# Introduction to statistics

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# Welcome everyone!

- Applied statistics using R via the RStudio interface.
  - 6 course days with lectures and (computer) exercises.
  - Frequentist statistics with univariate responses.
  - Statistical models for categorical and continuous data.

- Lectures and exercises given jointly for two courses:
  - Applied Statistics (Master Course, 7.5 ECTS).
  - Statistical methods for the Biosciences (PhD Course, 4.5 ECTS).

- Background:
  - Teaching level and course aims.
  - Data Science Laboratory
  - All course material based on previous years and graciously shared by Bo Markussen.

# Who are we?

- Anton Rask Lundborg:
  - Course lecturer.
  - Postdoc at MATH.
  - Mathematical education, PhD in statistics from the University of Cambridge.
  - Research on theoretical/methodological statistics with a focus on significance testing and variable importance with applications to causal inference.
  - My first time running the course, (gentle) feedback is welcome. ☺
  - Office 04.3.01, 3rd floor E-building at HCØ (Nørre Campus).

- Ulises Bercovich Szulmajster:
  - PhD student in statistics at KU-MATH.
  - Will be present at the exercise class in the afternoon.

# Course material

- Computer software:
  - R: www.r-project.org + RStudio: www.rstudio.com
- Main literature:
  - The slides!
  - The help pages in R.
  - Course book: Martinussen, Skovgaard, Sørensen, "A first guide to statistical computations in R", Biofolia 2012.
  - Sterne & Smith (2001), "Sifting the evidence—what's wrong with significance tests?", British Medical Journal, 226–231.
  - Gelman & Carlin (2014), "Beyond Power Calculations: Assessing Type S (Sign) and Type M (Magnitude) Errors", Perspectives on Psychological Science, 1–11.
- Also used:
  - Your old book on basic statistics.
  - Grolemund, Wickham (2017), R for Data Science, O'Reilly.
  - Wickham (2016), ggplot2, Springer.

# Statistical software for validity, reliability, reproducibility

Programming: R, SAS, Stata, Python, MatLab, ...

Menu based: Excel, Graphpad Prism, SPSS, SAS Enterprise, JMP, Stata, R-commander, ...

Pros and Cons:

| | Programming | Menu based |
|---|---|---|
| + | Full control, direct reproducibility | Good overview of models and possibilities |
| − | Syntax, commands, options, etc. | Mouse clicking, limited flexibility, reproducibility difficult |

RStudio: An interface to R successfully countering many of the cons of programming.

R markdown: File format for making dynamic documents that integrate code, output, graphs and text.

# Basic concepts of frequentist statistics

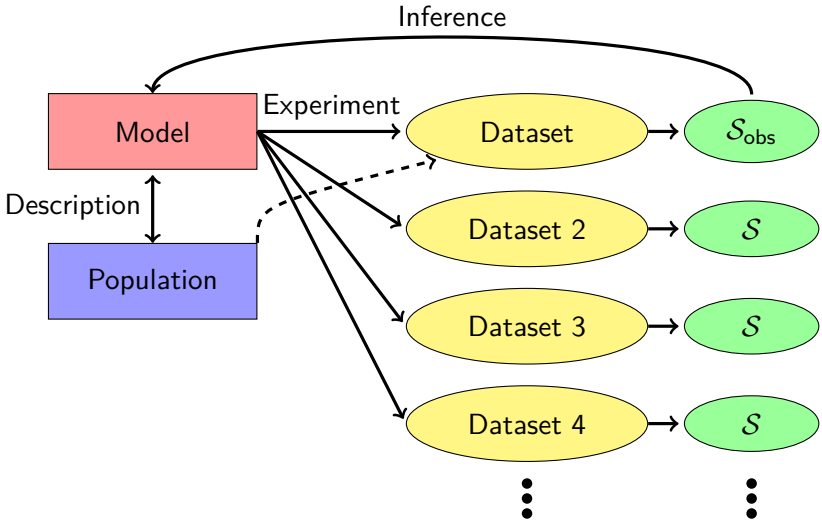
# Why do statistics? – To answer four important questions!

1. Is there an effect?
   - Answered by hypothesis testing via $p$-values.
2. Where is the effect?
   - Answered by $p$-values from post hoc analyses.
3. What is the effect?
   - Answered by confidence and prediction intervals.
4. Can the conclusions be trusted?
   - Answered by model validation.

