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Generalized linear model
an extension of the linear model

https://github.com/davemakowski

Outline

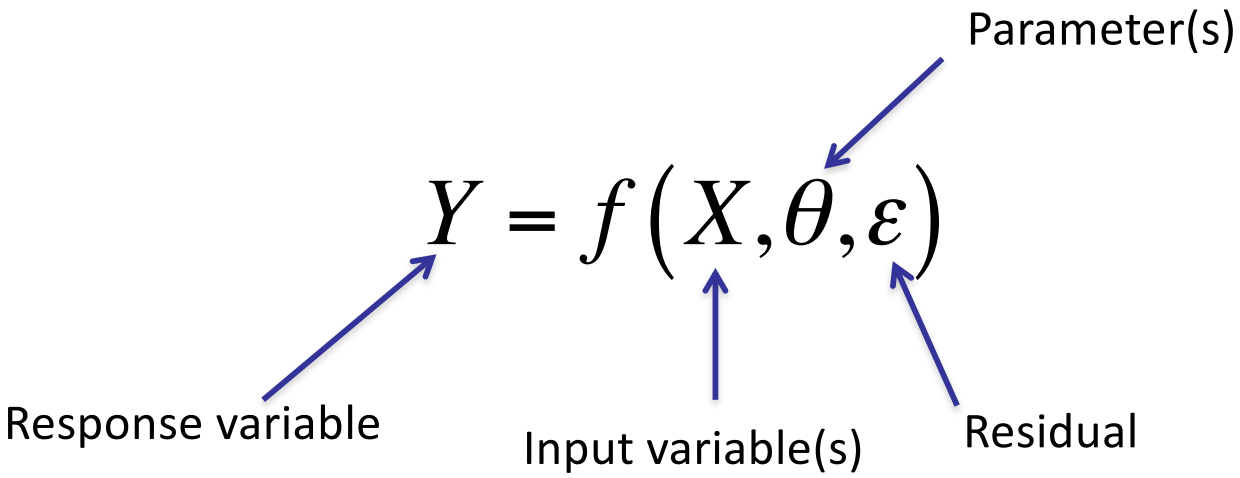
- Some reminders
- GLM: why and what
- Logistic and binomial models
- Poisson models

Some reminders

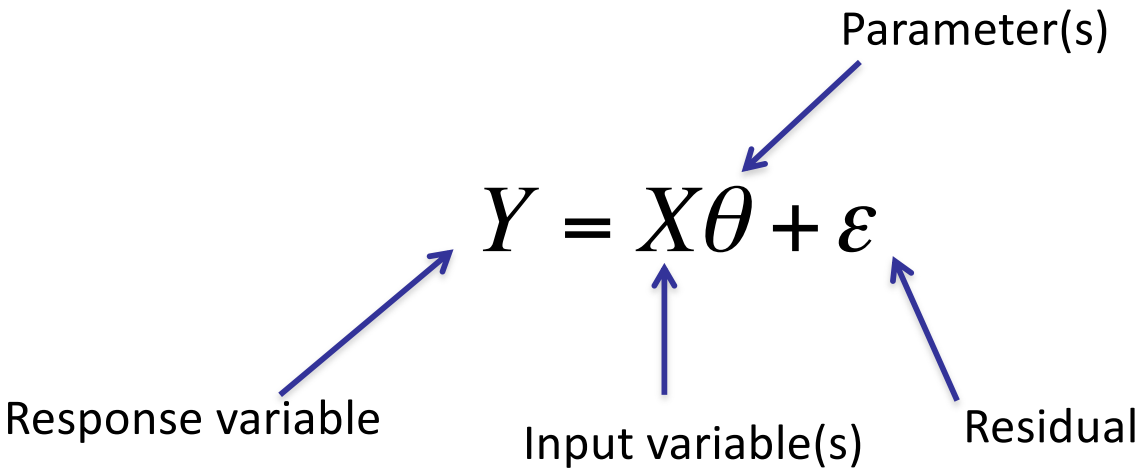
What is a statistical model?

- A particular type of mathematical model
- A model that includes observables (the measured variables)
- ... and unobservable elements (the parameters and some hidden variables)
- Some of these elements are random variables defined by probability laws.

What is a statistical model?



What is a statistical model?



What is a linear model?

$$\begin{pmatrix} y_1 \\ y_2 \\ \dots \\ y_N \end{pmatrix} = \begin{pmatrix} x_{11} & x_{12} & \dots & x_{1P} \\ x_{21} & x_{22} & \dots & x_{2P} \\ \dots & \dots & \dots & \dots \\ x_{N1} & x_{N2} & \dots & x_{NP} \end{pmatrix} \begin{pmatrix} \theta_1 \\ \theta_2 \\ \dots \\ \theta_P \end{pmatrix} + \begin{pmatrix} \varepsilon_1 \\ \varepsilon_2 \\ \dots \\ \varepsilon_N \end{pmatrix}$$

N observations of *Y*

Matrix of *N*P* values of the *P* input variables

P parameters

N residuals

$$y_2 = x_{21}\theta_1 + x_{22}\theta_2 + \ldots + x_{2P}\theta_P + \varepsilon_2$$

Many types of linear models

- A continuous explanatory variable

  Simple linear regression

- Several continuous explanatory variables

  Multiple linear regression

- One categorical explanatory variable

  One-way analysis of variance (ANOVA)

- Several categorical explanatory variables

  Analysis of variance with 2, 3... factors

- Continuous and categorical explanatory variables

  Analysis of covariance (ANCOVA)

Why are they useful?

- Testing a relationship between a response variable (Y) and one or more explanatory variables (X)

  Statistical test

- Quantifying the effect of X on Y

  Estimation and confidence interval

- Predicting Y as a function of X

  Prediction

Other types of statistical models

- **Generalized linear model** (GLM): useful to deal with categorical response variable *Y*
- Non-linear models: useful to deal with nonlinear responses
- Non-parametric models: avoid any strong assumption
- Mixed models: useful to deal with repeated/longitudinal data

What is a linear model?

$$\begin{pmatrix} y_1 \\ y_2 \\ \dots \\ y_N \end{pmatrix} = \begin{pmatrix} x_{11} & x_{12} & \dots & x_{1P} \\ x_{21} & x_{22} & \dots & x_{2P} \\ \dots & \dots & \dots & \dots \\ x_{N1} & x_{N2} & \dots & x_{NP} \end{pmatrix} \begin{pmatrix} \theta_1 \\ \theta_2 \\ \dots \\ \theta_P \end{pmatrix} + \begin{pmatrix} \varepsilon_1 \\ \varepsilon_2 \\ \dots \\ \varepsilon_N \end{pmatrix}$$

N observations of *Y*

Matrix of *N*P* values of the *P* input variables

P parameters

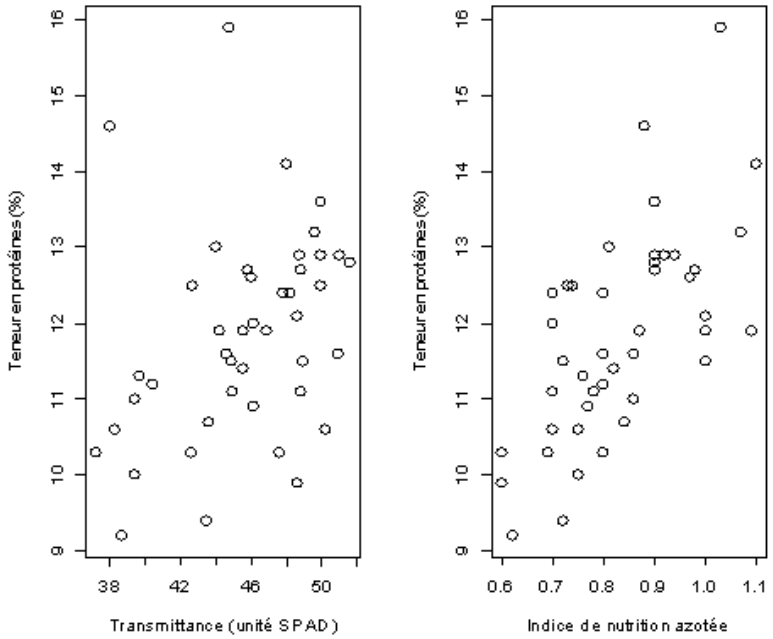
N residuals

Why linear models are so popular?

- Relevant in many cases
- Parameters are easy to estimate
- Many statistical tools are associated with linear models (tests etc.)
- Caution: its assumptions are not always verified.

Example: Linear models for predicting wheat grain protein contents (N=43, P=1, 2 or 3)

Y



X1 X2

Two linear models

```
Mod.1<-lm(TAB$TeneurPro~TAB$SPAD, data=TAB)
Mod.2<-lm(TAB$TeneurPro~TAB$INN, data=TAB)

summary(Mod.1)
summary(Mod.2)
```

Model 1

```
Call:
lm(formula = TAB$TeneurPro ~ TAB$SPAD, data = TAB)

Residuals:
    Min      1Q  Median      3Q     Max
-2.2791 -0.7759 -0.0530  0.5362  4.1580

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)   6.6901     2.3146   2.890  0.00613 **
TAB$SPAD      0.1129     0.0506   2.232  0.03113 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 1.31 on 41 degrees of freedom
Multiple R-squared: 0.1084,     Adjusted R-squared: 0.08661
F-statistic: 4.982 on 1 and 41 DF,  p-value: 0.03113
```

Model 2

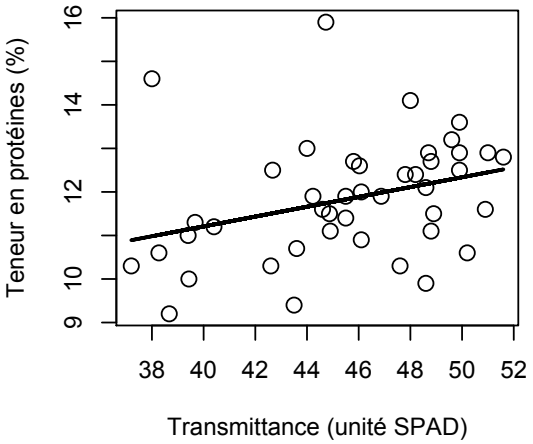
```
Call:
lm(formula = TAB$TeneurPro ~ TAB$INN, data = TAB)

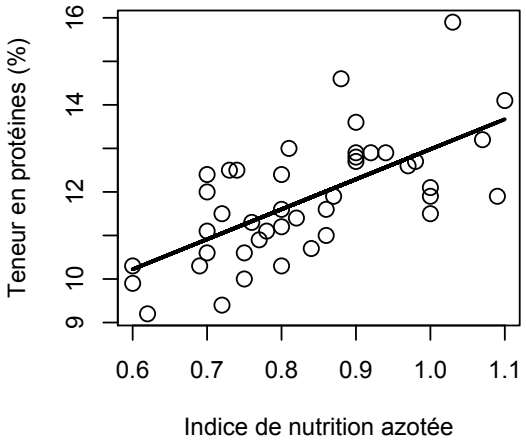
Residuals:
    Min      1Q  Median      3Q     Max
-1.7011 -0.5999 -0.1737  0.4900  2.7126

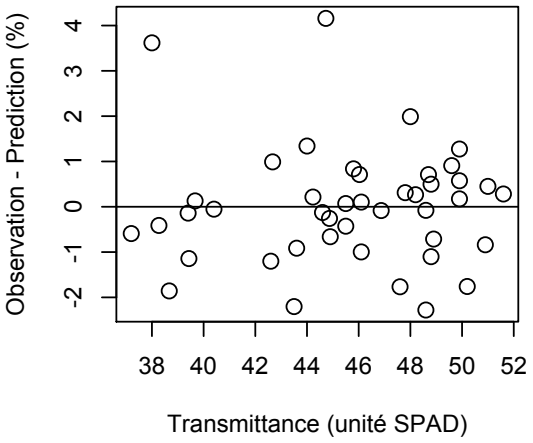
Coefficients:
             Estimate Std. Error. t value Pr(>|t|)
(Intercept)     6.085      1.040   5.852 7.02e-07 ***
TAB$INN         6.895      1.232   5.598 1.61e-06 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

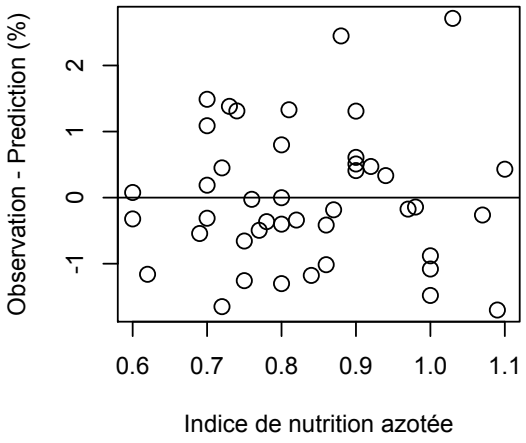
Residual standard error: 1.045 on 41 degrees of freedom
Multiple R-squared: 0.4332,     Adjusted R-squared: 0.4194
F-statistic: 31.33 on 1 and 41 DF,  p-value: 1.614e-06
```

Models 1 and 2









Limits of the linear model

$$y = \theta_0 + \theta_1 x_1 + \ldots + \theta_p x_p + \varepsilon$$

$$E(\varepsilon) = 0$$

$$E(y) = \theta_0 + \theta_1 x_1 + \ldots + \theta_p x_p$$

The average response is a linear combination of inputs and of parameters.

Limits of the linear model

- Not well adapted to deal with discrete response variables (e.g. 0/1, counting...).

- Not very flexible in terms of response function

Outline

- Some reminders
- GLM: why and what
- Logistic and binomial models
- Poisson models

Why GLM?

GLM: a standard approach to deal with categorical responses

- Binary data: 0/1, Yes/No
- Proportion data: *K* positive cases out of *N*
- Count data*: 0, 1, 2, …, K* occurences

GLM: a standard approach to deal with categorical responses

- Able to handle categorical data
- Include interpretable parameters
- Deal with some particular types of nonlinear responses
- More general than the linear model (LM is a special case of GLM)

Two components of a GLM

Deterministic component:

Express the expected values of the observations as a function of the inputs

Random component:

Describe the variability of the observations

Deterministic component based on a link function

The link function *g* is defined such as:

$$g\left[E\left(Y|X_1,\ldots,X_p\right)\right] = \theta_0 + \theta_1 X_1 + \cdots + \theta_p X_p$$

$$E\left(Y|X_1,\ldots,X_p\right) = g^{-1}\left(\theta_0 + \theta_1 X_1 + \cdots + \theta_p X_p\right)$$

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Examples of link functions commonly used:

g(y)=log(y)
g(y)=logit(y)=log(y/(1-y))

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Examples of link functions commonly used:

g(y)=log(y)

g(y)=logit(y)=log(y/(1-y))

$$E\left(Y|X_1,\ldots,X_p\right) = exp\left(\theta_0 + \theta_1 X_1 + \cdots + \theta_p X_p\right)$$

Deterministic component based on a link function

The link function *g* is defined such as:

$$g\left[E\left(Y|X_1,\ldots,X_p\right)\right] = \theta_0 + \theta_1 X_1 + \cdots + \theta_p X_p$$

$$E\left(Y|X_1,\ldots,X_p\right) = g^{-1}\left(\theta_0 + \theta_1 X_1 + \cdots + \theta_p X_p\right)$$

Examples of link functions commonly used:

g(y)=log(y)

g(y)=logit(y)=log(y/(1-y))

$$E\left(Y|X_1,\ldots,X_p\right) = \frac{exp\left(\theta_0 + \theta_1 X_1 + \cdots + \theta_p X_p\right)}{1 + exp\left(\theta_0 + \theta_1 X_1 + \cdots + \theta_p X_p\right)}$$

Random component based on the exponential family

- Describe the distribution of the data conditionnally to the inputs (i.e., distribution of $Y|X$)

- Distributions commonly used:
  - Bernouilli
  - Binomial
  - Poisson
  - (Gaussian)

Random component based on the exponential family

- Describe the distribution of the data conditionnally to the inputs (i.e., distribution of $Y|X$)

- Distributions commonly used:
  - Bernouilli: binary observations (0/1)
  - Binomial
  - Poisson
  - (Gaussian)

$$Y \sim B(\pi)$$

Probability of Y=1

Random component based on the exponential family

- Describe the distribution of the data conditionnally to the inputs (i.e., distribution of $Y|X$)

- Distributions commonly used:
  - Bernouilli
  - Binomial: number of « success » out of N
  - Poisson
  - (Gaussian)

$$Y \sim Bin(N, \pi)$$

Probability of « *success* »

