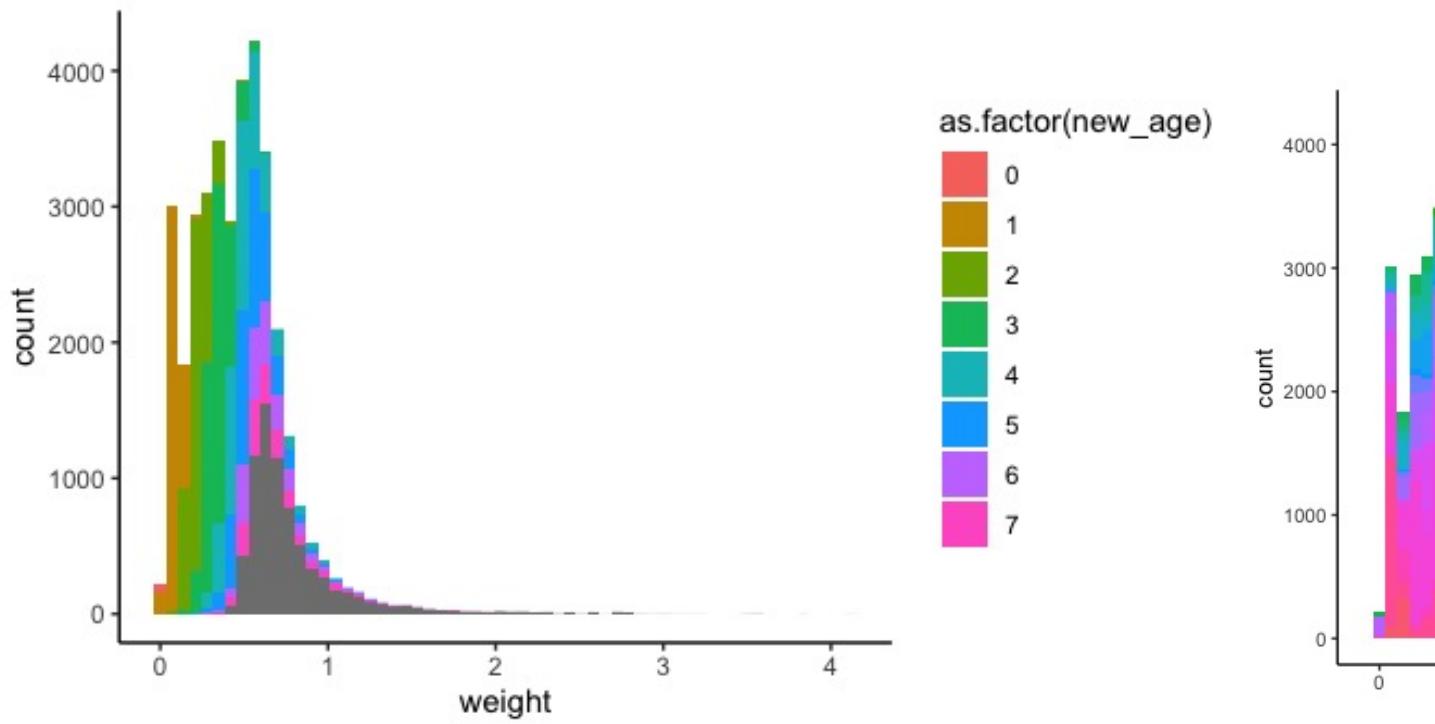
Fixed the distribution from gaussian to lognormal and re-ran the 4 models in brms. 1. Just age as a predictor

2. age with catch_year random effect
3. age with cohort random effect
4. age with both catch_year and cohort random effect

The posterior predictive check is much better when using the lognormal distribution, but there seems to be some bias in predictions as shown by the offset peaks.



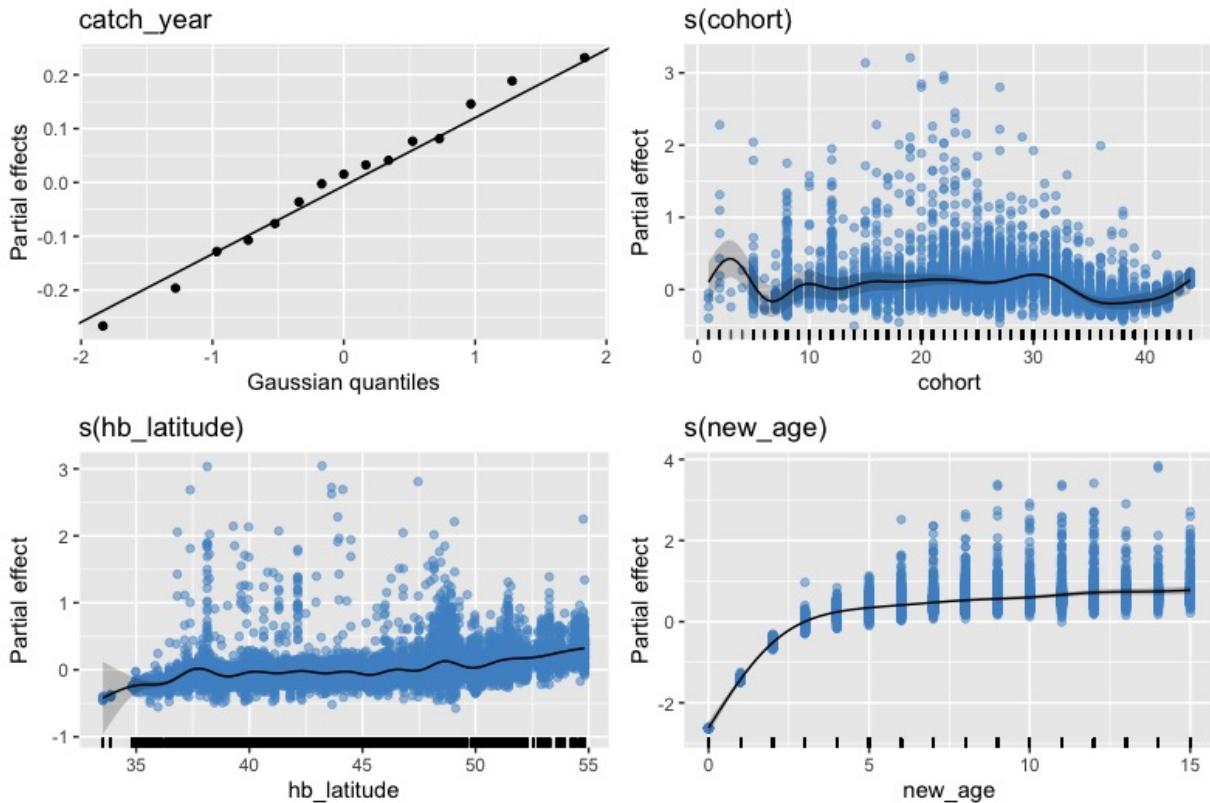
So, what are those peaks? Through some simple visualisation, it looks like the peaks are associated with ages as opposed to cohorts. The first peak is the age 1 individuals, the second peak is ages 2 and 3, and the third peak is a compilation of the rest of the ages.



Now I am on a quest to minimize the bias!

I am instead running more gams in mgcv since that has been much faster. In terms of the bias in the posterior predictive check, I originally thought a gamma distribution might be a better fit than the lognormal, but that doesn't seem to be the case when I looked at the outputs and GCV which is a leave one out cross-validation that acts similarly to the AIC. So, I continue to use a lognormal (or at least in the gam case, I am using a gaussian with log link - which hopefully is fine... couldn't find the lognormal distribution option in mgcv)

I also included a smoother on latitude to hopefully capture some of the residuals in the larger fish. Below is a plot of the partial effects for the gam with catch_year random effects, s(cohort), and s(latitude) and you can see the new_age is still underpredicting for those older ages



I also learned about new diagnostic checks using `gam.check` to determine if the number of knots is too low (predictors with $k > 1$ or a significant p-value)

Aug 8-13, 2022

Following the gams fit last week and the significance of at least a smoother on latitude, I am making the switch to sdm-TMB and going to start figuring out how to use it.

- check correlation structure

Notes on coordinate system for sdmTMB

- have to convert from LatLong to UTM which minimizes distortion and has attributes that make estimating distances easy and more accurate.
- Pacific Northwest is UTM zone 10 (EPSG: 32610)

I was on vacation from Thursday - Monday

Aug 16-19, 2022

The first thing I did was check correlation structure among key predictors from the data frame which included catch month, catch day, length, distance fished, latitude, longitude, catch year and cohort. Using the `cor()` function, there were a few correlations > 0.7 .

- latitude x catch month = 0.80
- latitude x longitude = 0.85
- cohort x catch year = 0.94

	catch_month	catch_day	length	distance_fished	hb_latitude
catch_month	1.00000000	-0.4828610987	0.3588093176	-0.05049285	0.80528335
catch_day	-0.48286110	1.0000000000	0.0003954114	0.01042608	-0.09679147
length	0.35880932	0.0003954114	1.0000000000	0.12335166	0.52282377
distance_fished	-0.05049285	0.0104260769	0.1233516592	1.00000000	-0.04962851
hb_latitude	0.80528335	-0.0967914679	0.5228237716	-0.04962851	1.00000000
hb_longitude	0.65202012	-0.0287545645	0.5055199224	-0.03191845	0.84940888
catch_year	-0.12630983	-0.0103531145	-0.3068209044	-0.01512864	-0.19213568
cohort	-0.23925645	-0.0183413984	-0.5154355845	-0.06526248	-0.30809197
	hb_longitude	catch_year	cohort		
catch_month	0.65202012	-0.12630983	-0.23925645		
catch_day	-0.02875456	-0.01035311	-0.01834140		
length	0.50551992	-0.30682090	-0.51543558		
distance_fished	-0.03191845	-0.01512864	-0.06526248		
hb_latitude	0.84940888	-0.19213568	-0.30809197		
hb_longitude	1.00000000	-0.14251631	-0.25922742		
catch_year	-0.14251631	1.00000000	0.94027636		
cohort	-0.25922742	0.94027636	1.00000000		

Big picture thinking

1. What are the local and regional trends in weight at age of Pacific Hake
2. Which covariates explain these changes and in what direction do they covary?
3. How strong are the latent spatial and spatiotemporal random effects? (maybe don't explicitly say this, but good to include in results)
4. To what extent does incorporating growth variation into the interpolation of missing data within the stock assessment affect the estimationg of management reference points?

Things to remember

- the data that I have is limited to the months of June - September when the acoustic trawl survey is sampling.

Variability can be partitioned into 4 ways (larsen et al 2001 - Designs for evaluating local and regional scale trends):

- Spatial: areas with increased condition in all years
- Temporal: changes throughout the populations range in a given year
- Spatiotemporal: areas with increased condition in a particular year
- Individual: residual variation in condition for each individual

Covariates to consider

- Temperature (at depth? SST?), PDO, ENSO (abiotic)
- Main food source (Euphasiid) or predator or competition from strong year classes (biotic)
- total catch? (fishing)

Questions for meeting with Kristin

- Do I need to standardize the data according to the CPUE? Saw this in the body condition sdmTMB

paper - might just be for density model

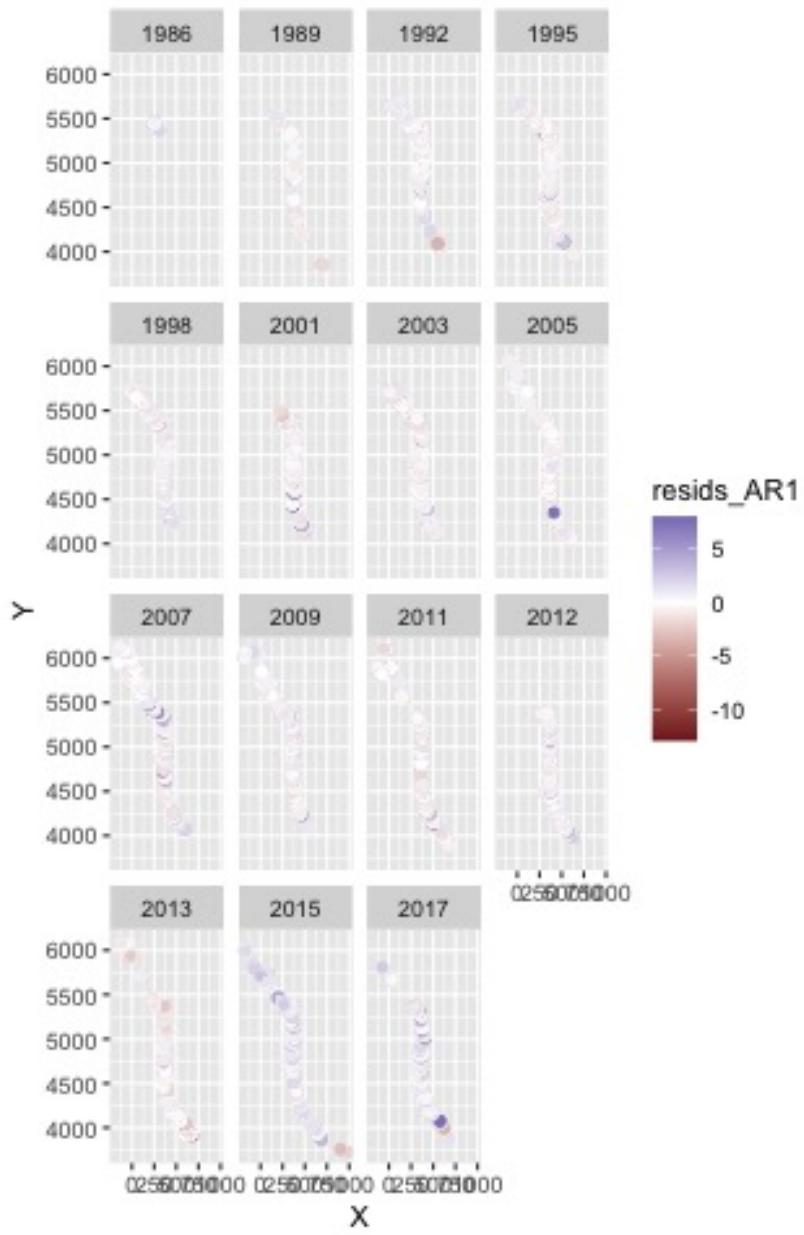
- Were there any changes in the net used for the acoustic-trawl survey that might influence the size of the fish being caught? Vessel-specific variation from year to year as well...
- Should we start to look into obtaining environmental data?
 - biomass at age for strong year classes

Explorations with sdmTMB

I am getting the hang of it. I started off with a very simple, non-spatial model where weight is predicted by age and cohort, with age and cohort as have a smoothing function. Then I turned on spatial, then the spatiotemporal random effect with an AR1 process. I tested two spatiotemporal models

m2: weight ~ s(age) + s(cohort)

```
> tidy(m2, "ran_pars", conf.int = TRUE)
      term   estimate std.error    conf.low    conf.high
1   range  95.6451287       NA  81.77952315 111.8616287
3     phi   0.1904433       NA   0.18902325  0.1918739
4 sigma_0  0.1148037       NA   0.07891091  0.1670223
5 sigma_E  0.2001517       NA   0.18132935  0.2209279
6     rho   0.1033049       NA  -0.09293560  0.2918195
> tidy(m2, conf.int = TRUE)
      term   estimate std.error conf.low conf.high
1 (Intercept) -0.9647078  0.02429143 -1.012318 -0.9170974
```

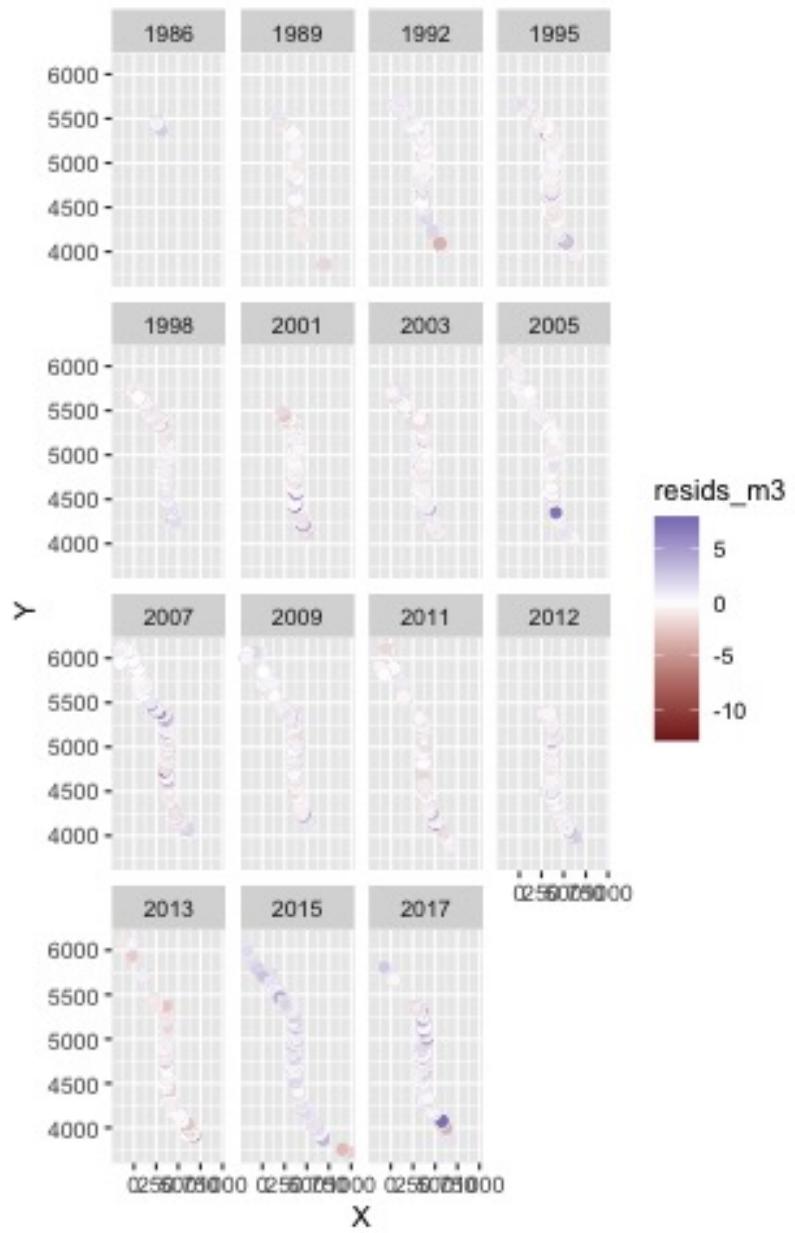


m3: weight ~ s(age) + s(cohort) + catch_month

```

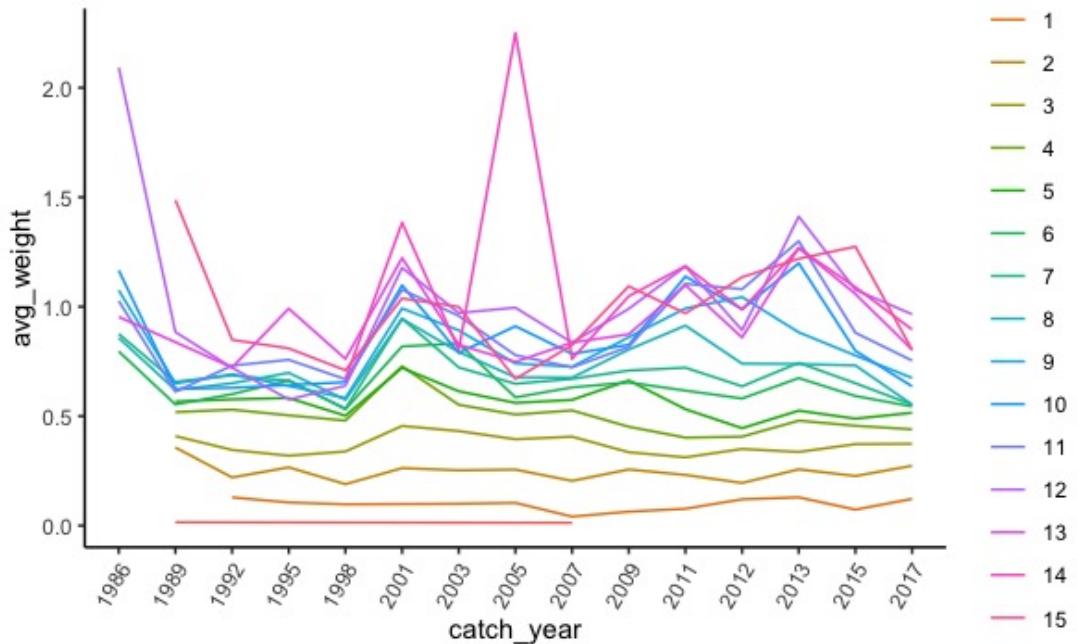
> tidy(m3, "ran_pars", conf.int = TRUE)
      term    estimate std.error    conf.low    conf.high
1   range  80.916372359        NA 69.14320482 94.6941834
3     phi   0.190359597        NA 0.18894111 0.1917887
4 sigma_0  0.043608373        NA 0.01513698 0.1256320
5 sigma_E  0.200755421        NA 0.18507765 0.2177612
6     rho   0.009789602        NA -0.16424999 0.1832381
> tidy(m3, conf.int = TRUE)
      term    estimate std.error    conf.low    conf.high
1 (Intercept) -1.7775624 0.10179888 -1.97708451 -1.5780402
2 catch_month  0.1094013 0.01363829  0.08267076  0.1361319

```

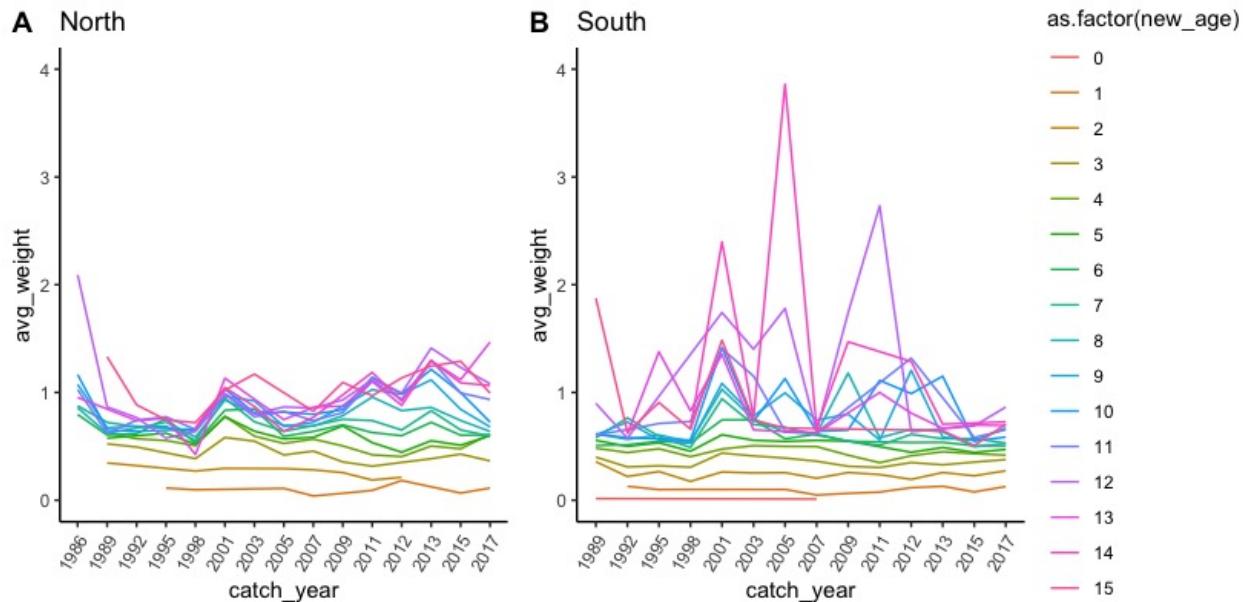


Catch month and latitude have a correlation of 0.8. Is it fine to still include if latitude is not considered a predictor, but rather a spatial random effect?

In terms of autocorrelation, I realize I never really looked at the time series of weight for each age to see if there are any long term declines or where the variability is most prominent.



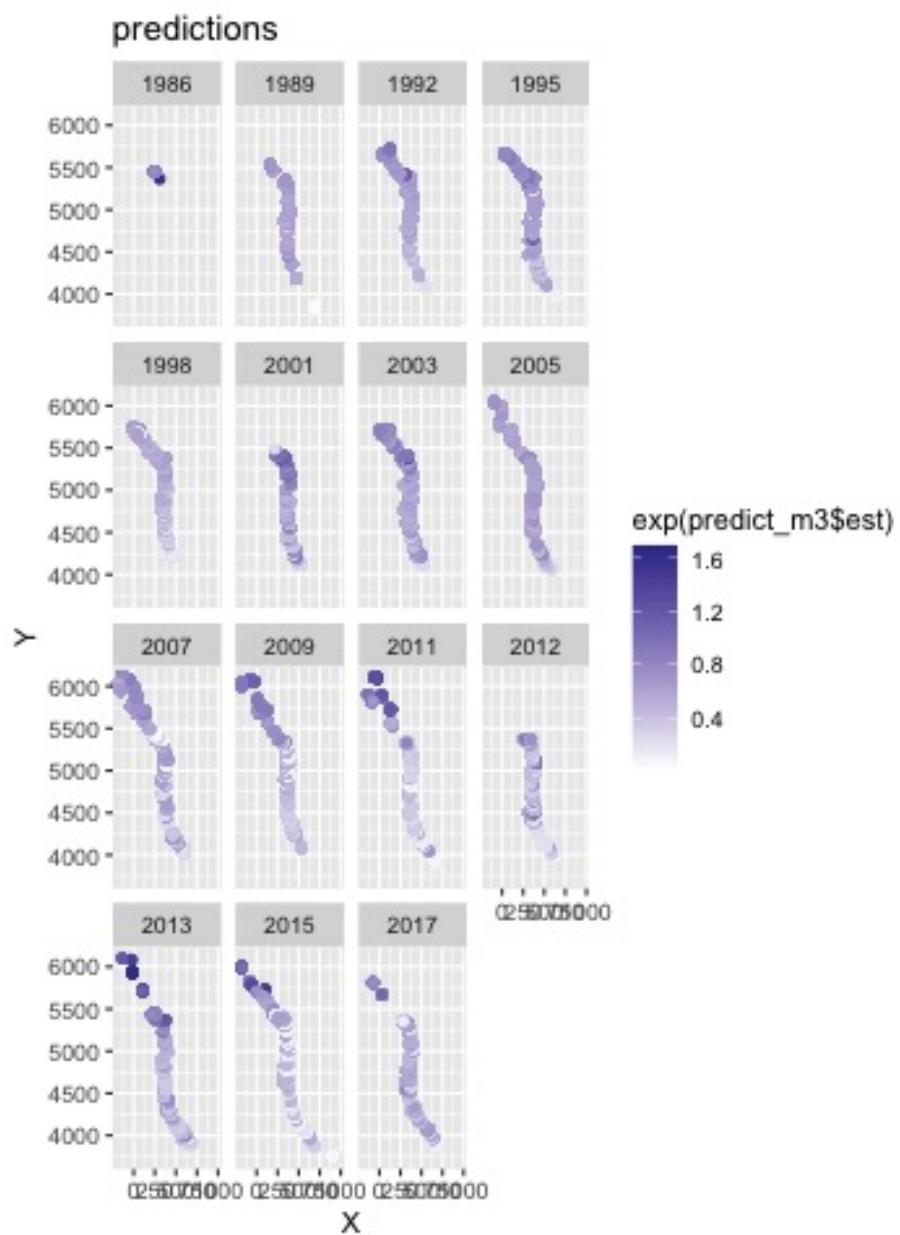
There also seems to be some differences when we split the data between north and south at the median point.
UTC 4957.963



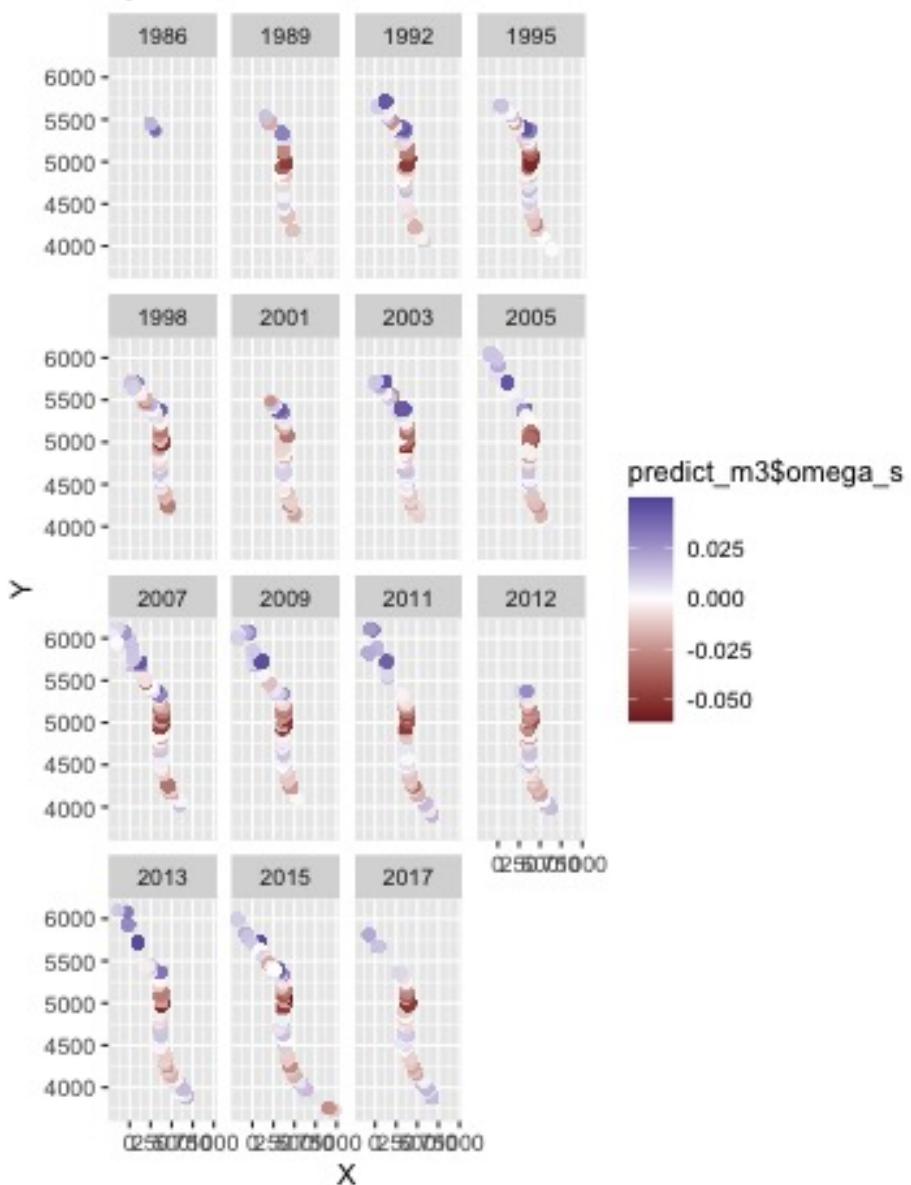
There is much greater variability in the older age classes of the south. Moreover, there may be a slightly increasing trend in the north.

Definitely worth looking at a longer time series of this - where is the fishery data again?

