Module 3: Linear Regression
TMA4268 Statistical Learning V2024

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Introduction

Learning material for this module

- @ISL: An Introduction to Statistical Learning, Chapter 3 (skip 3.5).

We need more statistical theory than is presented in the textbook, which you find in this module page.

What will you learn?

- Simple linear regression:
  - Model and assumptions
  - Least squares
  - Testing and confidence intervals

- Multiple linear regression:
  - The use of matrix algebra
  - Distribution of estimators
  - Assessing model fit, model selection
  - Confidence and prediction ranges

- Qualitative predictors

- Interactions

- Assessing model fit / residual analysis

Linear regression

- Very simple approach for *supervised learning.*

- Parametric.

- A quantitative response vs. one or several explanatory variables (quantitative or qualitative).

- Is linear regression too simple? Maybe, but very useful. Important to *understand* because many learning methods can be seen as generalization of linear regression.

Motivating example: Prognostic factors for body fat

(From Theo Gasser & Burkhardt Seifert *Grundbegriffe der Biostatistik*)

Body fat is an important indicator for overweight, but difficult to measure.

Question: Which factors allow for precise estimation (prediction) of body fat?

Study with 243 male participants, where body fat (%) and BMI and other predictors were measured. Some scatterplots[1]:

---
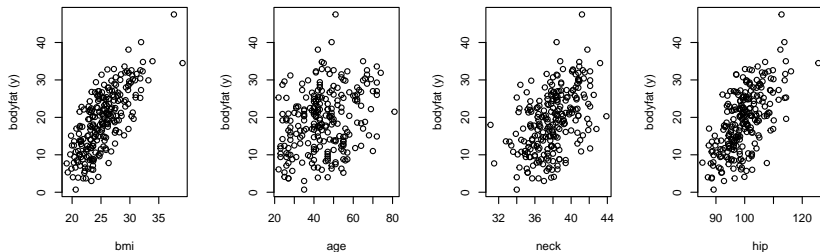
[1]The data to reproduce these plots and analyses can be found here:
https://github.com/stefaniemuff/statlearning/tree/master/3LinReg/data

For a good predictive model we need to dive into *multiple linear regression*. However, wer start with the simple case of *only one predictor variable*:
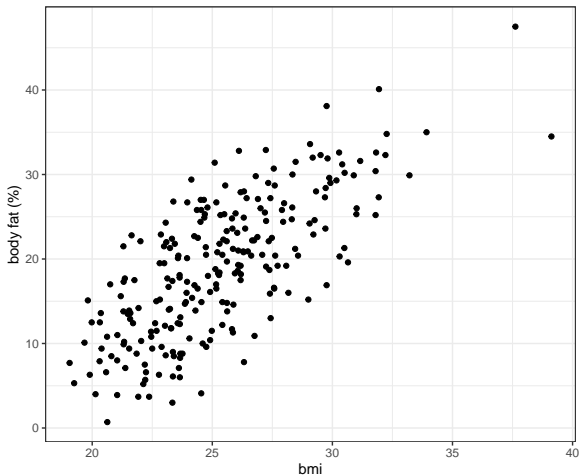
Interesting questions

1. How good is BMI as a predictor for body fat?
2. How strong is this relationship?
3. Is the relationship linear?
4. Are also other variables associated with `bodyfat`?
5. How well can we predict the bodyfat of a person?

Simple Linear Regression

- One quantitative response Y is modelled

- *One covariate x (=simple)*,

- and the relationship between Y and x is assumed to be *linear*.

Looking at the data it is obbious that the relationship is not perfectly linear. But we could assume it to be approximately linear. Such that, all instances of (x, Y), given by (x_i, y_i), $i = 1, ..., n$, lie around a straight line:

$$y_i \approx \beta_0 + \beta_1 x_i \ .$$
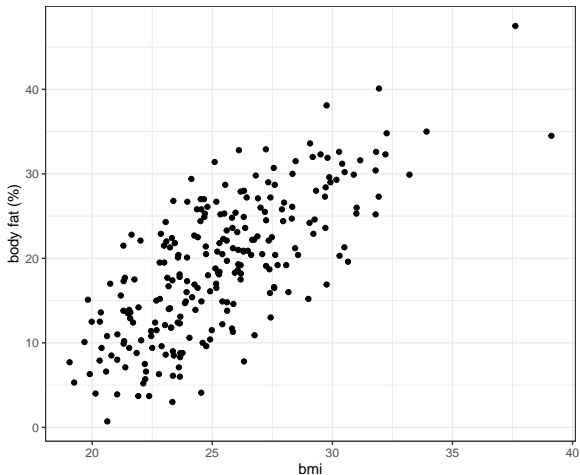
But which is the "true" or "best" line, if the relationship is not exact?
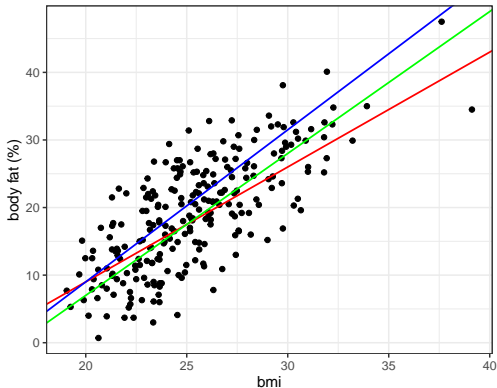
Task: Estimate the intercept and slope parameters (by "eye") and write it down (we will look at the "best" answer later).

$\rightarrow$ Mentimeter

It is obvious that

- the linear relationship does not describe the data perfectly.
- another realization of the data (other 243 males) would lead to a slightly different picture.

$\Rightarrow$ We need a **model** that describes the relationship between BMI and bodyfat.

The simple linear regression model

In the linear regression model the dependent variable Y is related to the independent variable x as

$$Y = \beta_0 + \beta_1 x + \varepsilon \ , \qquad \varepsilon \sim N(0, \sigma^2) \ .$$

In this formulation Y is a random variable $Y \sim N(\beta_0 + \beta_1 x, \sigma^2)$ where

$$Y \quad = \quad \underbrace{\text{expected value}}_{\mathsf{E}(Y) = \beta_0 + \beta_1 x} \quad + \quad \underbrace{\text{error}}_{\varepsilon} \ .$$

Note:
- The model for Y given x has *three parameters*: β_0 (intercept), β_1 (slope coefficient) and σ^2 .
- x is the *independent*/ *explanatory* / *regressor* variable.
- Y is the *dependent* / *outcome* / *response* variable.

Modeling assumptions

The central assumption in linear regression is that for any pairs
(x_i, Y_i), the error $\varepsilon_i \sim N(0, \sigma^2)$. This implies

a) The expected value of ε_i is 0: $\mathsf{E}(\varepsilon_i) = 0$.
b) All ε_i have the same variance: $\mathsf{Var}(\varepsilon_i) = \sigma^2$.
c) All ε_i are normally distributed.
d) ε is independent of any variable, observation number etc.
e) $\varepsilon_1, \varepsilon_2, \ldots, \varepsilon_n$ are independent of each other.

Visualization of the regression assumptions

The assumptions about the linear regression model lie in the error term

$$\varepsilon \sim N(0, \sigma^2) \ .$$
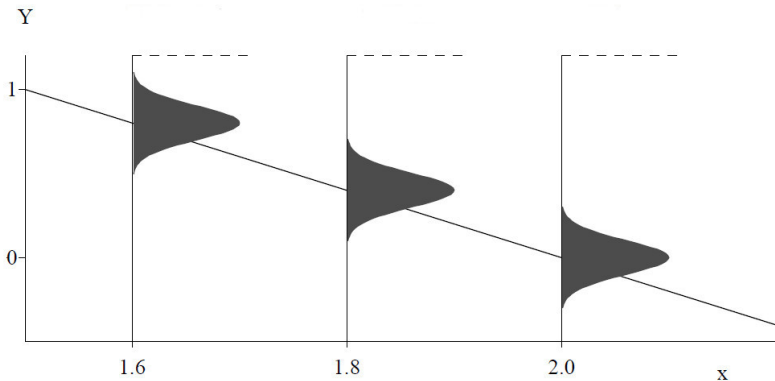
Note: The true regression line goes through $\mathsf{E}(Y|X = x)$.

Parameter estimation ("model fitting")

In a regression analysis, the task is to estimate the **regression coefficients** β_0, β_1 and the **residual variance** σ^2 for a given set of (x, y) data.

- **Problem:** For more than two points (x_i, y_i), $i = 1, \ldots, n$, there is generally no perfectly fitting line.

- **Aim**: We want to find the parameters (a, b) of the best fitting line $Y = a + bx + \epsilon$.

- **Idea:** Minimize the deviations between the data points (x_i, y_i) and the regression line.