Random component based on the exponential family

- Describe the distribution of the data conditionnally to the inputs (i.e., distribution of $Y|X$)

- Distributions commonly used:
  - Bernouilli
  - Binomial
  - Poisson: count data
  - (Gaussian)

$$Y \sim P(\lambda)$$

Mean number of occurences

Distribution	Mean	Variance
Gaussian	μ	σ^2
Bernouilli	π	$\pi(1-\pi)$
Binomial	$N\pi$	$N\pi(1-\pi)$
Poisson	λ	λ

Popular GLMs

Model	Link function	Distribution
Linear Gaussian	identity	Gaussian
Logistic regression Binomial model	logit	Bernouilli or Binomial
Poisson log linear	log	Poisson

Example 1: Effect of insecticide in mortality of caterpillars

	Log_2 (Dose insecticide)					
Sexe	0	1	2	3	4	5
M	1	4	9	13	18	20
F	0	2	6	10	12	16

Collett, 1991

Number of deaths out of 20 individuals

Probability of death = *f*(sex, dose)

```
Call:
glm(formula = propMort ~ ldose * sexe, family = binomial, weights = Freq)

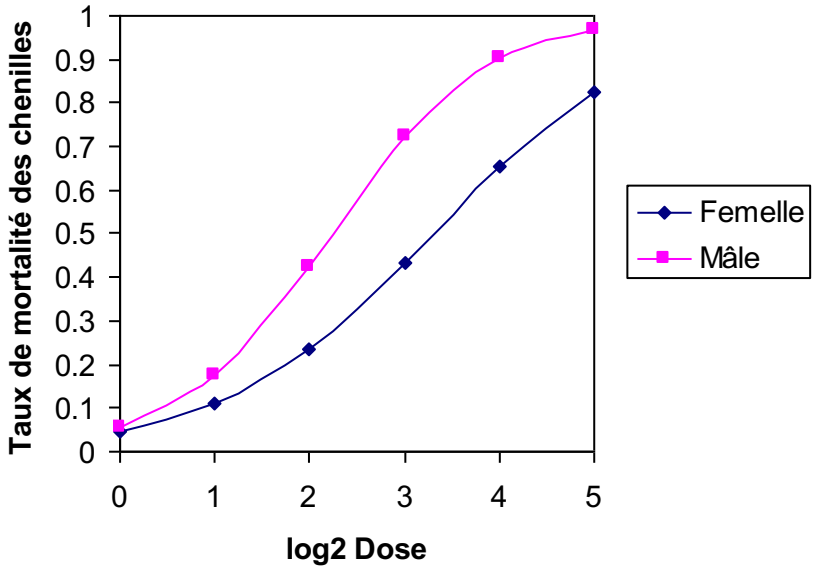
Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.39849  -0.32094  -0.07592   0.38220   1.10375

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -2.9935     0.5527  -5.416 6.09e-08 ***
ldose         0.9060     0.1671   5.422 5.89e-08 ***
sexeM         0.1750     0.7783   0.225    0.822
ldose:sexeM   0.3529     0.2700   1.307    0.191
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

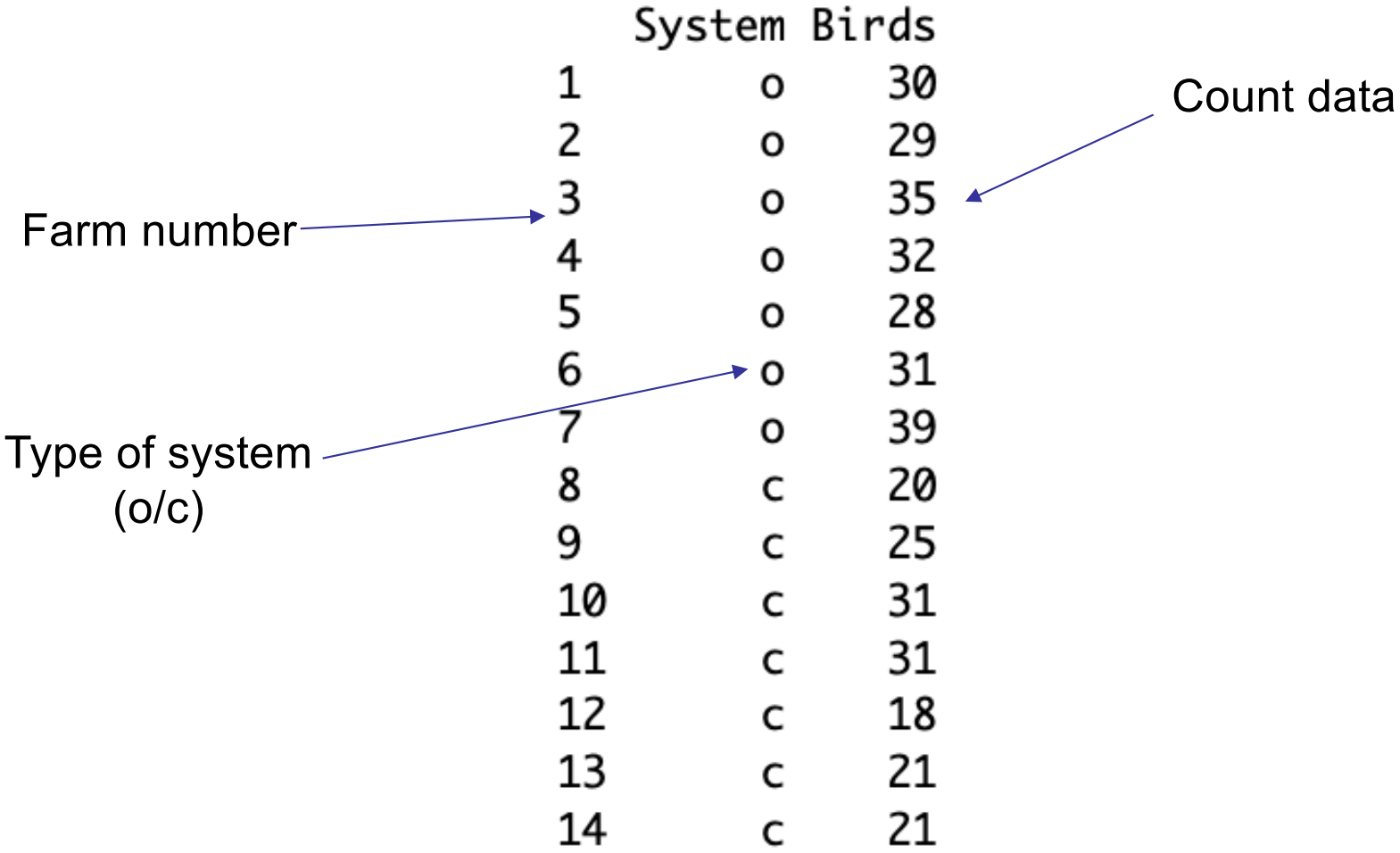
(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 124.8756  on 11  degrees of freedom
Residual deviance:   4.9937  on  8  degrees of freedom
AIC: 43.104

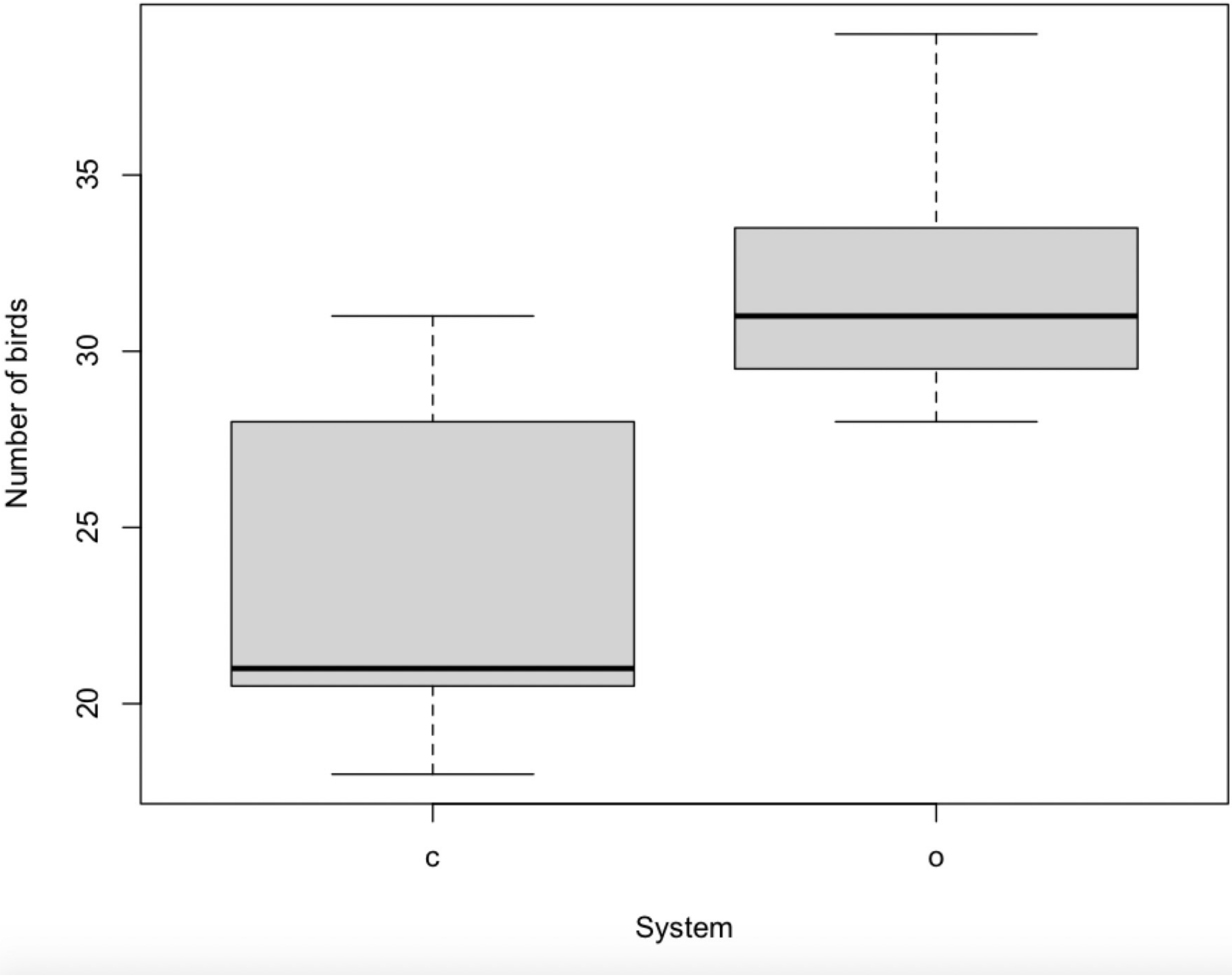
Number of Fisher Scoring iterations: 4
```



Example 2: Number of birds in Organic vs. Conventional farming



	System	Birds
1	o	30
2	o	29
3	o	35
4	o	32
5	o	28
6	o	31
7	o	39
8	c	20
9	c	25
10	c	31
11	c	31
12	c	18
13	c	21
14	c	21


Number of birds
20
25
30
35
c
o
System

GLM: Poisson log linear model

```
Call:
glm(formula = Birds ~ System, family = poisson)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.2541  -0.5973  -0.2675   0.4498   1.3973

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  3.17208    0.07738  40.992  < 2e-16 ***
Systemo      0.29365    0.10224   2.872  0.00408 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 17.9192  on 13  degrees of freedom
Residual deviance:  9.5801  on 12  degrees of freedom
AIC: 85.679

Number of Fisher Scoring iterations: 4
```

log(mean bird number) = Intercept + Systemo*X
= 3.17 for Conventional
= 3.17 + 0.29 = 3.46 for Organic

```
Call:
glm(formula = Birds ~ System, family = poisson)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.2541  -0.5973  -0.2675   0.4498   1.3973

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  3.17208    0.07738  40.992  < 2e-16 ***
Systemo      0.29365    0.10224   2.872  0.00408 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 17.9192  on 13  degrees of freedom
Residual deviance:  9.5801  on 12  degrees of freedom
AIC: 85.679

Number of Fisher Scoring iterations: 4
```

mean bird number = exp(Intercept + Systemo*X)
= 23.8 for Conventional
= 31.8 for Organic

```
Call:
glm(formula = Birds ~ System, family = poisson)

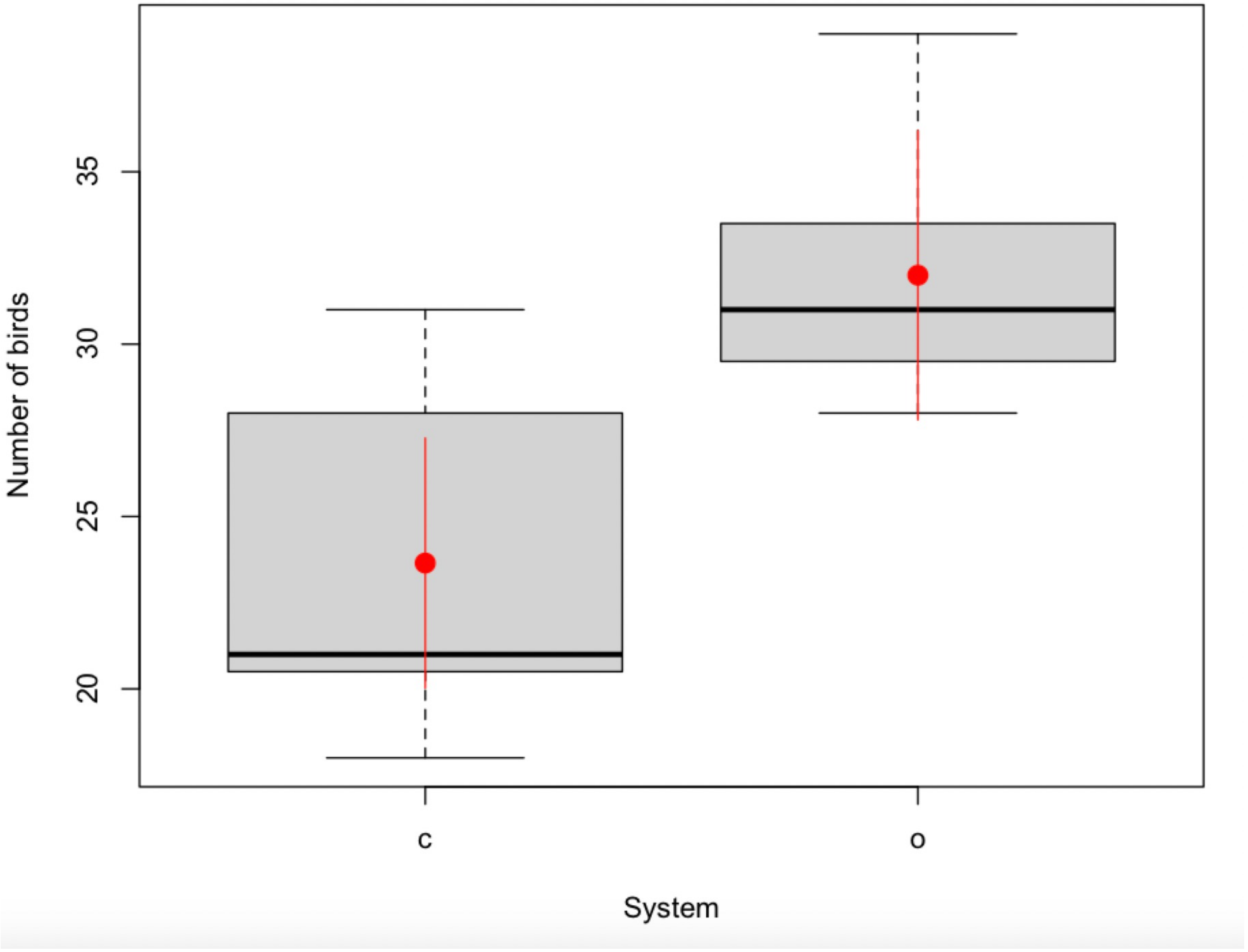
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.2541  -0.5973  -0.2675   0.4498   1.3973

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  3.17208    0.07738  40.992  < 2e-16 ***
Systemo      0.29365    0.10224   2.872  0.00408 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 17.9192  on 13  degrees of freedom
Residual deviance:  9.5801  on 12  degrees of freedom
AIC: 85.679

Number of Fisher Scoring iterations: 4
```


Number of birds
20
25
30
35
c
o
System

Example 3: modelling the effect of temperature on the survival of an invasive species

Data:

- Pieces of wood with heat treatment
- Five different temperatures tested
- Observations: Number of insects surviving heat treatment

