evropský sociální fond v ČR
EVROPSKÁ UNIE
MINISTERSTVO ŠKOLSTVÍ, MLÁDEŽE A TĚLOVÝCHOVY
OP Vzdělávání pro konkurenceschopnost

INVESTICE DO ROZVOJE VZDĚLÁVÁNÍ

Tento projekt je spolufinancován Evropským sociálním fondem a Státním rozpočtem ČR
InoBio – CZ.1.07/2.2.00/28.0018

Logistic regression

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Ing. Daniel Volařík, Ph.D.

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EUROPEAN UNION

MINISTRY OF EDUCATION, YOUTH AND SPORTS

OP Education for Competitiveness

INVESTMENTS IN EDUCATION DEVELOPMENT

Recup

- Linear model
  - Constant variance
  - Normality
  - independence
- Generalised linear models
  - Linear predictor
  - Link function
  - Distribution of errors (Gamma, Poisson, binomial)

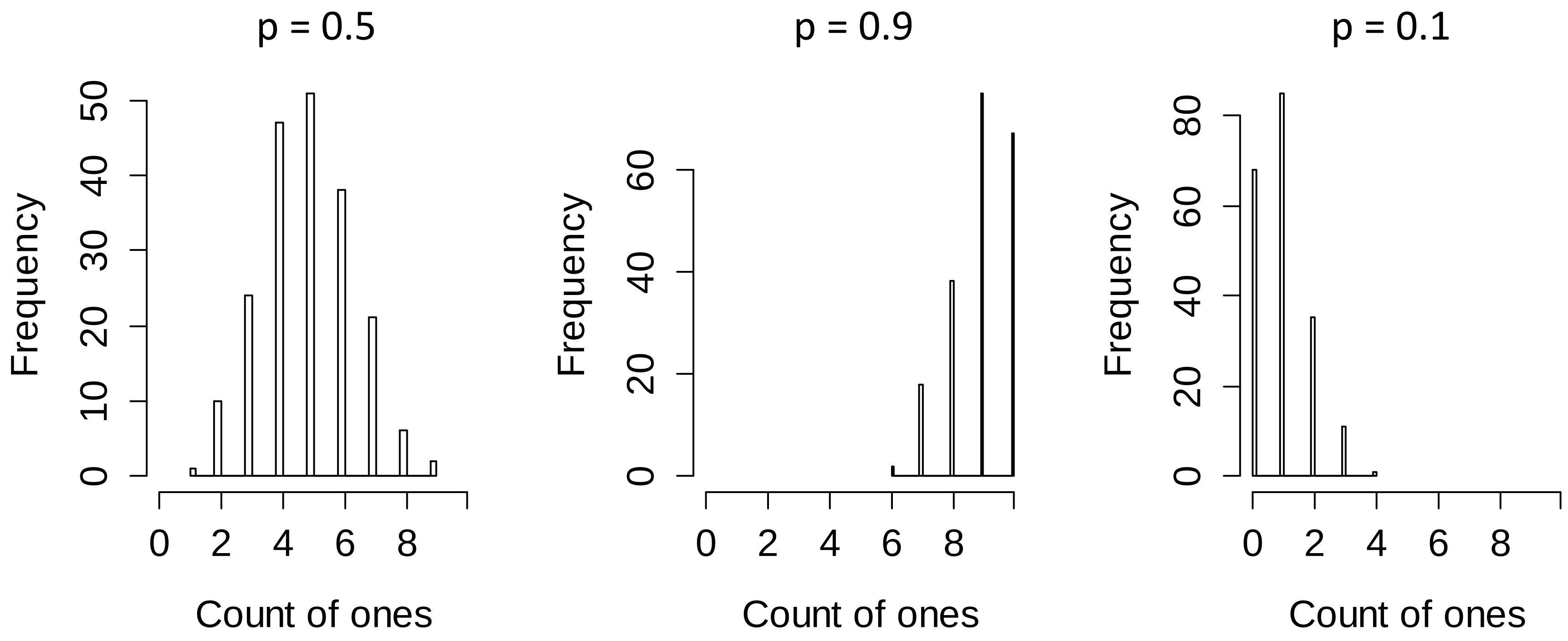
Logistic regression

- GLM with binomial error distribution
- Presence-absence data
- Proportional data

Binomial distribution

- A sequence of independent Bernoulli trials (like tossing a coin).
- A two-parameter distribution: the number of trials, *N*, and the probability of success, *p,* in any given trial.
- Mean is given by $N \times p$
- Variance by $N \times p \times (1 – p)$
- Assumption: probability of success does not change from trial to trial.

