Model checking

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Outline

You fitted a GAM, everything is fine, right? *Right*?

But what about?

- Smooth terms flexibility?
- Non-constant variance?
- Response distribution selection?
- Correlated covariates?

“perhaps the most important part of applied statistical modelling”

Simon Wood, Generalized Additive Models: An Introduction in R

Basis size (k)

- k ≈ number of basis functions
- Set k per term
- e.g. `s(x, k=10)` or `s(x, y, k=100)`
- Penalty removes “extra” wigglyness
  - *up to a point!*
- (But computation is slower with bigger k)

Default basis size

```r
b <- gam(Nhat ~ s(day), data=pop_unhappy, method="REML")
gam.check(b)
```

```

Method: REML   Optimizer: outer newton
full convergence after 6 iterations.
Gradient range [-0.004427235,0.003510967]
(score 6424.346 & scale 844.0966).
Hessian positive definite, eigenvalue range [3.647717,668.0272].
Model rank =  10 / 10

Basis dimension (k) checking results. Low p-value (k-index<1) may
indicate that k is too low, especially if edf is close to k'.

          k'   edf k-index p-value
s(day) 9.000 8.778   0.638       0
```

Increasing basis size

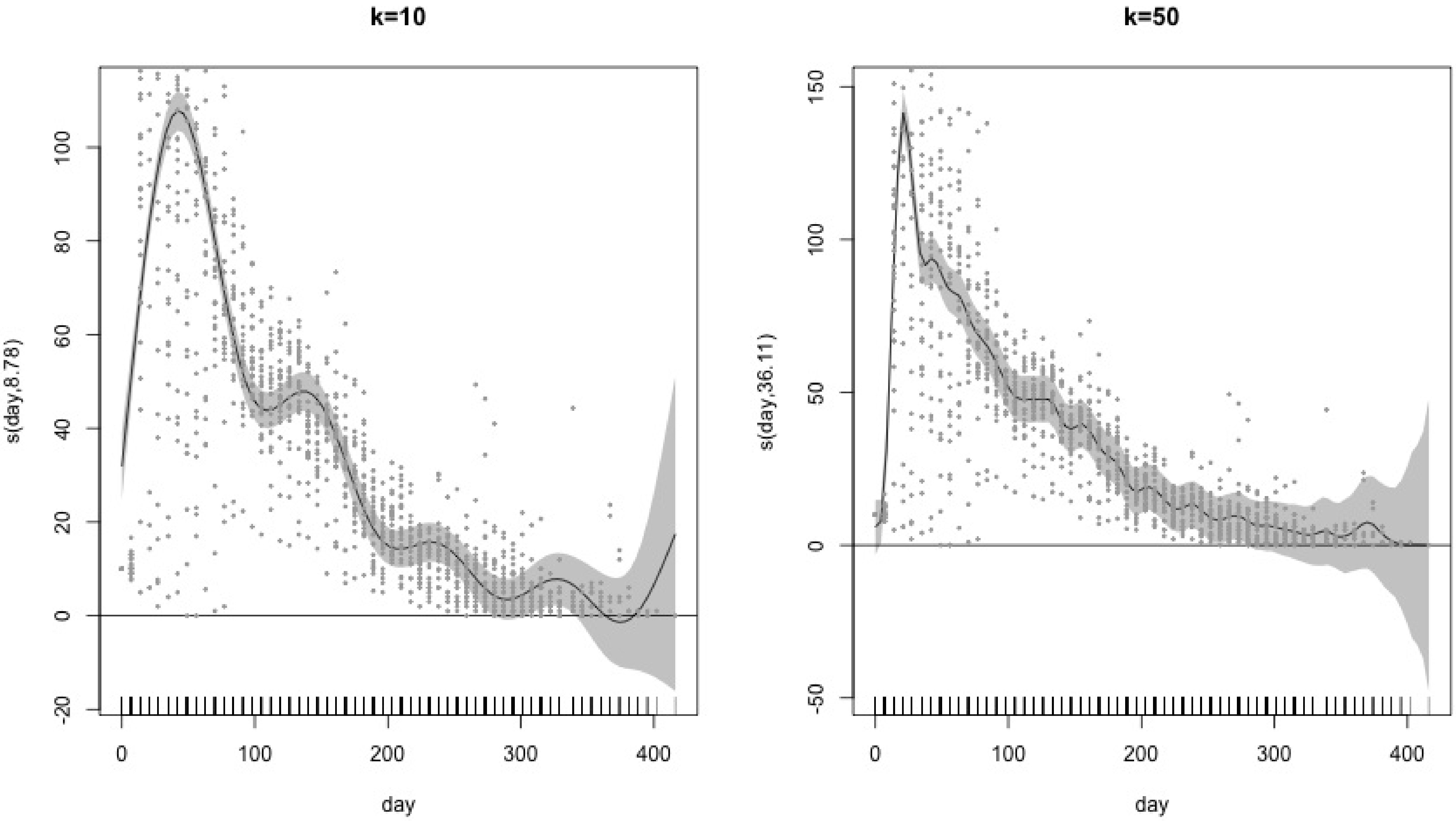
```r
b_50 <- gam(Nhat ~ s(day, k=50), data=pop_unhappy, method="REML")
gam.check(b_50)
```

```
Method: REML   Optimizer: outer newton
full convergence after 6 iterations.
Gradient range [-1.841561e-07,6.686406e-09]
(score 6296.597 & scale 647.8836).
Hessian positive definite, eigenvalue range [10.49952,668.4687].
Model rank =  50 / 50

Basis dimension (k) checking results. Low p-value (k-index<1) may
indicate that k is too low, especially if edf is close to k'.

           k'    edf k-index p-value
s(day) 49.000 36.110   0.847       0
```

Does it make a difference?!



General strategy

- leave k at default, see what happens
- double k depending on results from `gam.check`
- repeat

`?choose.k` has some good advice

Historical/philosophical note

- “Keep relationships simple and interpretable”
  - What does this mean?
  - Bias confirmation?
  - Limit model to get “clean” relationships?
- Some literature suggests “limit k=5” or somesuch
  - Original `gam` package for S+ had a default k=5
  - Coincidence?
  - (Simon Wood, pers. comm.)