Modèle Poisson log lineaire

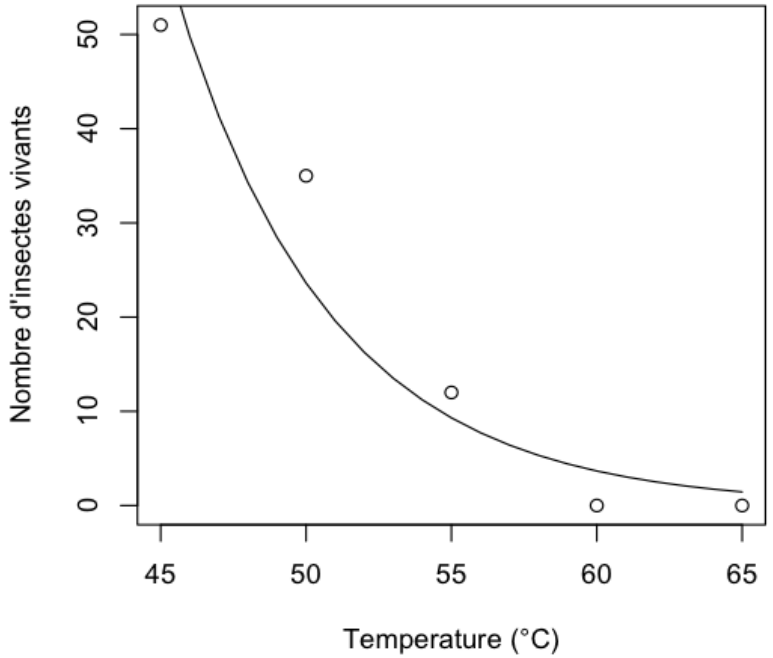
mean insect number = exp(Intercept + Slope*time)
= exp(12.5 - 0.19*Time)

Coefficients:

	Estimate	Std. Error	z value	Pr(>|z|)	
(Intercept)	12.47853	1.06901	11.673	<2e-16	***
X	-0.18633	0.02217	-8.406	<2e-16	***

Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

AIC: 36.62



Example 4: modelling the number of fires across time

Data:

- One site in the US (county) during several years
- Observations: number of fires every month

mean fire number = exp(Intercept + Slope*time)
= exp(0.87 + 0.0067*Time)

Modèle quasi-Poisson log lineaire

```
Call:
glm(formula = Y ~ X, family = "quasipoisson", data = DATA)

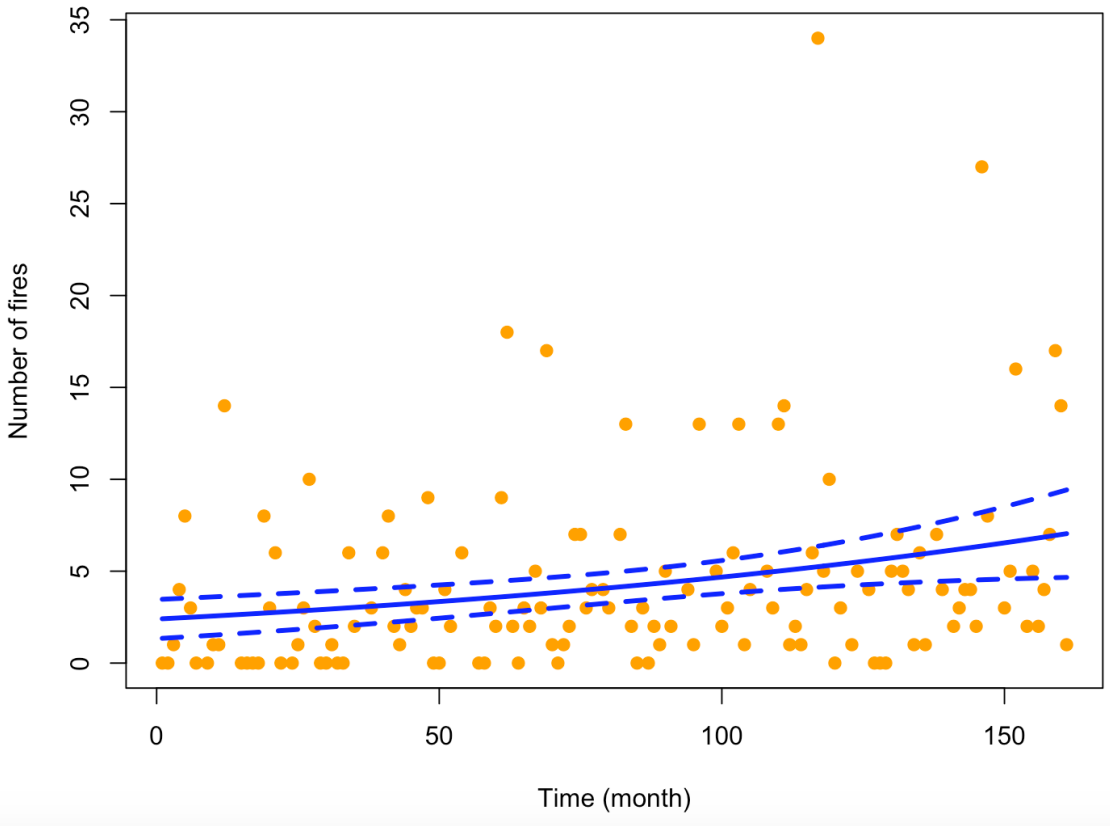
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-3.3712  -2.1217  -0.7257   0.3497   8.3430

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 0.872939   0.226930   3.847 0.000184 ***
X           0.006701   0.002154   3.110 0.002284 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for quasipoisson family taken to be 5.611049)

    Null deviance: 671.24  on 135  degrees of freedom
Residual deviance: 615.46  on 134  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 5
```



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- Poisson models

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  - Definition
  - Estimation
  - Test and deviance
  - Useful variants
  - Model selection

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Definition

Model	Link function	Distribution
Linear Gaussian	identity	Gaussian
Logistic regression Binomial model	logit	Bernouilli or Binomial
Poisson log linear	log	Poisson

Definition (binary observations)

Deterministic component

$$\log\left\{\frac{\pi}{1-\pi}\right\} = \theta_0 + \theta_1 x_1 + \ldots + \theta_p x_p$$

Random component

$$Y \sim B(\pi)$$

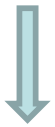
where Y is a binary observation (0 ou 1)

π is the probability of Y=1

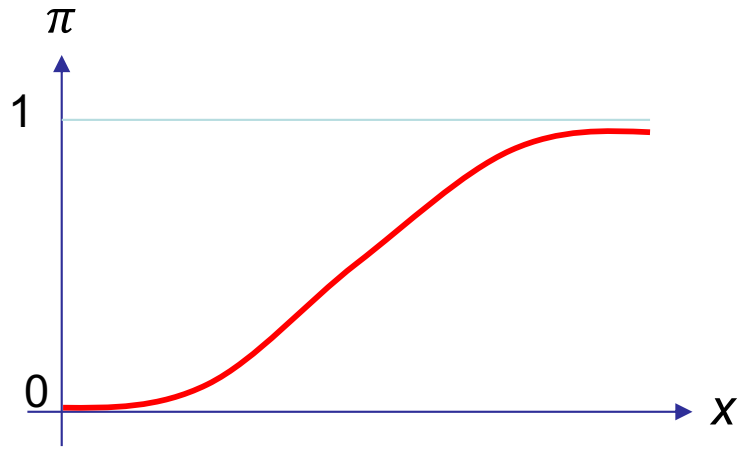
Definition (binary observations)

Deterministic component

$$\log\left\{\frac{\pi}{1-\pi}\right\} = \theta_0 + \theta_1 x_1 + \ldots + \theta_p x_p$$



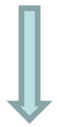
$$\pi = \frac{\exp\left(\theta_0 + \theta_1 x_1 + \ldots + \theta_p x_p\right)}{1 + \exp\left(\theta_0 + \theta_1 x_1 + \ldots + \theta_p x_p\right)}$$



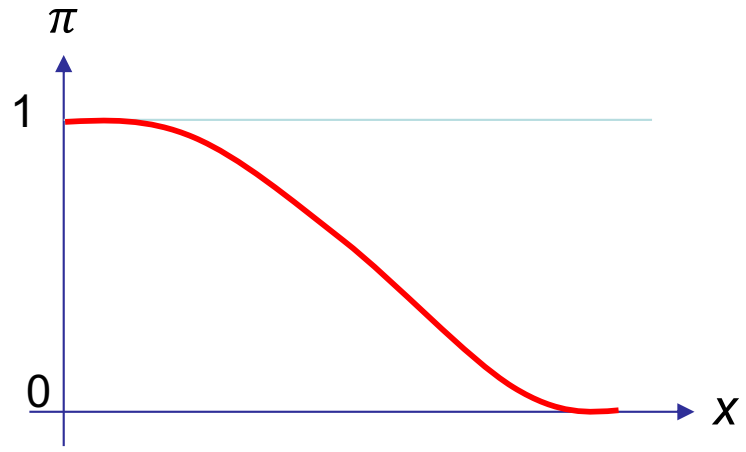
Definition (binary observations)

Deterministic component

$$\log\left\{\frac{\pi}{1-\pi}\right\} = \theta_0 + \theta_1 x_1 + \ldots + \theta_p x_p$$



$$\pi = \frac{\exp\left(\theta_0 + \theta_1 x_1 + \ldots + \theta_p x_p\right)}{1 + \exp\left(\theta_0 + \theta_1 x_1 + \ldots + \theta_p x_p\right)}$$



Definition (binomial observations)

Deterministic component

$$\log\left\{\frac{\pi}{1-\pi}\right\} = \theta_0 + \theta_1 x_1 + \ldots + \theta_p x_p$$

Random component

$$Y \sim Bin(N, \pi)$$

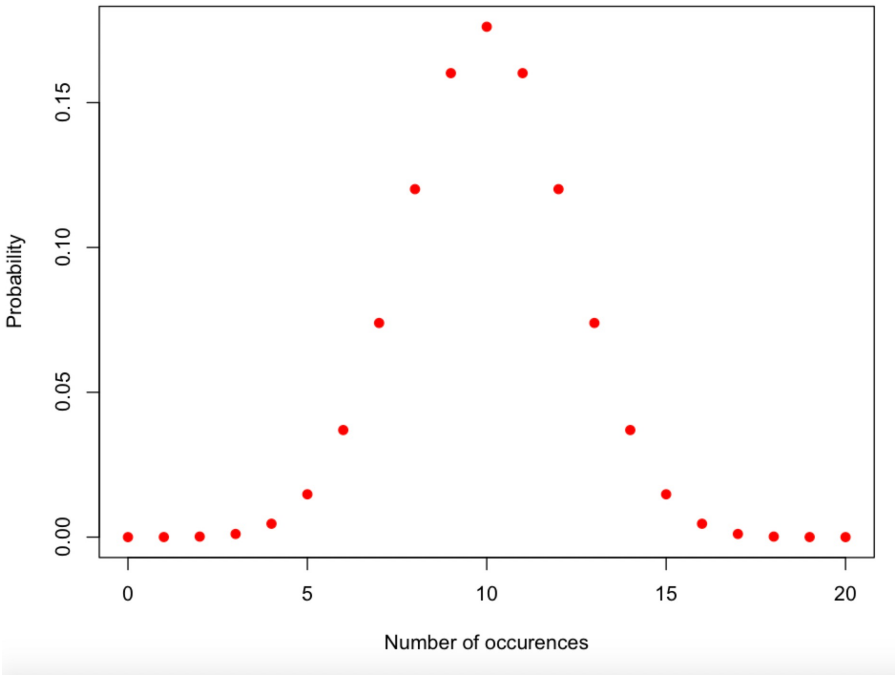
where Y is categorical variable ranging from 1 to N (0, 1, 2, …, N)

π is the probability of success

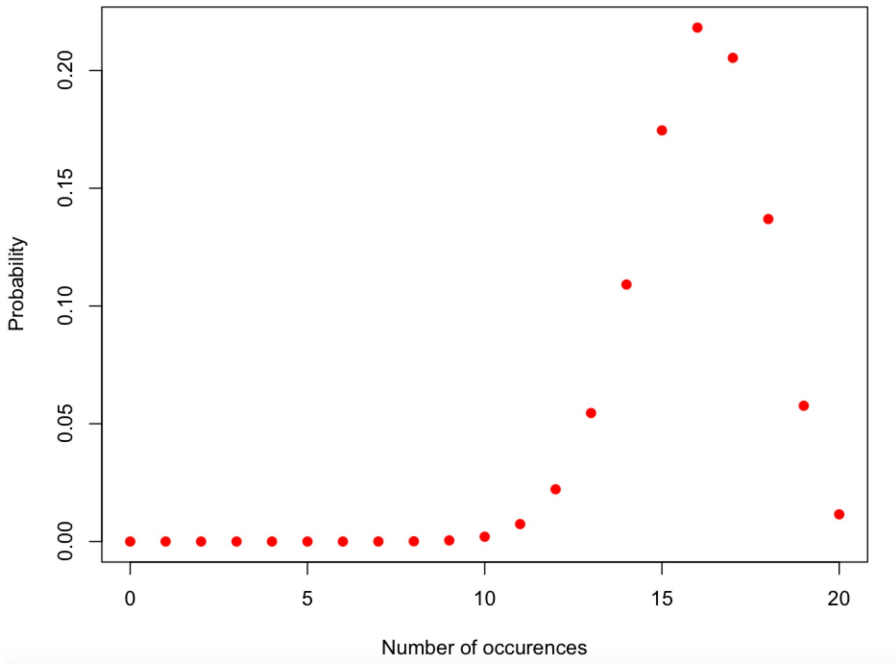
N is the sample size.

$$P(Y = m) = \binom{N}{m} \pi^m (1 - \pi)^{N-m}$$

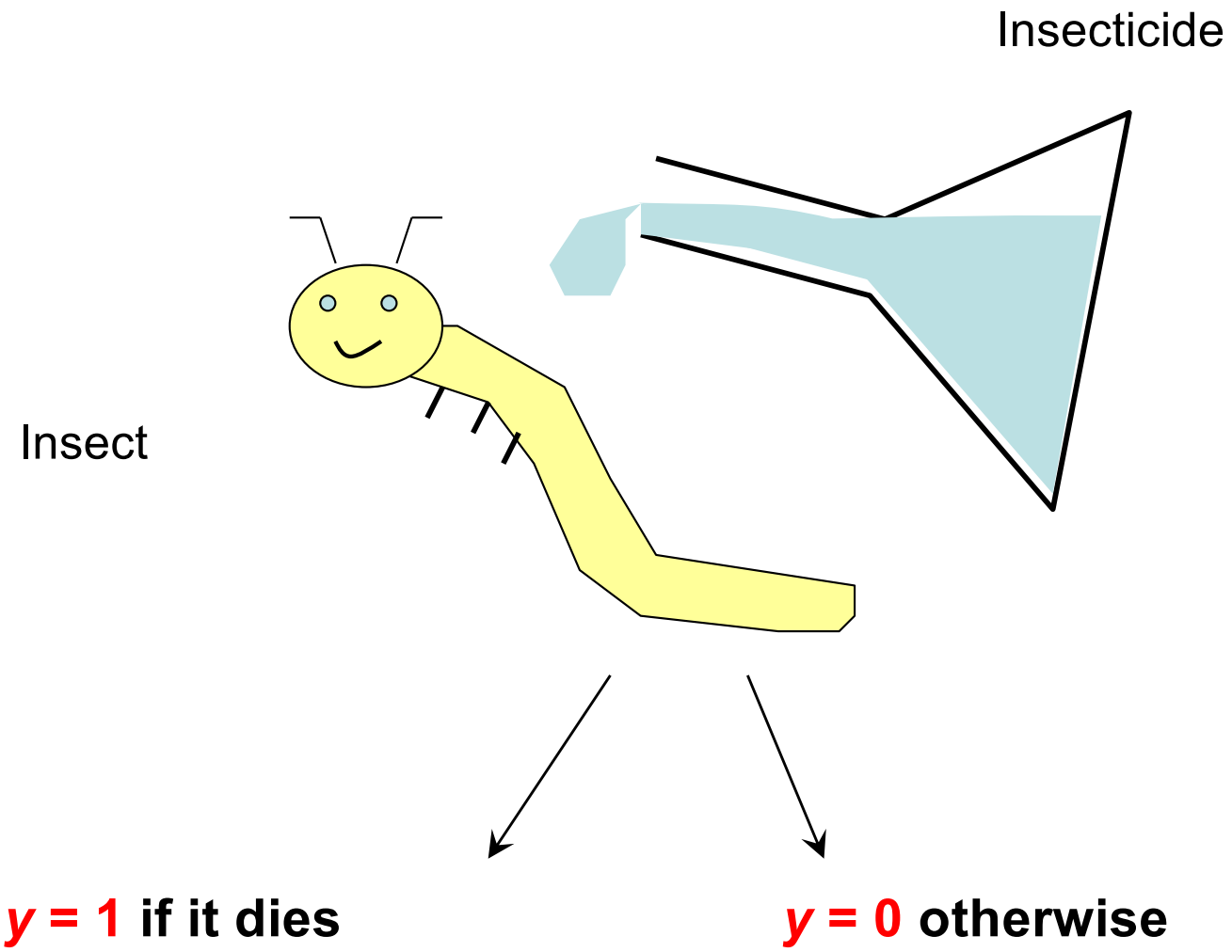
$\pi = 0.5, N = 20$



$\pi = 0.8, N = 20$



Example 1: Effect of insecticide in mortality of caterpillars



Example 1: Effect of insecticide in mortality of caterpillars

	Log_2 (Dose insecticide)					
Sexe	0	1	2	3	4	5
M	1	4	9	13	18	20
F	0	2	6	10	12	16

Collett, 1991

Number of deaths out of 20 individuals

Goal:

Assess the effect of insecticide on the death rate as a function of dose and sex

Models tested in example 1

Model 1. $$\log\left\{\frac{\pi}{1-\pi}\right\} = \theta_0 + \theta_1 x$$

Model 2. $$\log\left\{\frac{\pi}{1-\pi}\right\} = \theta_0 + \theta_1 sexe + \theta_2 x$$

Model 3. $$\log\left\{\frac{\pi}{1-\pi}\right\} = \theta_0 + \theta_1 sexe + \theta_2 x + \theta_3 sexe \times x$$

with *x* the value of log_2 *(dose of insecticide),*
sexe=1 for male
sexe=0 for female.

