

# Hake Notes

Andrea Odell

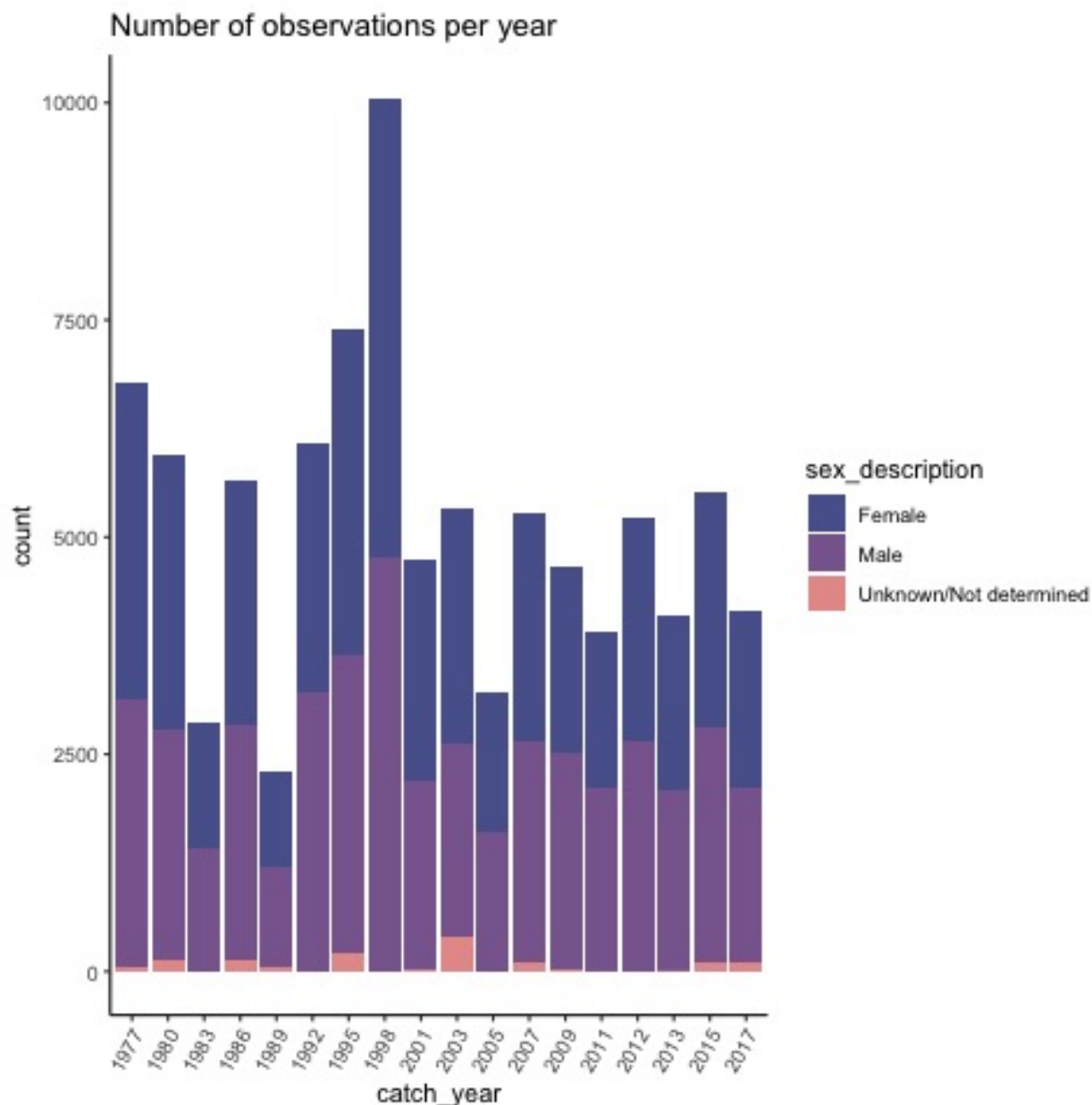
2022-07-04

## 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 . . . . .	30
Aug 22-29 . . . . .	39
Sept 12-16 . . . . .	48
Sept 19-23 . . . . .	49
Sept 26-30 . . . . .	51

### 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

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

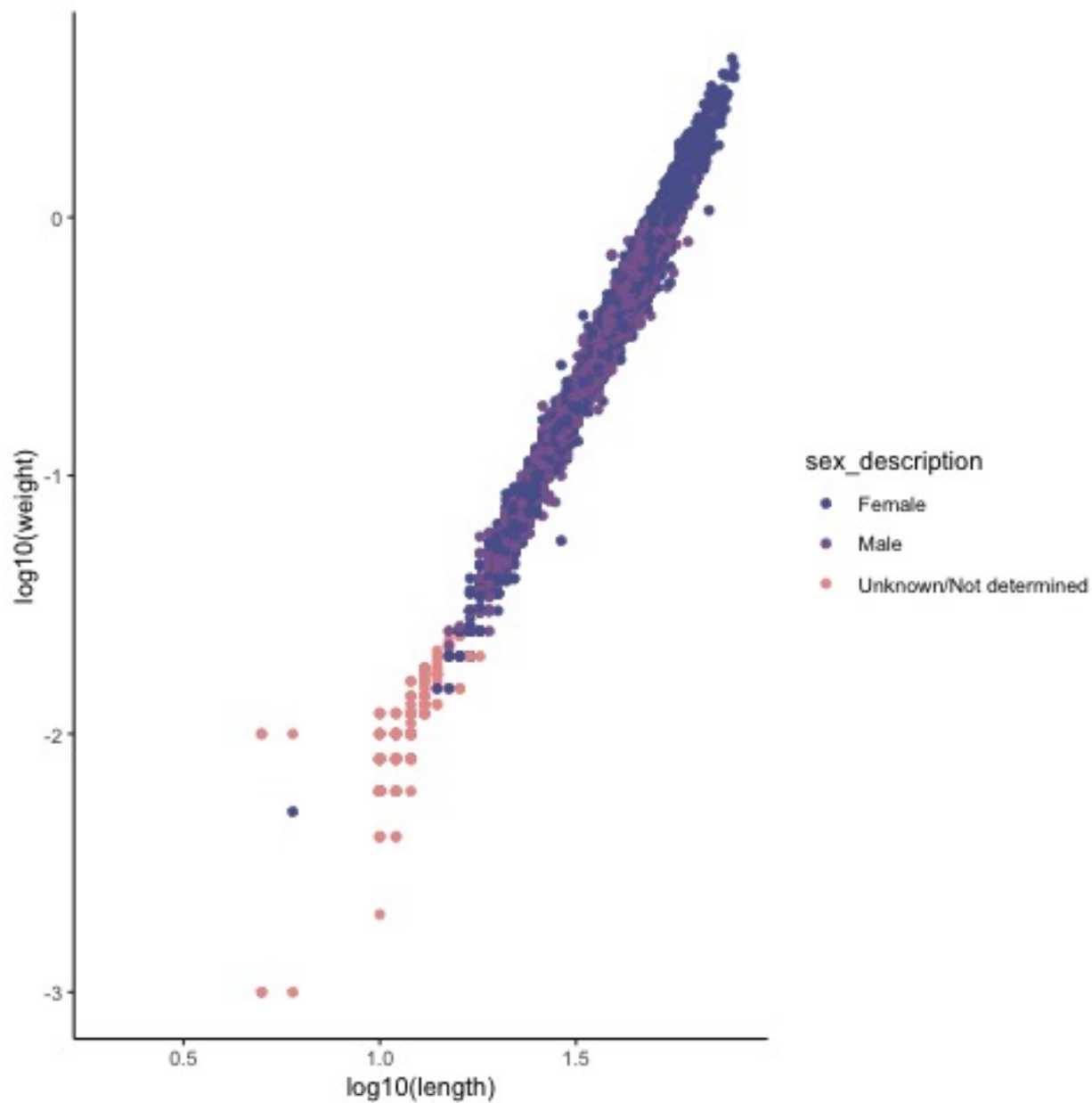
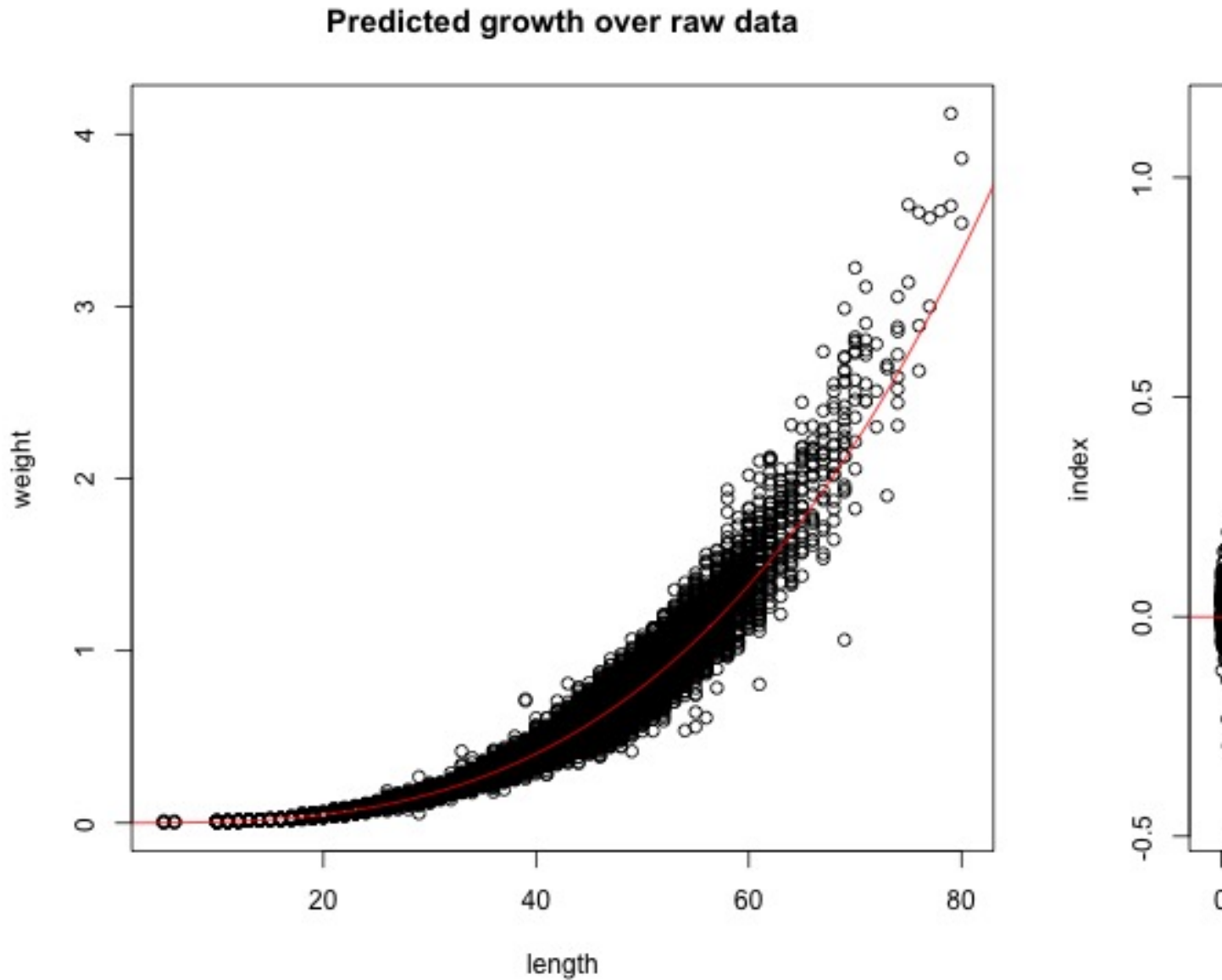


Figure 1: Log10-transformed length weight relationship



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?).

