Fitting GAMs in practice

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Overview

- Introduction to some data
- Fitting simple models
- Plotting simple models

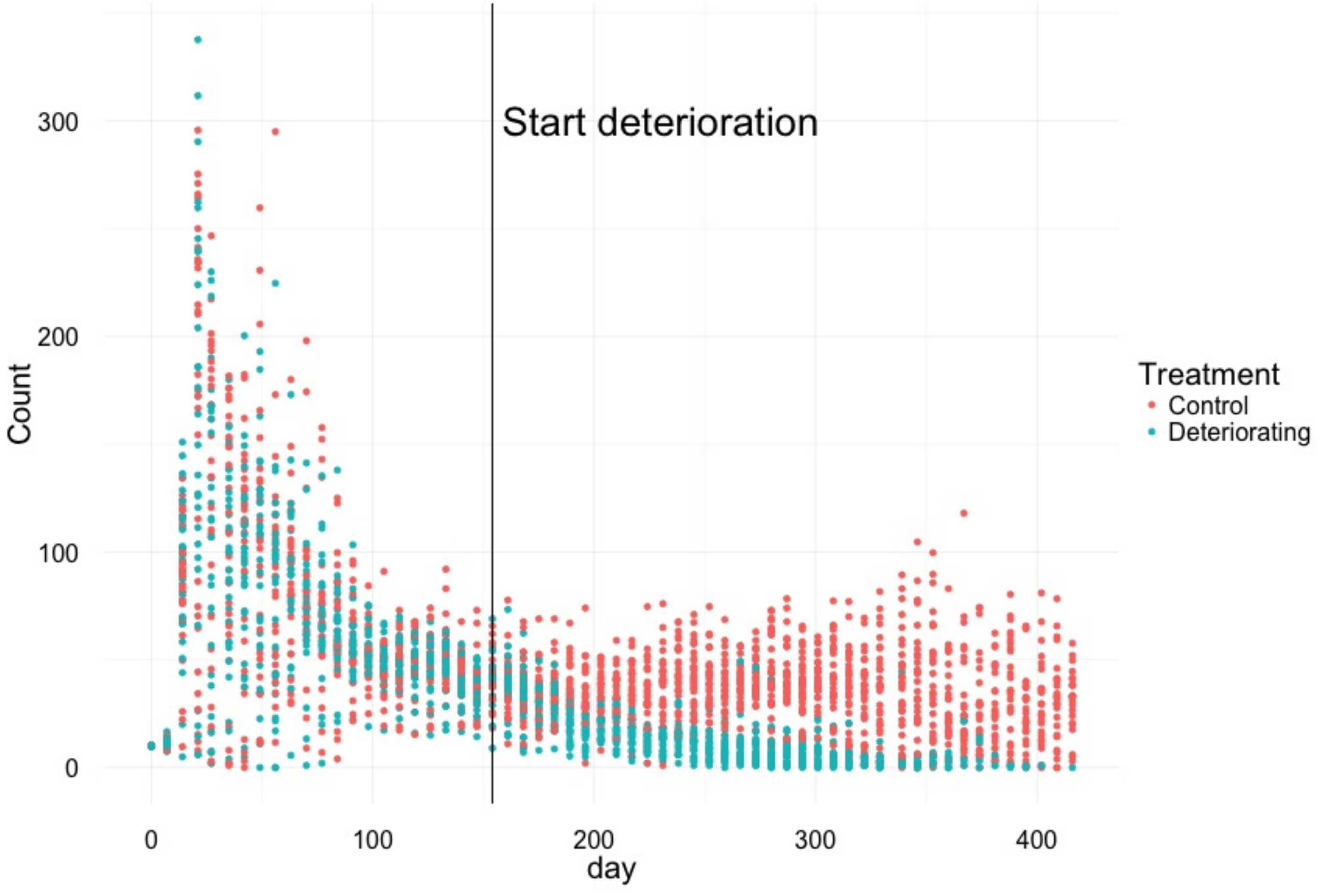
Data

Extinction experiment

- 60 populations of *Daphnia magna* in lab
- ½ in constant conditions, ½ in "deteriorating"
- Data from Drake & Griffen (Nature doi:10.1038/nature09389)

