

Beyond the exponential family

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Away from the exponential family

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- Has sufficient statistics: easier to estimate parameter variance
- ... but it doesn't describe everything
- mgcv has expanded to cover many new families
- Lets you model a much wider range of scenarios with smooths

What we'll cover

- “Counts”: Negative binomial and Tweedie distributions
- Modelling proportions with the Beta distribution
- Robust regression with the Student's t distribution
- Ordered and unordered categorical data
- Multivariate normal data
- Modelling extra zeros with zero-inflated and adjusted families
- *NOTE*: All the distributions we're covering here have their own quirks. Read the help files carefully before using them!

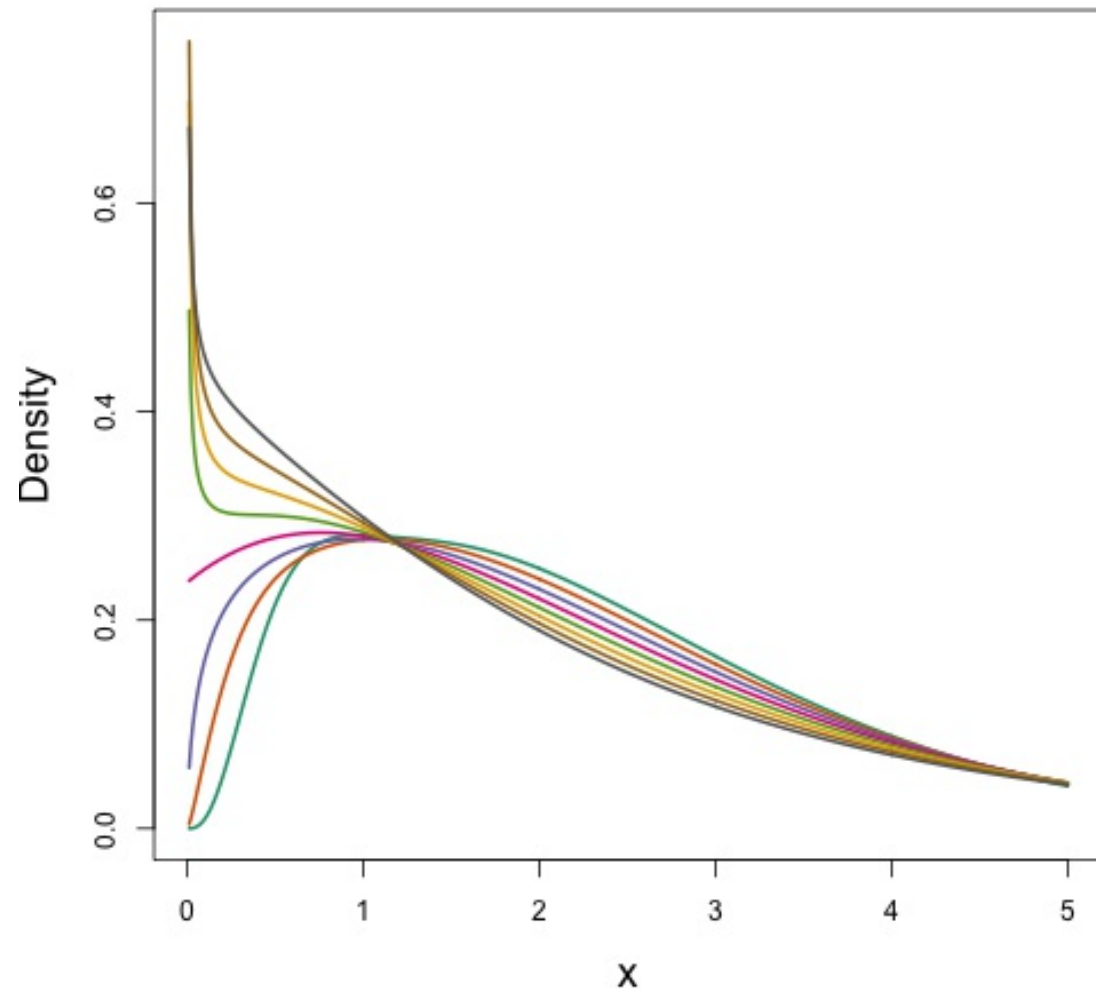
Modelling "counts"

Counts and count-like things

- Response is a count (not always integer)
- Often, it's mostly zero (that's complicated)
- Could also be catch per unit effort, biomass etc
- Flexible mean-variance relationship

