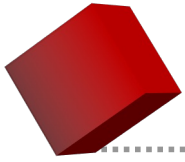


# Introduction to Linear Regression

Andrés Garchitorena

Institut de Recherche pour le Développement

*E2M2 Workshop  
Ranomafana, March 2024*



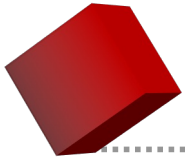
# Objectives of the lecture

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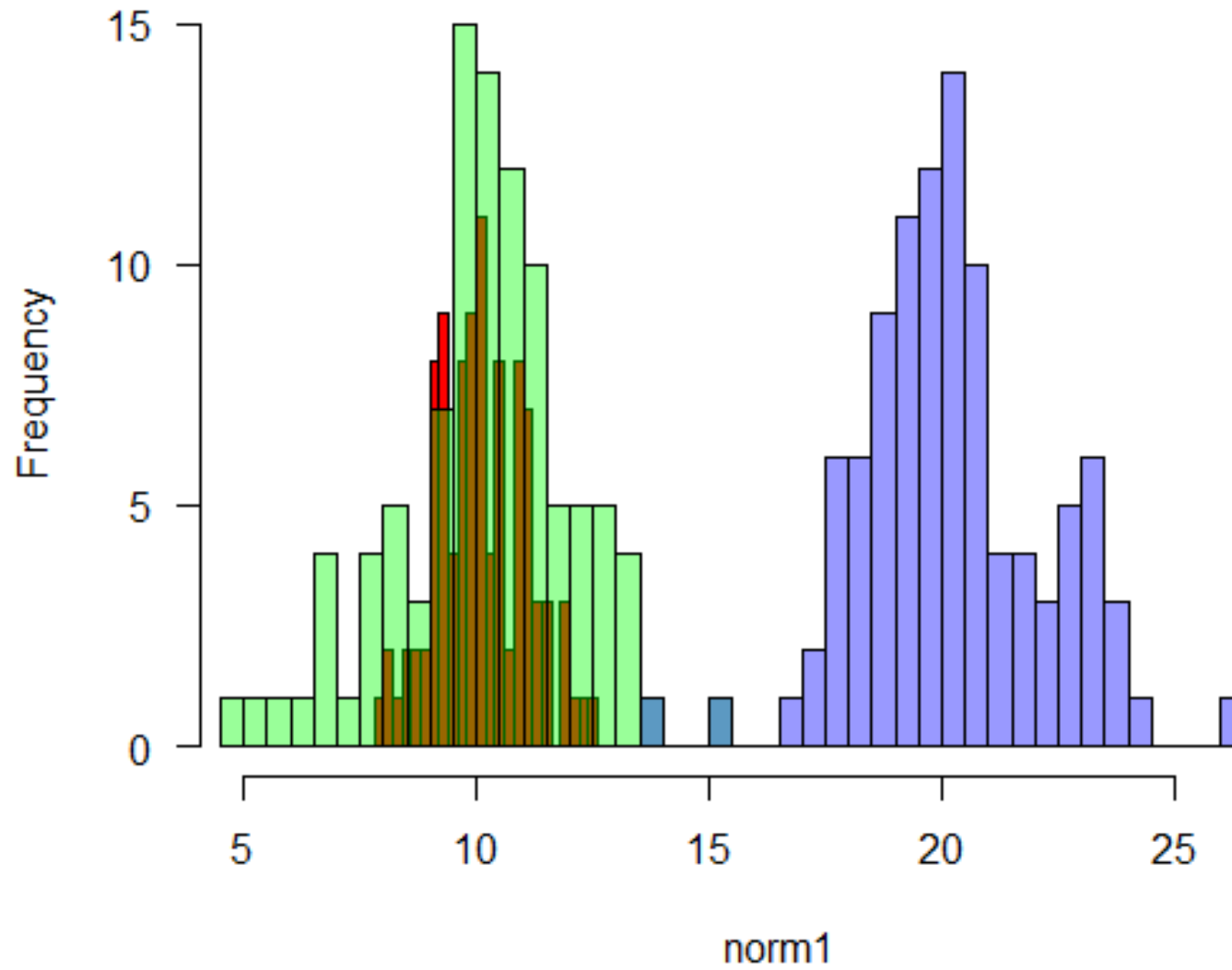
1. Remind some basic principles around linear regression and statistical models
2. Introduce the use of generalized linear models for the study of epidemiological questions
3. Provide an overview of the steps involved in developing a generalized linear model

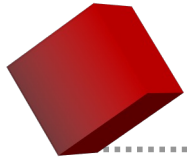
## 1. Univariate Linear Models

**SOME BASICS FIRST...**



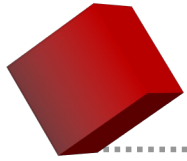
# Variables and distributions



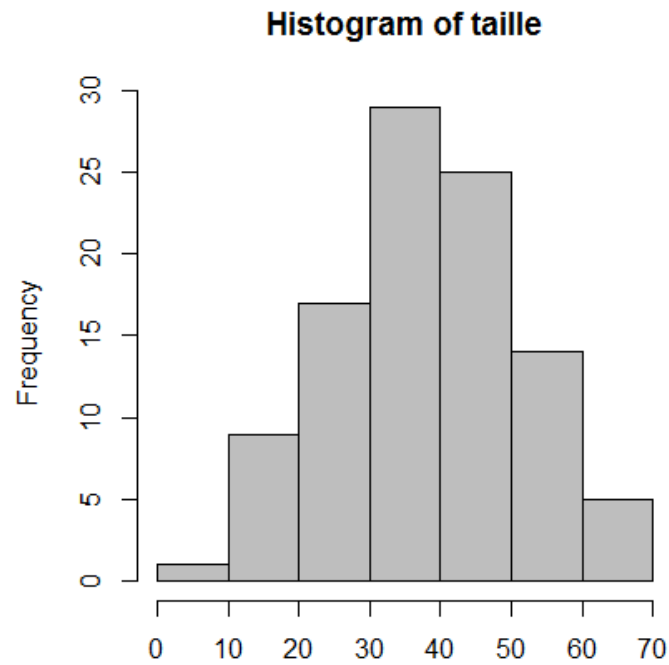


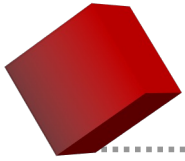
# Children height and determinants



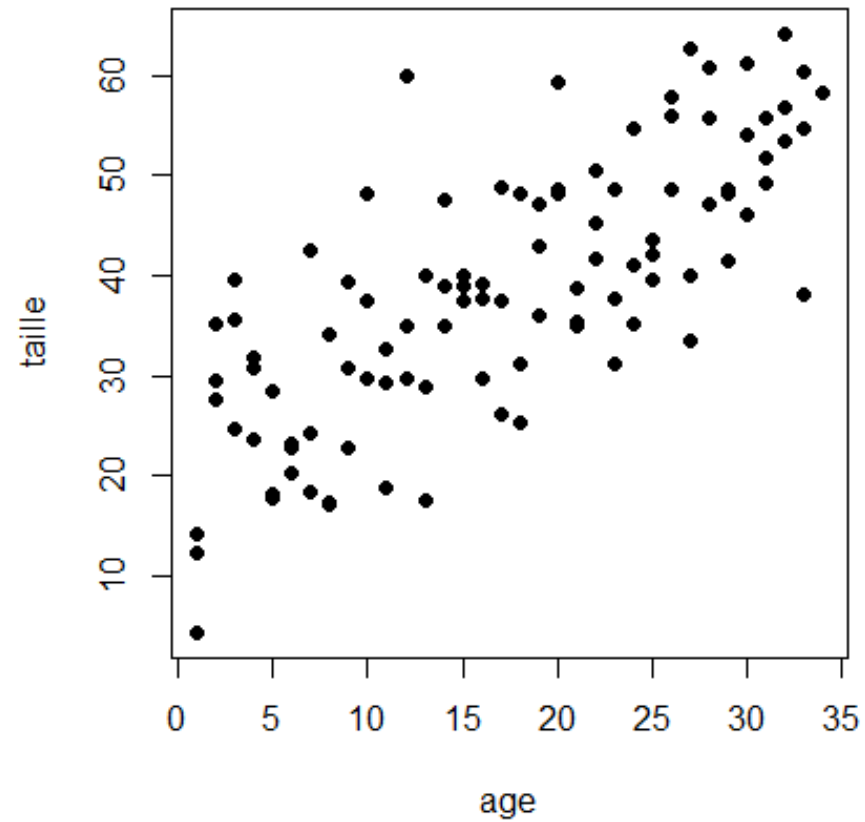


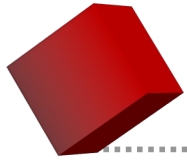
# Children height and determinants





# Children height and determinants



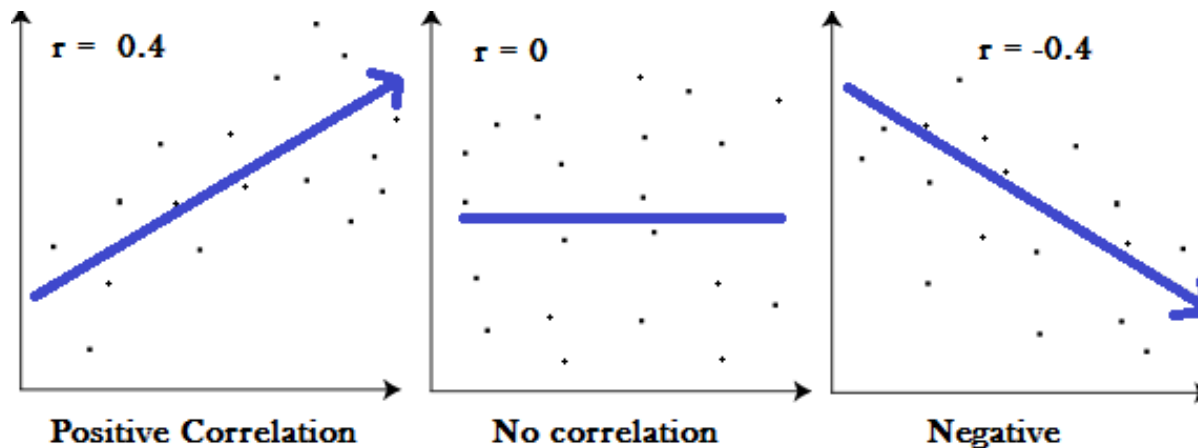


# Correlation tests (Michelle's presentation)

Correlation coefficient formulas are used to find how strong a relationship is between data. Most common for quantitative variables is Pearson's, but there are non-parametric alternatives