Remarks:

- Often "effect" should be replaced by "association". Causality $\neq$ correlation!
- Statistical models are also used for other purposes: Which ones?

# Overview of the statistical paradigm




Examples of $\mathcal{S}$ include estimators, confidence intervals, test statistics and $p$-values.

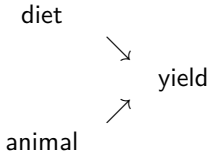
# Understanding hypothesis testing

## Motivating example: Permutation testing

# Does feed concentrate increase milk yield? – An interventional study

- Does feeding concentrate to dairy cows have an effect on milk yield?


We can illustrate this is in a causal diagram:

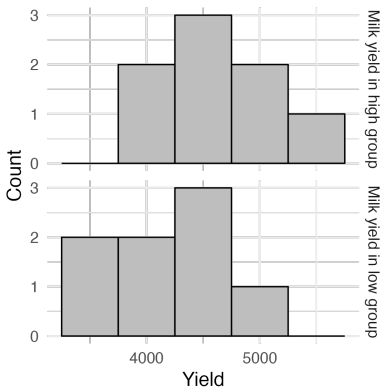



- Objective of the example:
  - Answer the posed question.
  - Learn basic concepts of hypothesis testing doing this.
  - First look at some R code.

# Does feeding concentrate influence milk yield?

Two groups of 8 cows, given low or high amounts of feed concentrate:

| Concentrate/day | Milk yield (kg) from week 1 to 36 (reference: V. Østergaard (1978)) | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| Low: 4.5 kg | 4132 | 3672 | 3664 | 4292 | 4881 | 4287 | 4087 | 4551 |
| High: 7.5 kg | 3860 | 4130 | 5531 | 4259 | 4908 | 4695 | 4920 | 4727 |

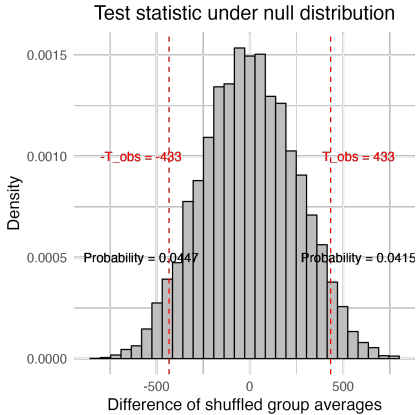



- Apparently there is an effect of feed concentrate.
- Confirmation by falsification of the null hypothesis of no effect.
- A test statistic summarizes the difference between groups, e.g.:

$$\begin{aligned} \mathcal{T}_{\text{obs}} &= \text{mean(high)} - \text{mean(low)} \\ &= 4629 - 4195 = 433 \end{aligned}$$

# Is the observed effect significant or due to randomness?

- Null hypothesis: Observed difference of average milk yield due to random allocation of 16 cows into two groups.
- We redo a random allocation 10,000 times and inspect the differences of average milk yields (see `feed_concentrate.R`).




The *p*-value is the probability of a more extreme test statistic than $\mathcal{T}_{\text{obs}}$,

$$\begin{aligned} p &= \text{Prob}(|\mathcal{T}| \geq |\mathcal{T}_{\text{obs}}|) \\ &= 0.0415 + 0.0447 \\ &= 0.0862 \end{aligned}$$

# R code for the permutation test

The code below is for illustration only, in practice use e.g. `wilcox.test()`.

```
# Read data and compute test statistic
low <- c(4132, 3672, 3664, 4292, 4881, 4287, 4087, 4551)
high <- c(3860, 4130, 5531, 4259, 4908, 4695, 4920, 4727)
yields <- c(low, high)

T_obs <- mean(high) - mean(low)

# Resample test statistic and compute p-values
N <- 10000
T_resamples <- replicate(N, {
  permuted_cows <- yields[sample(1:16)]
  group_1 <- permuted_cows[1:8]
  group_2 <- permuted_cows[9:16]
  mean(group_1) - mean(group_2)
})
(p_value_onesided <- mean(T_resamples >= T_obs))
(p_value_twosided <- mean(abs(T_resamples) >= abs(T_obs)))
```

# Summary of basic concepts

What did we learn from the milk yield example?

- Statistical hypothesis tests distinguish real effects from random variation.
- Scientific hypothesis supported by falsifying opposite hypothesis.
- Test statistic measures discrepancy between data and null hypothesis.
- $p$-value is the probability of larger discrepancy than the observed one.
- Small $p$-value $\Longrightarrow$ significance.
- The observed $p$-value, 0.0856, is not sufficiently small to claim statistical significance. What can we do about this? (Multiple valid answers!)

