vliruos
SHARING MINDS, CHANGING LIVES

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

•Statistics: 2011-2016, 2017.
•Statistics: 2017.
•Statistics for development : 2018-2022.

The >eR-Biostat initiative

Making R based education materials in statistics accessible for all

Basic concepts in statistical modeling using R: A Simple Logistic Regression

Developed by

Legesse Kassa Debusho (UNISA, South Africa), Ziv Shkedy (Hasselt University, Belgium)

and

Tadele Worku Mengesha (Gondar University), Abdisa Gurmessa (Jimma University)

https://erbiostat.wixsite.com/erbiostat

UPDATED: 2022

ER-BioStat

https://github.com/eR-Biostat

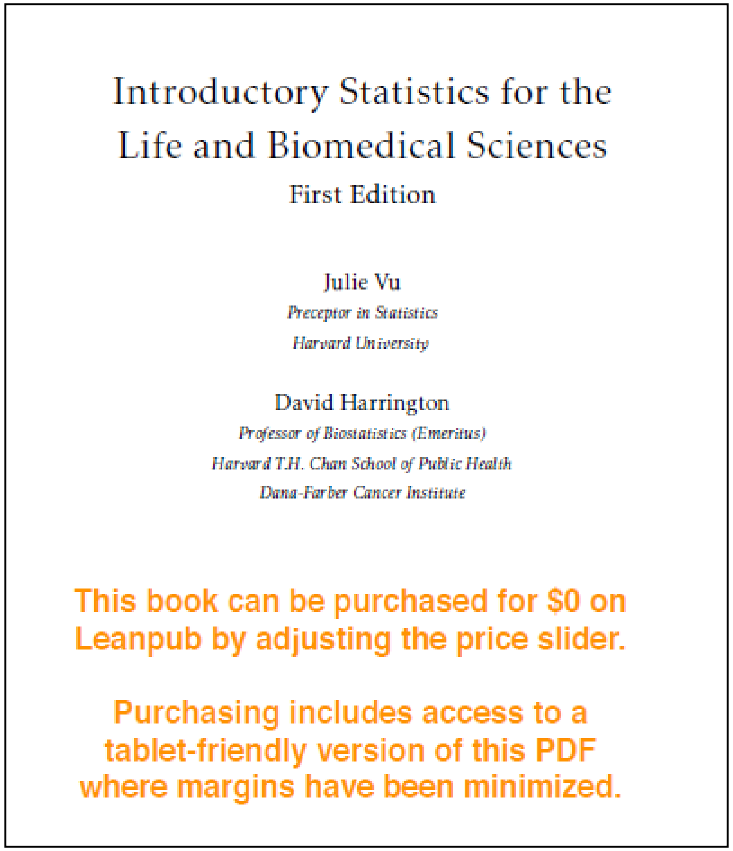
Email: erbiostat@gmail.com

@erbiostat

Contents

- Logistic regression:
  - Notation and model formulation.
    - Zero/one data.
    - Data in frequency tables.
  - Examples.
  - The glm() function in R.
  - Fitting logistic regression models using the glm() function in R: 5 examples.

Recommended reading



Introductory Statistics for the
Life and Biomedical Sciences
First Edition

Julie Vu
Preceptor in Statistics
Harvard University

David Harrington
Professor of Biostatistics (Emeritus)
Harvard T.H. Chan School of Public Health
Dana-Farber Cancer Institute

This book can be purchased for $0 on Leanpub by adjusting the price slider.

Purchasing includes access to a tablet-friendly version of this PDF where margins have been minimized.

- In this part of the course, we cover mainly Section 9.5.
- The examples that are used for illustration are not the same as the examples in the book.
- The book is available for free online:

https://www.openintro.org/book/biostat/

Section 9.5: introduction to logistic regression

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:

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

An 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 (=explanatory variable(s)).

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

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

Logistic regression model

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

Example:

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

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

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

Model formulation

Model formulation for zero/one (binary data)

$Y_i \sim B(1, \pi_i)$ The distribution of Y_i

$\pi = P(Y_i = 1)$=f$(predictor(s))$

$$\pi = \frac{e^{\alpha+\beta X}}{1+e^{\alpha+\beta X}}$$

The probability of success.

Dependency of Y_i on the predictor X_i

Our aim is to model the dependency of the response on the predictor, i.e., to estimate the unknown parameters α and β

The model consists of three components: the distribution of Y, the dependency of predictor(s) and the structure of the probability of success.

Binary data in frequency tables

Predictor	Response	Sample size
X_1	Y_1	n_1
X_2	Y_2	n_2
.	.	.
.	.	.
X_I	Y_I	n_I

A frequency table with I categories.

For each category X_i, there are n_i observations, each observation if a binary indicator:

$$Y_{ij} = \begin{cases} 1 & \pi \\ 0 & 1-\pi \end{cases}$$

The response Y_i is the sum of all 1s in the category:

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

Model formulation for data in frequency tables

$$Y_{ij} = \begin{cases} 1 & \pi \\ 0 & 1 - \pi \end{cases}$$

When data are given in frequency tables, there are n_i observations per category in the table.

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

Y_i is the number of 1s in the category.

$Y_i \sim B(n_i, \pi_i)$ The distribution of Y_i

$$\pi = P(Y_i = 1) = \text{f}(predictor(s))$$

$$\pi = \frac{e^{\alpha+\beta X}}{1+e^{\alpha+\beta X}}$$

Examples & notaions

Example 1: Smoked mice

- In order to investigate the influence of smoking on lung cancer a group of 55 mince were randomized into two treatment groups.
- In the first group (the treated group), each mouse was closed 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 cambers for 12 hours with out smoke.
- After one year an autopsy was carried out.
- The response is the present and absent of a tumour.
- The second variable in the data is the treatment group.

Smoked mice: the response variable

The question of primary interest is:

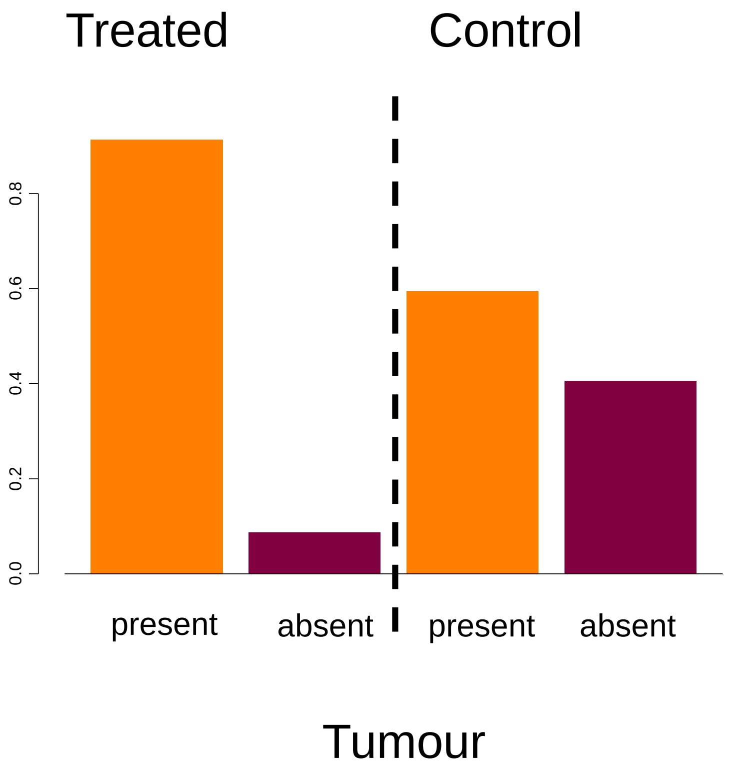
DOSE THE SMOKE INCREDSE THE RISK FOR CANCER ?

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

The response variable

Smoked mice: the data

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



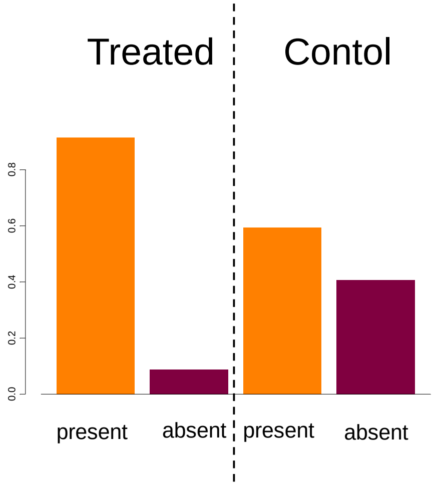
Smoked mice

	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 experiment.
- Individual data can be extracted from the table.
- In terms of statistical modelling, the response is binary (tumour absent/tumour present).
- 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 difference is only due to chance or if the smoke increase the risk for tumour.