Photo credit doi:10.1371/journal.pbio.0030253

Extinction experiment



Inferential goals

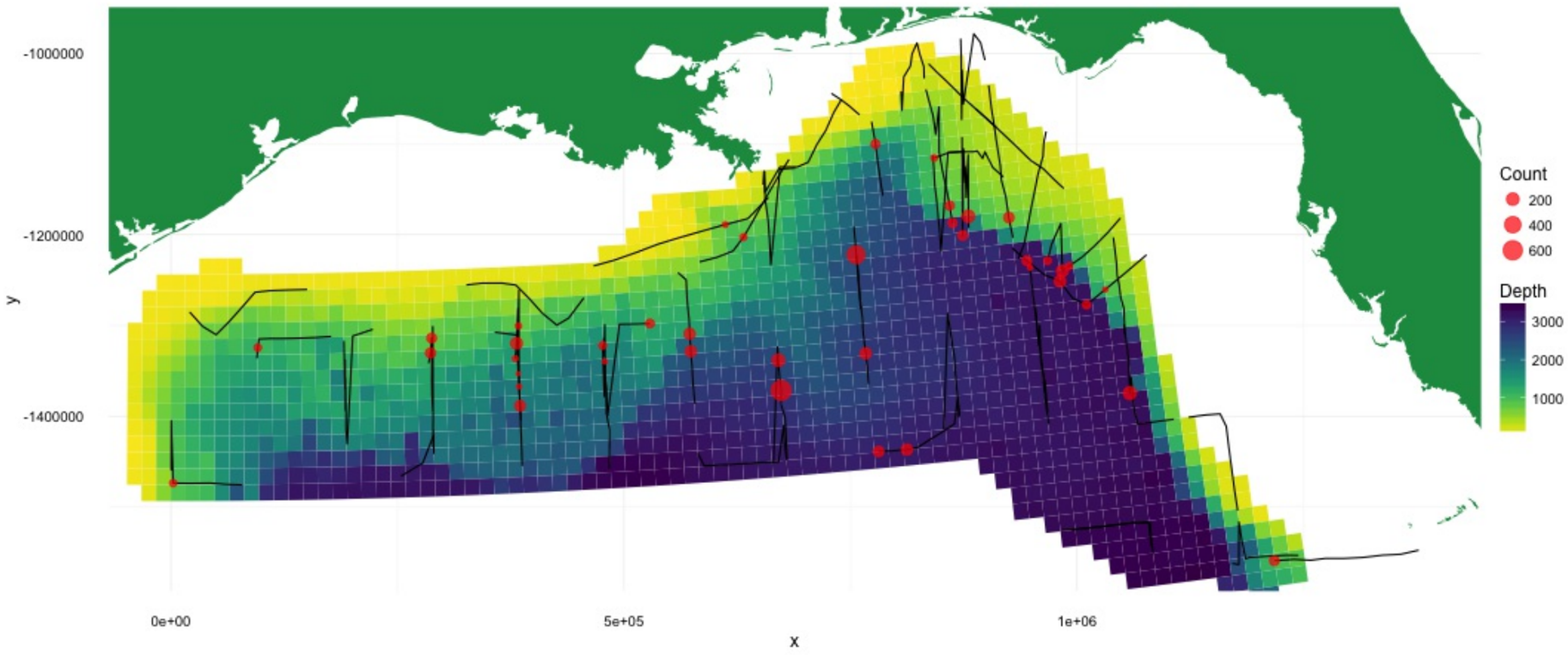
- Make sense of all these dots!
- What are the “average” trends?
  - (What are non-average trends?)
- When do the deteriorating populations go extinct on average?

Pantropical spotted dolphins

- Example taken from Miller et al (2013)
- Paper appendix has a better analysis
- Simple example here, ignoring all kinds of important stuff!

Inferential aims

- How many dolphins are there?
- Where are the dolphins?
- What are they interested in?



