vliruos

SHARING MINDS, CHANGING LIVES

This course was developed as a part of the VLIR-UOS Cross-Cutting project s:

- Statistics: 2011-2016, 2017.
- Statistics: 2017.
- Statistics for development : 2018-2020.

The >eR-Biostat initiative

Making R based education materials in statistics accessible for all

Applied Generalized Linear Models (GLM) using R (PART 1)

Developed by

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Reference list

- Main reference:
  - Dobson (2002): An introduction to generalized linear models.
- Other references:
  - McCillagh and Nelder (1983): Generalized linear models (first edition).
  - Collet D(1994): Modeling Binary data.
  - Lindsey (1997): Applying generalized linear models.

Software

- Two main R functions:
  - Linear models in R: the lm() function.
  - Generalized linear models in R: the glm() function in R.
- All R programs for the examples presented in the slides are available online.

Datasets

- Data are given as a part of R programs for the course.
- External datasets (which are not given as a part of the R code) and used for illustration are available online.

Topics (part 1)

1. Analysis of Variance
2. Linear regression models with normal error
3. Generalized linear models
4. Exponential Family
5. Generalized linear model function in R
6. Models for Binary data
7. Estimation and confidence intervals
8. Inference
9. Model Selection
10. Model diagnostic

Topics (part 2)

11. Poisson Regression
12. Beyond Poisson and binomial distributions:
    models with different link functions and/or distributions
13. Poisson regression and log linear models
14. Over dispersion

Chapter 1:
Analysis of Variance (ANOVA)

Donson: chapter 2

Lindsey: chapter 9

McCullagh & Nelder: chapter 3

Example 1: A Biopharmaceutical Problem

- A group of 24 rats were randomized into two treatment groups: active drug and placebo
- After the administration of the drug, the rat was placed on a surface, and the distanced traveled by the rat (in meters) was measured.

The data

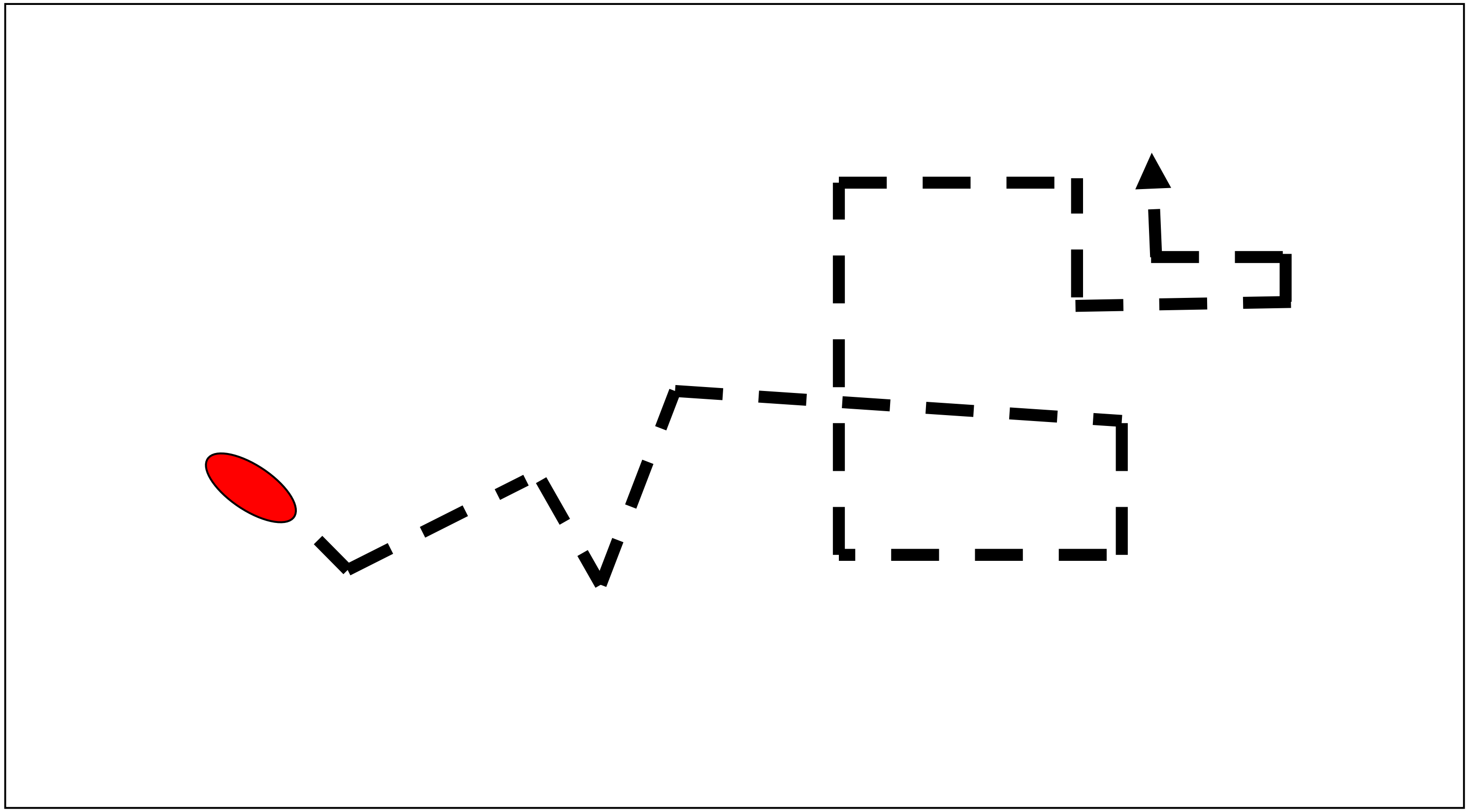
22	QNP	186.6145
11	QNP	103.3529
4	QNP	191.3850
16	QNP	334.9845
7	QNP	89.2831
13	QNP	345.5070
2	QNP	169.5161
20	QNP	173.1491
19	QNP	130.9634
8	QNP	363.4392
10	QNP	76.5340
24	QNP	202.1145
1	SALINE	12.8458
17	SALINE	44.3092
15	SALINE	41.3581
6	SALINE	24.5560
23	SALINE	61.5525
18	SALINE	38.8464
5	SALINE	27.0107
12	SALINE	45.9960
21	SALINE	13.7927
14	SALINE	42.4009
3	SALINE	17.5861
9	SALINE	11.7937

Response

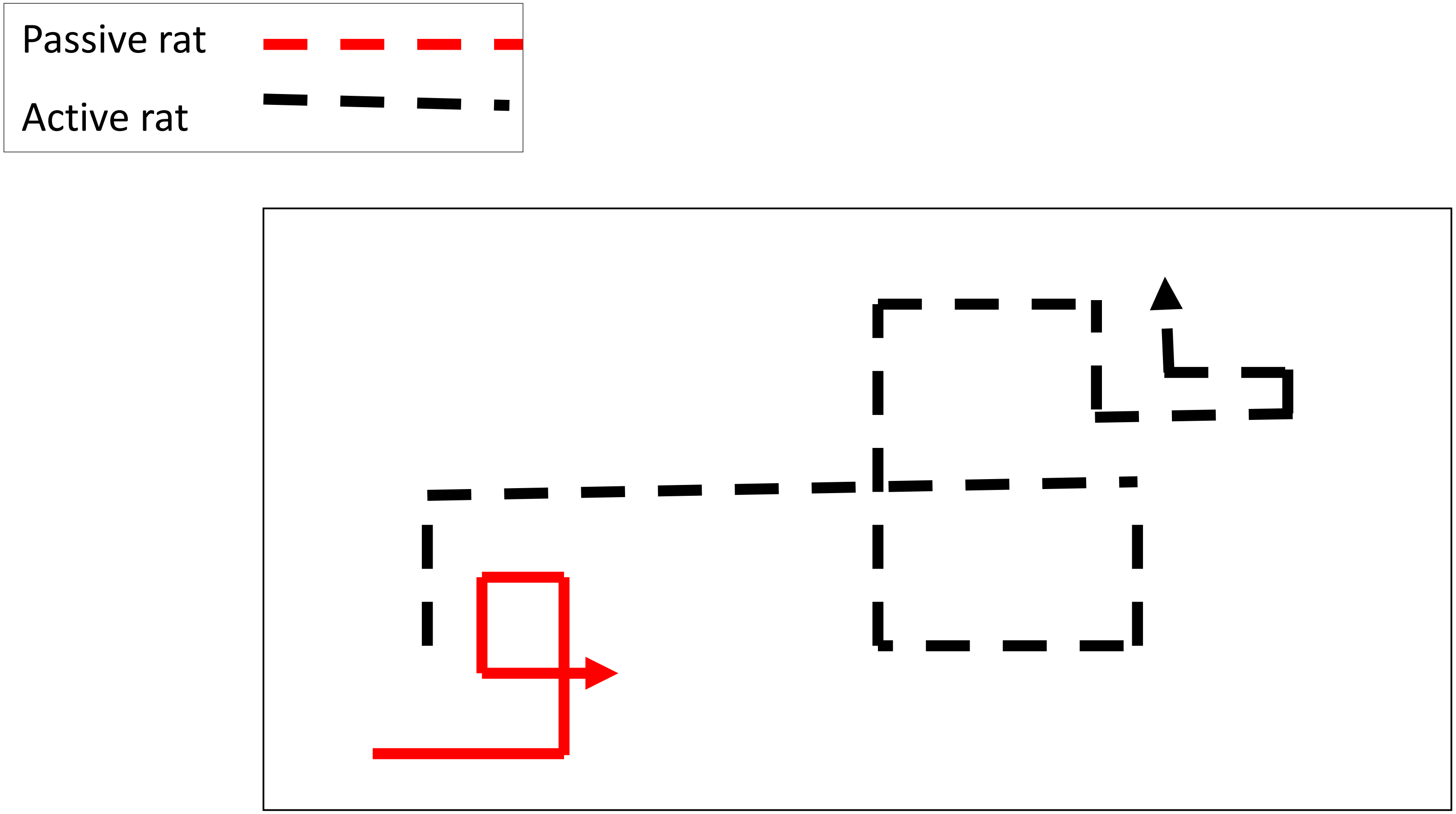
Treatment group

The Evaluation of the Rat performance in distance

Y_i is the distance traveled by the rat during the experiment.



Description of the Experiment



It is assumed that a successful drug increase the distance traveled by the rat.

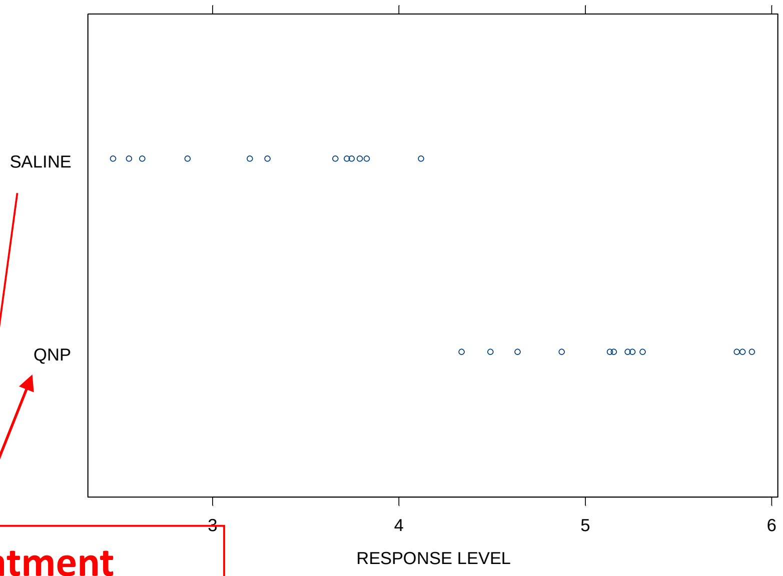
The Scientific Question

- Does the drug increase the distance traveled by the rat ?

A good drug is expected to improve the rats’ performance, i.e. to increase the distance travel by the rat

Graphical display of the data (1)

A strip plot



Treatment

groups

The response level (on log scale)

The data

22	QNP	186.6145
11	QNP	103.3529
4	QNP	191.3850
16	QNP	334.9845
7	QNP	89.2831
13	QNP	345.5070
2	QNP	169.5161
20	QNP	173.1491
19	QNP	130.9634
8	QNP	363.4392
10	QNP	76.5340
24	QNP	202.1145
1	SALINE	12.8458
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6	SALINE	24.5560
23	SALINE	61.5525
18	SALINE	38.8464
5	SALINE	27.0107
12	SALINE	45.9960
21	SALINE	13.7927
14	SALINE	42.4009
3	SALINE	17.5861
9	SALINE	11.7937

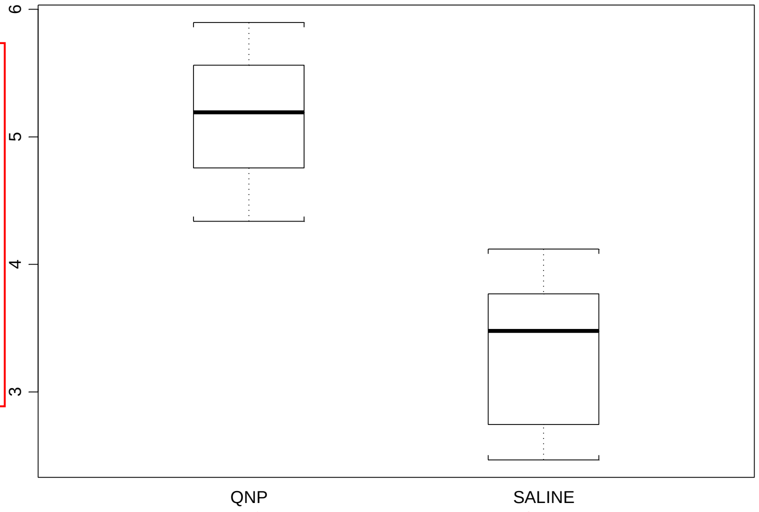
Response

Treatment group

Graphical display of the data (2)

A boxplot plot

The level (on log scaleresponse)



Treatment groups

22	QNP	186.6145
11	QNP	103.3529
4	QNP	191.3850
16	QNP	334.9845
7	QNP	89.2831
13	QNP	345.5070
2	QNP	169.5161
20	QNP	173.1491
19	QNP	130.9634
8	QNP	363.4392
10	QNP	76.5340
24	QNP	202.1145
1	SALINE	12.8458
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6	SALINE	24.5560
23	SALINE	61.5525
18	SALINE	38.8464
5	SALINE	27.0107
12	SALINE	45.9960
21	SALINE	13.7927
14	SALINE	42.4009
3	SALINE	17.5861
9	SALINE	11.7937

The data

Response

Treatment group

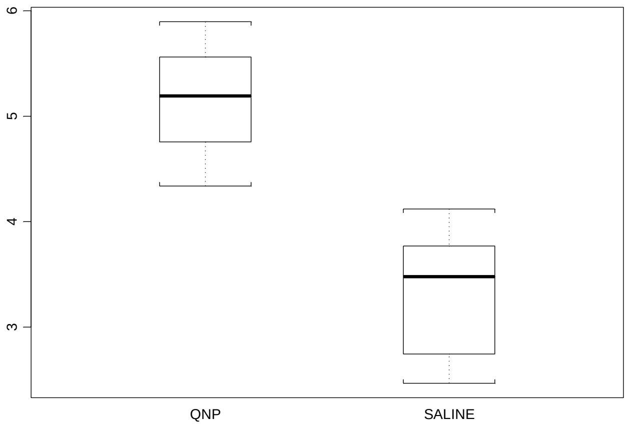
Boxplot by treatment group

The data in R:

```
> dist<-c(186.6145,103.3529,191.3850,334.9845,89.2831,
     345.5070,169.5161,173.1491,130.9634,363.4392,
     76.5340,202.1145,12.8458,44.3092,41.3581,24.5560,
     61.5525,38.8464,27.0107,45.9960,13.7927,42.4009,17.5861,
     11.7937)
> gr<-c(rep(0,12),rep(1,12))
```

The boxplot:

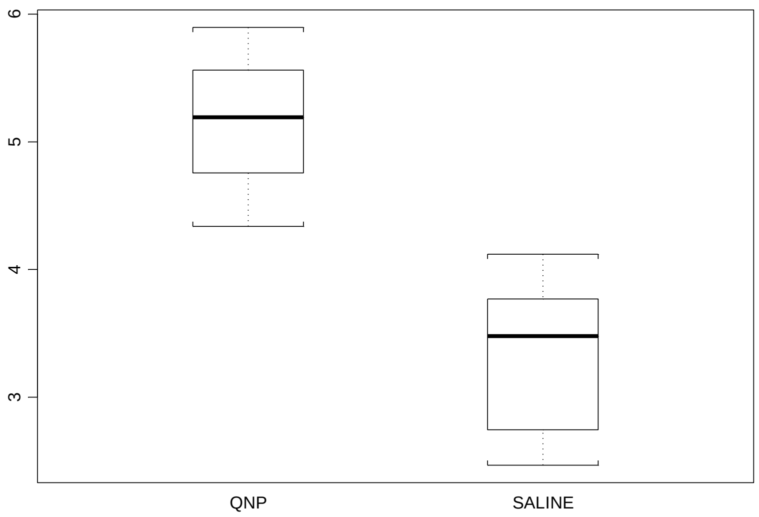
```
> boxplot(split(dist,gr))
```



Groups' means

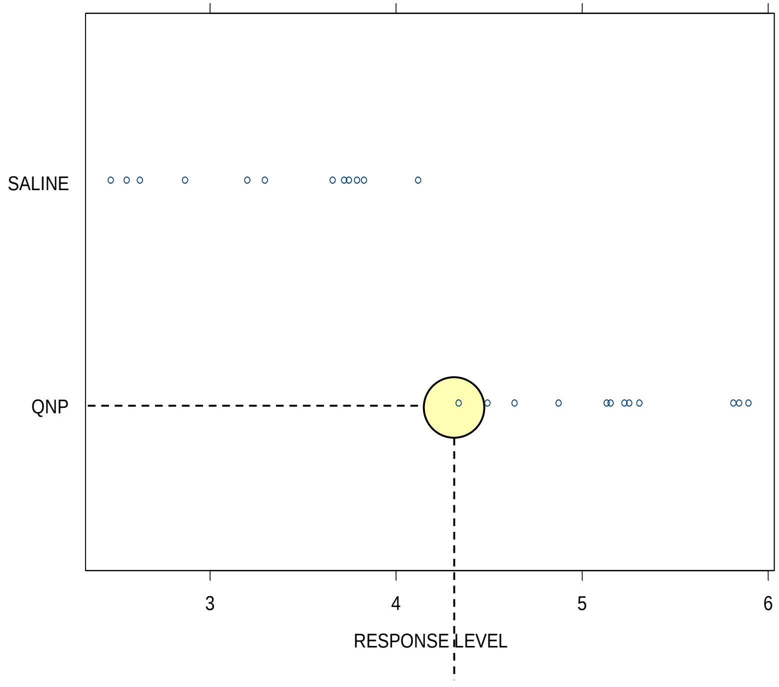
```
> tapply(dist,as.factor(gr),mean)
        0         1
197.23694  31.83734

> tapply(dist,as.factor(gr),median)
        0         1
179.88180  32.92855
```



ANOVA Terminology

- The distance traveled is the dependent variable. This is the response.
- The treatment group is the independent variable and it called the factor. In this example the factor has two levels.



(X_{11},Y_{11})

Data Structure

- We have two variables, the factor (x) and the response (Y).
- The value of X is equal for all subjects from the same treatment group. This value is the factor level.

22	QNP	186.6145
11	QNP	103.3529
4	QNP	191.3850
16	QNP	334.9845
7	QNP	89.2831
13	QNP	345.5070
2	QNP	169.5161
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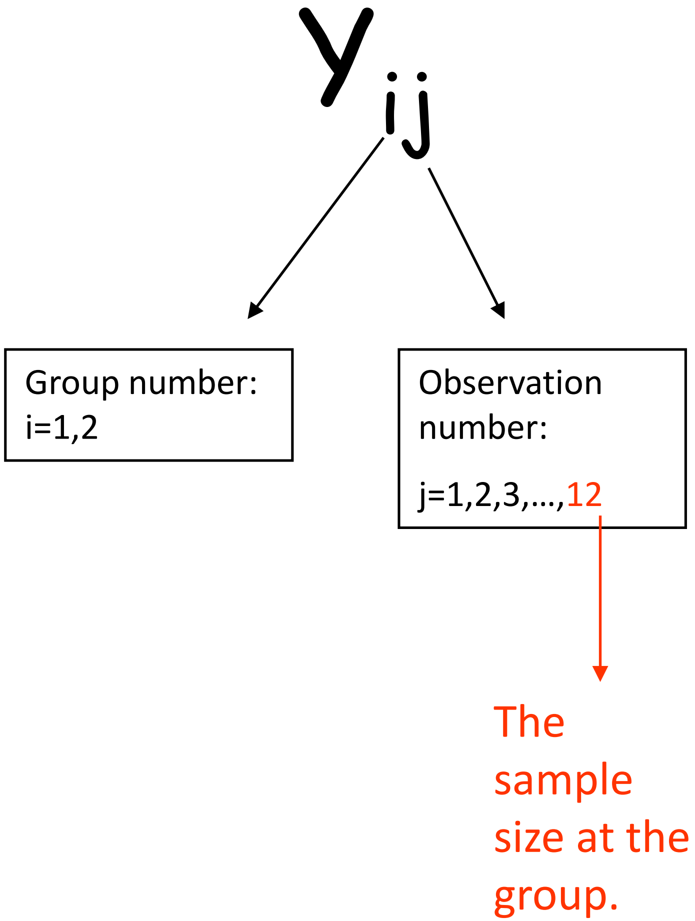
23	SALINE	61.5525
18	SALINE	38.8464
5	SALINE	27.0107
12	SALINE	45.9960
21	SALINE	13.7927
14	SALINE	42.4009
3	SALINE	17.5861
9	SALINE	11.7937

The factor: the treatment group

The response: the distance traveled (y_i)

Data Structure: notation (1)



y_{ij}

Group number: i=1,2

Observation number:

j=1,2,3,…,12

The sample size at the group.

22	QNP	186.6145
11	QNP	103.3529
4	QNP	191.3850
16	QNP	334.9845
7	QNP	89.2831
13	QNP	345.5070
2	QNP	169.5161
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12	SALINE	45.9960
21	SALINE	13.7927
14	SALINE	42.4009
3	SALINE	17.5861
9	SALINE	11.7937

Group 1:

i=1

n_1=12

Group 2:

i=2

n_2=12

Y_{212}: Observation number 12 in group 2

Data Structure: notation (2)

Number of Group: I

Sample size: n

n=n_1+n_2+,…,n_k

Overall mean: $\bar{Y}_{..}$

Mean of group i: $\bar{Y}_{i.}$

Sample size in group i: n_i

22	QNP	186.6145
11	QNP	103.3529
4	QNP	191.3850
16	QNP	334.9845
7	QNP	89.2831
13	QNP	345.5070
2	QNP	169.5161
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12	SALINE	45.9960
21	SALINE	13.7927
14	SALINE	42.4009
3	SALINE	17.5861
9	SALINE	11.7937

Group 1: The group mean

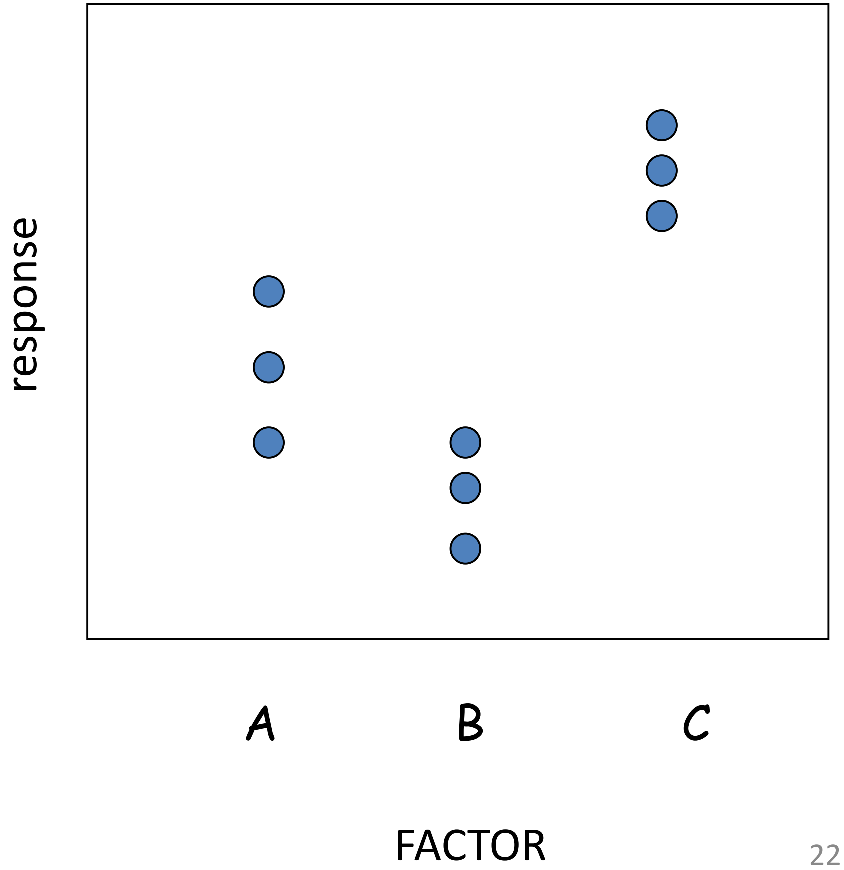
$$\bar{Y}_{1\cdot}$$

Group 2: The group mean

$$\bar{Y}_{2\cdot}$$

What is a One-Way ANOVA Model ?

- A One-Way ANOVA model is a statistical model which aims to explain the variability of the response variable.
- The question of primary interest is IF THE MEAN RESPONSE IS DIFFERENT across the factor levels.



one-way ANOVA: testing of hypotheses

H_0 & H_1

Testing of hypotheses

- The sample per treatment group (i. e, each level of the treatment factor) is a sample of a population.
- We want to test whether the means of the populations across the factor levels are equal or not.
- The averages of the populations are parameters (but unknown parameters). We want to estimate these parameters.

Populations and the factor levels (and assumptions)

Populations	Distribution of the populations
1) (QNP)	$N\left(\mu_1, \sigma^2\right)$
2) (SLINE)	$N\left(\mu_2, \sigma^2\right)$

population mean

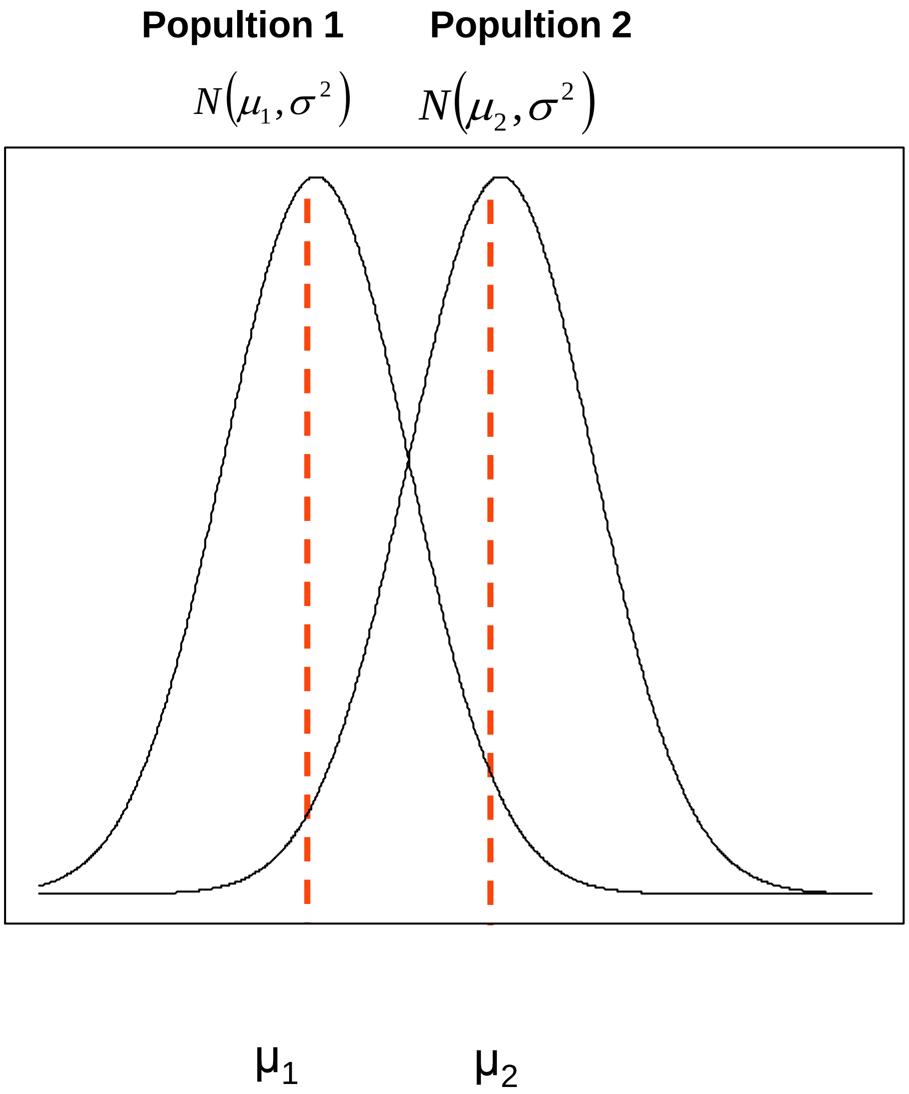
Population variance

- There are two factor levels (groups): active drug and placebo.
- Each subject within a treatment group is a random sample from a population.
- We assume that

$$\boxed{Y_{ij} \sim N\left(\mu_i, \sigma^2\right)}$$

Two populations

- We assume that the variance is constant (σ^2).
- The null hypothesis is not rejected if the means are equal



Formulation of the null hypothesis

The null hypothesis states that (for K populations) the average of the K populations is the same.

$$\boxed{H_0 : \mu_1 = \mu_2 = \ldots = \mu_K}$$

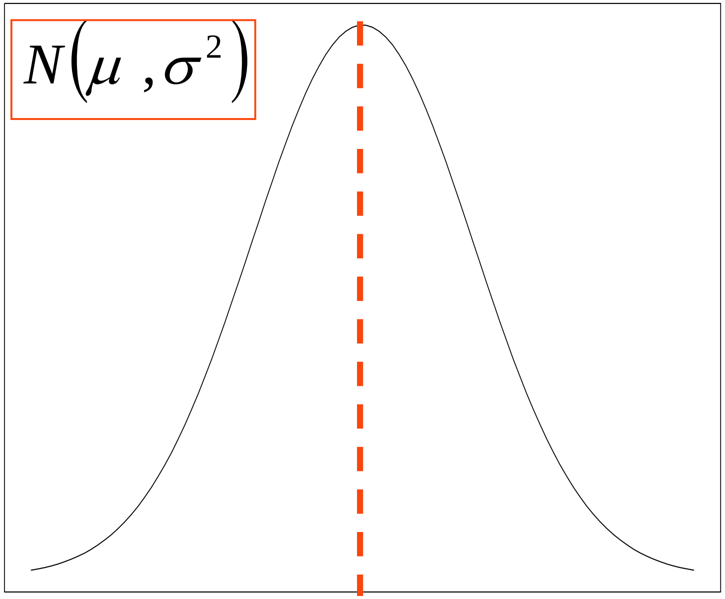
In other words, there is no effect of the treatment.

The null hypothesis

- Under the null hypothesis the means in the population are equal.
- This means that:

$$H_0 : \mu_1 = \mu_2 = \ldots = \mu_K$$

$$\boxed{Y_{ij} \sim N\left(\mu, \sigma^2\right)}$$



What is the alternative?

$$H_1 : \mu_i \neq \mu_l$$

For at elast one pair of *i* and *l* (*i,l=1,2,..K*)

$$\Rightarrow Y_{ij} \sim N\left(\mu_i, \sigma^2\right) \text{ and } Y_{lj} \sim N\left(\mu_l, \sigma^2\right)$$

$$\text{for } i \neq l, i, l = 1,2,\cdots,K$$

one-way ANOVA: inference

$H_0 \,\&\, H_1$

Two Sources of Variability

- The main concept in ANOVA models, and in particular One-way ANOVA is to decompose the total variability of the response into two parts.

total variabilty=variability within the groups + variability between the groups

- An ANOVA model is a model in which we explain the total variability with these two sources.

A very simple example

- One factor experimant.
- The factor has three levels (1,2,3).
- Three observation at each level.

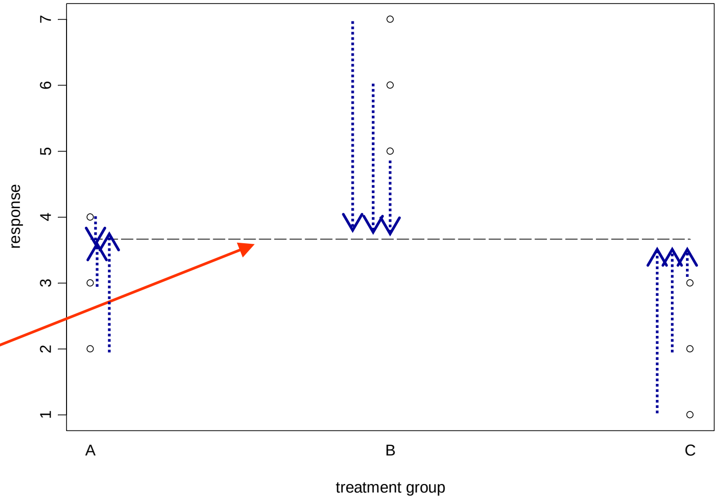
```
> resp<-c(2,3,4,5,6,7,1,2,3)
> gr<-c(1,1,1,2,2,2,3,3,3)
> data.frame(resp,gr)
  resp gr
1    2  1
2    3  1
3    4  1
4    5  2
5    6  2
6    7  2
7    1  3
8    2  3
9    3  3
```

group	Y_{ij}	Group mean
1 1 1	2 3 4	3
2 2 2	5 6 7	6
3 3 3	1 2 3	2

Overall mean: 3.6666

Two Sources of Variability: the total variability

The total sum of squares (SST) is the sum of squared distance between the observations from the overall mean.



The overall mean=3.66667

$$(2-3.666)^2+(3-3.666)^2+(4-3.666)^2+,\ldots,(2-3.666)^2+(3-3.666)^2=32$$

$$SST=\sum_{i=1}^{I}\sum_{j=1}^{n_i}\left(Y_{ij}-\overline{Y}_{..}\right)^2$$

Two Sources of Variability: the variability within the groups

The sum of squares within the groups is the sum of squared diffrence between the observations at each group to the group mean.