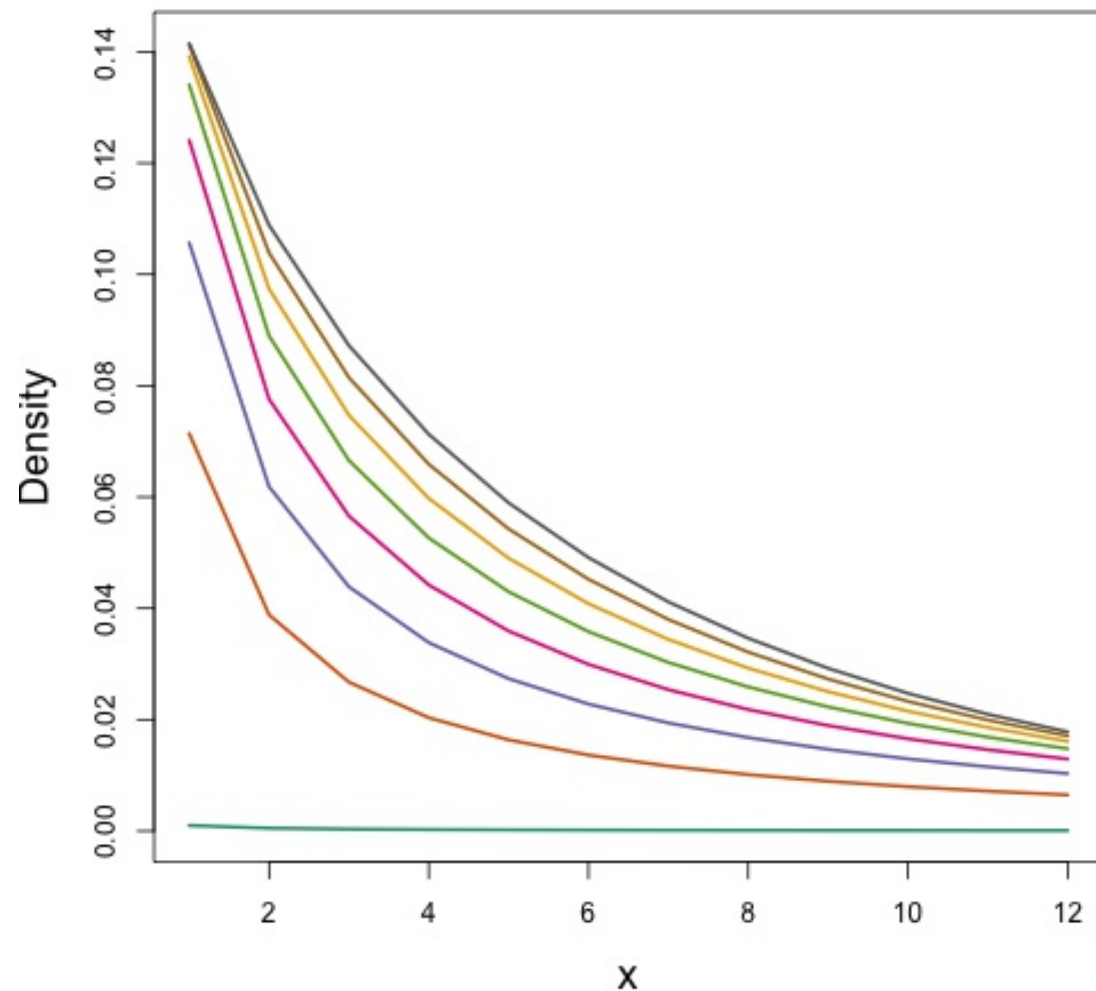


Tweedie distribution



- $\text{Var}(\text{count}) = \varphi(\text{count})^q$
- Common distributions are sub-cases:
 - $q = 1 \Rightarrow \text{Poisson}$
 - $q = 2 \Rightarrow \text{Gamma}$
 - $q = 3 \Rightarrow \text{Normal}$
- We are interested in $1 < q < 2$
- (here $q = 1.2, 1.3, \dots, 1.9$)
- `tw()`

Negative binomial



- $\text{Var}(\text{count}) = (\text{count}) + \kappa(\text{count})^2$
- Estimate κ
- Is quadratic relationship a “strong” assumption?
- Similar to Poisson:
 $\text{Var}(\text{count}) = (\text{count})$
- `nb()`