Response:

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

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 called seropositive.

Example 2: Serological data

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

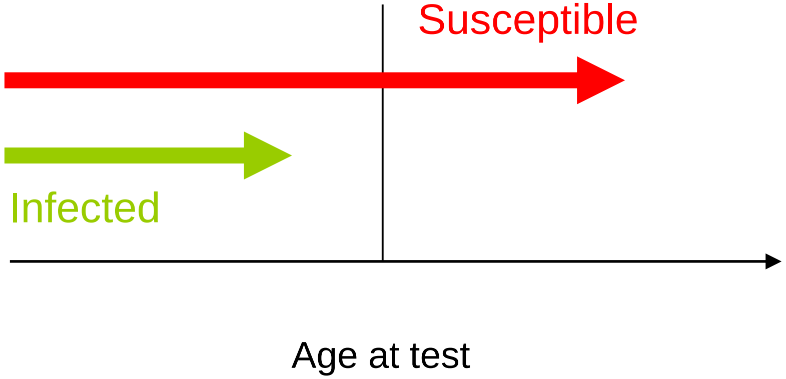
1. Age at test.
2. Infected or not.

- Prevalence of sero-positivity In the sample:

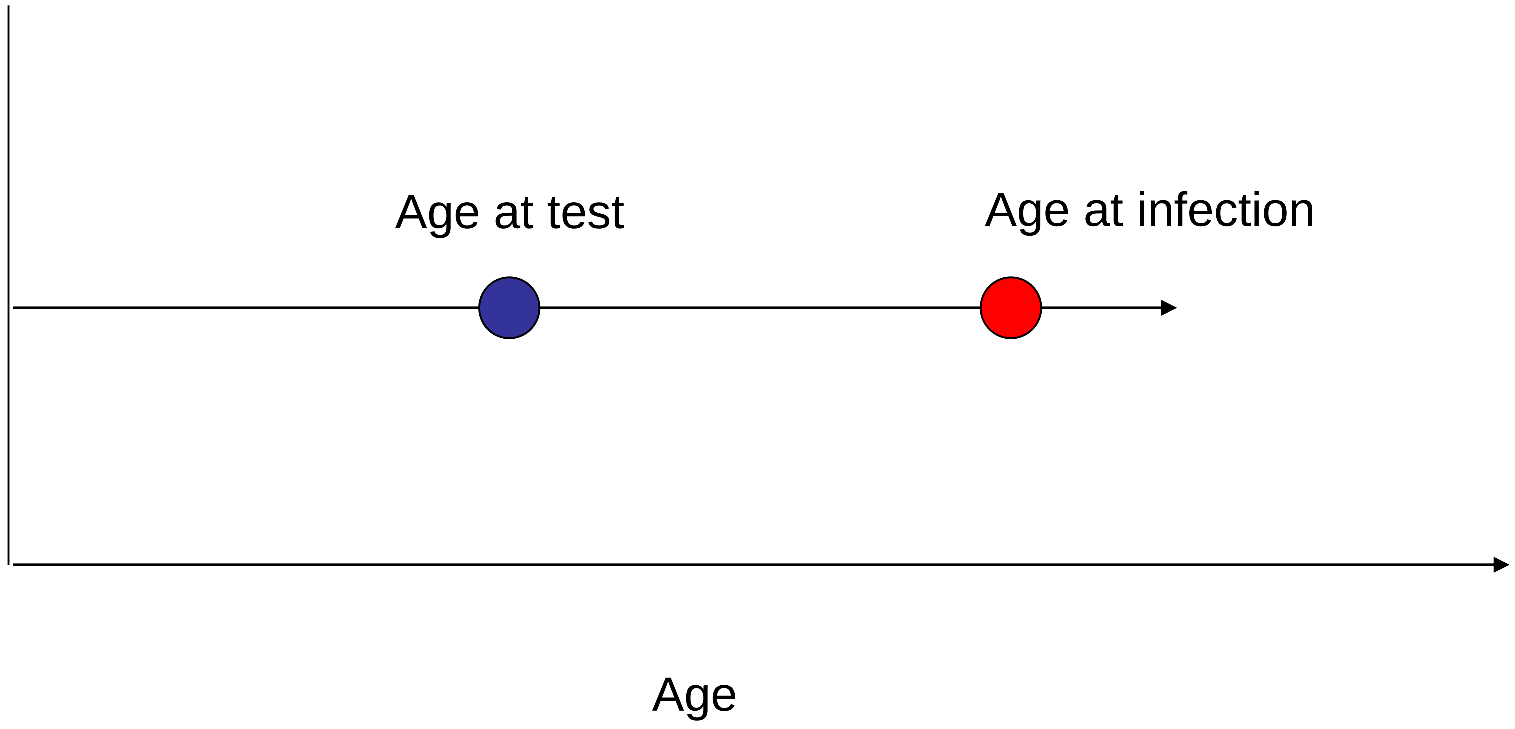
$$\pi(a)$$

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

- Sero-prevalnce data

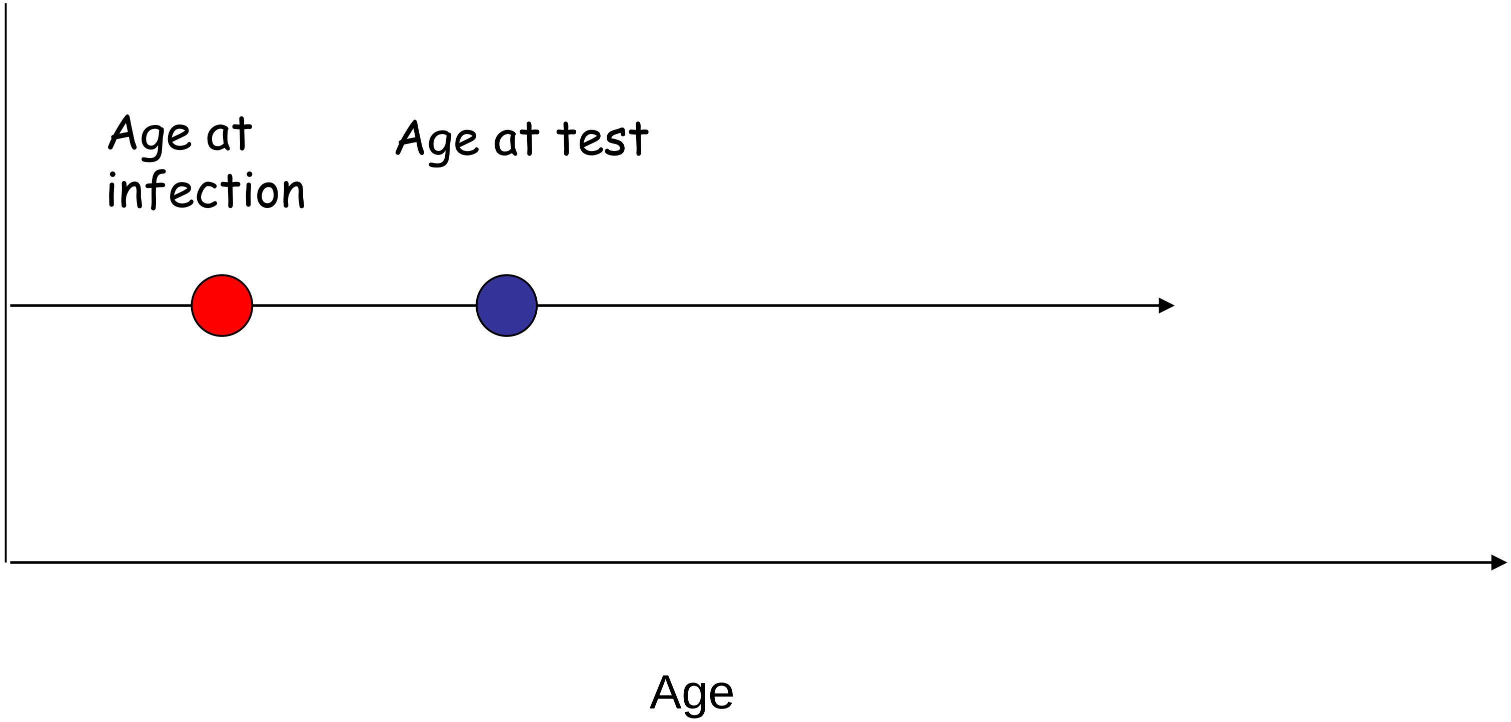


Current status data: sero-negative



- Sero-Negative: infected after the test.

