The >eR-Biostat initiative

Making R based education materials in statistics accessible for all

Basic concepts in statistical modeling using R: Simple Logistic Regression

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The course was developed as a part of the >eR-BioStat initiative.

External datasets are available in the GitHub page of the course.

E-learning system using R

Biostatistics

contents

- Logistic regression:
  - Examples.
  - The `glm()` function in R.
  - Fitting logistic regression models using the `glm()` function in R: 5 examples.

YouTube tutorials

- YouTube tutorials are available for:
  - Logistic Regression using R | Data Science | Machine Learning (host by Analytics University) : https://www.youtube.com/watch?v=nubin7hq4-s
  - Logistic Regression Analysis in R (host by Dr. Bo Han) : https://www.youtube.com/watch?v=eScK5w5JcHI
  - Statistics with R: Example of logistic regression (host by Phil Chan) https://www.youtube.com/watch?v=xEllScuasns

R program and Datasets

- Simple linear regression:
  - Introduction and model formulation.
  - Fitting a simple linear regression model using the lm() function in R.
  - Model diagnostic.
  - Model diagnostic in R.

Introduction

Introduction

- In health, education, medical and social sciences, we frequently deal with dichotomous or binary outcomes.
- For example, we may have data on presence (Yes) or absence (No) of an event. For example; presence or absence of :
  - ➢ Anaemia
  - ➢ Ebola
  - ➢ Diabetes

The response variabel

A binary variable:

$$Y_i = \begin{cases} 1 & \text{presence} \\ 0 & \text{absence} \end{cases}$$

A example:

$$Y_i = \begin{cases} 1 & \text{Diabetes} \\ 0 & \text{Healthy} \end{cases}$$

Bernoulli random variables

- Let $Y_1, Y_2, \ldots, Y_N$ represent a sample of Bernoulli random variables from N trials.

$$Y_i = \begin{cases} 1 \text{ if the outcome is postive/success} \\ \\ 0 \text{ if the outcome is negative/failure} \end{cases}$$

- Let $p = P(Y_i = 1)$ be the probability of success

- Let $(1 - p) = P(Y_i = 0)$ be the probability of failure

The predictor(s)

Our aim is to model the dependence of the probability of success upon known predictors.

$$Y_i = \begin{cases} 1 & \text{presence} \\ 0 & \text{absence} \end{cases} \quad \Rightarrow \quad P(Y_i = 1) = P(Y_i = \text{presence}) = \text{P(success)}$$

$$P(Y_i = 1) = f(predictors) = f(X_1, X_2, \ldots)$$

Logistic regression model

Our aim is to model the dependence of the probability of success on known predictors.

Example:

$$Y_i = \begin{cases} 1 & \text{Diabetes} \\ 0 & \text{Healthy} \end{cases}$$

$$P(Y_i = \text{Diabetes}) = \underbrace{f(predictors) = f(diet, age, ...)}$$

The model that we use to model the dependence between diabetes and the predictors is logistic regression model.

Examples

Example 1: Smoked mice

In order to investigate the infeluence of smoking on lung canser a group of 55 mince were randomized into two treatment groups.

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

The second group (the control group) were kept in thier cambers for 12 hours with out smoke.

Afrer One year an autopsy was carried out.

The response is the present and absent of a rumour.

The second variable in the data is the treatment group.

Smoked mice: the response variable

The question of primary interest is:

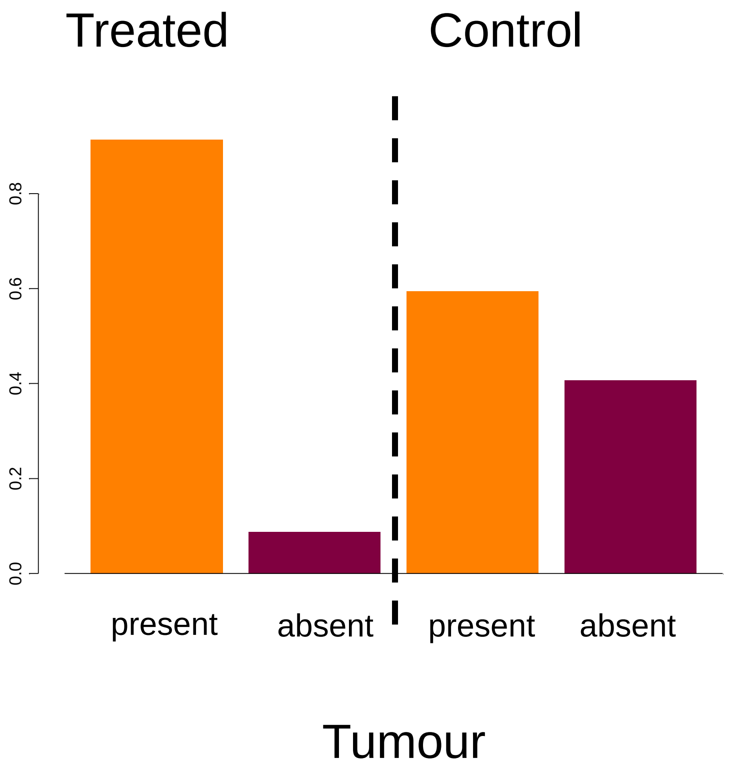
DOSE THE SMOKE INCREAE THE RISK FOR CANSER ?

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

The response variable

Smoked mice: the data

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



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.

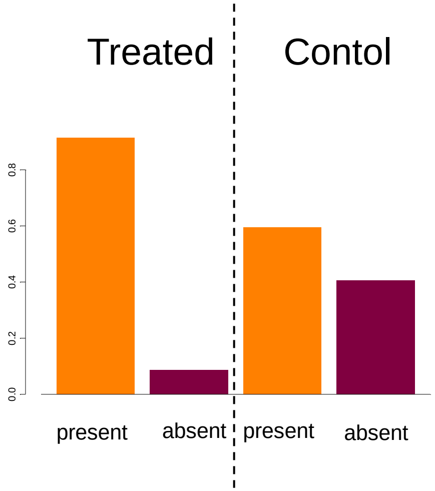
We do not have information about individuals in the sample, but only about the counts in different combinations of the experimant.

Individual data can be exracted from the table.

In terms of statistical modeling, the response is binary (tumour absent/tumour presnt).

The predictor, the treatment group, is also binary.

Response and predictor



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 differene is only due to chance or if thesmoke increase the risk for tumour.

Response:

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

Predicator:

$$Treatment_i(treated\,/\,control)$$

$$P(Y_i = 1) = P(tumour) = f(treatment)$$

Example 2: 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 2: Serological data

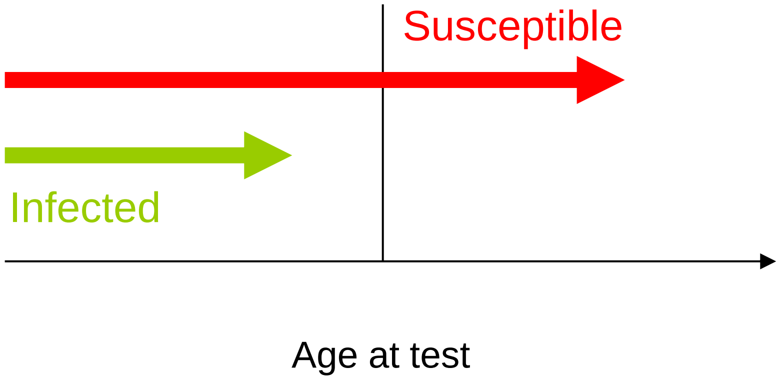
- A sample which taken at a certain time point.
- The information for each individual:

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

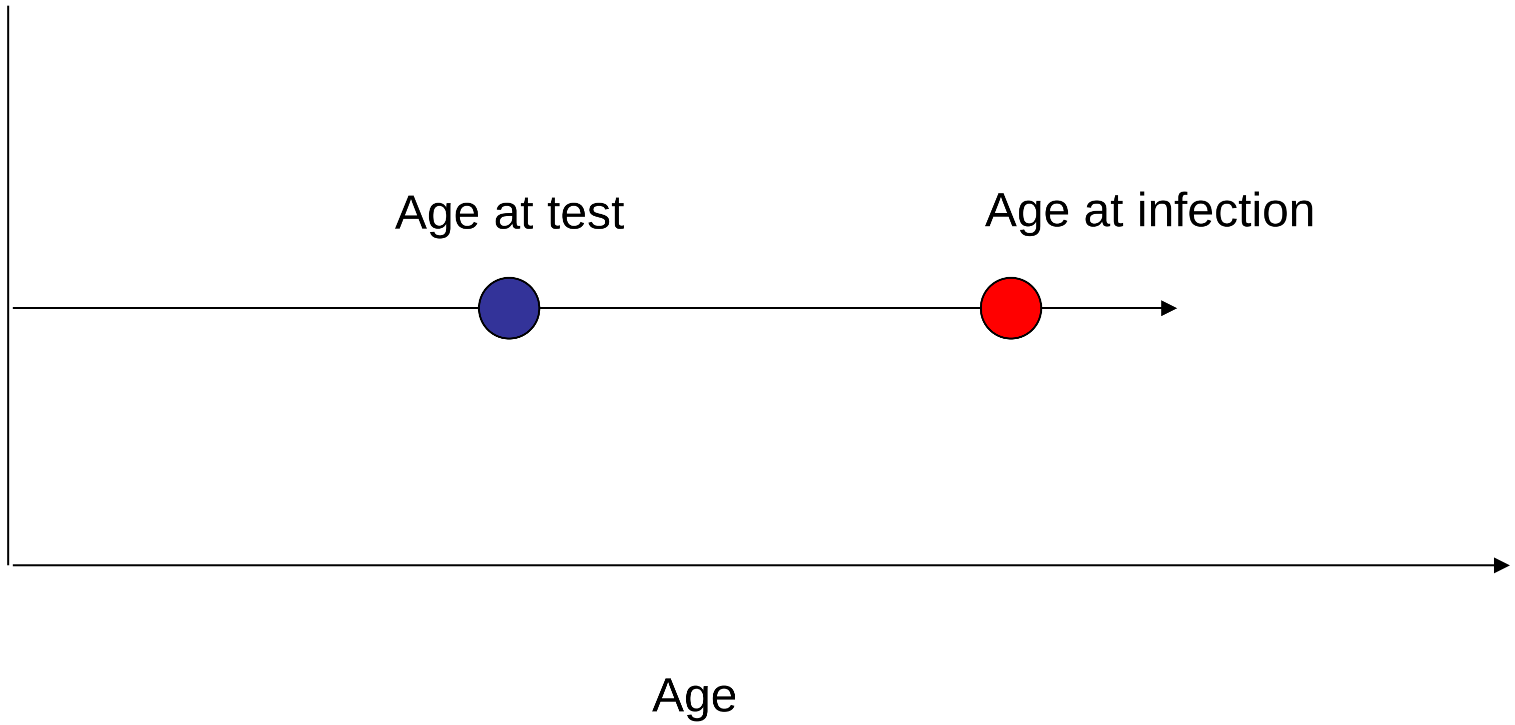
- Prevalence of sero-positivity In the sample: $\pi(a)$

