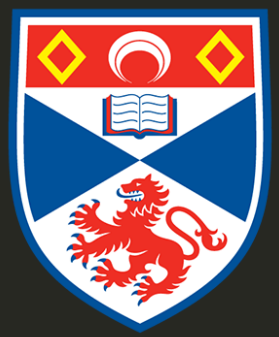
Lecture 4: Model checking



University of
St Andrews

"perhaps the most important part of applied statistical modelling"

Simon Wood

Model checking

- As with detection functions, checking is important
- Checking *doesn't* mean your model is **right**
- Want to know the model conforms to assumptions
- What assumptions should we check?

Convergence

Convergence

- Fitting the GAM involves an optimization
- By default this is REstricted Maximum Likelihood (REML) score
- Sometimes this can go wrong
- R will warn you!

A model that converges

```
gam.check(dsm_tw_xy_depth)
```

```
##
## Method: REML   Optimizer: outer newton
## full convergence after 7 iterations.
## Gradient range [-3.456333e-05,1.051004e-05]
## (score 374.7249 & scale 4.172176).
## Hessian positive definite, eigenvalue range [1.179219,301.267].
## Model rank =  39 / 39
##
## 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(x,y)   29.00 11.11    0.65  <2e-16 ***
## s(Depth)  9.00  3.84    0.81    0.37
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

A bad model

```
Error in while (mean(ldxx/(ldxx + ldss)) > 0.4) { :
  missing value where TRUE/FALSE needed
In addition: Warning message:
In sqrt(w) : NaNs produced
Error in while (mean(ldxx/(ldxx + ldss)) > 0.4) { :
  missing value where TRUE/FALSE needed
```

This is **rare**

The Folk Theorem of Statistical Computing

"most statistical computational problems are due not to the algorithm being used but rather the model itself"

Andrew Gelman

Folk Theorem anecdata

- Often if there are fitting problems, you're asking too much from your data
- Model is too complicated
- Too little data
- Try something simpler, see what happens

Basis size

Basis size (k)

- 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`)

Checking basis size

```
gam.check(dsm_x_tw)
```

```
##
## Method: REML   Optimizer: outer newton
## full convergence after 7 iterations.
## Gradient range [-3.196351e-06,4.485625e-07]
## (score 409.936 & scale 6.041307).
## Hessian positive definite, eigenvalue range [0.7645492,302.127].
## 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(x) 9.00 4.96    0.76    0.38
```

Increasing basis size