Residual checks

Residuals

- Deal with 2 types of residuals
    - Deviance
    - Randomized quantile
- Raw residuals are just (observed - fitted)
    - Analog to R^2
    - Difficult to assess mean-variance relationship graphically
    - Need to rescale so mean-variance is constant

Deviance residuals

- Deviance $\approx$ "R^2 for GAMs"
- Per-observation deviance $\approx$ raw resids?
- Multiply by sign of (observed-fitted)
- Should be Normal(0, 1) distributed

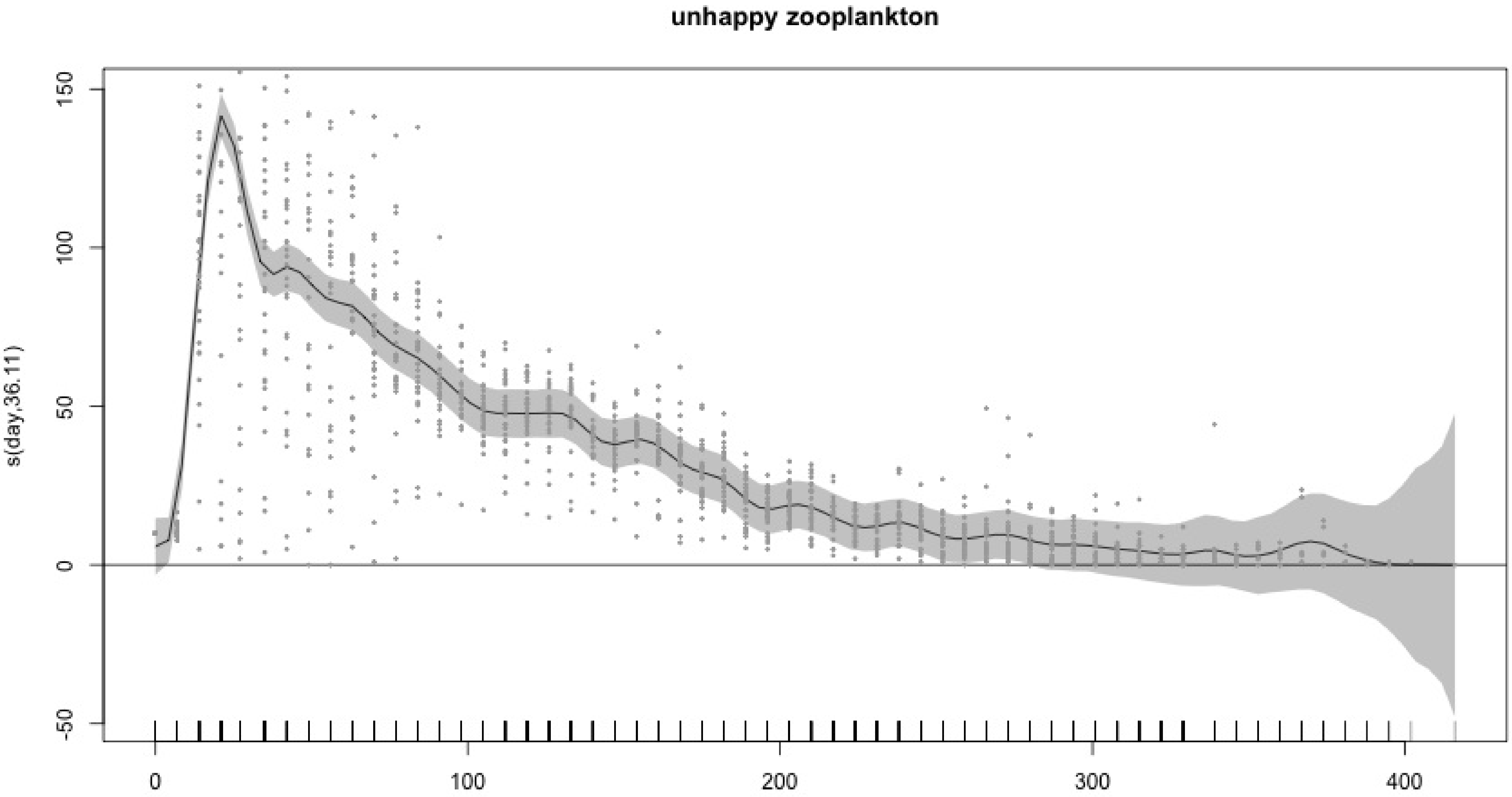
gam.check() plots

`gam.check()` creates 4 plots:

1. Quantile-quantile plots of residuals
2. Histogram of residuals
3. Residuals vs. linear predictor
4. Observed vs. fitted values