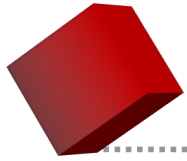
The formulas return a value between -1 and 1, where:

- 1 indicates a strong positive relationship
- -1 indicates a strong negative relationship
- 0 indicates no relationship

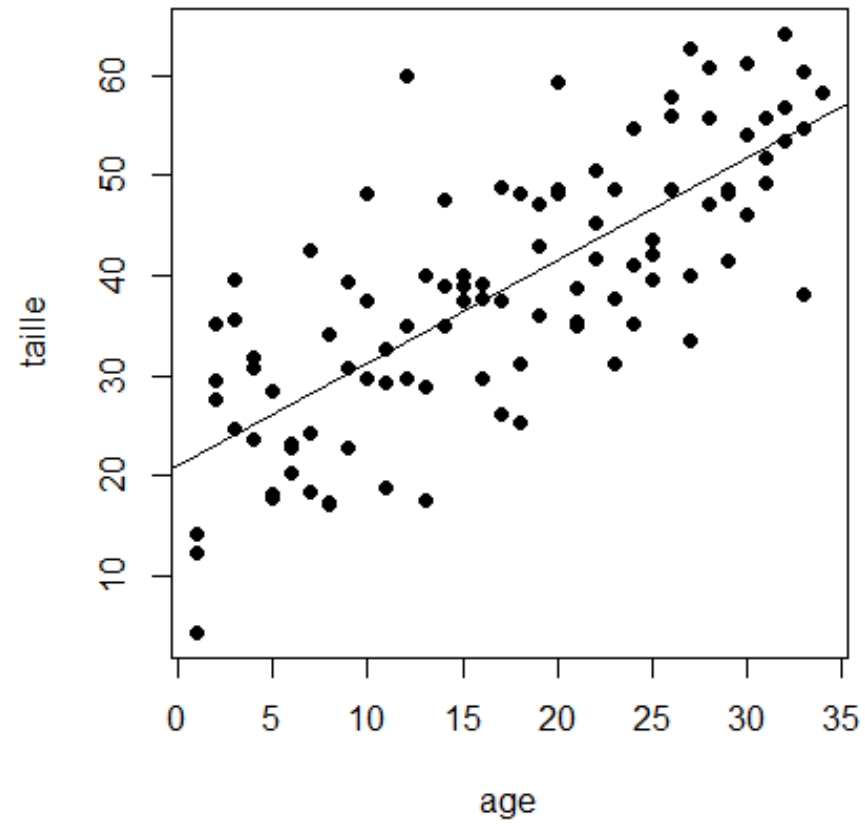


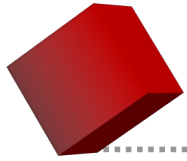
$$r = \frac{n(\sum xy) - (\sum x)(\sum y)}{\sqrt{[n\sum x^2 - (\sum x)^2][n\sum y^2 - (\sum y)^2]}}$$





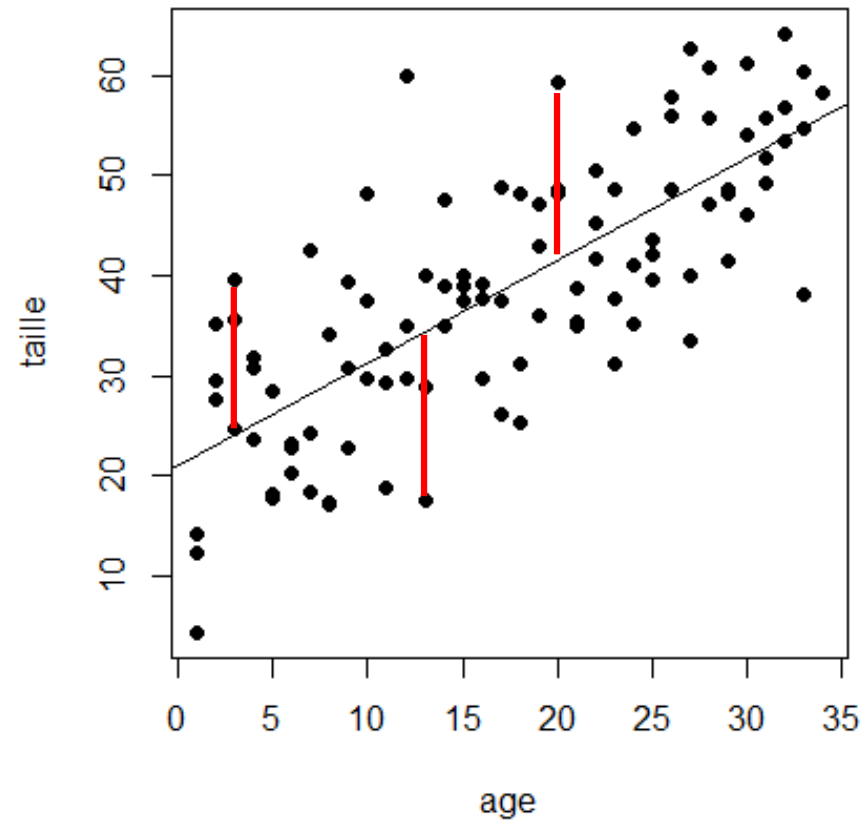
# Simple linear regression

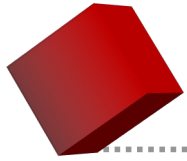




# Simple linear regression

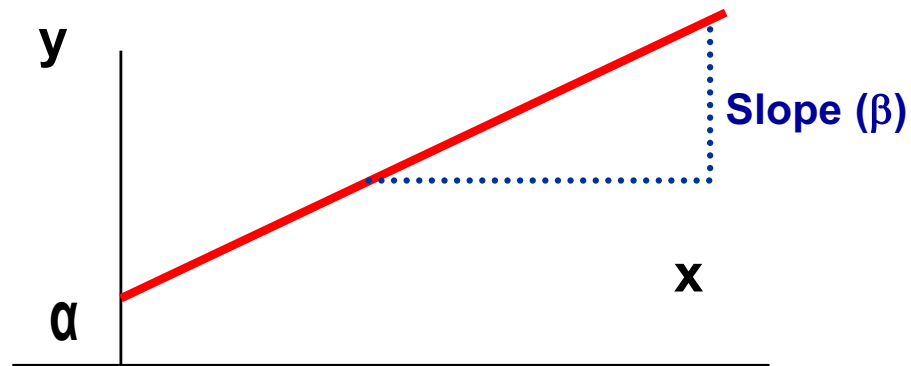
The goal is to minimize the difference between what we predict and what we observe



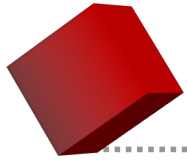


# Simple linear regression

- Relation between 2 continuous variables



- *Intercept ( $\alpha$ )*
  - Value of y when x is 0
- *Regression coefficient  $\beta_1$* 
  - Measures association between y and x
  - Amount by which y changes on average when x changes by one unit
- *Error ( $\varepsilon$ )*
  - Difference between the predicted values and observed values of y



## Simple linear regression

$$y = \alpha + \beta * x + \varepsilon$$

Response variable =

Systematic  
component

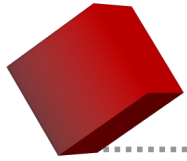
+

Residual  
component

Intercept and  
explanatory variables

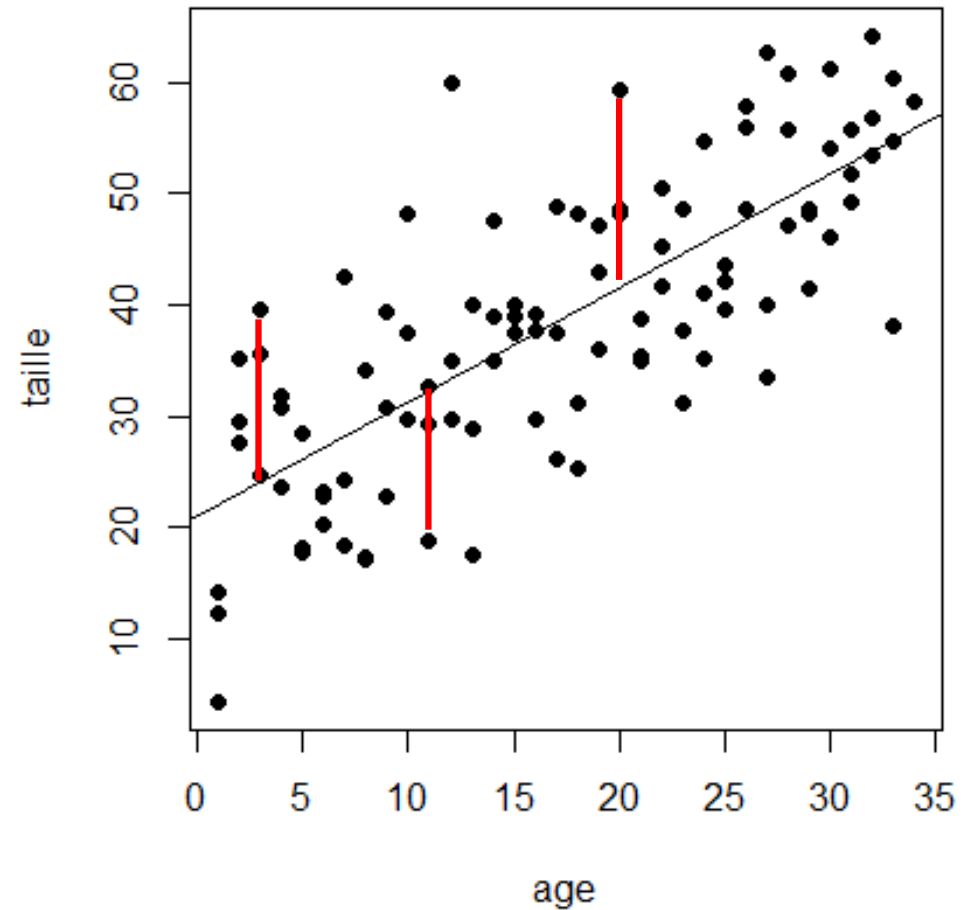
- Null mean
- Independence
- Fixed variance
- Normality

The R function to fit a linear model is `lm()` which uses the form  
**`fitted.model <- lm(formula, data=data.frame)`**



## Simple linear regression

$$\text{Taille (cm)} = 20 + 1.15 \times \text{Age (months)} + \text{Error}$$



A process is generally the result  
of several others...