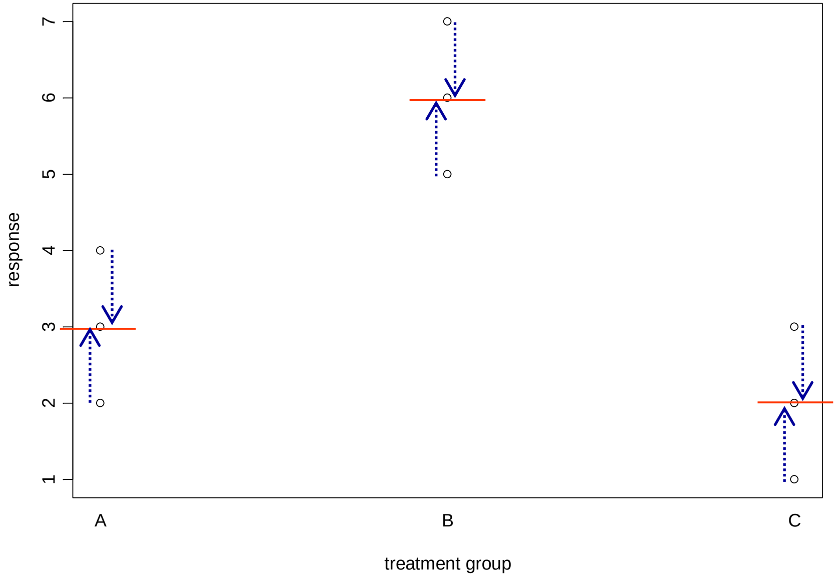
A $(2-3)^2+(3-3)^2+(4-3)^2 = 2$

B $(5-6)^2+(6-6)^2+(7-6)^2 = 2$

C $(1-2)^2+(2-2)^2+(3-2)^2 = 2$

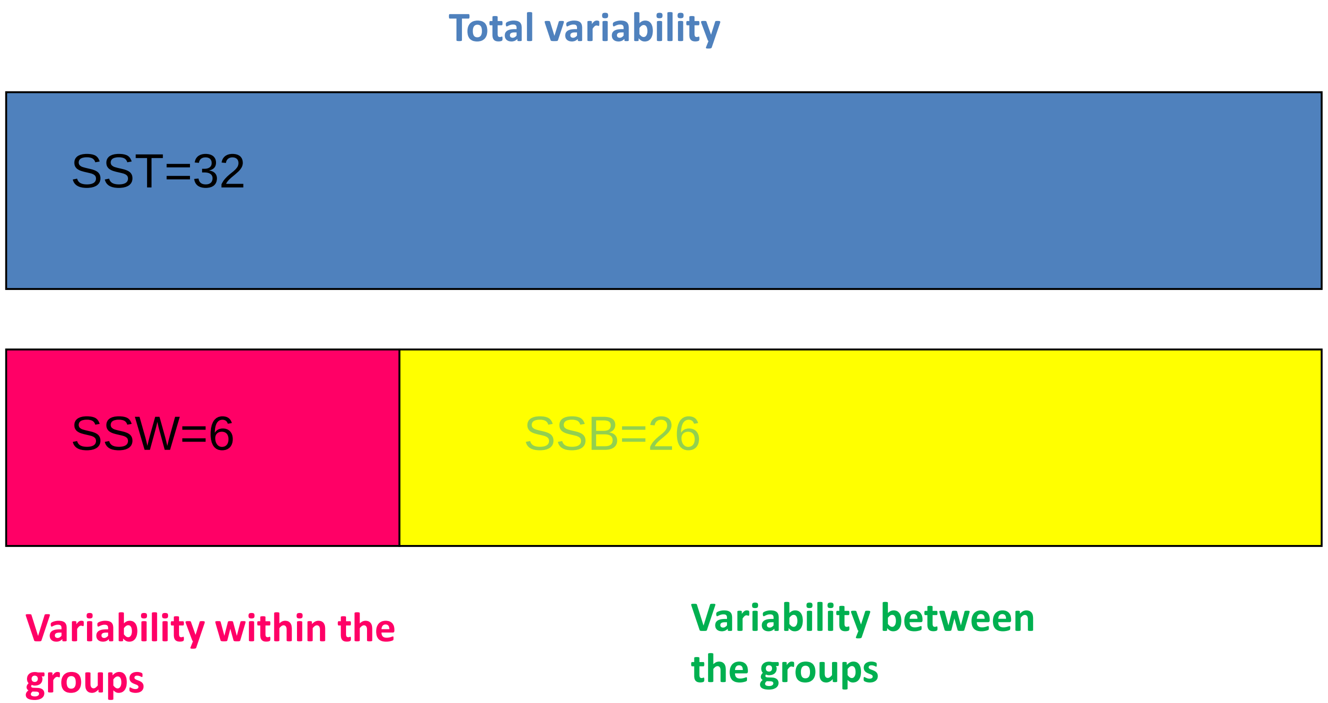
$$\overline{6}$$

$$SSW=\sum_{i=1}^{I}\sum_{j=1}^{n_i}\left(Y_{ij}-\bar{Y}_{i.}\right)^2$$



Groups means: 3 (group A), 6 (group B) and 2 (group C)

Two Sources of Variability



Total variability

SST=32

SSW=6

SSB=26

Variability within the groups

Variability between the groups

SST=SSW+SSB

In the slides for the class we use the notaions:

SST=SSE+SSTR

The function aov()in R

Analysis Of Variance:

$$\text{aov(}\underbrace{\text{response\textasciitilde predictor(s))}}_{Y_{ij} = \mu_i + \varepsilon_{ij}}$$

Two Sources of variability in R

```
> fit.1<-aov(resp~as.factor(gr))
```

```
> summary(fit.1)
              Df Sum Sq Mean Sq F value   Pr(>F)
as.factor(gr)  2     26      13      13 0.006592 **
Residuals      6      6       1
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

One-Way ANOVA model: model formulation

$$Y_{ij} = \mu_i + \varepsilon_{ij}$$

Parameters: fixed but unknown and needed to be estimated

Random error, assumed to follow normal distribution with constant varaince.

$$\varepsilon_{ij} \sim N\left(0, \sigma^2\right)$$

Model assumptions are:

1. The random error is normal distributed.
2. The varaince is constant across the factor levels.

The Null Hypothesis: No treatment effect

- For a model in which the factor has three levels we wish to test the null hypothesis:

$$H_0 : \mu_1 = \mu_2 = \mu_3$$

- This means that we want to test if the means across all factor levels are equal.

- Mind that: we test if the parameters (μ_j) are equal, not about the sample means ($\overline{Y}_j$).

Test Statistic F

Within group sum of squares

$$SSW = \sum_{i=1}^{I}\sum_{j=1}^{n_i}\left(Y_{ij} - \bar{Y}_{i.}\right)^2$$

Between group sum of squares

$$SSB = \sum_{i=1}^{I} n_i\left(\bar{Y}_{i.} - \bar{Y}_{..}\right)^2$$

$$F = \frac{SSB/(I-1)}{SSW/(N-I)} = \frac{MSB}{MSW}$$

The test statistic, F, is the ratio between the mean of the between sum of squares (SSB) and the mean of the within sum of squares.

Test Statistic in R

$$\frac{\text{Within group sum of squares/dgree of fredom}}{\text{Between group sum of squares/dgree of fredom}} = \frac{SSB/(I-1)}{SSW/(N-I)} = \frac{MSB}{MSW} = F$$

```
> fit.1<-aov(resp~as.factor(gr))
> summary(fit.1)
              Df Sum Sq Mean Sq F value   Pr(>F)
as.factor(gr)  2     26      13      13 0.006592 **
Residuals      6      6       1
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Analysis of example 1: distance in rat experiment

```
> fit.2<-aov(dist~as.factor(gr))
> summary(fit.2)
              Df Sum Sq Mean Sq F value    Pr(>F)
as.factor(gr)  1 164142  164142  32.131 1.062e-05 ***
Residuals     22 112389    5109
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

A typical example of one-way ANOVA (1)

- For an experimant with I treatments we have I groups
- Each group recive different treatment
- Sample size at each group: n_i
- We assume that each group is a sample from a population

Example 2: phosphate concentration in plasma (Table 6.18 in Dobson (2002))

- The respons variable is the concentrtion phosphate in the plasma.
- 3 treatmemts groups: Hyperinsulinemic obese (HZ), Non Hyperinsulinemic obese (NHZ), and Controls(R).

HZ	NHZ	R
2.3	3.0	3.0
4.1	4.1	2.6
4.2	3.9	3.1
4.0	3.1	2.2
4.6	3.3	2.1
4.6	2.9	2.4
3.8	3.3	2.8
5.2	3.9	3.5
3.1		2.9
3.7		2.6
3.8		3.1
		3.2

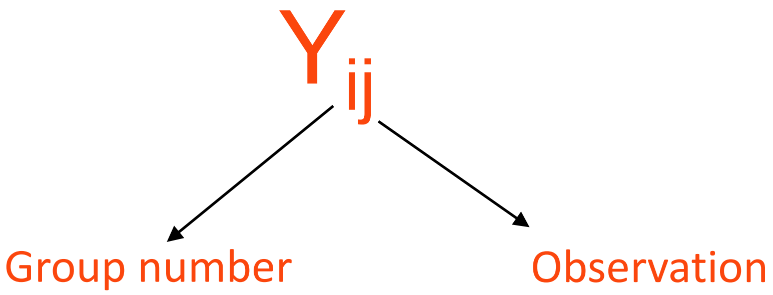
Data structure and notaion

Example of one-way ANOVA

HZ	NHZ	R
2.3	3.0	$\boxed{3.0}$
4.1	4.1	2.6
4.2	3.9	3.1
4.0	3.1	2.2
4.6	3.3	2.1
4.6	2.9	2.4
3.8	3.3	2.8
5.2	3.9	3.5
3.1		2.9
3.7		2.6
3.8		3.1
		3.2

Reaspone: Y_{ij}.

Y_{ij}= observation j in group i



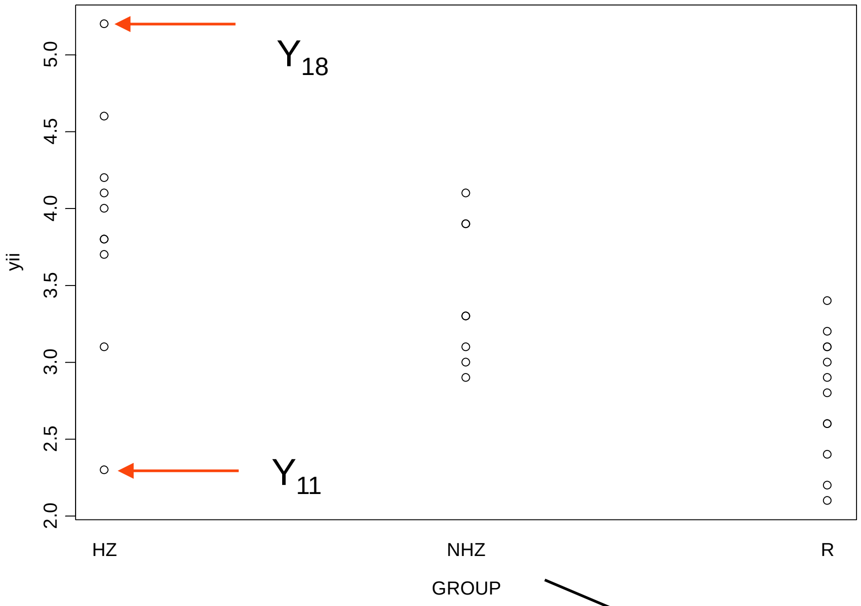
Y_{ij}

Group number

Observation

HZ i=1	NHZ i=2	R i=3
Y_{11}	Y_{21}	$\boxed{Y_{31}}$
Y_{12}	Y_{22}	Y_{32}
Y_{13}	Y_{23}	Y_{33}
Y_{14}	Y_{24}	Y_{34}
Y_{15}	Y_{25}	Y_{35}
Y_{16}	Y_{26}	Y_{36}
Y_{17}	Y_{27}	Y_{37}
Y_{18}	Y_{28}	Y_{38}
Y_{19}		Y_{39}
Y_{110}		Y_{310}
Y_{111}		Y_{311}
		Y_{312}

Scatterplot of the data



Y_{11}

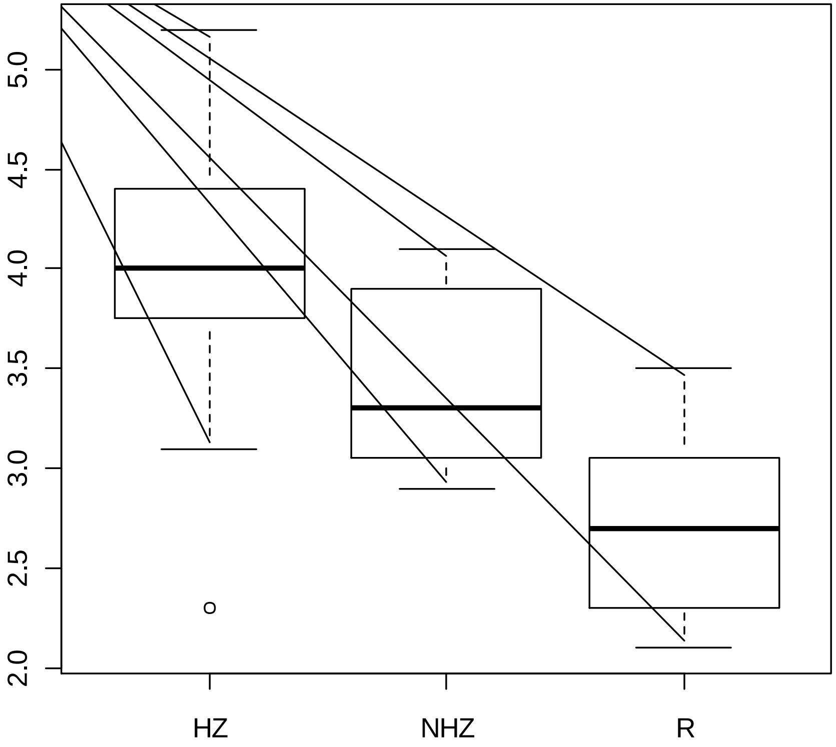
Y_{18}

HZ	NHZ	R
2.3	3.0	3.0
4.1	4.1	2.6
4.2	3.9	3.1
4.0	3.1	2.2
4.6	3.3	2.1
4.6	2.9	2.4
3.8	3.3	2.8
5.2	3.9	3.5
3.1		2.9
3.7		2.6
3.8		3.1
		3.2

Treatment group

Response values.

Boxplot of the data



Patterns in the medians

Variability.

Populatiions

population	distribution
1) (HZ)	$N\left(\mu_1,\sigma^2\right)$
2) (NHZ)	$N\left(\mu_2,\sigma^2\right)$
3) (R)	$N\left(\mu_3,\sigma^2\right)$

Mean in the population

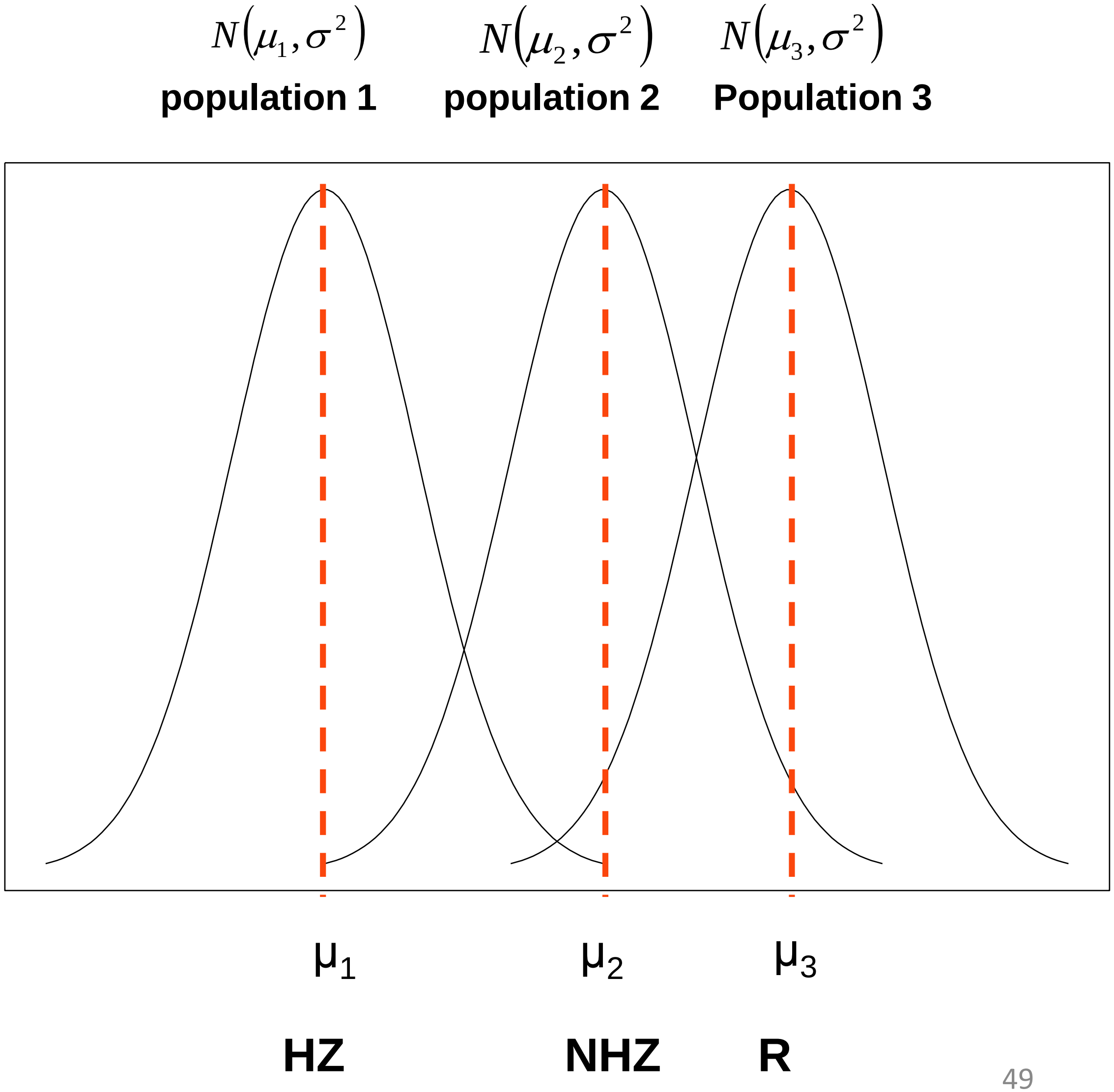
Variance in the population.

- Mean and variance in the population.
- Normal distribution.

$$\boxed{Y_{ij} \sim N\left(\mu_i,\sigma^2\right)}$$

Three populations

- Constant variance: σ^2.
- The null hypothesis



Formulation of the null hypothesis

Under the null hypothesis:

$$\boxed{H_0 : \mu_1 = \mu_2 = \mu_3}$$

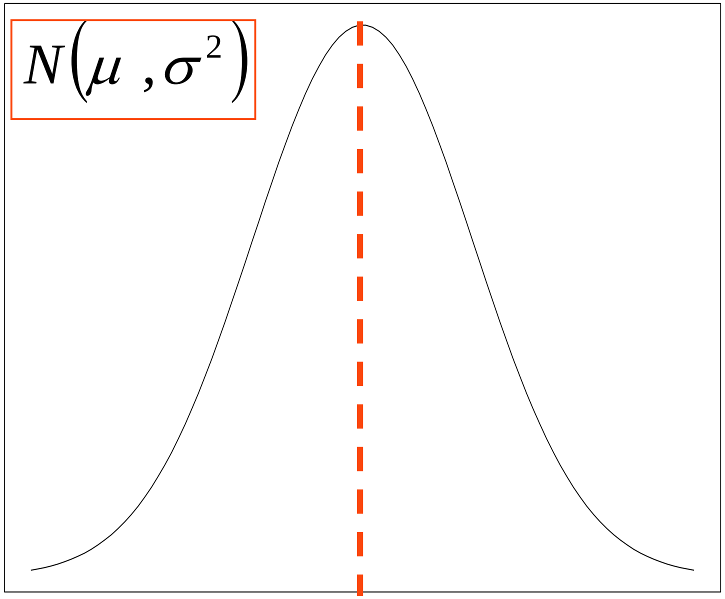
No effect of the treatment.

The null hypothesis

- Under the null hypothesis the means are equal

$$\boxed{Y_{ij} \sim N\left(\mu, \sigma^2\right)}$$

$$H_0 : \mu_1 = \mu_2 = \mu_3$$



μ

What is the alternative hypothesis ?

Under the alternative hypothsis

$$H_1 : \mu_i \neq \mu_l$$

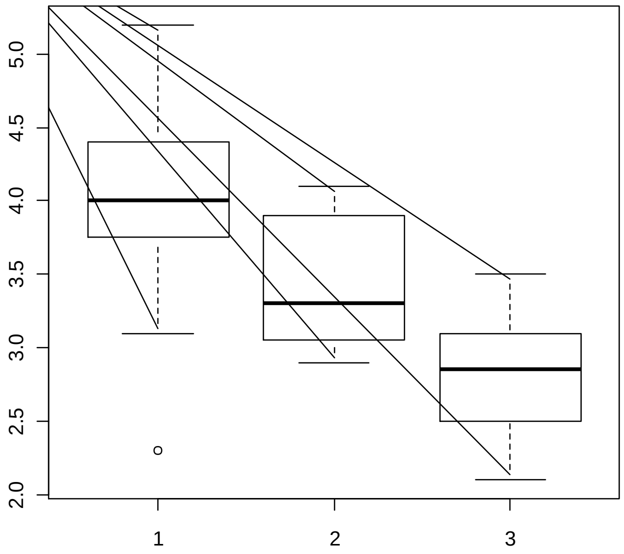
For at least one pair *i* and *l* (*i*,*l*=*1*,*2*,..*k*)

$\mu_1 \neq \mu_2$ and/or $\mu_1 \neq \mu_3$ and/or $\mu_2 \neq \mu_3$

Example 2: data in R

```
> con<-c(2.3,4.1,4.2,4.0,4.6,4.6,3.8,5.2,3.1,3.7,3.8,
+       3.0,4.1,3.9,3.1,3.3,2.9,3.3,3.9,
+       3.0,2.6,3.1,2.2,2.1,2.4,2.8,3.5,2.9,2.6,3.1,3.2)
> gr<-c(rep(1,11),rep(2,8),rep(3,12))
```

```
> boxplot(split(con,gr))
```



Analysis of variance in R

```
>fit.1<-aov(con~as.factor(gr))

> summary(fit.1)
              Df Sum Sq Mean Sq F value    Pr(>F)
as.factor(gr)  2 7.6926  3.8463  11.318 0.0002499 ***
Residuals     28 9.5152  0.3398
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

One-Way ANOVA model

- The one way ANOVA model is a statistical model which we use in order to test the null hypothesis that the mean response across the factor level equal.
- It does not tell us which one is different.

One-Way ANOVA model

- Post-hoc Pairwise comparisons and
- Multiplicity issues

Chapter 2:
Linear regression models with normal error

Donson: chapter 2.

Lindsey: chapter 9.

McCullagh & Nelder: chapter 3.

Simple linear regression model

$$\boxed{Y_i = \beta_0 + \beta_1 \times x_i + \varepsilon_i}$$

Y_i is the response variable.

x_i is the predictor (independent variable).

The observation is the pair (Y_i , x_i)..

Sample of size n: (Y_1 , x_1), (Y_2 , x_2),..., (Y_n , x_n)

β_0 and **β_1** are the unknown parameters of the model.

ε_i is a stochastic random variable (unobserved).

The error terms ε$_1$,ε$_2$,…,ε$_n$

$$\boxed{\varepsilon_i = Y_i - (\beta_0 + \beta_1 x_i)}$$

- We assume for ε$_1$,ε$_2$,…,ε$_n$

1 $\varepsilon_i \sim N(0, \sigma^2)$

$E(\varepsilon_i) = 0$

2

$Var(\varepsilon_i) = \sigma^2$

3

The distribution of the response

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

$$Y_i \sim N(\underbrace{\beta_0 + \beta_1 x_i}, \sigma^2) \qquad i = 1, \ldots, n$$

$$E[Y_i] = \beta_0 + \beta_1 x_i = \mu_i$$

$$Y_i \sim N(\mu_i, \sigma^2) \qquad i = 1, \ldots, n$$

The paraemters to be estimated

$$\boxed{Y_i = \beta_0 + \beta_1 x_i + \varepsilon_i}$$

- **β$_0$** en **β$_1$** are uknown parameters.
- **β$_1$** – the slope.
- **β$_0$** - the intercept.

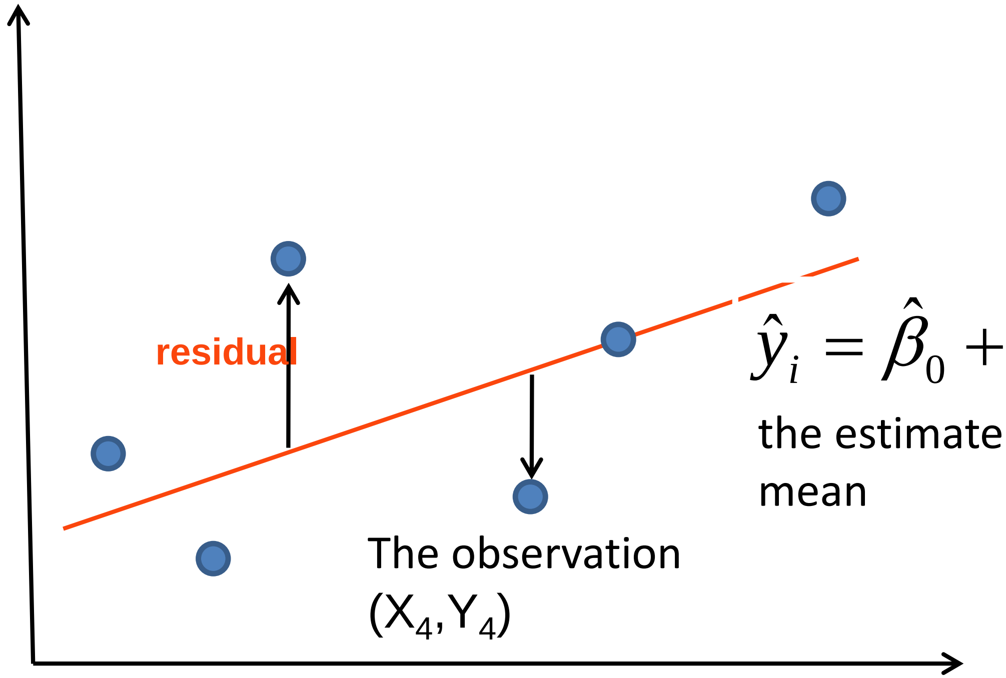
$$\boxed{\varepsilon_i \sim N(0, \sigma^2)}$$

The variance of the random error

$$\boxed{E(\varepsilon_i) = 0}$$

$$\boxed{Var(\varepsilon_i) = \sigma^2}$$

The residual



$$\hat{y}_i = \hat{\beta}_0 + \hat{\beta}_1 x_i$$

the estimated mean

$$r_i = y_i - (\underbrace{\hat{\beta}_0 + \hat{\beta}_1 x_i}_{\hat{y}_i})$$

The estimated mean

Matrix notaions

$$Y = X\beta + \varepsilon$$

$$Y = \begin{bmatrix} Y_1 \\ Y \\ \vdots \\ Y_n \end{bmatrix} \qquad X = \begin{bmatrix} X_{11} & & X_{p1} \\ & & \\ & & \\ X_{1n} & & X_{pn} \end{bmatrix} \qquad \beta = \begin{bmatrix} \beta_1 \\ \beta_2 \\ \vdots \\ \beta_p \end{bmatrix} \qquad \varepsilon = \begin{bmatrix} \varepsilon_1 \\ \varepsilon_2 \\ \vdots \\ \varepsilon_n \end{bmatrix}$$

Error structure (I)

$$E(Y) = E(X\beta) + E(\varepsilon) = X\beta = \mu$$

$$COV(Y) = \sigma^2 I$$

The response variables Y have equal variance they are uncorrelated (Identically Independently Distributed-iid).

Distribution of the response

Density function of the response

$$f(y) = \frac{1}{\sqrt{2\pi\sigma^2}} \exp\left(\frac{-(y-\mu)^2}{2\sigma^2} \right)$$

Likelihood function

$$L(y_1 .... y_n, \mu, \sigma^2) = \prod_{i=1}^{n} \frac{1}{\sqrt{2\pi\sigma^2}} \exp\left(\frac{-(y_i-\mu_i)^2}{2\sigma^2} \right)$$

Example 1: Plant weight data (Dobson)

Genetically similar seeds are randomly assigned to be raised either in

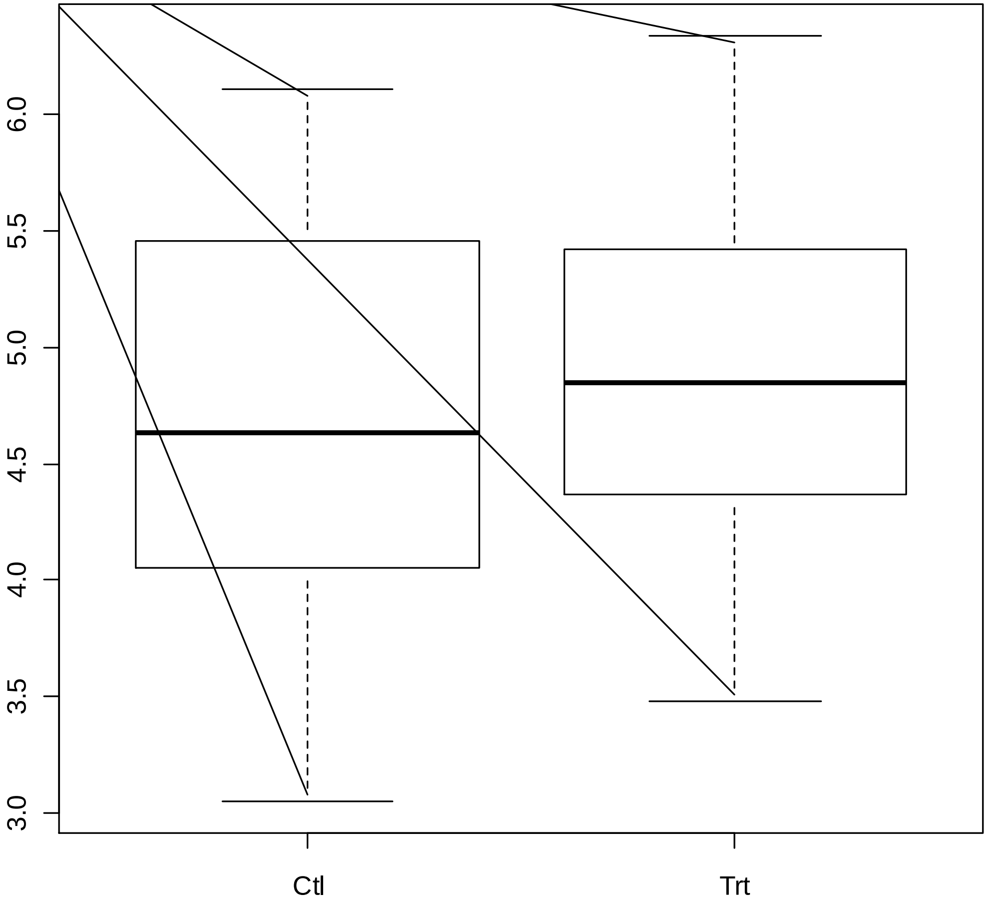
1. a nutritionally enriched environment (treatment)-treatment A in Dobson Table 6.6
2. standard conditions (control)

Response: dried weight in grams of the seeds.

Table 1.1: Plant weight from two different growing conditions

Control (1)	**4.17**	**5.58**	**5.18**	**6.11**	**4.50**	**4.61**	**5.17**	**4.53**	**5.33**	**5.14**
Treatment (2)	**4.81**	**4.17**	**4.41**	**3.59**	**5.87**	**3.83**	**6.03**	**4.89**	**4.32**	**4.69**

The data



The main question:
Are the mean in the two treatment groups equal ?

Model formulation (1): oneway ANOVA model

$$y_{ij} = \mu_i + \varepsilon_{ij}$$

$$\varepsilon_{ij} \sim N(0, \sigma^2)$$

Assumptions:

1. Normality
2. Constant variance.

See slide 34

Model formulation (2): linear regression model

$$y_i = \beta_0 + \beta_1 x_i + \varepsilon_i$$

$$x_i = \begin{cases} 1 & T \\ 0 & C \end{cases}$$

$$E(y_i) = \begin{cases} \beta_0 + \beta_1 x_i & T \\ \beta_0 & C \end{cases}$$

R-Code and Output

```
> ctl <- c(4.17,5.18,5.18,6.11,4.50,4.61,5.17,4.53,5.33,5.14)
> trt <- c(4.81,4.17,4.41,3.59,5.87,3.83,6.03,4.89, 4.32,4.69)
> group <- gl(2,20,labels=c("Ctl","Trt"))
> weight <- c(ctl,trt)
> cbind(weight,group)
```

gl() function generates factor levels

Table 1.1: Plant weight from two different growing conditions

Control (1)	**4.17**	**5.58**	**5.18**	**6.11**	**4.50**	**4.61**	**5.17**	**4.53**	**5.33**	**5.14**
Treatment (2)	**4.81**	**4.17**	**4.41**	**3.59**	**5.87**	**3.83**	**6.03**	**4.89**	**4.32**	**4.69**

The aov() and lm() functions in R

```
>lm(response ~ predictor(s))

>aov(response ~ factor(s))
```

One-way ANOVA as linear regression model

```
> fit.D9 <- lm(weight ~ group)
> summary(fit.D9)
Call:
lm(formula = weight ~ group)

Residuals:
    Min      1Q  Median      3Q     Max
-1.0710 -0.4692  0.0885  0.1983  1.3690

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   4.9920     0.2165  23.061 8.14e-15 ***
groupTrt     -0.3310     0.3061  -1.081    0.294
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.6845 on 18 degrees of freedom
Multiple R-squared:  0.06098,           Adjusted R-squared:  0.008817
F-statistic: 1.169 on 1 and 18 DF,  p-value: 0.2939
```

ANOVA model

```
> fit.aov<-aov(weight ~ group)
> summary(fit.aov)
            Df Sum Sq Mean Sq F value Pr(>F)
group        1  0.548  0.5478   1.169  0.294
Residuals   18  8.435  0.4686

> anova(fit.aov)
Analysis of Variance Table

Response: weight
          Df Sum Sq Mean Sq F value Pr(>F)
group      1 0.5478  0.5478   1.169 0.2939
Residuals 18 8.4349  0.4686
```

Example 2: Body weight and gestational age (section 2.2.2 in Dobson)

Birth weights (g) and estimated gestational age (weeks) of 12 male and female babies born in a certain hospital.

Two predictors: age and gender.

Birth weight and gestational age for male and female babies

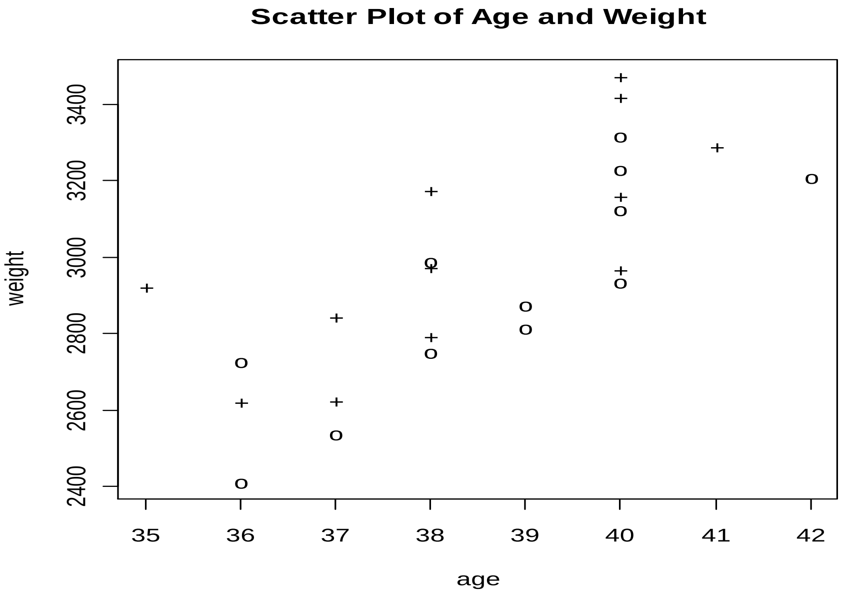
	Male		Female	
	Age (weeks)	Birth weight (g)	Age (weeks)	Birth weight (g)
	40	2968	40	3317
	38	2795	36	2729
	40	3163	40	2935
	35	2925	38	2754
	36	2625	42	3210
	37	2847	39	2817
	41	3292	40	3126
	40	3473	37	2539
	37	2628	36	2412
	38	3176	38	2991
	40	3421	39	2875
	38	2975	40	3231
Means	38.33	3024.00	38.75	2911.33

Data in R

```
> bage<-c(40,38,40,35,36,37,41,40,37,38,40,38)
> gage<-c(40,36,40,38,42,39,40,37,36,38,39,40)
> bwei<-c(2968,2795,3163,2925,2625,2847,3292,3473,2628,3176,3421,2975)
> gwei<-c(3317,2729,2935,2754,3210,2817,3126,2539,2412,2991,2875,3231)
> age<-c(bage,gage)
> weight<-c(bwei,gwei)
> gender <- gl(2,12,24,labels=c("M","F"))
> dat2<-data.frame(weight,age,gender)
>Dat2
 weight age gender
1    2968  40      M
2    2795  38      M
3    3163  40      M
4    2925  35      M
5    2625  36      M
6    2847  37      M
```

The data

```
> plot(age,weight,pch=" ", main="Scatter Plot of Age and Weight")
> points(age[gender=="F"],weight[gender=="F"],pch="o")
> points(age[gender=="M"],weight[gender=="M"],pch="+")
```



Does the growth rate equal for male and female ?

Model formulation

$$Y_{ij} \sim N(\mu_{ij}, \sigma^2) \qquad i = 1,\ldots,n,\ j = 1(M), 2(F).$$

$$E(Y_{ij}) = \mu_{ij}$$

- Mean structure:
  - 4 possible models.