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

- Sero-prevalnce data

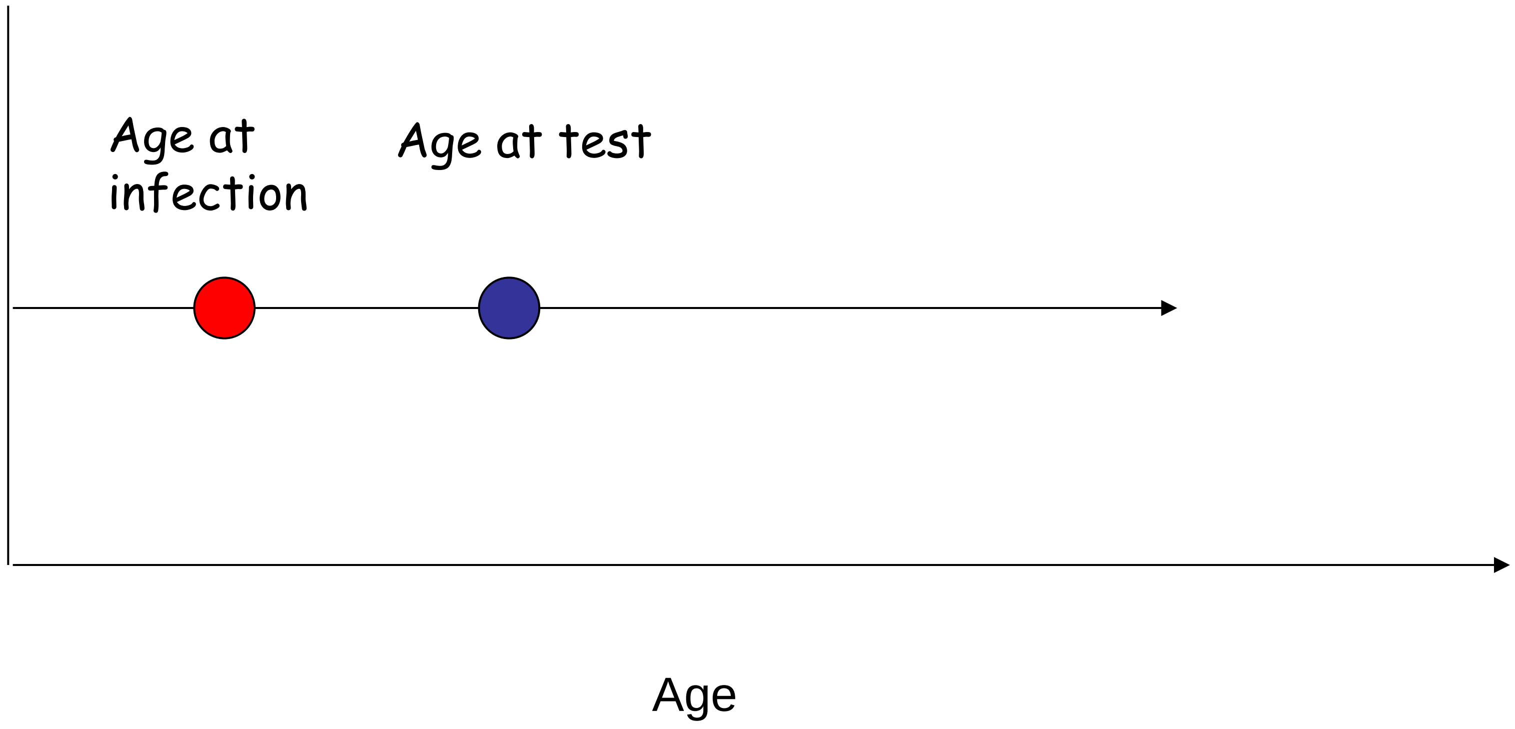


Current status data: sero-negative



- Sero-Negative: infected after the test.

Current status data: sero-positive



Age at infection

Age at test

Age

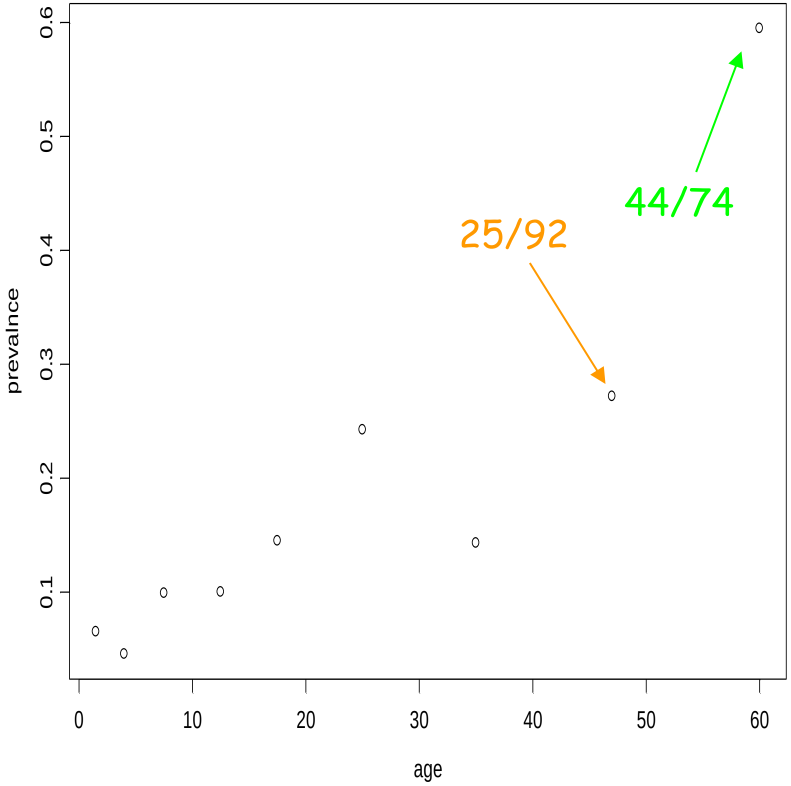
- Sero-Positive: infected after the test.

Example 2: Serological data

Malaria in Brasil

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

What is the relationship between infection and age ?



Example 2: 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

Response:

$$Y_{ij} = \begin{cases} 1 & Sero+ \\ 0 & Seto- \end{cases}$$

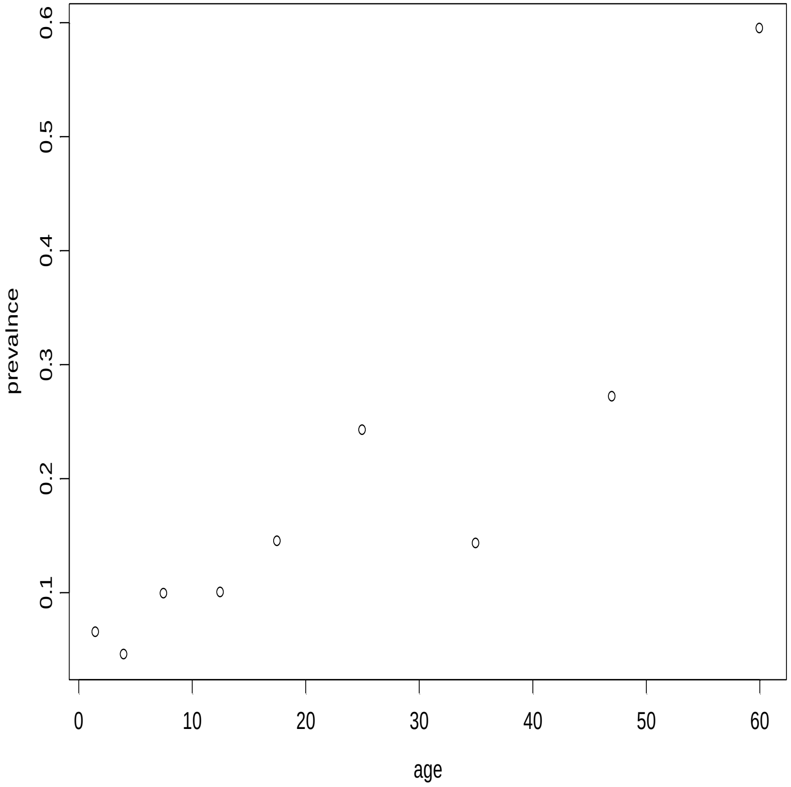
Number of Sero+ in age group j:

$$Y_j = \sum_{i=1}^{n_j} Y_i$$

Sample size at age group j:

$$n_j$$

Example 2: Serological data



Response: number of infected (sero+):

$$Y_j = \sum_{i=1}^{n_j} Y_i$$

Predictor: age

$$P(Y_i = 1) = P(sero+) = f(age)$$

Example 3: Bioassay

A bioassay experimant is an experimant designed to assess the potency of a compund by means of the response produced when it is administreted to a living organisim.