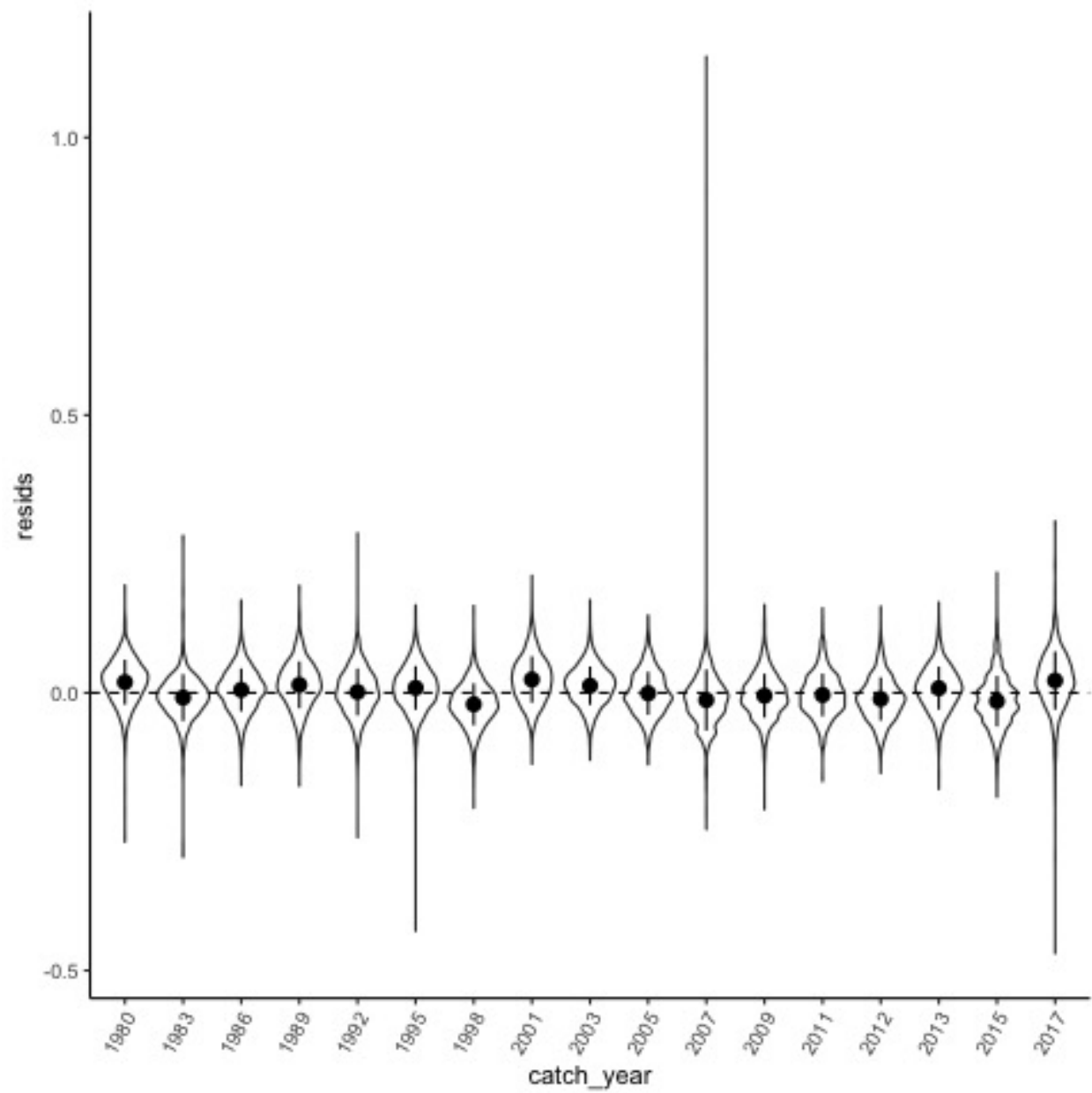


Figure 2: Summary of growth anomalies per year

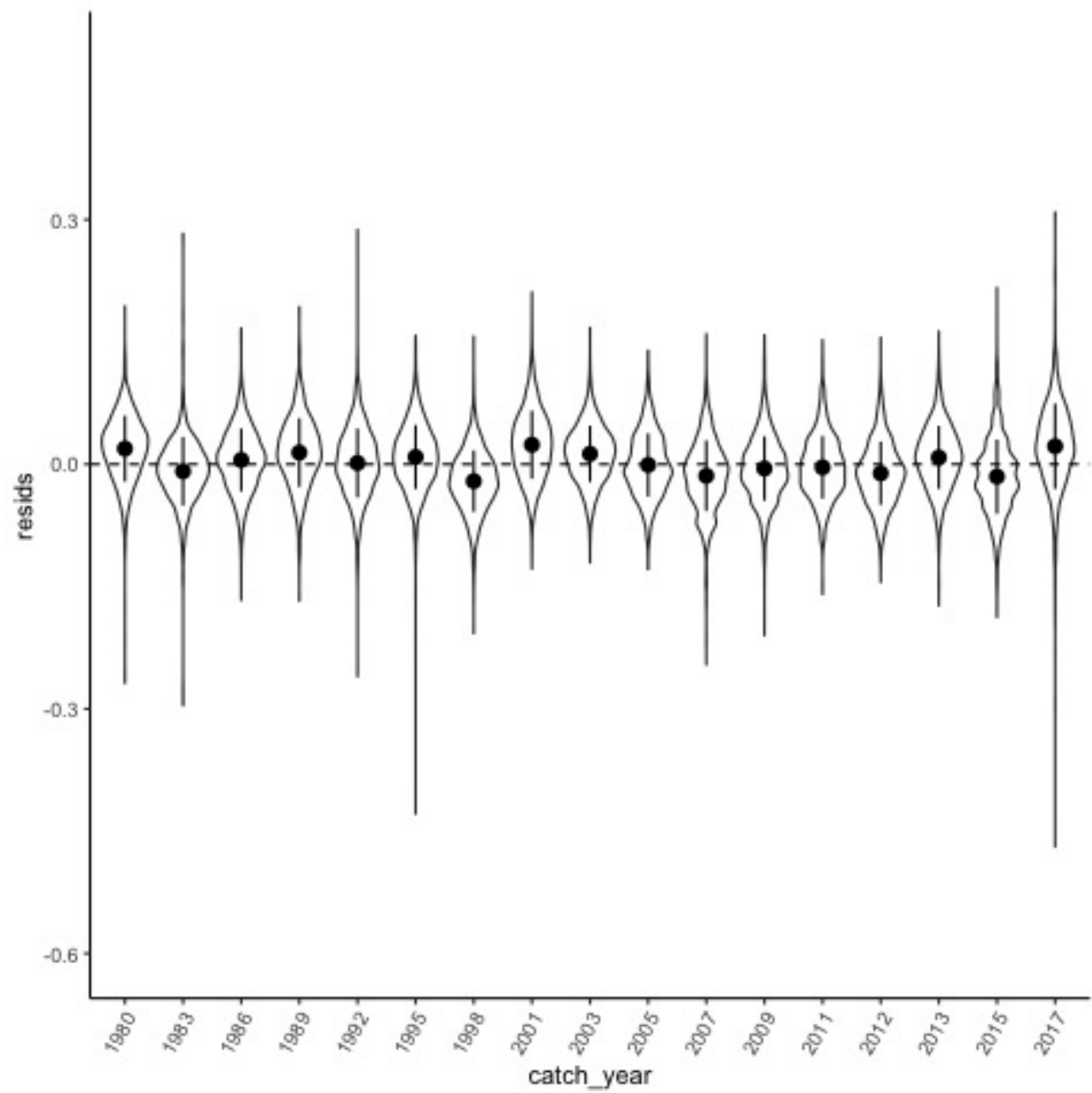


Figure 3: outlier removed

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

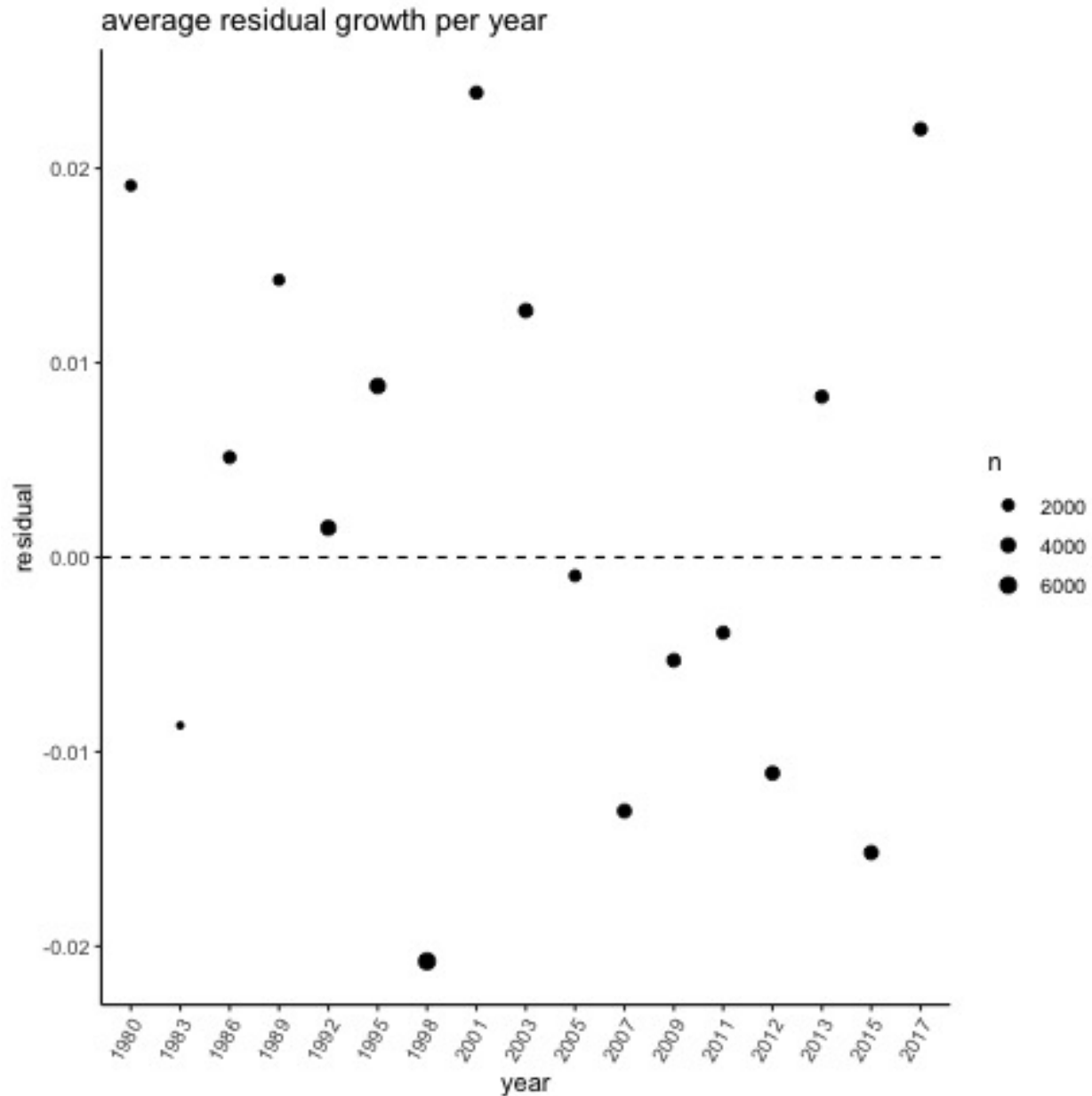


Figure 4: Avg growth anomalies per year

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

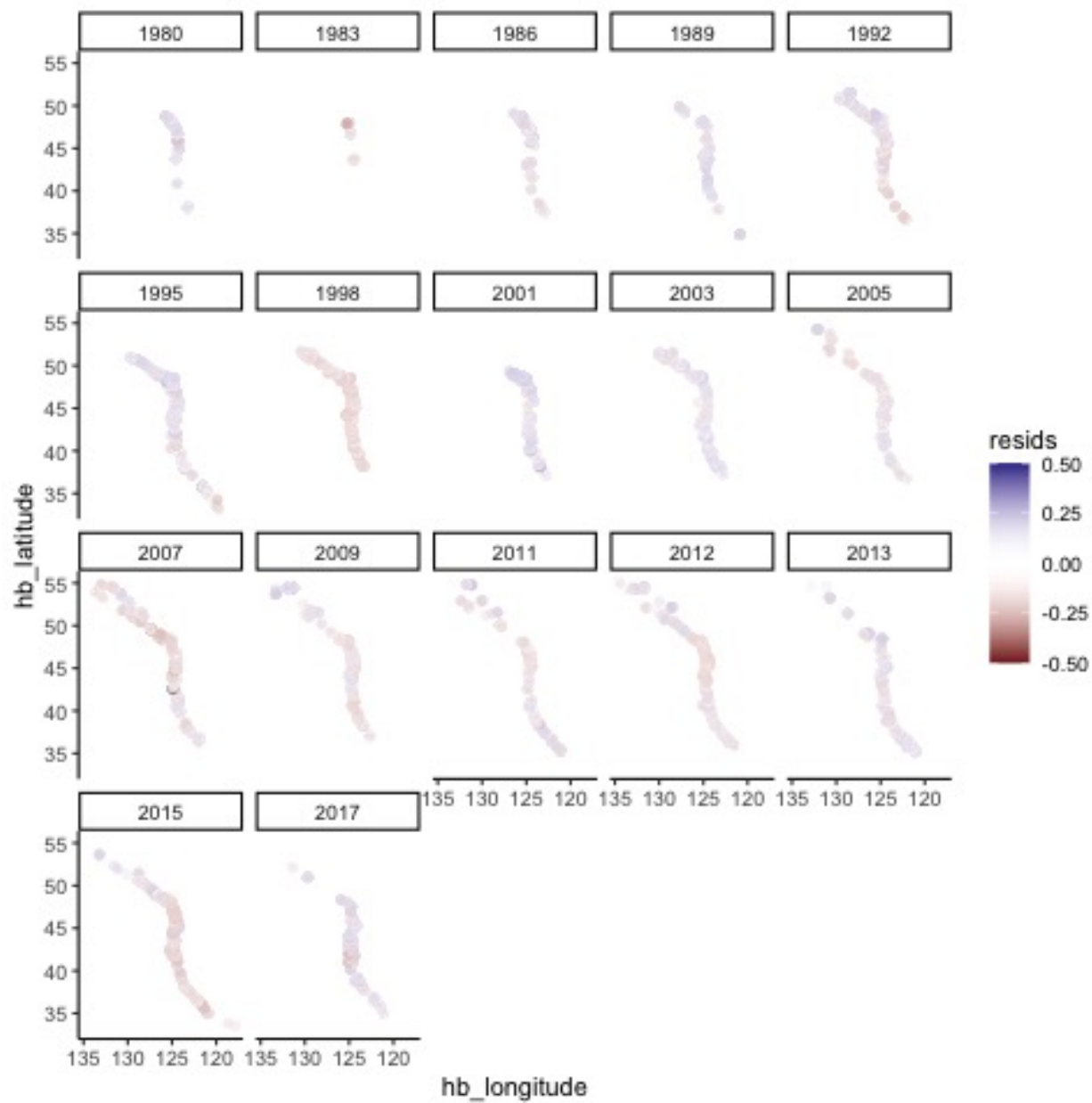


Figure 5: Spatial variation of growth anomalies by year



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.

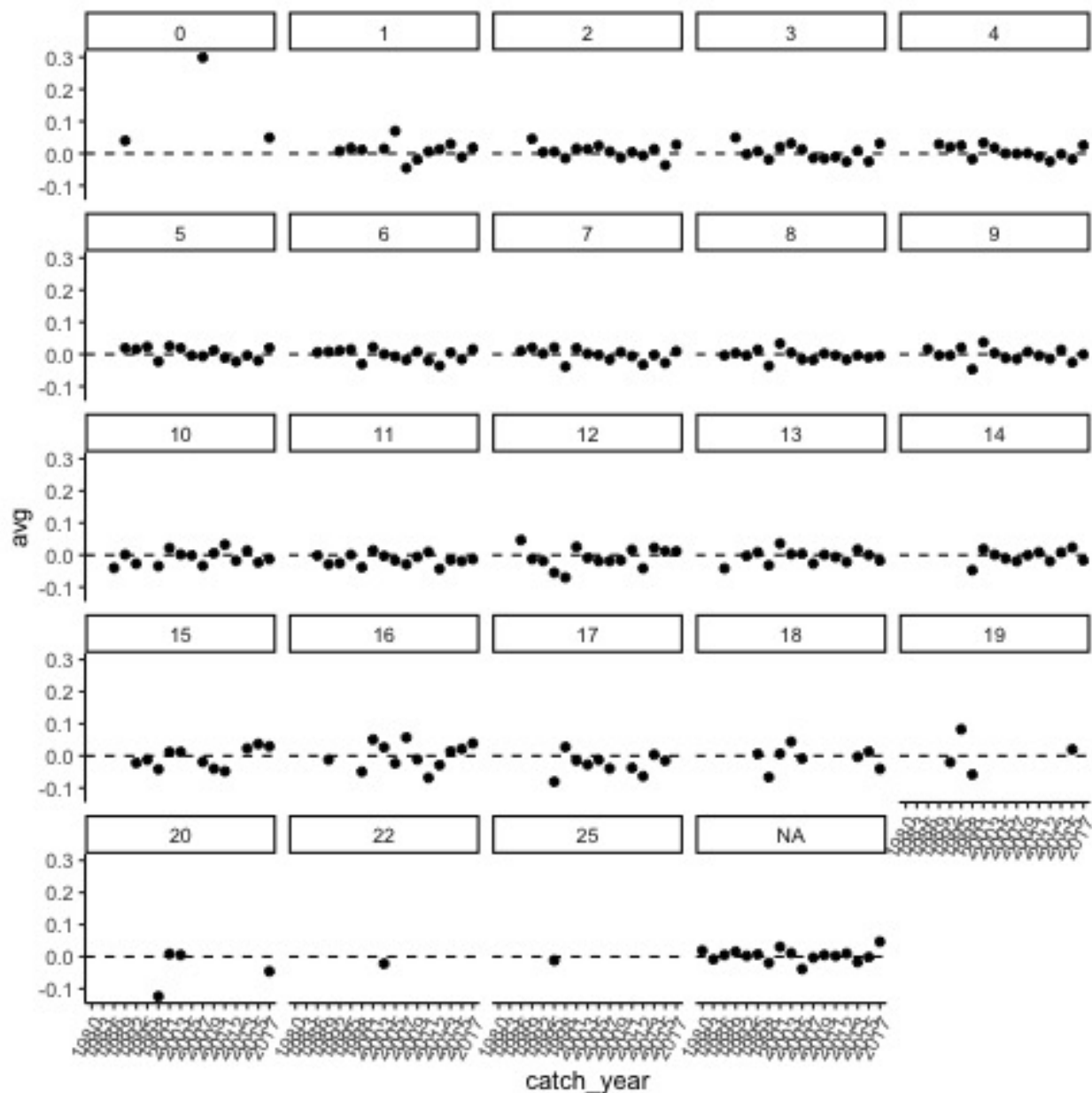


Figure 6: growth anomalies timeseries by age

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.

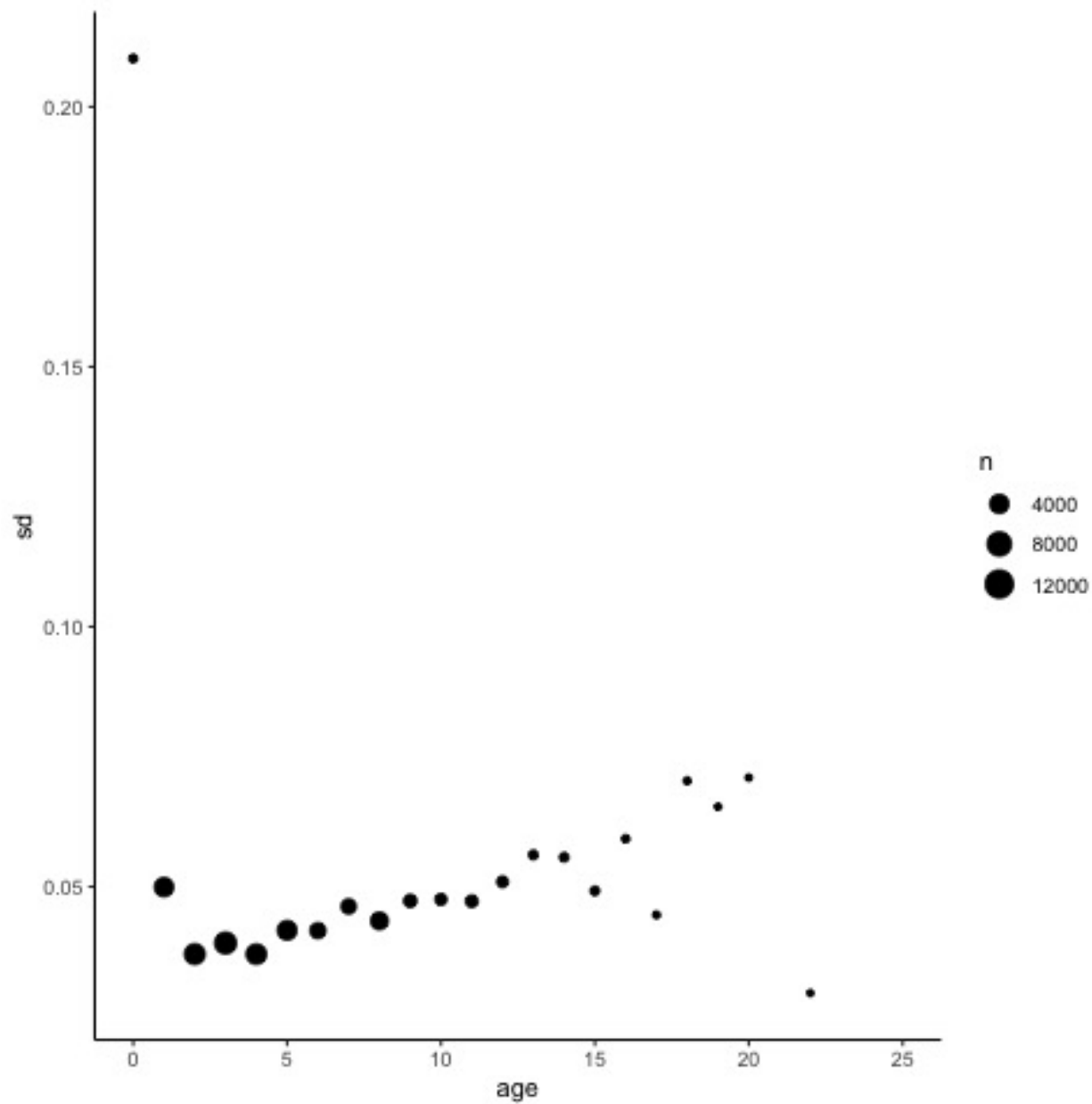


Figure 7: Variability of growth anomaly by age

## 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 subsetting 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.