Model 0: model formulation

Gender and age do not have influence on the response.

$$Y_{ij} \sim N(\mu, \sigma^2) \qquad i = 1, \ldots, n,\; j = 1(M), 2(F).$$

$$E(Y_{ij}) = \mu$$

```
fit.lm.0 <- lm(weight ~ 1,data=dat2)
```

Model 0: R output

```
> fit.lm.0 <- lm(weight ~ 1,data=dat2)

> summary(fit.lm.0)

Call:
lm(formula = weight ~ 1, data = dat2)

Residuals:
   Min      1Q  Median      3Q     Max 
-555.67 -182.92  -16.17  216.83  505.33 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept)  2967.67      57.58   51.54   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 282.1 on 23 degrees of freedom
```

Model 1: model formulation

Response is a function of age

$$Y_{ij} \sim N(\mu_i, \sigma^2) \qquad i = 1, \ldots, n\,,\ j = 1(M), 2(F).$$

$$\begin{aligned} E(Y_{ij}) = \mu_i &= \beta_0 + \beta_1 x_i \\ &= \beta_0 + \beta_1 Age_i \end{aligned}$$

```
fit.lm.1 <- lm(weight ~ age,data=dat2)
```

Model 1: R output

```
> summary(fit.lm.1)

Call:
lm(formula = weight ~ age, data = dat2)

Residuals:
    Min       1Q   Median       3Q      Max
-262.032 -158.292    8.355   88.147  366.496

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -1485.0      852.6  -1.742   0.0955 .
age            115.5       22.1   5.228 3.04e-05 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 192.6 on 22 degrees of freedom
Multiple R-squared: 0.554,      Adjusted R-squared: 0.5338
F-statistic: 27.33 on 1 and 22 DF,  p-value: 3.04e-05
```

Model 2: model formulation

Response is a function of age and gender

$$Y_{ij} \sim N(\mu_{ij}, \sigma^2) \qquad i = 1, \ldots, n, \; j = 1(M), 2(F).$$

$$E(Y_{ij}) = \mu_{ij} = \beta_0 + \beta_1 x_i + \beta_2 G_i$$

$$= \beta_0 + \beta_1 Age_i + \beta_2 genderF$$

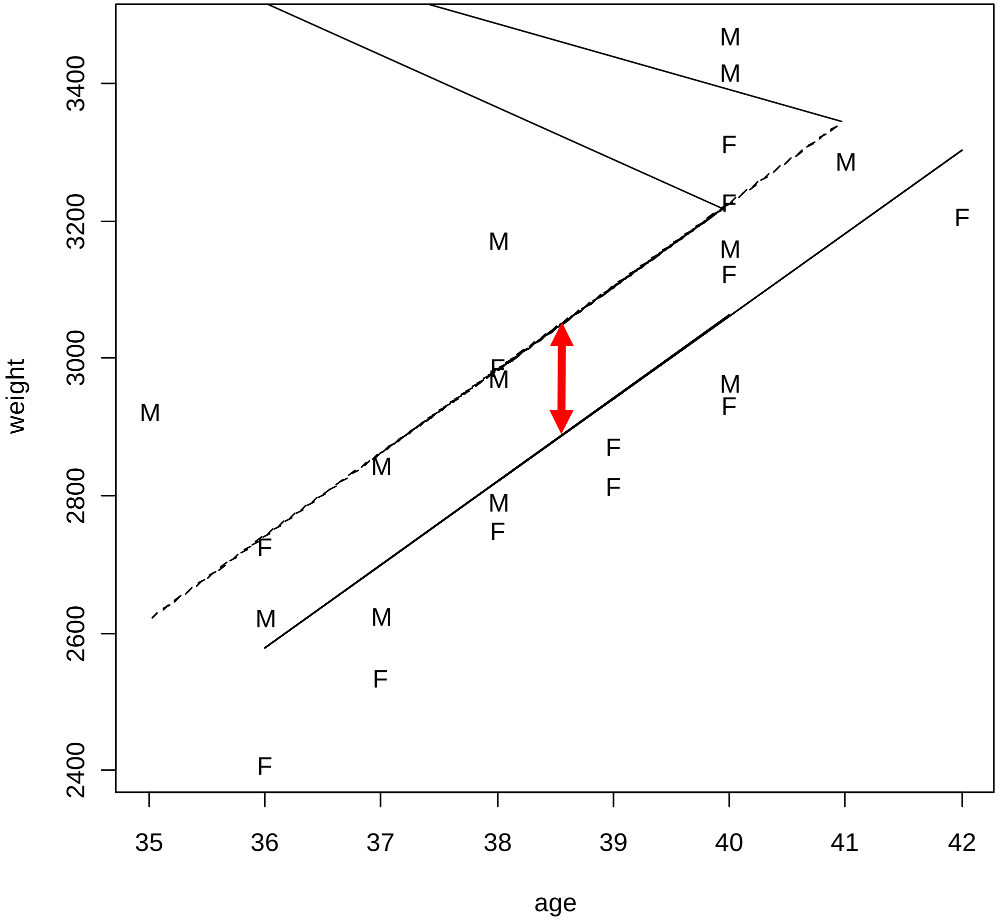
$$\text{where } genderF = \begin{cases} 1 & \text{, girl} \\ 0 & \text{, boy} \end{cases}$$

```
fit.lm.2 <- lm(formula = weight ~ age + gender, data = dat2)
```

Model 2: R output

```
summary(fit.lm.2)

Call:
lm(formula = weight ~ age + gender, data = dat2)

Residuals:
   Min      1Q  Median     3Q    Max 
-257.49 -125.28  -58.44  169.00  303.98 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) -1610.28     786.08  -2.049   0.0532 .  
age           120.89      20.46   5.908 7.28e-06 ***
genderF      -163.04      72.81  -2.239   0.0361 *  
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 177.1 on 21 degrees of freedom
Multiple R-squared:  0.64,	Adjusted R-squared: 0.6057 
F-statistic: 18.67 on 2 and 21 DF,  p-value: 2.194e-05
```

Data and predicted model (model 2)



```
Coefficients:
           Estimate Std. Error t value Pr(>|t|)
(Intercept) -1610.28     786.08  -2.049   0.0532 .
age           120.89      20.46   5.908 7.28e-06 ***
genderF      -163.04      72.81  -2.239   0.0361 *
```

For boys

$$Y_{ij}=-1610.28+120.89*Age$$

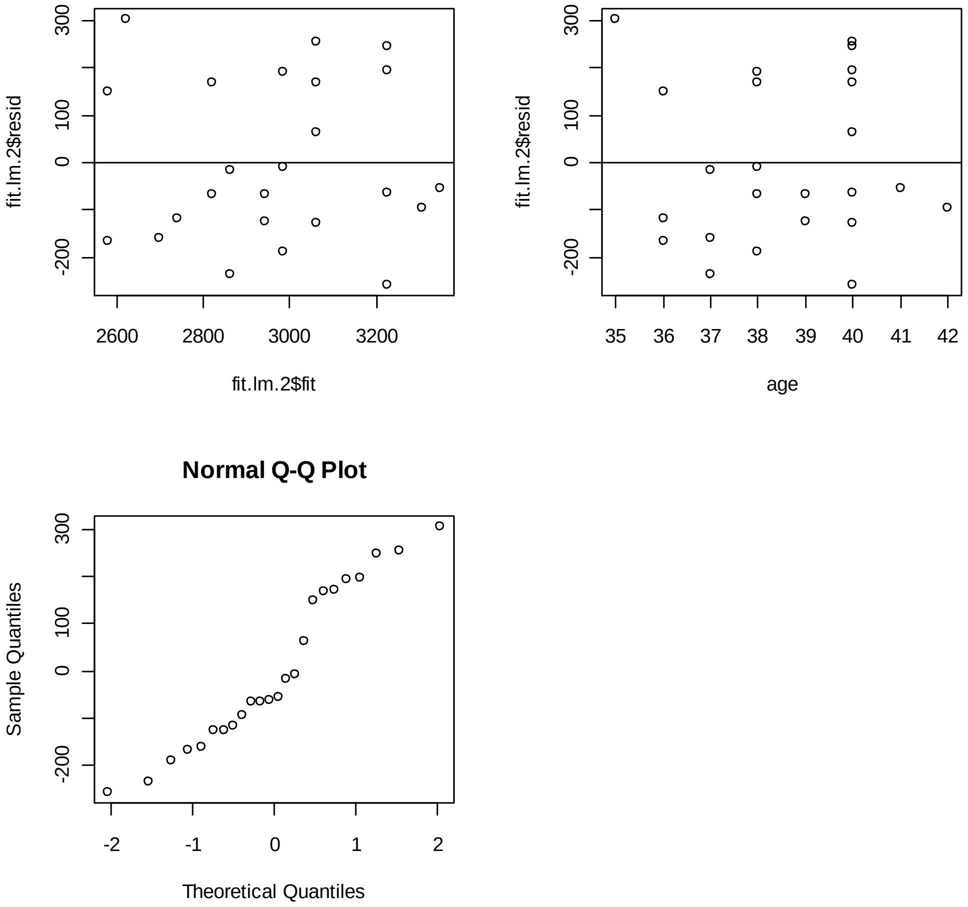
For girls

$$Y_{ij}=-1610.28+120.89*Age-163.04*(1)$$

$$=-1610.28-163.04+120.89*Age$$

$$=-1773.32+120.89*Age$$

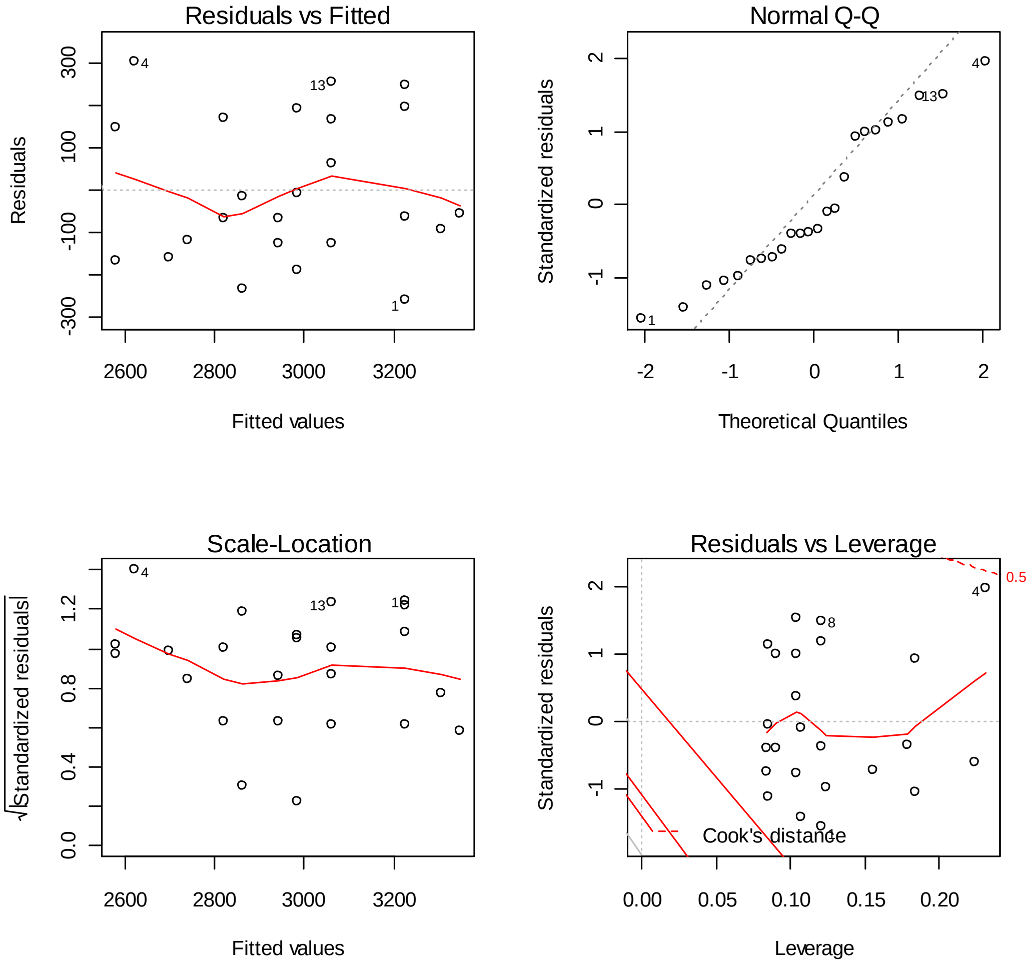
Diagnostic plots



```
par(mfrow=c(2,2))
plot(fit.lm.2$fit,fit.lm.2$resid)
abline(0,0)
plot(age,fit.lm.2$resid)
abline(0,0)
qqnorm(fit.lm.2$resid)
```

Diagnostic plots

> plot(fit.lm.4)



The likelihood function

Likelihood function

$$L(y_1....y_n,\mu,\sigma^2)=\left(\frac{1}{\sqrt{2\pi\sigma^2}}\right)^n\prod_{i=1}^n \exp\left(\frac{-(y_i-\mu_i)^2}{2\sigma^2}\right)$$

-2log(L)

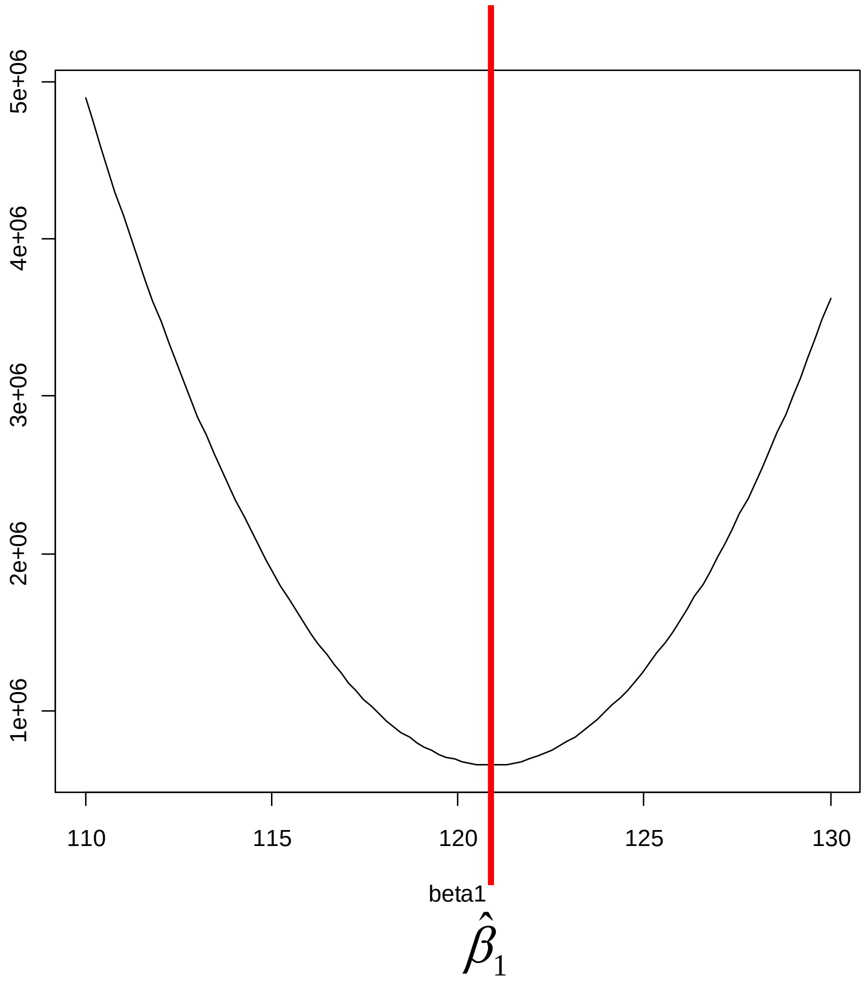
$$-2\ell = n\log(2\pi\sigma^2)+\sum_{i=1}^n \frac{-(y_i-\mu_i)^2}{\sigma^2}$$

The likelihood function

Maximizing the likelihood is equivalent to minimize the sum of squares

$$\sum_{j}\sum_{i=1}^{n}(y_{ij}-\mu_{ij})^2$$

The likelihood function



$$RSS(\mu) = \sum_{i=1}^{n} (y_i - (\hat{\beta}_0 + \beta_1 x_i + \hat{\beta}_2 G_i))^2$$

```
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -1610.28     786.08  -2.049   0.0532 .
age           120.89      20.46   5.908 7.28e-06 ***
genderF      -163.04      72.81  -2.239   0.0361 *
```

$$RSS(\mu) = \sum_{i=1}^{n} (y_i - (1610.2 + \beta_1 x_i + 163.04 G_i))^2$$

Model 2/3: model formulation

Let us consider two models

$$Y_{ij} \sim N(\mu_{ij}, \sigma^2)$$

$$E(Y_{ij}) = \mu_{ij} = \beta_{0j} + \beta_1 x_i \qquad E(Y_{ij}) = \mu_{ij} = \beta_{0j} + \beta_{1j} x_i$$

What is the difference between the models ?

Model 2 & 3: sum of squares

$$E(Y_{ij}) = \mu_{ij} = \beta_{0j} + \beta_1 x_{ij}$$

$$RSS_2(\mu_{ij}) = \sum_{i=1}^{n} (y_i - (\hat{\beta}_{0j} + \beta_1 x_{ij}))^2$$

3 parameters

$$E(Y_{ij}) = \mu_{ij} = \beta_{0j} + \beta_{1j} x_{ij}$$

$$RSS_3(\mu_{ij}) = \sum_{i=1}^{n} (y_i - (\hat{\beta}_{0j} + \beta_{1j} x_{ij}))^2$$

4 parameters

Model 2 & 3 in R

$$E(Y_{ij}) = \mu_{ij} = \beta_{0j} + \beta_1 x_{ij}$$

$$E(Y_{ij}) = \mu_{ij} = \beta_{0j} + \beta_{1j} x_{ij}$$

```
> fit.lm.2 <- lm(weight ~ age + gender,data=dat2)
> fit.lm.3 <- lm(weight ~ age + gender+age:gender,data=dat2)
```

Model 2 & 3 in R

$$E(Y_{ij}) = \mu_{ij} = \beta_{0j} + \beta_1 x_{ij}$$

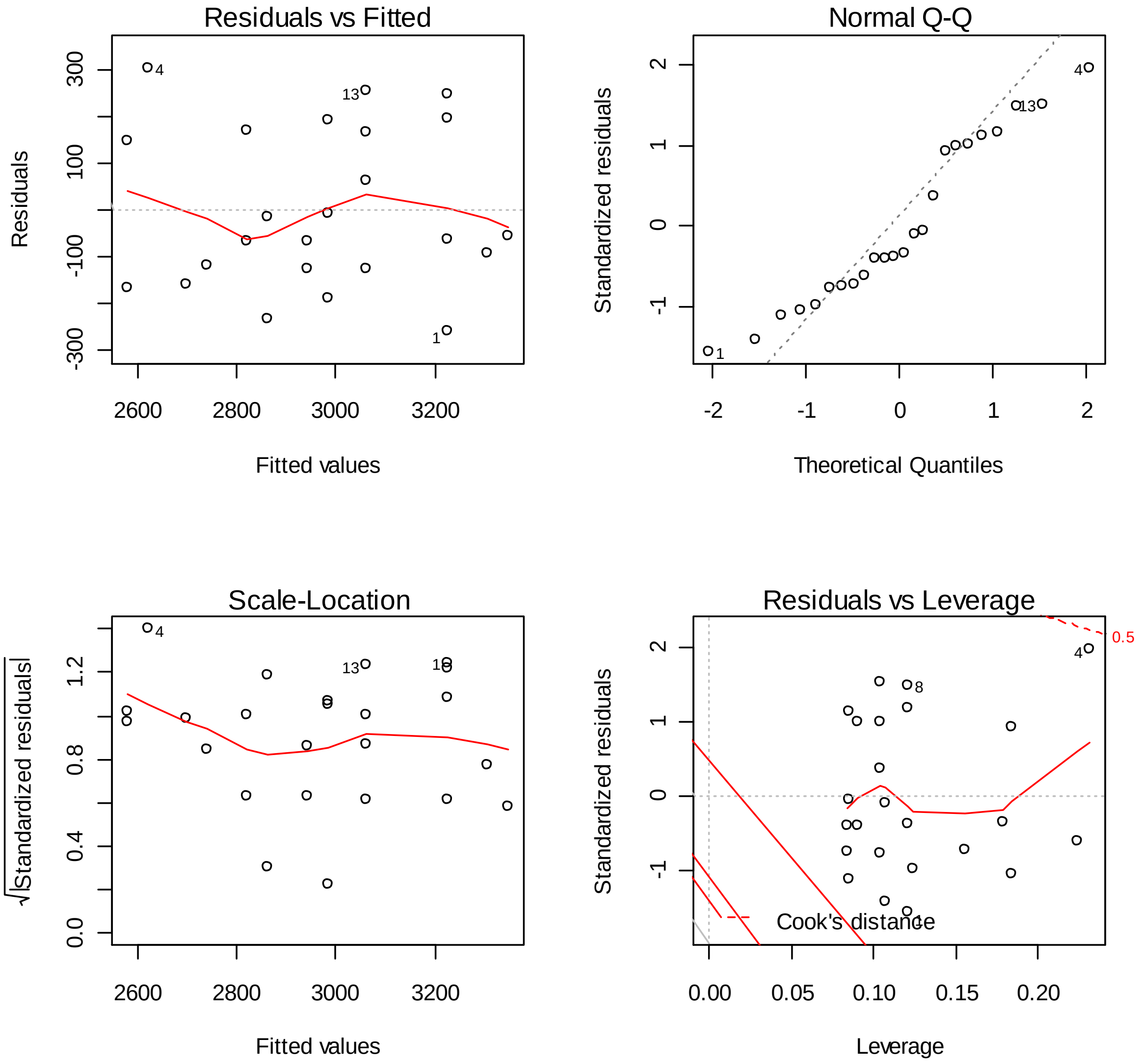
```
Call:
lm(formula = weight ~ age + gender, data = dat2)

Residuals:
    Min      1Q  Median      3Q     Max 
-257.49 -125.28  -58.44  169.00  303.98 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) -1610.28     786.08  -2.049   0.0532 .  
age           120.89      20.46   5.908 7.28e-06 ***
genderF      -163.04      72.81  -2.239   0.0361 *  
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 177.1 on 21 degrees of freedom
Multiple R-squared:  0.64,	Adjusted R-squared: 0.6057 
F-statistic: 18.67 on 2 and 21 DF,  p-value: 2.194e-05
```

Model 2 & 3 in R

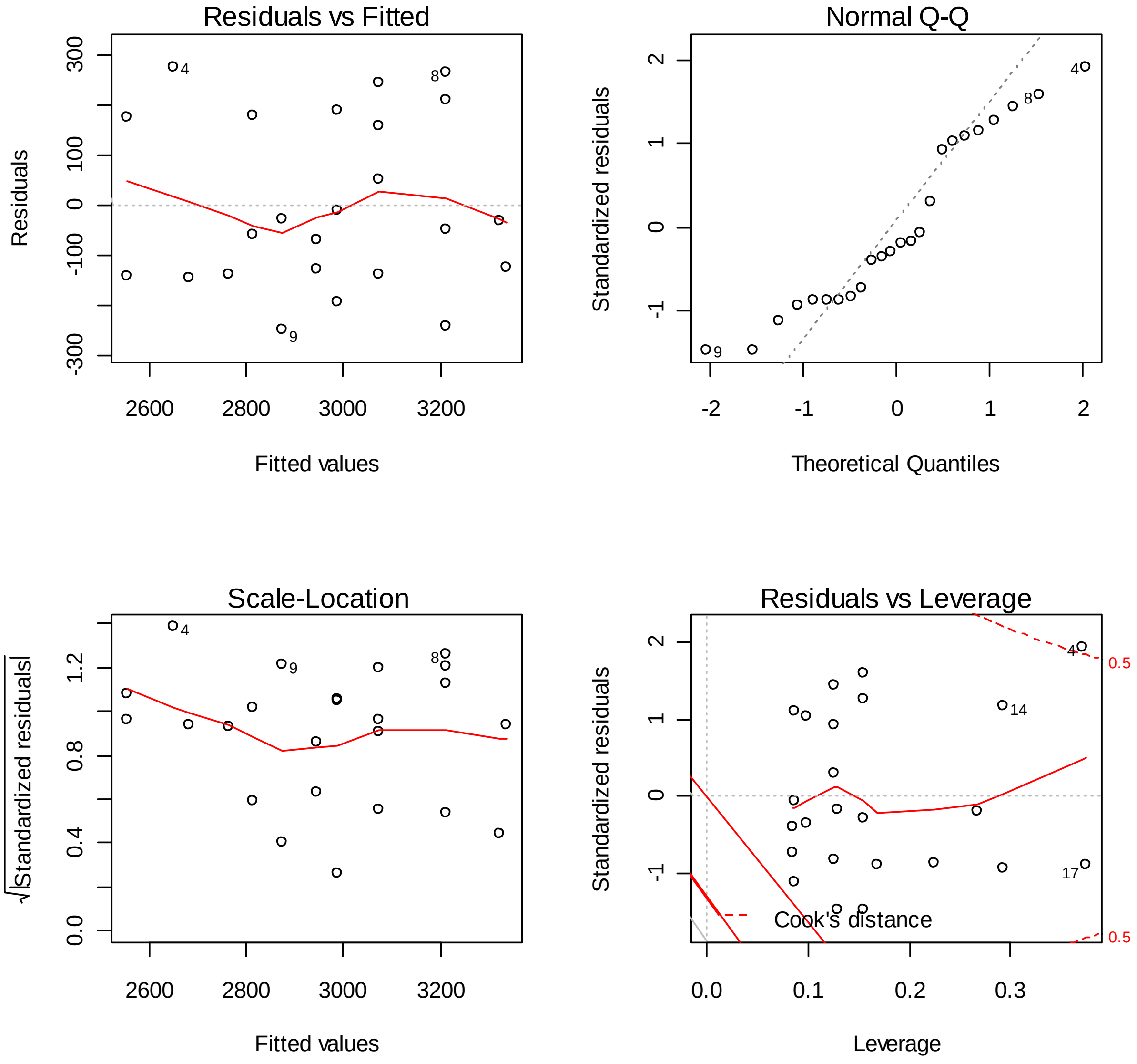
$$E(Y_{ij}) = \mu_{ij} = \beta_{0j} + \beta_1 x_{ij}$$

```
> summary(fit.lm.3)

Call:
lm(formula = weight ~ age + gender + age:gender, data = dat2)

Residuals:
   Min      1Q  Median      3Q     Max
-246.69 -138.11  -39.13  176.57  274.28

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -1268.67    1114.64  -1.138 0.268492
age           111.98      29.05   3.855 0.000986 ***
genderF      -872.99    1611.33  -0.542 0.593952
age:genderF    18.42      41.76   0.441 0.663893
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 180.6 on 20 degrees of freedom
Multiple R-squared: 0.6435,     Adjusted R-squared:  0.59
F-statistic: 12.03 on 3 and 20 DF,  p-value: 0.0001010
```

Diagnostic plot model 2



Diagnostic plot model 3



For both models: no systematic patterns in relation to fitted values.

Points in the QQ normal plot close to the line

Very little difference between the models.

Model 2 & 3: F test

$E(Y_{ij}) = \mu_{ij} = \beta_{0j} + \beta_1 x_{ij}$

$E(Y_{ij}) = \mu_{ij} = \beta_{0j} + \beta_{1j} x_{ij}$

The only different between the models is that model 3 has two different slopes.

We can formulate the following hypotheses

$$H_0 : E(Y_{ij}) = \beta_{0j} + \beta_1 x_{ij}$$
$$H_1 : E(Y_{ij}) = \beta_{0j} + \beta_{1j} x_{ij}$$

Model 2 & 3: F test

$$E(Y_{ij}) = \mu_{ij} = \beta_{0j} + \beta_1 x_{ij}$$

$$RSS_2(\mu_{ij}) = \sum_{i=1}^{n} (y_i - (\hat{\beta}_{0j} + \beta_1 x_{ij}))^2$$

3 parameters

$$RSS_2(\mu_{ij}) \text{ with (N - 3) df}$$

$$E(Y_{ij}) = \mu_{ij} = \beta_{0j} + \beta_{1j} x_{ij}$$

$$RSS_3(\mu_{ij}) = \sum_{i=1}^{n} (y_i - (\hat{\beta}_{0j} + \beta_{1j} x_{ij}))^2$$

4 parameters

$$RSS_3(\mu_{ij}) \text{ with (N - 4) df}$$

$$F = \frac{\left(RSS_2(\mu_{ij}) - RSS_3(\mu_{ij})\right)/(4-3)}{RSS_3(\mu_{ij})/(24-4)}$$

Under the null hypothesis

$$F \sim f(1{,}20)$$

Model 2 & 3: F test in R

$$RSS_2(\mu_{ij}) = \sum_{i=1}^{n}(y_i - (\hat{\beta}_{0j} + \beta_1 x_{ij}))^2$$

$$RSS_3(\mu_{ij}) = \sum_{i=1}^{n}(y_i - (\hat{\beta}_{0j} + \beta_{1j} x_{ij}))^2$$

$$F = \frac{\left(RSS_2(\mu_{ij}) - RSS_3(\mu_{ij})\right)/(4-3)}{RSS_3(\mu_{ij})/(24-4)}$$

```
> anova(fit.lm.2,fit.lm.3)
```

```
Analysis of Variance Table

Model 1: weight ~ age + gender
Model 2: weight ~ age + gender + age:gender
  Res.Df    RSS Df Sum of Sq      F Pr(>F)
1     21 658771
2     20 652425  1    6346.2 0.1945 0.6639
```

General F test

$$E(Y_{ij}) = \mu_{ij} = \beta_{0j} + \beta_1 x_{ij}$$

$$E(Y_{ij}) = \mu_{ij} = \beta_{0j} + \beta_{1j} x_{ij}$$

$$RSS_R(\mu_{ij}) = \sum_{i=1}^{n} (y_i - (\hat{\beta}_{0j} + \beta_1 x_{ij}))^2$$

$$RSS_F(\mu_{ij}) = \sum_{i=1}^{n} (y_i - (\hat{\beta}_{0j} + \beta_{1j} x_{ij}))^2$$

$$RSS_R(\mu_{ij}) \text{ with } \mathrm{df_R} = \mathrm{N - m}$$

$$RSS_F(\mu_{ij}) \text{ with } \mathrm{df_F} = \mathrm{N - (m + p)}$$

$$F = \frac{\left(RSS_R(\mu_{ij}) - RSS_F(\mu_{ij})\right) \big/ \left(df_R - df_F\right)}{RSS_F(\mu_{ij}) \big/ df_F}$$

Under the null hypothesis

$$F \sim f((df_R - df_F, df_F)$$

Chapter 3:
Generalized linear models

Donson: chapter 3.

Lindsey: chapter 1.

McCullagh & Nelder: chapter 2.

Generalized linear models (GLM)

A framework for model fitting.

Examples:

- when an outcome (a response) is measured as a success or failure.
- when we count the number of events over a fixed period.

Generalized linear models (GLM) are used to fit fixed effect models to certain types of data that are not normally distributed.

Generalized – not limited to normally distributed data.
Linear – models use a linear combination of variables to ‘predict’
the response.

Components of a GLM

1. **Random component-** the probability distribution of the response.

2. **Systematic component (linear predictor):** the predictor variables are (e.g., X_1, X_2, etc). These variable enter to the model in a linear manner.

$$\beta_0 + \beta_1 X_1 + \beta_2 X_2 + \ldots + \beta_k X_k$$

3. **Link function**-Specify the relationship between the mean random component (i.e., E(Y)) and the systematic component.

Example 1: linear regression models

Random component: the distribution of the response

$$Y_i \sim N(\beta_0 + \beta_1 X_i, \sigma_\varepsilon^2)$$

The systematic component: the linear predictor

$$E(Y_i) = \underbrace{\beta_0 + \beta_1 x_i}_{\text{Linear predictor}}$$

The link function

$$\eta = \beta_0 + \beta_1 X_i$$

$$g\big(E(Y_i)\big) = \eta$$

$$\underbrace{g = 1}_{\text{Link function}}, \text{ identity function}$$

Components of a GLM: linear regression models

For the case with p predictors (and p unknown parameters)

$$E(Y_i) = \mu_i = \underbrace{\sum_{j=1}^{p} \beta_j x_j}$$

$$\eta = \sum_{j=1}^{p} \beta_j x_j$$

The link function (=the link between the random and the systematic part)

$$Y_i \sim N(\mu_i, \sigma_\varepsilon^2)$$

$$g(\mu) = g\big(E(Y_i)\big) = \eta$$

$$g = 1$$

Example 2: binary data

Dichotomous (binary) with a fixed numbers of trials (Binomial distribution) Success/failure.

Dose response experiment (Table 7.2 in Dobson):

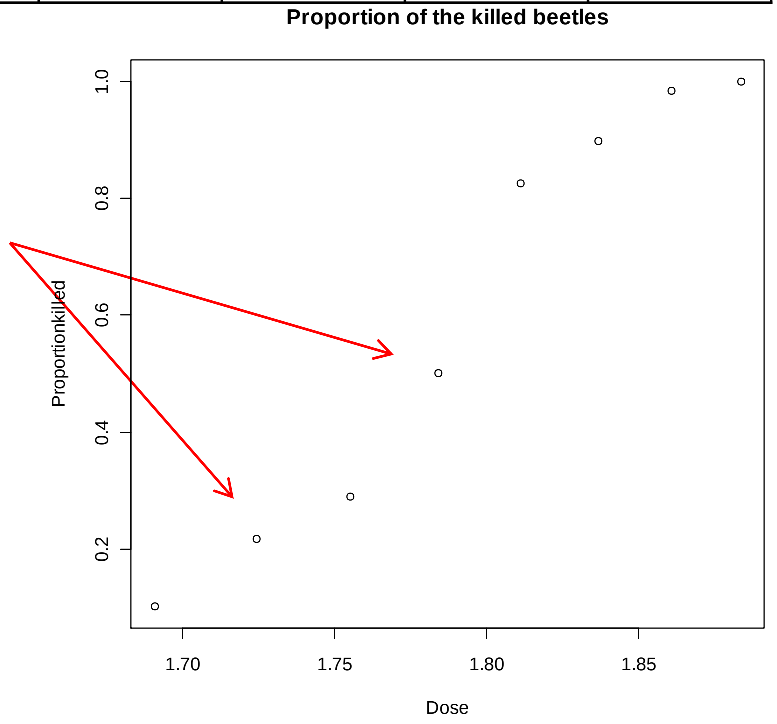
Dose	1.6907	1.7242	1.7552	1.7842	1.8113	1.8369	1.8610	1.8839
Beetles	59	60	62	56	63	59	62	60
Killed	6	13	18	28	52	53	61	60

Random component: example of binary data

Dose	1.6907	1.7242	1.7552	1.7842	1.8113	1.8369	1.8610	1.8839
Beetles	59	60	62	56	63	59	62	60
Killed	6	13	18	28	52	53	61	60

$$Y_{ij} = \begin{cases} 1 & alive \\ 0 & killed \end{cases}$$

$$\frac{\sum Y_{ij}}{n_j}$$



$$Y_{ij} \sim B(1, \pi_{ij})$$

$$E(Y_{ij}) = P(Y_{ij} = 1) = \pi_{ij}$$

Systematic component: dependency of the predictor – the linear predictor

The systematic component of the model consists of a set of explanatory variables and some linear function of them.

$$\pi_j = f(dose_i) = f(d_i)$$

$$\pi_j = f(d_i) = f(\underbrace{\beta_0 + \beta_1 d_j}_{\text{The linear predictor}})$$

The Link function

The expected values of the response variable

$$E(Y_{ij}) = \pi_j$$

The systematic part

$$\pi_j = f(\beta_0 + \beta_1 d_j) = f(\eta)$$

$$\pi_j = \frac{e^{\beta_0 + \beta_1 d_j}}{1 + e^{\beta_0 + \beta_1 d_j}}$$

The logistic function to describe the mean, E(Y_{ij}), as a function of the linear predictor

$$g(E(Y_{ij})) = g(\pi_j) = \eta$$

Values between 0 and 1

The Link function (logit link function for binary data)

The link between the expected values of the response variable and the linear predictor

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

$$\log\left(\frac{\pi_j}{1-\pi_j}\right) = \log\left(e^{\beta_0+\beta_1 d_j}\right)$$

$$\Rightarrow g\left(\pi_j\right) = \log\left(e^{\beta_0+\beta_1 d_j}\right) = \beta_0 + \beta_0 d_j = \eta$$

Example 3: count data

- In a list of 41 events, respondents were asked to note which had occurred within the last 18 months.
- The result is given as:

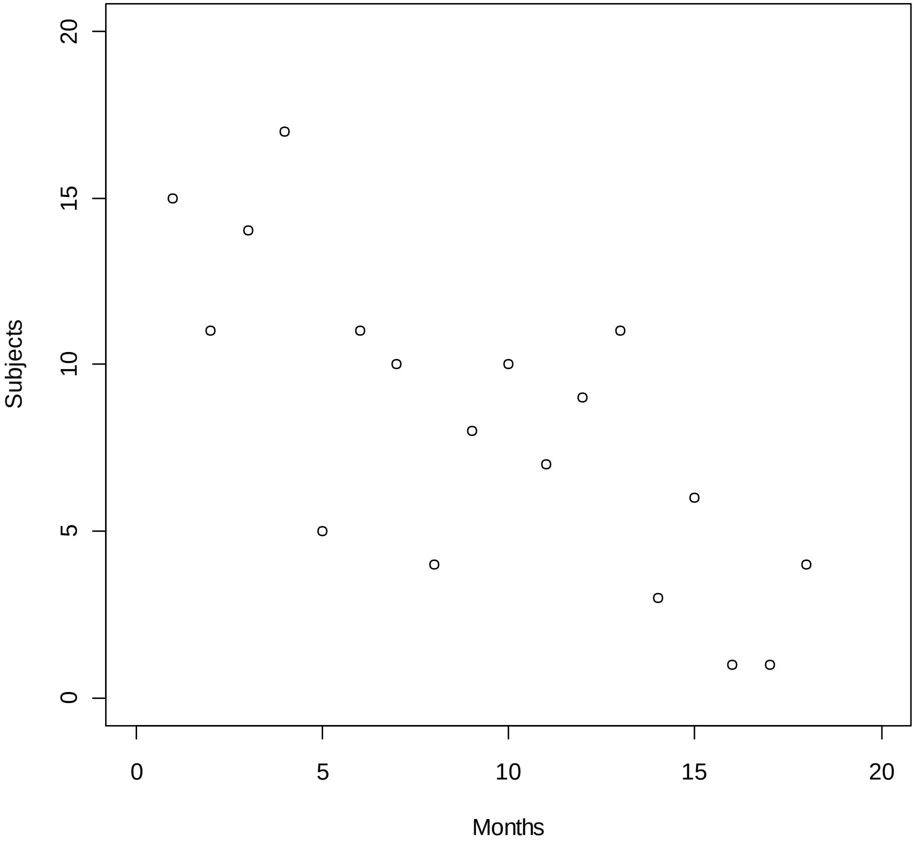
Month	1	2	3	4	5	6	7	8	9
Respondents	15	11	14	17	5	11	10	4	8
Month	10	11	12	13	14	15	16	17	18
Respondents	10	7	9	11	3	6	1	1	14

$$Y_t \sim Poisson(\mu(t))$$

Random component: example of count data

$$Y_t \sim Poisson(\mu_t)$$

$$E(Y_t) = \mu_t$$



Systematic component: dependency of the predictor – the linear predictor

$$\mu_t = f(time) = f(t) = f(\underbrace{\beta_0 + \beta_1 t}_{\text{The linear predictor}}) = f(\eta)$$

$$\mu_t = f(\beta_0 + \beta_1 t) = e^{\beta_0 + \beta_1 t}$$

The Link function: count data (log link)

The expected values of the response variable

$$E(Y_t) = \mu_t$$

The systematic part

$$\mu_t = e^{\beta_0 + \beta_1 t}$$

$$g(E(Y_t)) = g(\mu_t) = \eta$$

$$g(\mu_t) = \log(\mu_t) = \log(e^{\beta_0 + \beta_1 t}) = \beta_0 + \beta_1 t = \eta$$

Example 4: mortality rate (Table 3.2, Dobson)

Number of deaths from coronary heart diseases and population size per 5 years age group in new south Wales, Australia 1991.