```
dsm_x_tw_k <- dsm(count~s(x, k=20), ddf.obj=df,
                  segment.data=segs, observation.data=obs,
                  family=tw())
gam.check(dsm_x_tw_k)
```

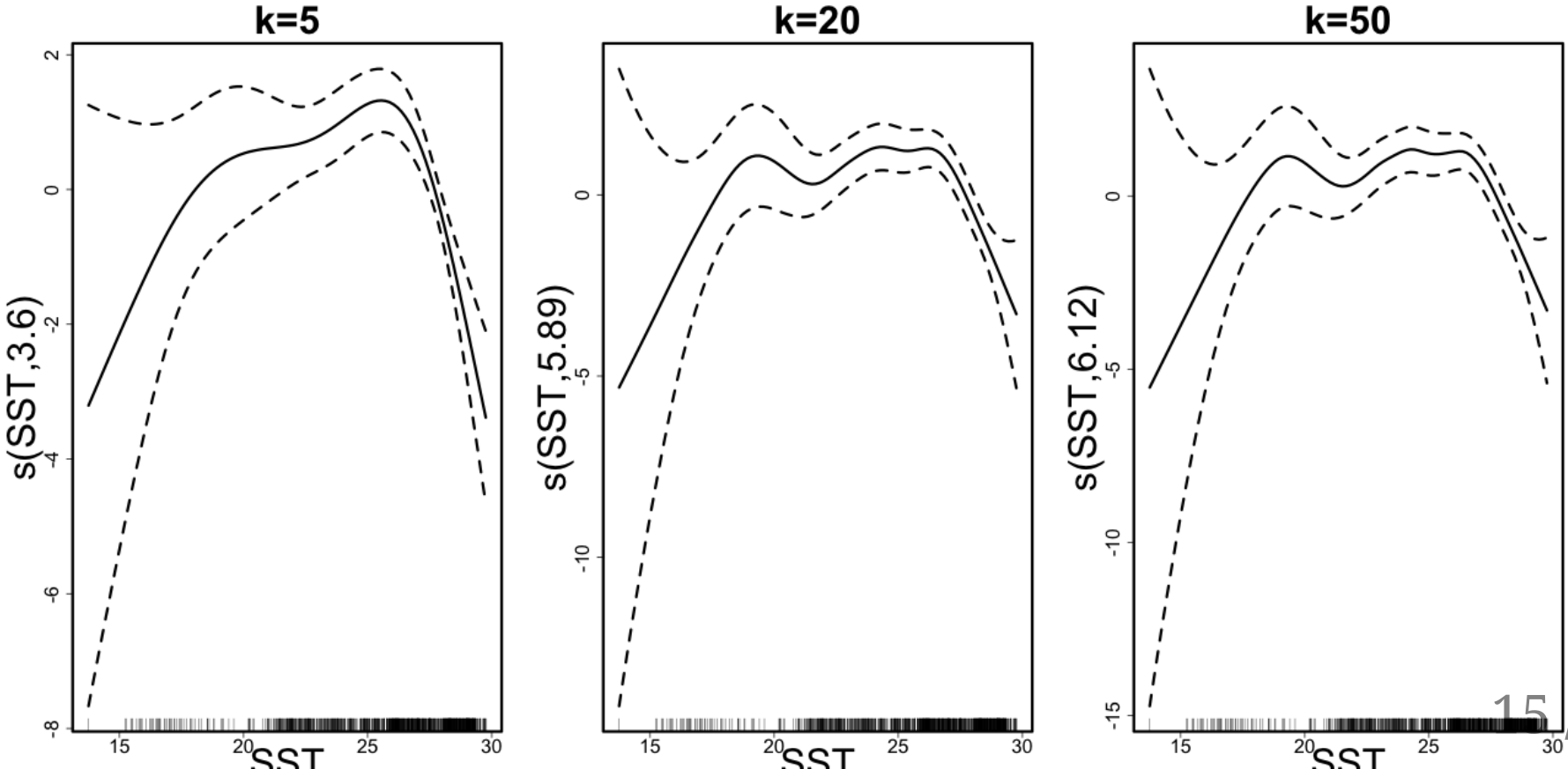
```
##
## Method: REML   Optimizer: outer newton
## full convergence after 7 iterations.
## Gradient range [-2.30124e-08,3.930703e-09]
## (score 409.9245 & scale 6.033913).
## Hessian positive definite, eigenvalue range [0.7678456,302.0336].
## Model rank =  20 / 20
##
## Basis dimension (k) checking 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(x) 19.00  5.25    0.76    0.35
```

Sometimes basis size isn't the issue...

- Generally, double `k` and see what happens
- Didn't increase the EDF much here
- Other things can cause low "`p-value`" and "`k-index`"
- Increasing `k` can cause problems (nullspace)

k is a maximum

- Don't worry about things being too wiggly