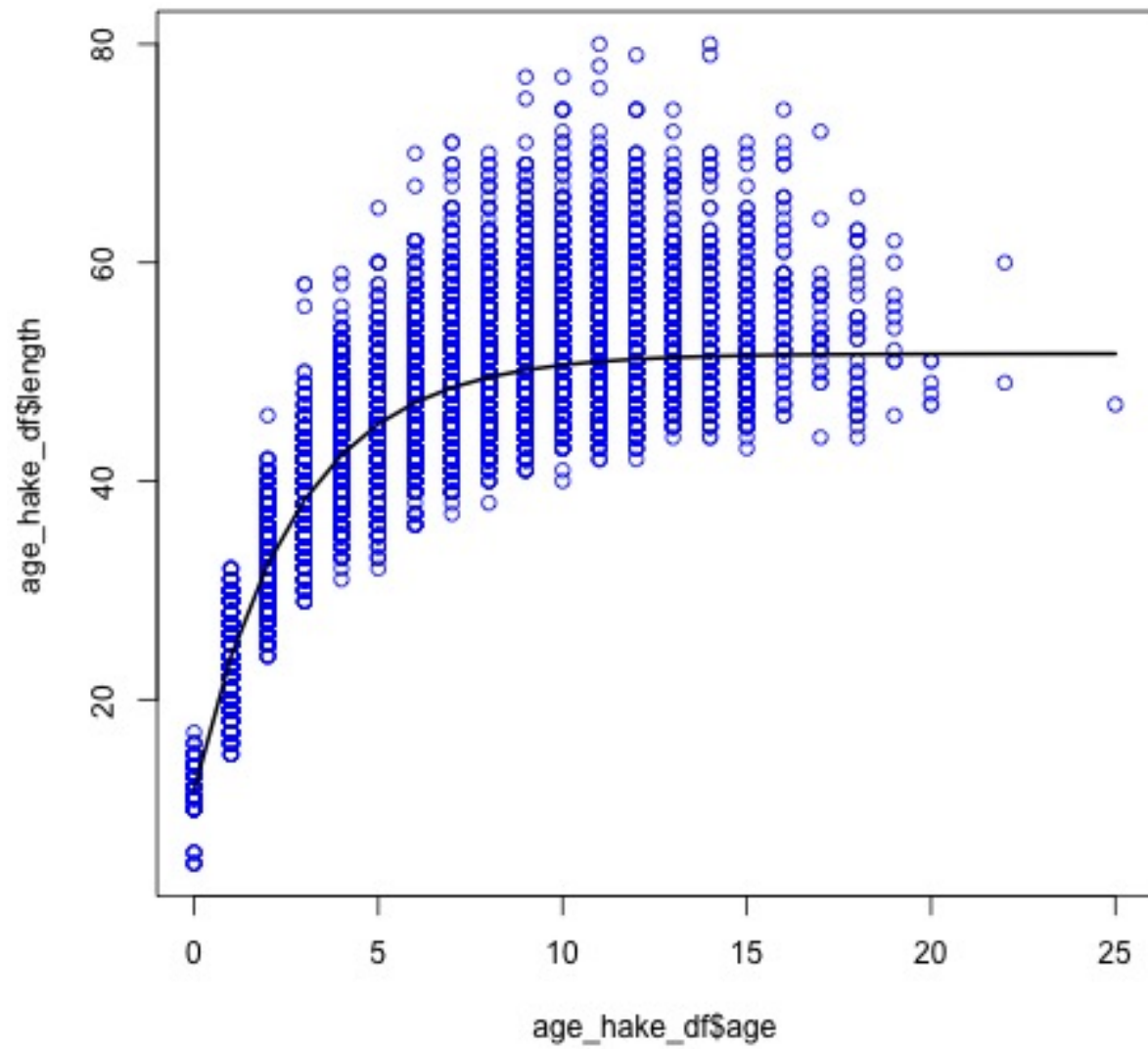
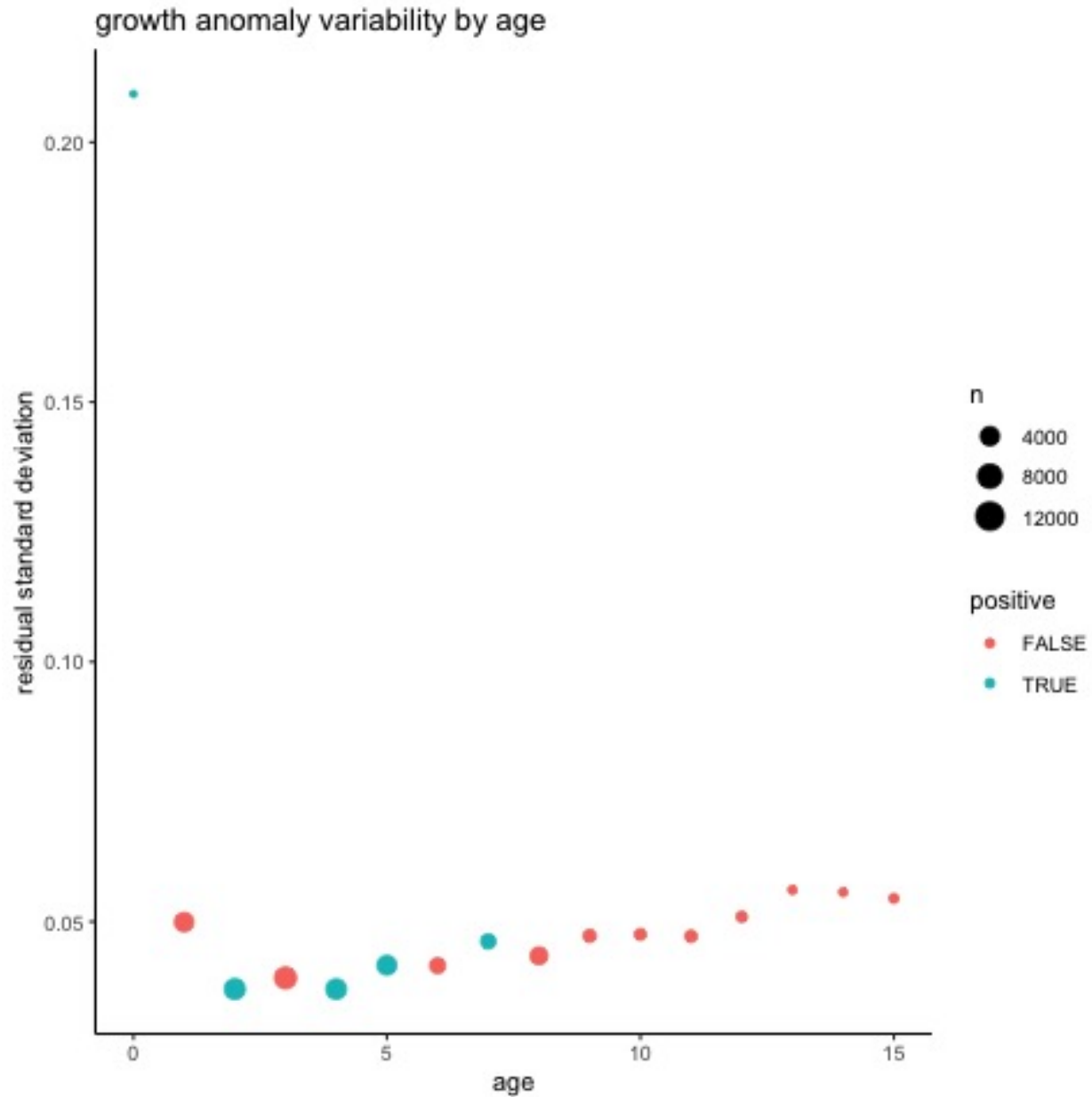
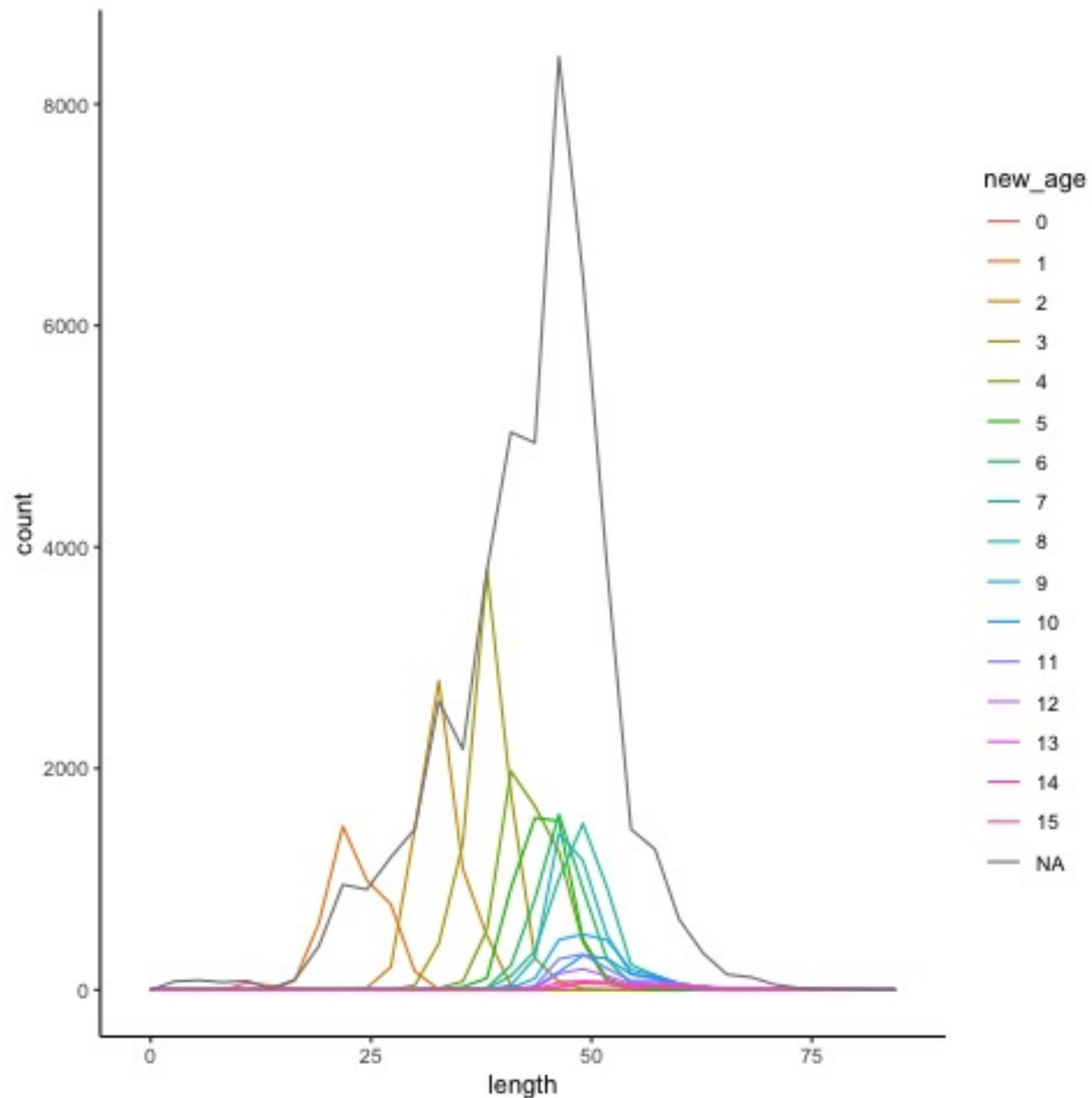


Figure 8: Growth curve to whole data



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 lie stages, stay fatter throughout their life?
  - Ultimately, how can we develop a model that goes into the MSE?
- Next steps:

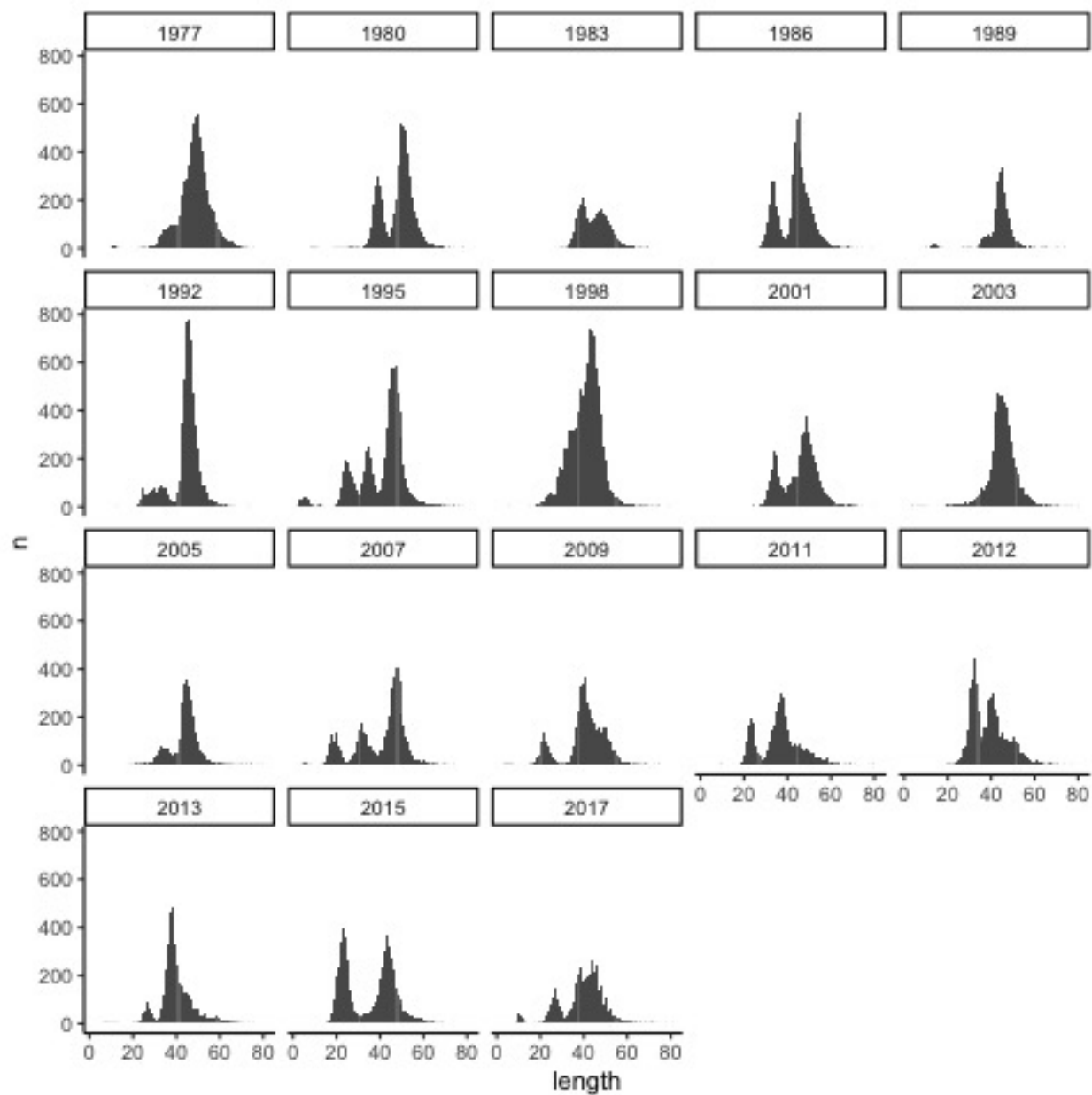
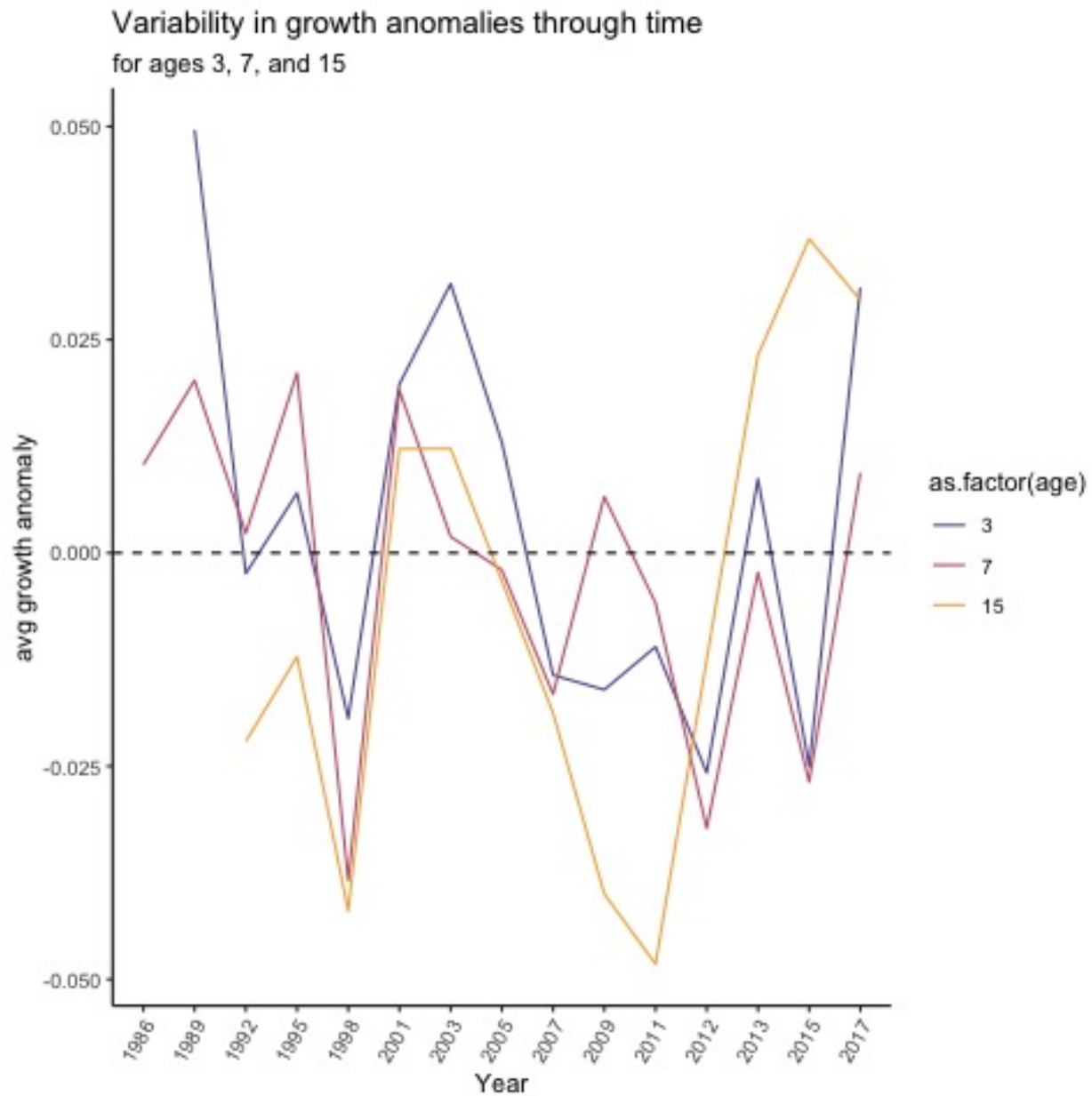


Figure 9: Length frequencies by year

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

July 11-15, 2022

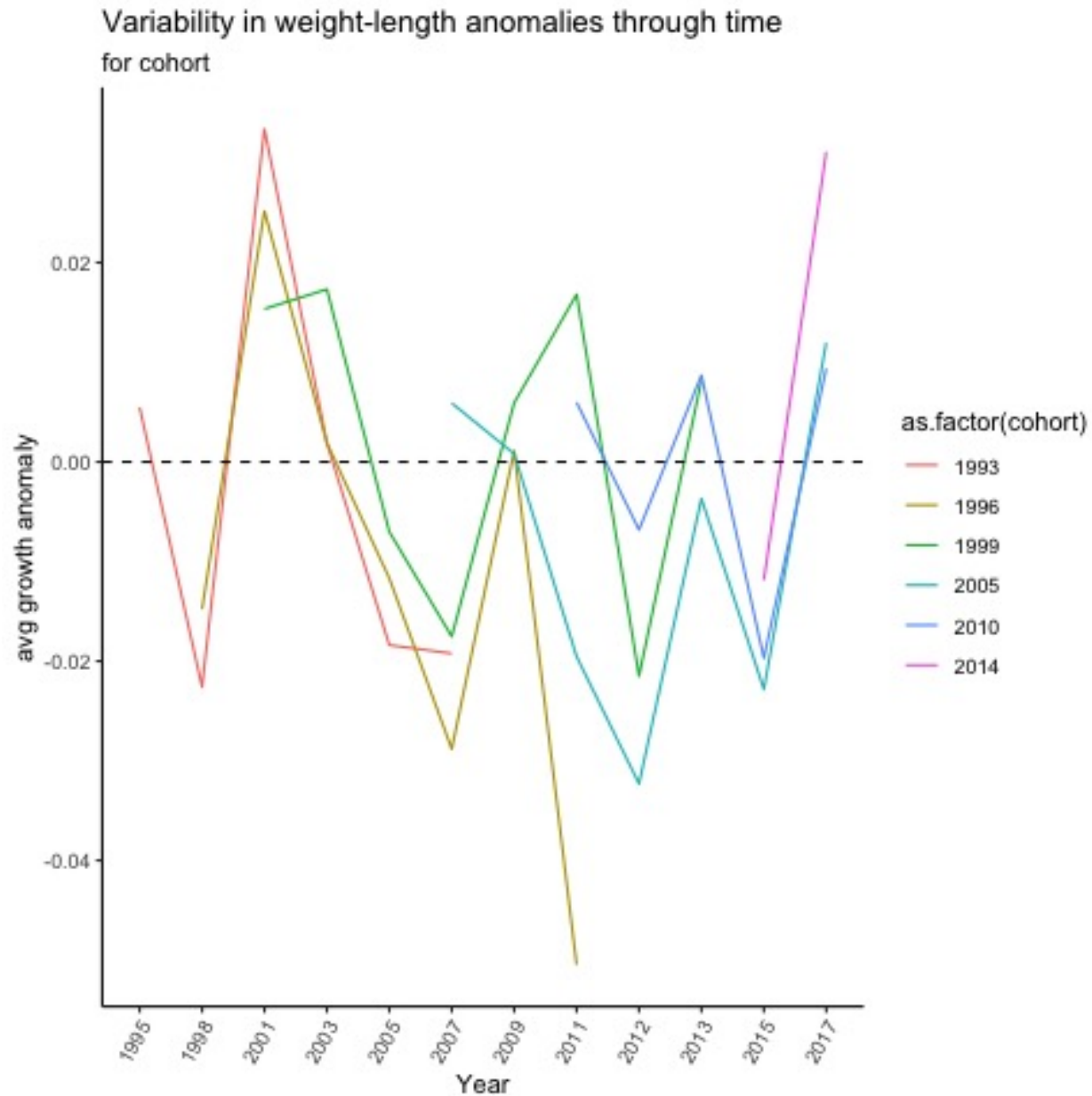
How do weight-length anomalies vary through time for a specific age?



