# Session regression I: simple linear regression

### Learning outcomes

- understand simple linear regression model incl. terminology and mathematical notations
- estimate model parameters and their standard error
- use model for checking the association between x and y
- use model for prediction
- asses model accuracy with RSE and R<sup>2</sup>
- check model assumptions
- to be able to use 1m function in R for model fitting, obtaining confidence interval and predictions

#### Introduction

Quiz: What do we already know about simple linear regression?

#### Description

- Simple linear regression is a statistical method that allows us to summarize and study relationships between two continuous (quantitative, numerical) variables
  - one variable, denoted x is regarded as the *predictor*, *explanatory*, or *indepedent variable*, e.g. body weight (kg)
  - the other variable, denoted y, is regarded as the *response*, *outcome*, or *dependent variable*, e.g. plasma volume (liters)
- It is used to estimate the best-fitting straight line to describe the association

#### Used for to answer questions such as:

- is there a relationship between x exposure (e.g. body weight) and y outcome (e.g. plasma volume)?
- how strong is the relationship between the two variables?
- what will be a predicted value of the y outcome given a new set of exposure values?
- how accurately can we predict the outcome?

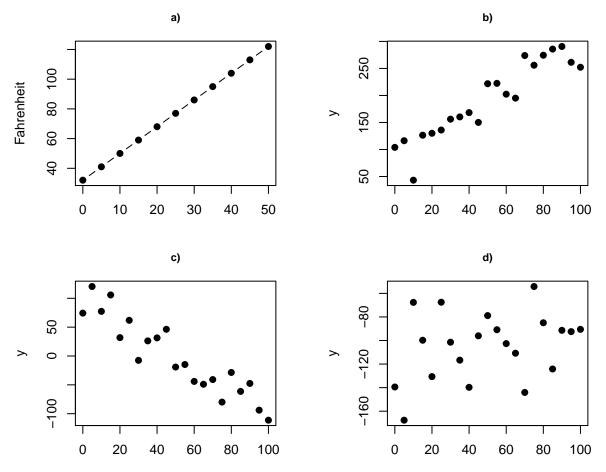


Figure 1: Deterministic vs. statistical relationship: a) deterministic: equation exactly describes the relationship between the two variables e.g. Fahrenheit = 9/5 \* Celcius + 32; b) statistical relationship between x and y is not perfect (increasing), c) statistical relationship between x and y is not perfect (decreasing), d) random signal

#### Example data

Example data contain the body weight (kg) and plasma volume (liters) for eight healthy men.

```
weight <- c(58, 70, 74, 63.5, 62.0, 70.5, 71.0, 66.0) # body weight (kg)
plasma <- c(2.75, 2.86, 3.37, 2.76, 2.62, 3.49, 3.05, 3.12) # plasma volume (liters)
```

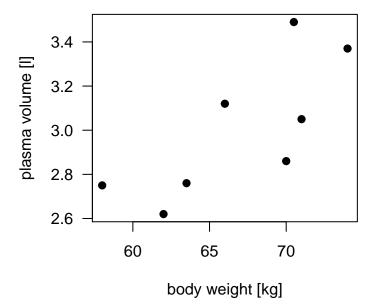


Figure 2: Scatter plot of the data shows that high plasma volume tends to be associated with high weight and \*vice verca\*.

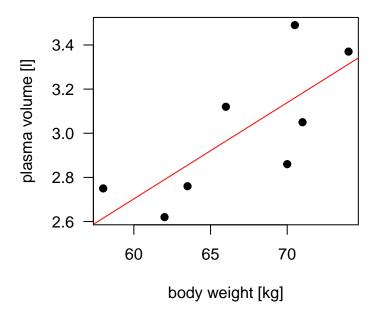


Figure 3: Scatter plot of the data shows that high plasma volume tends to be associated with high weight and \*vice verca\*. Linear regrssion gives the equation of the straight line that best describes how the outcome changes (increase or decreases) with a change of exposure variable (in red)

The equation of the regression line is:

$$y = \beta_0 + \beta_1 x$$

or mathematically using matrix notation

$$Y = \beta_0 + \beta_1 X$$

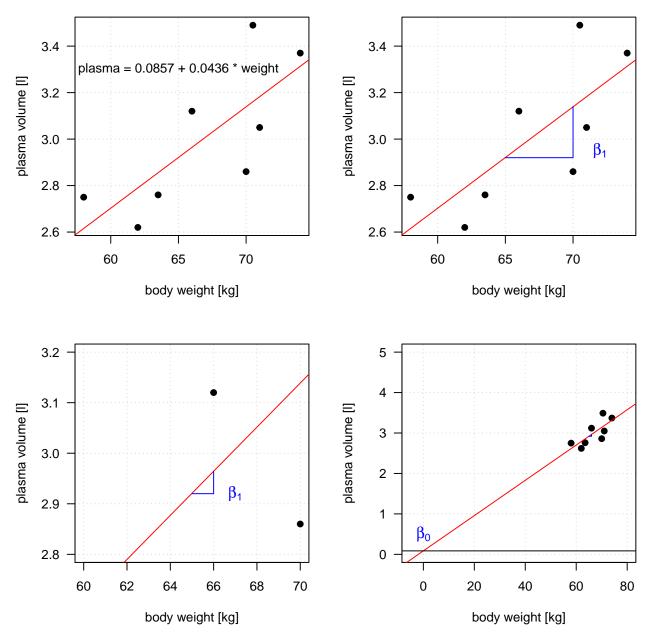
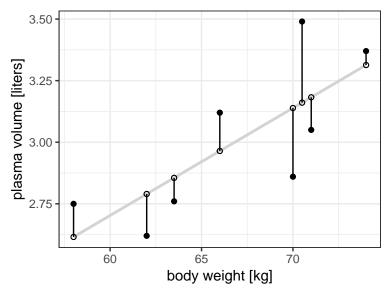


Figure 4: Scatter plot of the data shows that high plasma volume tends to be associated with high weight and \*vice verca\*. Linear regrssion gives the equation of the straight line that best describes how the outcome changes (increase or decreases) with a change of exposure variable (in red). Parameters explanation

### Quiz: regression model parameters

## Estimating model coefficients

In practice,  $\beta_0$  and  $\beta_1$  are usually unknown. The best-fitting line is derived using the method of **least** squares, i.e. by finding the values of the parameters  $\beta_0$  and  $\beta_1$  tht minimize the sum of the squared vertical distances of the points from the line.



Let  $(x_1, y_1), (x_2, y_2), ..., (x_n, y_n)$  represent n observation pairs, each of which consists of a measurement of X and Y, e.g. in our example we have 8 pairs of observations, e.g. (58, 2.75), (70, 2.86) etc.

```
weight <- c(58, 70, 74, 63.5, 62.0, 70.5, 71.0, 66.0) # body weight (kg)
plasma <- c(2.75, 2.86, 3.37, 2.76, 2.62, 3.49, 3.05, 3.12) # plasma volume (liters)
```

We seek to find coefficients estimates  $\hat{\beta}_0$  and  $\hat{\beta}_1$  such that liner model fits the available data well, i.e. such that the resulting line is as close as possible to the 8 data points.

There are a number of ways of measuring *closeness*. By far the most common approach involves minimizing the *least squares* criterion.

Let  $\hat{y}_i = \hat{\beta}_0 + \hat{\beta}_1 x_i$  be the prediction Y based on the *i*th value of X. Then  $\epsilon_i = y_i - \hat{y}_i$  represents the *i*th residual, i.e. the difference between the *i*th observed response value and the *i*th response value that is predicted by the linear model.

RSS, the residual sum of squares is defined as:

$$RSS = \epsilon_1^2 + \epsilon_2^2 + \dots \epsilon_n^2$$

or equivalently as:

$$RSS = (y_1 - \hat{\beta}_0 - \hat{\beta}_1 x_1)^2 + (y_2 - \hat{\beta}_0 - \hat{\beta}_1 x_2)^2 + \dots + (y_n - \hat{\beta}_0 - \hat{\beta}_1 x_n)^2$$

The least squares approach chooses  $\hat{\beta}_0$  and  $\hat{\beta}_1$  to minimize the RSS. With some calculus one gets:

$$\hat{\beta}_1 = \frac{\sum_{i=1}^n (x_i - \overline{x})(y_i - \overline{y})}{\sum_{i=1}^n (x_i - \overline{x})^2}$$
$$\hat{\beta}_0 = \overline{y} - \hat{\beta}_1 \overline{x}$$

where  $\overline{y} = \frac{1}{n} \sum_{i=1}^{n} y_i$  and  $\overline{x} = \frac{1}{n} \sum_{i=1}^{n} x_i$  are the sample means.