# Conclusion from a hypothesis test

- $p$-value measures disagreement with $H_0$ (not the same as importance!):

  small $p$: disagreement=reject

  large $p$: agreement=cannot reject

  Conventional labelling ("." in some R outputs):

| | |
|---|---|
| $p > 0.05$ : NS | (non-significant) |
| $0.05 < p < 0.10$ : . | (significant at 10% level) |
| $0.01 < p < 0.05$ : * | (significant at 5% level) |
| $0.001 < p < 0.01$ : ** | (significant at 1% level) |
| $p < 0.001$ : *** | (significant at 0.1% level) |

- Small $p$ = strong evidence against $H_0$. If $p = 0.2\%$, say, then
  - either $H_0$ is false
  - or $H_0$ is true and we have been unlucky! (risk $= 2/1000$)
  - or we have tested too many hypotheses (say 1000)
  - or the model is wrong (conclusion cannot be trusted)

# Checkpoint

- Questions?
- Next, we discuss the building blocks of a dataset: Observations, variables, and variable types.
- This corresponds to tidy data in the tidyverse invented by Hadley Wickham.

Time for a break!

# Tidy data

# Data example 1

Setup: A feature is measured for a collection of molecules without and with some modification. We have one or several repetitions for each combination of modification and molecule.

Scientific question: Does the modification have an impact of the individual molecules and for all molecules in general?

Here a data example in a non-tidy organization:

| Without | With |
|---|---|
| 0.0 | 20.0 |
| 48.0 | 33.0 |
| 0.0, 76.2, 82.1, 57.9, 78.4 | 76.0 |
| 0.0 | 47.0 |
| 0.0 | 69.0 |
| 9.0 | 16.0 |

# Data example 2

Setup: Multiple features are measured in an experiment, e.g. br6 and br74, with multiple repetitions.

Challenge: There are systematic differences between repetitions due to experimental environments and molecule synthesizing batches.

Data example in a non-tidy organization. There are two repetitions of br6 and br74, and each row is one molecule:

| br6_rep1 | br74_rep1 | br6_rep2 | br74_rep2 |
|---|---|---|---|
| 0.6423 | 0.6129 | 0.5507 | 0.5359 |
| 0.4004 | 0.2456 | 0.3336 | 0.2749 |
| 0.1135 | 0.0403 | 0.0424 | 0.0529 |

# What is a tidy data organization?

A data matrix (think of a spreadsheet like Excel) such that

1. each column is a variable, i.e. a (physical) quantity that can be measured or chosen by design in the experiment,
2. each row is an observation, i.e. the values of the variables for a particular experimental unit,
3. all the relevant information is explicitly represented in the data matrix, e.g. not implicitly given by ordering of rows or columns.

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Exercise: Which of these properties are violated by the non-tidy data organizations shown in Data Example 1 and 2?

# Tidy vs. non-tidy data: Data example 1

## A tidy data organization:

| Molecule | Modification | Feature |
|---|---|---|
| A | without | 0.0 |
| A | with | 20.0 |
| B | without | 48.0 |
| B | with | 33.0 |
| C | without | 0.0 |
| C | without | 76.2 |
| C | without | 82.1 |
| C | without | 57.9 |
| C | without | 78.4 |
| C | with | 76.0 |
| D | without | 0.0 |
| D | with | 47.0 |
| E | without | 0.0 |
| E | with | 69.0 |
| F | without | 9.0 |
| F | with | 16.0 |

## A non-tidy data organization:

| Without | With |
|---|---|
| 0.0 | 20.0 |
| 48.0 | 33.0 |
| 0.0, 76.2, 82.1, 57.9, 78.4 | 76.0 |
| 0.0 | 47.0 |
| 0.0 | 69.0 |
| 9.0 | 16.0 |

# Tidy vs. non-tidy data: Data example 2

A tidy data organization:

| Molecule | br6 | br74 |
|---|---|---|
| A | 0.6423 | 0.6129 |
| A | 0.5507 | 0.5359 |
| B | 0.4004 | 0.2456 |
| B | 0.3336 | 0.2749 |
| C | 0.1135 | 0.0403 |
| C | 0.0424 | 0.0529 |