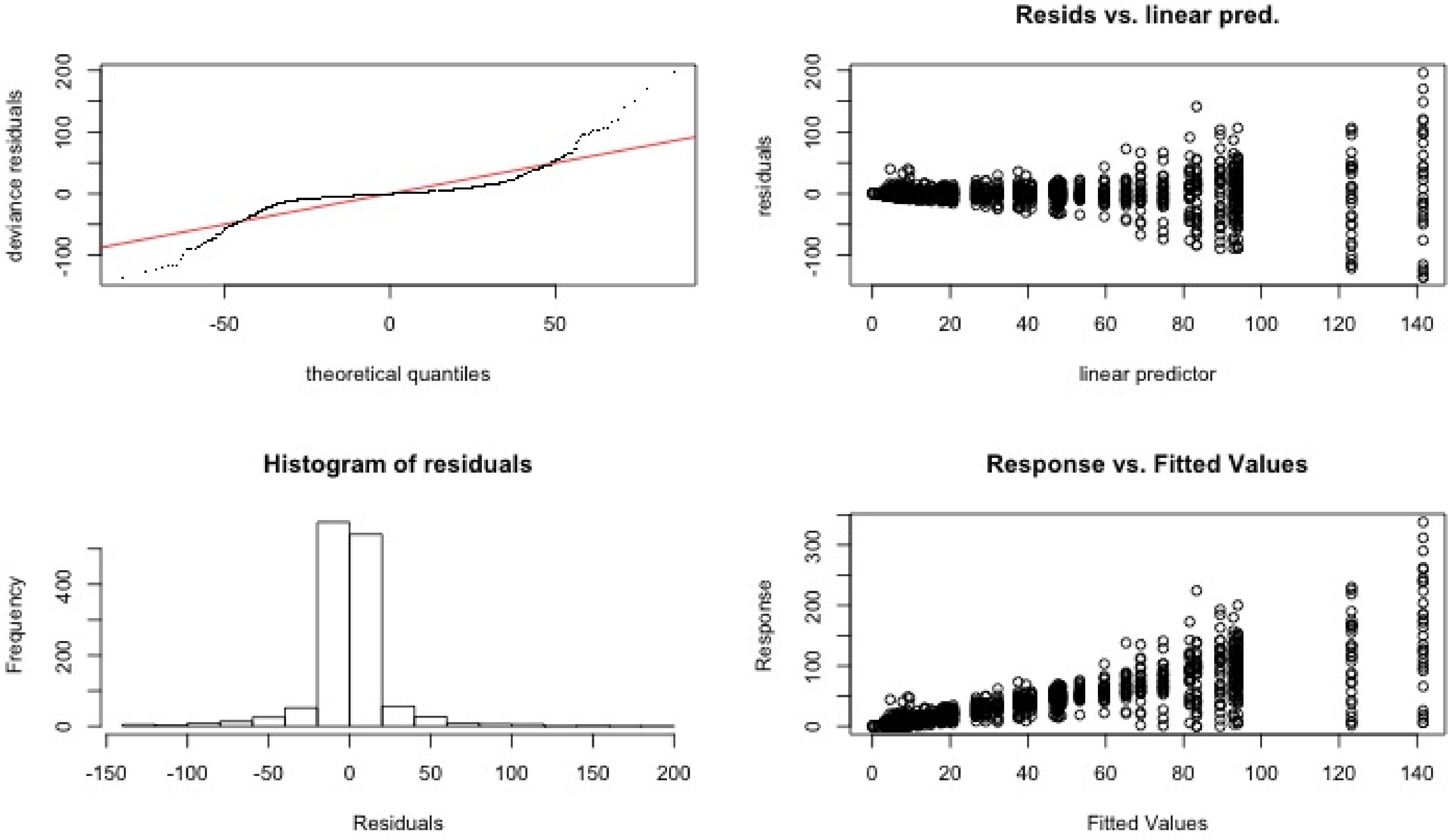
Checking response distribution

- Left side of `gam.check` plots
- Examples from the Drake & Griffen data
- Looking at the "deteriorating" populations



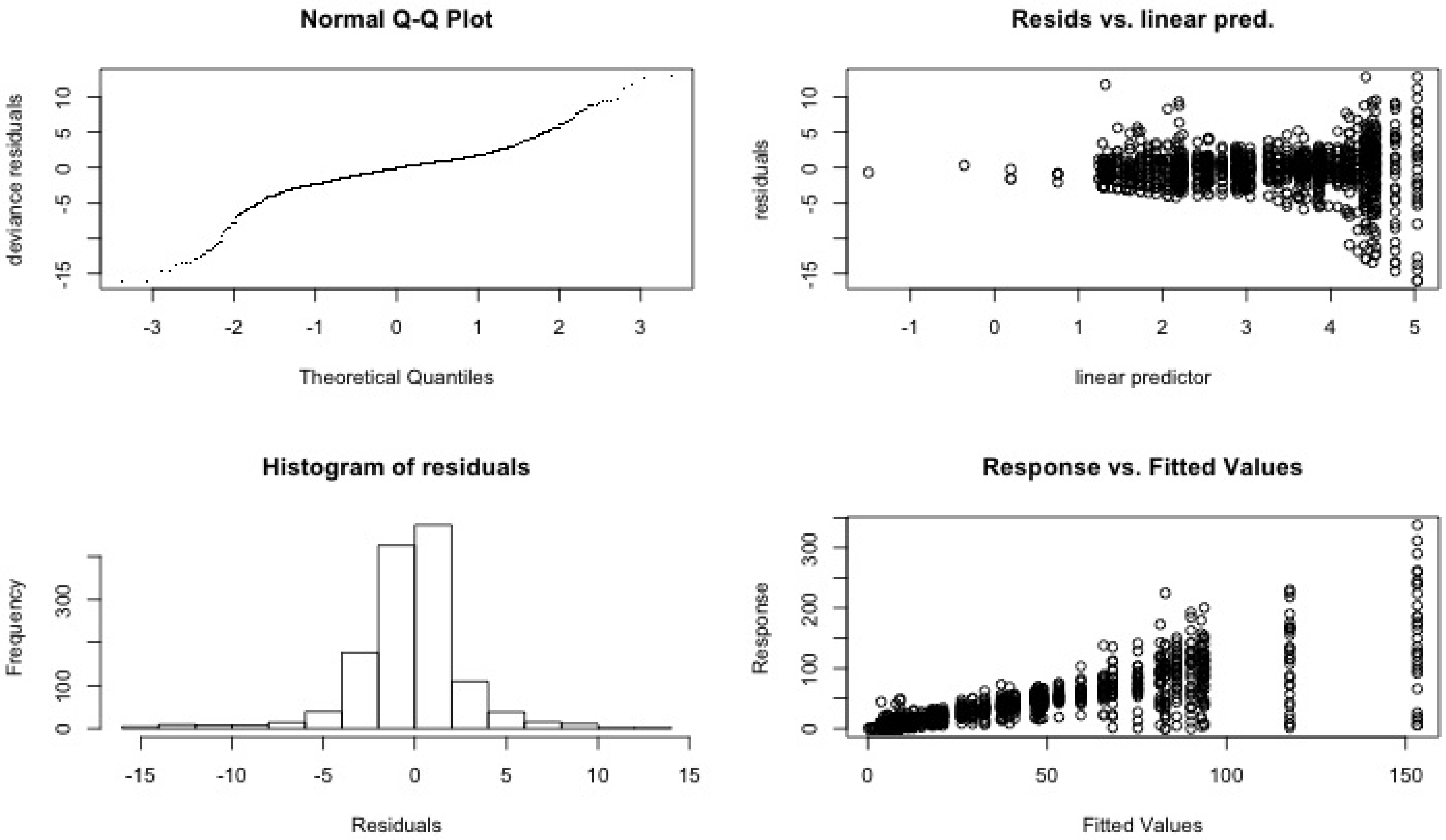
Normal response with count data

```
b <- gam(Nhat ~ s(day, k=50), data=pop_unhappy, method="REML")
```