Outline

- Logistic and binomial models
  - Definition
  - Estimation
  - Test and deviance
  - Useful variants
  - Model selection

- Poisson models
  - Definition
  - Estimation
  - Test and deviance
  - Useful variants
  - Model selection

Estimation of the parameters by maximum likelihood

Objective: Find the parameter values maximizing the probability of the data conditionnally to the parameters.

$$\text{Likelihood}=L\left(\theta_0,\theta_1,\ldots,\theta_p\right)=\text{Prob}\left(y_1,\ldots,y_N \middle| \theta_0,\theta_1,\ldots,\theta_p\right)$$

Likelihood for the bernouilli-logit model

$$\pi\left(x_{i,1},\ldots,x_{i,p};\theta_1,\ldots,\theta_p\right)=\frac{\exp\left(\theta_0+\theta_1 x_{1,i}+\ldots+\theta_p x_{p,i}\right)}{1+\exp\left(\theta_0+\theta_1 x_{1,i}+\ldots+\theta_p x_{p,i}\right)}$$

Likelihood= $\mathrm{Prob}\left(\mathrm{y}_1,\ldots,\mathrm{y}_N\,\middle|\,\theta_0,\theta_1,\ldots,\theta_p\right)=$

$$\prod_{i=1}^{N}\pi\left(x_{i,1},\ldots,x_{i,p};\theta_1,\ldots\theta_p\right)^{yi}\left[1-\pi\left(x_{i,1},\ldots,x_{i,p};\theta_1,\ldots\theta_p\right)\right]^{1-yi}$$

Likelihood for the bernouilli-logit model

$$\pi\left(x_{i,1},...,x_{i,p};\theta_1,...,\theta_p\right)=\frac{\exp\left(\theta_0+\theta_1 x_{1,i}+...+\theta_p x_{p,i}\right)}{1+\exp\left(\theta_0+\theta_1 x_{1,i}+...+\theta_p x_{p,i}\right)}$$

Likelihood= $\mathrm{Prob}\left(y_1,...,y_N\,\middle|\,\theta_0,\theta_1,...,\theta_p\right)=$

$$\prod_{i=1}^{N}\pi\left(x_{i,1},...,x_{i,p};\theta_1,...\theta_p\right)^{yi}\left[1-\pi\left(x_{i,1},...,x_{i,p};\theta_1,...\theta_p\right)\right]^{1-yi}$$

0/1 0/1

- The same type of likelihood function can be expressed for binomial models as well.
- The parameter values can be estimated by maximizing this function, using an iterative algorithm (Newton-Raphson).
- In most cases, it works well, but not always…

Models tested in example 1

Model 1. $$\log\left\{\frac{\pi}{1-\pi}\right\} = \theta_0 + \theta_1 x$$

Model 2. $$\log\left\{\frac{\pi}{1-\pi}\right\} = \theta_0 + \theta_1 sexe + \theta_2 x$$

Model 3. $$\log\left\{\frac{\pi}{1-\pi}\right\} = \theta_0 + \theta_1 sexe + \theta_2 x + \theta_3 sexe \times x$$

with *x* the value of log_2 *(dose of insecticide),*
sexe=1 for male
sexe=0 for female.

glm(formula, family=binomial(link= ‘logit’), data…)

Or

glm (formula, family=binomial, data…)

```
#####Data
ldose=c(0:5, 0:5)
sexe=factor(c(rep("M",6), rep("F", 6)))
nombMort=c(1,4,9,13,18,20,0,2,6,10,12,16)
nombViv=20-nombMort
Reponse=cbind(nombMort,nombViv)

#####Option 1 (numbers)
Modele=glm(Reponse~ldose*sexe,family=binomial)
summary(Modele)

######Option 2 (proportions)
propMort=nombMort/20
Freq=rep(20,12)

Modele=glm(propMort~ldose*sexe,family=binomial,weight=Freq)
summary(Modele)
```

```
Call:
glm(formula = propMort ~ ldose * sexe, family = binomial, weights = Freq)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.39849  -0.32094  -0.07592   0.38220   1.10375

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -2.9935     0.5527  -5.416 6.09e-08 ***
ldose         0.9060     0.1671   5.422 5.89e-08 ***
sexeM         0.1750     0.7783   0.225    0.822
ldose:sexeM   0.3529     0.2700   1.307    0.191
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 124.8756  on 11  degrees of freedom
Residual deviance:   4.9937  on  8  degrees of freedom
AIC: 43.104

Number of Fisher Scoring iterations: 4
```

```
Call:
glm(formula = propMort ~ ldose * sexe, family = binomial, weights = Freq)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.39849  -0.32094  -0.07592   0.38220   1.10375

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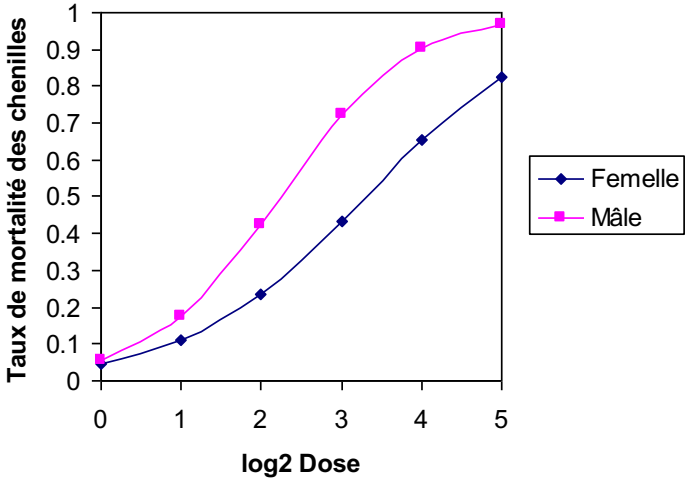

$$\pi\left(x_{i,1},\ldots,x_{i,p};\theta_1,\ldots,\theta_p\right)=\frac{\exp\left(\theta_0+\theta_1 x_{1,i}+\ldots+\theta_p x_{p,i}\right)}{1+\exp\left(\theta_0+\theta_1 x_{1,i}+\ldots+\theta_p x_{p,i}\right)}$$

Odds and odds ratio

$$\log\left(\frac{\pi}{1-\pi}\right)=\theta_0+\theta_1 x$$

$$\text{Odds}=\frac{\pi}{1-\pi}=\exp(\theta_0+\theta_1 x)$$

$$\text{Odds ratio}=\frac{\exp(\theta_0+\theta_1(x+1))}{\exp(\theta_0+\theta_1 x)}=\frac{\exp(\theta_0+\theta_1 x+\theta_1)}{\exp(\theta_0+\theta_1 x)}=\exp(\theta_1)$$

θ_1 =log(Odds ratio)

$\theta_1 > 0$	x increases the probability
$\theta_1 < 0$	x decreases the probability
$\theta_1 = 0$	No effect

```
Call:
glm(formula = propMort ~ ldose * sexe, family = binomial, weights = Freq)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.39849  -0.32094  -0.07592   0.38220   1.10375

Coefficients:
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(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 124.8756  on 11  degrees of freedom
Residual deviance:   4.9937  on  8  degrees of freedom
AIC: 43.104

Number of Fisher Scoring iterations: 4
```

- Positive effect of dose on the probability of death
- Positive effect of « male » on the probability of death
- Effect of dose is stronger for male

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```
Call:
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AIC: 43.104

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```

?

Wald test

$$H_0: \theta = 0$$

$$z = \frac{\hat{\theta}}{\sqrt{\widehat{var}(\hat{\theta})}}$$

Parameter estimate

Standard error

$$z^2 \sim \chi^2_{1ddl}$$

```
> 1-pchisq((-5.416)^2,df=1)
[1] 6.09471e-08
> 1-pchisq(5.422^2,df=1)
[1] 5.893588e-08
> 1-pchisq(0.225^2,df=1)
[1] 0.8219793
> 1-pchisq(1.307^2,df=1)
[1] 0.1912127
```

```
Call:
glm(formula = propMort ~ ldose * sexe, family = binomial, weights = Freq)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.39849  -0.32094  -0.07592   0.38220   1.10375

Coefficients:
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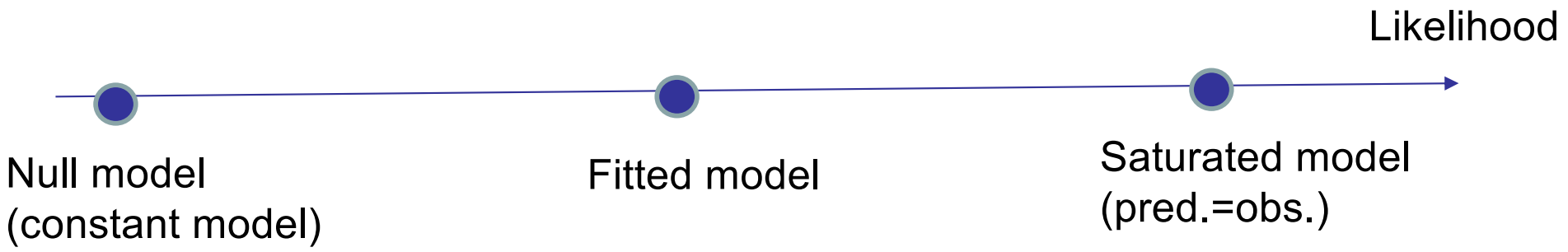
AIC: 43.104

Number of Fisher Scoring iterations: 4
```

?

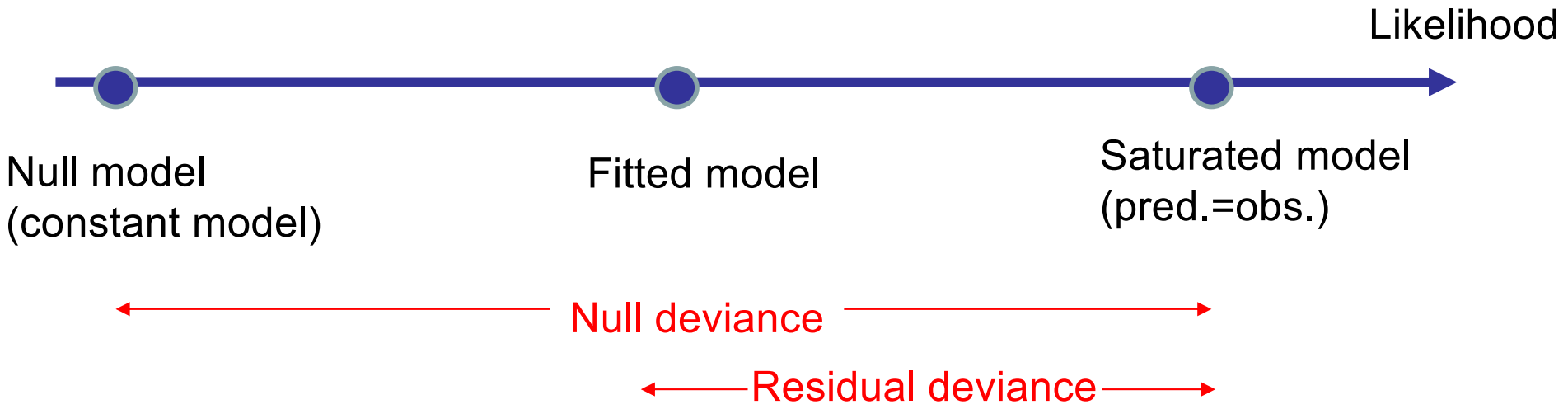
Deviance

- Measure the quality of a model compared to a « perfect » model (« saturated »)
- Generalization of the residual sum of squares
- Expressed from the likelihood
- Key quantity to compare models
- Lower deviance, better fit



Null and residual deviances

- Measure the quality of a model compared to a « perfect » model (« saturated »)
- Generalization of the residual sum of squares
- Expressed from the likelihood
- Key quantity to compare models
- Lower deviance, better fit



Null and residual deviances

- Measure the quality of a model compared to a « perfect » model (« saturated »)
- Generalization of the residual sum of squares
- Expressed from the likelihood
- Key quantity to compare models
- Lower deviance, better fit

$$Null\ Deviance = 2\{log[likelihood(Model_{saturated})] - log[likelihood(Model_{null})]\}$$

$$Residual\ Deviance = 2\{log[likelihood(Model_{saturated})] - log[likelihood(Model_{fitted})]\}$$

$$Pseudo\ R^2 = 1 - \frac{Residual\ deviance}{Null\ deviance}$$

Akaike Information Criterion (AIC)

$$-2\log(Likelihood) + 2Number\ of\ parameters$$

Quality of fit – Penalty depending on the complexity

```
Call:
glm(formula = propMort ~ ldose * sexe, family = binomial, weights = Freq)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.39849  -0.32094  -0.07592   0.38220   1.10375

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -2.9935     0.5527  -5.416 6.09e-08 ***
ldose         0.9060     0.1671   5.422 5.89e-08 ***
sexeM         0.1750     0.7783   0.225    0.822
ldose:sexeM   0.3529     0.2700   1.307    0.191
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 124.8756  on 11  degrees of freedom
Residual deviance:   4.9937  on  8  degrees of freedom
AIC: 43.104

Number of Fisher Scoring iterations: 4
```

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  - Definition
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- Poisson models
  - Definition
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  - Useful variants
  - Model selection

Some useful variants

- Deterministic component
  - Polynomials (quadratic, cubic …)
  - Other link functions (e.g., probit)

    ```
    glm(formula, family=binomial(link='probit'), data)
    ```
  - Non-parametric response (R package mgcv)

- Random component
  - Add random parameters (see the course « Mixed models »)
  - Use Beta binomial instead of binomial (useful to deal with overdispersion)

Outline

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  - Useful variants
  - Model selection

Selection based on the likelihood ratio test

- Useful to compare two models, *Model 1* and *Model 2*, when *Model 1* is embedded in *Model 2*

- Rely on *T* = Deviance(*Model 1*) – Deviance(*Model 2*)

$$T \sim \chi^2_{k\ ddl}$$

where *k* is the number of additional parameters in *Model 2*

Models tested in example 1

Model 1. $$\log\left\{\frac{\pi}{1-\pi}\right\} = \theta_0 + \theta_1 x$$

Model 2. $$\log\left\{\frac{\pi}{1-\pi}\right\} = \theta_0 + \theta_1 sexe + \theta_2 x$$

Model 3. $$\log\left\{\frac{\pi}{1-\pi}\right\} = \theta_0 + \theta_1 sexe + \theta_2 x + \theta_3 sexe \times x$$

with *x* the value of log_2 *(dose of insecticide),*
sexe=1 for male
sexe=0 for female.