Data in R:

```
> age<-c(32,37,42,47,52,57,62,67)
> deaths<-c(1,5,5,12,25,38,54,65)
> pop<-c(17742,16554,16059,13083,10784,9645,10706,9933)
> data.frame(age,deaths,pop,(deaths/pop)*100000)
  age deaths   pop          rate per year
1  32      1 17742           5.636343
2  37      5 16554          30.204180
3  42      5 16059          31.135189
4  47     12 13083           91.722082
5  52     25 10784           231.824926
6  57     38  9645         393.986522
7  62     54 10706          504.390062
8  67     65  9933         654.384375
```

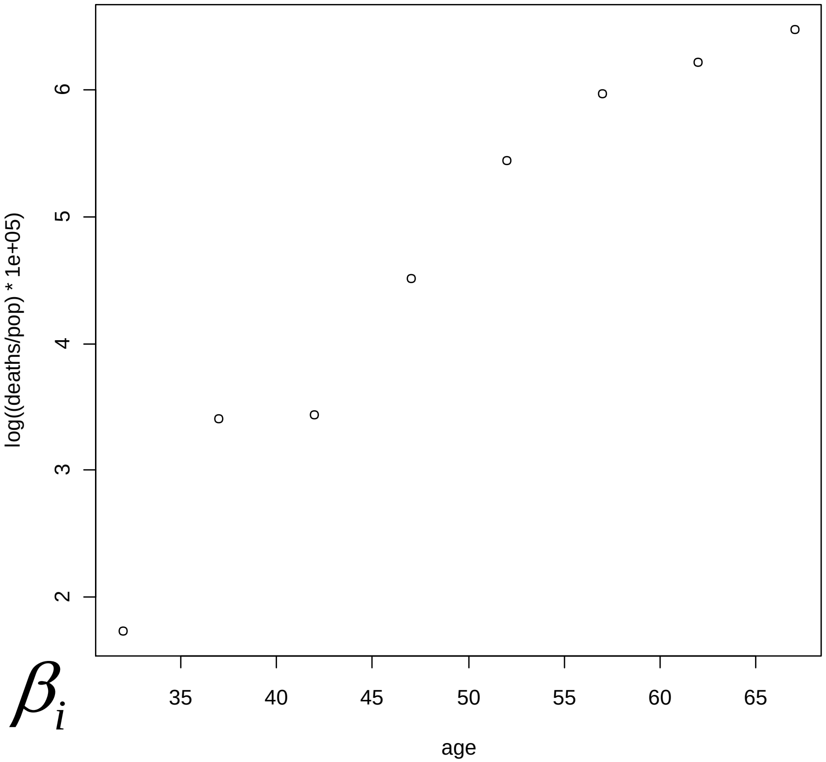
Random component: example of count data

$$Y_i \sim Poisson(\mu_i)$$

$$E(Y_i) = \mu_t$$

$$\mu_i = n_i e^{\beta_i}$$

$$g(\mu_i) = \log(\mu_i) = \log(n_i) + \beta_i$$



Chapter 4:
The Exponential family

Donson: chapter 3.

Lindsey: chapter 1.

McCullagh & Nelder: chapter 2.

The exponential family

Most of the commonly used statistical distributions, e.g. Normal, Binomial and Poisson, are members of the exponential family of distributions.

$$f(y) = \exp\left\{ \frac{y_i\theta_i - b(\theta_i)}{a_i(\phi)} + c(y_i, \phi) \right\}$$

Where Ø is the dispersion parameter and θ is the canonical parameter and

a_i(Ø), b(θ_i) and c(y_i, Ø) are known functions

The Exponential family

- The parameters θ_i and Ø are essentially location and scale parameters.
- It can be shown that if Y_i has a distribution in the exponential family then it has mean and variance

$$\mathrm{E}(Y_i) = \mu_i = b(\theta_i)$$

And

$$Var(Y_i) = \sigma_i^2 = b''(\theta_i) a_i(\phi_i)$$

Example: normal distribution

$$f(y_i;\mu_i,\sigma^2)=\frac{1}{\sqrt{2\pi\sigma^2}}e^{\frac{-(y_i-\mu_i)^2}{2\sigma^2}}$$

$$=\exp\left\{\left[y_i\mu_i-\frac{\mu_i^2}{2}\right]\frac{1}{\sigma^2}-\frac{y_i^2}{2\sigma^2}-\frac{1}{2}\log(2\pi\sigma^2)\right\}$$

$$\Downarrow$$

$$\theta_i=\mu_i,$$

$$b(\theta_i)=\theta_i^2/2$$

$$a_i(\phi)=\sigma^2$$

$$c(y_i,\ \phi)=-\left[y_i^2/\phi+\log(2\pi\phi)\right]/2\,.$$

Example: Bernoulli distribution

$$Y = \begin{cases} 1 & if \text{ even of interest has occured} \\ 0 & \text{Otherwise} \end{cases}$$

$$p(y \mid \theta) = \theta^{y}(1-\theta)^{1-y} = \exp\{y \log \frac{\theta}{1-\theta} + \log(1-\theta)\}$$

⇓

$$a = 1$$

$$b(\theta) = \log(1+\exp(\theta))$$

$$c(y) = 1$$

$$E(y) = \mu = b'(\theta) = e^{\theta}(1+\exp(\theta))^{-1}$$

$$\text{var}(y) = \mu(1-\mu)$$

Example: Binomial distribution

$$Z_i = \begin{cases} 1 \\ 0 \end{cases} \Longrightarrow Y_i = \sum_{i=1}^{n} Z_i \Longrightarrow Y_i \sim B(n, \pi_i)$$

$$p(y_i \mid \theta) = \binom{n_i}{y_i} \theta^{y_i} (1-\theta)^{n-y} =$$

$$\exp\left\{ y_i \log\left[\frac{\theta_i}{1-\theta_i}\right] + n_i \log(1-\theta_i) + \log\binom{n_i}{y_i} \right\}$$

$$a_i(\phi) = 1, \quad b(\theta_i) = \log(1+\exp(\theta_i))$$

$$c(y) = \log\binom{n_i}{y_i}$$

$$E(y) = \mu = b'(\theta_i) = e^{\theta}(1+\exp(\theta_i))^{-1}$$

$$\operatorname{var}(y) = \mu(1-\mu)/n$$

Poisson distribution

$$Y_i \sim Poisson(\mu)$$

$$f(y_i, \theta_i) = e^{-\theta_i} \frac{\theta_i^{y_i}}{y_i!} \exp\{y_i \log\theta_i - \theta_i - \log(y_i!)\}$$

$$a_i(\phi) = 1$$
$$b(\theta) = \exp(\theta)$$
$$c(y) = -\log(y!)$$
$$E(y) = \mu = b'(\theta) = \exp(\theta)$$
$$\operatorname{var}(y) = \mu$$

Gamma distribution

$$f\,(y_i\,;\,\mu_i\,,\nu) = \left(\frac{\nu}{\mu_i}\right)\frac{{y_i}^{\nu-1} e^{\frac{\nu\ y_i}{\mu_i}}}{\Gamma(\nu)}$$

$$= \exp\left\{\begin{array}{l}\left[-\,y_i\,/\,\mu_i - \log(\mu_i\,)\right]\nu + (\nu - 1)\log(\,y_i\,) \\ +\,\nu\log(\nu) - \log\left[\Gamma(\nu)\right]\end{array}\right\}$$

where

$$\theta_i = -1/\,\mu_i,$$

$$b\,(\theta_i) = -\log(-\theta_i\,)$$

$$a_i\,(\phi) = 1/\nu,\ \ and$$

$$c\ \ (y_i,\ \phi) = (\nu - 1)\log(\ y_i\,) + \nu\log(\ \nu) - \log\left[\Gamma(\nu)\right].$$

The Canonical link function: Poisson distribution

The canonical link function is given by

$$g(b^{'}) = X\beta = \theta$$

Where **b** is obtained from the general exponential density form .

The link function

$$Y_i \sim Poisson(\mu)$$

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

$$a_i(\phi) = 1$$

$$\boxed{b(\theta) = \exp(\theta)}$$

$$c(y) = -\log(y!)$$

$$\boxed{E(y) = \mu = b'(\theta) = \exp(\theta)}$$

$$\operatorname{var}(y) = \mu$$

The canonical link function: Binomial distribution

$$Z_i = \begin{cases} 1 \\ 0 \end{cases} \Rightarrow Y_i = \sum_{i=1}^{n} Z_i \Rightarrow Y_i \sim B(n, \pi_i)$$

$$p(y_i \mid \theta) = \exp\left\{ y_i \log\left[\frac{\theta_i}{1-\theta_i}\right] + n_i \log(1-\theta_i) + \log\binom{n_i}{y_i} \right\}$$

The link function

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

$$a_i(\phi) = 1, \quad b(\theta_i) = \log(1+\exp(\theta_i))$$

$$c(y) = \log\binom{n_i}{y_i}$$

$$\log\left(\frac{\mu}{1-\mu}\right) = \log\left(\frac{\dfrac{e^{\theta}}{1+e^{\theta}}}{\dfrac{1}{1+e^{\theta}}}\right) = \log\left(e^{\theta}\right) \Leftarrow E(y) = \mu = b'(\theta_i) = e^{\theta_i}(1+\exp(\theta_i))^{-1}$$

$$\operatorname{var}(y) = \mu(1-\mu)/n$$

The canonical link function: Normal distribution

$$f(y_i;\mu_i,\sigma^2)=\frac{1}{\sqrt{2\pi\sigma^2}}e^{\frac{-(y_i-\mu_i)^2}{2\sigma^2}}$$

$$=\exp\left\{\left[y_i\mu_i-\frac{\mu_i^{\ 2}}{2}\right]\frac{1}{\sigma^2}-\frac{y_i^{\ 2}}{2\sigma^2}-\frac{1}{2}\log(2\pi\sigma^2)\right\}$$

$$Y_i \sim N(\mu,\sigma^2)$$

$$g(\mu)=1\times\mu$$

$$\theta_i=\mu_i,$$

$$b(\theta_i)=\theta_i^{\ 2}/2$$

$$\mu=b^{'}(\theta_i)=\frac{2\theta}{2}$$

Canonical link function

Table showing the distribution with their link function and its name

Distribution	Link function ($g(\mu)$)	Name
Bernoulli	$\log(\mu/(1-\mu))$	Logit
Binomial	$\log(\mu/(k-\mu))$	Logit
Negative Binomial	$\log(\mu/(k+\mu))$	Logit
Poisson	$\log(\mu)$	Log
Gamma/ Exponential	$1/\mu$	Inverse
Normal	μ	Identity

Chapter 5
Generalized linear model function in R

The glm() Function

Generalized linear models can be fitted in R using the glm() function, which is similar to the lm function for fitting linear models.

The arguments to a glm() call are as follows:

```
glm(formula,family,link,data,...)
```

The first argument of the function is a model formula, which defines the response and linear predictor.

From glm() function we have the following family

Family	Default Link Function
binomial	(link = "logit")
gaussian	(link = "identity")
Gamma	(link = "inverse")
inverse.gaussian	(link = "1/mu^2")
poisson	(link = "log")
quasi	(link = "identity", variance = "constant")
quasibinomial	(link = "logit")
quasipoisson	(link = "log")

Link Function

- The link function links the response mean μ to the linear predictor η.
- Identity: $g(\mu) = \mu$
- Log: $g(\mu) = \log(\mu)$
- Logit: $g(\mu) = \log\left(\dfrac{\mu}{1-\mu}\right)$
- Probit : $g(\mu) = \phi^{-1}(\mu)$
- Comp. Log-log: $g(\mu) = \log(-\log(1-\mu))$
- Power: $g(\mu) = \mu^{\lambda}$, Where λ is the value in the power entry field.

Mainly for binary data (we will speak about this in a later stage in the course)

Link Function and distribution

- For each response distribution in the exponential family, there exists a special link function, the canonical link, for which θ=η .The canonical links expressed in terms of the mean parameter μ are
- Normal: $g(\mu) = \mu$
- Inverse Gaussian $g(\mu) = \mu^{-2}$
- Gamma $g(\mu) = \mu^{-1}$
- Poisson $g(\mu) = \log(\mu)$
- Binomial $g(\mu) = \log\left(\frac{\mu}{1-\mu}\right)$

- **Note** Some links are not appropriate for all distributions; logit, probit, and complementary log-log links are only appropriate for the binomial distribution.

Example: binary data with logit link

- Model with Binomial family and logit link function
- Fitting the model with the glm() function:

```
> model1 <- glm(Y ~ X*d, family=binomial(link=logit))
```

$$\eta = \beta_0 + \beta_1 x_i + \beta_2 d_{ij} + \beta_3 x_i * d_{ij}$$

A model with two predictors and interaction.

Alternative code

```
> model1<- glm(y ~ X+d+X:d, family=binomial(link=logit))
```

Extractor functions in R

- The glm function returns an object of class c("glm", "lm").
- There are several glm or lm methods available for accessing/displaying components of the glm object, including:
  - residuals()
  - fitted()
  - predict()
  - coef()
  - deviance()
  - formula()
  - summary()

Extractor functions in R

- Summary to obtain more detailed information about the model :
- residuals or resid, for the deviance residuals
- fitted or fitted.values, for the fitted values (estimated probabilities)
- predict, for the linear predictor (estimated logits)
- coef or coefficients, for the coefficients, and
- deviance, for the deviance.

The predict() function in R

- The predict() function obtains predictions and optionally estimates standard errors of those prediction from a fitted glm objects.

- The general call is;

```
predict(object, newdata = NULL, type = c("link", "response", "terms"), se.fit = FALSE,
dispersion = NULL, terms = NULL, na.action = na.pass, ...)
```

The update() function in R

- The update () function in R can be used to modify a fitted model by dropping some of the terms.

- The general call of the function is given as:

```
Update(old model, ~, . - or + the term we want to drop/ad)
```

Chapter 6:
Models for Binary data

Donson: chapter 7.

Lindsey: chapter 2.

McCullagh & Nelder: chapter 4.

Binary data

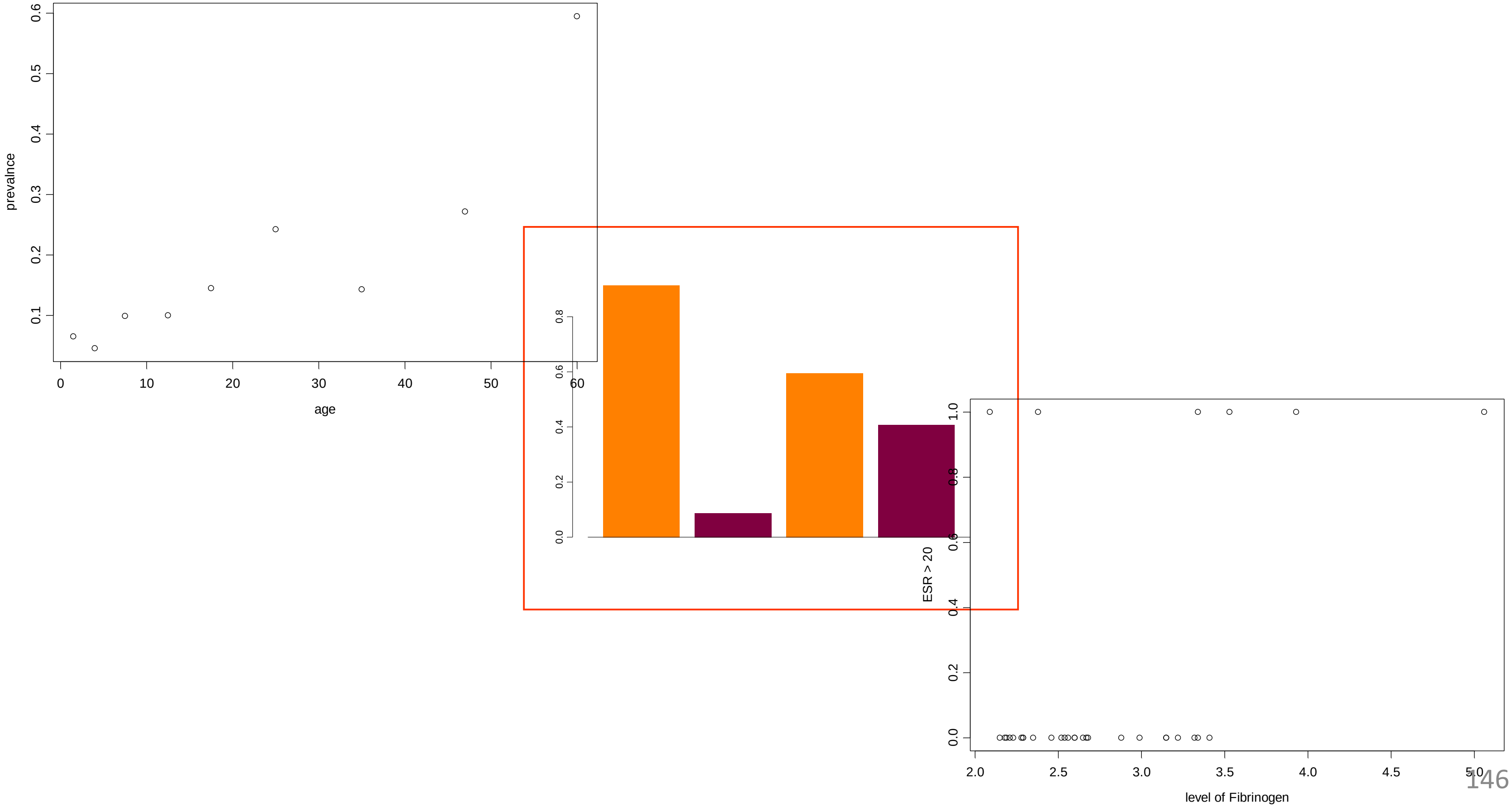
- Binary data may occur in two forms
  - ungrouped in which the variable can take one of two values, say success/failure
  - grouped in which the variable is the number of successes in a given number of trials
- The natural distribution for such data is the *Binomial (n, p) distribution;* where in the first case n = 1

Exploring Binary Data

If our aim is to model a binary response, we would first like to explore the relationship between that response and potential explanatory variables.

- When the explanatory variables are categorical, a simple approach is to calculate proportions within subgroups of the data.
- When some of the explanatory variables are continuous, plots can be more helpful.

Example tour



Example 1: The Aspirin and Myocardial Infarction Data

- Relationship between aspirin use and heart attacks
- 5-year randomized study
- does regular aspirin intake reduces mortality from cardiovascular disease?

	Myocardial Infarction		
Group	Yes	No	**Total**
Placebo	189	10845	11034
Asprin	104	10933	11037

Example 1: The Aspirin and Myocardial Infarction Data

The question of primary interest is:

Does regular aspirin intake reduces mortality from cardiovascular disease?

$$Y_i = \begin{cases} 1 & \text{Myocardial Infarction} \quad Yes \\ 0 & \text{Myocardial Infarction} \quad No \end{cases}$$

The response variable

Example 2: smoked mice

In order to investigate the influence of smoking on lung cancer a group of 55 mice were randomized into two treatment groups.

In the first group (the treated group), each animal was enclosed in a chamber that was filled with the smoke of one cigarette every hour in 12 hours day.

The second group (the control group) were kept in their chambers for 12 hours with out smoke. After one year an autopsy was carried out.

The response is the present and absent of a tumor.

The second variable in the data is the treatment group.

Example 2: smoked mice

The question of primary interest is:

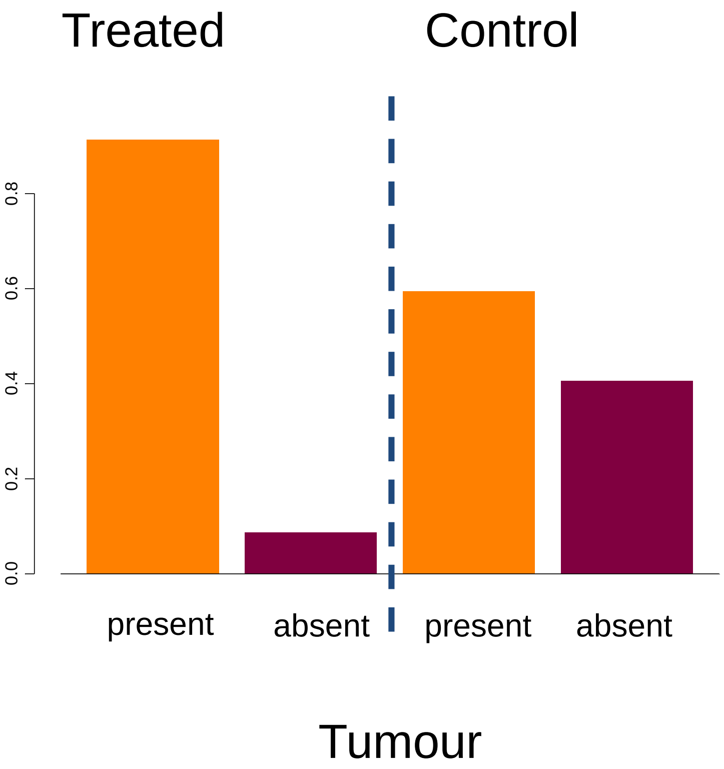
DOSE SMOKE INCREAE THE RISK FOR CANCER ?

$$Y_i = \begin{cases} 1 & tumour \quad present \\ 0 & tumour \quad absent \end{cases}$$

The response variable

Example 2: smoked mice

	Tumour present	Tumour absent	Total
Treated	21	2	23
Contol	19	13	32
Total	20	15	55



Example 2: smoked mice

	Tumour present	Tumour absent	Total
Treated	21	2	23
Contol	19	13	32
Total	20	15	55

We want to model the probability to develop a tumour given the treatment group.

This is an example of grouped data.

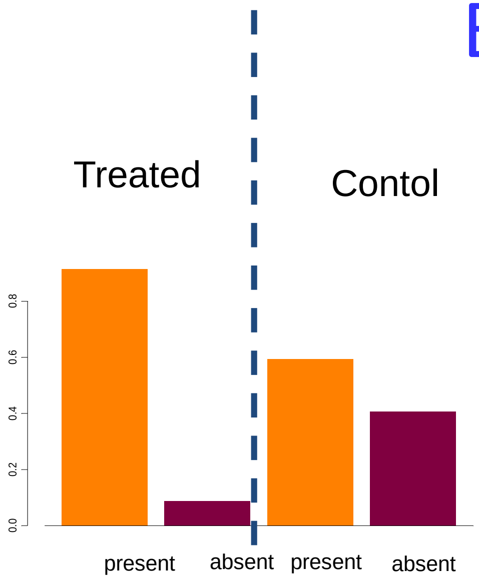
We do not have information about individuals in the sample, but only about the counts in different combinations of the experiment.

Individual data can be extracted from the table.

In terms of statistical modeling, the response is binary (tumor absent/tumor present).

The predictor, the treatment group, is also binary.

Example 2: smoked mice



In the treated group, 21/23 (91%) of the mice develop tumour. In the control group only 19/32 (59%).

The aim of the analysis is to determine if this difference is only due to chance or if the smoke increase the risk for tumour.

Example 3: Serological data

Antibodies produced in response to an infectious disease like malaria remain in the body after the individual has recovered from the disease. A serological test detects the presence or absence of such antibodies. An individual with such antibodies is termed seropositive.

Example 3: Serological data

- A sample which taken at a certain time point.
- The information for each individual:

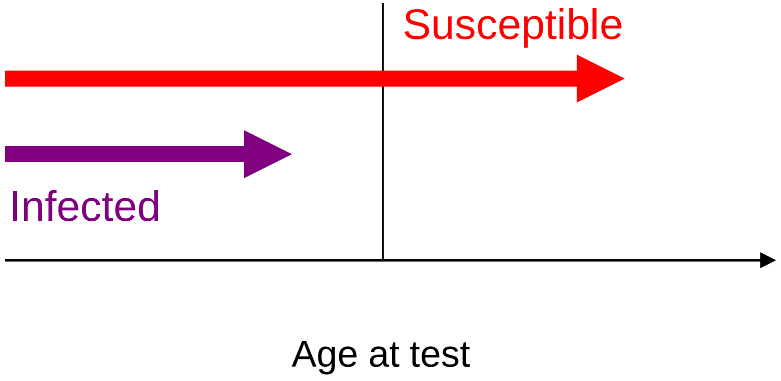
1. Age at test.
2. Infected or not.

- Prevalence of sero-positivity In the sample:

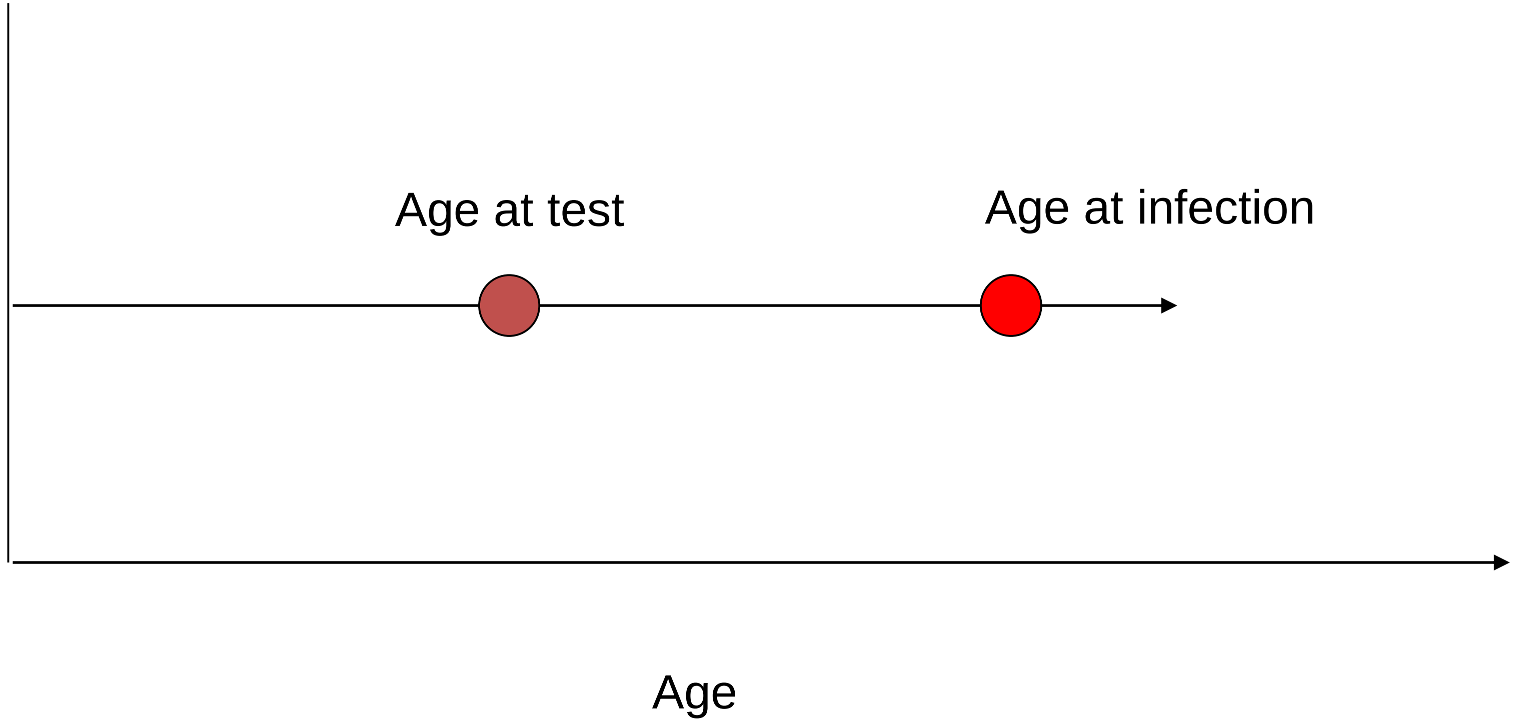
$$P(a)$$

This is the probability to become infected before the age at test.

- Sero-prevalnce data

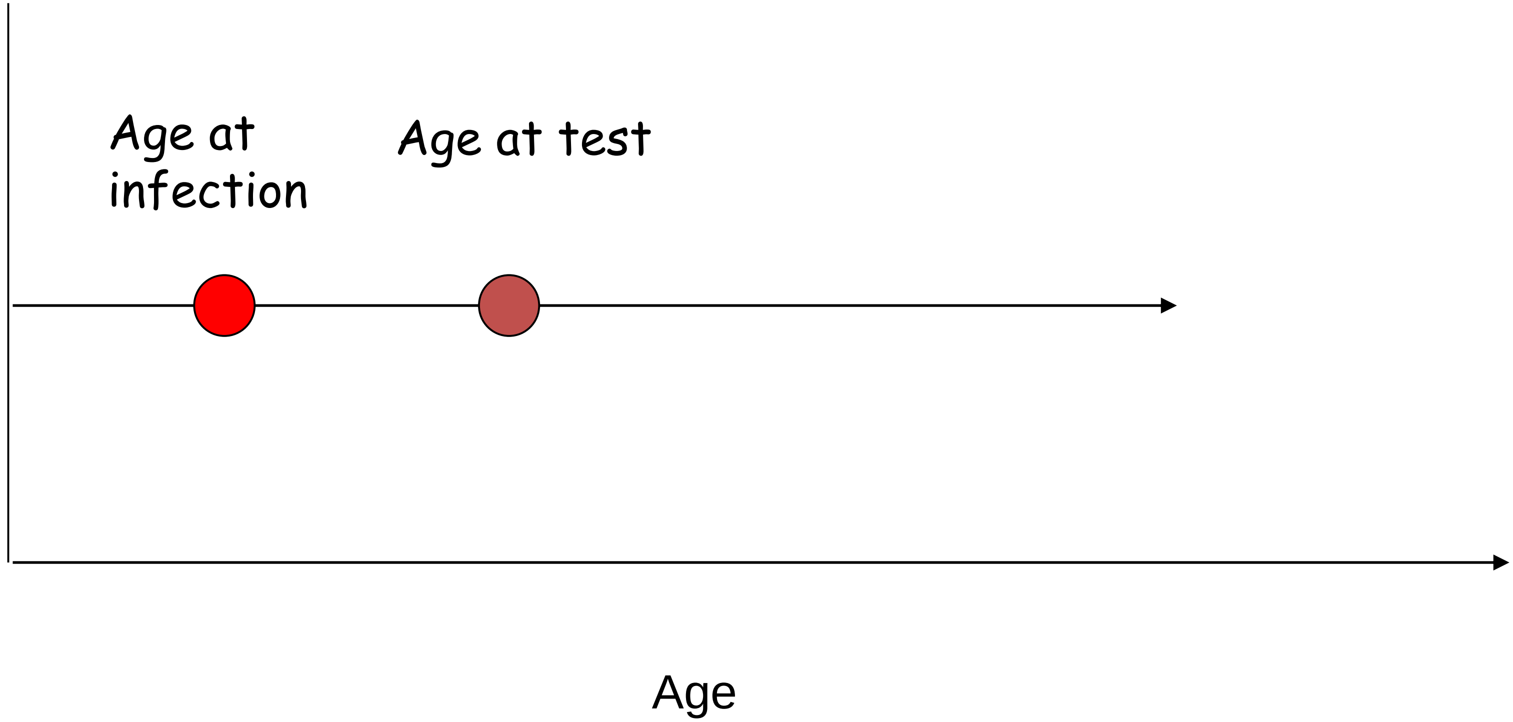


Example 3: serological data



- Sero-Negative: infected after the test.

Example 3: serological data



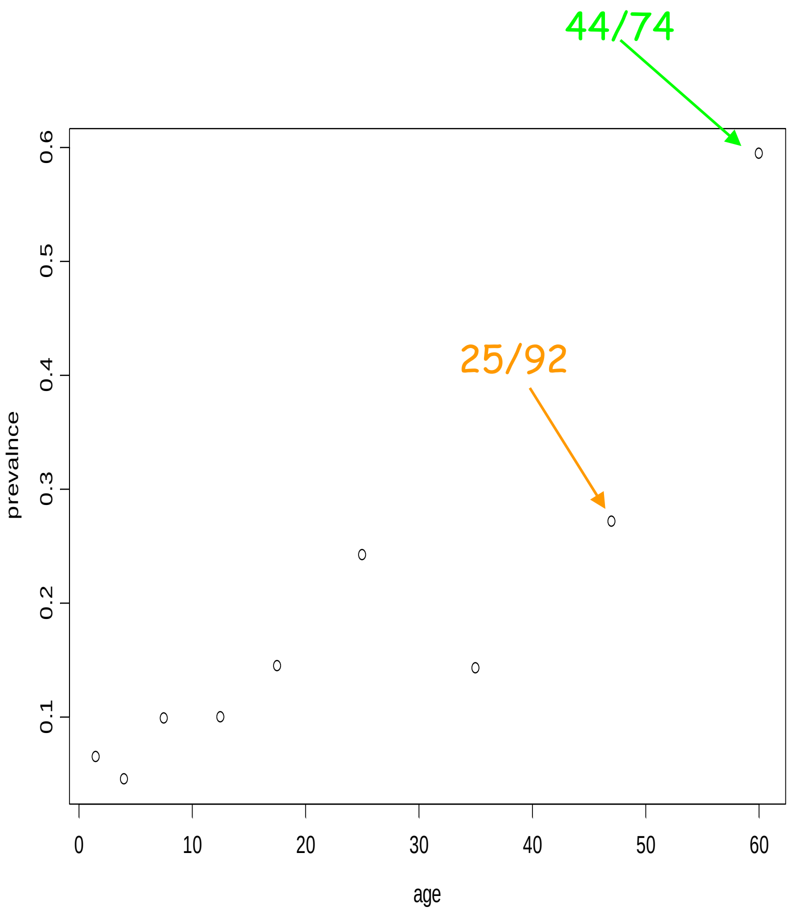
- Sero-Positive: infected before the test.