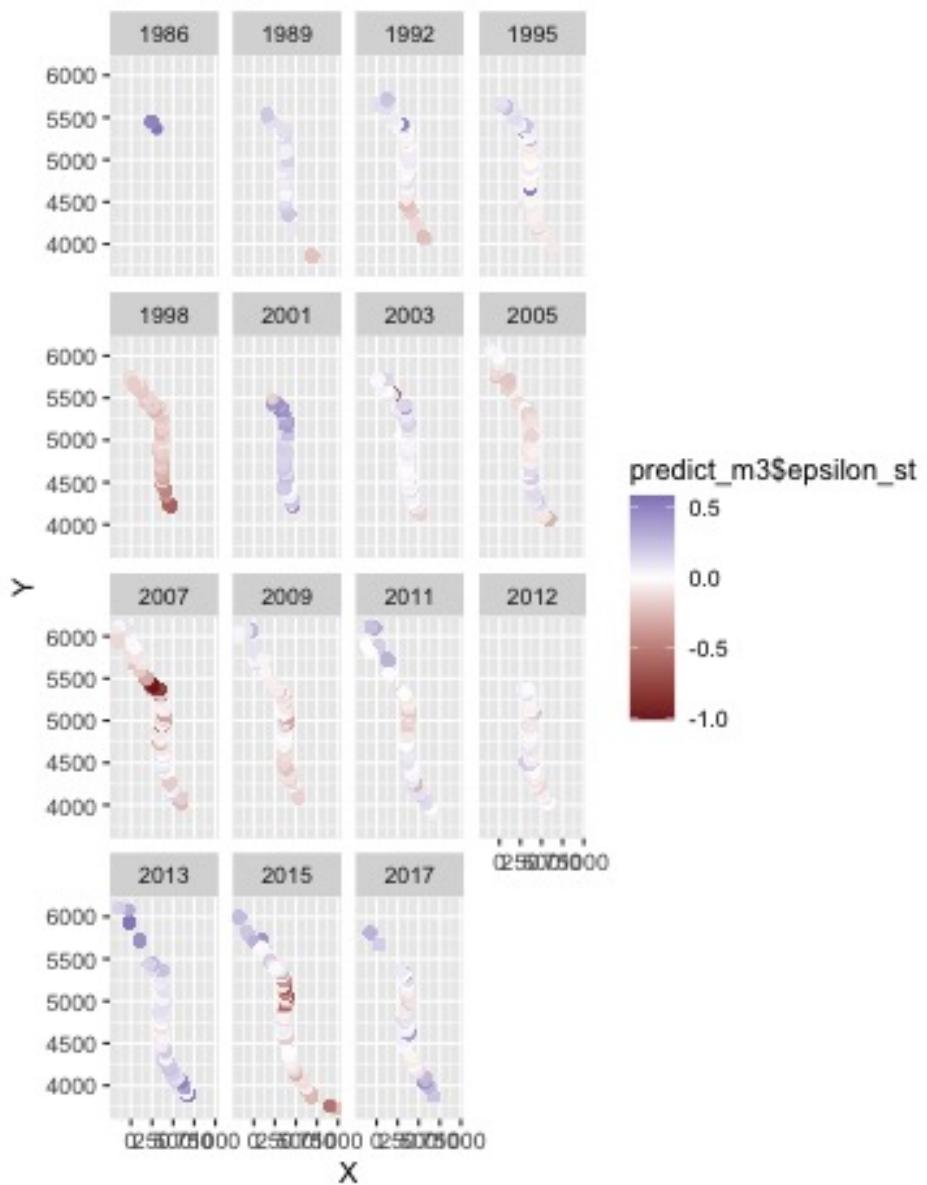
Now looking at the outputs of m3



spatial random effects



spatiotemporal random effects



Next week:

- time varying intercept model and compare to gams
- add a smoother on catch_year
- biomass of cohort in that year rather than cohort

Aug 22-29, 2022

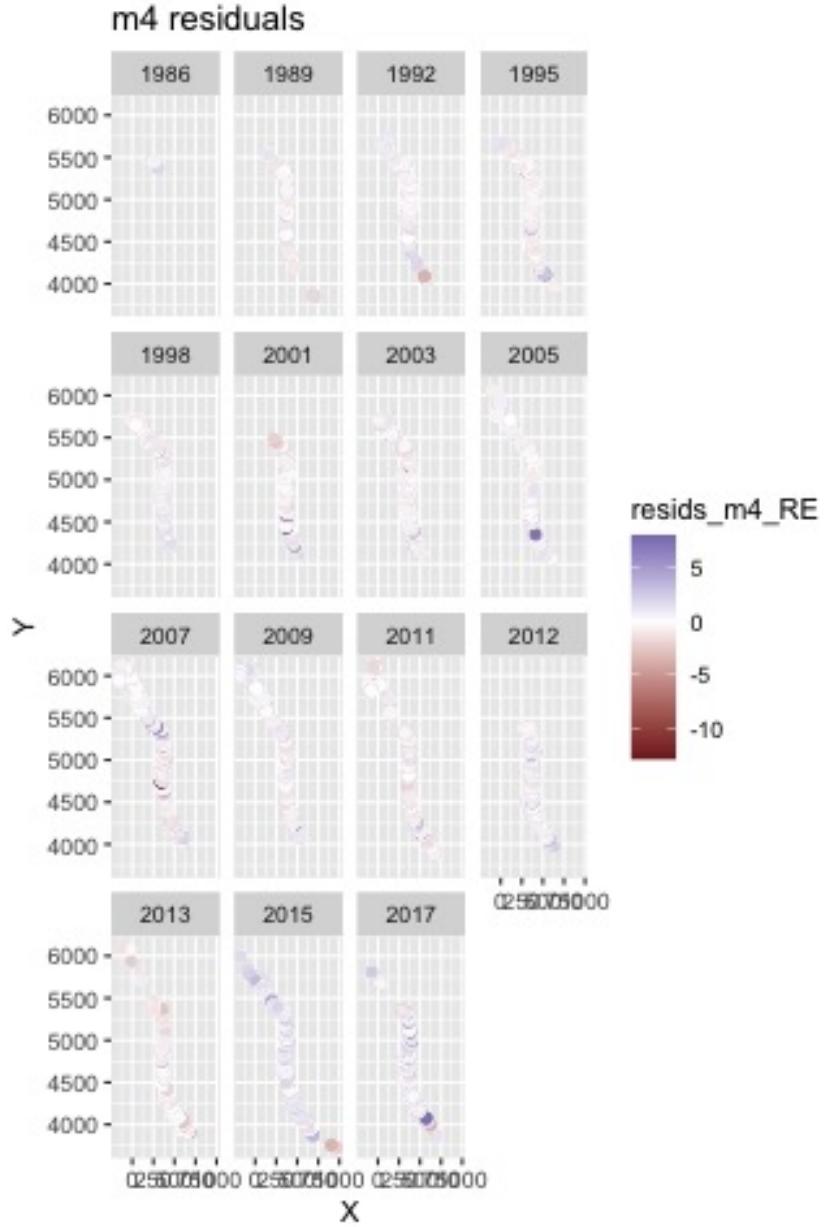
There are a few ways to include time-varying intercepts

- `as.factor(year)` I tried this and the model didn't converge very well
- `(1 | year)` I tried this as well and the model didn't converge very well

- time_varying = ~ 1 This one worked the best. It follows a random walk

`m4 = weight ~ 0 + s(new_age) + s(cohort) + catch_month with time-varying intercept`

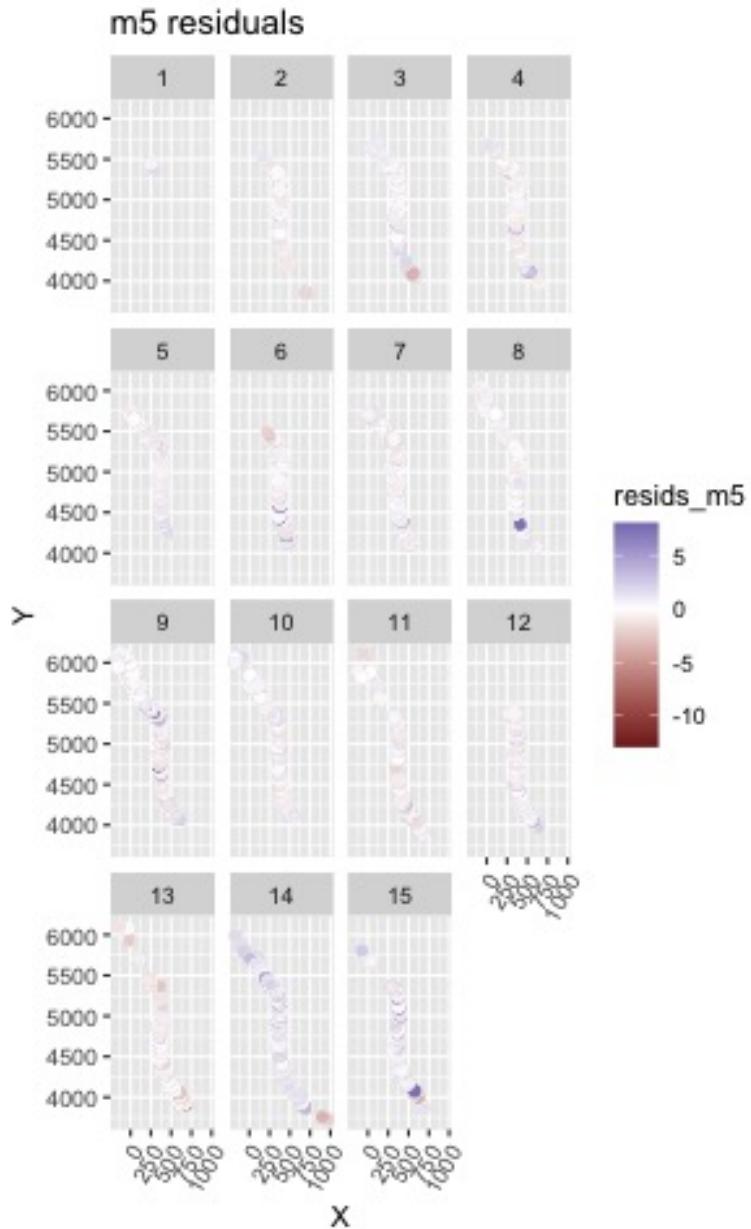
However, it doesn't look like it improved the residuals very much...



Could it be that one of the predictors is time-varying rather than the intercept?

I also tried including a smoother on catch_year in addition to the time-varying intercept and that doesn't seem to capture the differences in weight in 2013-2015

`m5 = weight ~ 0 + s(new_age) + s(cohort) + catch_month + s(catch_year) with a time-varying intercept`



Also tried a model that didn't include a smoother on catch year but instead created a separate slope for the smoother on new_age. I did this because I was hoping to capture the variability in more recent years that we saw in the observed weight at age in the north above.

Potentially include age as a time-varying slope to account for the changes in weight at age in more recent years? unfortunately can't include smoothers in the time-varying argument, but instead can use independent slopes for each year s(new_age, by = catch_year)

```
m6 = weight ~ 0 + s(new_age, by = catch_year) + s(cohort) + catch_month with time-varying intercept
```

This model did not converge (non-positive Hessian definite)

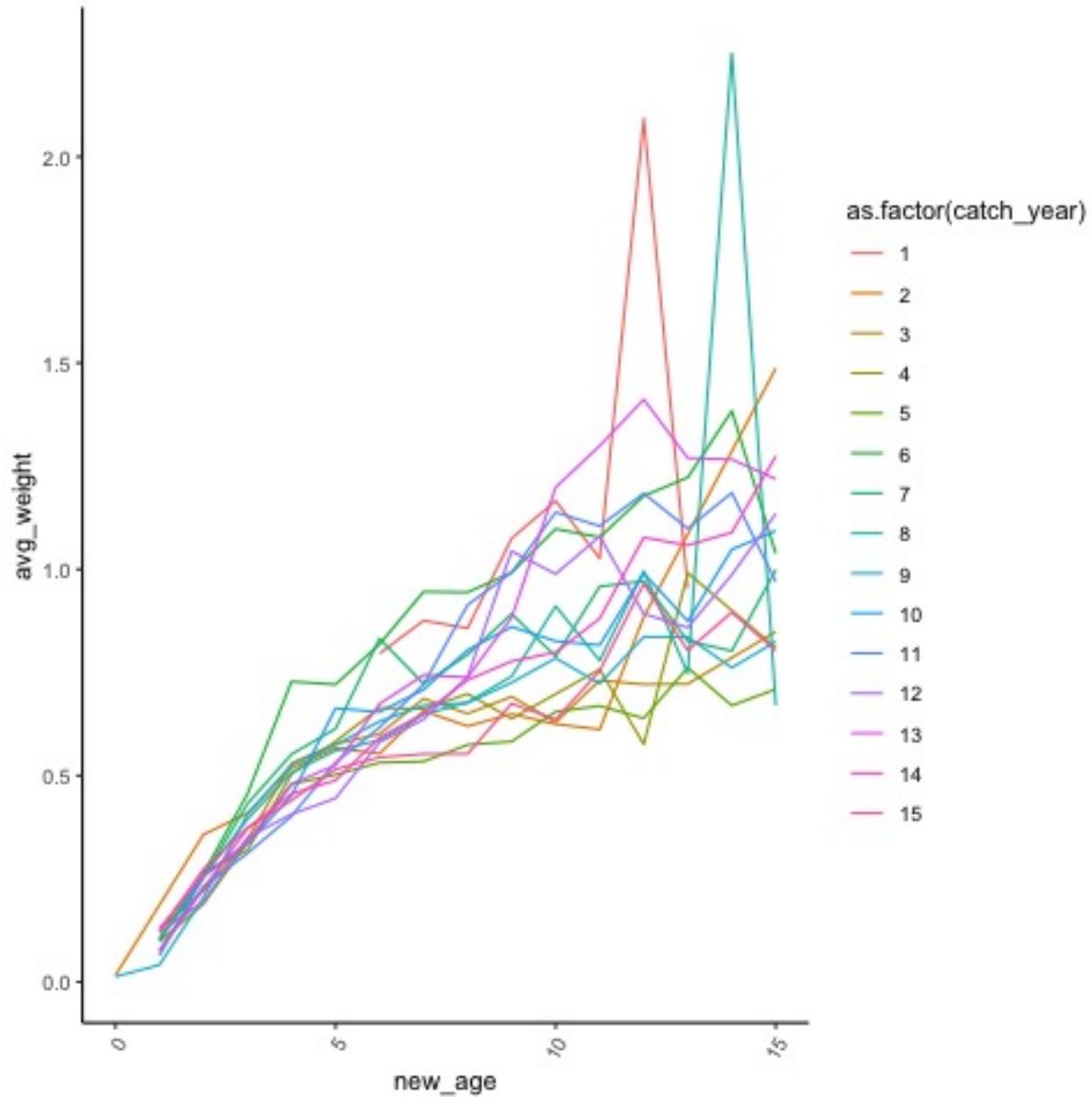
Tried removing the smoother on cohort,

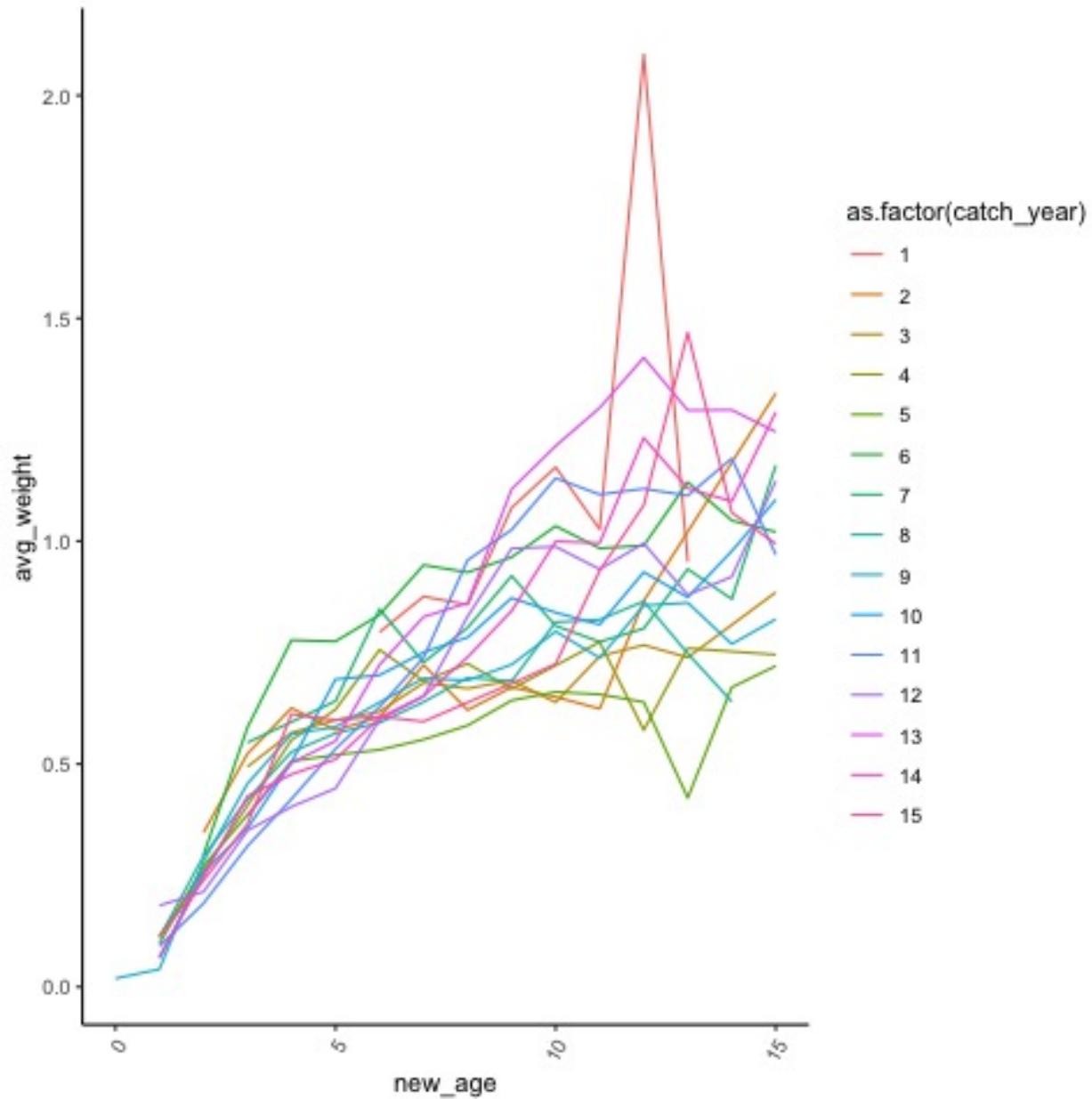
```
m7 = weight ~ 0 + s(new_age, by = catch_year) + catch_month with time-varying intercept
```

This model converged, but it still doesn't capture the residuals in the more recent years.

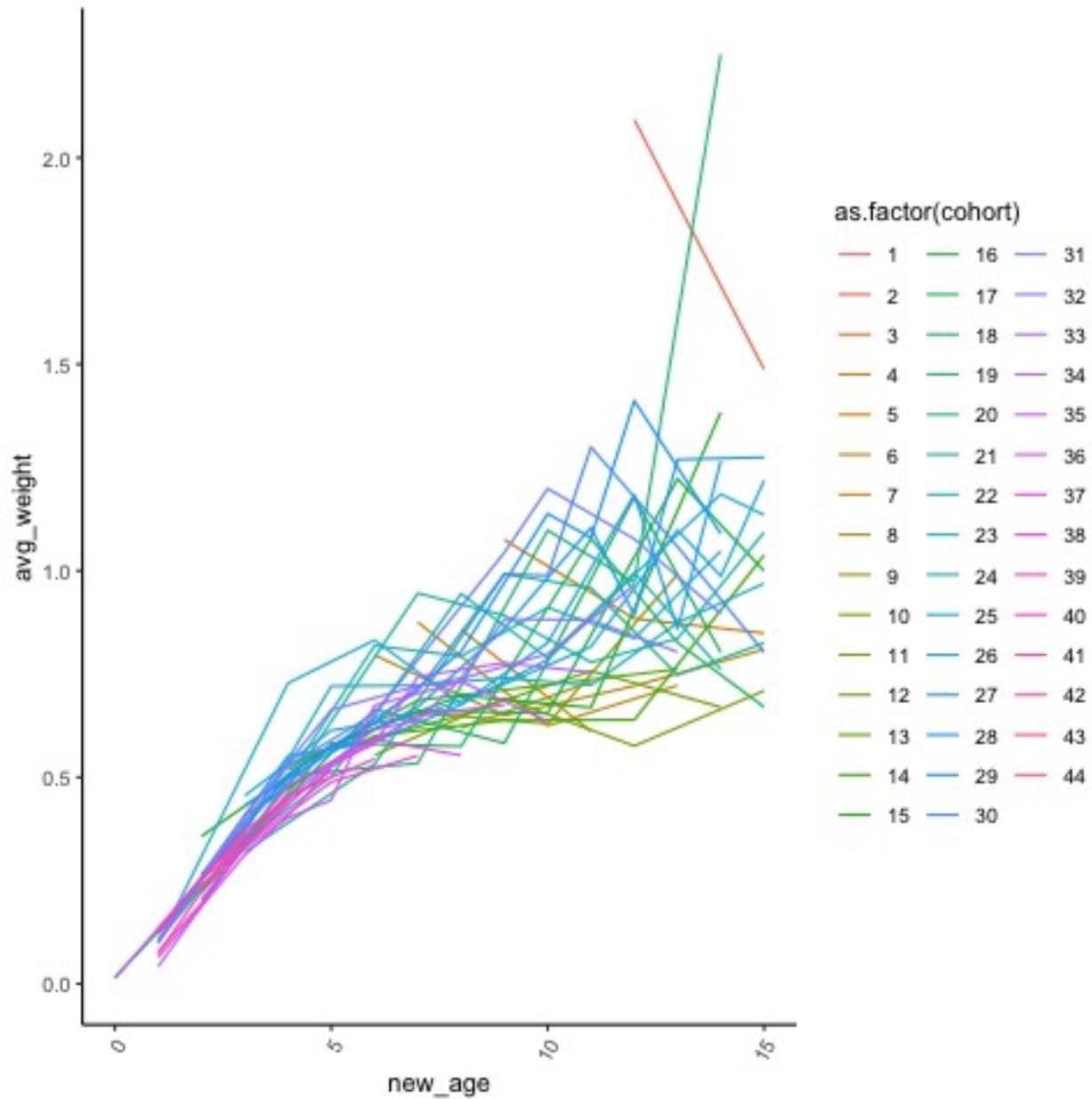
Also, realized the maximum residual is "Inf". I just don't think any of these models are doing too well, so I am stepping back and looking at the data once again.

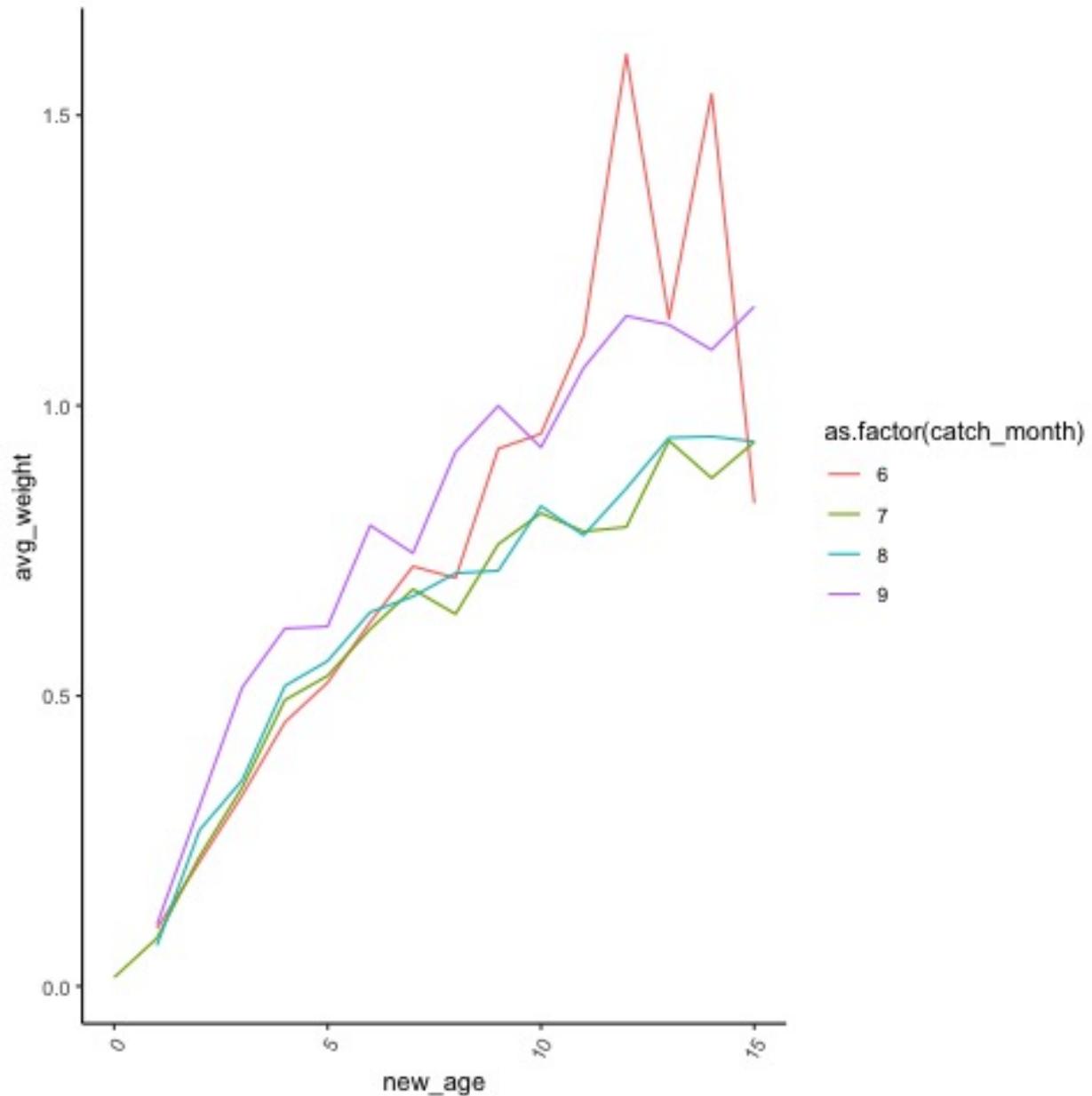
This first plot is weight at age curves by year. and the next one is just for the northern individuals.



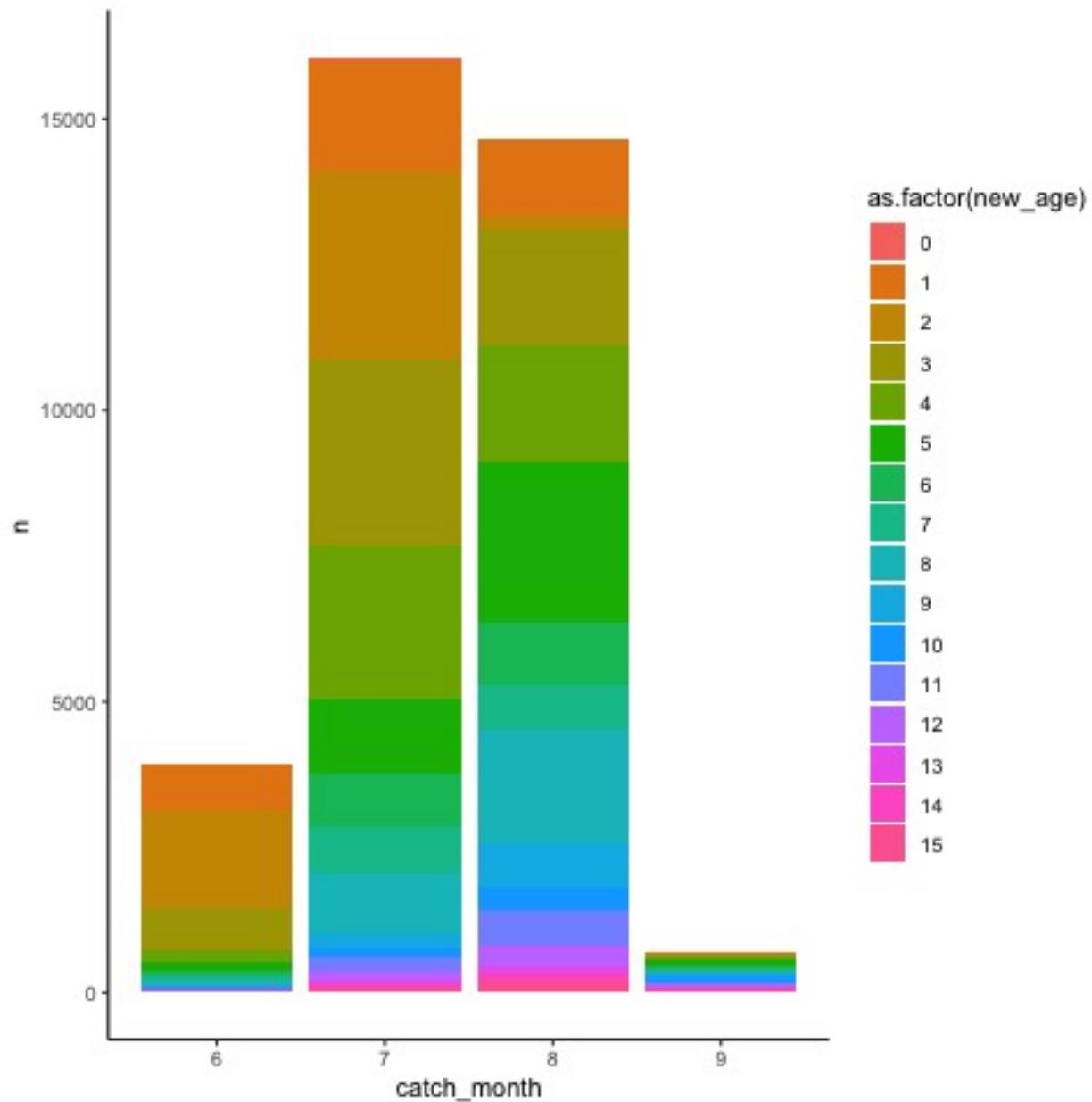


Then, by cohort

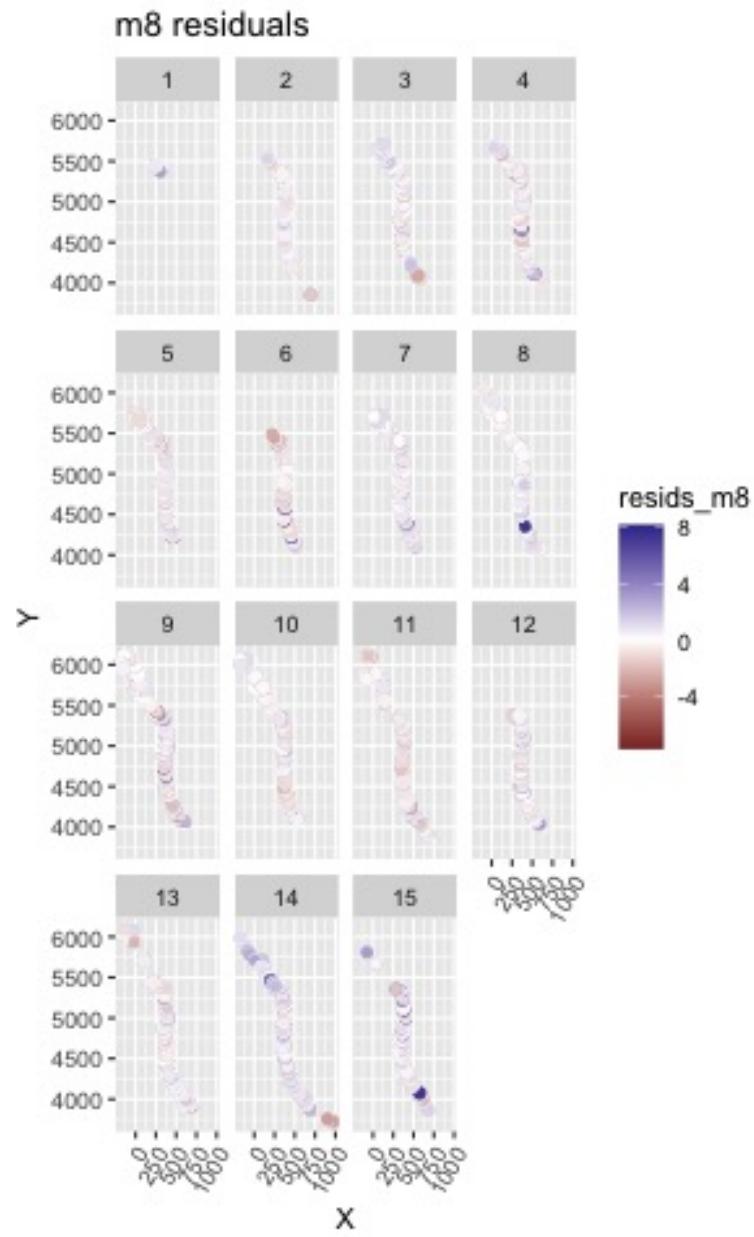




But as a caveat, here are how many observations of each age are sampled per month. Month 6 and 9 are very lightly sampled, so take with caution.

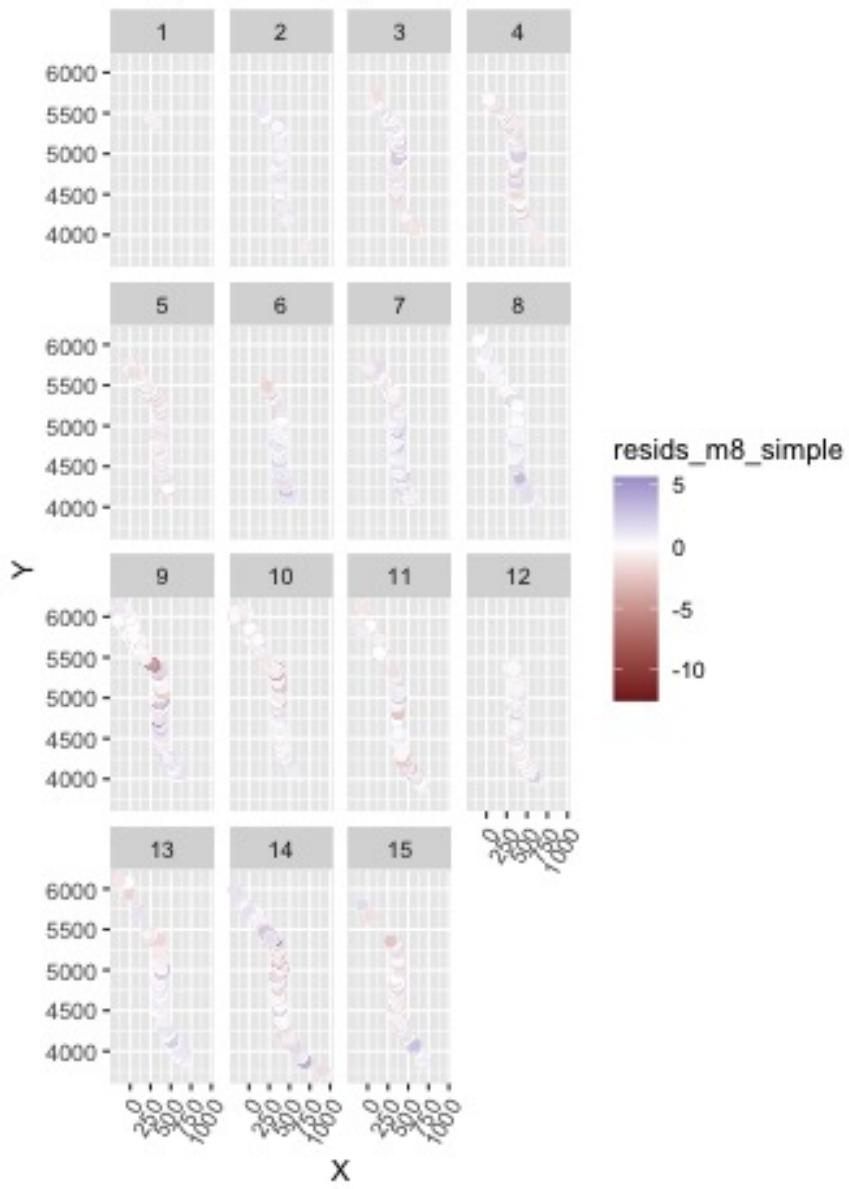


m8 = weight ~ s(new_age, by = catch_year) Just spatial (not spatiotemporal)



Okay, but even simpler, the spatial model with `weight ~ new_age` seems to minimize the residuals quite a bit.

weight ~ new_age as spatial model



Meeting with Kristin

- catch_month currently is a fixed linear effect, but the data tell us otherwise. Maybe best to consider it as a random effect
- Does it need the spatial part or the spatiotemporal part or either? - what are the temporal trends and potential covariates (qualitatively)
- standard deviation of the catch month random effect vs intercept, vs others to see how much those matter compared to the spatiotemporal.
- try to fit catch_month random effect, and then add the time-varying (but potentially confounded)
- sub-areas within a region - weight-at-age curve for canadian vs US
- fishery data - can't fit spatial model, but we know that the canadian fishery fishes in canada and the us fishery fishes in US, so we can at least have that spatial component (which for the MSE is relevant)
- malick - relationships with temperature.