But what are we actually going to minimize?

Least squares

Remember the **Least Squared Method**. Graphically, we are
minimizing the sum of the squared distances over all points:
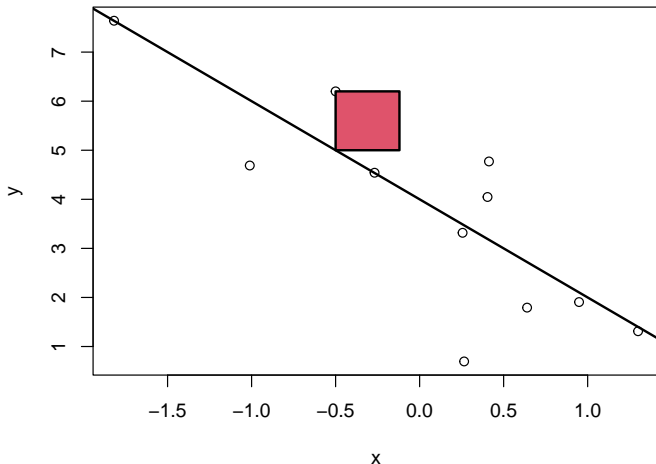
- Mathematically, a and b are estimated such that the sum of *squared vertical distances* (residual sum of squares)

$$\text{RSS} = \sum_{i=1}^{n} e_i^2 \,, \qquad \text{where} \quad e_i = y_i - (a + bx_i)$$

is minimized.

- The respective "best" estimates are called $\hat{\beta}_0$ and $\hat{\beta}_1$.

- We can predict the value of the response for a (new) observation of the covariate at x.
$$\hat{y} = \hat{\beta}_0 + \hat{\beta}_1 x.$$

- The i-th *residual* of the model is the difference between the i-th *observed* response value and the i-th *predicted* value, and is written as:
$$e_i = Y_i - \hat{y}_i.$$

- We may regard the residuals as *predictions* (not estimates) of the error terms ε_i.

(The error terms are random variables and can not be estimated - they can be predicted. It is only for parameters that we speak about estimates.)

Least squares estimators:

Using n observed independent data points

$$(x_1, y_1), (x_2, y_2), ..., (x_n, y_n) ,$$

we aim at finding a and b such that

$$RSS = \sum_{i=1}^{n} (y_i - a - bx_i)^2 = \min$$

to do this we need to solve the linear system

$$\frac{\partial RSS}{\partial a} = -2 \sum_{i=1}^{n} (y_i - a - bx_i) = 0$$

$$\frac{\partial RSS}{\partial b} = -2 \sum_{i=1}^{n} (y_i - a - bx_i) = 0$$

(1)

Least squares estimators:

The system can be solved analytically and the least squares estiamtes for simple linear regression are given as

$$\hat{\beta}_0 = \bar{y} - \hat{\beta}_1 \bar{x}$$
$$\hat{\beta}_1 = \frac{\sum_{i=1}^{n}(x_i - \bar{x})(y_i - \bar{y})}{\sum_{i=1}^{n}(x_i - \bar{x})^2} = \frac{\mathsf{Cov}(x,y)}{\mathsf{Var}(x)} \tag{2}$$

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

This is something you should have proven in your previous statistics classes; if you forgot how to get there, please check again, e.g. in chapter 11 of the book by @walepole.etal, see here.

Maximum likelihood estimator

Another method to estimate α, β, σ^2 when we assume that

$$y_i \sim \mathcal{N}(\alpha + \beta x_i, \sigma^2), \ i = 1 \dots, n$$

is to maximise the **likelihood** function:

$$L(\alpha, \beta, \sigma^2; y_1, \dots, y_n) = \prod_i f(y_i; \alpha, \beta, \sigma^2)$$

where

$$f(y; \alpha, \beta, \sigma^2) = \frac{1}{\sqrt{2\sigma^2}} \exp\{-\frac{1}{2\sigma^2}(y - \alpha - \beta x)^2\}$$

This gives the same result as the previous slide.

This is something you should know from TMA4240/4245; if you forgot how to get there, please check again, e.g. in chapter 11 of the book by @walepole.etal, see here.

Do-it-yourself "by hand"

Go to the Shiny gallery and try to "estimate'' the correct parameters.

You can do this here:

https://gallery.shinyapps.io/simple_regression/

Example continued: Body fat

Assume a linear relationship between the % bodyfat (`bodyfat`) and the BMI (`bmi`), we can get the LS estimates using R as follows:

```r
r.bodyfat = lm(bodyfat ~ bmi, data = d.bodyfat)
```

The estimates (and more information) can be obtained as follows:

```r
summary(r.bodyfat)$coef
```

```
##              Estimate Std. Error   t value      Pr(>|t|)
## (Intercept) -26.984368  2.7689004 -9.745518  3.921511e-19
## bmi           1.818778  0.1083411 16.787522  2.063854e-42
```

We see that the model fits the data quite well. It captures the essence. It looks that a linear relationship between `bodyfat` and `bmi` is a good approximation.
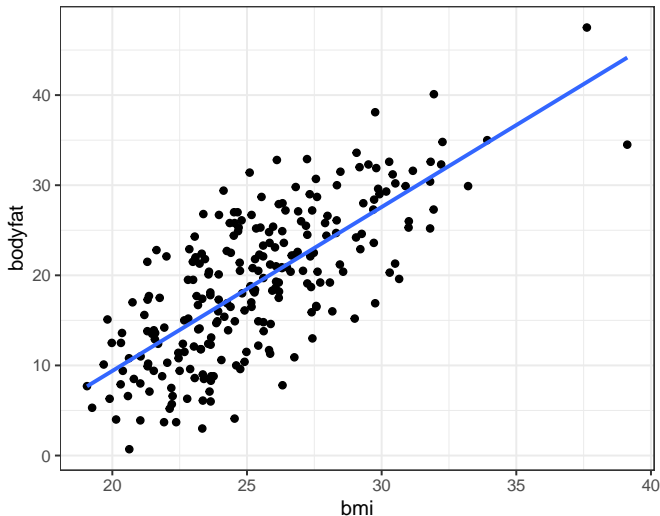
Questions:

- The blue line gives the estimated model. Explain what the line means in practice. Is this result plausible?

- Compare the estimates for β_0 and β_1 to the estimates you gave at the beginning - were you close?

- How does this relate to the *true* (population) model?

- **What could the regression line look like if another set of 243 males were used for estimation?**

Uncertainty in the estimates $\hat{\beta}_0$ and $\hat{\beta}_1$

Note: $\hat{\beta}_0$ and $\hat{\beta}_1$ are themselves *random variables* and as such contain *uncertainty*!

Let us look again at the regression output, this time only for the coefficients. The second column shows the standard error of the estimate:

```
summary(r.bodyfat)$coef
```

```
##               Estimate Std. Error   t value      Pr(>|t|)
## (Intercept) -26.984368  2.7689004 -9.745518 3.921511e-19
## bmi           1.818778  0.1083411 16.787522 2.063854e-42
```

$\rightarrow$ The logical next question is: what is the distribution of the estimates?

Distribution of the estimators for $\hat{\beta}_0$ and $\hat{\beta}_1$

To obtain an intuition, we generate data points according to model

$$y_i = 4 - 2x_i + \varepsilon_i , \quad \varepsilon_i \sim N(0, 0.5^2).$$

In each round, we estimate the parameters and store them:

```
set.seed(1)
niter <- 1000
pars <- matrix(NA, nrow = niter, ncol = 2)
for (ii in 1:niter) {
    x <- rnorm(100)
    y <- 4 - 2 * x + rnorm(100, 0, sd = 0.5)
    pars[ii, ] <- lm(y ~ x)$coef
}
```

Doing it 1000 times, we obtain the following distributions for $\hat{\beta}_0$ and $\hat{\beta}_1$:
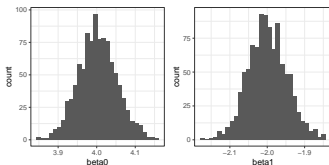
Accuracy of the parameter estimates

- The standard errors of the estimates are given by the following formulas:

$$\mathsf{Var}(\hat{\beta}_0) = \mathrm{SE}(\hat{\beta}_0)^2 = \sigma^2 \Big[\frac{1}{n} + \frac{\bar{x}^2}{\sum_{i=1}^n (x_i - \bar{x})^2}\Big]$$

and

$$\mathsf{Var}(\hat{\beta}_1) = \mathrm{SE}(\hat{\beta}_1)^2 = \frac{\sigma^2}{\sum_{i=1}^n (x_i - \bar{x})^2}.$$

- $\mathsf{Cov}(\hat{\beta}_0, \hat{\beta}_1)$ is in general different from zero.