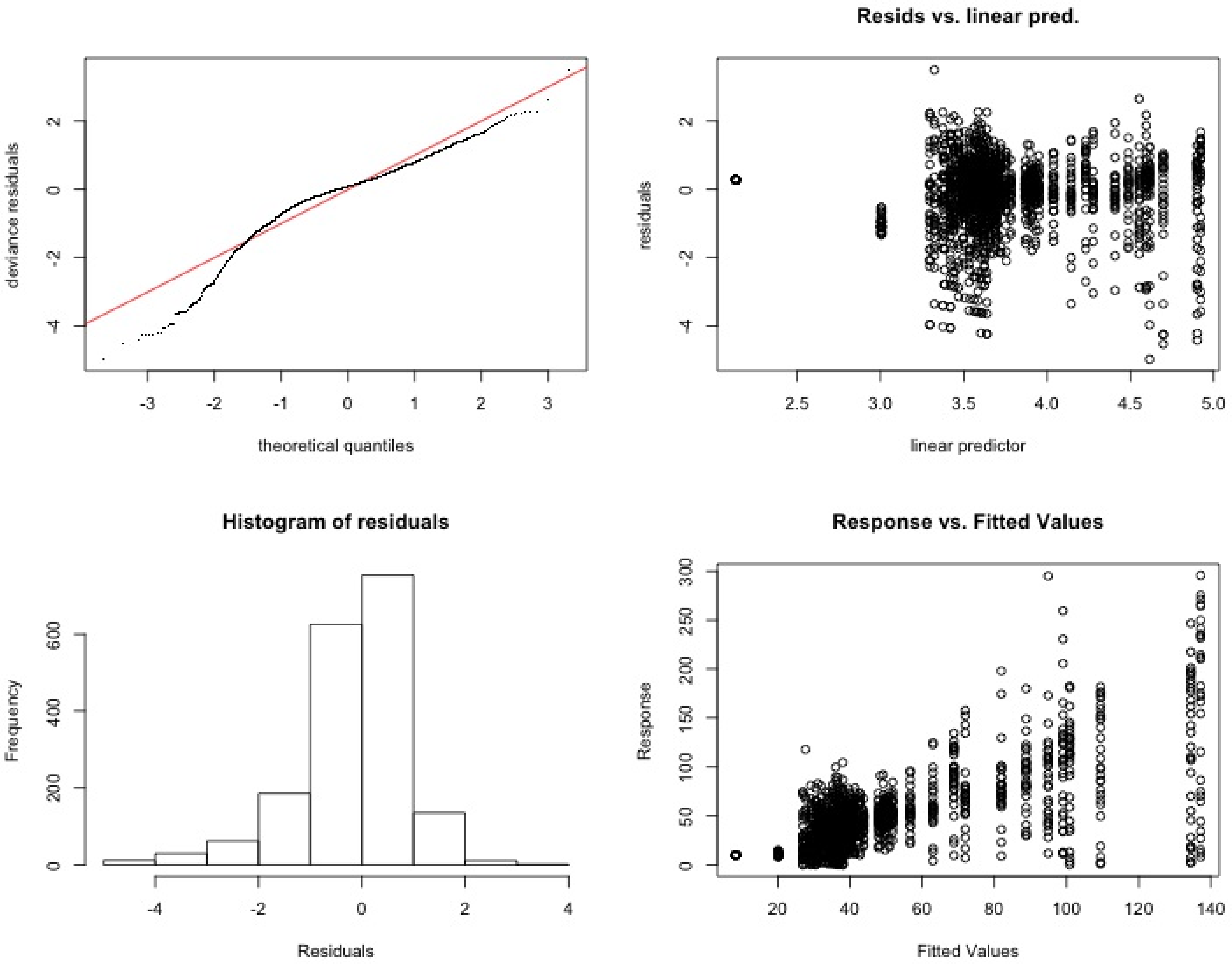
What about a count distribution?

```
b_quasi <- gam(Nhat ~ s(day, k=50), data=pop_unhappy,
method="REML", family=quasipoisson())
```



What about a fancier count distribution?

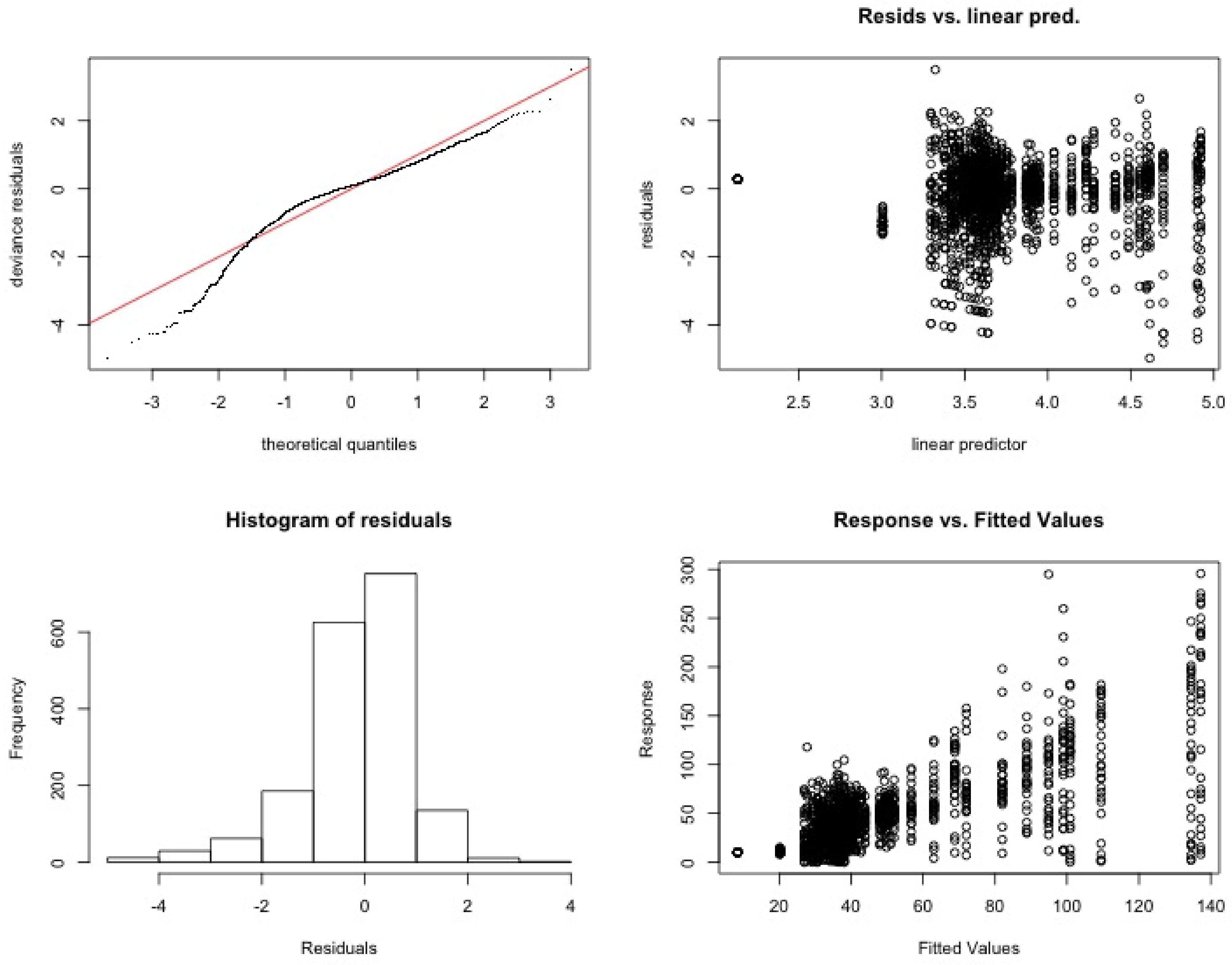
```
b_nb <- gam(Nhat ~ s(day, k=50), data=pop_happy, method="REML",
family=nb())
```



