

Analyses of *Analyses of* **continuous II**

Gamma & Lognormal distributions

- Gamma and lognormal data arise:
 - precise measurements of small quantities (concentration), weight, time, etc.
 - measurements are continuous
 - negative values and zeros are not allowed
 - distribution is skewed to the right

Lognormal model

- logarithmic transformation of measurements will homogenise variance and adjust asymmetry of distribution
- moments - 2 parameters (μ_{tr}, σ_{tr})
 - while on log scale variance is independent of mean, on original scale variance is a function of expected mean

$$E(y) = \exp\left(\mu_{tr} + \frac{\sigma_{tr}^2}{2}\right)$$

$$Var(y) = \exp(\sigma_{tr}^2 - 1)\exp(2\mu_{tr} + \sigma_{tr}^2)$$

- predicted values: $\exp(Q) = \text{median}$

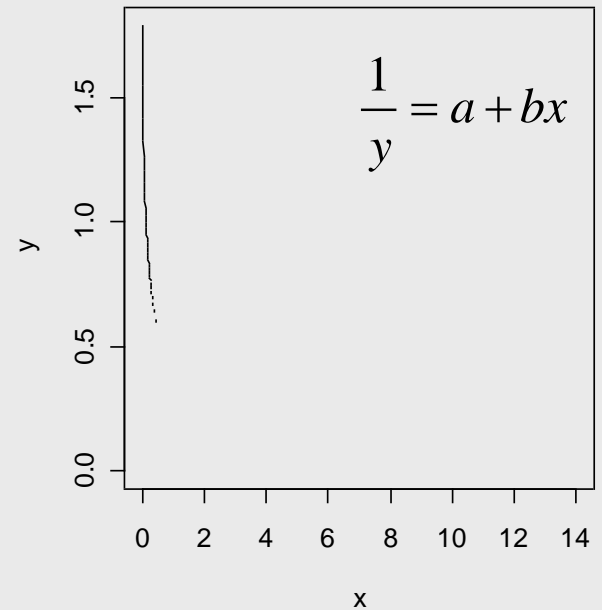
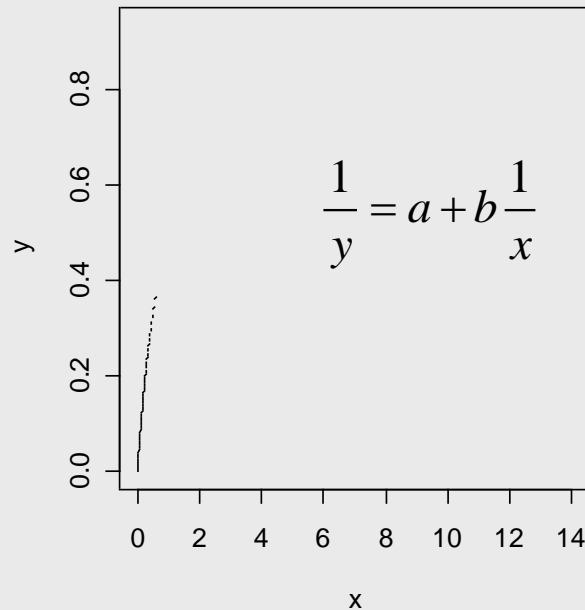
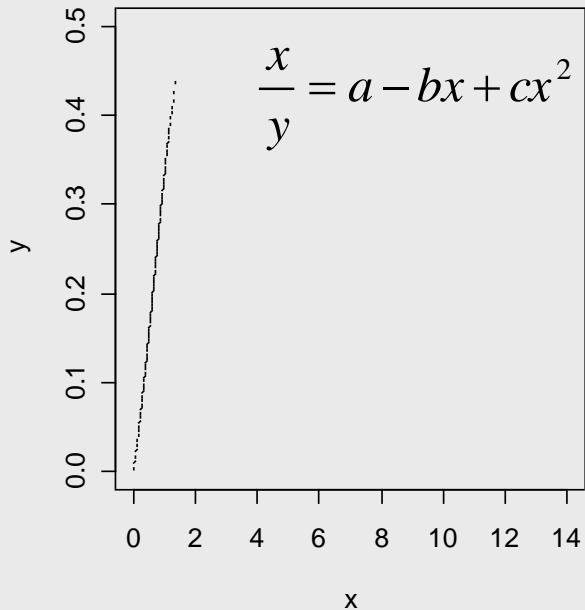
Gamma model

- used to model inverse polynomials moments - 2 parameters (μ, φ)

$$E(y) = \mu$$

$$\text{Var}(y) = \varphi\mu^2$$

- dispersion parameter (φ) = $\text{Var}(y) / \mu^2$



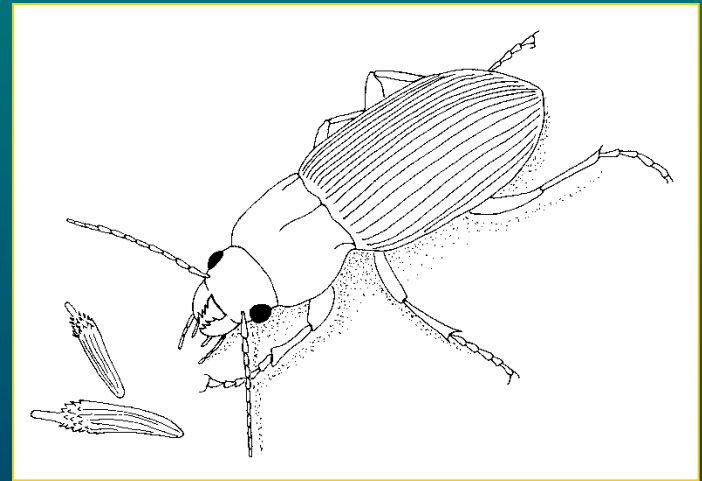
Analytical methods

- **Welch test** (`t.test`) to compare two means with heterogenous variances
- `glm(formula, Gamma(link= ...))`
- links:
 - **inverse** (default) $\frac{1}{y}$
 - **logarithmic** (`log`)
 - **identity** (`identity`)
- `lm(log(y) ~ ...)`

Simple Regression

Background

In euryphagous predators the size of prey is positively related to their body size. There is an upper limit due to e.g. morphological constraints.



Design

In the laboratory, acceptance of food was studied in 36 species of granivorous beetles. Each carabid beetle was offered seeds of various sizes [g]. Preferred seed size was recorded. For each beetle body size [mm] was recorded too.

Hypotheses

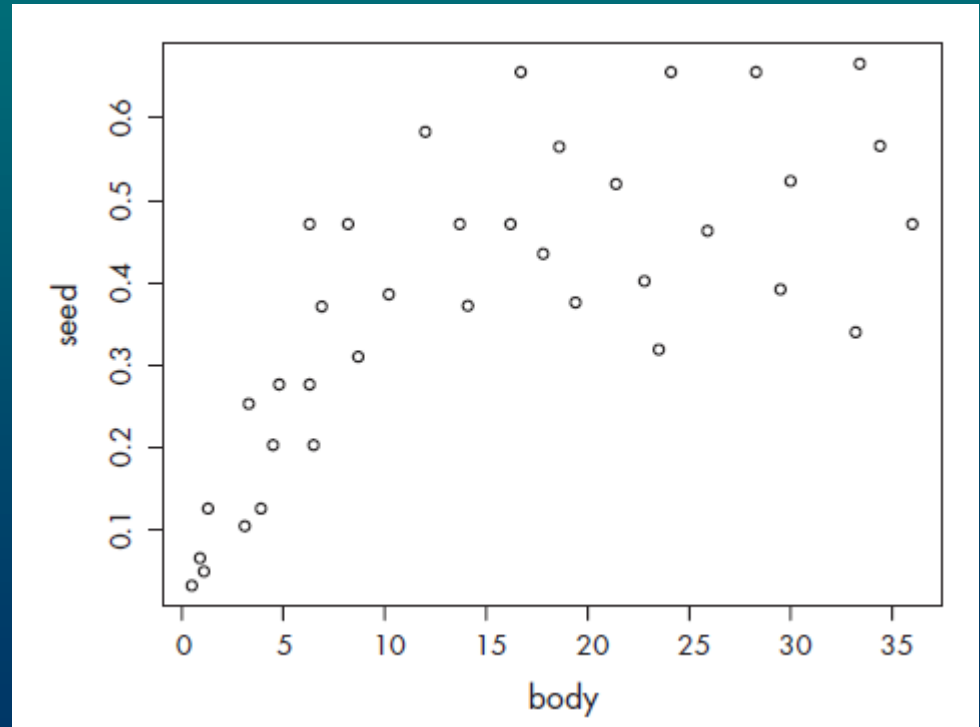
Is size of seeds related to the carabid body size?

What is the shape of the relationship?

Variables

body

seed



$$\frac{1}{\mu_i} = \alpha + \beta \frac{1}{body_i},$$

kde $seed_i \sim \text{Gama}(\mu_i, \varphi)$, nezávisle pro každého jedince.

```
> m1 <- glm(seed ~ I(1/body), family=Gamma)
```

```
> anova(m1, test="F")
```

Analysis of Deviance Table

Model: Gamma, link: inverse

Response: seed

Terms added sequentially (first to last)

	Df	Deviance	Resid.	Df	Resid. Dev	F	Pr(>F)
NULL				35	15.3681		
I(1/body)	1	8.3662		34	7.0019	42.624	1.787e-07 ***

$$\frac{1}{\mu_i} = \alpha + \beta \frac{1}{body_i} + \gamma \frac{1}{body_i^2},$$

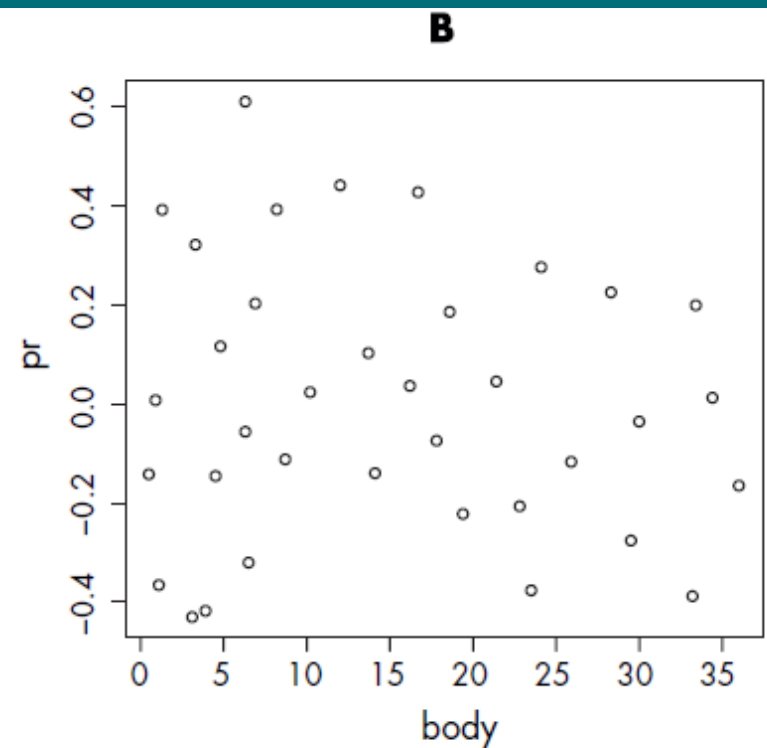
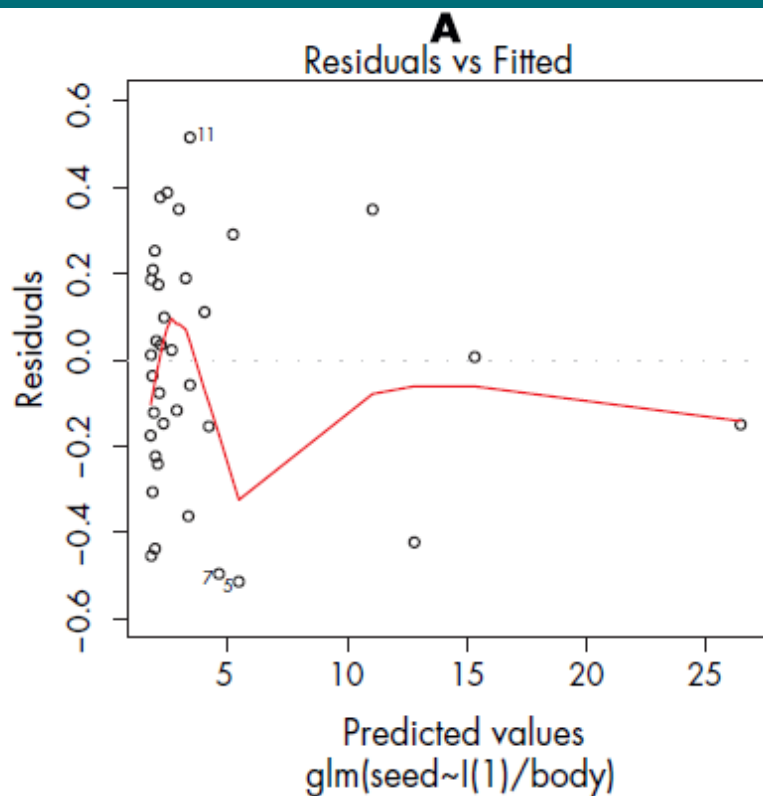
$seed_i \sim \text{Gama}(\mu_i, \varphi)$, nezávisle pro každého jedince.


```
> m2 <- glm(seed ~ I(1/body) + I(1/body^2), Gamma)
> anova(m1, m2, test="F")
Analysis of Deviance Table
```

Model 1: seed ~ I(1/body)

Model 2: seed ~ I(1/body) + I(1/body^2)

	Resid. Df	Resid. Dev	Df	Deviance	F	Pr(>F)
1	34	7.0019				
2	33	7.0016	1	0.0003	0.0013	0.9713



```

> summary(m1)

Call:
glm(formula = seed ~ I(1/body), family = Gamma)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-0.7530027  -0.4237538   0.0008676   0.2527096   0.7024871

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   1.7418     0.3162   5.508 3.76e-06 ***
I(1/body)    11.8626     2.4463   4.849 2.69e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Gamma family taken to be 0.1962785)

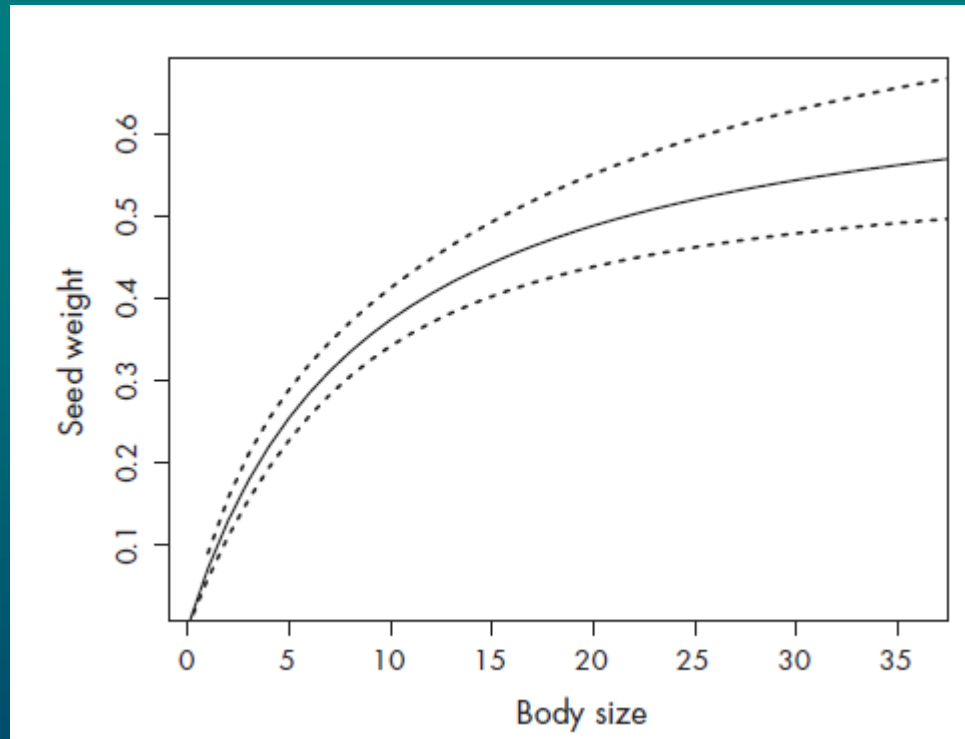
Null deviance: 15.3681  on 35  degrees of freedom
Residual deviance:  7.0019  on 34  degrees of freedom
AIC: -49.676

```

Coefficient of determination: $(15.3681 - 7.0019) / 15.3681 = 0.54$.

Asymptote: $1/1.7418 = 0.574$,

$$\frac{body}{1.742body + 11.86}$$



$$seed_i = \alpha + \beta body_i + \gamma body_i^2 + \varepsilon_i,$$

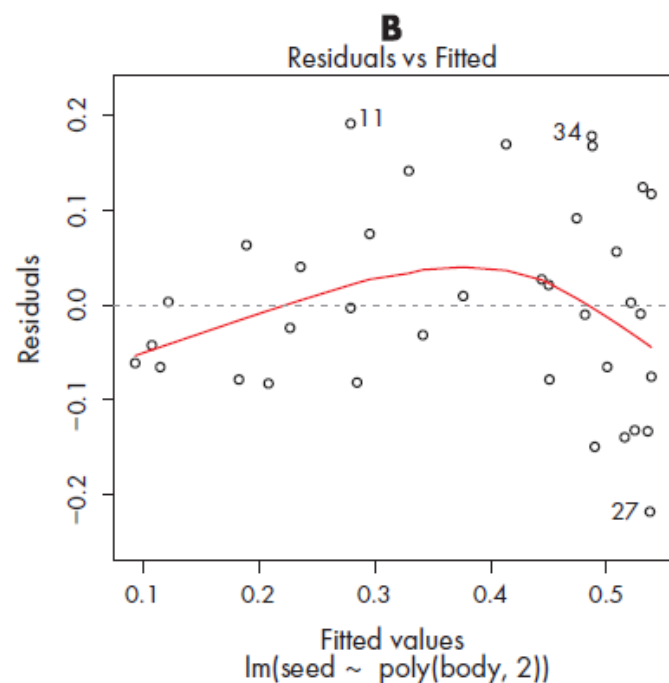
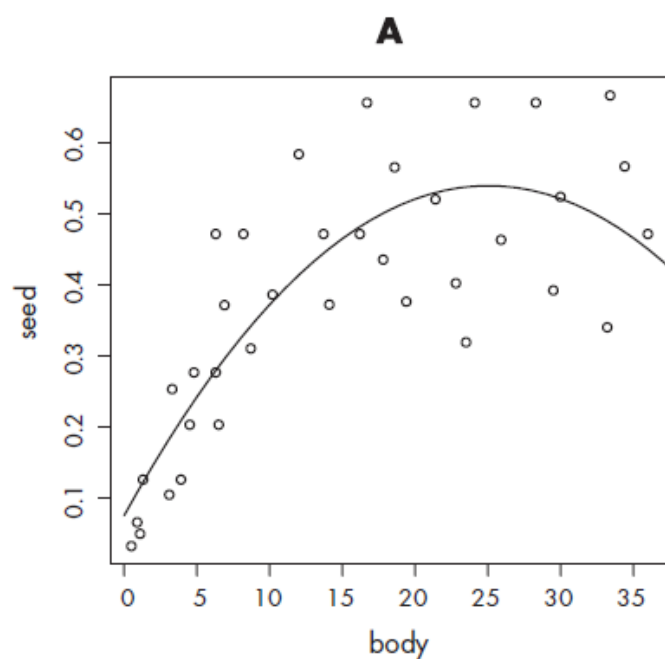
kde $\varepsilon_i \sim N(0, \sigma^2)$, nezávisle pro jednotlivé jedince.

```

> m3 <- lm(seed ~ poly(body,2))
> summary(m3)
...
Coefficients:
                Estimate Std. Error t value Pr(>|t|)
(Intercept)      0.30842   0.02318  13.305 8.17e-15 ***
poly(body, 2)1   0.55682   0.13908   4.004 0.000333 ***
poly(body, 2)2  -0.41591   0.13908  -2.990 0.005235 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.1391 on 33 degrees of freedom
Multiple R-Squared:  0.4307,    Adjusted R-squared:  0.3962
F-statistic: 12.49 on 2 and 33 DF,  p-value: 9.173e-05

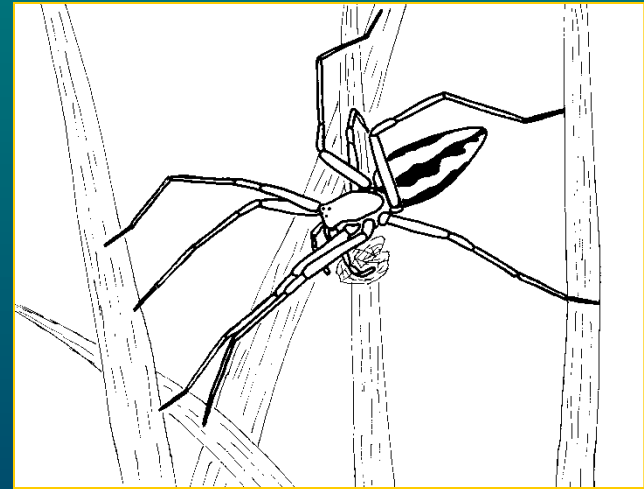
```



2-way ANOVA

Background

In the gift-giving spider a male brings a prey to a female in order to avoid being cannibalised. Several variables can potentially influence how quickly female will accept the gift.



Design

In the laboratory, effect of two variables was studied: satiation of female (satiated, starved) and their mating experience (mated, virgin). Time [s] of the gift presentation was recorded. Experiment was fully factorial, for each combination 10 males and females were used.

