

## Load packages and data

```
library(data.table); library(qgam); library(mgcViz); library(ggplot2)

lengths <- fread('data/derived/lengths (qaqc).csv')
```

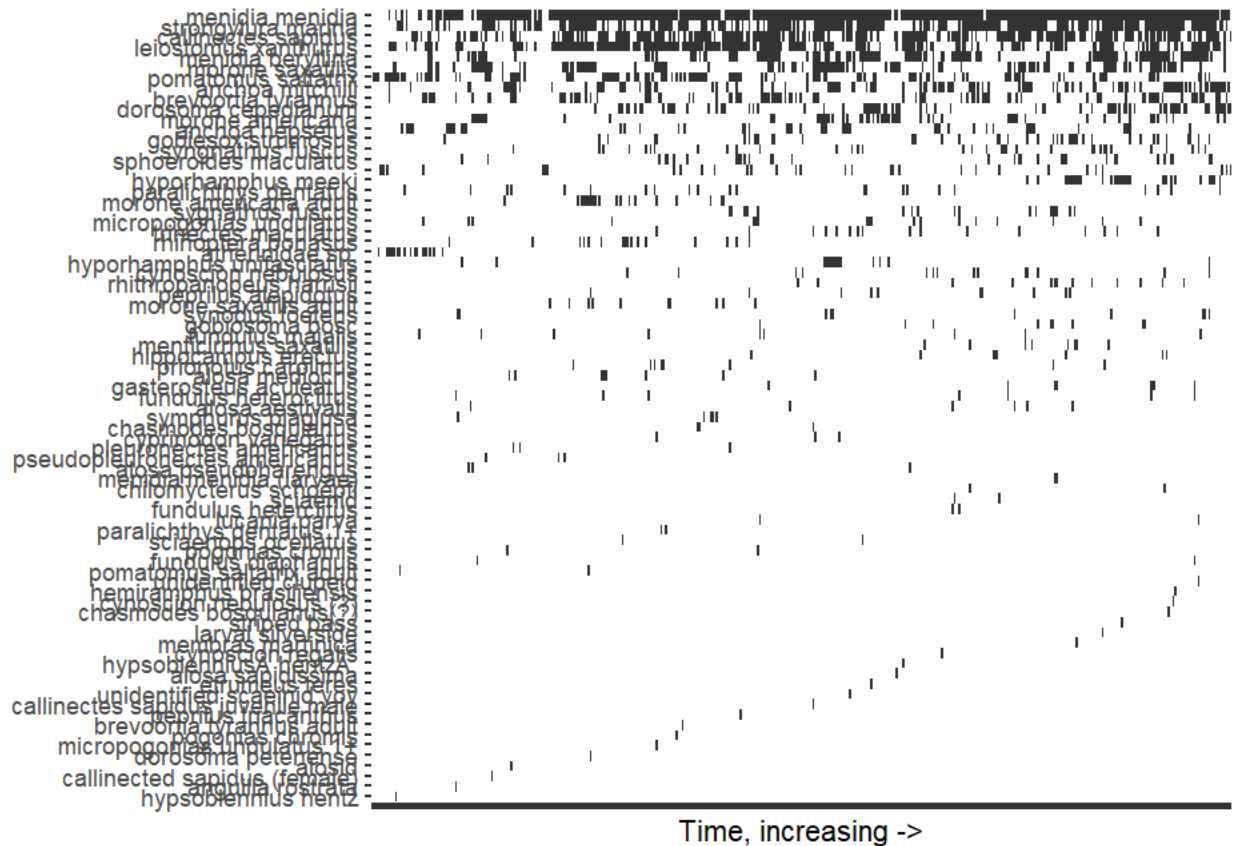
## Update to the observation raster:

```
l_summary <- lengths[, .N, by = c('scientific', 'wk', 'year')]
setorder(l_summary, year, wk)

plot_order <- l_summary[, .(incidence = sum(.N)), by = 'scientific']
setorder(plot_order, incidence)

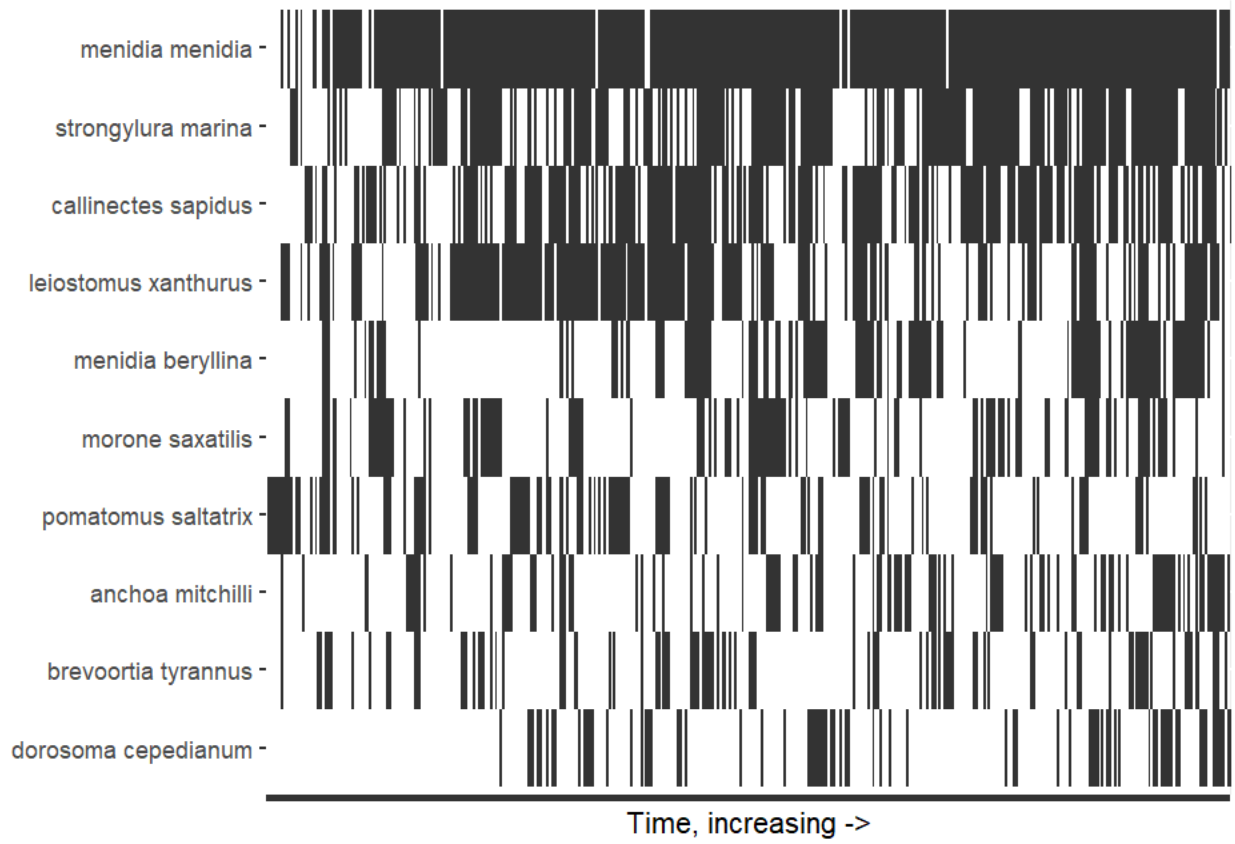
l_summary[, scientific := factor(scientific, order = T,
                                levels = plot_order$scientific)]

ggplot(data = l_summary) +
  geom_raster(aes(y = scientific, x = interaction(wk, year))) +
  labs(x = 'Time, increasing ->', y = NULL) +
  theme(axis.text.x = element_blank())
```



