Linear models and generalized linear models

in R

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What is a linear regression

Simple linear regression

$$Y_i = \beta_0 + \beta_1 x_i + \epsilon$$
$$\epsilon \sim N(0, \sigma^2_\epsilon)$$

or in distributional notation

$$Y \sim N(\beta_0 + \beta_1 x, \sigma^2_\epsilon)$$

General linear model

$$Y_i = \beta_0 + \beta_1 x_{1i} + \beta_1 x_{2i} + \ldots + \epsilon$$
$$\epsilon \sim N(0, \sigma^2_\epsilon)$$

and

$$Y \sim N(\beta_0 + \beta_1 x_{1i} + \beta_1 x_{2i} + \ldots, \sigma^2)$$

Linear model assumptions

Some are made on the residuals and others on the independent variables.
None are made on the (unconditionned) dependent variable.

Residuals are assumed to:

- have a mean of zero
- be independent
- be normally distributed
- be homoscedastic

Independent variables are assumed to:

- have a linear relation with Y
- be measured without error
- to be independent from each other

Maximum likelihood

Technique used for estimating the parameters of a given distribution, using some observed data

For Example: Population is known to follow a “normal distribution” but “mean” and “variance” are unknown, MLE can be used to estimate them using a limited sample of the population.

Likelihood vs probability

We maximize the likelihood and make inferences on the probability

Likelihood

$$L(parameters|data)$$

How likely it is to get those parameters given the data.

Probability

$$P(data|null\,parameters)$$

Probability to get the data given the null parameters. Or how probable it is to get those data according to the null model.

Maximum likelihood approach

$$L(parameters|data) = \prod_{i=1}^{n} f(data_i|parameters)$$

where f is the probability density function of your model.

Working with product is more painful than with sum, we can take the log:

$$ln(L(parameters|data)) = \sum_{i=1}^{n} ln(f(data_i|parameters))$$

Need to solve:

$$\frac{\delta ln(L(parameters|data)}{\delta parameters} = 0$$

For multiple regression, the parameters βs are given by $\beta = (X^T X)^{-1} X^T y$

Equivalent to minimizing residuals (but you don't want to see the proof)

Doing linear models in R

Simply use `lm()` function. It works for everything anova, ancova, t-test.

We will use data of sturgeon measurements at different locations in Canada.

```r
dat <- read.csv("data/lm_example.csv")
str(dat)
```

```
## 'data.frame':    92 obs. of  4 variables:
##  $ year   : int  1978 1978 1978 1978 1978 1978 1978 1978 1978 1978 ...
##  $ fklngth: num  41.9 50.2 50.2 47.3 49.6 ...
##  $ locate : chr  "NELSON      " "LOFW        " "LOFW        " "NELSON      " ...
##  $ age    : int  11 24 23 20 23 20 23 19 17 14 ...
```

Fitting a model and checking assumptions

First we load the needed packages for:

- data manipulation: `tidyverse`
- fancy plots: `ggplot2`
- type III anova: `car`
- fancy and nicer visual assumptions checks: `performance`
- formal assumptions tests: `lmtest`

```r
library(car)
library(performance)
library(lmtest)
library(tidyverse)
```

Data exploration

R Code

Plot

```r
ggplot(data = dat, aes(x = age, y = fklngth)) +
  facet_grid(. ~ locate) +
  geom_point() +
  stat_smooth(method = lm, se = FALSE) +
  stat_smooth(se = FALSE, color = "red") +
  labs(
    y = "Fork length",
    x = "Age"
  )
```

Creating log10 transform

```
dat <- dat %>%
  mutate(
    lage = log10(age),
    lfkl = log10(fklngth)
  )
```

Data exploration: with log

Code

Plot

```
ggplot(data = dat, aes(x = lage, y = lfkl)) +
  facet_grid(. ~ locate) +
  geom_point() +
  stat_smooth(method = lm, se = FALSE) +
  stat_smooth(se = FALSE, color = "red") +
  labs(
    y = "log 10 Fork length",
    x = "Log 10 Age"
  )
```

Fit the model

```
m1 <- lm(lfkl ~ lage + locate + lage:locate, data = dat)
summary(m1)
```

```
## 
## Call:
## lm(formula = lfkl ~ lage + locate + lage:locate, data = dat)
## 
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -0.09375 -0.01864 -0.00253  0.02090  0.08030 
## 
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)    
## (Intercept)              1.24287    0.04370  28.443  < 2e-16 ***
## lage                     0.31431    0.03292   9.546 3.08e-15 ***
## locateNELSON             0.19295    0.06331   3.048  0.00304 ** 
## lage:locateNELSON       -0.14276    0.04902  -2.912  0.00455 ** 
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.02823 on 88 degrees of freedom
## Multiple R-squared:  0.5664,	Adjusted R-squared:  0.5516 
## F-statistic: 38.31 on 3 and 88 DF,  p-value: 6.197e-16
```