Hypotheses

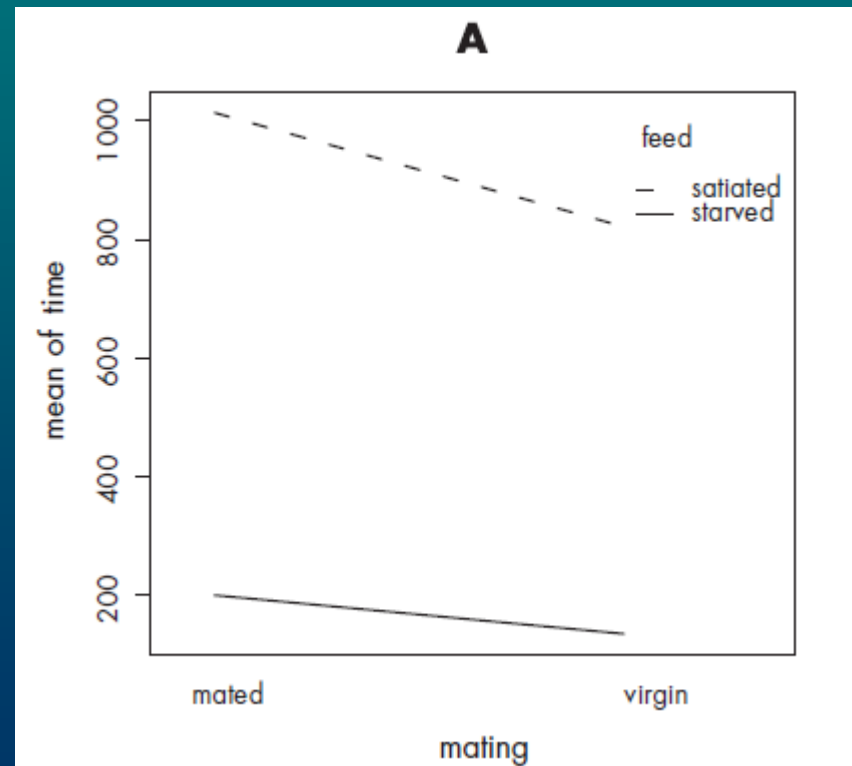
Is presentation time affected by any of the two variables?

If it is what is the difference between factor levels?

Variables

MATING: mated, virgin

FEED: satiated, starved
time



$$time_{ijk} = \alpha + MATING_j + FEED_k + MATING:FEED_{jk} + \varepsilon_{ijk},$$

s $\varepsilon_{ijk} \sim N(0, \sigma^2)$, nezávisle pro jednotlivá pozorování.

```
> m1 <- lm(time ~ mating*feed)
```

```
> anova(m1)
```

```
Analysis of Variance Table
```

```
Response: time
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
mating	1	165122	165122	0.2558	0.616098
feed	1	5625000	5625000	8.7142	0.005528 **
mating:feed	1	40322	40322	0.0625	0.804058
Residuals	36	23237845	645496		

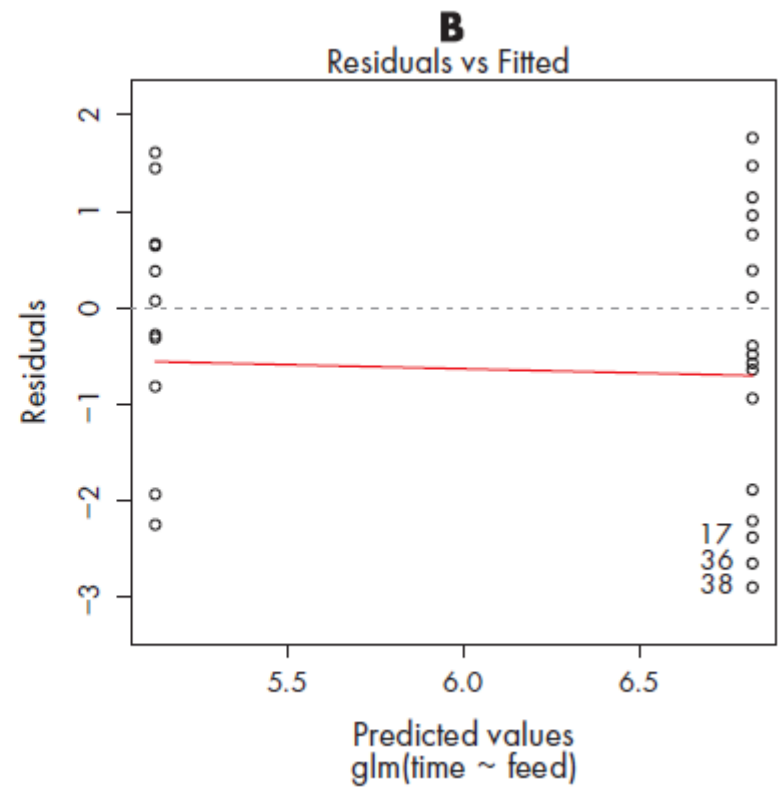
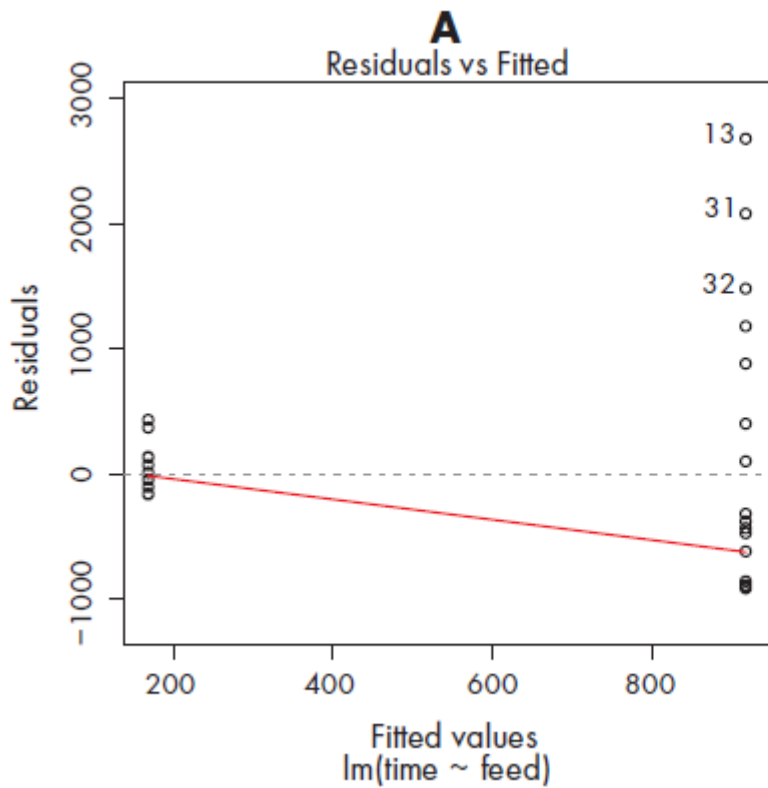
```
> anova(m3)
```

```
Analysis of Variance Table
```

```
Response: time
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
feed	1	5625000	5625000	9.1177	0.004507 **
Residuals	38	23443290	616929		

```
---
```



$\log(\mu_{jk}) = \alpha + \text{MATING}_j + \text{FEED}_k + \text{MATING:FEED}_{jk}$,
 $s \text{ time}_{jk} \sim \text{Gama}(\mu_{jk}, \varphi)$, nezávisle pro jednotlivá pozorování,

```

> m4 <- glm(time ~ mating*feed, Gamma(link=log))
> anova(m4, test="F")
...

```

	Df	Deviance	Resid.	Df	Resid.	Dev	F	Pr(>F)
NULL				39		122.018		
mating	1	0.564		38		121.454	0.3888	0.5368618
feed	1	26.258		37		95.196	18.1021	0.0001425 ***
mating:feed	1	0.083		36		95.113	0.0570	0.8126218

```

---
```

```

> anova(m6, test="F")
...

```

	Df	Deviance	Resid.	Df	Resid.	Dev	F	Pr(>F)
NULL				39		122.018		
feed	1	25.922		38		96.096	20.3	6.138e-05 ***

```

---
```

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

```
> summary(m6)
...
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   6.8222     0.2527  26.999 < 2e-16 ***
feedstarved  -1.6982     0.3573  -4.752 2.87e-05 ***
---
```

```
> exp(6.8222)
[1] 918.0024
> exp(6.8222-1.6982)
[1] 168.0061
> tapply(time, feed, mean)
satiated  starved
    918      168
```

$$\log(\text{time}_{ijk}) = \alpha + \text{MATING}_j + \text{FEED}_k + \text{MATING:FEED}_{jk} + \varepsilon_{ijk}$$

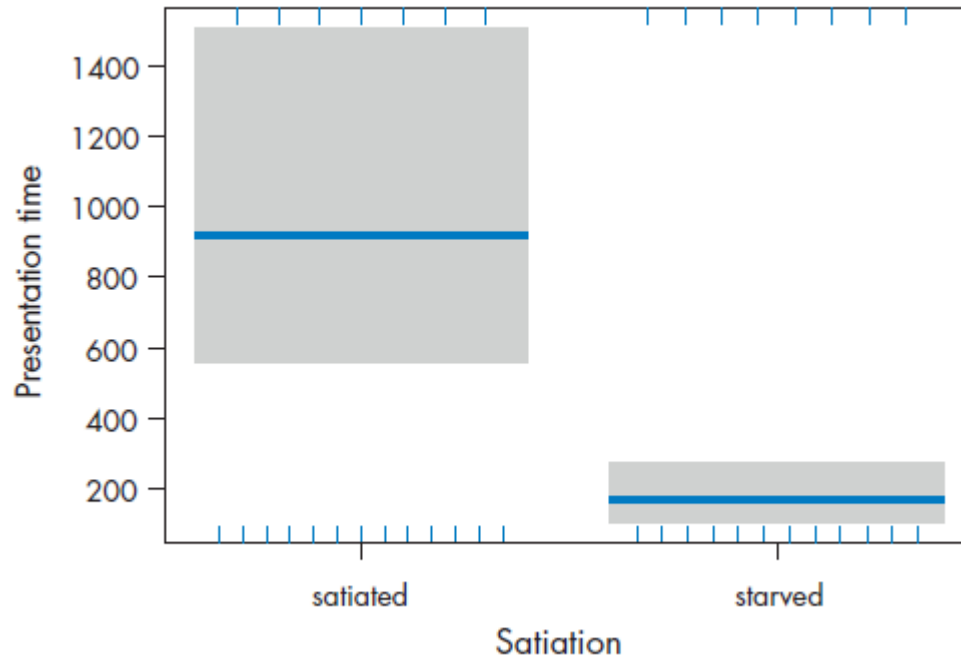
s $\varepsilon_{ijk} \sim N(0, \sigma^2)$, nezávisle pro jednotlivá pozorování.

```
> m7 <- lm(log(time) ~ mating*feed)
> anova(m7)
Analysis of Variance Table

Response: log(time)
          Df  Sum Sq Mean Sq F value  Pr(>F)
mating     1   11.432   11.432   2.7578 0.10547
feed       1   19.262   19.262   4.6468 0.03787 *
mating:feed 1    0.019    0.019   0.0045 0.94681
Residuals 36 149.226    4.145
---
```

```
> m8 <- lm(log(time) ~ feed)
> summary(m8)
```

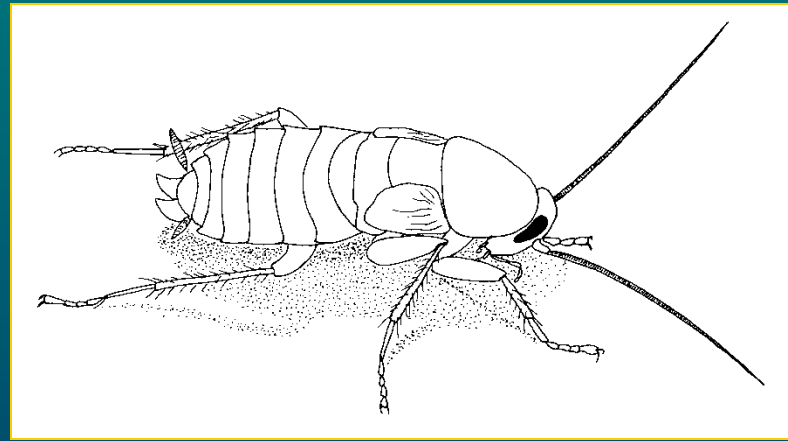
```
Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)   5.4658     0.4598   11.887 2.27e-14 ***
feedstarved  -1.3879     0.6503   -2.134  0.0393  *
```



2-way ANCOVA

Background

The nutritional quality of the diet affects growth of organisms in a various ways. To find optimal diet for cockroaches the following experiments was performed.



Design

Effect of five diet types (control, lipid1, lipid2, protein1, protein2) was tested on body weight [g] of male and female cockroaches. For each diet 10 females and 7 males were used. Their body weight [g] was recorded before and after the experiment.

Hypotheses

Is weight influenced by the diet type?

If so which diet resulted in largest weight?

Is weight on diets similar for males and females?

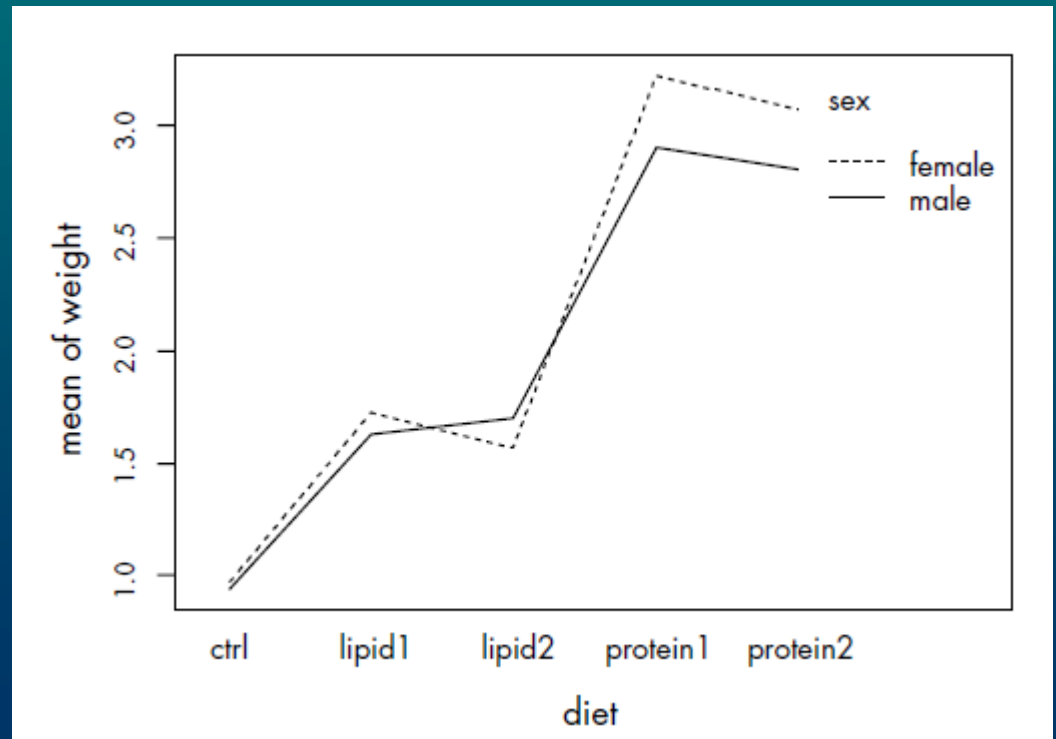
Variables

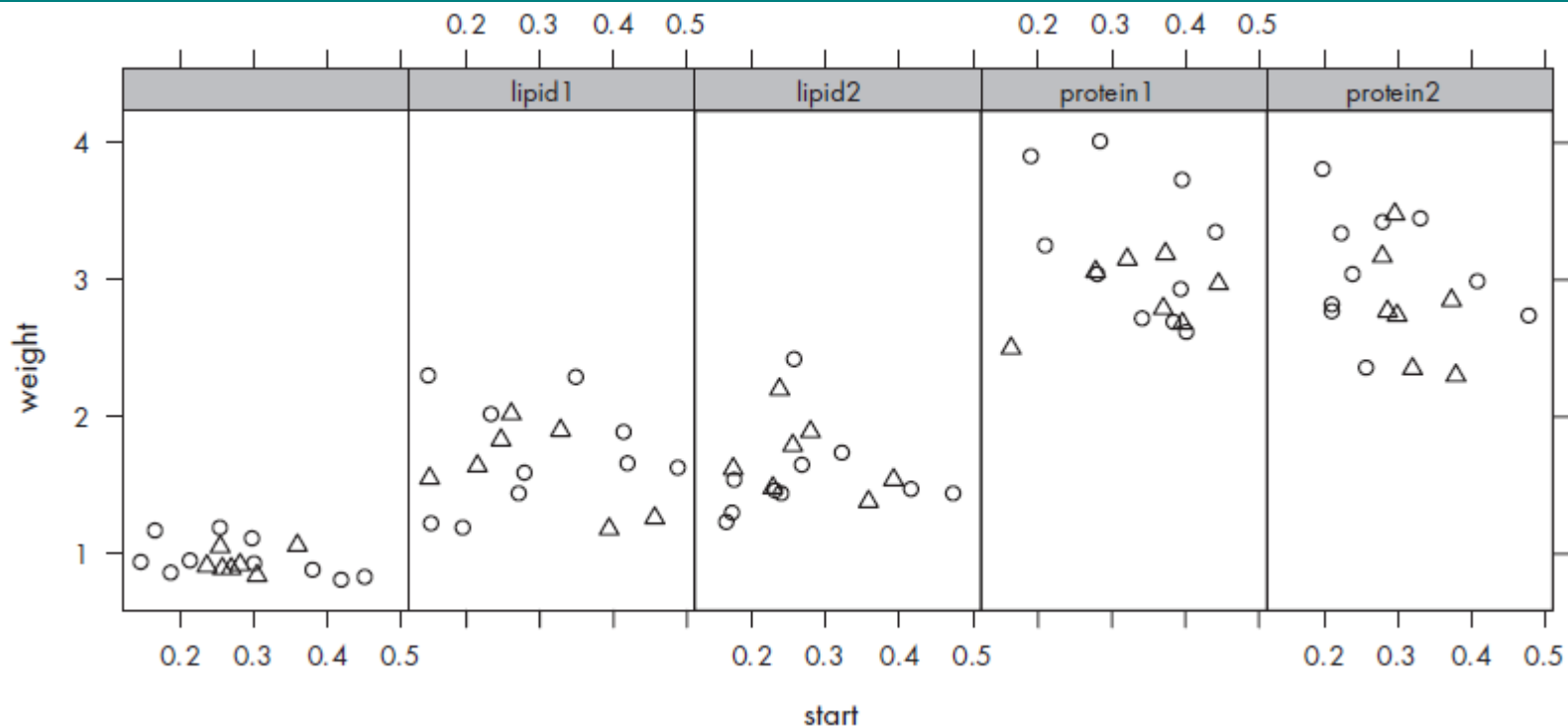
DIET: control, lipid1, lipid2, protein1, protein2

SEX: male, female

start

weight





$$\log(\text{weight}_{ijk}) = \alpha + \text{DIET}_j + \text{SEX}_k + \beta \text{start}_i + \text{DIET:SEX}_{jk} + \delta_{j1} \text{start}_i + \delta_{1k} \text{start}_i + \delta_{jk} \text{start}_i + \varepsilon_{ijk},$$

kde $\varepsilon_{ijk} \sim N(0, \sigma^2)$, nezávisle pro jednotlivá měření.

```
> m1 <- lm(log(weight) ~ diet*sex*start)
```

```
> anova(m1)
```

```
Analysis of Variance Table
```

```
Response: log(weight)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
diet	4	16.1349	4.0337	150.3981	<2e-16	***
sex	1	0.0261	0.0261	0.9732	0.3275	
start	1	0.0455	0.0455	1.6956	0.1975	
diet:sex	4	0.0866	0.0217	0.8073	0.5250	
diet:start	4	0.0244	0.0061	0.2272	0.9222	
sex:start	1	0.0315	0.0315	1.1743	0.2825	
diet:sex:start	4	0.1829	0.0457	1.7048	0.1596	
Residuals	65	1.7433	0.0268			

```
---
```

```
> anova(lm(log(weight) ~ sex*diet*start))
```

```
Analysis of Variance Table
```

```
Response: log(weight)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
sex	1	0.0261	0.0261	0.9732	0.3275	
diet	4	16.1349	4.0337	150.3981	<2e-16	***
start	1	0.0455	0.0455	1.6956	0.1975	
sex:diet	4	0.0866	0.0217	0.8073	0.5250	
sex:start	1	0.0196	0.0196	0.7302	0.3959	
diet:start	4	0.0363	0.0091	0.3382	0.8512	
sex:diet:start	4	0.1829	0.0457	1.7048	0.1596	
Residuals	65	1.7433	0.0268			

$$\log(\text{weight}_{ijk}) = \alpha + \text{DIET}_j + \text{SEX}_k + \beta \text{start}_i + \gamma \text{start}_i^2 + \text{DIET:SEX}_{jk} + \delta_{j1} \text{start}_i + \delta_{1k} \text{start}_i + \delta_{jk} \text{start}_i + \omega_{j1} \text{start}_i^2 + \omega_{1k} \text{start}_i^2 + \omega_{jk} \text{start}_i^2 + \varepsilon_{ijk}, \quad (9-13)$$

kde $\varepsilon_{ijk} \sim N(0, \sigma^2)$, nezávisle pro jednotlivá měření.

```
> m2 <- lm(log(weight) ~ diet*sex*poly(start,2))
```

```
> anova(m1, m2)
```

Analysis of Variance Table

Model 1: log(weight) ~ diet * sex * start

Model 2: log(weight) ~ diet * sex * poly(start, 2)

	Res.Df	RSS	Df	Sum of Sq	F	Pr(>F)
1	65	1.7433				
2	55	1.4122	10	0.33113	1.2896	0.2592

```
> anova(m3)
```

Analysis of Variance Table

Response: log(weight)

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
diet	4	16.1349	4.0337	144.4941	<2e-16	***
sex	1	0.0261	0.0261	0.9350	0.3369	
start	1	0.0455	0.0455	1.6290	0.2061	
diet:sex	4	0.0866	0.0217	0.7756	0.5448	
diet:start	4	0.0244	0.0061	0.2183	0.9274	
sex:start	1	0.0315	0.0315	1.1282	0.2919	
Residuals	69	1.9262	0.0279			

```
> summary(m8)
```

```
Call:
```

```
lm(formula = log(weight) ~ diet)
```

```
Residuals:
```