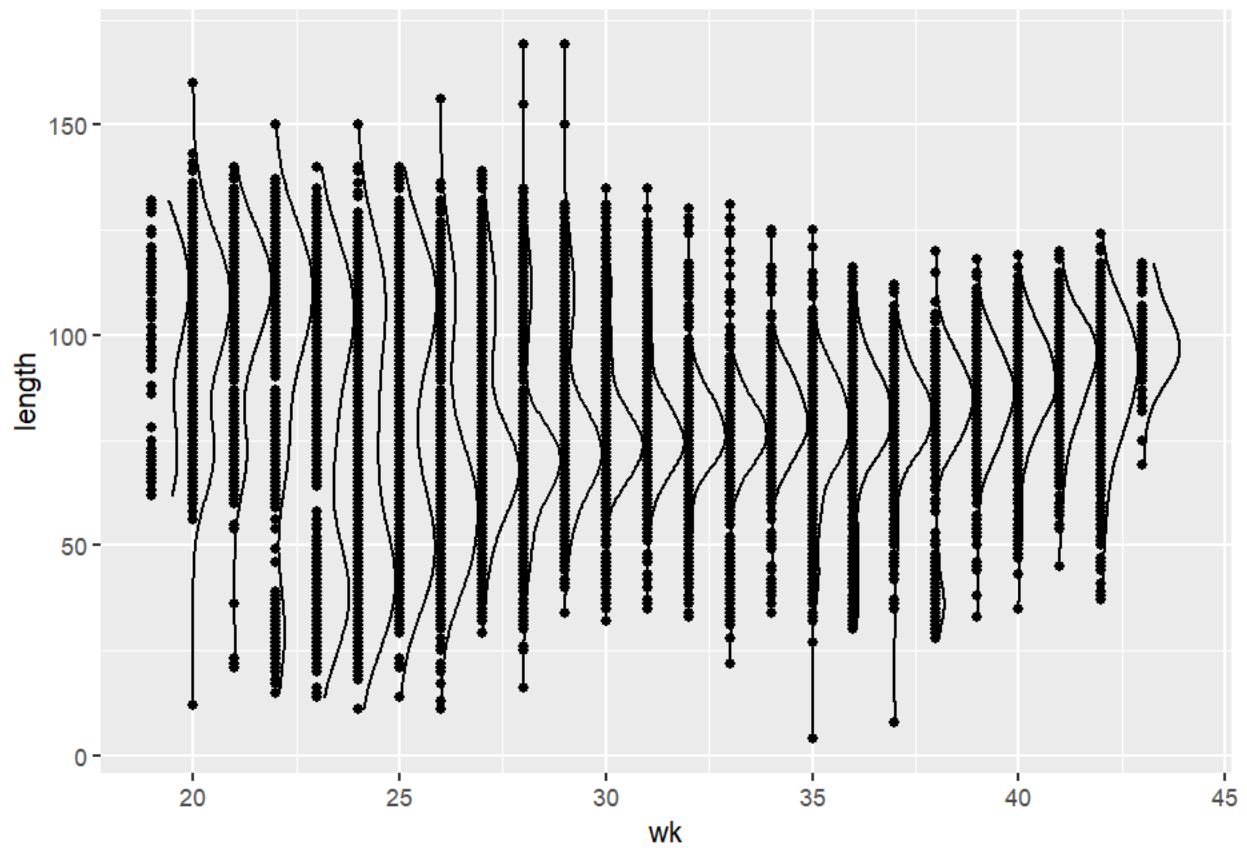
## Focusing on the most-frequent 10

```
ggplot(data = l_summary[scientific %in% tail(plot_order, 10)$scientific,]) +  
  geom_raster(aes(y = scientific, x = interaction(wk, year))) +  
  labs(x = 'Time, increasing ->', y = NULL) +  
  theme(axis.text.x = element_blank())
```



