

Intermediate statistics: data analysis in practice

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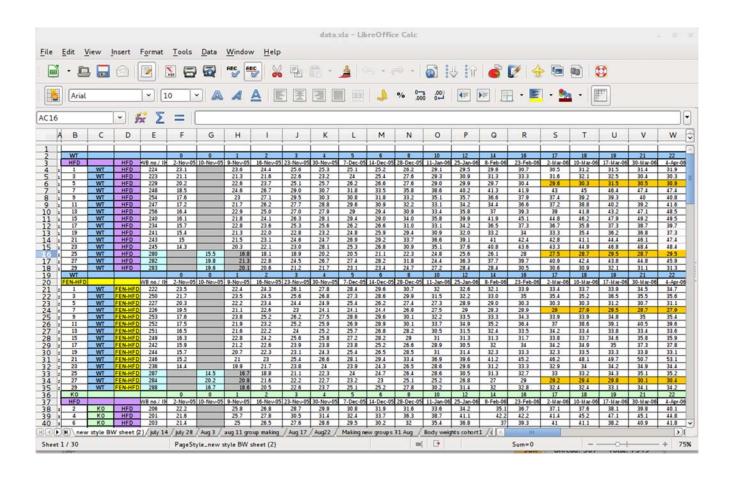


Swiss Institute of Bioinformatics

What do you think is easy and what do you think is complicated with data analysis?

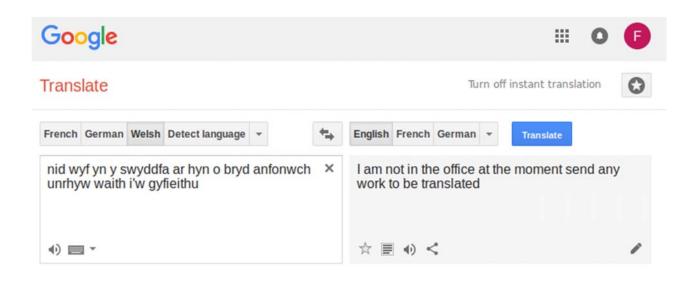
- Exploratory data analysis
- Data summarization: mean, median, SD, SEM, CI
- Graphics, tables
- Statistical tests
 - Student's t-tests (one- and two-sample, paired)
 - Wilcoxon
 - Fisher's exact test
 - Chi-square
 - ANOVA
- Correlation, linear regression
- Principal component analysis (PCA)

What are the general steps of data analysis?





Nid wyf yn y swyddfa ar hyn o bryd. Anfonwch unrhyw waith i'w gyfieithu

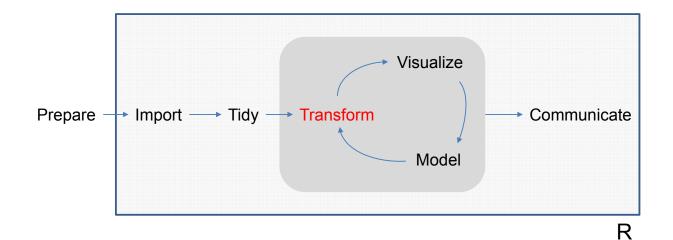


Some important rules of statistical analysis

Know the story around the data

Ask concrete questions

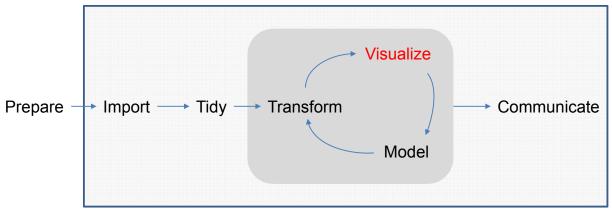
Always look at the data!



Should we really "transform" the data?