	Min	1Q	Median	3Q	Max
	-0.33311	-0.09764	-0.02934	0.11146	0.41505

```
Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	-0.05319	0.03967	-1.341	0.184	
dietlipid1	0.55181	0.05610	9.836	2.02e-15	***
dietlipid2	0.52190	0.05610	9.303	2.23e-14	***
dietprotein1	1.17298	0.05610	20.908	< 2e-16	***
dietprotein2	1.12984	0.05610	20.139	< 2e-16	***

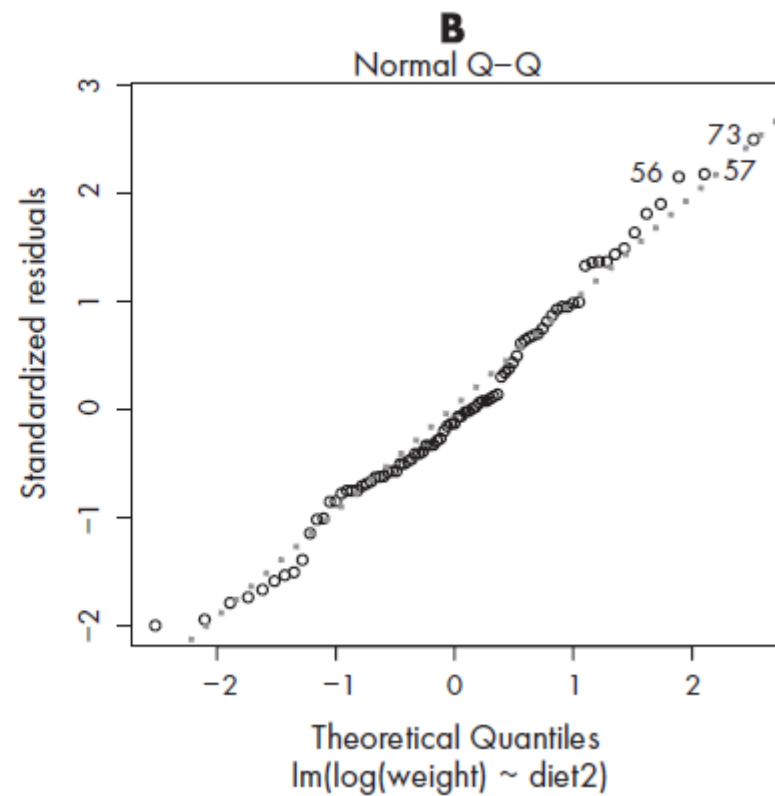
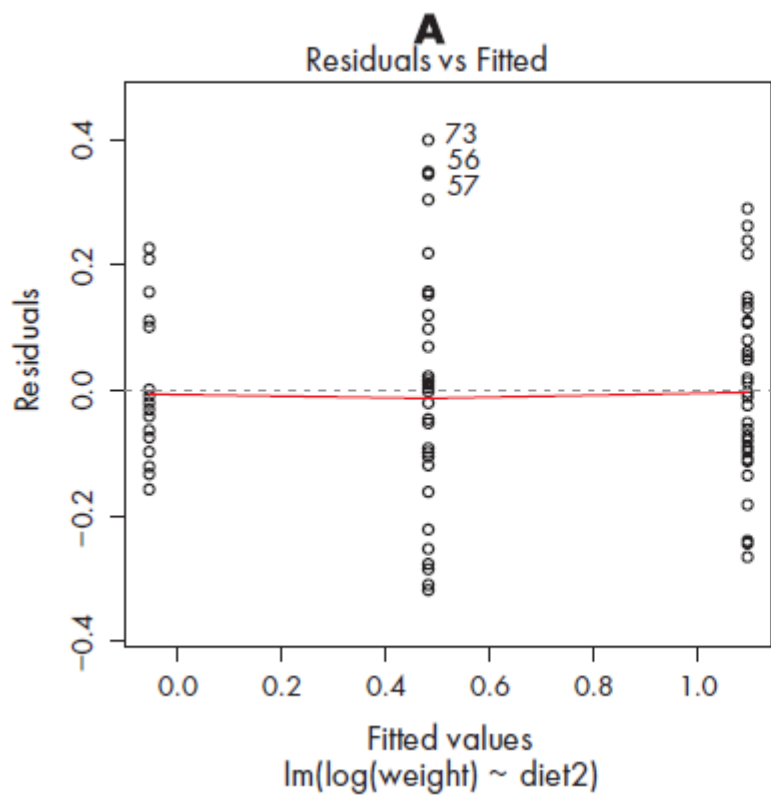
```
---
```

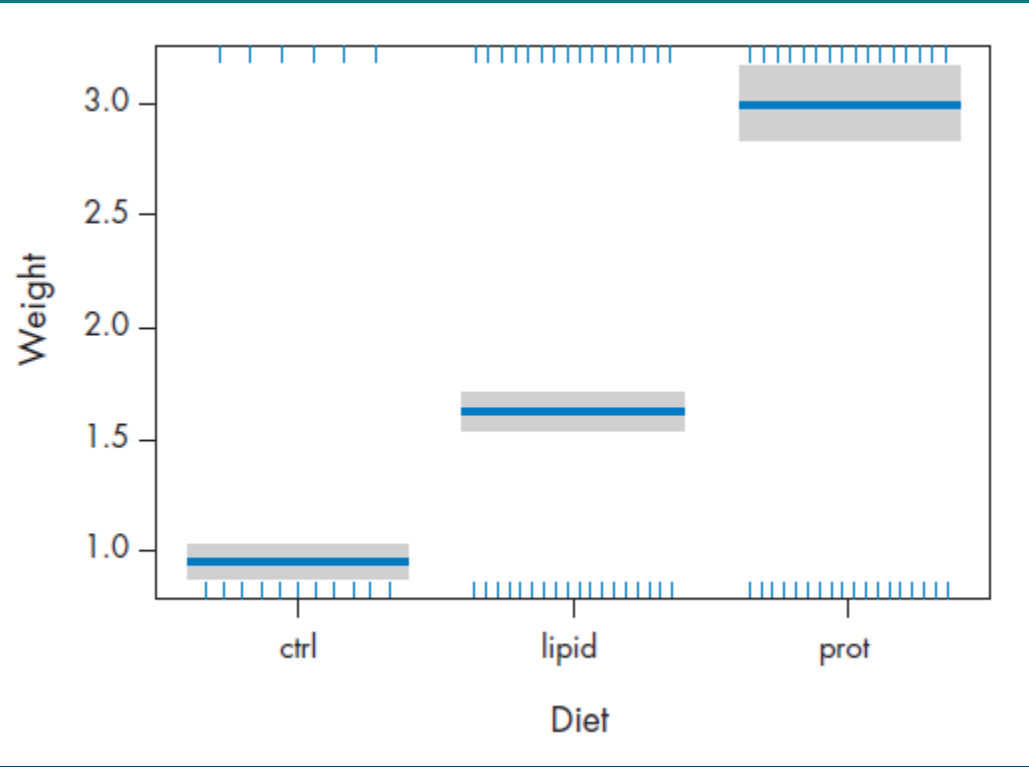
```
> summary(m9)
```

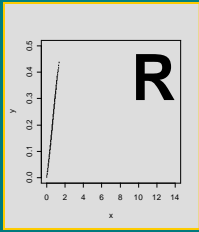
```
...
```

```
Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	-0.05319	0.03940	-1.35	0.181	
diet2lipid	0.53686	0.04825	11.13	<2e-16	***
diet2prot	1.15141	0.04825	23.86	<2e-16	***







Analyses

Analyses

*of counts *

Poisson distribution

- Poisson data arise when data are:
 - counts/frequencies of individuals, species, cells
 - events of behaviour, etc.
 - always positive integers
 - counts are often low (including 0)
- we count how many times an event occurred but we do not know how often it did not occur (we do not know n)
- moment: $E(y) = \mu = Var(y)$

Analytical methods

- χ^2 test (**chisq.test**) to analyse 2-dimension tables
- Fisher exact test (**fisher.test**) to analyse 2x2 tables
- Mantel-Haenszel test (**mantelhaen.test**) to analyse 3-dimension tables for independence
- Log-linear analysis (**loglin**) to study complex frequency tables
- Contingency tables (**xtabs**) to study effect of factors
- Standard regression (**lm**) can be used after transformation

- squareroot transformation

$$\sqrt{y}$$

- can predict values out of bounds (negative)

- Poisson GLM (**glm**) to study effect of both factorial and continuous predictors

Poisson model

- `glm(..., family = poisson(link=...))`

link functions:

- logarithmic (`log`)
- squareroot (`sqrt`)
- identity (`identity`)

- estimated parameters are on logarithmic scale $(-\infty, +\infty)$

- inverse function to log is exp

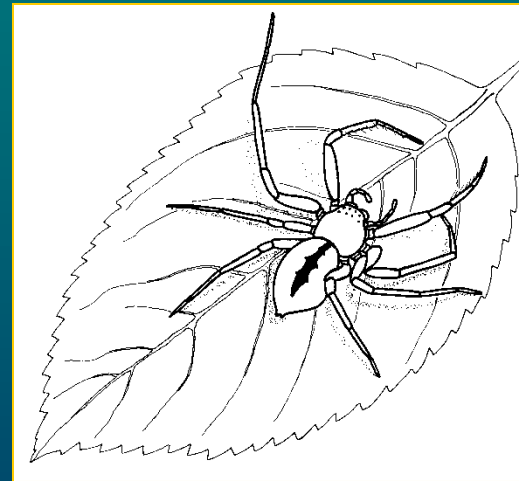
e^{θ}

1-way ANOVA

Background

Diversity of organisms changes with the age of the habitat.

According to the intermediate disturbance hypothesis, the diversity increases and then decreases with age, thus being highest at medium age.



Design

In 15 apple orchards diversity of arachnids was studied on trees. The orchards were of variable age, classified into 3 classes: 0-9, 10-19 and 20-30 years old. Each class was represented by 5 orchards.

Hypotheses

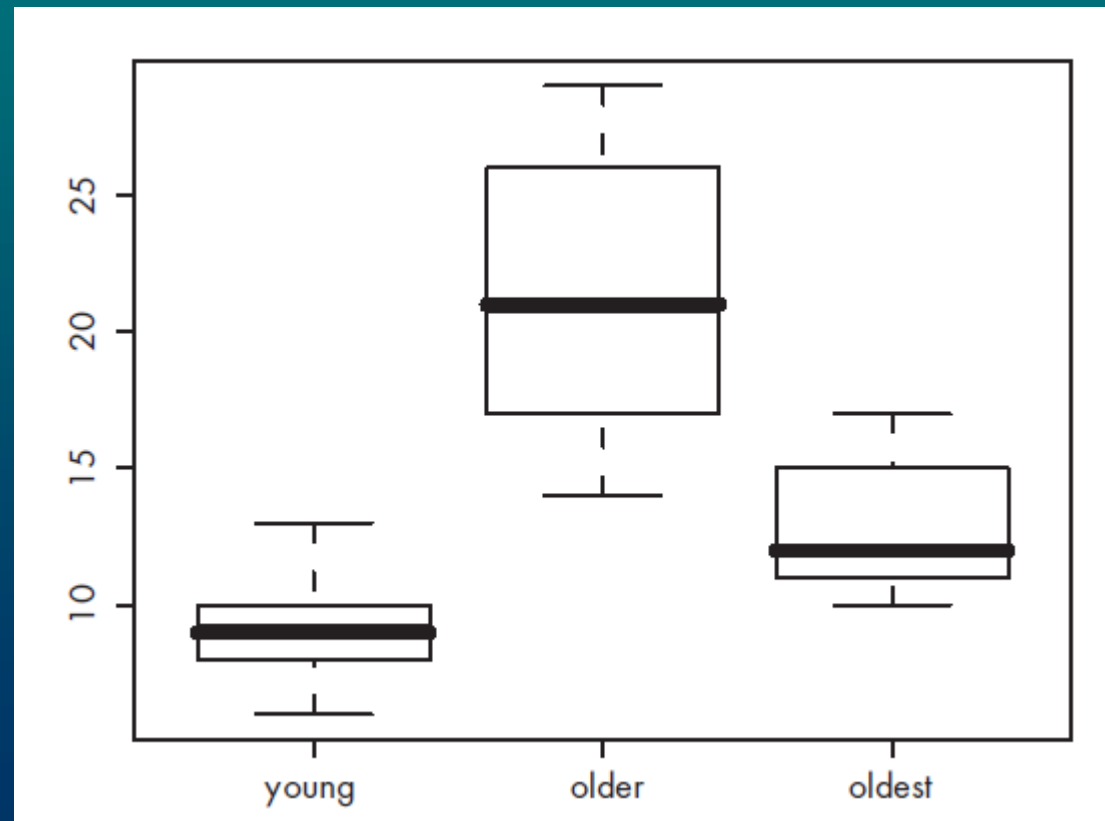
Is diversity related to the age of orchards?

What is the trend of change?

Variables

ORCHARD: young, older, oldest

divers



$$\log(\mu_j) = \alpha + ORCHARD_j,$$

kde $divers_j \sim Poi(\mu_j)$, nezávisle pro jednotlivé sady.

```
> m1 <- glm(divers ~ orchard, family=poisson)
```

```
> anova(m1, test="Chi")
```

Analysis of Deviance Table

Model: poisson, link: log

Response: divers

Terms added sequentially (first to last)

	Df	Deviance	Resid. Df	Resid. Dev	P(> Chi)
NULL			14	38.964	
orchard	2	26.246	12	12.718	1.999e-06

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)	
(Intercept)	2.2192	0.1474	15.051	< 2e-16	***
orchardolder	0.8442	0.1763	4.788	1.68e-06	***
orchardoldest	0.3457	0.1927	1.794	0.0727	.

```
> contrasts(orchard) <- "contr.helmert"
> m2 <- glm(divers ~ orchard, family=poisson)
> summary(m2)
...
Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)  2.61585     0.07186  36.404 < 2e-16 ***
orchard1     0.42209     0.08815   4.788 1.68e-06 ***
orchard2    -0.02545     0.05072  -0.502  0.616
```

```
> orchard1 <- ordered(orchard)
> m3 <- glm(divers ~ orchard1, family=poisson)
```

```
> summary(m3)
...
Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)  2.61585     0.07186  36.404 < 2e-16 ***
orchard1.L   0.24448     0.13624   1.794  0.0727 .
orchard1.Q  -0.54813     0.11144  -4.919 8.71e-07 ***
```

```

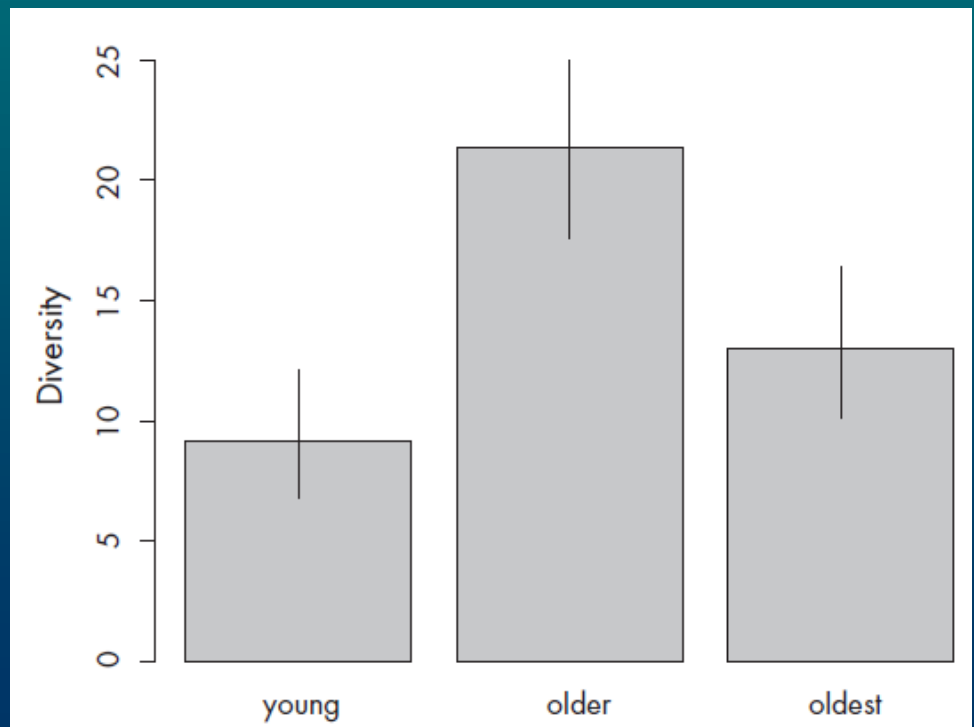
> m3 <- glm(divers ~ orchard - 1, poisson)
> summary(m3)
...
Coefficients:
              Estimate Std. Error z value Pr(>|z|)
orchardyoung    2.21920    0.14744   15.05  <2e-16 ***
orchardolder    3.06339    0.09667   31.69  <2e-16 ***
orchardoldest   2.56495    0.12403   20.68  <2e-16 ***

```

```

> exp(confint(m3))
Waiting for profiling to be done...
              2.5%      97.5%
orchardyoung   6.790864 12.12010
orchardolder  17.597063 25.71441
orchardoldest 10.090235 16.42096

```



Over- / under-dispersion

- arises when dispersion parameter φ $\varphi = \text{Var}(y)/\text{E}(y) \neq 1$

i.e. the residual deviance is not similar to the residual degrees of freedom

$$E(y) = \text{Var}(y) = \mu$$

- overdispersion: variance is larger $\rightarrow \varphi > 1$
- underdispersion: variance is smaller $\rightarrow \varphi < 1$

- causes:

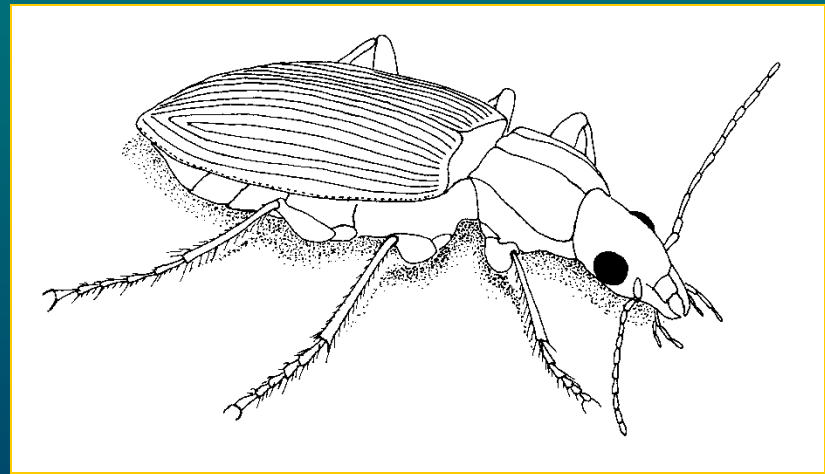
- if the distribution is aggregated
- if counts are not independent
- lack of important variables, etc.
- suspicious data

- solution: use **quasipoisson** family
- this will influence SE of parameter estimates
 - if $\varphi > 1$ then SE will be larger
 - if $\varphi < 1$ then SE will be smaller
- without correction for overdispersion there would be too many false positive results (in favour of H_A)
- when using **quasipoisson** χ^2 - and z- tests have to change to F- and t- tests

Multiple Regression

Background

Abundance of carabid beetles in cereals depends on abiotic and biotic factors. If we understand how abiotic factors influence abundance of carabids then we can adapt certain management practices to increase the abundance when needed.



Design

In the field, on 21 wheat plots the abundance of carabid beetles was studied by means of pitfall traps. At every site average day temperature [$^{\circ}\text{C}$] and average sun activity [W/m^2] was recorded.

Hypotheses

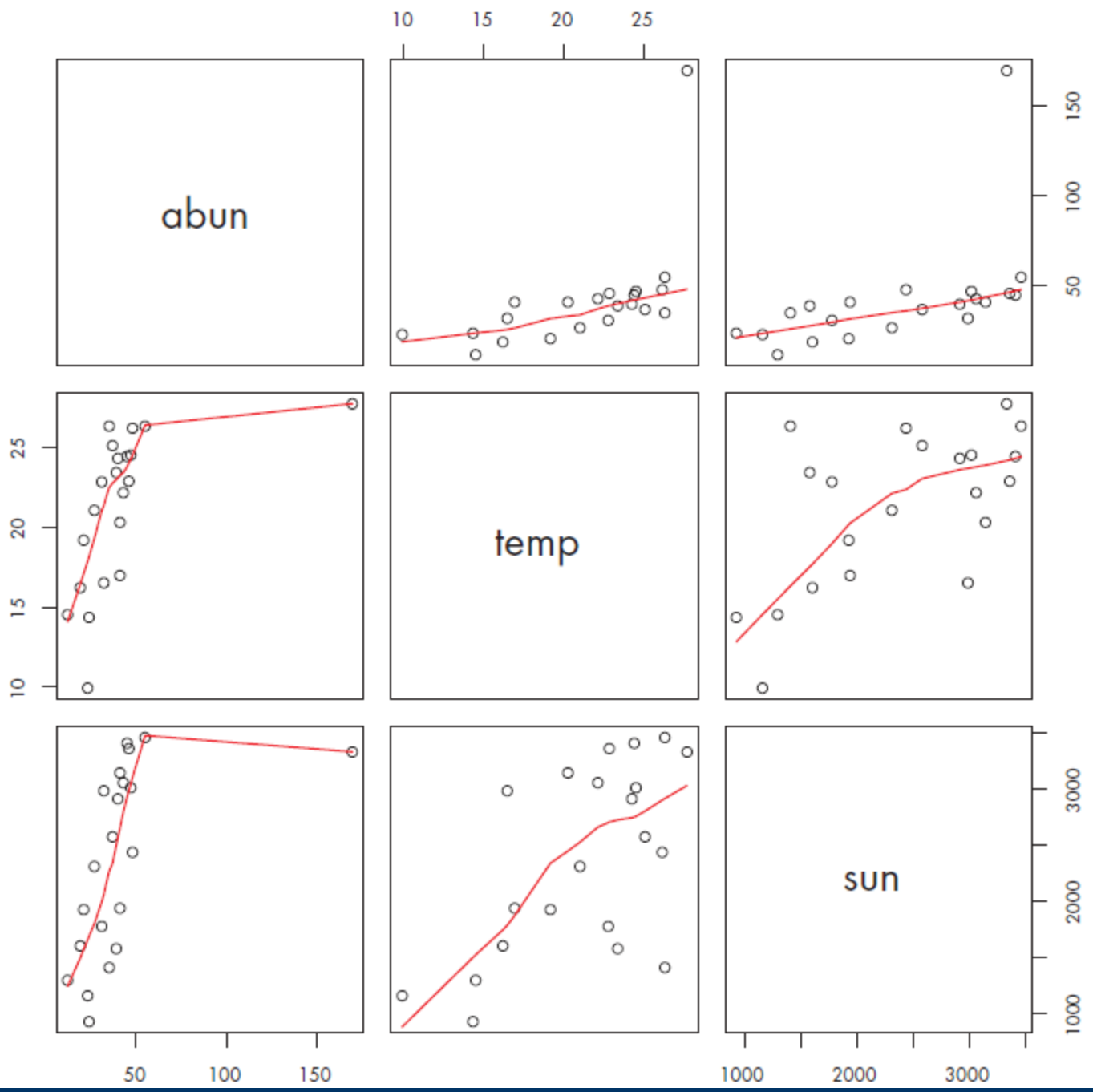
Was abundance of beetles affected by any of the two variables?
If so what is the model of the relationship?