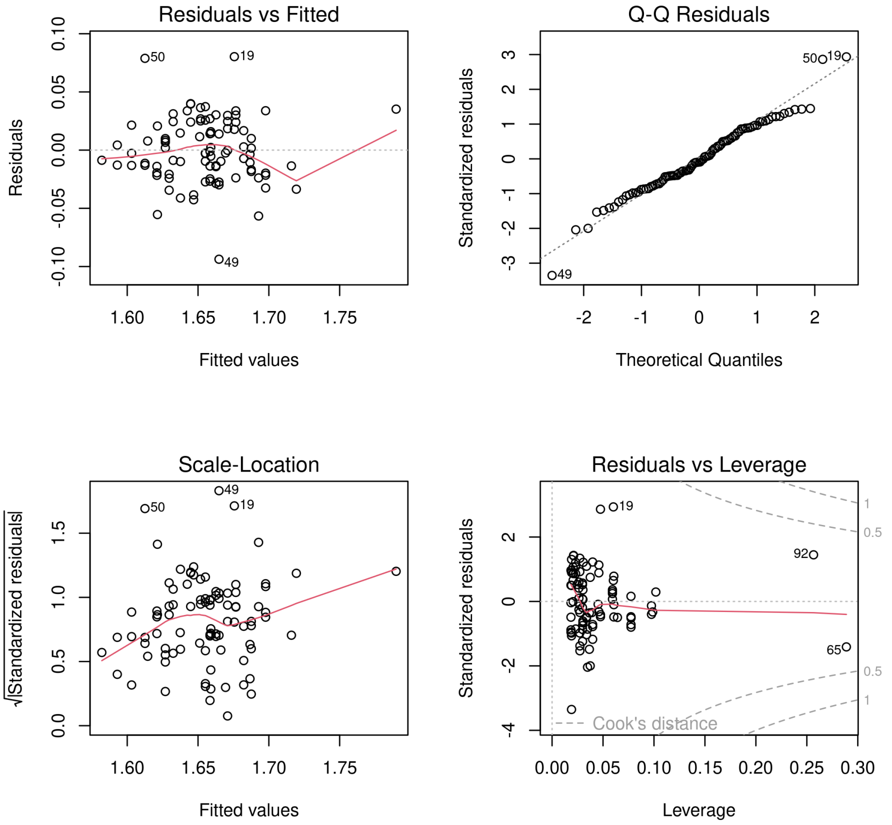
Anova for factors

```
Anova(m1, type = 3)
```

```
## Anova Table (Type III tests)
##
## Response: lfkl
##              Sum Sq Df  F value    Pr(>F)
## (Intercept) 0.64467  1 809.0107 < 2.2e-16 ***
## lage        0.07262  1  91.1310 3.079e-15 ***
## locate      0.00740  1   9.2901  0.003042 **
## lage:locate 0.00676  1   8.4815  0.004546 **
## Residuals   0.07012 88
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

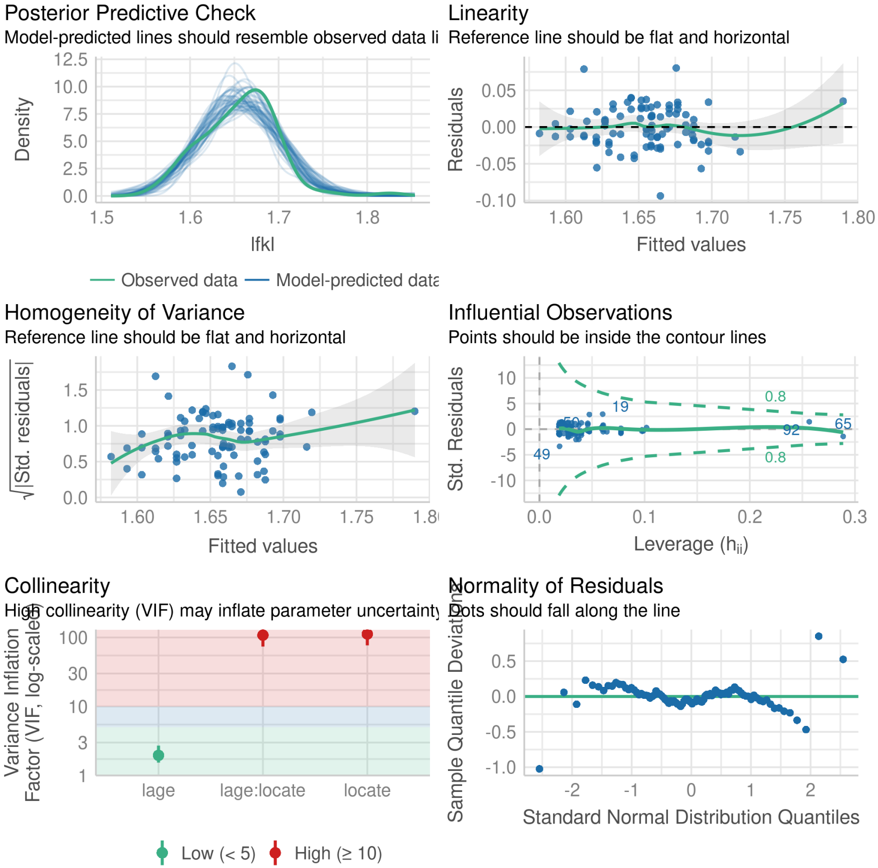
Assumptions (classic plot)

```r
par(mfrow = c(2, 2))
plot(m1)
```



Assumptions (Nicer plot)

```
check_model(m1)
```



Formal tests

Normality of residuals

```
shapiro.test(residuals(m1))
```

```
##
##     Shapiro-Wilk normality test
##
## data:  residuals(m1)
## W = 0.97639, p-value = 0.09329
```

Formal tests

Heteroscedasticity

```
bptest(m1)
```

```
##
##      studentized Breusch-Pagan test
##
## data:  m1
## BP = 1.8366, df = 3, p-value = 0.607
```

Formal tests

Linearity