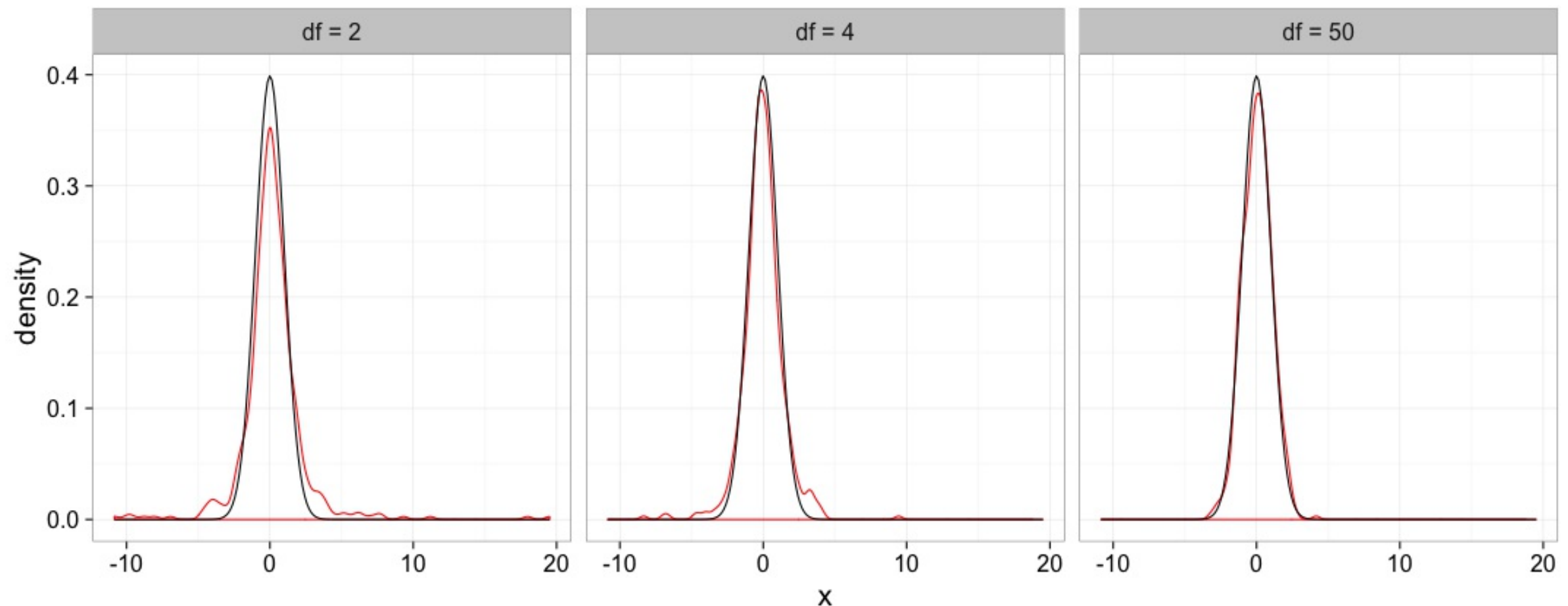
Modelling proportions

The Beta distribution

Modelling outliers

The student-t distribution

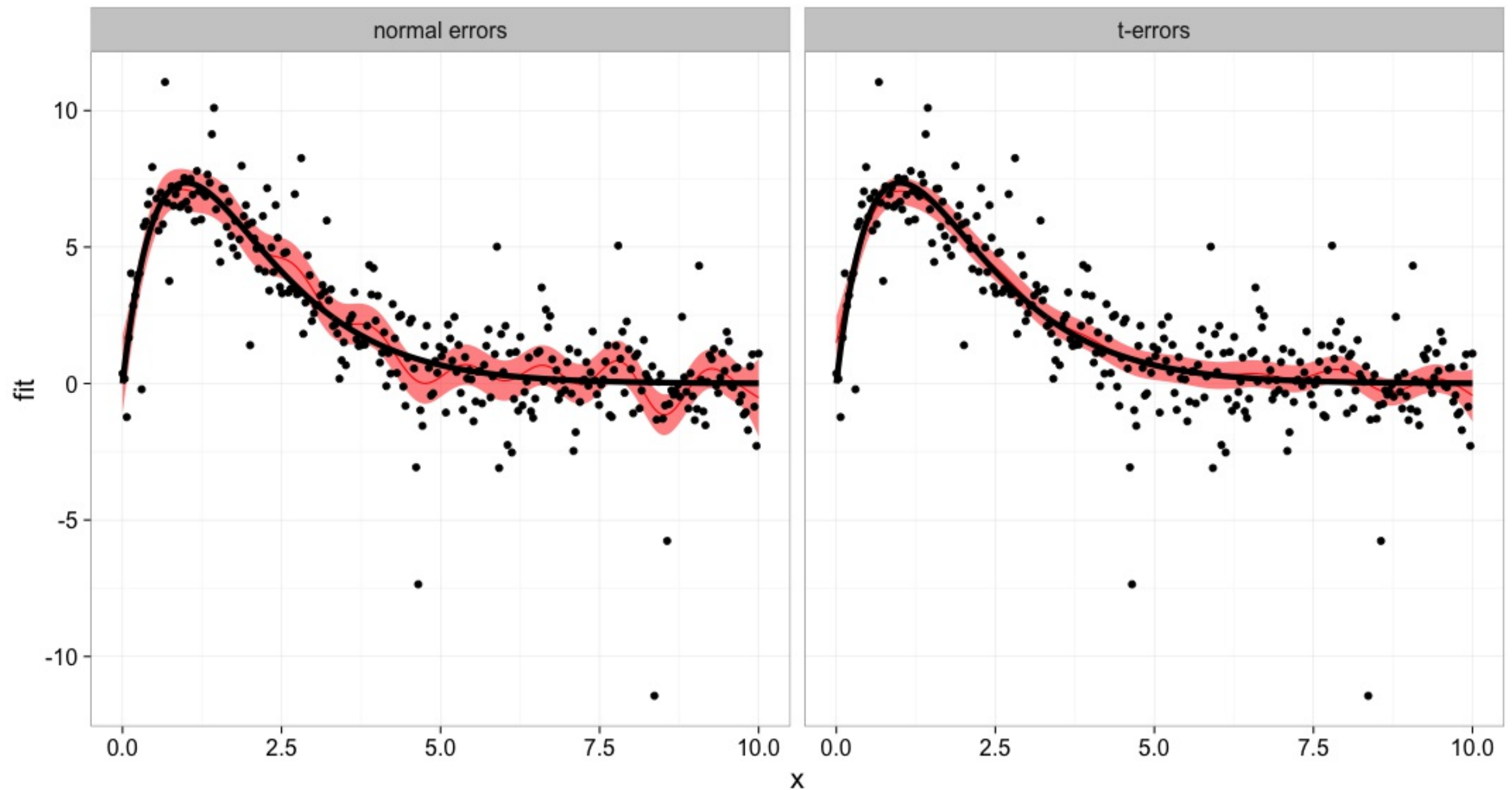
- Models continuous data w/ longer tails than normal
- Far less sensitive to outliers
- Has one extra parameter: df.
- bigger df: t dist approaches normal



The student-t distribution: Usage

```
set.seed(4)
n=300
dat = data.frame(x=seq(0,10,length=n))
dat$f = 20*exp(-dat$x)*dat$x
dat$y = 1*rt(n,df = 3) + dat$f
norm_mod = gam(y~s(x,k=20), data=dat,
family=gaussian(link="identity"))
t_mod = gam(y~s(x,k=20), data=dat, family=scat(link="identity"))
```

The student-t distribution: Usage



The student-t distribution: Usage

Family: Scaled $t(2.976, 0.968)$
Link function: identity

Formula:
 $y \sim s(x, k = 20)$

Parametric coefficients:

| | Estimate | Std. Error | z value | Pr(> z) | |
|-------------|----------|------------|---------|----------|-----|
| (Intercept) | 2.02664 | 0.06853 | 29.57 | <2e-16 | *** |

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Approximate significance of smooth terms:

| | edf | Ref.df | Chi.sq | p-value | |
|------|-------|--------|--------|---------|-----|
| s(x) | 13.27 | 15.71 | 1221 | <2e-16 | *** |

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

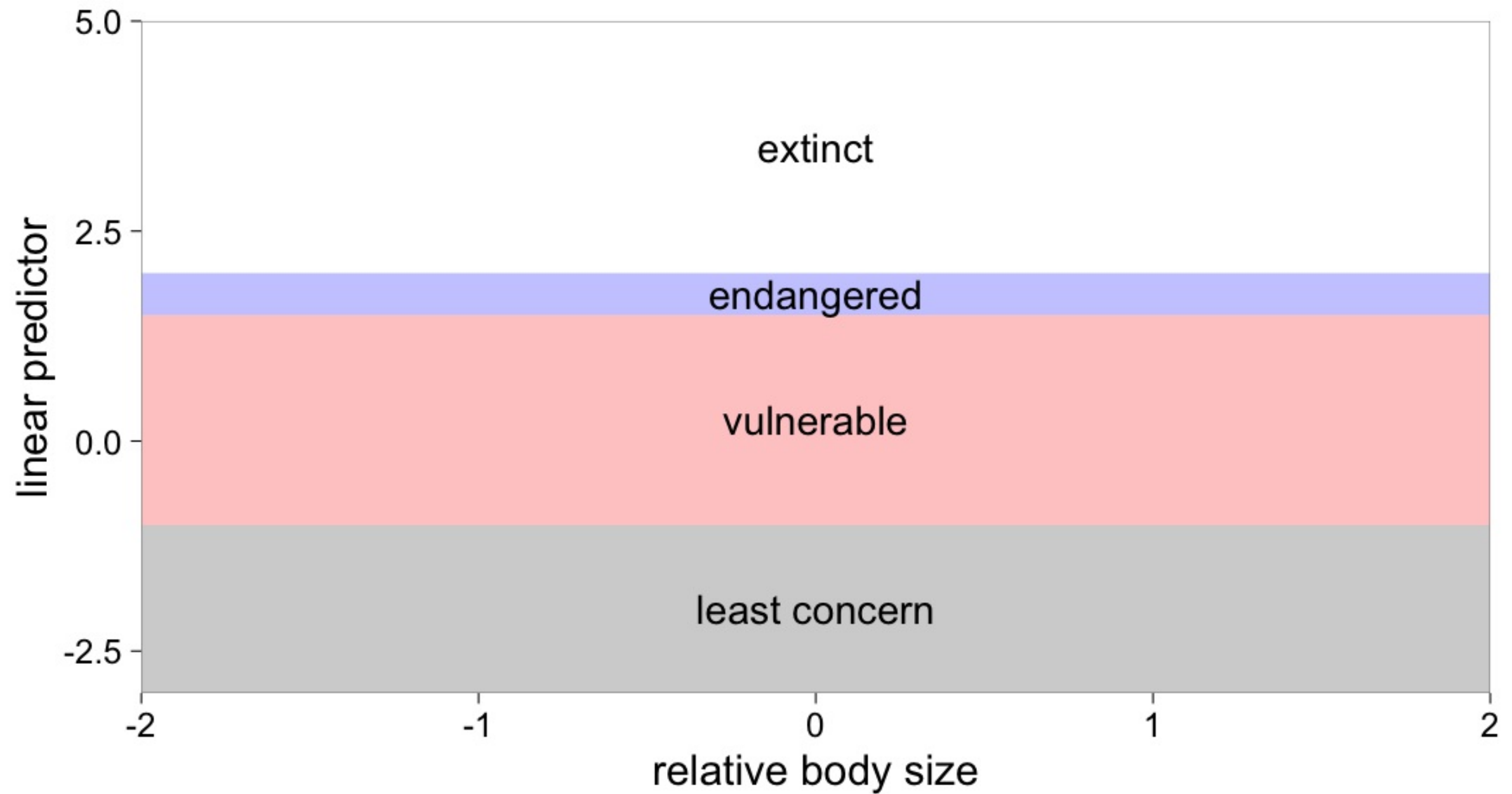
R-sq.(adj) = 0.695 Deviance explained = 63.1%
-REML = 546.75 Scale est. = 1 n = 300