In this eaxmple the protective effect of a particular serum (serum 32) on the bacterium associated with the occurrence of pneumonia is under investigation.

Study design:

The esperimant consist of 5 groups of 40 mice. Each group was injcted with combination of an infecting dose of a cluture of pneumococci and one of five doses of the anti pneumococcus serum.

Bioassay data: response and predictor

The response of the number of deaths within 7 days from injection.

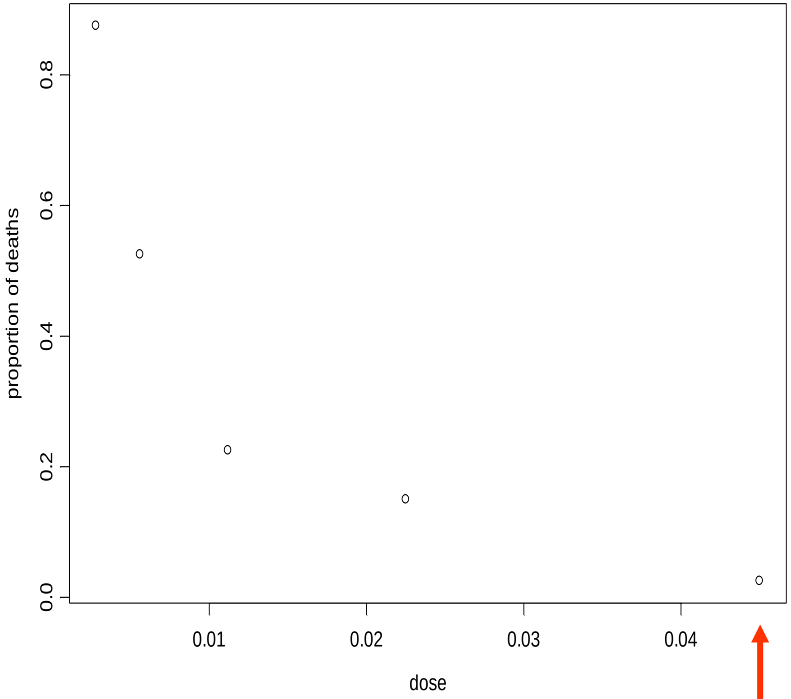
The dose level is the predictor.

The question of primary interest:

What is the relationship between the injected dose and the number of deaths ?

Example 3: the data

Dose of serum	Number of deaths	Sample size
0.0028	35	40
0.0056	21	40
0.0112	9	40
0.0225	6	40
0.0450	1	40



Example 3: the data

Dose of serum	Number of deaths	Sample size
0.0028	35	40
0.0056	21	40
0.0112	9	40
0.0225	6	40
0.0450	1	40

Response:

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

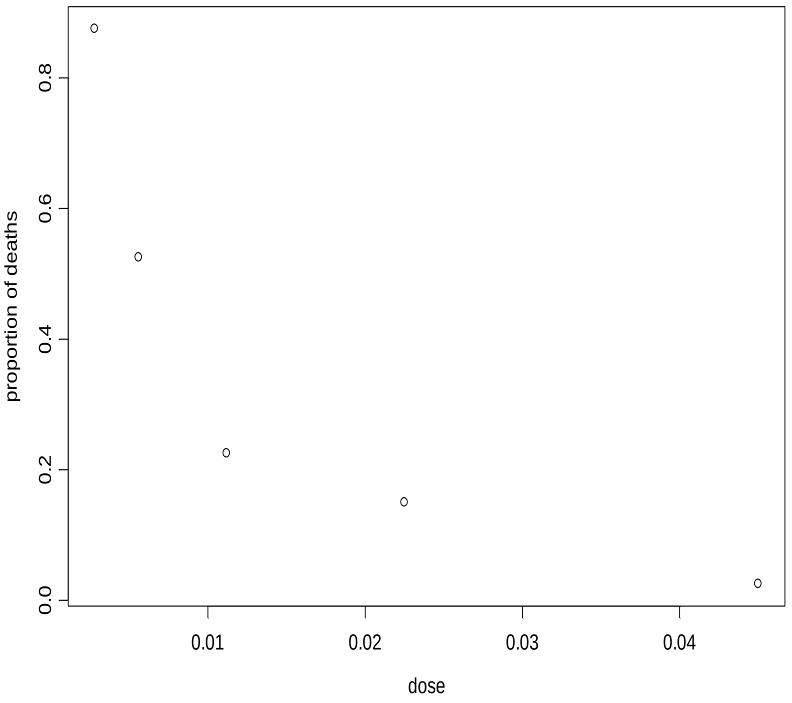
Number of deaths in dose level j:

$$Y_j = \sum_{i=1}^{n_j} Y_i$$

Sample size at dose level j:

$$n_j$$

Example 3: response and predictor



Response: number of deaths at each dose level:

$$Y_j = \sum_{i=1}^{n_j} Y_i$$

Predictor: dose

$$P(Y_i = 1) = P(death) = f(dose)$$

Example 4: Determination of ESR

The erythocte sedimentation rate (ESR) is the rate at which red blood cells settle out of suspensin in blood plasme when measured under standard condition.

The ESR increase if the levels of certian proteins in the blood increase.

Rheumatic diseases, chronis dideases and infections increase these proteins level.

From that reason the determination of the ESR is one of the most commenly used screening tests performed on samples bloods.

Determination of ESR: The data

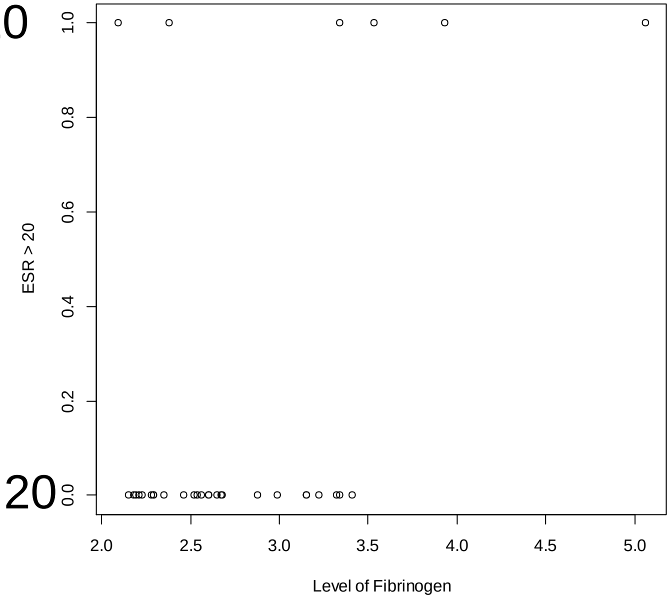
```
  Individual  Fib  Glob Y
1           1 2.52   38 0
2           2 2.56   31 0
3           3 2.19   33 0
4           4 2.18   31 0
5           5 3.41   37 0
.           . .      .  .
.           . .      .  .
.           . .      .  .
19         19 2.60   38 0
20         20 2.23   37 0
21         21 2.88   30 0
22         22 2.65   46 0
23         23 2.09   44 1
24         24 2.28   36 0
25         25 2.67   39 0
26         26 2.29   31 0
27         27 2.15   31 0
28         28 2.54   28 0
29         29 3.93   32 1
30         30 3.34   30 0
31         31 2.99   36 0
32         32 3.32   35 0
```

An example of individual data. For each subject we have the response and the proteins level.

Does the Fibrinogen level (proteins in the blood) infeleune the ESR rate ?