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\_wtatage()
    - \* 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

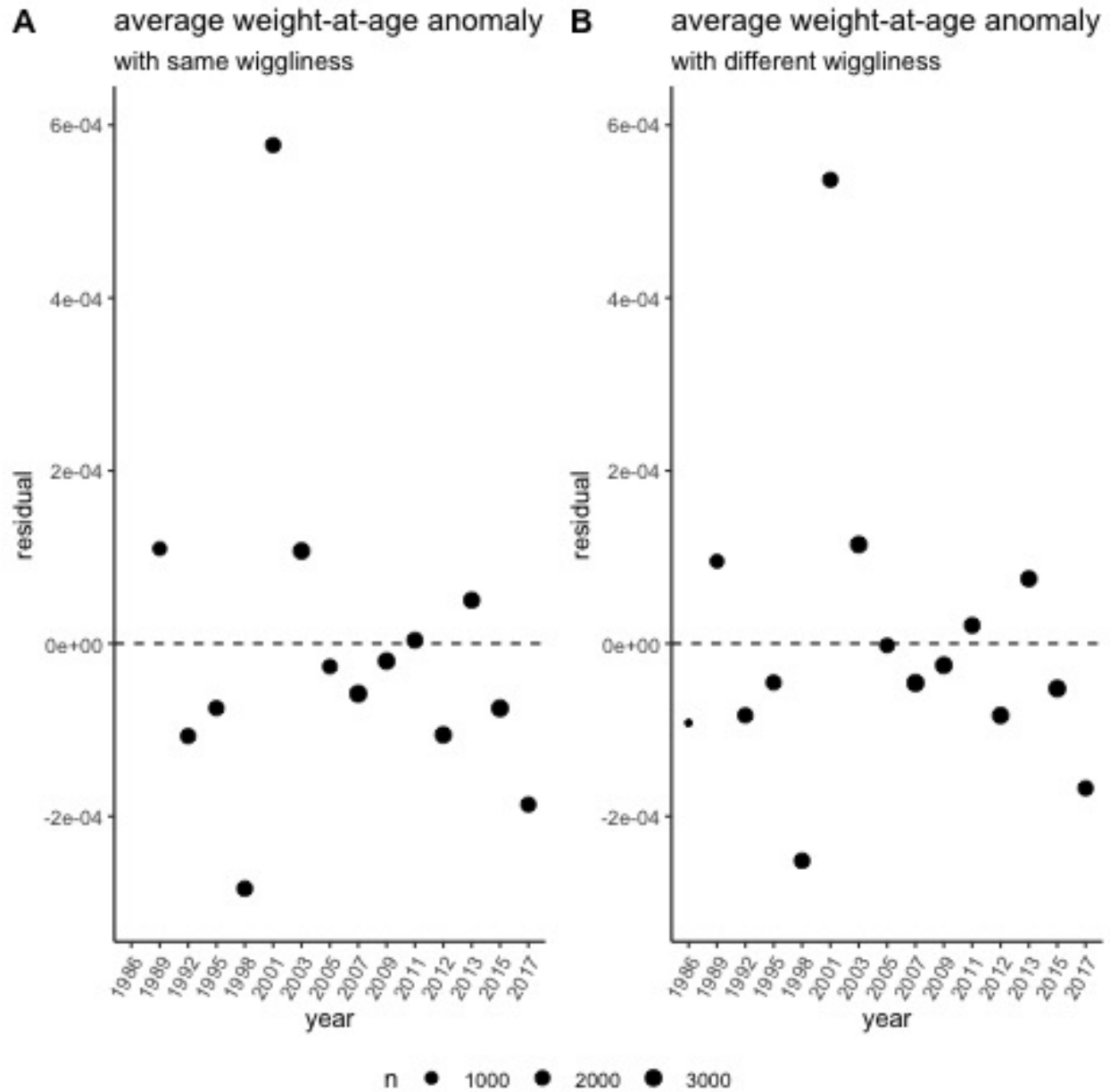
```
gam_out <- gam(weight ~ s(new_age), data = hake_weight_age_df, method = "REML")
```

2. GAM with group-level smoothers with different wiggleness 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 wiggleness 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")
```

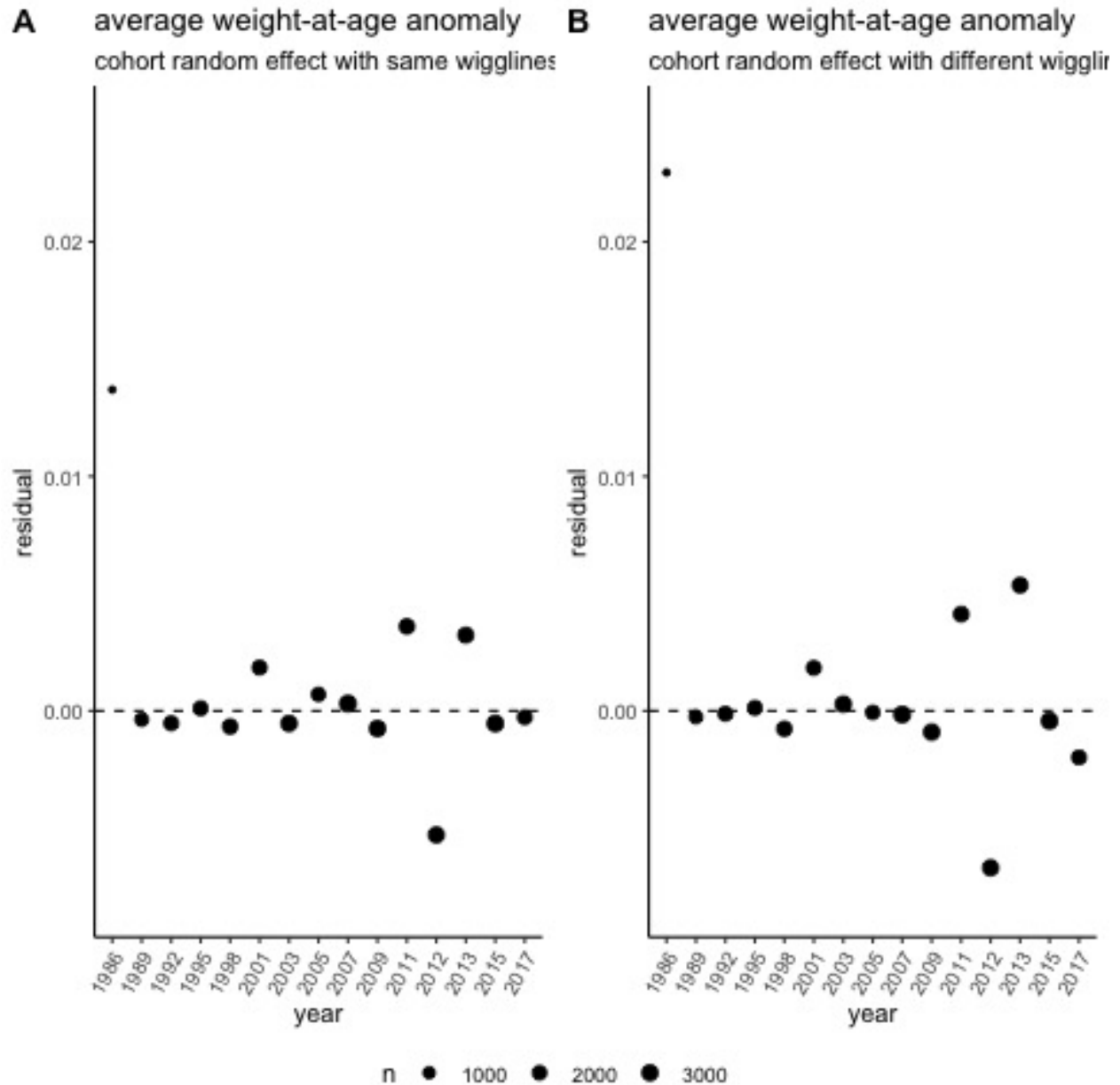


4. GAM with group-level smoothers with different wigginess for cohort

```
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 wigginess 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")
```



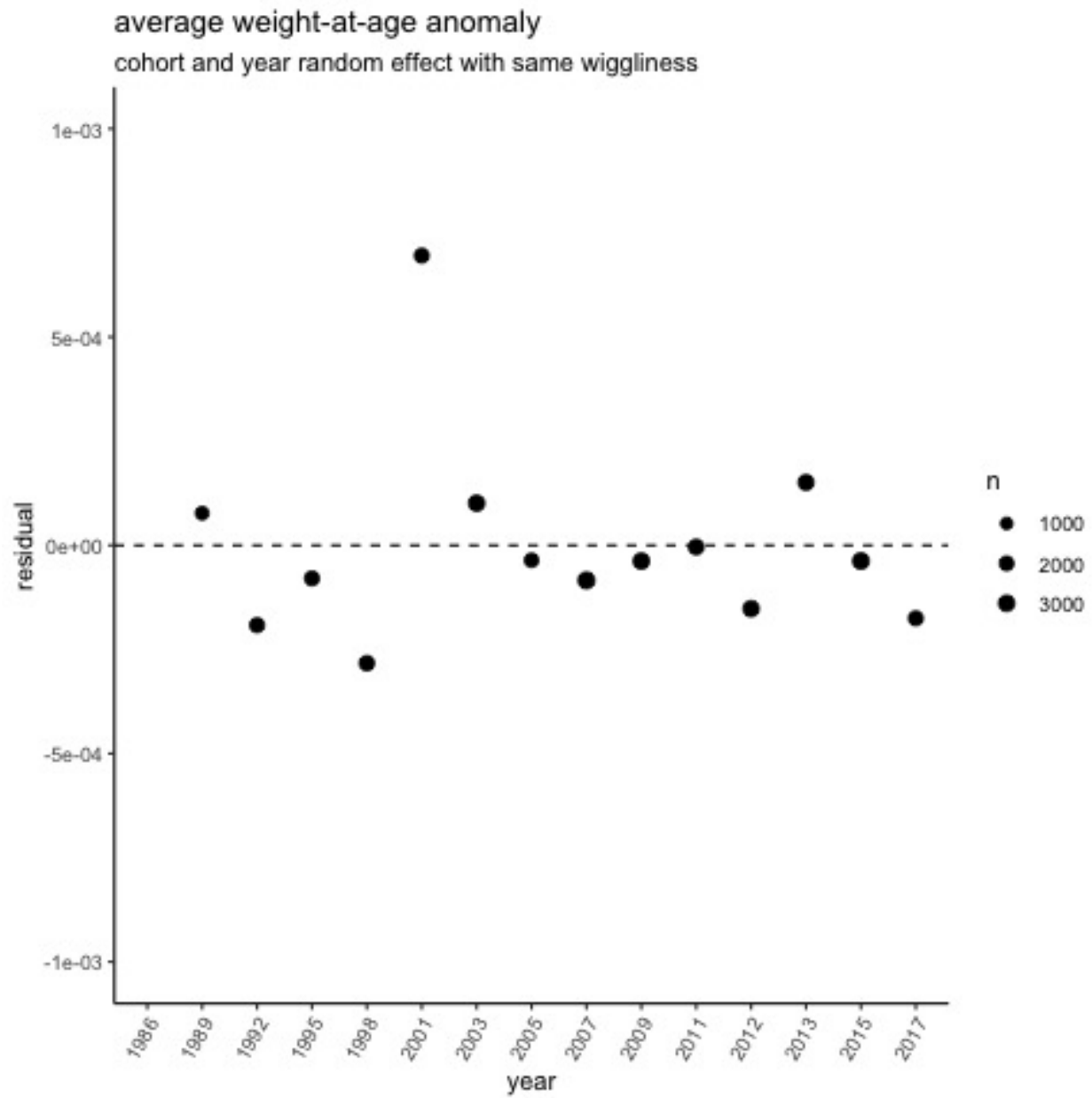
July 18-22, 2022

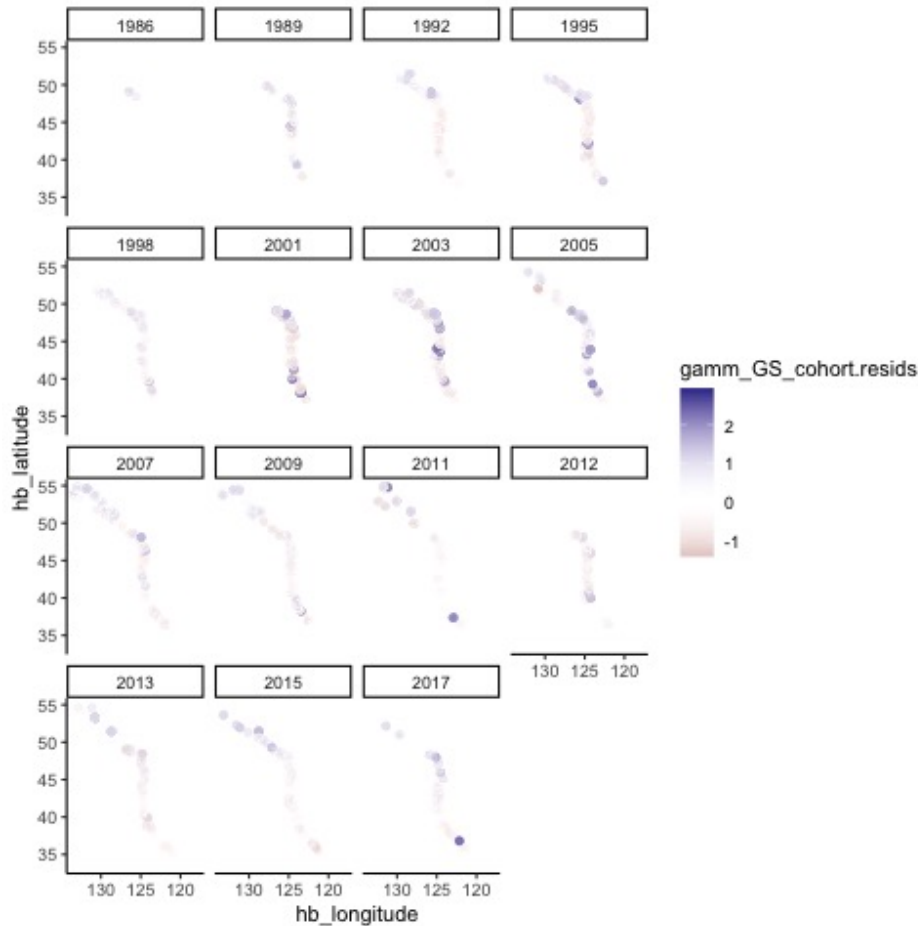
Of all 5 models, `gamm_GS_cohort_out` had the smallest AIC value.

- 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 wiggleness 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")
```





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 wiggleness (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 Mallick 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 wiggleness” where each cohort and year had their own wiggleness/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

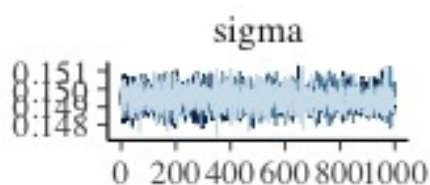
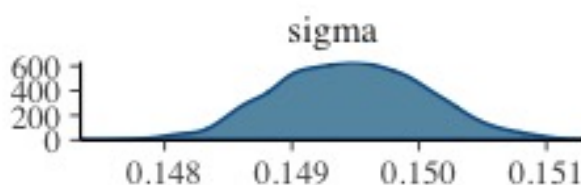
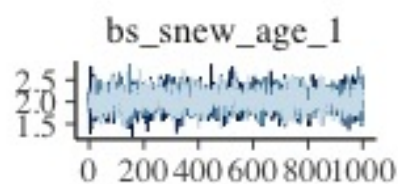
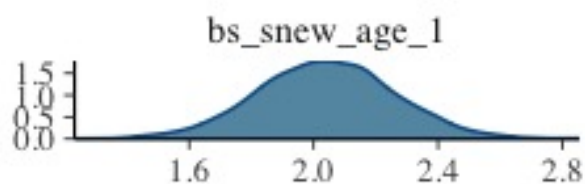
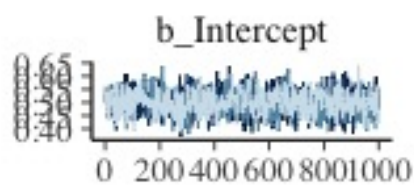
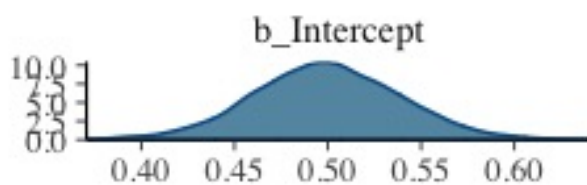
```
gamm_year_brm_out = brm(bf(weight ~ s(new_age) + s(catch_year, bs="re")),  
                        data = hake_weight_age_df, family = gaussian(), cores = 4,  
                        iter = 2000, warmup = 1000, chains = 4)
```