Modelling multi-dimensional data

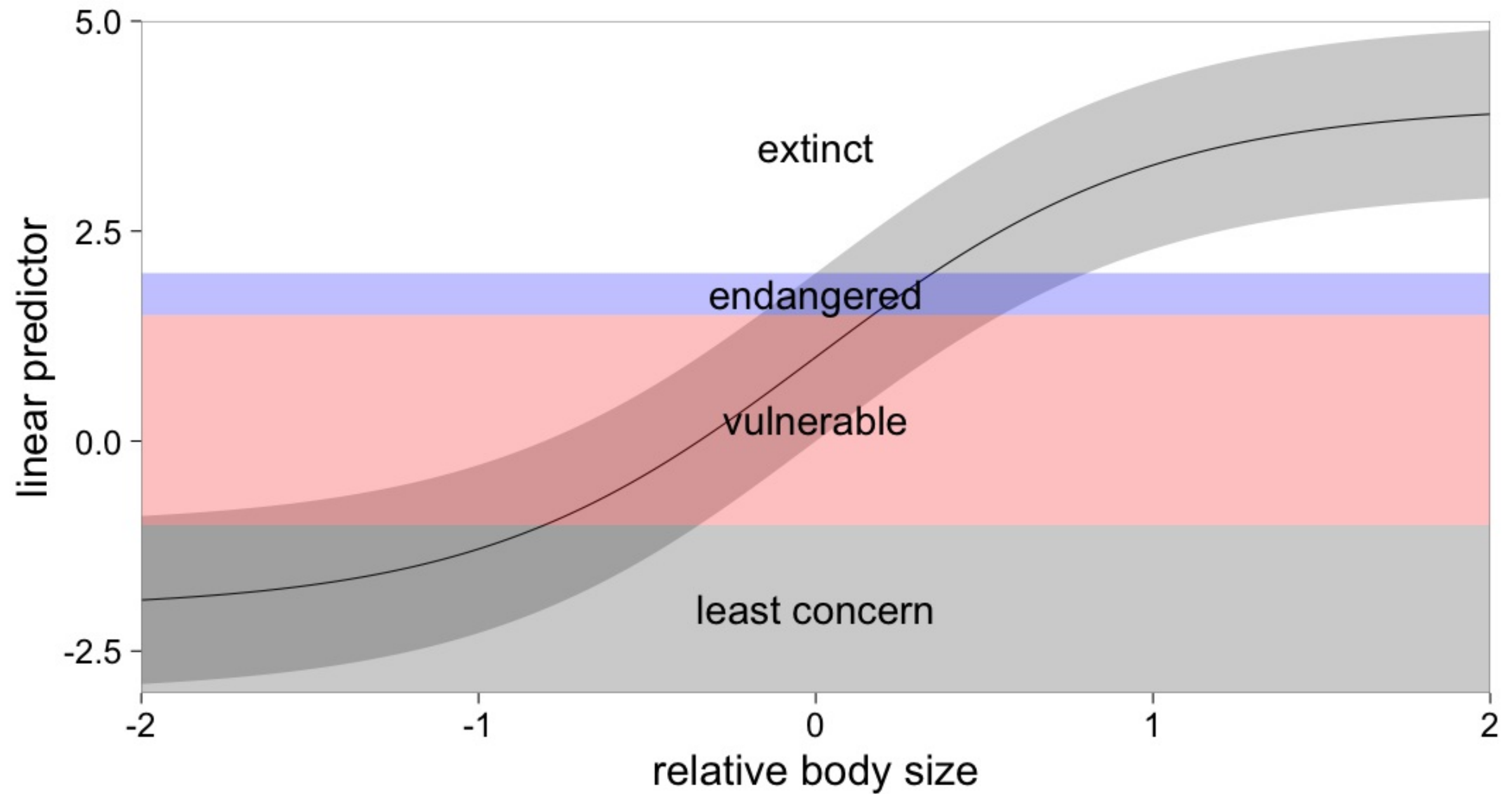
Ordered categorical data

- Assumes data are in discrete categories, and categories fall in order
- e.g.: conservation status: “least concern”, “vulnerable”, “endangered”, “extinct”
- fits a linear latent model using covariates, w/ threshold for each level
- First cut-off always occurs at -1