Example 4: determination of ESR

ESR > 20



ESR <= 20

Response:

$$Y_i = \begin{cases} 1 & ESR > 20 \\ 0 & ESR \leq 20 \end{cases}$$

Predictor: Fibrinogen level.

$$P(Y_i = 1) = P(ESR > 20) = f\,(\text{Fibrinogen level})$$

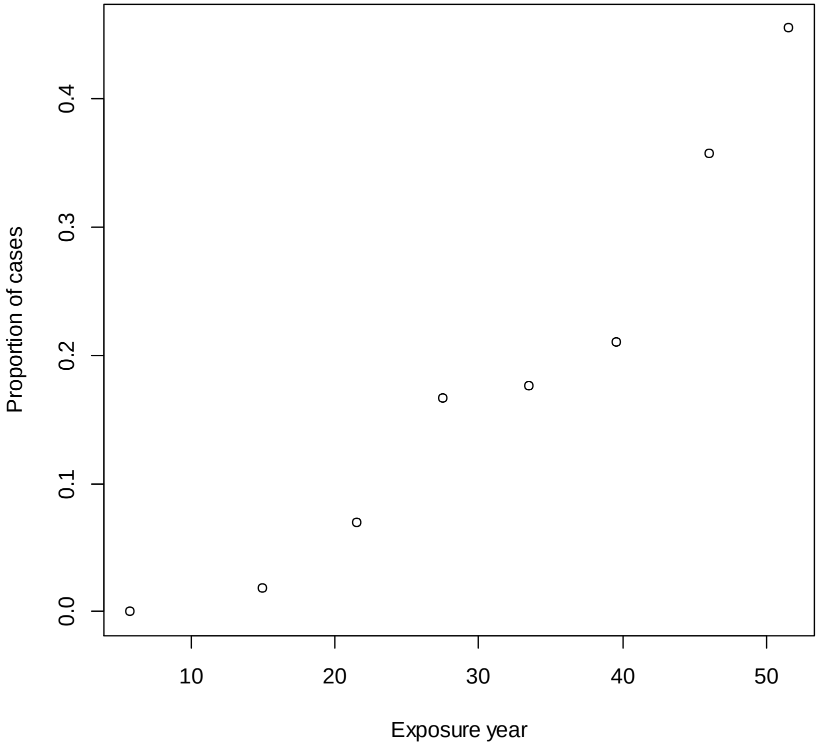
Example 5: Pneumoconiosis amongst coal miners

Pneumoconiosis amongst groups of coal miners with varying exposure to coal dust.

Does exposure time increase the probability to have the disease ?

The data

```
 Years Cases Miners
1   5.8     0     98
2  15.0     1     54
3  21.5     3     43
4  27.5     8     48
5  33.5     9     51
6  39.5     8     38
7  46.0    10     28
8  51.5     5     11
```

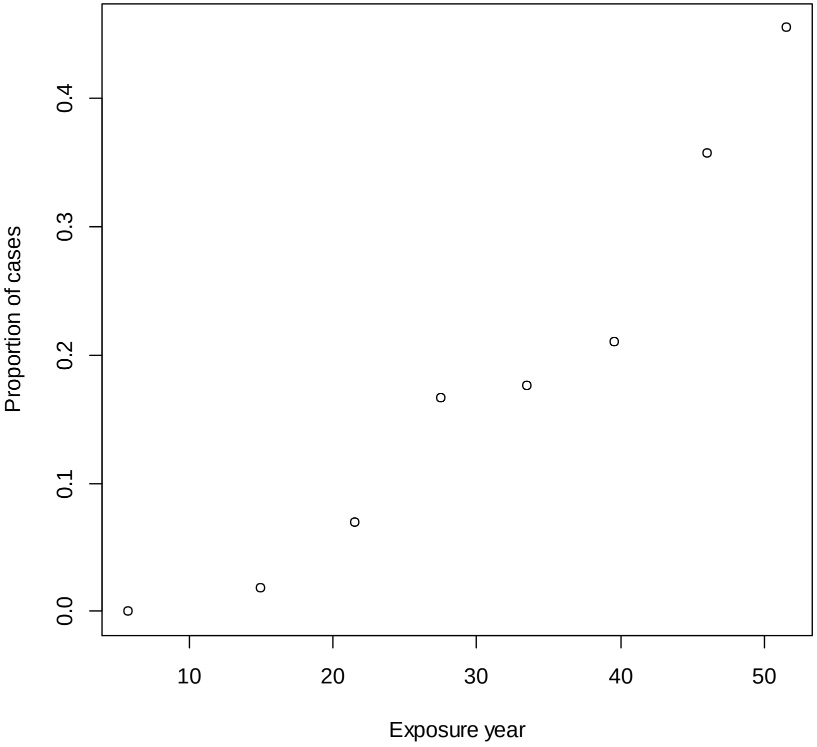


Example 5: response and predictor

Response:

$$Y_i = \begin{cases} 1 \\ 0 \end{cases}$$

Predictor: years of exposure to coal dust.



$$P(Y_i = 1) = P(\text{Pneumoconiosis}) = f(time)$$

Fitting logistic regression models using the glm( ) function in R

The glm() Function in R

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

- Arguments in the `glm()` call are as follows:

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

The glm() Function in R

- For binary data, the general call of the glm() function has the form

```
glm(formula, family=binomial(link = "logit"))
```

this defines a logistic regression model, i.e. a model for binary data with logit link finction.

The glm() Function: zero/one data.

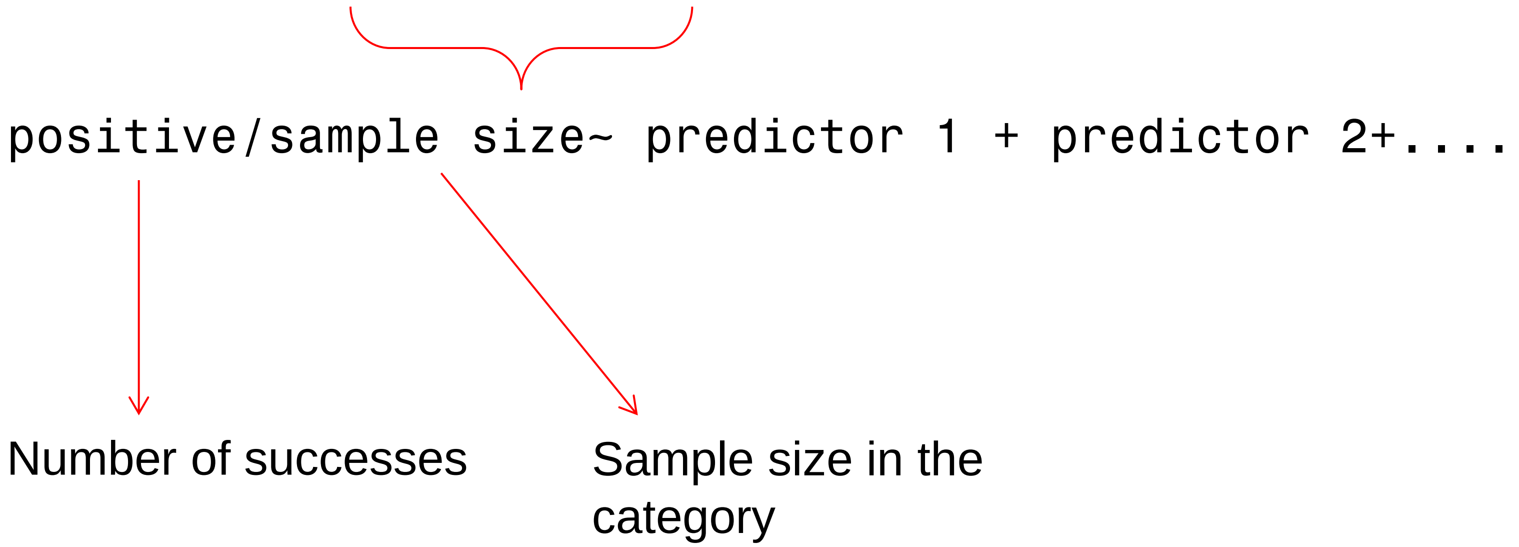
- For a zero/one data (for example the ESR data):

$$\texttt{glm(}\underbrace{\texttt{formula,}}_{\texttt{respone}\sim\texttt{predictor 1 + predictor 2+}_{\top}\texttt{.}}\texttt{family,link,data,...)}$$

The glm() Function: grouped data

- For grouped data (for example, the serological data)

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



```
positive/sample size~ predictor 1 + predictor 2+....
```

Number of successes

Sample size in the category

Fitting logistic regression models using glm( ) function in R: 4 examples

Example 1: Smoked mice

The question of primary interest is:

DOSE THE SMOKE INCREAE THE RISK FOR CANSER ?

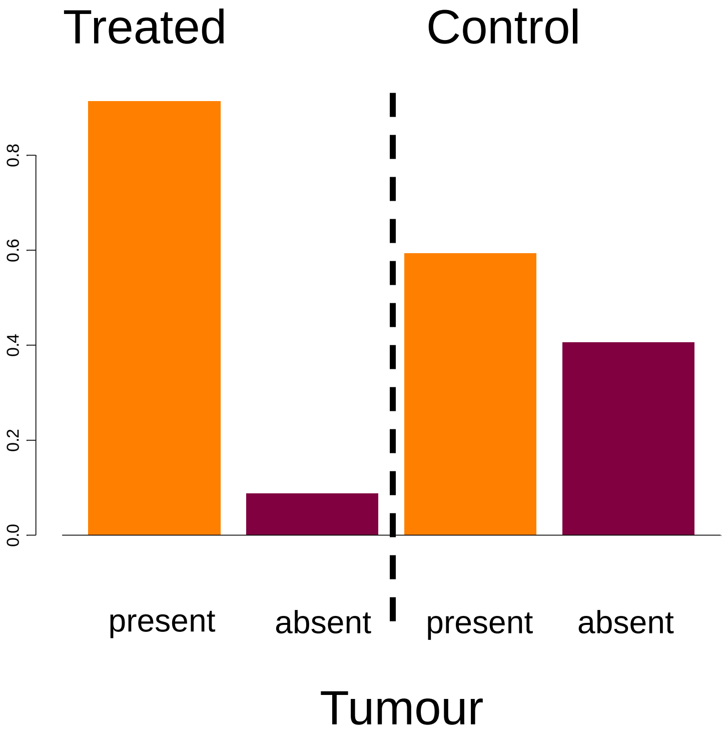
$$Y_i = \begin{cases} 1 \quad \mathit{tumour} \quad \mathit{present} \\ 0 \quad \mathit{tumour} \quad \mathit{absent} \end{cases}$$