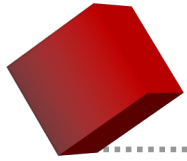
1. Univariate  
Linear Models



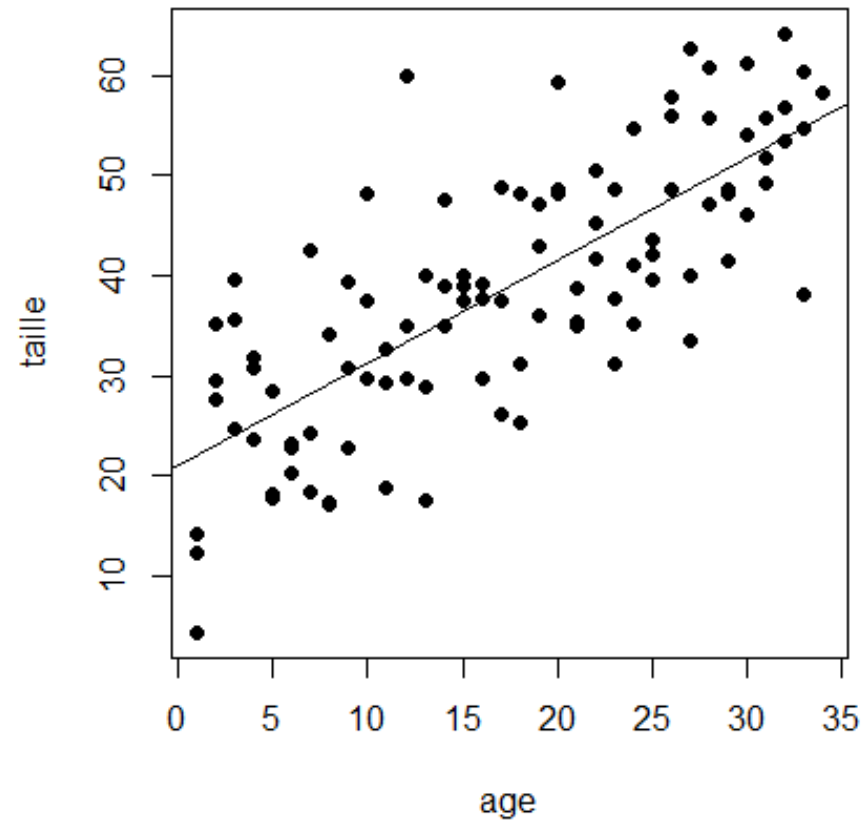
```
graph TD; A[1. Univariate Linear Models] --> B[2. Multivariate Linear Models];
```

2. Multivariate  
Linear Models

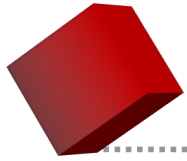
# INTRODUCING MULTIVARIATE LINEAR MODELS