Sept 12-16, 2022

Prior to this week, I have settled on a model `weight ~ 0 + s(new_age) + s(cohort) + (1 | catch_month) + (1 | catch_year)` and have tried three versions: spatiotemporal, spatial, and without random fields.

	df	AIC
m4.spatiotemporal	11	-84642.87
m4.spatial.only	9	-79002.06
m4.no.spatiotemp	7	-71673.21

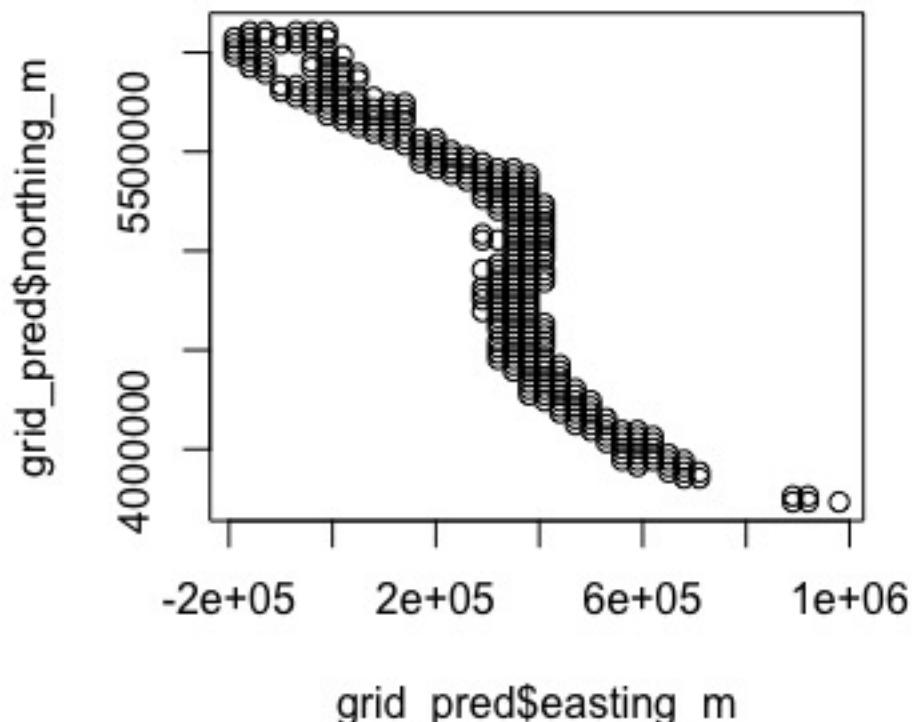
According to AIC, the spatiotemporal model was the best model. It also converged very nicely.

Questions for Kristin

1. how to make a mesh over the survey area?
 - plot the random effect levels for the `catch_month` -github action knit rmarkdown

Sept 19-23, 2022

Trying to learn how to create a spatial domain, following code that Malick provided (in the `malick_code` folder of the project).



I was able to make a spatial domain following Michael Malick's code, however, when I go to make predictions on those new data, an error pops up saying

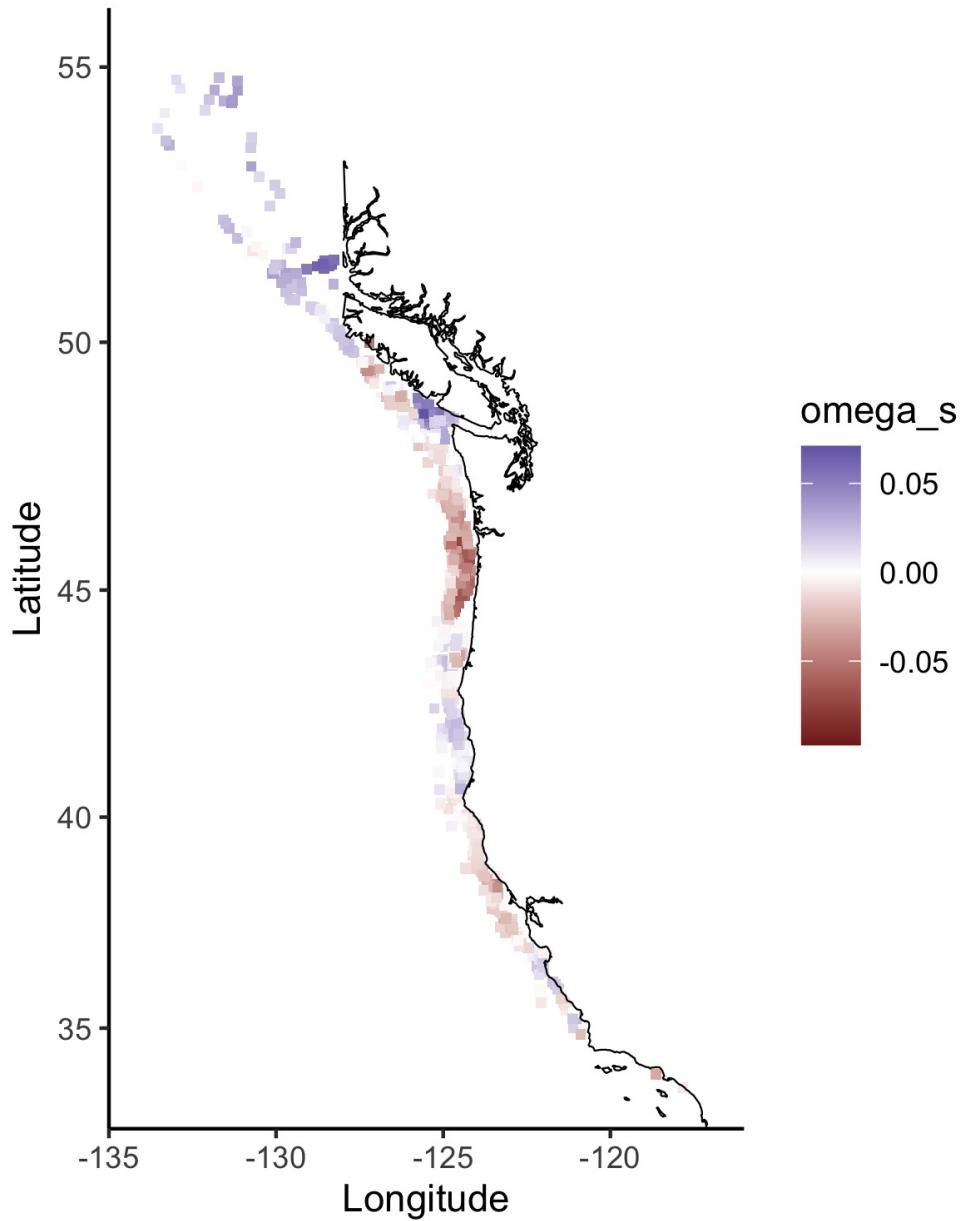
Error in vapply(RE_names, function(x) as.integer(nd[[x]]) - 1L, rep(1L, values must be length 4575, but FUN(X[[1]])) result is length 0

I tried reformatting the dataset, making sure that the UTM coordinates were aligned and that time was modeled (i.e. can't be considered as a factor class). Not entirely sure what else it could be. Either way, decided to continue making maps using the observed datapoints.

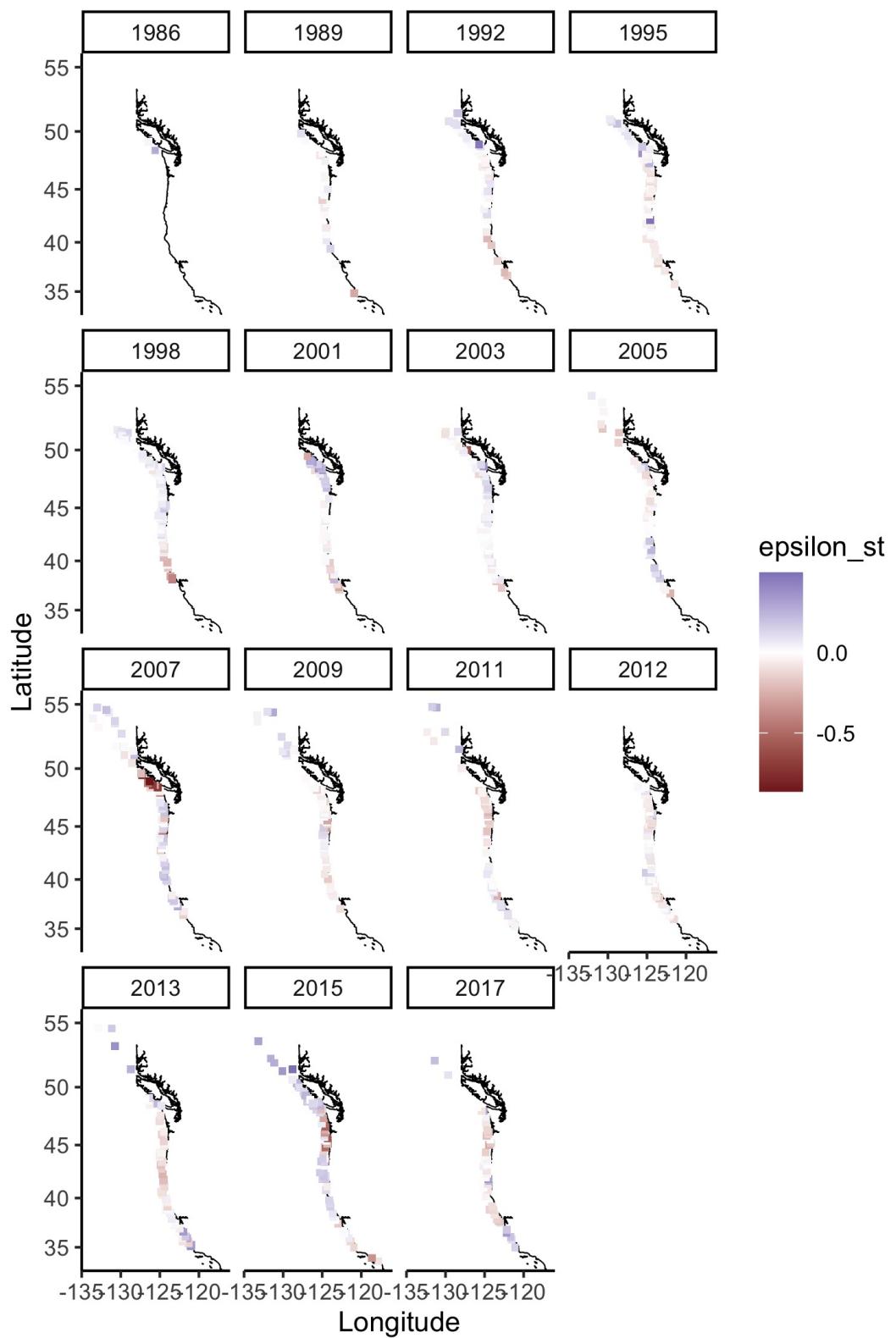
Because time needed to be modeled (not considered a factor class), I had to restructure my model. It still had spatial and spatiotemporal random effects.

`weight ~ 0 + s(new_age) + s(cohort) + (1 | catch_month)` with time-varying intercept (~1) following a random walk.

I overlayed some of the predictions over the map of the coastline and some interesting patterns arise, especially with spatial random effects.

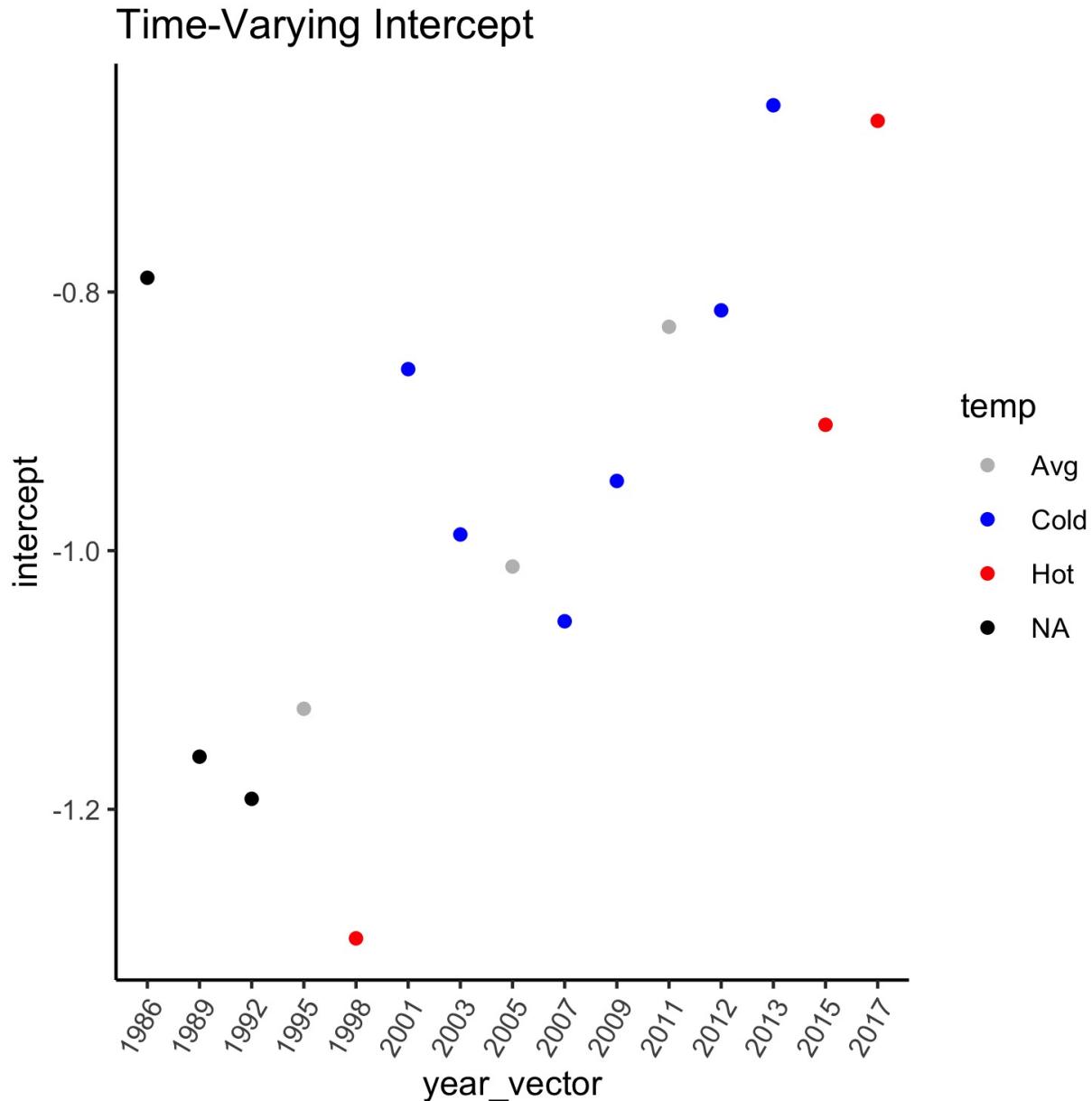


There is a very interesting spatial trend! It looks like the hake are lighter than average in areas nearby where freshwater meets the ocean (columbia river basin and san joaquin river basin) and a patch of heavier than average hake at the entrance (or exit?) of the strait of juan de fuca. Through quick search, it looks like there is a patch of greater primary productivity at the entrance of the strait of juan de fuca similar to where we see the patch of heavier than average fish (Davis, K. A., N. S. Banas, S. N. Giddings, S. A. Siedlecki, P. MacCready, E. J. Lessard, R. M. Kudela, and B. M. Hickey (2014), Estuary-enhanced upwelling of marine nutrients fuels coastal productivity in the U.S. Pacific Northwest, *J. Geophys. Res. Oceans*, 119, 8778–8799)



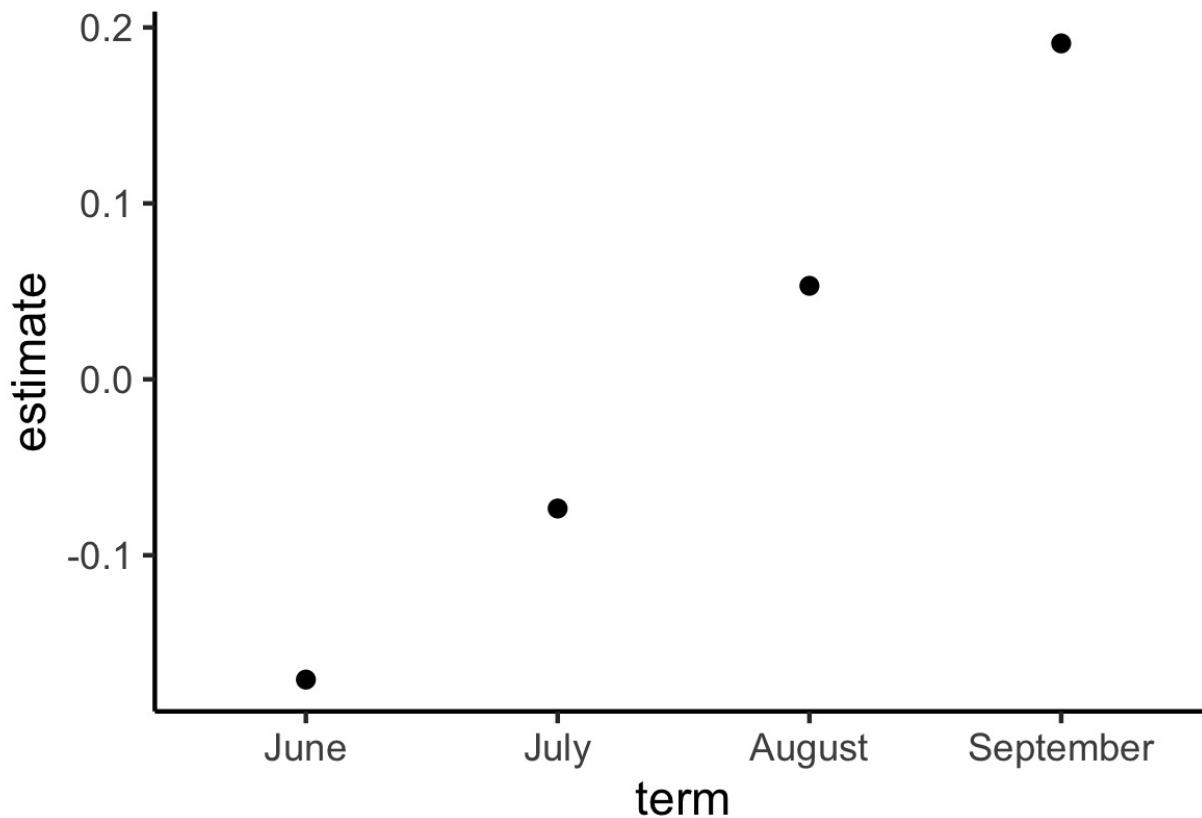
Sept 26-30, 2022

Looking at the time-varying intercepts, there is quite a clear temporal trend revealing pacific hake are becoming heavier than average! The information on temperature anomaly is pulled from Malick et al. (2020). The trend doesn't appear to be strongly tied to temperature, at least when visualized this way.



Malick et al. 2020 looked at whether the relationship between temperature and biomass remained stationary across life stages by splitting the data up into 3 age groups (age 2, 3-4, and 5+) and running the statistical model. Potentially something I can do...

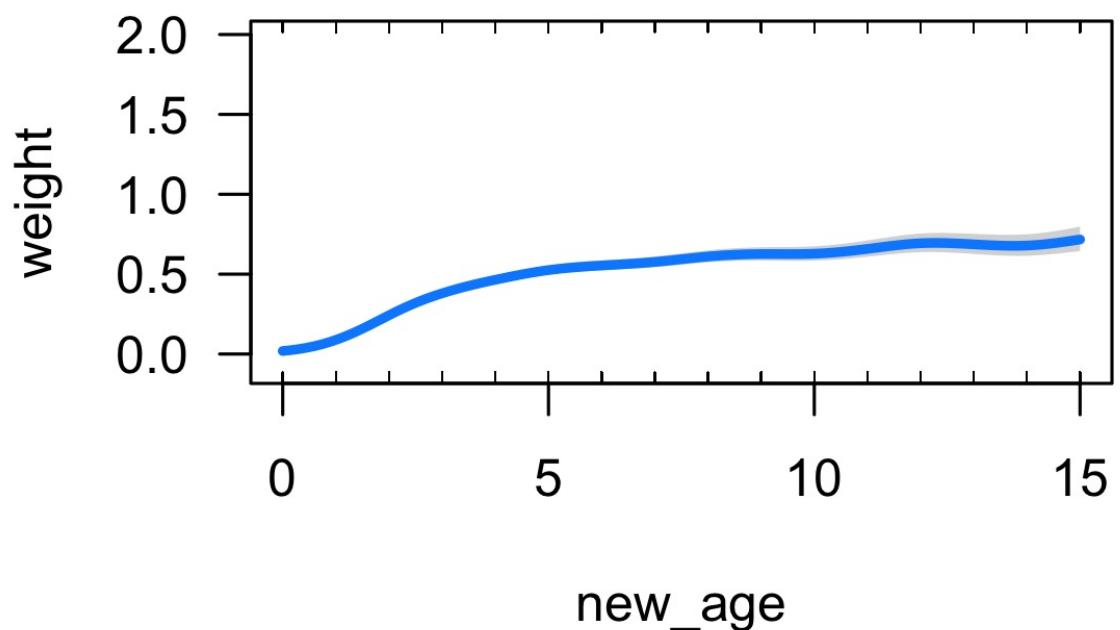
Month Time-Varying Intercept



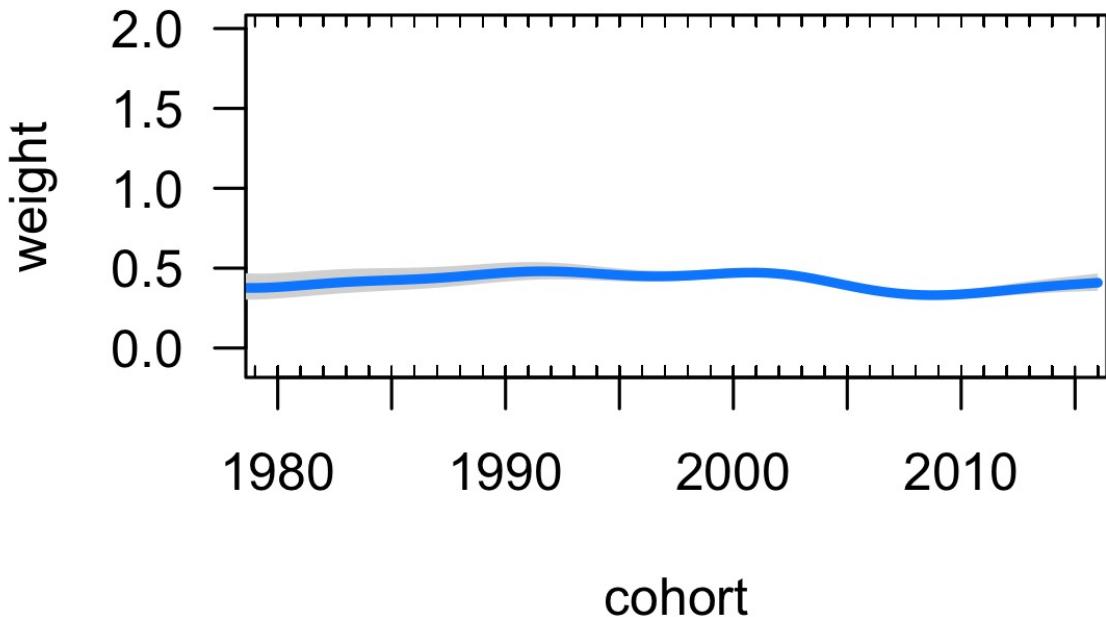
When looking at the varying intercepts associated with month, there seems to be a linear increase according to the model. Previously, when just visualizing the data, there was a nonlinear trend in weight at age between months so we decided to treat `catch_month` as a random effect. This could be the result of uneven sample sizes which is accounted for as a random effect in the sdmTMB model. Might be worth switching cohort back to being a linear effect.

GAMS

weight-at-age smoothed function - scale



cohort smoothed function



The linear component of age is positive (~ 20) and the linear component of cohort is negative (~ -5). With age, that checks out (weight should be positively associated with age), but it seems as though there is a negative trend with cohorts - so more recent cohorts are trending lighter than average when compared to previous cohorts. This is interesting to think about in conjunction with the time-varying intercept, where hake are trending heavier than average through the time-series. However, there is greater uncertainty in more recent cohorts because of fewer years available to estimate weight-at-age. The standard deviation of the weights for each smoothing function is greater for age than for cohort, which I interpret as the extent of wigginess.

After realizing that `catch_month` has a linear effect on weight, I reran the model with `catch_month` as a linear predictor `weight ~ 0 + s(new_age) + s(cohort) + catch_month` with time varying intercept. I ran two versions of this model: spatial + spatiotemporal (m4.2) and just spatiotemporal (no spatial; m4.3). I did this because the spatial standard deviation (`omega_s`) was fairly low compared to the spatiotemporal standard deviation (`epsilon_st`) and one of the vignettes mentioned not to run a spatial model when the spatiotemporal SD was much larger than the spatial SD. When I ran those two new models, the AIC indicated that m4.2 was the best model, m4.3 was <1 AIC value larger so there wasn't too much of a difference but this model had a few errors when looking at model diagnostics. The original model I was using where `catch_month` was a random effect was ~15 AIC values greater than the other models.

The only change that occurred in the outputs/coefficients when switching `catch_month` to a linear predictor was that the coefficient values for the time-varying intercepts shifted to smaller numbers, but the trend remained the same. Everything else remained the same and instead `catch_month` has a linear effect of 0.13.

Things to remember

- Cohort effects - is there density dependence? i.e. in years with high recruitment and consequently more

competition for resources, do those cohorts remain lighter than average?

- Pacific Hake also have spatial structure (larger, older fish travel more northward) - be mindful of how that might influence what we see. Is that captured in the spatial sd? or in catch_month (which is associated with space because sampling occurs more northward each month)

Model Validation? - AIC - well-documented biases with mixed effects models - k-fold cross validation (<https://pbs-assess.github.io/sdmTMB/articles/cross-validation.html>) - tmbstan package to sample from joint posterior, evaluate accuracy of laplace approximation or perform posterior predictive checks - residuals: MCMC avoids statistical issues but is slower - simulate.sdmTMB() can simulate from fitted models and sdmTMB_simulate() can simulate entirely new data to ensure identifiability, evaluate bias and precision in estimates, or evaluate consequences of model misspecification.

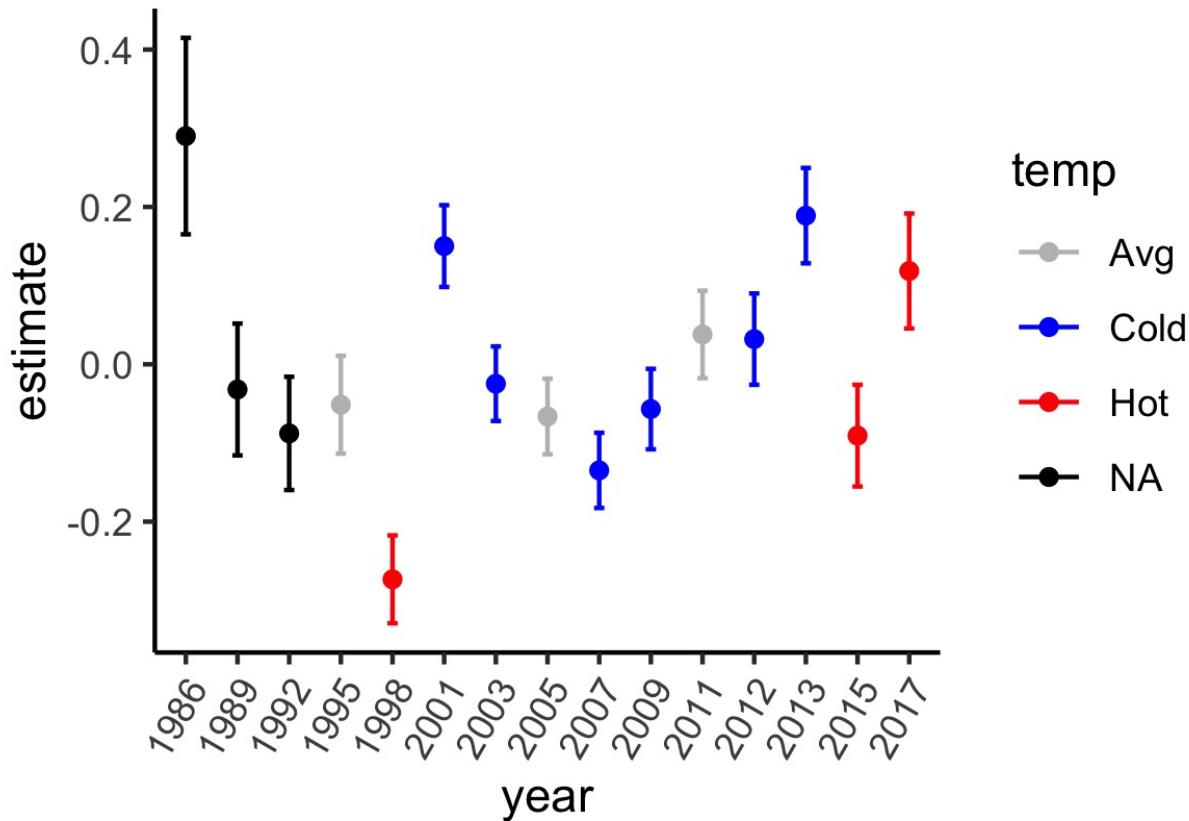
There are also codes for each ship that sampled. It looks like there are 6 unique ship codes. Might be worth including ship_code as a covariate to account for ship-ship variation?

In terms of predicting over the spatial domain, the reason it is not working right now is because each spatial coordinate is being predicted by all of the years, months, cohorts, and ages. What might need to be done is instead figure out potential drivers for spatial variation which could be included into the model, so the predictors only have one value at each spatial coordinate.