The response variable

Data structure in R

```
> mice <- data.frame(Treatm=c("Treated", "Control"),
+             Tumour = c(21,19), Total = c(23,32))
> attach(mice)
> mice
```

```
   Treatm  Tumour Total
1 Treated      21    23
2 Control      19    32
```



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

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

Number of subjects with tunour

$$Y_i = \sum X_i$$

Distribution of Y

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

The model for P

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

EXAMPLE 1: SMOKED MICE

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

Fitting the model with the glm() function:

```
> fit2.mice <- glm(cbind(Tumour ,Total-Tumour)~factor(Treatm),
                    data = mice, family = binomial("logit"))
```

$$\log it\left(P_i\right) = \alpha + \beta \times treatment$$

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

$$P_i = \frac{e^{\alpha+\beta\times treatment_i}}{1+e^{\alpha+\beta\times treatment_i}}$$

R output

```
> summary(fit2.mice)

Call:
glm(formula = cbind(Tumour, Total - Tumour) ~ factor(Treatm),
    family = binomial("logit"), data = mice)

Deviance Residuals:
[1]  0  0

Coefficients:
                      Estimate Std. Error z value Pr(>|z|)
(Intercept)             0.3795     0.3599   1.054   0.2917
factor(Treatm)Treated   1.9719     0.8229   2.396   0.0166 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 7.6349  on 1  degrees of freedom
Residual deviance: 0.0000  on 0  degrees of freedom
AIC: 10.421

Number of Fisher Scoring iterations: 4
```

The odds ratio

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

$$OR = \frac{21 \times 13}{19 \times 2}$$

```
> OR1<-(21*13)/(19*2)
> OR1
[1] 7.184211
> log(OR1)
[1] 1.971886
```

```
> summary(fit2.mice)$coeff
                         Estimate Std. Error  z value  Pr(>|z|)
(Intercept)             0.3794896  0.3599370 1.054322 0.2917354
factor(Treatm)Treated   1.9718856  0.8229056 2.396248 0.0165639
```

$$\hat{\beta} = \log(OR)$$

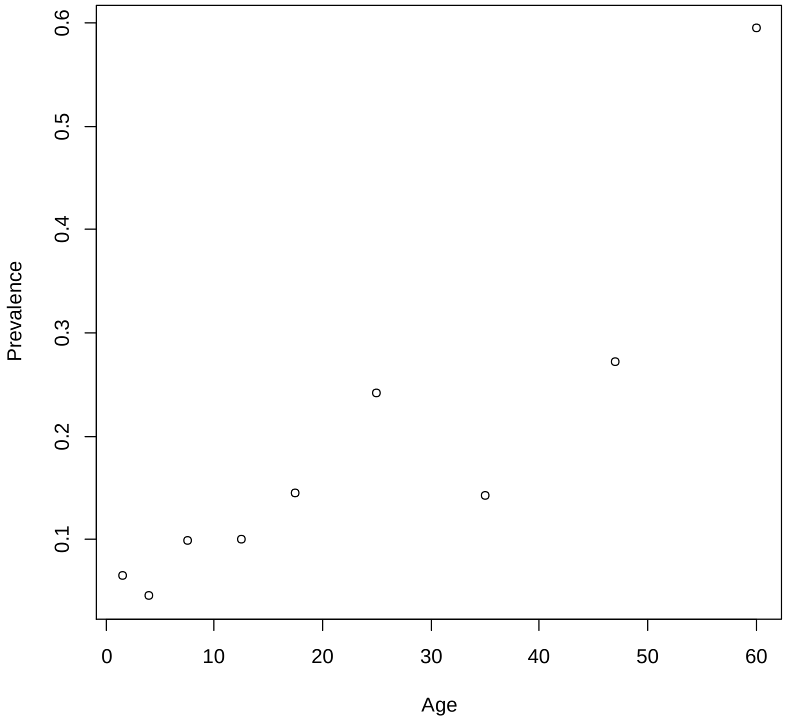
$$OR = \exp(1.971886) = 7.184.$$

Example 2 (Serological data): Data structure in R

```
Serolog <- read.table('c:/... /Serological.txt',
+                 header = TRUE, na.strings = "NA", dec = ".")
> attach(Serolog)
> print(Serolog)


   Age   N pos
1  1.5 123   8
2  4.0 132   6
3  7.5 182  18
4 12.5 140  14
5 17.5 138  20
6 25.0 161  39
7 35.0 133  19
8 47.0  92  25
9 60.0  74  44
```

Example 2: Serological data

```
p <- pos/N
plot(p ~ Age, xlab = "Age",
     ylab = "Prevalence")
```



Model formulation

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

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

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

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

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

glm( ) function in R

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

pos/N

```
> fit.Sero <- glm(pos/N ~ Age, data = Serolog, family = binomial)
```

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

model pos/N=age

Parameters estimate

```
> summary(fit.Sero)

Call:
glm(formula = pos/N ~ Age, family = binomial, data = Serolog)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-0.24363  -0.09726   0.01479   0.06756   0.19568

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -2.79677    1.79832  -1.555    0.120
Age          0.04718    0.04668   1.011    0.312

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 1.31775  on 8  degrees of freedom
Residual deviance: 0.18094  on 7  degrees of freedom
AIC: 8.0619

Number of Fisher Scoring iterations: 5
```

$$\log it\left(\hat{P}_i\right) = \widehat{\alpha} + \hat{\beta} \times age$$

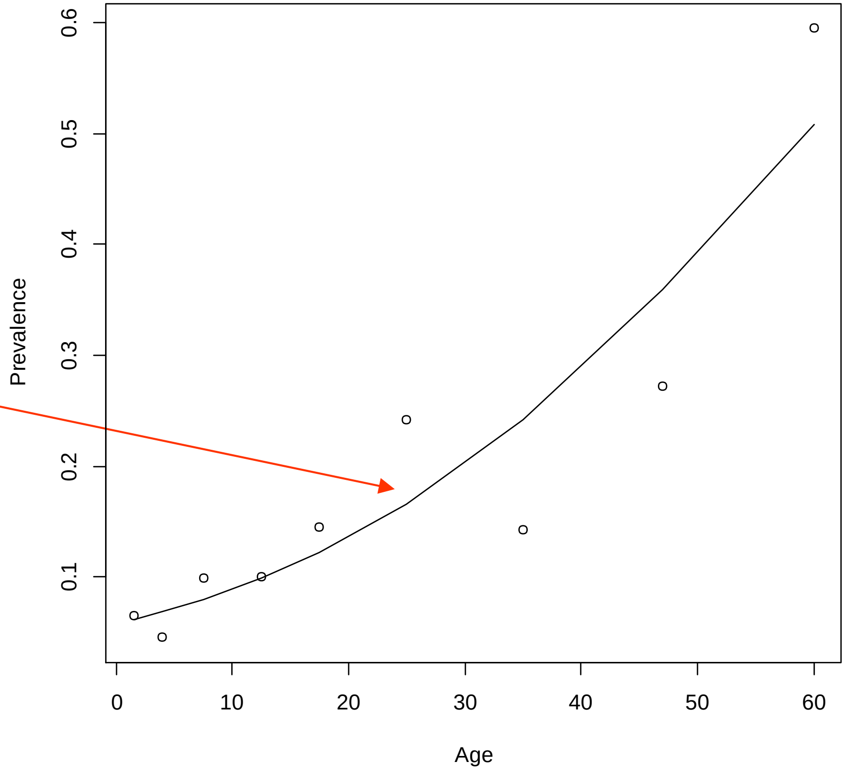
$$\log it\left(\hat{P}_i\right) = 2.71 + 0.044 \times age$$

Data and predicted values

```
> p <- pos/N
> plot(p ~ Age, xlab = "Age", ylab = "Prevalence")
> lines(Age, fit.Sero$fit)
```

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

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



Example 3: Bioassay

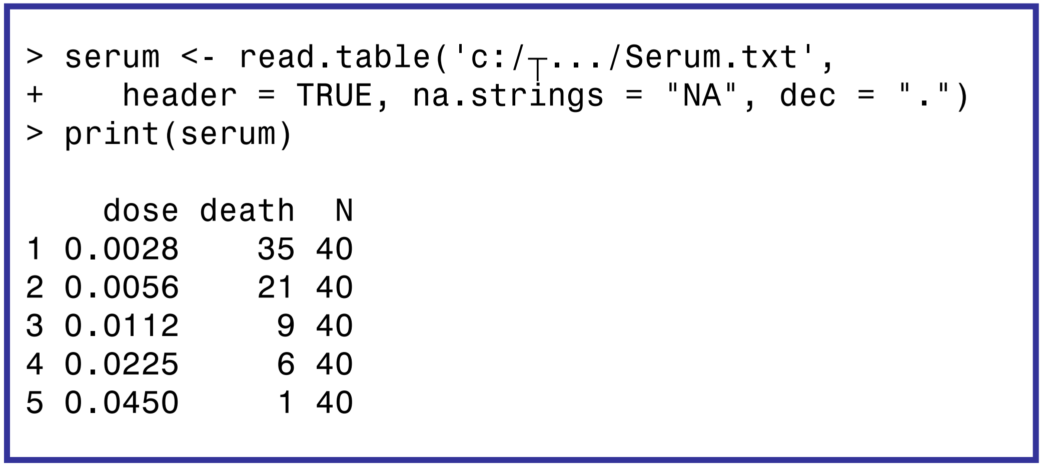
The response of the number of deaths within 7 days from injection.

The dose level is the predictor.