Ordered categorical data

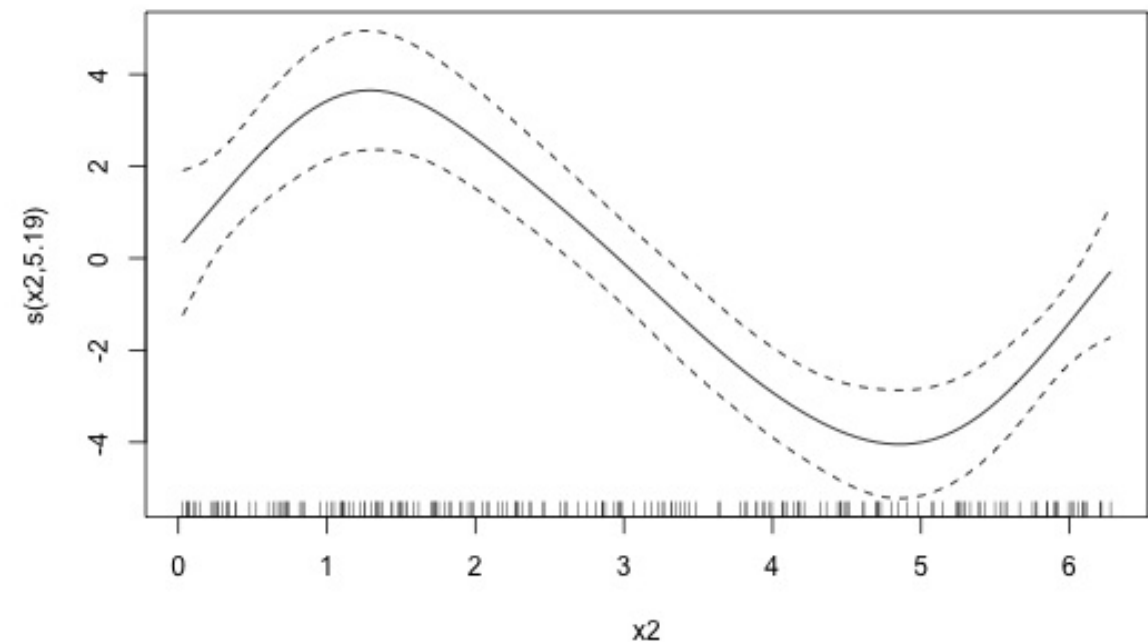
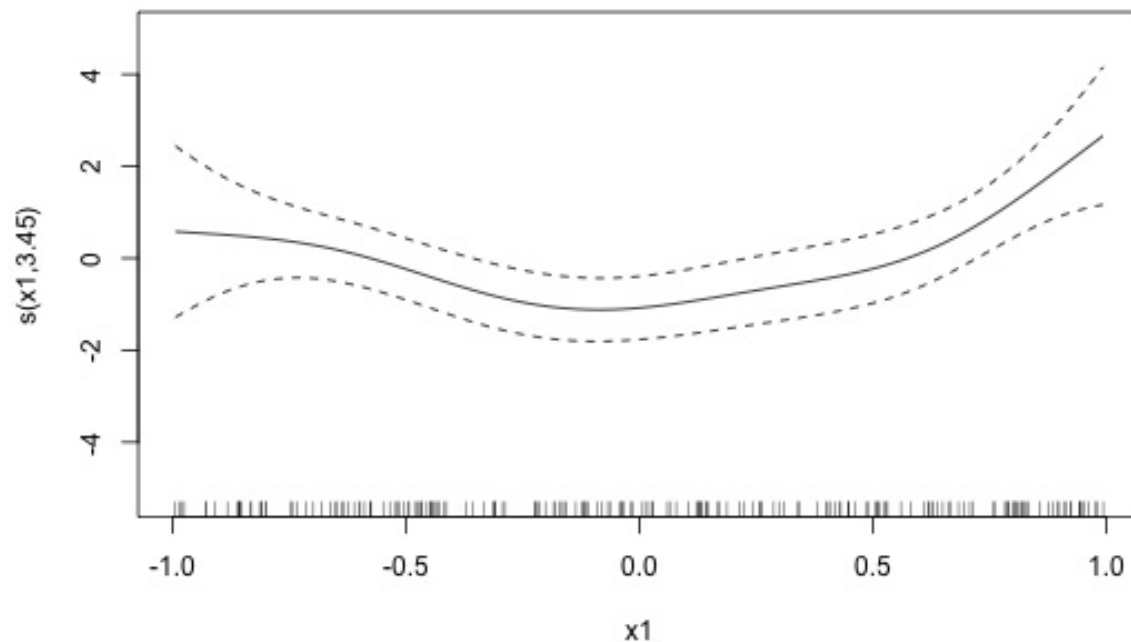


Ordered categorical data



Using ocat

```
n= 200  
dat = data.frame(x1 = runif(n,-1,1),x2=2*pi*runif(n))  
dat$f = dat$x1^2 + sin(dat$x2)  
dat$y_latent = dat$f + rnorm(n,dat$f)  
dat$y = ifelse(dat$y_latent<0,1, ifelse(dat$y_latent<0.5,2,3))  
ocat_model = gam(y~s(x1)+s(x2), family=ocat(R=3),data=dat)  
plot(ocat_model,page=1)
```



Using ocat

```
summary(ocat_model)
```

```
Family: Ordered Categorical(-1,-0.09)
Link function: identity
```

```
Formula:
y ~ s(x1) + s(x2)
```

```
Parametric coefficients:
```

| | Estimate | Std. Error | z value | Pr(> z) |
|-------------|----------|------------|---------|----------|
| (Intercept) | 0.5010 | 0.2792 | 1.794 | 0.0727 |

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Approximate significance of smooth terms:
```

| | edf | Ref.df | Chi.sq | p-value | |
|-------|-------|--------|--------|----------|-----|
| s(x1) | 3.452 | 4.282 | 18.67 | 0.00133 | ** |
| s(x2) | 5.195 | 6.270 | 84.34 | 1.09e-15 | *** |

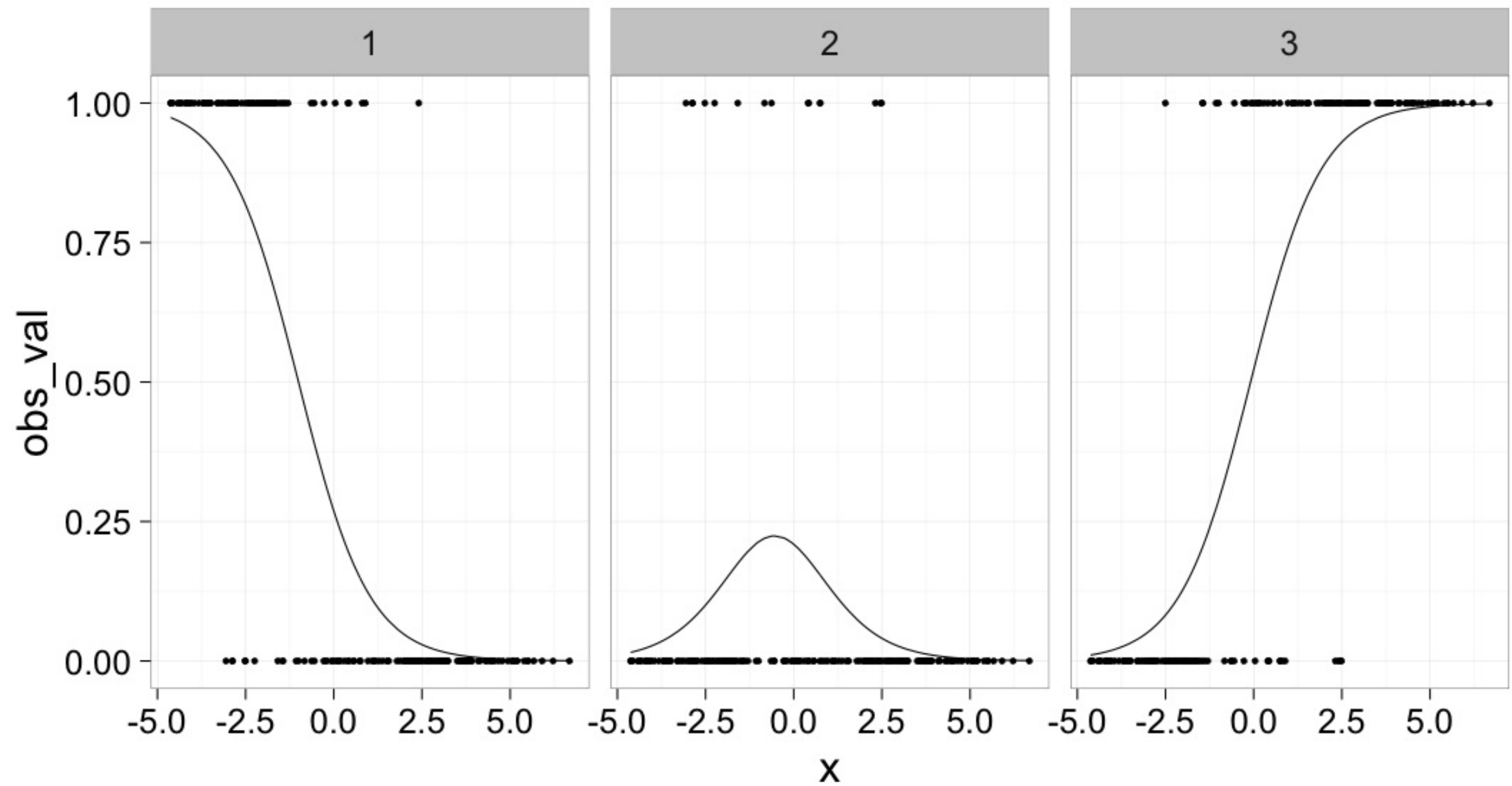
```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Deviance explained = 57.7%
```