Notes for Meeting with Kristin - negative time-varying intercepts - Intro to sdmTMB vignette also has time-varying coefficients that are all negative. I also kinda wonder if this has something to do with how they are calculated. In the output, it shows (Intercept)-1991 as the parameter name, so is it subtracting from the “current” year? - Originally I have the intercept as a time-varying parameter (random walk), but I tried other ways to vary the intercept - `as.factor(catch_year)` (i.e. IID) - did not converge - `(1 | catch_year)` random effect

When we assume catch_year is a random effect

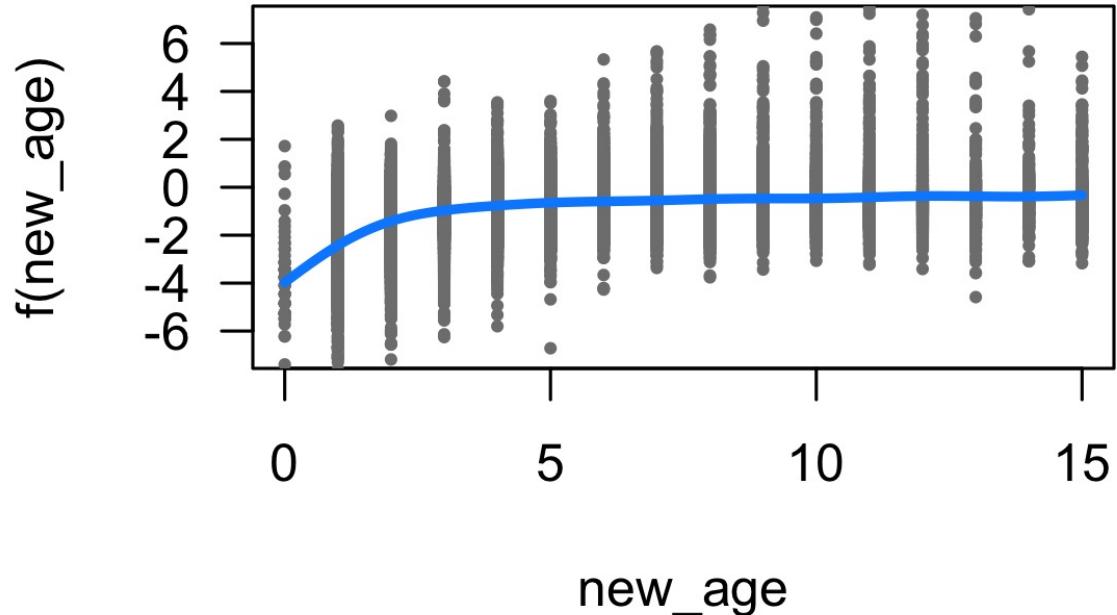
catch_year as random effect



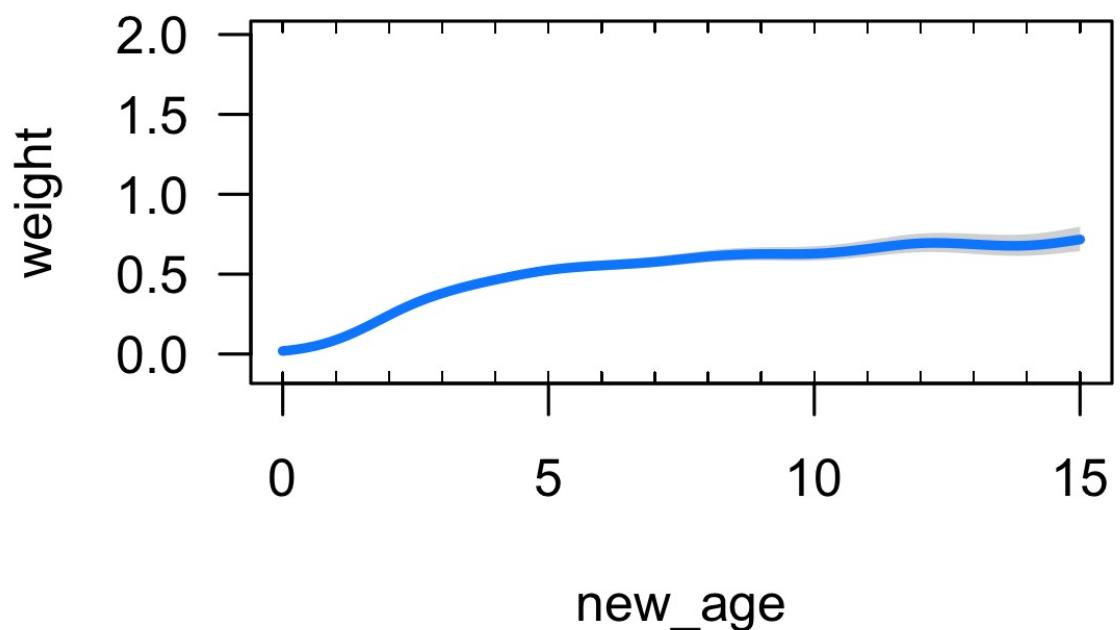
So, I think the question is, should we assume time as a random effect or as a random walk? The reason why I switched to time as a random walk is because in order to make predictions, “time needs to be modeled” (i.e. not a random effect)

For the GAMs, I scaled them according to the response variable “weight” because I thought that would be easier to interpret. Below are both the scaled and unscaled GAM plots. I reran these plots using the newest model with catch_year as a random effect

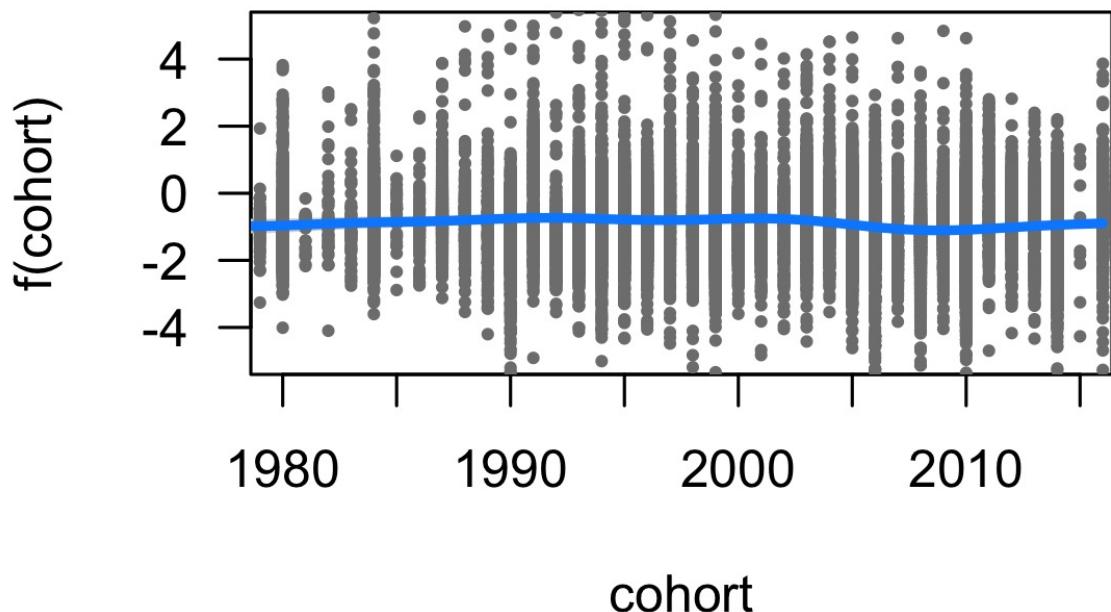
weight-at-age smoothed function



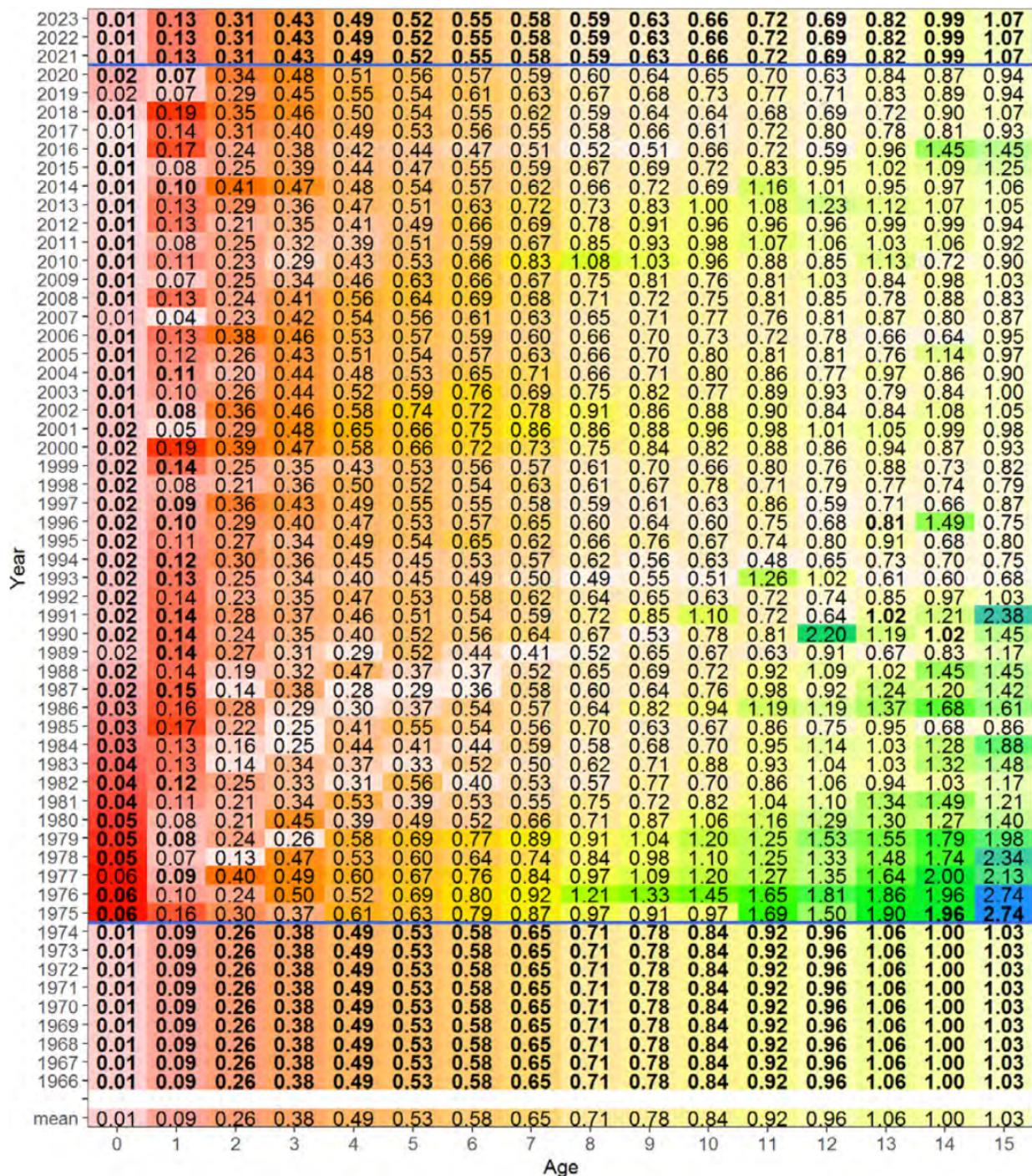
weight-at-age smoothed function - scale



cohort smoothed function



Oct. 24-28, 2022



This is a clear example of the sensitivity of weight at age matrix to the data quality used to generate it. The opaqueness of the colors indicate the relative size, such that more translucent fish are lighter than those more intense colors. In those early years (late 70s), the matrix indicates the weight at each age are relatively heavier than recent years. **HOWEVER**, this is a direct result of the sampling that occurred in that year (primarily speaking about 1976 survey). The sampling occurred largely in northern Washington and Canada, where my preliminary spatial exploration of weight trends indicates is where heavier hake tend to reside.

This leads to an overestimation of weight at age for those years and the surrounding ages and years where missing data are interpolated.

Nov. 2022 - Jan 2023

During this time I was working on the NMFS-SG Joint Fellowship Application

Feb. 2023 - Jul. 2023

During this time I was focusing on my Qualifying Exam and Chapter 1 of my dissertation
I was then awarded the NMFS-SG Fellowship!

August 2023

Notes from meeting with Kristin 08/02/23

- Something to consider: Having age, year, and cohort within the same model may be confounding.
Might need to pick just 2 covariates since cohort is a function of age and year.
- Next Steps:
 - Run models with age as a required covariate (because we are dealing with weight-at-age) paired with either cohort or year. Do this without spatial or spatiotemporal random effects. Determine best fit model
 - Add spatial and/or spatiotemporal random effects to the best model.
- Still waiting on data from more recent years and the fishery-dependent data. Kristin is putting in a request for that.
- Thoughts on PICES presentation
 - 3 solid results figures
 - What's next - could be discussed as part of context or at the end
 - Think about environmental covariates

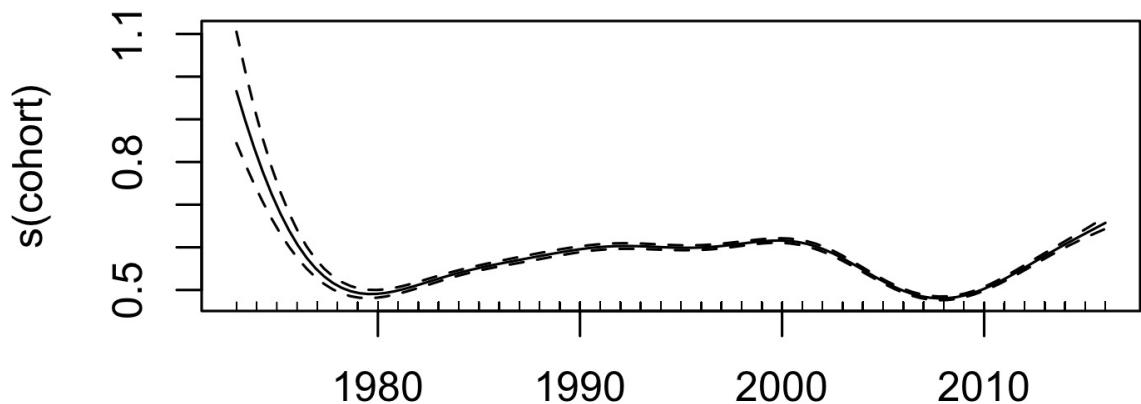
I continued to work in the sdm-TMB.r script. I created a new section titled **Pairwise covariate model exploration** where I begin the model exploration Kristin and I spoke about (see notes above).

I am starting out with 3 main model configurations before incorporating the spatial and spatiotemporal random effects. This includes:

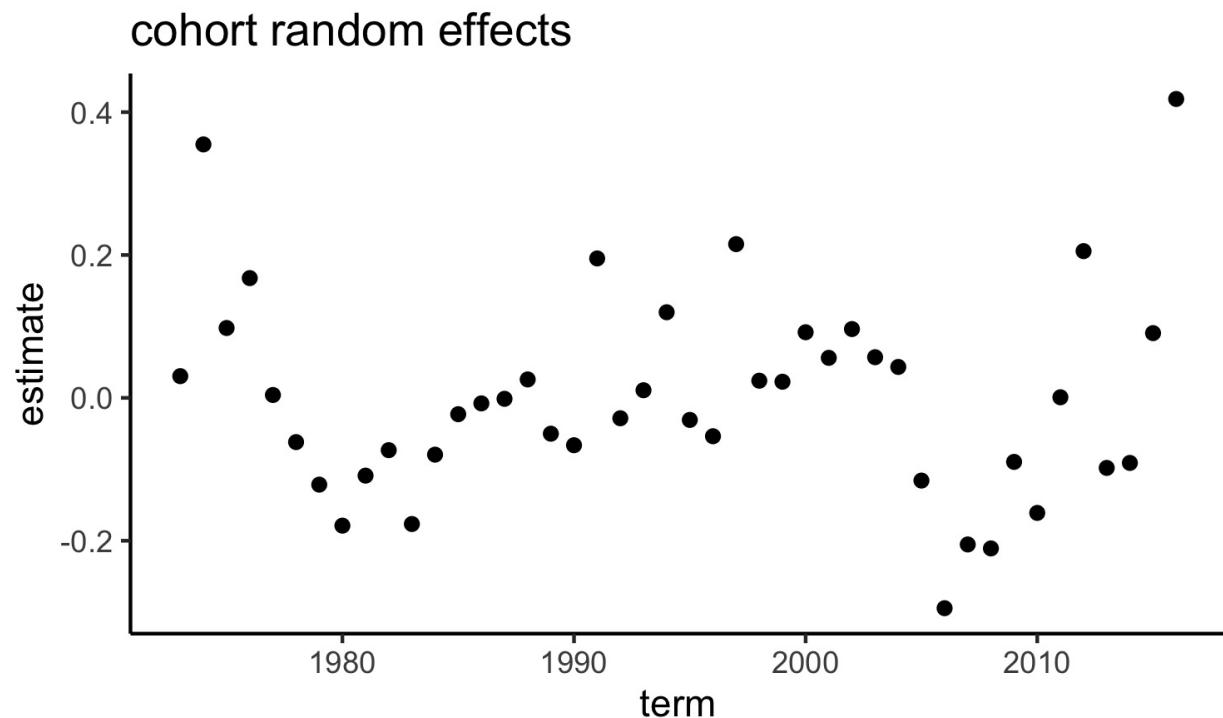
1. `m_age <- weight ~ s(age)`
2. `m_age_cohort <- weight ~ s(age) + cohort`
3. `m_age_year <- weight ~ s(age) + year`

For model 1, I tested the fit to a lognormal link log and a gamma link log. The lognormal link log was a better fit according to AIC which was the case in previous model iterations.

For model 2, I tested the fit with a smoother on cohort and cohort as a random effect. The random effect model was a better fit according to AIC (>3000). However, to me it makes more sense to have cohort as a smoother since the effect on cohort one year to the next might be correlated? Not sure. Maybe this data doesn't support that.

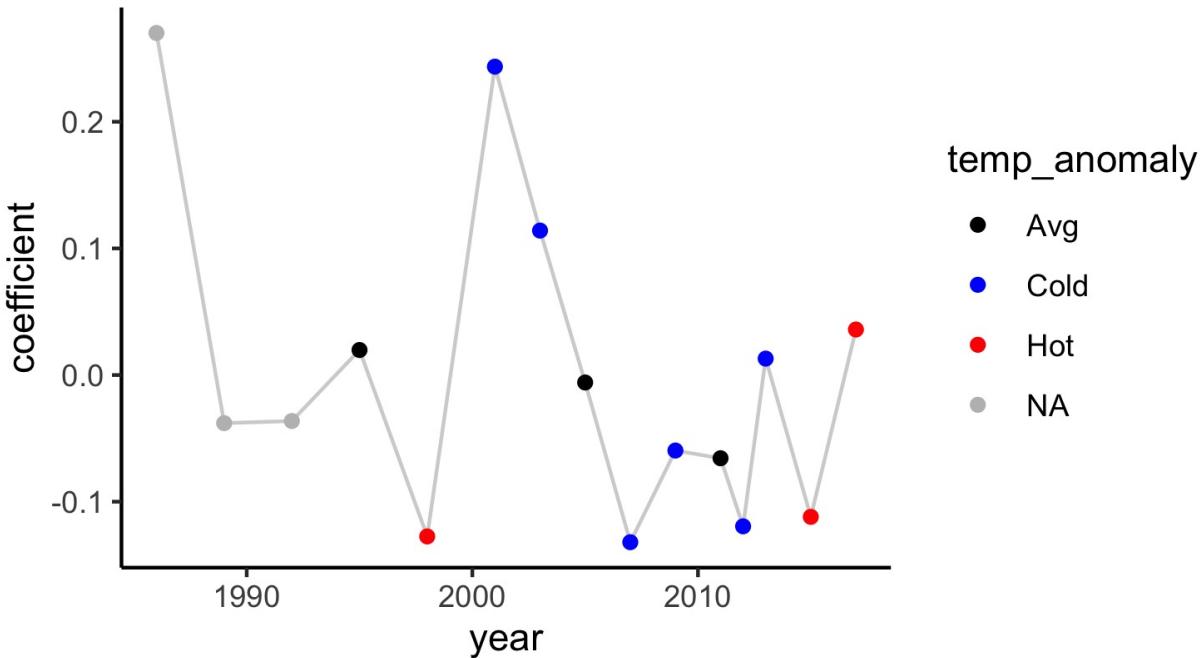


cohort

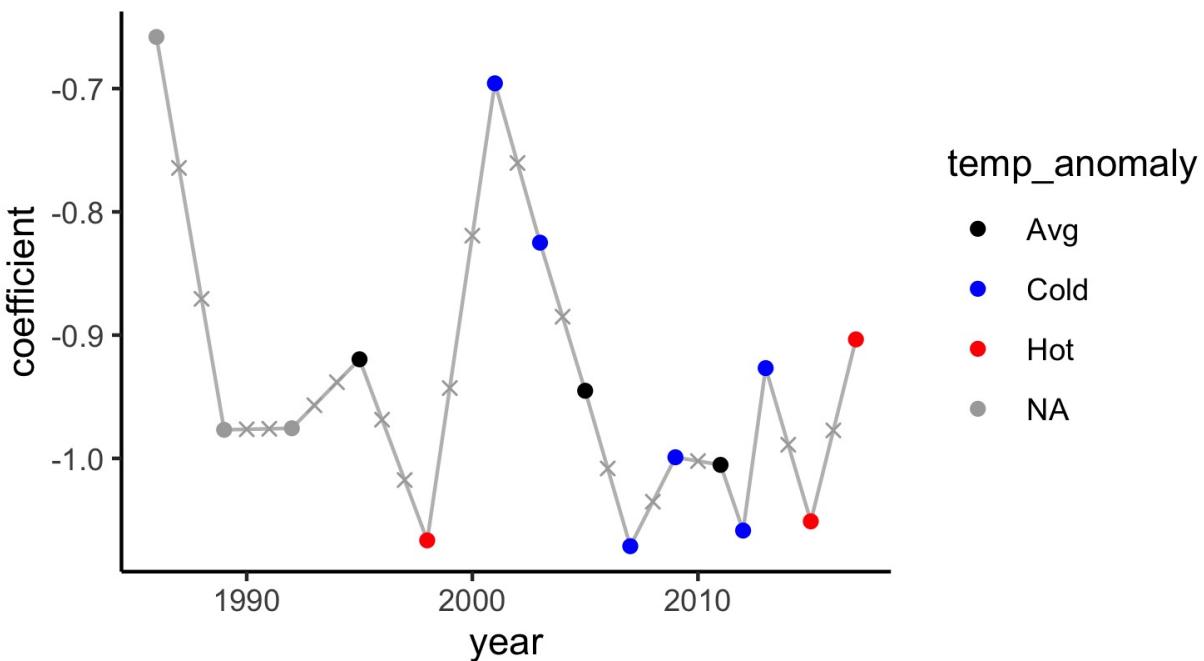


For model 3, I tested the fit with year as a random effect and as a random walk. The random effect model was a slightly better fit (5 AIC). However, I received a warning saying the models were not all fitted to the same number of observations. Couldn't quite figure out why that may be. It has to do with the year as random walk model and could potentially be because the random walk interpolates into the "extra time" (i.e years without data)

Year as Random Effect



Year as Random Walk



Between the five different models - $s(\text{age})$, $s(\text{age}) + s(\text{cohort})$, $s(\text{age}) + (1 | \text{cohort})$, $s(\text{age}) + (1 | \text{year})$, and $s(\text{age}) + \text{rw}(\text{year})$ - The $s(\text{age}) + (1 | \text{cohort})$ model was the best fit (>2000) followed by $s(\text{age}) + \text{rw}(\text{year})$, $s(\text{age}) + (1 | \text{year})$, $s(\text{age}) + s(\text{cohort})$, and $s(\text{age})$.

Adding spatial and spatiotemporal random effects

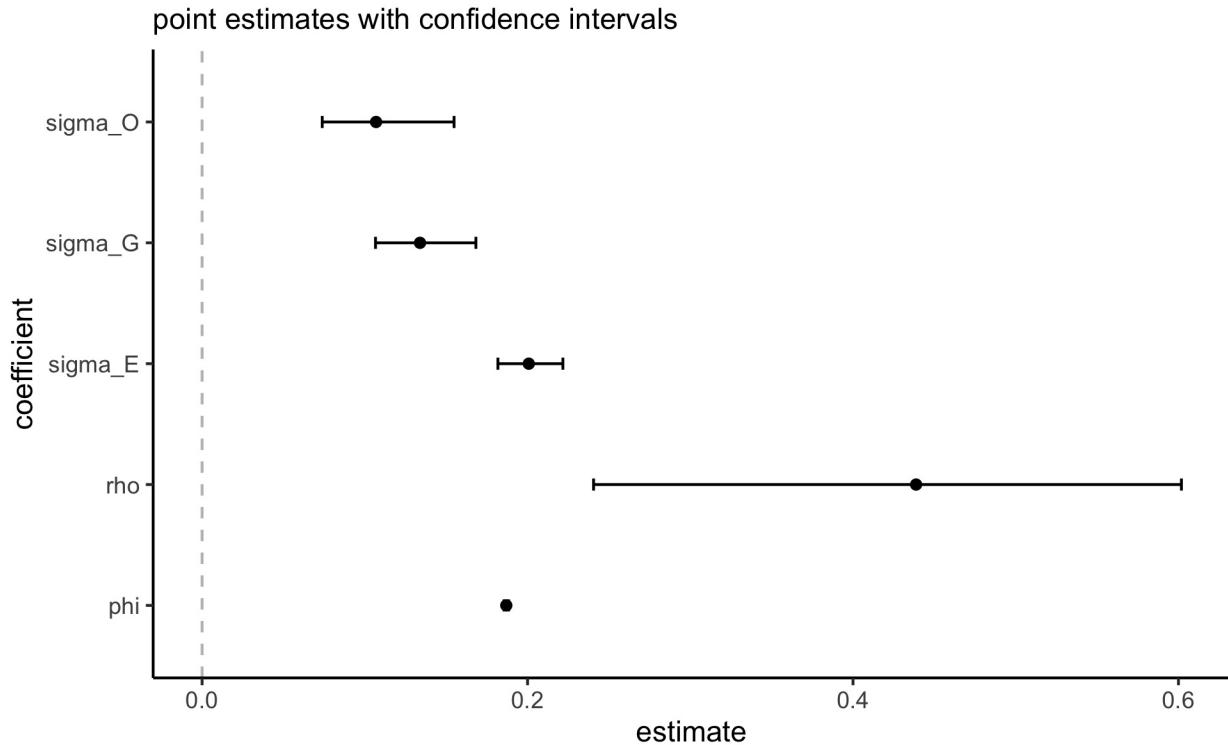
Since I have identified $s(\text{age}) + (1 | \text{cohort})$ as the best supported model, I will add spatial and spa-

tiotemporal random effects

1. $s(\text{age}) + (1 | \text{cohort})$
2. $s(\text{age}) + (1 | \text{cohort}) + \omega_s$
3. $s(\text{age}) + (1 | \text{cohort}) + \epsilon_{s,t}$
4. $s(\text{age}) + (1 | \text{cohort}) + \omega_s + \epsilon_{s,t}$

For the spatiotemporal models, I tested both IID and AR1 processes. Of these models, the model with spatial and spatiotemporal (AR1) random effects was the best fitting model.

Cohort as random effect



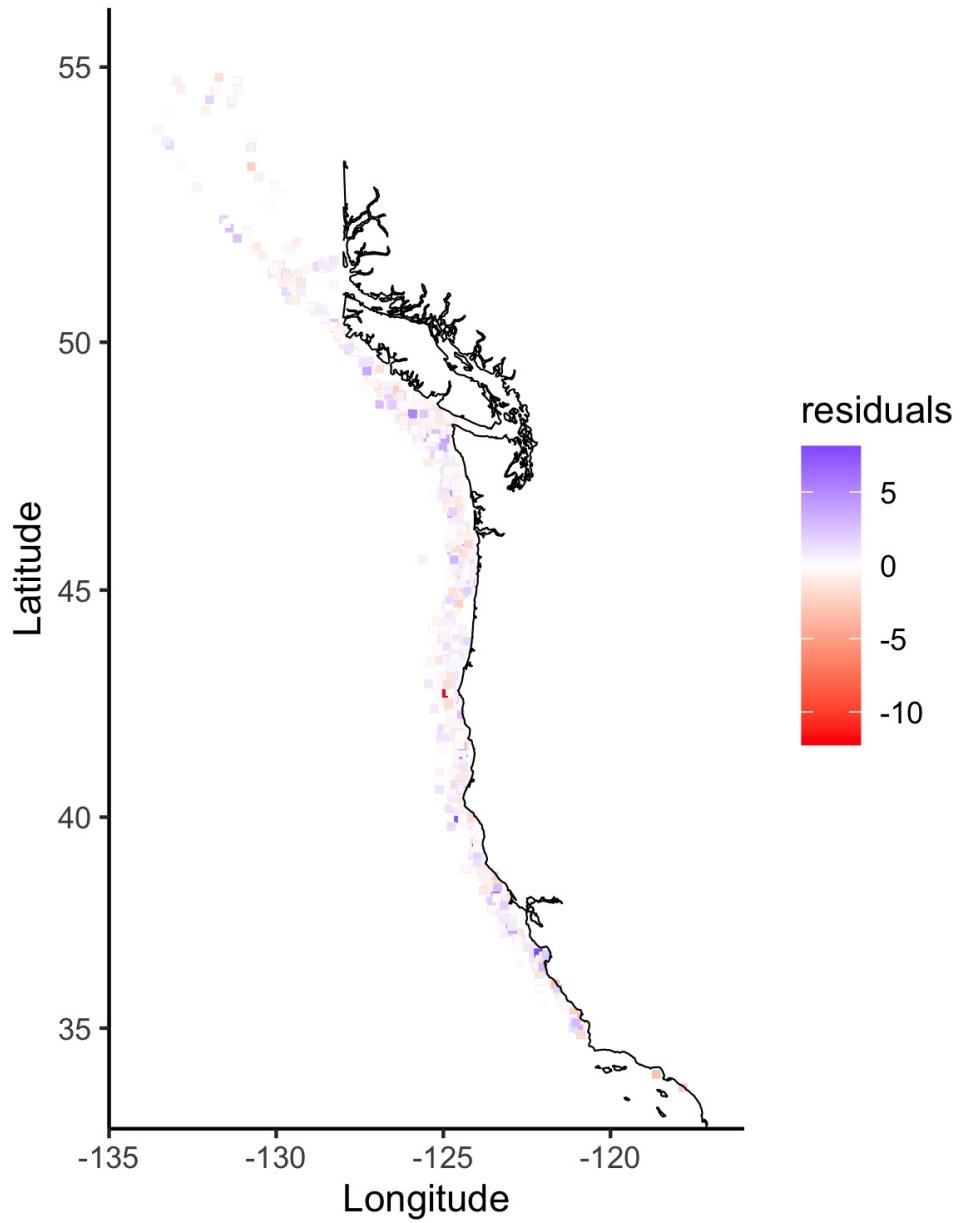
σ_O = spatial random field marginal variance

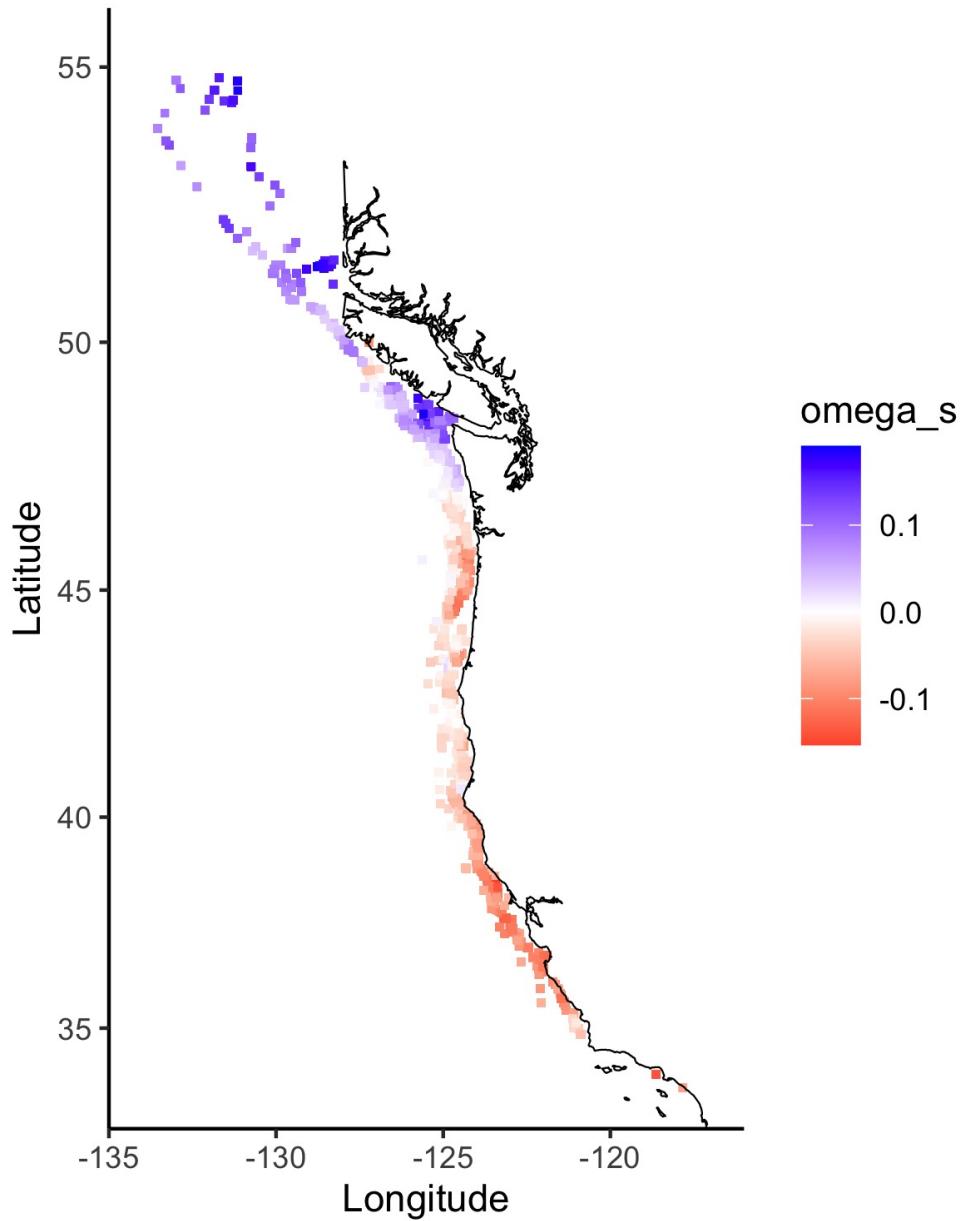
σ_G = IID random intercept variance (cohort intercepts)

σ_E = spatiotemporal random field marginal variance

ρ = spatiotemporal AR1 correlation

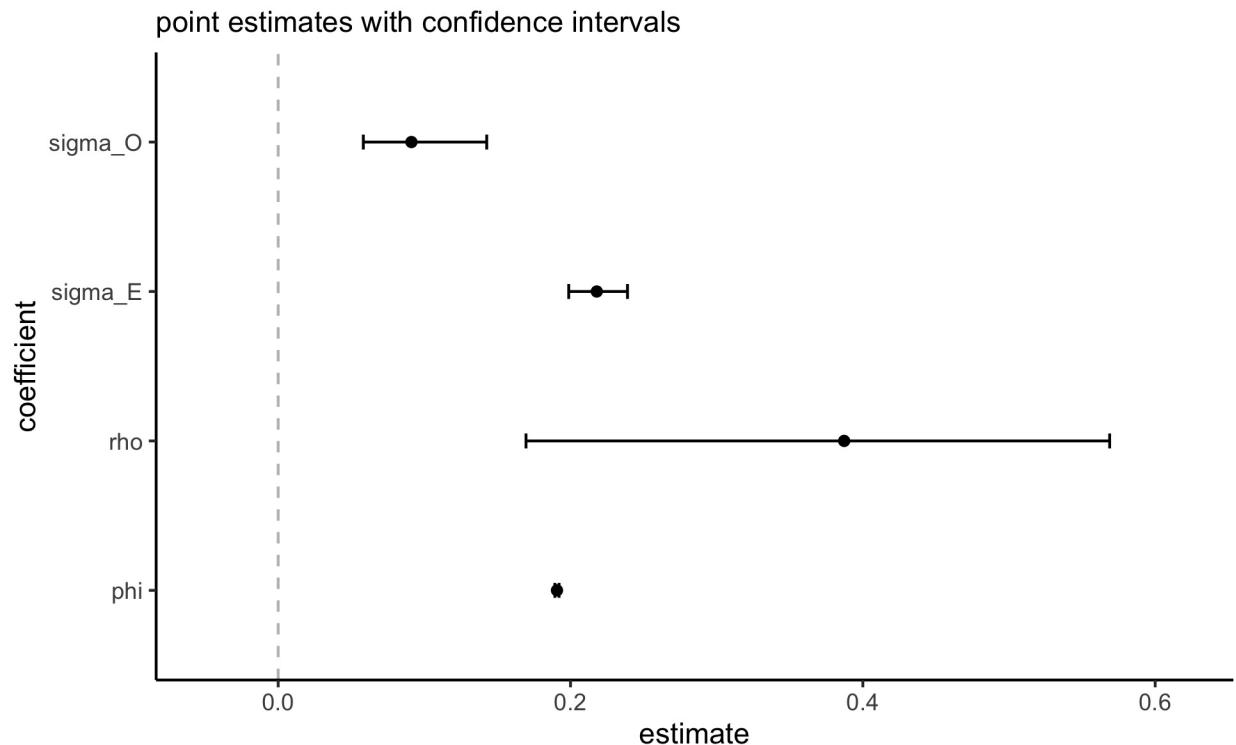
ϕ = dispersion parameter for lognormal distribution