Example 3: Serological data of malaria

- In this example the information about each subject in the experiment is the disease status (infected or not by malaria) and the age group of the subject.
- The variables are: the sample size, the number of sero-positive at each sample size (=the number of infected subjects) and the age.

Example 3: serological data

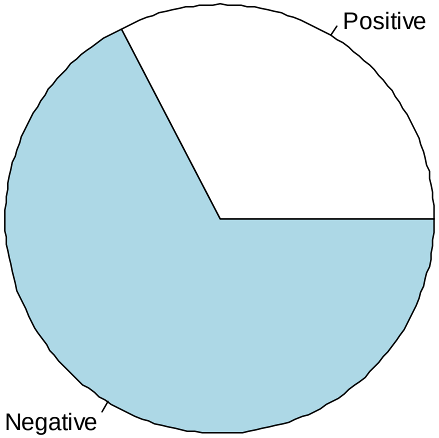
Age group	Mid age	Sero positive	Sample size
	1.5	8	123
	4.0	6	132
	7.5	18	182
	12.5	14	140
	17.5	20	138
	25.0	39	161
	35.0	19	133
	47.0	25	92
	60.0	44	74



Example 4: HIV data

- Consider the HIV data set and the model for HIV (the outcome variable, yes/no or 1/0).
- Covariates:
- ……, age group (also coded 1/0).
- Age group was coded 1 for people younger than 40.7 years
- Age

- Response: HIV status (32.6% are positive).

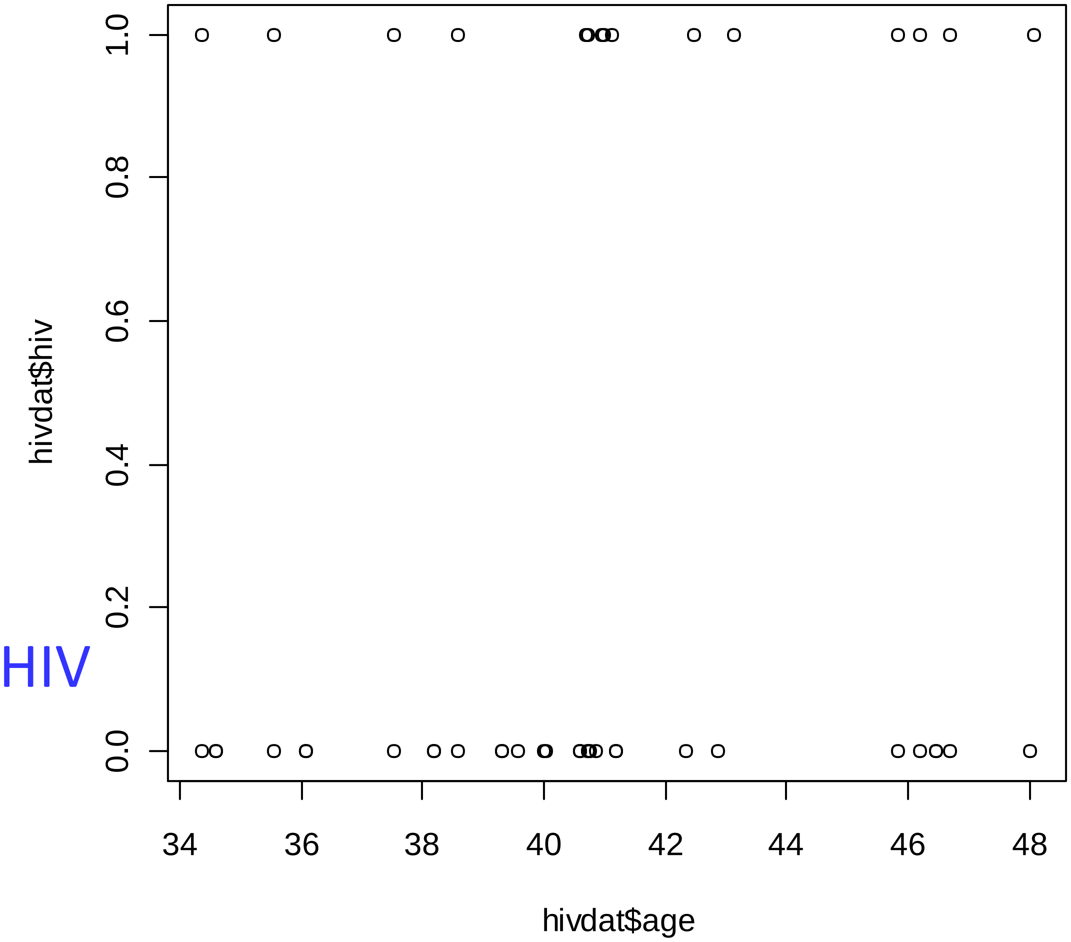


Example 4: HIV data

```
> par(mfrow=c(1,1))
> plot(hivdat$age,hivdat$hiv)
```

- Continuous predictor.
- Age as predictor variable.
- Response: HIV STATUS

Does the probability to be HIV positive depends on age ?



Example 5: toxicity example (Budworm)

Collett (1991) describes an experiment on the toxicity of the pyrethoid trans - cypermethrin to the tobacco budworm.

Batches of 20 moths of each sex were exposed to varying doses of the pyrethoid for three days and the number of dead or knocked down in each batch was recorded:

Sex	Dose (μ g)					
	1	2	4	8	16	32
Male	1	4	9	13	18	20
Female	0	2	6	10	12	16

Predictor: log(dose)

Example 6: Heart Disease (Dipankar Bandyopadhyay, Ph.D.)

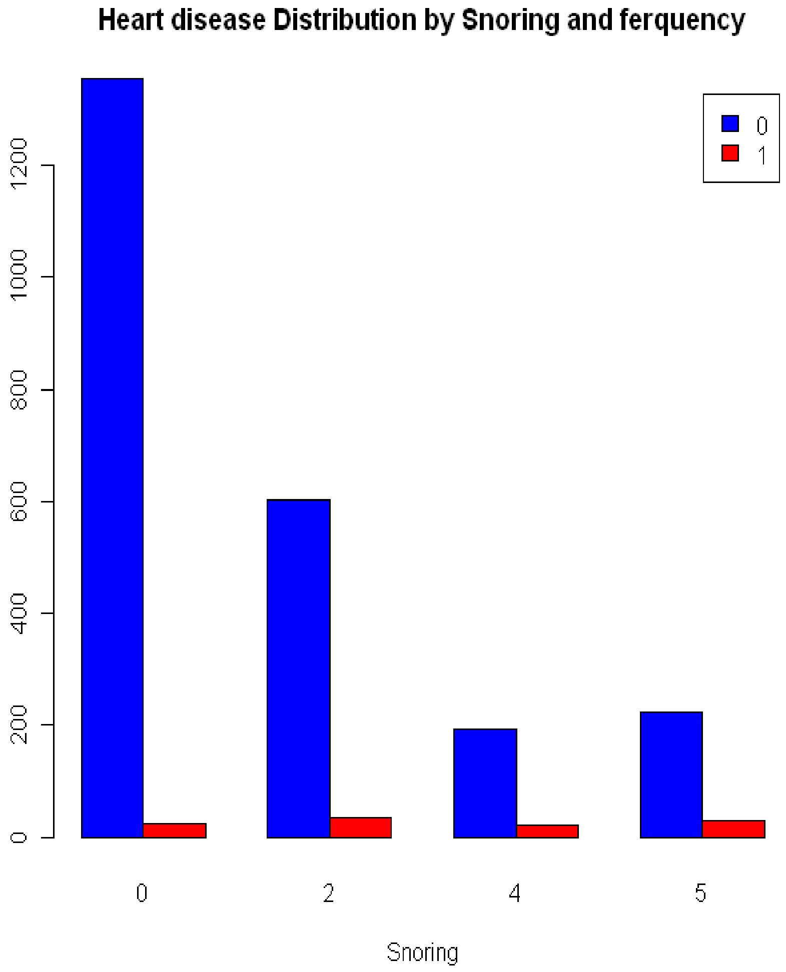
Our outcome is heart disease, and in order to use the ordinal levels of snoring, we need to select scores.

A set (0, 2 , 4, 5) seems to capture the relative magnitude of the differences among the categories.

	Heart Disease		Proportion
Snoring	Yes	No	Yes
Never	24	1355	0.017
Occationally	35	603	0.055
Nearly every night	21	192	0.099
Every Night	30	224	0.118

Example 6: Heart Disease data

```
> par(mfrow=c(1,1))
> plot(snoring,dhyes)
```



- Categorical predictor.
- Snoring as predictor variable.
- Response: Heart disease (yes|No)

Does the probability to be heart disease depends on snoring ?

Modeling Binary data

Binary data

$$Z_i = \begin{cases} 1 & P \\ 0 & 1-P \end{cases}$$

The observation is a binary variable with takes the value of 1 with probability P.

$$Z_1, Z_2, Z_3 \ldots Z_{n_i}$$

P is the success probability, i.e. P(Z=1).

$$E(Z_i) = P_i$$

The expected value of Z is equal to P.

The sum of binary random variables

$$\boxed{Z_i = \begin{cases} 1 & P \\ 0 & 1-P \end{cases}}$$

$$\boxed{Z_1, Z_2, Z_3 \ldots Z_{n_i}}$$

$$\boxed{E(Z_i) = P_i}$$

$$\boxed{Y_i = \sum_{i=1}^{n_i} Z_i}$$

$$\boxed{Y_i \sim Bin(n_i, P_i)}$$

Often we want to model the sum of the binary variables Y.

If Z~B(1,P) then Y~B(n,P).

E(Z)=P and E(Y)=nP.

Example 1: The Aspirin and Myocardial Infarction Data

The question of primary interest is:

does regular aspirin intake reduces mortality from cardiovascular disease?

$$Z_i = \begin{cases} 1 & \mathit{cardiovascular} \quad \mathit{present} \\ 0 & \mathit{cardiovascular} \quad \mathit{absent} \end{cases}$$

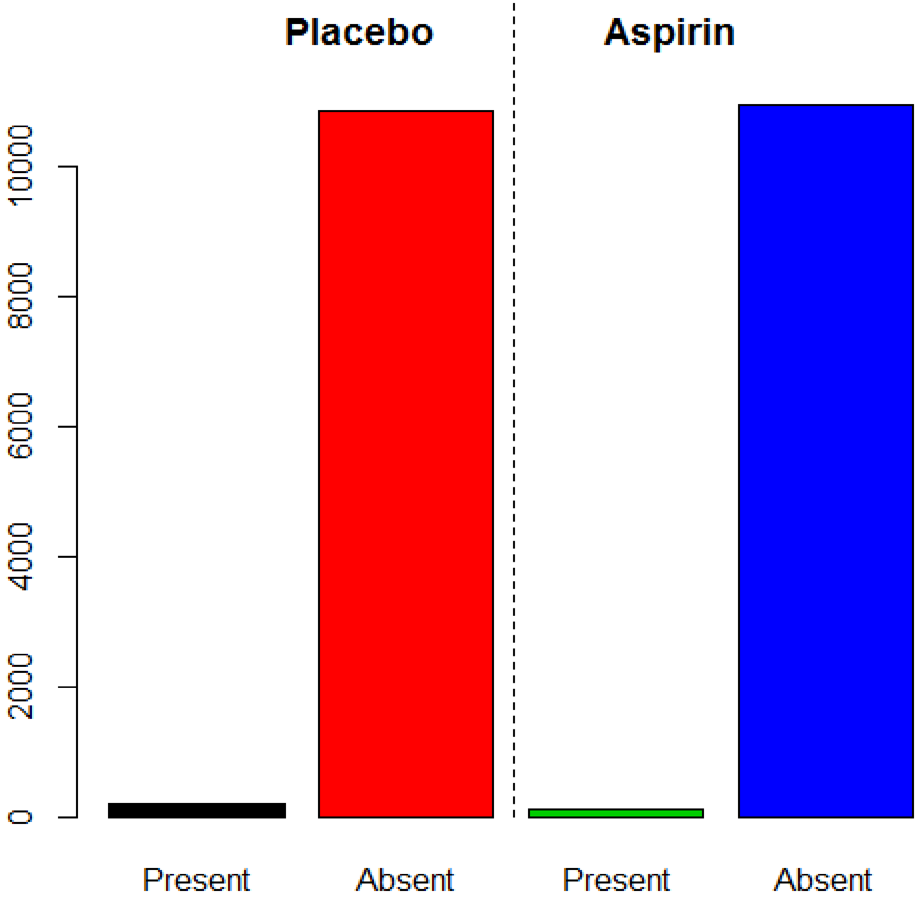
The probability of sucsses

- The probability of success P(Z=1). This is the probability to have cardiovascular disease. We want to see if Aspirin intake has an effect on the probability to have Myocardial infarction.

EXAMPLE 1: Aspirin

The Data

Myocardial Infarction			
Group	Yes	No	Total
Placebo	189	10845	11034
Aspirin	104	10933	11037



EXAMPLE 1: Aspirin

Data in R

```
> resp<-as.factor(c(rep(1,189),rep(0,10845),rep(1,104),rep(0 ,10933)))
> trt<-as.factor(c(rep(1,189),rep(1,10845),rep(2,104),rep(2,10933)))
```

Myocardial Infarction			
Group	Yes	No	Total
Placebo	189	10845	11034
Aspirin	104	10933	11037

$$trt_i = \begin{cases} 1 & Aspirin \\ 2 & Placebo \end{cases}$$

$$resp_i = \begin{cases} 1 & Yes \\ 0 & No \end{cases}$$

Data structure:

```
> cbind(resp,trt)
     resp trt
[1,]       2  1
[2,]       2  1
[3,]       2  1
[4,]       2  1
[5,]       2  1
[6,]       2  1
          .  .
          .  .
[22066,]   1  2
[22067,]   1  2
[22068,]   1  2
[22069,]   1  2
[22070,]   1  2
[22071,]   1  2
```

Sample size → [22071,]

Data structure in R

- Data are given in table format.
- The variable count is the number of cases in each category.

```
> table(trt,resp)
      resp
trt     0     1
  1 10845   189
  2 10933   104
>
```

Model formulation

We want to model the probability to have Myocardial infarction given the aspirin intake.

The model for P- logit transformation

$$\log it(P) = \beta_0 + \beta j$$

```
< fit.myoc<-glm(resp~trt,family=binomial(link = "logit"))
```

EXAMPLE 1: Aspirin

The estimated model in R

```
> summary(fit.myoc)

Call:
glm(formula = resp ~ as.factor(trt), family = binomial(link = "logit"))

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-0.1859  -0.1859  -0.1376  -0.1376   3.0544

Coefficients:
                Estimate Std. Error z value Pr(>|z|)
(Intercept)     -4.04971    0.07337 -55.195  < 2e-16 ***
as.factor(trt)2 -0.60544    0.12284  -4.929 8.28e-07 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 3114.7  on 22070  degrees of freedom
Residual deviance: 3089.3  on 22069  degrees of freedom
AIC: 3093.3

Number of Fisher Scoring iterations: 7
```

$\hat{\beta}_0$

$\hat{\beta}$

$$\log it\left(\hat{P}_i\right) = \hat{\beta}_0 + \hat{\beta} \times Aspirin$$

EXAMPLE 1: Aspirin

How do we interpreat the parameters from the output above ?

The parameter estimate for the effect of the placebo group is -4.04971. The parameter estimate for the effect of the Aspirin intake is -0.60544.

The odds ratio, θ, is equal to 0.5458342. If θ < 1 than the odds for a Myocardial infarction in the Aspirin intake group is smaller than the odds for Myocardial infarction in the placebo group. This means that the aspirin reduces the risk of myocardial infarction.

EXAMPLE 1: Aspirin

Example 2: smoked mice

The question of primary interest is:

DOSE THE SMOKE INCREAE THE RISK FOR CANSER ?

$$Z_i = \begin{cases} 1 \quad tumour \quad present \\ 0 \quad tumour \quad absent \end{cases}$$

The response variable

The probability of sucsses

- The probability of success P(Z=1). This is the probability to have tumour. We want to see if treatment (smoke) has an effect on the probability to develop a tumour.

EXAMPLE 2: SMOKED MICE

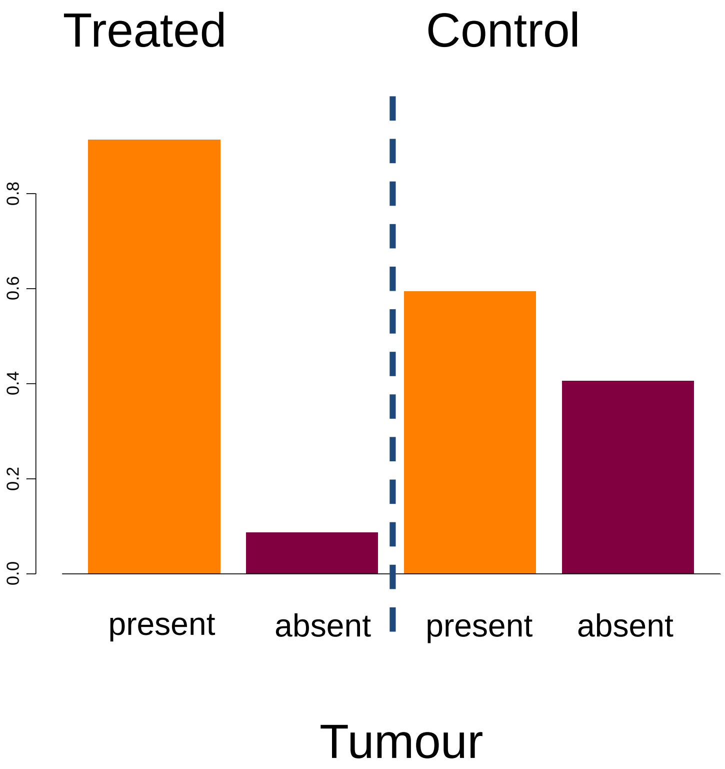
Data structure in R

- Data are given in table format.
- The variable count is the number of cases in each category.

```
> table(trti,resp)
    resp
trti  0  1
   1 21  2
   2 19 13
```

The Data

	Tumour present	Tumour absent	Total
Treated	21	2	23
Contol	19	13	32
Total	20	15	55



EXAMPLE 2: SMOKED MICE

Model formulation

	Tumour present	Tumour absent	Total
Treated	21	2	23
Contol	19	13	32
Total	20	15	55

We want to model the probability to develop a tumour given the treatment group.

The individual data

$$Z_i = \begin{cases} 1 & tumour \quad present \\ 0 & tumour \quad absent \end{cases}$$

Number of subjects with tumour

$$Y_i = \sum Z_i$$

Distribution of Y

$$Y_i \sim B(n_i \, , \quad P_i)$$

The model for P- logit transformation

$$\log it(P) = \beta_0 + \beta j$$

EXAMPLE 2: SMOKED MICE

The probability

$$P = \frac{e^{\beta_0 + \beta_j}}{1 + e^{\beta_0 + \beta_j}}$$

The parameter β_j is the treatment effect.

Note that we have two treatment groups and it is dummy coding for treatment effect, the $\beta_{control} = \beta_0$

EXAMPLE 2: SMOKED MICE

The probability

$$\begin{tikzcd}
 & P = \dfrac{e^{\beta_0 + \beta_{treatment}}}{1 + e^{\beta_0 + \beta_{treatment}}} \\
P = \dfrac{e^{\beta_0 + \beta_j}}{1 + e^{\beta_0 + \beta_j}} \arrow[ur] \arrow[dr] & \\
 & P = \dfrac{e^{\beta_0}}{1 + e^{\beta_0}}
\end{tikzcd}$$

The probability to have tumor for the treatment group.

The probability to have tumor for the control group.

Logistic regression in R

	Tumour present	Tumour absent	Total
Treated	21	2	23
Contol	19	13	32
Total	20	15	55

```
fit.mice<-glm(resp~trti,family=binomial(link = "logit"))
```

$$\log it(P_i) = \beta_0 + \beta \times treatment$$

model status= treat

The estimated model in R

```
> summary(fit.mice)

Call:
glm(formula = resp ~ trti, family = binomial(link = "logit"))

Deviance Residuals:
    Min       1Q   Median       3Q      Max  
-1.0211  -1.0211  -0.4265   1.3422   2.2101  

Coefficients:
            Estimate Std. Error z value Pr(>|z|)   
(Intercept)  -2.3514     0.7400  -3.177  0.00149 **
trti2         1.9719     0.8229   2.396  0.01656 * 
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

$\hat{\beta}_0$

$\hat{\beta}$

$$\log it\left(\hat{P}_i\right) = \hat{\beta}_0 + \hat{\beta} \times treatment$$

How do we interpreat the parameters ?

```
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -2.3514     0.7400  -3.177  0.00149 **
trti2        1.9719     0.8229   2.396  0.01656 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

The parameter estimate for the effect of the control group is -2.3514. The parameter estimate for the effect of the treatment group (the smoked group) is equal to 1.9719.

➔ The probability of tumour in control and treatment groups are 0.086955 and 0.406247, respectively.

➔ The odds of tumour in control and treatment groups are 0.095236 and 0.684203, respectively.

How do we interpreat the parameters ?

➔ The probability of tumour in control and treatment groups are 0.086955 and 0.406247, respectively.

➔ The odds of tumour in control and treatment groups are 0.095236 and 0.684203, respectively.

➔ The odds ratio θ is 7.184314.

➔ If θ > 1 than the odds for a tumour in the treatment group is larger than the odds for a tumour in the control group. This means that the probability for tumour in the treatment group is LARGER than the probability for tumour in the control group.

The odds ratio: estimation

```
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -2.3514     0.7400  -3.177  0.00149 **
trti2         1.9719     0.8229   2.396  0.01656 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

For a factor predictor variable,

$$\theta = \exp(\beta).$$

In our example: $\theta = \exp(1.9719) = 7.184314$.

The odds ratio: point estimator

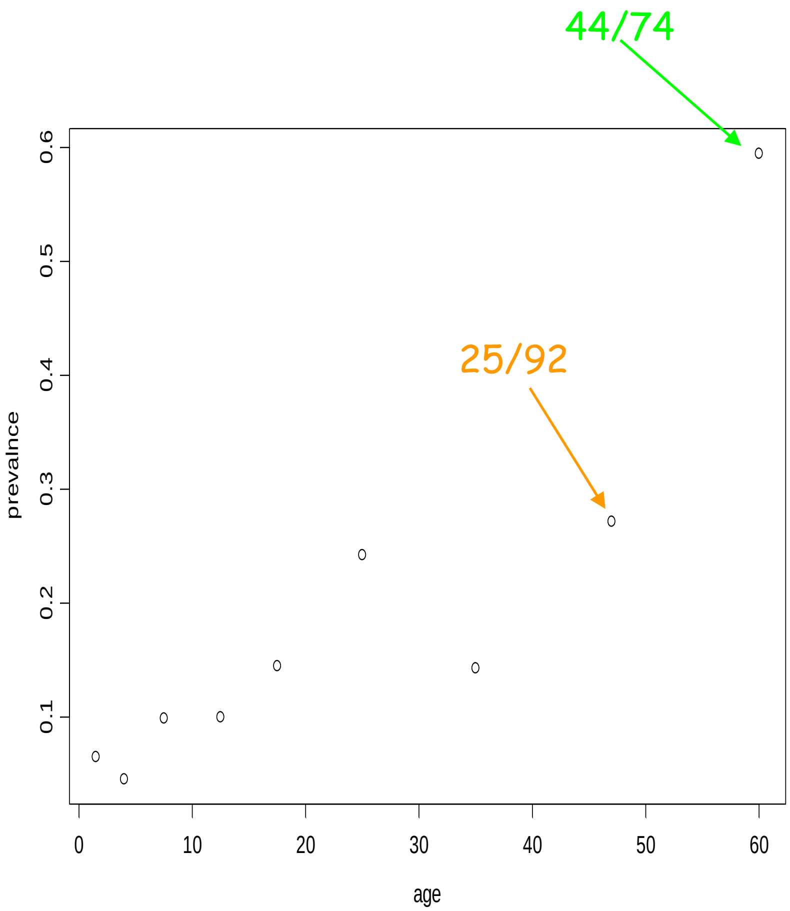
The inverse of the odds ratio, θ, is equal to 0.139.

➔ The odds for a tumour in the control group is smaller than the odds for a tumour in the treatment group. This means that the probability for tumour in the control group is SMALLER than the probability for tumour in the treatment group.

EXAMPLE 2: SMOKED MICE

Example 3: serological data

Age group	Mid age	Sero positive	Sample size
	1.5	8	123
	4.0	6	132
	7.5	18	182
	12.5	14	140
	17.5	20	138
	25.0	39	161
	35.0	19	133
	47.0	25	92
	60.0	44	74



Example 3: Data structure in R

- This is an example in which the predictor (age) is continuous.
- We want to model the probability of infection as a function of age.

```
cbind(agei,posi,negi)
     agei posi negi
 [1,]  1.5    8  115
 [2,]  4.0    6  126
 [3,]  7.5   18  164
 [4,] 12.5   14  126
 [5,] 17.5   20  118
 [6,] 25.0   39  122
 [7,] 35.0   19  114
 [8,] 47.0   25   67
 [9,] 60.0   44   30
```

Example 3: serological data

Mid age	Sero positive	Sample size
1.5	8	123
4.0	6	132
7.5	18	182
12.5	14	140
17.5	20	138
25.0	39	161
35.0	19	133
47.0	25	92
60.0	44	74

$$Z_i = \begin{cases} 1 & sero \quad pos. \\ 0 & sero \quad neg. \end{cases}$$

$$\boxed{Y_i = \sum Z_i}$$

Number of sero-positive at each age group

$$Y_i \sim B(\boxed{n_i ,} \quad P_i)$$

n_i: sample size at each age group

P_i is the probability to be infected (the prevalence). We use logistic regression in order to model the prevalence as a function of age

$$\log it(P_i) = \beta_0 + \beta \times \boxed{age}$$

The probability of infection

$$P = \frac{e^{\beta_0 + \beta\ age}}{1 + e^{\beta_0 + \beta\ age}}$$

If β>0 then there is a positive association between the probability and age. This means that the probability of infection increase with age.

If β<0 then there is a negative association between the probability and age. This means that the probability of infection decrease with age.

EXAMPLE 3: serological data

Logistic regression in R

$$Y_i \sim B(n_i\,, \quad P_i)$$

pos/N

```
fit.malaria<-glm(cbind(posi,negi)~agei,
          family=binomial(link="logit"))
```

$$\log it(P_i) = \beta_0 + \beta \times age$$

model pos/N=age

Parameters estimate

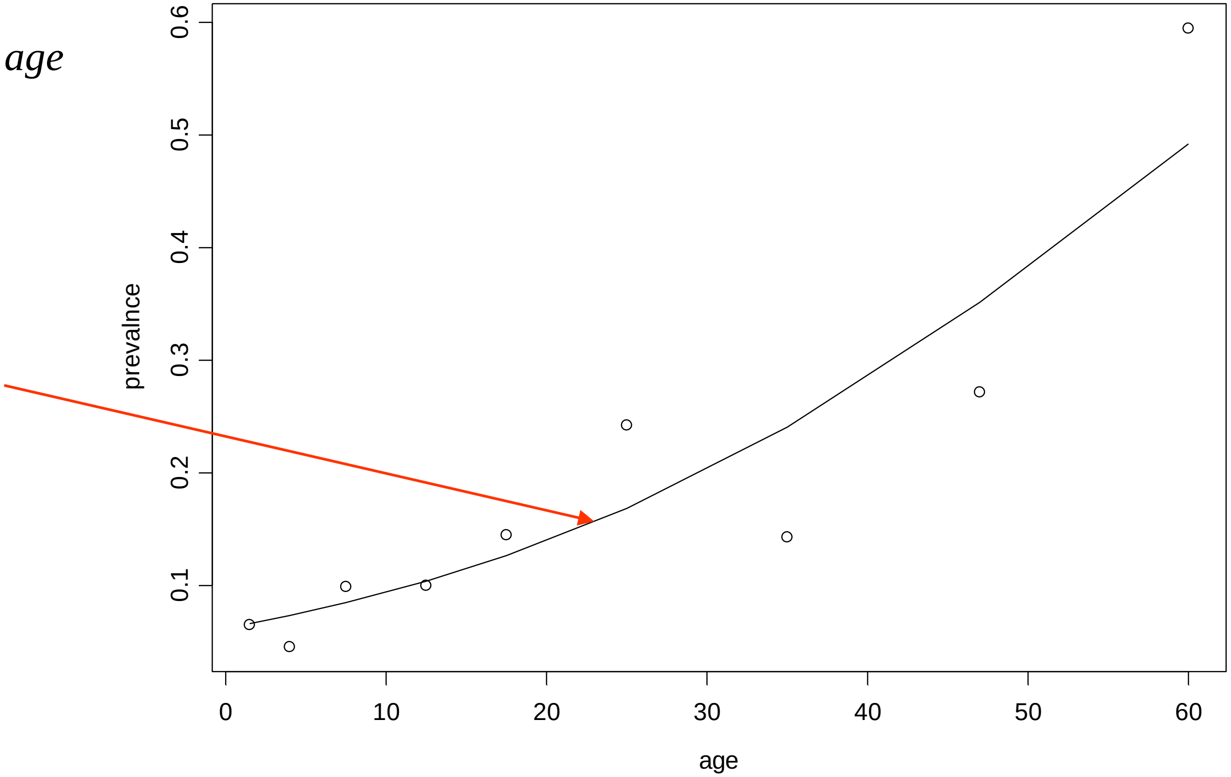
$$\begin{array}{rcccccl} \log it\left(\hat{P}_i\right) &=& a &+& b &\times& age\\ & & \downarrow & & \downarrow & & \\ \log it\left(\hat{P}_i\right) &=& -2.71 &+& 0.044 &\times& age \end{array}$$

```
> summary(fit.malaria)

Call:
glm(formula = cbind(posi, negi) ~ agei, family = binomial(link = "logit"))

Deviance Residuals:
    Min        1Q    Median       3Q       Max
-2.78685  -1.31863  -0.05053   0.66752   2.38275

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -2.714074   0.151740 -17.886   <2e-16 ***
agei         0.044672   0.004511   9.904   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Data and predicted values

$$\log it\left(\hat{P}_i\right) = -2.71 + 0.044 \times age$$

$$\hat{P}_i = \frac{e^{-2.71+0.044\times age}}{1+e^{-2.71+0.044\times age}}$$



EXAMPLE 3: serological data

The odds ratio: point estimator

```
> exp(0.044672)
[1] 1.045685
```

How to calculate the odds ratio ?

The odds ratio is given by

$\theta=\exp(\beta)$.

In our example $\theta=\exp(0.0447)=1.046$.

Implies per unit increase of age the odds to be infected by malaria increase by 4.6%

Example 4: HIV data

- Dependency of the probability to be HIV positive on different covariates.

$$Y_i = \begin{cases} 1 & HIV + \\ 0 & HIV - \end{cases}$$

$$Y_i \sim B(1, \pi)$$

$$X_i = age_i$$

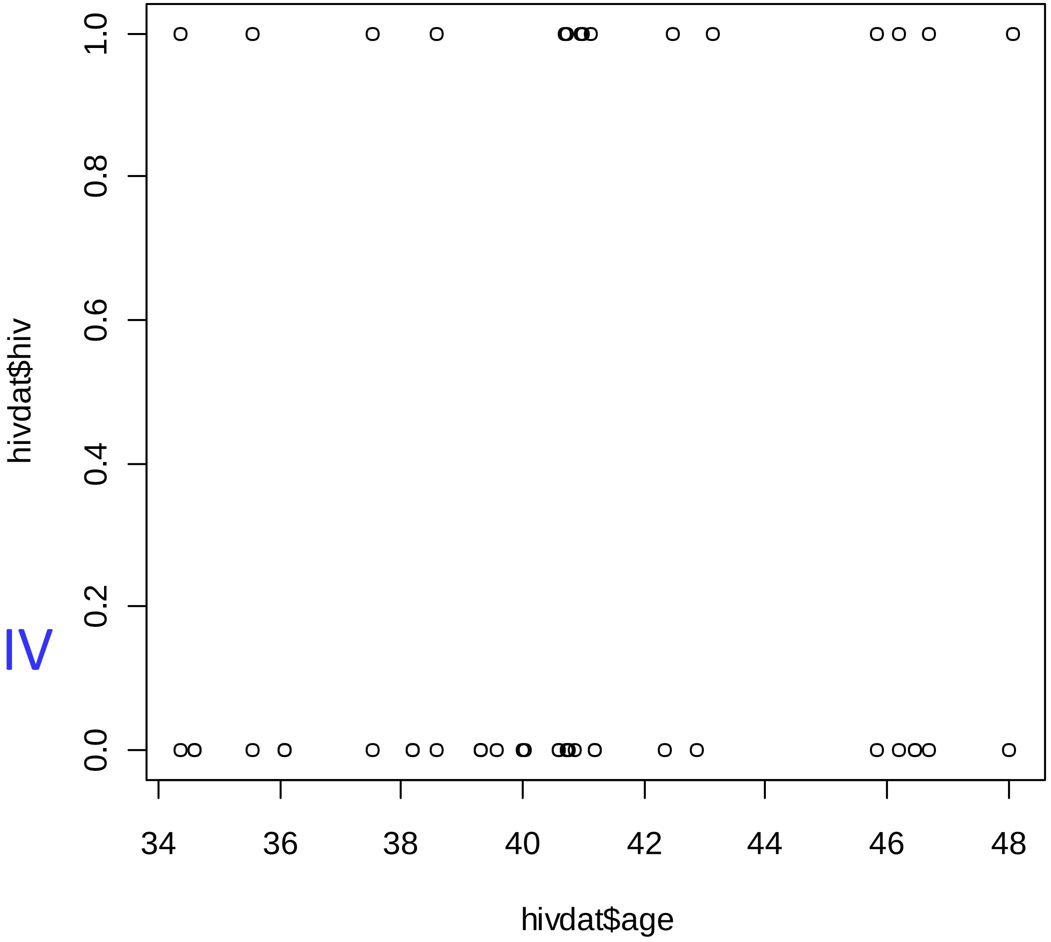
Does the probability to be HIV positive depends on age

Example 4: HIV data

```
> par(mfrow=c(1,1))
> plot(hivdat$age,hivdat$hiv)
```

- Continuous predictor.
- Age as predictor variable.
- Response: HIV STATUS

Does the probability to be HIV positive depends on age ?