```
-REML = 97.38 Scale est. = 1
```

```
n = 200
```

Using ocat

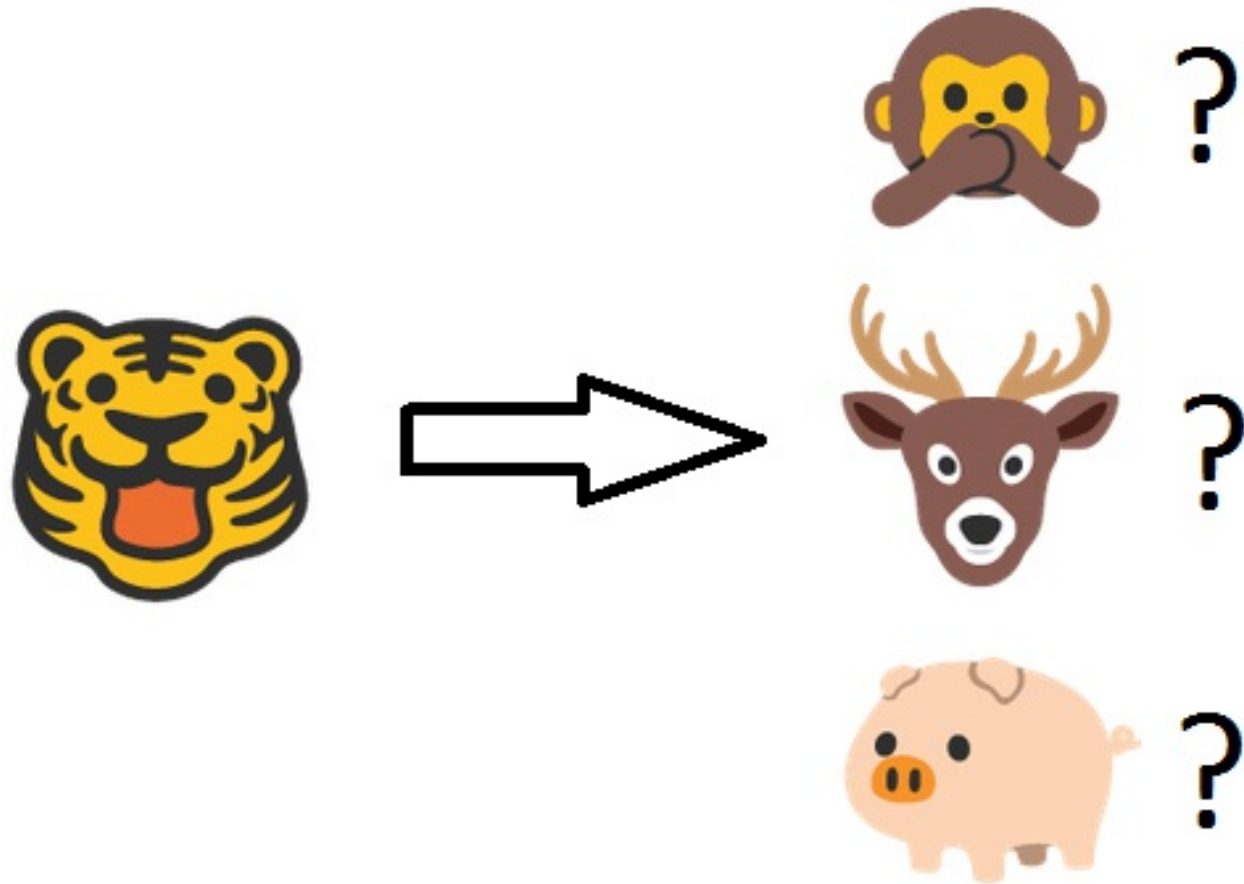


Unordered categorical data

- What do you do if categorical data doesn't fall in a nice order?

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- $p(y = i|\mathbf{x}) = \exp(\mu_i(\mathbf{x})) / (1 + \sum_j \exp(\mu_j(\mathbf{x})))$
- $\mu_i(\mathbf{x}) = s_{1,j}(x_1) + s_{2,j}(x_2)$
- $p(y = 0|\mathbf{x}) = 1 / (1 + \sum_j \exp(\mu_j(\mathbf{x})))$

Using the multinom function



= 0



= 1



= 2