Note: We will *derive a general version* of these formulas for multiple linear regression, because without matrix notation this is very cumbersome.

Under the assumption that $\varepsilon \sim N(0, \sigma^2)$, and assuming $\hat{\beta}_0$ and $\hat{\beta}_1$ are estimated as in formulas (1) and (2), we have in addition that

$$\hat{\beta}_0 \sim N(\beta_0, \sigma^2_{\beta_0}) \quad \text{and} \quad \hat{\beta}_1 \sim N(\beta_1, \sigma^2_{\beta_1}) \ .$$

Again: We will derive this in the multiple linear regression version in more generality (see recommended exercise 3).

Design issue with data collection

Recall that

$$\text{SE}(\hat{\beta}_1)^2 = \frac{\sigma^2}{\sum_{i=1}^{n}(x_i - \bar{x})^2} \ ,$$

thus for a given σ^2, the standard error is only dependent on the *design* of the x_i's!

- Would we like the $\text{SE}(\hat{\beta}_1)^2$ large or small? Why?
- If it is possible for us to choose the x_i's, which strategy should we use to choose them?

Residual standard error (RSE)

- **Problem**: σ is usually not known, but needs to be estimated[2].
- Remember: The residual sum of squares is
  RSS $= \sum_{i=1}^{n}(y_i - \hat{\beta}_0 - \hat{\beta}_1 x_i)^2$.
- An estimate of σ, the residual standard error, RSE, is given by

$$\hat{\sigma} = \text{RSE} = \sqrt{\frac{1}{n-2}\text{RSS}} = \sqrt{\frac{1}{n-2}\sum_{i=1}^{n}(y_i - \hat{y}_i)^2} \ .$$

- What are the characteristcs of $\hat{\sigma}^2$?
  - Unbiased estimator for σ^2
  - $\frac{n-2}{\sigma^2}\hat{\sigma}^2 \sim \chi_{n-2}^2$

---

[2] σ^2 is the *irreducible error* variance.

Estimated Variance for β_1

- So actually we have

$$\hat{\text{SE}}(\hat{\beta}_1)^2 = \frac{\hat{\sigma}^2}{\sum_{i=1}^{n}(x_i - \bar{x})^2} \ ,$$

but we usually just write $\text{SE}(\hat{\beta}_1)^2$ (without the extra hat).

The estimated standard errors can be seen using the `summary()` function:

```
summary(r.bodyfat)$coef
```

```
##              Estimate Std. Error   t value     Pr(>|t|)
## (Intercept) -26.984368  2.7689004 -9.745518 3.921511e-19
## bmi           1.818778  0.1083411 16.787522 2.063854e-42
```

Testing and Confidence Intervals

After the regression parameters and their uncertainties have been
estimated, there are typically two fundamental questions:

1. **"Are the parameters compatible with some specific value?"**

Typically, the question is whether the slope β_1 might be 0 or not, that
is: "Is x an informative predictor or not?"

$\rightarrow$ This leads to a **statistical test**.

2. **"Which values of the parameters are compatible with the data?"**

$\rightarrow$ This leads us to determine **confidence intervals**.

Let's first go back to the output from the bodyfat example:

```
summary(r.bodyfat)$coef
```

```
##              Estimate Std. Error   t value     Pr(>|t|)
## (Intercept) -26.984368  2.7689004 -9.745518 3.921511e-19
## bmi          1.818778  0.1083411 16.787522 2.063854e-42
```

Besides the estimate and the standard error (which we discussed before), there is a t value and a probability Pr(>|t| that we need to understand.

How do these things help us to answer the two questions above?

Testing the effect of a covariate

Remember: in a statistical test you first need to specify the *null hypothesis*.

Here, typically, the null hypothesis is

$$H_0 : \quad \beta_1 = 0 \ .$$

In words: H_0 = "There is no relationship between X and Y." [3]

Here, the *alternative hypothesis* is given by

$$H_A : \quad \beta_1 \neq 0$$

---

[3]You could also test against another null hypothesis, like $\beta_1 = c$.

Remember: To carry out a statistical test, we need a *test statistic*. This is some type of **summary statistic** that follows a known distribution under H_0.

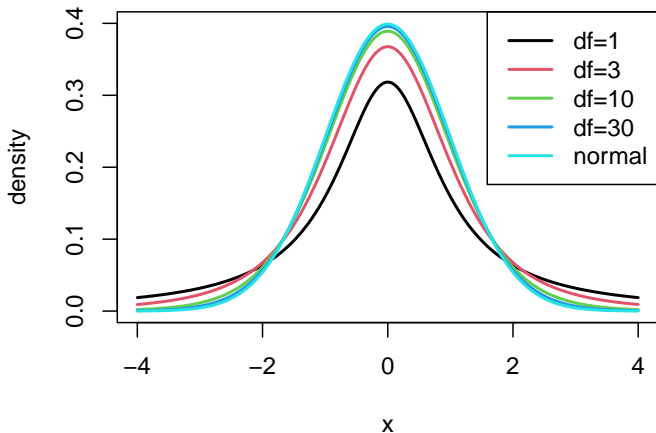For our purpose, we use the so-called T**-statistic**

$$T = \frac{\hat{\beta}_1}{SE(\hat{\beta}_1)} \; .$$

Note: If you want to test against another value than $\beta_1 = 0$, the formula is

$$T = \frac{\hat{\beta}_1 - c}{SE(\hat{\beta}_1)} \; .$$

Where does this come from??

Recap: The t-distribution

- The t-distribution has heavier tails than the normal distribution.
- For df ≥ 30 the t and Normal distribution are pretty similar.

Distribution of parameter estimators

We will *derive a general version* for multiple linear regression!

Brief recap: Under H_0, T has a t-distribution with $n-2$ degrees of freedom ($n =$ number of data points; compare to Chapter 8.6 in @walepole.etal).

Hypothesis tests for bodyfat example

So let's again go back to the bodyfat regression output:

```
summary(r.bodyfat)$coef
```

```
##               Estimate Std. Error   t value     Pr(>|t|)
## (Intercept) -26.984368   2.7689004 -9.745518 3.921511e-19
## bmi           1.818778   0.1083411 16.787522 2.063854e-42
```

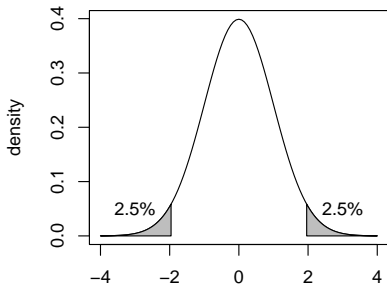**Q**: Check how the `Estimate`, `Std. Error` and `t value` relate.

- The last column contains the *p-values* of the tests with H_0: $\beta_0 = 0$ and $\beta_1 = 0$, respectively.
- The *p*-value for `bmi` is very small ($p < 0.0001$). **What does this mean?**
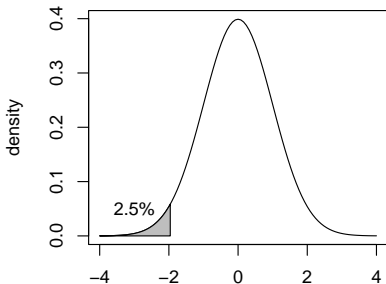
Recap: Formal definition of the p-value

The p-value is the probability to observe a data summary (e.g., an average) that is at least as extreme as the one observed, given that the Null Hypothesis is correct.

Example (normal distribution): Assume the observed test-statistic leads to a z-value = -1.96 $\Rightarrow$ $P(|z| \geq 1.96) = 0.05$ and $P(z \leq -1.96) = 0.025$.

Cautionary notes regarding p-values:

- The (mis)use of p-values is heavily under critique in the scientific world!
- Simple yes/no decisions do often stand on very wiggly scientific ground.

We will discuss this a bit in the final module 12. The topic is connected to good/bad research practice, problems with "reproducibility'' and scientific progress in general. See e.g. here:

- The p-value statement by ASA: https://amstat.tandfonline.com/doi/full/10.1080/00031305.2016.1154108#.Xh16iuExnhM
- Ideas to redefine what "statistical significane'' means: https://www.nature.com/articles/s41562-017-0189-z
- Recently written with some co-authors: https://www.cell.com/trends/ecology-evolution/fulltext/S0169-5347(21)00284-6

Confidence intervals

- Confidence intervals (CIs) are a much more informative way to report results than p-values!

- The t-distribution[4] can be used to create confidence intervals for the regression parameters. The lower and upper limits of a 95% confidence interval for β_j are

$$\hat{\beta}_j \pm t_{(1-\alpha/2), n-2} \cdot \text{SE}(\hat{\beta}_j) \quad j = 0, 1.$$

- Interpretation of this confidence interval:
  - There is a 95% probability that the interval will contain the *true* value of β_j.
  - **It is the range of parameter estimates that are *compatible with the data*** .