EXAMPLE 4: HIVdata

Model formulation

$$
\begin{aligned}
&Y_i \sim B(1, \pi) \\
&E(Y_i) = \pi \\
&\pi = f(X_i) = f(age_i)
\end{aligned}
$$

The GLM

$$
\left.
\begin{aligned}
&Y_i \sim B(1, \pi) \\
&E(Y_i) = \pi \\
&\pi = \frac{e^{\beta_0 + \beta_1 X_i}}{1 + e^{\beta_0 + \beta_1 X_i}}
\end{aligned}
\right\}
\quad g(E(Y_i)) = g(\pi_i) = \beta_0 + \beta_1 X_i
$$

The GLM in R

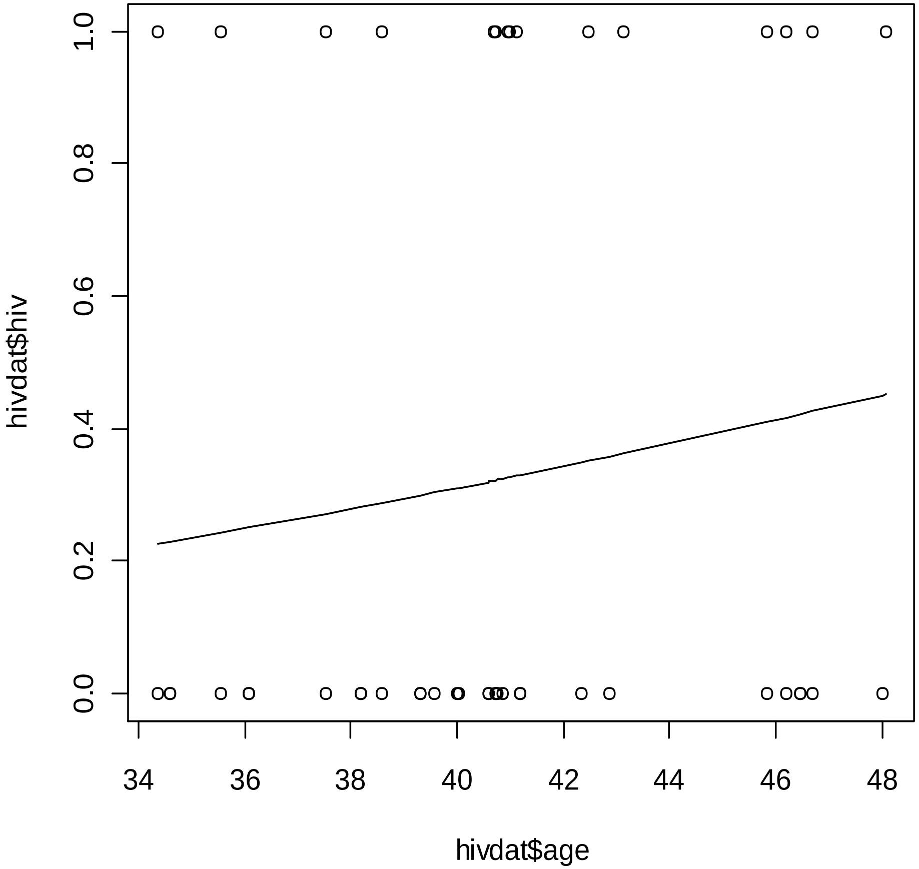
```
> hiv.fit1 <- glm(hiv ~ age, family=binomial(link = "logit"),
                data= hivdat)
> summary(hiv.fit1)

Call:
glm(formula = hiv ~ age, family = binomial(link = "logit"), data = hivdat)

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -3.79597    3.43622  -1.105    0.269
age          0.07492    0.08314   0.901    0.367

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

The data and fitted model plot

```
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -3.79597    3.43622  -1.105    0.269
age          0.07492    0.08314   0.901    0.367
```

$$g(\pi_i) = -3.79 + 0.0749 \times age_i$$

$$\pi_i = \frac{e^{-3.79+0.0749\times age_i}}{1+e^{-3.79+0.0749\times age_i}}$$



EXAMPLE 4: HIVdata

The odds ratio: point estimator

```
> exp(0.07492)
[1] 1.077798
```

How to calculate the odds ratio ?

θ=exp(β).

In our example θ=exp(0.07492)=1.07798.

As age increases by one unit the odds to be HIV positive increase by 7.8%

EXAMPLE 4: HIVdata

Example 5: toxicity example (Budworm)

Collett (1991) describes an experiment on the toxicity of the pyrethoid trans - cypermethrin to the tobacco budworm.

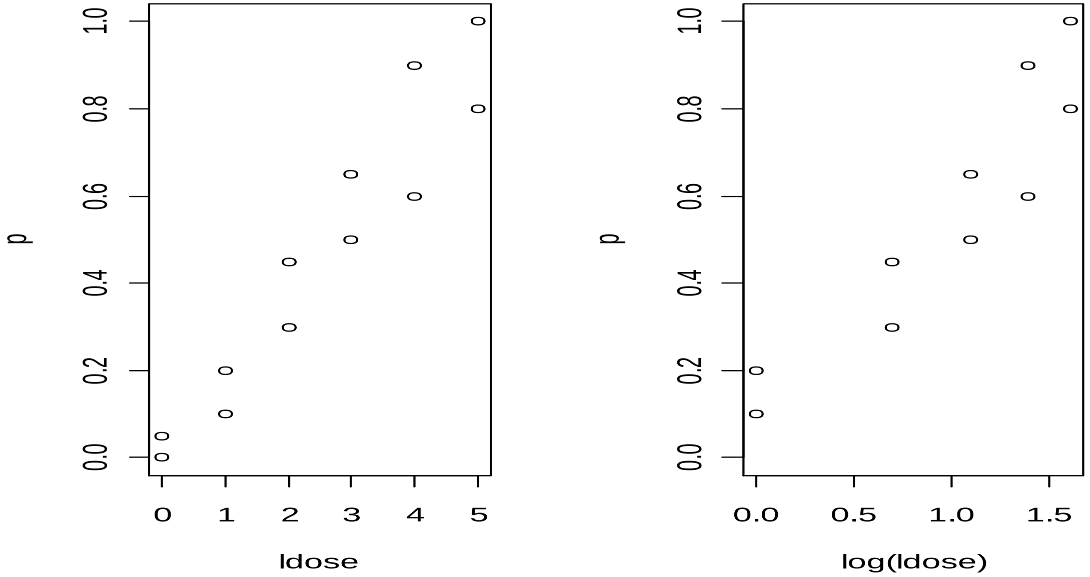
Batches of 20 moths of each sex were exposed to varying doses of the pyrethoid for three days and the number knocked out in each batch was recorded:

Sex	Dose (μ g)					
	1	2	4	8	16	32
Male	1	4	9	13	18	20
Female	0	2	6	10	12	16

Predictor: log(dose)

Data and Plot in R

```
> ldose <- rep(0:5, 2)
> numdead <- c(1, 4, 9, 13, 18, 20, 0, 2, 6, 10, 12, 16)
> sex <- factor(rep(c("M", "F"), c(6, 6)))
> SF <- cbind(numdead, numalive=20-numdead)
> p<-numdead/20
> par(mfrow=c(1,2))
> plot(p ~ ldose)
> plot(p ~ log(ldose))
```



EXAMPLE 5: toxicity

Model formulation

the expected values of

The response variable

$$E(Y_{ij}) = P(Y_{ij} = 1) = \pi_j$$

$$P(Y_{ij} = 1) = P(\text{knocked out })$$

The systematic part

$$\pi_j = f(dose \quad gender)$$

$$\eta = dose + gender + dose * gender$$

$$g(E(Y_{ij})) = g(\pi_j) = \eta$$

Model formulation

Distribution of the response

$$Y_{ij} \sim Bin(n(d_j), \pi_j)$$

$$P(Y_{ij} = 1) = P(\text{ko}) = \pi_j$$

The linear predictor

$$\eta = \beta_0 + \beta_1 G_i + \beta_2 d_{ij} + \beta_3 G_i \times d_{ij}$$

$$E(Y_{ij}) = \pi_j = \frac{e^{\beta_0 + \beta_1 G_i + \beta_2 d_{ij} + \beta_3 G_i \times d_{ij}}}{1 + e^{\beta_0 + \beta_1 G_i + \beta_2 d_{ij} + \beta_3 G_i \times d_{ij}}} = \frac{e^{\eta}}{1 + e^{\eta}}$$

$$g(E(Y_{ij})) = g(\pi_j) = \eta$$

Model with Binomial family and logit link function

Fitting the model with the glm() function:

```
> budworm.lg <- glm(SF ~ sex*ldose, family=binomial)
```

$$\eta = \beta_0 + \beta_1 G_i + \beta_2 d_{ij} + \beta_3 G_i \times d_{ij}$$

Alternative code

```
> budworm.lg <- glm(SF ~ sex+ldose+sex:ldose, family=binomial)
```

R output

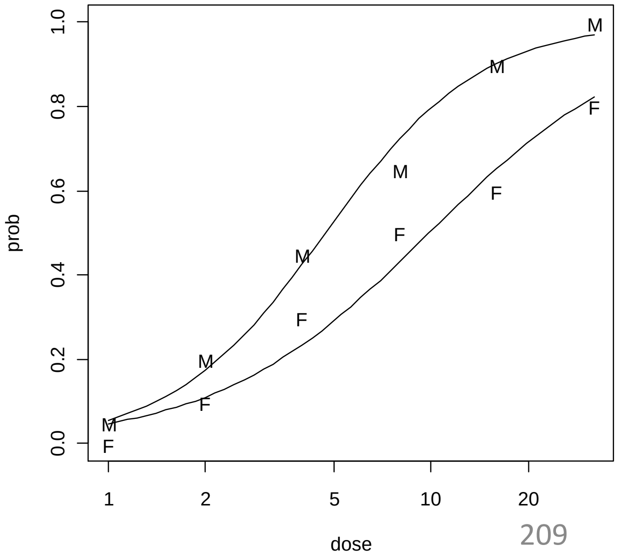
```
Call:
glm(formula = SF ~ sex * ldose, family = binomial)


Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -2.9935     0.5527  -5.416 6.09e-08 ***
sexM          0.1750     0.7783   0.225    0.822
ldose         0.9060     0.1671   5.422 5.89e-08 ***
sexM:ldose    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
```

Exp(0.906)=2.47 implies unit increase of dose increase the number of knocked out 2.47 times

EXAMPLE 5: toxicity

Plot of observed and predictive probability of death for male and female budworms

```
> plot(c(1,32), c(0,1), type = "n", xlab = "dose",
+     ylab = "prob", log = "x")
> text(2^ldose, numdead/20, as.character(sex))
> ld <- seq(0, 5, 0.1)
> lines(2^ld, predict(budworm.lg, data.frame(ldose=ld,
+   sex=factor(rep("M", length(ld)), levels=levels(sex))),
+   type = "response"))
> lines(2^ld, predict(budworm.lg, data.frame(ldose=ld,
+   sex=factor(rep("F", length(ld)), levels=levels(sex))),
+   type = "response"))
```



EXAMPLE 5: toxicity

Example 6:Heart Disease(Dipankar Bandyopadhyay, Ph.D.)

	Heart Disease		Proportion
Snoring	Yes	No	Yes
Never	24	1355	0.017
Occationally	35	603	0.055
Nearly every night	21	192	0.099
Every Night	30	224	0.118

Our outcome is heart disease, and in order to use the ordinal levels of snoring, we need to select scores.

A set (0, 2 , 4, 5) seems to capture the relative magnitude of the differences among the categories.

Data structure in R

- Data are given in table format.
- The variable count is the number of cases in each category.

```
> table(snoring,dhyes)
       dhyes
snoring    0    1
      0 1355   24
      2  603   35
      4  192   21
      5  224   30
```

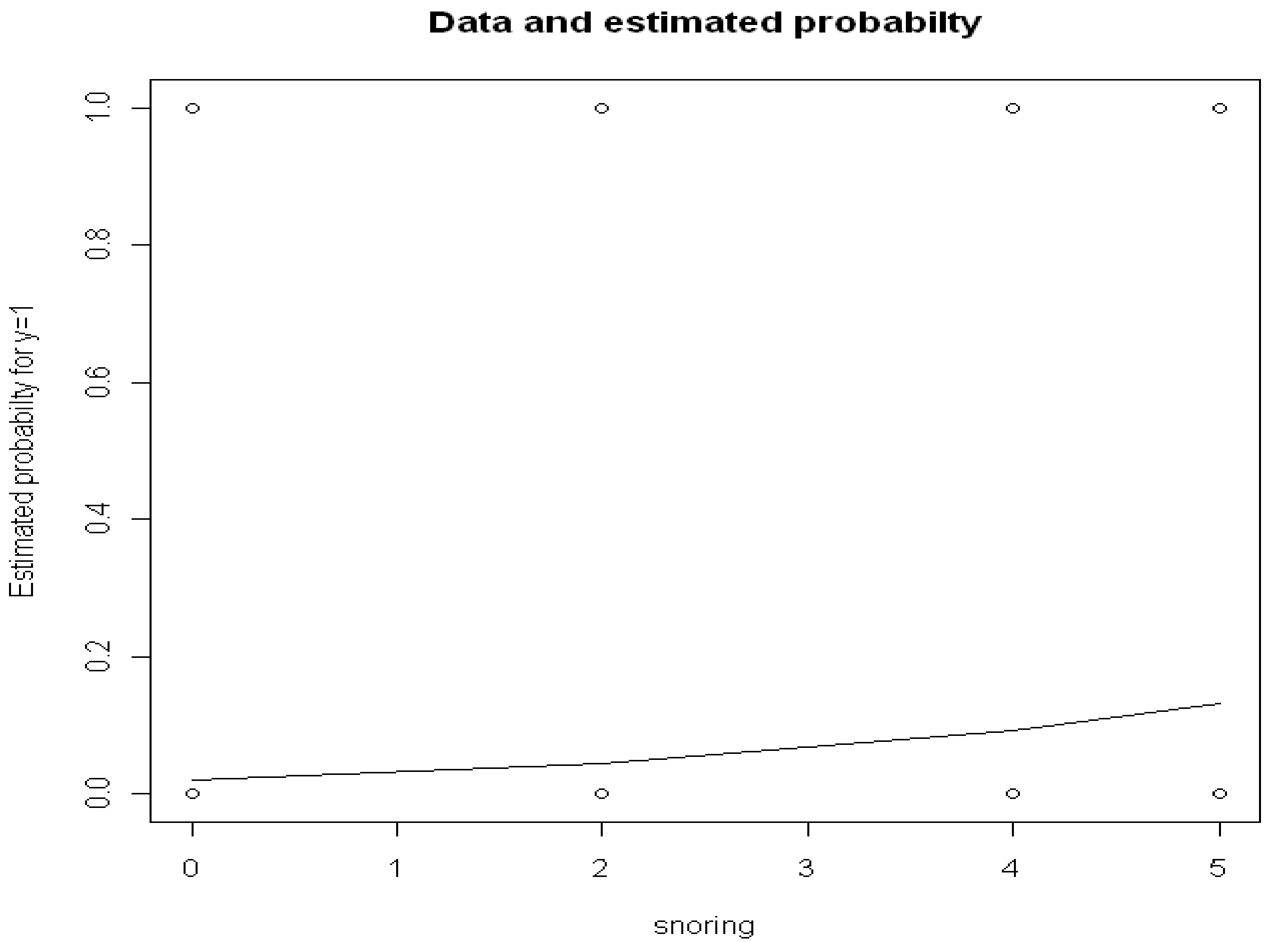
```
> fit.snoring<-glm(dhyes~as.factor(snoring),family=binomial(link="logit"))
```

The estimated model in R

```
> summary(fit.snoring)

Call:
glm(formula = dhyes ~ as.factor(snoring), family = binomial(link = "logit"))

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-0.5014  -0.3359  -0.1874  -0.1874   2.8464

Coefficients:
                   Estimate Std. Error z value Pr(>|z|)
(Intercept)         -4.0335     0.2059 -19.590  < 2e-16 ***
as.factor(snoring)2   1.1869     0.2695   4.404 1.06e-05 ***
as.factor(snoring)4   1.8205     0.3086   5.900 3.64e-09 ***
as.factor(snoring)5   2.0231     0.2832   7.144 9.06e-13 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 900.83  on 2483  degrees of freedom
Residual deviance: 834.92  on 2480  degrees of freedom
AIC: 842.92

Number of Fisher Scoring iterations: 6
```

EXAMPLE 6: heart Desease

Data and predicted probability



EXAMPLE 6: heart Desease

The estimated model in R

```
➢fit.snoringCont<-glm(dhyes~snoring,family=binomial(link="logit"))
➢summary(fit.snoringCont)

➢Call:
glm(formula = dhyes ~ snoring, family = binomial(link = "logit"))

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-0.5331  -0.3010  -0.2036  -0.2036   2.7882

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -3.86625    0.16621 -23.261  < 2e-16 ***
snoring      0.39734    0.05001   7.945 1.94e-15 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 900.83  on 2483  degrees of freedom
Residual deviance: 837.73  on 2482  degrees of freedom
AIC: 841.73

Number of Fisher Scoring iterations: 6
```

$$\log it\left(\hat{P}_i\right) = -3.87 + 0.397 \times Snoring$$

EXAMPLE 6: heart Desease

Chapter 7:
Estimation and confidence Interval

Donson: chapter 4.

Lindsey: chapter 2.

McCullagh & Nelder: chapter 4.

Estimation of model parameters

A single algorithm can be used to estimate the parameters of an exponential family using maximum likelihood.

The log-likelihood for the samples $y_1, \mathrm{y}_2, \ldots., \mathrm{y}_\mathrm{n}$ is

$$l = \sum_{i=1}^{n} \frac{y_i \theta_i - b(\theta_i)}{\phi_i} + c(y_i, \theta_i)$$

The maximum likelihood estimates are obtained by solving the score equation

$$U(\beta_j) = \frac{\partial l}{\partial \beta_j} = \sum_{i=1}^{n} \frac{y_i - \mu_i}{\phi_i V(\mu_i)} \times \frac{x_{ij}}{g'(\mu_i)} = 0$$

For parameters $\beta_{j.}$

The score function

We assume that

$$\phi_i = \frac{\phi}{a_i}$$

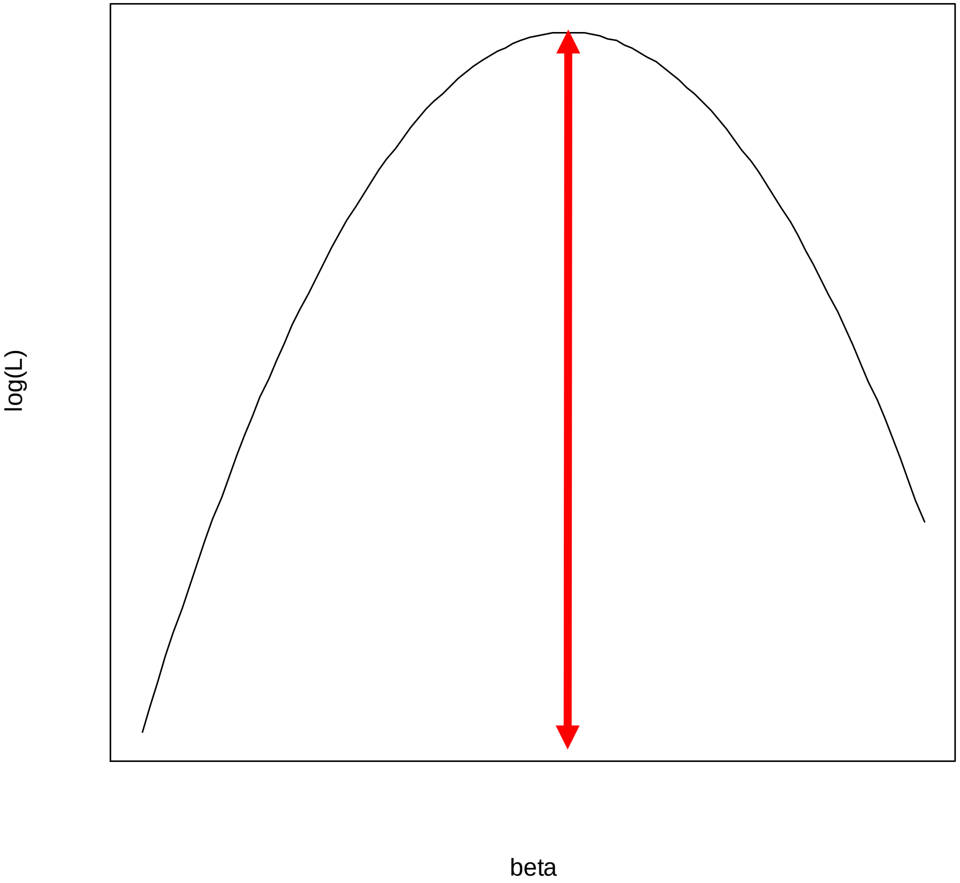
Where *ϕ* is a single dispersion parameter and a_i are known ***prior weights***; for example binomial proportions with known index n_i have *ϕ=1* and a_i=n_i

The estimating equations are then

$$\frac{\partial l}{\partial \beta_j} = \sum_{i=1}^{n} \frac{a_i (y_i - \mu_i)}{V(\mu_i)} \times \frac{x_{ij}}{g'(\mu_i)} = 0$$

Which does not depend on ϕ (which may be unknown)

The score function



At the maximum:

$$U(\beta_j) = \frac{\partial l}{\partial \beta_j} = 0$$

Example : toxicity example (Budworm)

Predictor: log(dose)

Sex	Dose (μ g)					
	1	2	4	8	16	32
Male	1	4	9	13	18	20
Female	0	2	6	10	12	16

See example 5 in Chapter 6

$$\eta = \beta_0 + \beta_1 G_i + \beta_2 d_{ij} + \beta_3 G_i \times d_{ij}$$

```
> budworm.lg <- glm(SF ~ sex+ldose+sex:ldose, family=binomial)
```

The R output

Parameter estimates:

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

Partial t-tests test the significance of each coefficient in the presence of others. Thus, only intercept and ldose were found to be significant at 5% level of significance.

Fisher scoring

The score function

$$U = \frac{d\ell}{d\beta}$$

The first derivative of the score

$$U^{'} = \frac{dU}{d\beta}$$

A general method of solving score equations is the iterative algorithm ***Fisher's Method of scoring*** (derived from a Taylor's expansion of U(**β)**)

$$\beta^{(r+1)} = \beta^{(r)} + \frac{U^{(r)}(\beta)}{U^{'(r)}(\beta)}$$

Fisher scoring

The score function

$$U = \frac{d\ell}{d\beta}$$

The expected value of the score

$$E(U) = 0$$

The variance of the score

$$Var(U) = E(U^2) - [E(U)]^2 = E(U^2)$$

$$E(U^2) = -E\left(\frac{\partial U}{\partial \beta}\right) = I(\beta)$$

Update in the rth iteration

$$\beta^{(r+1)} = \beta^{(r)} + \frac{U^{(r)}(\beta)}{I^{(r)}(\beta)}$$

Fisher scoring

With some mathematics it can be shown that

$$\beta^{(r+1)} = \left(X^{T} W^{(r)} X\right)^{-1} X^{T} W^{(r)} z^{(r)}$$

That is the score equations for a weighted least squares regression of **$\mathbf{z}^{(\mathbf{r})}$** on **X** with weights $W^{(r)}$=diag(w_i), where

$$z_i^{(r)} = \eta_i^{(r)} + \left(y_i - \mu_i^{(r)}\right) g'\left(\mu_i^{(r)}\right)$$

$$w_i^{(r)} = \frac{a_i}{V\left(\mu_i^{(r)}\right)\left(g'\left(\mu_i^{(t)}\right)\right)^2}$$

Standard errors

The estimates $\hat{\beta}$ have the usual properties of maximum likelihood estimators. In particular, $\hat{\beta}$ is asymptotically

$$N(\beta, i^{-1})$$

Where

$$i(\beta) = \phi^{-1} X^T W X$$

Standard errors for β_j may therefore be calculated as the square roots of the diagonal elements of

$$\hat{\text{cov}}(\hat{\beta}) = \phi(X^T \hat{W} X)^{-1}$$

In which $\phi(X^T \hat{W} X)^{-1}$ is a by-product of the final ***IWLS*** Iteration. If ϕ is unknown, an estimate is required.

Standard error

There are practical difficulties in estimating the dispersion *ϕ* by Maximum likelihood.

Therefore it is usually estimated by ***method of moments.*** If β was known an unbiased estimate of $\phi = \{a_i \operatorname{var}(Y)\}/v(\mu_i)$

Would be

$$\frac{1}{n}\sum_{i=1}^{n}\frac{a_i(y_i-\mu_i)^2}{V(\mu_i)}$$

Allowing for the fact that β must be estimated we obtain

$$\frac{1}{n-p}\sum_{i=1}^{n}\frac{a_i(y_i-\mu_i)^2}{V(\mu_i)}$$

R output for the toxicity example

```
Call:
glm(formula = SF ~ sex * ldose, family = binomial)

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -2.9935     0.5527  -5.416 6.09e-08 ***
sexM          0.1750     0.7783   0.225    0.822
ldose         0.9060     0.1671   5.422 5.89e-08 ***
sexM:ldose    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: the beetle data

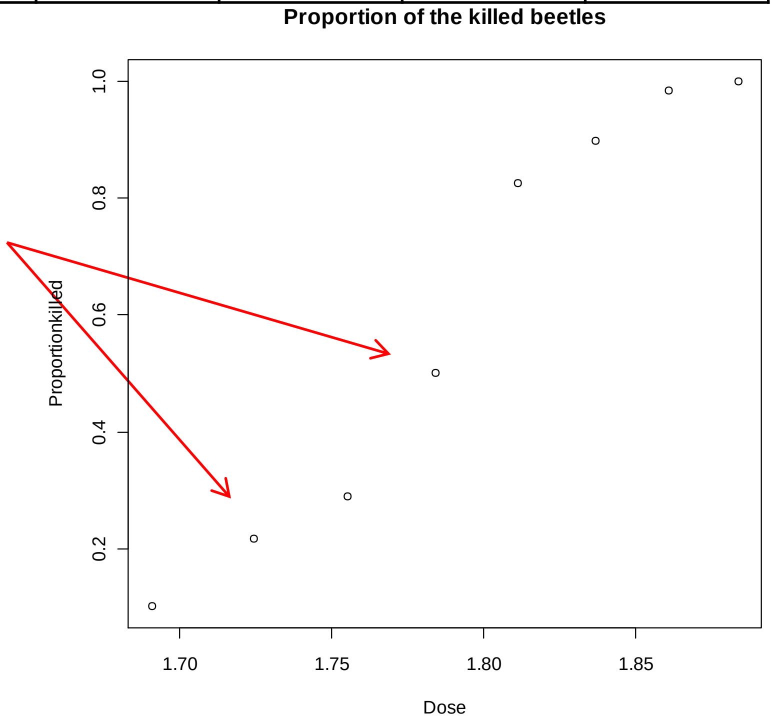
Dose	1.6907	1.7242	1.7552	1.7842	1.8113	1.8369	1.8610	1.8839
Beetles	59	60	62	56	63	59	62	60
Killed	6	13	18	28	52	53	61	60

$$Y_{ij} = \begin{cases} 1 & alive \\ 0 & killed \end{cases}$$

$$\frac{\sum Y_{ij}}{n_j}$$

$$Y_{ij} \sim B(1, \pi_{ij})$$

$$E(Y_{ij}) = P(Y_{ij} = 1) = \pi_{ij}$$



The Link function and linear predictor

The expected values of the response variable

$$E(Y_{ij}) = \pi_j$$

The systematic part

$$\pi_j = f(\beta_0 + \beta_1 d_j) = f(\eta)$$

$$\pi_j = \frac{e^{\beta_0 + \beta_1 d_j}}{1 + e^{\beta_0 + \beta_1 d_j}}$$

The logistic function to describe the mean, $E(Y_{ij})$, as a function of the linear predictor

Values between 0 and 1

$$g(E(Y_{ij})) = g(\pi_j) = \eta$$

The model in R

```
> model.conf <-glm(cbind(killed,unkilled)~Dose, family=binomial("cloglog"),
                   data=beetle)
```

```
> summary(model.conf)

Call:
glm(formula = cbind(killed, unkilled) ~ Dose, family = binomial("cloglog"),
    data = beetle)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-0.80329  -0.55135   0.03089   0.38315   1.28883

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -39.572      3.240  -12.21   <2e-16 ***
Dose          22.041      1.799   12.25   <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: 284.2024  on 7  degrees of freedom
Residual deviance:   3.4464  on 6  degrees of freedom
AIC: 33.644

Number of Fisher Scoring iterations: 4
```

Confidence interval

- A (1-α)100% confidence interval for the parameter of the model can be defined as:

$$(\beta_i \pm Z_{\alpha/2} \times se(\beta_i))$$

```
> C.I<-c(model.conf$coeff[2]-1.96*1.799,model.conf$coeff[2]+1.96*1.799)

> C.I
    Dose     Dose 
18.51513 25.56721 
```

95% C.I for the slope.

$$\exp\{\beta_i \pm Z_{\alpha/2} \times se(\beta_i)\}$$

Confidence interval in R

Confidence interval in R can be defined using the formula:

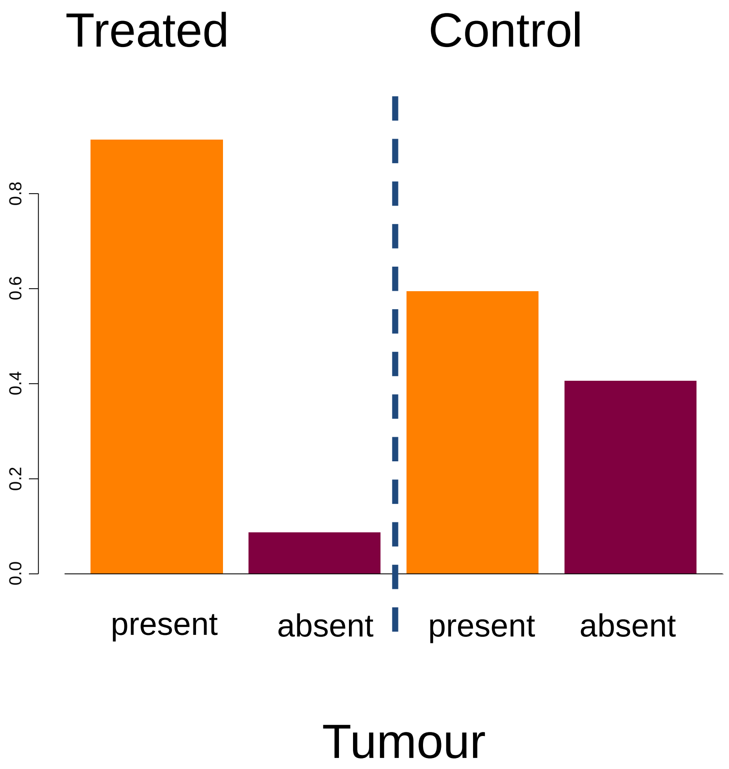
```
> confint(object, parm, level = 0.95, ...)
```

If the parm option is missed, then R will compute confidence interval for all parameters in the model.

```
>library(MASS)

> model.conf <-glm(cbind(killed,unkilled)~Dose, family=binomial("cloglog"), data=beetle)

> confint(model.conf, level=0.95)
Waiting for profiling to be done...
            2.5 %    97.5 %
(Intercept) -46.2037 -33.53869
Dose        18.6903  25.72251
```

Example : mice data

	Tumour present	Tumour absent	Total
Treated	21	2	23
Contol	19	13	32
Total	20	15	55



Model formulation

	Tumour present	Tumour absent	Total
Treated	21	2	23
Contol	19	13	32
Total	20	15	55

We want to model the probability to develop a tumour given the treatment group.

The individual data

$$Z_i = \begin{cases} 1 & tumour \quad present \\ 0 & tumour \quad absent \end{cases}$$

Number of subjects with tumour

$$Y_i = \sum Z_i$$

Distribution of Y

$$Y_i \sim B(n_i \,, \quad P_i)$$

The model for P- logit transformation

$$\log it(P) = \beta_0 + \beta_j$$

How do we interpreat the parameters ?

```
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -2.3514     0.7400  -3.177  0.00149 **
trti2         1.9719     0.8229   2.396  0.01656 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

The parameter estimate for the effect of the control group is -2.3514. The parameter estimate for the effect of the treatment group (the smoked group) is equal to 1.9719.

Example : mice data

```
> library(MASS)
>fit.mice<-glm(resp~trti,family=binomial(link = "logit"))

> confint(fit.mice, level=0.95)
Waiting for profiling to be done...
                  2.5 %    97.5 %
(Intercept) -4.1843896 -1.125530
trti2        0.5295788  3.909658
```

Interpretation

The odds ratio, θ, is equal to exp(1.9719)=7.18. If θ > 1 than the odds for a tumour in the control group is smaller than the odds for a tumour in the treatment group.

```
> exp(1.9719)
[1] 7.184314
```

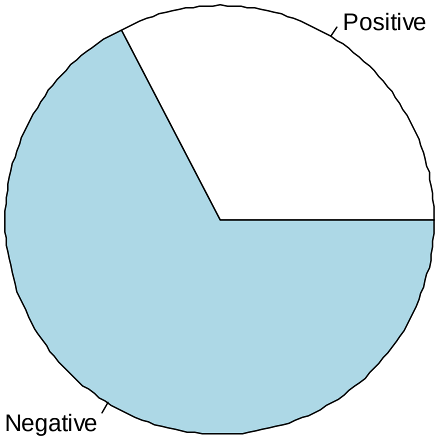
95% C.I for the odds ratio:

```
> exp(confint(fit.mice, level=0.95))
Waiting for profiling to be done...
                2.5 %     97.5 %
(Intercept) 0.0152315  0.3244804
trti2       1.6982169 49.8818870
```

Example 4: HIV data

- Consider the HIV data set and the model for HIV (the outcome variable, yes/no or 1/0).
- Covariates:
- age group (also coded 1/0).
- Age group was coded 1 for people younger than 40.7 years
- Age

- Response: HIV status (32.6% are positive).

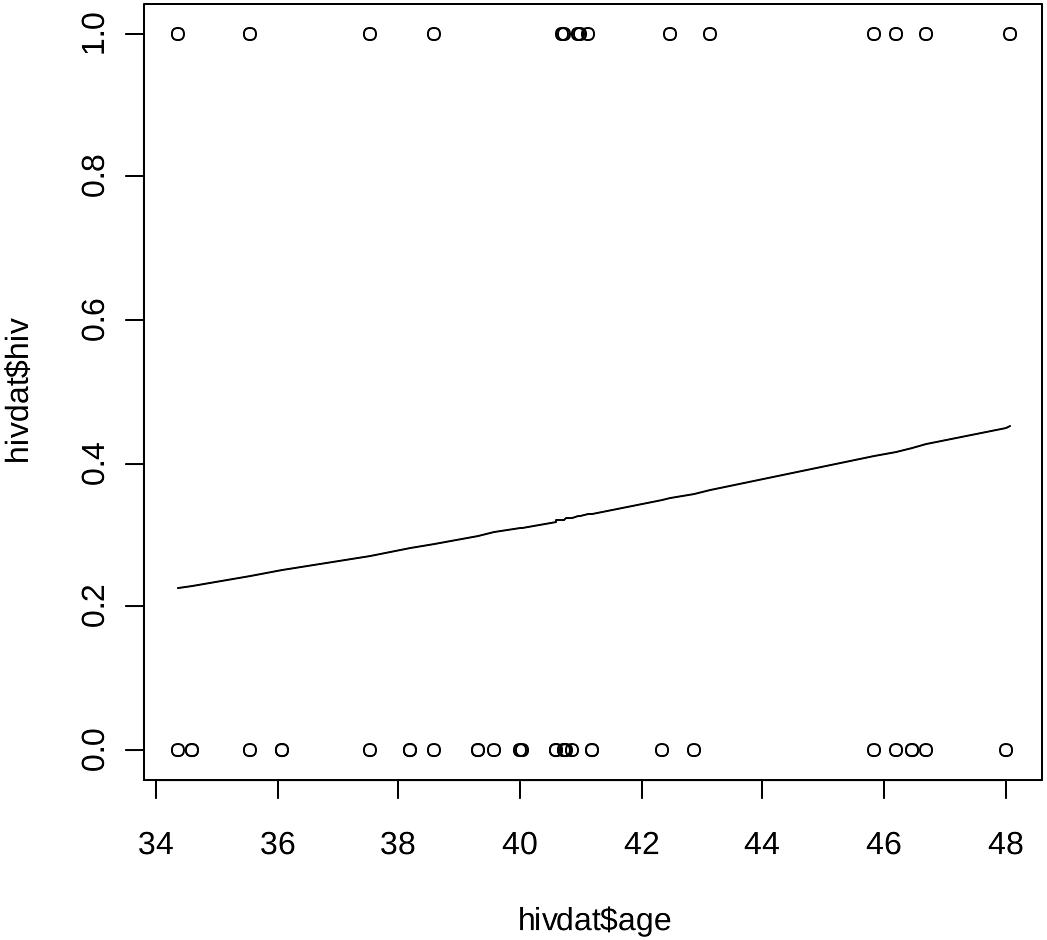


Example 3: HIV data

```
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -3.79597    3.43622  -1.105    0.269
age          0.07492    0.08314   0.901    0.367
```

$$g(\pi_i) = -3.79 + 0.0749 \times age_i$$

$$\pi_i = \frac{e^{-3.79+0.0749\times age_i}}{1+e^{-3.79+0.0749\times age_i}}$$



95% C.I for the parameter estimates

```
> confint(hiv.fit1 , level=0.95)
Waiting for profiling to be done...
                 2.5 %    97.5 %
(Intercept) -10.86100806 2.8239564
age         -0.08678935 0.2445192
```

95% C.I for the odds ratio

```
> exp(confint(hiv.fit1, level=0.95))
Waiting for profiling to be done...
                   2.5 %    97.5 %
(Intercept) 1.919217e-05 16.843358
age         9.168702e-01  1.277007
```

$$\exp\{\beta_i \pm Z_{\alpha/2} \times se(\beta_i)\}$$

Chapter 8
Inference

Donson: chapter 5.

Lindsey: chapter 9.

McCullagh & Nelder: chapter 3.

Inference

$$\eta_i = \beta_0 + \beta_1 x_{1i} + \beta_2 x_{2i} + \ldots + \beta_p x_{pi}$$

$$H_0 : \beta_j = 0$$

$$H_0 : \beta_j \neq 0$$

We can test the above hypothesis using:

1. Wald test
2. Likelihood ratio test

Wald Test

Asymptotic distribution of the ML estimator

$$\hat{\beta} \sim N(\beta, \phi(X'WX)^{-1})$$

We wish to test the null hypothesis

$$H_o : \beta_j = 0 \qquad versus \qquad H_1 : \beta_j \neq 0$$

Test statistic

$$Z_j = \frac{\hat{\beta}_j}{\sqrt{\phi(X'\hat{W}X)_{jj}^{-1}}} \quad , \quad Z_j \sim N(0,1)$$

Which is asymptotically N(0,1) under H_o

Example : toxicity example (Budworm)

Predictor: log(dose)

Sex	Dose (μ g)					
	1	2	4	8	16	32
Male	1	4	9	13	18	20
Female	0	2	6	10	12	16

See example 5 in Chapter 6

$$\eta = \beta_0 + \beta_1 G_i + \beta_2 d_{ij} + \beta_3 G_i \times d_{ij}$$