= $f(\text{tree cover, road distance})$



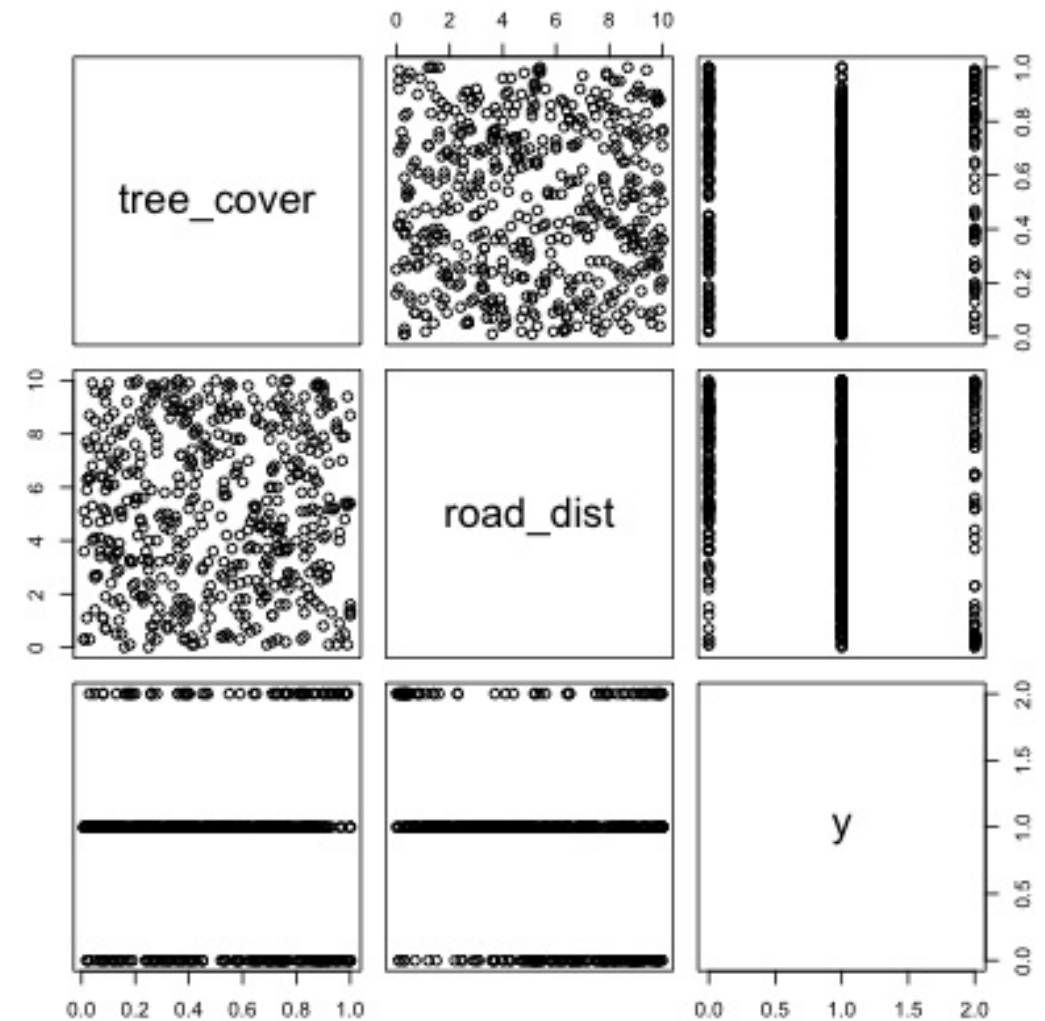
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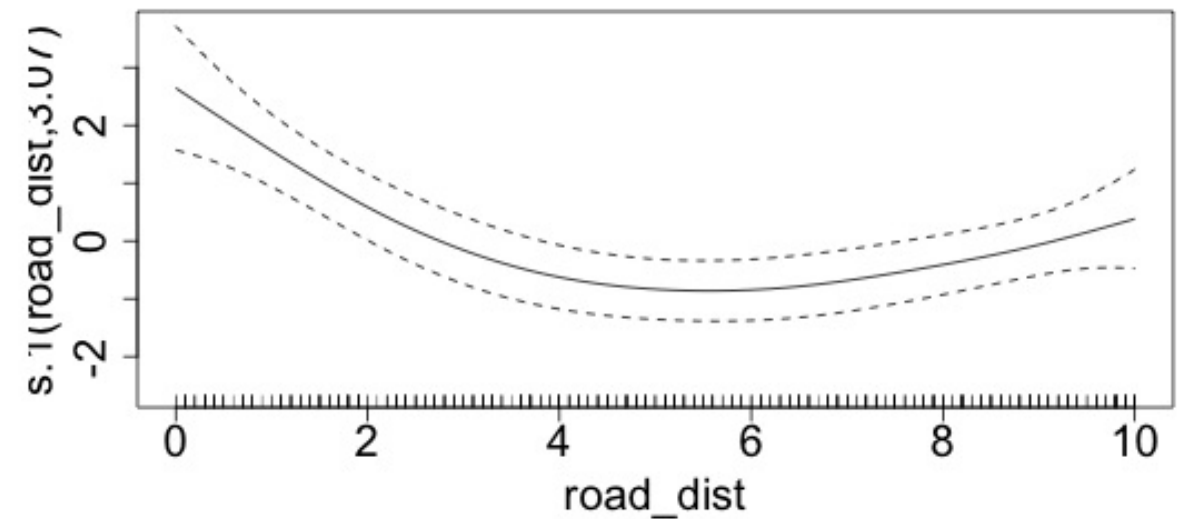
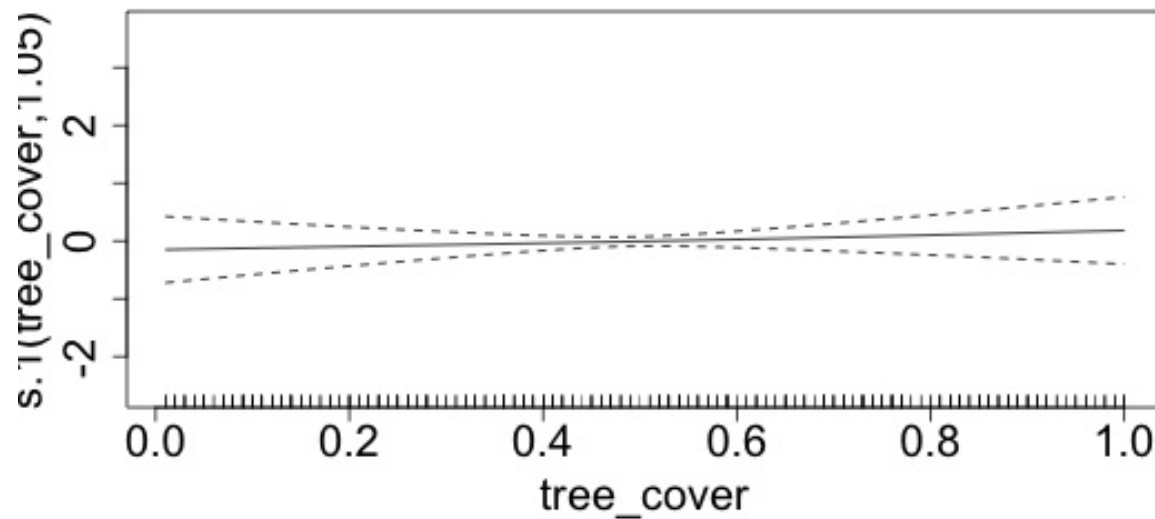
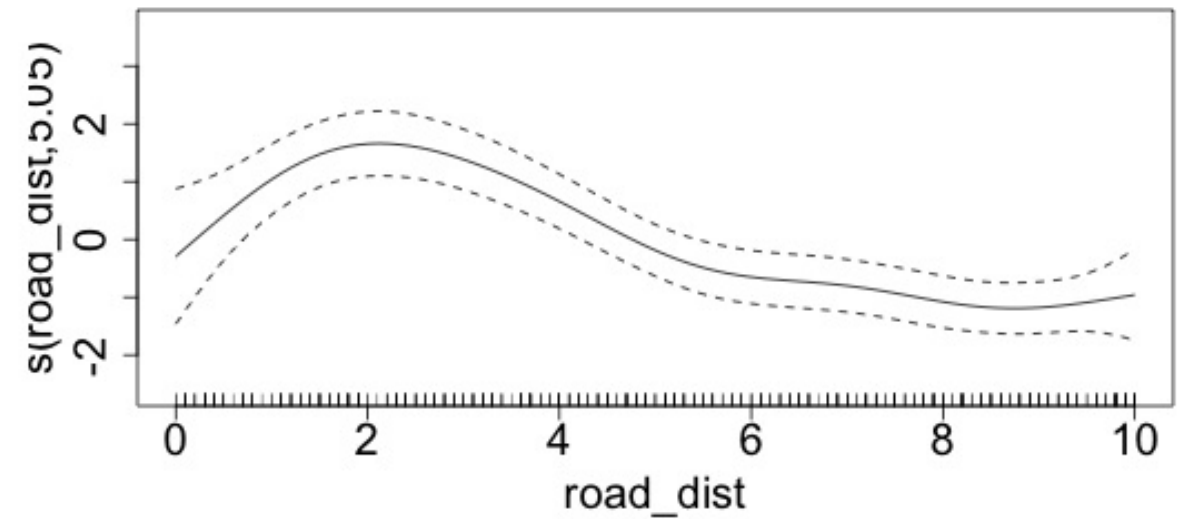
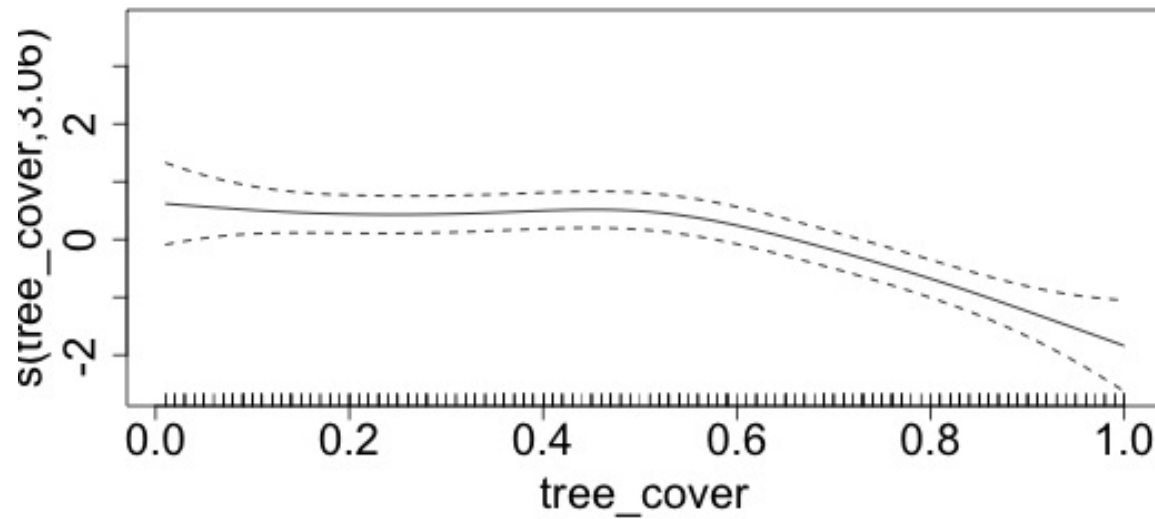
```
head(model_dat)
```

| | tree_cover | road_dist | y |
|---|------------|-----------|---|
| 1 | 0.51 | 8.6 | 1 |
| 2 | 0.31 | 9.9 | 0 |
| 3 | 0.43 | 8.2 | 1 |
| 4 | 0.69 | 2.9 | 1 |
| 5 | 0.09 | 0.7 | 1 |
| 6 | 0.23 | 5.6 | 1 |