---

[4]If n is large, the normal approximation to the t-distribution can be used (and is used in the textbook).

Doing this for the bodfat example "by hand'' is not hard. We have
$241 (= 243 - 2)$ degrees of freedom:

```
coefs <- summary(r.bodyfat)$coef
beta <- coefs[2, 1]
sdbeta <- coefs[2, 2]
beta + c(-1, 1) * qt(0.975, 241) * sdbeta
```

```
## [1] 1.605362 2.032195
```

We can directly ask R to give us the CIs:

```
confint(r.bodyfat, level = c(0.95))
```

```
##                    2.5 %     97.5 %
## (Intercept) -32.438703 -21.530032
## bmi           1.605362   2.032195
```

Interpretation:

For an increase in the bmi by one index point, roughly ... percentage points more bodyfat are expected, and all true values for β_1 between ... and ... are ....

Model accuracy

Measured by

1. The **residual standard error (RSE)**, which provides an **absolute measure** of *lack of fit* (see above).

2. The **coefficient of determination** R^2, which measures the proportion of y's variance explained by the model (between 0 and 1), is a **relative measure** of *lack of fit*:

$$R^2 = \frac{\text{TSS} - \text{RSS}}{\text{TSS}} = 1 - \frac{\text{RSS}}{\text{TSS}} = 1 - \frac{\sum_{i=1}^{n}(y_i - \hat{y}_i)^2}{\sum_{i=1}^{n}(y_i - \bar{y}_i)^2},$$

where

$$\text{TSS} = \sum_{i=1}^{n}(y_i - \bar{y})^2$$

is the *total sum of squares*, a measure for the total variability in Y.

R^2 in simple linear regression

Note: In simple linear regression, R^2 is the squared correlation between the independent and the dependent variable.

Verify this by comparing R^2 from the bodyfat output to the squared correlation between the two variables:

```
summary(r.bodyfat)$r.squared
## [1] 0.5390391
cor(d.bodyfat$bodyfat, d.bodyfat$bmi)^2
## [1] 0.5390391
```

Summary: Simple Linear Regression

- The statistical model:

$$y_i = \alpha + \beta x_i + \epsilon_i, \ \epsilon_i \sim (0, \sigma^2) \ \epsilon_i \perp \epsilon_j, \ i \neq j$$

- Parameter estimate

$$\hat{\beta}_0 = \bar{y} - \hat{\beta}_1 \bar{x} \sim \mathcal{N}(\beta_0, \frac{\sigma^2 \sum x_i^2}{n \sum (x_i - \bar{x})^2})$$

$$\hat{\beta}_1 = \frac{\sum_{i=1}^{n}(x_i - \bar{x})(y_i - \bar{y})}{\sum_{i=1}^{n}(x_i - \bar{x})^2} \sim \mathcal{N}(\beta_1, \frac{\sigma^2}{\sum (x_i - \bar{x})^2})$$

(3)

- Interpretation of the parameters
- Derive confidence intervals and test
- Model accuracy

Multiple Linear Regression

Remember that the bodyfat dataset contained much more information than only bmi and bodyfat:

- `bodyfat`: % of body fat.
- `age`: age of the person.
- `weight`: body weighth.
- `height`: body height.
- `bmi`: bmi.
- `abdomen`: circumference of abdomen.
- `hip`: circumference of hip.

Model

We assume

$$Y = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + ... + \beta_p X_p + \varepsilon , \qquad (4)$$

where X_j is the jth predictor and β_j the respective regression coeffficient.

Assume we have n sampling units $(x_{1i}, ... , x_{pi}, y_i)$, $1 \leq i \leq n$, such that each represents an instance of equation (3), we can use the data matrix

$$\mathbf{X} = \begin{bmatrix} 1 & x_{11} & ... & x_{1p} \\ 1 & x_{21} & ... & x_{2p} \\ \vdots & ... & ... & \vdots \\ 1 & x_{n1} & ... & x_{np} \end{bmatrix}$$

to write the model in matrix form:

$$\mathbf{Y} = \mathbf{X}\beta + \varepsilon$$

Notation

- $\mathbf{Y}$: $(n \times 1)$ vector of responses (e.g., bodyfat).

- $\mathbf{X}$: $(n \times (p+1))$ design matrix, and x_i^T is a $(p+1)$-dimensional row vector for observation i.

- β : $((p+1) \times 1)$ vector of regression parameters $(\beta_0, \beta_1, ..., \beta_p)^\top$.

- ε : $(n \times 1)$ vector of random errors.

- We assume that pairs (x_i^T, y_i) $(i = 1, ..., n)$ are measured from *independent* sampling units.

Remark: other books, including the book in TMA4267 and TMA4315 define p to include the intercept. This may lead to some confusion about p or $p+1$ in formulas...

Classical linear model

$$\mathbf{Y} = \mathbf{X}\beta + \varepsilon$$

Assumptions:

1. $\mathsf{E}(\varepsilon) = 0$.

2. $\mathsf{Cov}(\varepsilon) = \mathsf{E}(\varepsilon\varepsilon^T) = \sigma^2 I$.

3. The design matrix has full rank, rank$(\mathbf{X}) = p + 1$. (We assume $n >> (p+1)$.)

The classical *normal* linear regression model is obtained if additionally

4. $\varepsilon \sim N_n(0, \sigma^2\mathbf{I})$ holds. Here N_n denotes the n-dimensional multivarate normal distribution.

The interpretation of the coefficients β_j is now as following: holding all other covariates fixed, what is the average effect on Y of a one-unit increase in the jth covariate.

The bodyfat example for two predictors

We are looking at the regression model

$$Y = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + \varepsilon \ ,$$

with bodyfat as the response (Y) and `bmi` and `age` as X_1 and X_2.

The regression

```
r.bodyfat = lm(bodyfat ~ bmi + age, data = d.bodyfat)
```

The *design matrix*:

```
head(model.matrix(r.bodyfat))
```

```
##   (Intercept)   bmi age
## 1           1 23.65  23
## 2           1 23.36  22
## 3           1 24.69  22
## 4           1 24.91  26
## 5           1 25.54  24
## 6           1 26.48  24
```

Distribution of the response vector

Assume that

$$\mathbf{Y} = \mathbf{X}\beta + \varepsilon \ , \quad \varepsilon \sim N_n(\mathbf{0}, \sigma^2 \mathbf{I}) \ .$$

Q:
- What is the expected value $\mathsf{E}(\mathbf{Y})$?
- The covariance matrix $\mathsf{Cov}(\mathbf{Y})$ given $\mathbf{X}$?
- Thus what is the distribution of $\mathbf{Y}$?

A:
$$\mathbf{Y} \sim N_n(\mathbf{X}\beta, \sigma^2\mathbf{I})$$

Parameter estimation for β

In multiple linear regression, the parameter vector β is estimated with *maximum likelihood* and *least squares*. These two methods give the same estimator when we assume the normal linear regression model.

With least squares, we minimize the RSS for a multiple linear regression model:

$$\text{RSS} = \sum_{i=1}^{n}(y_i - \hat{y}_i)^2 = \sum_{i=1}^{n}(y_i - \hat{\beta}_0 - \hat{\beta}_1 x_{i1} - \hat{\beta}_2 x_{i2} - ... - \hat{\beta}_p x_{ip})^2$$

$$= \sum_{i=1}^{n}(y_i - x_i^T \hat{\beta})^2 = (\mathbf{Y} - \mathbf{X}\hat{\beta})^T (\mathbf{Y} - \mathbf{X}\hat{\beta})$$

The estimator is found by solving the system of $(p+1)$ equations

$$\frac{\partial \text{RSS}}{\partial \beta} = \mathbf{0} \ .$$

$\rightarrow$ Derivation on the board.