Translating maths into R

A simple example:

$$y_i = \beta_0 + s(x) + s(w) + \epsilon_i$$

where $\epsilon_i \sim N(0, \sigma^2)$

Let's pretend that $y_i \sim \text{Normal}$

- linear predictor: `formula = y ~ s(x) + s(w)`
- response distribution: `family=gaussian()`
- data: `data=some_data_frame`

Putting that together

```
my_model <- gam(y ~ s(x) + s(w),
                family = gaussian(),
                data = some_data_frame,
                method = "REML")
```

- `method="REML"` uses REML for smoothness selection (default is `"GCV.Cp"`)

What about a practical example?

Simple extinction example

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

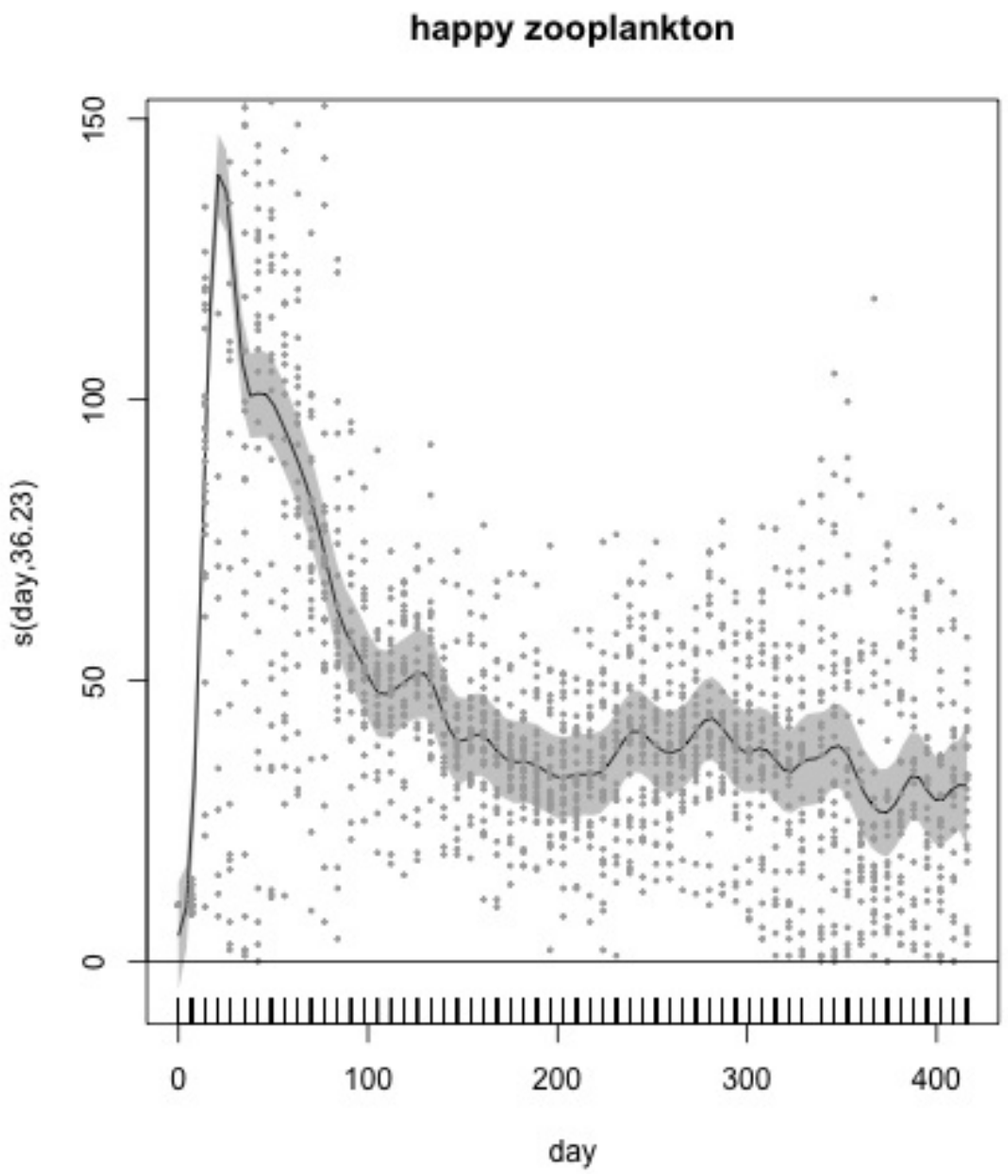
- Fit 2 models, one to control group, one to experimental group
- `Nhat` is the count of *D. magna* (estimated from 3 censuses)
- Model as a function of `day`