A non-tidy data organization:

| br6_rep1 | br74_rep1 | br6_rep2 | br74_rep2 |
|---|---|---|---|
| 0.6423 | 0.6129 | 0.5507 | 0.5359 |
| 0.4004 | 0.2456 | 0.3336 | 0.2749 |
| 0.1135 | 0.0403 | 0.0424 | 0.0529 |

# Wide data vs. long data: Data example 2 (both tidy!)

Wide data organization:

| Molecule | br6 | br74 |
|---|---|---|
| A | 0.6423 | 0.6129 |
| A | 0.5507 | 0.5359 |
| B | 0.4004 | 0.2456 |
| B | 0.3336 | 0.2749 |
| C | 0.1135 | 0.0403 |
| C | 0.0424 | 0.0529 |

Long data organization:

| Molecule | Experiment | Feature | Y |
|---|---|---|---|
| A | 1 | br6 | 0.6423 |
| A | 1 | br74 | 0.6129 |
| A | 2 | br6 | 0.5507 |
| A | 2 | br74 | 0.5359 |
| B | 3 | br6 | 0.4004 |
| B | 3 | br74 | 0.2456 |
| B | 4 | br6 | 0.3336 |
| B | 4 | br74 | 0.2749 |
| C | 5 | br6 | 0.1135 |
| C | 5 | br74 | 0.0403 |
| C | 6 | br6 | 0.0424 |
| C | 6 | br74 | 0.0529 |

- When more features are measured, the organization to the left becomes wider, whereas the organization to the right becomes longer.
- Advice: Use physical (and concise) names, and not generic names like $Y$ as done above.

# Exercise: Rows and Columns, Observations and Variables

| Group I | Group II | Group III |
|---|---|---|
| 243 | 206 | 241 |
| 251 | 210 | 258 |
| 275 | 226 | 270 |
| 291 | 249 | 293 |
| 347 | 255 | 328 |
| 354 | 273 | |
| 380 | 285 | |
| 392 | 295 | |
| | 309 | |

Table shows red cell folate levels ($\mu$g/l).

Reference: Amess et al. (1978), Megaloblastic haemopoiesis in patients receiving nitrous oxide, Lancet, 339-342.

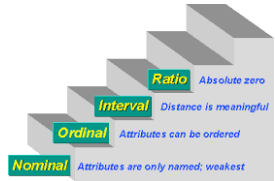
- Are these the same dataset?
- What are the variables? How many observations are there?

| Group | Level |
|---|---|
| I | 243 |
| I | 251 |
| I | 275 |
| I | 291 |
| I | 347 |
| I | 354 |
| I | 380 |
| I | 392 |
| II | 206 |
| II | 210 |
| II | 226 |
| II | 249 |
| II | 255 |
| II | 273 |
| II | 285 |
| II | 295 |
| II | 309 |
| III | 241 |
| III | 258 |
| III | 270 |
| III | 293 |
| III | 328 |

# Variable types

# Four categories of variable types with increasing structural information

- Example of a nominal variable:
  - Color (red, green, purple).
- Example of an ordinal variable:
  - Status (healthy, slight symptoms, severe symptoms, dead).
- Example of an interval variable:
  - Temperature measured in degrees of Celsius.
- Examples of ratio variables:
  - Temperature measured in Kelvin.
  - Height (measured in cm).
  - Money on my bank account (measured in Danish kroner).




- Nominal and ordinal variables are subtypes of categorical variables.
- Interval and ratio variables are subtypes of continuous variables.

# Table of Variables

# Table of Variables

A summary of tidy data in form of another table with one row per variable and 4 columns with meta-information:

1. Variable: The name of the variable in the dataset.
2. Type: The variable type (nominal, ordinal, interval or ratio).
3. Range: State the levels (separated by "," and "$<$" for nominal and ordinal variables, respectively) and range [min; max] for continuous variables.
4. Usage: The role of the variable in the statistical analysis (fixed effect, random effect, response, correlation effect, subject id, not used, ...)

Today we have only seen fixed effect and response. The response variable is characterized by:

- This is what we are interested in.
- This is what we want to predict knowing the other variables.
- This is where the random variation matters to us.