Current status data: sero-positive



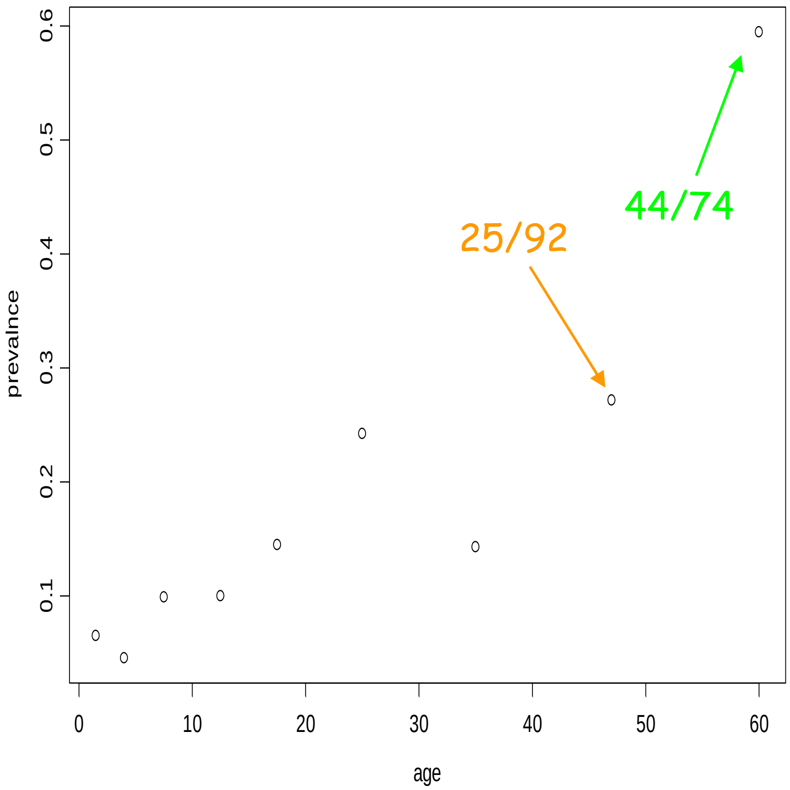
- Sero-Positive: infected after the test.

Example 2: Serological data

Malaria in Brasil

Age group	Mid age	Sero positive	Sample size
1	1.5	8	123
2	4.0	6	132
3	7.5	18	182
4	12.5	14	140
5	17.5	20	138
6	25.0	39	161
7	35.0	19	133
8	47.0	25	92
9	60.0	44	74

What is the relationship between infection and age ?



44/74

25/92

Example 2: Serological data

Age group	Mid age	Sero positive	Sample size
1	1.5	8	123
2	4.0	6	132
3	7.5	18	182
4	12.5	14	140
5	17.5	20	138
6	25.0	39	161
7	35.0	19	133
8	47.0	25	92
9	60.0	44	74

Response:

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

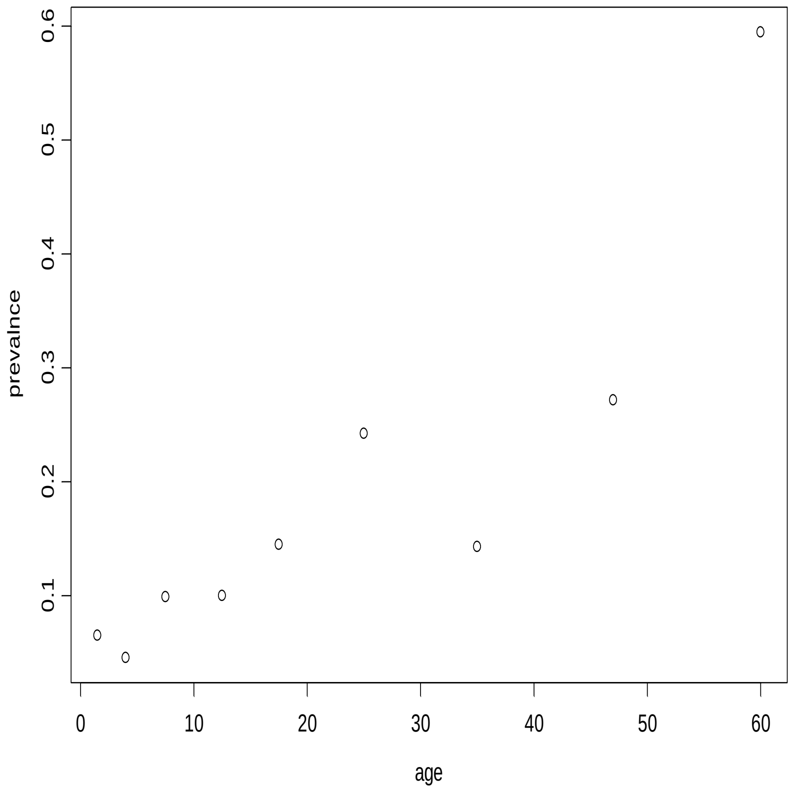
Number of Sero+ in age group i:

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

Sample size at age group i:

$$n_i$$

Example 2: Serological data



What is the relationship between the age and the probability to be infected ?

Response: number of infected (sero+):

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

Predictor: age.

We want to model the probability to be infected as a function of the age.

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

Example 3: Bioassay data

- A bioassay experiment is an experiment designed to assess the potency of a compound by means of the response produced when it is administrated to a living organism.

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

- Study design:
  - The experiment consist of 5 groups of 40 mice.
  - Each group was injected with combination of an infecting dose of a culture of pneumococci and one of five doses of the anti pneumococcus serum.

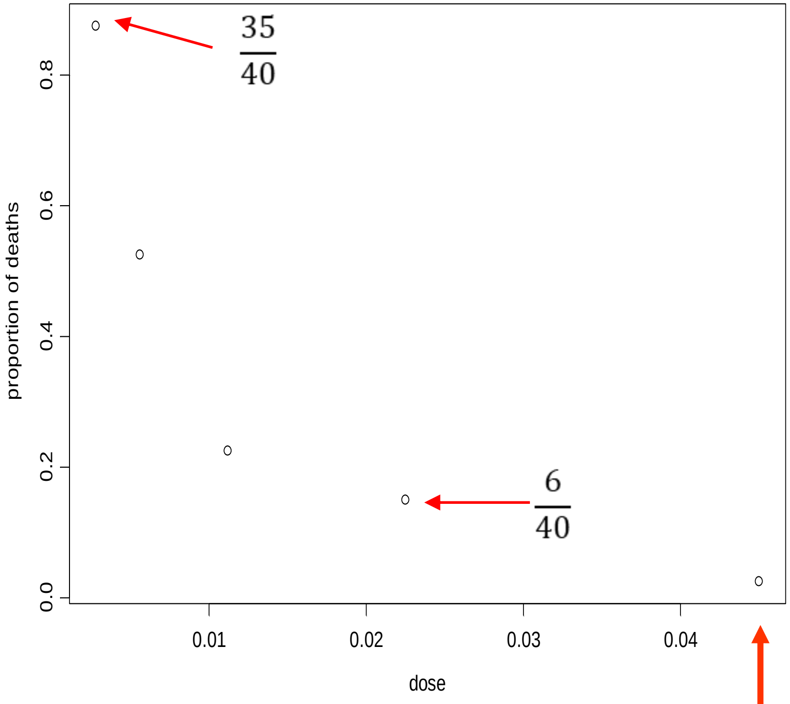
Bioassay data: response and predictor

- 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

- A frequency table with 5 categories.
- 40 subjects per category.