Variables

temp

sun

abun



$$\log(\mu_i) = \alpha + \beta_1 \text{temp}_i + \beta_2 \text{sun}_i + \delta \text{temp}_i \text{sun}_i,$$

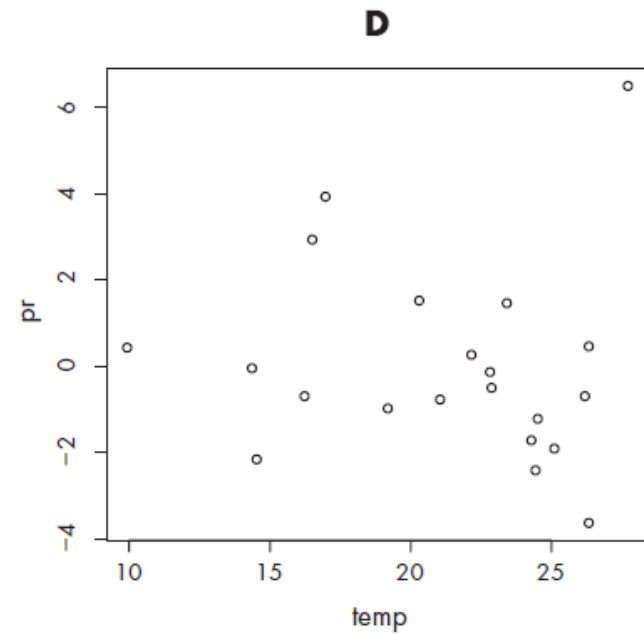
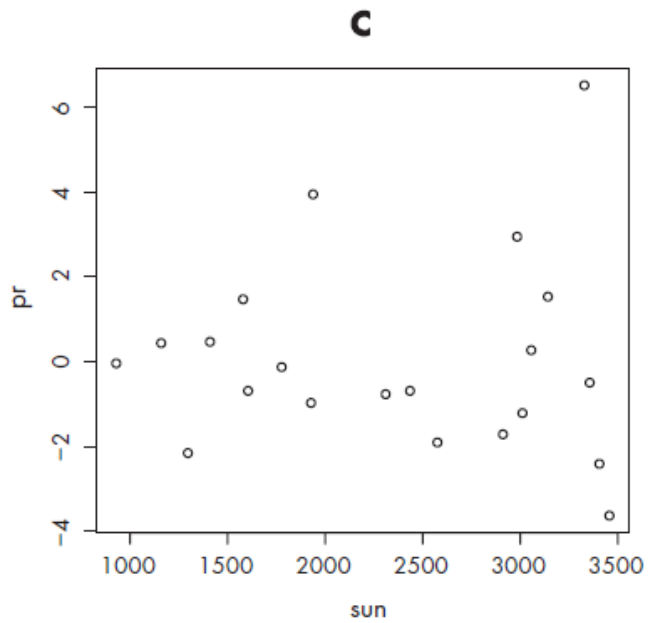
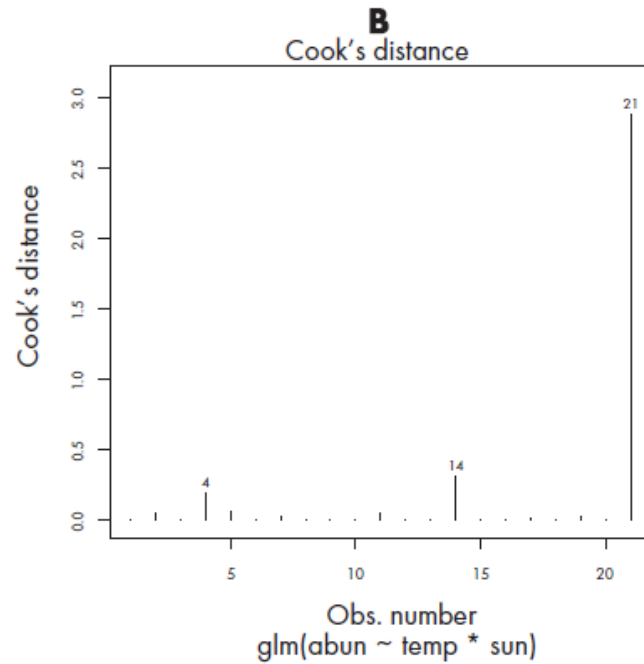
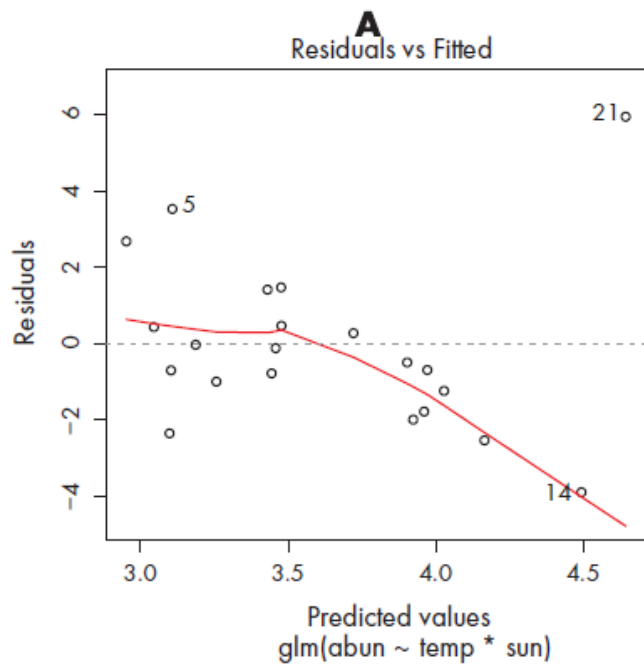
kde $abun_i \sim \text{Poi}(\mu_i)$, nezávisle pro jednotlivé porosty.

```
> m1 <- glm(abun ~ temp*sun, family=poisson)
> summary(m1)
...
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  4.195e+00  4.745e-01   8.840 < 2e-16 ***
temp         -5.386e-02  2.258e-02  -2.385  0.0171 *
sun          -1.151e-03  2.364e-04  -4.869 1.12e-06 ***
temp:sun      6.257e-05  1.006e-05   6.221 4.95e-10 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 317.229  on 20  degrees of freedom
Residual deviance:  98.657  on 17  degrees of freedom

> m2 <- update(m1, family=quasipoisson)
> anova(m2, test="F")
...
      Df Deviance Resid. Df Resid. Dev      F    Pr(>F)
NULL                20      317.23
temp                1      153.10    19      164.12 24.5836 0.0001196 ***
sun                 1       27.90    18      136.23  4.4796 0.0493541 *
temp:sun            1       37.57    17       98.66  6.0324 0.0251002 *
---
```



```

> m3 <- glm(abun ~ temp*sun, poisson, subset=-21)
> anova(m3, test="Chi")
...
      Df Deviance Resid. Df Resid. Dev P(>|Chi|)
NULL                19      75.292
temp      1    40.291      18      35.001 2.188e-10
sun       1    12.165      17      22.836 4.870e-04
temp:sun  1     0.117      16      22.719    0.732
> m4 <- update(m3, ~.-temp:sun)
> anova(m4, test="Chi")
...
      Df Deviance Resid. Df Resid. Dev P(>|Chi|)
NULL                19      75.292
temp      1    40.291      18      35.001 2.188e-10
sun       1    12.165      17      22.836 4.870e-04

```

```

> library(car)
> Anova(m4)
Analysis of Deviance Table (Type II tests)

Response: abun
      LR Chisq Df Pr(>Chisq)
temp  12.567  1  0.0003926 ***
sun   12.165  1  0.0004870 ***
---

```

```
> vif(m4)
      temp      sun
1.325588 1.325588
```

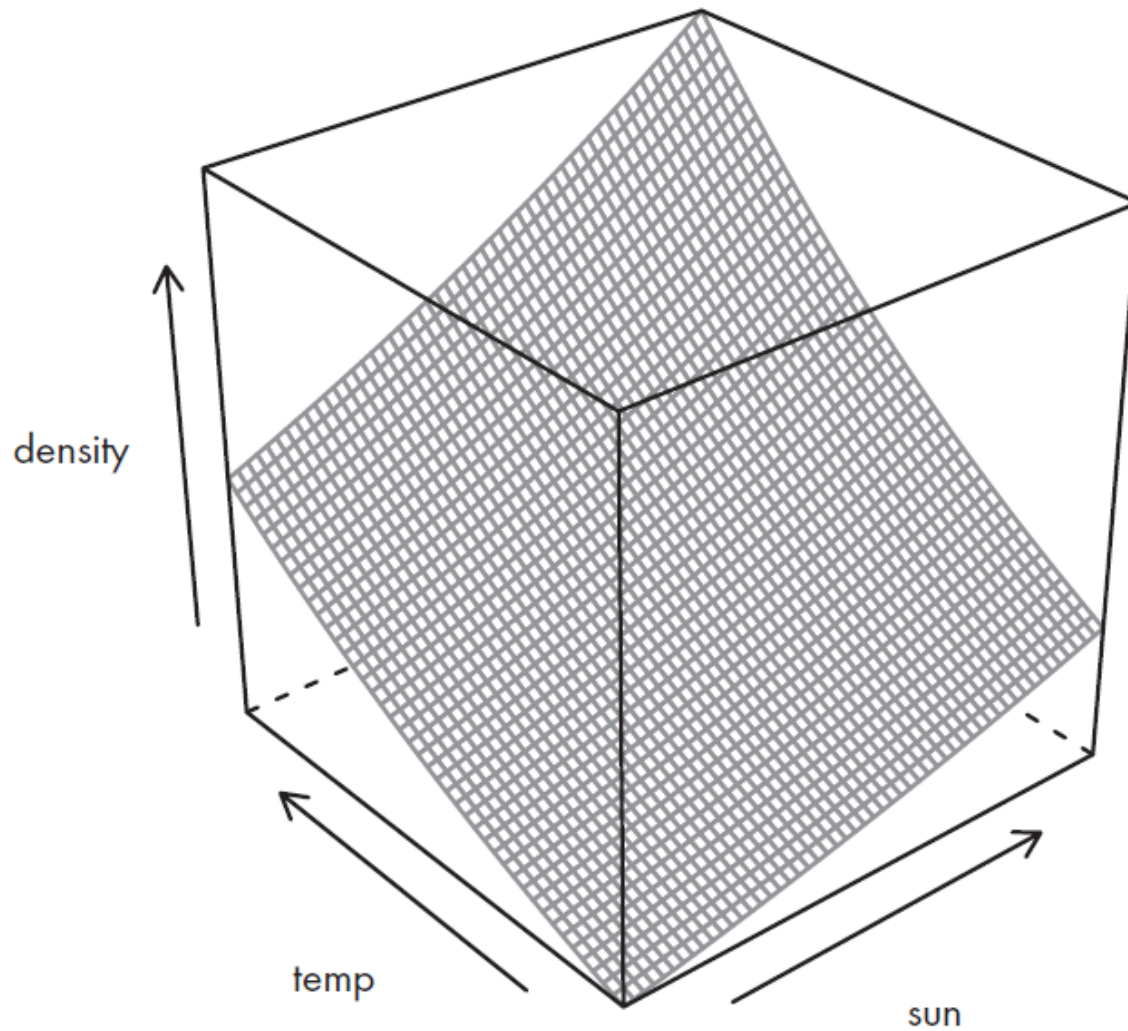
```
> summary(m4)
```

```
...
Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept) 2.283e+00  2.088e-01  10.933  < 2e-16 ***
temp         3.781e-02  1.070e-02   3.534 0.000409 ***
sun          1.954e-04  5.655e-05   3.455 0.000550 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 75.292  on 19  degrees of freedom
Residual deviance: 22.836  on 17  degrees of freedom
AIC: 135.76
```

```
> (75.292-22.836)/75.292
[1] 0.6967008
```

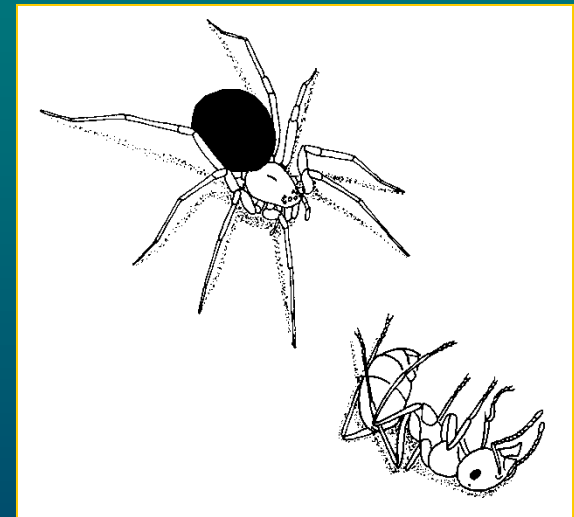


$$\exp(2.283 + 0.038sun + 0.0002temp).$$

1-way ANCOVA

Background

Some spiders are specialised in their diet. Specialisation can involve evolution of physiological and behavioural traits, such as prey-specific venom and number of attacks.



Design

In the lab, the number of attacks of an ant-eating spider on ants of two subfamilies was observed. For each subfamily 20 species of ants were used. Each ant species was tested once. For each ant body size was recorded as it may influence its susceptibility to venom.

Hypotheses

Was the number of attack related to ant size?

Was the number of attacks similar for ants of both subfamilies?

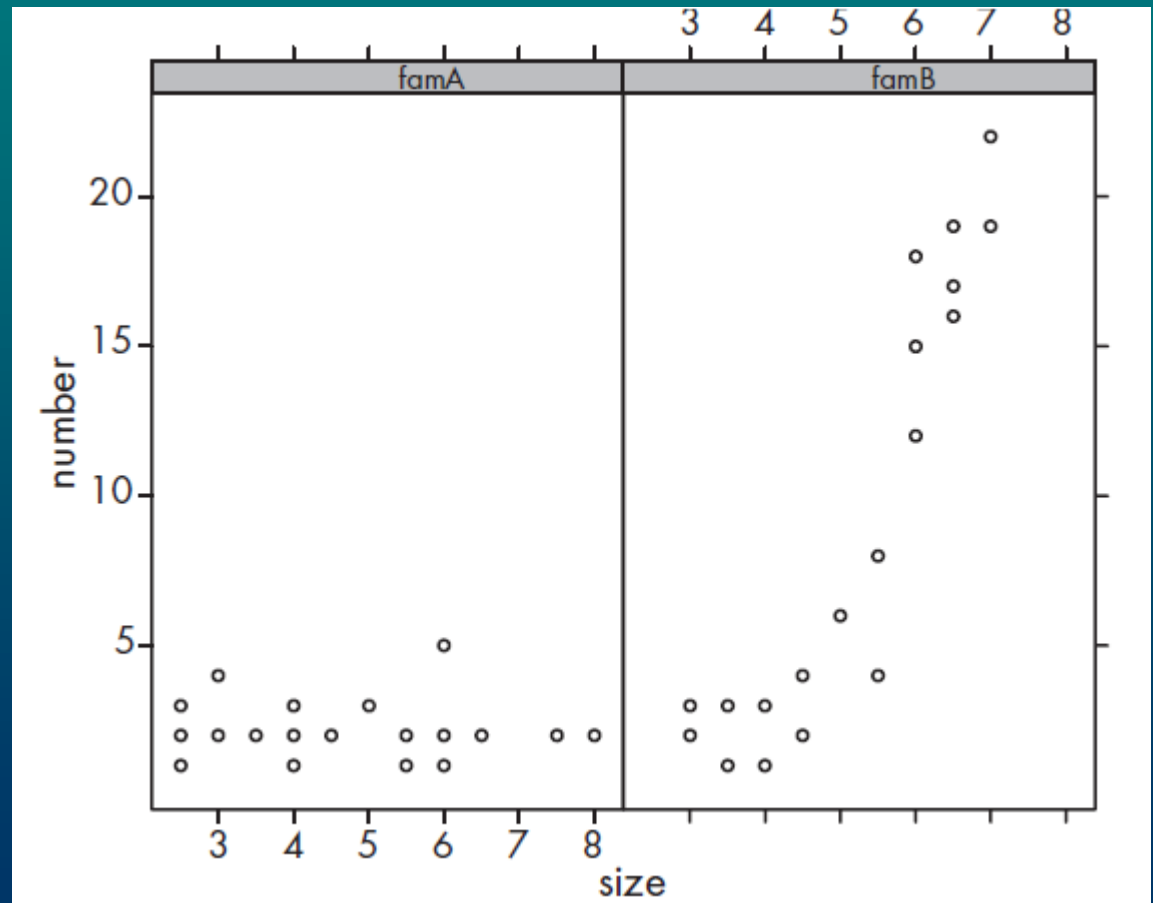
What is the shape of the relationship?

Variables

ANT: famA, famB

size

number



$$\log(\mu_{ij}) = \alpha + ANT_j + \beta size_i + \delta_j size_i,$$

kde $number_{ij} \sim Poi(\mu_{ij})$, nezávisle pro jednotlivá pozorování.

```
> m1 <- glm(number ~ size*ant, family=poisson)
> anova(m1, test="Chi")
...
      Df Deviance Resid. Df Resid. Dev P(>|Chi|)
NULL           39      215.561
size           1       93.395      38      122.167 4.284e-22
ant            1       75.555      37       46.612 3.554e-18
size:ant       1       25.804      36       20.808 3.779e-07
```

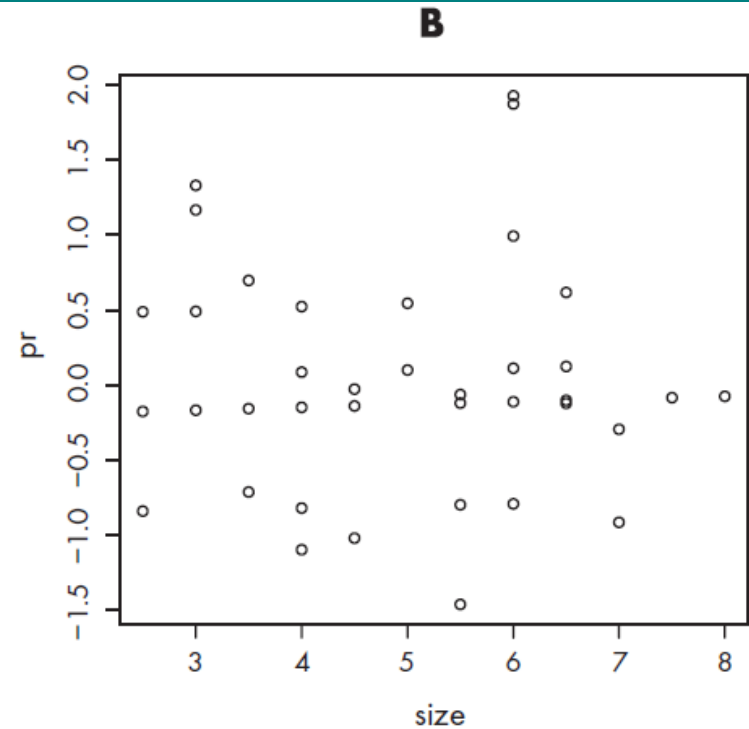
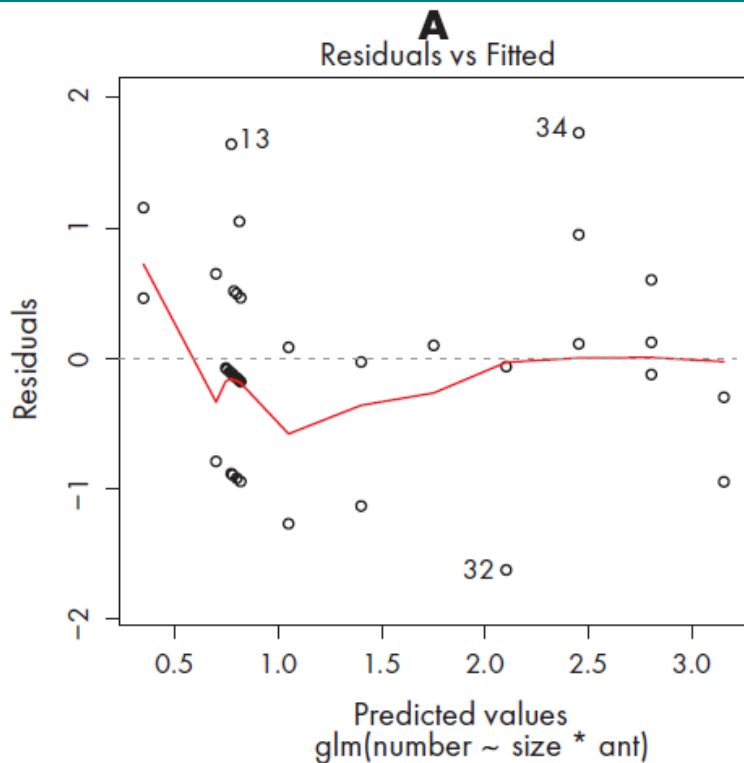
```

> summary(m1)
...
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  0.89794    0.64904   1.383 0.166512
size        -0.02154    0.12456  -0.173 0.862735
antfamB     -2.66924    0.80637  -3.310 0.000932 ***
size:antfamB  0.70407    0.14579   4.829 1.37e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 215.561  on 39  degrees of freedom
Residual deviance:  20.808  on 36  degrees of freedom
AIC: 153.15