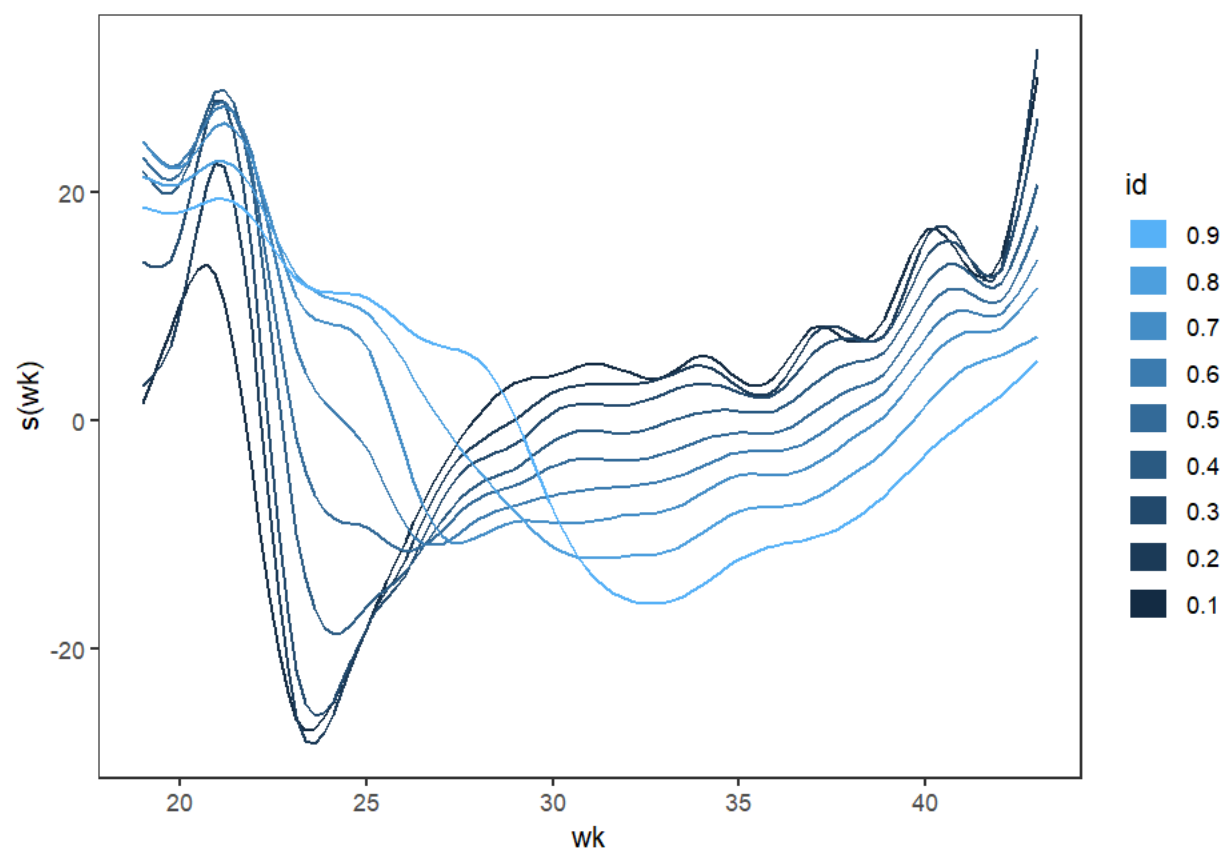
menidia menidia

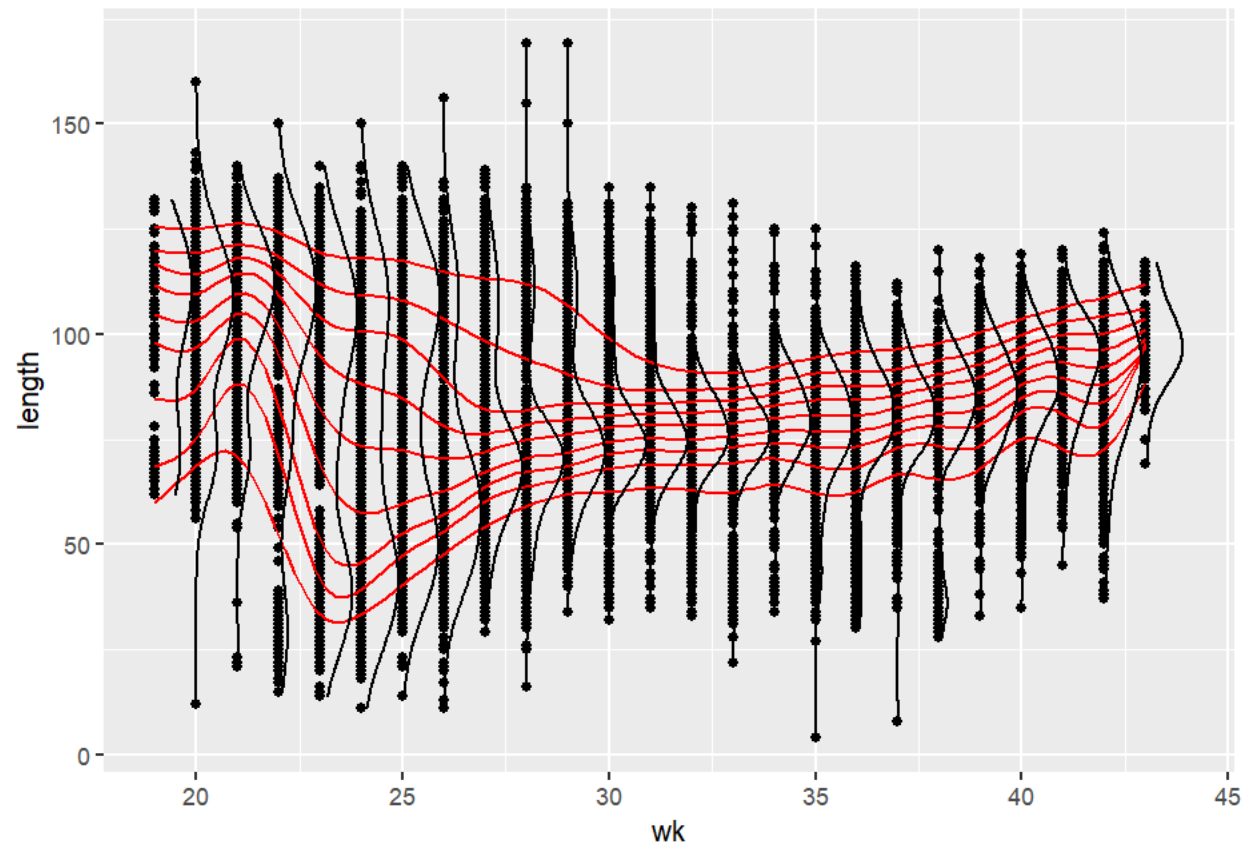
Raw length frequency



### Quantile regression

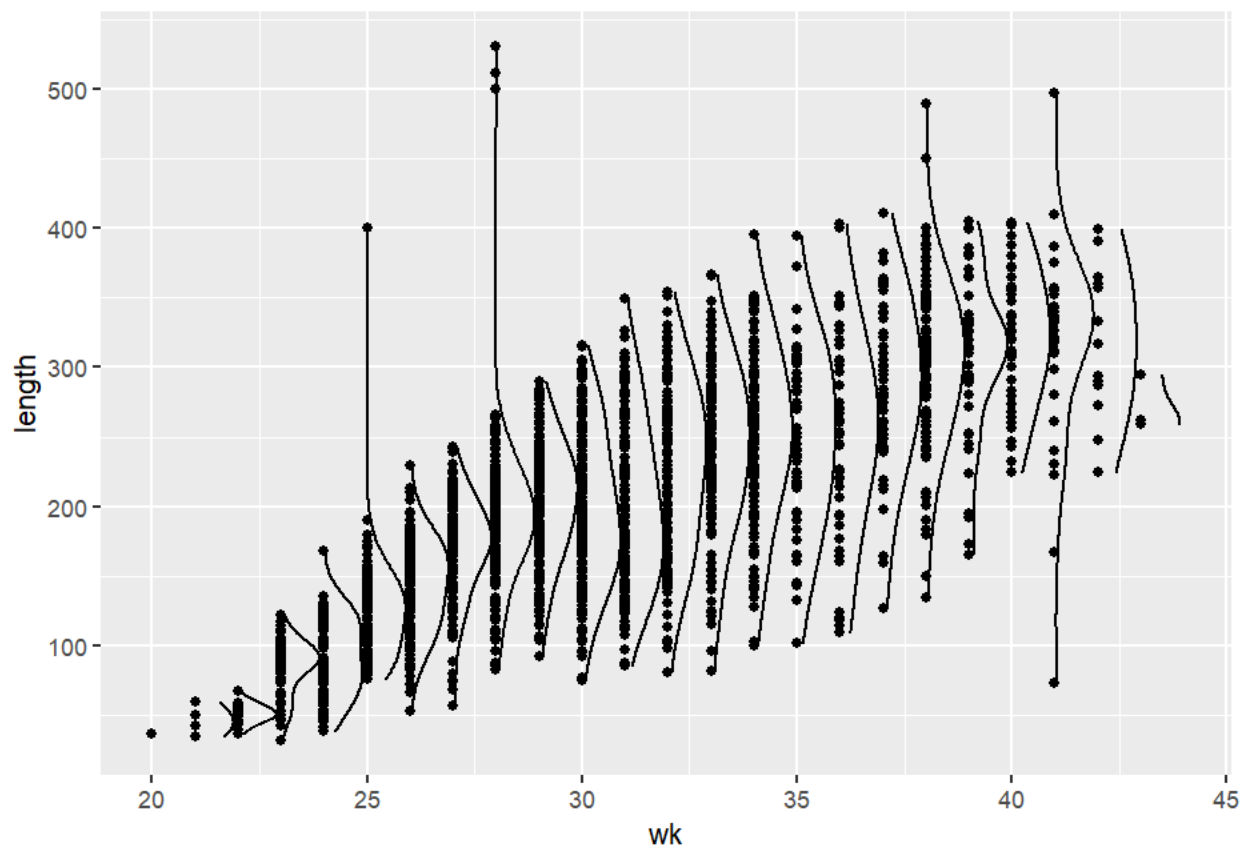
Estimating learning rate. Each dot corresponds to a loss evaluation. qu = 0.5.....done qu = 0.4.....done qu = 0.6.....done qu = 0.3.....done qu = 0.7.....done qu = 0.2.....done qu = 0.8.....done qu = 0.1.....done qu = 0.9.....done