Summing up:

The least squares and maximum likelihood estimator for β:
is given like
$$\hat{\beta} = (\mathbf{X}^T\mathbf{X})^{-1}\mathbf{X}^T\mathbf{Y} \ .$$

Example continued

```
r.bodyfat3 <- lm(bodyfat ~ bmi + age + neck + hip + abdomen, data = d.bodyfat)
summary(r.bodyfat3)
```

```
##
## Call:
## lm(formula = bodyfat ~ bmi + age + neck + hip + abdomen, data = d.bodyfat)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -9.3727 -3.1884 -0.1559  3.1003 12.7613
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -7.74965    7.29830  -1.062  0.28939
## bmi          0.42647    0.23133   1.844  0.06649 .
## age          0.01457    0.02783   0.524  0.60100
## neck        -0.80206    0.19097  -4.200 3.78e-05 ***
## hip         -0.31764    0.10751  -2.954  0.00345 **
## abdomen      0.83909    0.08418   9.968  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.392 on 237 degrees of freedom
## Multiple R-squared:  0.7185, Adjusted R-squared:  0.7126
## F-statistic:   121 on 5 and 237 DF,  p-value: < 2.2e-16
```

Reproduce the values under `Estimate` by calculating without the use
of `lm`.

```
X = model.matrix(r.bodyfat3)
Y = d.bodyfat$bodyfat
betahat = solve(t(X) %*% X) %*% t(X) %*% Y
print(betahat)
```

```
##                  [,1]
## (Intercept) -7.74964673
## bmi          0.42647368
## age          0.01457356
## neck        -0.80206081
## hip         -0.31764315
## abdomen      0.83909391
```

Distribution of the regression parameter estimator

Given
$$\hat{\beta} = (\mathbf{X}^T\mathbf{X})^{-1}\mathbf{X}^T\mathbf{Y} \ ,$$

what are
- The mean $\mathsf{E}(\hat{\beta})$?
- The covariance matrix $\mathsf{Cov}(\hat{\beta})$?
- The distribution of $\hat{\beta}$?

Hint: Use that
- $\hat{\beta} = \mathbf{C}\mathbf{Y}$ with $\mathbf{C} = (\mathbf{X}^T\mathbf{X})^{-1}\mathbf{X}^T$.
- $\mathbf{Y} \sim N_n(\mathbf{X}\beta, \sigma^2\mathbf{I})$.

Answers:

See Problem 2 of recommended exercise 3 (and the respective solutions) to derive that

$$\widehat{\beta} \sim N_{p+1}(\beta, \underbrace{\sigma^2(\mathbf{X}^T\mathbf{X})^{-1}}_{\text{covariance matrix}}) \ .$$

The covariance matrix of $\hat{\beta}$ in R

The covariance matrix for the $\hat{\beta}$ can be obtained as follows:

```
vcov(r.bodyfat3)
##              (Intercept)           bmi           age          neck           hip
## (Intercept) 53.26521684  0.6774596810 -0.0780438125 -0.7219656479 -0.548205733
## bmi          0.67745968  0.0535131152  0.0005729015 -0.0120408637 -0.005804073
## age         -0.07804381  0.0005729015  0.0007745054 -0.0003432518  0.001523951
## neck        -0.72196565 -0.0120408637 -0.0003432518  0.0364680351 -0.002715930
## hip         -0.54820573 -0.0058040729  0.0015239515 -0.0027159299  0.011558850
## abdomen      0.16457979 -0.0110809165 -0.0011917596 -0.0007706161 -0.004570722
##                 abdomen
## (Intercept)  0.1645797895
## bmi         -0.0110809165
## age         -0.0011917596
## neck        -0.0007706161
## hip         -0.0045707222
## abdomen      0.0070861066
```

How does this compare to simple linear regression? Not so easy to see a connection!

$$\hat{\beta}_0 = \bar{Y} - \hat{\beta}_1 \bar{x} \text{ and } \hat{\beta}_1 = \frac{\sum_{i=1}^{n}(x_i - \bar{x})(Y_i - \bar{Y})}{\sum_{i=1}^{n}(x_i - \bar{x})^2},$$

$$\hat{\beta} = (\mathbf{X}^T\mathbf{X})^{-1}\mathbf{X}^T\mathbf{Y}.$$

Exercise: Verify the connection using $\beta = (\beta_0, \beta_1)^\top$ and
$$\mathbf{X} = \begin{bmatrix} 1 & x_{11} \\ 1 & x_{21} \\ 1 & \vdots \\ 1 & x_{n1} \end{bmatrix}.$$

Four important questions

1. Is at least one of the predictors $X_1, \ldots, X_p$ useful in predicting the response?

2. Do all the predictors help to explain Y, or is only a subset of predictors useful?

3. How well does the model fit the data?

4. Given a set of predictor variables, how accurate is our prediction?

1. Relationship between predictors and response?

Question is whether we could as well omit all predictor variables at the same time, that is

$$H_0 : \beta_1 = \beta_2 = ... = \beta_p = 0$$

vs.

$$H_1 : \text{at least one } \beta_j \text{ is non-zero.}$$

To answer this, we need the F-statistic

$$F = \frac{(\text{TSS} - \text{RSS})/p}{\text{RSS}/(n-p-1)} \sim F_{p,(n-p-1)} \; ,$$

where total sum of squares $\text{TSS} = \sum_i (y_i - \bar{y})^2$, and residual sum of squares $\text{RSS} = \sum_i (y_i - \hat{y}_i)^2$. Under the Normal regression assumptions, F follows an $F_{p,(n-p-1)}$ distribution (see @walepole.etal, Chapter 8.7).

- If H_0 is true, F is expected to be ≈ 1.

- Otherwise, we expect that the numerator is larger than the denominator (because the regression then explains a lot of variation) and thus F is greater than 1. For an observed value f_0, the p-value is given as

$$p = P(F_{p,n-p-1} > f_0) \; .$$

Checking the F-value in the R output:

```
summary(r.bodyfat)
```

```
##
## Call:
## lm(formula = bodyfat ~ bmi + age, data = d.bodyfat)
##
## Residuals:
##      Min      1Q   Median       3Q      Max
## -12.0415  -3.8725  -0.1237   3.9193  12.6599
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -31.25451    2.78973 -11.203  < 2e-16 ***
## bmi           1.75257    0.10449  16.773  < 2e-16 ***
## age           0.13268    0.02732   4.857 2.15e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.329 on 240 degrees of freedom
## Multiple R-squared:  0.5803, Adjusted R-squared:  0.5768
## F-statistic: 165.9 on 2 and 240 DF,  p-value: < 2.2e-16
```

Conclusion?

More complex hypotheses

Sometimes we don't want to test if all β's are zero at the same time, but only a subset $1, \ldots, q$:

$$H_0 : \beta_1 = \beta_2 = \cdots = \beta_q = 0$$

vs.

$$H_1 : \text{at least one different from zero.}$$

Again, the F-test can be used, but now F is calculated like

$$F = \frac{(\text{RSS}_0\text{-RSS})/(q)}{\text{RSS}/(n - p - 1)} \sim F_{q, n-p-1} \ ,$$

where
- Large model: RSS with $p + 1$ regression parameters
- Small model: RSS_0 with $p + 1 - q$ regression parameters

Example in R

- **Question:** Do `weight` and `height` explain something of `bodyfat`, on top of the variables `bmi` and `age`?
- Fit both models and use the `anova()` function to carry out the F-test:

```r
r.bodyfat.small = lm(bodyfat ~ bmi + age, data = d.bodyfat)
r.bodyfat.large = lm(bodyfat ~ bmi + age + weight + height, data = d.bodyfat)
anova(r.bodyfat.small, r.bodyfat.large)
```

```
## Analysis of Variance Table
##
## Model 1: bodyfat ~ bmi + age
## Model 2: bodyfat ~ bmi + age + weight + height
##   Res.Df    RSS Df Sum of Sq      F Pr(>F)
## 1    240 6816.2
## 2    238 6702.9  2    113.28 2.0112 0.1361
```

Inference about a single predictor β_j

A special case is

$$H_0 : \beta_j = 0 \quad \text{vs.} \quad H_1 : \beta_j \neq 0$$

- Nothing new: We did it for simple linear regression!
- This makes sense: it is known that (or you can try to show it yourself)

$$F_{1,n-p-1} = t^2_{n-p-1} \ ,$$

thus we can use a T-statistic with $(n - p - 1)$ degrees of freedom to get the p-value.

Going back again:

```r
summary(r.bodyfat)$coef
```

```
##               Estimate Std. Error    t value     Pr(>|t|)
## (Intercept) -31.2545057 2.78973238 -11.203406 1.039096e-23
## bmi           1.7525705 0.10448723  16.773060 2.600646e-42
## age           0.1326767 0.02731582   4.857137 2.149482e-06
```

However:

Only checking the individual p-values is dangerous. **Why?**

Inference about β_j: confidence interval

- Using that

$$T_j = \frac{\hat{\beta}_j}{\text{SE}(\hat{\beta}_j)} \sim t_{n-p-1} \ ,$$

we can create confidence intervals for β_j in the same manner as we did for simple linear regression (see slide 41). For example, when using the typical confidence level $\alpha = 0.05$ we have

$$\hat{\beta}_j \pm t_{0.975,n-p-2} \cdot \text{SE}(\hat{\beta}_j) \ .$$

```
confint(r.bodyfat)
```
```
##                  2.5 %      97.5 %
## (Intercept) -36.7499929 -25.7590185
## bmi           1.5467413   1.9583996
## age           0.0788673   0.1864861
```

2. Deciding on important variables

Overarching question:

<div align="center">

Which model is the best?