```
pairs(model_dat)
```

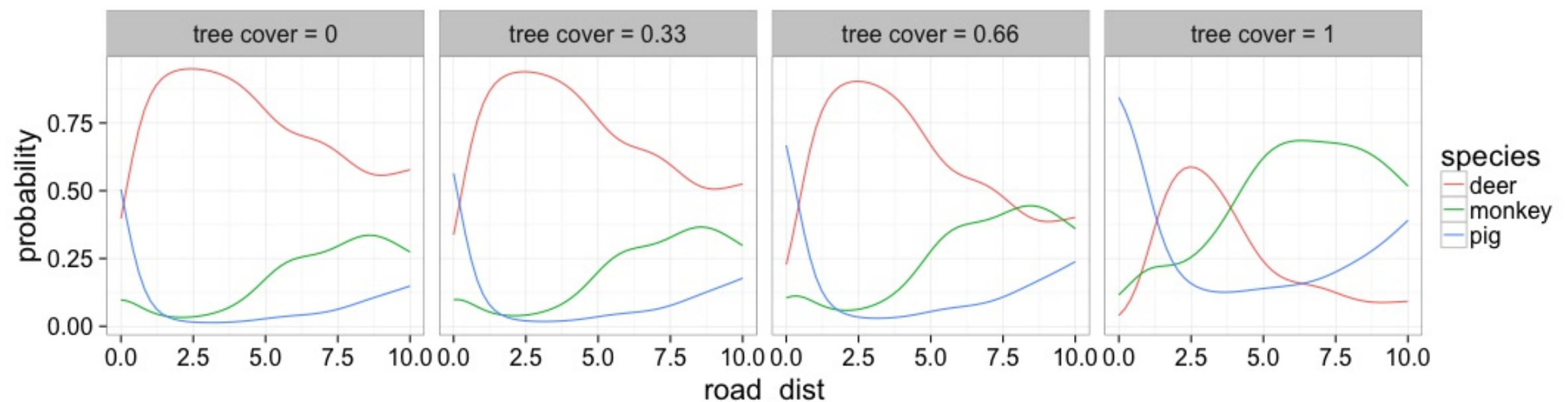


Using the multinom function



Understanding the results

```
multinom_pred_data = as.data.frame(expand.grid(road_dist
=seq(0,10,length=50),
                                             tree_cover
=c(0,0.33,0.66,1)))
multinom_pred = predict(multinom_model, multinom_pred_data,type =
"response")
colnames(multinom_pred) = c("monkey","deer","pig")
multinom_pred_data = cbind(multinom_pred_data,multinom_pred)
multinom_pred_data_long = multinom_pred_data %>%
  gather(species, probability, monkey, deer,pig)%>%
  mutate(tree_cover =paste("tree cover = ", tree_cover,sep=""))
ggplot(aes(road_dist,
probability,color=species),data=multinom_pred_data_long)+
  geom_line()+
  facet_grid(.~tree_cover)+
  theme_bw(20)
```



Other multivariate distributions
to check out

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- mgcv code: `formula=list(y1~s(x1)+s(x2), y2 = s(x1)+s(x3)), family = mvn(d=2)`

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- mgcv code: `formula = y~s(x1)+s(x2), weights=censor.var, family=cox.ph`
- `censor.var = 0` if censored, 1 if not

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The end of the distribution zoo

That's the end of this section! We convene after lunch (1:00 PM). You'll get to work through a few more advanced examples of your choice.