```



```
> m2 <- glm(number ~ poly(size,2)*ant, poisson)
```

```
> anova(m1, m2, test="Chi")
```

Analysis of Deviance Table

Model 1: number ~ size * ant

Model 2: number ~ poly(size, 2) * ant

	Resid. Df	Resid. Dev	Df	Deviance	P(> Chi)
1	36	20.8084			
2	34	20.7673	2	0.0411	0.9797

$$\sqrt{\text{number}_i} = \alpha + \beta \text{size}_i + \gamma \text{size}_i^2 + \varepsilon_i,$$

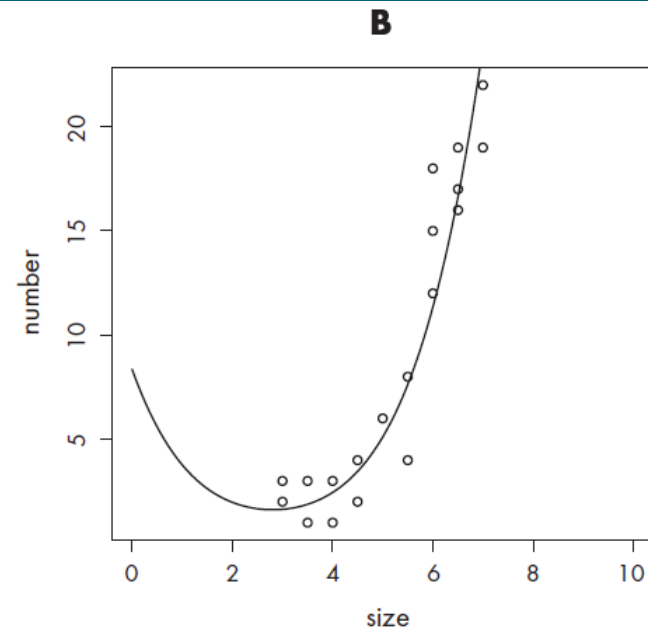
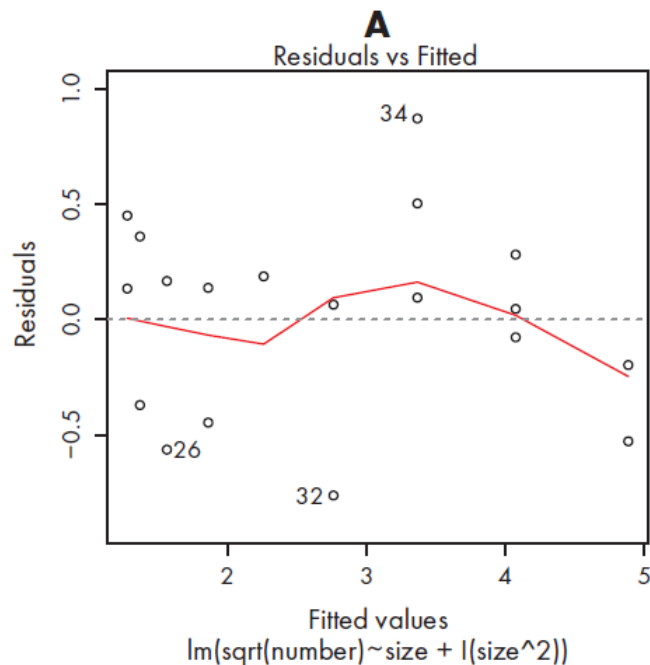
kde $\varepsilon_i \sim N(0, \sigma^2)$, nezávisle pro jednotlivá pozorování.

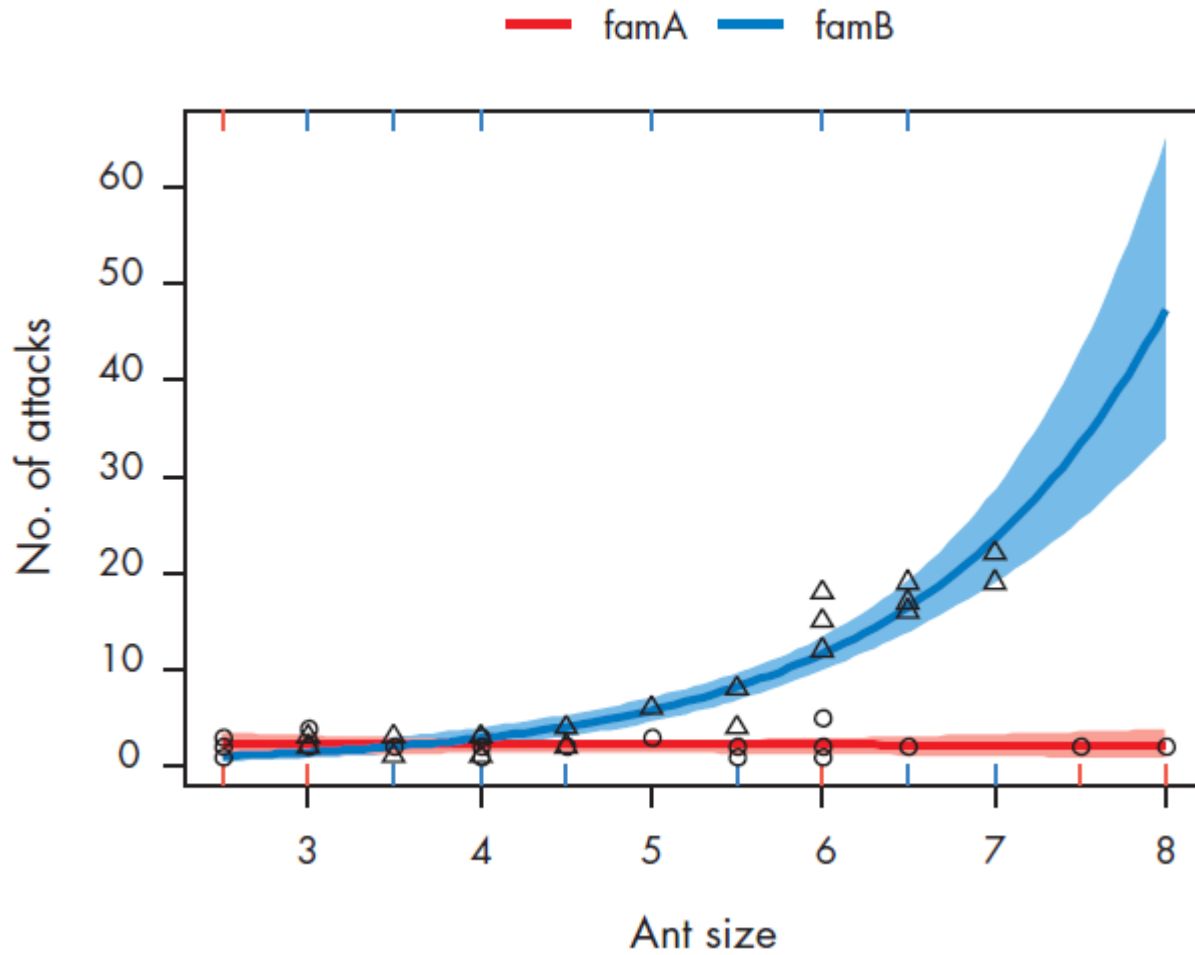
```
> m3 <- lm(sqrt(number) ~ size + I(size^2), subset=(ant=="famB"))
> anova(m3)
```

Analysis of Variance Table

Response: sqrt(number)

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
size	1	28.3476	28.3476	161.0631	4.253e-10	***
I(size^2)	1	1.1930	1.1930	6.7783	0.01855	*
Residuals	17	2.9921	0.1760			





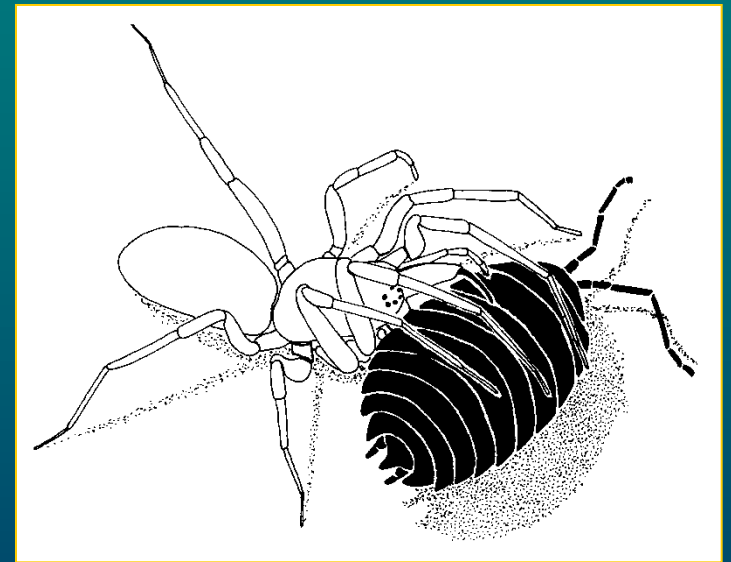
$$number = e^{-1.77 + 0.68size}$$

$$number = e^{0.89}$$

3-way ANOVA

Background

Some predators use conditional strategies to catch prey. The use of strategy often depends on the characteristics of prey.



Design

In the field, it was observed which of three strategies spiders used to capture prey. For each trial, size (two size classes) and movement (slow or fast) of prey was recorded. Altogether 88 trials were observed.

Hypotheses

Is use of strategy influenced by prey size and its movement?

If so which prey is captured by strategy A, B and C?

Variables

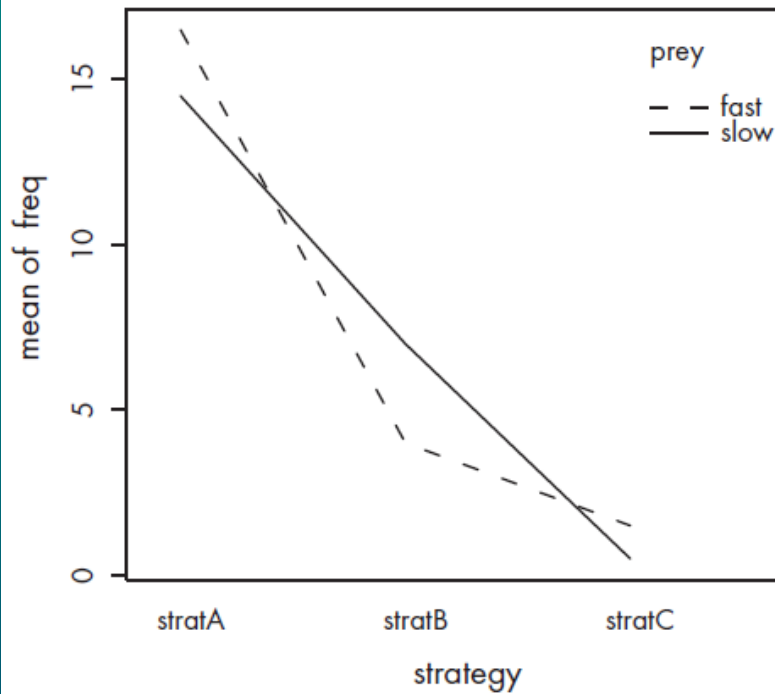
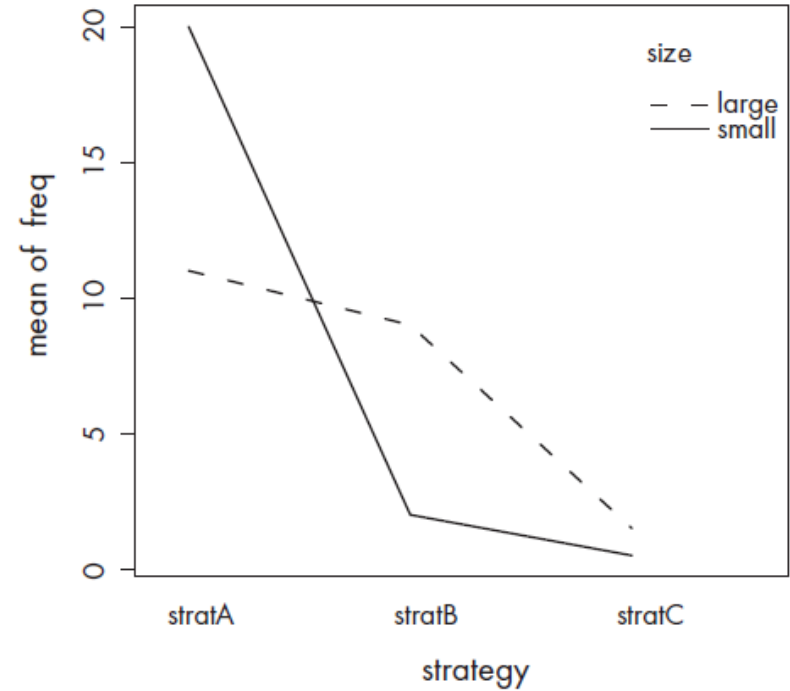
PREY: fast, slow

SIZE: large, small

STRATEGY: stratA, stratB, stratC

freq

	slow		fast	
	small	large	small	large
stratA	19	10	21	12
stratB	4	10	0	8
stratC	0	1	1	2

A**B**

$$\log(\mu_{ijk}) = \alpha + STRATEGY_i + SIZE_j + PREY_k + STRATEGY:PREY_{ik} +$$

$$STRATEGY:SIZE_{ij} + SIZE:PREY_{jk} + STRATEGY:SIZE:PREY_{ijk},$$
 kde $freq_{ijk} \sim Poi(\mu_{ijk})$, nezávisle pro jednotlivá pozorování.

```
> m1 <- glm(freq ~ strategy*size*prey, family=poisson)
> summary(m1)
```

Call:

```
glm(formula = freq ~ strategy * size * prey, family = poisson)
```

Deviance Residuals:

```
[1] 0 0 0 0 0 0 0 0 0 0 0 0 0
```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.485e+00	2.887e-01	8.608	<2e-16
strategystratB	-4.055e-01	4.564e-01	-0.888	0.3744
strategystratC	-1.792e+00	7.638e-01	-2.346	0.0190
sizesmall	5.596e-01	3.619e-01	1.546	0.1220
preyslow	-1.823e-01	4.282e-01	-0.426	0.6702
strategystratB:sizesmall	-2.594e+01	6.965e+04	-0.000372	0.9997
strategystratC:sizesmall	-1.253e+00	1.277e+00	-0.981	0.3266
strategystratB:preyslow	4.055e-01	6.390e-01	0.635	0.5257
strategystratC:preyslow	-5.108e-01	1.297e+00	-0.394	0.6938
sizesmall:preyslow	8.224e-02	5.325e-01	0.154	0.8773
strategystratB:sizesmall:preyslow	2.438e+01	6.965e+04	0.000350	0.9997
strategystratC:sizesmall:preyslow	-2.269e+01	6.965e+04	-0.000326	0.9997

```
> anova(m1, test="Chi")
```

```
...
```

	Df	Deviance	Resid.	Df	Resid. Dev	P(> Chi)
NULL				11	87.966	
strategy	2	64.205		9	23.761	1.143e-14
size	1	0.045		8	23.715	0.831
prey	1	0.000		7	23.715	1.000
strategy:size	2	15.939		5	7.776	3.458e-04
strategy:prey	2	2.962		3	4.814	0.227
size:prey	1	0.507		2	4.307	0.476
strategy:size:prey	2	4.307		0	3.033e-10	0.116

```
> m2 <- update(m1, ~.-strategy:size:prey)
```

```
> anova(m2, test="Chi")
```

```
...
```

	Df	Deviance	Resid.	Df	Resid. Dev	P(> Chi)
NULL				11	87.966	
strategy	2	64.205		9	23.761	1.143e-14
size	1	0.045		8	23.715	0.831
prey	1	0.000		7	23.715	1.000
strategy:size	2	15.939		5	7.776	3.458e-04
strategy:prey	2	2.962		3	4.814	0.227
size:prey	1	0.507		2	4.307	0.476

```
> m3 <- update(m2, ~.-strategy:prey)
```

```
> anova(m3, test="Chi")
```

```
...
```

	Df	Deviance	Resid.	Df	Resid. Dev	P(> Chi)
NULL				11	87.966	
strategy	2	64.205		9	23.761	1.143e-14
size	1	0.045		8	23.715	0.831
prey	1	0.000		7	23.715	1.000
strategy:size	2	15.939		5	7.776	3.458e-04
size:prey	1	0.045		4	7.731	0.831

```
> summary(m3)
```

```
Call:
```

```
glm(formula = freq ~ strategy + size + prey + strategy:size +  
     size:prey, family = poisson)
```

```
Deviance Residuals:
```

1	2	3	4	5	6	7
-0.3233	1.2076	-1.0111	-0.2297	0.3990	-0.4079	0.3227
8	9	10	11	12		
-1.9777	0.6395	0.2194	-0.4077	0.3585		

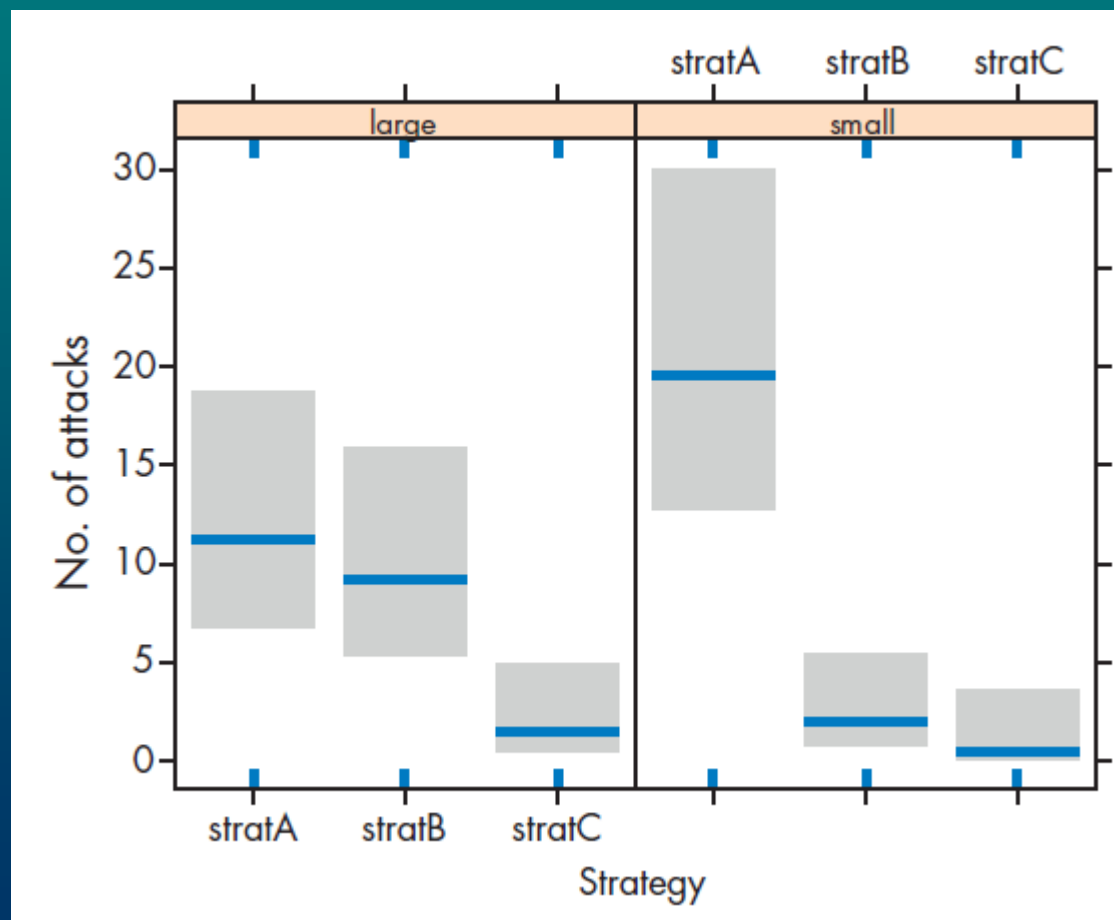
```
Coefficients:
```

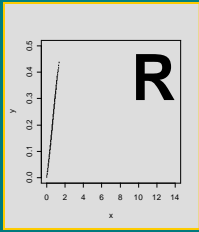
	Estimate	Std. Error	z value	Pr(> z)	
(Intercept)	2.42088	0.26010	9.307	< 2e-16	***
strategystratB	-0.20067	0.31782	-0.631	0.527782	
strategystratC	-1.99243	0.61546	-3.237	0.001207	**
sizesmall	0.55237	0.34042	1.623	0.104669	
preyslow	-0.04652	0.30508	-0.152	0.878805	
strategystratB:sizesmall	-2.10191	0.61318	-3.428	0.000608	***
strategystratC:sizesmall	-1.69645	1.18481	-1.432	0.152193	
sizesmall:preyslow	0.09097	0.42662	0.213	0.831142	

```
> attacks <- tapply(predict(m3,type="response"), list(size,strategy), mean)
```

```
> attacks
```

	stratA	stratB	stratC
large	11	9	1.5
small	20	2	0.5





Analyses

Analyses

of counts **||**

Negative-binomial distribution

- NB is a parametric alternative to Poisson model with overdispersion
- distribution of y is strongly asymmetric with many zeros
- NB has two parameters, μ and θ
- moments:

$$E(y) = \mu$$

$$Var(y) = \mu + \frac{\mu^2}{\theta}$$

- θ is aggregation parameter $(0, \infty)$
- if $\theta \geq 1$.. random distribution, $\theta < 1$.. aggregated distribution

- θ can be estimated from

$$\hat{\theta} = \frac{\bar{y}^2}{s^2 - \bar{y}}$$

NB model

`glm.nb(formula)` from *MASS* library

- links:

`log` (default)

`sqrt`

`identity`

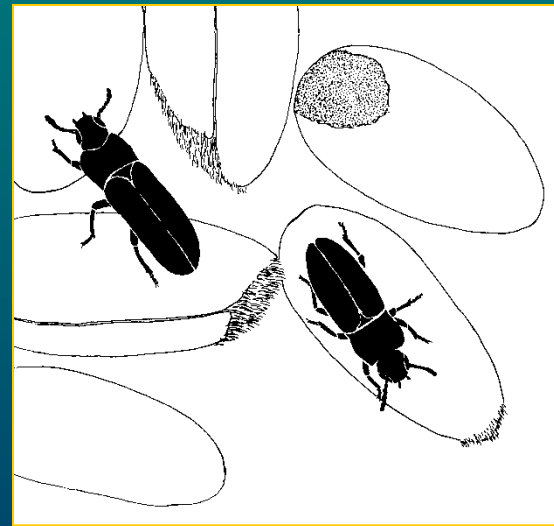
- begin with Poisson model, if overdispersion is large switch to

`glm.nb`

1-way ANOVA

Background

Grain beetles are serious pests in grain stores. They may occur not only in the grain but also in crevices of corridors. It is essential to know where they occur before control methods are applied.