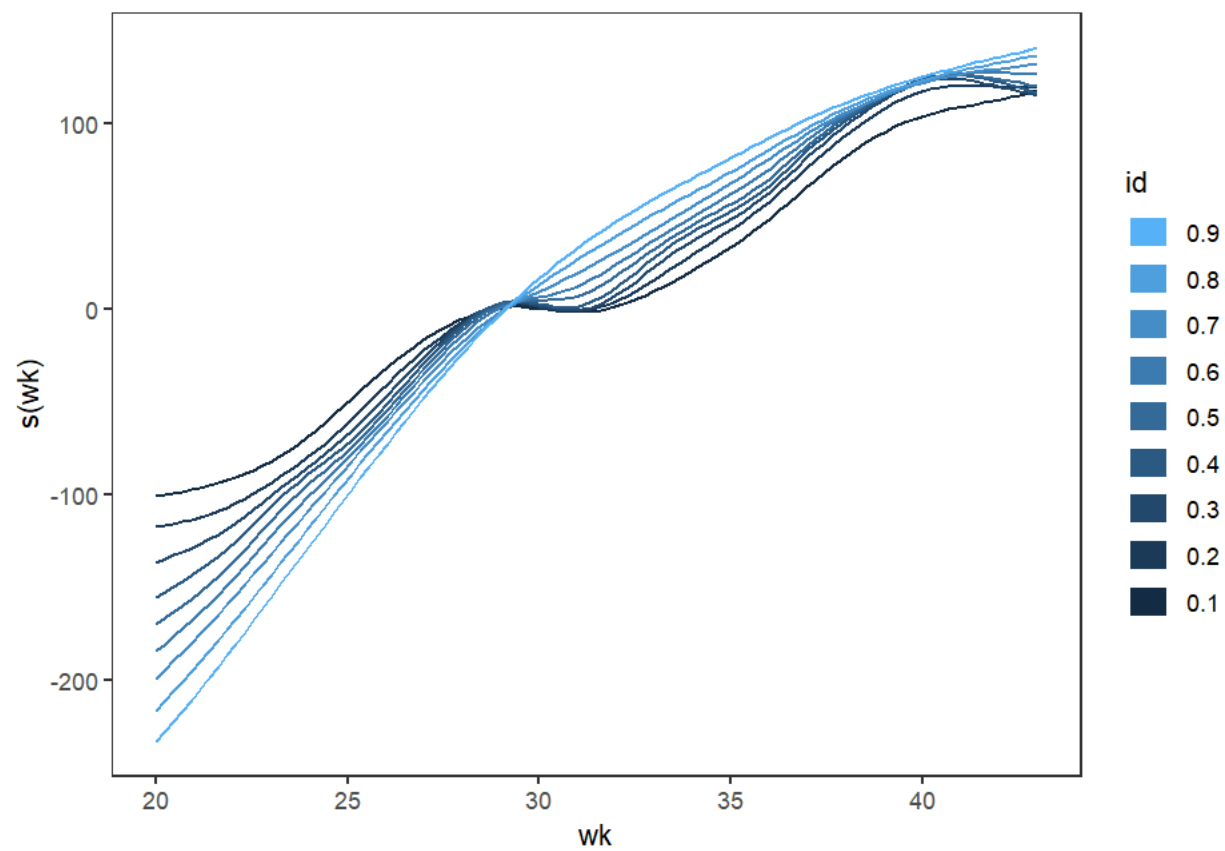
## strongylura marina

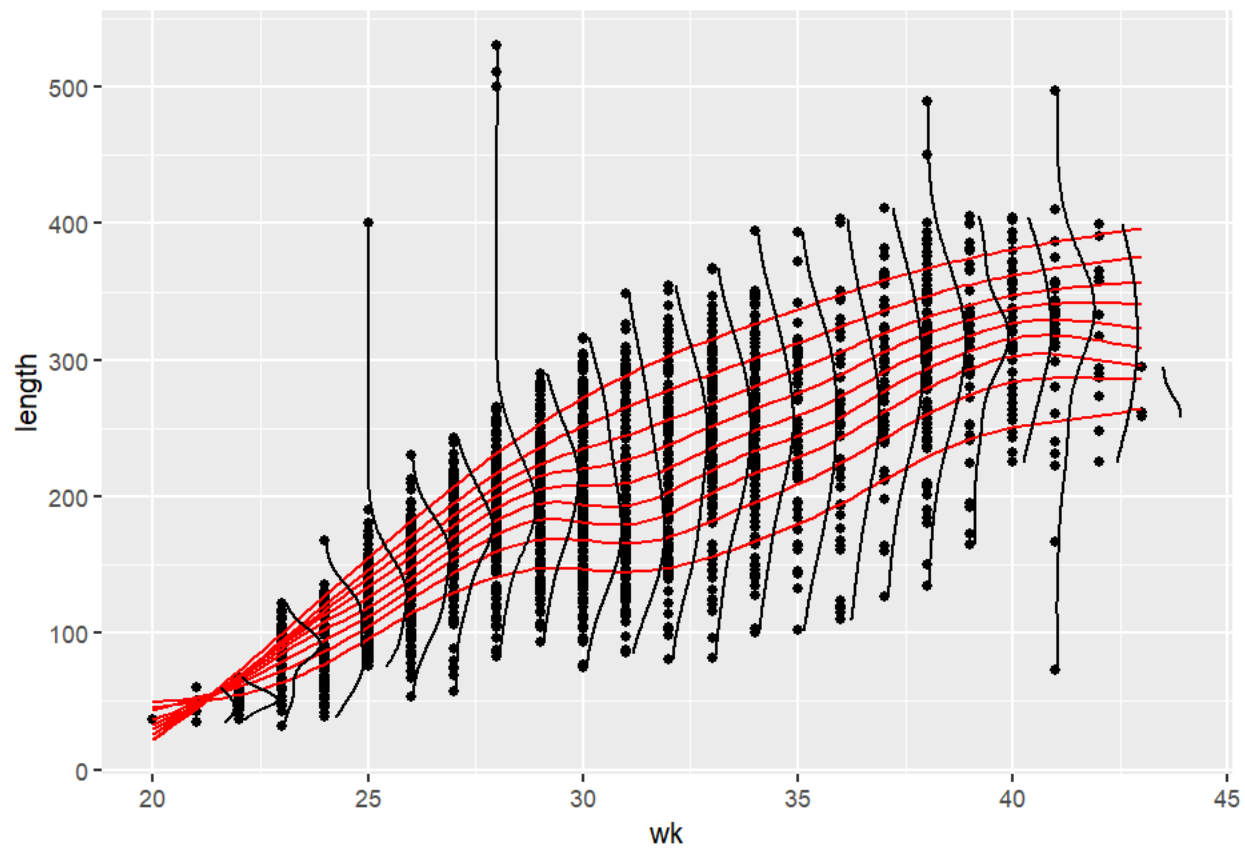
Raw length frequency



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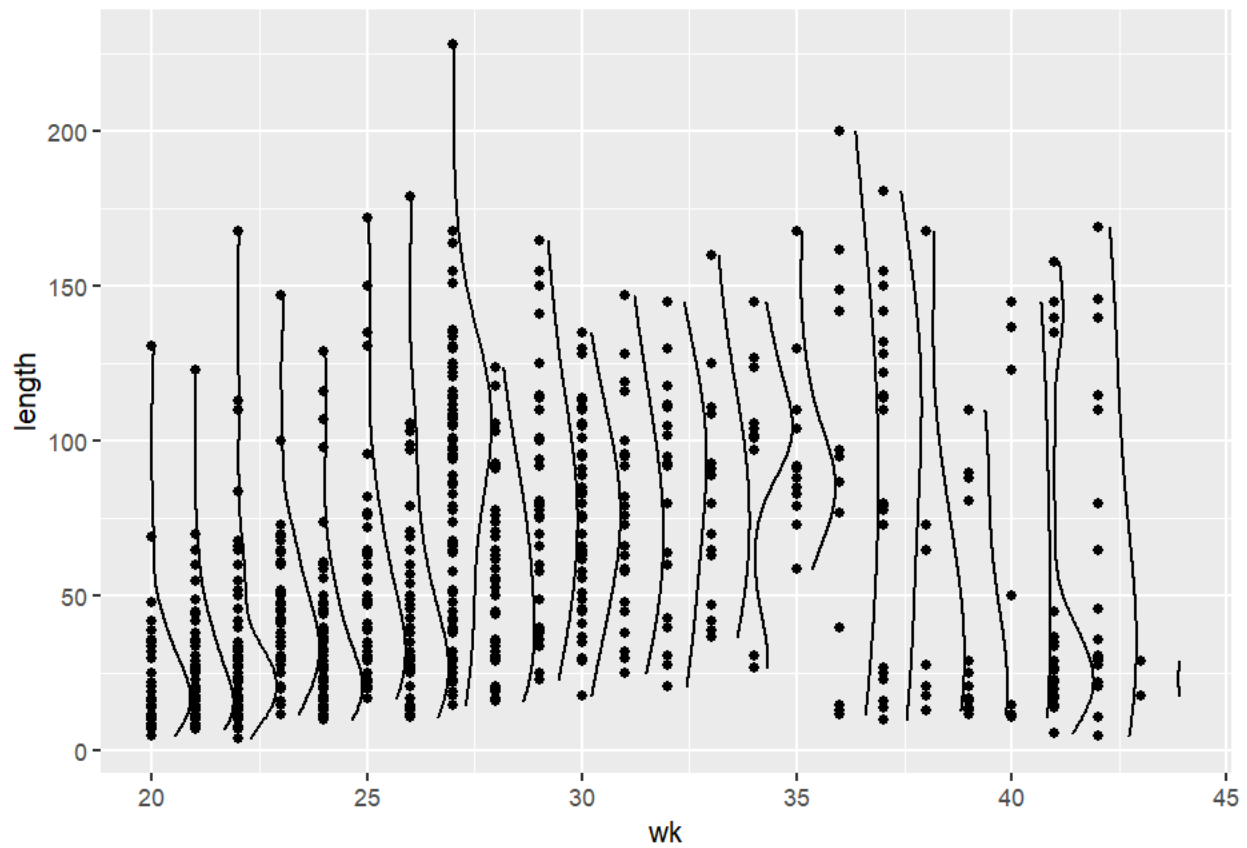