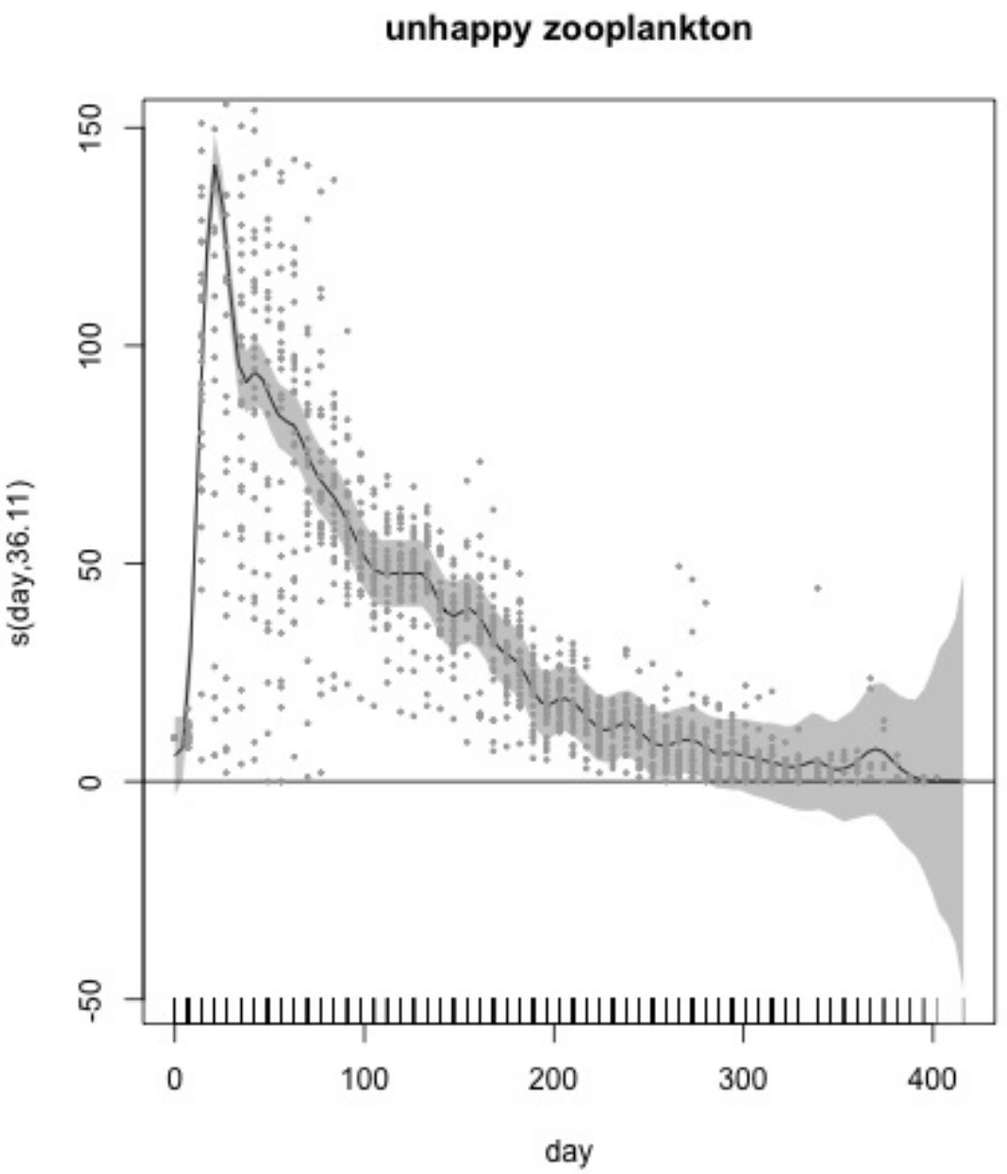
What did that do?

```
summary(dmagna_unhappy)
```

```
Family: gaussian
Link function: identity

Formula:
Nhat ~ s(day, k = 50)

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  38.9173     0.6959   55.93   <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(day) 36.11  42.04 60.94  <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

R-sq.(adj) =  0.657   Deviance explained = 66.6%
-REML = 6296.6  Scale est. = 647.88    n = 1338
```

Cool, but what about a plot?