```r
resettest(m1, power = 2:3, type = "fitted", data = dat)
```

```
## 
##      RESET test
## 
## data:  m1
## RESET = 1.6953, df1 = 2, df2 = 86, p-value = 0.1896
```

Generalized linear models

Generalized linear models

An extension to **linear models**

GLM expresses the transformed conditional expectation of the dependent variable `Y` as a linear combination of the regression variables `X`

Model has 3 components

- a dependent variable Y with a response distribution to model it: **Gaussian**, **Binomial**, **Bernouilli**, **Poisson**, **negative binomial**, **zero-inflated …**, **zero-truncated …**, …
- linear predictors (or independent variables)

$$\eta = \beta_0 + \beta_1 X_1 + \ldots + \beta_k X_k$$

- a link function such that

$$E(Y|X) = \mu = g^{-1}(\eta)$$

Dependent variable

- when continuous and follows *conditional* normal distribution, called **Linear regression**
- Binary outcomes (success/failure), follows a *Binomial distribution*, called **Logistic regression**
- Count data (number of events), follows a *Poisson*, called **Poisson regression**

Classic link functions

- Identity link (form used in linear regression models)

$$g(\eta) = \mu$$

- Log link (used when μ cannot be negative, *e.g.* Poisson data)

$$g(\eta) = log(\mu)$$

Logit link (used when \mu is bounded between 0 and 1, *e.g.* binary data)

$$g(\eta) = log\left(\frac{\mu}{1-\mu}\right)$$

Linear regression

- Y: continuous
- Response distribution: Gaussian
- Link function: identity

$$g(\eta) = \mu$$
$$\mu(X_1, \ldots, X_k) = \beta_0 + \beta_1 X_1 + \ldots + \beta_k X_k$$

Logistic regression

- Y: binary or proportion
- Response distribution: Binomial or bernoulli
- Link function: logit

$$g(\eta) = ln\left(\frac{\mu}{1-\mu}\right)$$

$$\mu(X_1, \ldots, X_k) = \frac{1}{1 + e^{-(\beta_0 + \beta_1 X_1 + \ldots + \beta_k X_k)}}$$

Poisson regression

- Y: discrete variable (integers)
- Response distribution: Poisson or Negative binomial
- Link function: natural logarithm

$$g(\eta) = ln(\mu)$$

$$\mu(X_1, \ldots, X_k) = e^{\beta_0 + \beta_1 X_1 + \ldots + \beta_k X_k}$$

Model assumptions

- Easy answer none or really few
- More advanced answer I am not sure, it is complicated
- Just check residuals I as usual
- Technically only 3 assumption:
  - **Variance is a function of the mean specific to the distribution used**
  - observations are independent
  - linear relation on the latent scale

GLMs do not care if the residual errors are Gaussian as long as the specified mean-variance relationship is satisfied by the data

- what about DHaRMA ? It's complicated

Choosing a link function

A link function should map the stuctural component from $(-\infty, \infty)$ to the distribution interval (*e.g.* (0,1) for binomial)

So number of link function possible is extremley large.

Choice of **link** function heavily influenced by field tradiditon

For binomial models

- **logit** assume modelling probability of an observation to be one
- **probit** assume binary outcome from a hidden gaussian variable (*i.e.* threshold model)
- **logit** & **probit** are really similar, both are symmetric but **probit** tapers faster. **logit** coefficient easier to interpret directly
- **cologlog** not-symmetrical

Logistic regression

Data

Here is some data to play with from a study on bighorn sheep.

We will look at the relation between reproduction and age

Loading ans tweaking the data

```
mouflon0 <- read.csv("data/mouflon.csv")
mouflon <- mouflon0 %>%
  arrange(age) %>%
  mutate(
    reproduction = case_when(
      age >= 13 ~ 0,
      age <= 4 ~ 1,
      .default = reproduction
    )
  )
```

First plot

Code

Plot

```r
bubble <- data.frame(
  age = rep(2:16, 2),
  reproduction = rep(0:1, each = 15),
  size = c(table(mouflon$age, mouflon$reproduction))
) %>%
  mutate(size = ifelse(size == 0, NA, size))
ggplot(
  bubble,
  aes(x = age, y = reproduction, size = size)
) +
  geom_point(alpha = 0.8) +
  scale_size(range = c(.1, 20), name = "Nb individuals")
```

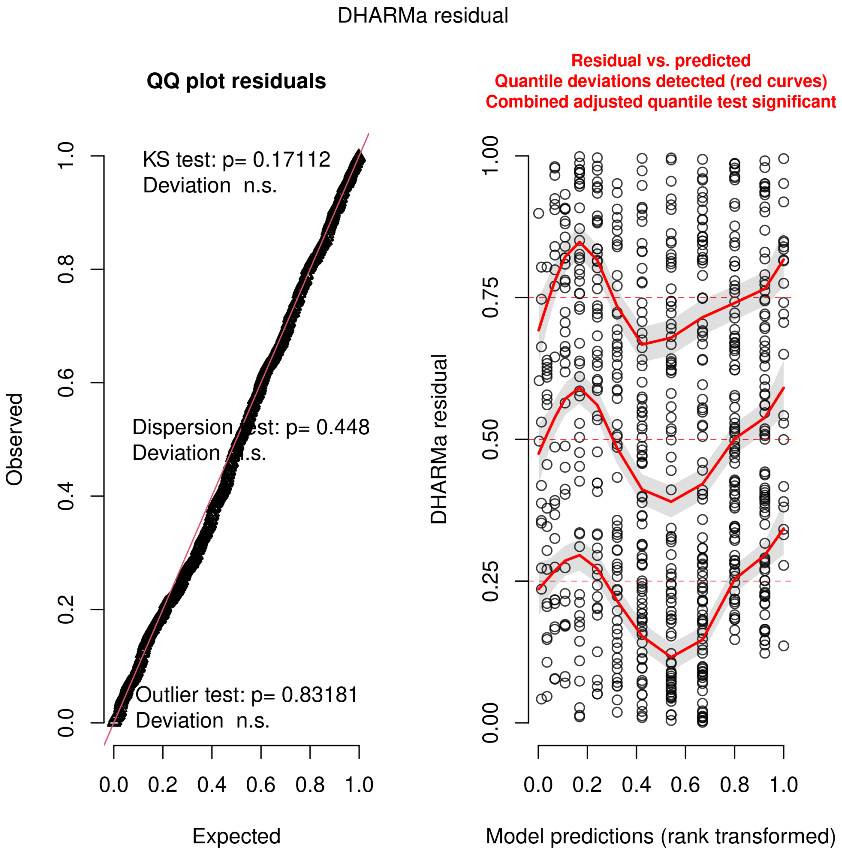
Fitting the logistic regression