```
> budworm.lg <- glm(SF ~ sex+ldose+sex:ldose, family=binomial)
```

Variance/covariance matrix of the estimates in R (for the toxicity example)

Variance covariance matrix for the parameter estimates

$$V = \phi(X'WX)^{-1}$$

```
> summary(budworm.lg)$cov.unscaled
            (Intercept)       sexM        ldose  sexM:ldose
(Intercept)   0.3054769 -0.3054769 -0.08394089  0.08394089
sexM         -0.3054769  0.6057665  0.08394089 -0.18661802
ldose        -0.0839409  0.0839409  0.02792296 -0.02792296
sexM:ldose    0.0839409 -0.1866180 -0.02792296  0.07289473
```

Variance/covariance matrix

- The variance can be written in terms of μ and the canonical link function g as:

$$\mathrm{var}(y) = a g'^{-1}(\mu)$$

- The variance matrix

$$\mathrm{var}(y) = V$$

- Fixed effect models assumes that the observations are uncorrelated, therefore the variance matrix is diagonal.

- Diagonal terms=variances of each parameter

Wald test in R (toxicity example)

```
Call:
glm(formula = SF ~ sex * ldose, family = binomial)


Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -2.9935     0.5527  -5.416 6.09e-08 ***
sexM          0.1750     0.7783   0.225    0.822
ldose         0.9060     0.1671   5.422 5.89e-08 ***
sexM:ldose    0.3529     0.2700   1.307    0.191
---
```

The likelihood ratio statistic

Consider two models:

The model with the maximum number of parameters that can be estimated: the saturated model.
The model of interest with k parameters.

The likelihood ratio:

$$\lambda = \frac{L(\hat{\beta}_{\max})}{L(\hat{\beta})}$$

The likelihood ratio statistic

The likelihood ratio provides a goodness to fit of the model of interest.

Log likelihood ratio

$$\log(\lambda) = \ell(\hat{\beta}_{\max}; y) - \ell(\hat{\beta}; y)$$

Large value of log(λ) indicates a poor fit.

The deviance

2Log likelihood ratio

$$D = 2\log(\lambda) = 2\left\lfloor \ell(\hat{\beta}_{\max}; y) - \ell(\hat{\beta}; y) \right\rfloor$$

Large value of deviance indicates a poor fit.

The deviance

Let us assume that we have two models: M1 and M2.

Deviance of M1:

$$D_{M1} = 2\log(\lambda) = 2\left\lfloor \ell(\hat{\beta}_{\max}; y) - \ell(\hat{\beta}_{M1}; y) \right\rfloor$$

Deviance of M2:

$$D_{M2} = 2\log(\lambda) = 2\left\lfloor \ell(\hat{\beta}_{\max}; y) - \ell(\hat{\beta}_{M2}; y) \right\rfloor$$

The deviance

The difference between the deviance of M1 and M2:

$$\Delta D = D_{M1} - D_{M2} = 2\left[\ell(\hat{\beta}_{\max}; y) - \ell(\hat{\beta}_{M1}; y)\right] - 2\left[\ell(\hat{\beta}_{\max}; y) - \ell(\hat{\beta}_{M2}; y)\right]$$

$$\Delta D = D_{M1} - D_{M2} = 2\left[\ell(\hat{\beta}_{M1}; y) - \ell(\hat{\beta}_{M2}; y)\right]$$

Likelihood ratio test

Consider two model with the following linear predictors:

$$\underbrace{\eta = \beta_0 + \beta_1 G_i + \beta_2 d_{ij}}_{\text{Full model}} \qquad \underbrace{\eta = \beta_0 + \beta_2 d_{ij}}_{\text{Redcued model}}$$

$$H_0 : \beta_1 = 0$$

$$H_0 : \beta_1 \neq 0$$

Model formulation

Model 1 → $\eta = \beta_0 + \beta_1 \times \log(dose)$

Model 2 → $\eta = \beta_0 + \beta_1 \times sex + \beta_2 \times \log(dose)$

Model 3 → $\eta = \beta_0 + \beta_1 \times sex + \beta_2 \times \log(dose) + \beta_3 \times sex \times \log(dose)$

Model 1 in R

```
> budworm.lg1 <- glm(SF ~ ldose, family=binomial)
> summary(budworm.lg1)
Call:
glm(formula = SF ~ ldose, family = binomial)
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.7989  -0.8267  -0.1871   0.8950   1.9850
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -2.7661     0.3701  -7.473 7.82e-14 ***
ldose        1.0068     0.1236   8.147 3.74e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 124.876  on 11  degrees of freedom
Residual deviance:  16.984  on 10  degrees of freedom
AIC: 51.094
```

Model 2 in R

```
> budworm.lg2 <- glm(SF ~ sex + ldose, family=binomial)
> summary(budworm.lg2)
Call:
glm(formula = SF ~ sex + ldose, 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 ***
sexM          1.1007     0.3558   3.093  0.00198 **
ldose         1.0642     0.1311   8.119 4.70e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 124.876  on 11  degrees of freedom
Residual deviance:   6.757  on  9  degrees of freedom
AIC: 42.867

Number of Fisher Scoring iterations: 4
```

The likelihood ratio test in R

```
> anova(budworm.lg1,budworm.lg2)
Analysis of Deviance Table

Model 1: SF ~ ldose
Model 2: SF ~ sex + ldose
  Resid. Df Resid. Dev Df Deviance
1        10    16.9840
2         9     6.7571  1   10.227
```

The likelihood ratio test

The difference between the deviance of M1 and M2:

$$\Delta D = D_{M1} - D_{M2} = 2\left\lfloor \ell(\hat{\beta}_{M1}; y) - \ell(\hat{\beta}_{M2}; y) \right\rfloor$$

Under the null hypothesis:

$$\Delta D = D_{M1} - D_{M2} \sim \chi^2_{(p-q)}$$

The likelihood ratio test in R

```
> anova.glm(budworm.lg1,budworm.lg2,test="Chisq")
Analysis of Deviance Table

Model 1: SF ~ ldose
Model 2: SF ~ sex + ldose
  Resid. Df Resid. Dev Df Deviance P(>|Chi|)
1        10    16.9840
2         9     6.7571  1   10.227  0.001384 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Model formulation

Model 1 → $\eta = \beta_0 + \beta_1 \times \log(dose)$

Model 2 → $\eta = \beta_0 + \beta_1 \times sex + \beta_2 \times \log(dose)$

Model 3 → $\eta = \beta_0 + \beta_1 \times sex + \beta_2 \times \log(dose) + \beta_3 \times sex \times \log(dose)$

Model 3 in R

```
> budworm.lg3<- glm(SF ~ sex*ldose, family=binomial)
> summary(budworm.lg3)
Call:
glm(formula = SF ~ sex * ldose, family = binomial)
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 ***
sexM          0.1750     0.7783   0.225    0.822
ldose         0.9060     0.1671   5.422 5.89e-08 ***
sexM:ldose    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
```

Likelihood ratio test

$$\eta = \beta_0 + \beta_1 sex + \beta_2 \log(d)$$

$$\eta = \beta_0 + \beta_1 sex + \beta_2 \log(d) + \boxed{\beta_3 sex \log(d)}$$

$$H_0 : \beta_3 = 0$$

$$H_1 : \beta_3 \neq 0$$

Model 2 versus model 3

```
> anova.glm(budworm.lg2,budworm.lg3,test="Chisq")
Analysis of Deviance Table

Model 1: SF ~ sex + ldose
Model 2: SF ~ sex * ldose
  Resid. Df Resid. Dev Df Deviance P(>|Chi|)
1        9     6.7571
2        8     4.9937  1   1.7633    0.1842
```

We cannot reject the null hypothesis

ANOVA() in R

```
> anova.glm(budworm.lg1,budworm.lg2,budworm.lg3,test="Chisq")



Analysis of Deviance Table

Model 1: SF ~ ldose
Model 2: SF ~ sex + ldose
Model 3: SF ~ sex * ldose
  Resid. Df Resid. Dev Df Deviance P(>|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
```

The update() function in R

- The update () function in R can be used to modify a fitted model by dropping some of the terms.

- The general formulation of the function is given as:

Update(old model, ~, . - or + the term we want to drop/ad)

The update() function in R: example

We would like to drop the interaction term of model 3:

$$\eta = \beta_0 + \beta_1 \times sex + \beta_2 \times \log(d) + \boxed{\beta_3 \times sex \times \log(d)}$$

```
updatefit<-update(budworm.lg3,~. -sex:ldose)
```

The original model

The update() function in R: example

$$\eta = \beta_0 + \beta_1 \times sex + \beta_2 \times \log(d) + \beta_3 \times sex \times \log(d) \Rightarrow \eta = \beta_0 + \beta_1 \times sex + \beta_2 \times \log(d)$$

```
> summary(updatefit)
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -3.4732     0.4685  -7.413 1.23e-13 ***
sexM          1.1007     0.3558   3.093  0.00198 **
ldose         1.0642     0.1311   8.119 4.70e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
(Dispersion parameter for binomial family taken to be 1)
    Null deviance: 124.876  on 11  degrees of freedom
Residual deviance:   6.757  on  9  degrees of freedom
AIC: 42.867

Number of Fisher Scoring iterations: 4
```

Chapter 9:
Model Selection

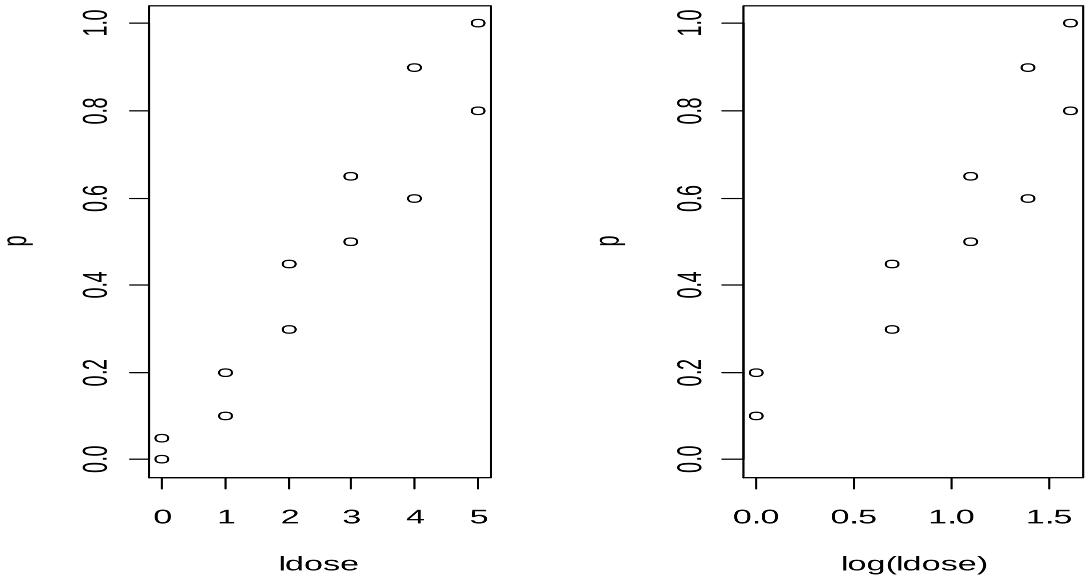
Donson: chapter 4.

Lindsey: chapter 3 (3.3.2 + A.1.4).

McCullagh & Nelder: chapter 2.

Example 1: Budworm Data and Plot in R

```
> ldose <- rep(0:5, 2)
> numdead <- c(1, 4, 9, 13, 18, 20, 0, 2, 6, 10, 12, 16)
> sex <- factor(rep(c("M", "F"), c(6, 6)))
> SF <- cbind(numdead, numalive=20-numdead)
> p<-numdead/20
> par(mfrow=c(1,2))
> plot(p ~ ldose)
> plot(p ~ log(ldose))
```



Example 1: model formulation

Model 1 →

$$\eta = \beta_0 + \beta_1 \times \log(d)$$

2 parameters

Model 2 →

$$\eta = \beta_0 + \beta_1 \times sex + \beta_2 \times \log(d)$$

3 parameters

Model 3 →

$$\eta = \beta_0 + \beta_1 \times sex + \beta_2 \times \log(d) + \beta 3 \times sex \times \log(d)$$

4 parameters

Example of three nested models.

Deviance

The deviance of a model is defined as

$$D = 2\phi(l_{sat} - l_{\mathrm{mod}})$$

Where l_{mod} is the log-likelihood of the fitted model and l_{sat} is the log-likelihood of the ***saturated model.***

In the saturated model, the number of parameters is equal to the number of observations, so

$$\hat{y} = y$$

For linear regression with Normal data, the deviance is equal to the residual sum of squares

Likelihood and the number of parameters

```
> budworm.lg1 <- glm(SF ~ ldose, family=binomial)
> budworm.lg2 <- glm(SF ~ sex + ldose, family=binomial)
> budworm.lg3<- glm(SF ~ sex*ldose, family=binomial)
>
> >
> logLik(budworm.lg1)
'log Lik.' -23.54722 (df=2)
> logLik(budworm.lg2)
'log Lik.' -18.43373 (df=3)
> logLik(budworm.lg3)
'log Lik.' -17.55206 (df=4)
```

-log(L) increases as the number of parameters increases.

Deviance and the number of parameters

```
> budworm.lg1$null.deviance
[1] 124.8756
> budworm.lg1$deviance
[1] 16.98403
> budworm.lg2$null.deviance
[1] 124.8756
> budworm.lg2$deviance
[1] 6.757064
> budworm.lg3$null.deviance
[1] 124.8756
> budworm.lg3$deviance
[1] 4.993727
```

Deviance decreases as the number of parameters increases.

Akaike Information Criterion (AIC)

- The Akaike information criterion (AIC) defines as:

$$AIC = -2\log(likelihood) + 2.p$$

- The model with minimal AIC tries to find an optimal compromise between model fit and model complexity.

- The R function stepAIC() of the package MASS provides such a functionality.

- The direction option specifies the strategy.

Goodness-of-fit and model complexity

$$AIC = -\underbrace{2\log(likelihood)}_{\text{Goodness-of-fit}} + \underbrace{2.p}_{\text{Complexity}}$$

```
> extractAIC(budworm.lg1, k=2)
[1]  2.00000 51.09443
> extractAIC(budworm.lg2, k=2)
[1]  3.00000 42.86747
> extractAIC(budworm.lg3, k=2)
[1]  4.00000 43.10413
```

Goodness-of-fit and model complexity

```
> summary(budworm.lg3)

Call:
glm(formula = SF ~ sex * ldose, family = binomial)
AIC: 43.104


> library(MASS)
> stepAIC(budworm.lg3, direction = "backward")
Start:  AIC=43.1
SF ~ sex * ldose
```

Starting point

```
           Df Deviance    AIC
- sex:ldose  1   6.7571 42.867
<none>           4.9937 43.104

Step:  AIC=42.87
SF ~ sex + ldose
```

In the first step the interaction is dropped

```
        Df Deviance     AIC
<none>         6.757  42.867
- sex    1   16.984  51.094
- ldose  1  118.799 152.909

Call:  glm(formula = SF ~ sex + ldose, family = binomial)

Coefficients:
(Intercept)        sexM       ldose
    -3.473        1.101       1.064
```

Final model

```
Degrees of Freedom: 11 Total (i.e. Null);  9 Residual
Null Deviance:      124.9
Residual Deviance: 6.757       AIC: 42.87
```

Model selection

- The basic idea of the procedure is to start from a given model (null model) and take a series of steps by either deleting or adding a term in the model from a list of candidates for inclusion, called the *scope* of the search and defined by a model formula.

The criteria seen before will be used in model selection

which involves

  - choice of distribution and link function
  - covariate(s) to include in the model

Example 2: data and model formulation

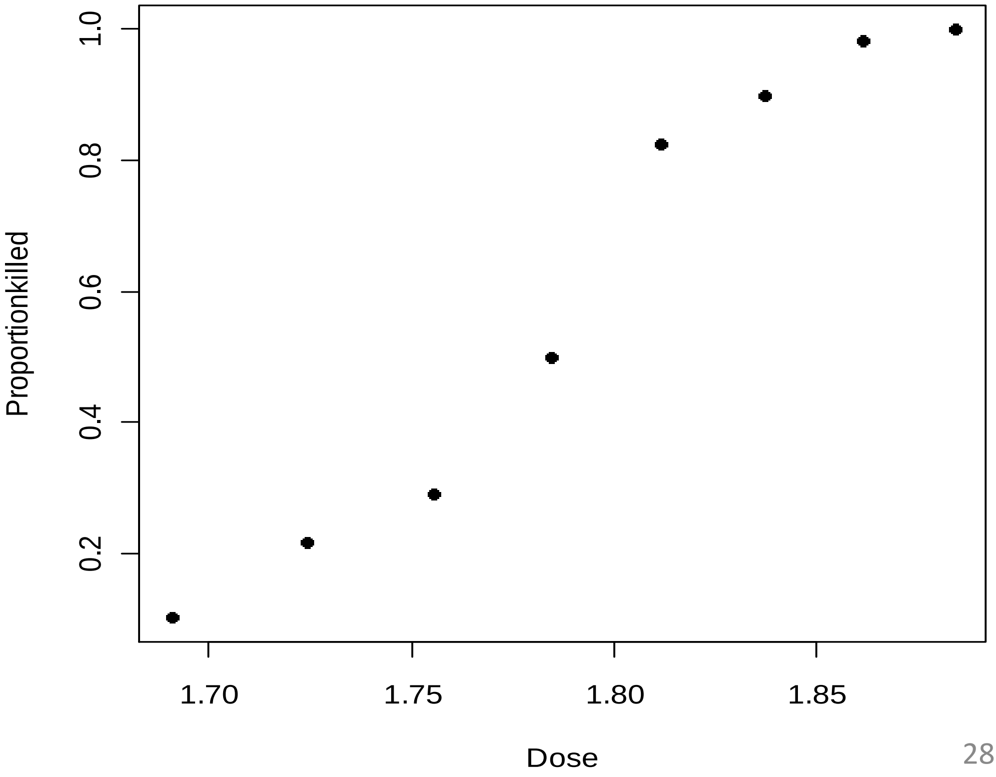
```
beetle<-read.table("C:......./beetle.txt", header = TRUE)
attach(beetle)
Proportionkilled<-killed/beetles
plot(Proportionkilled~Dose, main="Proportion of the killed beetles")
```

$$Y_i \sim Bin(\pi(d_i), n_i)$$

$$g(\pi(d_i)) = \beta_0 + \beta_1 d_i$$

g is the link function:

- logit.
- probit.
- cloglog.



Model with logit link

$$g(\pi_i) = \log(\frac{\pi_i}{1-\pi_i}) = \beta_0 + \beta_1 d_i$$

Where

$$\pi_i = \frac{\exp(\beta_0 + \beta_1 d_i)}{1 + \exp(\beta_0 + \beta_1 d_i)}$$

Model 1: binomial with logit link

```
> t1 <-glm(cbind(killed,unkilled)~Dose, family=binomial("logit"))
➢    summary(t1)
➢    Call:
glm(formula = cbind(killed, unkilled) ~ Dose, family = binomial("logit"))

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.5941  -0.3944   0.8329   1.2592   1.5940

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -60.717      5.181  -11.72   <2e-16 ***
Dose          34.270      2.912   11.77   <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: 284.202  on 7  degrees of freedom
Residual deviance:  11.232  on 6  degrees of freedom
AIC: 41.43
Number of Fisher Scoring iterations: 4
```

Model with probit link

$$\Phi^{-1}(\pi_i) = \beta_0 + \beta_1 d_i$$

Where

$$\Phi = \int_{-\infty}^{\beta_0 + \beta d_i} \frac{1}{\sqrt{2\pi}} \exp(-\frac{1}{2} z^2) dz$$

Model2: with probit link

```
> t2 <-glm(cbind(killed,unkilled)~Dose, family=binomial("probit"))
> summary(t2)
Call:
glm(formula = cbind(killed, unkilled) ~ Dose, family = binomial("probit"))

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.5714  -0.4703   0.7501   1.0632   1.3449
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -34.935      2.648  -13.19   <2e-16 ***
Dose          19.728      1.487   13.27   <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: 284.202  on 7  degrees of freedom
Residual deviance:  10.120  on 6  degrees of freedom
AIC: 40.318

Number of Fisher Scoring iterations: 4
```

Model with c-log-log link

$$g(\pi_i) = \log(-\log(1-\pi_i)) = \beta_0 + \beta_1 d_i$$

Where

$$\pi_i = 1 - e^{-(\beta_0 + \beta d_i)}$$

$$1-\pi_i = e^{-e^{(\beta_0+\beta d_i)}}$$

$$\log(1-\pi_i) = -e^{(\beta_0+\beta d_i)}$$

$$\log(-\log(1-\pi_i)) = \log(e^{(\beta_0+\beta d_i)}) = \beta_0 + \beta d_i$$

Model 3: with cloglog link

```
> t3 <-glm(cbind(killed,unkilled)~Dose, family=binomial("cloglog"))
> summary(t3)

Call:
glm(formula = cbind(killed, unkilled) ~ Dose, family = binomial("cloglog"))

Deviance Residuals:
    Min       1Q    Median      3Q      Max
-0.80329  -0.55135   0.03089   0.38315   1.28883

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -39.572      3.240  -12.21   <2e-16 ***
Dose          22.041      1.799   12.25   <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: 284.2024  on 7  degrees of freedom
Residual deviance:   3.4464  on 6  degrees of freedom
AIC: 33.644

Number of Fisher Scoring iterations: 4
```

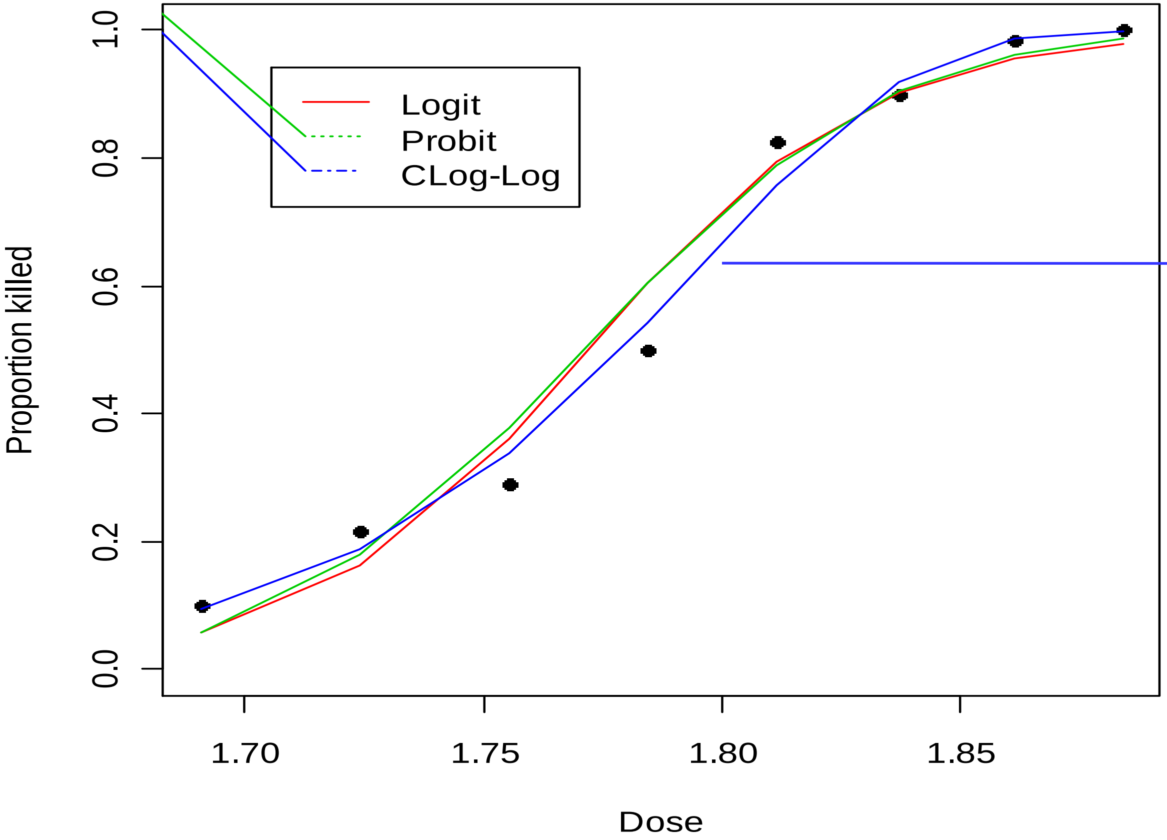
Model selection based on AIC

- Selection of terms for deletion or inclusion is based on Akaike's information criterion (AIC).
- In R, the function “extractAIC(model) will give AIC .

Model	Likelihood	No parameters	AIC
Logit	-18.71513	2	41.43
Probit	-18.15890	2	40.318
Clolog	-14.82224	2	33.44

- According to the AIC criteria, the model with cloglog link function will be chosen as a good model.

Plot of the estimated models



Best model

```
> extractAIC(t1, k=2)
[1]  2.00000 41.43027
> extractAIC(t2, k=2)
[1]  2.0000 40.3178
> extractAIC(t3, k=2)
[1]  2.00000 33.64448
```

Chapter 10:
Model diagnostic

```
> library(boot)
> library(graphics)
```

Donson: chapter 7.

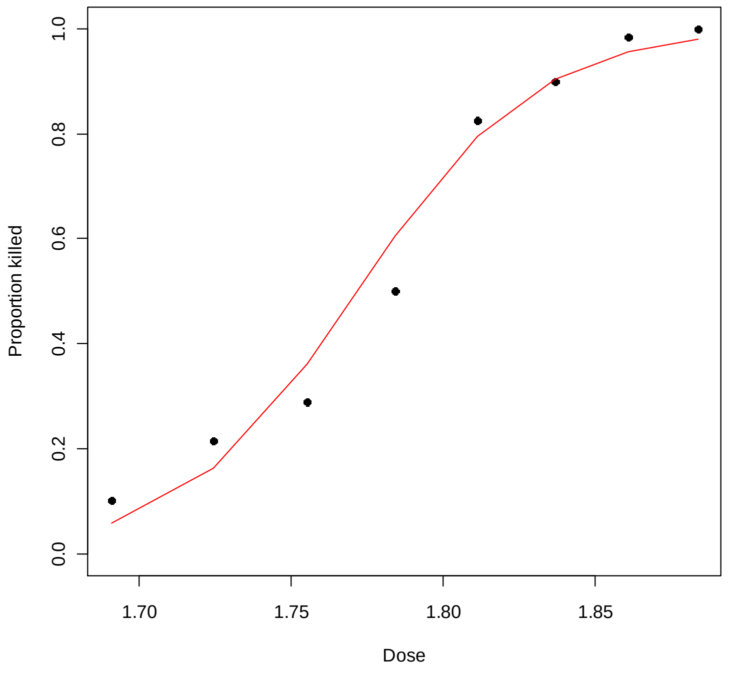
Lindsey: Appendix B.

McCullagh & Nelder: chapter 2.

Example 1: the beetle example

Consider beetle example with the logit model

$$g(\pi_i) = \log(\frac{\pi_i}{1-\pi_i}) = \beta_0 + \beta_1 d_i$$



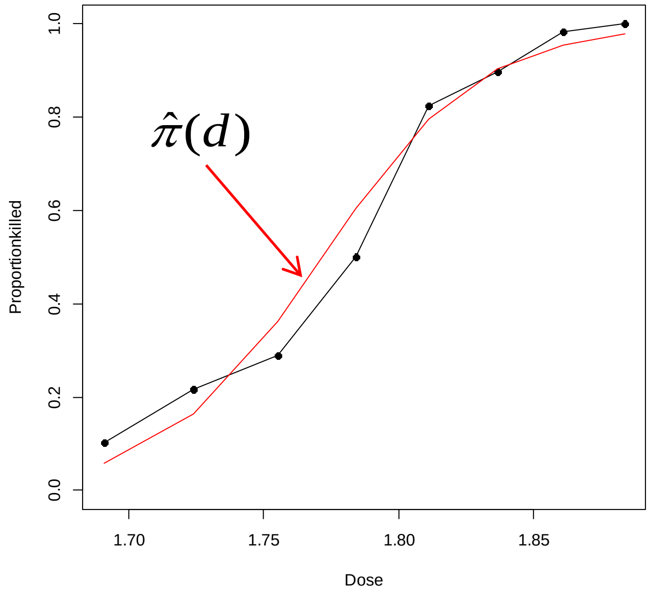
Example 1: the beetle example in R

```
> t1 <-glm(cbind(killed,unkilled)~Dose, family=binomial("logit"))
```

```
> summary(t1)

Call:
glm(formula = cbind(killed, unkilled) ~ Dose, family = binomial("logit"))

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.5941  -0.3944   0.8329   1.2592   1.5940

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -60.717      5.181  -11.72   <2e-16 ***
Dose          34.270      2.912   11.77   <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: 284.202  on 7  degrees of freedom
Residual deviance:  11.232  on 6  degrees of freedom
AIC: 41.43
```

$$\hat{\beta}_0 = -60.71$$

$$\hat{\beta}_1 = 34.27$$



Residual Analysis

Several kinds of residuals can be defined for GLMs:

- ***Raw response:*** $R_i = y_i - \hat{\mu}_i$
- ***working:*** from the working response in the IWLS algorithm
- ***Pearson***

$$r_i^{\ P} = \frac{y_i - \hat{\mu}_i}{\sqrt{V(\hat{\mu}_i)}}$$

- Such that $\sum_i (r_i^{\ P})^2$ equals the generalized Pearson statistic
- ***deviance :*** $r_i^{\ D}$ such that $\sum_i (r_i^{\ P})^2$ equals the deviance.

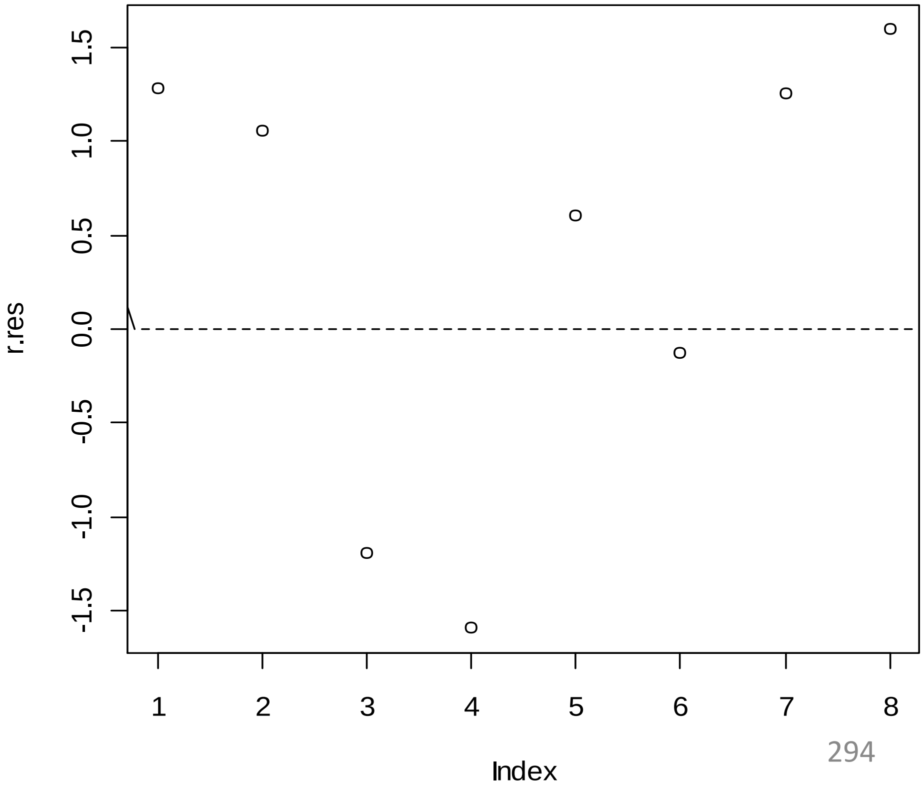
These definitions are all equivalent for Normal models

Raw residuals in R

The raw residual is defined as:

$$r_i = y_i - \hat{\mu}_i$$

```
library(boot)
library(graphics)
r.res<-resid(t1)
par(mfrow=c(2,2))
plot(r.res)
abline(h=0, lty=2)
```



For binary data, these residuals are not really informative

why not ?

