Other useful models

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Outline

- Models so far
- Other GLMs
- Other useful models
- Some other approaches (**tomorrow**)

Generalised linear models so far

- Linear regression
- Binomial regression
- Poisson regression
- Negative-binomial regression (for fixed dispersion)

Other GLMS not covered so far

- Gamma regression
- Log-normal regression
- Inverse Gaussian regression
- Tweedie regression
- Multinomial regression
- Ordinal regression
- Conway-Maxwell-Poisson regression (not included here)

Other useful models

- beta regression
- beta-binomial regression (overdispersed binomial, not covered here)
- Zero-inflated models
- Hurdle models

Other useful methods

more tomorrow

GLMs for positive continuous data

Data bounded at zero $y_i > 0$, and might or might not include zeros.

- Usually (right) skewed
- Variance increases with mean

E.g.,:

- Biomass
- Size measurements
- Nitrogen in soil
- Amount of rainfall
- Insurance claims

Options:

- Log-normal regression
- Inverse Gaussian GLM
- Gamma GLM
- **Tweedie GLMs**

Our example data: soil nitrogen

Originally by Lane et al. (2002)

- Soil nitrogen in kilograms per hectare
- Nitrogen fertilizer dose in kilograms per hectare

Fert	Source	SoilN
0	0	4.53
0	0	5.46
0	0	4.77
48	0	6.17
48	0	9.30
48	0	8.29
96	0	11.30
96	0	16.58

Log-normal regression

Connected to the normal distribution, in the sense:

$$\begin{aligned} \log(y_i) &\sim \mathcal{N}(\mu_i, \sigma^2) \\ y_i &\sim \mathcal{L}ognormal(\mu_i, \sigma^2) \end{aligned} \tag{1}$$

- So, easy to fit!
- I don't generally recommend response transformations
- Two parameters: μ_i and σ^2
- $\mathbb{E}(y_i|x_i) = \exp(\mu_i + \frac{\sigma^2}{2})$
- var$(y_i|x_i) = \{\exp(\sigma^2) - 1\}\exp(2\mu_i + \sigma^2)$

We are not modeling the mean but the location parameter μ_i

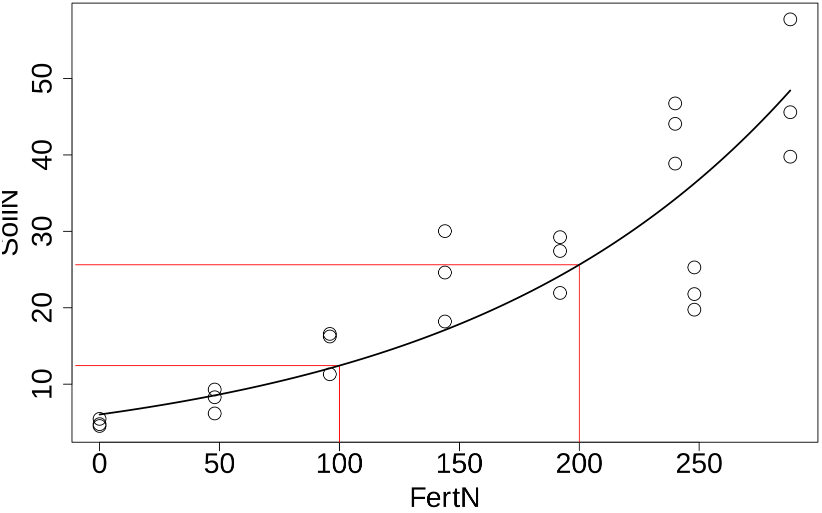
Log-normal regression in R

```
model1 <- lm(log(SoilN)~Fert, data = nitrogen)
fitted <- exp(predict(model1)) #We need to backtransform ours
cbind(est=coef(model1), confint(model1))
```

```
##                     est       2.5 %      97.5 %
## (Intercept) 1.796792406 1.553746377 2.039838436
## Fert        0.007234334 0.005914211 0.008554456
```