Binomial error distribution



- All examples are from samples with N = 10
- Each sampling has 200 runs
- In R you can explore this using rbinom() function

Presence-absence data

- binary (0 or 1) responses such as presence versus absence of an organism, alive versus dead, male versus female and so on.
- Binary data can only take two possible values - zero or one - and can therefore not be normally distributed.
- Special version of the binomial distribution known as the Bernoulli distribution where the number of trials is one (n = 1).

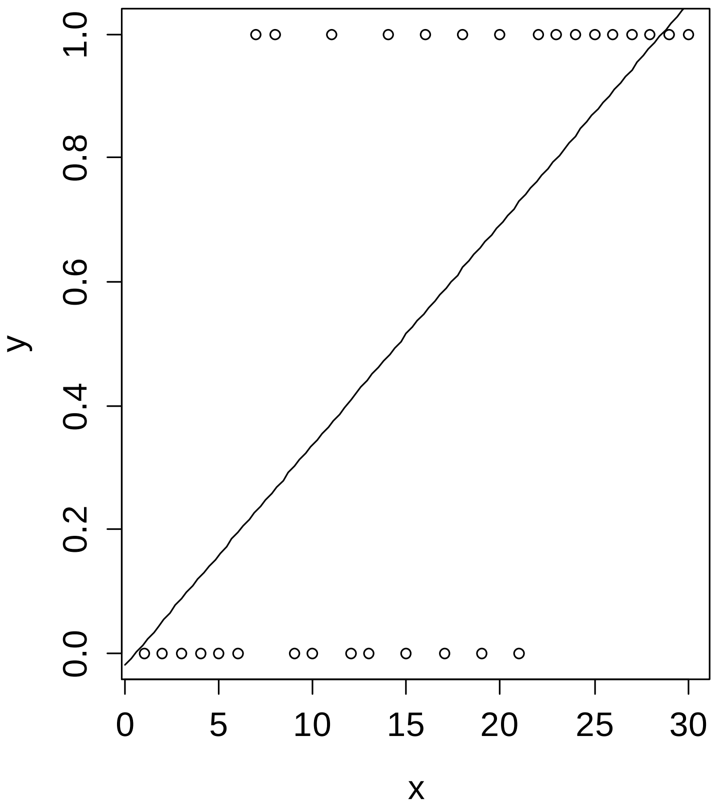
Proportional data

- For example we sample N animals for presence-absence of some disease, or we sample N trees weather they are dead or alive
- We have proportion of animals with disease or proportion of dead trees
- binomial distribution

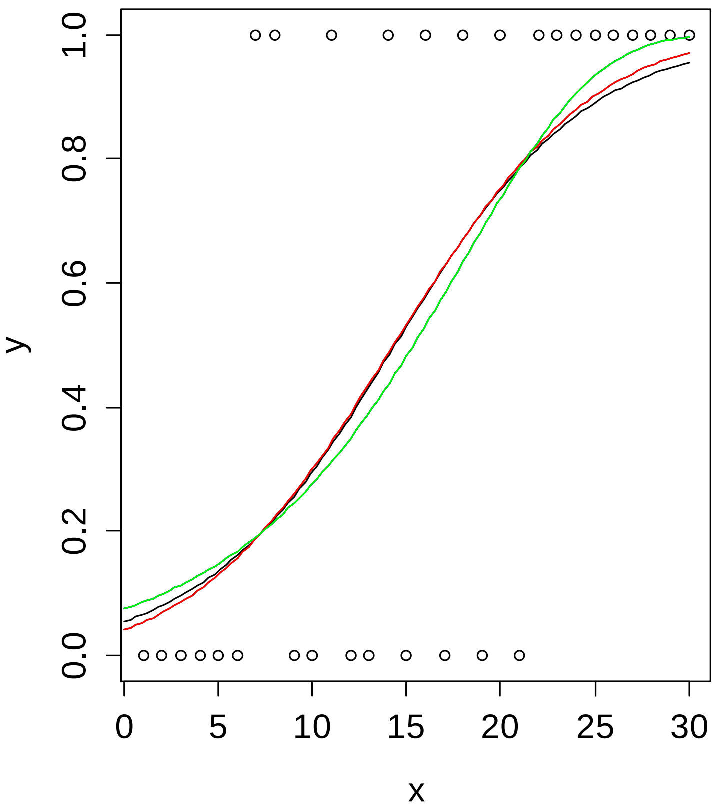
Link functions

- logit: $\mathrm{g}(p) = \log\left(\frac{p}{1-p}\right)$
- probit: $\mathrm{g}(p) = \phi^{-1}(p)$, where ϕ is the cumulative density function of the standard normal distribution
- cloglog – complementary log-log:
$$\mathrm{g}(p) = \log(-\log(1-p))$$
- Sigmoidal shape curves bounded between 0 and 1
- Differente links have slightly differente shape
- Cloglog could be good choise when there is considerable more zeros than ones or vice versa.