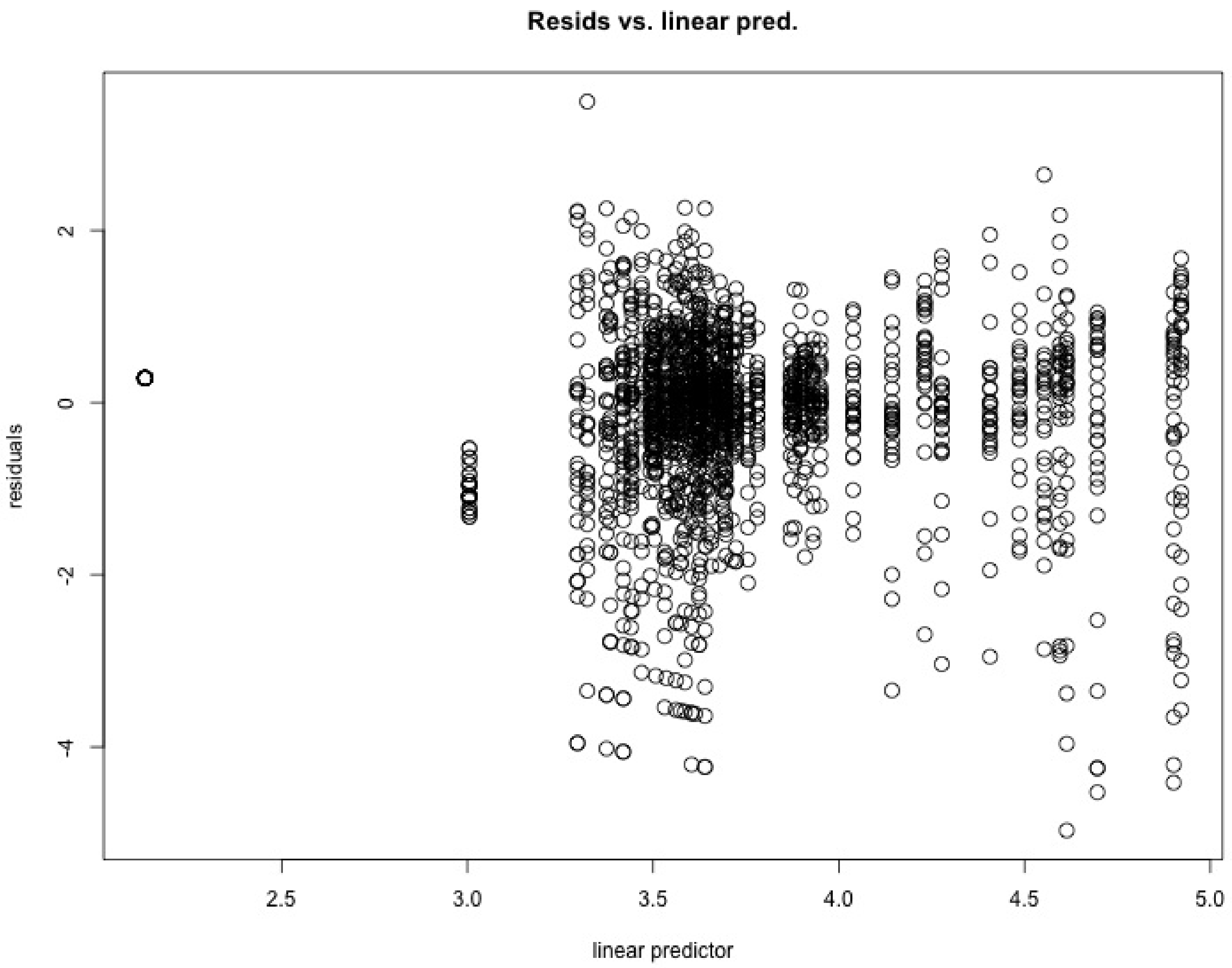
Variance relationships

- Heteroskedasticity
- Do we know that the mean-variance relationship is right?
- Deviance resids should give us constant variance if model correct?
- Right column of `gam.check`:
  - residuals vs. linear prediction == cloud
  - Response vs. fitted == line-ish