- Soil nitrogen increases with supplied nitrogen
- $\log(2)/0.007234334 \approx 95$
- Soil nitrogen doubles for almost every 100 kg/hectare fertilizer

Log-normal regression: results



Inverse Gaussian GLM

- Sharper peak and heavier tails than log-normal
- Often used in presence of extreme events

$$\frac{1}{\mathbb{E}(y_i|\mathbf{x}_i)^2} = \alpha + \mathbf{x}_i\boldsymbol{\beta}$$
$$\mathbb{E}(y_i|\mathbf{x}_i) = \frac{1}{(\alpha + \mathbf{x}_i\boldsymbol{\beta})^2} \tag{2}$$

- parameters: location μ_i and dispersion ϕ
- canonical link: squared inverse
- alternatively inverse, log-link

$\text{var}(y_i|\mathbf{x}_i) = \frac{\mu_i^3}{\phi}$

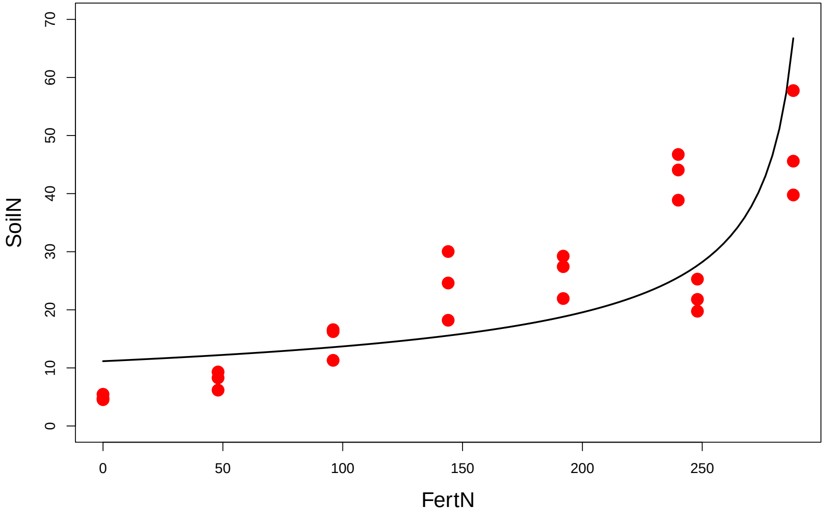
Inverse Gaussian GLM in R

```
model2 <- glm(SoilN~Fert, data = nitrogen, family = "inverse.gaussian")
summary(model2)
```

```
##
## Call:
## glm(formula = SoilN ~ Fert, family = "inverse.gaussian", data = nitrogen)
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  8.039e-03  1.728e-03   4.652 0.000123 ***
## Fert        -2.714e-05  6.202e-06  -4.375 0.000241 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for inverse.gaussian family taken to be 0.01367622)
##
##     Null deviance: 0.72554  on 23  degrees of freedom
## Residual deviance: 0.37002  on 22  degrees of freedom
## AIC: 185.12
##
## Number of Fisher Scoring iterations: 6
```