The question of primary interest:

What is the relationship between the injected dose and the number of deaths ?

Data structure in R

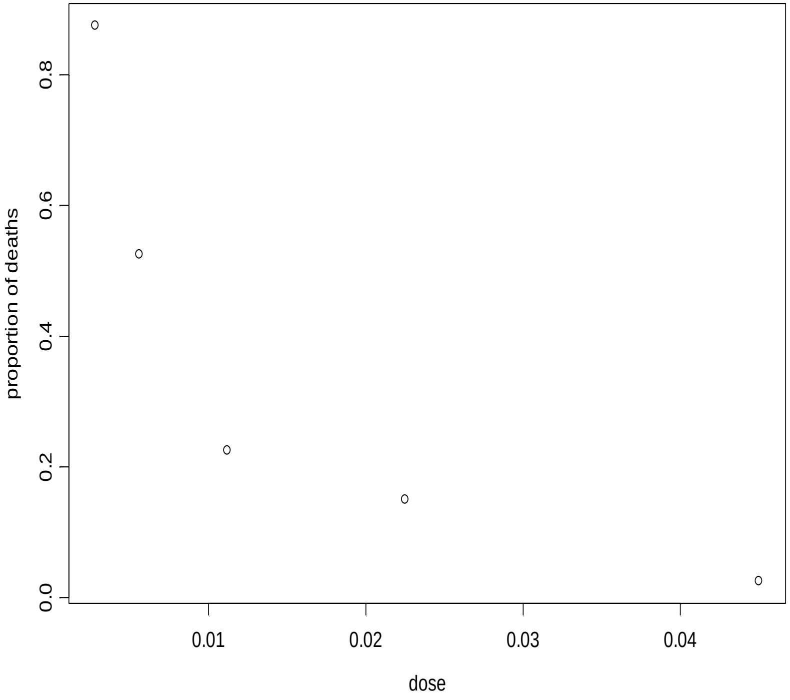


```
> serum <- read.table('c:/.../Serum.txt',
+    header = TRUE, na.strings = "NA", dec = ".")
> print(serum)

    dose death  N
1 0.0028    35 40
2 0.0056    21 40
3 0.0112     9 40
4 0.0225     6 40
5 0.0450     1 40
```

Dose of serum	Number of deaths	Sample size
0.0028	35	40
0.0056	21	40
0.0112	9	40
0.0225	6	40
0.0450	1	40

The data

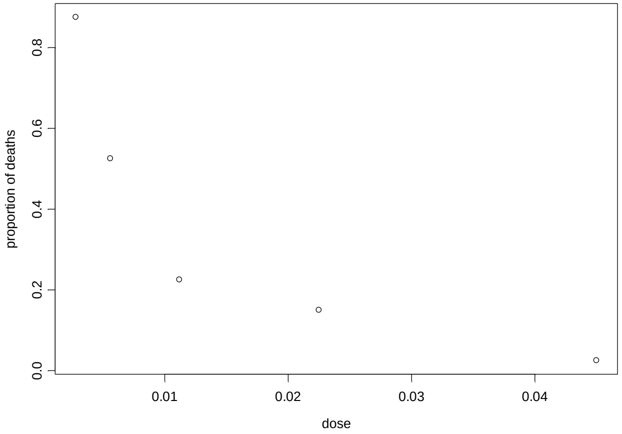
```
> print(serum)
    dose death  N
1 0.0028    35 40
2 0.0056    21 40
3 0.0112     9 40
4 0.0225     6 40
5 0.0450     1 40


> plot(death/N  ~ ldose,
   data = serum, xlab = "Dose",
   ylab = "Proportion of deaths")
```



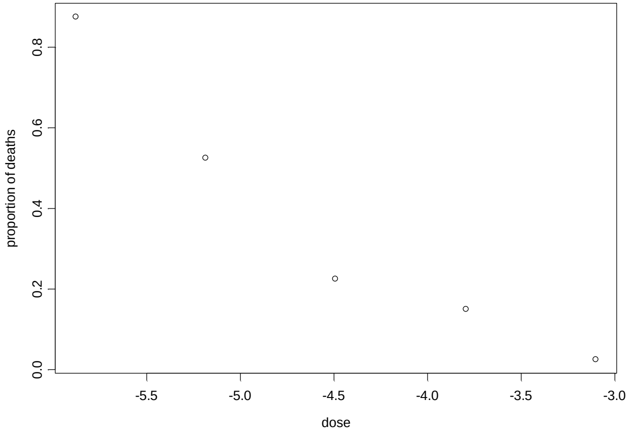
EXAMPLE 3: bioassay

Using log(dose) as predictor

Original scale



Log scale



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

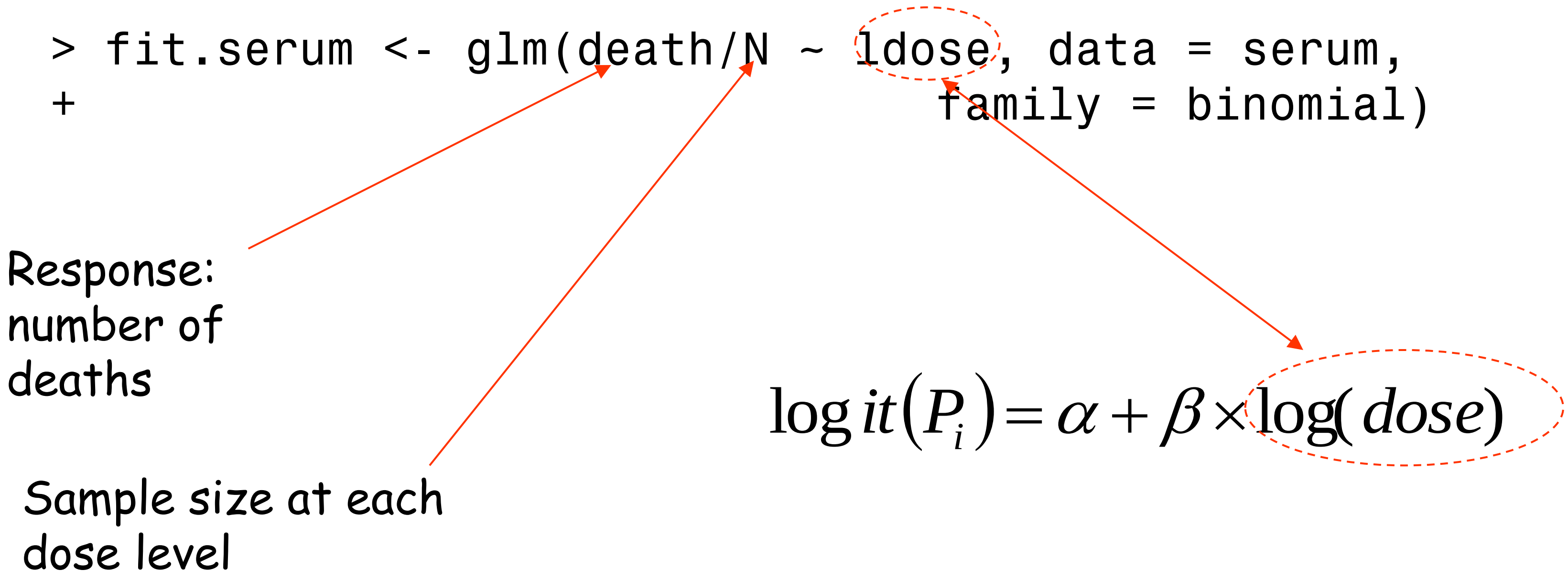
Y: Number of deaths

$$\log it(P_i) = \alpha + \beta \times \boxed{\log(dose)}$$

The model is fitted with dose on log scale

$$P_i = \frac{e^{\alpha+\beta\times\log(dose)}}{1+e^{\alpha+\beta\times\log(dose)}}$$

R script for the model



```
> fit.serum <- glm(death/N ~ ldose, data = serum,
+                       family = binomial)
```

Response: number of deaths

Sample size at each dose level

$$\log it(P_i) = \alpha + \beta \times \log(dose)$$

```
 print(serum)
    dose death  N
1 0.0028    35 40
2 0.0056    21 40
3 0.0112     9 40
4 0.0225     6 40
5 0.0450     1 40
```

Outout

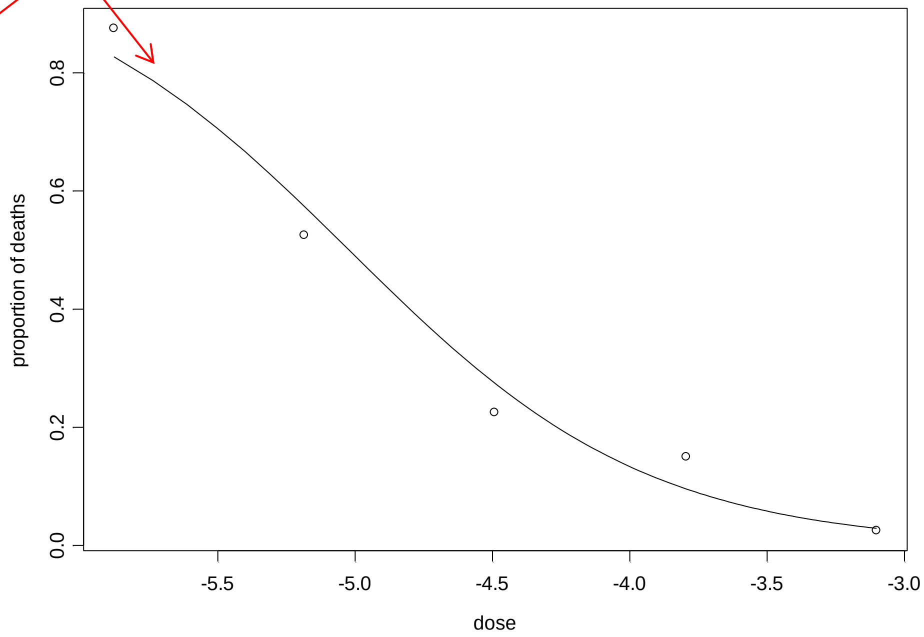
```
> summary(fit.serum)

Call:
glm(formula = death/N ~ ldose, family = binomial, data = serum)

Deviance Residuals:
       1         2         3         4         5
 0.13193  -0.09818  -0.11361   0.17236  -0.02366

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)   -9.189      7.938  -1.158    0.247
ldose         -1.830      1.610  -1.136    0.256

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 2.251289  on 4  degrees of freedom
Residual deviance: 0.070222  on 3  degrees of freedom
```