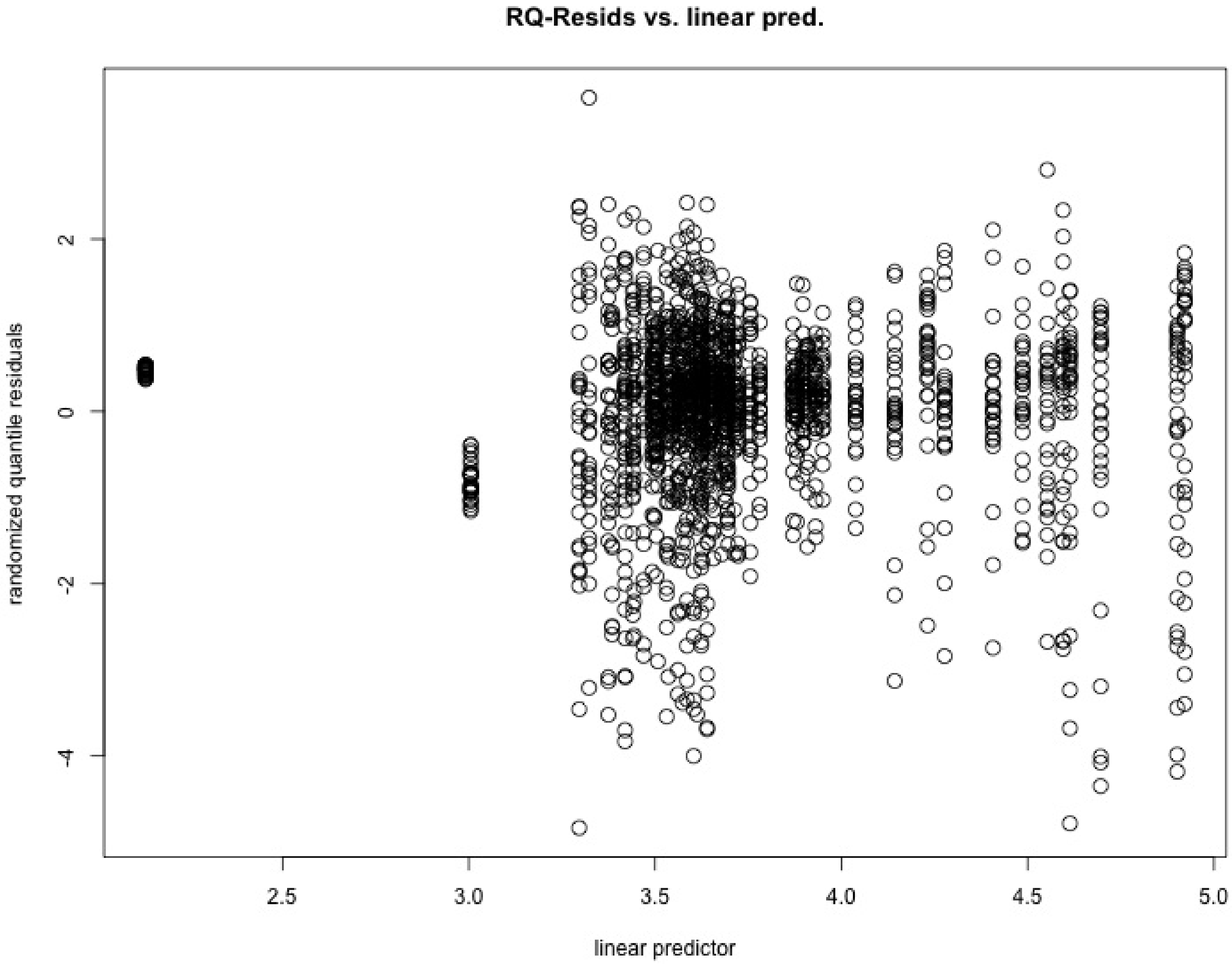
Mean-variance incorrect



Close up


Resids vs. linear pred.
residuals
2
0
-2
-4
2.5
3.0
3.5
4.0
4.5
5.0
linear predictor