#### 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)
```

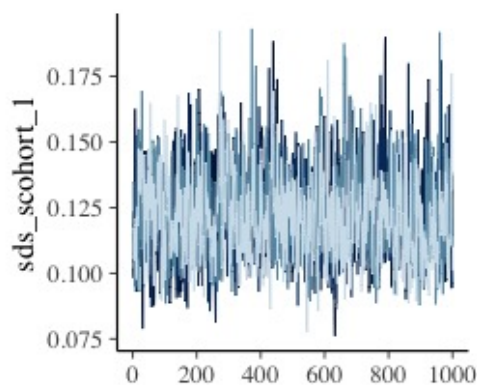
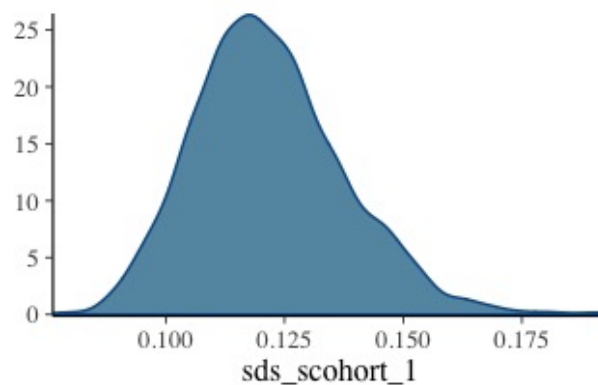
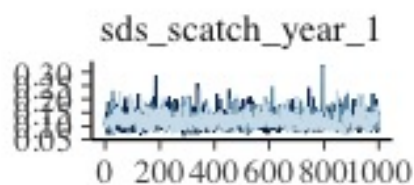
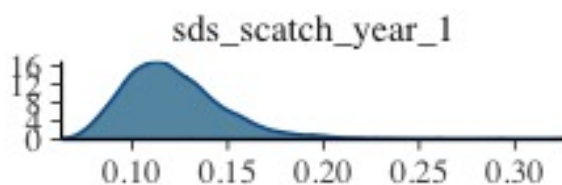
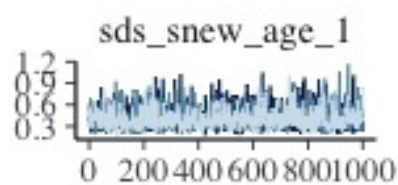
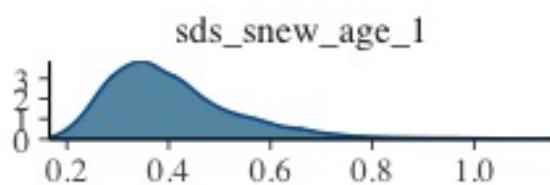
Model comparisons: elpd\_diff se\_diff gamm\_year\_cohort\_out 0.0 0.0 gamm\_year\_brm\_out -1632.4 110.9

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



Chain

- 1
- 2
- 3
- 4



Chain

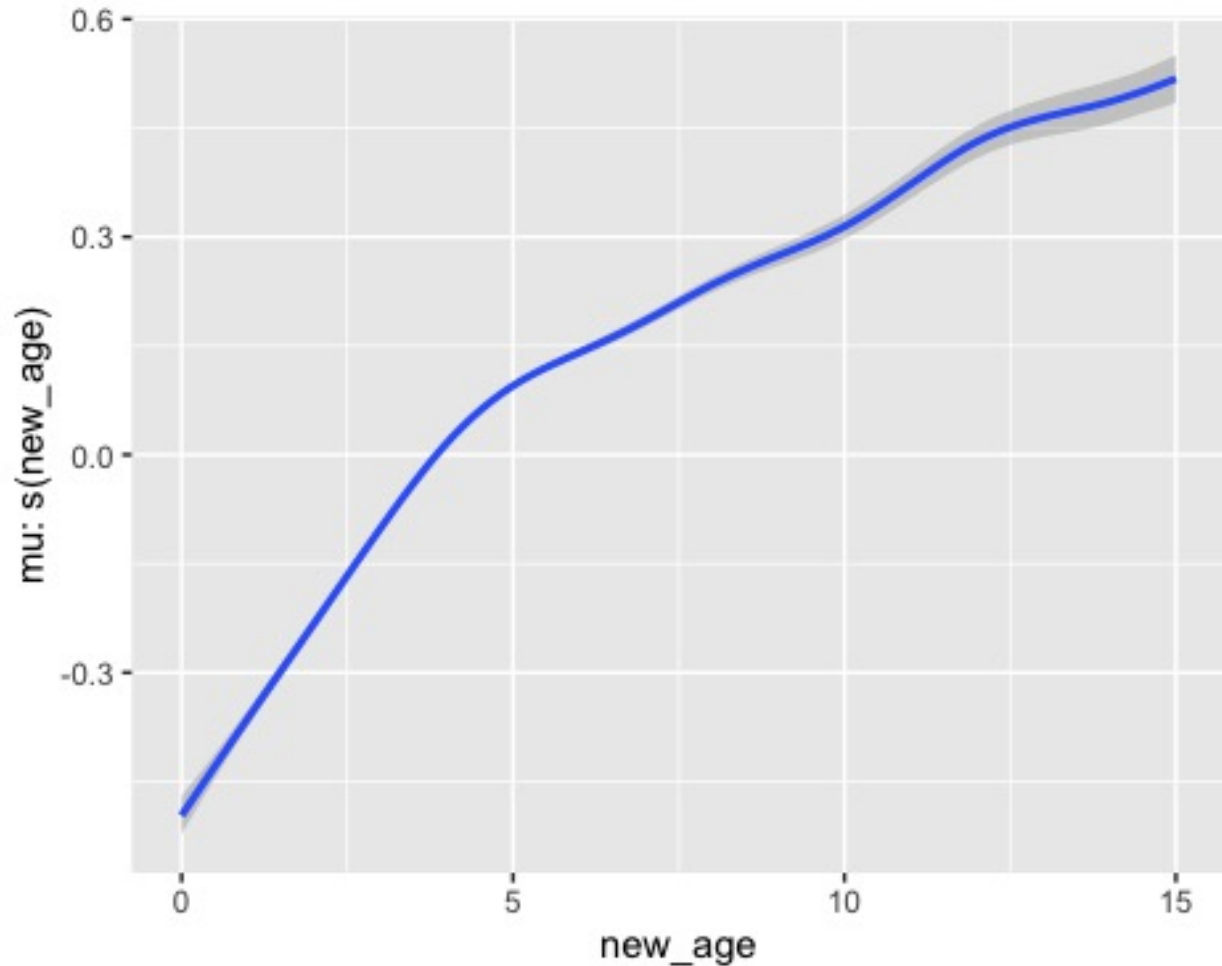
- 1
- 2
- 3
- 4

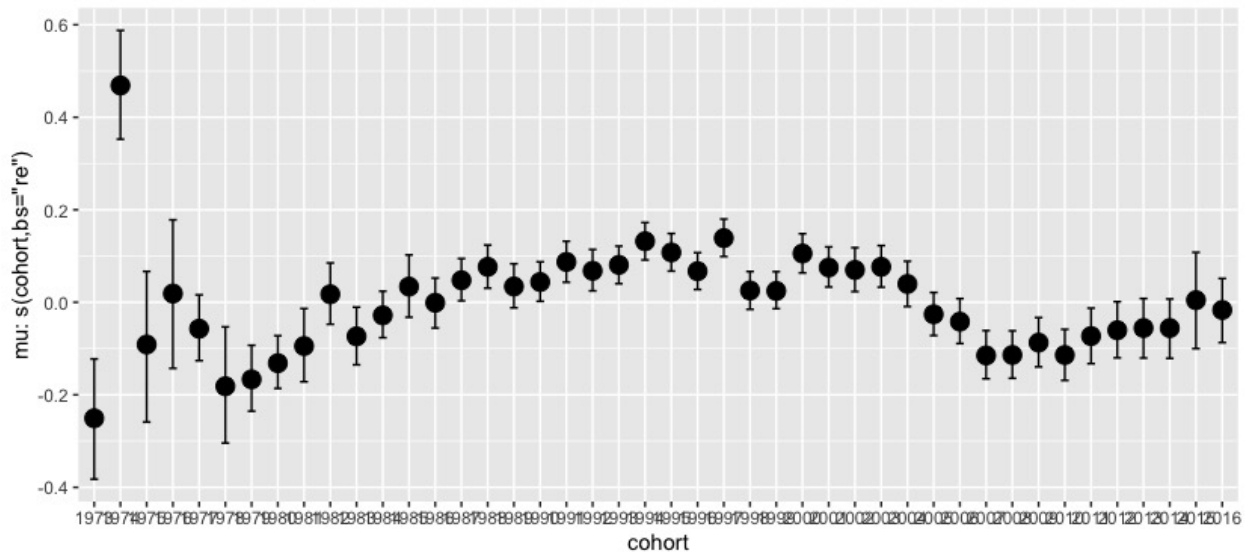
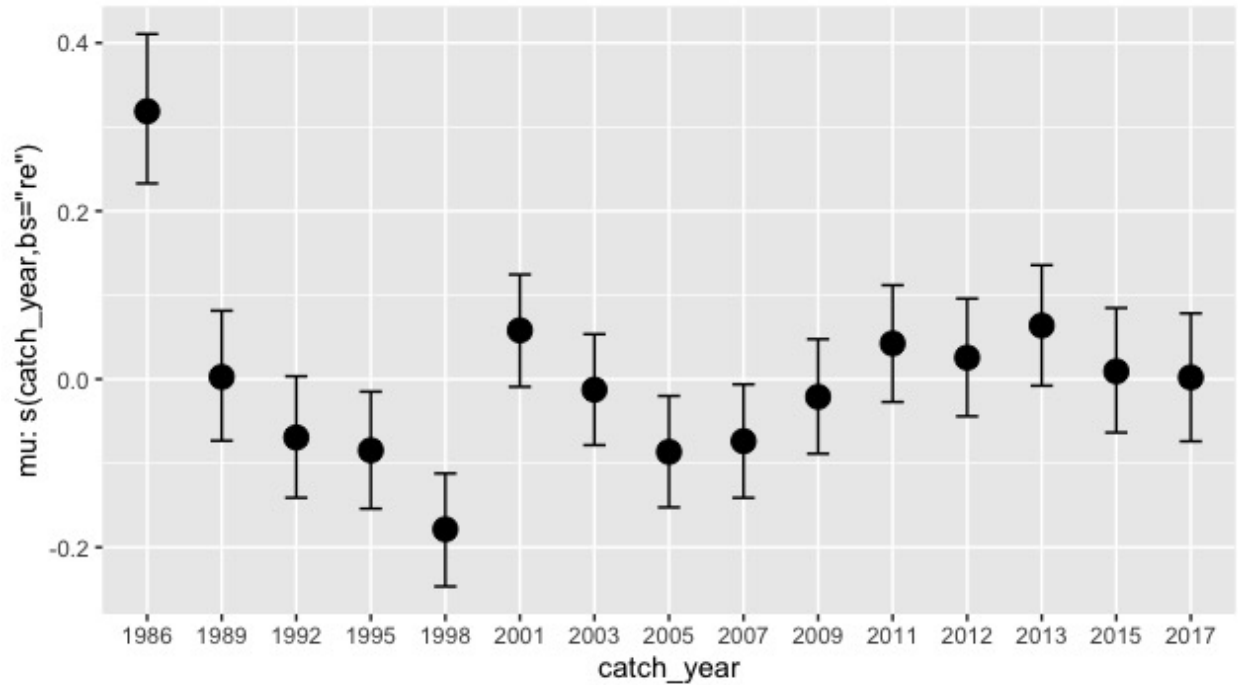


Density and traceplots look good - got the hairy caterpillars

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

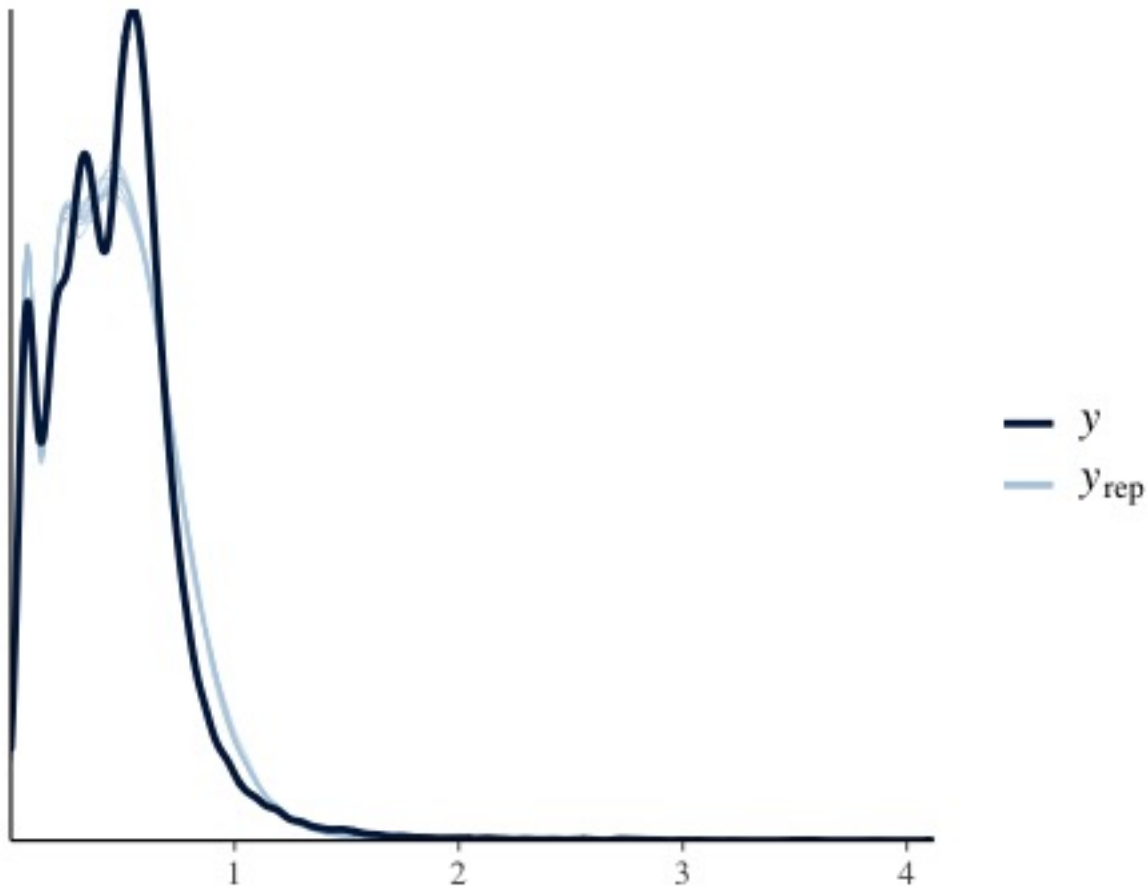
### Notes from presentation

- 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?

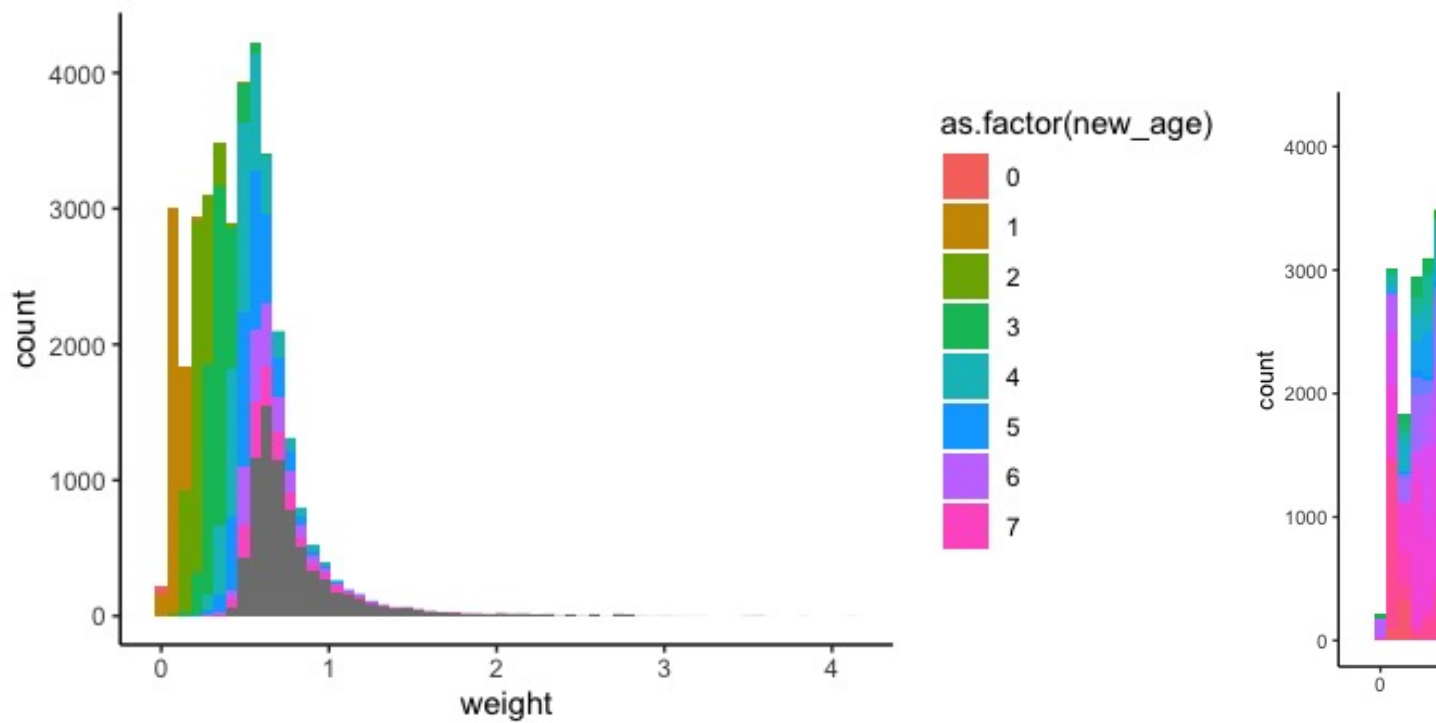
- Motivations for population dynamics fellowship
  - Lay the groundwork for what we might build into a forecast (so instead of interpolating, we can extrapolate)
  - They want to include an internally estimate weight at age into FIMS, and so this work can directly inform how they do that

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.



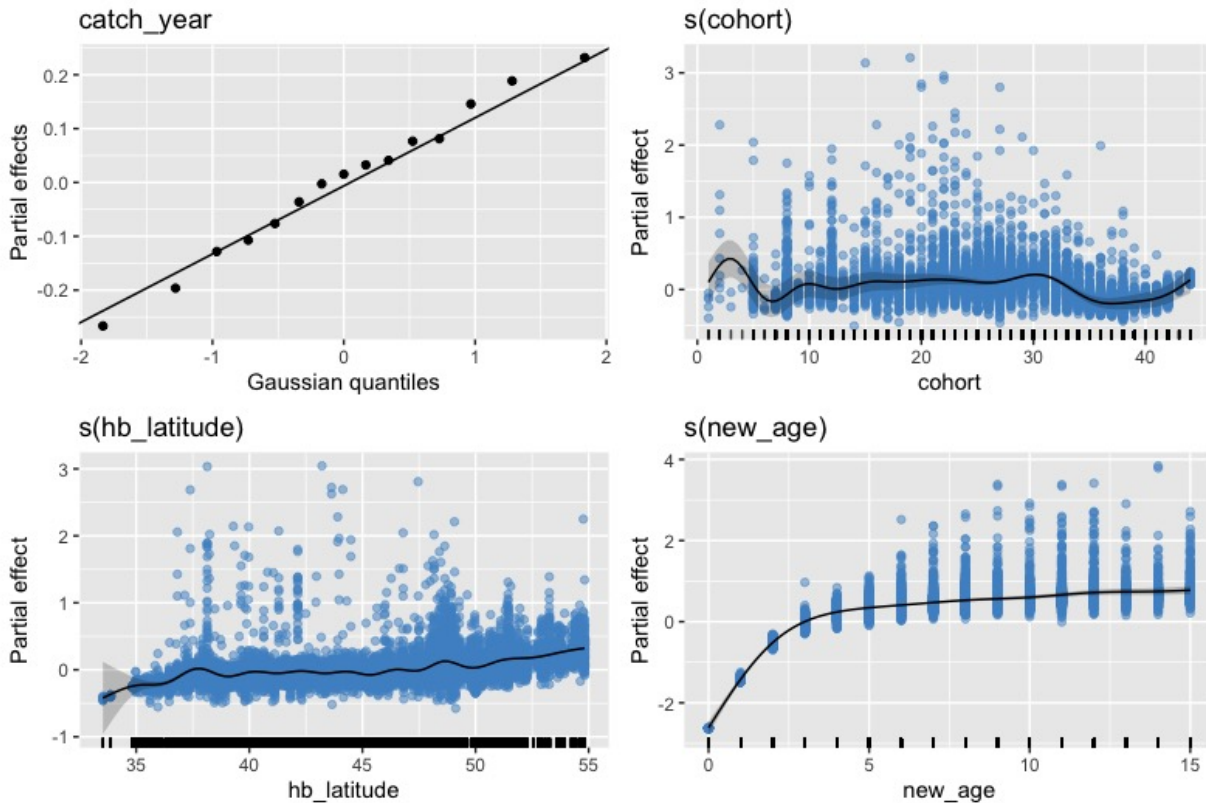
So, what are those peaks? Through some simple visualisation, it looks like the peaks are associated with ages as opposed to cohorts. The first peak is the age 1 individuals, the second peak is ages 2 and 3, and the third peak is a compilation of the rest of the ages.



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

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 estimation 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

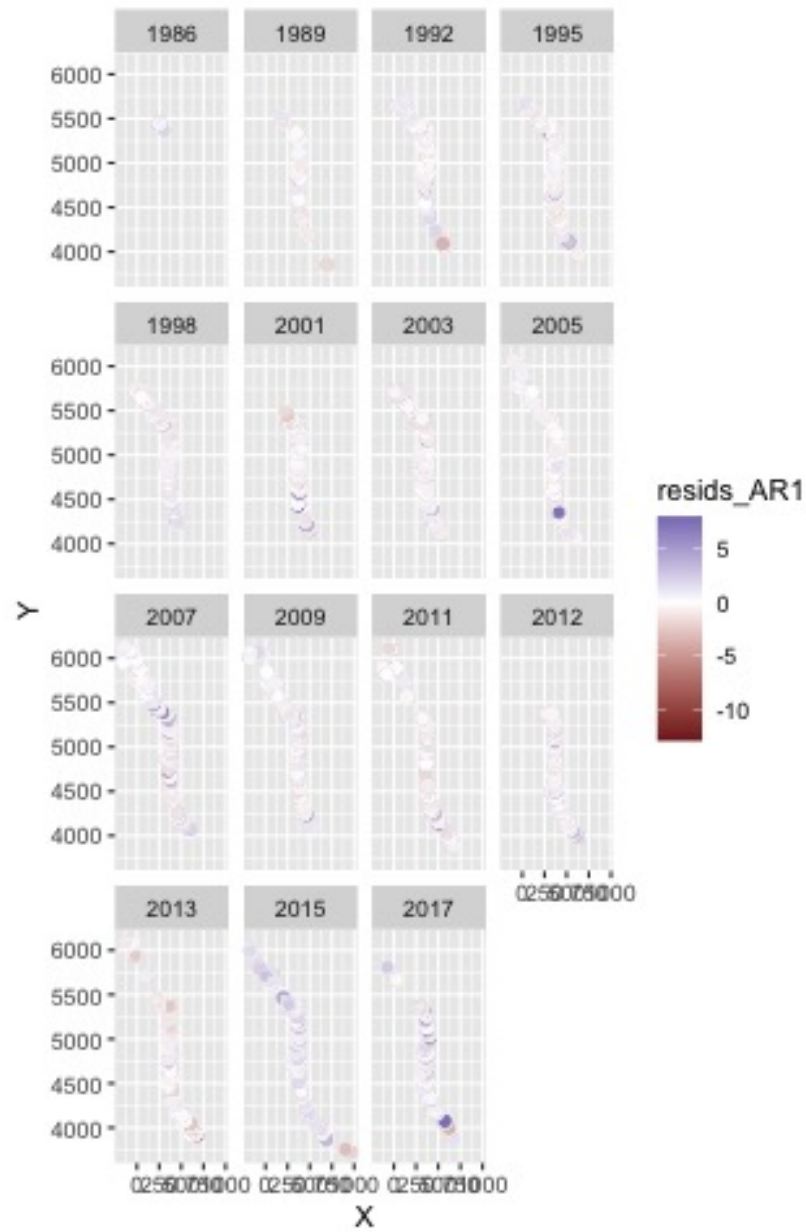
#### *Explorations with sdmTMB*

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
```