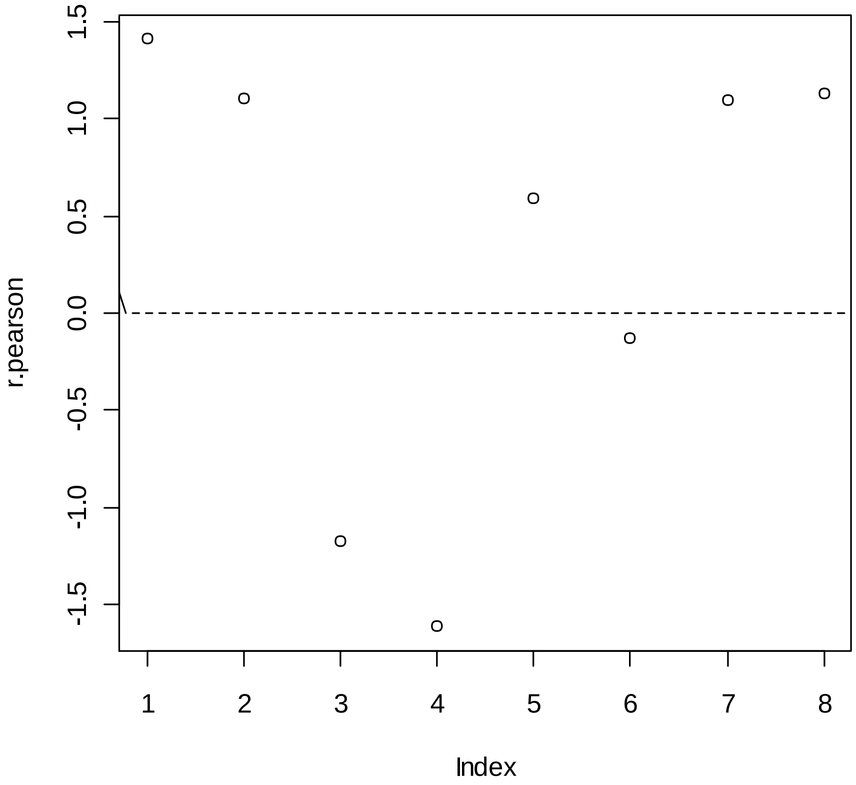
Pearson residual in R

Pearson residual :

$$r_i^{\,P} = \frac{y_i - \hat{\mu}_i}{\sqrt{V(\hat{\mu}_i)}}$$

$$\sum_i (r_i^{\,P})^2$$

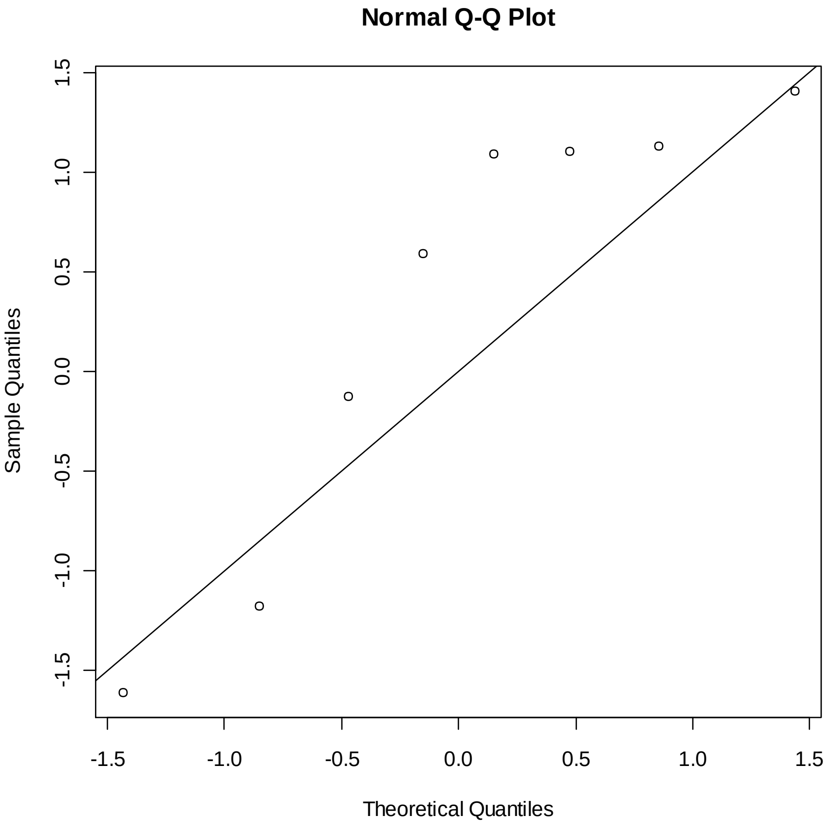
```
>r.pearson<-resid(t1, type="pearson")
> plot(r.pearson)
> abline(h=0, lty=2)
```



Pearson residuals

$$r_i^{\ P} = \frac{y_i - \hat{\mu}_i}{\sqrt{V(\hat{\mu}_i)}} \sim N(0,1)$$

```
> par(mfrow=c(1,1))
> qqnorm(r.pearson)
> abline(0,1)
```



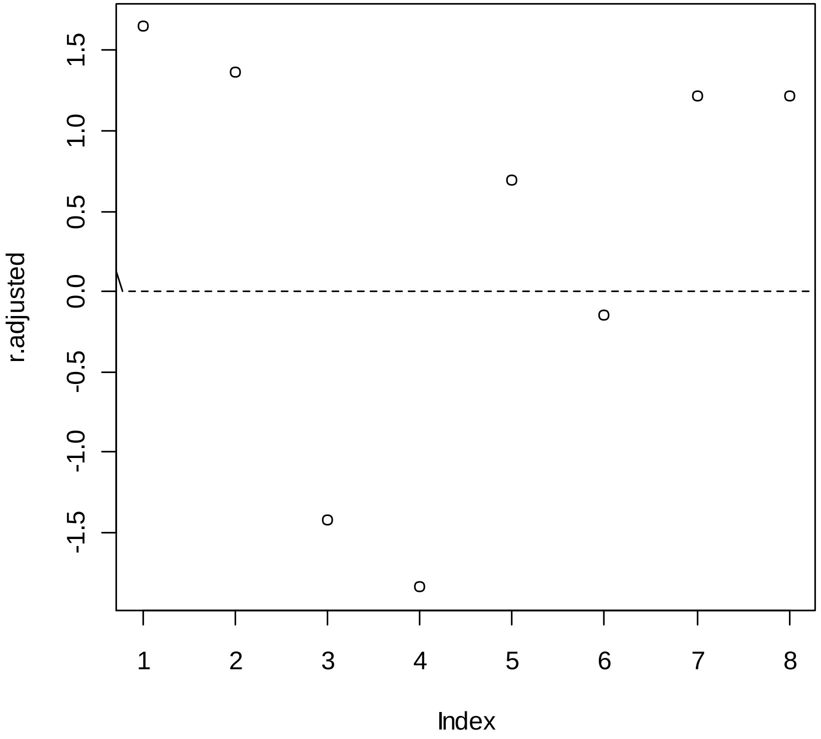
Adjusted residual in R

The adjusted residual

$$e_i{}^a = \frac{e_i{}^p}{(1-H_{ii})^{1/2}}$$

see slide 299

```
> hii <- hatvalues(t1)
> r.adjusted <- r.pearson/sqrt(1 - hii)
> plot(r.adjusted)
> plot(r.adjusted)
> abline(h = 0, lty = 2)
```



Deviance residual

$$r_i^{\,d} = sign(Y_i - n_i \hat{p}_i)\;(2y_i \ln\left(\frac{Y_i}{n_i \hat{p}_i}\right) + 2(n_i - y_i)\ln\left(\frac{n_i - Y_i}{n_i(1-\hat{p}_i)}\right))$$

$$\Rightarrow D = \sum_{i=1}^{n} (r_i^{\,D})^2$$

High leverage and influential points in logistic regression

$$\text{Linear models:}$$

$$\mathrm{Y} = \mathrm{X}\beta + \varepsilon \qquad \hat{\beta} = (\mathrm{X}^{\mathrm{t}}\mathrm{X})^{-1} X^{t} Y \qquad \hat{Y} = \mathrm{X}\hat{\beta} = HY,$$

$$H = X(\mathrm{X}^{\mathrm{t}}\mathrm{X})^{-1} X^{t} \qquad H^{2} = H$$

$$\Rightarrow = Y - \hat{Y} = (I - H)Y$$

$$= (I - H)(Y - \hat{Y}) \qquad \text{since } \mathrm{H}\hat{\mathrm{Y}} = \mathrm{H}(\mathrm{HY}) = \mathrm{H}^{2}Y = HY = \hat{Y}$$

$$= (I - H)(\hat{e})$$

$$\Rightarrow \text{raw} \quad \text{residuals} \quad \text{satisfy} \quad \hat{e} = (I - H)\hat{e}$$

$$\text{logistic} \quad \text{regression}$$

$$e^{P} = (I - H)e^{P} \;, where \quad e_{i}^{P} = \frac{Y_{i} - n_{i}\hat{p}_{i}}{(n_{i}\hat{p}_{i}(1 - \hat{p}_{i}))^{1/2}}$$

(Reference: Pregibon (1981))

High leverage points in logistic regression

$$e^P = \underbrace{(I - H)}_{M} e^P \quad \Rightarrow \quad e_i^{\,a} = \frac{e_i^{\,p}}{(1 - H_{ii})^{1/2}}$$

M spans residual space **e^P**.

This suggests that small m_{ii} (or large h_{ii}) should be useful in detecting extreme points in the design space X.

We have

$$\sum_{i=1}^{n} h_{ii} = p$$

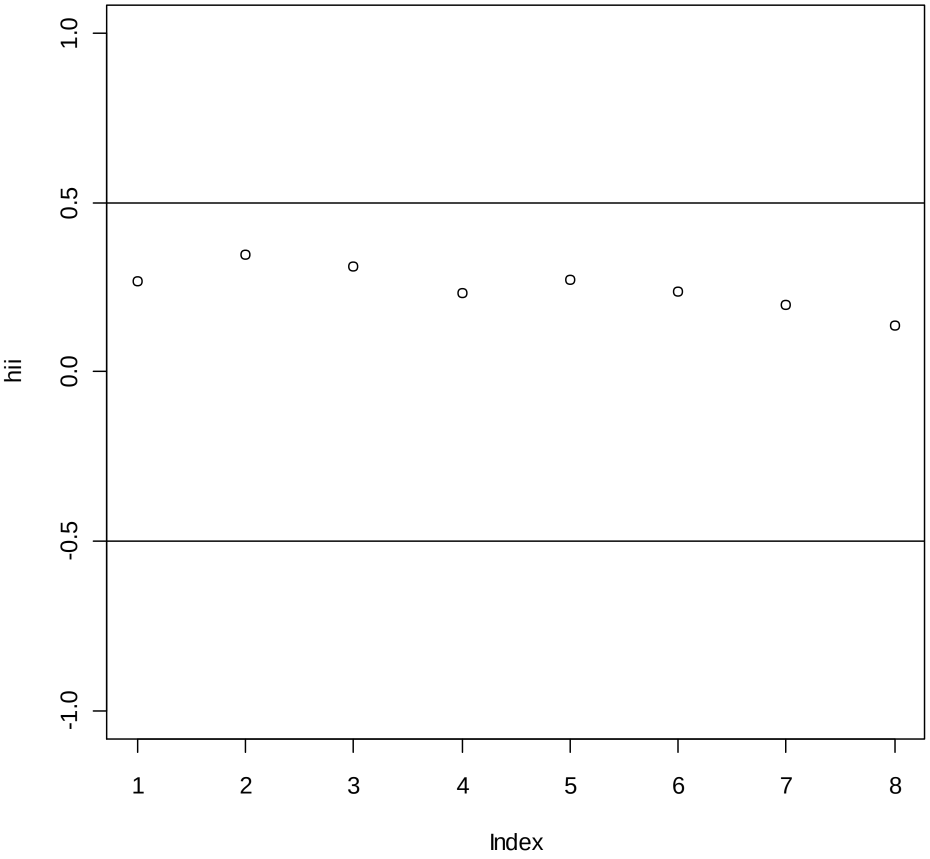
Therefore we consider

$$h_{ii} > \frac{2p}{n}$$

as "high leverage points".

High leverage points in logistic regression

```
> hii <- hatvalues(t1)
> sum(hii)
[1] 2
> plot(hii,ylim=c(-1,1))
> 2*2/8
[1] 0.5
> abline(0.5,0)
> abline(-0.5,0)
```



Cook’s distance in logistic regression

Using LRT it can be shown that

$$\left\{\beta :\ -2\ln\{\frac{L(\beta)}{L(\hat{\beta})}\} \leq \chi^{2}{}_{1-\alpha,p}\right\} \text{ is an approx.100 } (1\text{-}\alpha)\%\,\text{CI} \quad \text{for } \beta$$

$$\Rightarrow D_i = -2\left\{\ln\frac{L(\beta)}{L(\hat{\beta}}\right\}$$

measures change in the parameter when ith observation removed; difficult to calculate.

Cook’s distance…

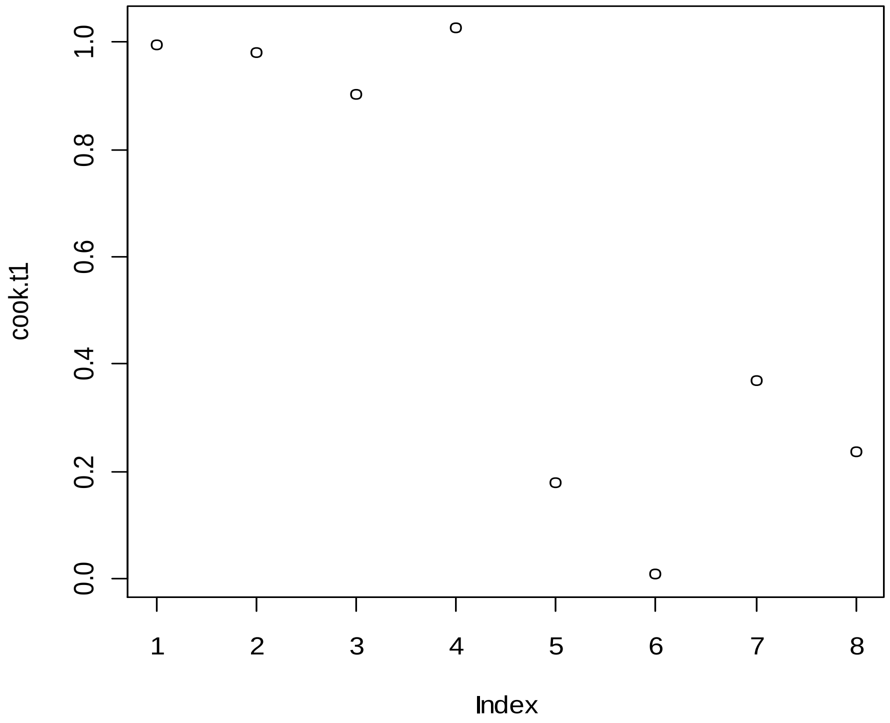
- Using Taylor expansion we have:

$$\left\{ \beta : \; -2\ln\{\frac{L(\beta)}{L(\hat{\beta}}\} \leq {\chi^2}_{1-\alpha,p} \right\} \approx \left\{ \beta : (\beta - \hat{\beta})^{\mathrm{t}} \mathrm{X}^{\mathrm{t}} \hat{\mathrm{D}} \mathrm{X}(\beta - \hat{\beta}) \leq {\chi^2}_{1-\alpha,p} \right\}$$

$$\Rightarrow D_i \approx (\hat{\beta}_{-i} - \hat{\beta})^{\mathrm{t}} \mathrm{X}^{\mathrm{t}} \hat{\mathrm{D}} \mathrm{X}(\hat{\beta}_{-i} - \hat{\beta})$$

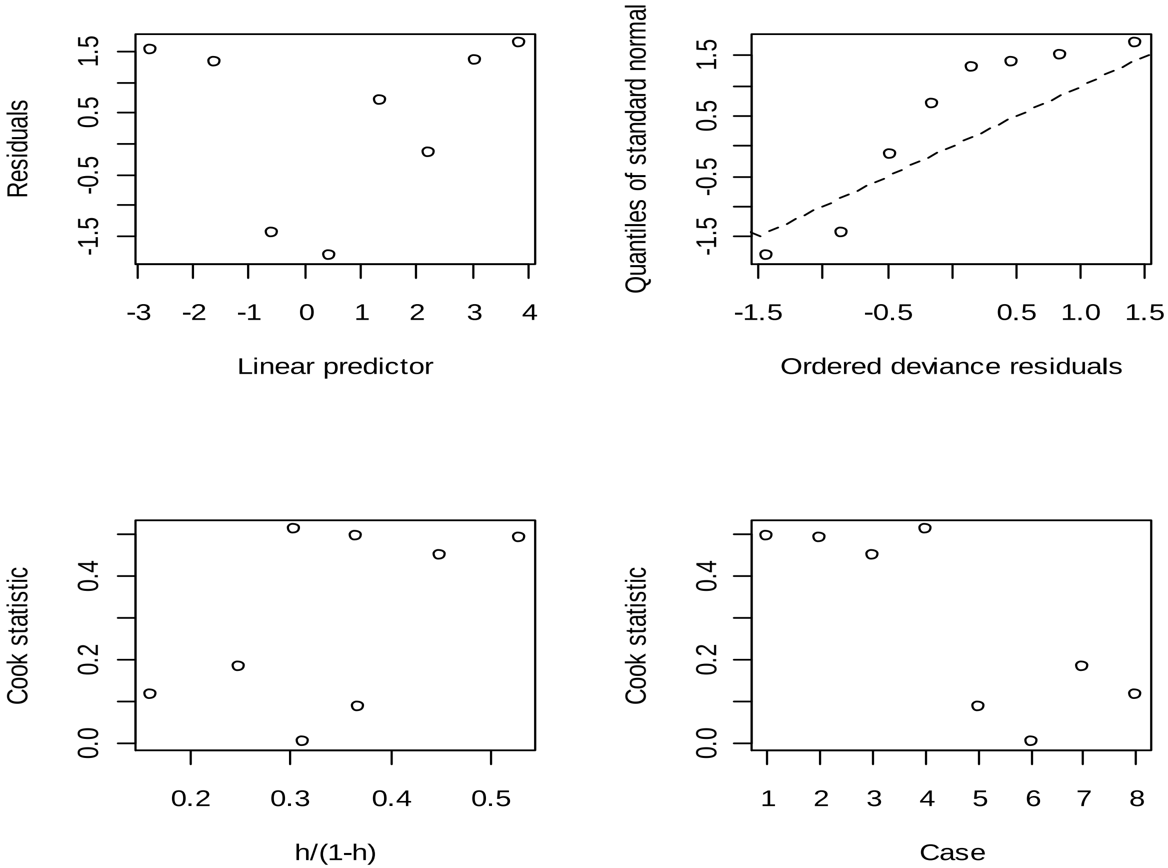
Cook's distance in R

```
> p.t1 <- length(coef(t1))
> cook.t1 <- ((r.pearson^2) * hii)/((1 - hii)^2)
> cook.t11 <- cooks.distance(t1) * p.t1
> plot(cook.t1)
```



Diagnostic with R: the beatle data with logit link function

```
> library(boot)
> glm.diag.plots(beatlefit)
```



summary

- Model formulation: distribution, linear predictor and link functions.
- Estimation and inference.
- Model selection.
- Model diagnostic.

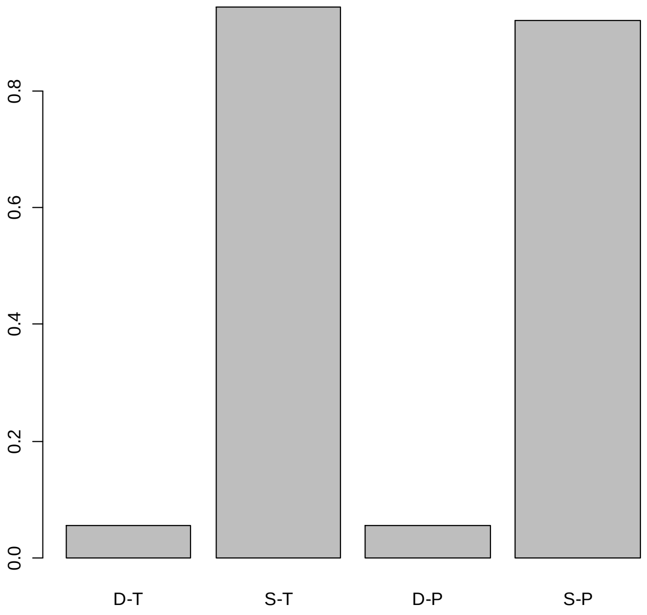
Extra Example

Effect of drug on cardiac death (McCullagh & Nelder 1983)

Effect of drug on cardiatic deaths

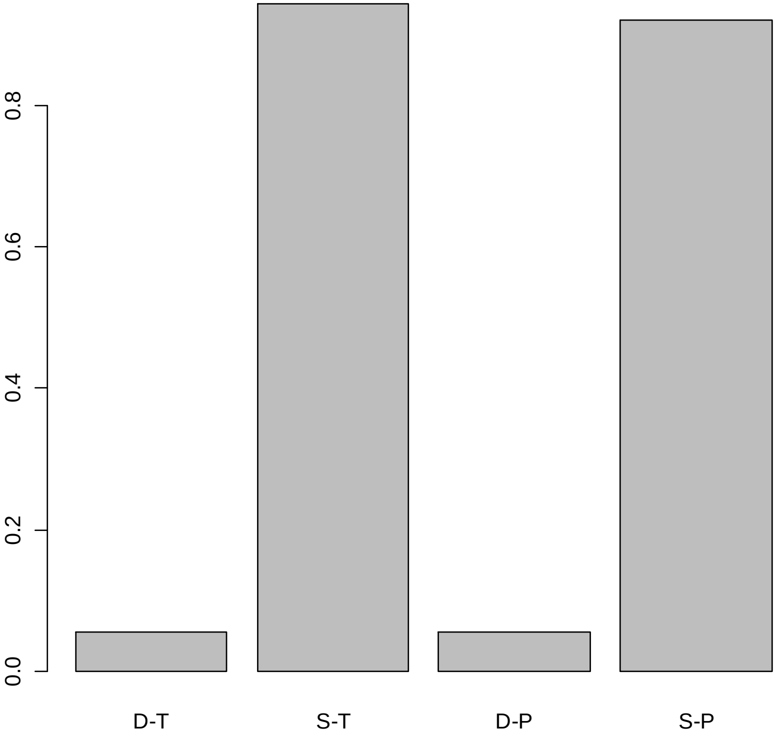
Study of the effect of a drug on cardiac death.

Patients treated with:
Drug: sulphinpyrazone.
Placebo.
Number of deaths and survivors (from the total) were recorded.



Effect of drug on cardiatic deaths

```
>d<-c(41,60)
>s<-c(692,682)
> n<-c(733,742)
> gr<-c("T","P")
> cbind(d,s,n)
     d   s   n
[1,] 41 692 733
[2,] 60 682 742
```



2 X 2 table

$$\begin{array}{ccc} y_{00} & y_{01} & n_1 \\ y_{10} & y_{11} & n_2 \\ m & n-m & n \end{array} \qquad \begin{array}{ccc} \pi_{00} & \pi_{01} & \pi_{0.} \\ \pi_{10} & \pi_{11} & \pi_{1.} \\ \pi_{.0} & \pi_{.1} & 1 \end{array}$$

$$OR = \frac{\dfrac{\pi_{00}}{1-\pi_{00}}}{\dfrac{\pi_{10}}{1-\pi_{10}}}$$

2 X 2 table

$$\begin{array}{ccc} \pi_{00} & \pi_{01} & \pi_{0.} \\ \pi_{10} & \pi_{11} & \pi_{1.} \\ \pi_{.0} & \pi_{.1} & 1 \end{array}$$

$$\hat{\pi}_{00} = \frac{y_{00}}{n_1}, 1 - \hat{\pi}_{00} = \frac{y_{01}}{n_1}$$

$$\hat{\pi}_{10} = \frac{y_{10}}{n_2}, 1 - \hat{\pi}_{10} = \frac{y_{11}}{n_2}$$

$$OR = \frac{\dfrac{\pi_{00}}{1-\pi_{00}}}{\dfrac{\pi_{10}}{1-\pi_{10}}}$$

$$OR = \frac{\dfrac{y_{00}}{y_{01}}}{\dfrac{y_{10}}{y_{11}}} = \frac{y_{00} \times y_{11}}{y_{01} \times y_{10}}$$

The odds ratio

$$\begin{array}{ccc} y_{00} & y_{01} & n_1 \\ y_{10} & y_{11} & n_2 \\ m & n-m & n \end{array}$$

```
> cbind(d,s,n)
      d   s   n
[1,] 41 692 733
[2,] 60 682 742
```

T

C

deaths

totals

$$OR = \varphi = \frac{y_{00} \times y_{11}}{y_{01} \times y_{10}}$$

$$\varphi = \frac{41 \times 682}{60 \times 692} = 0.6735$$

$$\log(\varphi) = -0.3953$$

What does an OR=0.6735 mean ?

Conditional likelihood for 2 X 2 table

$$\begin{array}{ccc} y_{00} & y_{01} & n_1 \\ y_{10} & y_{11} & n_2 \\ m & n-m & n \end{array}$$

$$y_{00} \sim B(n_1, \pi_{00})$$

$$y_{10} \sim B(n_2, \pi_{10})$$

$$\boxed{y_{00} + y_{10} = m}$$

Conditional likelihood for 2 X 2 table

$$\begin{array}{ccc} y_{00} & y_{01} & n_1 \\ y_{10} & y_{11} & n_2 \\ m & n-m & n \end{array}$$

$$y_{00} \sim B(n_1, \pi_{00})$$

$$y_{10} \sim B(n_2, \pi_{10})$$

$$\boxed{y_{00} + y_{10} = m}$$

$$x_i = \begin{cases} 1 & T \\ 0 & P \end{cases}$$

Conditional likelihood for 2 X 2 table

$$y_{00} \sim B(n_1, \pi_{00})$$

$$y_{10} \sim B(n_2, \pi_{10})$$

$$x_i = \begin{cases} 1 & T \\ 0 & P \end{cases}$$

$$y_i \sim B(n_i, \pi_i)$$

$$g(\pi_i) = \beta_0 + \beta_1 x_i$$

$$\pi_i = \begin{cases} \dfrac{e^{\beta_0+\beta_1}}{1+e^{\beta_0+\beta_1}} & T \\ \dfrac{e^{\beta_0}}{1+e^{\beta_0}} & P \end{cases}$$

The odds ratio

$$\varphi = OR = \frac{\dfrac{\pi_1}{1-\pi_1}}{\dfrac{\pi_2}{1-\pi_2}} = \frac{e^{\beta_0+\beta_1}}{e^{\beta_0}} = e^{\beta_1}$$

$$\log(\varphi) = \beta_1$$

Inference

$$y_i \sim B(n_i, \pi_i)$$

$$g(\pi_i) = \beta_0 + \beta_1 x_i$$

$$H_0 : \pi_T = \pi_P$$

$$H_1 : \pi_T \neq \pi_P$$

$$H_0 : \beta_1 = 0$$

$$H_1 : \beta_1 \neq 0$$

$$H_0 : \varphi = e^{\beta_1} = 1$$

$$H_1 : \varphi = e^{\beta_1} \neq 1$$

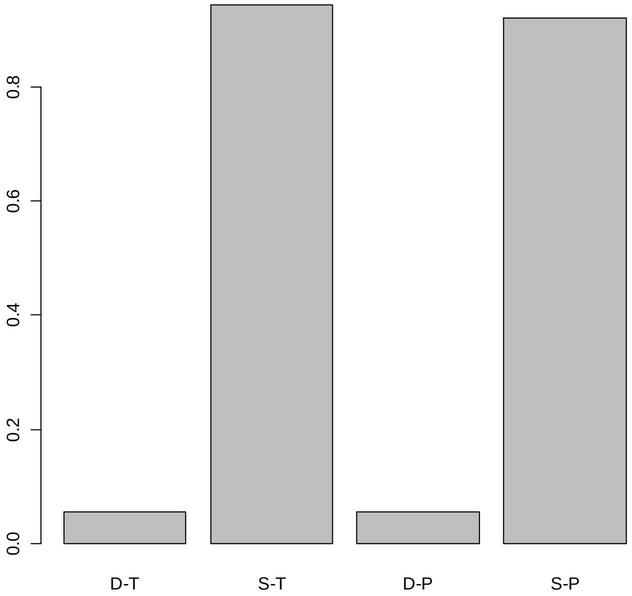
R output

```
Call:
glm(formula = d/n ~ gr, family = "binomial")

Deviance Residuals:
[1]  0  0

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -2.4307     3.6680  -0.663    0.508
grT          -0.3953     5.6912  -0.069    0.945

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 4.9015e-03  on 1  degrees of freedom
Residual deviance: 2.4213e-16  on 0  degrees of freedom
AIC: 4.2838
```

Effect of drug on cardiac deaths

```
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -2.4307     3.6680  -0.663    0.508
grT          -0.3953     5.6912  -0.069    0.945
```

We cannot reject the null hypothesis.



Example

Habitat preferences of lizards

(McCullagh & Nelder 1983)

Section 4.6, page 128 (first edition)

Habitat preferences of lizards

- A study consists of two lizards type: Grohami and Opalinus.
- Response: number of sites (from the total) occupied by Grahami lizards.

- Covariates:

1. Height of the site (H).
2. Diameter (D).
3. Sun condition of the site (S, sun/ shade).
4. Time of the day (T).

Habitat preferences of lizards

```
> habitat
   G Total  S  D  H     T
1  20    22 S1 D1 H1 Early
2   8     9 S1 D1 H1   Mid
3   4     8 S1 D1 H1  Late
4  13    13 S1 D1 H2 Early
5   8     8 S1 D1 H2   Mid
6  12    12 S1 D1 H2  Late
7   8    11 S1 D2 H1 Early
8   4     5 S1 D2 H1   Mid
9   5     8 S1 D2 H1  Late
10  6     6 S1 D2 H2 Early
11  0     0 S1 D2 H2   Mid
12  1     2 S1 D2 H2  Late
13 34    45 S2 D1 H1 Early
14 69    89 S2 D1 H1   Mid
15 18    28 S2 D1 H1  Late
16 31    36 S2 D1 H2 Early
17 55    59 S2 D1 H2   Mid
18 13    16 S2 D1 H2  Late
19 17    32 S2 D2 H1 Early
20 60    92 S2 D2 H1   Mid
21  8    16 S2 D2 H1  Late
22 12    13 S2 D2 H2 Early
23 21    26 S2 D2 H2   Mid
24  4     8 S2 D2 H2  Late
```

S: sun conditions sun / shade).
D: diameter (<2 / > 2).
H: hight (< 5 / > 5).
T: time of day (early/ mid day/late).

Habitat preferences of lizards: model formulation

$$y_{ijkl} \sim B(n_{ijkl}, \pi_{ijkl})$$

Total sample size.

Number of sites occupied by Grahami lizards.

$\pi_{ijkl} =$ The probability that a site is occupied by Grahami lizards.

$$\begin{aligned} g(\pi_{ijkl}) &= \mu + \alpha_i + \beta_j + \gamma_k + \delta_l + \ldots \\ &= \beta_0 + \beta_1 S + \beta_2 D + \beta_3 H + \beta_4 T + \cdots \end{aligned}$$

Habitat preferences of lizards: model formulation in R

Main effects model in R

$$g(\pi_{ijkl}) = \mu + \alpha_i + \beta_j + \gamma_k + \delta_l$$

```
> f1<-glm((G/Total)~H+D+S+T,family="binomial",data=habitat)
```

R output

```
> summary(f1)

Call:
glm(formula = (G/Total) ~ H + D + S + T, family = "binomial",
    data = habitat)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-0.50878  -0.11019   0.02009   0.26466   0.52322

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)   2.0618     1.4060   1.466    0.143
HH2           1.0631     1.1222   0.947    0.343
DD2          -0.8798     1.0841  -0.812    0.417
SS2          -0.6415     1.0884  -0.589    0.556
TLate        -1.2054     1.2761  -0.945    0.345
TMid          0.0587     1.4590   0.040    0.968

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 4.6730  on 22  degrees of freedom
Residual deviance: 1.5417  on 17  degrees of freedom
  (1 observation deleted due to missingness)
AIC: 28.658
```

Interpretation

```
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)   2.0618     1.4060   1.466    0.143
HH2           1.0631     1.1222   0.947    0.343
DD2          -0.8798     1.0841  -0.812    0.417
SS2          -0.6415     1.0884  -0.589    0.556
TLate        -1.2054     1.2761  -0.945    0.345
TMid          0.0587     1.4590   0.040    0.968
```

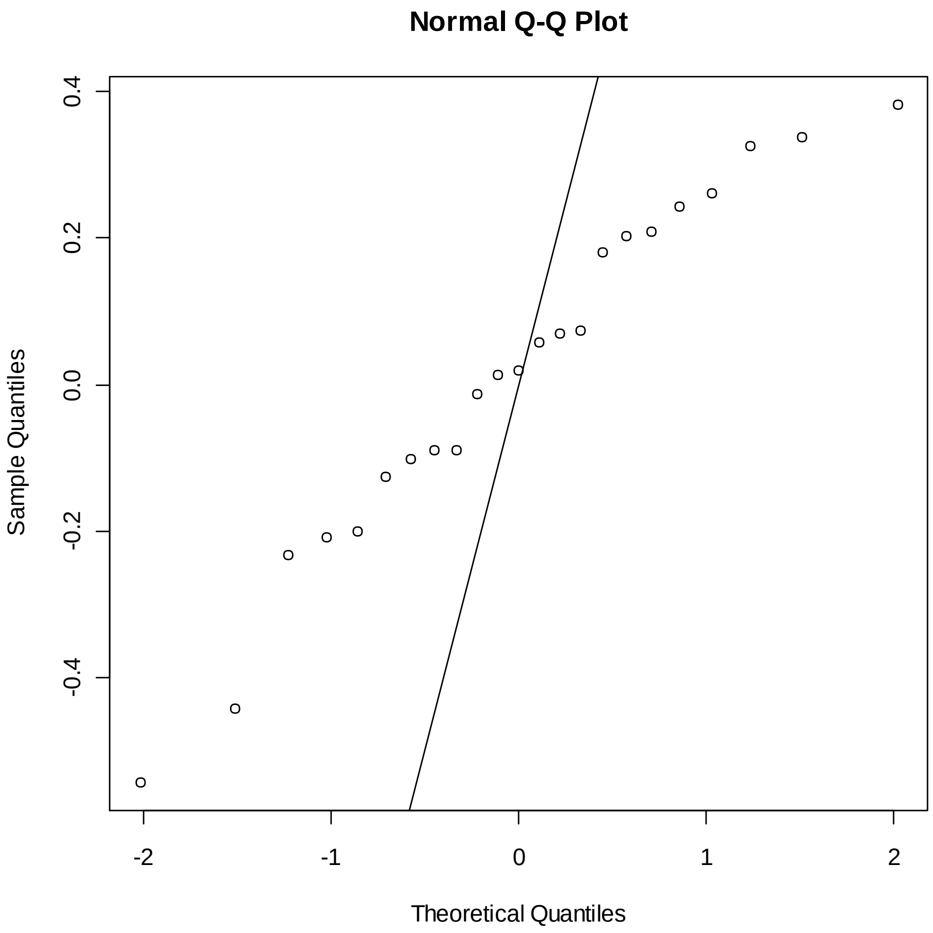
All the parameters estimates are not significant.

We will look at this problem again when we will speak about over/under dispersion of binomial data.

diagnostic

```
>r.pearson<-resid(f1, type="pearson")
> par(mfrow=c(1,1))
> qqnorm(r.pearson)
> abline(0,1)
```

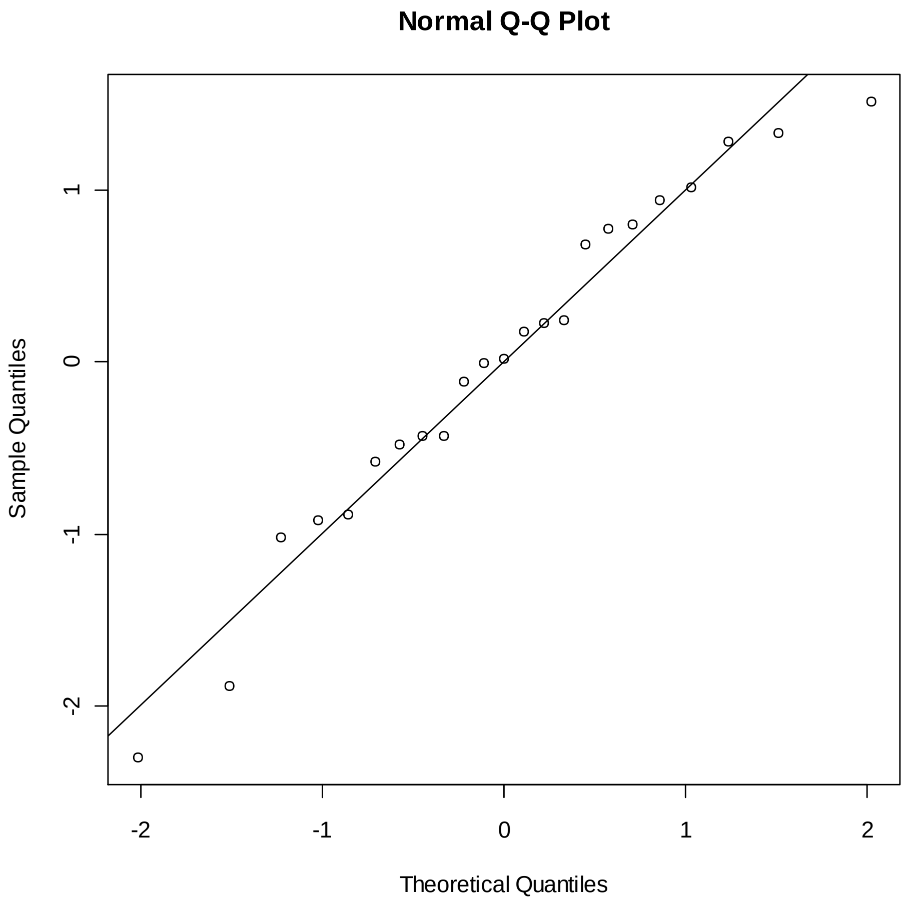
$$r_i^{\,P} = \frac{y_i - \hat{\mu}_i}{\sqrt{V(\hat{\mu}_i)}} \sim N(0,1)$$



diagnostic

```
> mean(r.pearson)
[1] 0.01454735
> var(r.pearson)
[1] 0.05871372

>r.s<-(r.pearson-mean(r.pearson))/
     sqrt((var(r.pearson)))

> qqnorm(r.s)
> abline(0,1)
```

The variance of pearson residual is much smaller than 1



Models with two-way interactions

$$g(\pi_{ijkl}) = \mu + \alpha_i + \beta_j + \gamma_k + \delta_l + \alpha\beta_{ij}$$

```
f2<-glm((G/Total)~H+D+S+T+T*S,family="binomial",data=habitat)
f3<-glm((G/Total)~H+D+S+T+T*H,family="binomial",data=habitat)
f4<-glm((G/Total)~H+D+S+T+T*D,family="binomial",data=habitat)
f5<-glm((G/Total)~H+D+S+T+S*H,family="binomial",data=habitat)
f6<-glm((G/Total)~H+D+S+T+S*D,family="binomial",data=habitat)
f7<-glm((G/Total)~H+D+S+T+H*D,family="binomial",data=habitat)
```

Model selection: the deviance

```
> deviance(f1)
[1] 1.541658
> deviance(f2)
[1] 1.379657
> deviance(f3)
[1] 1.327497
> deviance(f4)
[1] 1.526889
> deviance(f5)
[1] 1.518356
> deviance(f6)
[1] 1.538425
> deviance(f7)
[1] 1.364903
```

```
f3<-glm((G/Total)~H+D+S+T+T*H,
        family="binomial“
        ,data=habitat)
```

Model selection: AIC

```
 extractAIC(f1)
[1]  6.00000 28.65782
> extractAIC(f2)
[1]  8.00000 32.57349
> extractAIC(f3)
[1]  8.00000 32.40805
> extractAIC(f4)
[1]  8.00000 32.52206
> extractAIC(f5)
[1]  7.00000 30.74255
> extractAIC(f6)
[1]  7.00000 30.77231
> extractAIC(f7)
[1]  7.00000 29.69527
```

$$g(\pi_{ijkl}) = \mu + \alpha_i + \beta_j + \gamma_k + \delta_l$$

The main effect model is the model with the smallest AIC.