# Children height and determinants

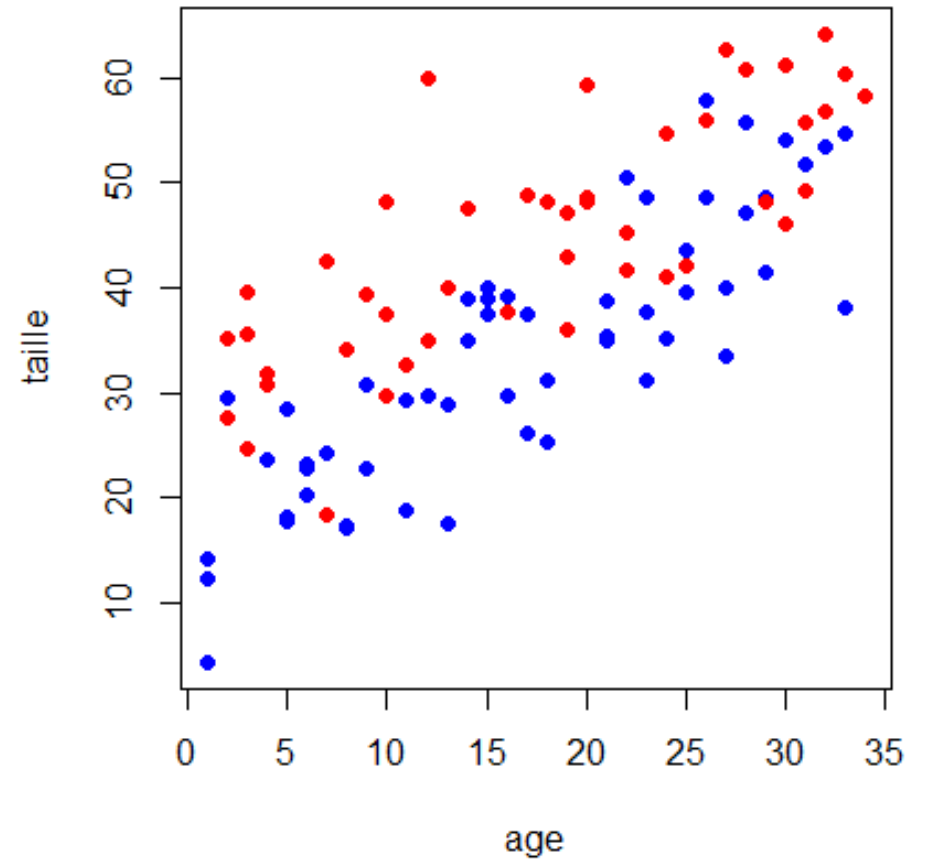


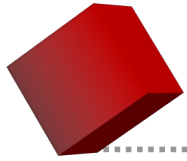




# Children height and determinants

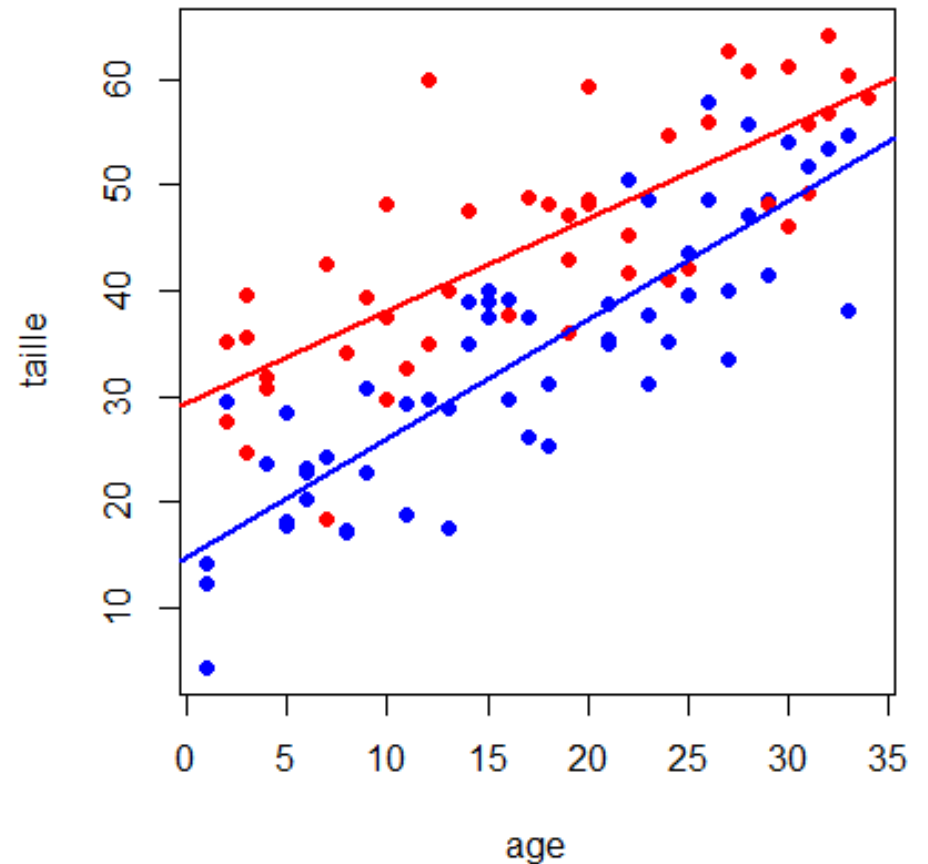
## The effect of gender



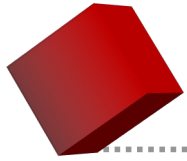


# Children height and determinants

## The effect of gender

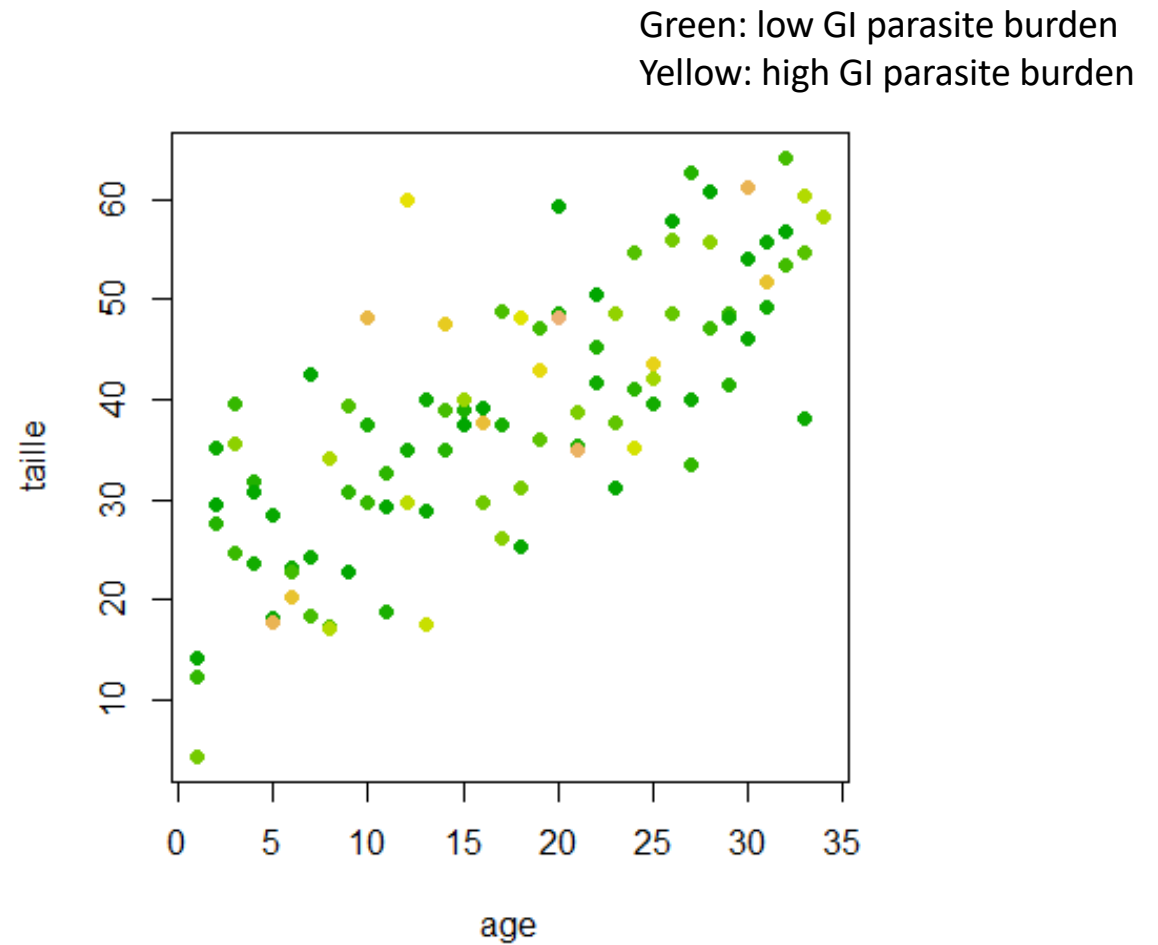


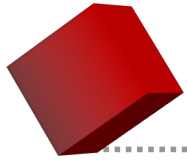
$$\text{Taille} = 15 + 1.15 \times \text{Age (months)} + 15 \times \text{Sexe (Female)} + \text{Error}$$



# Children height and determinants

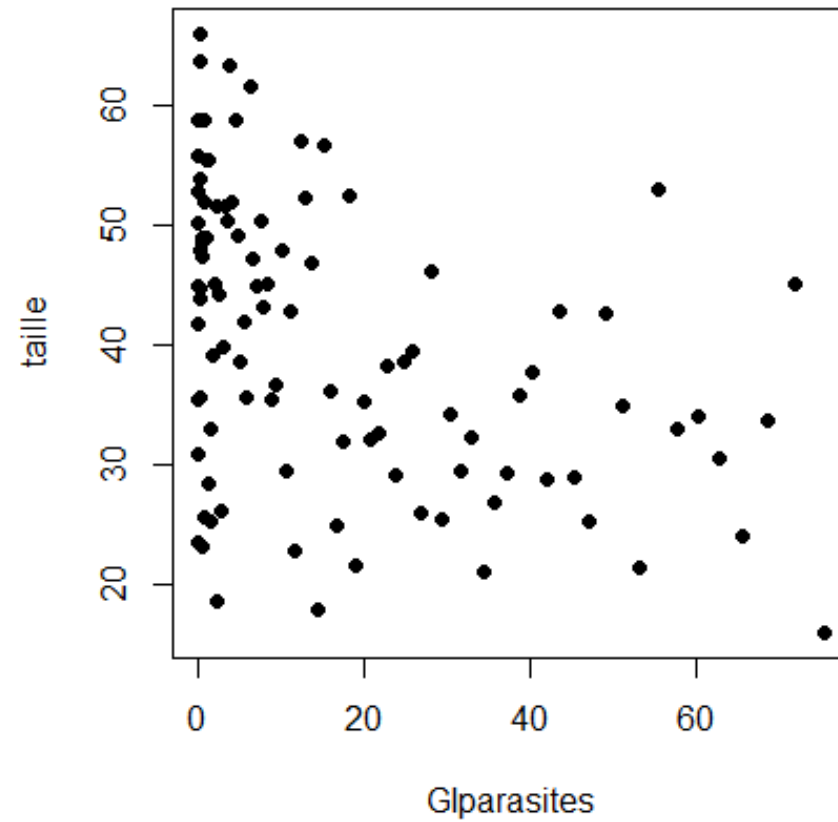
## The effect of parasites

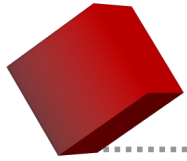




# Children height and determinants

## The effect of parasites



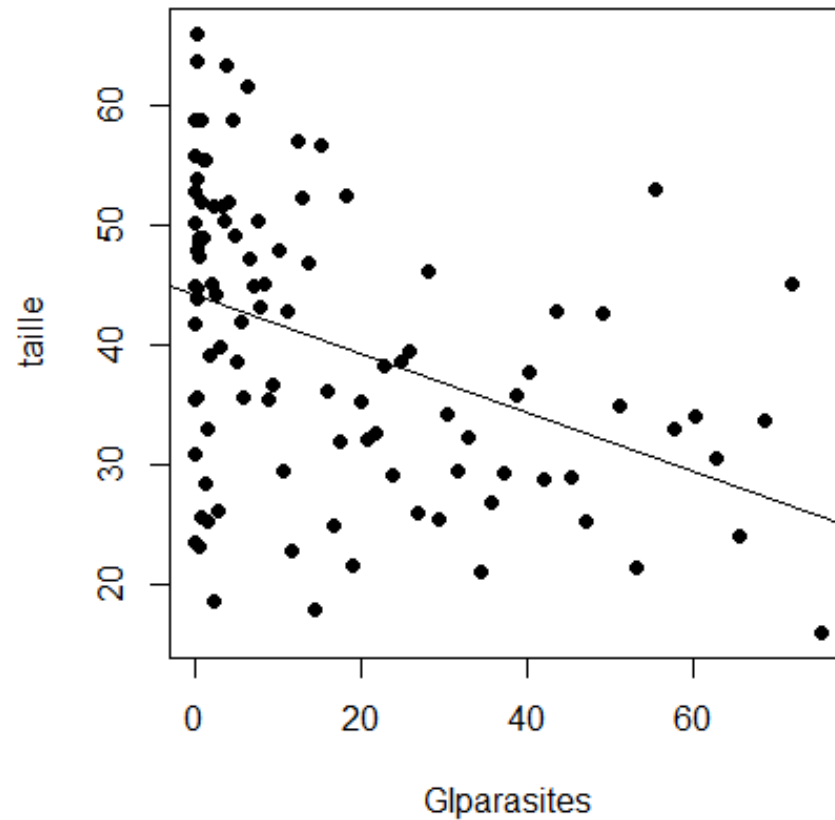


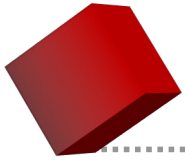
# Children height and determinants

## The effect of parasites



$$\text{Taille} = 45 - 0.3 \times \text{Nb Parasites} + \text{Error}$$



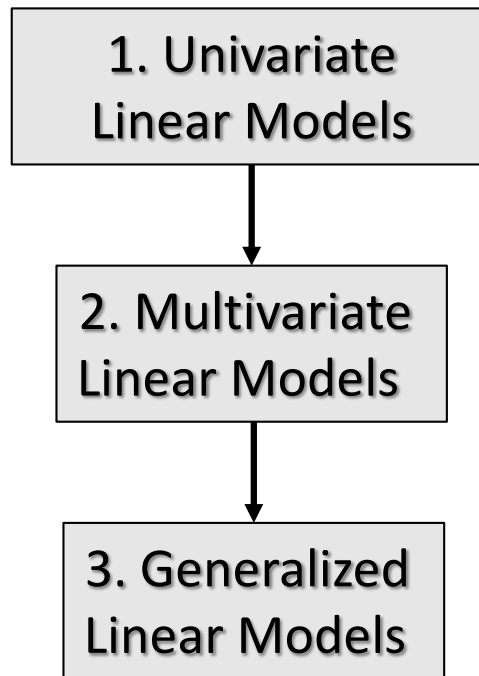


# Multiple linear regression

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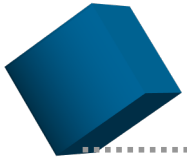
- Generalization of simple regression
- To describe the relationship between
  - The response variable,  $y$
  - The explanatory variables,  $x = (x_1, x_2, \dots, x_n)$
- The model:  $y = \alpha + \beta_1 * x_1 + \dots + \beta_n * x_n + \varepsilon$   
with  $\varepsilon \sim N(0, \sigma^2)$
- We generally select the model that best fits the data (best explains observed patterns) with the smallest number of variables

Unfortunately, not all things in  
life are normal...