Interpretation is -very- difficult with inverse-type link functions

Inverse Gaussian GLM: results



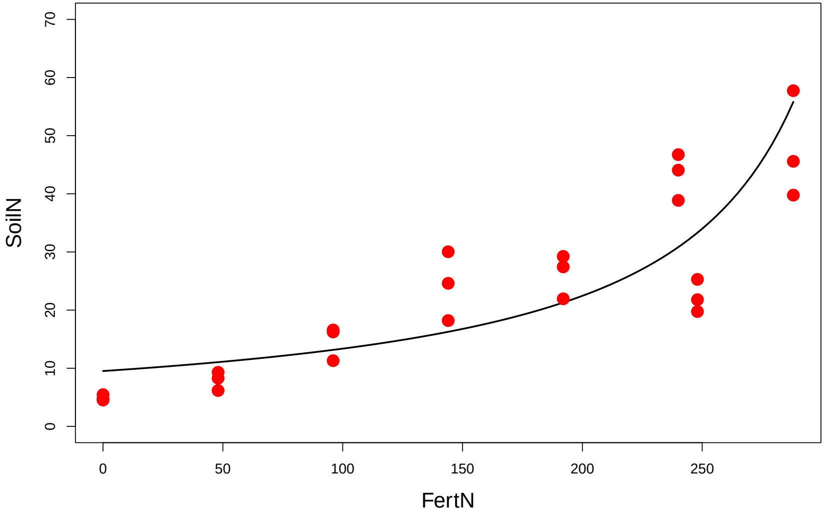
Gamma GLM

- (negative) Inverse link is canonical
  - provide starting positive values `mustart`
- Log-link is more stable

```
model3 <- glm(SoilN~Fert, data = nitrogen, family = "Gamma")
summary(model3)
```

```
##
## Call:
## glm(formula = SoilN ~ Fert, family = "Gamma", data = nitrogen)
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.050e-01  1.170e-02   8.977 8.28e-09 ***
## Fert        -3.025e-04  4.605e-05  -6.569 1.32e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.1512009)
##
##     Null deviance: 11.5897  on 23  degrees of freedom
## Residual deviance:  3.4555  on 22  degrees of freedom
## AIC: 168.93
##
```

Gamma GLM: results



Tweedie distributions

Many of the distributions so far are special forms of the Tweedie family of distributions:

$\mathrm{var}(y_i|\mathbf{x}_i) = \mu_i^{\xi}\phi$

- Normal distribution $\xi = 0$
- Poisson distribution $\xi = 1$
- Gamma distribution $\xi = 2$
- Inverse Gaussian distribution $\xi = 3$

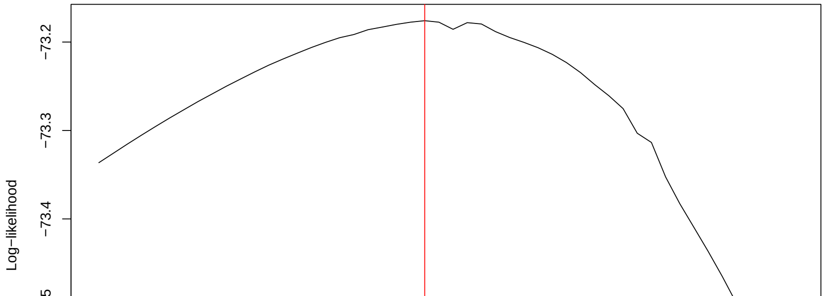
With Tweedie we can:

- Analyse positive continuous data (with zeros!)
- Counts

Tweedie GLM in R: finding ξ

```
## 2.01 2.06 2.11 2.16 2.21 2.26 2.31 2.36 2.41 2.46 2.51 2.5
## ................................Done.
```

```
## 3.022245 3.032245 3.042245 3.052245 3.062245 3.072245 3.08
## ..............................................................
```