# Data example 2 revisited

## Dataset in wide format:

| molecule | br6 | br74 |
|---|---|---|
| A | 0.6423 | 0.6129 |
| A | 0.5507 | 0.5359 |
| B | 0.4004 | 0.2456 |
| B | 0.3336 | 0.2749 |
| C | 0.1135 | 0.0403 |
| C | 0.0424 | 0.0529 |

## Table of Variables:

| Variable | Type | Range | Usage |
|---|---|---|---|
| molecule | nominal | A, B, C | fixed effect |
| br6 | ratio | [0.0424; 0.6423] | response |
| br74 | ratio | [0.0403; 0.6129] | response |

Quiz: Can you imagine a situation, where that variables have different uses, e.g. where br6 is a fixed effect?

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## Dataset in long format:

| molecule | experiment | feature | Y |
|---|---|---|---|
| A | 1 | br6 | 0.6423 |
| A | 1 | br74 | 0.6129 |
| A | 2 | br6 | 0.5507 |
| A | 2 | br74 | 0.5359 |
| B | 3 | br6 | 0.4004 |
| B | 3 | br74 | 0.2456 |
| B | 4 | br6 | 0.3336 |
| B | 4 | br74 | 0.2749 |
| C | 5 | br6 | 0.1135 |
| C | 5 | br74 | 0.0403 |
| C | 6 | br6 | 0.0424 |
| C | 6 | br74 | 0.0529 |

## Table of Variables:

| Variable | Type | Range | Usage |
|---|---|---|---|
| molecule | nominal | A, B, C | fixed effect |
| experiment | nominal | 6 levels | random effect |
| feature | nominal | br6, br74 | fixed effect |
| Y | ratio | [0.0403; 0.6423] | response |

# Checkpoint

- Questions?
- Next, we continue with a short introduction to R and RStudio.
- After this we discuss *t*-tests and data transformations (you might know much of this already).

Time for a break!

# Introduction to R

The RStudio interface consists of $4 = 2 \times 2$ windows:

| | |
|---|---|
| Upper-left | The editor, where you write your R programs. |
| Lower-left | The console, where code is executed and results are printed. |
| Upper-right | Overview of objects (variables, vectors, matrices, data frames, lists, functions, "results", etc.) in the (global-) environment. |
| Lower-right | Miscellaneous: overview of working directory, history of plots, administration of packages, and help pages. |

- R is a full-scale object-oriented programming language.
- In R your data is typically stored in either vectors, matrices, or most commonly in data frames (tidyverse introduces a variant of dataframes; tibbles).
- Results from analyses are stored in associated objects (for well-programmed functions):
  - E.g. a call to the `lm()` function results in an `lm`-object.
  - Such objects may be printed, summarized and/or plotted.

# Functions and R packages

R contains many predefined functions for doing statistical computations:

- Standard functions: `mean()`, `sd()`, ...
  - These functions may be used without any further ado.
  - Includes so-called generic functions: `print()`, `summary()`, `plot()`, ...
- Functions from pre-installed packages: `MASS::boxcox()`, `cluster::agnes()`, ...
  - The package may be loaded in an R session: e.g. `library(MASS)`.
- Functions from other packages: `nlme::lme()`, `LabApplStat::DD()`, ...
  - The package must be installed once before it can be loaded and used: preferably done using the Install Packages button.
  - Ability to install packages is vital for the functionality of R.
  - Unfortunately, problems installing packages have become more prevalent (possible solutions: "Run as Administrator" + ask for help!)

# $t$-tests

# Systematic effects vs. Random variation

- Systematic effects: Mean properties of the population. Often the object of interest.
  - For instance the expected life span of men and women, or the difference between the effect of two drugs.

- Random variation: The dispersion of the data points around the systematic properties.
  - Natural variation in the population.
  - Measurement errors.
  - Difference between a complex world and a simple model.

- Hypothesis testing: Are the systematic effects significant, or can they be explained by the random variation?

# Data example 3: Change in glucose level – One sample $t$-test

- For 8 diabetics the one-hour change in plasma glucose level after some glucose treatment was measured:

```
> change <- c(0.77, 5.14, 3.38, 1.44, 5.34, -0.55, -0.72, 2.89)
> mean(change)
[1] 2.21125
> sd(change)
[1] 2.36287
```

- Did the treatment change the plasma glucose level?

- We will review and apply fundamental statistical concepts such as statistical model, null hypotheses, test statistics, $p$-values, confidence intervals.