# INTRODUCING GENERALIZED LINEAR MODELS



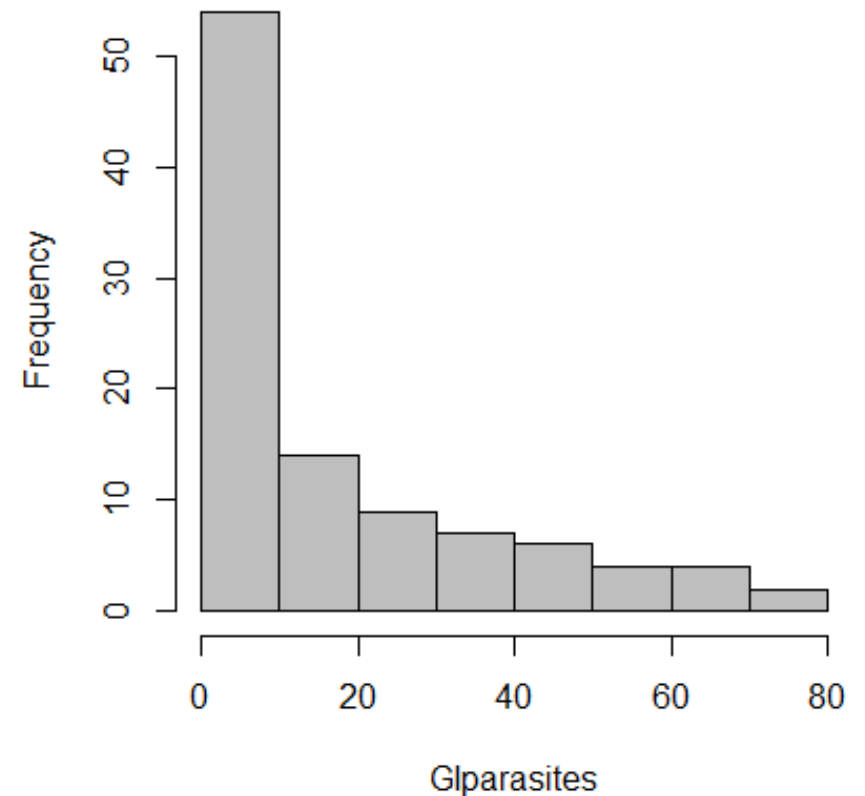


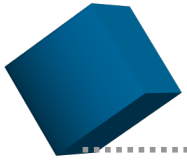
## Count data



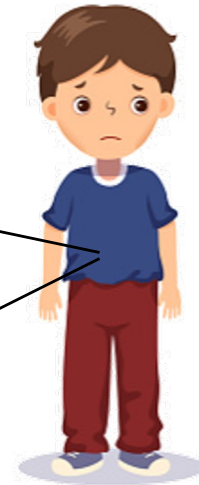
**Histogram of GIParasites**

- Cannot be negative
- Discrete values
- The lower the values, the « less normal » they generally are.
- Examples:
  - Number of individuals of a species X
  - Number of people with a disease X

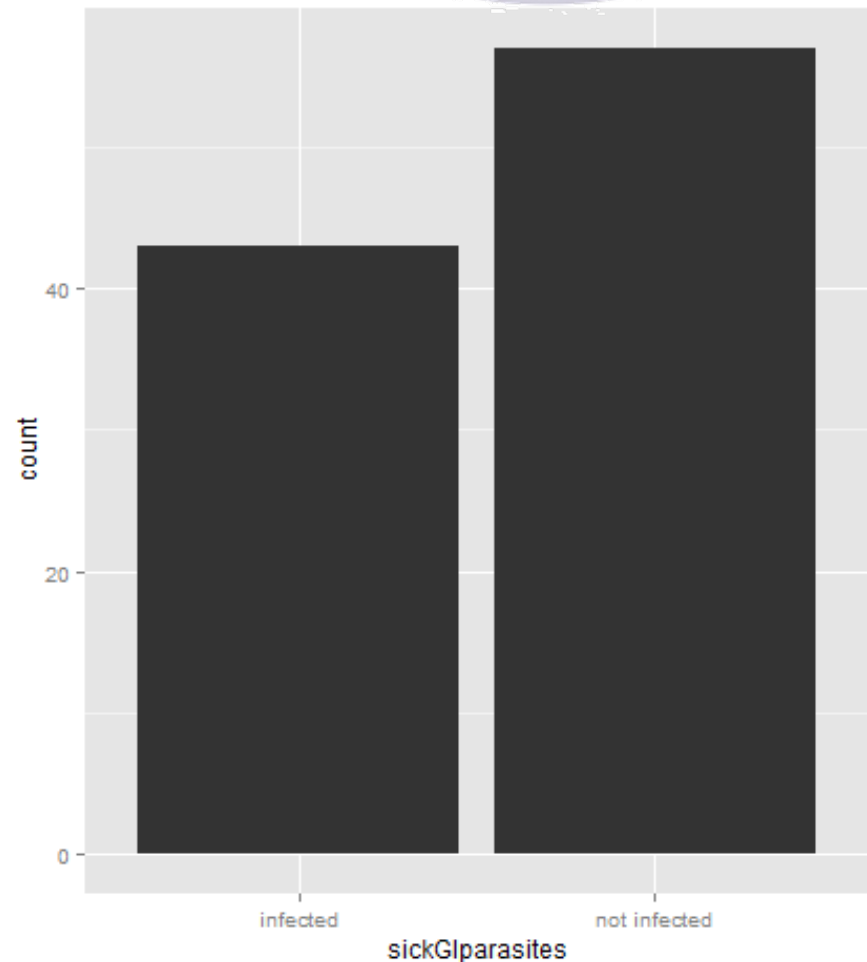


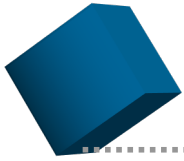


## Binary data (events)



- Values either 1 or 0 (either happened or not happened)
- The outcome variable is the number of successes /failures
- Examples:
  - Presence of a disease
  - Presence of a species



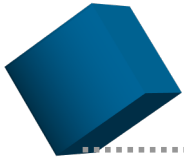


## Limitations of linear models

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- In these types of situations, general linear models are not appropriate because:
  - The range of Y is restricted (e.g. binary, count)
  - The variance of Y depends on the mean
- **Generalized linear models** extend the linear model framework to address both of these issues by using a **linear predictor** and a **link function**

The R function to fit a general linear model is `glm()` which uses the form **`fitted.model <- glm(formula, family="model family", data=data.frame)`**



## Generalized linear modeling

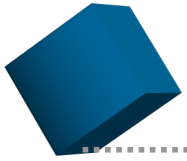
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- One generalization of multiple linear regression. Response,  $y$ , predictor variables  $x_1, x_2, \dots$ . The distribution of  $Y$  depends on the  $X$ 's through a single linear function, the “linear predictor”

$$\nu = \beta_1 x_1 + \beta_2 x_2 + \dots + \beta_p x_p$$

- A link function describes how the mean  $E(Y) = \mu$ , depends on the linear predictor  $\nu$ .

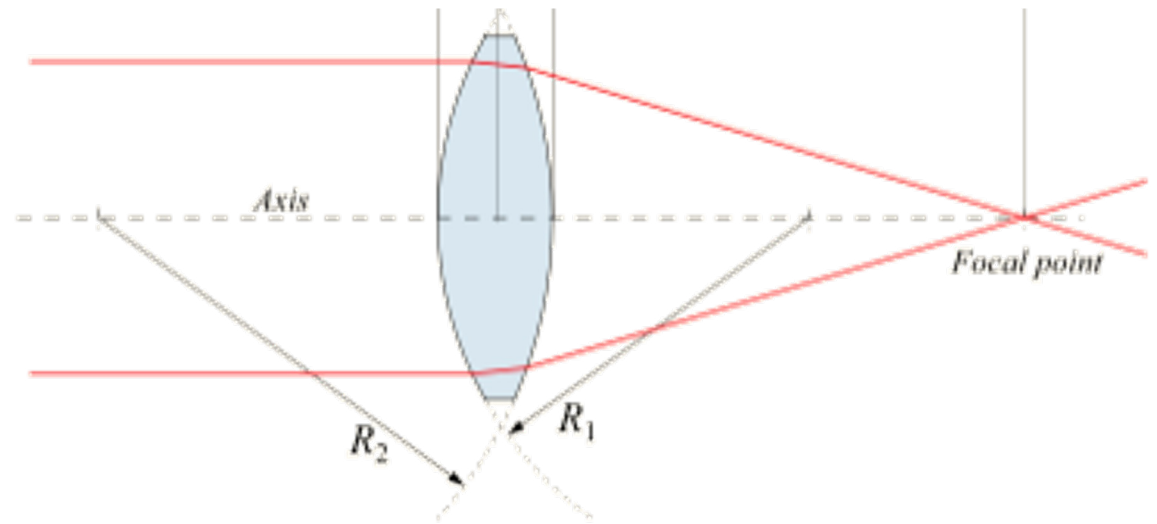
$$\mu = m(\nu), \quad \nu = m^{-1}(\mu) = l(\mu)$$