Randomized quantile residuals

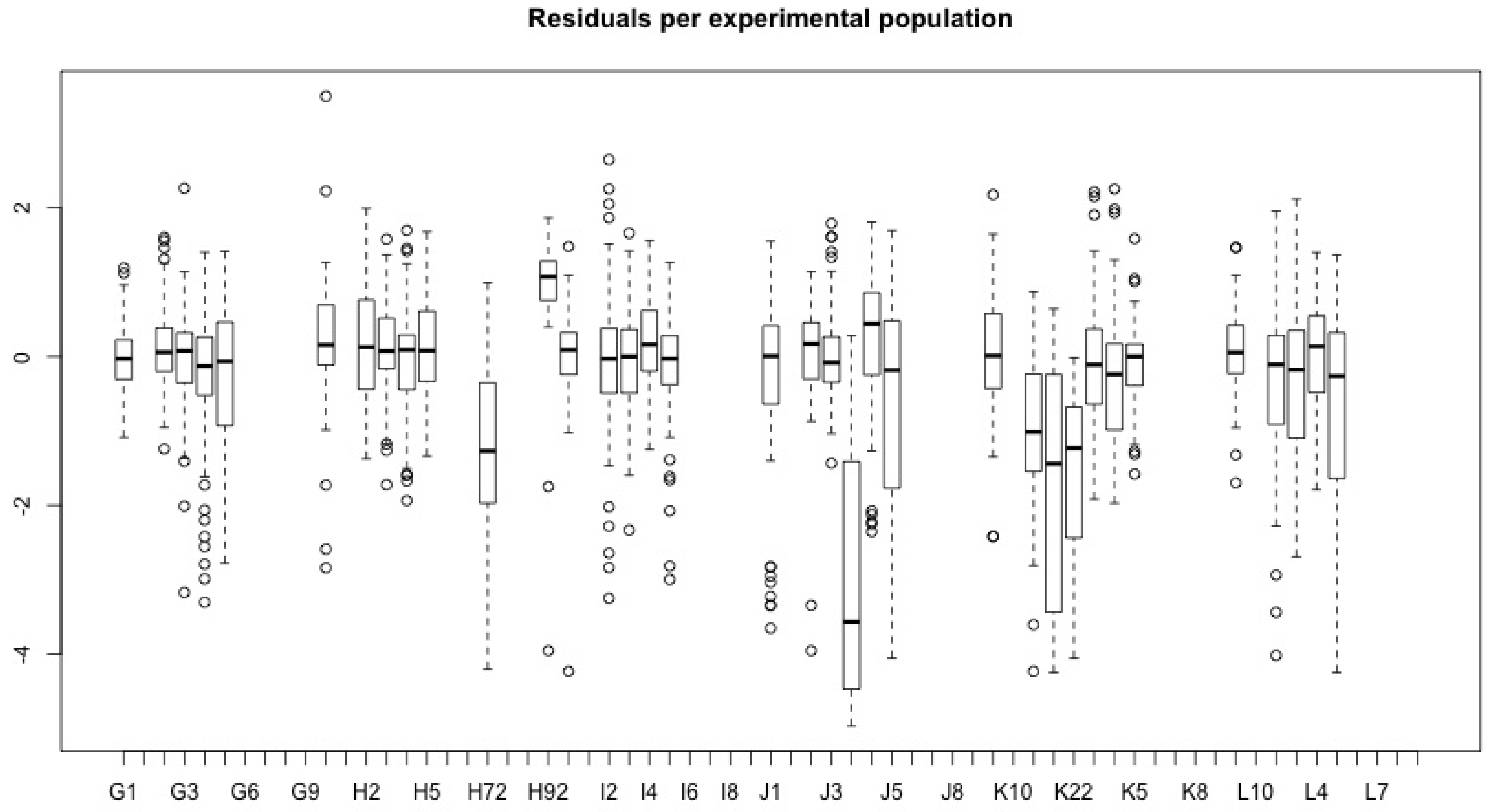


Shortcomings

- Deviance resids vs. linear predictor is victim of artifacts
- Need an alternative
- "Randomised quantile residuals" (*experimental*)
  - `rqresiduals` in `statmod`
  - Exactly normal residuals … if the model is right!
  - `rqgam.check` in `dsm` (ignore left side plots!)

These plots are just the start

- Need to go further
- Look at aggregations of residuals by other variables



Residual checking as art form

- Residuals can tell you a **lot** about your model
- No general method
  - Depends on data
  - Depends on inferential goals
- Highlight model deficiencies
- Inform what to do next; which other questions are interesting

Tobler’s first law of geography

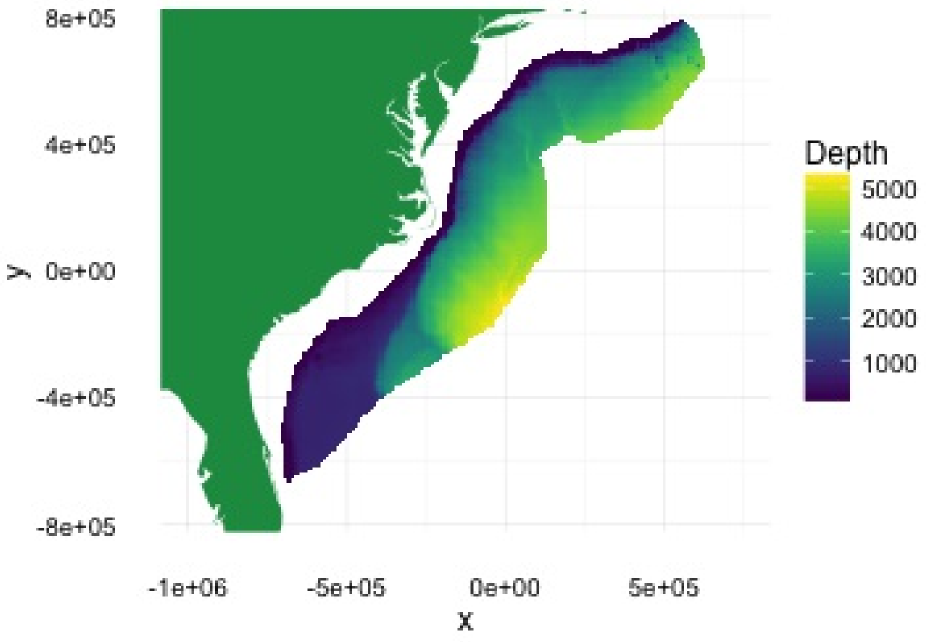
“Everything is related to everything else, but near things are more related than distant things”

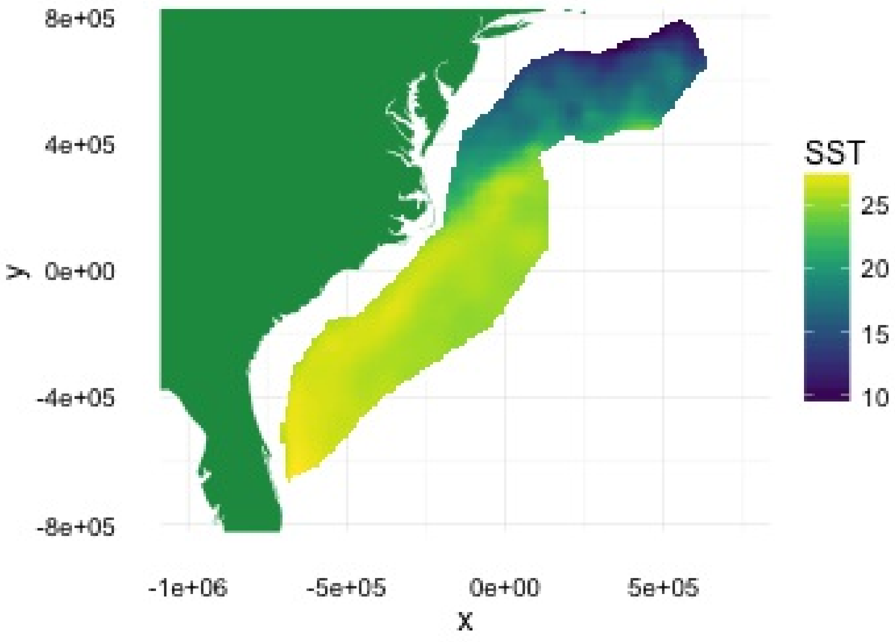
Tobler (1970)