- k gives the maximum complexity
- Penalty deals with the rest



Residuals

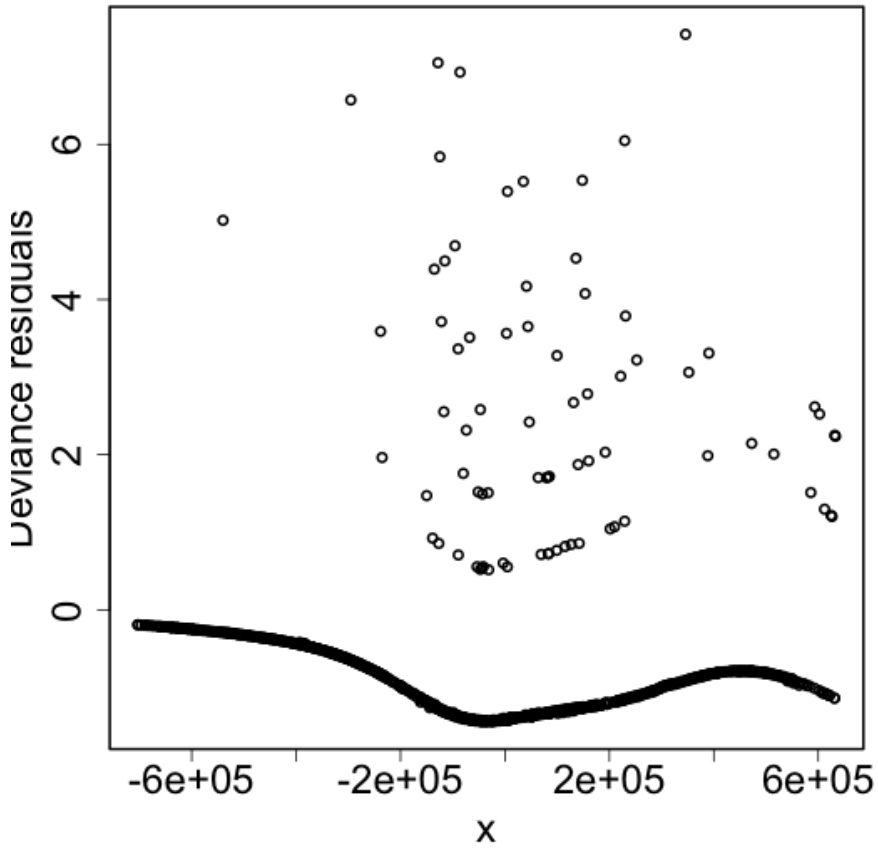
What are residuals?

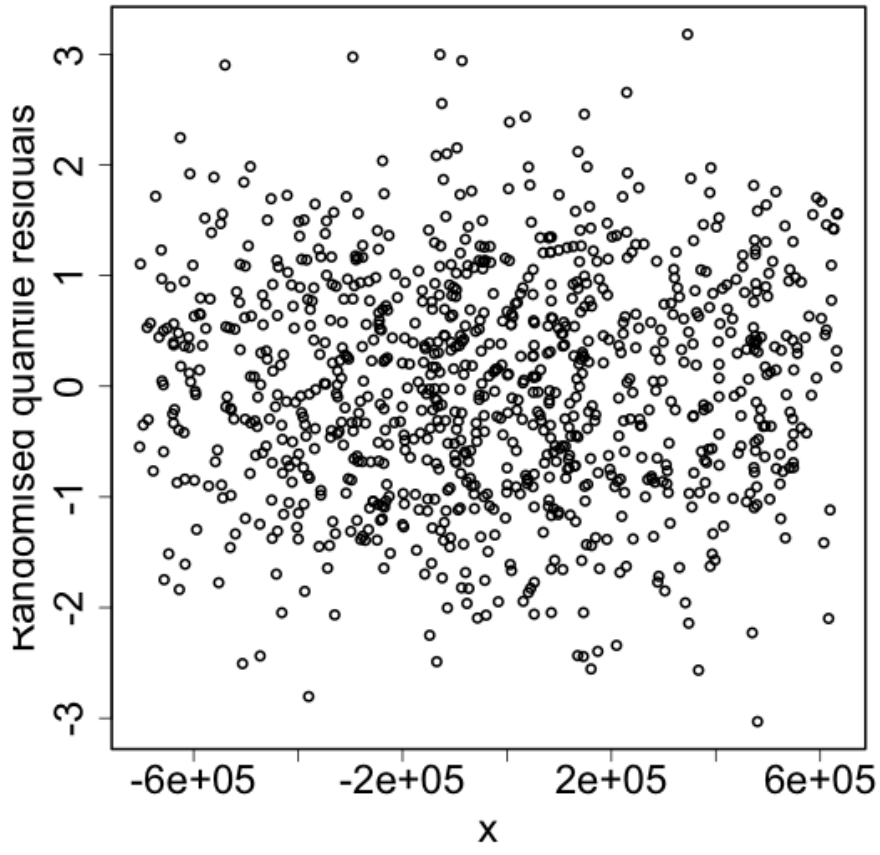
- Generally residuals = observed value - fitted value
- BUT hard to see patterns in these "raw" residuals
- Need to standardise $\Rightarrow$ **deviance residuals**
- Expect these residuals $\sim N(0, 1)$

Why are residuals important?

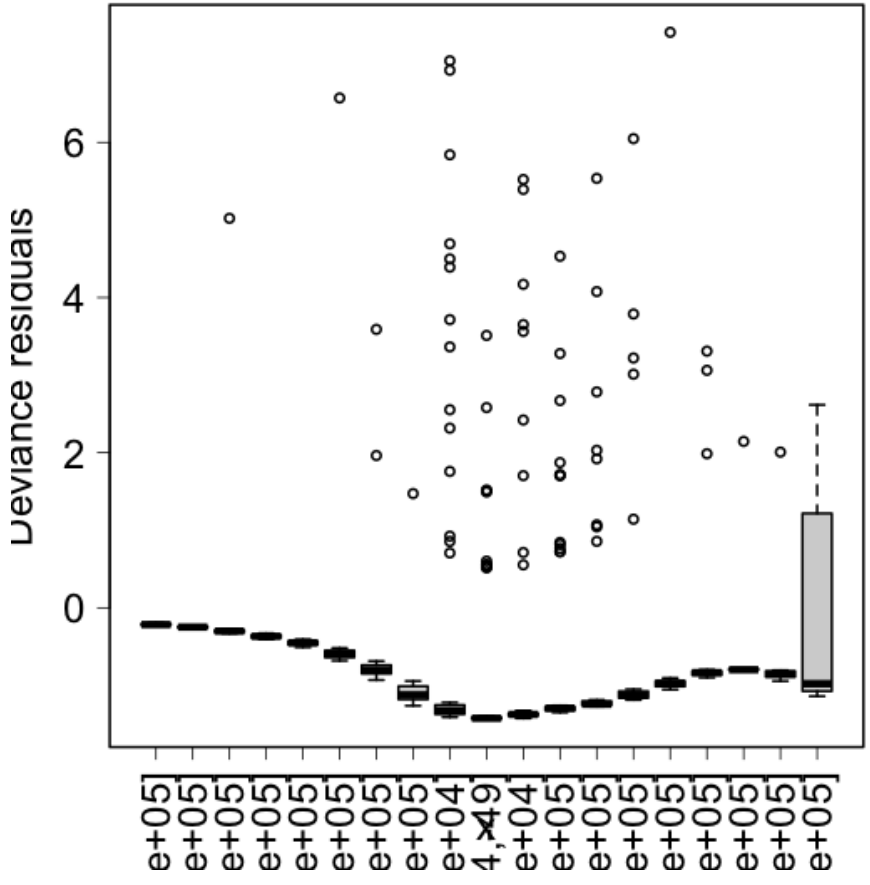
- Structure in the residuals means your model didn't capture something
- Maybe a missing covariate
- Model doesn't describe the data well

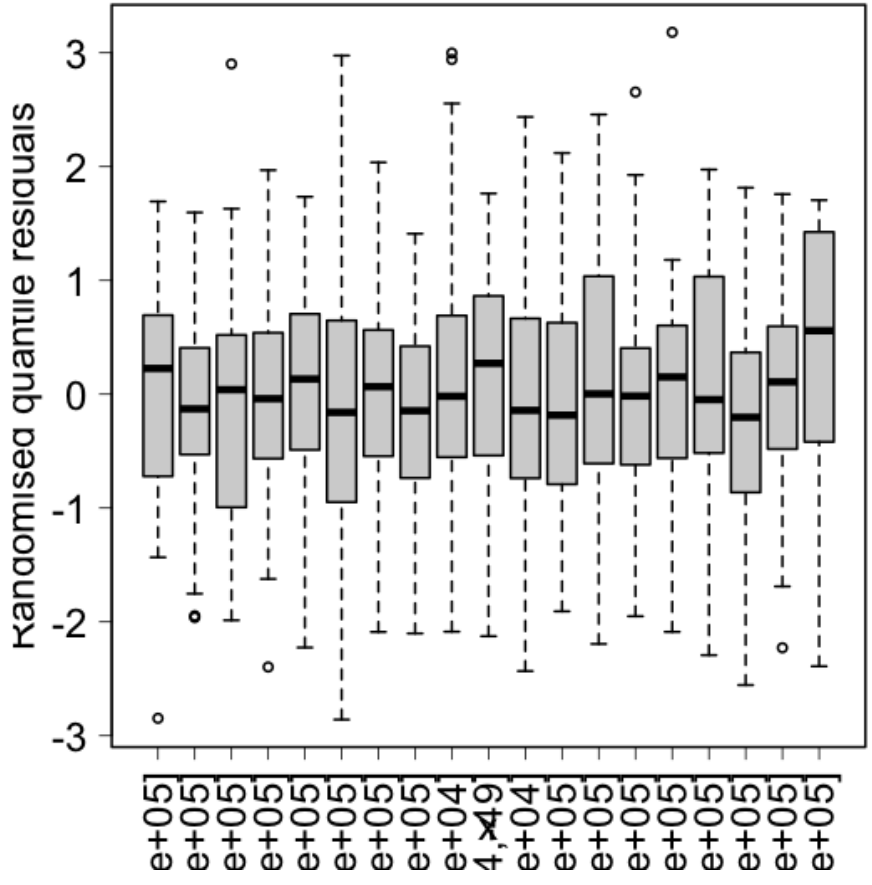
Residuals vs. covariates





Residuals vs. covariates (boxplots)





Fitting to residuals

- Refit our model but with the residuals as response
- Response is normal (for deviance residuals)
- What pattern is left in the residuals?

Example

- Example model with `NPP` and `Depth`