```
m1 <- glm(reproduction ~ age,
  data = mouflon,
  family = binomial
)
summary(m1)
```

```
##
## Call:
## glm(formula = reproduction ~ age, family = binomial, data = mouflon)
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  3.19921    0.25417   12.59   <2e-16 ***
## age         -0.36685    0.03287  -11.16   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 928.86  on 715  degrees of freedom
## Residual deviance: 767.51  on 714  degrees of freedom
##   (4 observations deleted due to missingness)
## AIC: 771.51
##
## Number of Fisher Scoring iterations: 4
```

Checking assumptions

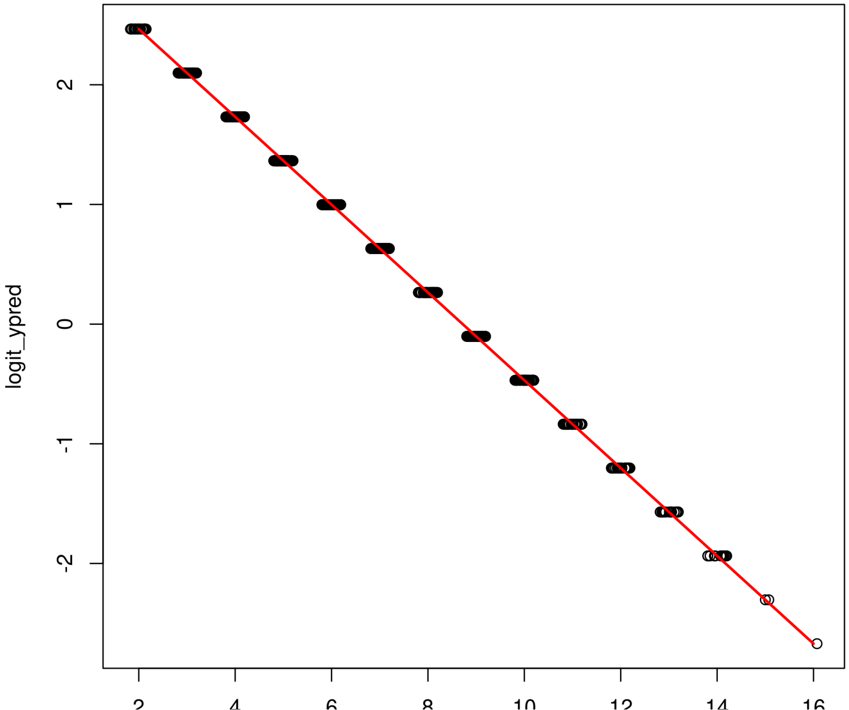
```
simulationOutput <- simulateResiduals(m1)
plot(simulationOutput)
```



Plotting predictions

plotting the model prediction on the link (latent) scale

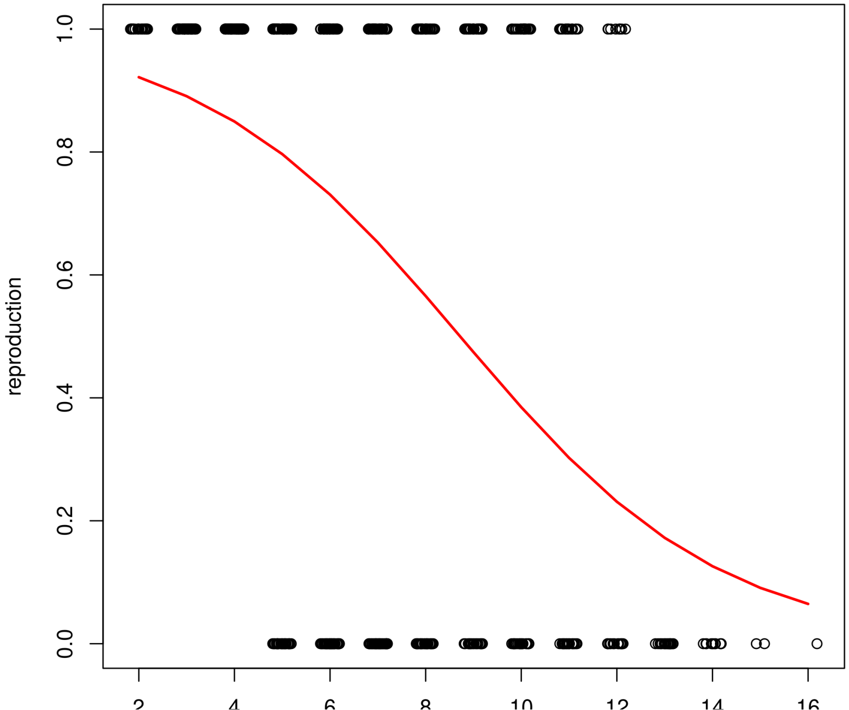
```
mouflon$logit_ypred <- 3.19921 - 0.36685 * mouflon$age
plot(logit_ypred ~ jitter(age), mouflon)
points(mouflon$age, mouflon$logit_ypred, col = "red", type = "l", lwd = 2)
```



Plotting predictions

plotting on the observed scale

```
mouflon$ypred <- exp(mouflon$logit_ypred) / (1 + exp(mouflon$logit_ypred))
plot(reproduction ~ jitter(age), mouflon)
points(mouflon$age, mouflon$ypred, col = "red", type = "l", lwd = 2)
```



Plotting predictions

but it can be much simpler

Code

Plot