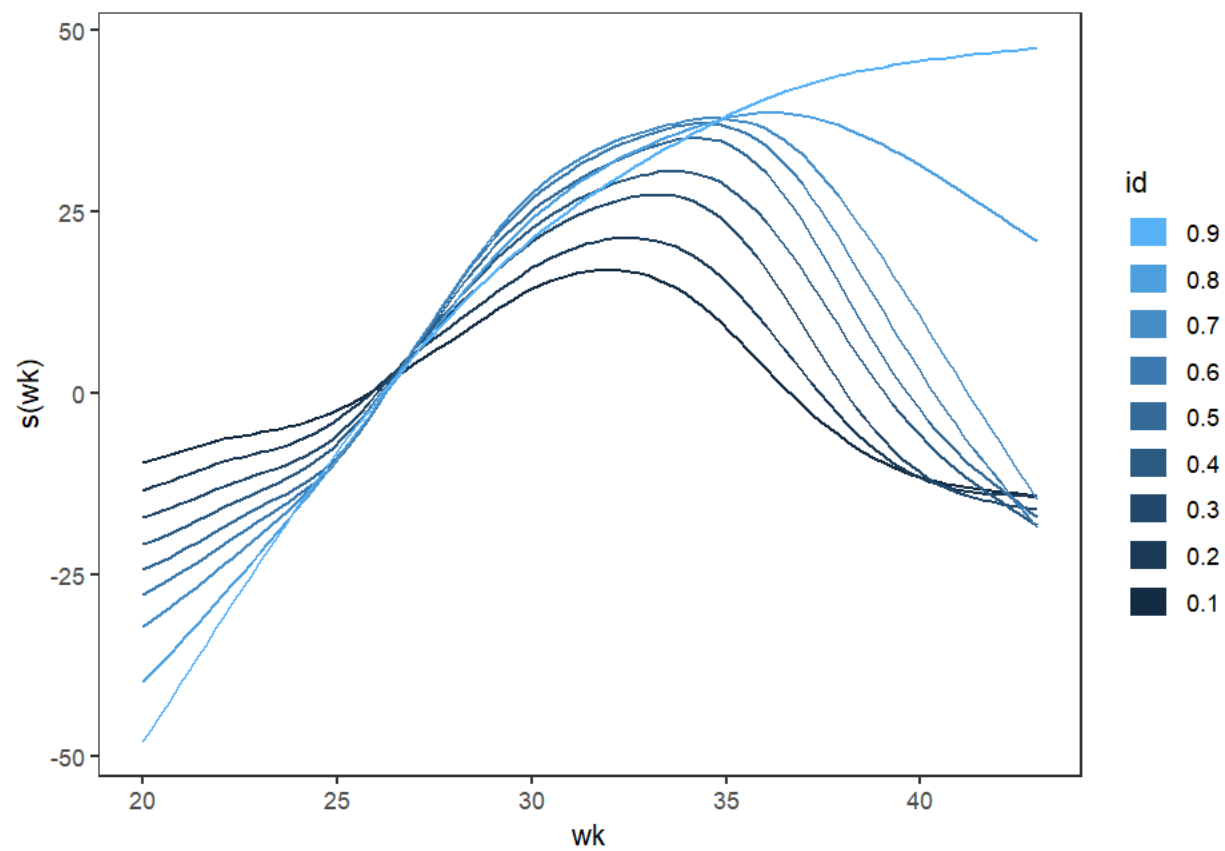
## callinectes sapidus

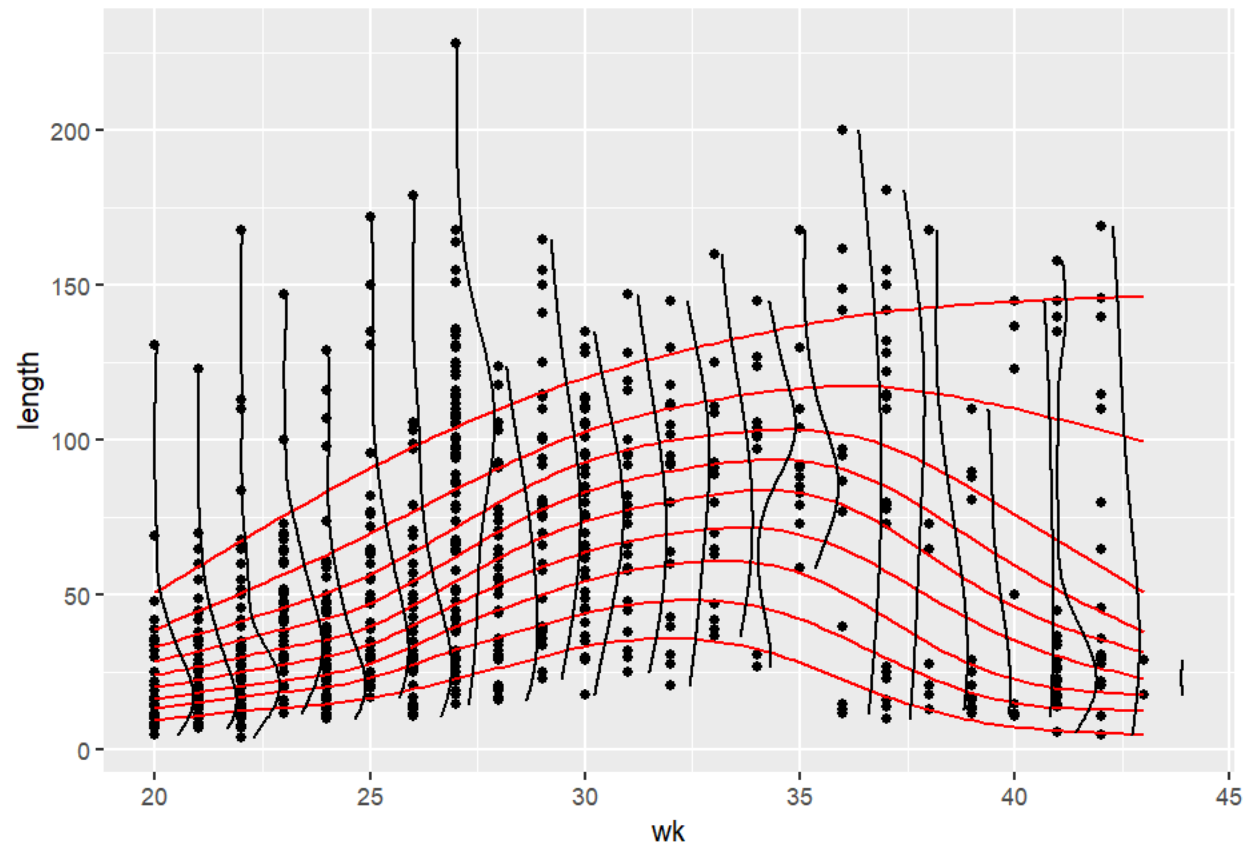
Raw length frequency



### Quantile regression