How did we do that?

```
plot(dmagna_unhappy, main="unhappy zooplankton",
shift=mean(pop_unhappy$Nhat), scale=0, shade=TRUE)
abline(h=0)
```

- `scale=0` puts each term on it's own y axis
- Terms are centred, need `shift=` to re-centre (don't in models w/ > 1 term!)
- `shade=TRUE` makes +/-2 se into shaded area
- `main=` sets title, as usual

A simple dolphin model

```
library(mgcv)
dolphins_depth <- gam(count ~ s(depth) + offset(off.set),
                      data = mexdolphins,
                      family = quasipoisson(),
                      method = "REML")
```

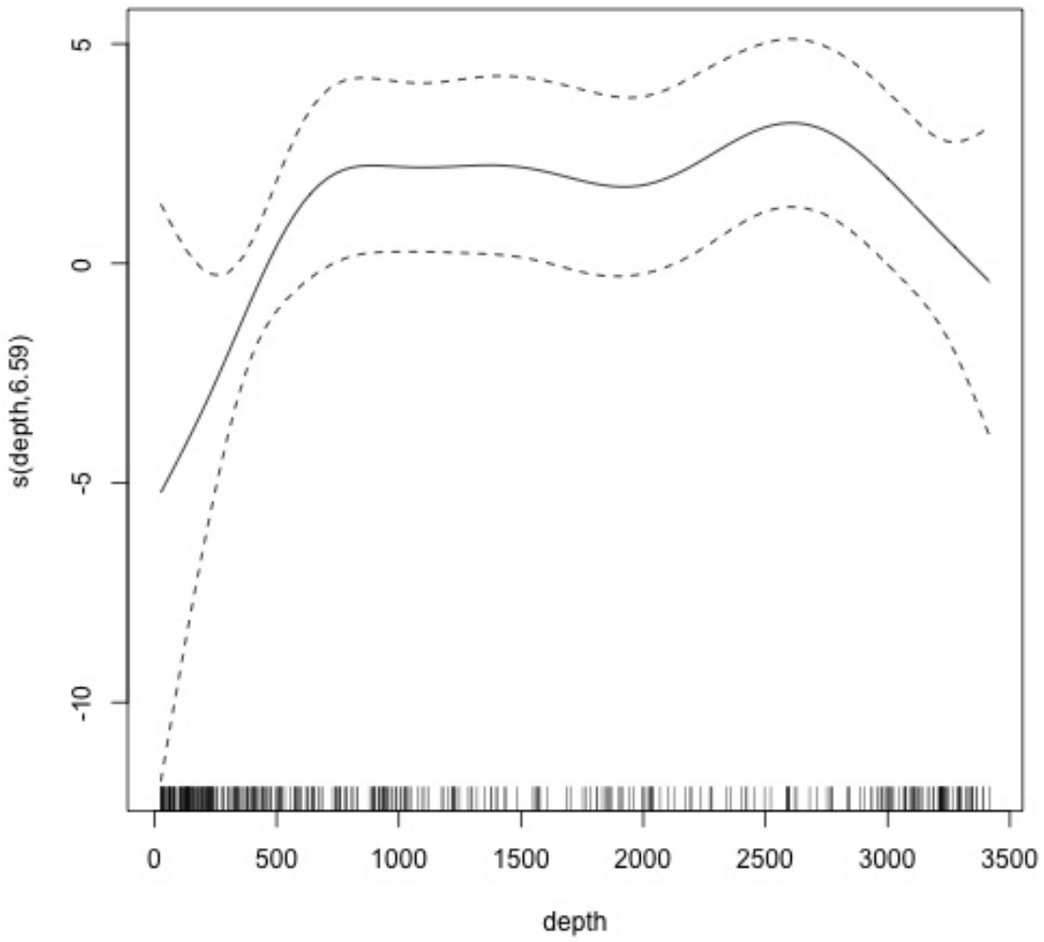
- count is a function of depth
- `off.set` is the effort expended
- we have count data, try quasi-Poisson distribution