</div>

But:

- Not clear what *best* means → we need an objective criterion, like AIC, BIC, Mallows C_p, adjusted R^2.
- There are usually **many** possible models. For p predictors, we can build 2^p different models.
- **Cautionary note**: Model selection can also lead to biased parameters estimates.

→ This topic is the focus of Module 6.

3. Model Fit

We can again look at the two measures from simple linear regression:

- An absolute measure of lack of fit is again given by the estimate of σ, the residual standard error (RSE)

$$\hat{\sigma} = \text{RSE} = \sqrt{\frac{\text{RSS}}{n - p - 1}} \ .$$

- R^2 is again the fraction of variance explained (no change from simple linear regression)

$$R^2 = \frac{\text{TSS} - \text{RSS}}{\text{TSS}} = 1 - \frac{\text{RSS}}{\text{TSS}} = 1 - \frac{\sum_{i=1}^{n}(y_i - \hat{y}_i)^2}{\sum_{i=1}^{n}(y_i - \bar{y}_i)^2} \ .$$

Simply speaking: "The higher R^2, the better."

However: Caveat with R^2

Let us look at the R^2s from the three bodyfat models

model 1: $y \sim bmi$
model 2: $y \sim bmi + age$
model 3: $y \sim bmi + age + neck + hip + abdomen$

```
summary(r.bodyfatM1)$r.squared
```
```
## [1] 0.5390391
```
```
summary(r.bodyfatM2)$r.squared
```
```
## [1] 0.5802956
```
```
summary(r.bodyfatM3)$r.squared
```
```
## [1] 0.718497
```

The models explain 54%, 58% and 72% of the total variability of y.
It thus *seems* that larger models are "better''. However, R^2 does
always increase when new variables are included, but this does not
mean that the model is more reasonable.

Adjusted R^2

When the sample size n is small with respect to the number of variables m included in the model, an *adjusted R^2* gives a better ("fairer") estimation of the actual variability that is explained by the covariates:

$$R_a^2 = 1 - (1 - R^2)\frac{n-1}{n-p-1}$$

R_a^2 **penalizes for adding more variables** if they do not really improve the model!

$\rightarrow R_a$ may decrease when a new variable is added.

Model fit – in a broader sense

We will look at model validation / model checking later.

4. Predictions: Two questions

1. **Which other regression lines are compatible with the observed data?**

$\rightarrow$ We can use $\hat{\beta}_0, \dots, \hat{\beta}_p$ to estimate the *least squares plane*

$$\hat{Y} = \hat{\beta}_0 + \hat{\beta}_1 X_1 + \dots + \hat{\beta}_p X_p$$

as an approximation of $f(X) = \beta_0 + \beta_1 X_1 + \dots + \beta_p X_p$. This leads to the *confidence interval*.

2. **Where do future observations with a given x coordinate lie?**

$\rightarrow$ Even if we could predict $\hat{Y} = f(X)$, the *true* value $Y = f(X) + \varepsilon$ varies around $\hat{Y}$. We can compute a *prediction interval* for new observations Y.
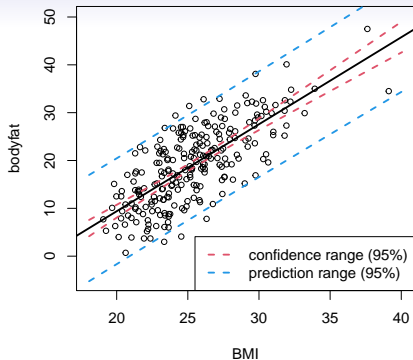
- Plotting the confidence and prediction intervals around all predicted values $\hat{Y}_0$ one obtains the **confidence range** or **confidence band** for the expected values of Y.

Note: The prediction range is much broader than the confidence range. Why?

Calculation of the confidence intervals/range

- Given a realization of $X_1, \dots, X_p$, say $x_1^{(0)}, \dots x_p^{(0)}$. The question is:

  Where does $\hat{y}_0 = \hat{\beta}_0 + \hat{\beta}_1 x_1^{(0)} + \dots \hat{\beta}_p x_p^{(0)}$ lie with a certain confidence (i.e., 95%)?

- This question is not trivial, because $\hat{\beta}_0, \dots \hat{\beta}_p$ are estimates from the data and contain uncertainty.

- For the confidence range, only the uncertainty in the estimates $\hat{\beta}_0, \dots \hat{\beta}_p$ matters.

Calculation of the prediction intervals/range

- Given a new value of $X_1, \ldots, X_p$, say $x_1^{(0)}, \ldots x_p^{(0)}$. The question is:

  Where does a future observation y_0 lie with a certain confidence (i.e., 95%)?

- To answer this question, we have to sum uncertainty over two components:
  1. the *uncertainty in the predicted value* $\hat{y}_0 = \hat{\beta}_0 + \hat{\beta}_1 x_1^{(0)} + \ldots \hat{\beta}_p x_p^{(0)}$ (due to uncertainty in $\hat{\beta}$).
  2. the *irreducible error* $\varepsilon_0 \sim N(0, \sigma^2)$.

- The *prediction intervals and range are always wider than the confidence intervals and range.*

- Confidence and prediction intervals for given data points can be
  found in R using `predict` on an `lm` object (make sure that
  `newdata` is a `data.frame` with the same names as the original
  data).

```
fit = lm(bodyfat ~ bmi + age + abdomen, data = d.bodyfat)
newobs = d.bodyfat[1, ]
predict(fit, newdata = newobs, interval = "confidence", type = "response")

##        fit      lwr      upr
## 1 13.17595 11.99122 14.36069
predict(fit, newdata = newobs, interval = "prediction", type = "response")

##        fit      lwr     upr
## 1 13.17595 3.951613 22.4003
```

Finally, we need to keep in mind that the model we work with is only an *approximation of the reality.* In fact,

In 2014, David Hand wrote:

> *In general, when building statistical models, we must not forget that the aim is to understand something about the real world. Or predict, choose an action, make a decision, summarize evidence, and so on, but always about the real world, not an abstract mathematical world: our models are not the reality – a point well made by George Box in his often-cited remark that "all models are wrong, but some are useful".*

[@box1979]

Extensions of the linear model

Extensions that make the linear model very powerful:

- Binary covariates (e.g., male/female, smoker/non-smoker)

- Categorical covariates (e.g., black/white/green)?

- Interaction terms

- Non-linear terms

Binary predictors

So far, the covariates X were always continuous.

In reality, there are no restrictions assumed with respect to the X variables.

One very frequent data type are **binary** variables, that is, variables that can only attain values 0 or 1.

If the binary variable x is the only variable in the model $Y_i = \beta_0 + \beta_1 x_i + \varepsilon_i$, the model has only two predicted outcomes (plus error):

$$Y_i = \left\{ \begin{array}{ll} \beta_0 + \varepsilon_i & \text{if } x_i = 0 \ , \\ \beta_0 + \beta_1 + \varepsilon_i & \text{if } x_i = 1 \ . \end{array} \right.$$

Example: Credit card data analysis in Section 3.3.1 in the ISLR book.

Qualitative predictors with more than 2 levels

More generally, a covariate may indicate a **category**, for instance the species of an animal or a plant. This type of covariate is called a **factor**. The trick: convert a factor variable X with k levels (for instance 3 species) into k dummy variables X_j with

$$x_{ij} = \begin{cases} 1, & \text{if the } i\text{th observation belongs to group } j. \\ 0, & \text{otherwise.} \end{cases}$$

Each of the covariates $x_1, \dots, x_k$ can then be included as a binary variable in the model

$$y_i = \beta_0 + \beta_1 x_1 + \dots + \beta_k x_k + \varepsilon_i \ .$$

However: this model is *not identifiable*.[5]

---

[5]What does that mean? I could add a constant to $\beta_1, \beta_2, \dots \beta_k$ and subtract it from β_0, and the model would fit equally well to the data, so it cannot be decided which set of the parameters is best.

Solution: One of the k categories must be selected as a *reference category* and is *not included in the model*. Typically: the first category is the reference, thus $\beta_1 = 0$.

The model thus discriminates between the factor levels, such that (assuming $\beta_1 = 0$)

$$y_i = \left\{ \begin{array}{ll} \beta_0 + \varepsilon, & \text{if } x_{i1} = 1 \\ \beta_0 + \beta_2 + \varepsilon, & \text{if } x_{i2} = 1 \\ ... \\ \beta_0 + \beta_k + \varepsilon, & \text{if } x_{ik} = 1 \end{array} \right. .$$

!Important to remember!
(Common aspect that leads to confusion!)

A factor covariate with k factor levels requires $k-1$ parameters!