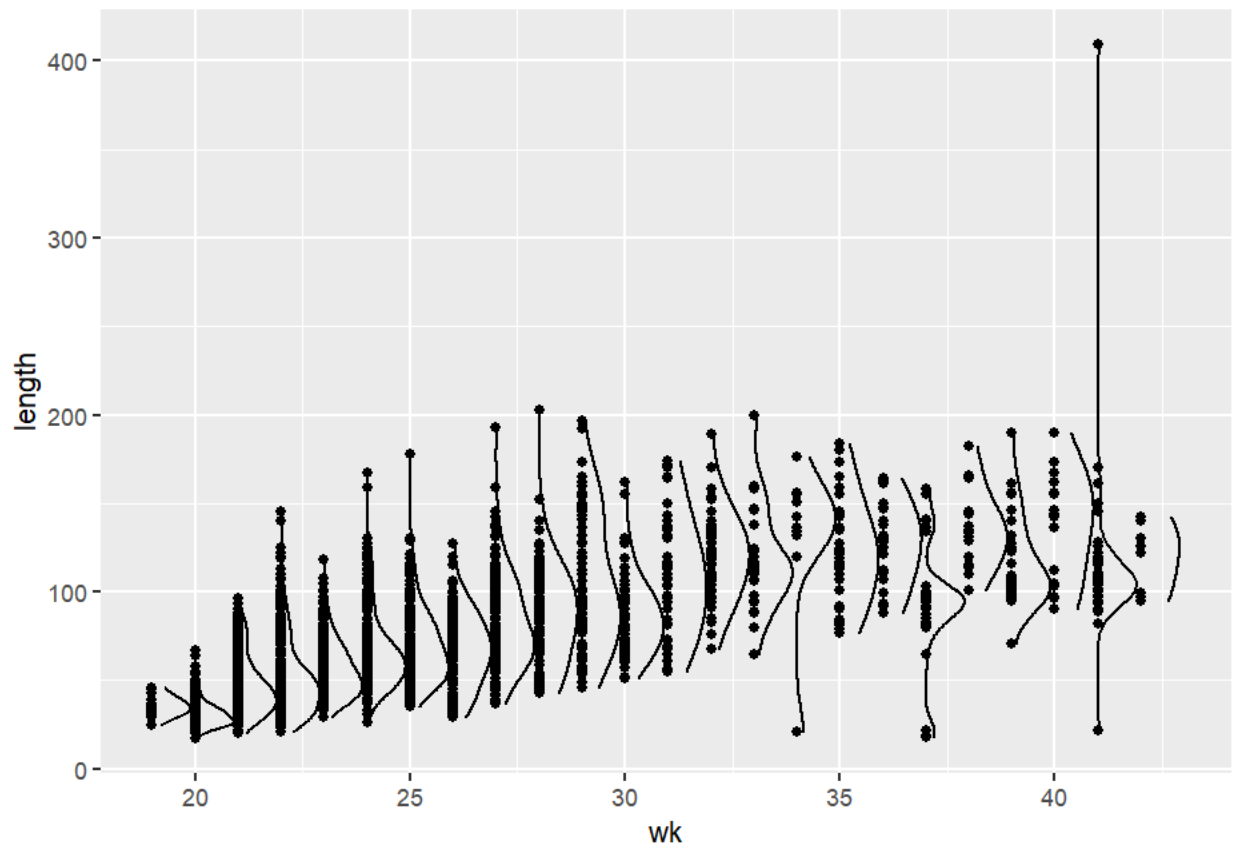
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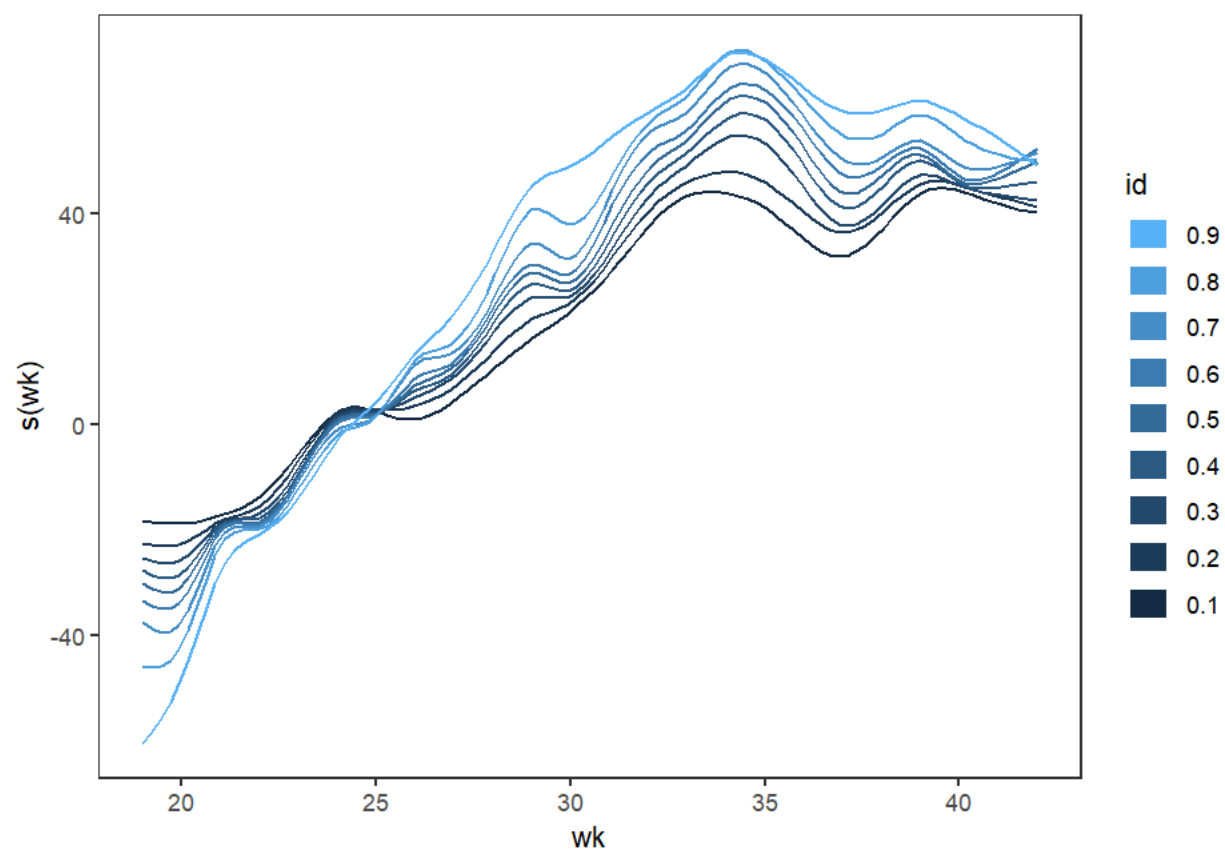
## leiostomus xanthurus