Link functions – example



Linear regression



GLM

Logit – black curve

Probit – red curve

Cloglog – green curve

Inverse link – antilogit

- $\log\left(\frac{p}{1-p}\right)$ = A + B*x
- If you want to make predictions on probability scale, you have to use inverse link – in case to logit it is antilogit
- $\left(\mathrm{logit}^{-1} = \frac{1}{1+ e^{-(linear\ predictor)}}\right)$

Overdispersion

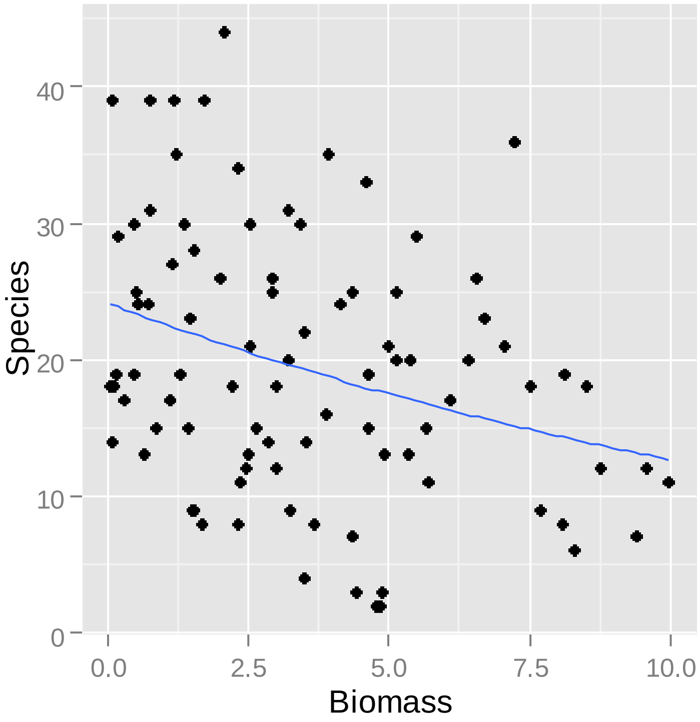
- In binomial distribution, mean is given by $N \times p$, variance by $N \times p \times (1 – p)$,
- for binary data mean is given by p and variance by p × (1-p)
- Overdispersion – when the variance is higher than expected
- (underdispersion – variance is lower than expected)
- Causes of overdispersion:
  - Important covariates or interactions are missing, outliers, wrong link function, non-linear effect entered as linear effect, …
  - When we can not find any of previos causes, it is real overdispersion – the variance is really larger than expected

Overdispersion - solution

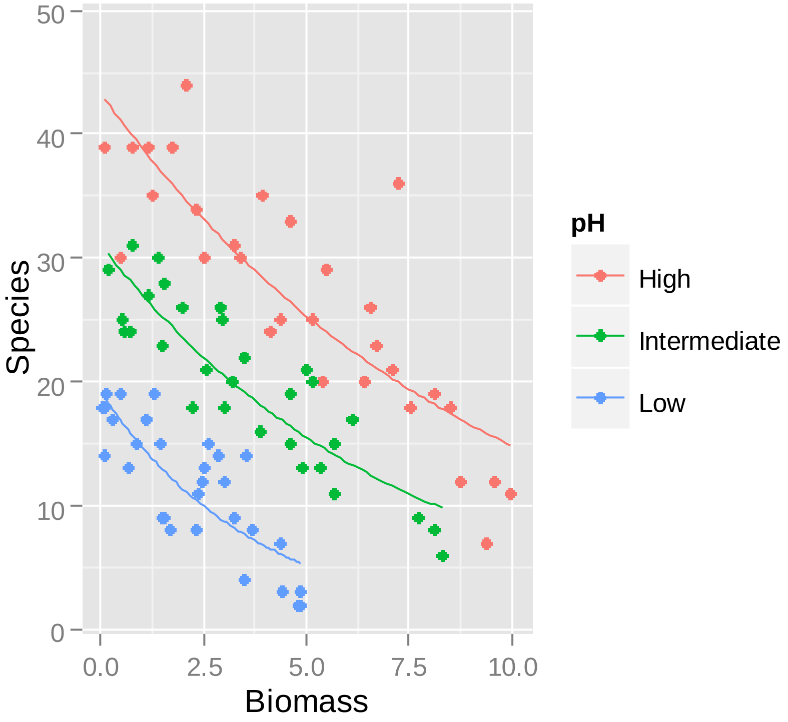
- We can detect overdispersion by comparing residual deviance with residual degrees of freedom – they should be approximately equal
- Quasi-binomial distribution
- Dispersion parameter ϕ