$\rightarrow$ The *degrees of freedom* of the fitted model are therefore reduced by $k-1$.

Example

We are now using the `Credit` dataset from the `ISLR` library.

```
library(ISLR)
data(Credit)
head(Credit)
## ID Income Limit Rating Cards Age Education Gender Student Married Ethnicity
## 1 1 14.891 3606 283 2 34 11 Male No Yes Caucasian
## 2 2 106.025 6645 483 3 82 15 Female Yes Yes Asian
## 3 3 104.593 7075 514 4 71 11 Male No No Asian
## 4 4 148.924 9504 681 3 36 11 Female No No Asian
## 5 5 55.882 4897 357 2 68 16 Male No Yes Caucasian
## 6 6 80.180 8047 569 4 77 10 Male No No Caucasian
## Balance
## 1 333
## 2 903
## 3 580
## 4 964
## 5 331
## 6 1151
```

Question: Do the Balances differ for different Ethnicities
(Caucasian/Asian/Afro-American)?

```
library(GGally)
ggpairs(Credit[, c("Ethnicity", "Balance")], aes(colour = Ethnicity))
```
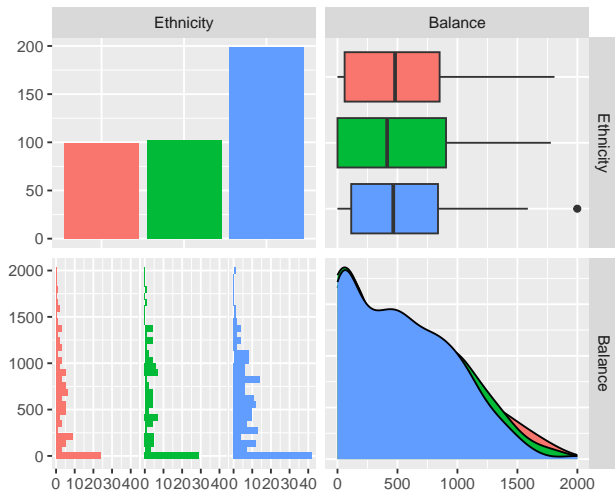
In R, a factor covariate can be used in the same way as a continuous predictor:

```r
r.lm <- lm(Balance ~ Ethnicity, data = Credit)
summary(r.lm)$coef
```

```
##                    Estimate Std. Error    t value      Pr(>|t|)
## (Intercept)        531.00000   46.31868 11.4640565 1.774117e-26
## EthnicityAsian     -18.68627   65.02107 -0.2873880 7.739652e-01
## EthnicityCaucasian -12.50251   56.68104 -0.2205766 8.255355e-01
```

Interpretation? Do the ethnicities really differ? Check also the F-test in the last line of the summary output.

$$\hat{y}_i = \begin{cases} & \text{if } i \text{ is Asian} \\ & \text{if } i \text{ is Caucasian} \\ & \text{if } i \text{ is Afro-American} \end{cases}$$

Sidenote: The "reference category"

In the above example we do not see a result for the
`EthnicityAfrican American`. Why?

- `African American` is chosen to be the reference category.
- The results for `EthnicityAsian` and `EthnicityCaucasian` are
  differences with respect to the reference cateogry.
- R chooses the reference category in alphabetic order! This is
  sometimes not a relevant category.
- You can change the reference category:

```r
library(dplyr)
Credit <- mutate(Credit, Ethnicity = relevel(Ethnicity, ref = "Caucasian"))
r.lm <- lm(Balance ~ Ethnicity, data = Credit)
summary(r.lm)$coef
```

```
##                             Estimate Std. Error    t value      Pr(>|t|)
## (Intercept)               518.497487   32.66986 15.8708211 2.824537e-44
## EthnicityAfrican American  12.502513   56.68104  0.2205766 8.255355e-01
## EthnicityAsian             -6.183762   56.12165 -0.1101850 9.123184e-01
```

Note: The differences are now with respect to the Caucasian category – the
model is however exactly the same!

Testing for a categorical predictor

Question: Is a qualitative predictor needed in the model?

For a predictor with more than two levels (like Ethnicity above), the Null Hypothesis is whether

$$\beta_1 = ... = \beta_{k-1} = 0$$

at the same time.

$\rightarrow$ We again need the F-test[6], as **always when we test for more than one $\beta_j = 0$ *simultaneously*!**

In R, this is done by the `anova()` function:

```
anova(r.lm)
## Analysis of Variance Table
##
## Response: Balance
##              Df   Sum Sq Mean Sq F value Pr(>F)
## Ethnicity     2    18454    9227  0.0434 0.9575
## Residuals   397 84321458  212397
```

---

[6]remember that the F-test is a generalization of the t-test!

Interactions: Removing the additivity assumption

We again look at the `Credit` dataset. We want to model the `Balance` as a function of `Income` and wheter the person is a student or not.

The model is given as

$$\text{Balance}_i = \beta_0 + \beta_1 \cdot \text{Income}_i + \beta_2 \cdot \text{Student}_i + \varepsilon_i ,$$

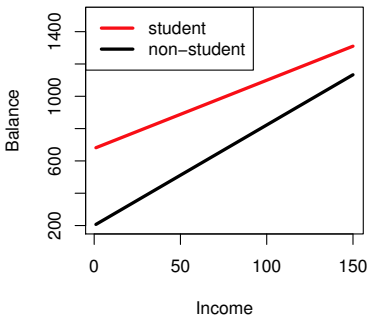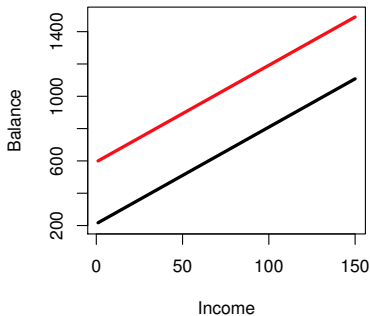where `Student` is a binary variable. Thus we have a model that looks like

$$\text{Balance}_i = \begin{cases} \beta_0 + \beta_2 + \beta_1 \cdot \text{Income}_i + \varepsilon_i , & \text{if } i \text{ is a student,} \\ \beta_0 + \quad\quad \beta_1 \cdot \text{Income}_i + \varepsilon_i & \text{otherwise.} \end{cases}$$

In R, we simply add `Student` to the model:

```r
r.lm <- lm(Balance ~ Income + Student, Credit)
```

Caveat: This model assumes that students and non-students have the same slope for `Income`. Realistic?

Let's look at the graphs:

$\rightarrow$ We want a model that allows for different slopes!

Interaction terms

We formulate a new model that includes the interaction term
(Income · Student):

$$\text{Balance}_i = \beta_0 + \beta_1 \cdot \text{Income}_i + \beta_2 \cdot \text{Student}_i + \beta_3 \cdot \text{Income}_i \cdot \text{Student}_i + \varepsilon_i \ ,$$

Thus we have a model that allows for different intercept *and* slope for
the two groups:

$$\text{Balance}_i = \left\{ \begin{array}{ll} \beta_0 + \beta_2 + (\beta_1 + \beta_3) \cdot \text{Income}_i + \varepsilon_i \ , & \text{if } i \text{ is a student,} \\ \beta_0 + \qquad \beta_1 \cdot \text{Income}_i + \varepsilon_i & \text{otherwise.} \end{array} \right.$$

In R, this is again quite simple:

```r
r.lm <- lm(Balance ~ Income * Student, Credit)
summary(r.lm)$coef
```

```
##                     Estimate  Std. Error   t value     Pr(>|t|)
## (Intercept)       200.623153  33.6983706  5.953497 5.789658e-09
## Income              6.218169   0.5920936 10.502003 6.340684e-23
## StudentYes        476.675843 104.3512235  4.567995 6.586095e-06
## Income:StudentYes  -1.999151   1.7312511 -1.154743 2.488919e-01
```

Interpretation:

We allow the model to depend on the binary variable `Student`, such that

For a student: $\hat{y} = 200.6 + 476.7 + (6.2 + \text{-}2.0) \cdot \text{Income}$

For a non-Student: $\hat{y} = 200.6 + (6.2) \cdot \text{Income}$

Question: Is the interaction relevant here?

The hierarchical principle

If we include an interaction in a model, we should also include the main effects, even if the p-values associated with the coefficients of the main effects are large (see p.89 in ISLR book).

More interactions

We can include interactions also between
- two continuous variables.
- a categorical variable with more than 2 levels and a continuous variable.

$\rightarrow$ See problem 1 in recommended exercises 3 (important)!

Non-linear terms

Linear regression is even more powerful!

- We have seen that it is possible to include continuous, binary or factorial covariates in a regression model.