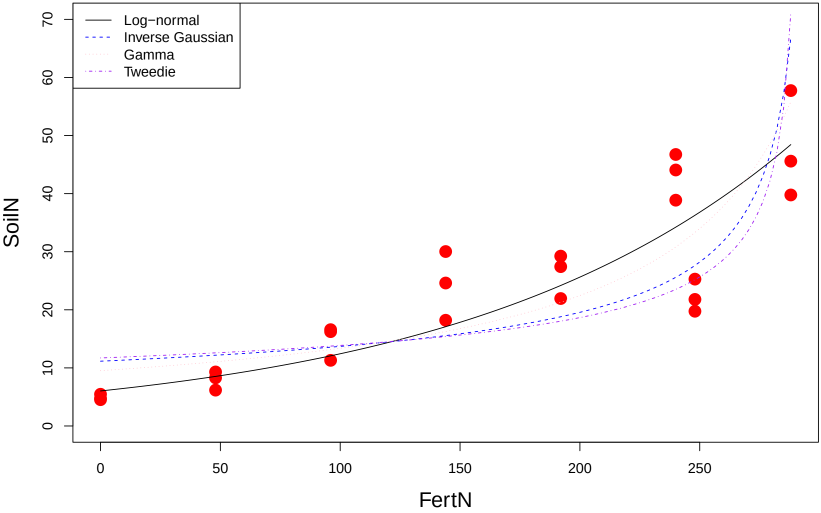


Tweedie GLM in R: fitting

```
model4 <- glm(SoilN~Fert, data = nitrogen, family = statmod::tweedie(var.power = out.est2$xi.max))
summary(model4)
```

```
##
## Call:
## glm(formula = SoilN ~ Fert, family = statmod::tweedie(var.power = out.est2$xi.max),
##     data = nitrogen)
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  2.175e-03  6.002e-04   3.624  0.00150 **
## Fert        -7.467e-06  2.113e-06  -3.535  0.00186 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Tweedie family taken to be 0.004092795)
##
##     Null deviance: 0.20212  on 23  degrees of freedom
## Residual deviance: 0.12582  on 22  degrees of freedom
## AIC: NA
##
## Number of Fisher Scoring iterations: 6
```

All together



Conclusion

- They can be relatively similar, but link function matters.
- **Mind the tail behavior**

Tweedie for flexible modeling of positive data (potentially with zeros)

GLMs for categorical data

Binomial models assume **dichotomy**. Alternative: **polychotomy**, multiple groups.

Multinomial

Gives the number of successes for a set of outcomes (instead of either success or fail)

Figure 1: We roll a dice many times, and count the number of times it hits each side. If we only throw the dice once, the throw follows a **categorical distribution**.

Multinomial logistic regression

The model we assume is:

$$\begin{aligned} \mathsf{pr}(y_{ij}) = \pi_{ij} &= \frac{\exp(\eta_{ij})}{1+\exp(\eta_{ij})} \\ \log(\frac{\pi_{ij}}{1-\pi_{ij}}) &= \eta_{ij} = \mathbf{x}_{ij}\boldsymbol{\beta}_j \end{aligned} \tag{3}$$

- E.g., probability of observing species at a site.
- We could fit multiple binomial models
  - Gets a bit messy: $y_{i1}|N_i \sim \mathcal{B}in(\pi_{i1}; N_i)$
  - $y_{i2}|N_i - y_{i1} \sim \mathcal{B}in(\pi_{ij}; N_i - y_{i1})$
- Equivalent to using a Poisson regression with fixed total

Cumulative link models

- Add order to the probabilities

Ordinal: proportional odds

More commonly, the categories are ordered.

$$\mathsf{pr}(y_i \leq j) = \sum_{k=1}^{j} \mathsf{pr}(y_k) = \frac{\exp(\theta_j + \boldsymbol{\beta}^\top \mathbf{x}_i)}{1 + \exp(\theta_j + \boldsymbol{\beta}^\top \mathbf{x}_i)} \tag{4}$$

- E.g., cover classes

Ordinal: proportional odds

Referred to as "proportional odds" because:

$$\frac{\pi_{ij}/(1-\pi_{ij})}{\pi_{i+1j}/(1-\pi_{i+1j})} = \exp\{\boldsymbol{\beta}(\mathbf{x}_{ij} - \mathbf{x}_{i+1j})\} \tag{5}$$

the log-odds is proportional to the difference in the covariates.

Ordinal example: vegetation data

```
data(dune,dune.env,package="vegan")
data <- cbind(y=as.factor(dune$Bracruta), dune.env)
(model5 <- MASS::polr(y~A1, data = data))
```