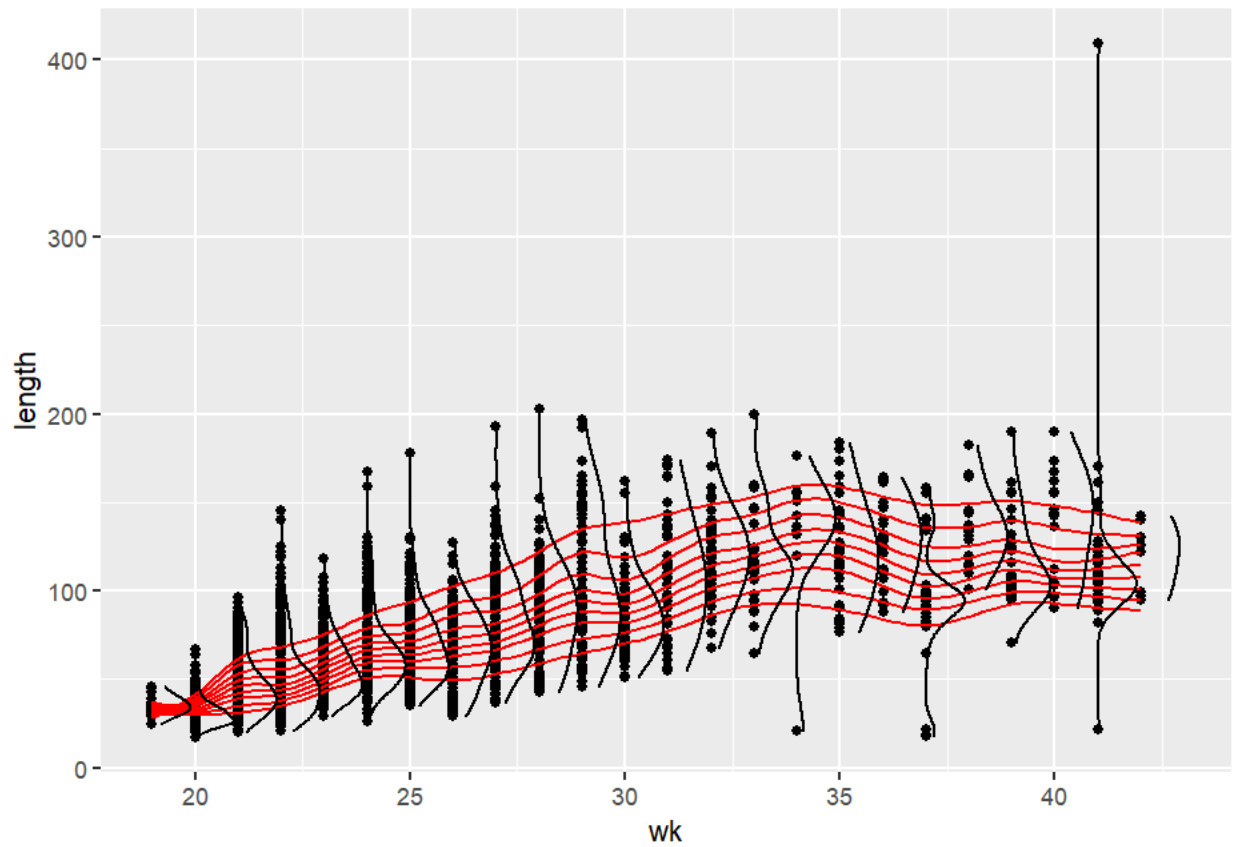
### Raw length frequency



### Quantile regression

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Raw length frequency

Quantile regression

Estimating learning rate. Each dot corresponds to a loss evaluation.  $qu = 0.5$ .

`## Error in chol.default(iS): the leading minor of order 3 is not positive definite`