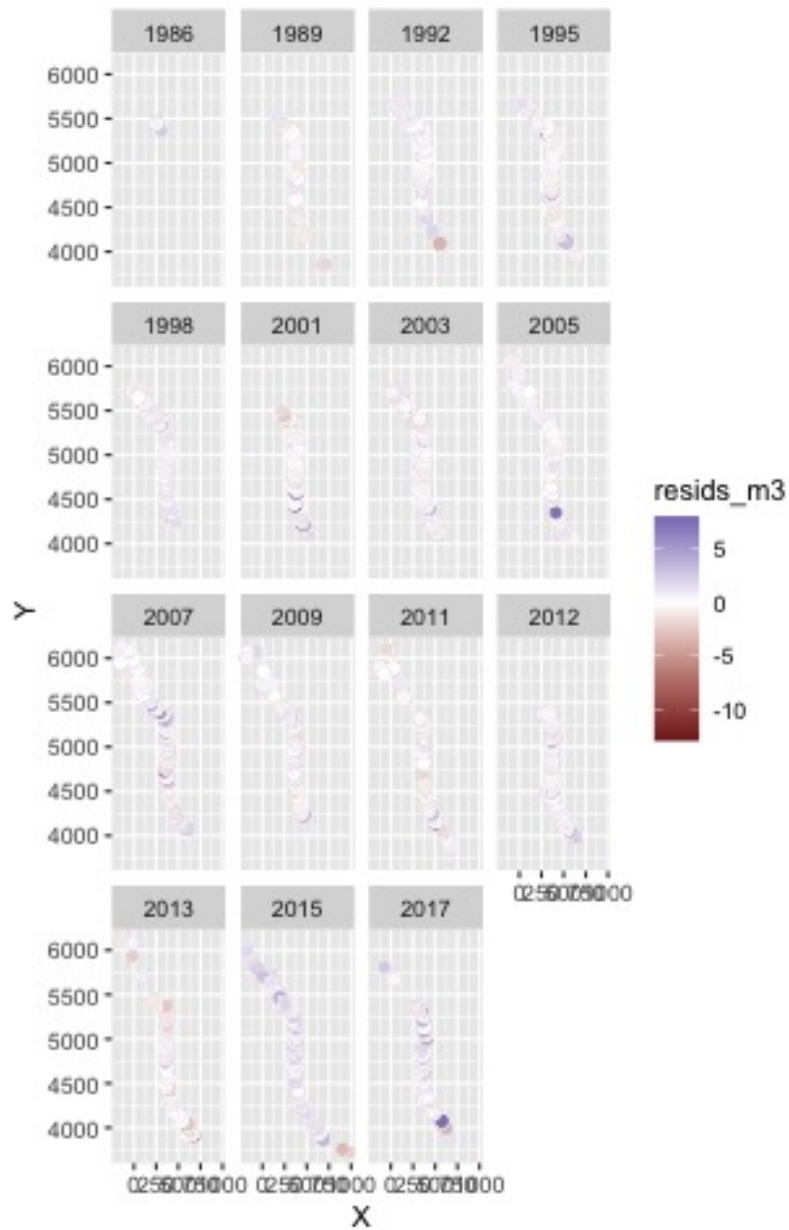


m3: weight ~ s(age) + s(cohort) + catch\_month

```

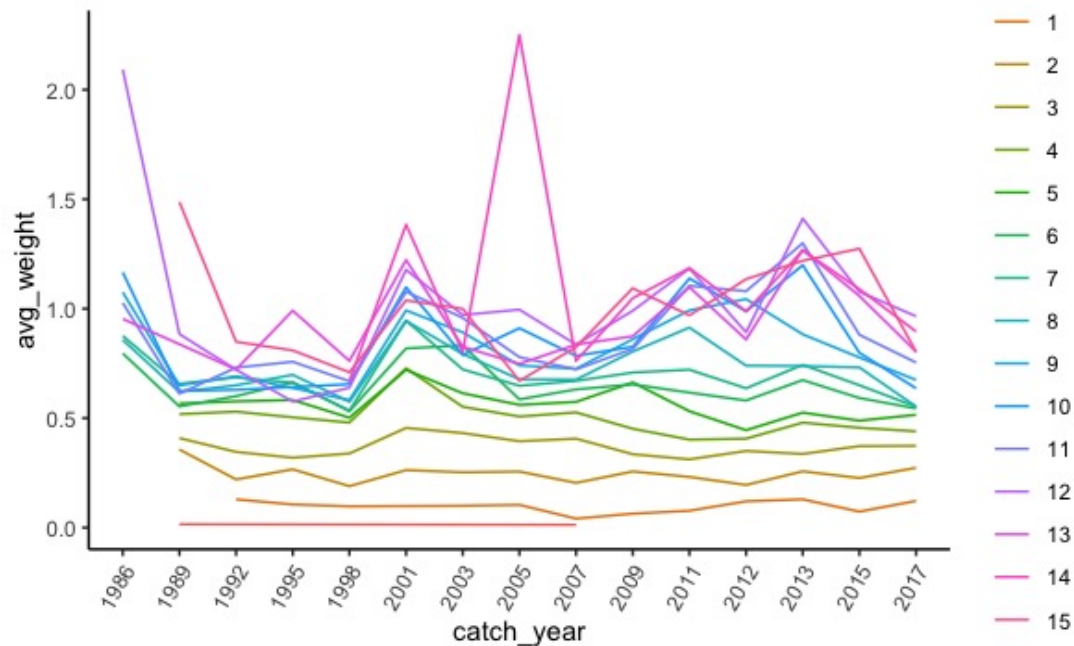
> tidy(m3, "ran_pars", conf.int = TRUE)
  term      estimate std.error   conf.low conf.high
1 range 80.916372359      NA 69.14320482 94.6941834
3  phi  0.190359597      NA  0.18894111  0.1917887
4 sigma_0 0.043608373      NA  0.01513698  0.1256320
5 sigma_E 0.200755421      NA  0.18507765  0.2177612
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

```

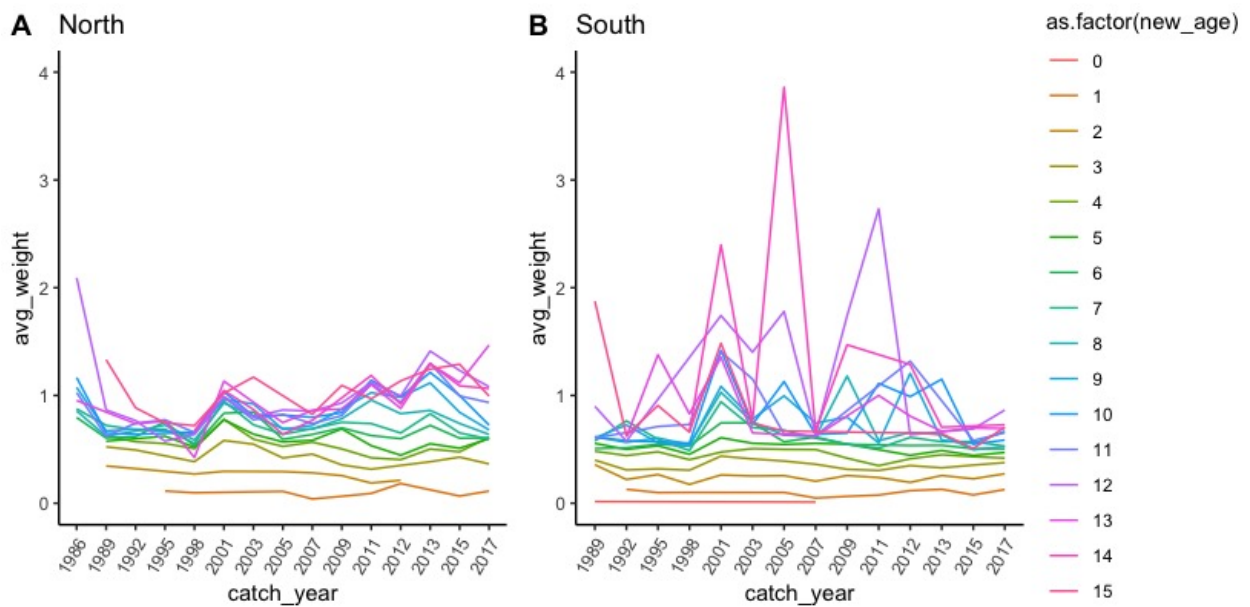


Catch month and latitude have a correlation of 0.8. Is it fine to still include if latitude is not considered a predictor, but rather a spatial random effect?

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.



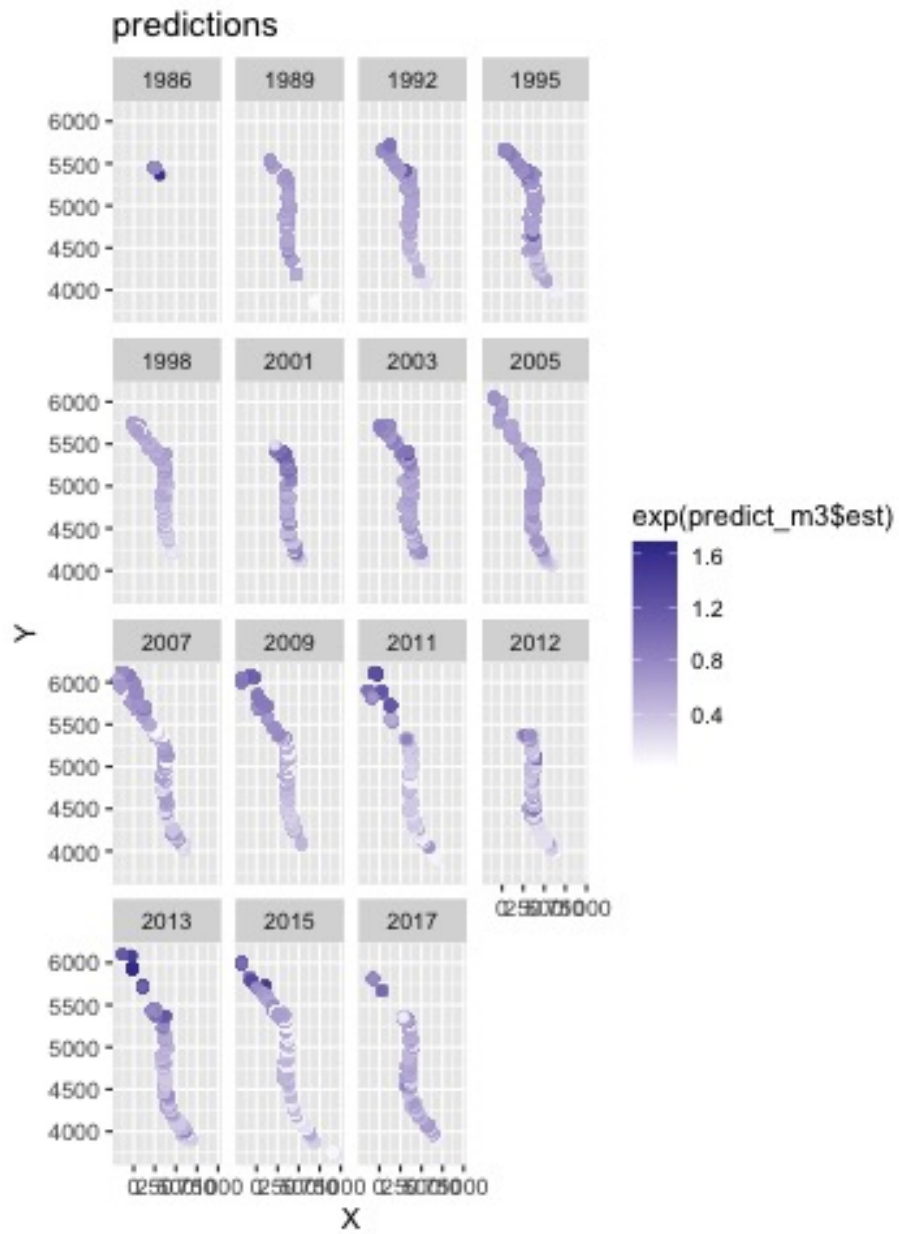
There also seems to be some differences when we split the data between north and south at the median point.  
UTC 4957.963

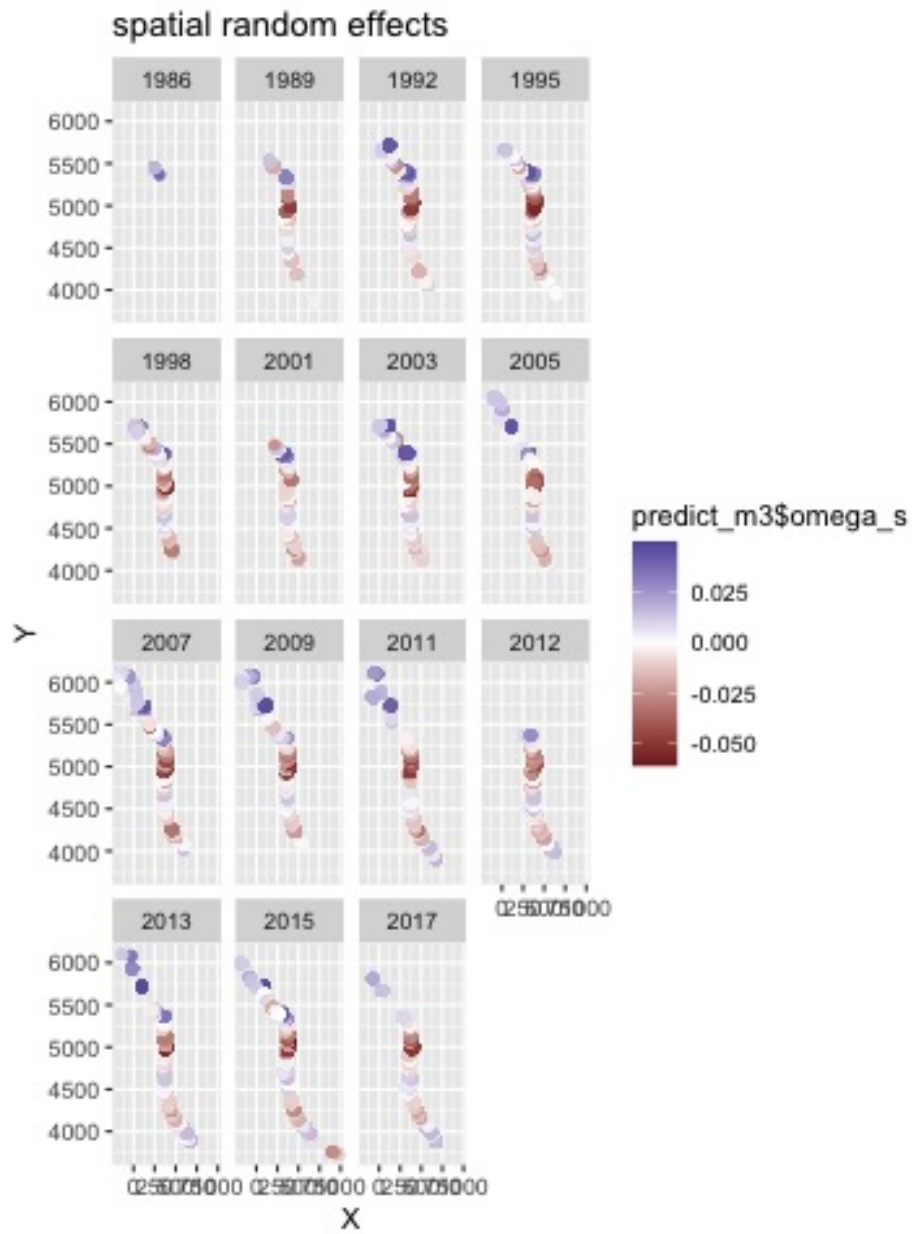


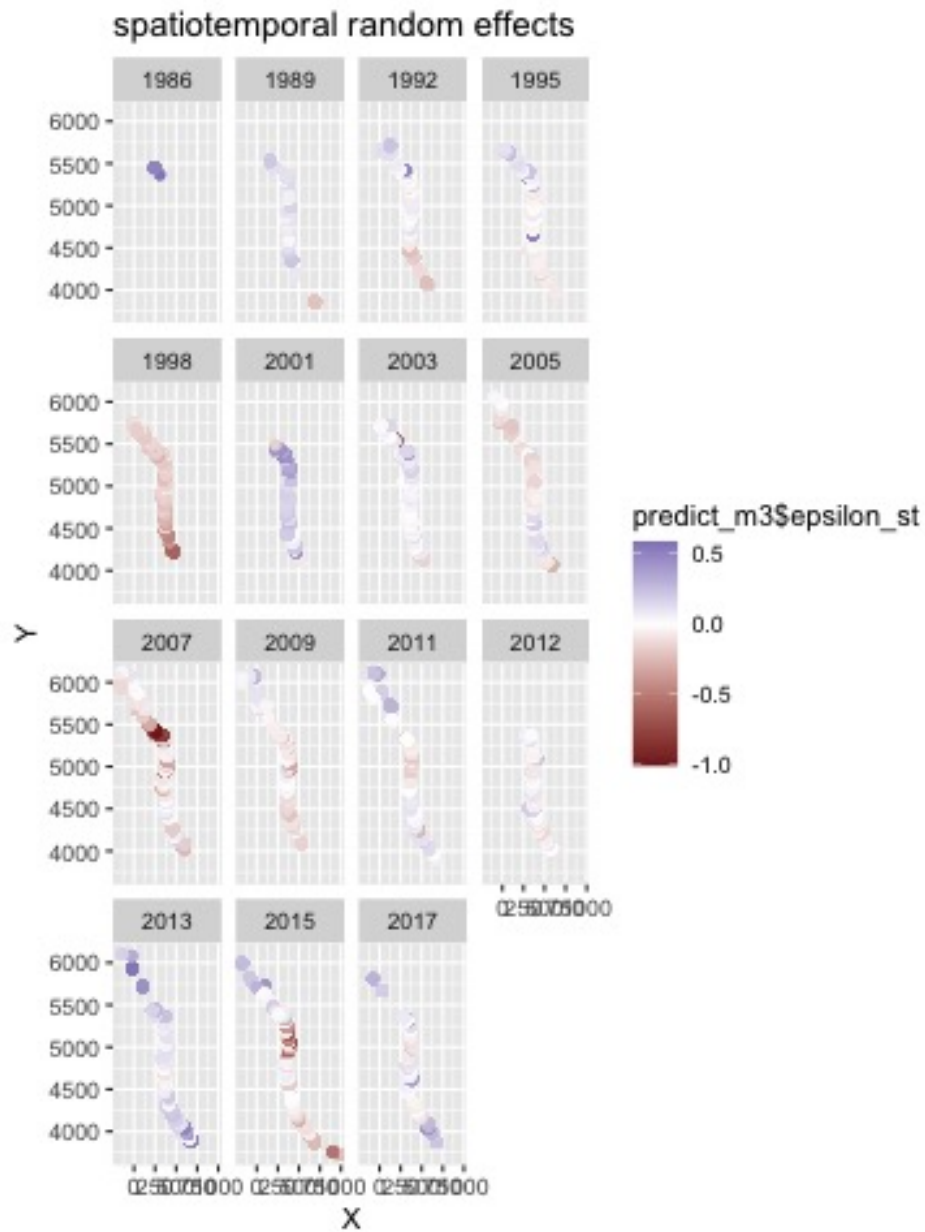
There is much greater variability in the older age classes of the south. Moreover, there may be a slightly increasing trend in the north.