What did that do?

```
summary(dolphins_depth)
```

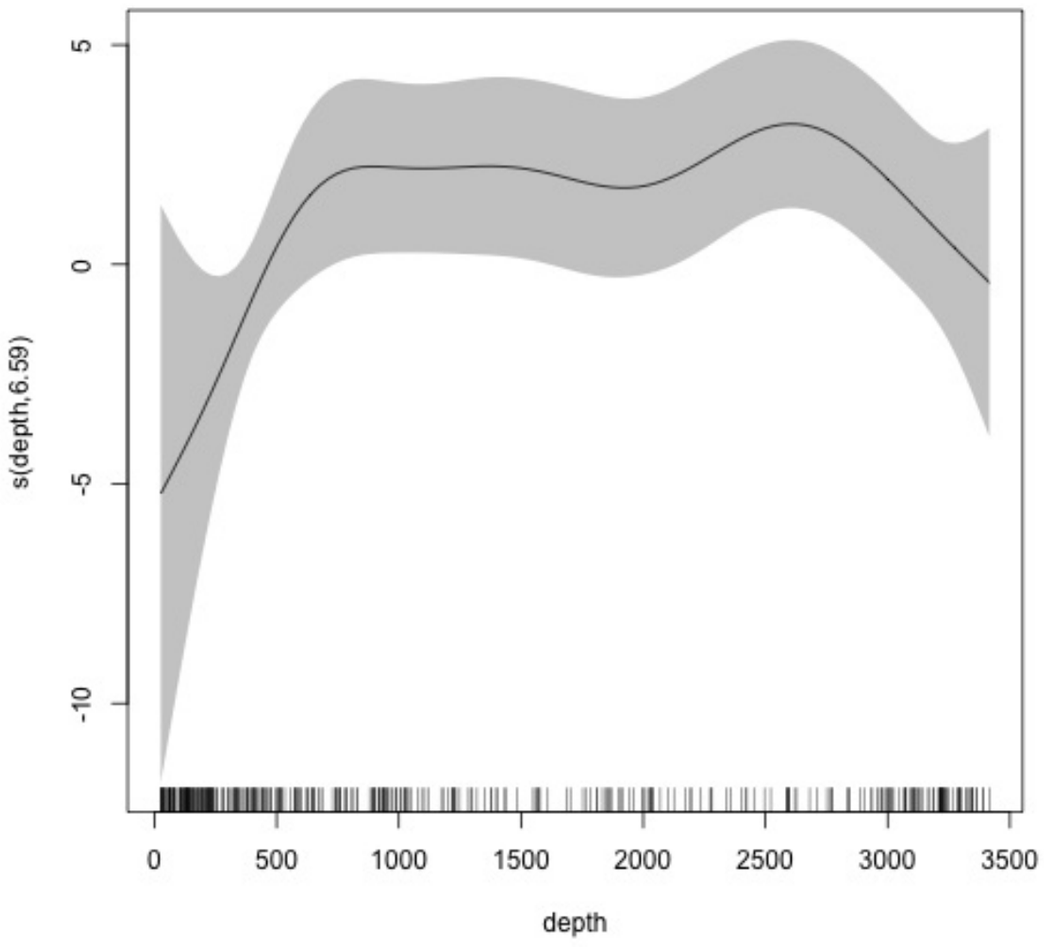
```
Family: quasipoisson
Link function: log

Formula:
count ~ s(depth) + offset(off.set)

Parametric coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) -18.2344     0.8949  -20.38   <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) 6.592  7.534 2.329  0.0224 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

R-sq.(adj) =  0.0545   Deviance explained = 26.4%
-REML = 948.28  Scale est. = 145.34    n = 387
```

Plotting



- `plot(dolphins_depth)`
- Dashed lines indicate +/- 2 standard errors
- Rug plot
- On the link scale
- EDF on y axis

Plotting (shaded se)