Design

Density of grain beetles was surveyed in a grain store by means of sticky traps. Traps were installed in two places: 25 traps in the corridors and 25 traps in the grain. After few days number of beetles was recorded.

Hypotheses

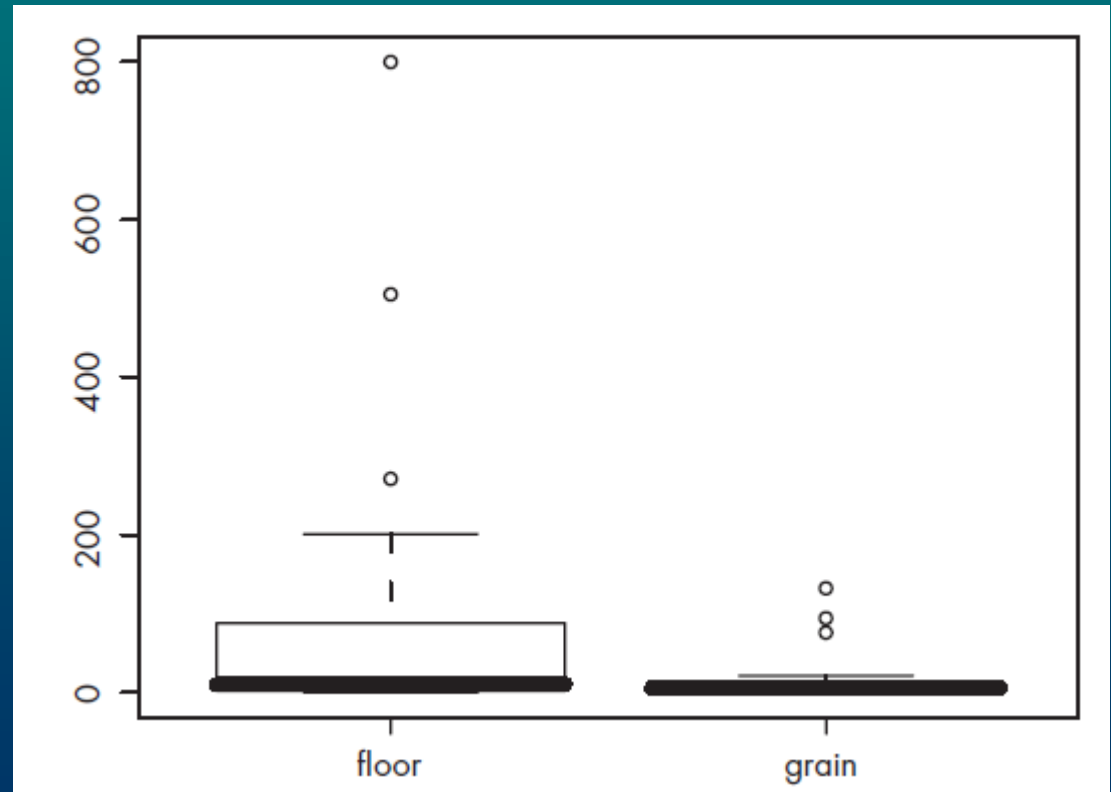
Is density of beetles similar on both places?

If not how different it is?

Variables

PLACE: floor, grain

density



$$\log(\mu_j) = \alpha + PLACE_j,$$

kde $density_j \sim Poi(\mu_j)$, nezávisle pro jednotlivé pasti.

```
> m1 <- glm(density ~ place, family=quasipoisson)
> anova(m1, test="F")
...
      Df Deviance Resid. Df Resid. Dev      F Pr(>F)
NULL           49      8026.5
place    1     1350.1       48     6676.4 6.0434 0.01762 *
---
```

```
> summary(m1)
...
Coefficients:
      Estimate Std. Error t value Pr(>|t|)
(Intercept)   4.5161     0.3125  14.45  <2e-16 ***
placegrain   -1.6280     0.7715  -2.11   0.0401 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for quasipoisson family taken to be 223.3983)
```

$$\log(\mu_j) = \alpha + PLACE_j,$$

kde $density_j \sim NB(\mu_j, \theta)$, nezávisle pro jednotlivé pasti.

```
> tapply(density, place, var)/tapply(density, place, mean)
      floor      grain
386.58096  60.20546
```

```
> tapply(density, place, function(x) mean(x)^2/(var(x)-mean(x)))
      floor      grain
0.2372524 0.3033504
```

```
> library(MASS)
> m2 <- glm.nb(density ~ place)
> anova(m2)
```

```
Analysis of Deviance Table
```

```
Model: Negative Binomial(0.3318), link: log
```

```
Response: density
```

```
Terms added sequentially (first to last)
```

	Df	Deviance	Resid.	Df	Resid.	Dev	P(> Chi)
NULL				49		70.174	
place	1	9.877		48		60.297	0.002

```
Warning message:
```

```
In anova.negbin(m2) : tests made without re-estimating 'theta'
```

```
> summary(m2)
```

```
Call:
```

```
glm.nb(formula = density ~ place, init.theta = 0.331844006124825,  
        link = log)
```

```
Coefficients:
```

	Estimate	Std. Error	z value	Pr(> z)	
(Intercept)	4.5161	0.3478	12.984	< 2e-16	***
placegrain	-1.6280	0.4937	-3.297	0.000976	***

```
---
```

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

```
(Dispersion parameter for Negative Binomial(0.3318) family taken to be 1)
```

```
Null deviance: 70.174  on 49  degrees of freedom  
Residual deviance: 60.297  on 48  degrees of freedom  
AIC: 430.95
```

```
Number of Fisher Scoring iterations: 1
```

```
Theta: 0.3318  
Std. Err.: 0.0610
```

```
2 x log-likelihood: -424.9480
```

```
> a <- split(x=density, f=place)
```

```
> m3 <- glm.nb(floor ~ 1)
```

```
> summary(m3)
```

```
...
```

```
Null deviance: 31.307 on 24 degrees of freedom
```

```
Residual deviance: 31.307 on 24 degrees of freedom
```

```
AIC: 245.47
```

```
Number of Fisher Scoring iterations: 1
```

```
Theta: 0.2915
```

```
Std. Err.: 0.0719
```

```
2 x log-likelihood: -241.4670
```



```
> m4 <- glm.nb(grain ~ 1)
> summary(m4)
...
Null deviance: 29.197 on 24 degrees of freedom
Residual deviance: 29.197 on 24 degrees of freedom
AIC: 186.78

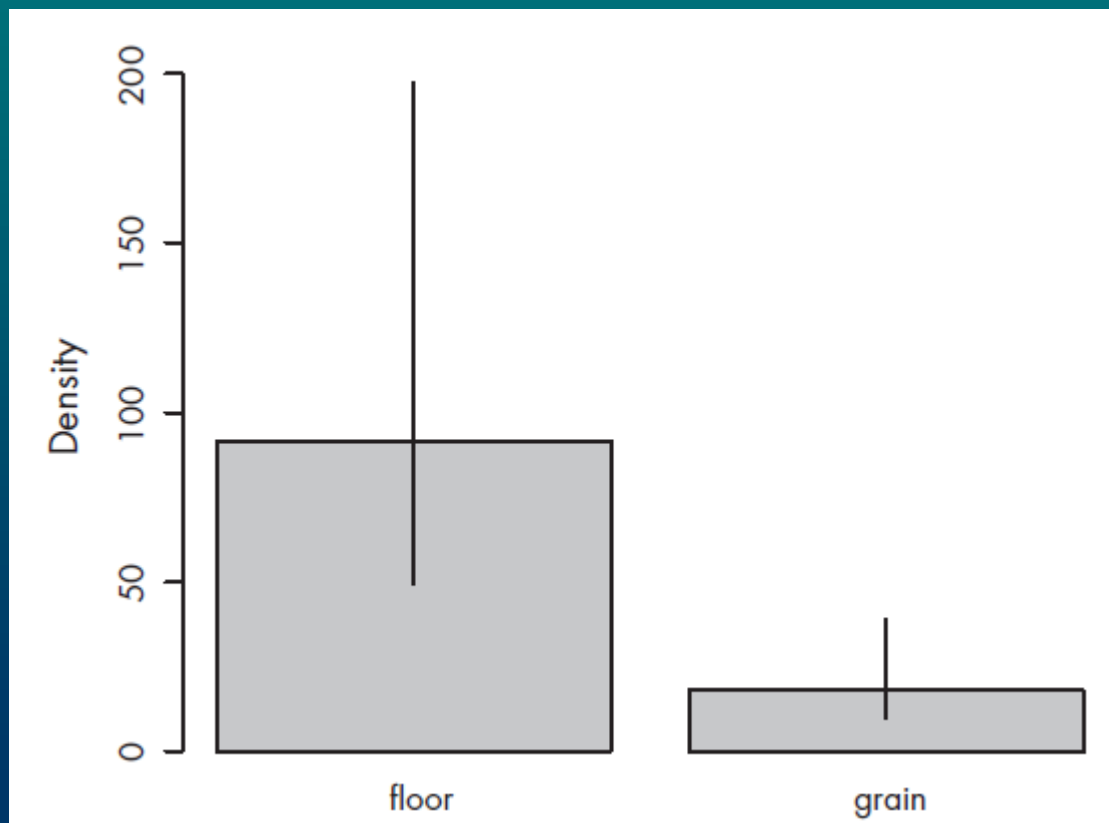
Number of Fisher Scoring iterations: 1

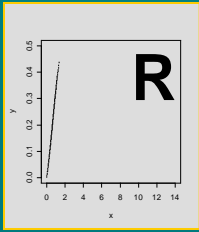
            Theta: 0.399
        Std. Err.: 0.111

2 x log-likelihood: -182.780
```

```
> 1-pchisq(0.701,1)
[1] 0.4024479
```

```
> m5 <- glm.nb(density ~ place-1)
> exp(confint(m5))
Waiting for profiling to be done...
              2.5%      97.5%
placefloor  49.57777 197.24605
placegrain   9.67290  38.87768
```





Analyses of *proportions*

Stano Pekár

Binomial distribution

■ Binomial data arise:

- when we count response to a certain stimulus → **dose-response studies**
- whenever we record whether an event has occurred or not within a known population (n)
- events: death, birth, germination, attack, consumption, reaction, etc.
- there are no classical replications - records are clustered to p or q
- p .. probability of successes, q .. probability of failures
- clustering of responses:

$$p = \frac{100}{200} + \frac{200}{300} = \frac{300}{500} = 0.6$$

~~$$p = \frac{0.5 + 0.667}{2} = 0.58$$~~

- distribution is bounded [$0 < p < 1$]
- variance is not constant, maximal when $p = q = 0.5$
- moments

$$E(y) = n\pi$$

$$Var(y) = n\pi(1 - \pi)$$

- estimated parameters are on logit scale $(-\infty, +\infty)$
- logistic model will always asymptote at 0 and 1

$$\log\left(\frac{p}{1-p}\right) = a + bx$$

- predicted values are then always within $[0, 1]$

- inverse function to logit is anti-logit where Q is a parameter estimate

$$\hat{y} = \frac{1}{1 + e^{-Q}}$$

- odds ratio

$$\frac{p}{1-p} = e^{-Q}$$

Analytical methods

- **Exact binomial test** (`binom.test`) to compare a single proportion
- **Proportion test** (`prop.test`) to compare two proportions
- **Contingency tables** (`xtabs`) to study effect of factors
- **Logistic regression** to study effect of continuous predictors
- **Standard regression** (`lm`) can be used after transformation
 - angular transformation $\arcsin \sqrt{p}$
 - can predict values out of bounds (negative or >1)
- **Binomial GLM** (`glm`) to study effect of both factorial and continuous predictors

Binomial model

• `glm(..., family = binomial(link=...))`

link functions:

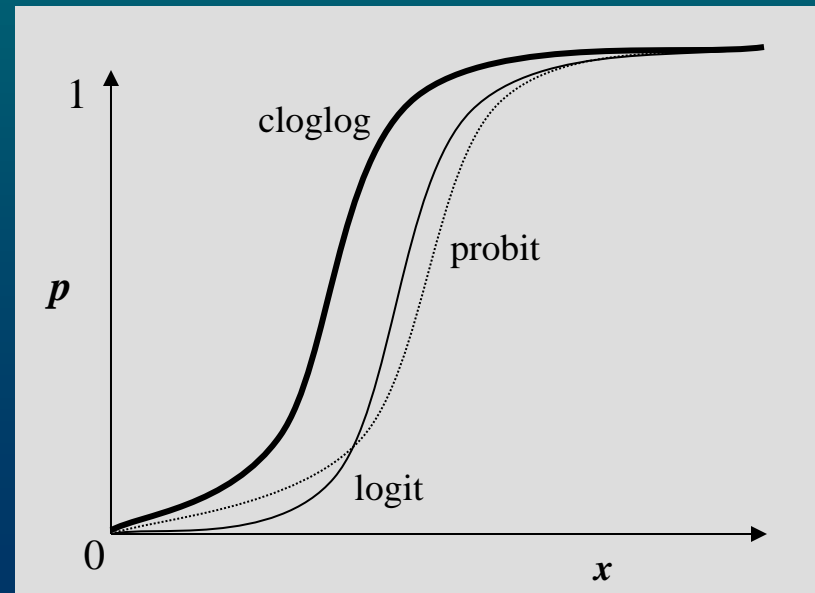
- logit (logit)

$$\log\left(\frac{p}{1-p}\right)$$

- probit (probit)

- complementary logit (cloglog)

$$\log(-\log(1-p))$$



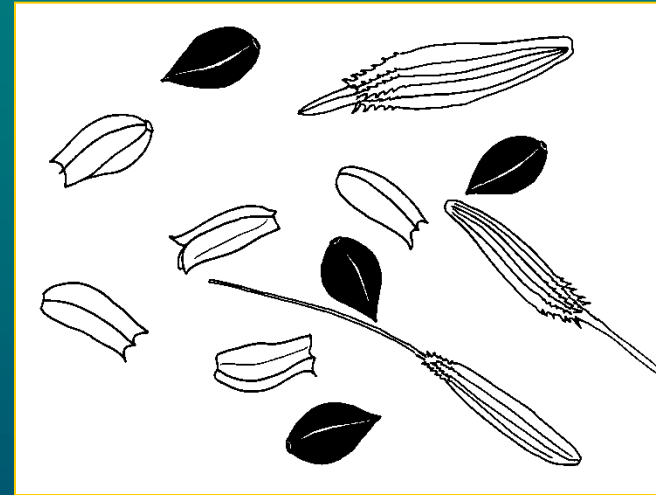
Data format:

- **Binomial distribution** ... individuals within a group are homogenous
 - two vectors $(y, n-y)$ or (y, n) of integers
- **Bernoulli (binary) distribution** ... individuals within a group are heterogenous, each characterised by a continuous character
 - $n = 1$
 - single vector of 0's or 1's

1-way ANOVA

Background

Some weed seeds may germinate following water priming (by rain) more than others thus attaining likely competitive advantage.



Design

The effect of water priming on the germination of weed seeds of 4 genera was studied in the laboratory. Each of 5 days 400 seeds of each genus were sown (200 seeds on control and 200 seeds on wet soil). Altogether 2000 seeds per genus were sown. Germination was recorded thereafter. Based on assumption of similar conditions during 5 days, data from 5 days were pooled.

Hypotheses

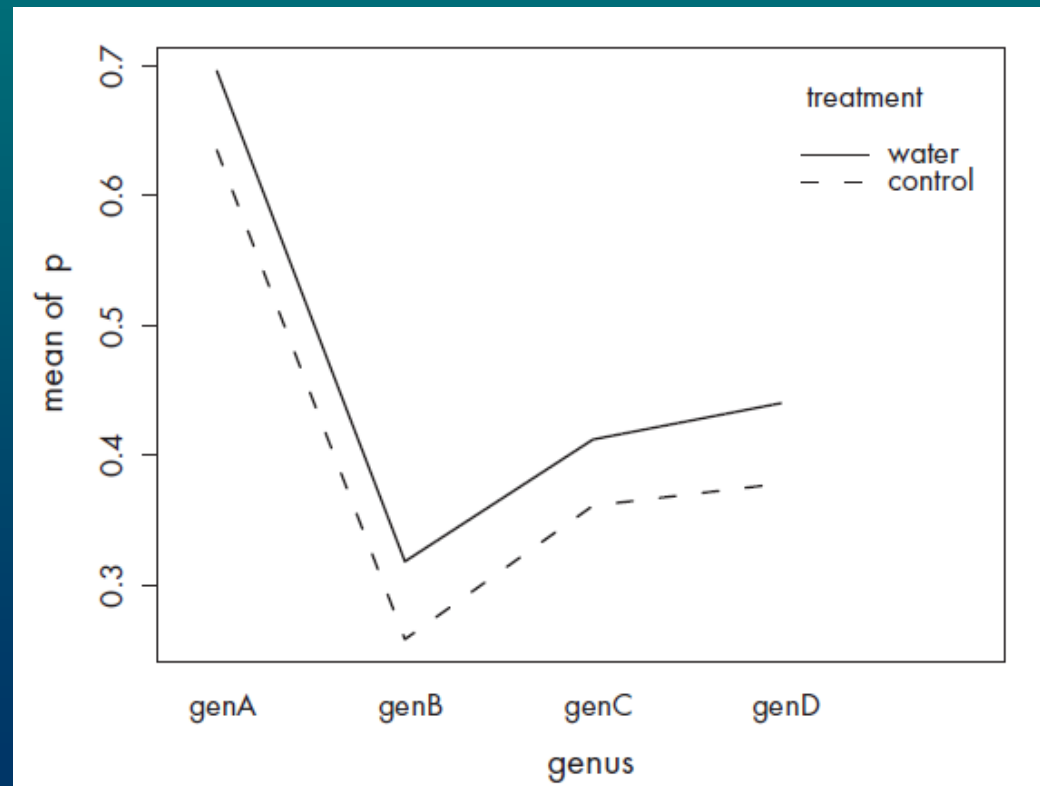
- Does water priming promote germination?
- If it does was the effect similar for all four genera?
- Which species germinated most and least?

Variables:

TREATMENT: control, water

GENUS: genA, genB,
genC, genD

germ
n



$$\log\left(\frac{\pi_{jk}}{1 - \pi_{jk}}\right) = \alpha + TREATMENT_j + GENUS_k + TREATMENT:GENUS_{jk},$$

kde $germ_{jk} \sim Bin(\pi_{jk}, n_{jk})$, nezávisle pro jednotlivé půdy.

```
> y <- cbind(germ, n-germ)
> m1 <- glm(y ~ genus*treatment, family=binomial)
> anova(m1, test="Chi")
```

Analysis of Deviance Table

Model: binomial, link: logit

Response: y

Terms added sequentially (first to last)

	Df	Deviance	Resid. Df	Resid. Dev	P(> Chi)
NULL			7	669.34	
genus	3	638.74	4	30.60	4.026e-138
treatment	1	30.23	3	0.37	3.840e-08
genus:treatment	3	0.37	0	1.212e-13	0.95

```
> m2 <- update(m1, ~.-genus:pesticide)
> summary(m2)
...
```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)	
(Intercept)	0.56138	0.05256	10.681	<2e-16	***
genusgenB	-1.59933	0.06860	-23.313	<2e-16	***
genusgenC	-1.15462	0.06614	-17.457	<2e-16	***
genusgenD	-1.06030	0.06583	-16.106	<2e-16	***
treatmentwater	0.25859	0.04710	5.491	4e-08	***

```
> 1/(1+ exp(-0.56138))
[1] 0.6367718
> 1/(1 + exp(-0.56138+1.59933))
[1] 0.2615457
```

```

> genus1 <- genus
> levels(genus1)
[1] "genA" "genB" "genC" "genD"
> levels(genus1)[3:4] <- "genCD"
> m3 <- glm(y ~ genus1 + treatment, binomial)
> anova(m2, m3, test="Chi")

```

Analysis of Deviance Table

Model 1: $y \sim \text{genus} + \text{treatment}$

Model 2: $y \sim \text{genus1} + \text{treatment}$

	Resid. Df	Resid. Dev	Df	Deviance	P(> Chi)
1	3	0.37316			
2	4	2.49523	-1	-2.12207	0.14519

```

> summary(m3)

```

...