```
# get data
refit_dat <- dsm_depth_npp$data
# make residuals column
refit_dat$resid <- residuals(dsm_depth_npp)
# fit a model (same model)
resid_fit <- gam(resid~s(Depth, bs="ts", k=20) +
                         s(NPP, bs="ts", k=20),
                 family=gaussian(), data=refit_dat, method="REML")
```

summary(resid_fit)

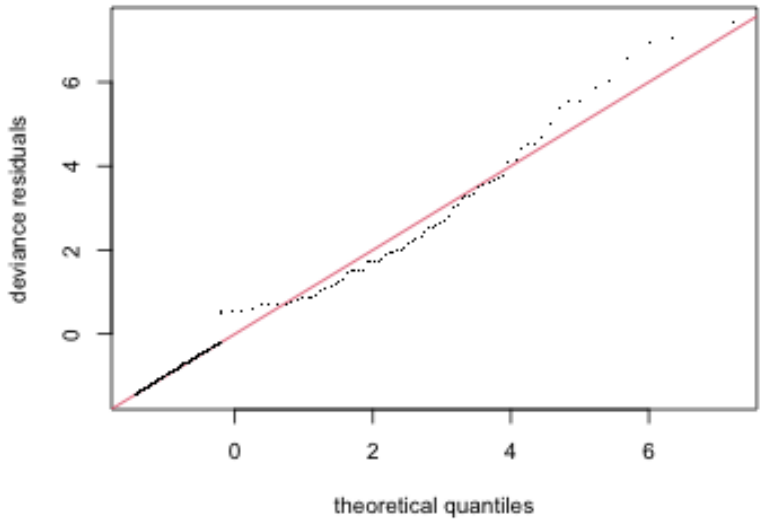
```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## resid ~ s(Depth, bs = "ts", k = 20) + s(NPP, bs = "ts", k = 20)
##
## Parametric coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.49454    0.03274   -15.1   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##              edf Ref.df     