```
dat_predict <- data.frame(
  age = seq(min(mouflon$age), max(mouflon$age), length = 1
) %>%
  mutate(
    reproduction = predict(m1, type = "response", newdata
  )

ggplot(mouflon, aes(x = age, y = reproduction)) +
  geom_jitter(height = 0.01) +
  geom_line(data = dat_predict, aes(x = age, y = reproduct
```

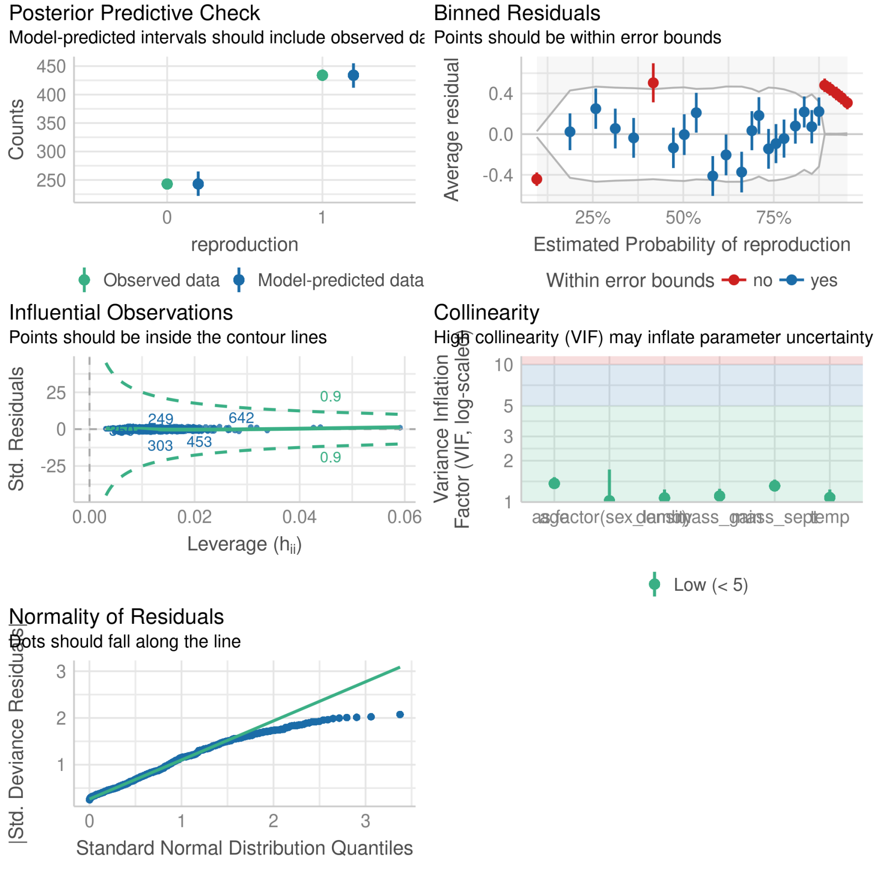
Your turn

we can do the same things with more complex models

```
m2 <- glm(
  reproduction ~ age + mass_sept + as.factor(sex_lamb) +
    mass_gain + density + temp,
  data = mouflon,
  family = binomial
)
```

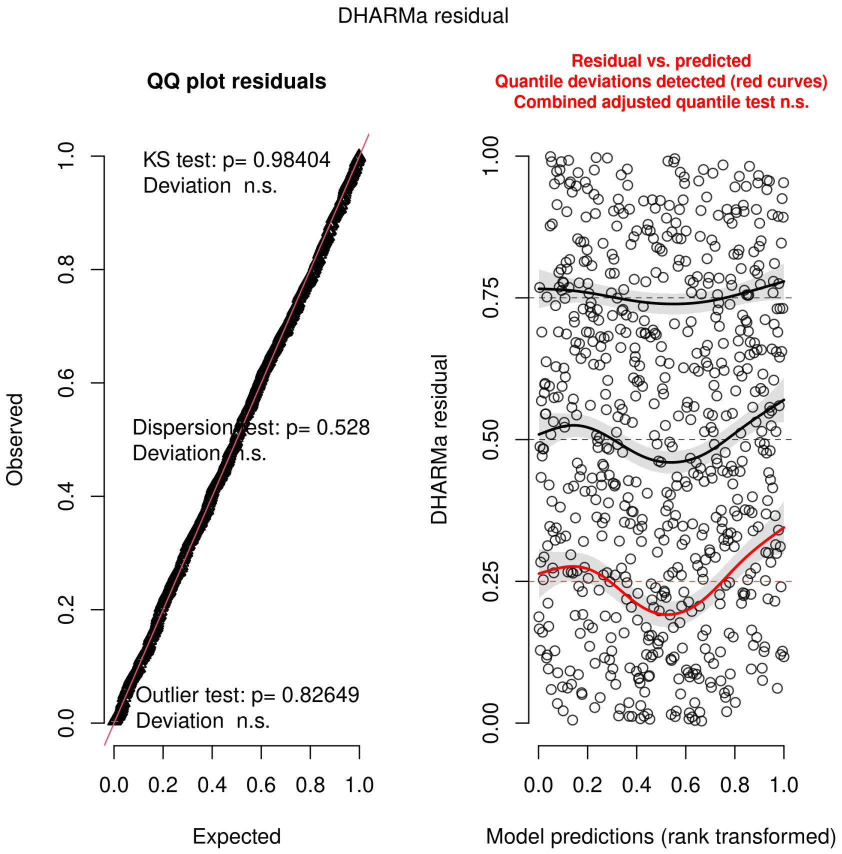
check model