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	0.56141	0.05256	10.68	< 2e-16 ***
genus1genB	-1.59933	0.06860	-23.31	< 2e-16 ***
genus1genCD	-1.10723	0.05749	-19.26	< 2e-16 ***
treatmentwater	0.25852	0.04709	5.49	4.02e-08 ***

```

> genus2 <- genus1
> levels(genus2)
[1] "genA" "genB" "genCD"
> levels(genus2)[2:3] <- "genBCD"
> m4 <- glm(y ~ genus2 + treatment, binomial)
> anova(m3, m4, test="Chi")

```

Analysis of Deviance Table

Model 1: y ~ genus1 + treatment

Model 2: y ~ genus2 + treatment

	Resid. Df	Resid. Dev	Df	Deviance	P(> Chi)
1	4	2.495			
2	5	73.684	-1	-71.189	3.246e-17

```

> ge <- tapply(predict(m3,type="response"), list(treatment,genus1), mean)

```

```

> ge

```

	genA	genB	genCD
control	0.6367787	0.2615513	0.366835
water	0.6942213	0.3144487	0.428665

Effect size

- statistical and biological effects are not identical
- statistical effects are affected by precision of measurements, number of measurements, type of test
- Cohen's coefficient:

$$h = \left| 2 \arcsin \sqrt{p_1} - 2 \arcsin \sqrt{p_2} \right|$$

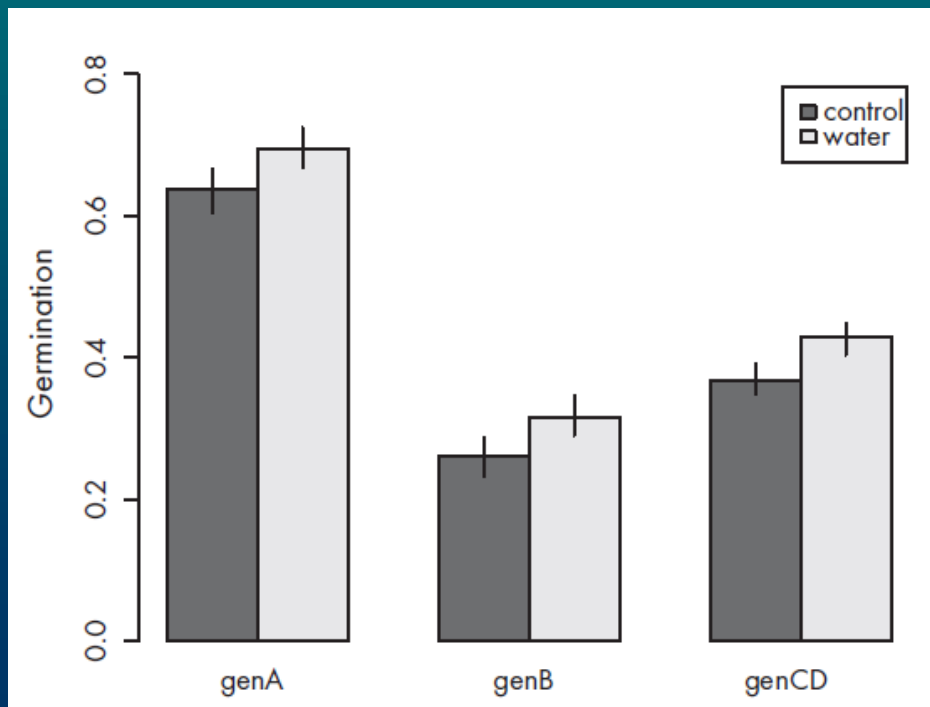
- $h < 0.2$... weak effect
- $h > 0.8$... strong effect

```
> abs(2*asin(sqrt(ge[1,1]))-2*asin(sqrt(ge[2,1])))  
[1] 0.1218512
```

```
> both <- paste(pesticide,genus1)
> m4 <- glm(y ~ factor(both) - 1, binomial)
> 1/(1+exp(-confint(m4)))
```

Waiting for profiling to be done...

	2.5%	97.5%
factor(both) control genA	0.6048442	0.6644666
factor(both) control genB	0.2315221	0.2857134
factor(both) control genCD	0.3485230	0.3908104
factor(both) water genA	0.6670153	0.7239840
factor(both) water genB	0.2896266	0.3473026
factor(both) water genCD	0.4044330	0.4477560



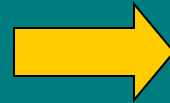
Over- / under-dispersion

- arises when dispersion parameter φ $\varphi = \text{Var}(y)/\text{E}(y) \neq 1$
 - overdispersion: variance is larger $\rightarrow \varphi > 1$
 - underdispersion: variance is smaller $\rightarrow \varphi < 1$
- causes:
 - if the model is misspecified
 - lacks important explanatory variables
 - relative frequency is not constant within a group
- solution: use **quasibinomial** family in which variance is estimated as $\text{Var}(y) = n\pi(1-\pi)\varphi$ instead of $\text{Var}(y) = n\pi(1-\pi)$

- this will influence SE of parameter estimates

- if $\varphi > 1$ then SE will be larger

- if $\varphi < 1$ then SE will be smaller



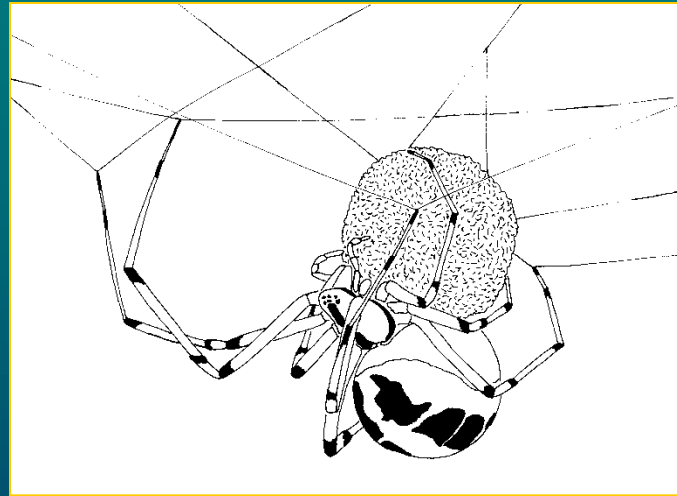
changes P values

- when using **quasibinomial** χ^2 - and z- tests
have to change to F- and t- tests

Regression

Background

Production of eggsac is influenced by a number of variables, such as body size, i.e. amount of consumed food. For an experimental study we need to be able to predict probability of production at a range of body sizes.



Design

In the laboratory, production of eggsacs was studied in a spider with a variable body size [mm]. As the body size was measured with the precision of 0.5 mm, all 160 individuals were classified into size classes each containing 15 to 30 specimens. Females that produced eggsacs were recorded.

Hypotheses

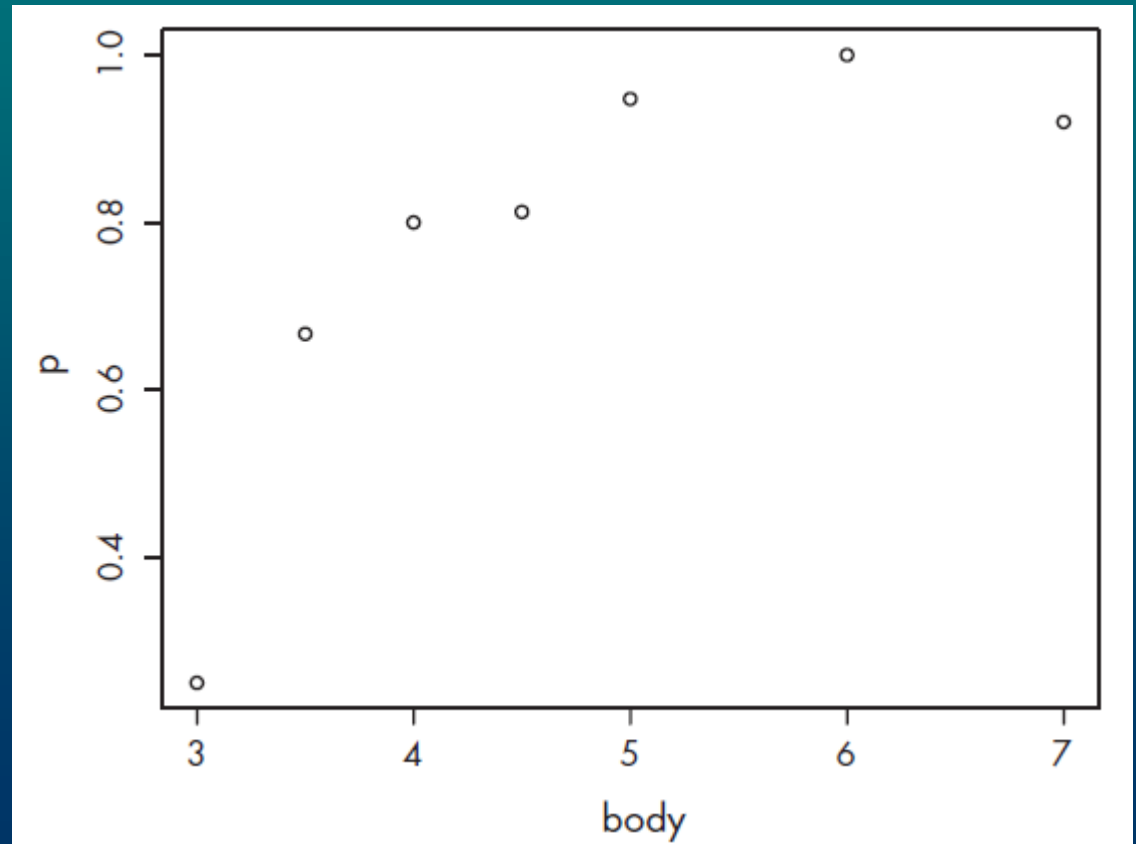
- Is eggsac production related to the body size?
- If it is what is the shape of the relationship?
- What is the model that can be used to predict eggsac production for spider sizes of 3–12 mm?

Variables:

body

n

eggs



$$\arcsin \sqrt{p_i} = \alpha + \beta \text{body}_i + \gamma \text{body}_i^2 + \varepsilon_i,$$

kde $\varepsilon_i \sim N(0, \sigma^2)$, nezávisle pro jednotlivé pavouky.

```
> tr <- asin(sqrt(p))  
> m1 <- lm(tr ~ body + I(body^2), weights=n)  
> summary(m1)
```

Coefficients:

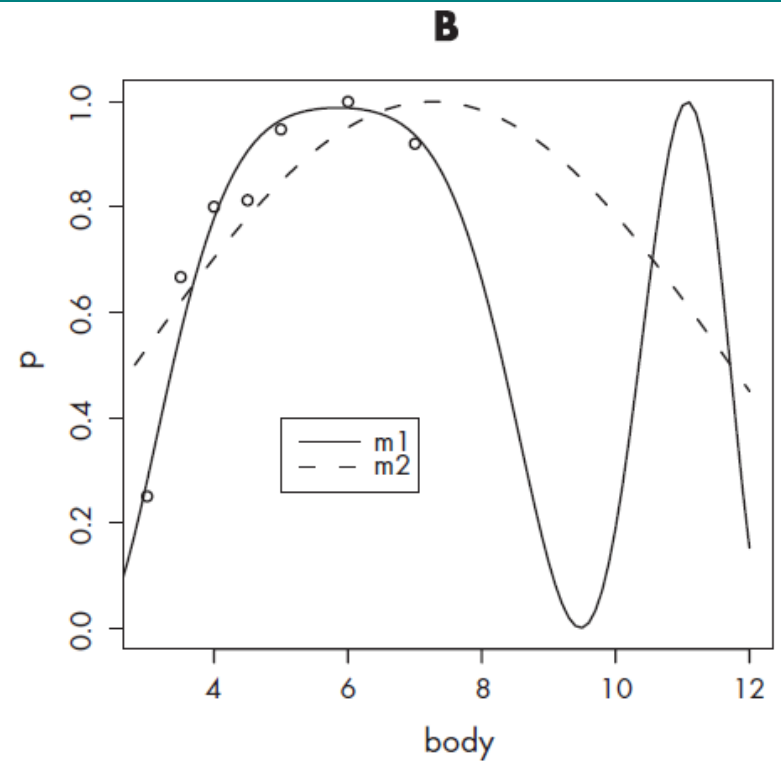
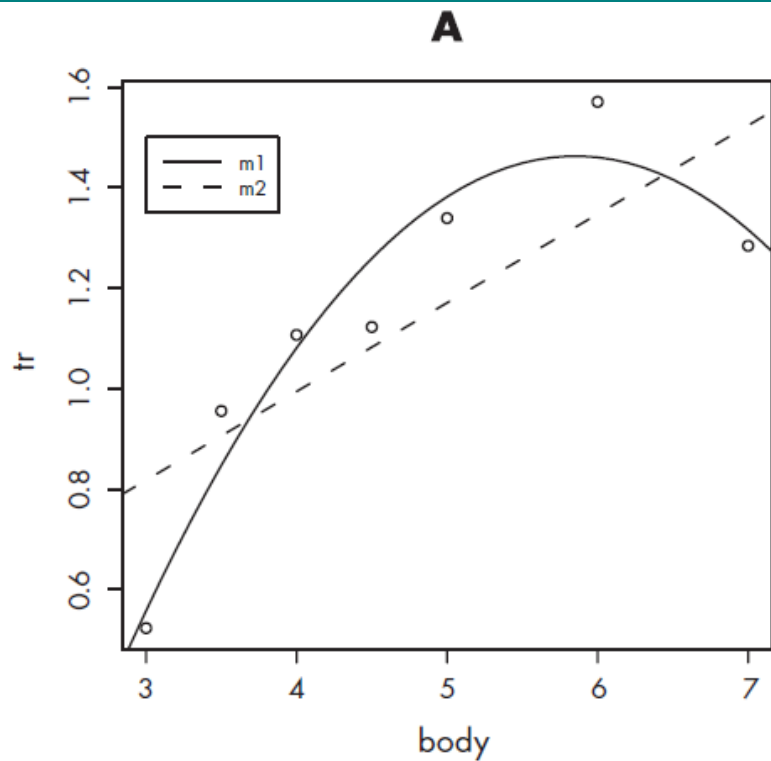
	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	-2.34592	0.59329	-3.954	0.01676	*
body	1.30161	0.24776	5.254	0.00628	**
I(body^2)	-0.11121	0.02433	-4.571	0.01025	*

```
> m2 <- update(m1, ~.-I(body^2))  
> summary(m2)
```

...

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	0.28836	0.31429	0.918	0.4010	
body	0.17649	0.06279	2.811	0.0375	*



$$\log\left(\frac{\pi_i}{1 - \pi_i}\right) = \alpha + \beta body_i + \gamma body_i^2,$$

kde $eggs_i \sim Bin(\pi_i, n_i)$, nezávisle pro jednotlivé pavouky.

```

> y <- cbind(eggs, n-eggs)
> m3 <- glm(y ~ body + I(body^2), family=binomial)
> summary(m3)
...
Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept) -13.7857      3.8482  -3.582 0.000340 ***
body         5.7218       1.6771   3.412 0.000645 ***
I(body^2)   -0.4825       0.1695  -2.846 0.004427 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 44.2136  on 6  degrees of freedom
Residual deviance:  3.3357  on 4  degrees of freedom

```

```

> summary(m4)
...
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -3.9270     1.1038  -3.558 0.000374 ***
body           1.2079     0.2756   4.383 1.17e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 44.214  on 6  degrees of freedom
Residual deviance: 11.072  on 5  degrees of freedom

```

```

> m5 <- update(m4, family=quasibinomial)

```

```

> summary(m5)

```

```

(Dispersion parameter for quasibinomial family taken to be 3.332466)

```

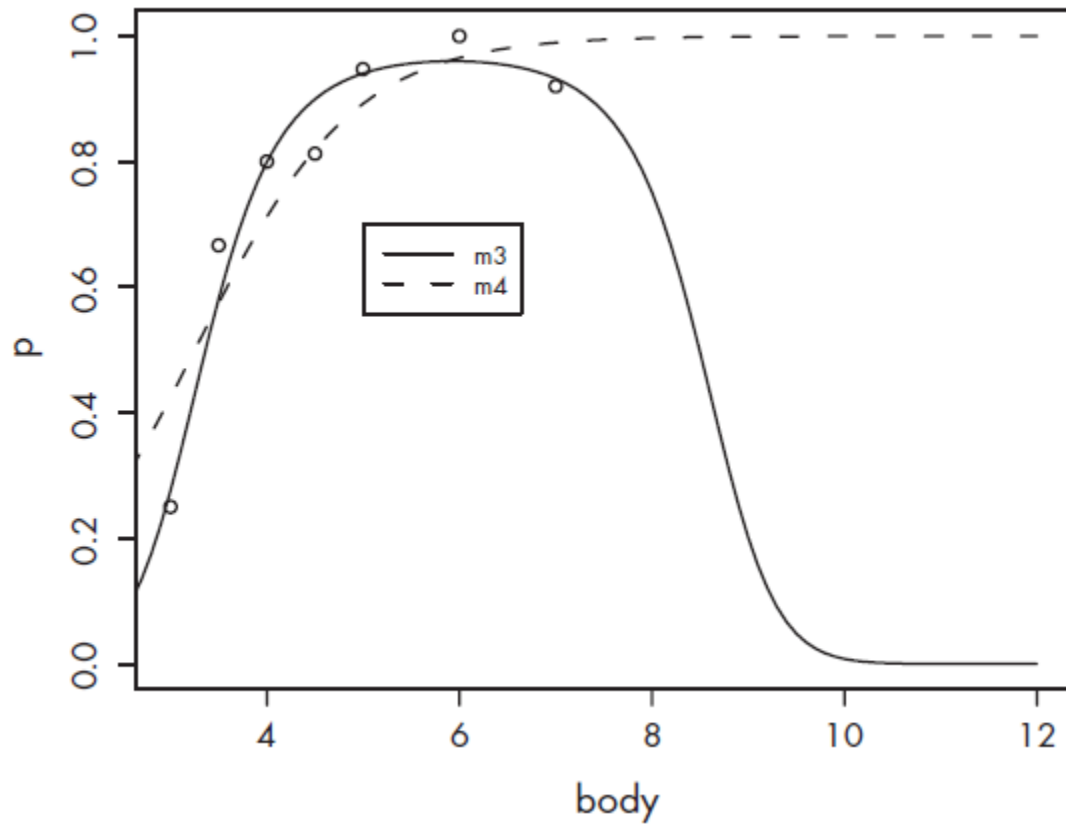
```

> anova(m5, test="F")

```

```

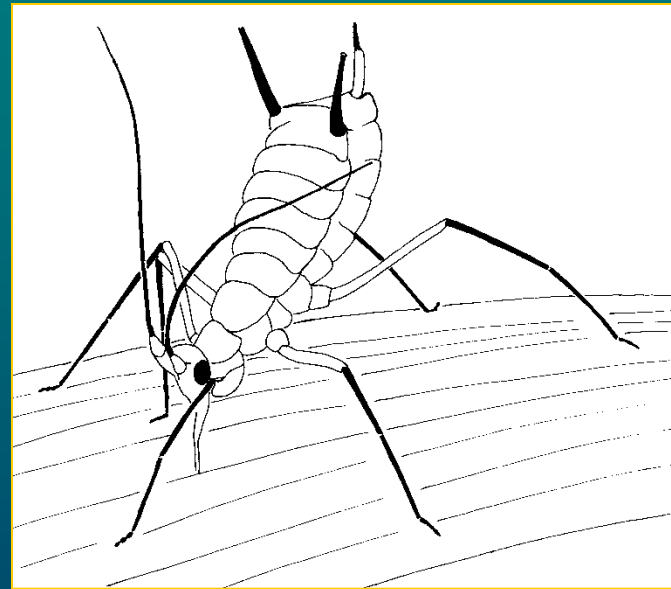
...
      Df Deviance Resid. Df Resid. Dev      F Pr(>F)
NULL           6      44.214
body  1      33.141           5      11.072 9.945 0.02528 *
```

1-way ANCOVA

Background

Synthetic insecticides often have a species-specific efficiency. The recommended doses or concentrations then have to be adjusted.



Design

In the laboratory an effect of an insecticide on the mortality of two aphid species was studied. The insecticide was applied at 6 concentrations [ppm]. Each concentration was tested on 30 individuals of both aphid species.

Hypotheses

- Is mortality affected by the concentration?
- Was the efficiency similar for both species?
- What is the LC_{50} (i.e. 50% lethal concentration) for both species?