- Even *transformations* of covariates can be included in (almost) any form. For instance the square of a variable X^2

$$y_i = \beta_0 + \beta_1 x_i + \beta_2 x_i^2 + \varepsilon_i \ ,$$

which leads to a **quadratic** or **polynomial** regression (if higher order terms are used).

- Other common transformations are:
  - log
  - $\sqrt{\cdot\cdot}$
  - sin, cos,

How can a *quadratic* regression be a *linear regression*??

Note:

The word *linear* refers to the *linearity in the coefficients*, and not on a linear relationship between Y and $X_1, \ldots, X_p$!

Question: When would we need such a regression? Well, sometimes the world is not linear. In particular, if

- there is a theoretical/biological/medical reason to believe in a non-linear relationship, or
- the residual analysis indicates that there are non-linear associations in the data.

$\rightarrow$ In the later modules, we will discuss other more advanced non-linear approaches for addressing this issue.

Challenges - for model fit

1. Non-linearity of data
2. Correlation of error terms
3. Non-constant variance of error terms
4. Non-Normality of error terms
5. Outliers
6. High leverage points
7. Collinearity

Recap of modelling assumptions in linear regression

To make valid inference from our model, we must check if our model assumptions are fulfilled![7]

The assumption in linear regression is that the residuals follow a $N(0, \sigma^2)$ distribution, implying that :

1. The expected value of ε_i is 0: $\mathsf{E}(\varepsilon_i) = 0$.
2. All ε_i have the same variance: $\mathsf{Var}(\varepsilon_i) = \sigma^2$.
3. The ε_i are normally distributed.
4. The ε_i are independent of each other.

---

[7]What is the problem if the assumptions are violated?

# Model checking tool I: Tukey-Anscombe diagram

The *Tukey-Anscombe* diagram plots the residuals against the fitted values. For the bodyfat data it looks like this:
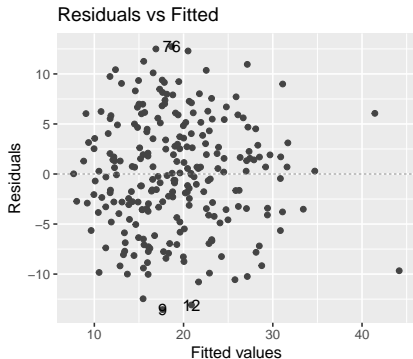
This plot is ideal to check if assumptions 1. and 2. (and partially 4.) are met. Here, this seems fine.

Model checking tool II: The QQ-diagram

To check assumption 3., the quantiles of the observed distribution are plotted against the quantiles of the respective theoretical (normal) distribution:
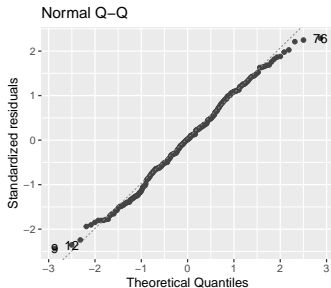

If the points lie approximately on a straight line, the data is fairly normally distributed. This is often "tested'' by eye, and needs some experience.

Model checking tool III: The scale-location plot

The scale-location plot is particularly suited to check the assumption of equal variances (homoscedasticity; assumption 2.).

The idea is to plot the square root of the (standardized) residuals $\sqrt{|\tilde{r}_i|}$ against the fitted values $\hat{y}_i$. There should be *no trend*:
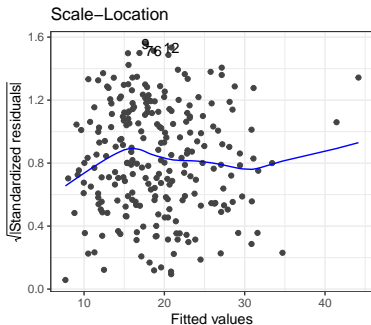
Model checking tool IV: The leverage plot

- Mainly useful to determine outliers.

- To understand the leverage plot, we need to introduce the idea of the **leverage**.

- In simple regression, the leverage of individual i is defined as

$$H_{ii} = \frac{1}{n} + \frac{(x_i - \overline{x})^2}{\sum_{i'}(x_{i'} - \overline{x})^2} \ . \tag{5}$$

Q: When are leverages expected to be large/small?

**Illustration**: Data points with x_i values far from the mean have a stronger leverage effect than when $x_i \approx \overline{x}$:
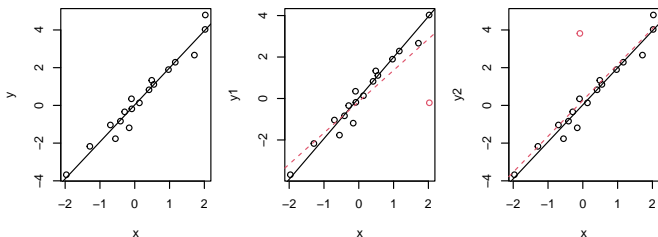
The outlier in the middle plot "pulls'' the regression line in its direction and biases the slope.

http://students.brown.edu/seeing-theory/regression-analysis/index.html to do it manually! [8]

---

[8]You may choose "Ordinary Least Squares" and then click on "I" for the Ascombe quartett example. Drag points to see what happens with the regression line.

In the leverage plot, (standardized) residuals $\tilde{r}_i$ are plotted against the leverage H_{ii} (still for the bodyfat):

Residuals vs Leverage
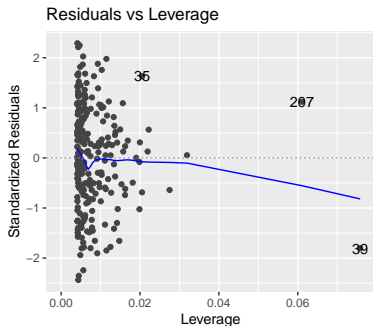
Critical ranges are the top and bottom right corners! Why?

Leverages in multiple regression

- Leverage is defined as the diagonal elements of the so-called *hat matrix* $\mathbf{H}$[9], i.e., the leverage of the i-th data point is H_{ii} on the diagonal of $\mathbf{H} = \mathbf{X}(\mathbf{X^T X})^{-1}\mathbf{X^T}$.

- Exercise: Verify that formula (4) comes out in the special case of simple linear regression.

- A large leverage indicates that the observation (i) has a large influence on the estimation results, and that the covariate values (x_i) are unusual.

---

[9]Do you remember why $\mathbf{H}$ is called *hat matrix*?

Different types of residuals?

It can be shown that the vector of residuals, $\mathbf{e} = (e_1, e_2, \dots, e_n)$ have a normal (singular) distribution with

- $\mathsf{E}(\mathbf{e}) = \mathbf{0}$
- $\mathsf{Cov}(\mathbf{e}) = \sigma^2(\mathbf{I} - \mathbf{H})$,

where $\mathbf{H} = \mathbf{X}(\mathbf{X}^T\mathbf{X})^{-1}\mathbf{X}^T$.

This means that the residuals (possibly) have different variance, and may also be correlated.

Q: Why is that a problem?

A:

- To check the model assumptions we want to look at the distribution of the error terms ε_i, to check that our errors are independent, homoscedastic (same variance for each observation), and not dependent on our covariates.

- However, we only have the residuals e_i, the "predictions" for ϵ_i.

- It would have been great if the e_i have the same properties as ϵ_i.

$\rightarrow$ To make the e_i more "like ϵ_i", we use *standardized* or *studentized residuals*.

Standardized residuals:

$$\tilde{r}_i = \frac{e_i}{\hat{\sigma}\sqrt{1 - H_{ii}}}$$

where H_{ii} is the ith diagonal element of the hat matrix **H**.

In R you can get the standardized residuals from an lm-object (named fit) by rstandard(fit).

Studentized residuals:

$$r_i^* = \frac{e_i}{\hat{\sigma}_{(i)}\sqrt{1 - H_{ii}}}$$

where $\hat{\sigma}_{(i)}$ is the estimated error variance in a model with observation number i omitted. It can be shown that it is possible to calculated the studentized residuals directly from the standardized residuals.

In R you can get the studentized residuals from an lm-object (named fit) by rstudent(fit).

Diagnostic plots in R

See exercises: We use `autoplot()` from the `ggfortify` package in R to plot the diagnostic plots.

Collinearity

In brief, collinearity refers to the situation when two or more predictors are correlated, thus encode (partially) for the same information.

Problems:
- Reduces the accuracy of the estimated coefficients $\hat{\beta}_j$ (large SE!).
- Consequently, reduces power in finding effects (p-values become larger).

Solutions:
- Detect it by calculating the *variance inflation factor* (VIF).
- Remove the problematic variable.
- Or combine the collinear variables into a single new one.

Todo: Read in the course book p.99-102 (self-study).

Further reading

- Videoes on YouTube by the authors of ISL, Chapter 3

References