Overdispersion

- Nice example from yesterday



Residual deviance: 407.67
on 88 degrees of freedom



Residual deviance: 83.20
on 84 degrees of freedom

Logistic regression in R

- Function glm() with parameters:
  - Formula (for linear predictor – the same as in lm()
  - Family – binomial
  - Link function – one of logit, probit, cloglog
- Example:

```
glm(response ~ x + z, data = data,
 family = binomial(link = "logit"))
```

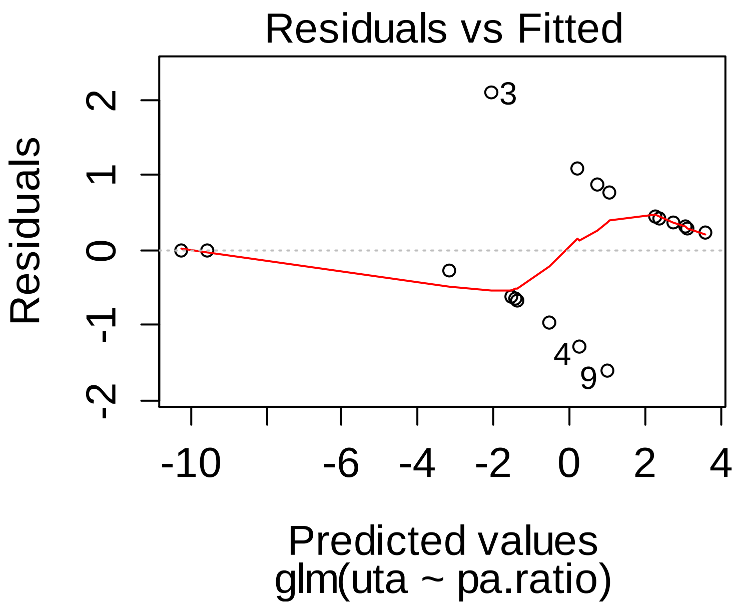
- For presence-absence data, the response is vector of zeros and ones
- For proportional data, the response is a list of two vector – one with positive cases and one with negative

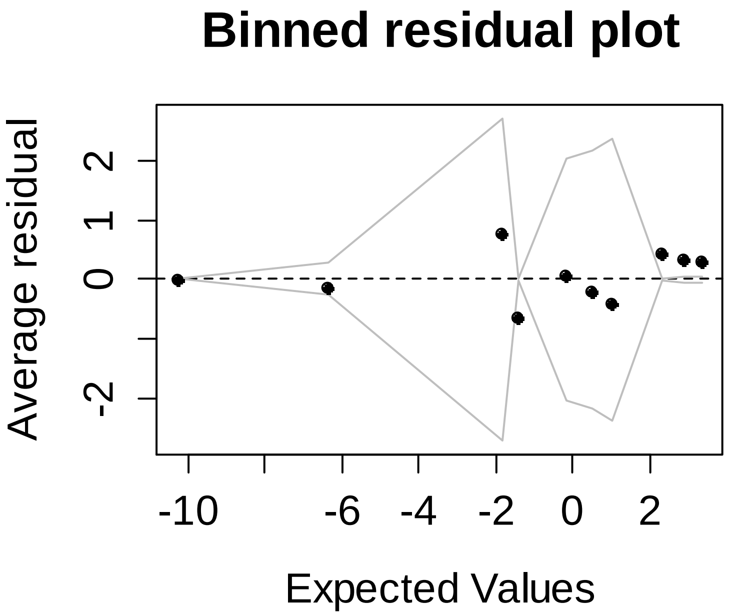
```
Response = cbind(positive_cases, negative_cases)
```

Model checking

- Check for equality of residual deviance and residual degrees of freedom for proportional data.
- binned plot
  - plots of raw residuals from logistic regression are usually not useful – because data are discrete and so are residuals
  - Instead we can plot binned (grouped) residuals vs fitted values
  - There is a degree of arbitraries in the size of bins
  - In R function binnedplot from arm package

Model checking





- Lines in the binned residual plot are +/- 2 standard-error bounds within which 95% of the binned residuals are expected to lie if the model is ‘true’

Exercices

- Presence-absence of lizards Uta in relation to perimeter-to-area ratio
- Proportional data – germination of Orobanche seed stimulated by extract of cucumber and beam