Response:

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

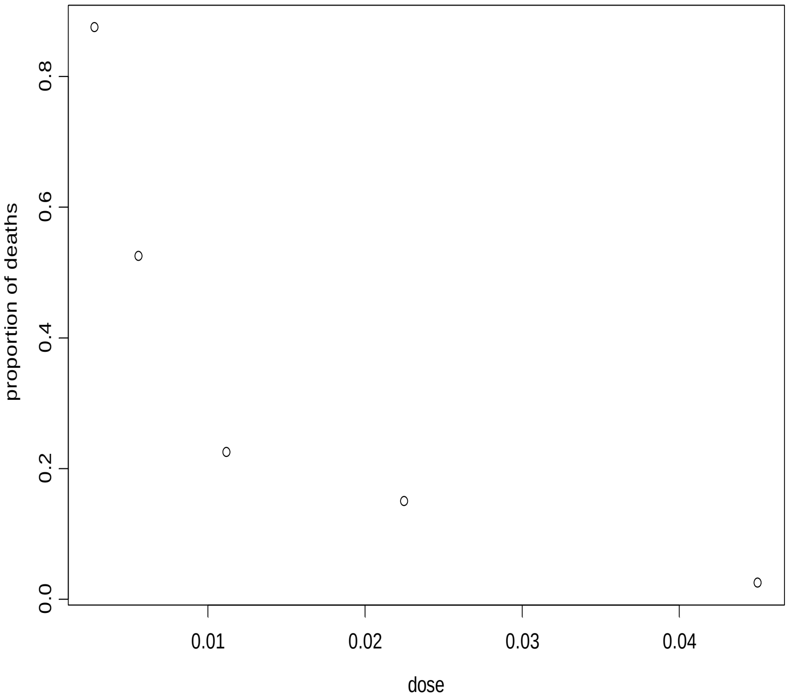
Number of deaths in dose level i:

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

Sample size at dose level i:

$$n_i$$

Example 3: response and predictor



Response: number of deaths at each dose level:

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

Predictor: dose.

The model:

$$P(Y_{ij} = 1) = P(death) = f(dose)$$

Example 4: determination of ESR

- The erythocte sedimentation rate (ESR) is the rate at which red blood cells settle out of suspension in blood plasma when measured under standard condition.
- The ESR increase if the levels of certain proteins in the blood increase.
- Rheumatic diseases, chronic diseases and infections increase these proteins level.
- From that reason the determination of the ESR is one of the most commonly used screening tests performed on samples bloods.

Determination of ESR: the data

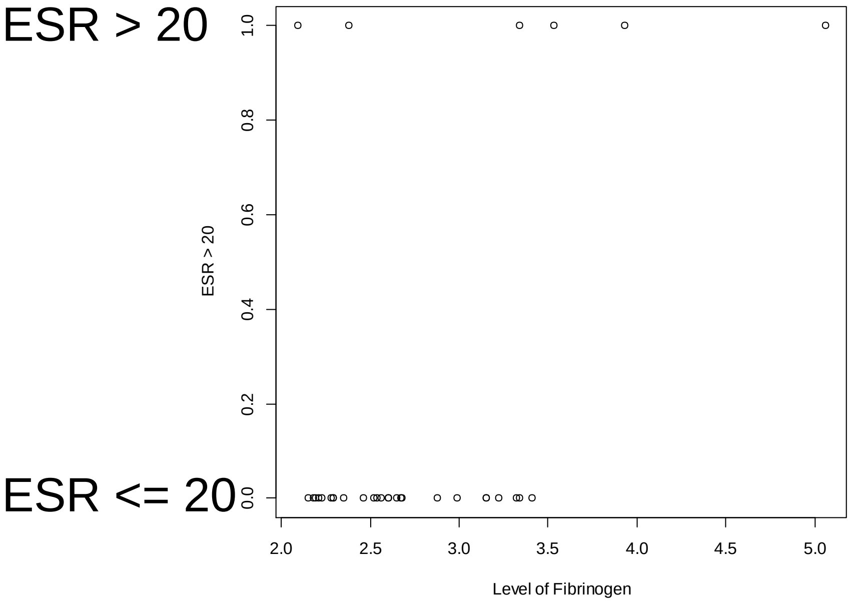
	Individual	**Fib**	Glob	Y
1	1	2.52	38	0
2	2	2.56	31	0
3	3	2.19	33	0
4	4	2.18	31	0
5	5	3.41	37	0
.	.	.	.	.
.	.	.	.	.
.	.	.	.	.
19	19	2.60	38	0
20	20	2.23	37	0
21	21	2.88	30	0
22	22	2.65	46	0
23	23	2.09	44	1
24	24	2.28	36	0
25	25	2.67	39	0
26	26	2.29	31	0
27	27	2.15	31	0
28	28	2.54	28	0
29	29	3.93	32	1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

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

- Data:
  - Fib: Fibrinogen level.
  - Glob:
  - Y: 0/1 indicator for ESR.

Example 4: determination of ESR



Response:

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

Predictor: Fibrinogen level.

A model for the probability that ESR>20:

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

Example 5: Pneumoconiosis amongst coal miners

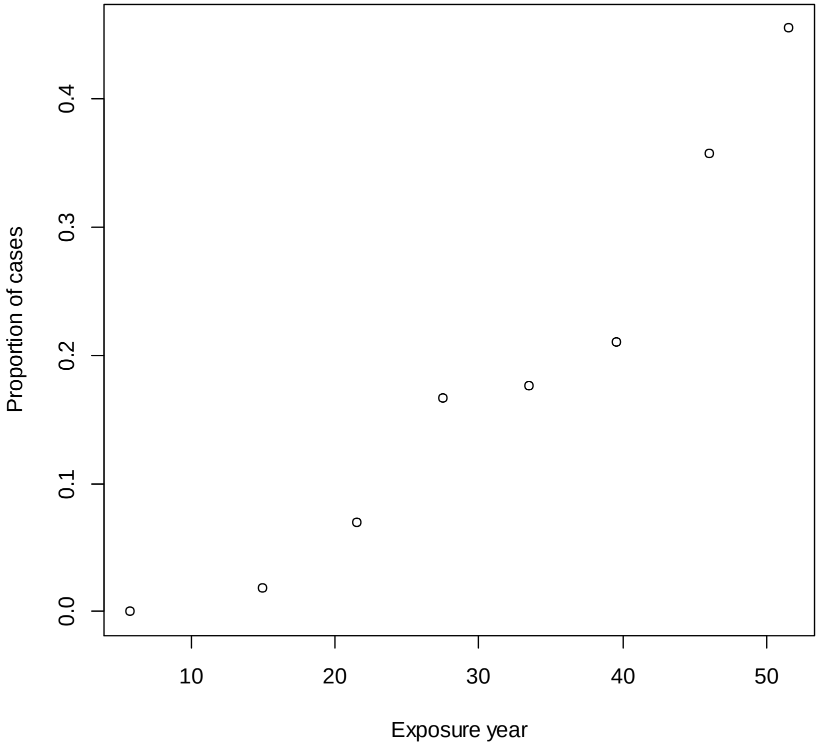
- Pneumoconiosis amongst groups of coal miners with varying exposure time to coal dust.
- Does exposure time increase the probability to have the disease ?