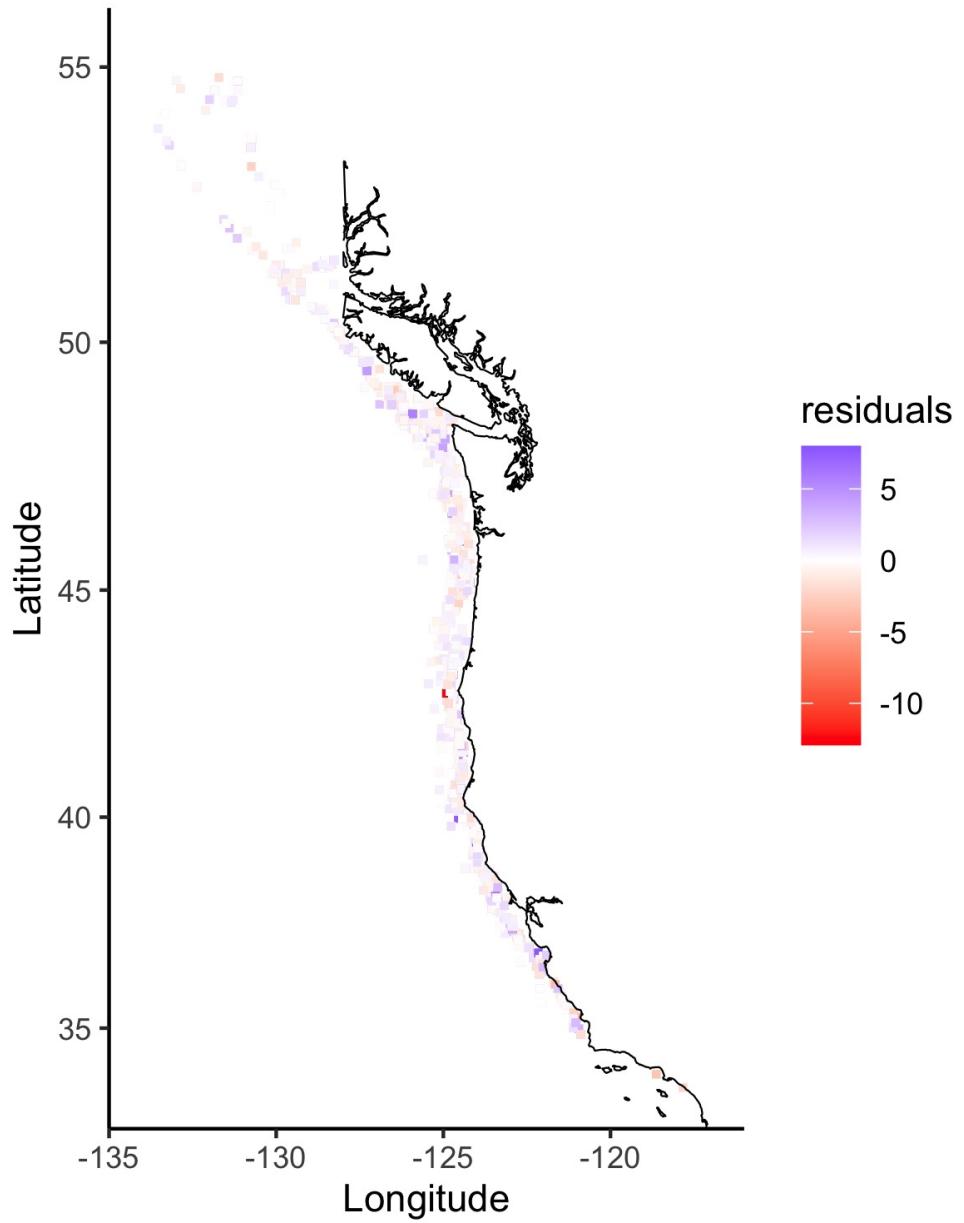


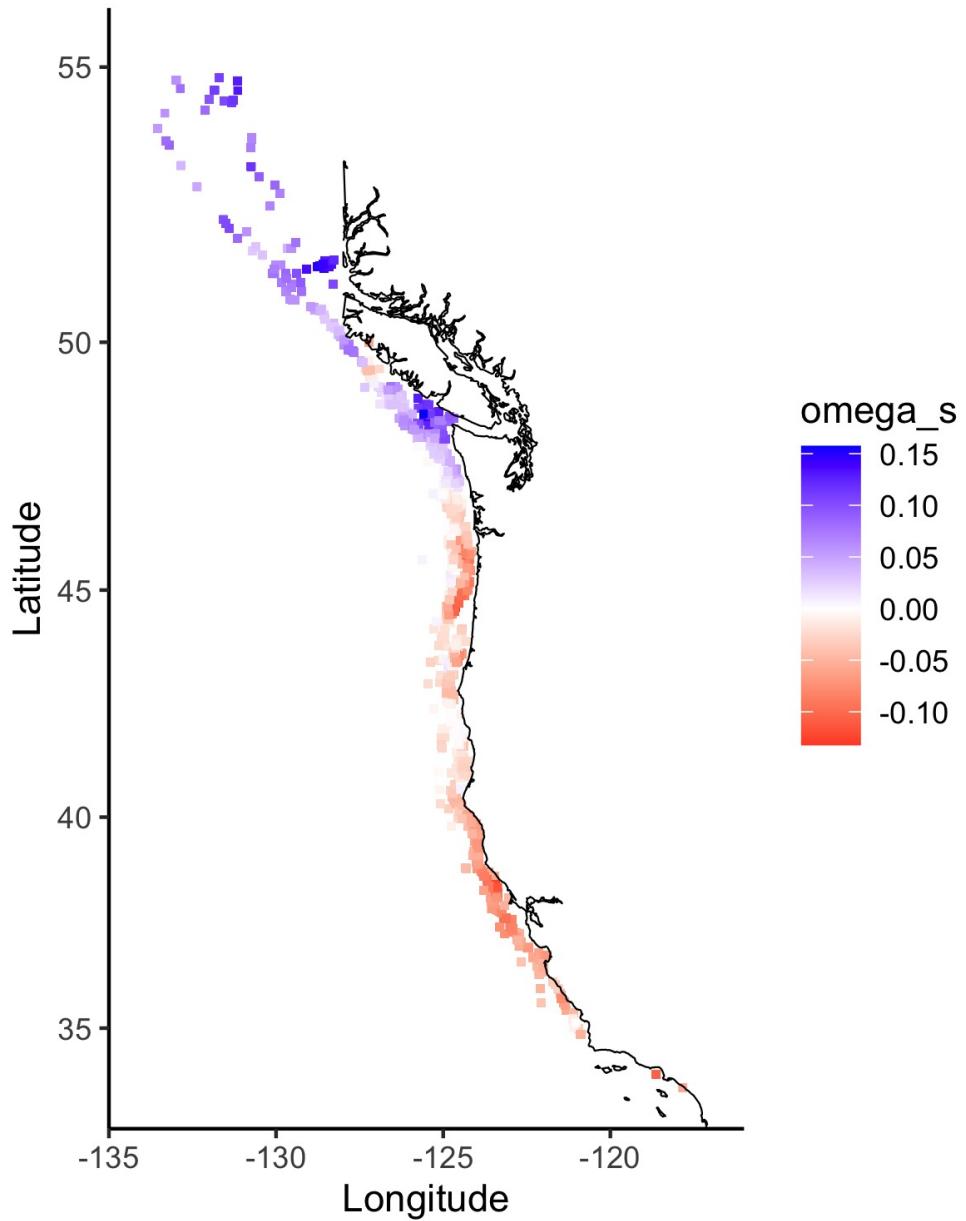


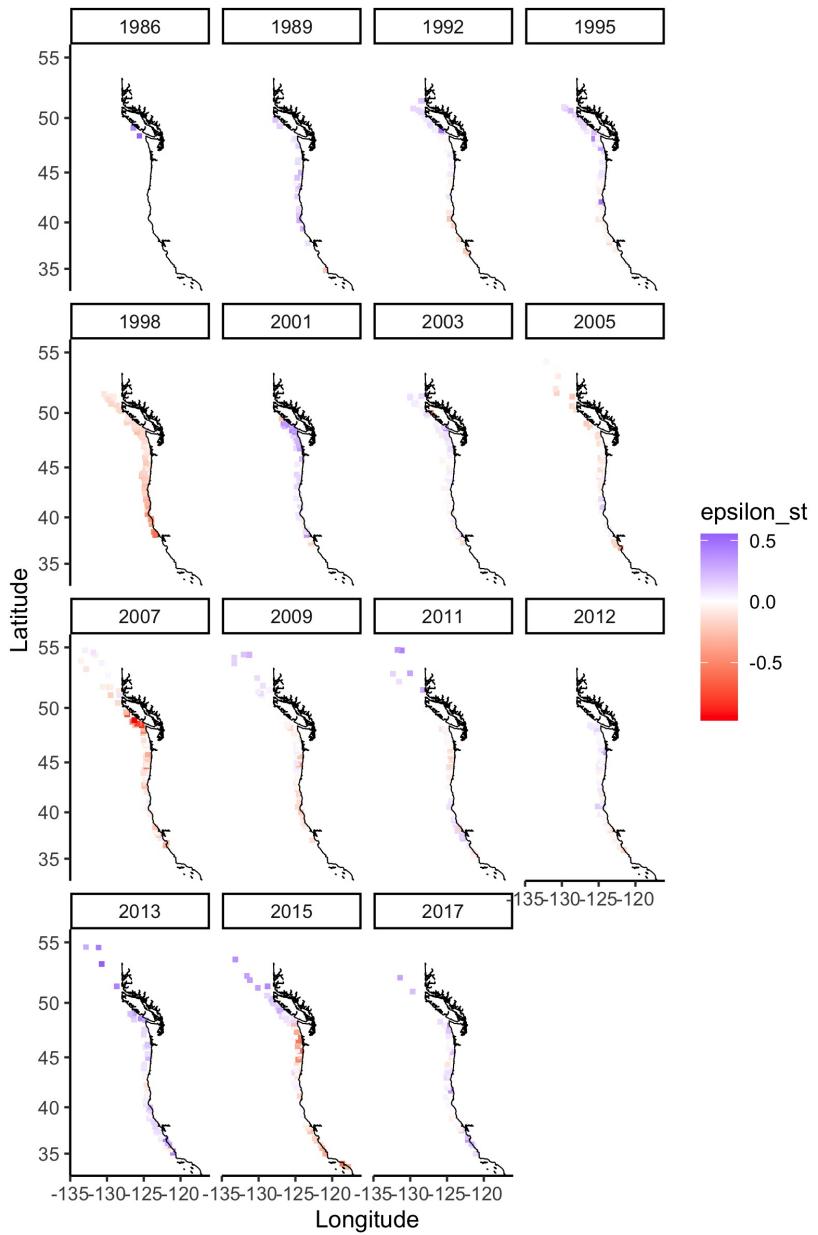
cohort as smoother

However, I wanted to explore the model that treated cohort as a smoother since we can expect the cohort effects may exhibit some autocorrelation.









Meeting w/ Kristin 08/22/23

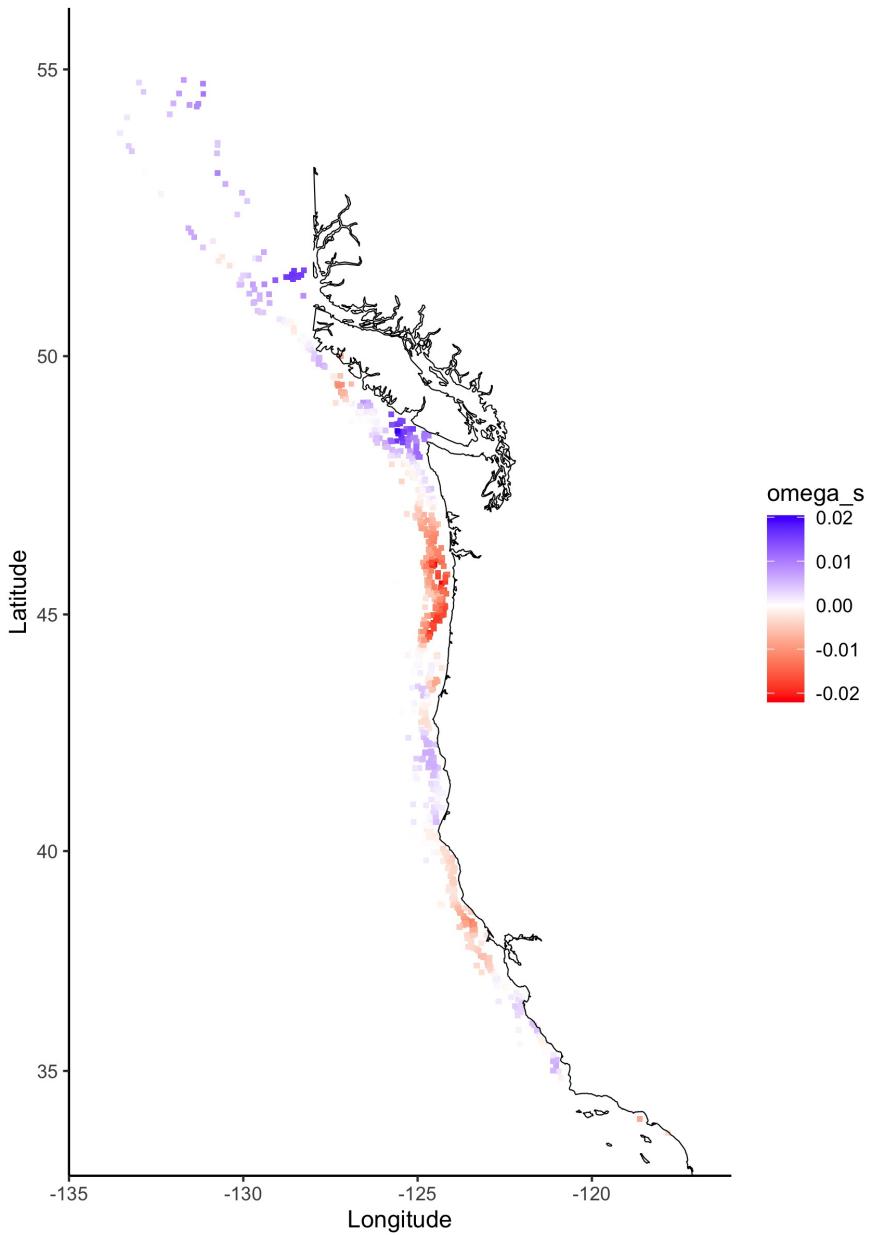
- Include month effect in the model - remove seasonal pattern in sampling design from the model
 - Is it best to include? Think about it!
- prediction grid - check mike malick code
 - look for helper functions to create a coarser grid

September 2023

Adding month and sex effects

Adding month as a linear predictor was a better fit to the data according to AIC and also reduced the unexplained spatial variance which we would expect. Because of this, the remaining spatial trends (a SD of only 0.03) revealed stronger spatial patterning as seen before.

`weight ~ s(age) + s(cohort) + catch_month`



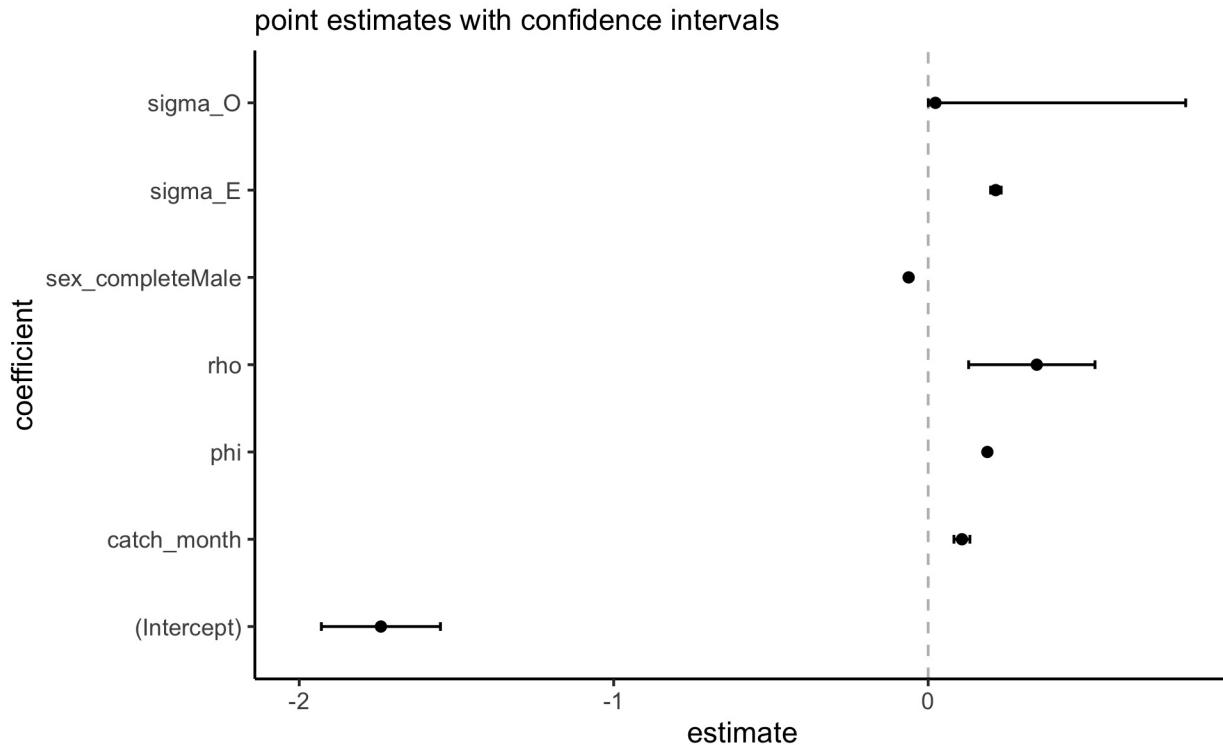
When adding sex effects, there are two approaches that I thought would be fair to take. To handle sex as a linear predictor, or to allow the smoother on age to interact with sex. For the interaction on smoother, I specify a “by” variable which generates an indicator vector for each level of the factor (male and female). Basically, each factor level, male and female, will have its own smooth. One thing to note, though, is that because centering constraints are applied to the smooths, we should include the by variable as a parametric term. But it wouldn’t converge haha.

In order to do this, I needed to make some minor changes to the dataset. There were 138 unsexed observations out of 35,348 (< 1%) and about 90% of these observations are in early age classes (0 and 1). So, I randomly assigned male and female at a 50/50 probability following the assumption that negligible sex-specific mortality has yet occurred and sex-ratio for juveniles are 1:1 (Zamora Garcia et al. 2020). I opted for these changes, as opposed to dropping the unsexed observations from the dataset, because they make a decent portion of the age-0 class which may drive the structure of the weight-at-age curve.

```
weight ~ s(new_age) + s(cohort) + catch_month + sex_complete
```

```
weight ~ s(new_age, by = sex_complete) + s(cohort) + catch_month + sex_complete
```

AIC model comparison indicates that sex as a linear predictor is a better fit to the data. Adding sex as a linear predictor didn't change any of the spatial trends, as we might expect. However, the confidence interval around the spatial SD is quite large but it does not overlap with 0.

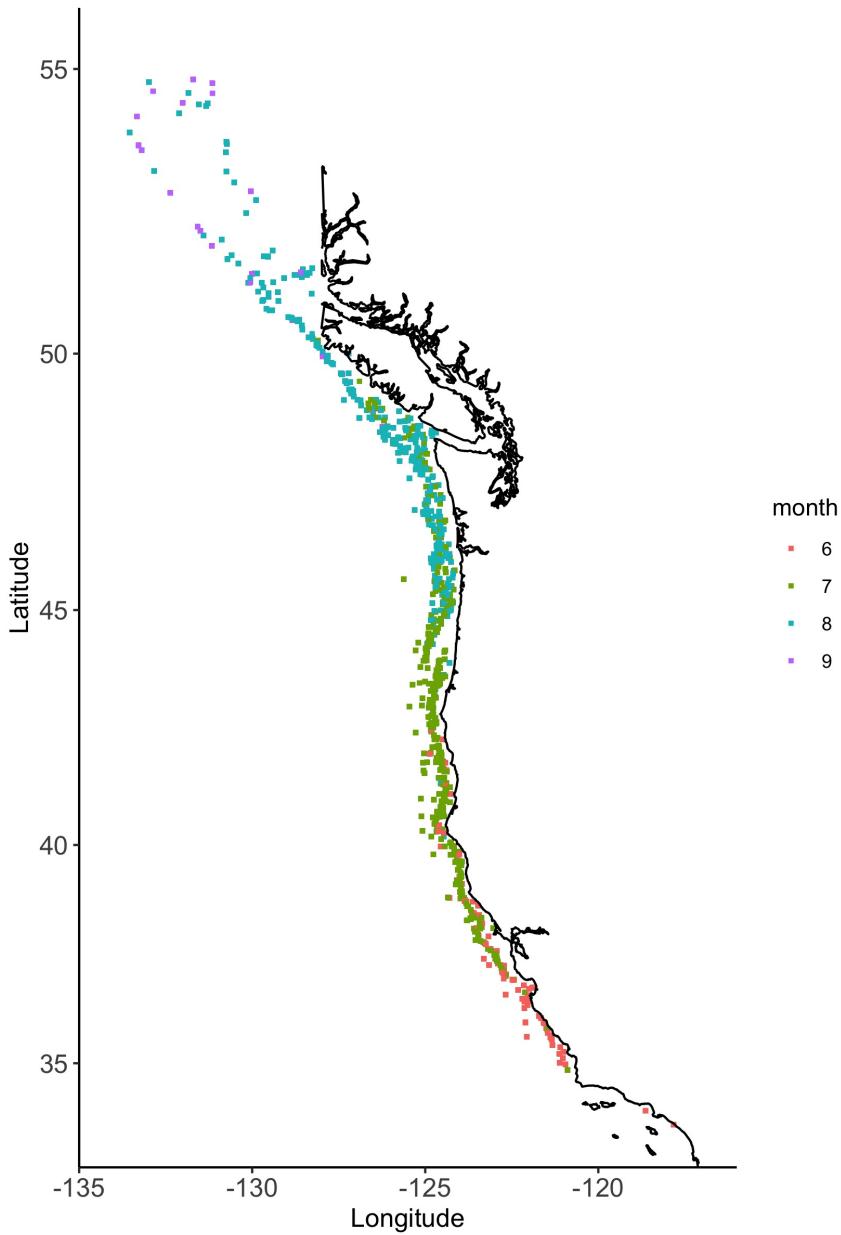


Prediction Grid

I created a dataset with all the unique year, age, cohort, month, and sex combinations. This led to ~850 unique combinations. I then extracted all of the unique spatial coordinates in which data was collected aggregated across all years. This was ~1000 unique combinations. I merged these datasets together such that each unique year, age, ..., sex combination was paired with all the unique coordinates, expanding the prediction grid to ~860,000 points. Not sure if this was correct

To do:

- take all the non-spatial covariate without the spatial RE and spatiotemporal RE and sequentially add them in
- pred_grid - use malick code to create a coarse spatial grid
 - make sure the coordinates and zone aligns



Month covariate acts as a proxy of seasonal, size-structured migration.

How to deal with unequal sample sizes for month? Shouldn't do random effect because too few categories.

Notes from sdmTMB workshop recording

- range (matern): distance at which points are effectively independent
- sigma_o (spatial SD): magnitude of spatial decay

I revisited the models and decided to omit sex as a covariate. It was causing issues in estimating the spatial RE while also not reducing the estimate of dispersion of the error distribution. So now moving forward I am using `weight ~ s(new_age) + s(cohort) + catch_month + omega_s + epsilon_st`.

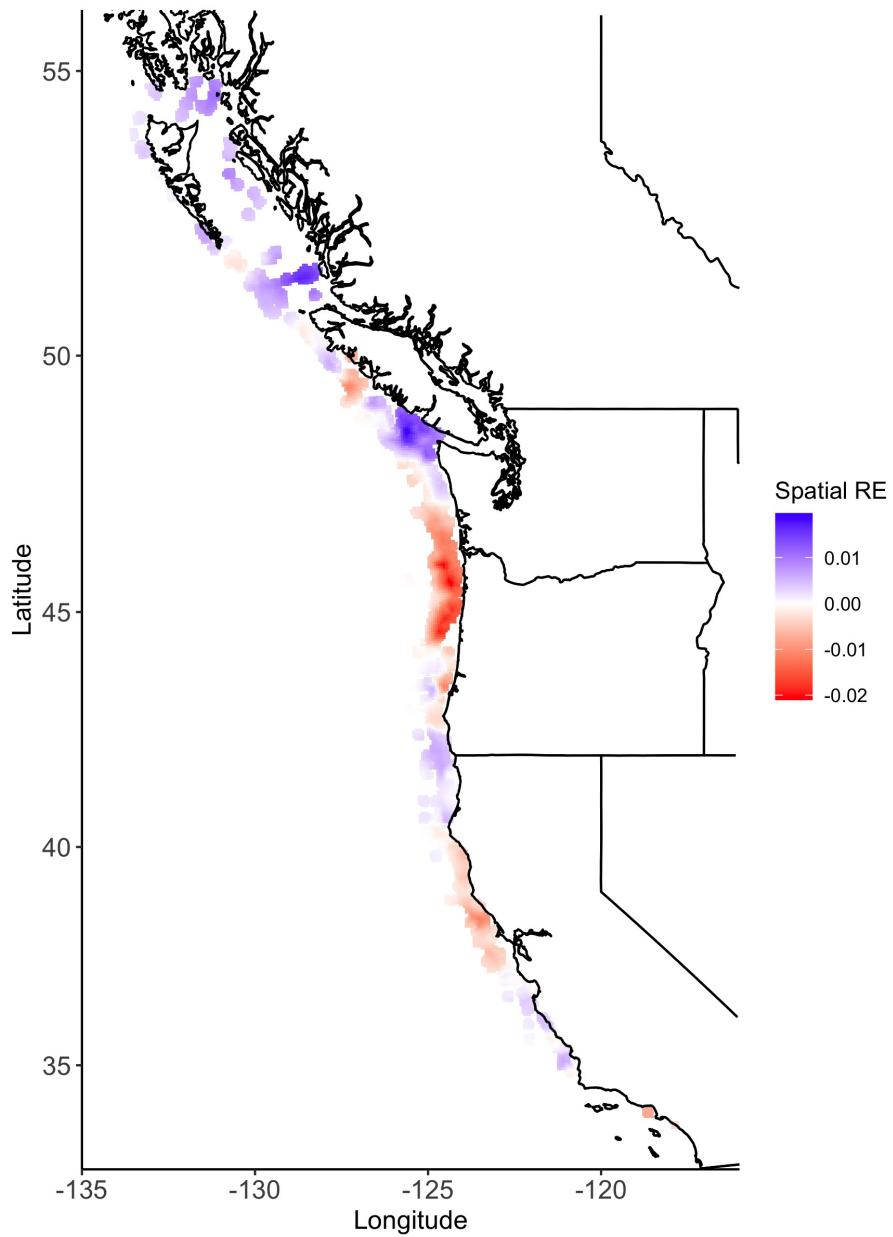
I still can't sort out how to interpret some of the coefficients. I tried centering the data so that I can interpret the intercept as the expected weight when all covariates are set to their mean, but the intercept is still negative.

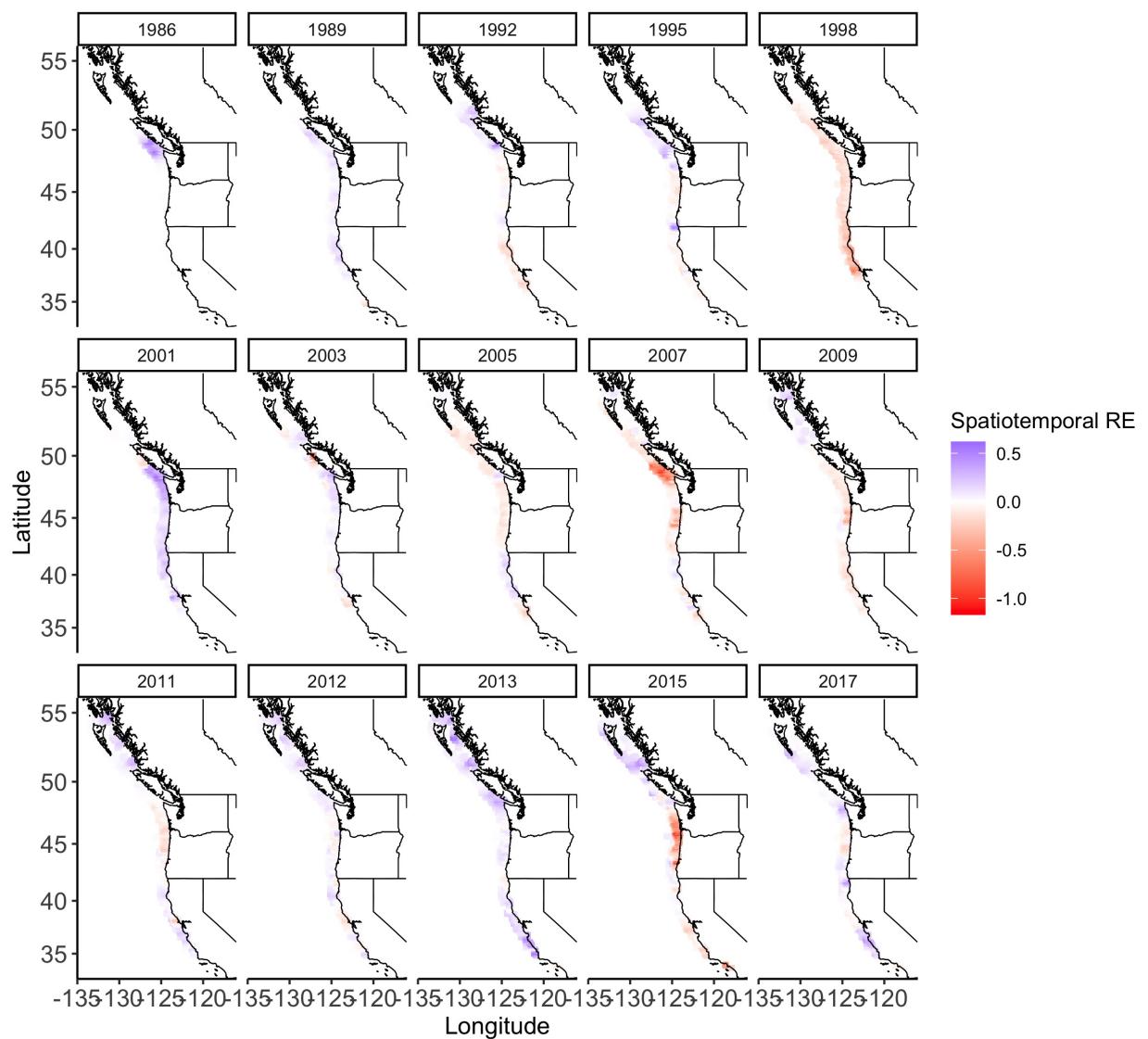
	term	estimate	std.error	conf.low	conf.high
1	range	77.8073197		65.1299399	92.9523199
3	phi	0.1905955		0.1891731	0.1920286
4	sigma_O	0.0261371		0.0015133	0.4514302
5	sigma_E	0.2152964		0.1990331	0.2328885
6	rho	0.3463787		0.1301139	0.5311817
11	(Intercept)	-1.7940204	0.0975290	-1.9851736	-1.6028671
2	catch_month	0.1105113	0.0130639	0.0849066	0.1361160

centered data					
	term	estimate	std.error	conf.low	conf.high
1	range	130.7975524		109.0223766	156.9219113
3	phi	0.1927765		0.1913348	0.1942290
4	sigma_O	0.0191793		0.0000018	205.5399998
5	sigma_E	0.3016991		0.2738805	0.3323433
6	rho	0.4469190		0.2536323	0.6058865
11	(Intercept)	-0.9717936	0.0232897	-1.0174405	-0.9261467
2	catch_month_cent	0.0895983	0.0138490	0.0624547	0.1167419

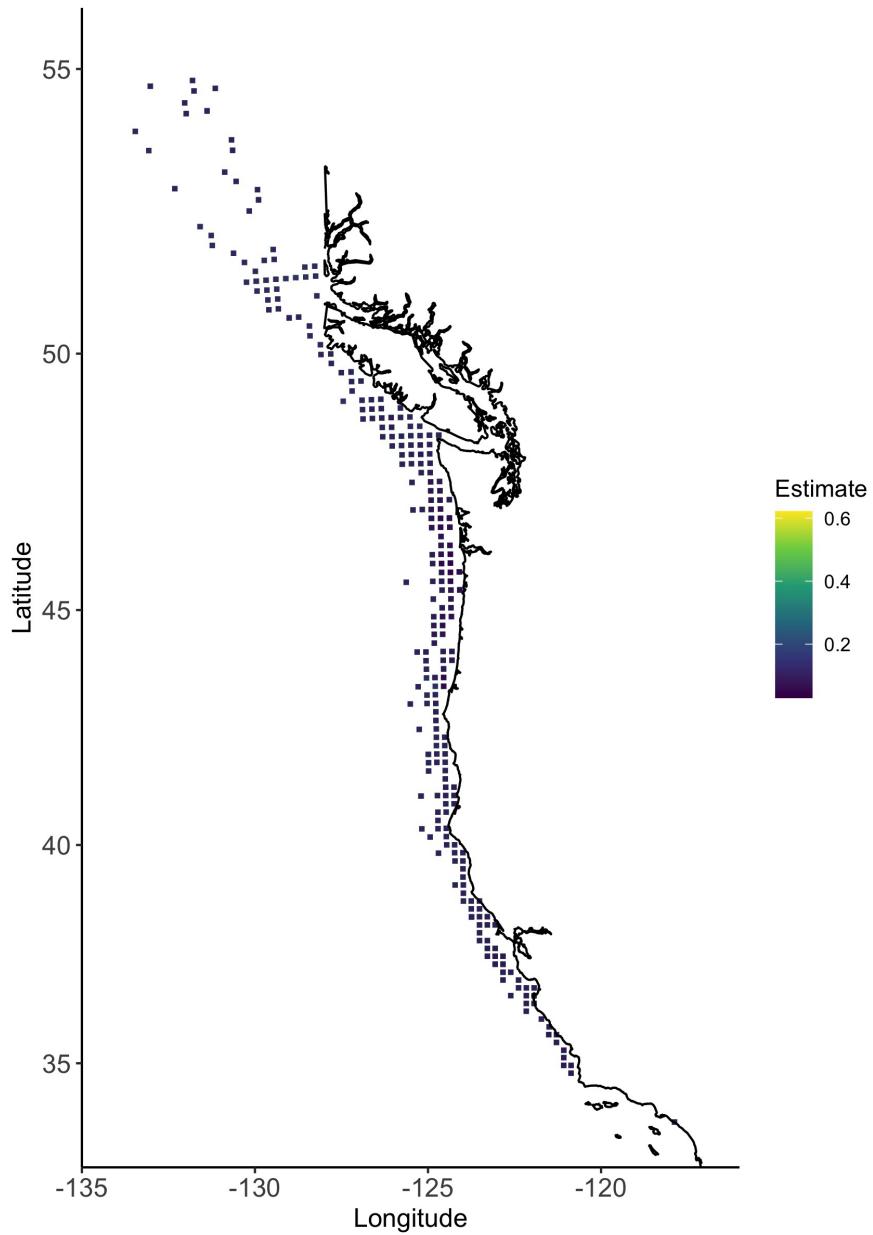
I ran the non-centered model with the prediction grid I created. The prediction grid consists of each unique age, year, month, cohort combination at each spatial location (537,372 spatial points).