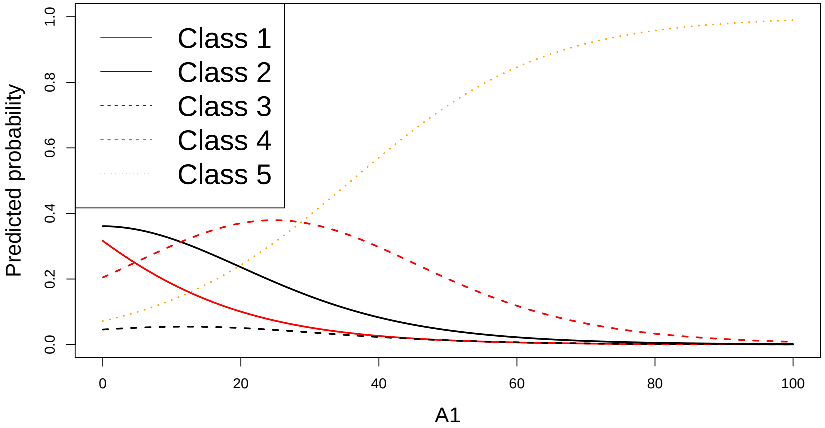
```
## Call:
## MASS::polr(formula = y ~ A1, data = data)
##
## Coefficients:
##         A1
## 0.07104338
##
## Intercepts:
##        0|2        2|3        3|4        4|6
## -0.7704179  0.7426109  0.9615655  2.5585698
##
## Residual Deviance: 57.48771
## AIC: 67.48771
```

Example: vegetation data

```
predict(model5,type="probs")
```

```
##            0         2          3         4          6
## 1  0.2750122 0.3576581 0.04925726 0.2317706 0.08630192
## 2  0.2652086 0.3558300 0.05000602 0.2386505 0.09030488
## 3  0.2542818 0.3532918 0.05080543 0.2465371 0.09508384
## 4  0.2556313 0.3536348 0.05070893 0.2455506 0.09447432
## 5  0.2282902 0.3449388 0.05251291 0.2662255 0.10803261
## 6  0.2542818 0.3532918 0.05080543 0.2465371 0.09508384
## 7  0.2750122 0.3576581 0.04925726 0.2317706 0.08630192
## 8  0.2556313 0.3536348 0.05070893 0.2455506 0.09447432
## 9  0.2624490 0.3552399 0.05021166 0.2406205 0.09147894
## 10 0.2679868 0.3563901 0.04979663 0.2366821 0.08914442
## 11 0.2652086 0.3558300 0.05000602 0.2386505 0.09030488
## 12 0.2346085 0.3472870 0.05212735 0.2613202 0.10465704
```

Ordinal example: vegetation data



Note that ordering has introduced some shapes.

Proportions: brief mentioning

Sometimes, mistakenly, logistic regression is referred to as "modeling proportions"

- Binomial responses are dichotomous (either 0 or 1)
- Proportions usually include 0 and/or 1, but also everything between

$$y_i \sim \mathcal{B}eta(\mu_i, \phi) \tag{6}$$

- "beta regression", which is not a GLM
- various packages implement it
- Require data between 0 and 1 (i.e., without 0 or 1)

When there are zeros and/or ones..zero-inflated models or hurdle models (ZIB or ordered beta regression).

Excess zeros

When there are more zeros than the selected distribution can generate.

- Can be accounted for with additional model terms (covariate)
- Alternatively:
  - Zero-inflated models
  - Hurdle models
  - Negative-binomial models: can handle excess zeros very well

1) Zero-inflated models: another process generates additional zeros (e.g., colonisation vs. abundance)

- e.g., Species abundance

2) Hurdle models: only one of the two processes generates values below the hurdle

Zero-inflation (Poisson)

$$y_i \sim ZIP(\lambda_{ij}, \pi_i) \tag{7}$$

$$y_i|\nu_j \sim \begin{cases} pPois(\lambda_i) & \text{if } y_i > 0 \\ \begin{cases} p\exp(-\lambda_i) & \text{if } \nu_i = 1 \\ 1 - p & \text{if } \nu_i = 0 \end{cases} & \text{if } y_i = 0 \end{cases} \tag{8}$$

- can choose to separately model p as a logistic regression
- quadratic mean-variance as in NB