F p-value
## s(Depth) 2.56621     19 1.230 4.9e-06 ***
## s(NPP)   0.03322     19 0.002   0.316
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.0241   Deviance explained = 2.67%
## -REML =   1362  Scale est. = 1.0174    n = 949
```

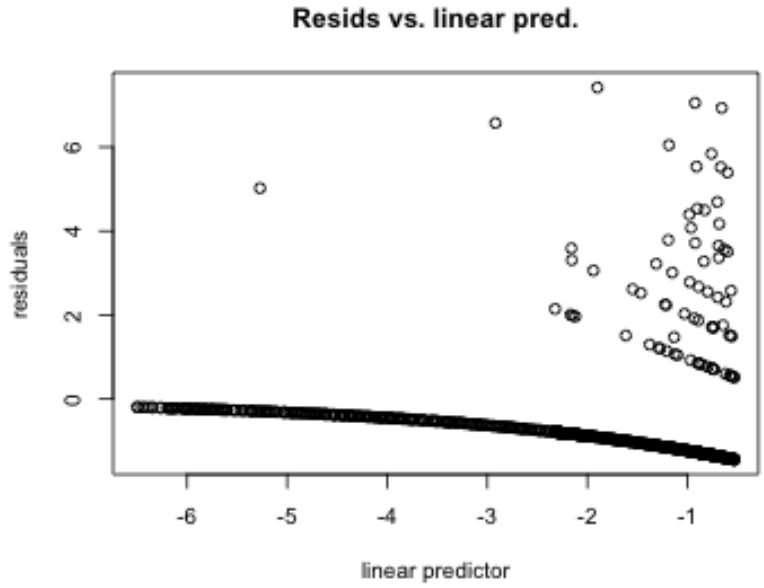
What's going on there?

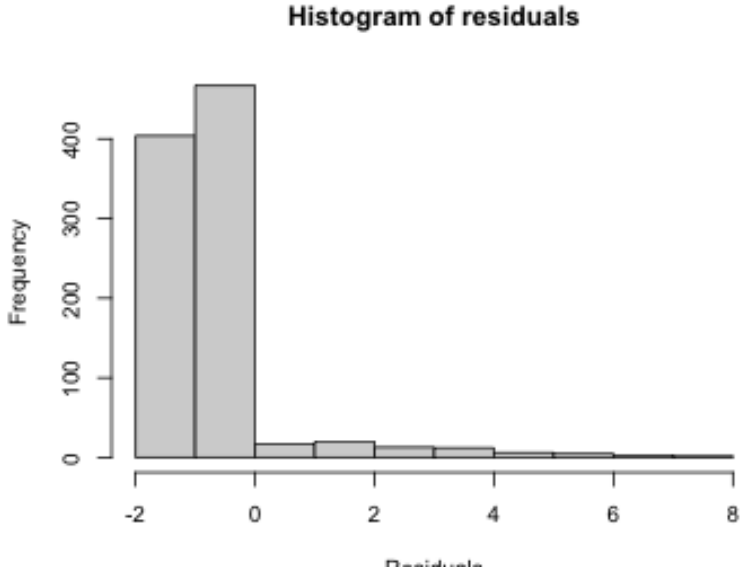
- Something unexplained going on?
- Maybe `Depth` + `NPP` is not enough?
  - Add other smooths (`s(x, y)?`)
- Increase `k`?

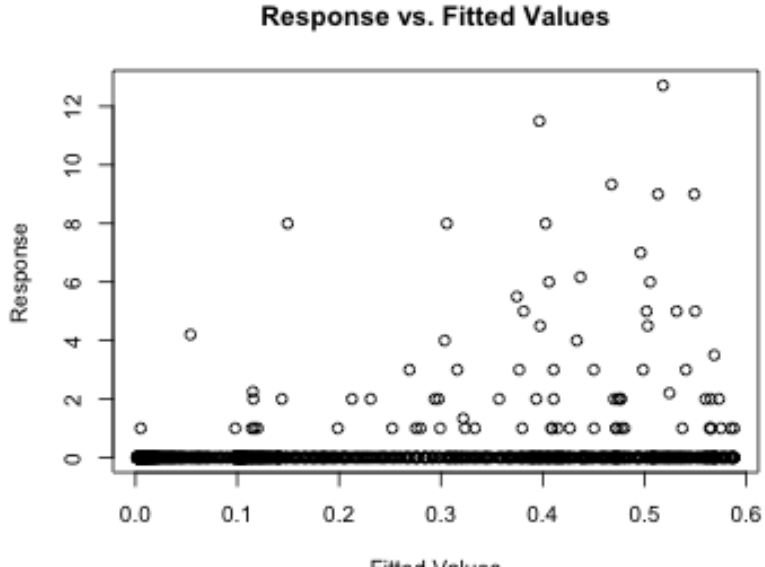
Other residual checking

gam.check


deviance residuals
0
2
4
6
theoretical quantiles


Resids vs. linear pred.
residuals
0
2
4
6
-6
-5
-4
-3
-2
-1
linear predictor