```
check_model(m2)
```



with DHaRMA

```
simulationOutput <- simulateResiduals(m2)
plot(simulationOutput)
```



Poisson regression

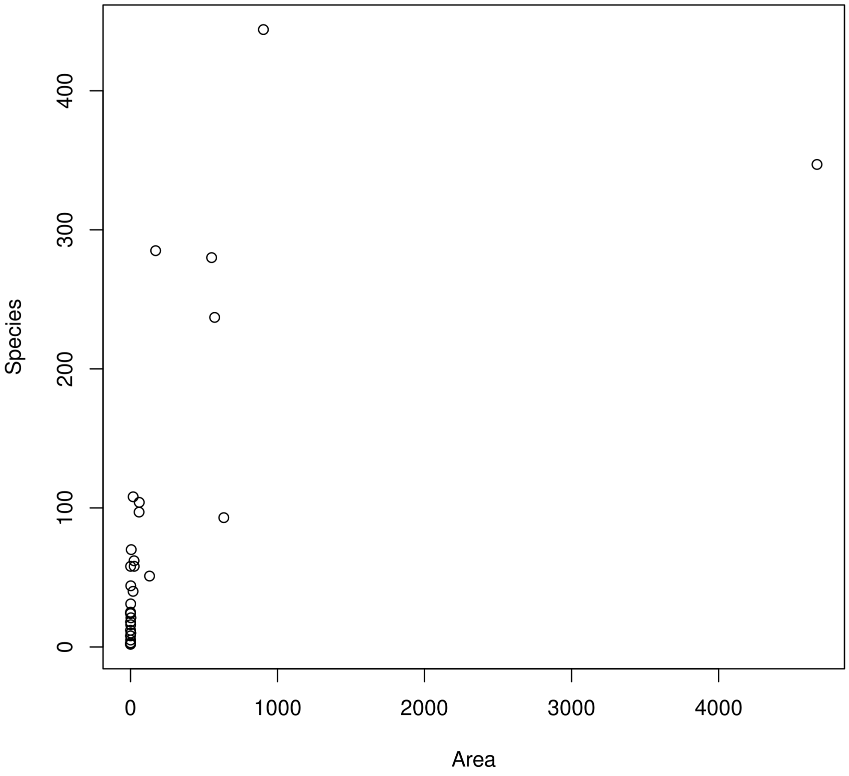
Data

data on galapagos islands species richness

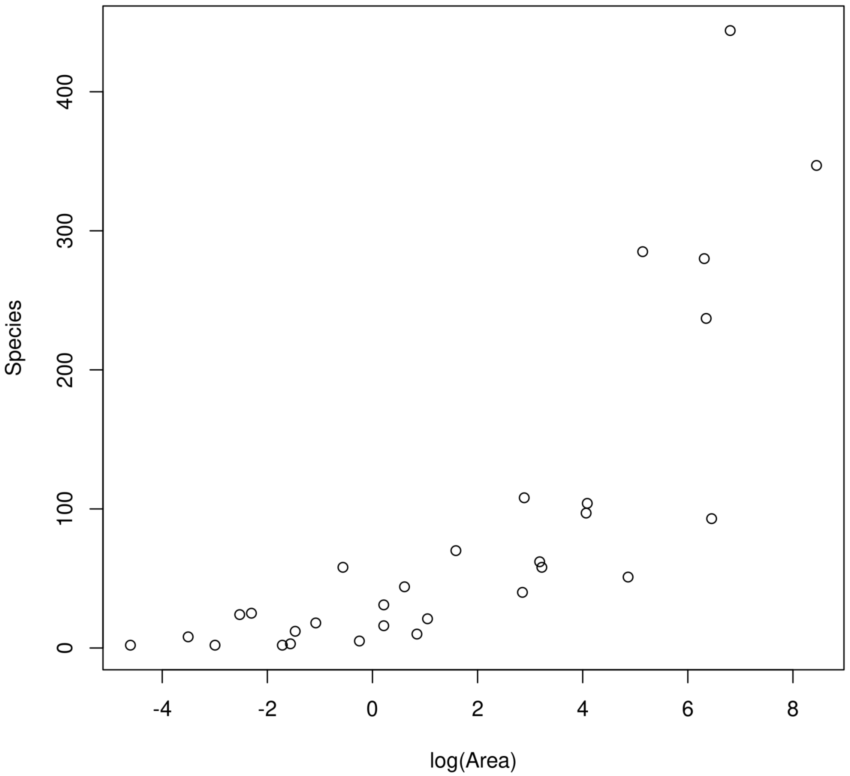
Fit 3 models:

- model of total number of species
- model of proportion of endemics to total
- model of species density

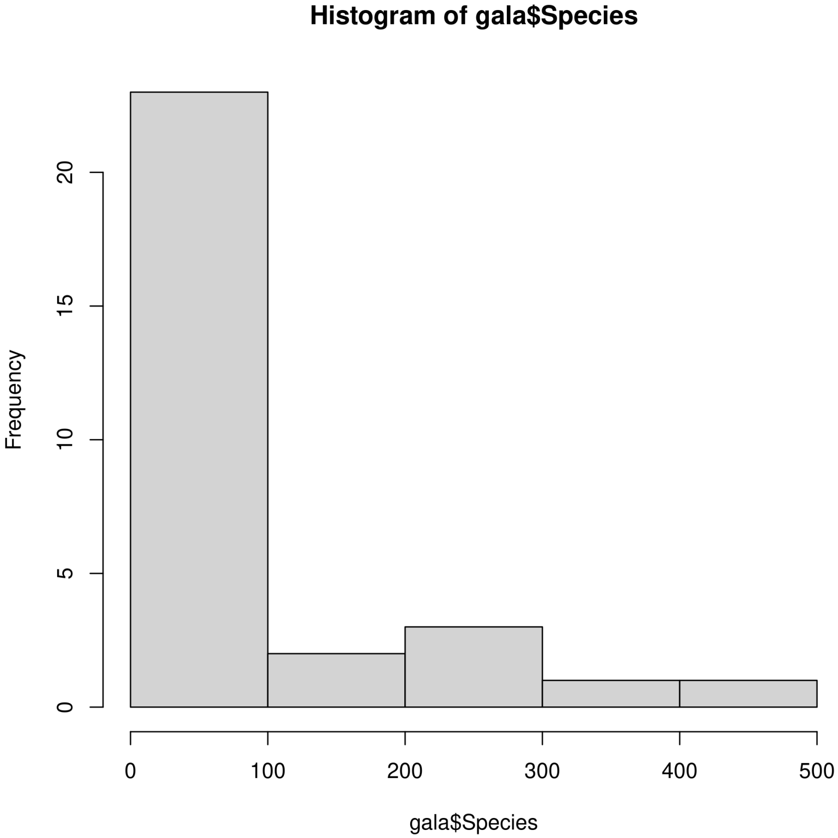
```r
gala <- read.csv("data/gala.csv")
plot(Species ~ Area, gala)
```