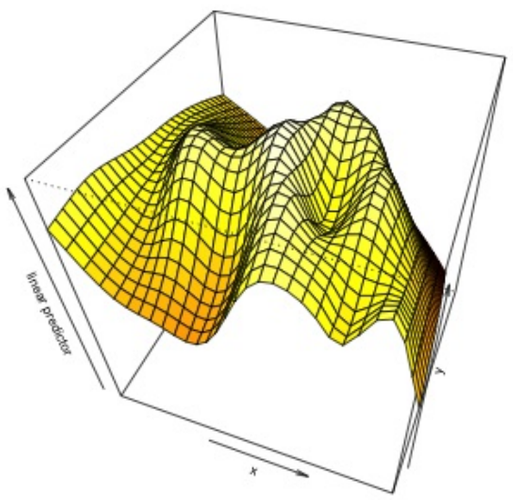
- `plot(dolphins_depth, shade=TRUE)`
- `?plot` has a **lot** of options
- `plotdat <- plot(model)` gives you the data that generates the plot

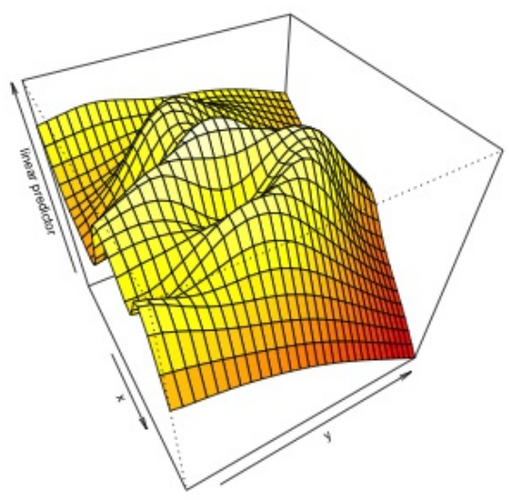
Thin plate regression splines

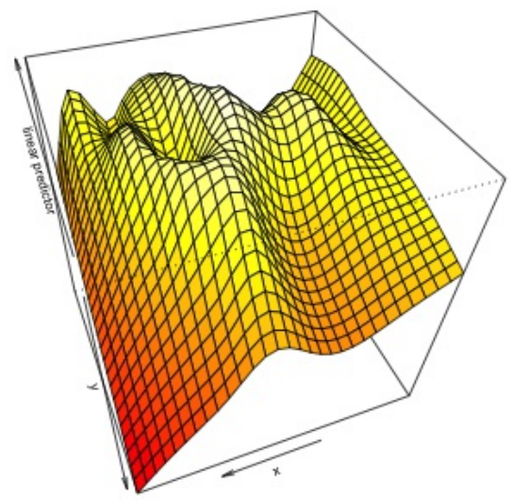
- Default basis
- One basis function per data point
- Reduce # basis functions (eigendecomposition)
- Fitting on reduced problem
- Multidimensional
- Wood (2003)

Bivariate terms

- Assumed an additive structure
- No interaction
- We can specify `s(x,y)` (and `s(x,y,z,...)`)
- (Assuming *isotropy* here…)







Adding a term

- Add a **surface** for location (x and y)
- Just use + for an extra term

```
dolphins_depth_xy <- gam(count ~ s(depth) + s(x, y) +
offset(off.set),
                  data = mexdolphins,
                  family=quasipoisson(), method="REML")
```

Summary

```
summary(dolphins_depth_xy)
```

```
Family: quasipoisson
Link function: log

Formula:
count ~ s(depth) + s(x, y) + offset(off.set)

Parametric coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) -19.1933     0.9468  -20.27   <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)  6.804  7.669 1.461   0.191
s(x,y)   23.639 26.544 1.358   0.114

R-sq.(adj) =   0.22   Deviance explained = 49.9%
-REML =  923.9  Scale est. = 79.474    n = 387
```