↓

predictor

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
```



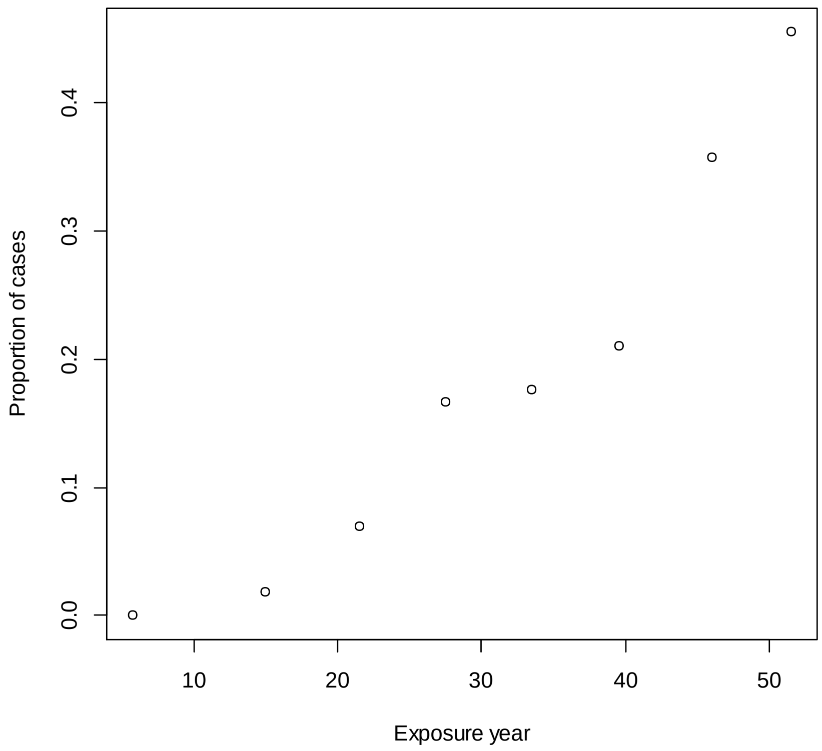
- Predictor: exposure time in years.
- Response: disease.
- Data:
  - Cases: number of miners with disease (Y_i).
  - Miners: number of miners in the category (n_i).

Example 5: response and predictor

Response:

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

$$Y_i = \sum_{j=1}^{n_i} Y_{ij} \Leftrightarrow Y_i \sim B(n_i, \pi_i)$$



Predictor: years of exposure to coal dust.

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

Summary: a logistic regression model

Data in table format

$$Y_{ij} = \begin{cases} 1 & \pi \\ 0 & 1-\pi \end{cases}$$

$$Y_i = \sum_{i=1}^{n_i} Y_{ij} \Longleftrightarrow Y_i \sim B(n_i, \pi_i)$$

Zero/One data

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

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

The model for the probability (as a function of the predictor):

$$\pi_i = \frac{e^{\alpha+\beta X_i}}{1+e^{\alpha+\beta X_i}}$$

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 function.

$$\left.\begin{array}{l} Y_{ij} = \begin{cases} 1 & \pi \\ 0 & 1-\pi \end{cases} \\ \\ Y_i = \sum_{i=1}^{n_i} Y_{ij} \Leftrightarrow Y_i \sim B(n_i, \pi_i) \end{array}\right\} \text{family=binomial}$$

$$\left.\pi_i = \frac{e^{\alpha+\beta X_i}}{1+e^{\alpha+\beta X_i}} \Rightarrow log\left(\frac{\pi_i}{1-\pi_i}\right) = \alpha + \beta X_i \right\} \text{link = "logit"}$$

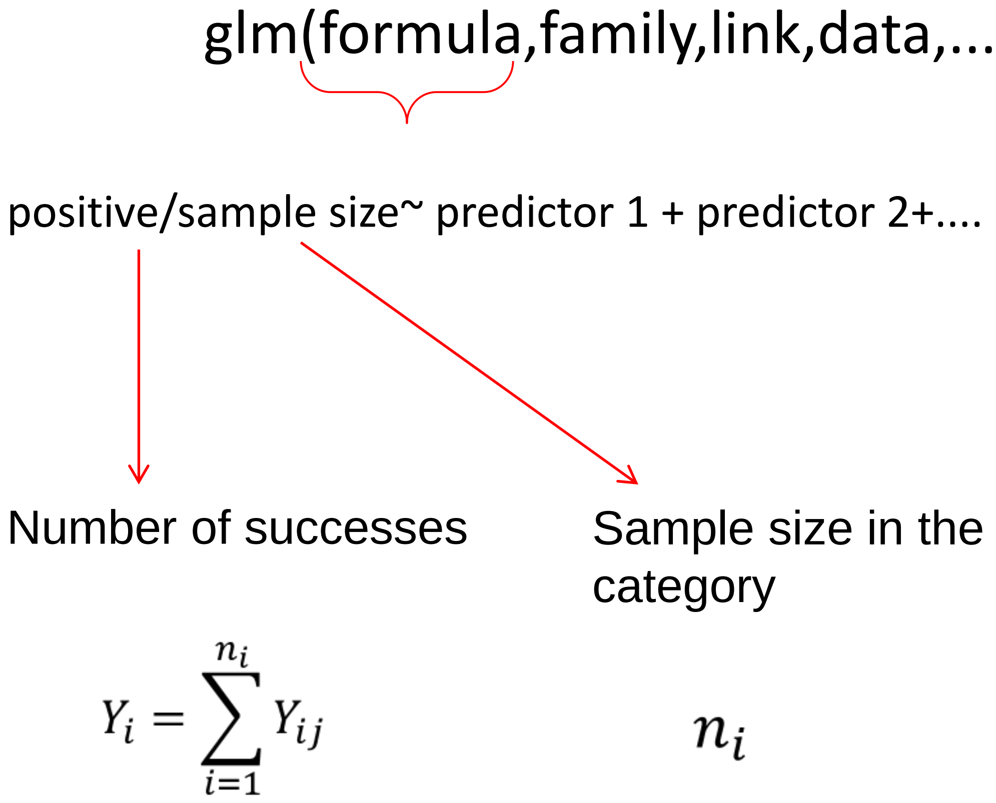
The glm() Function: zero/one data.

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

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

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

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

Sample size in the category

$$n_i$$

Fitting logistic regression models using the glm( ) function in R: 5 examples

Example 1: Smoked mice

The question of primary interest is:

DOSE THE SMOKE INCREASE THE RISK FOR CANCER ?

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

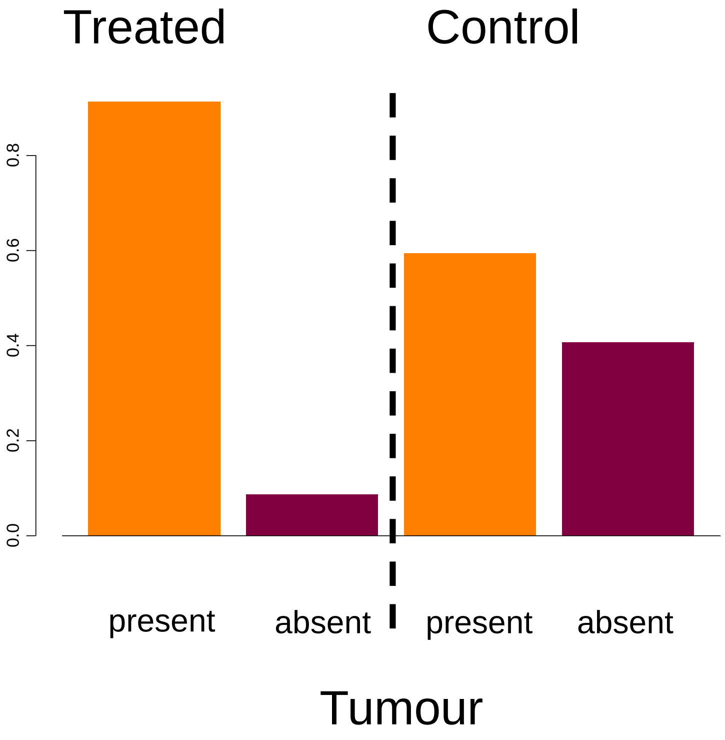
The response variable

EXAMPLE 1: SMOKED MICE

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 (i.e. cancer) given the treatment group.
- Predictor: treatment group (X_i).

$$X_i = \begin{cases} 1 & Treatment \\ 0 & Control \end{cases}$$

The individual data

$$Y_{ij} = \begin{cases} 1 & Cancer \\ 0 & No\ cancer \end{cases}$$

Number of subjects with tunour

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

Distribution of Y

$$Y_i \sim B(n_i, \pi_i)$$

The model for the probability:

$$\pi_i = \frac{e^{\alpha+\beta X_i}}{1+e^{\alpha+\beta X_i}} \Rightarrow log\left(\frac{\pi_i}{1-\pi_i}\right) = \alpha + \beta X_i$$

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"))
```