```
#####Data
ldose=c(0:5, 0:5)
sexe=factor(c(rep("M",6), rep("F", 6)))
nombMort=c(1,4,9,13,18,20,0,2,6,10,12,16)
nombViv=20-nombMort
Reponse=cbind(nombMort,nombViv)

Model_1=glm(Reponse~ldose,family=binomial)

Model_2=glm(Reponse~ldose+sexe,family=binomial)

Model_3=glm(Reponse~ldose*sexe,family=binomial)

anova(Model_1,Model_2, Model_3, test="LRT")
```

```
> anova(Model_1,Model_2, Model_3, test="LRT")
Analysis of Deviance Table

Model 1: Reponse ~ ldose
Model 2: Reponse ~ ldose + sexe
Model 3: Reponse ~ ldose * sexe
  Resid. Df Resid. Dev Df Deviance Pr(>Chi)
1        10    16.9840
2         9     6.7571  1  10.2270 0.001384 **
3         8     4.9937  1   1.7633 0.184209
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

```
> summary(Model_2)

Call:
glm(formula = Reponse ~ ldose + sexe, family = binomial)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.10540  -0.65343  -0.02225   0.48471   1.42944

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -3.4732     0.4685  -7.413 1.23e-13 ***
ldose         1.0642     0.1311   8.119 4.70e-16 ***
sexeM         1.1007     0.3558   3.093  0.00198 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 124.8756  on 11  degrees of freedom
Residual deviance:   6.7571  on  9  degrees of freedom
AIC: 42.867

Number of Fisher Scoring iterations: 4
```

Selection based on AIC

```
> AIC(Model_1,Model_2,Model_3)
         df      AIC
Model_1   2 51.09443
Model_2   3 42.86747
Model_3   4 43.10413
```

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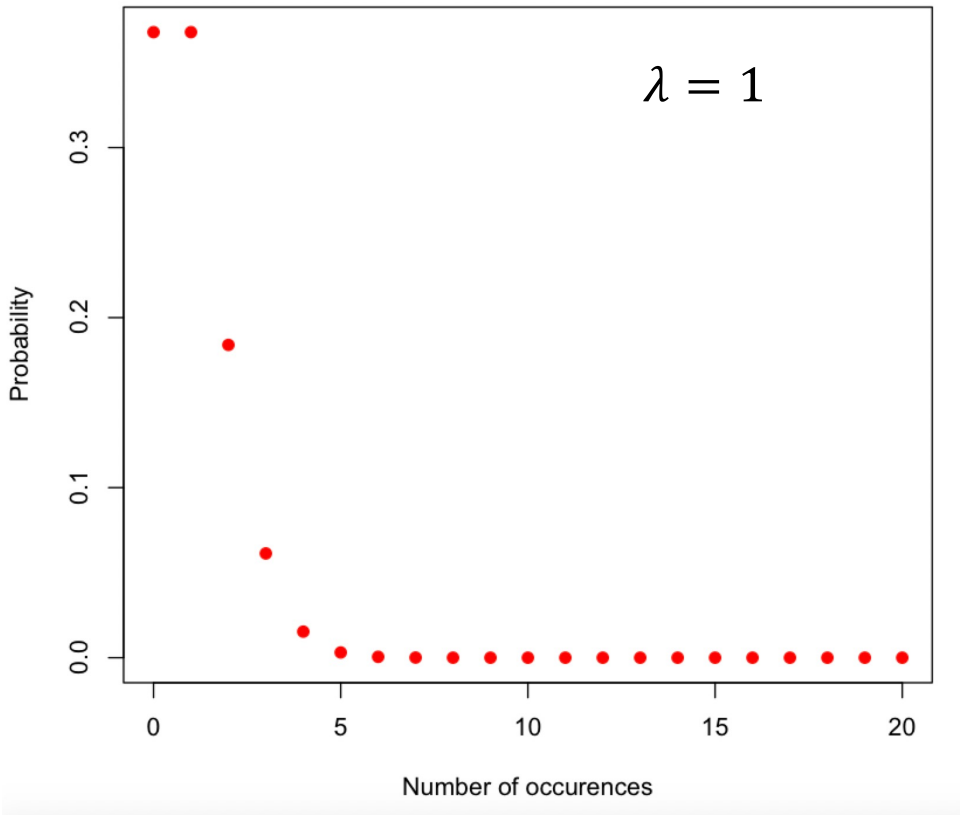
  - Definition
  - Estimation
  - Test and deviance
  - Useful variants
  - Model selection

Definition

Model	Link function	Distribution
Linear Gaussian	identity	Gaussian
Logistic regression Binomial model	logit	Bernouilli or Binomial
Poisson log linear	log	Poisson

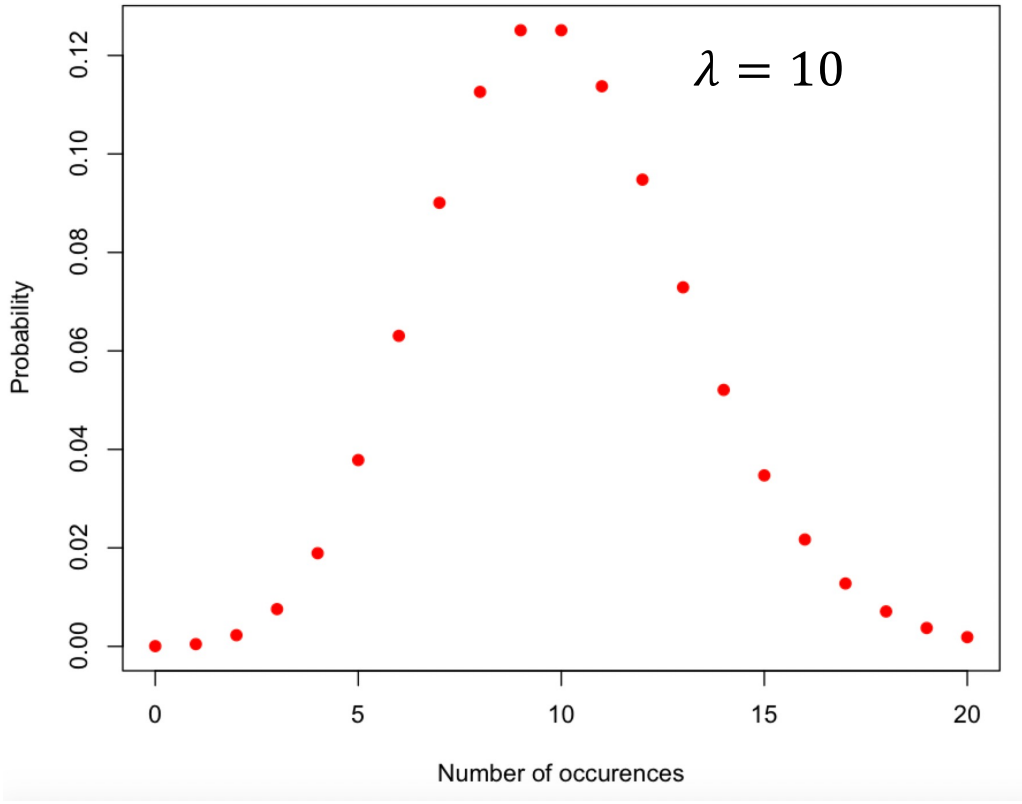
Distribution	Mean	Variance
Gaussian	μ	σ^2
Bernouilli	π	$\pi(1-\pi)$
Binomial	$N\pi$	$N\pi(1-\pi)$
Poisson	λ	λ

$$p\left(y=m\middle|\lambda\right)=\exp\left(-\lambda\right)\lambda^{m}/m!$$



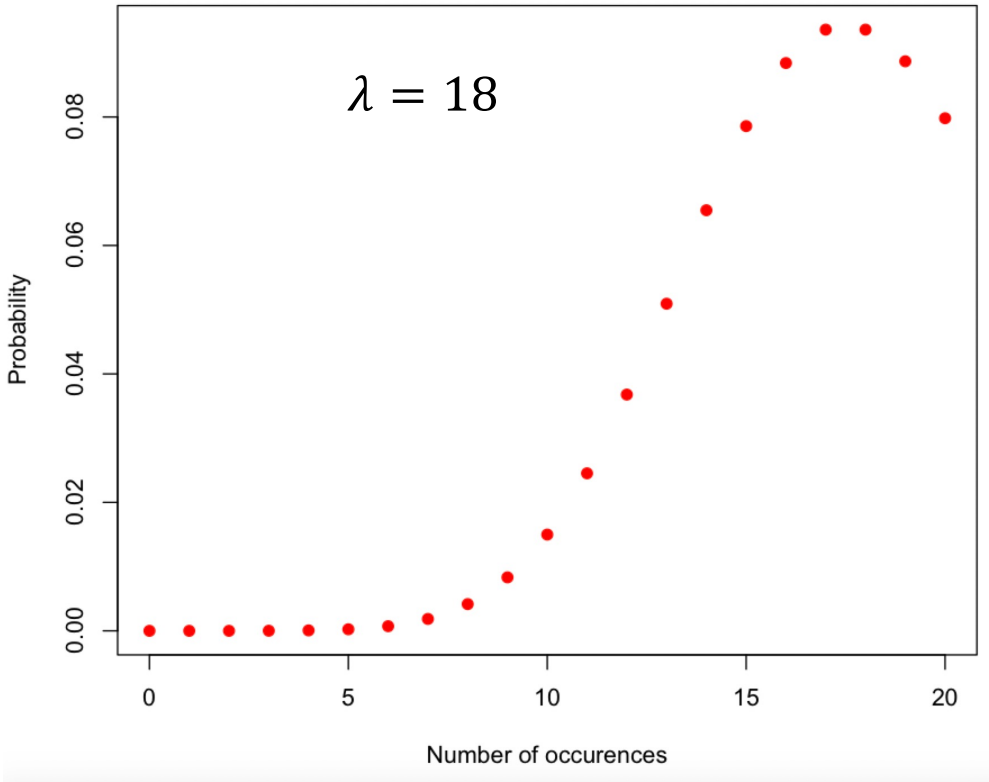
Distribution	Mean	Variance
Gaussian	μ	σ^2
Bernouilli	π	$\pi(1-\pi)$
Binomial	$N\pi$	$N\pi(1-\pi)$
Poisson	λ	λ

$$p\left(y=m\middle|\lambda\right)=\exp\left(-\lambda\right)\lambda^{m}/m!$$



Distribution	Mean	Variance
Gaussian	μ	σ^2
Bernouilli	π	$\pi(1-\pi)$
Binomial	$N\pi$	$N\pi(1-\pi)$
Poisson	λ	λ

$$p\left(y=m\middle|\lambda\right)=\exp\left(-\lambda\right)\lambda^{m}/m!$$



Model Poisson log linear

Deterministic component

$$g\left[E\left(y\right)\right] = \log\left[E\left(y\right)\right] = \theta_0 + \theta_1 x_1 + \ldots + \theta_p x_p$$

$$E(y) = \exp\left(\theta_0 + \theta_1 x_1 + \ldots + \theta_p x_p\right)$$

Random component

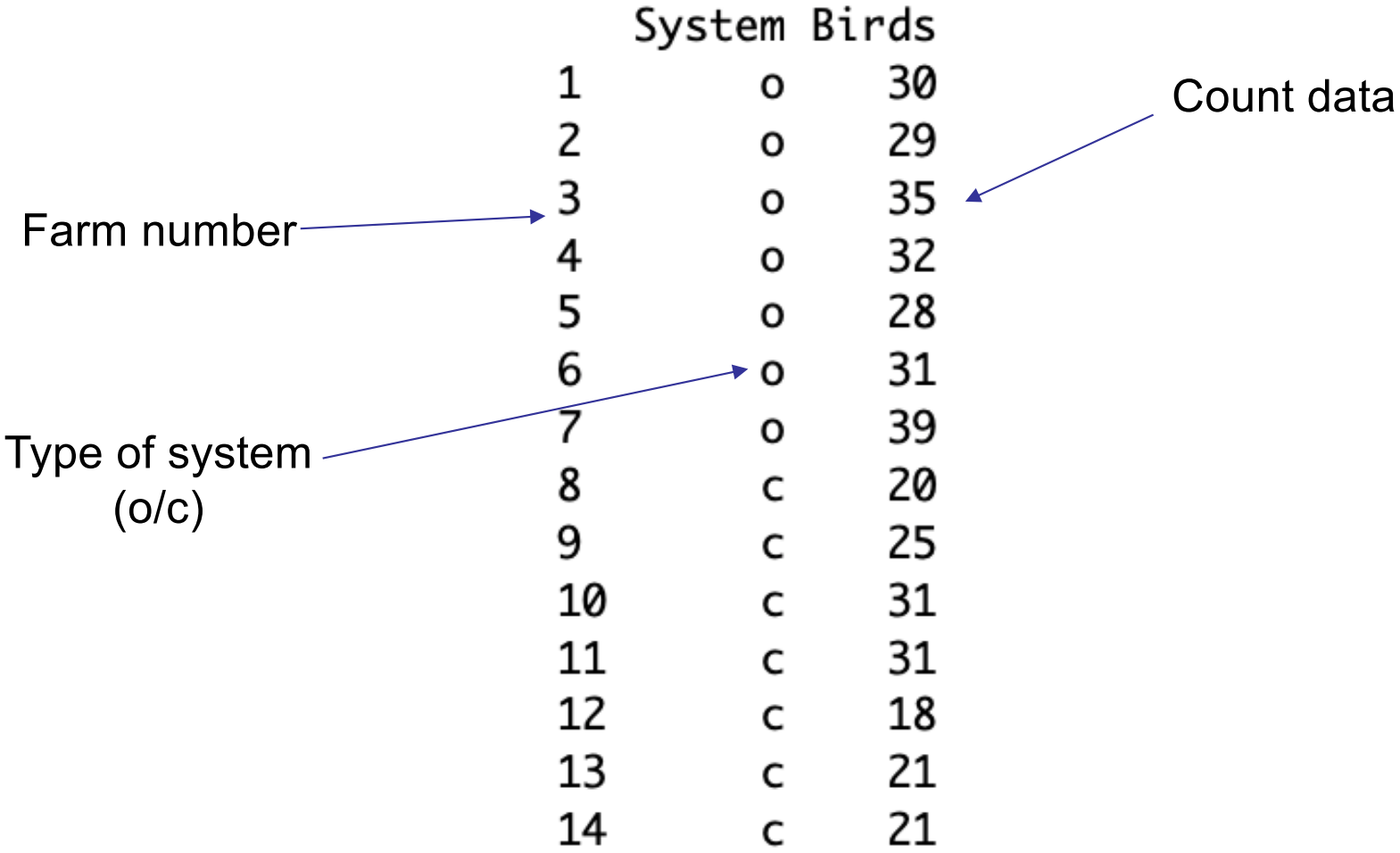
$$y \sim Poisson\left(\lambda\right)$$

where *y* is a number of occurrences (ex: number of birds,number of insects, number of fires etc.)