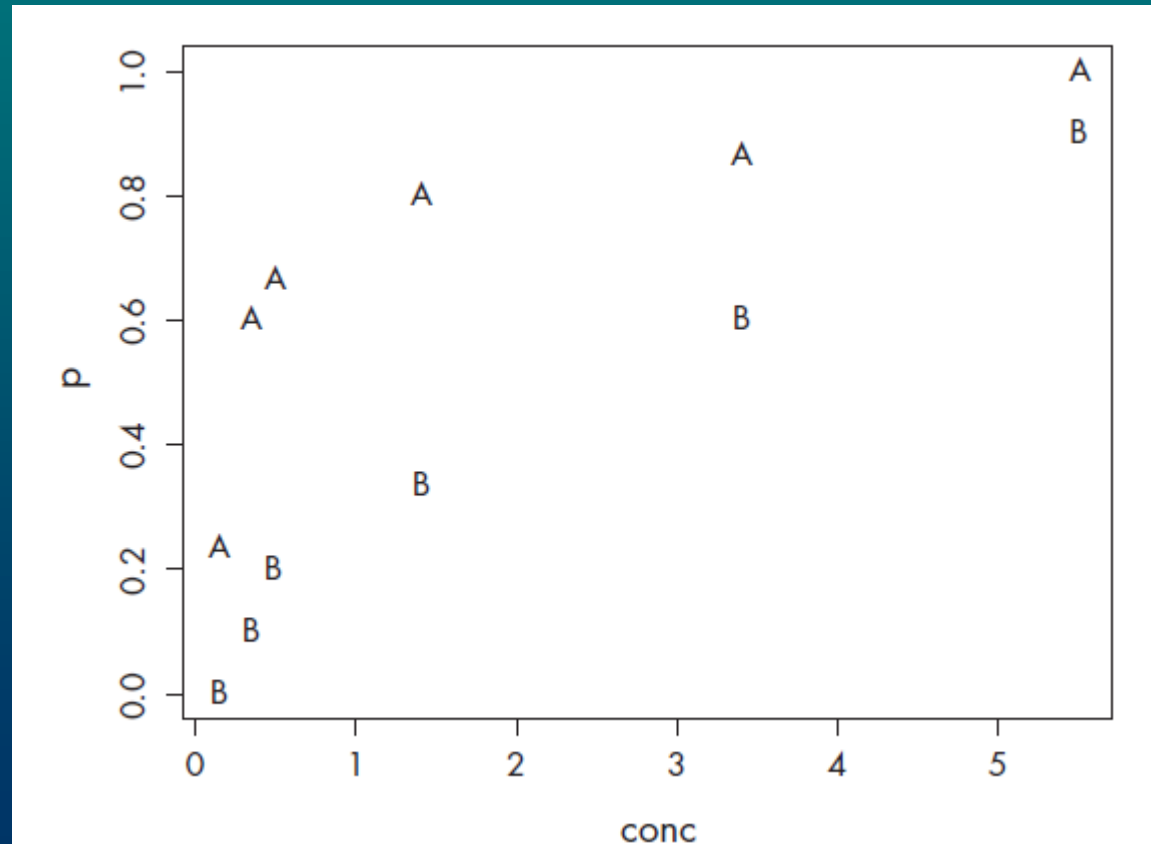
Variables:

SPECIES: A, B

conc

n

dead



$$\log\left(\frac{\pi_{ij}}{1 - \pi_{ij}}\right) = \alpha + SPECIES_j + \beta \log(\text{conc}_i) + \delta_j \log(\text{conc}_i),$$

kde $dead_{ij} \sim \text{Bin}(\pi_{ij}, n_{ij})$, nezávisle pro jednotlivá pozorování.

```
> y <- cbind(dead, n-dead)
> m1 <- glm (y ~ log(conc)*species, binomial)
> anova(m1)
...
              Df Deviance Resid. Df Resid. Dev P(>|Chi|)
NULL                               11      185.807
log(conc)                1    110.170           10      75.638 8.996e-26
species                   1     62.087            9      13.551 3.286e-15
log(conc):species        1      1.343            8      12.207    0.246
```

```
> m2 <- update(m1, ~.-log(conc):species)
> anova(m2)
...
              Df Deviance Resid. Df Resid. Dev P(>|Chi|)
NULL                               11      185.807
log(conc)                1    110.170           10      75.638 8.996e-26
species                   1     62.087            9      13.551 3.286e-15
```

```
> summary(m2)
```

```
...
```

```
Coefficients:
```

	Estimate	Std. Error	z value	Pr(> z)	
(Intercept)	1.3825	0.2201	6.280	3.39e-10	***
log(conc)	1.2328	0.1348	9.146	< 2e-16	***
speciesB	-2.2117	0.3180	-6.955	3.52e-12	***

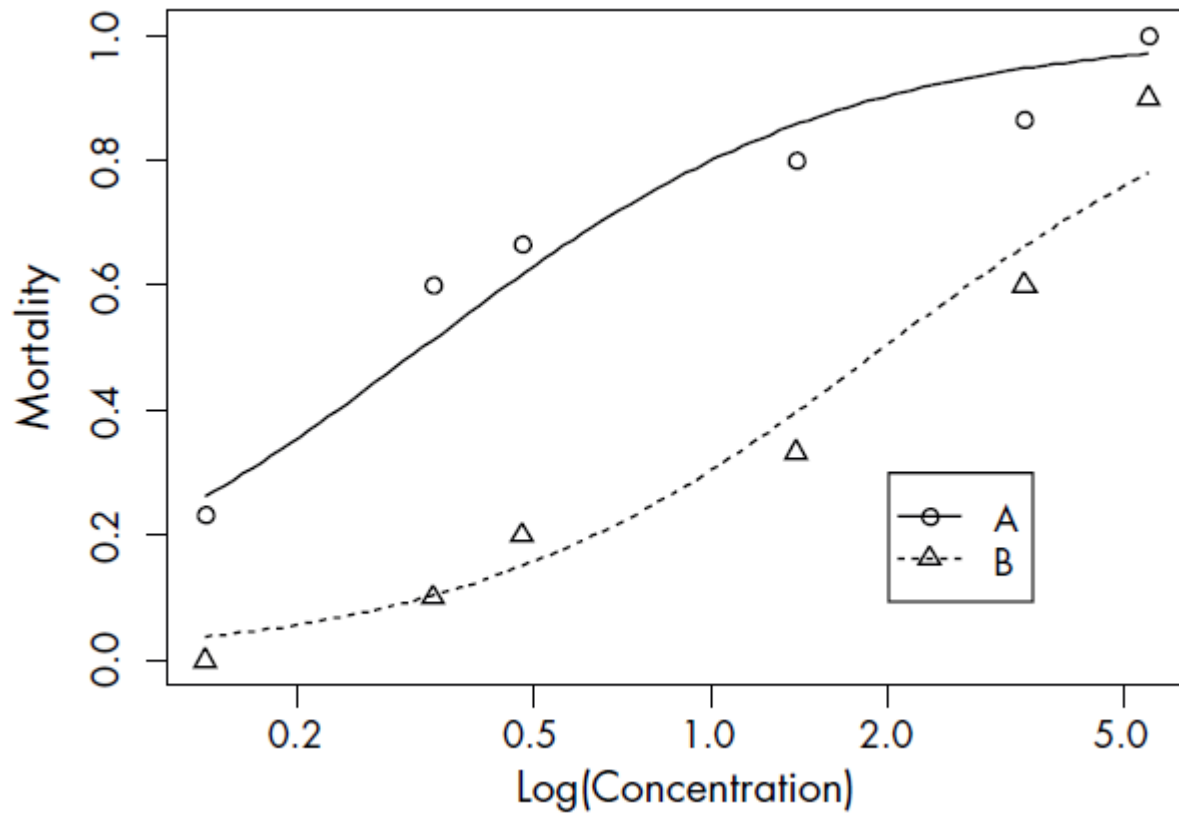
```
---
```

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

```
(Dispersion parameter for binomial family taken to be 1)
```

```
Null deviance: 185.807 on 11 degrees of freedom  
Residual deviance: 13.551 on 9 degrees of freedom
```

$$100/(1 + \exp(-1.383 - 1.233\log(\text{conc})))$$



$$100/(1 + \exp(0.829 - 1.233\log(\text{conc})))$$

$$LC_{50} = \exp\left(-\frac{a}{b}\right)$$

```
> m3 <- glm(y ~ species + log(conc) - 1, binomial)
> summary(m3)
```

...

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)	
speciesA	1.3825	0.2201	6.280	3.39e-10	***
speciesB	-0.8293	0.2020	-4.106	4.02e-05	***
log(conc)	1.2328	0.1348	9.146	< 2e-16	***

```
> library(MASS)
> dose.p(m3, cf=c(1,3), p=0.5)
```

	Dose	SE
p = 0.5:	-1.121418	0.1627097

$$\exp(-1.121) = 0.326$$

```
> dose.p(m3, cf=c(2,3), p=0.5)
```

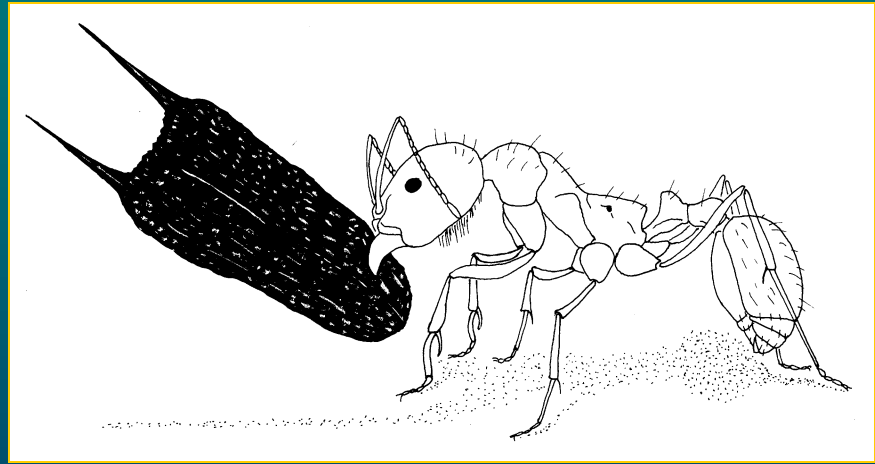
	Dose	SE
p = 0.5:	0.6726813	0.159251

$$\exp(0.673) = 1.96.$$

1-way Binary ANCOVA

Background

Granivorous ants collect various seeds and bring them into nest. Sympatrically occurring species may show trophic niche partitioning related to the size of collected seeds.



Design

Seed preference of two ant species was studied in the laboratory. Each of 25 ants of both species was offered seeds of variable size expressed as its weight [mg]. Response of ants was classified as “yes” or “no” if it took or refused to take a seed, respectively.

Hypotheses

- Is acceptance related to the seed size?
- Did both species have similar preference for seed sizes?
- If not what is the threshold size of seeds for both species?

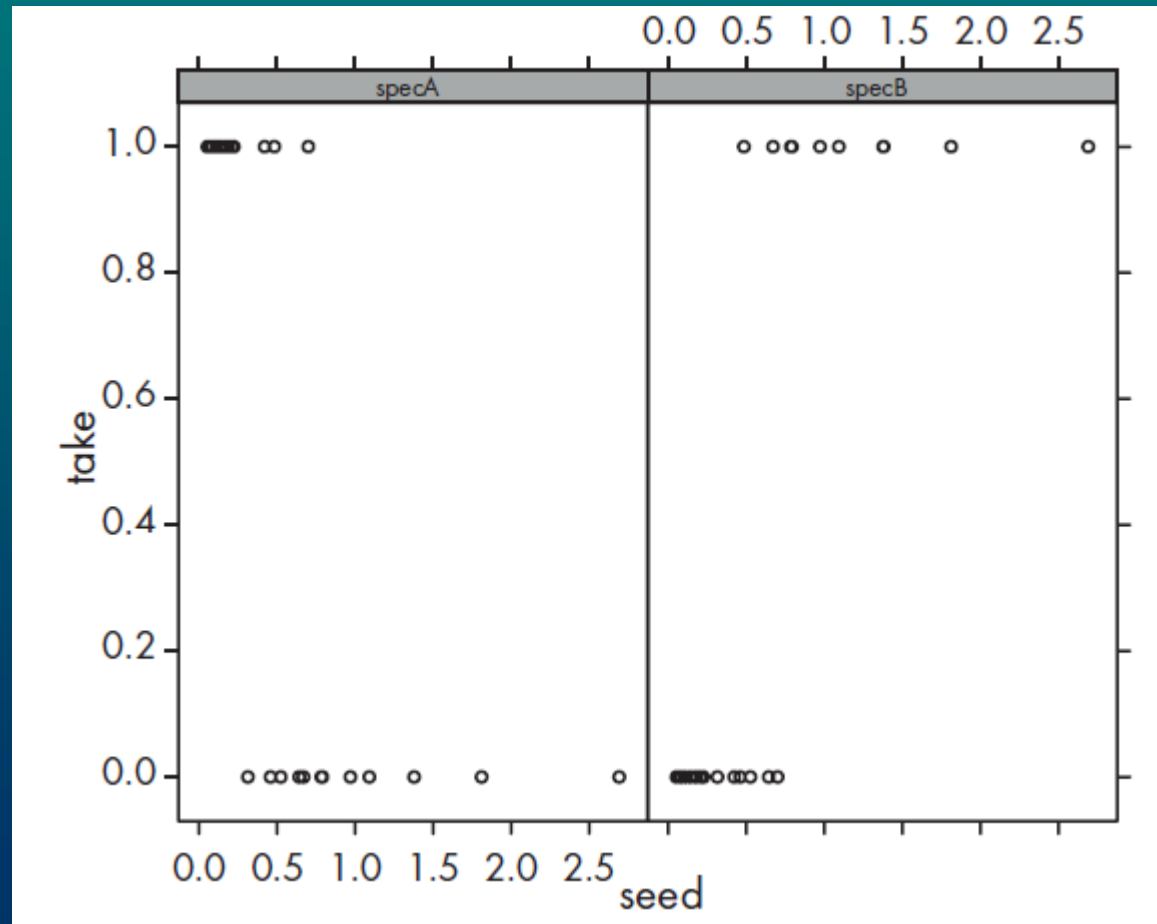
(The threshold size is defined as a size that is accepted with higher than 90% probability)

Variables:

SPECIES: specA, specB

seed

take



$$\log\left(\frac{\pi_{ij}}{1 - \pi_{ij}}\right) = \alpha + \text{SPECIES}_j + \beta_{\text{seed}}_{ij} + \delta_j \text{seed}_{ij},$$

kde $\text{take}_{ij} \sim \text{Bin}(\pi_{ij}, 1)$, nezávislé pro jednotlivé mravence.

```
> m1 <- glm(take ~ seed*species, family=binomial)
> summary(m1)
...
Coefficients:
                Estimate Std. Error z value Pr(>|z|)
(Intercept)         4.012      1.646    2.437  0.01480 *
seed                -8.346      3.315   -2.517  0.01182 *
speciesspecB       -10.957      3.697   -2.964  0.00304 **
seed:speciesspecB   19.147      6.141    3.118  0.00182 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 68.593  on 49  degrees of freedom
Residual deviance: 24.726  on 46  degrees of freedom
```

```
> anova(m1, test="Chi")
```

```
...
```

	Df	Deviance	Resid.	Df	Resid. Dev	P(> Chi)
NULL				49	68.593	
seed	1	0.054		48	68.539	0.817
species	1	0.325		47	68.214	0.568
seed:species	1	43.488		46	24.726	4.267e-11

```
> m2 <- glm(take ~ log(seed)*species, binomial)
```

```
> AIC(m1, m2)
```

	df	AIC
m1	4	32.72631
m2	4	32.23823

```
> m3 <- glm(take ~ seed*species, binomial(link=cloglog))
```

```
> AIC(m3)
```

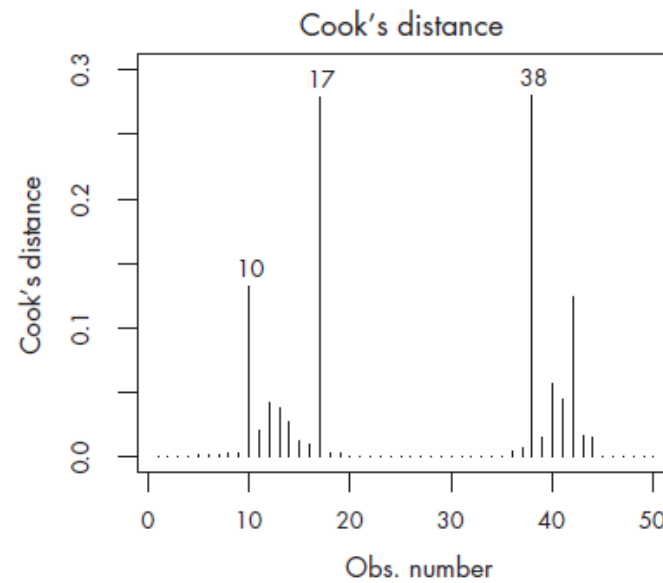
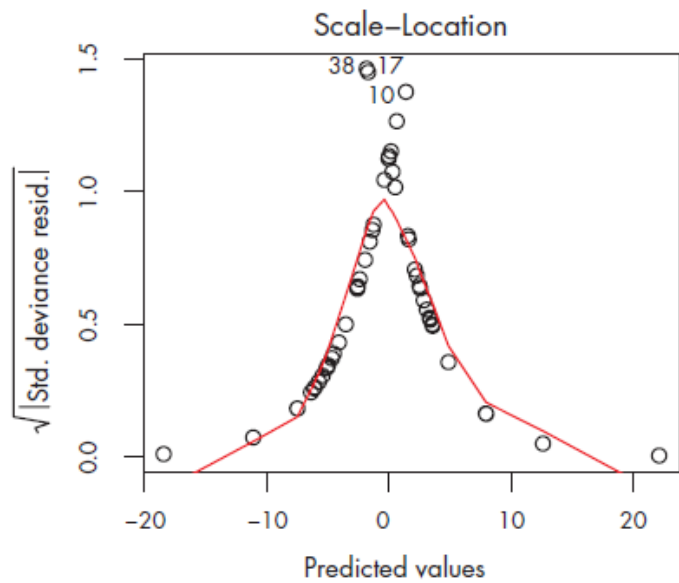
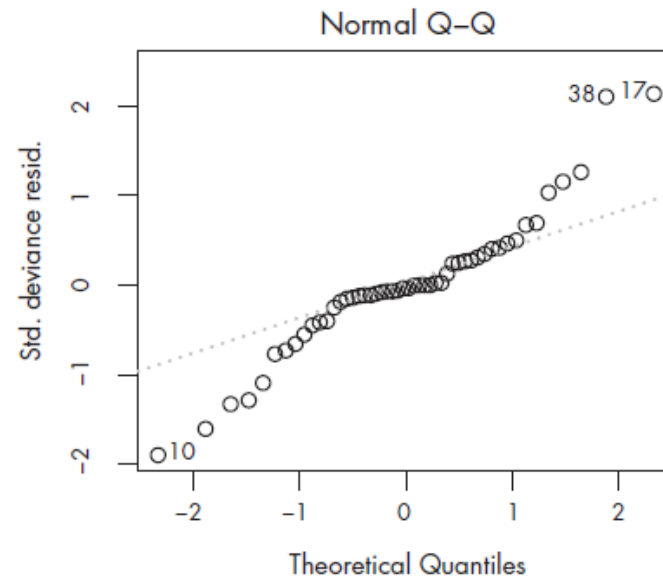
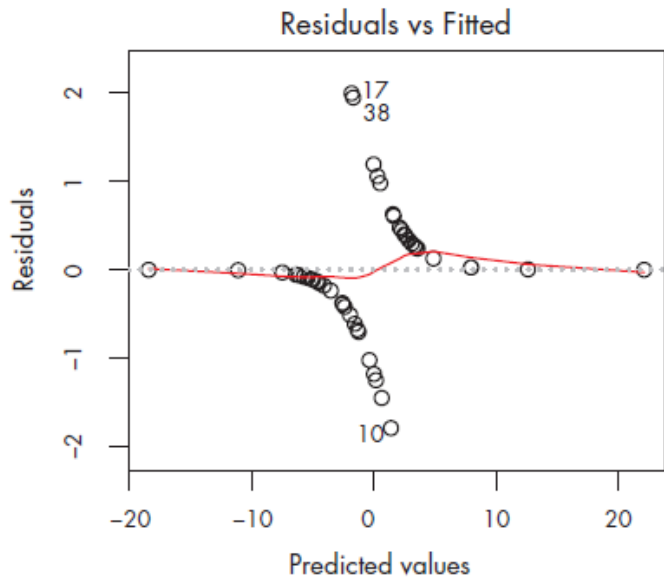
```
[1] 31.63241
```

Coefficient of determination

- several for GLM models
- McFaden's coefficient – based on likelihood of models
- ranges from 0 to 1

$$\rho^2 = 1 - \frac{\text{LogLik}_M}{\text{LogLik}_{M0}}$$

```
> m4 <- glm(take ~ 1, binomial)
> 1-logLik(m1)/logLik(m4)
'logLik' 0.6395213 (df=4)
```



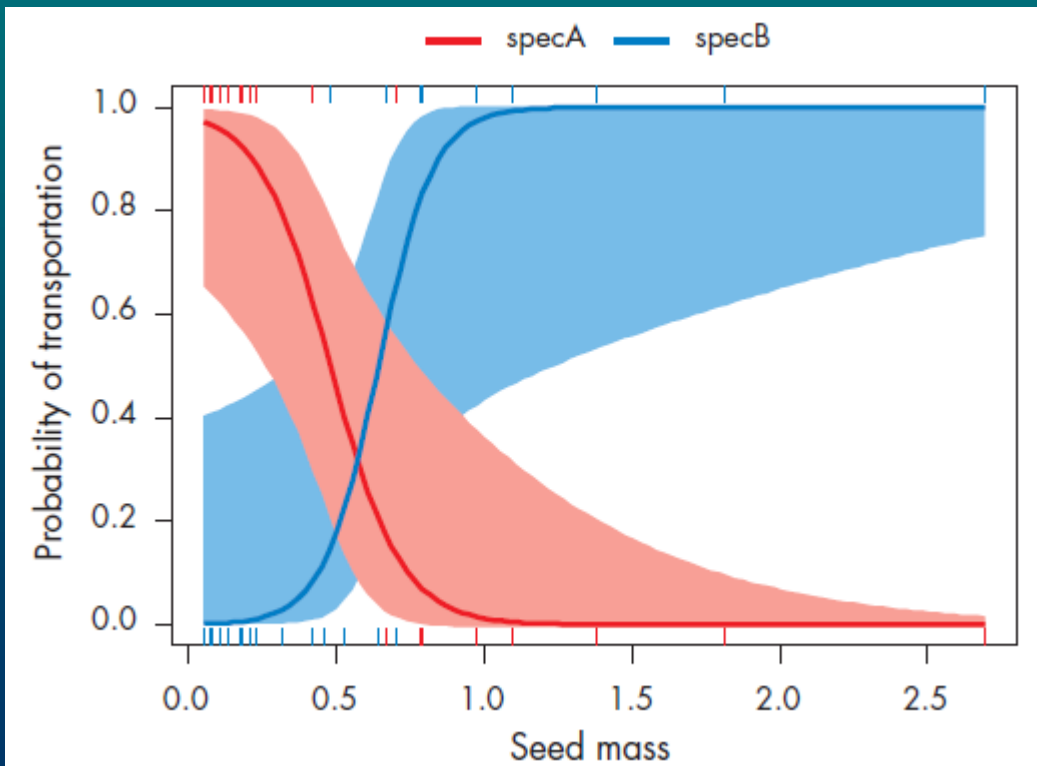
$$x = \frac{\log(0.9/0.1) - a}{b}$$

```
> (log(0.9/0.1) - 4.012) / -8.346
```

```
[1] 0.2174425
```

```
> (log(0.9/0.1) - 4.012 + 10.957) / (-8.346 + 19.147)
```

```
[1] 0.8464239
```



$$\frac{1}{1 + \exp(6.945 - 10.8 \text{seed})}$$

$$\frac{1}{1 + \exp(-4.012 + 8.346 \text{seed})}$$