$$log\left(\frac{\pi_i}{1-\pi_i}\right)= \alpha + \beta X_i$$

$$Y_i \sim B(n_i, \pi_i)$$

$$\pi_i = \frac{e^{\alpha+\beta X_i}}{1 + e^{\alpha+\beta X_i}}$$

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
```

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

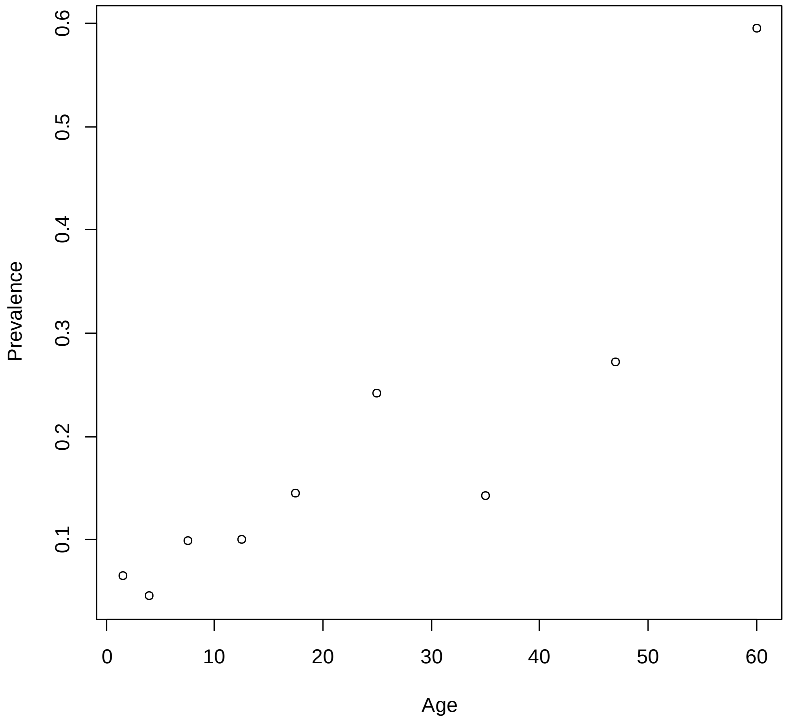
$$OR = \exp(1.971886) = 7.184.$$

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

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

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

Number of sero-positive at each age group

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

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

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

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)
```

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

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
```

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

$$\downarrow \qquad \downarrow$$

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

Data and predicted values

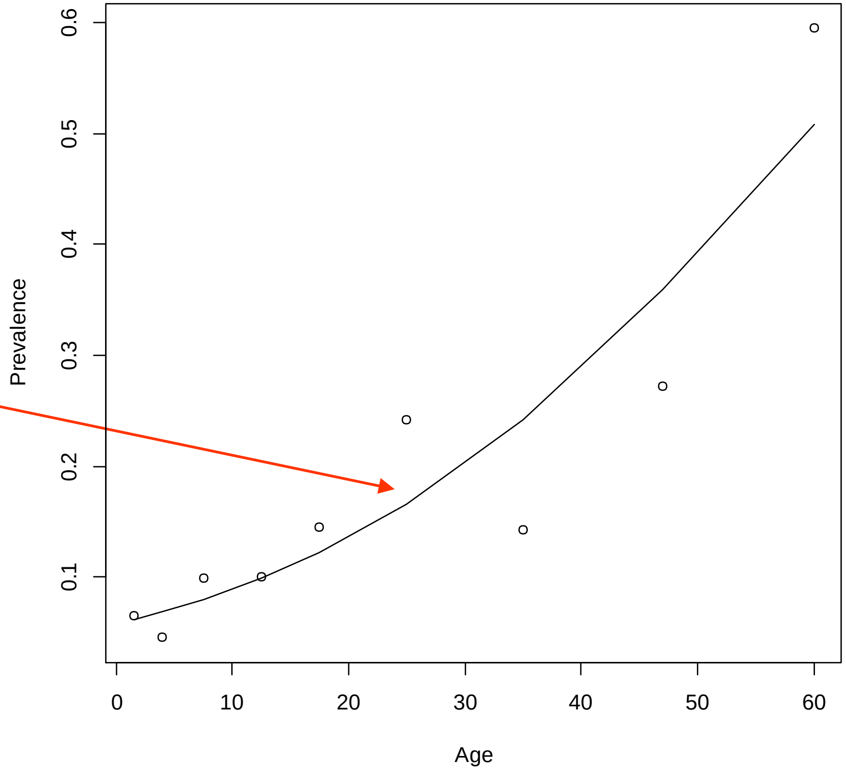
```
> p <- pos/N
> plot(p ~ Age, xlab = "Age", ylab = "Prevalence")
> lines(Age, fit.Sero$fit)
```

Predicted values:

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

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

fit.Sero$fit



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

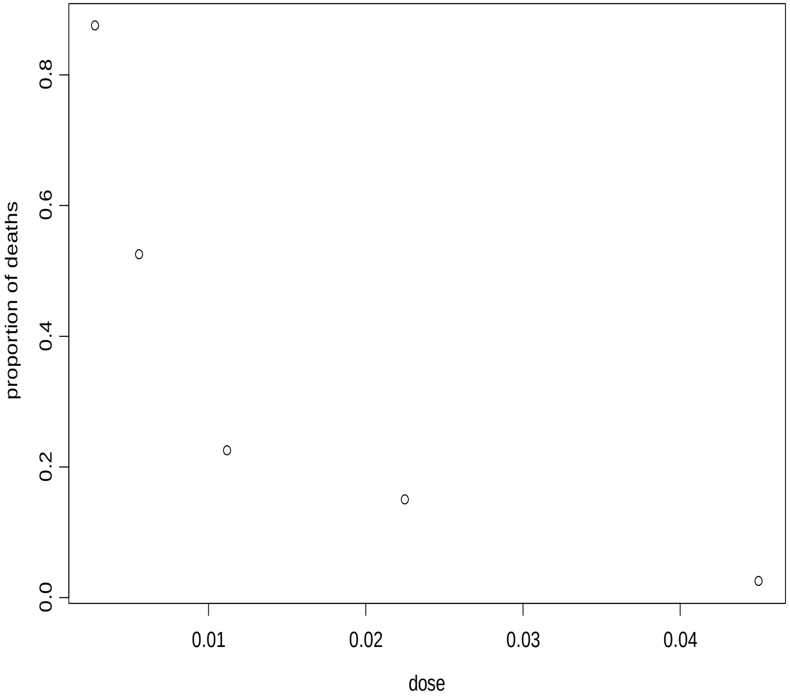
```
> serum <- read.table('c:/....../Serum.txt',
+    header = TRUE, na.strings = "NA", dec = ".")
> print(serum)

    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

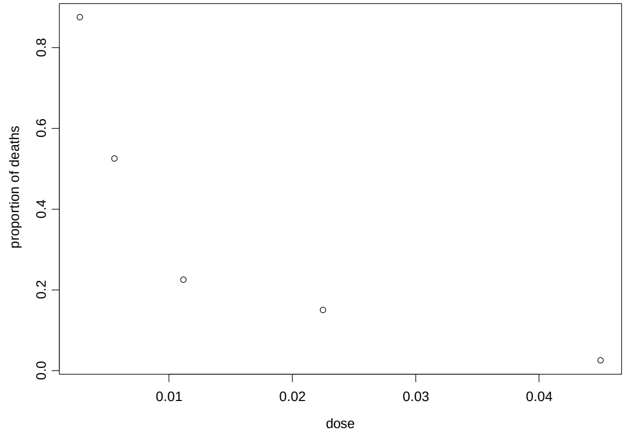
```
> print(serum)
    dose death  N
1 0.0028    35 40
2 0.0056    21 40
3 0.0112     9 40
4 0.0225     6 40
5 0.0450     1 40
```