The spatial and spatiotemporal random effects fields look great.

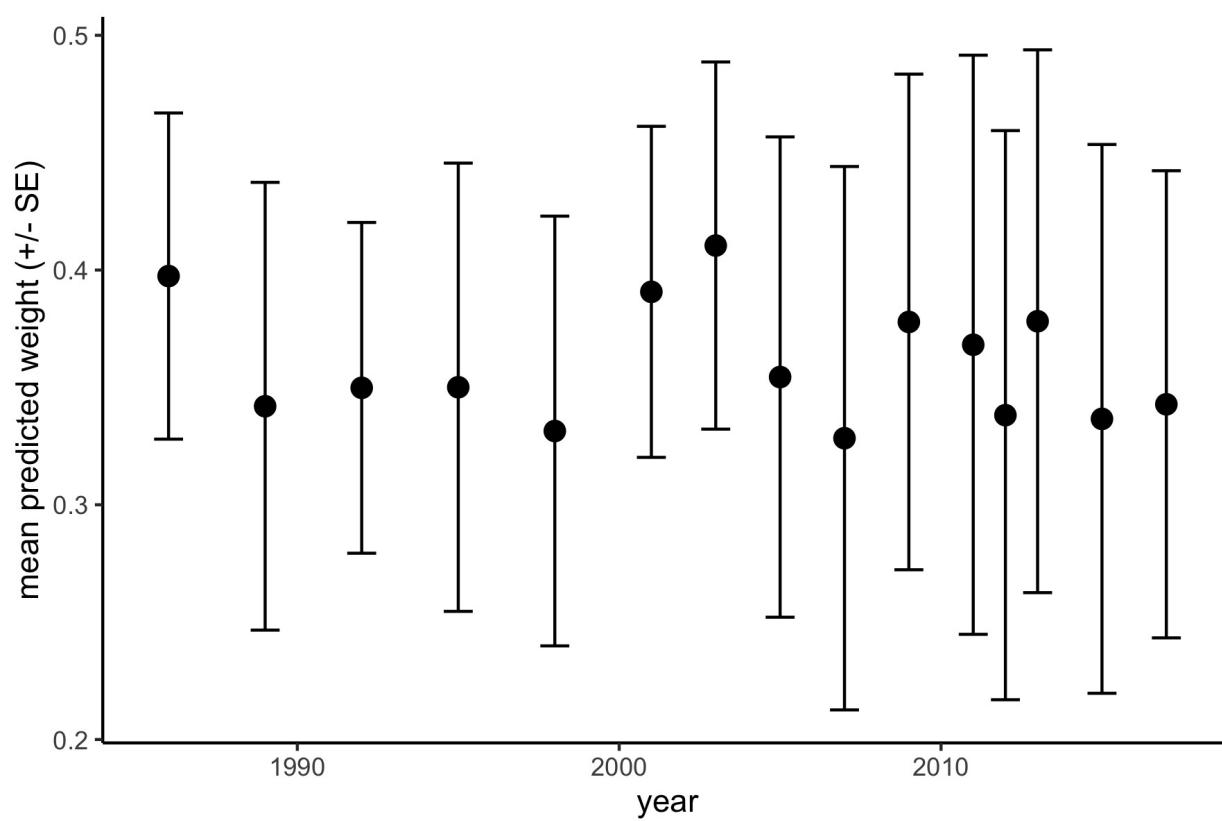
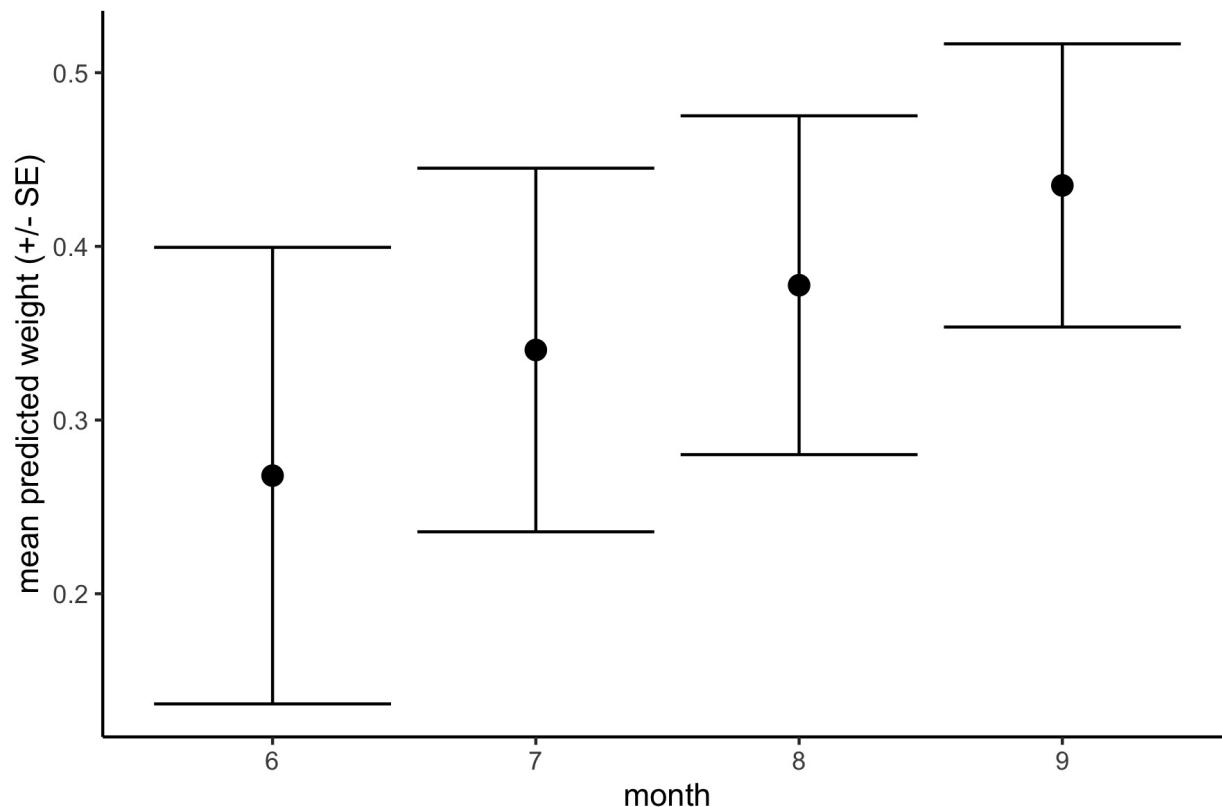


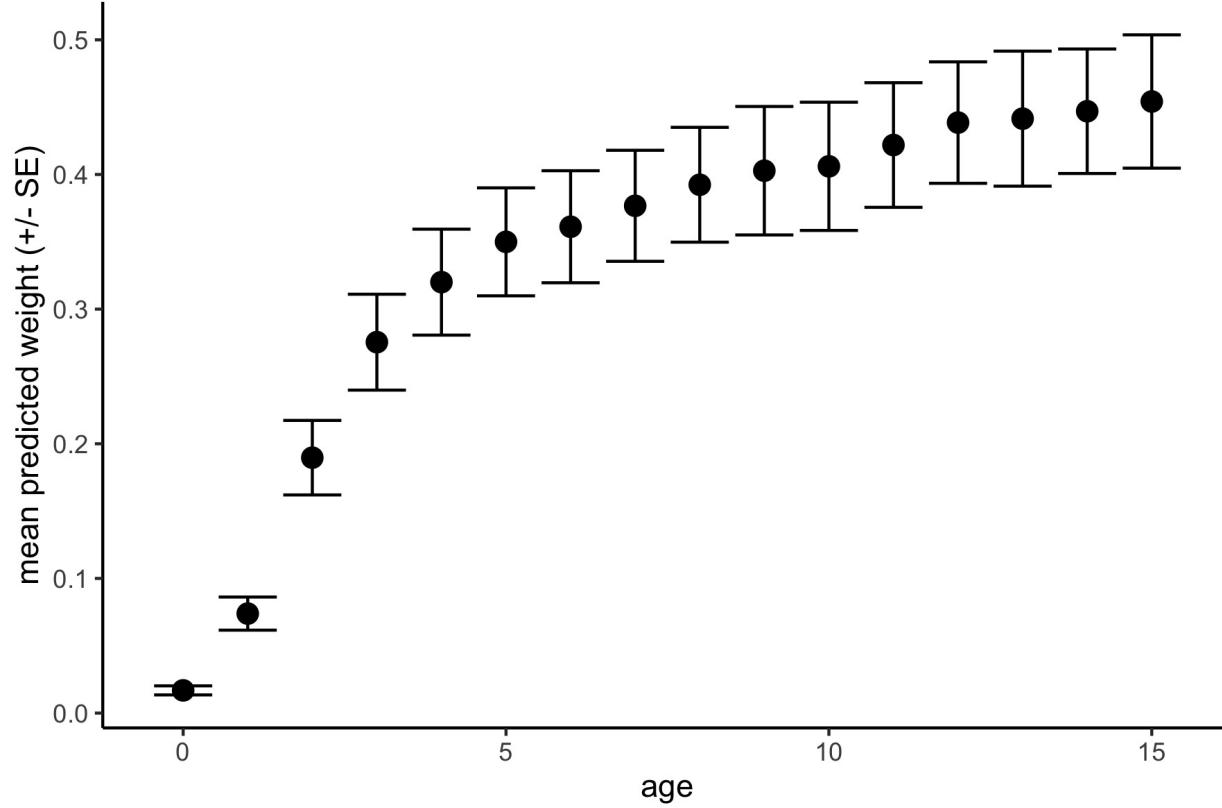
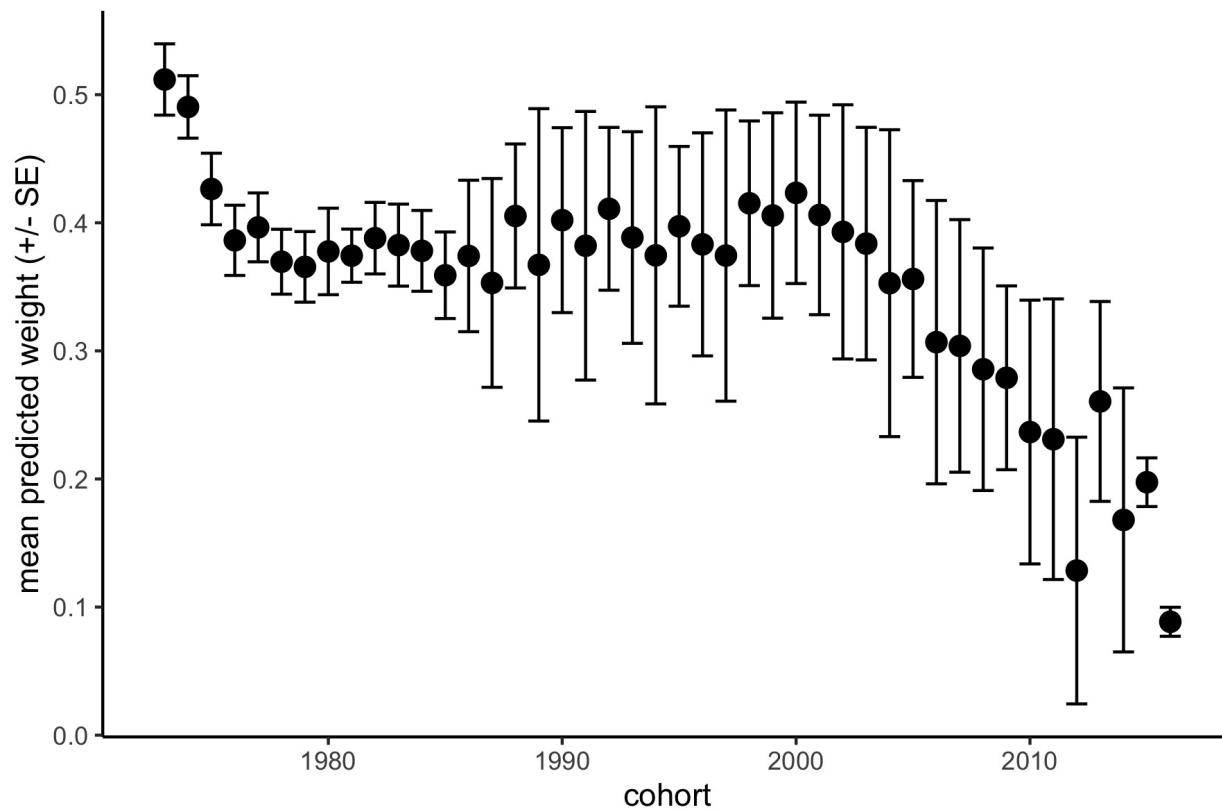


However, we can't explore the predictions (estimate, non RE estimate, RE estimates) because all of the data is available at each spatial location so the estimates are stacked on top of each other.

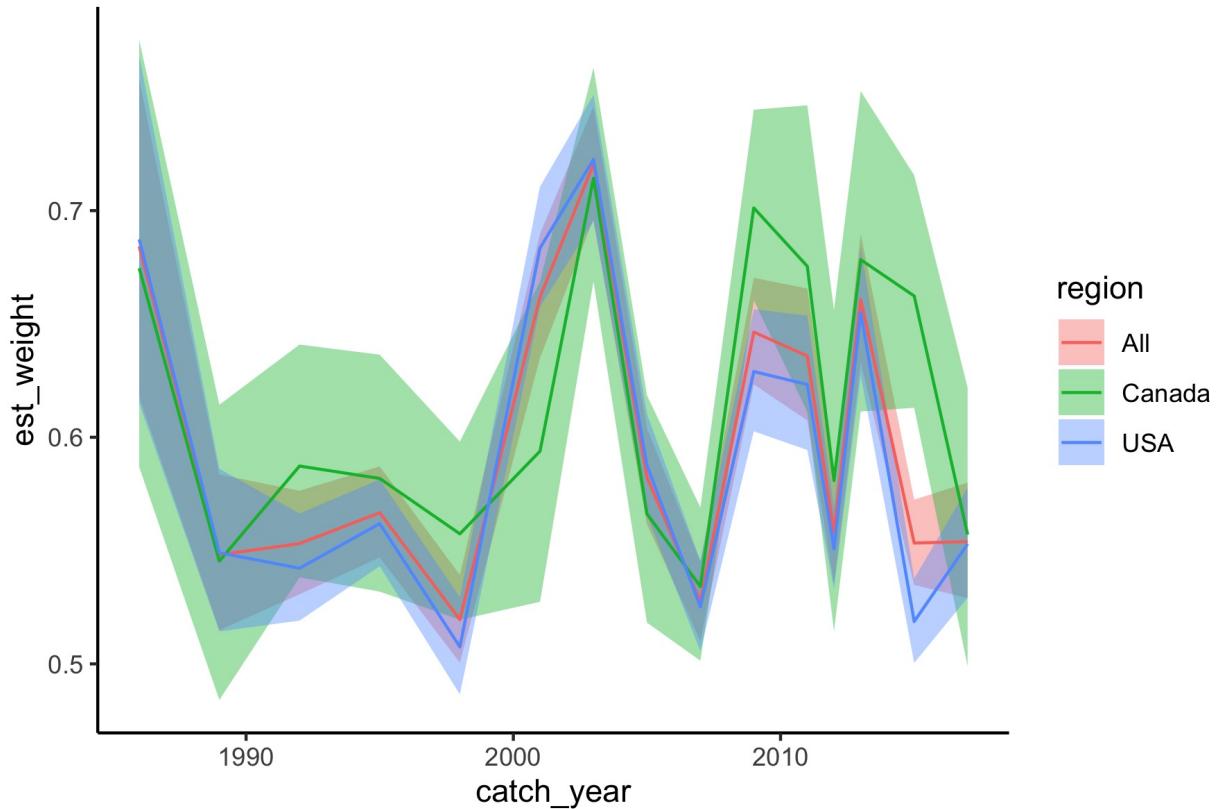


Also, here's a look at the effect of month and year on the predicted weight.



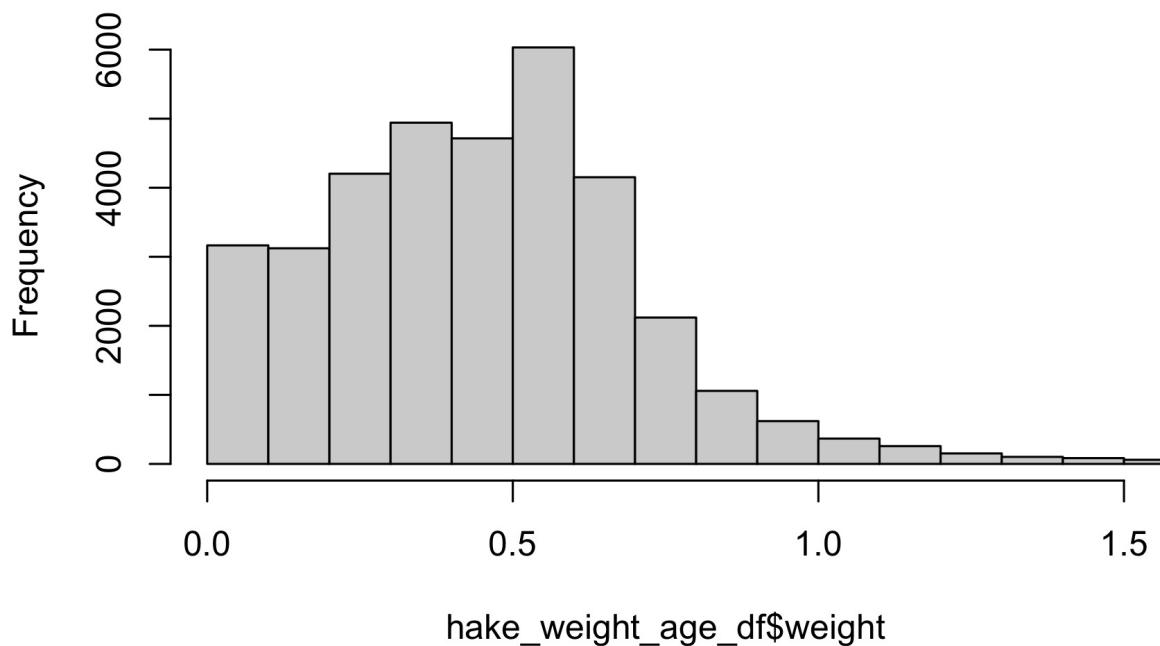


The index of weight across years for the whole spatial domain and split between USA and Canada.

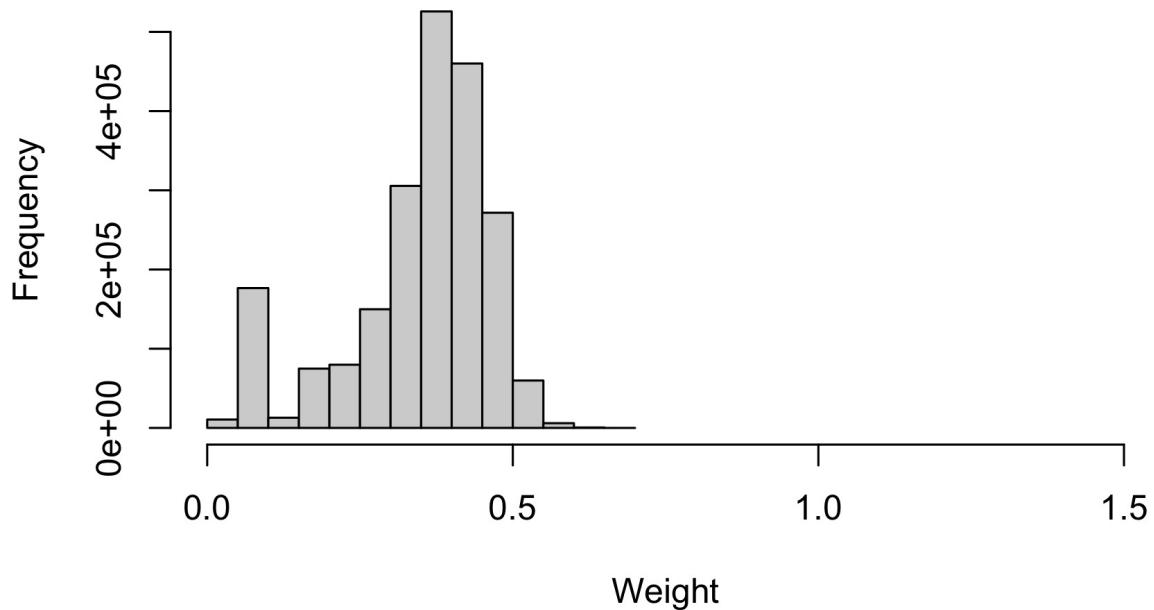


The prediction grid used to create this index is essentially a unique combination of all covariates made available at each spatial location. So, the index now looks similar between the USA and Canada since the data available in each country is the same.

Observed Weights

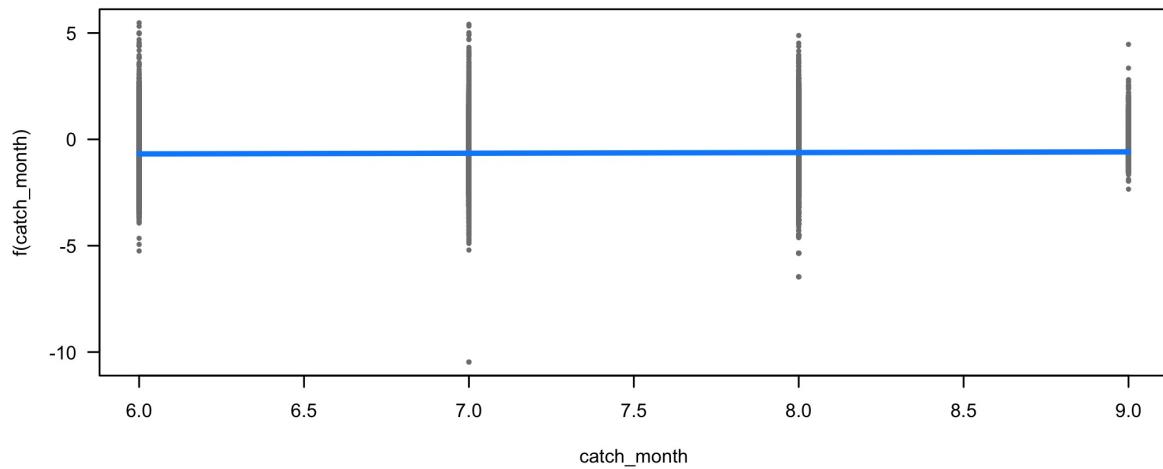
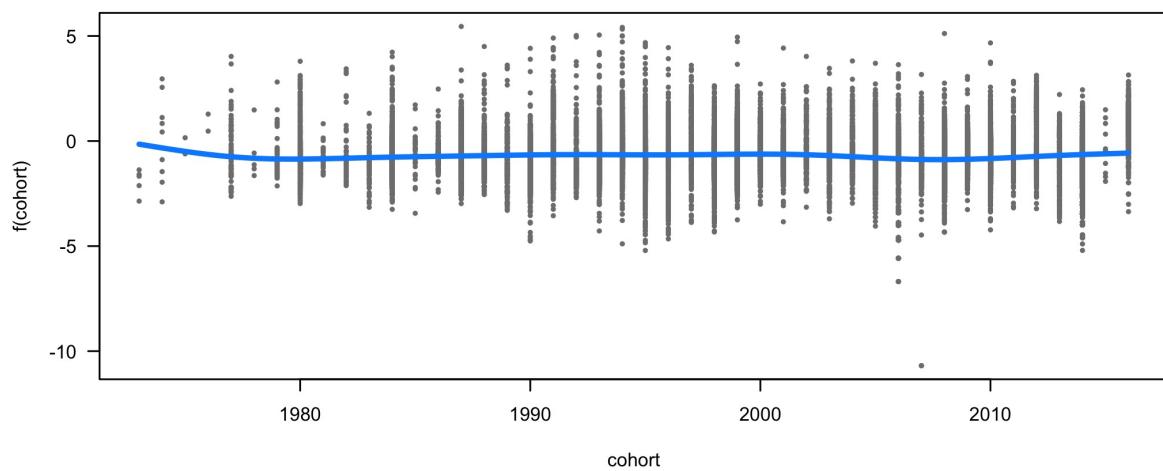
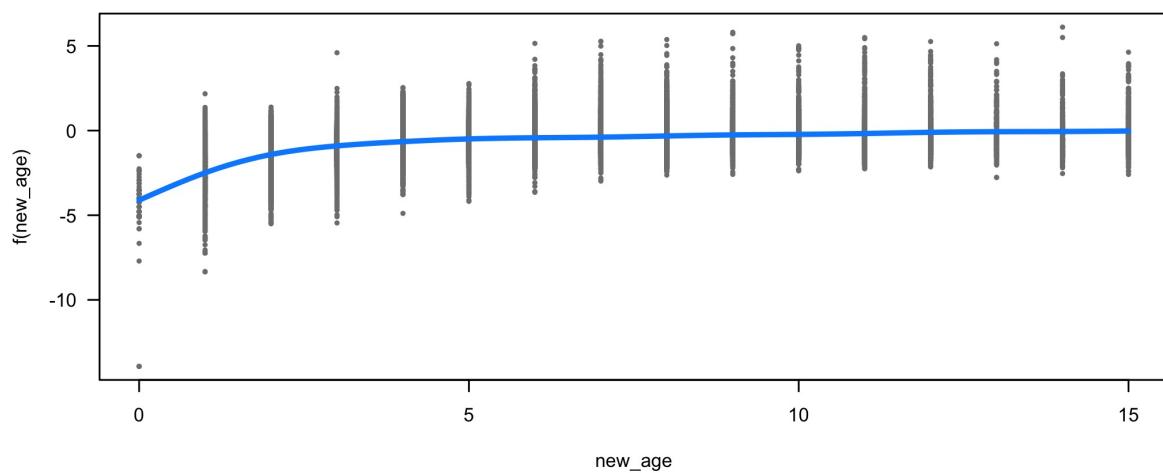


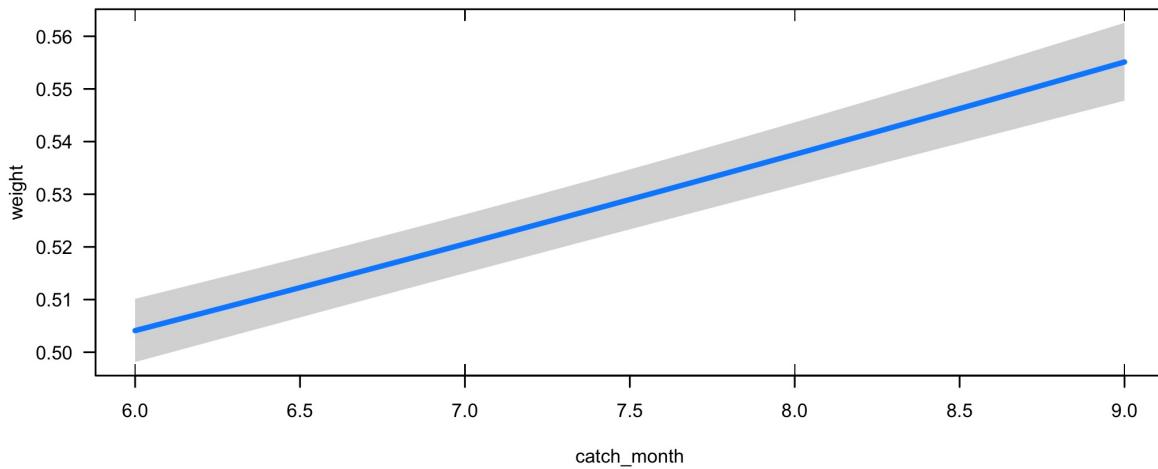
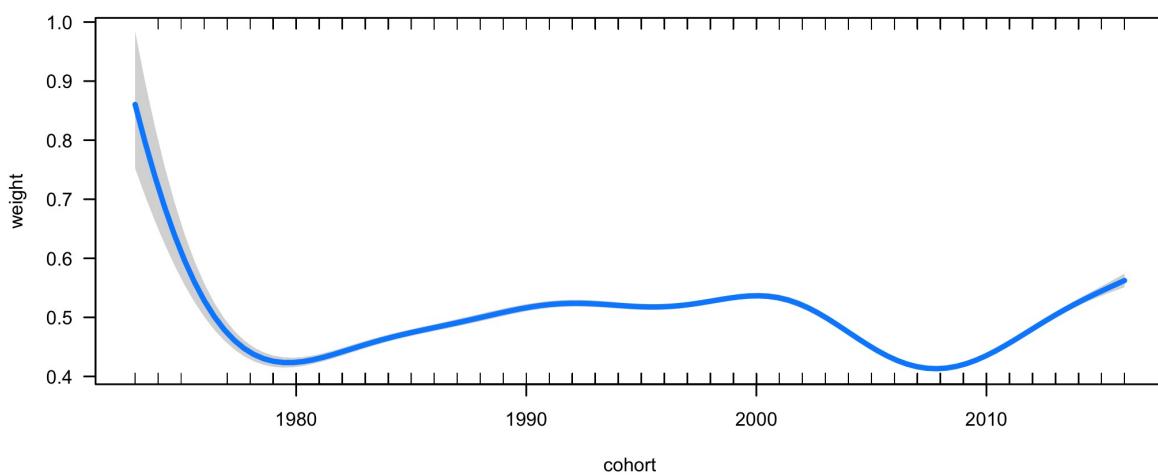
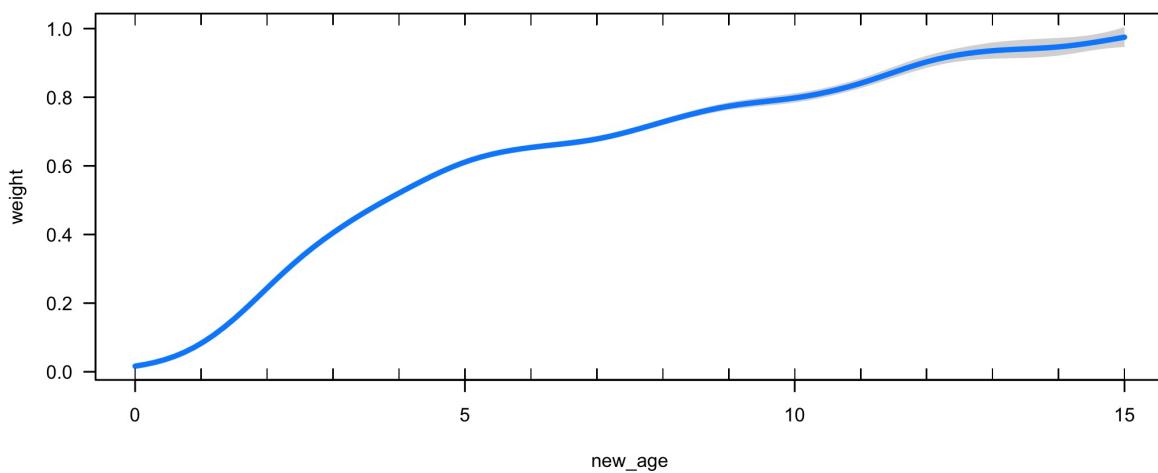
Predicted Weights