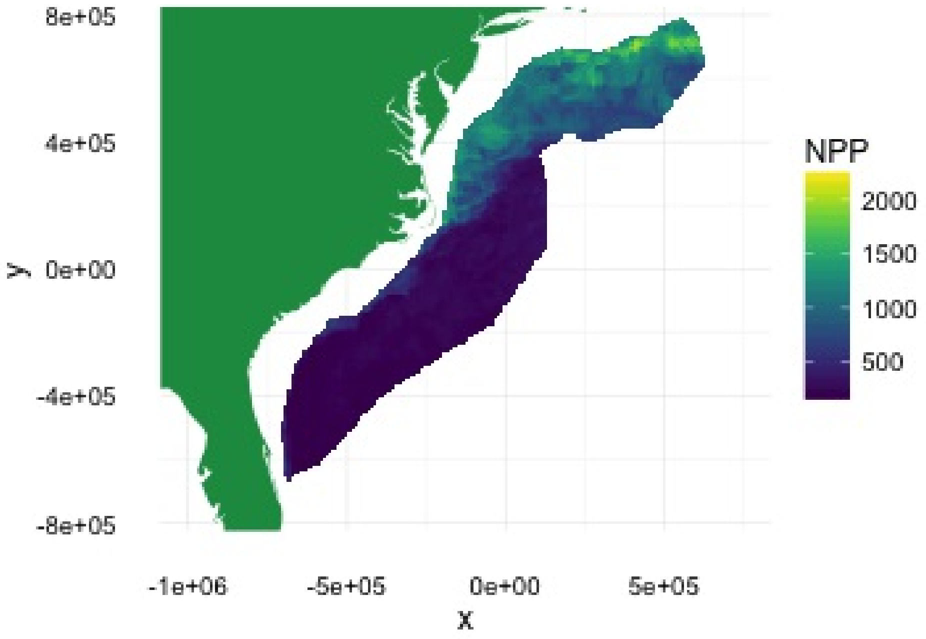
Concurvity

- We all know correlated covariates are bad
- What about non-linear correlations?
- Can we describe covariates as functions of each other?
- Important for model selection — sensitivity analysis

Example - US East coast



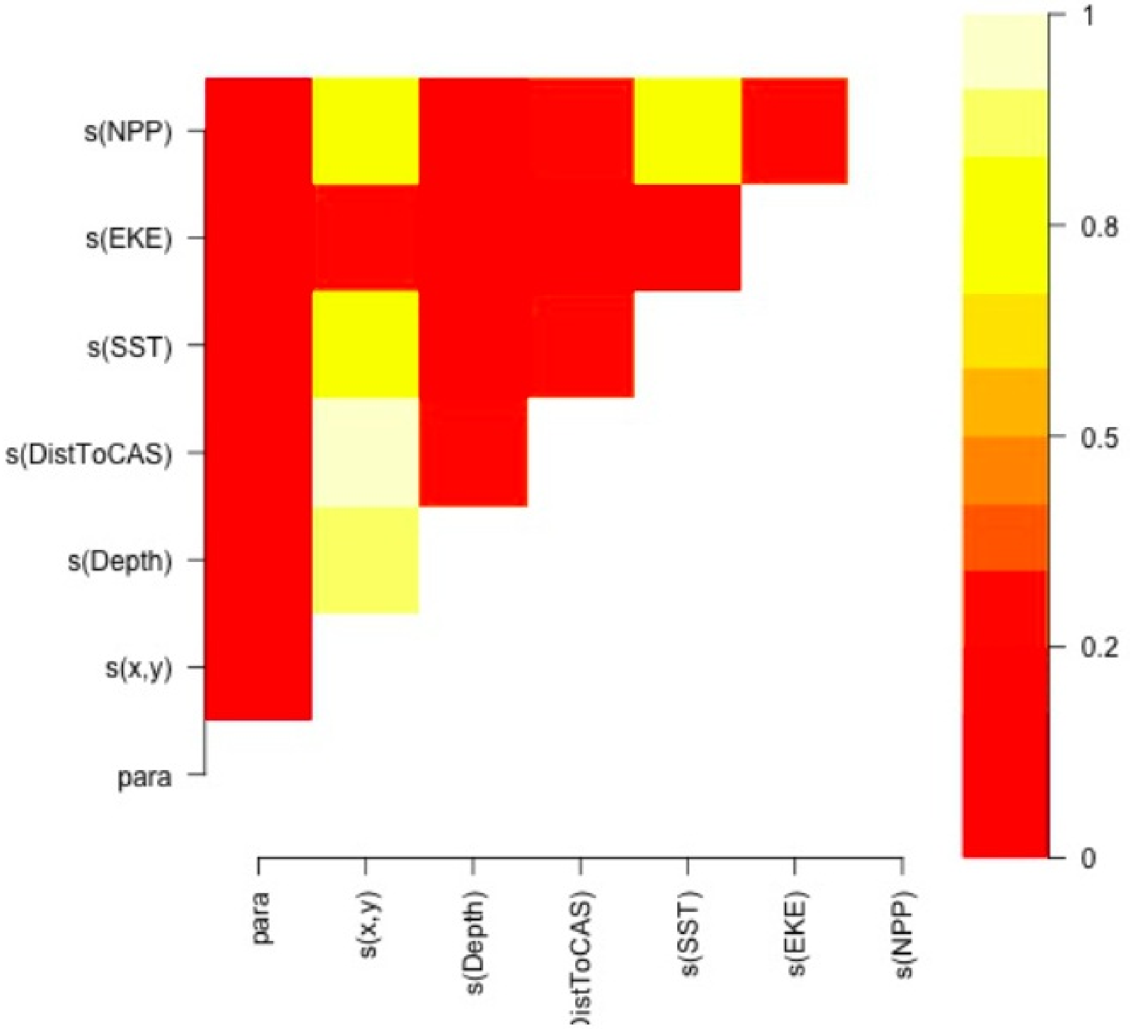




Checking for concurvity

- Measures, for each smooth term, how well this term could be approximated by
  - `concurvity(model, full=TRUE)`: some combination of all other smooth terms
  - `concurvity(model, full=FALSE)`: each of the other smooth terms in the model (useful for identifying which terms are causing issues)

Plotting concurvity



- We can visualise
- `vis.concurvity` on course site

Concurvity: things to remember

- Can make your model unstable to small changes
- `cor(data)` not sufficient: use the `concurvity(model)` function
- Not always obvious from plots of covariates or smooths