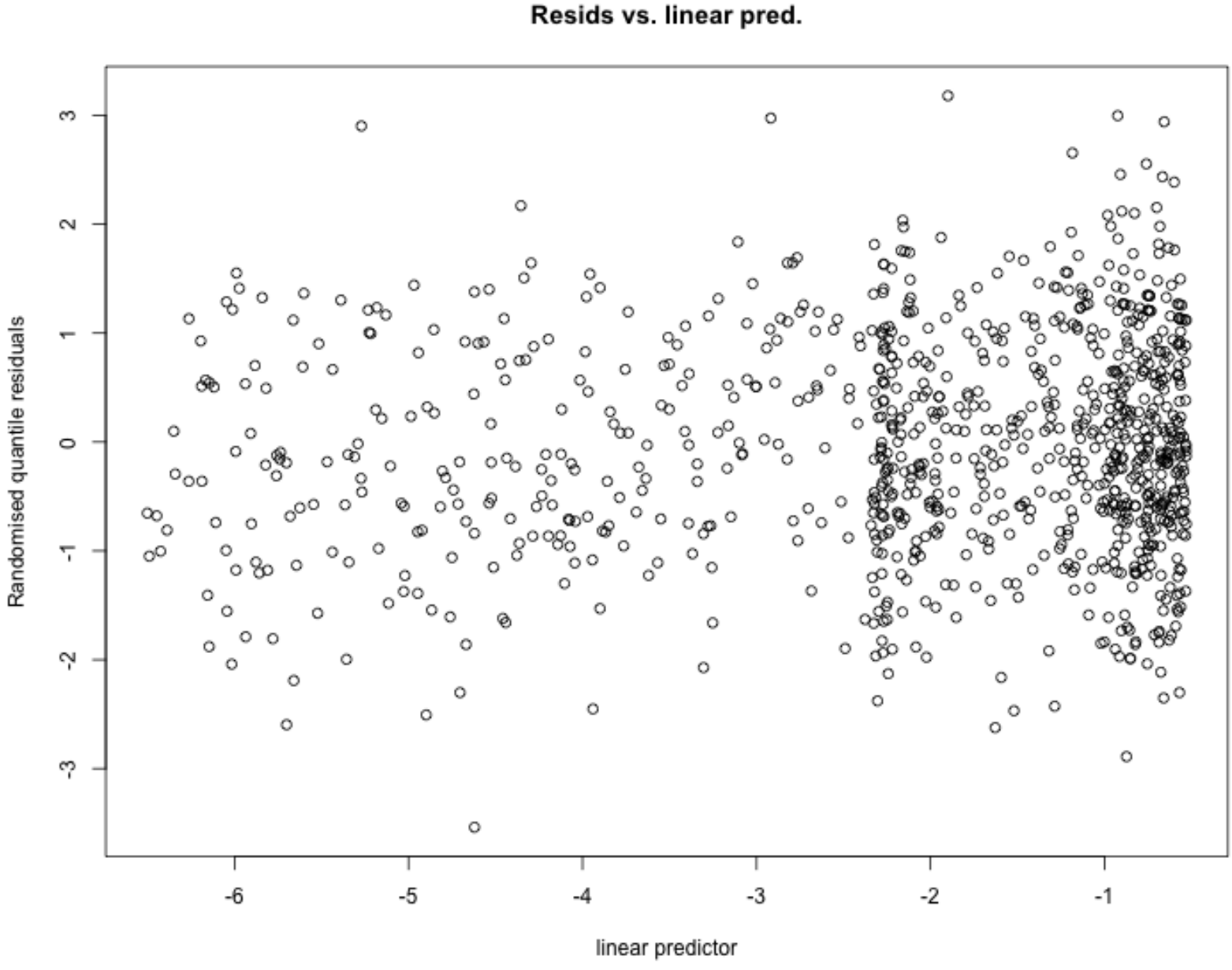

Histogram of residuals
Frequency
0
100
200
300
400
-2
0
2
4
6
8


Response vs. Fitted Values
Response
0
2
4
6
8
10
12
0.0
0.1
0.2
0.3
0.4
0.5
0.6

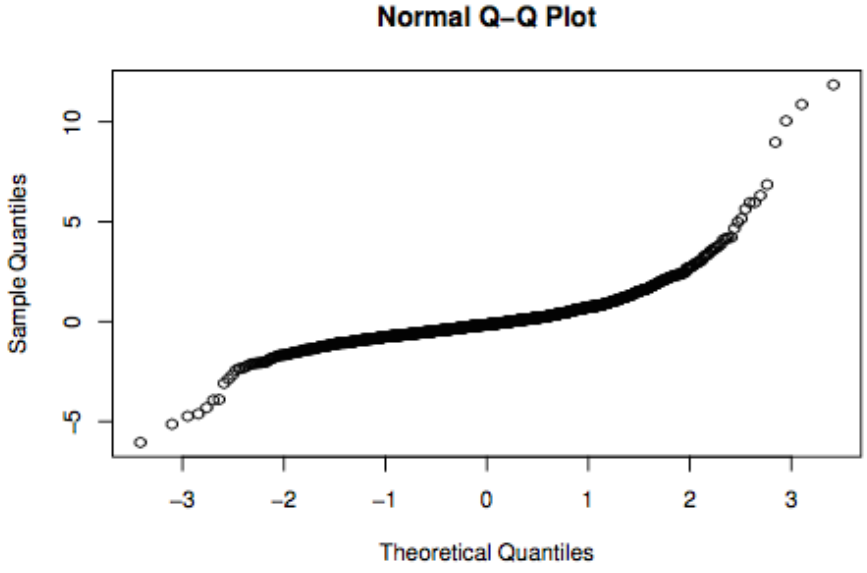
Shortcomings

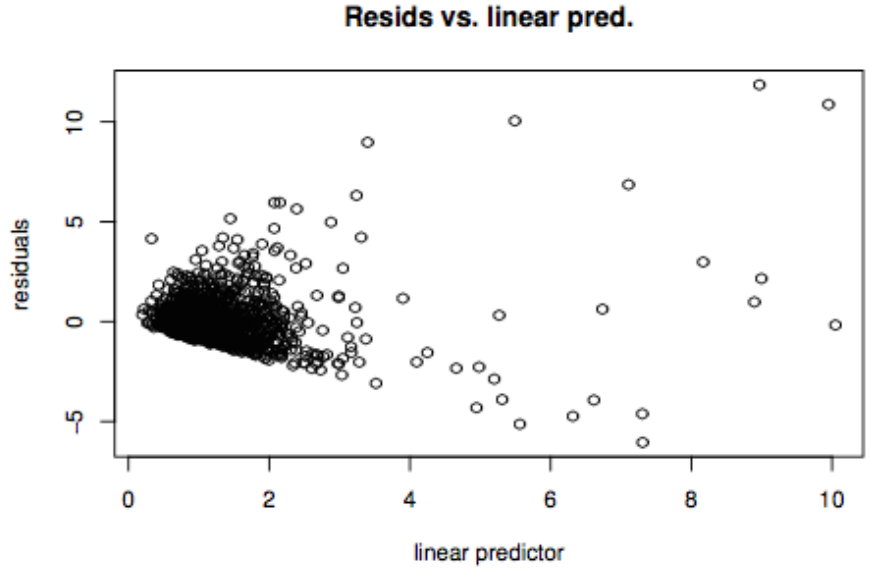
- `gam.check` can be helpful
- "Resids vs. linear pred" is victim of artifacts
- Need an alternative
- "Randomised quanitle residuals"
  - `rqgam.check`
  - Exactly normal residuals

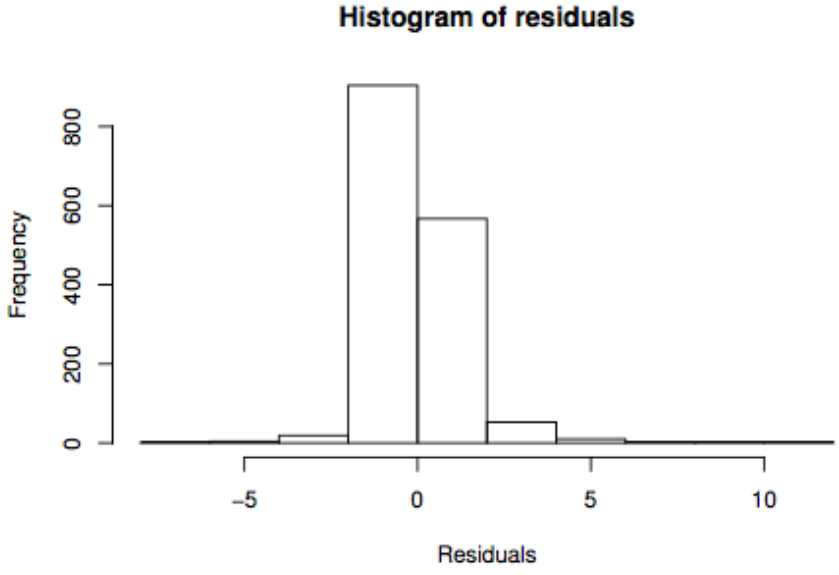
Randomised quantile residuals

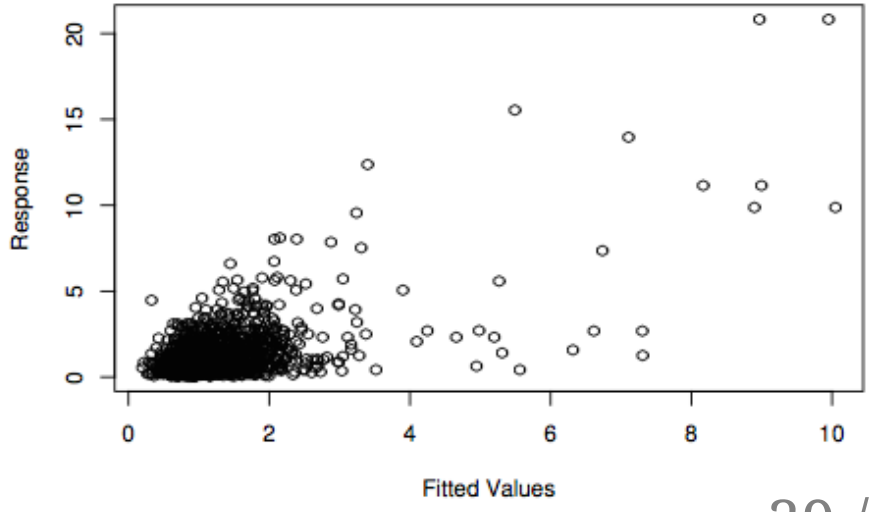


Example of "bad" plots

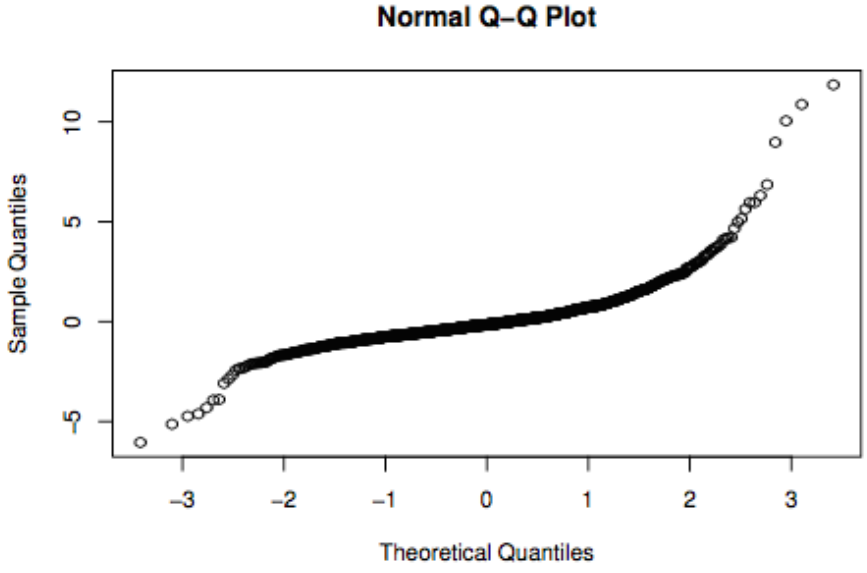