Revisiting GAMs

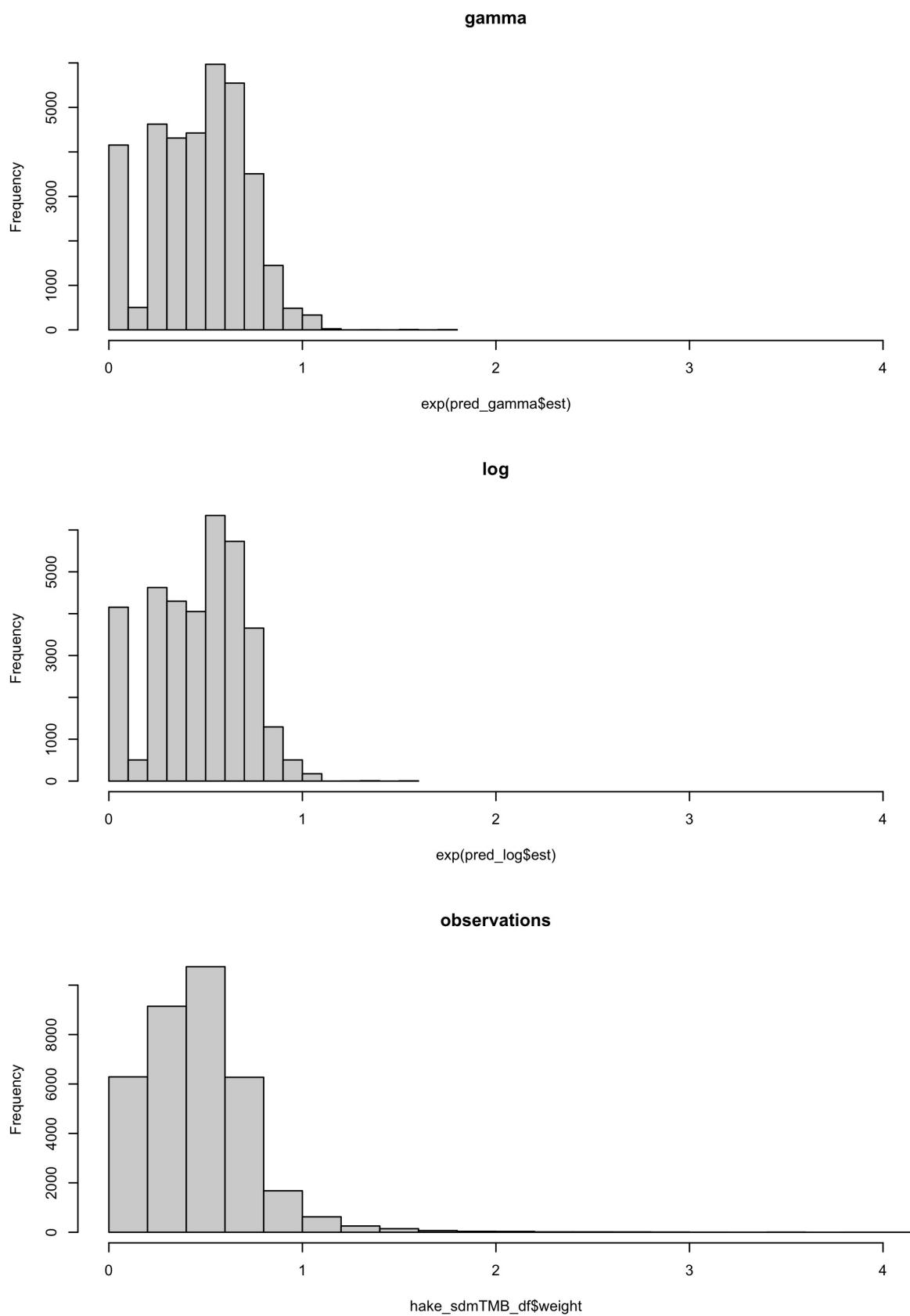
- The GAM in my model uses a thin plate regression spline. This approach is often considered universally optimal and does not require the user to specify the number of knots used to estimate the spline. This minimizes the knot placement and selection issue that is more common in other penalizing approaches. It instead uses a truncated eigen decomposition to achieve rank reduction.
- I tried cubic regression spline as well, varying the number of knots. However, this approach did not seem to support the data visually, often with wigginess occurring where it is biologically irrelevant.
- I created plots of the GAMs, in both the original format (scaled to the linear predictor which is better for observing model fit and outliers) and scaled to the response variable (better for communicating model results)





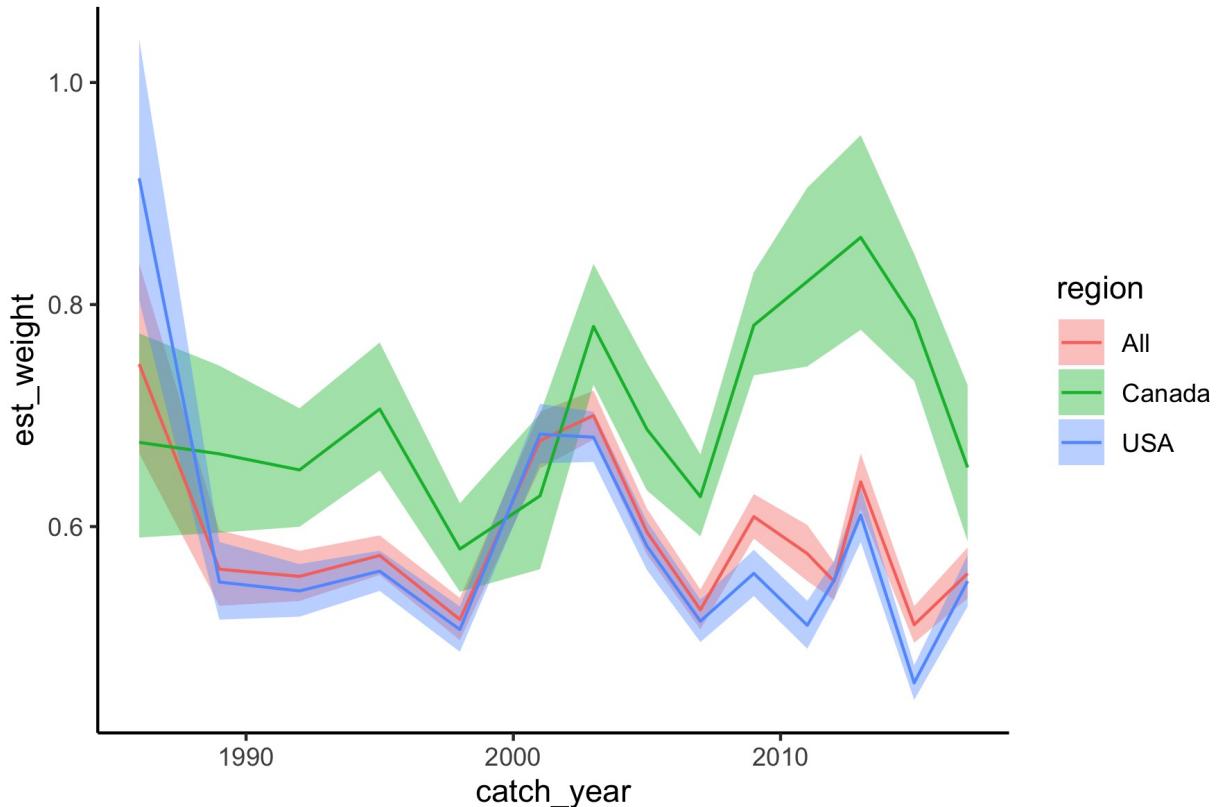
The above plots are for the model using a log-link lognormal error structure. The log link means that we transform the systematic function (i.e. the predictors) by taking the log of it. If X is the systematic function, it would be $\log(X)$, so the linear predictors are exponentiated.

I also tested the model with a log-link gamma error structure because looking at the histogram of predicted weights against the observations, it looked like the gamma did a better job capturing the lighter weights and the log of the weights had a left-skew which is also better captured by a gamma distribution. I also tried taking the log of weights and fitting a gamma distribution to it, but because of the gamma and lognormal distribution requirement for data to be positive, I did not pursue this path further.



Revisiting Index

Because of the way the index was generated, the indices between Canada and USA were very similar (see notes above). So, I wanted to try to make the predictions grid more characteristic of what we would see in the natural world. So, when I created the prediction grid, I split the observations between USA and Canada, expanded each countries unique combination of data to the spatial locations available in each country, and then merged the two predictions grids. That way, the unique combinations in that country were available in that country only. This resulted in the index below -



PICES presentation title - Spatiotemporal trends in weight and its potential implications for stock assessments - Spatiotemporal trends in weight and its potential implications for empirical weight at age

Adding sex back into the model I was previously having issues fitting sex into the model. Turns out my mesh was way too small (cutoff = 10km) and causing convergence issues. So, I decreased the resolution of the mesh and tried a few different sizes (cutoff = 20, 30, 50). With 20 and 30, the outputs were fairly similar. With 50, the range increased pretty dramatically and some of the coefficients shifted a bit. I think the cutoff value of 50 might be too large and not allowing the model to accurately estimate the range. The model with 20km cutoff size was a better fit to the data, but it did increase run time. So I decided to settle with cutoff = 30.

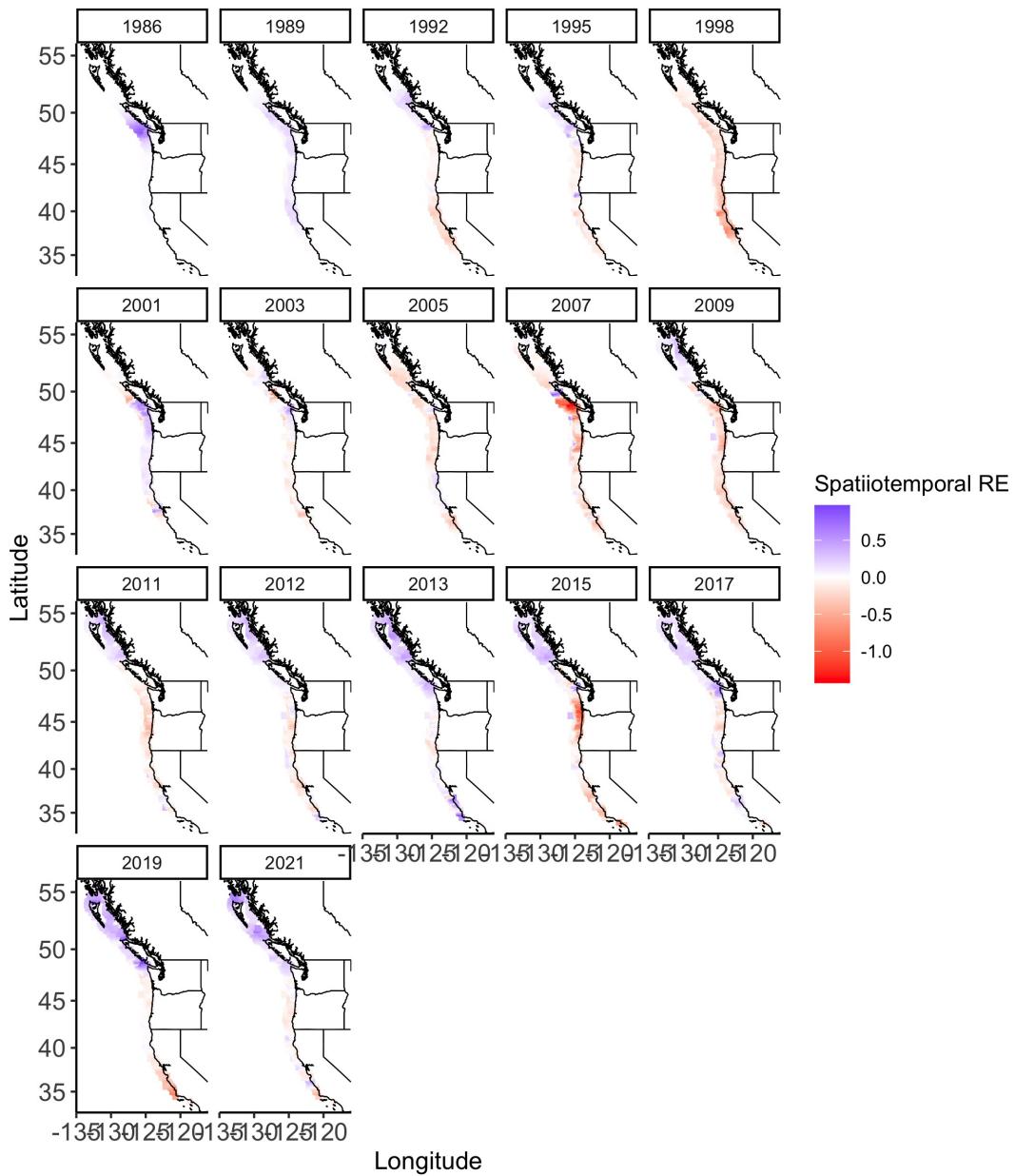
With cutoff = 30, I fit the model with no spatial or spatiotemporal RE, with only spatial RE, with only spatiotemporal RE, and with both spatial and spatiotemporal random effects.

The model with only spatiotemporal RE was the best fitting model, beating the model with spatial and spatiotemporal RE by just 2 AIC values. The spatial and spatiotemporal RE model did not converge well and had a hard time estimating the spatial SD, which was very small anyway.

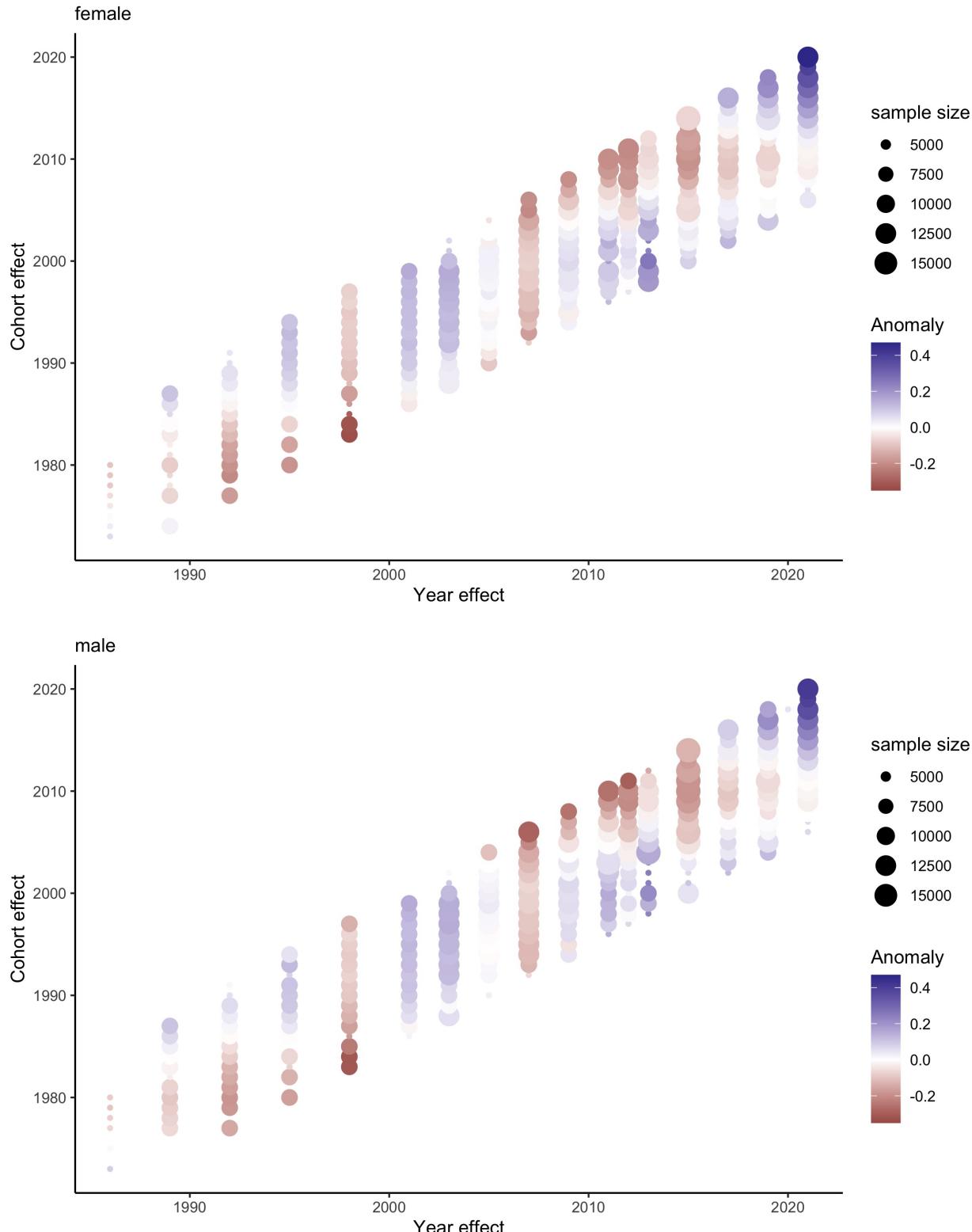
October 2023

Below are some figures of the predictions from the spatiotemporal only model. I added sex back in as a by factor in the age GAM.

spatiotemporal random effects - this plot shows the spatiotemporal random effects across the whole spatial domain



Year and Cohort Anomalies - This plot shows the weight anomalies for a given age. On the x-axis, we have year effects which visualize impacts along vertical slice. So, years 1998 and 2007 had lighter than the average individuals in that age class across all cohorts. On the y-axis is the cohort effect, whuich visualize impact along a horizontal slice. For example, 2007 and 2008 cohorts remain fairly small across years, while 1998 cohort remains fairly large with the exception of 2005 and 2007 overall smaller fish.

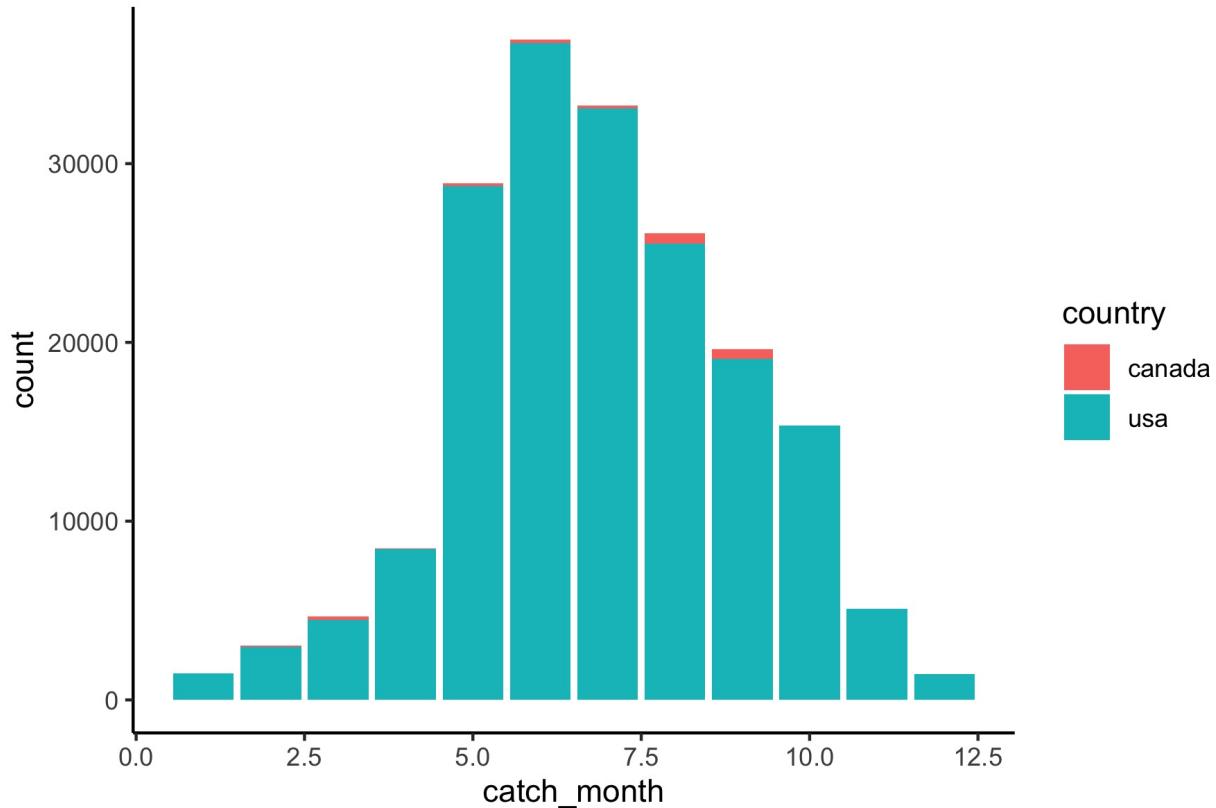


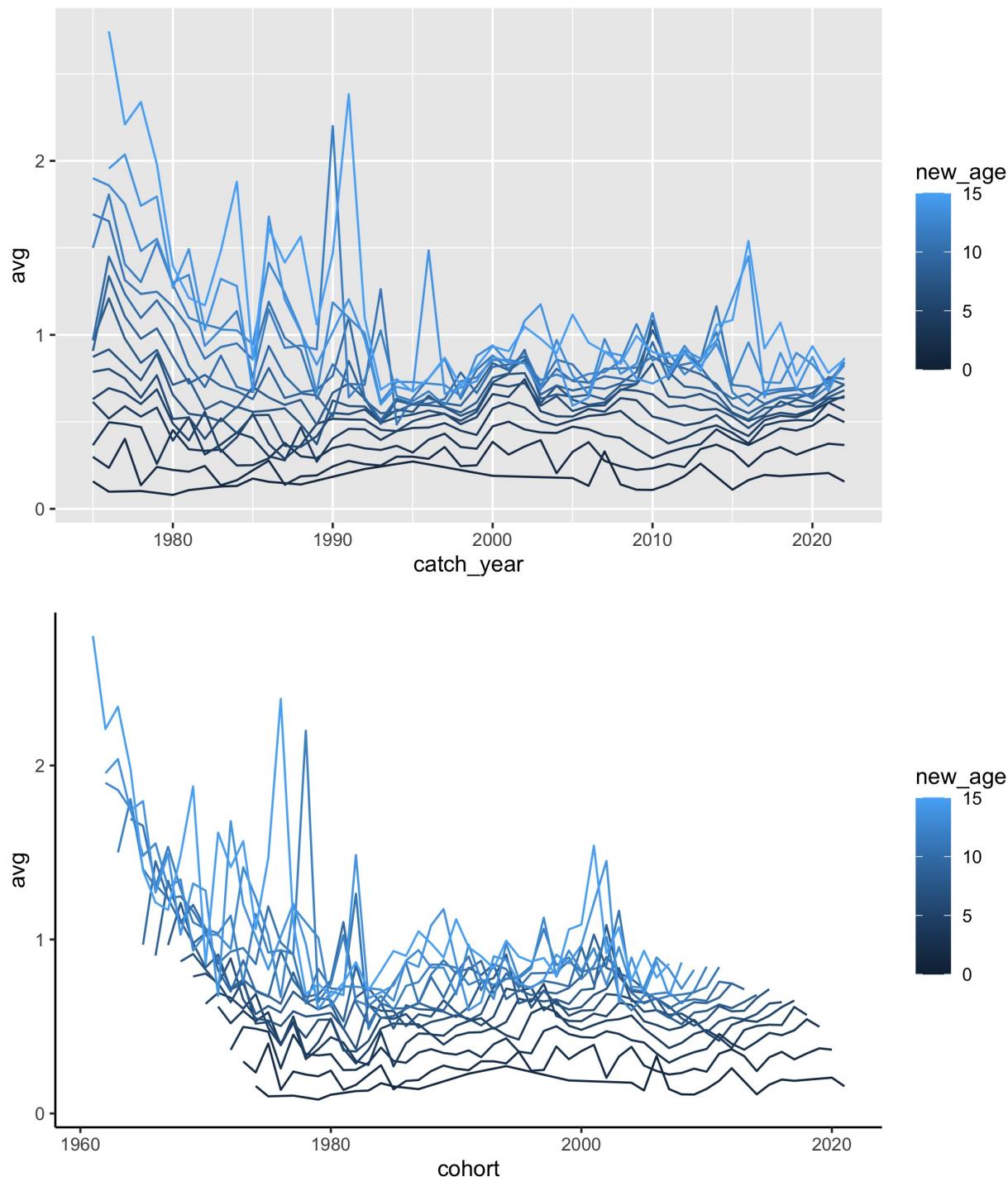
I have also fit a statistical model to the fishery data. I started off with just age as a predictor and it did not converge. I tested out a number of models 1) sex as a by factor in age gam 2) sex as a linear predictor 3) smoother on cohort 4) smoother on month 5) year as random effect. I also tried adding country as a categorical predictor but it did not work - the undefined sex factor is characteristic of the entire canadian

fishery, and so I think sex is already capturing the difference seen in Canada.

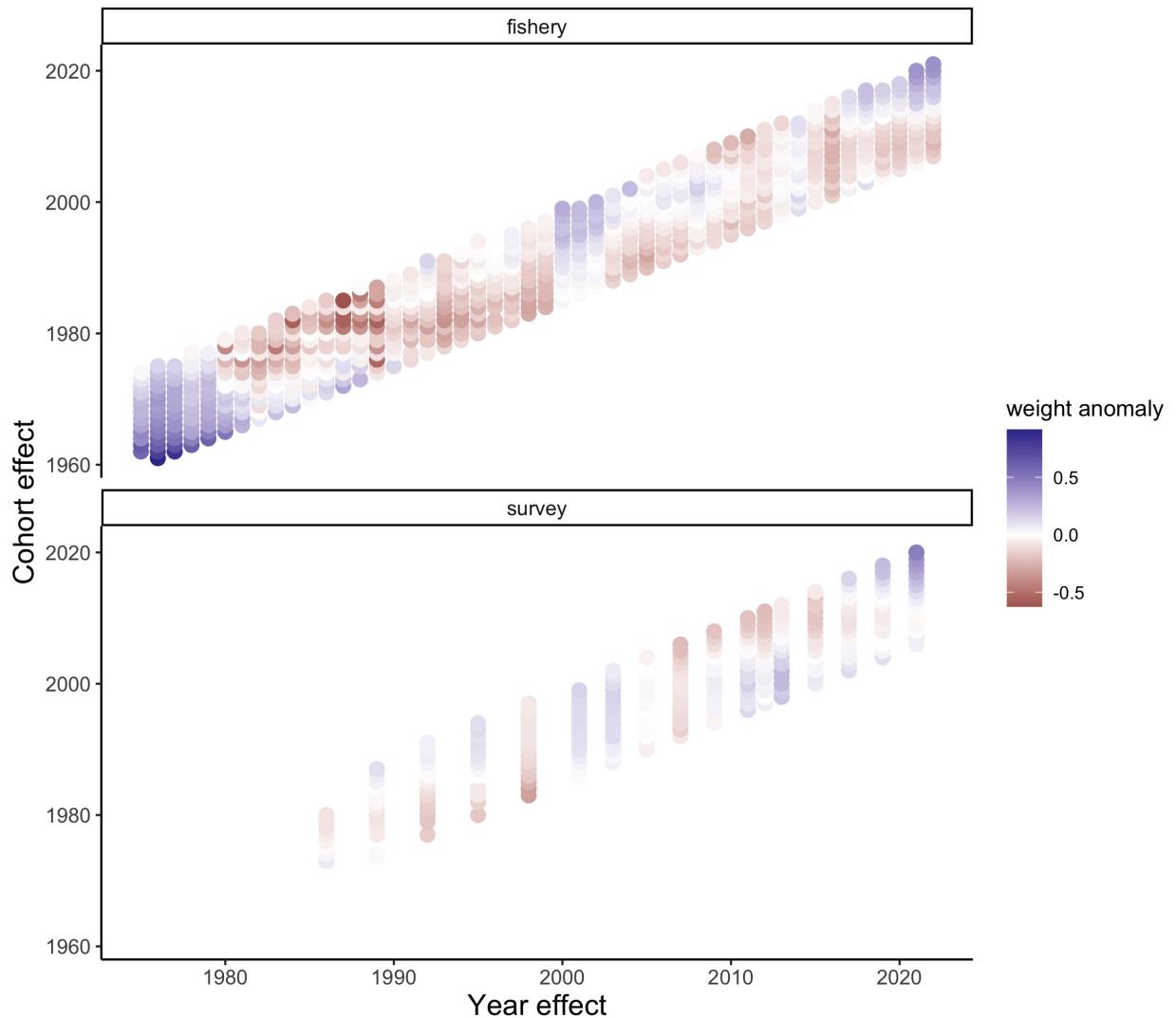
The model I settled on was `weight ~ s(new_age, by = sex_description) + s(cohort) + sex_description + s(catch_month) + (1 | fcatch_year)` which was ~10K AIC values less than the next best fit model.