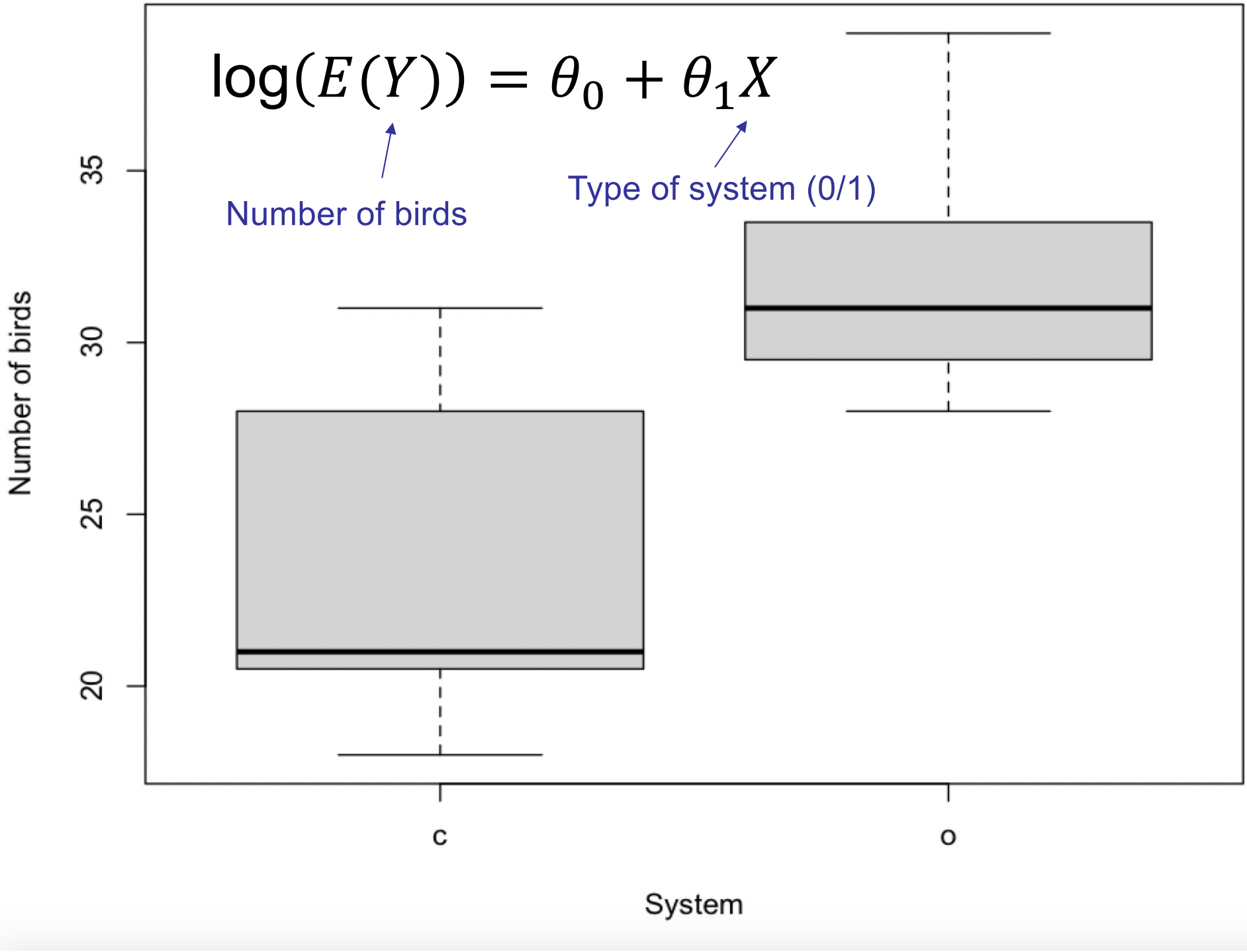
$$E\left(y\right) = \lambda$$

$$p\left(y = m \middle| \lambda\right) = \exp\left(-\lambda\right)\lambda^m / m!$$

Example 2: Number of birds in Organic vs. Conventional farming



	System	Birds
1	o	30
2	o	29
3	o	35
4	o	32
5	o	28
6	o	31
7	o	39
8	c	20
9	c	25
10	c	31
11	c	31
12	c	18
13	c	21
14	c	21


$\log(E(Y)) = \theta_0 + \theta_1 X$
Number of birds
Type of system (0/1)
Number of birds
35
30
25
20
c
o
System

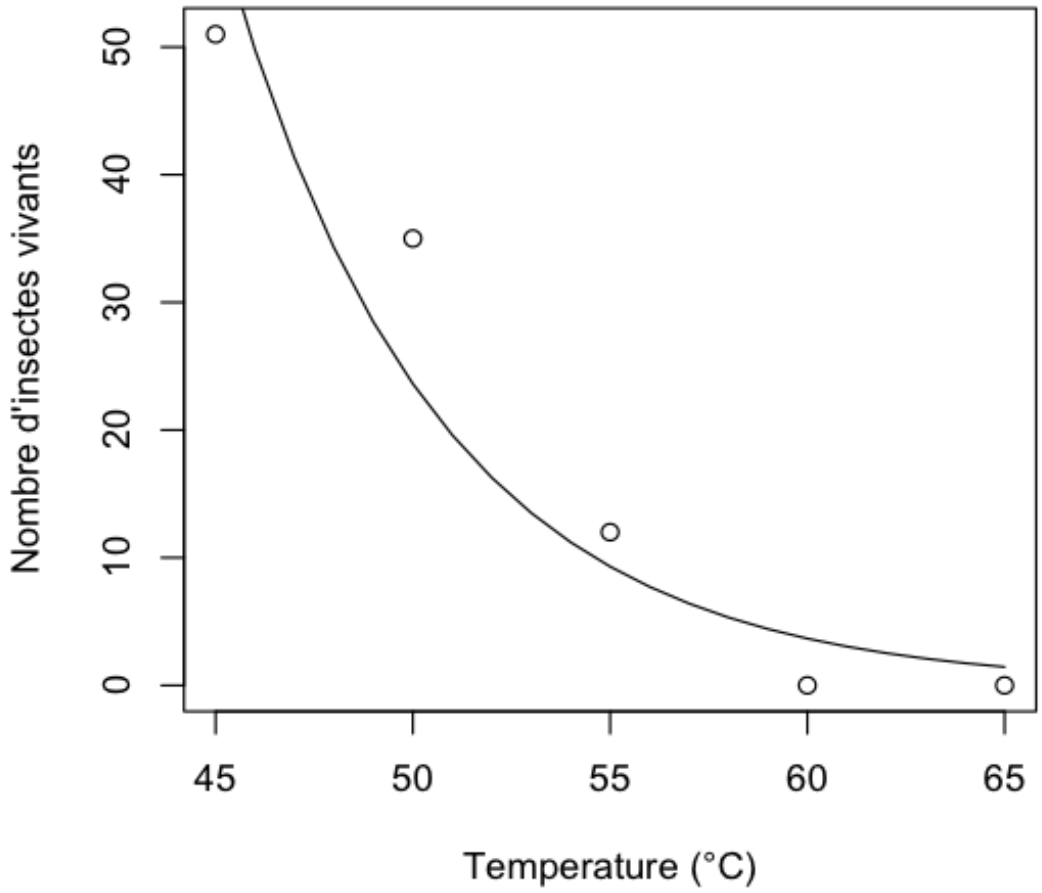
Example 3: modelling the effect of temperature on the survival of an invasive species

- We are interested in an insect pest called *Agrilus planipennis* that attacks ash wood.
- Data is available from the experiment conducted by Myers et al (2009) Pieces of ash wood were exposed to five different temperatures for 30 min.
- The number of live insects measured on the pieces of wood after the heat treatment was equal to 51, 35, 12, 0, 0 per m^2 of wood for temperatures 45, 50, 55, 60, 65◦C respectively

$$\log(E(Y)) = \theta_0 + \theta_1 X$$

Number of insects

Temperature



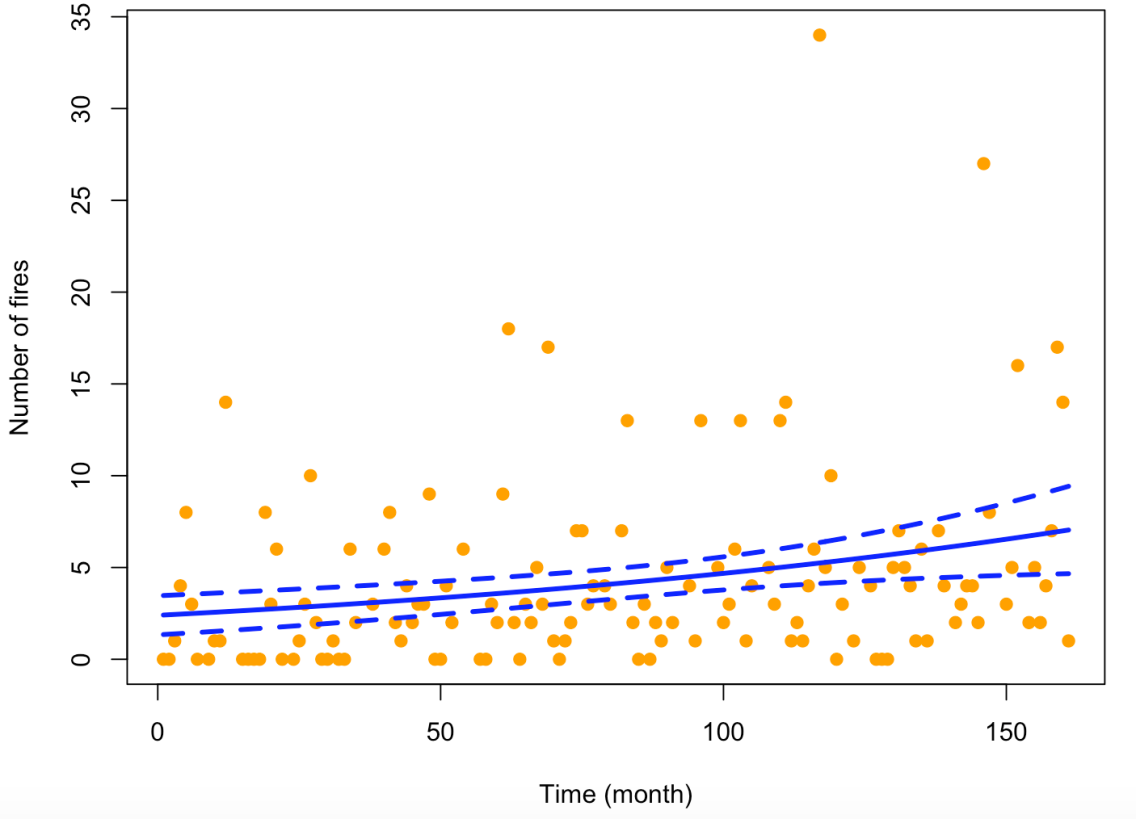
Example 4: modelling the number of fires across time

Data:

- One site in the US (county) during several years
- Observations: number of fires every month

$$\log(E(Y)) = \theta_0 + \theta_1 X$$

Number of fires Time (in months)



Outline

- Logistic and binomial models
  - Definition
  - Estimation
  - Test and deviance
  - Useful variants
  - Model selection

- Poisson models
  - Definition
  - Estimation
  - Test and deviance
  - Useful variants
  - Model selection

Example 2: Number of birds in Organic vs. Conventional farming

```
Birds=c(30, 29, 35, 32, 28, 31, 39, 20, 25, 31, 31, 18, 21, 21)
System=c("o", "o", "o", "o", "o", "o","o","c", "c", "c", "c", "c", "c","c")

data.frame(System, Birds)

Mod<-glm(Birds~System, family=poisson)
summary(Mod)

predict(Mod, type="response", se.fit=T)

par(mfrow=c(1,1))

plot(Birds~as.factor(System), xlab="System", ylab="Number of birds")

points(c(1,2),c(23.65, 32), pch=19, cex=1.5, col="red")

lines(c(1,1),c(23.65-1.96*1.85, 23.65+1.96*1.85), col="red")
lines(c(2,2),c(32-1.96*2.14, 32+1.96*2.14), col="red")
```

```
> summary(Mod)

Call:
glm(formula = Birds ~ System, family = poisson)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.2541  -0.5973  -0.2675   0.4498   1.3973

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  3.17208    0.07738  40.992  < 2e-16 ***
Systemo      0.29365    0.10224   2.872  0.00408 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

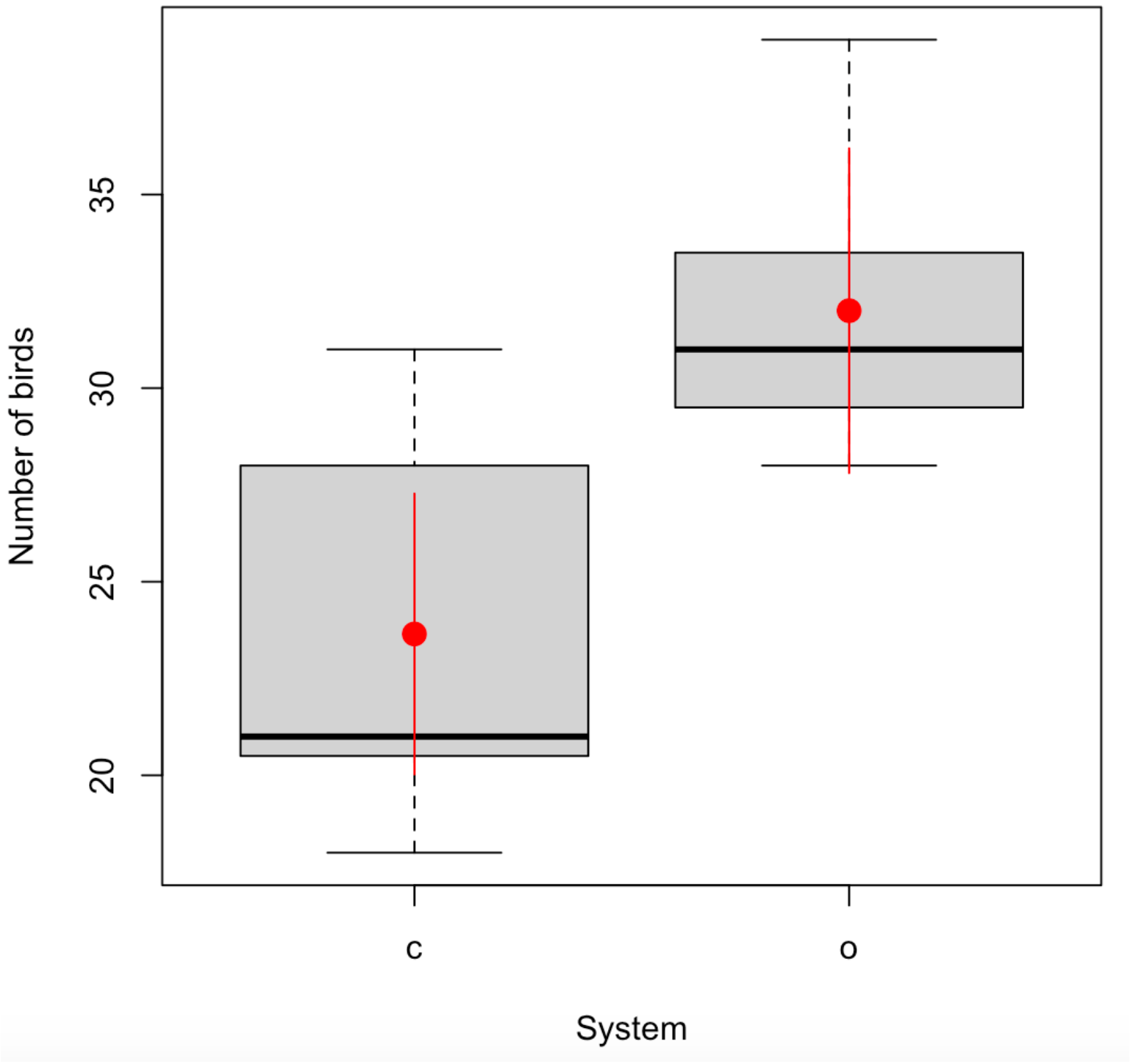
(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 17.9192  on 13  degrees of freedom
Residual deviance:  9.5801  on 12  degrees of freedom
AIC: 85.679

Number of Fisher Scoring iterations: 4

>
> predict(Mod, type="response", se.fit=T)
$fit
       1        2        3        4        5        6        7        8        9
32.00000 32.00000 32.00000 32.00000 32.00000 32.00000 32.00000 23.85714 23.85714
      10       11       12       13       14
23.85714 23.85714 23.85714 23.85714 23.85714

$se.fit
       1        2        3        4        5        6        7        8        9
2.138090 2.138090 2.138090 2.138090 2.138090 2.138090 2.138090 1.846121 1.846121
      10       11       12       13       14
1.846121 1.846121 1.846121 1.846121 1.846121
```


Number of birds
20
25
30
35
c
o
System

Example 3: modelling the effect of temperature on the survival of an invasive species

```
X = c(45, 50, 55, 60, 65)
Y = c(51, 35, 12, 0, 0)

Model <- glm(Y~X, family=poisson)
summary(Model)

plot(X,Y, xlab="Temperature (C)",ylab="Number of insects")
lines(45:65,exp(coef(Model)[1]+coef(Model)[2]*45:65), col="red")
```

```
Call:
glm(formula = Y ~ X, family = poisson)

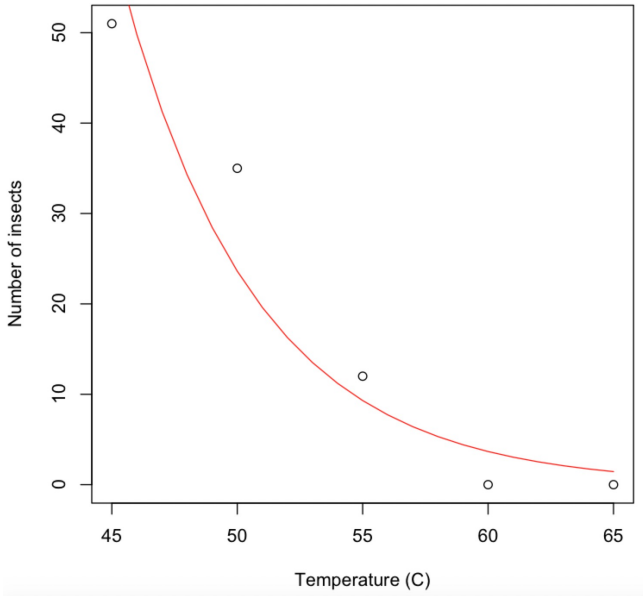
Deviance Residuals:
      1       2       3       4       5
-1.1886  2.1833  0.8455 -2.7074 -1.6992

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) 12.47853    1.06901  11.673   <2e-16 ***
X           -0.18633    0.02217  -8.406   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 126.355  on 4  degrees of freedom
Residual deviance:  17.112  on 3  degrees of freedom
AIC: 36.62

Number of Fisher Scoring iterations: 5
```