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

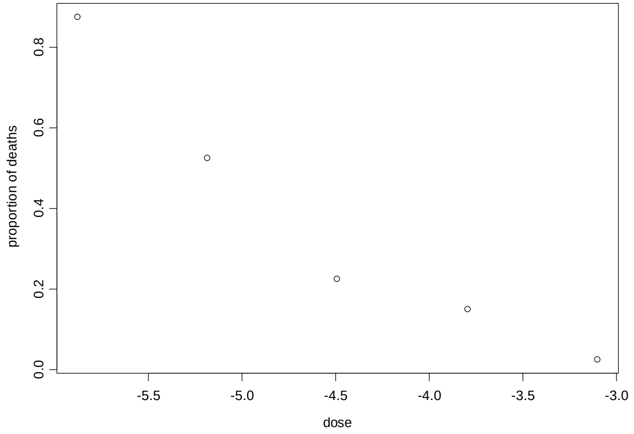


Using log(dose) as predictor

Original scale



Log scale



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

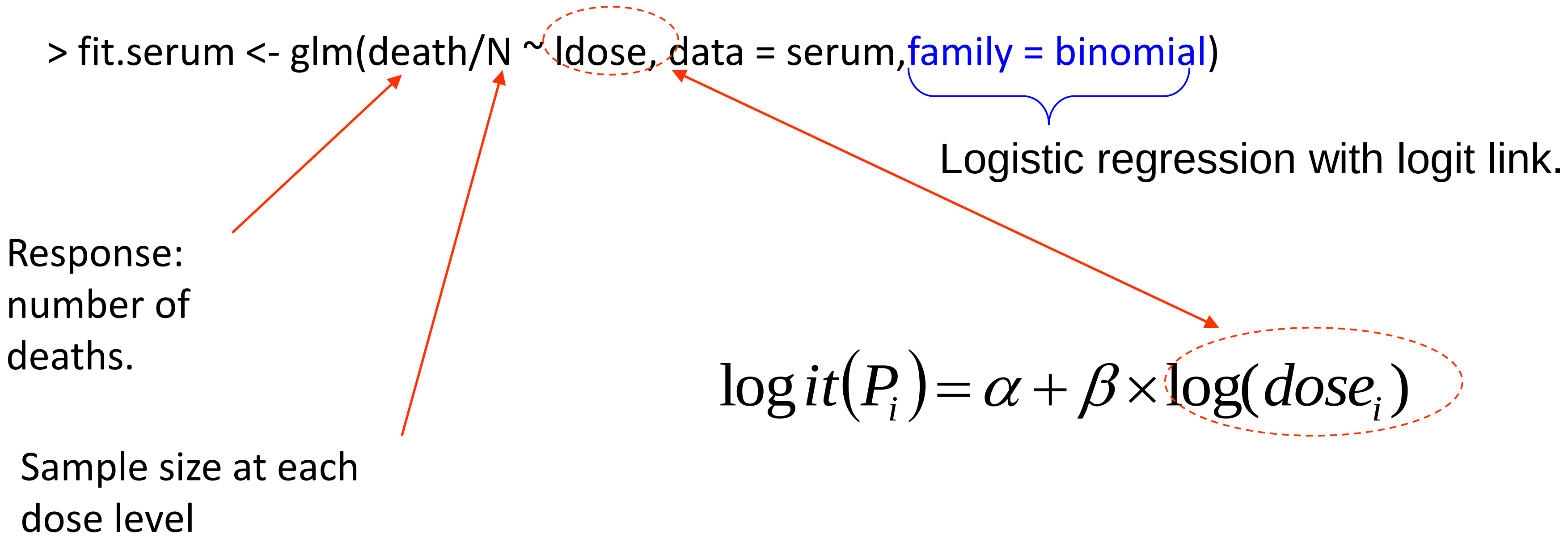
Y: Number of deaths

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

The model is fitted with dose on log scale:

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

R script for the model



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

Logistic regression with logit link.

Response: number of deaths.

Sample size at each dose level

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

```
  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

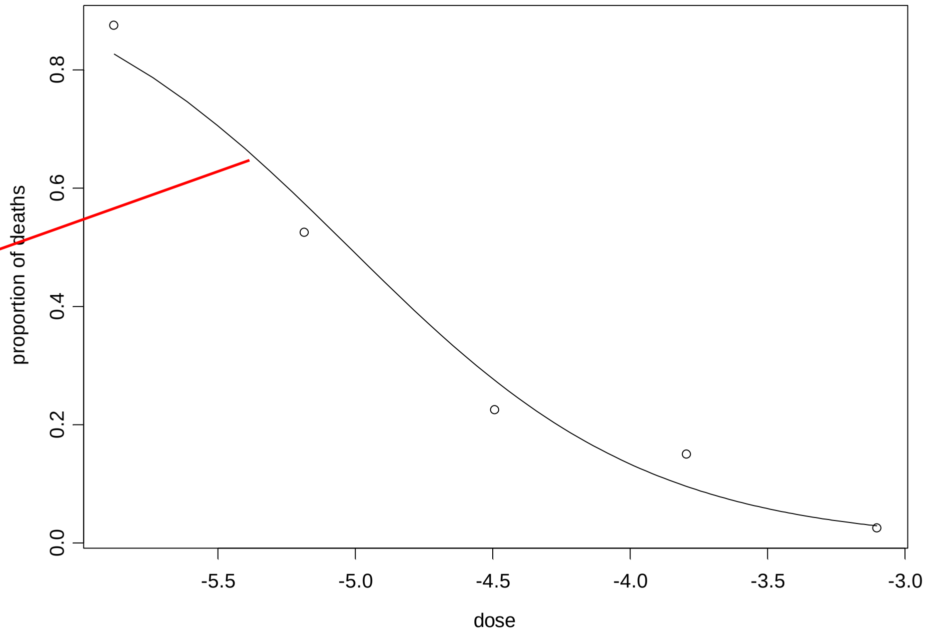
```
> summary(fit.serum)

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:

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



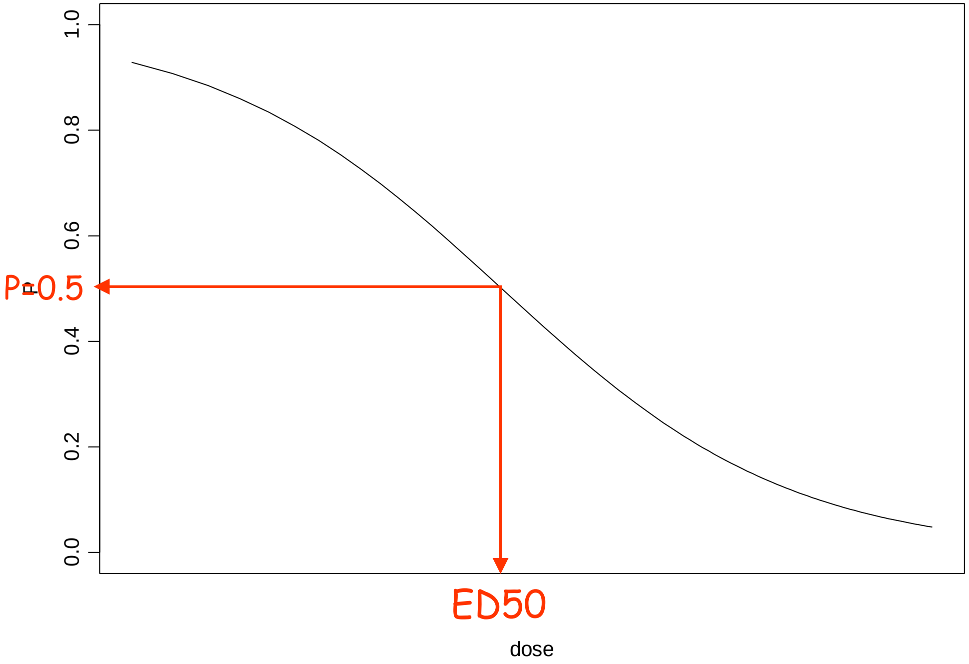
ED50

Consider the follwoing logistic regression model:

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

With

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



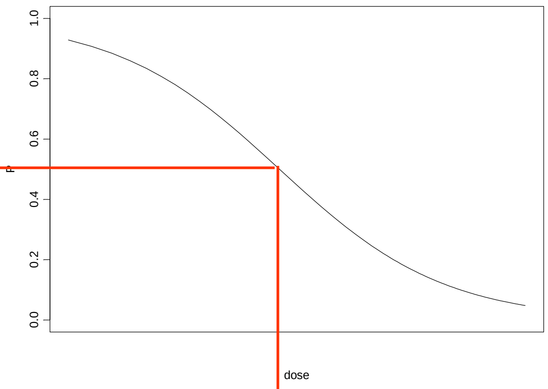
The ED50 is the dose level for which the probability for a response is equal to 0.5, this means that

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

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

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

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).