# Fundamental statistical concepts

- Models are described by parameters. In data example 1 these are the mean $\mu$ and the standard deviation $\sigma$. We have the model:

$$Y_1, \ldots, Y_n \quad \text{i.i.d. } \mathcal{N}(\mu, \sigma^2)$$

- A statistical hypothesis is a simplifying statement about the model. Often formulated in terms of the parameters, e.g.

$$\text{Null hypothesis } H_0\text{: } \mu = 0, \qquad \text{Alternative } H_A\text{: } \mu \neq 0$$

- Test statistic $T$ is a function of the data. Actual value denoted $t_{\text{obs}}$.
  - If $T$ measures disagreement with $H_0$ and if $t_{\text{obs}}$ is too extreme, then we reject $H_0$.
  - If the observed data is conceived as being random, then $T$ becomes a random variable with a probability distribution.
  - Extremeness quantified by the *p*-value, calculated assuming $H_0$ is true,

$$p = \mathbb{P}(T \text{ more extreme than } t_{\text{obs}})$$

# One sample $t$-test – model: $Y_1, \ldots, Y_n$ i.id. $\mathcal{N}(\mu, \sigma^2)$

- Given prefixed value $\mu_0$, often 0, we pose the hypothesis $H_0$: $\mu = \mu_0$.

$$\text{Estimates:} \qquad \widehat{\mu} = \overline{Y} = \frac{1}{n}\sum_{i=1}^{n} Y_i, \qquad \widehat{\sigma}^2 = s^2 = \frac{1}{n-1}\sum_{i=1}^{n}(Y_i - \overline{Y})^2$$

- Test statistic and $p$-value for one-sided test, $H_A$: $\mu > \mu_0$,

$$T = \frac{\overline{Y} - \mu_0}{s/\sqrt{n}} \sim t_{\text{df}=n-1}, \qquad p = \mathbb{P}(t_{\text{df}=n-1} > t_{\text{obs}})$$

- Test statistic and $p$-value for two-sided test, $H_A$: $\mu \neq \mu_0$,

$$T = \frac{\overline{Y} - \mu_0}{s/\sqrt{n}} \sim t_{\text{df}=n-1}, \qquad p = \mathbb{P}(|t_{\text{df}=n-1}| > |t_{\text{obs}}|)$$

# Data example 3: Change in glucose level

- For 8 diabetics the one-hour change in plasma glucose level after some glucose treatment was measured:

```
> change <- c(0.77, 5.14, 3.38, 1.44, 5.34, -0.55, -0.72, 2.89)
> mean(change)
[1] 2.21125
> sd(change)
[1] 2.36287
```

- Did treatment change plasma glucose level in data example 3 (see `glucose.R`)?

$$t_{\text{obs}} = 2.21 \cdot \sqrt{8}/2.36 = 2.65, \qquad p = 2 \cdot \mathbb{P}(T_{\text{df}=7} > 2.65) = 0.03$$

Quiz: Is there anything special about the way these data were computed? (Hint: how are the changes computed?)

# Data example 4: phosphorus concentration in lakes – two sample $t$-test

We now consider an example with two independent samples (allowing different sizes).

```
> lakes
# A tibble: 627 x 2
   location     phosphorus
   <chr>             <dbl>
 1 East-Denmark    255
 2 East-Denmark    102.
 3 East-Denmark    166.
 4 East-Denmark     42.5
 5 East-Denmark    102.
 6 East-Denmark     60.6
 7 East-Denmark     89.8
 8 East-Denmark    182.
 9 East-Denmark    243.
10 East-Denmark     30.9
# ... with 617 more rows
```

- Is there a difference between East-Denmark (235 observations) and West-Denmark (392 observations)?
- Let us write up a statistical model and do the analysis using R.

# Statistical analysis of two independent normal samples

Statistical model:

$$\text{First population} \sim \mathcal{N}(\mu_1, \sigma_1^2), \qquad \text{Second population} \sim \mathcal{N}(\mu_2, \sigma_2^2)$$

Sequence of hypothesis [usually we skip (I) and simply use (IIb)]:

(I) $H_0$: $\sigma_1 = \sigma_2$

(II) $H_0$: $\mu_1 = \mu_2$

- (IIa) Assuming equal standard deviations $\sigma_1 = \sigma_2$.
- (IIb) Not assuming equal standard deviations.

Available statistical tests:

(I) `var.test()`, `bartlett.test()`, `lawstat::levene.test()`, `fligner.test()`, and many more.

- Don't do too many tests. Preferably only one test. Why?

(II) $t$-test, slightly different form in (IIa) and (IIb).