Example 4: modelling the number of fires across time

```
> summary(Mod)

Call:
glm(formula = Y ~ X, family = "poisson", data = DATA)

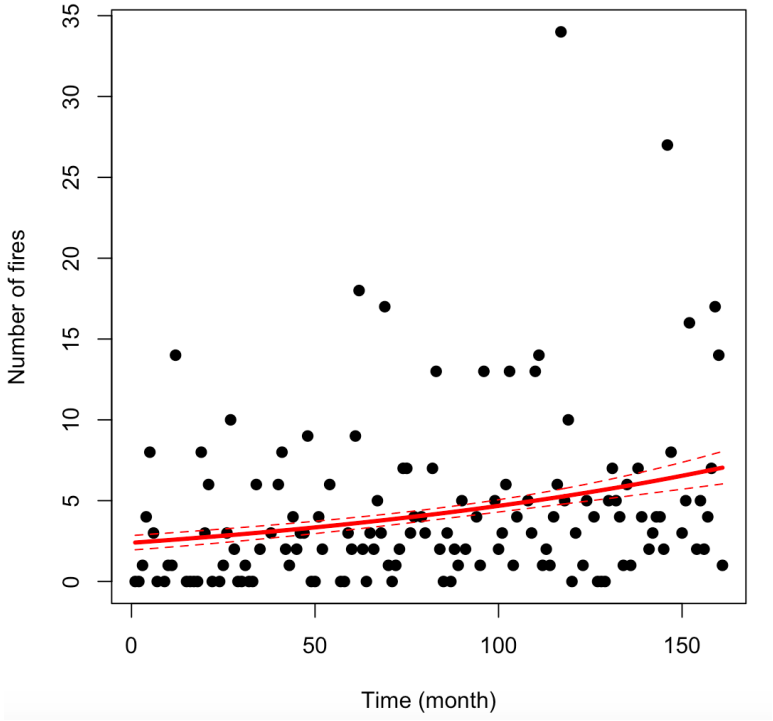
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-3.3712  -2.1217  -0.7257   0.3497   8.3430

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept) 0.8729387  0.0958008   9.112  < 2e-16 ***
X           0.0067010  0.0009095   7.367 1.74e-13 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 671.24  on 135  degrees of freedom
Residual deviance: 615.46  on 134  degrees of freedom
AIC: 972.87

Number of Fisher Scoring iterations: 5
```



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Test and deviance

Similar to what we have seen for the binomial model

- Wald test
- Null deviance, residual deviance
- Likelihood ratio test
- AIC

Special attention should be given to overdispersion

Overdispersion

What is it?

- Poisson models assume that the mean and the variance are equal
- This assumption is often wrong: Variance > Mean

How can we detect it?

- Compare the residual deviance to the ddl
- *Residual deviance* >> *ddl* indicates overdispersion

What can we do?

- Adapt the model by adding an extra-parameter
- Change the probability distribution

  Poisson ⟹ Negative binomial

Distribution	Mean	Variance
Gaussian	μ	σ^2
Bernouilli	π	$\pi(1-\pi)$
Binomial	$N\pi$	$N\pi(1-\pi)$
Poisson	λ	λ
Negative binomial	$r\ (1-\pi)/\pi$	$r\ (1-\pi)/\pi^2$

Example 4: modelling the number of fires across time

```
> summary(Mod)

Call:
glm(formula = Y ~ X, family = "poisson", data = DATA)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-3.3712  -2.1217  -0.7257   0.3497   8.3430

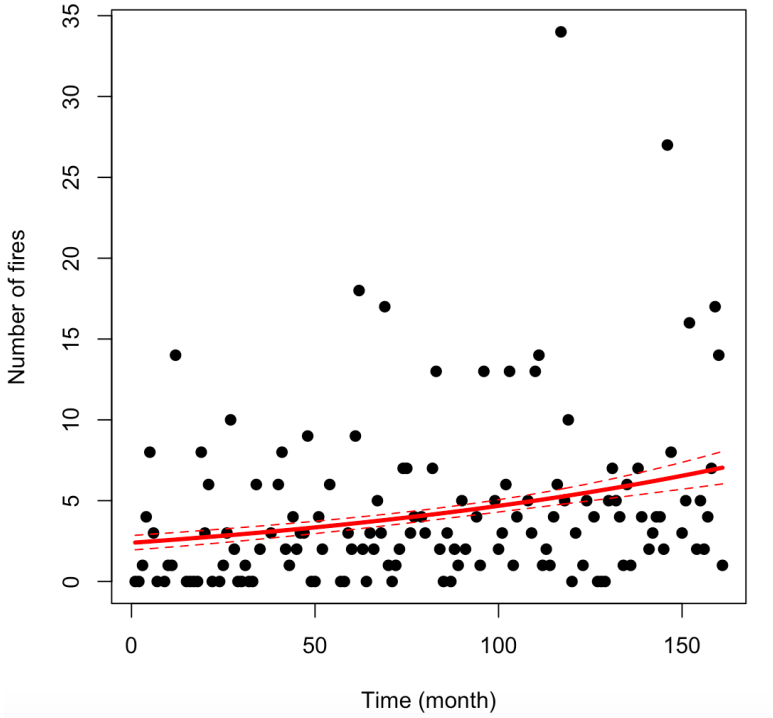
Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept) 0.8729387  0.0958008   9.112  < 2e-16 ***
X           0.0067010  0.0009095   7.367 1.74e-13 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 671.24  on 135  degrees of freedom
Residual deviance: 615.46  on 134  degrees of freedom
AIC: 972.87

Number of Fisher Scoring iterations: 5
```

$$\frac{615}{134} = 4{,}5$$



Quasi-poisson

Variance = K x Mean

```
> summary(Mod)

Call:
glm(formula = Y ~ X, family = "quasipoisson", data = DATA)

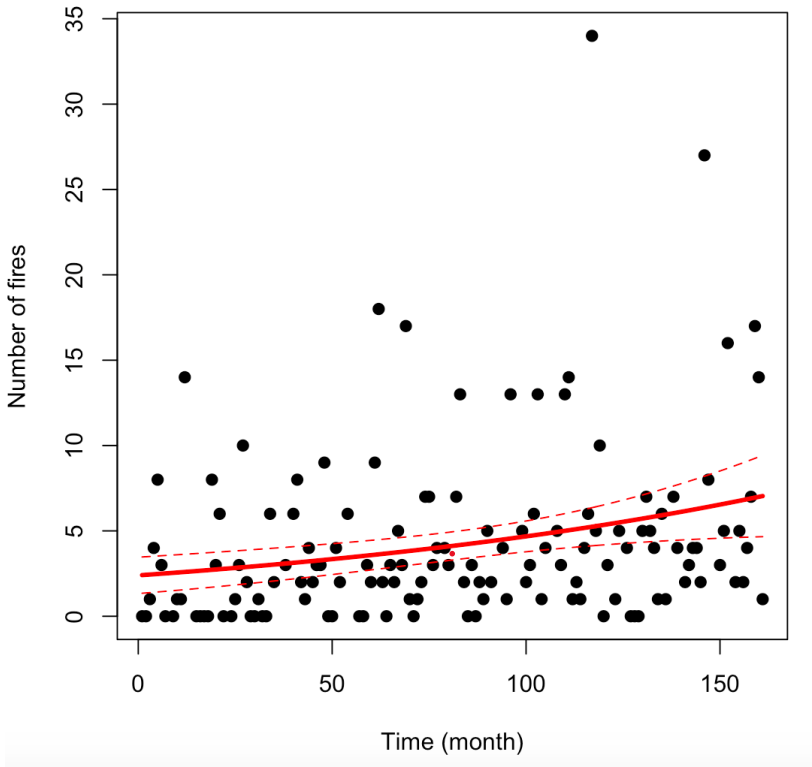
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-3.3712  -2.1217  -0.7257   0.3497   8.3430

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 0.872939   0.226930   3.847 0.000184 ***
X           0.006701   0.002154   3.110 0.002284 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for quasipoisson family taken to be 5.611049)

    Null deviance: 671.24  on 135  degrees of freedom
Residual deviance: 615.46  on 134  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 5
```



Distribution	Mean	Variance
Gaussian	μ	σ^2
Bernouilli	π	$\pi(1-\pi)$
Binomial	$N\pi$	$N\pi(1-\pi)$
Poisson	λ	λ

Distribution	Mean	Variance
Gaussian	μ	σ^2
Bernouilli	π	$\pi(1-\pi)$
Binomial	$N\pi$	$N\pi(1-\pi)$
Poisson	λ	λ
Negative binomial	$r\,(1-\pi)/\pi$	$r\,(1-\pi)/\pi^2$

Negative binomial

```
library(MASS)

Model_nb<-glm.nb(Y~X, data=DATA)
summary(Model_nb)
```

```
> summary(Model_nb)

Call:
glm.nb(formula = Y ~ X, data = DATA, init.theta = 1.102557845,
    link = log)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-2.0048  -1.0392  -0.3590   0.1711   2.6435

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) 0.858679   0.190632   4.504 6.66e-06 ***
X           0.006864   0.001988   3.453 0.000555 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(1.1026) family taken to be 1)

    Null deviance: 165.29  on 135  degrees of freedom
Residual deviance: 153.57  on 134  degrees of freedom
AIC: 693.88

Number of Fisher Scoring iterations: 1


              Theta:  1.103
          Std. Err.:  0.181

 2 x log-likelihood:  -687.884
```

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Some useful variants

- Deterministic component
  - Polynomials
  - Non-parametric response (mgcv)
  - Offset
- Random component
  - Negative binomial
  - Zero-inflated
  - Additional random effects (mixed models)

Offset

- Useful when the count data are collected at different scales
- Can be easily included in a model using glm()

Example

We want to estimate the effect of temperature on the number of covid19 cases in cities of different sizes.

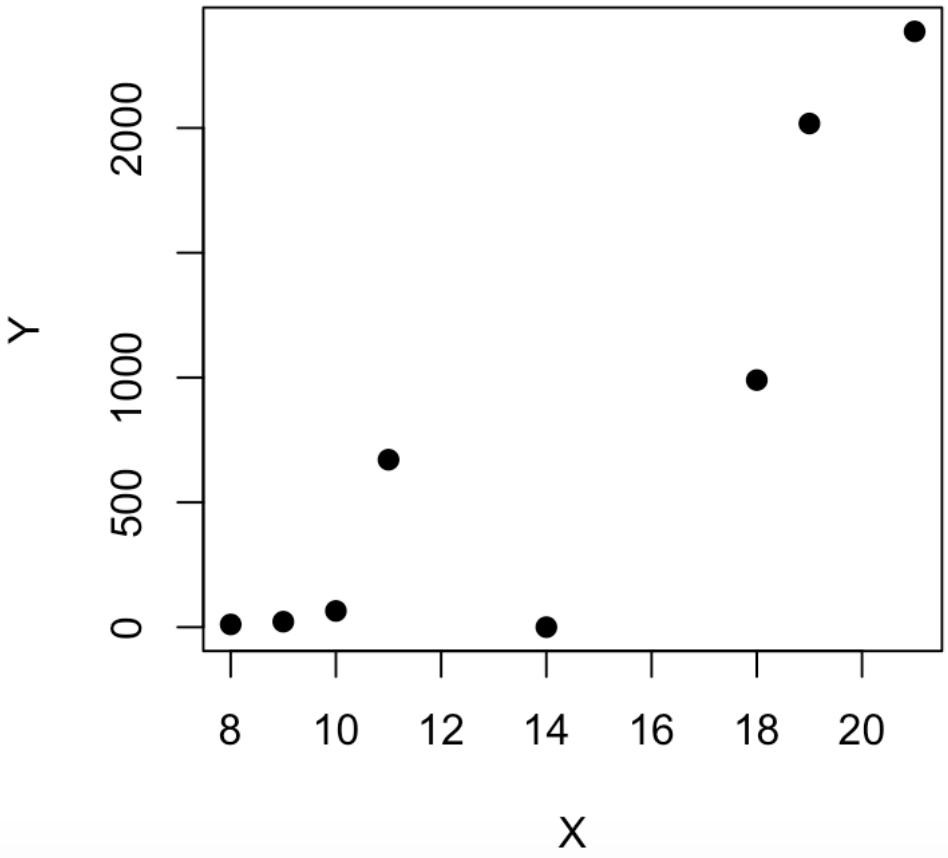
We have *N* observations of covid19-case numbers (*Y*) in *N* cities of different sizes *S* and temperatures *X*

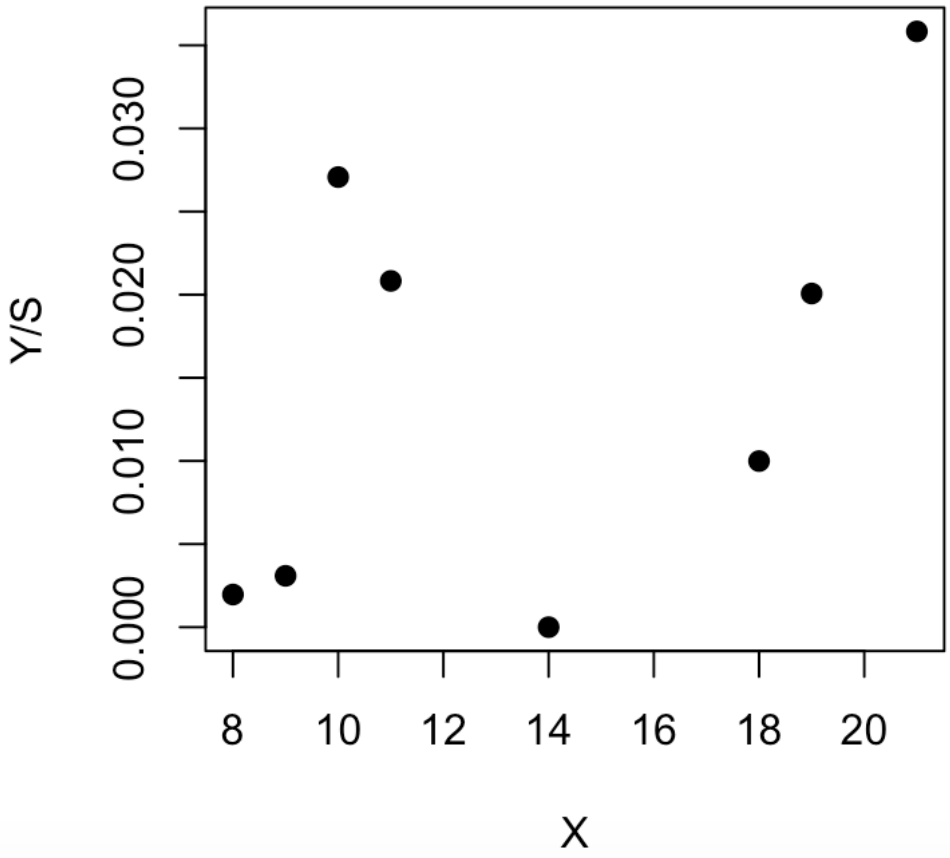
$$log[E(Y)] = log(S) + \theta_0 + \theta_1 X$$

$$E(Y) = S \times \exp(\theta_0 + \theta_1 X)$$

```
S=c(1100, 5602, 100551, 99090, 32218, 2401, 7123,66612)
X=c(14, 8, 19, 18, 11, 10, 9, 21)
Y=c(0, 11, 2018, 990, 671, 65, 22, 2387)

par(mfrow=c(1,2))
plot(X,Y, pch=19)
plot(X,Y/S, pch=19)
```





```
Mod_1=glm(Y~X, family=poisson)
summary(Mod_1)

Mod_2=glm(Y~X+ offset(log(S)), family=poisson)
summary(Mod_2)

Mod_3=glm(Y~X, family=quasipoisson)
summary(Mod_3)

Mod_4=glm(Y~X+offset(log(S)), family=quasipoisson)
summary(Mod_4)
```

$$log[E(Y)] = log(S) + \theta_0 + \theta_1 X$$

```
> summary(Mod_1)

Call:
glm(formula = Y ~ X, family = poisson)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-28.1721   -9.6856   -5.9444   -0.0256   28.2420

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) 2.228884   0.075293   29.60   <2e-16 ***
X           0.268188   0.003991   67.19   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 9023.5  on 7  degrees of freedom
Residual deviance: 2018.7  on 6  degrees of freedom
AIC: 2074

Number of Fisher Scoring iterations: 6
```

```
> Mod_2=glm(Y~X+ offset(log(S)), family=poisson)
> summary(Mod_2)

Call:
glm(formula = Y ~ X + offset(log(S)), family = poisson)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-23.050   -5.722   -3.762    9.556   16.632

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept) -5.591646   0.091655  -61.01   <2e-16 ***
X            0.091033   0.004882   18.65   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 1641.5  on 7  degrees of freedom
Residual deviance: 1224.8  on 6  degrees of freedom
AIC: 1280.1

Number of Fisher Scoring iterations: 5
```

```
> Mod_3=glm(Y~X, family=quasipoisson)
> summary(Mod_3)

Call:
glm(formula = Y ~ X, family = quasipoisson)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-28.1721   -9.6856   -5.9444   -0.0256   28.2420

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  2.22888    1.42066   1.569   0.1677
X            0.26819    0.07531   3.561   0.0119 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for quasipoisson family taken to be 356.0194)

    Null deviance: 9023.5  on 7  degrees of freedom
Residual deviance: 2018.7  on 6  degrees of freedom
AIC: NA
```

```
> Mod_4=glm(Y~X+offset(log(S)), family=quasipoisson)
> summary(Mod_4)

Call:
glm(formula = Y ~ X + offset(log(S)), family = quasipoisson)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-23.050   -5.722   -3.762    9.556   16.632

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -5.59165    1.32085  -4.233  0.00548 **
X            0.09103    0.07035   1.294  0.24325
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for quasipoisson family taken to be 207.6794)

    Null deviance: 1641.5  on 7  degrees of freedom
Residual deviance: 1224.8  on 6  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 5
```