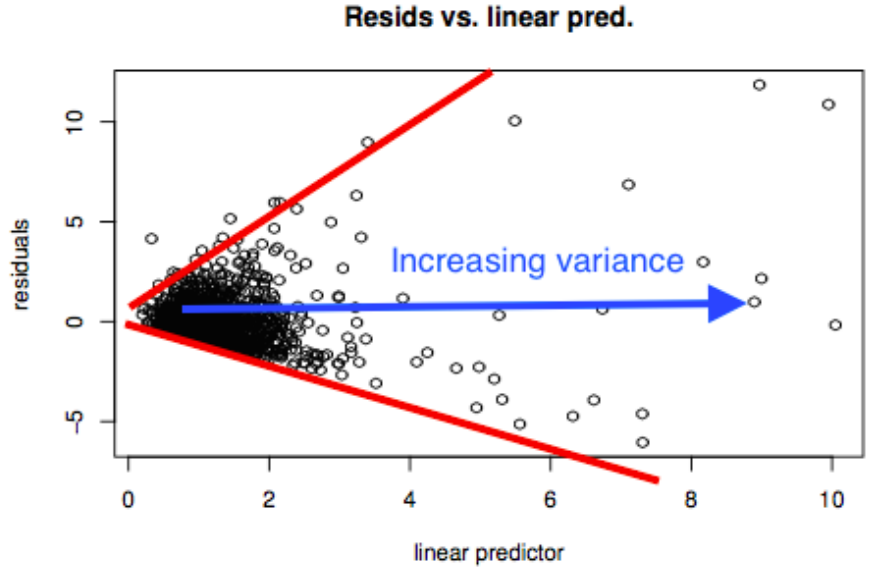


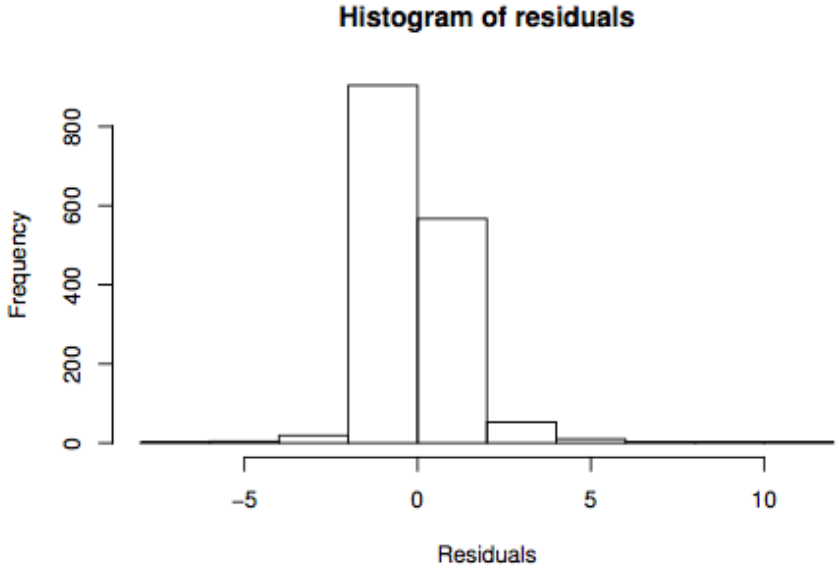


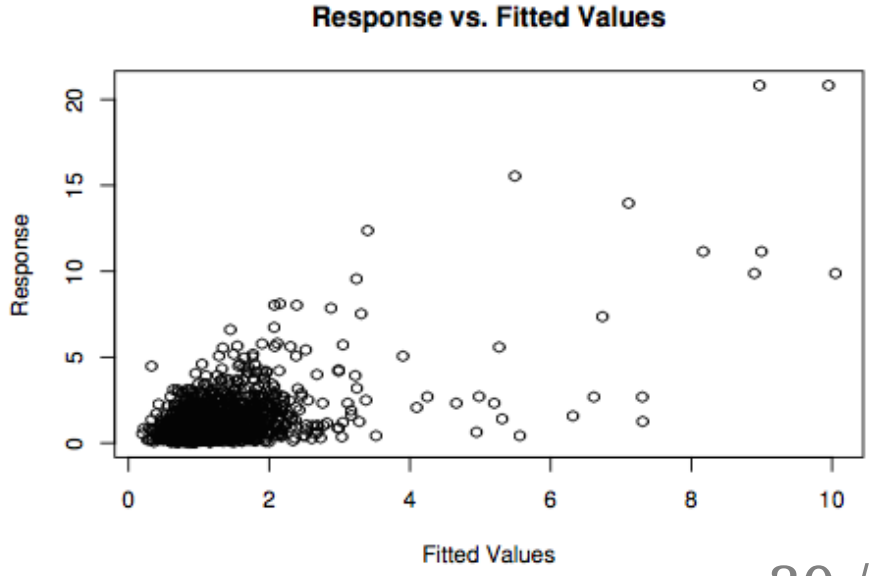


Example of "bad" plots









Residual checks

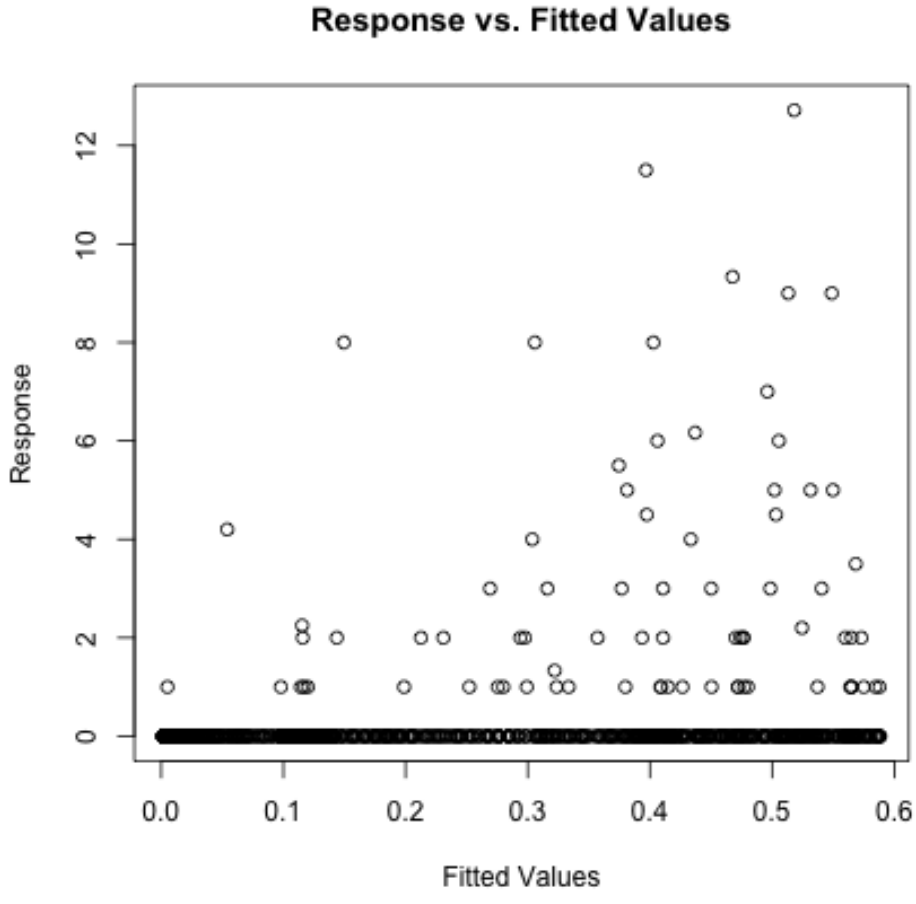
- Looking for patterns (not artifacts)
- This can be tricky
- Need to use a mixture of techniques
- Cycle through checks, make changes recheck

Observed vs. expected

class: inverse, middle, center

Response vs. fitted values

- `gam.check` "response vs. fitted values"
- BUT smooths are "wrong" everywhere in particular



Summarize over covariate chunks

- On average the smooth is right
- Check aggregations of count
- Here detection function has Beaufort as factor