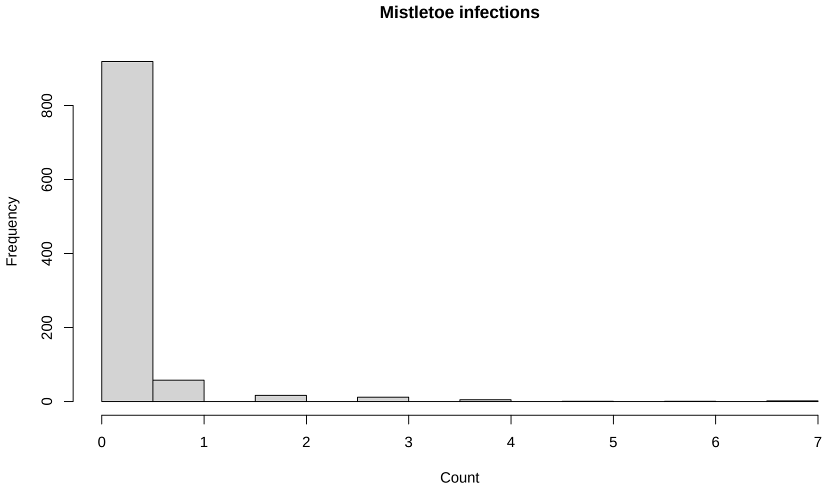
Example: Mistletoe infection data

Mistletoe data covered in Zuur (2021)

- Count of mistletoe infections in a tree stand
- DBH, tree infected or not, size of largest mistletoe

CI_stem	N12	No.of.mistletoes	Stand	ID	DBH	Distance.fror
5.343255	36	1	äobes	921	26	
4.771435	32	2	äobes	923	27	
5.856576	32	0	äobes	920	25	
5.093324	39	0	äobes	916	25	
6.452976	32	0	äobes	918	24	
5.598422	32	0	äobes	917	26	
5.301989	32	0	äobes	919	28	
6.384254	29	0	äobes	913	20	

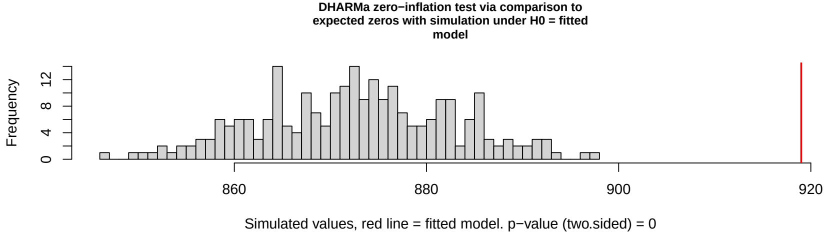
Example: Mistletoe infections



Example: Mistletoe infections

```
model6 <- glm(No.of.mistletoes~DBH, family="poisson", data = data)
```

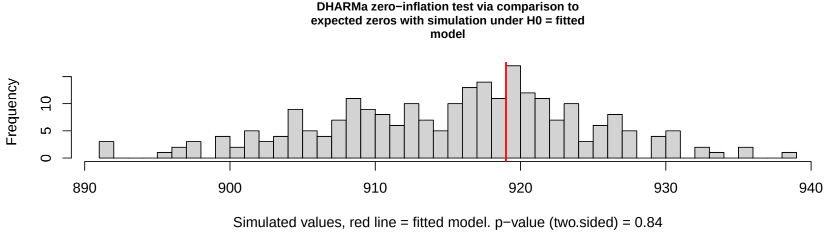
```
DHARMa::testZeroInflation(model6)
```




```
##
##  DHARMa zero-inflation test via comparison to expected zeros with
##  simulation under H0 = fitted model
##
## data:  simulationOutput
## ratioObsSim = 1.0525, p-value < 2.2e-16
```

Example: Mistletoe infections

```
model7 <- glmmTMB::glmmTMB(No.of.mistletoes~DBH,ziformula=~1, family="poisson", data = data)
```




```
##
##  DHARMa zero-inflation test via comparison to expected zeros with
##  simulation under H0 = fitted model
##
## data:  simulationOutput
## ratioObsSim = 1.0035, p-value = 0.84
## alternative hypothesis: two.sided
```

Summary

- At least not mentioned: Generalized and Conway-Maxwell Poisson
- Ordered beta
- Truncation