# Assumptions and checking for Normality

All *t*-tests (and other "normal" models) are only valid under certain assumptions:

- Assumptions
  - The response variable (more precisely, the error terms) are normally distributed.
  - Possibly homogeneity of variance (homoscedasticity), meaning that the variance of the response variable is constant over the observed range of some other variable. This is (I) on slide 40.

- Checking for Normality
  - Visual inspection : `QQ-plot`.
  - Goodness-of-fit tests: `Shapiro-Wilks test`, `Kolmogorov-Smirnov test`, `Cramer-von Mises test`, `Anderson-Darling test`.

Shapiro-Wilks and Kolmogorov-Smirnov tests are available in `base R`, the others in the package `nortest`.

# Transforming data

When the normality assumption is not satisfied, it can be useful to transform the data.

- Standard transformations (for $x > 0$):
  - `log` transform: $x \mapsto \log(x) = y$.
  - Square root transformation: $x \mapsto \sqrt{x} = y$.
  - The inverse transformation: $x \mapsto \frac{1}{x} = y$.
    This transformation changes the order of the observations.
  - Box-Cox transformation with index $\lambda$:

$$x \mapsto y_\lambda = \begin{cases} \frac{x^\lambda - 1}{\lambda} & , \quad \lambda \neq 0 \\ \log(x) & , \quad \lambda = 0. \end{cases}$$

    Note the order of the observations is changed when $\lambda < 0$.
    Some particular cases:

| $\lambda = -1$ | $\lambda = 0$ | $\lambda = 0.33$ | $\lambda = 0.5$ | $\lambda = 1$ |
|---|---|---|---|---|
| *Inverse* | log | *cubic root* | *square root* | *no transformation* |

- Arcus sinus transformation (for $x \in [0, 1]$):
  - $x \mapsto \arcsin(\sqrt{x})$.
  - May be appropriate when $x$ measures proportion of successes from a number of trials.

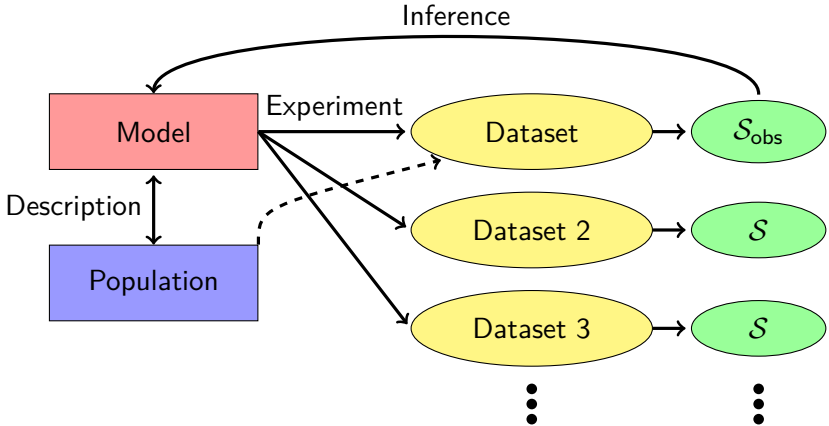
# Data example 4: Using R – `lakes.R`

- Reading an Excel sheet.
- Validation of normality:
  - Graphical: `qqnorm(); abline(mean(),sd())`
  - Shapiro-Wilks test: `shapiro.test()`
  - Kolmogorov-Smirnov test: `ks.test(,"pnorm",mean(),sd())`

  Statisticians often prefer the graphical method as it reveals more than the $p$-value of a normality test.
- Data transformation.
- The actual two sample $t$-test.
- Keyboard shortcuts (Windows): `Ctrl-Enter`, `Ctrl-Shift-Enter`, `Ctrl-1`, `Ctrl-2`

# Summary + Exercises

# Today's summary: Model, data, statistic




- What is the distribution of the $p$-value?
- Where do standard deviation and standard error reside?
- What is the interpretation of a confidence interval?

# Homework

- Exercise class November 22 from 14.00 to 16.45.
  - Exercise sheets: `ex_day1.pdf`, `ggplot2_exercise.pdf`
  - Exercises not completed at class should be completed at home.

- Before the lectures on November 29 you should read the papers:
  - Sterne & Smith (2001), "Sifting the evidence—what's wrong with significance tests?", British Medical Journal, 226–231.
  - Gelman & Carlin (2014), "Beyond Power Calculations: Assessing Type S (Sign) and Type M (Magnitude) Errors", Perspectives on Psychological Science, 1–11.