```
obs_exp(dsm_bad, "Beaufort_f")
```

```
##              [0,1]    (1,2]    (2,3]    (3,4]    (4,5]
## Observed   1.00000 95.45000 103.5500 34.70000 4.000000
## Expected 20.28781 54.57573 136.3581 53.98742 5.949304
```

```
obs_exp(dsm_good, "Beaufort_f")
```

```
##              [0,1]    (1,2]    (2,3]    (3,4]    (4,5]
## Observed  1.0000 95.45000 103.5500 34.70000 4.000000
## Expected 6.8887 45.18587 118.5747 53.81458 4.909644
```

Observed vs. expected for environmental covariates

- Just need to specify the cutpoints

```
obs_exp(dsm_bad, "Depth", c(0, 1000, 2000, 3000, 4000, 6000))
```

```
##          (0,1e+03] (1e+03,2e+03] (2e+03,3e+03] (3e+03,4e+03] (4e+03,6e+03]
## Observed   4.00000      52.53333     139.16667      35.00000       8.00000
## Expected  85.65231      37.98341      63.40892      53.78726      30.32642
```

```
obs_exp(dsm_good, "Depth", c(0, 1000, 2000, 3000, 4000, 6000))
```

```
##          (0,1e+03] (1e+03,2e+03] (2e+03,3e+03] (3e+03,4e+03] (4e+03,6e+03]
## Observed  4.000000      52.53333      139.1667      35.00000      8.000000
## Expected  5.308628      48.14915      128.7962      38.76013      8.359456
```

Summary

- Convergence
  - Rarely an issue
- Basis size
  - k is a maximum
  - Double and see what happens
- Residuals
  - Deviance and randomised quantile
  - check for artifacts
- Observed vs. expected
  - Compare aggregate information