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- Poisson models
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  - Estimation
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Model selection

- Deviance
- Likelihood ratio test
- AIC
- Check overdispersion

Summary

- Specify the objective of your analysis
- Look at you data
  - With yes/no data, try Bernouilli models
  - With proportions, try Binomial models
  - With count data, try Poisson models
- Define several models including 0, 1, 2, …, inputs
- Fit the models
- Test the different variants
- Check overdispersion
- Interpret results and conclude

Exercise

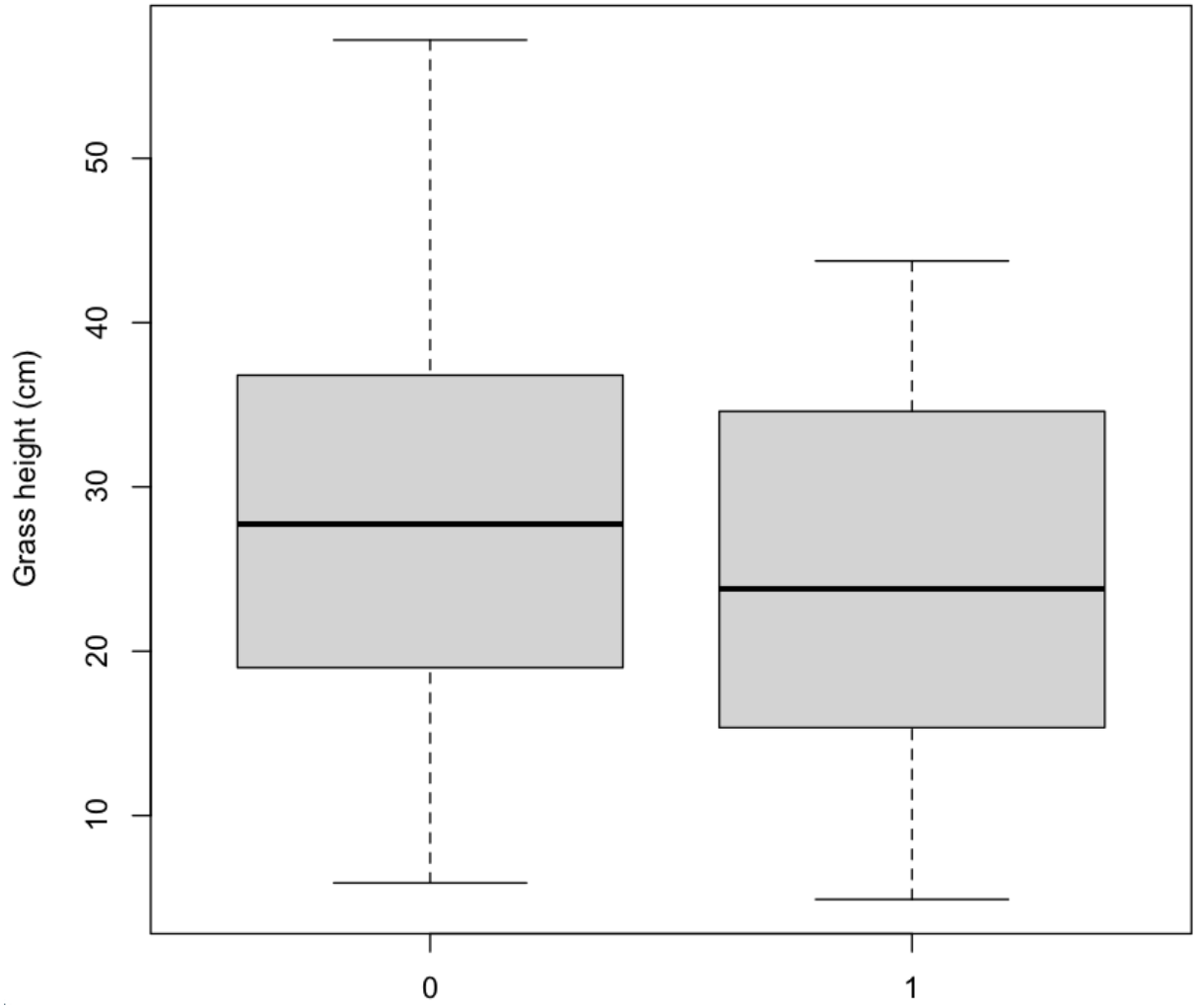
Objective:

Assess whether the probability of presence of the bird *Tringa totanus* is higher in grassland with high vs. low grass height

```
> DATA
    Presence HauteurHerbe
1          0        48.80
2          0        15.70
3          0        15.40
4          0        22.80
5          1        30.40
6          1        34.30
7          0        31.30
8          1        12.80
9          1         4.90
10         0        26.30
11         0        10.40
12         0        42.90
13         0        24.20
14         0        16.70
15         0        27.70
16         0        33.30
```

```
> dim(DATA)
[1] 424   2
```

```
> summary(DATA)
    Presence       HauteurHerbe
Min.   :0.0000   Min.   : 4.90
1st Qu.:0.0000   1st Qu.:18.70
Median :0.0000   Median :27.00
Mean   :0.1203   Mean   :27.89
3rd Qu.:0.0000   3rd Qu.:36.48
Max.   :1.0000   Max.   :57.20
```



Questions

1. Define one or several models
2. How to estimate the model parameters?

```
> Mod<-glm(Presence~HauteurHerbe, data=DATA, family="binomial")
> summary(Mod)

Call:
glm(formula = Presence ~ HauteurHerbe, family = "binomial", data = DATA)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-0.6797  -0.5541  -0.4730  -0.4102   2.2831

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)  -1.16333    0.38712  -3.005  0.00265 **
HauteurHerbe -0.03123    0.01423  -2.195  0.02813 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 311.63  on 423  degrees of freedom
Residual deviance: 306.59  on 422  degrees of freedom
AIC: 310.59

Number of Fisher Scoring iterations: 5
```

```
> Mod0<-glm(Presence~1, data=DATA, family="binomial")
> summary(Mod0)

Call:
glm(formula = Presence ~ 1, family = "binomial", data = DATA)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-0.5063  -0.5063  -0.5063  -0.5063   2.0581

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -1.9898     0.1493  -13.33   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

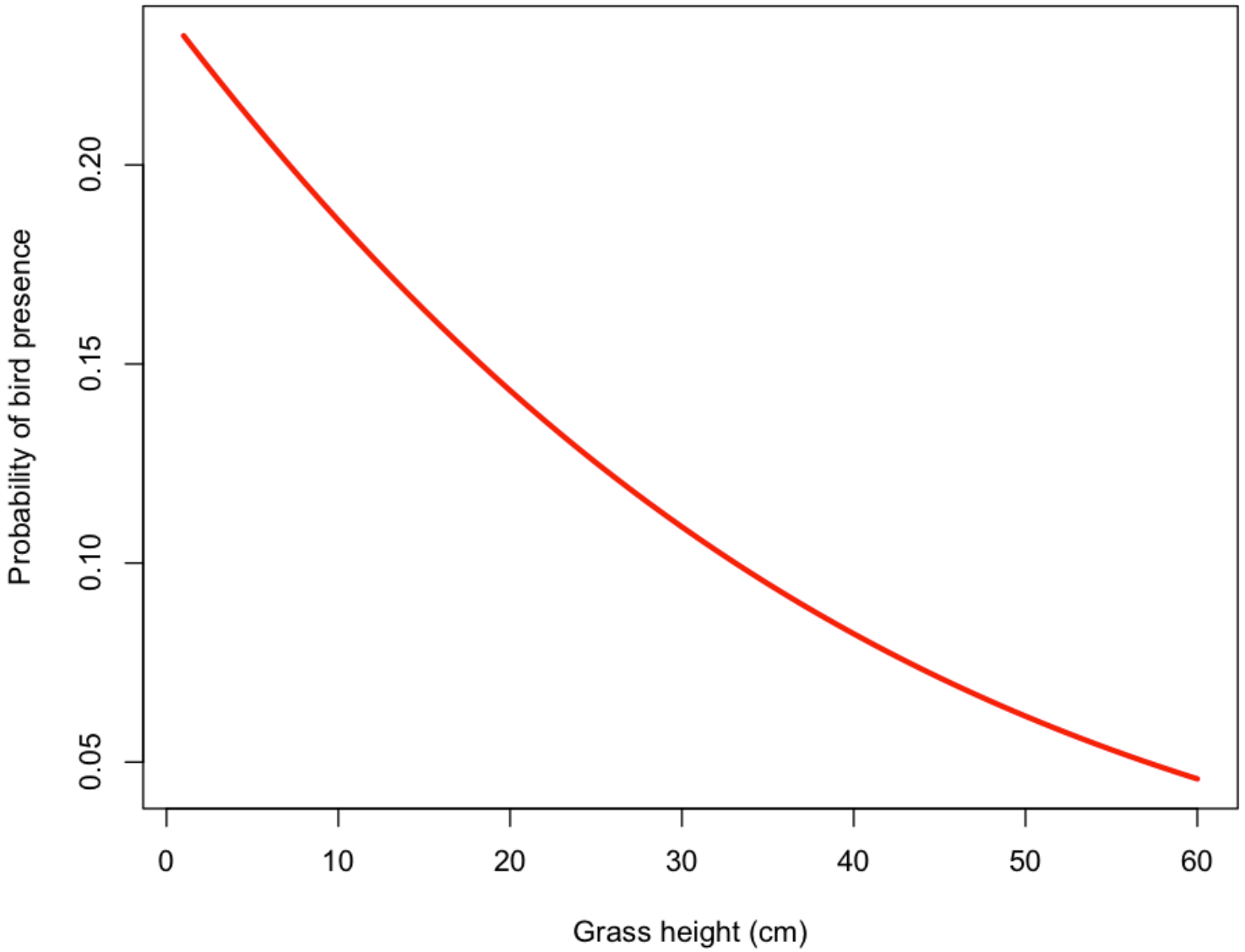
    Null deviance: 311.63  on 423  degrees of freedom
Residual deviance: 311.63  on 423  degrees of freedom
AIC: 313.63

Number of Fisher Scoring iterations: 4
```

Questions

1. Define one or several models
2. How to estimate the model parameters?
3. Is the effect of grass height significant?
4. Is its effect positive or negative on bird presence probability?

```
Proba<-predict(Mod, newdata=data.frame(HauteurHerbe=1:60),type="response")
plot(1:60, Proba, xlab="Grass height (cm)", ylab="Probability of bird presence", type="l", lwd=3, col="red")
```



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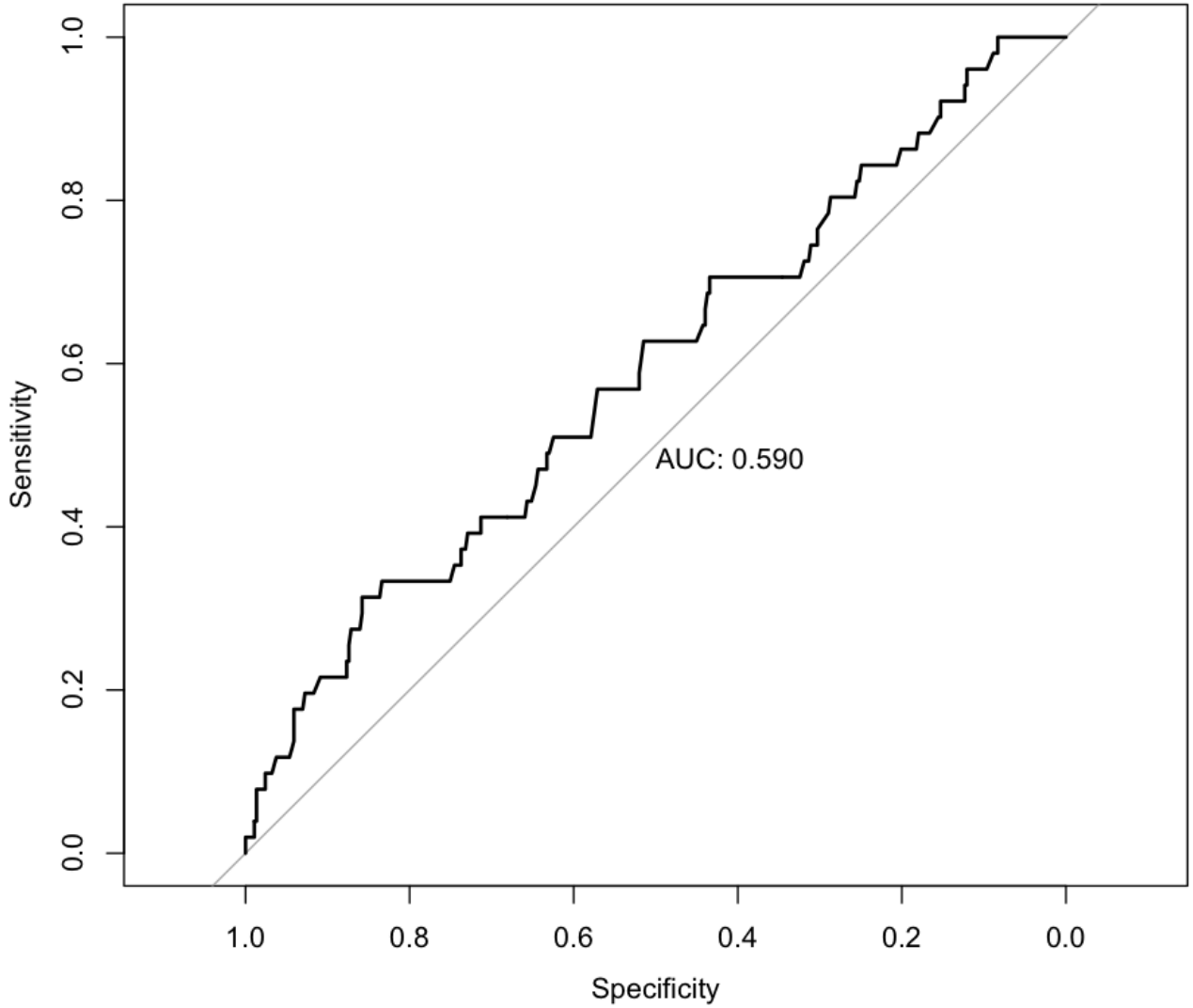
5. What is the probability of bird presence for a grass height of 30cm?

```
library(pROC)
Pred=predict(Mod, type="response")
roc1=roc(DATA$Presence~Pred)
plot(roc1, print.auc=T)
```



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5. What is the probability of bird presence for a grass height of 30cm?
6. Is the model reliable for predicting bird presence?