```
plot(Species ~ log(Area), gala)
```



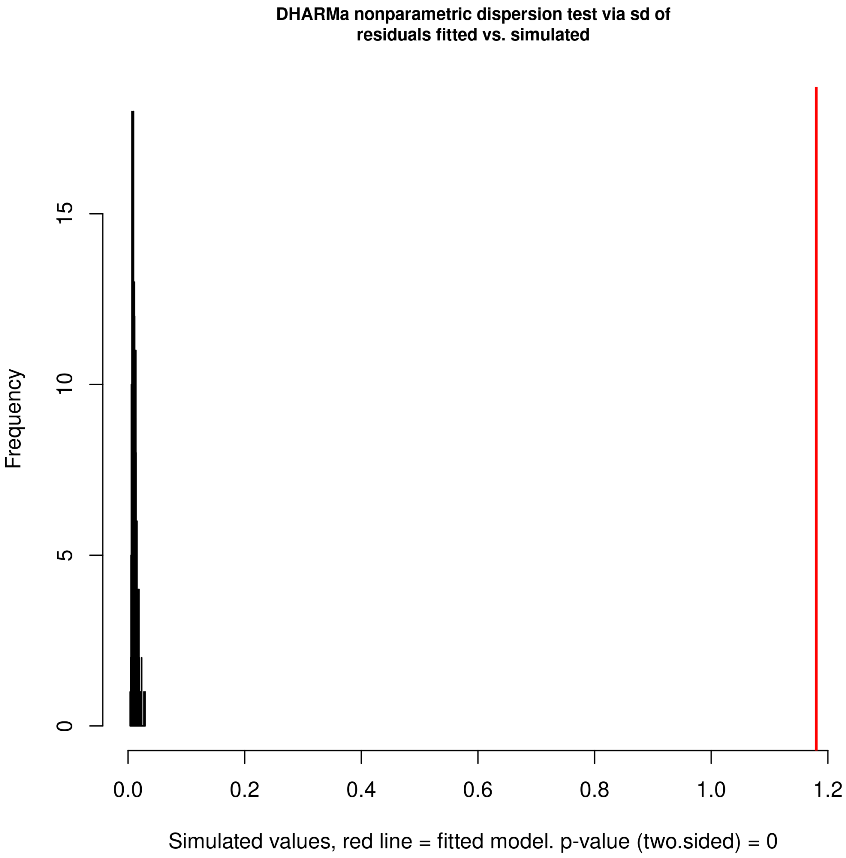
```
hist(gala$Species)
```



```
modpl <- glm(Species ~ Area + Elevation + Nearest, family = poisson, gala)
summary(modpl)
```

```
##
## Call:
## glm(formula = Species ~ Area + Elevation + Nearest, family = poisson,
##     data = gala)
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept)  3.548e+00  3.933e-02  90.211  < 2e-16 ***
## Area        -5.529e-05  1.890e-05  -2.925  0.00344 **
## Elevation    1.588e-03  5.040e-05  31.502  < 2e-16 ***
## Nearest      5.921e-03  1.466e-03   4.039 5.38e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 3510.7  on 29  degrees of freedom
## Residual deviance: 1797.8  on 26  degrees of freedom
## AIC: 1966.7
##
## Number of Fisher Scoring iterations: 5
```

```
res <- simulateResiduals(modpl)
testDispersion(res)
```

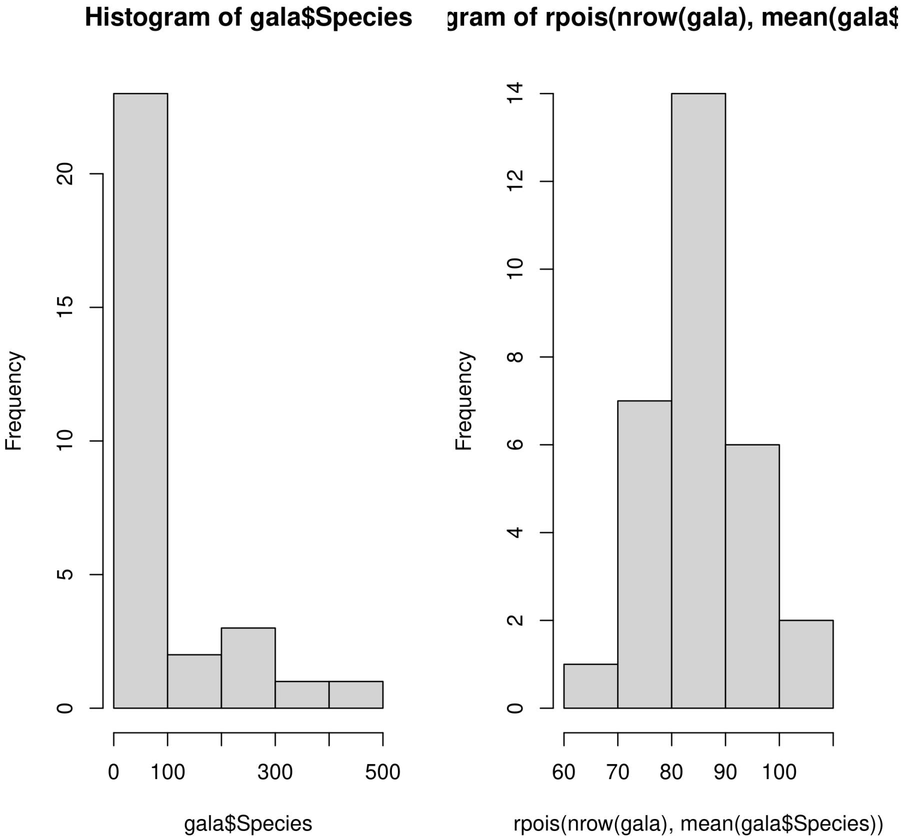