Data and fitted model

```
> plot(death/N  ~ ldose, data = serum, xlab = "Dose",
       ylab = "Proportion of deaths")
> lines(serum$ldose, fit.serum$fit)
```

Fitted values:

$$\hat{P}_i = \frac{e^{-9.189-1.830\times\log(dose)}}{1+e^{-9.189-1.830\times\log(dose)}}$$



ED50

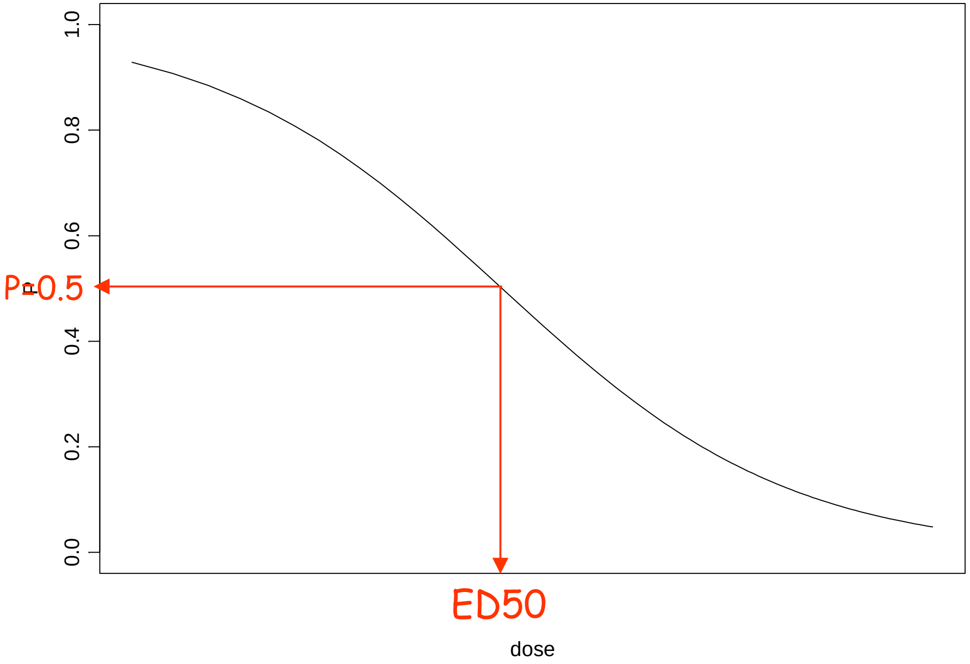
Consider the follwoing logistic regression model:

$$\log it\left(P_i\right) = \alpha + \beta \times \log(dose)$$

With

$$P_i = \frac{e^{\alpha+\beta\times dose}}{1+e^{\alpha+\beta\times dose}}$$

The ED50 is the dose level for which the probability for a response is equal to 0.5, this means that

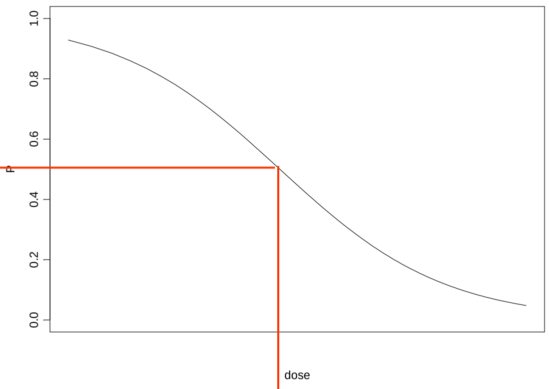


$$0.5 = \frac{e^{\alpha+\beta\times\log(dose)}}{1+e^{\alpha+\beta\times\log(dose)}}$$

This dose level is the ED50 (on log scale)

How to calculate the ED50 ?

$$0.5 = \frac{e^{\alpha+\beta\times ED50}}{1+e^{\alpha+\beta\times ED50}} \longleftarrow 0.5 = \frac{e^{\alpha+\beta\times dose}}{1+e^{\alpha+\beta\times dose}}$$



ED50

Logit of 0.5:

$$\log it(0.5) = \log\left(\frac{0.5}{1-0.5}\right) = \log(1) = 0$$

Logit of P:

$$\log it(P) = \log\left(\frac{P}{1-P}\right) = \alpha + \beta \times dose$$

For P=0.5, dose=ED50, this maens that

$$\alpha + \beta \times ED50 = 0 \dashrightarrow ED50 = -\frac{\alpha}{\beta}$$

Example 4: Determination of ESR

- The erythocte sedimentation rate (ESR) is the rate at which red blood cells settle out of suspensin in blood plasme when measured under standard condition.
- Response: binary (zero/one).

Data structure in R

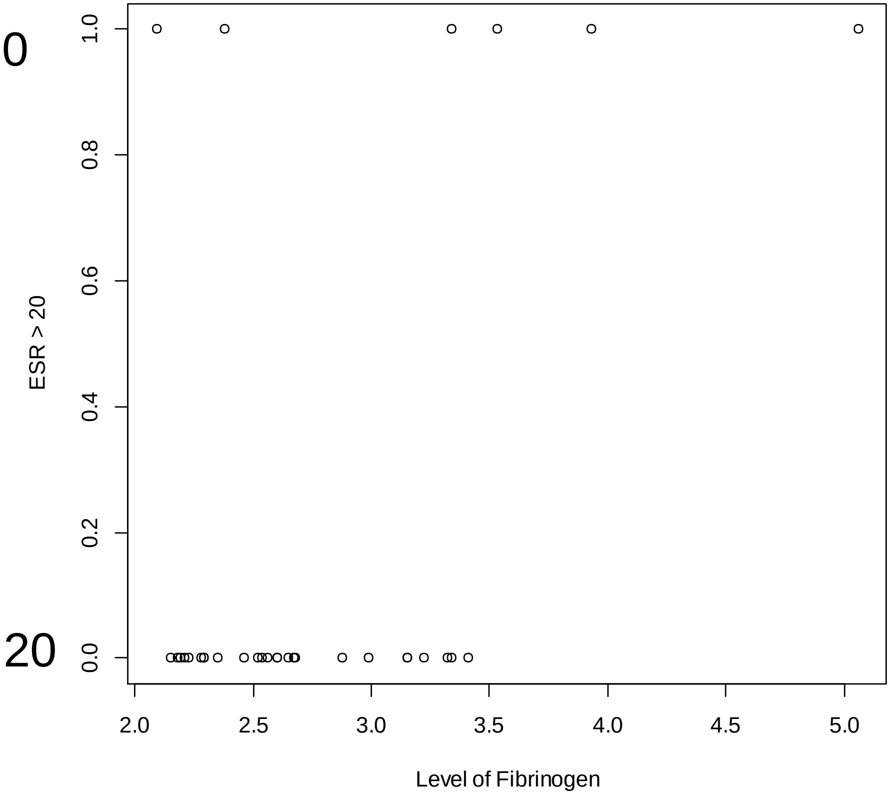
```
> serum <- read.table('c:/..../Serum.txt',
+    header = TRUE, na.strings = "NA", dec = ".")
> print(serum)

    dose death  N
1 0.0028    35 40
2 0.0056    21 40
3 0.0112     9 40
4 0.0225     6 40
5 0.0450     1 40
```

The data: zero/one data

```
> plot(Y ~ Fib, data = esr, xlab = "Level of Fibrinogen",
        ylab = "ESR > 20")
```

ESR > 20

ESR <= 20



```
> print(esr)
   Individual  Fib Glob Y
1           1 2.52   38 0
2           2 2.56   31 0
3           3 2.19   33 0
.
.
13         13 5.06   37 1
14         14 3.34   32 1
15         15 2.38   37 1
16         16 3.15   36 0
17         17 3.53   46 1
18         18 2.68   34 0
19         19 2.60   38 0
```