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

Now looking at the outputs of m3







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**

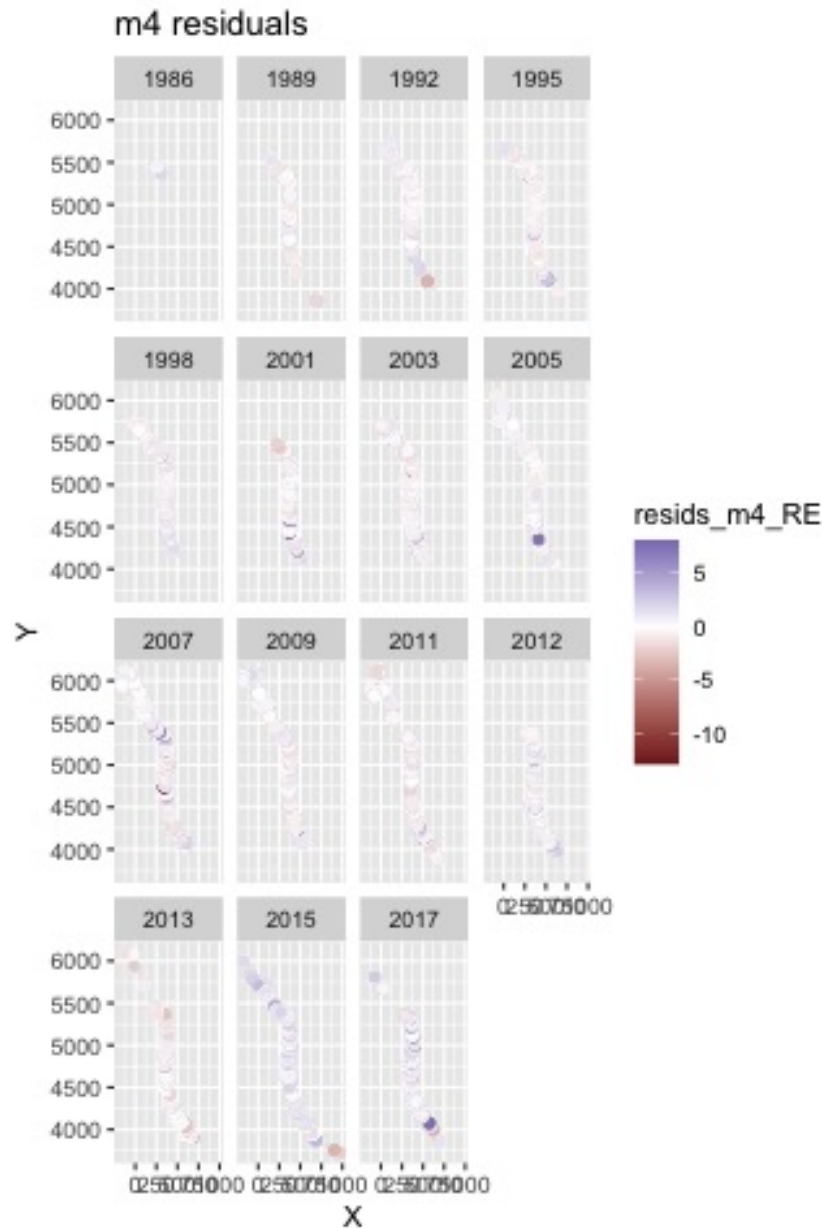
There are a few ways to include time-varying intercepts

- `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...

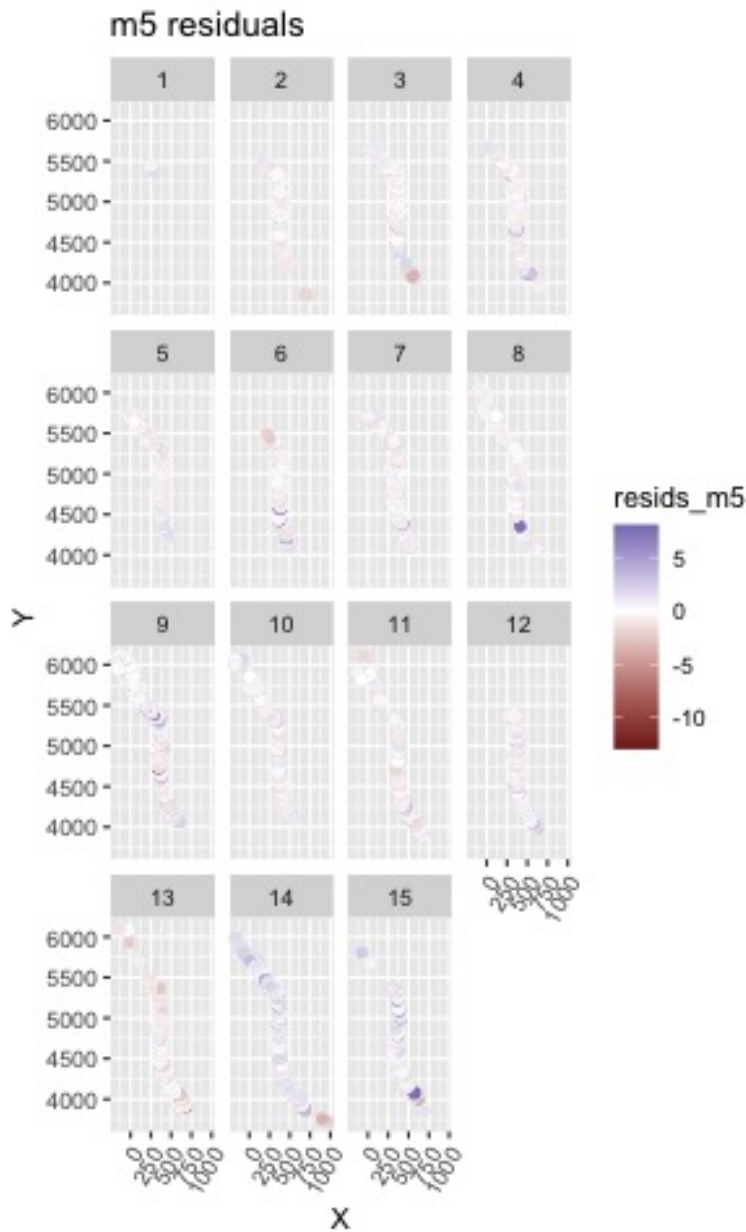


Could it be that one of the predictors is time-varying rather than the intercept?