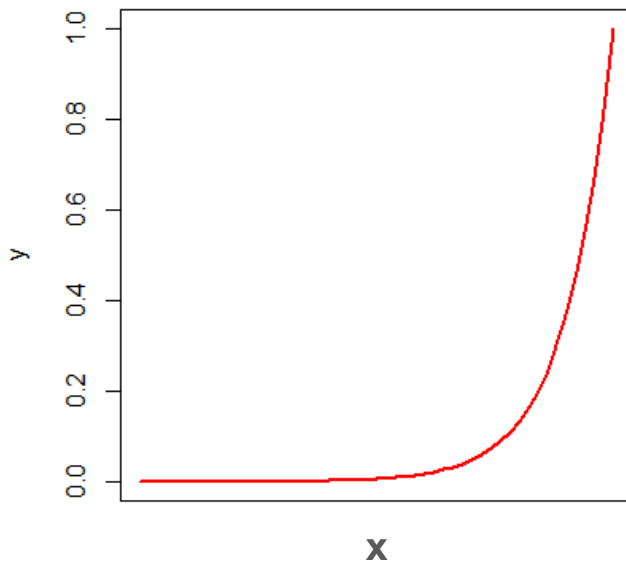
# Generalized linear modeling

## Most common families and links

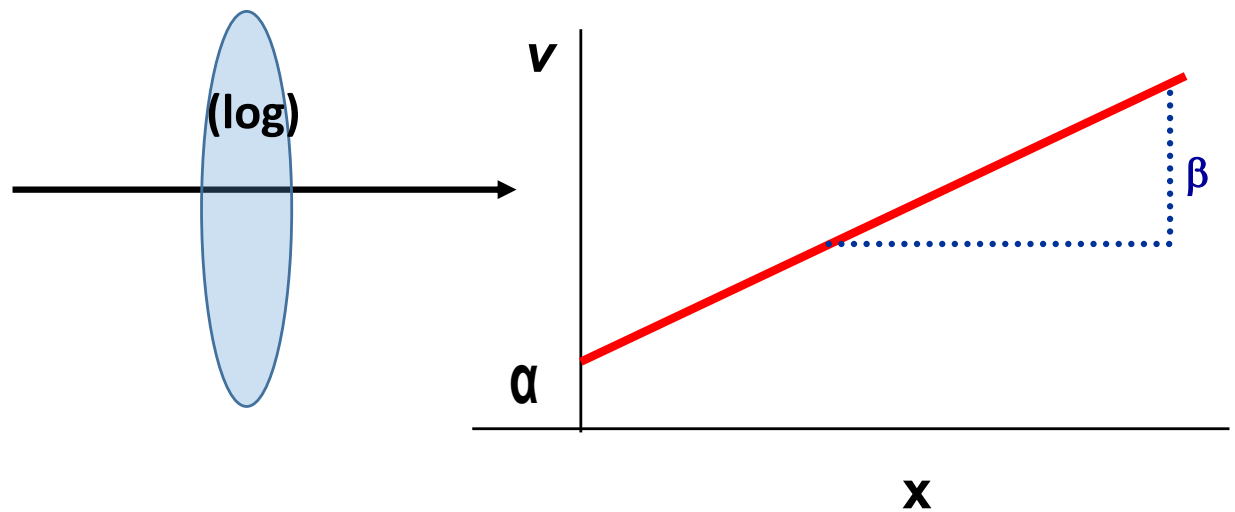
- Gaussian: identity
- Poisson: log
- Binomial: logit
- Negative binomial: log

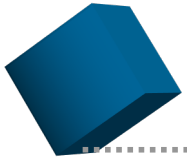


$$Y = e^{(\alpha + \beta x)}$$



$$V = \alpha + \beta x$$

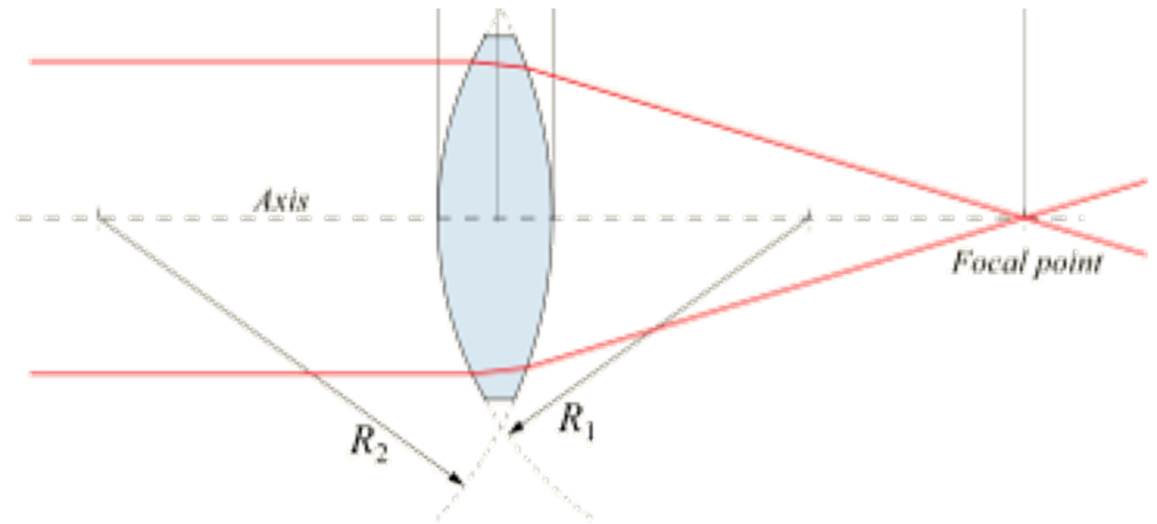




# Generalized linear modeling

## Most common families and links

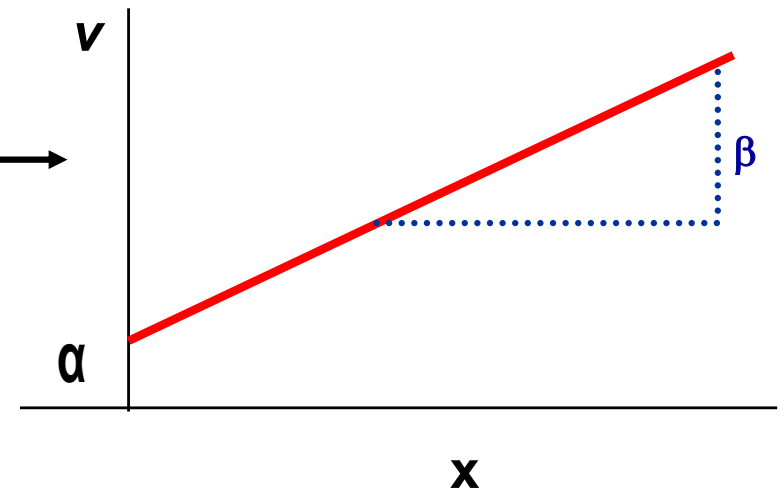
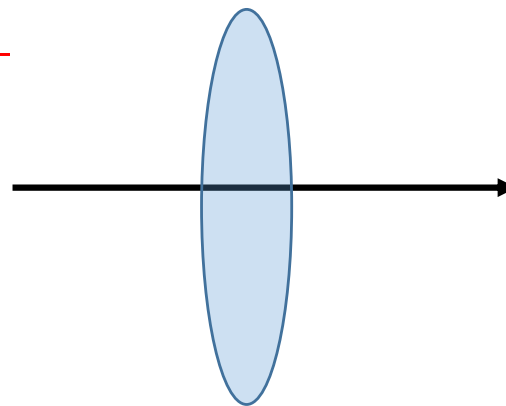
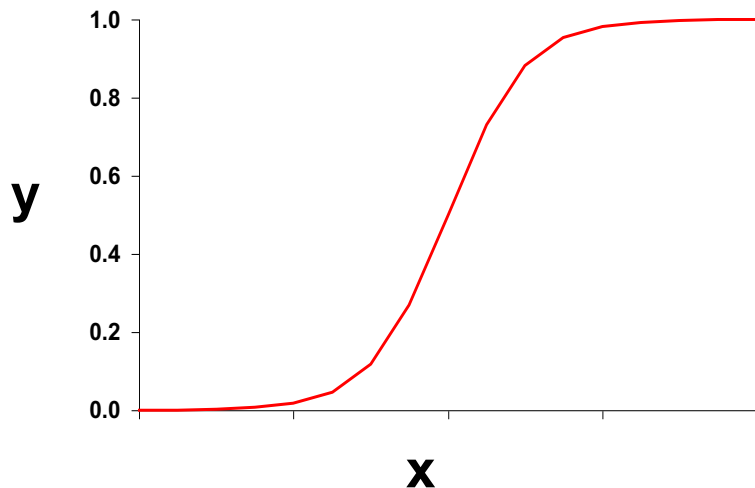
- Gaussian: identity
- Poisson: log
- Binomial: logit
- Negative binomial: log

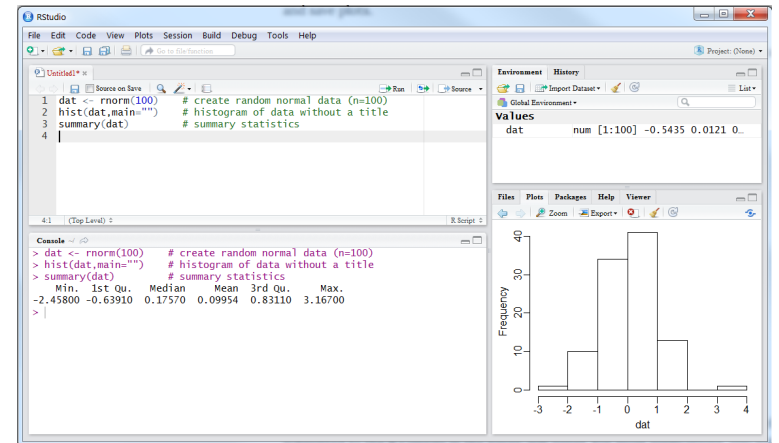
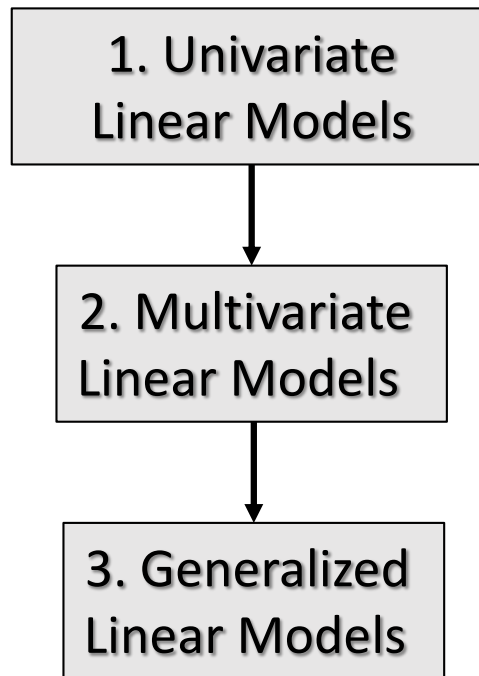


$$P(y|x) = \frac{e^{\alpha + \beta x}}{1 + e^{\alpha + \beta x}}$$

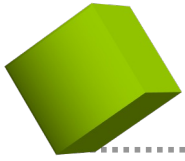
(logit)