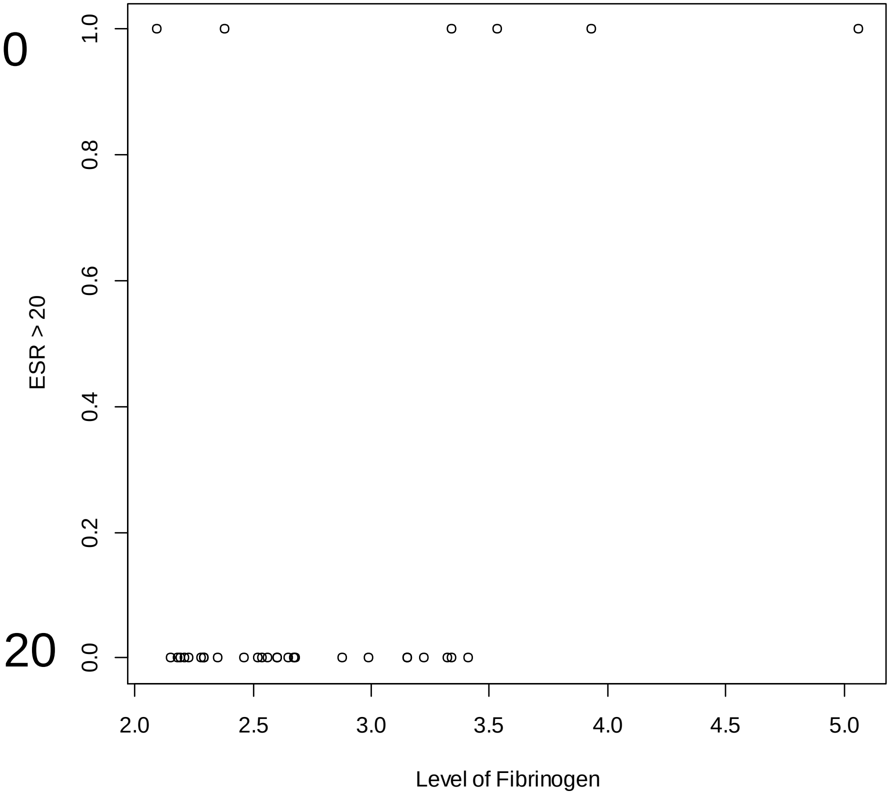
Data structure in R

```
> 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
```

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

R script for the model

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

Y ~ Fib

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

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

response

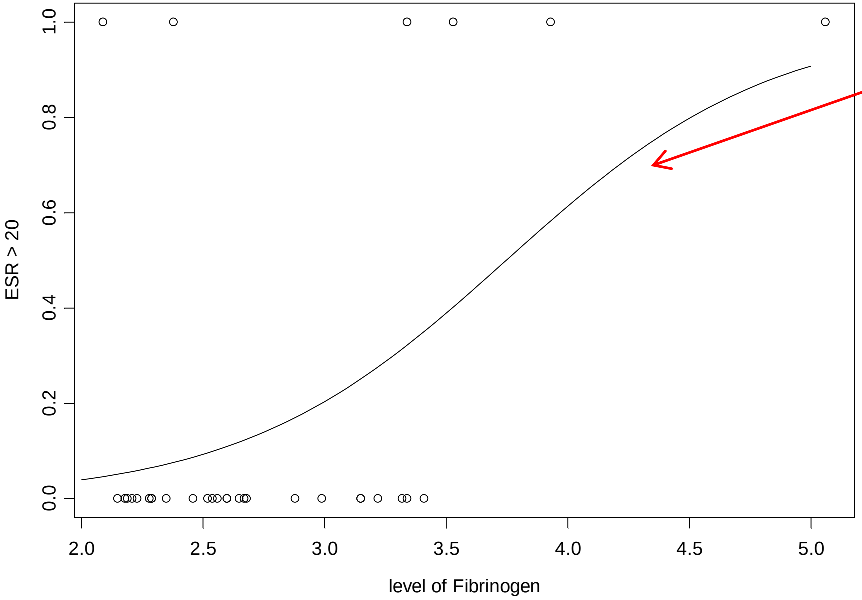
predictor

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)
```



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

```
> 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
```

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

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

Example 5: Pneumoconiosis amongst coal miners

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

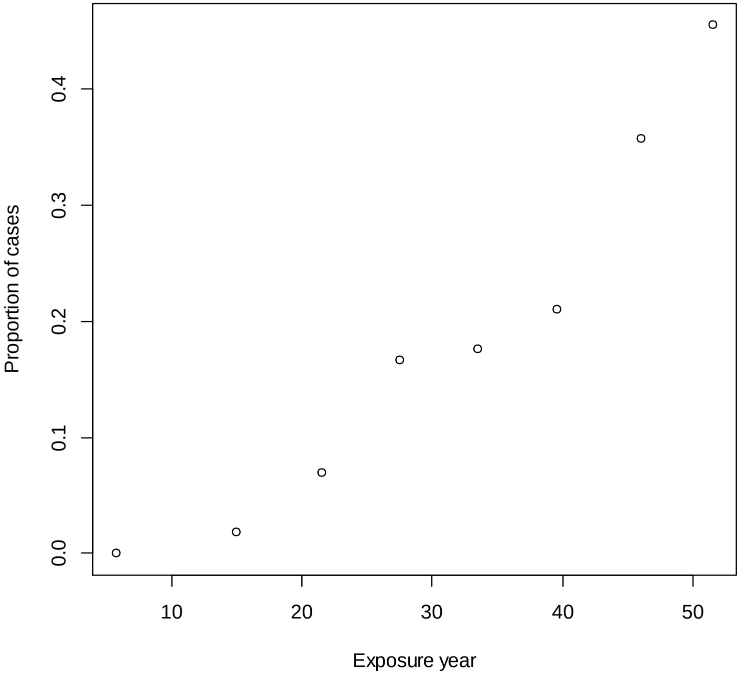
Does exposure time increase the probability to have the disease ?

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
```

n_i

Y_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

⇩

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

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
```

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

$$\downarrow \quad \downarrow$$

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

Data and predicted model

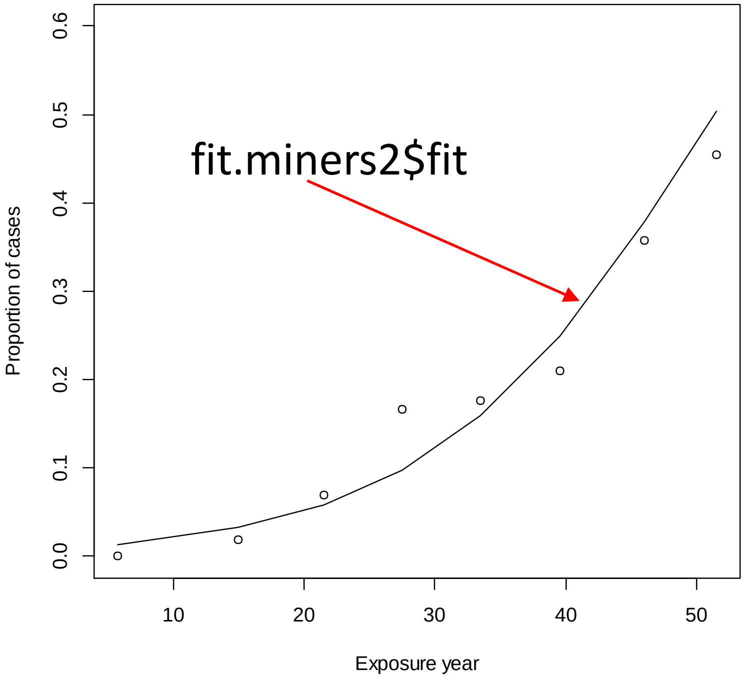
```
> plot(Years,Cases/Miners, xlab = "Exposure year",
      ylab = "Proportion of cases",ylim=c(0,0.6))
> lines(Years,fit.miners2$fit)
```

```
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 ***
```

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

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

$$\hat{P}_i = \frac{e^{\hat{\alpha}+\hat{\beta}\times Exposure_i}}{1+e^{\hat{\alpha}+\hat{\beta}\times Exposure_i}}$$ =fit.miners2$fit



fit.miners2$fit