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  $s(\text{new\_age}, \text{by} = \text{catch\_year})$

```
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)

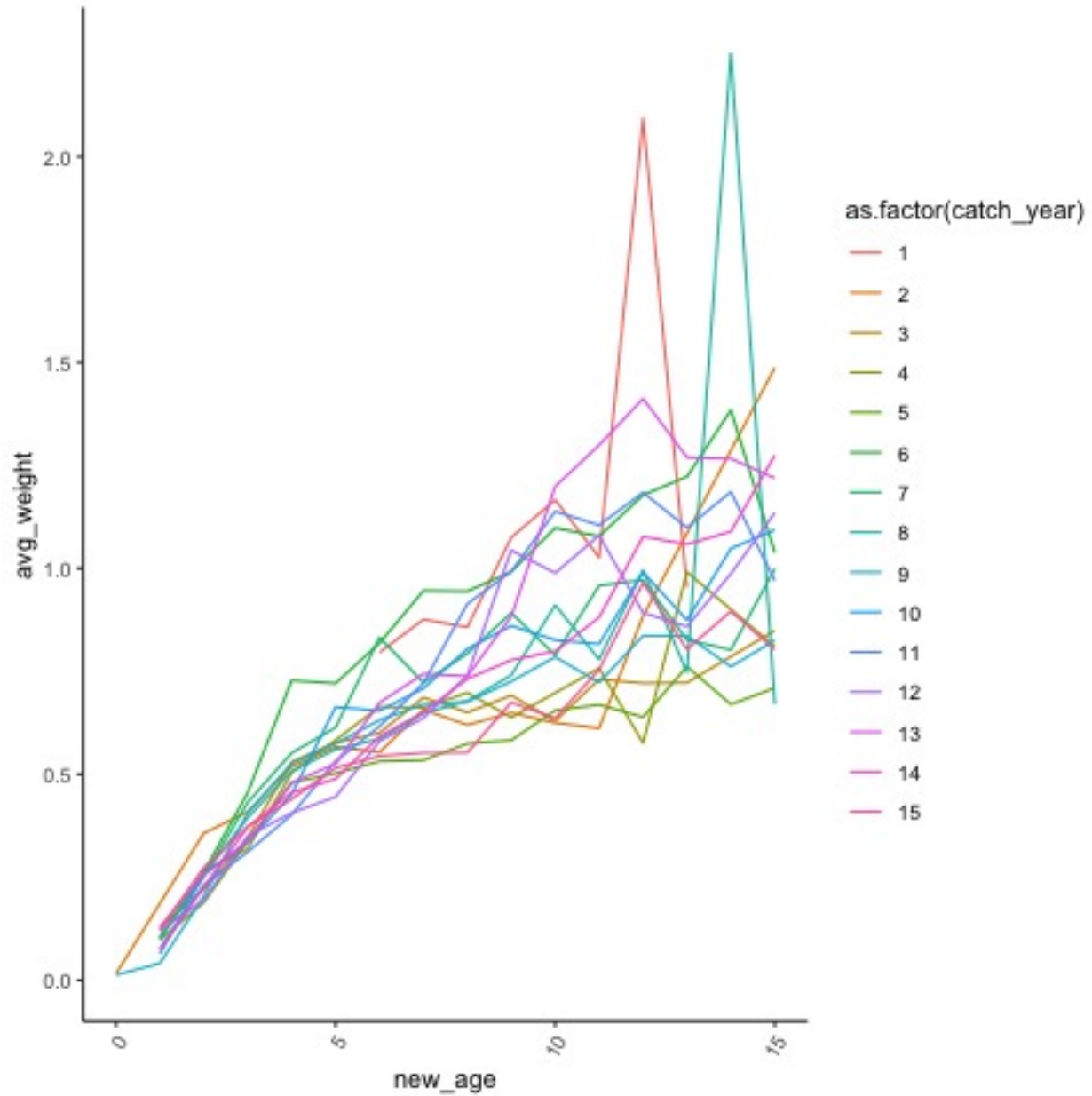
Tried removing the smoother on cohort,

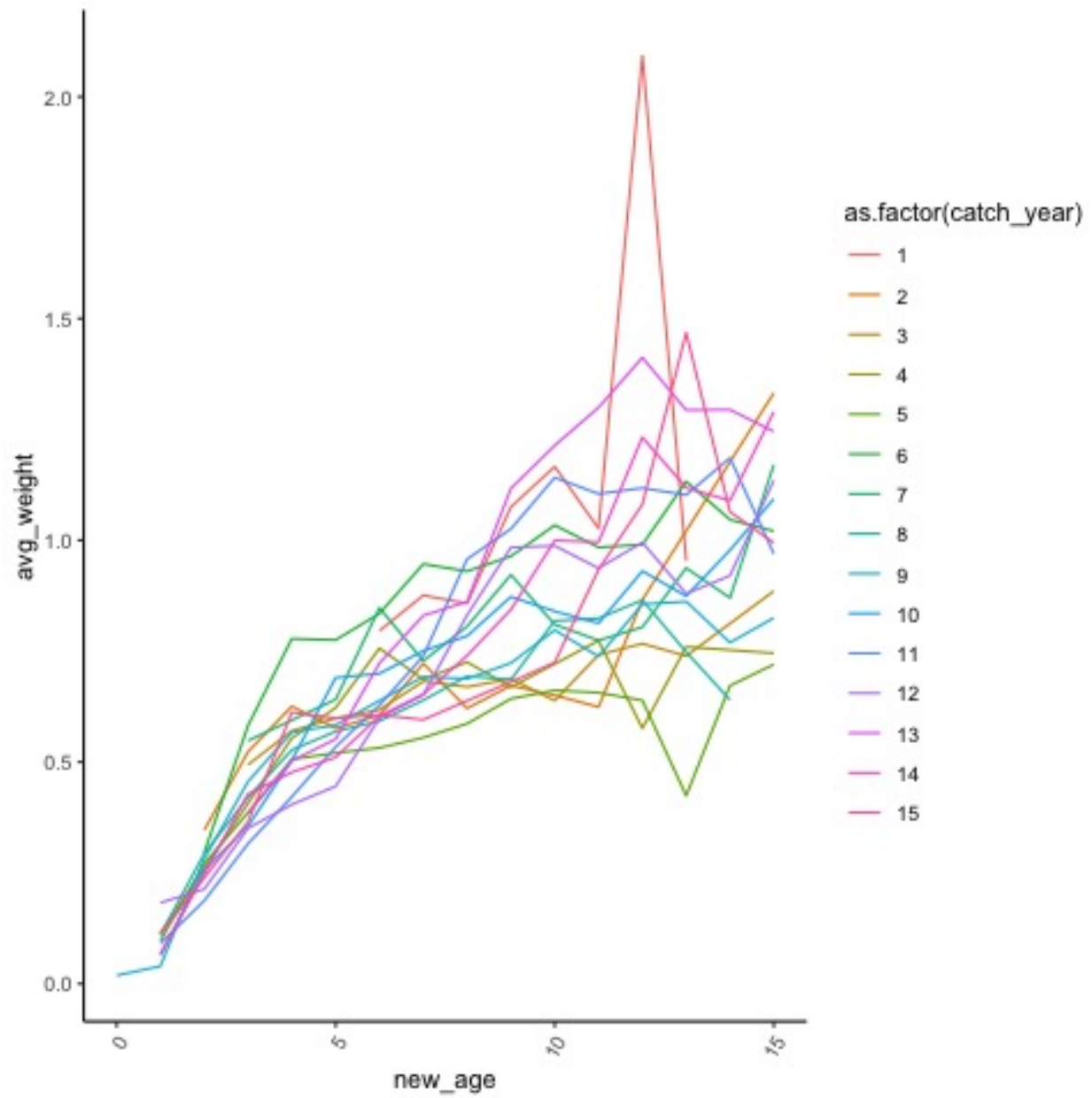
```
m7 = weight ~ 0 + s(new_age, by = catch_year) + catch_month with time-varying intercept
```

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

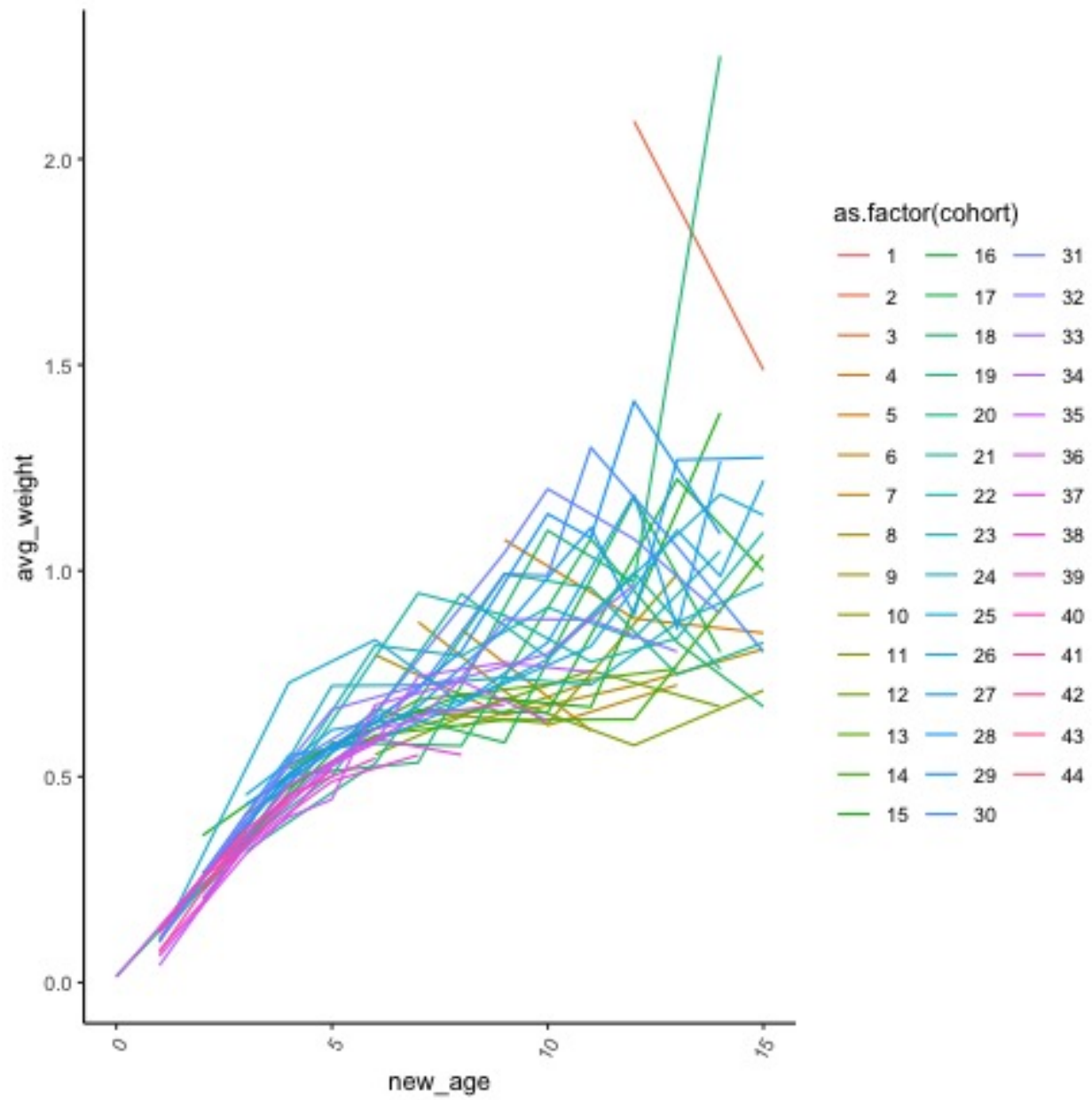
Also, realized the maximum residual is "Inf". I just don't think any of these models are doing too well, so I am stepping back and looking at the data once again.

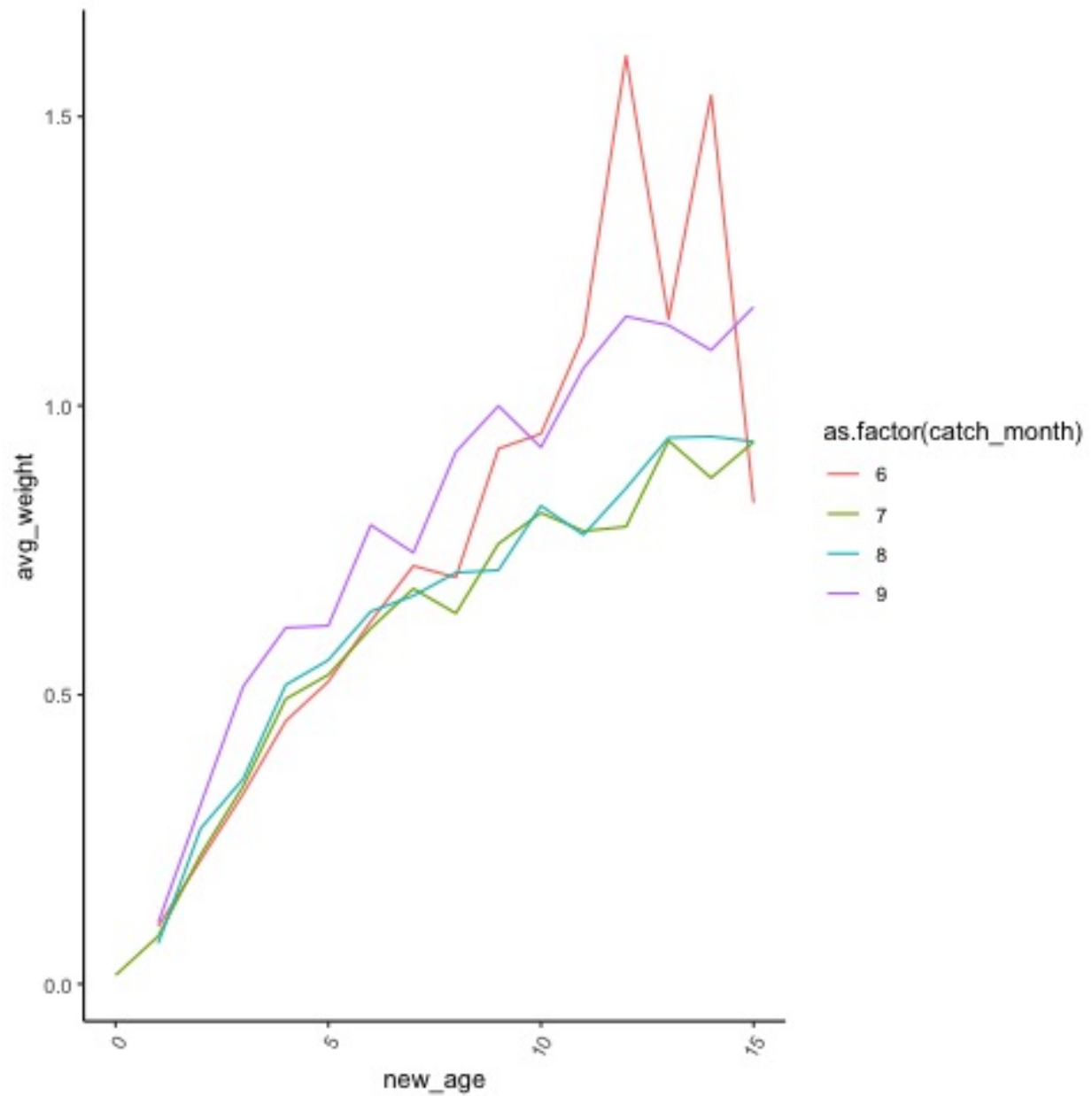
This first plot is weight at age curves by year. and the next one is just for the northern individuals.



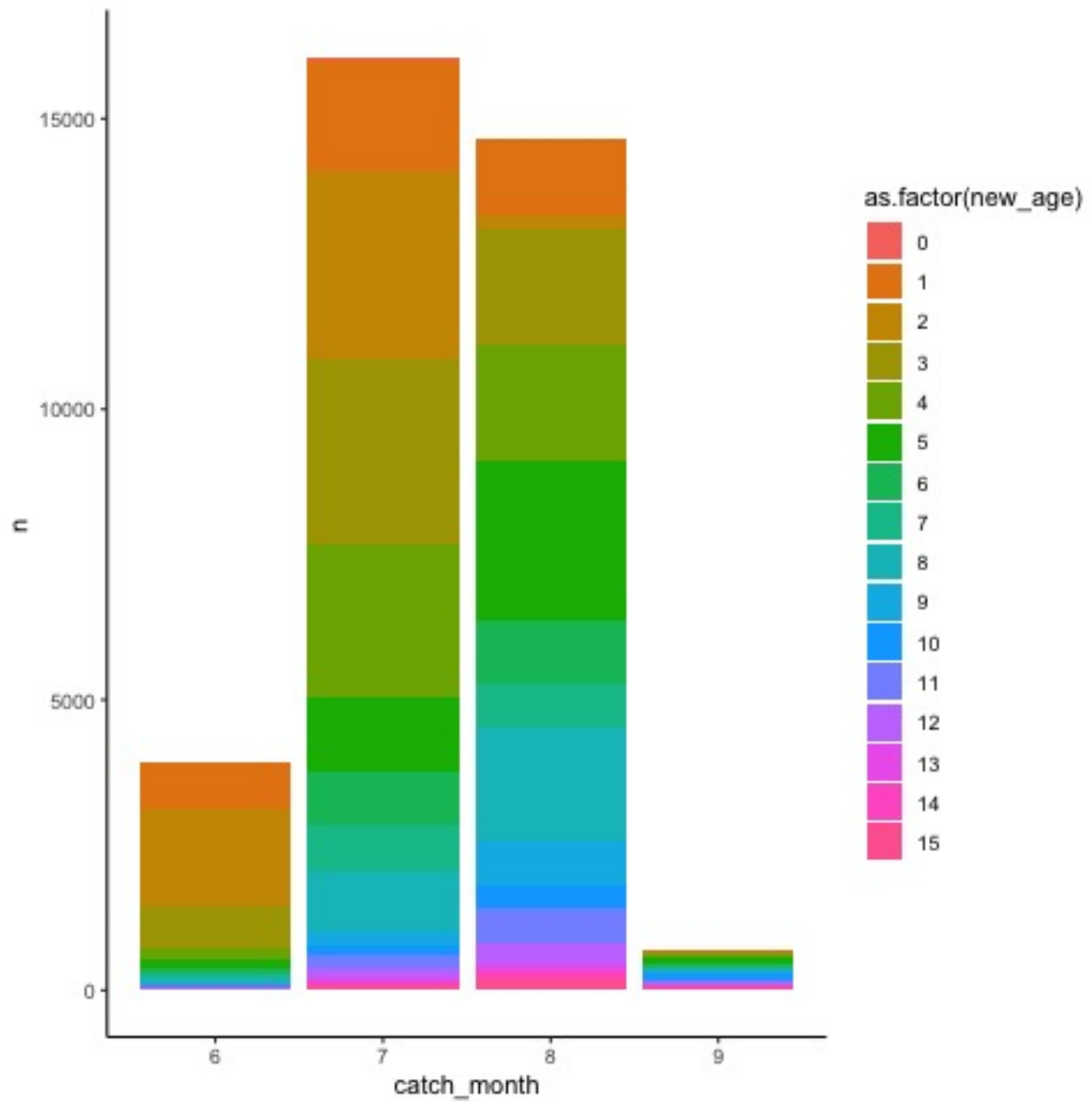


Then, by cohort

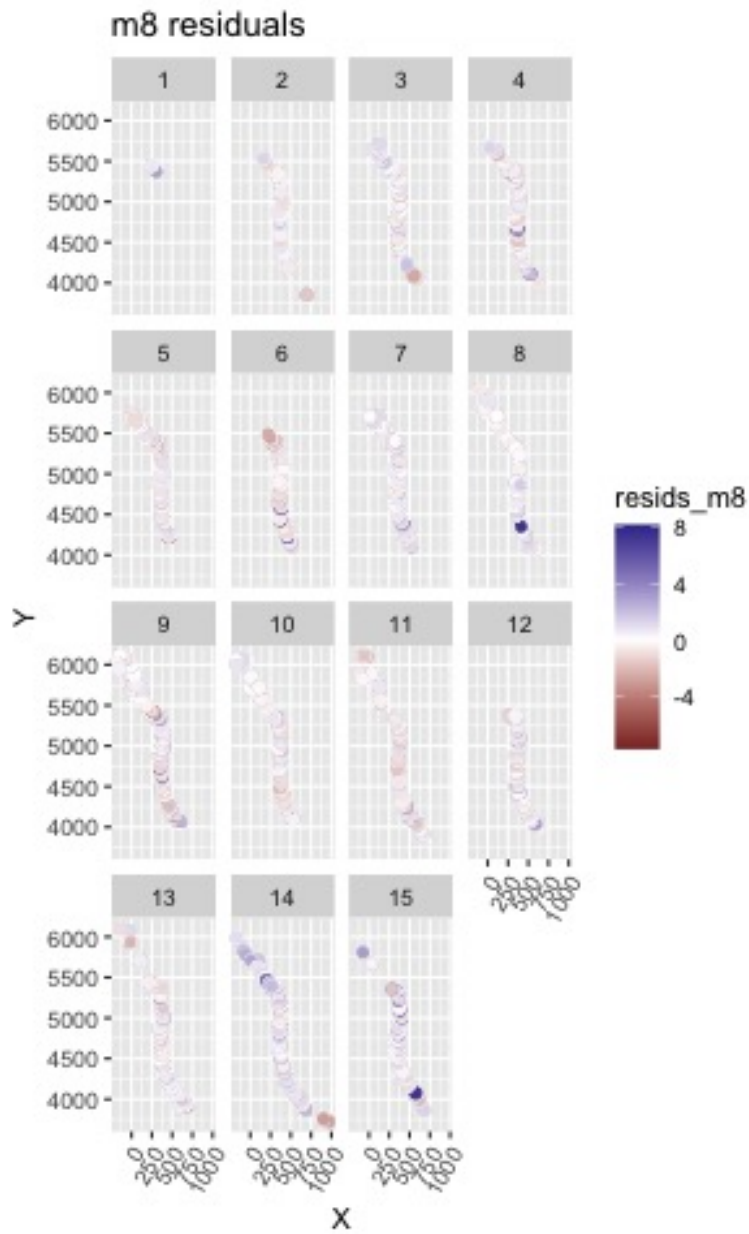




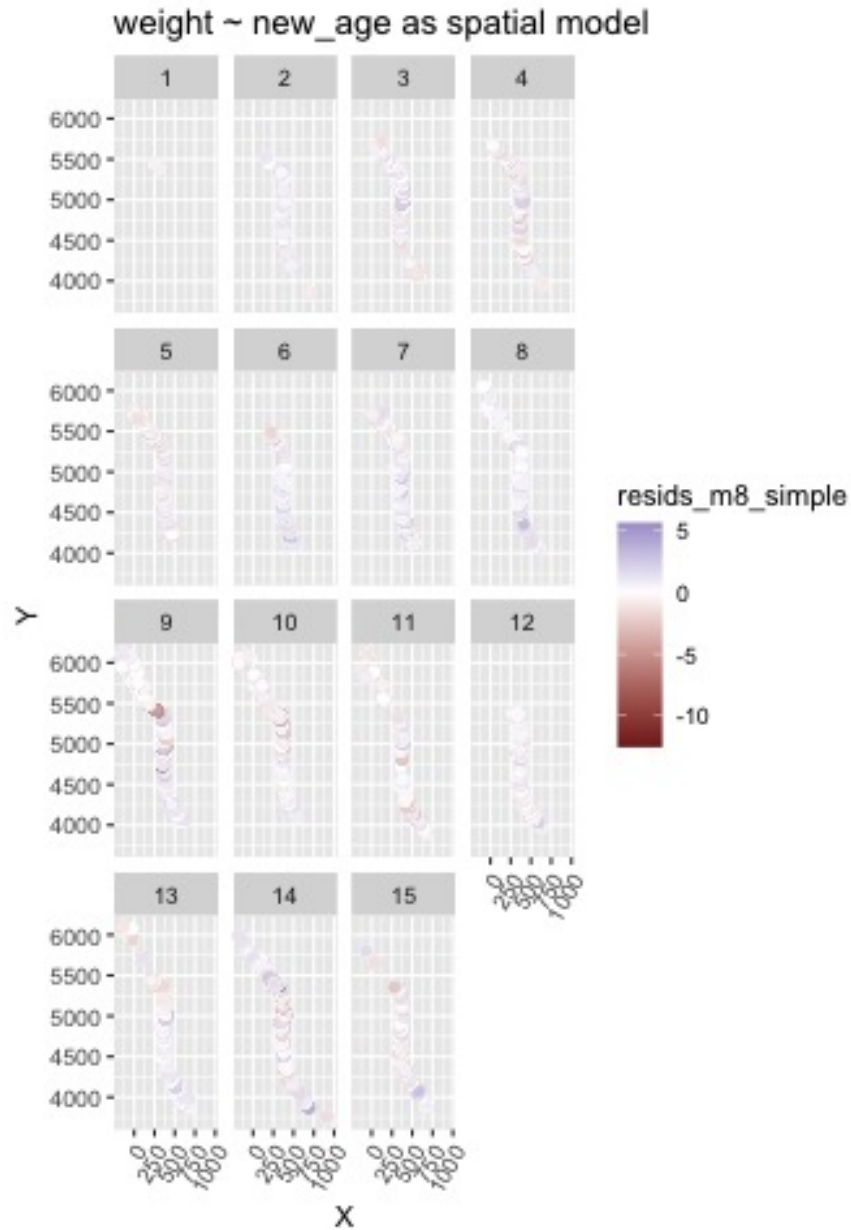
But as a caveat, here are how many observations of each age are sampled per month. Month 6 and 9 are very lightly sampled, so take with caution.



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.



*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

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

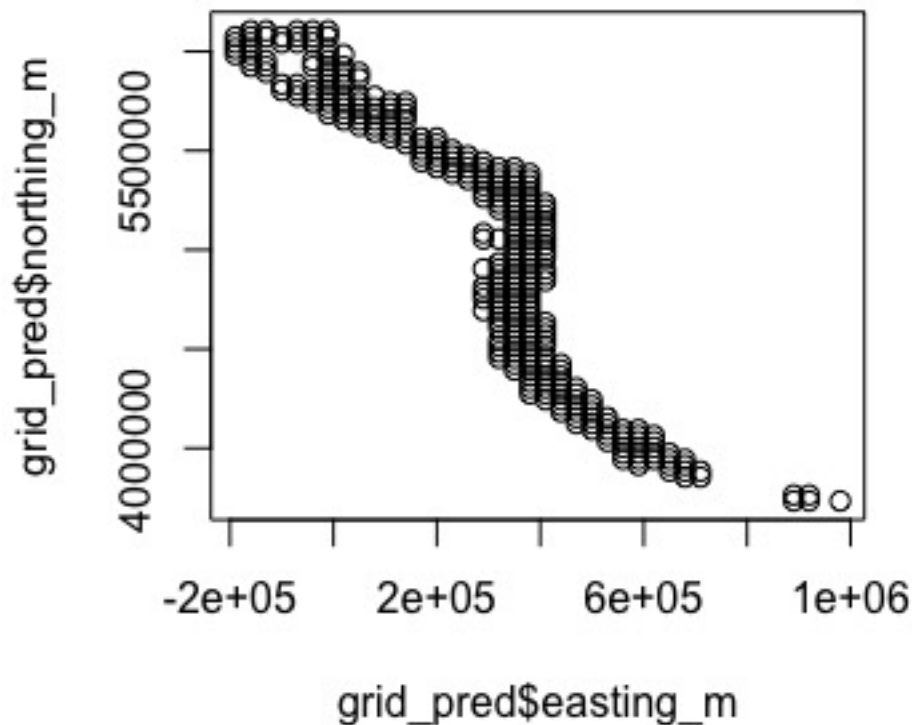
According to AIC, the spatiotemporal model was the best model. It also converged very nicely.

*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**

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

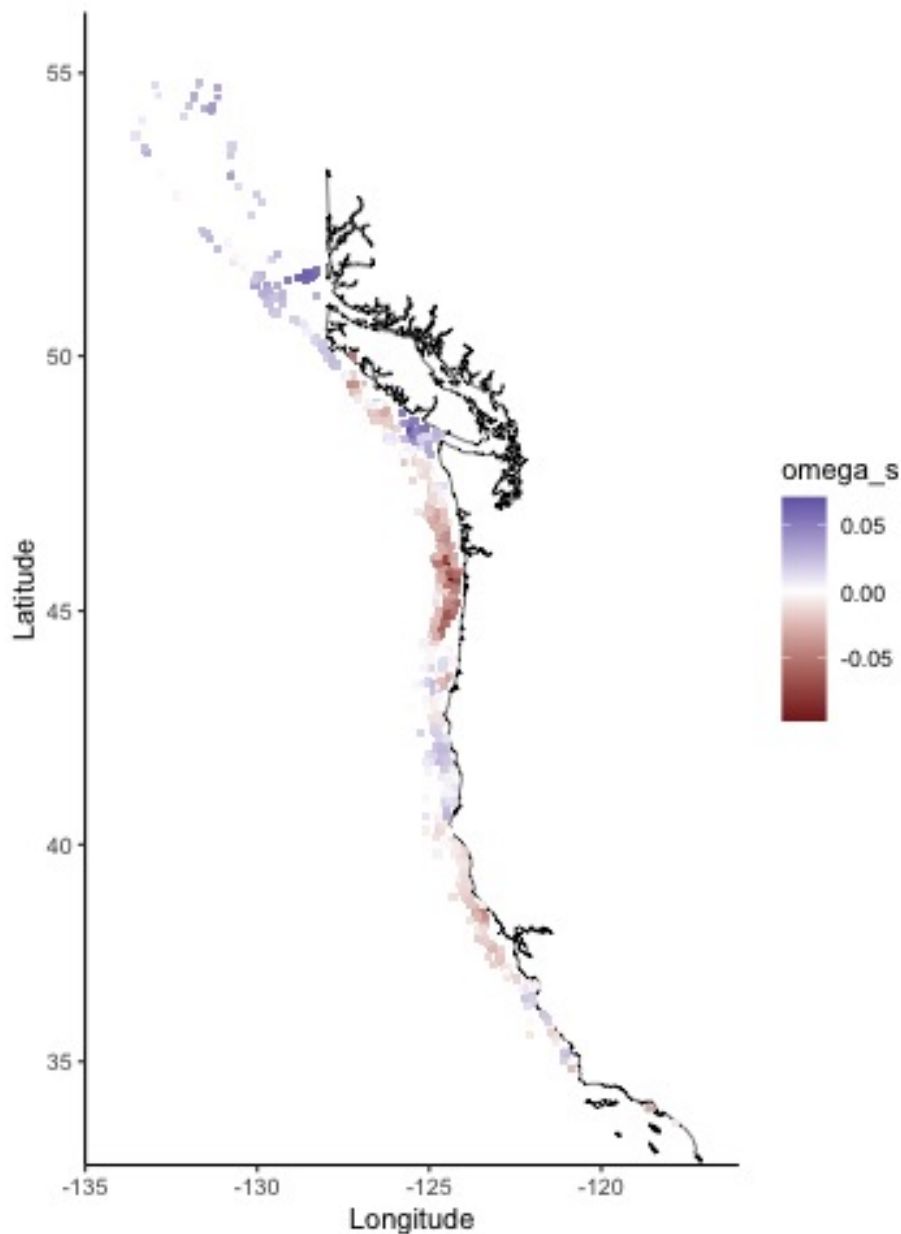
`FUN(X[[1]])` result is length 0

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.

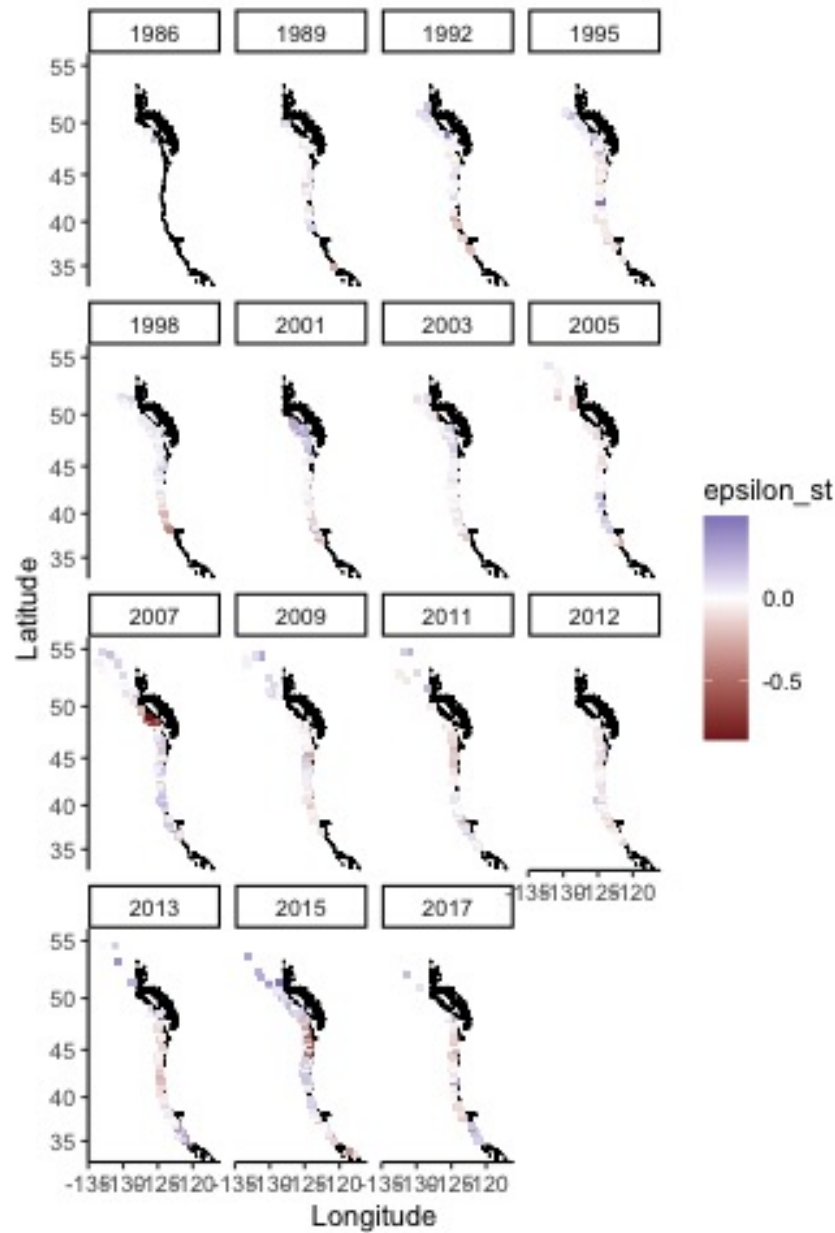
`weight ~ 0 + s(new_age) + s(cohort) + (1 | catch_month)` with time-varying intercept ( $\sim 1$ ) following a random walk.

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 where

freshwater meets the ocean (columbia river basin and san joaquin river basin).



### Sept 26-30

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.