```
##
##      DHARMa nonparametric dispersion test via sd of residuals fitted vs.
##      simulated
##
## data:  simulationOutput
## dispersion = 110.32, p-value < 2.2e-16
```

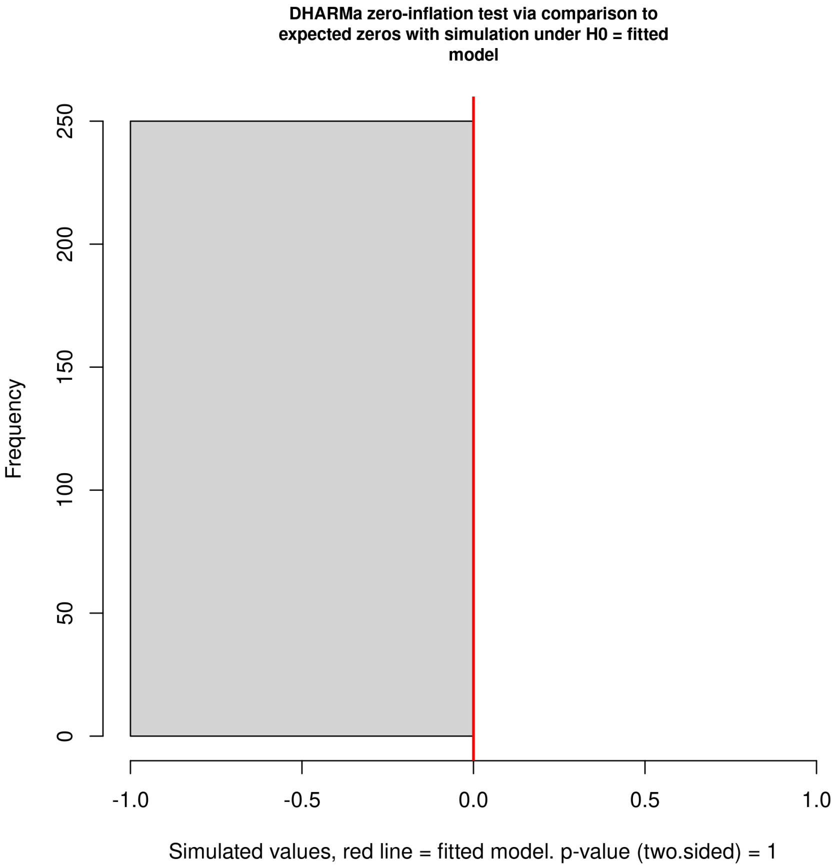
```
c(mean(gala$Species), var(gala$Species))
```

```
## [1]    85.23333 13140.73678
```

```
par(mfrow=c(1,2))
hist(gala$Species)
hist(rpois(nrow(gala), mean(gala$Species)))
```

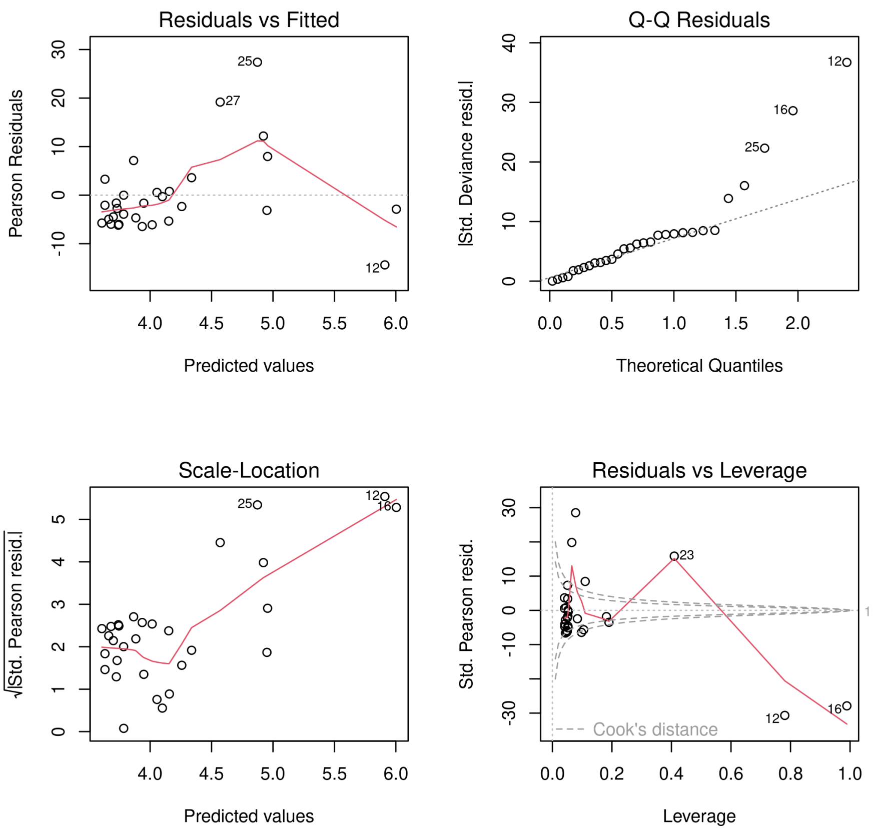


```
testZeroInflation(res)
```



```
##
##      DHARMa zero-inflation test via comparison to expected zeros with
##      simulation under H0 = fitted model
##
## data:  simulationOutput
## ratioObsSim = NaN, p-value = 1
## alternative hypothesis: two.sided
```

```
par(mfrow = c(2, 2))
plot(modpl)
```



Happy coding