Pen and Paper exercise: Estimating model coefficients

# Hypothesis testing

### Accuracy of the coefficient estimates

- The calculated  $\hat{\beta}_0$  and  $\hat{\beta}_1$  are estimates of the population values of the intercept and slope and are, therefore, subject to sampling variation
- Their precision is measure by their standard errors

$$s.e(\hat{\beta}_0) = s * \sqrt{\left[\frac{1}{n} + \frac{x_i^2}{\sum_{i=1}^n (x_i - \overline{x})^2}\right]}$$

$$s.e(\hat{\beta}_1) = \frac{s}{\sqrt{\sum_{i=1}^{n} (x_i - \overline{x})^2}}$$

where, s is the standard deviation of the points about the line. It has (n-2) degrees of freedom, i.e. the sample size minus the number of regression coefficients

$$s = \sqrt{\left[\frac{\sum_{i=1}^{n} (y_i - \overline{y})^2 - \overline{\beta_1} \sum_{i=1}^{n} (x_i - \overline{x})^2}{n - 2}\right]}$$

Pen and Paper exercise: Accuracy of the coefficient estimates

#### Confidence interval

- Standard errors can be used to compute confidence interval.
- A 95% confidence interval is defined as a range of values such that with 95% probability, the range will contain the true unknown value of the parameter.
- The range is defined in terms of lower and upper limits computed from the data. For linear regression, the 95% confidence intervals takes form:

$$[\hat{\beta}_1 - 2 * s.e.(\hat{\beta}_1), \hat{\beta}_1 + 2 * s.e.(\hat{\beta}_1)]$$

and

$$[\hat{\beta}_1 - 2 * s.e.(\hat{\beta}_0), \hat{\beta}_1 + 2 * s.e.(\hat{\beta}_0)]$$

## Hypothesis testing

- Standard errors can also be used to perform hypothesis testing on the coefficients.
- The most common hypothesis test involves testing the null hypothesis of:

 $H_0$ : There is no relationship between X and Y

versus the alternative hypothesis

 $H_0$ : There is some relationship between X and Y

Mathematically, this corresponds to testing

$$H_0: \beta_1 = 0$$

versus

$$H_0: \beta_1 \neq 0$$

since if

$$\beta_1 = 0$$

then the model

$$Y = \beta_0 + \beta_1 X + \epsilon$$

reduces to

$$Y = \beta_0 + \epsilon$$

To test the null hypothesis we need to determine whether  $\hat{\beta}_1$ , our estimate of  $\beta_1$ , is sufficiently far from zero that we can be confident that  $\beta_1$  is non-zero.

How far is far enough? This depends on the accuracy of  $\hat{\beta}_1$ , that is standard error  $s.e.(\hat{\beta}_1)$ . If  $s.e.(\hat{\beta}_1)$  is small, then small values of  $\hat{\beta}_1$  may provide strong evidence that  $\hat{\beta}_1 \neq 0$  and *vice verca*. In practice, we compute a t-statistics given by

$$t = \frac{\hat{\beta}_1 - 0}{s.e.(\hat{\beta}_1)}$$

which measures the standard deviations that  $\hat{\beta}_1$  is away from 0.

If there really is no relationship between X and Y, then we this will have a t-distribution with n-2 degrees of freedom. From previous sessions, we now know how to compute probability of observing any value equal to |t|. We call this probability the p-value.

We can interpret the p-value as follows: a small p-value indicates that it is unlikely to observe such a substantial association between X and Y due to chance, i.e. in the absence of any real association. We therefore can reject the null hypothesis.

Typical p-value cutoffs for rejecting the null hypothesis are 5 or 1%. Pen and Paper exercise: Hypothesis testing

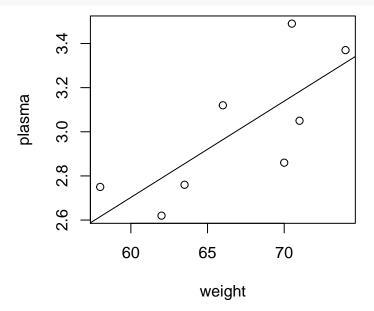
### Live coding demo

##

```
weight \leftarrow c(58, 70, 74, 63.5, 62.0, 70.5, 71.0, 66.0)
plasma \leftarrow c(2.75, 2.86, 3.37, 2.76, 2.62, 3.49, 3.05, 3.12)
plot(weight, plasma)
reg <- lm(plasma~weight)
summary(reg)
##
## Call:
## lm(formula = plasma ~ weight)
##
## Residuals:
##
                   1Q
                        Median
                                      3Q
                                              Max
  -0.27880 -0.14178 -0.01928 0.13986
                                         0.32939
##
##
## Coefficients:
##
               Estimate Std. Error t value Pr(>|t|)
                0.08572
                            1.02400
                                      0.084
                                               0.9360
## (Intercept)
## weight
                0.04362
                                      2.857
                                               0.0289 *
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
```

```
## Residual standard error: 0.2188 on 6 degrees of freedom
## Multiple R-squared: 0.5763, Adjusted R-squared: 0.5057
## F-statistic: 8.16 on 1 and 6 DF, p-value: 0.02893
```

abline(reg)



# Prediction example

• by hand and live demo

# Assessing the Accuracy of the Model & Correlation

# Assumptions