R script for the model

```
> fit.esr <- glm(Y ~ Fib, data = esr, family = binomial)
```

$$Y_i = \begin{cases} 1 & ESR > 20 \\ 0 & ESR \le 20 \end{cases}$$

predictor

Y ~ Fib

$$\Downarrow$$

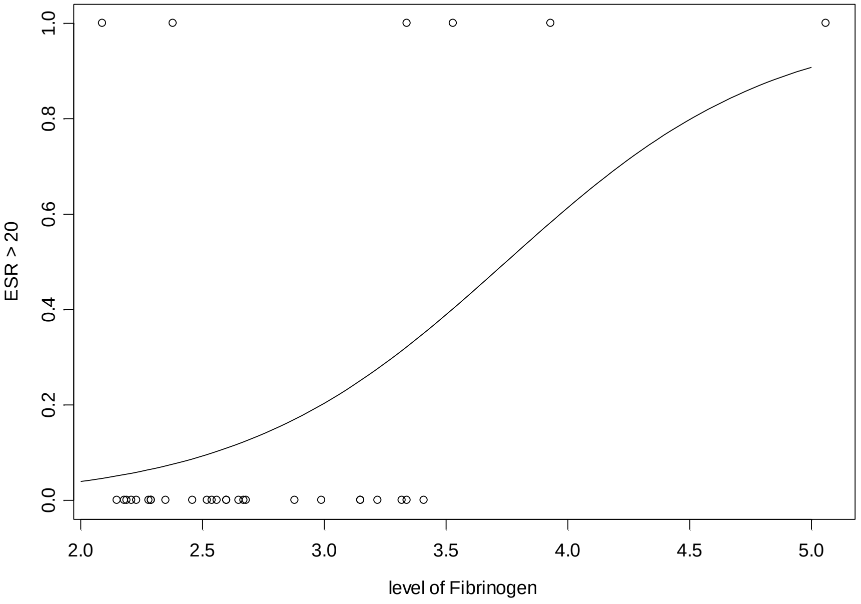
$$\log it\left(P_i\right) = \alpha + \beta \times Fib_i$$

R output

```
Call:
glm(formula = Y ~ Fib, family = binomial, data = esr)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-0.9298  -0.5399  -0.4382  -0.3356   2.4794

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -6.8451     2.7703  -2.471   0.0135 *
Fib           1.8271     0.9009   2.028   0.0425 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 30.885  on 31  degrees of freedom
Residual deviance: 24.840  on 30  degrees of freedom
AIC: 28.84

Number of Fisher Scoring iterations: 5
```

Data and fitted model

```
> plot(Y ~ Fib, data = esr, xlab = "Level of Fibrinogen",
       ylab = "ESR > 20")
> lines(Fib, fit.esr$fit)
```



$$\hat{P}_i = \frac{e^{\hat{\alpha}+\hat{\beta}\times Fib_i}}{1+e^{\hat{\alpha}+\hat{\beta}\times Fib_i}}$$

```
> summary(fit.esr)$coeff

              Estimate Std. Error   z value   Pr(>|z|)
(Intercept) -6.845075  2.7702849 -2.470892 0.01347765
Fib          1.827081  0.9008553  2.028162 0.04254367
```

$$\hat{\alpha} = \text{-}6.845075$$

$$\hat{\beta} = 1.827081$$

Example 5: Pneumoconiosis amongst coal miners

Pneumoconiosis amongst groups of coal miners with varying exposure to coal dust.

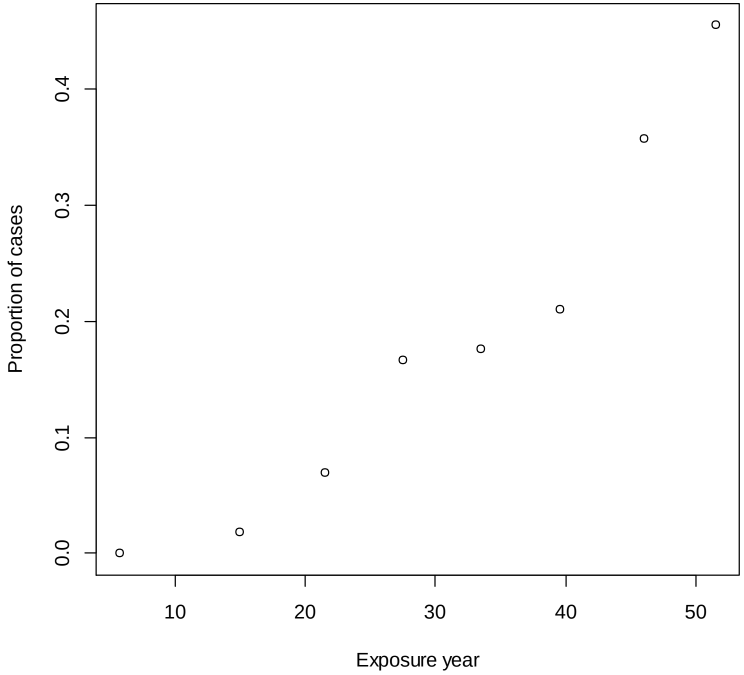
Does exposure time increase the probability to have the disease ?

A YouTube tutorial:

Statistics with R: Example of logistic regression (host by Phil Chan):
https://www.youtube.com/watch?v=xEllScuasns

Data structure in R

```
> Years<-c(5.8,15.0,21.5,27.5,33.5,39.5,46.0,51.5)
> Cases<-c(0,1,3,8,9,8,10,5)
> Miners<-c(98,54,43,48,51,38,28,11)
> CW<-cbind(Cases,Miners-Cases)
> CW
     Cases
[1,]     0 98
[2,]     1 53
[3,]     3 40
[4,]     8 40
[5,]     9 42
[6,]     8 30
[7,]    10 18
[8,]     5  6
```



```
> plot(Years,Cases/Miners, xlab = "Exposure year", ylab = "Proportion of cases")
```

Variables and model formulation

```
> data.frame(Years,Cases,Miners)


  Years Cases Miners
1   5.8     0     98
2  15.0     1     54
3  21.5     3     43
4  27.5     8     48
5  33.5     9     51
6  39.5     8     38
7  46.0    10     28
8  51.5     5     11
```

Y_i n_i

$$Y_{ij} = \begin{cases} 1 & \text{Pneumoconiosis} \\ 0 & \text{healthy} \end{cases}$$

$$Y_i = \sum_{j=1}^{n_i} Y_{ij}$$

Number of infected at each exposure group

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

n_i: sample size at each exposure group

We use logistic regression to model the probability of infection a function of exposure time in years:

$$\log it(P_i) = \alpha + \beta \times Exposure_i$$

R script for the model

```
> fit.miners2 <- glm(CW~ Years, family = binomial)
```

```
> CW
      Cases
[1,]      0 98
[2,]      1 53
[3,]      3 40
[4,]      8 40
[5,]      9 42
[6,]      8 30
[7,]     10 18
[8,]      5  6
```

```
CW ~ Years
```

⇩

$$\log it\left(P_i\right) = \alpha + \beta \times Exposure_i$$

Predictor: exposure time in years

R output

```
> summary(fit.miners2)

Call:
glm(formula = CW ~ Years, family = binomial)

Deviance Residuals:
    Min        1Q    Median        3Q       Max
-1.6625   -0.5746   -0.2802   0.3237   1.4852

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -4.79648    0.56859  -8.436  < 2e-16 ***
Years        0.09346    0.01543   6.059 1.37e-09 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 56.9028  on 7  degrees of freedom
Residual deviance:  6.0508  on 6  degrees of freedom
AIC: 32.877

Number of Fisher Scoring iterations: 4
```

$$\log it\left(\hat{P}_i\right) = \hat{\alpha} + \hat{\beta} \times \exp osure$$

$$\log it\left(\hat{P}_i\right) = \text{-}4.79648 + 0.09346 \times \exp osure$$

Data and predicted model

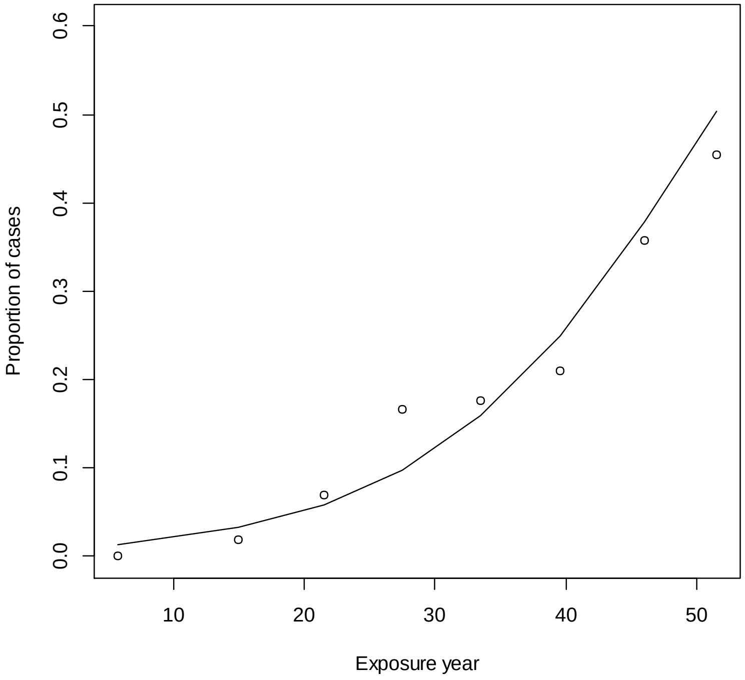
```
> plot(Years,Cases/Miners, xlab = "Exposure year",
       ylab = "Proportion of cases",ylim=c(0,0.6))
> lines(Years,fit.miners2$fit)
```

```
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -4.79648    0.56859  -8.436  < 2e-16 ***
Years        0.09346    0.01543   6.059 1.37e-09 ***
```

$$\hat{\alpha} = -4.79648$$

$$\hat{\beta} = 0.09346$$

$$\hat{P}_i = \frac{e^{\hat{\alpha} + \hat{\beta} \times Exposure_i}}{1 + e^{\hat{\alpha} + \hat{\beta} \times Exposure_i}}$$


Proportion of cases
Exposure year