Fishery data exploration

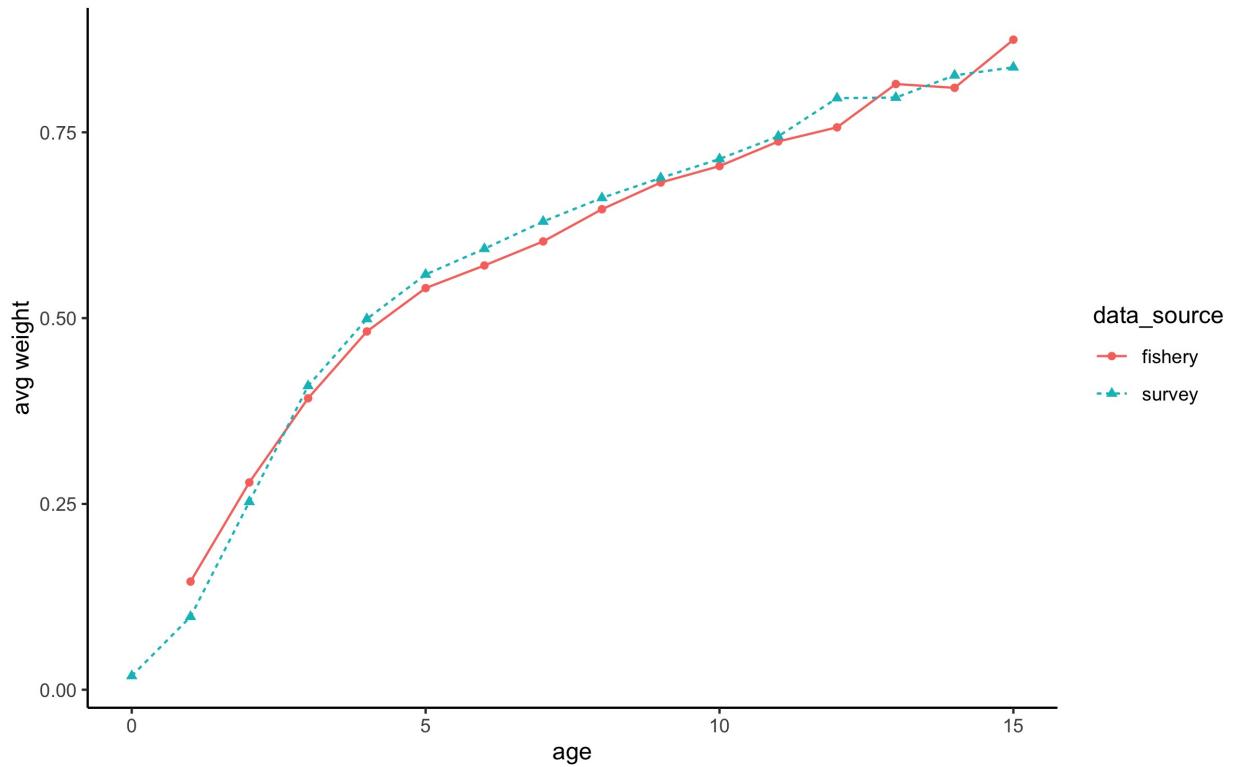




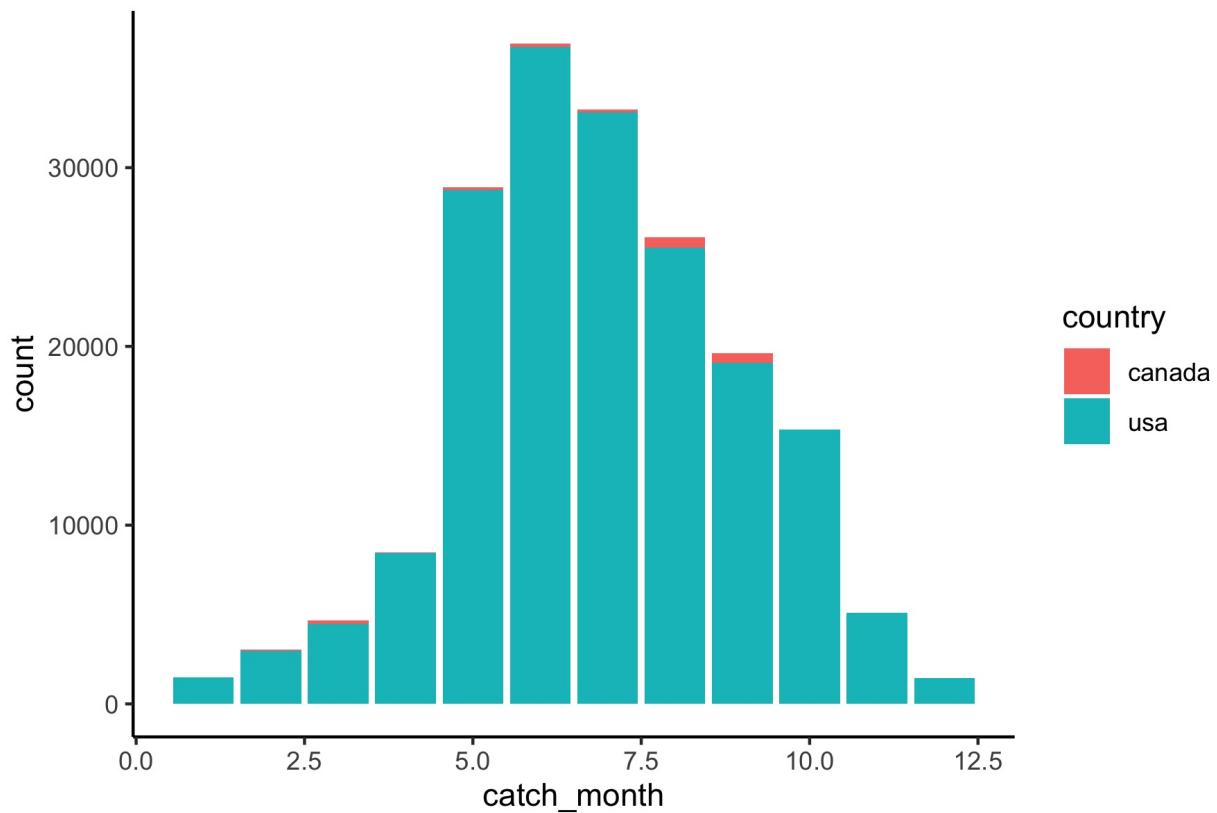
fishery vs survey data



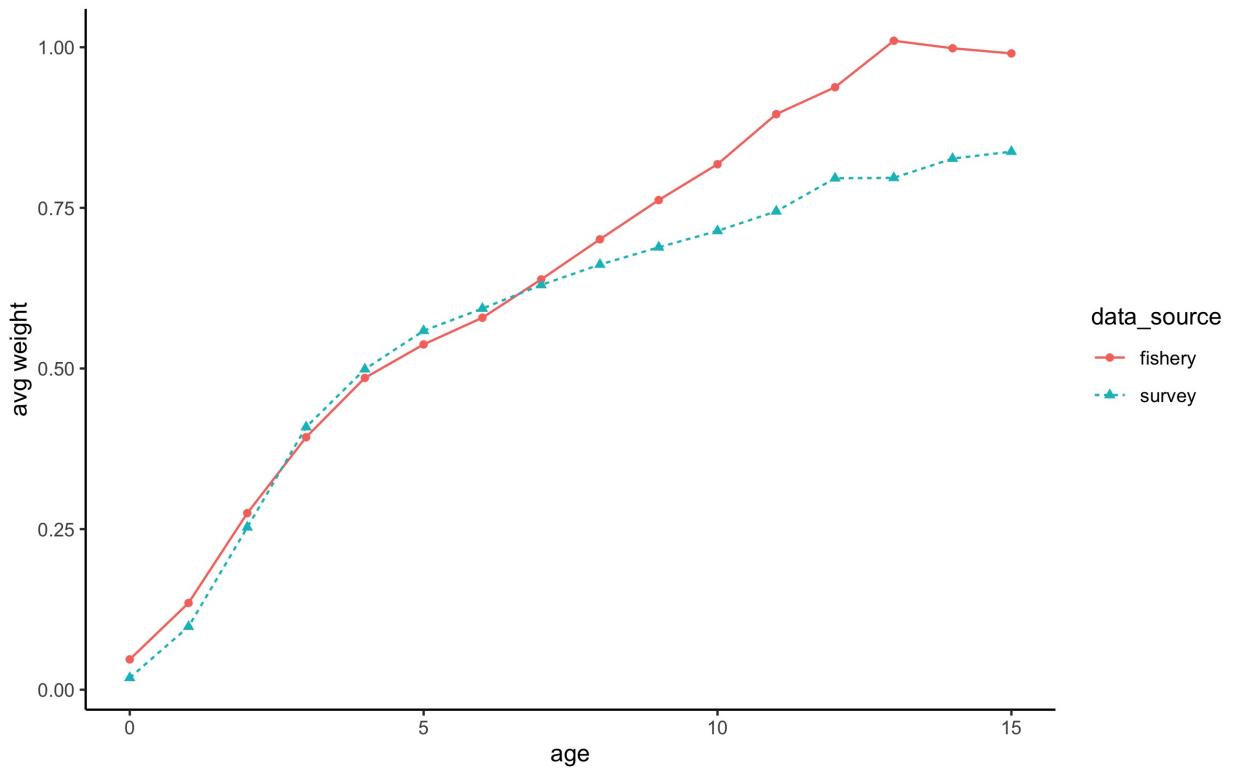
Below is the predicted weight-at-age between the two sources of data for 1986 and on. There is no survey data previous to 1986 and the fishery data reveals much heavier than average fish in those early years which had driven differences between the fishery and survey (see next plots below)



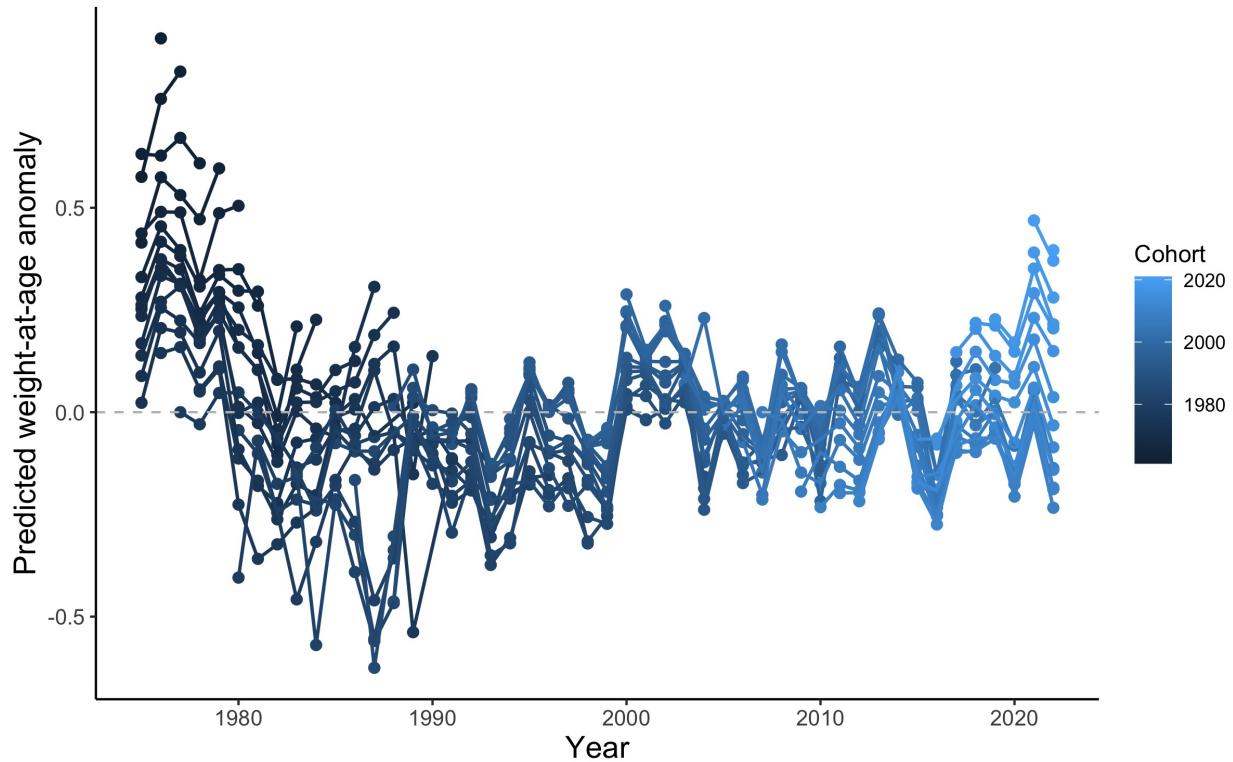
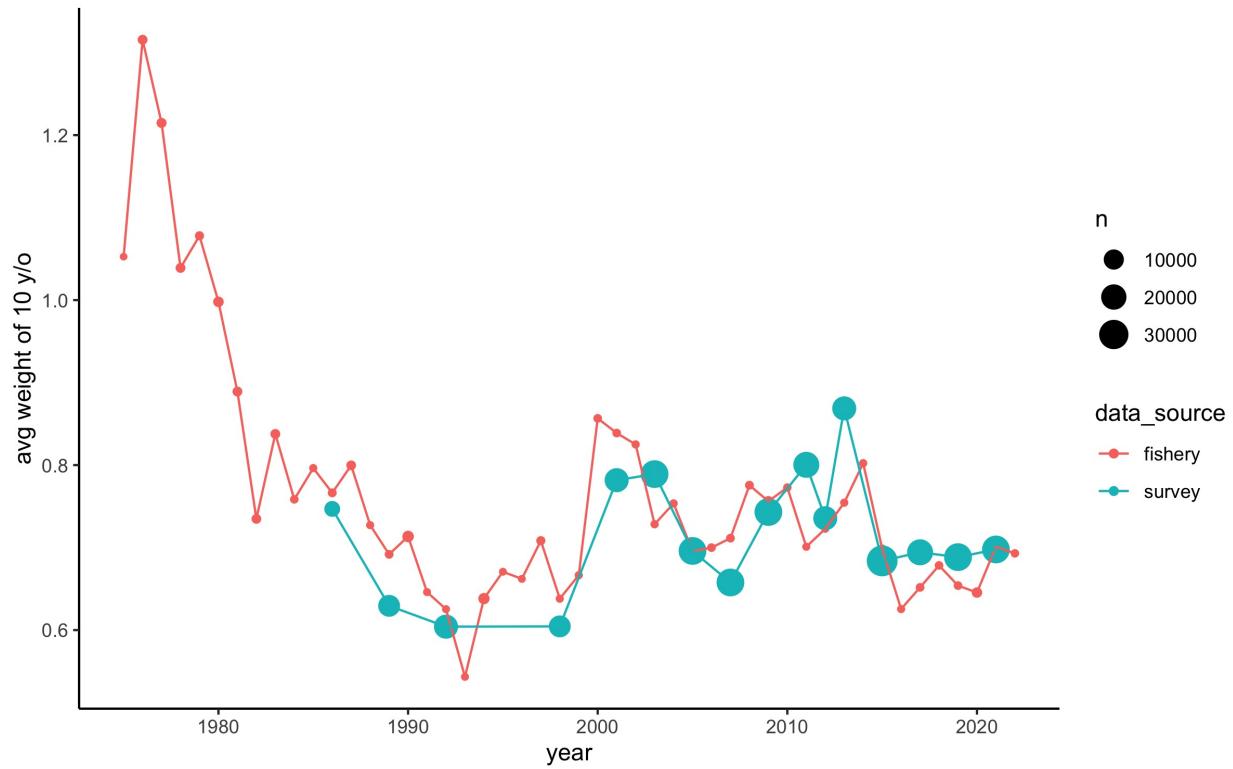
Limited differences potentially due to the fishing methods used (trawls are fairly unselective) and the fact that the fisheries operate largely during the summer (when survey operates) which might limit seasonal variation between the two data sources.



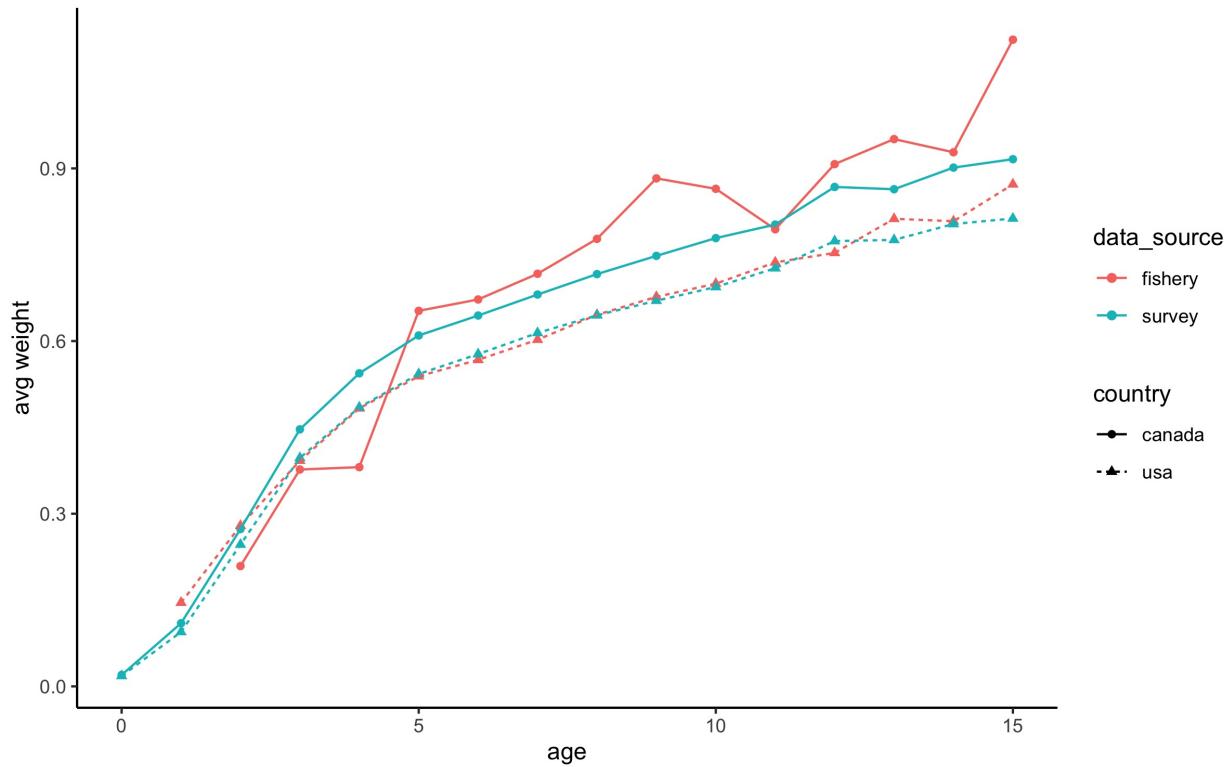
Here is the predicted weight-at-age for all years combined



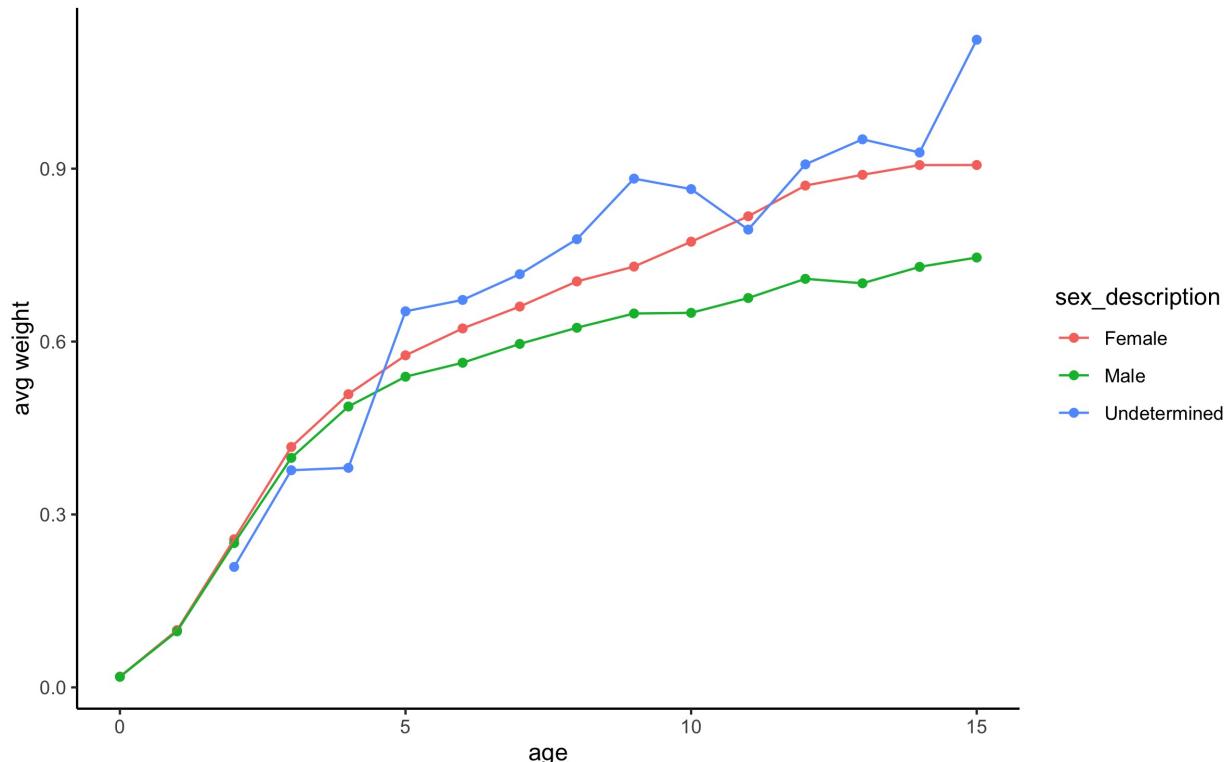
and as you can see from this timeseries of weights for a 10 year old between the data sources, the fishery data in the early years reveal much heavier than average individuals



Differences in weight-at-age are seen between countries

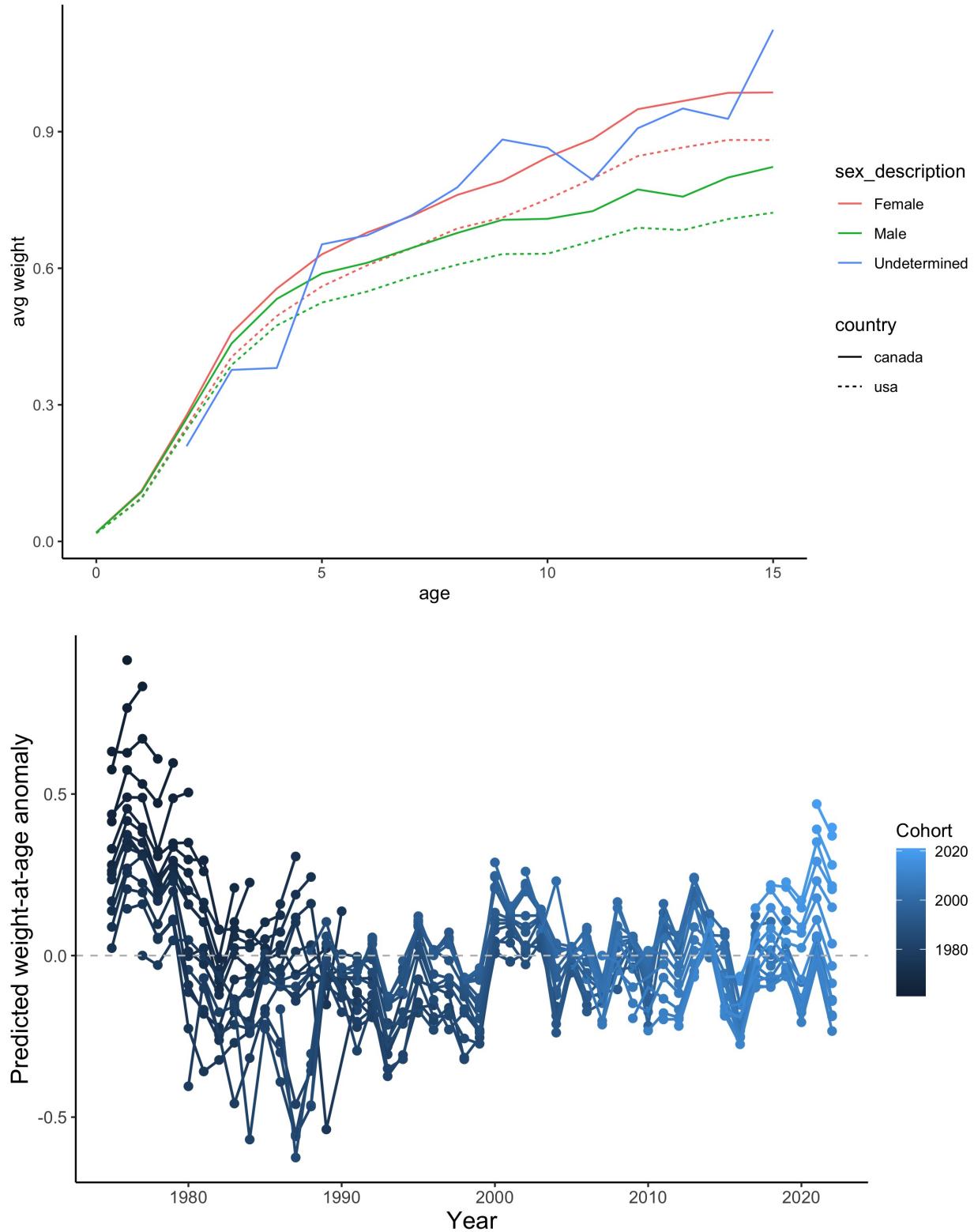


Differences seen by sex



The unsexed fish in this case come solely from the Canadian Fishery. At first glance, it may seem like the Canadian fishery (i.e. unsexed) catches mostly females based off of the weight-at-age curve. When we

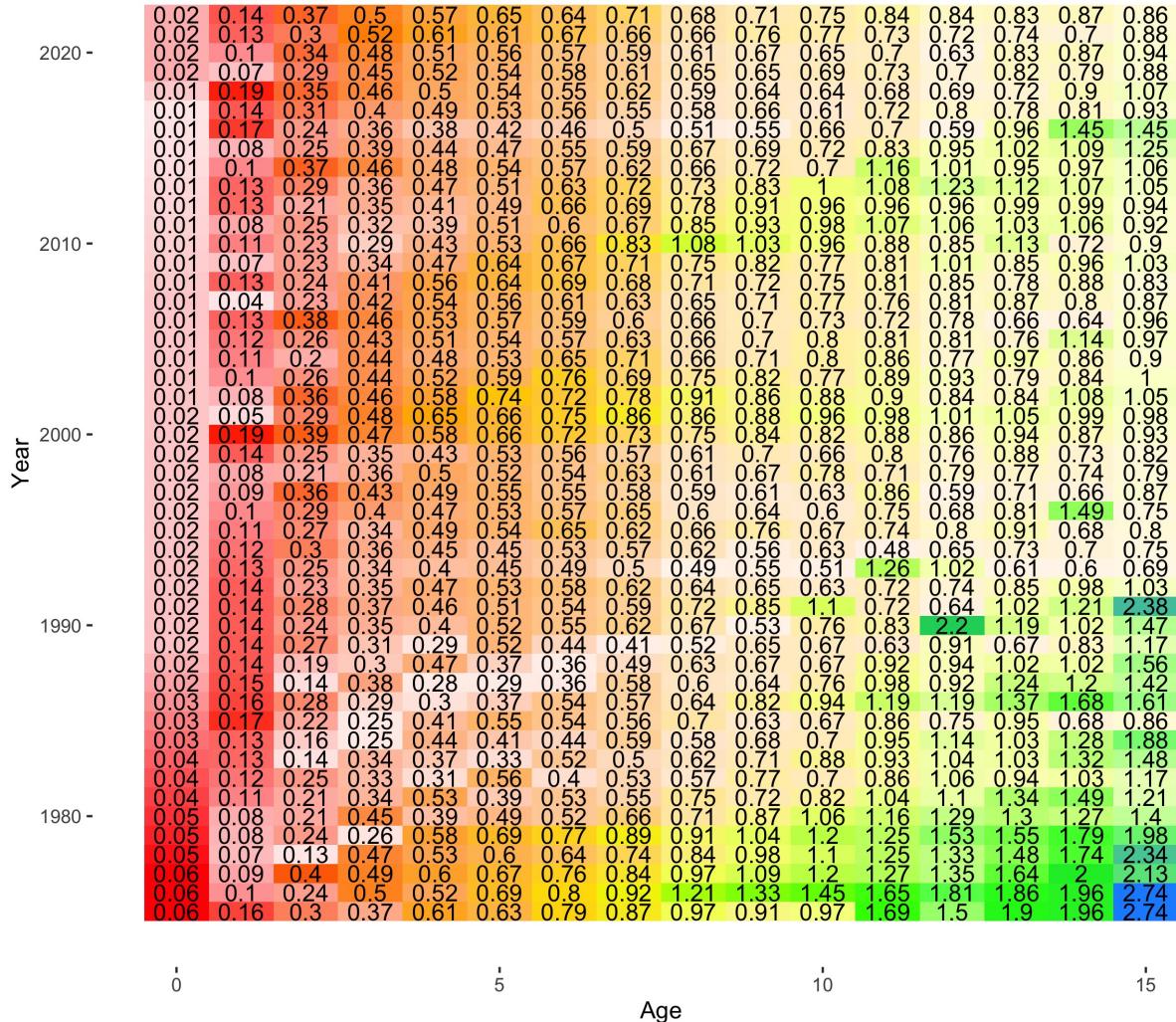
look further into the unsexed weight-at-age curve adn split the data by country, we see that the unsexed weight-at-age follow the Canadian females closely. This could mean that the Canadian Fishery may be catching proportionally more females, or it could mean they just happen to be catching really large males.



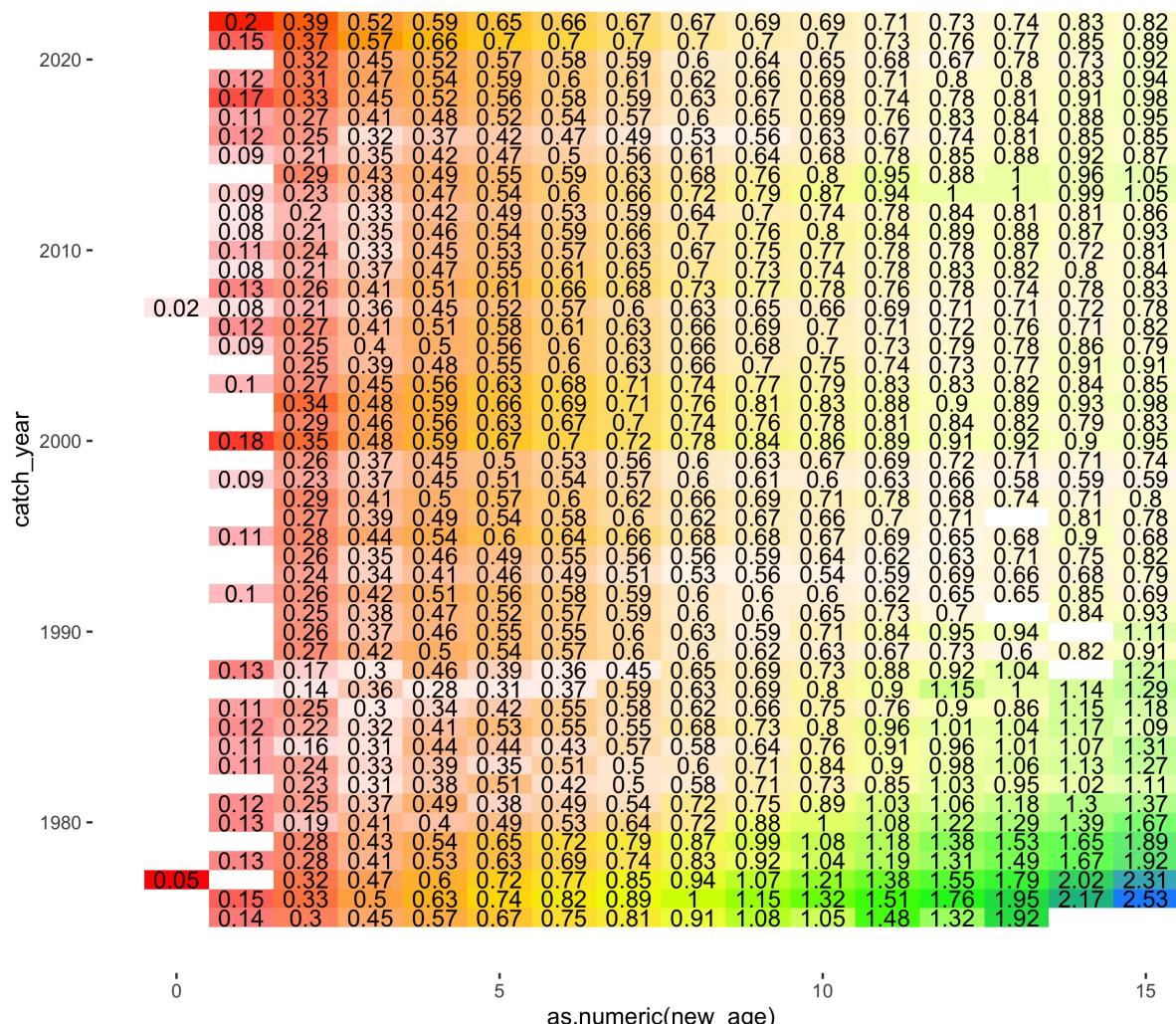
Check sample size in each variable (cohort x year)

Differences between model predictions and current EWAA

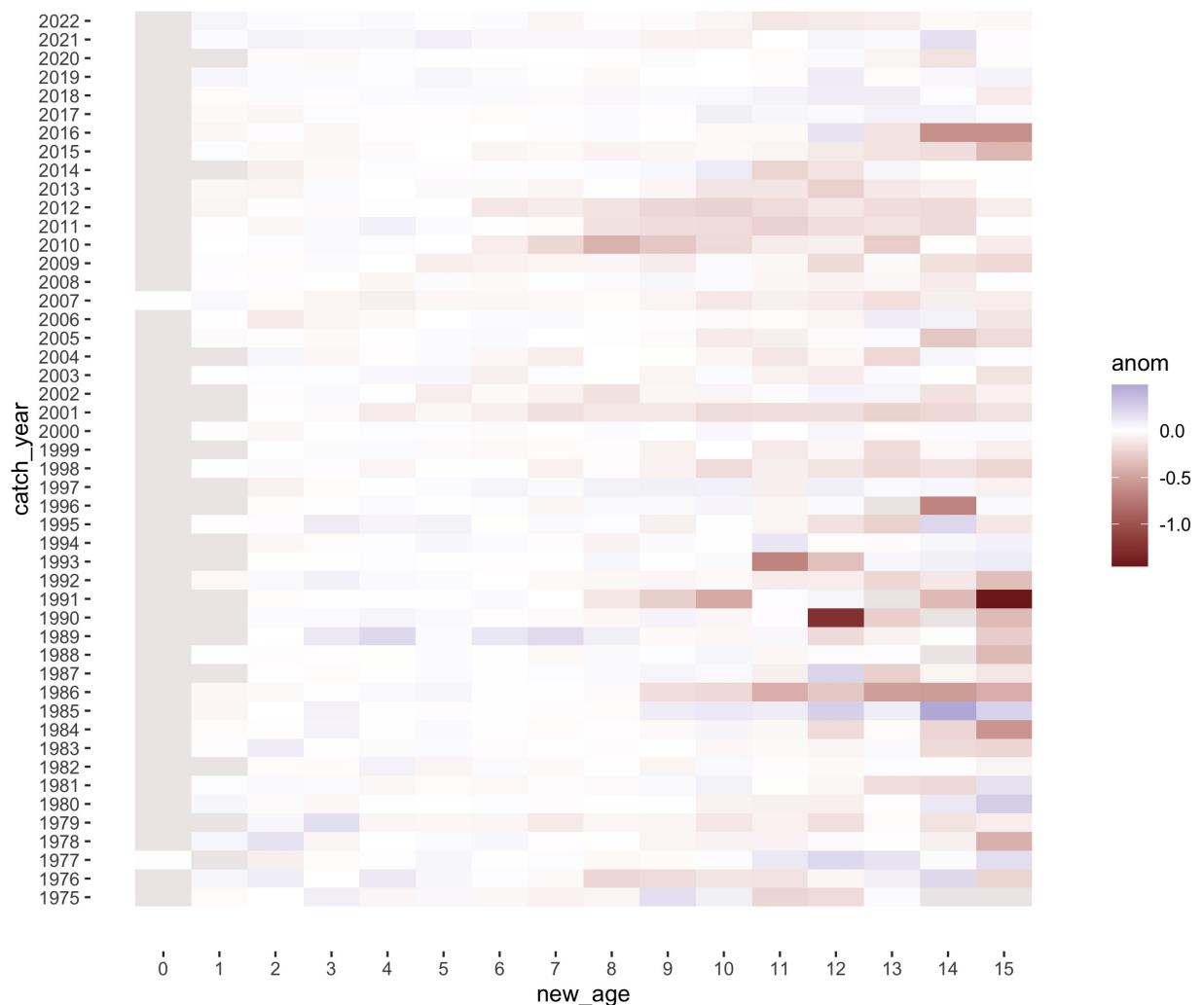
Below are the heatmaps for the currently used empirical weight at age from the hake assessment github



and here's a similar heatmap but using the predictions from the fishery and survey models. I pooled together all of the predictions from both the models. I did not apply any weight to either. The survey predictions dataset was MUCH larger than the fishery predictions dataset due to the fact that the survey data was expanded spatially and the fishery data was not. Once the data was pooled, I grouped by age and year and simply took the average to create the empirical weight-at-age.



Below is now the matrix showing the deviations between predictions and the observations (i.e. the two heatmaps).



Also created this fun map which shows how the survey spatial coverage changes from year to year. Some years miss Canada, which means they're missing larger fish and potentially skewing the ewaa toward lighter weight-at-age fish. I still need to add the year labels...