$$V = \alpha + \beta x$$





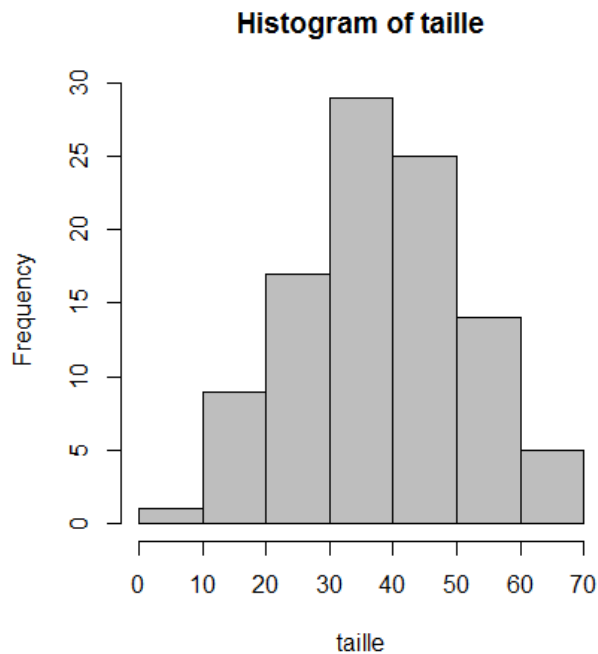
**STEPS IN DEVELOPMENT OF  
STATISTICAL MODELS**



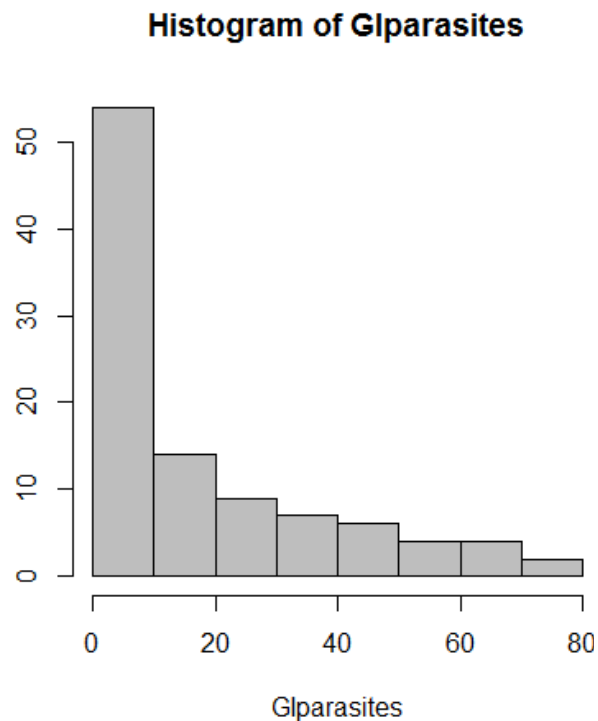
# Database construction and descriptive analyses

- Distribution of the response variable
- Distribution of the explanatory variables

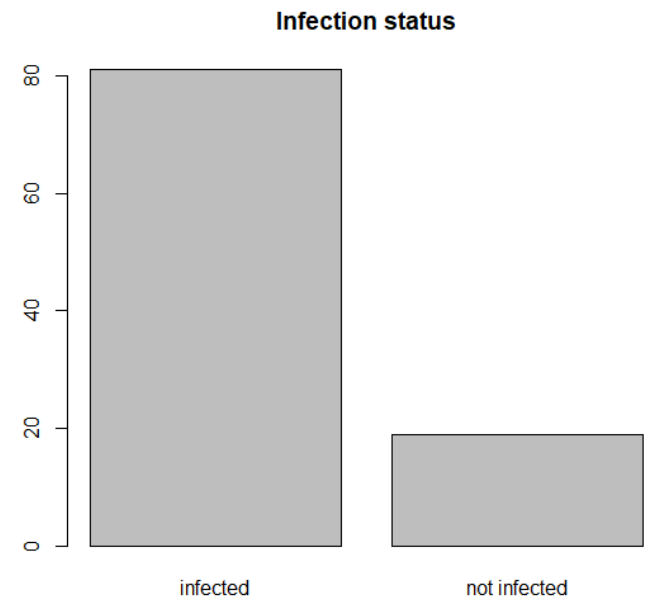
`hist(mydata$var)`



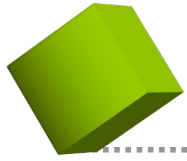
`hist(mydata$var)`



`plot(mydata$var)`



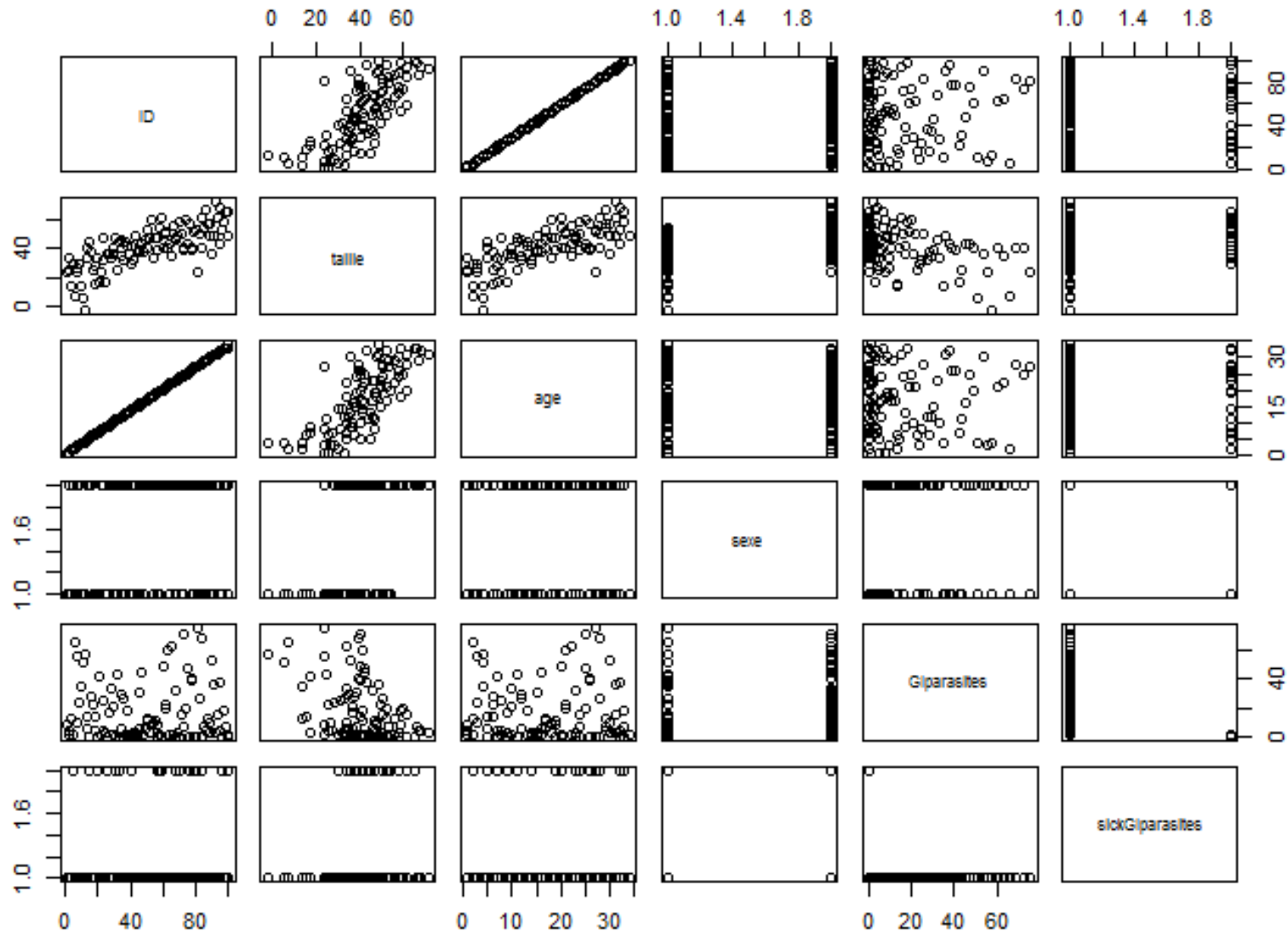


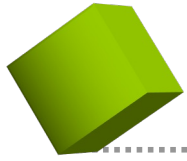


# Database construction and descriptive analyses

- Relationships between the variables

`pairs(mydata)`





## Univariate analyses

- Quantify the strength of the relationship between the response variable and each explanatory variable
- Test the significance of the relationship between the response variable and each explanatory variable

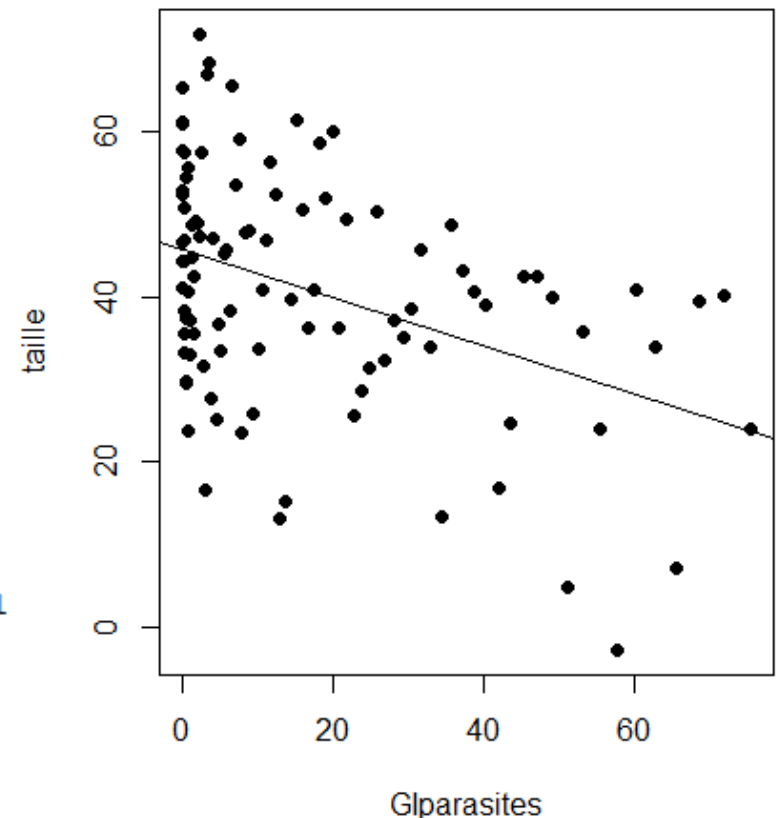
Model1 = lm(taille~Giparasites, data=mydata)  
summary (Model1)