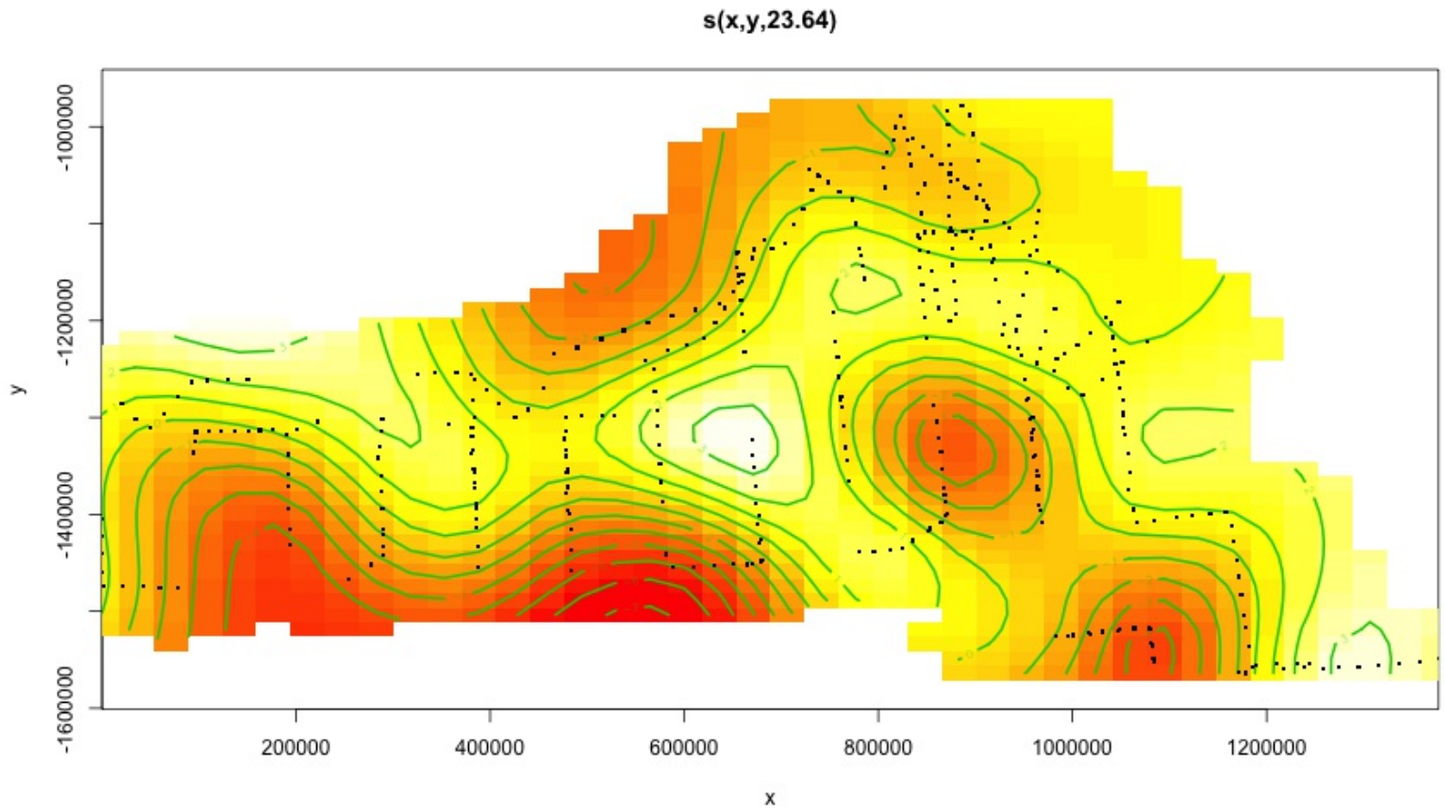
Plot x,y term

```
plot(dolphins_depth_xy, select=2, cex=3, asp=1, lwd=2, scheme=2)
```

- `scale=0`: each plot on different scale
- `select=` picks which smooth to plot
- `scheme=2` much better for bivariate terms
- `vis.gam()` also useful

Plot x,y term

```
plot(dolphins_depth_xy, select=2, cex=3, asp=1, lwd=2, scheme=2)
```



Fitting/plotting GAMs summary

- `gam` does all the work
- very similar to `glm`
- `s` indicates a smooth term
- `summary`, `plot` methods