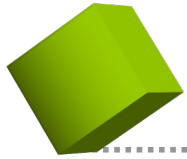
```
call:
lm(formula = taille ~ Giparasites)

Residuals:
    Min       1Q   Median       3Q      Max
-31.605  -8.351   1.113   9.901  26.528

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  45.8267    1.7154  26.714  < 2e-16 ***
Giparasites  -0.2927    0.0651  -4.495 1.91e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 13.07 on 98 degrees of freedom
Multiple R-squared:  0.171,    Adjusted R-squared:  0.1625
F-statistic: 20.21 on 1 and 98 DF, p-value: 1.906e-05
```





## Multivariate analyses

- Quantify the relationship between the response variable and a set of explanatory variables

```
Model1 = lm(taille~age+sexe+GIparasites, data=mydata)
summary (m1)
```

```
Call:
lm(formula = taille ~ age + sexe + GIparasites, data = mydata)

Residuals:
    Min       1Q   Median       3Q      Max
-16.9962  -2.6011  -0.1584   3.7331  12.0600

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  21.94145    1.28143   17.12  <2e-16 ***
age           1.02365    0.05584   18.33  <2e-16 ***
sexeMale     10.88561    1.09295    9.96  <2e-16 ***
GIparasites  -0.29930    0.02652  -11.28  <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

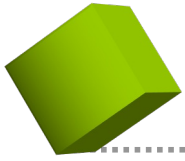
Residual standard error: 5.323 on 96 degrees of freedom
Multiple R-squared:  0.8653,    Adjusted R-squared:  0.8611
F-statistic: 205.5 on 3 and 96 DF,  p-value: < 2.2e-16
```

- Select the set of predictors that best explains the response variable (backwards, forward, stepwise)

```
drop1 (m1)
```

```
add1 (m1)
```

```
step (m1)
```

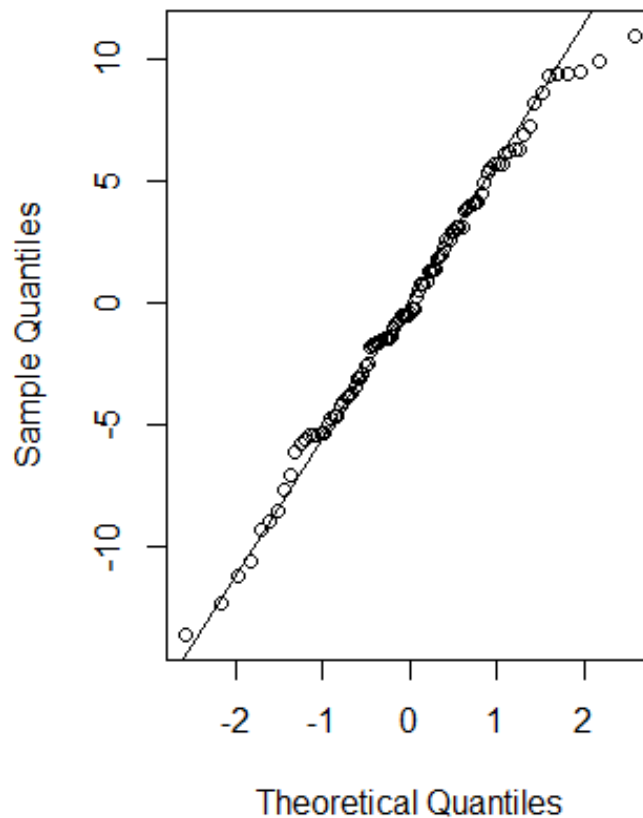


# Model validation

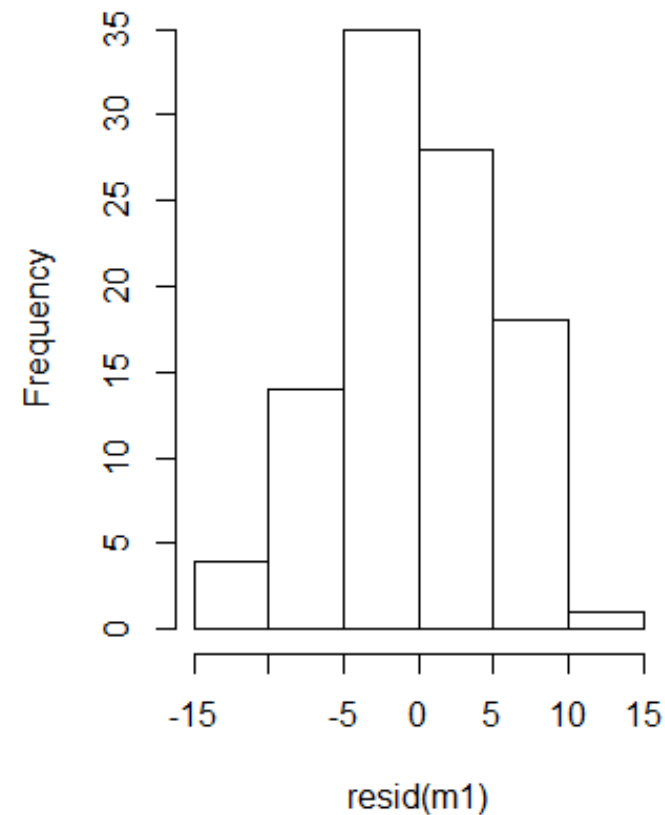
- Check that model assumptions have not been violated

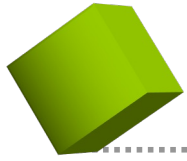
## Normality of residuals

**Normal Q-Q Plot**



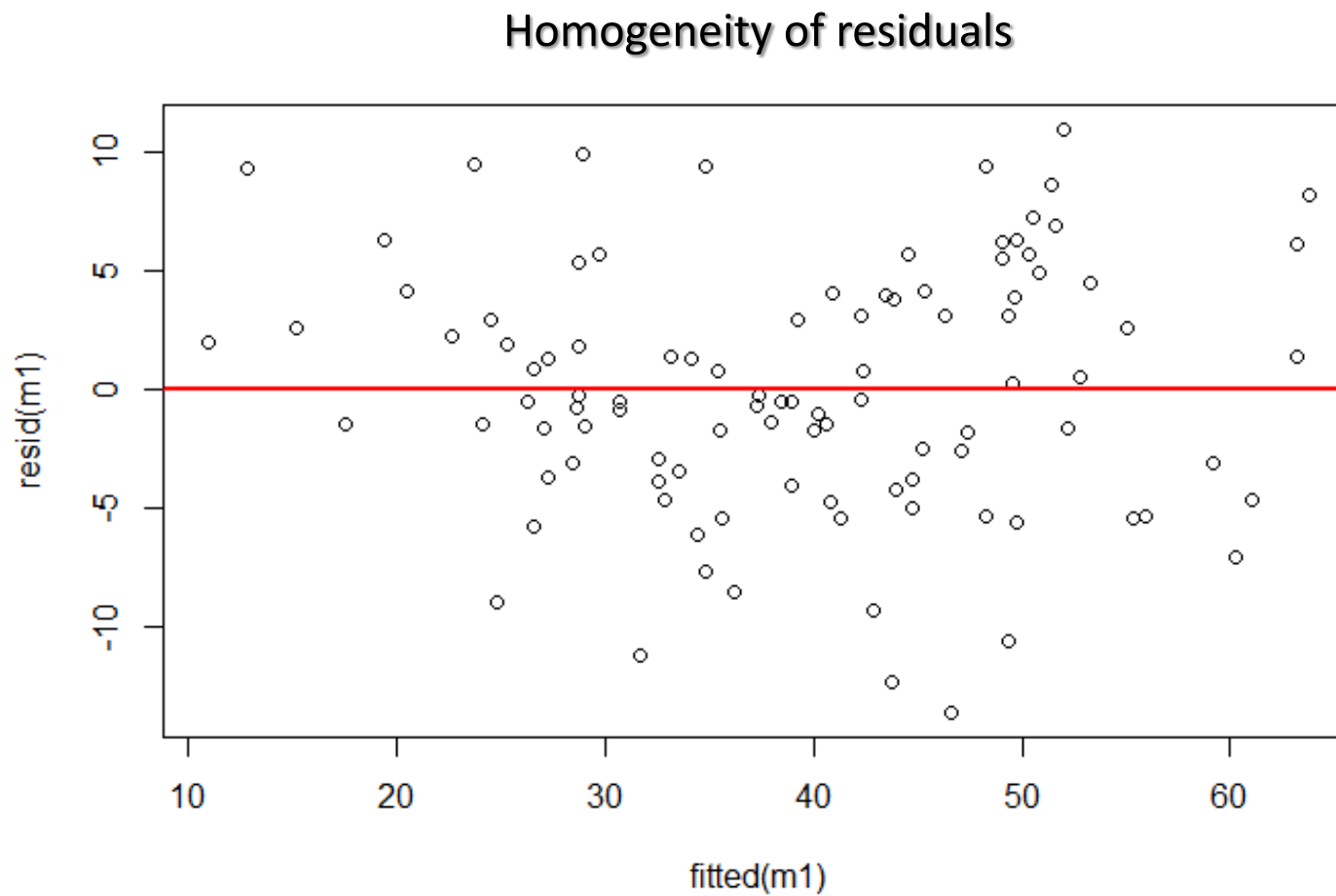
**Histogram of resid(m1)**





## Model validation

- Check that model assumptions have not been violated



# Correlation & Linear Regression in Epidemiology

Andrés Garchitorena

Researcher, Institut de Recherche pour le Développement

*Institut Pasteur Madagascar  
Antananarivo, Juin 2020*