- Summarization: mean, median, etc
- Create new variables:
 - Combine variables (height+weight → BMI)
 - Change the scale of a variable or units
 - Normalize
 - Log-transform
- Aggregate data

Data analysis workflow

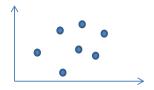


R

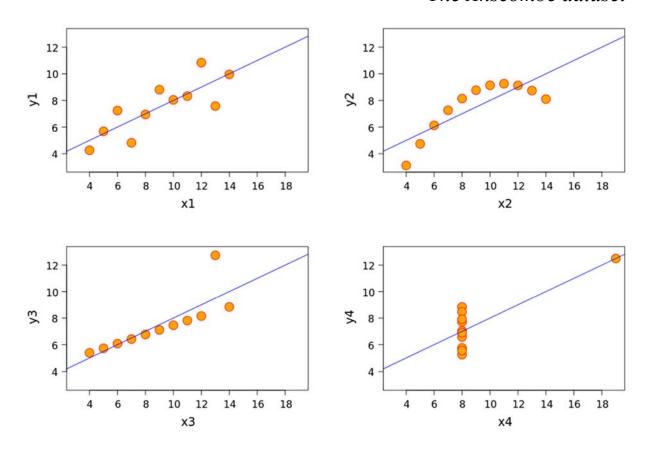
| | X1 | X2 | ХЗ | X4 | Y1 | Y2 | Y3 | Y4 |
|--------------------|-----|-----|-----|-----|-----------|-----|-----------|-----------|
| Mean | 9.0 | 9.0 | 9.0 | 9.0 | 7.5 | 7.5 | 7.5 | 7.5 |
| Standard deviation | 3.3 | 3.3 | 3.3 | 3.3 | 2.0 | 2.0 | 2.0 | 2.0 |

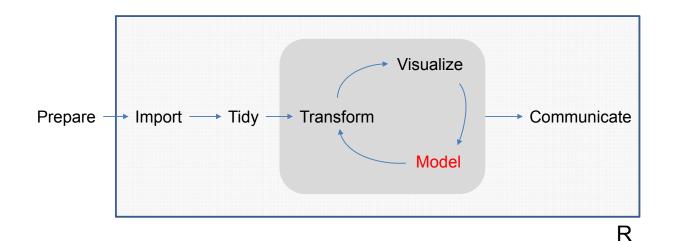
| | X1 vs Y1 | X2 vs Y2 | X3 vs Y3 | X4 vs Y4 |
|-----------------|--------------|--------------|--------------|--------------|
| Correlation | 0.81 | 0.81 | 0.81 | 0.81 |
| Regression line | Y = 3 + 0.5x |

Can we guess what the scatterplots look like?



The Anscombe dataset





Adapted from Hadley Wickham

Here:

a model provides a summary/explanation of a dataset

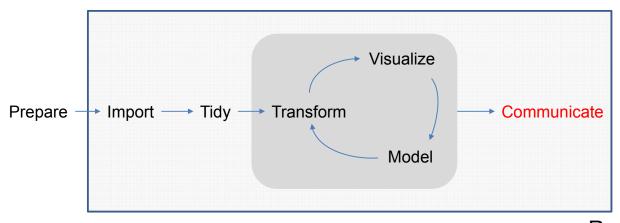
Explains true signal vs noise

One rule:

Keep it simple

(although this is not universally agreed)

Data analysis workflow



R

Flipped classroom?

How we are going to work

- Work in groups of 5 (5 groups in total)
- Get a project to work on (it may or may not be the same for all groups)
- Work on the analysis within the group, and prepare an *informal* presentation of the results
- Don't discuss only the results, but also the methods and the issues you've encountered.
- · Ask for feedback if you are stuck or if you hesitate
- Groups will then present and we will discuss the topics afterwards.

Schedule

| 9:00 | Welcome and introduction |
|-------|-----------------------------|
| 10:00 | Coffee break |
| 10:15 | Work in group (qPCR data) |
| 12:00 | Lunch |
| 13:00 | Presentation: knitr |
| 13:30 | Work in group |
| 14:30 | Coffee break |
| 14:45 | Presentation and discussion |
| 15:30 | Work in group (dataset 2) |

First dataset: qPCR dataset

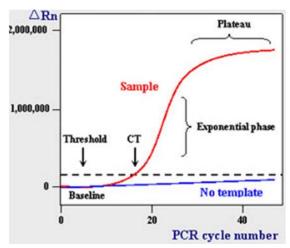
- Measure of gene expression in mice
- Two variables of interest:
 - Genotype: WT/KO mice for the MAF1 gene
 - Treatment: either normal food (control) or fasting (treated)
- We are interested in the expression of gene AKT
- 3 biological replicates for each group
- 3 technical replicates for each biological replicate

Our questions

- In MAF1 WT mice, is there a difference in AKT expression depending on the treatment?
- Does the effect of the treatment depend on the MAF genotype (WT/KO)?

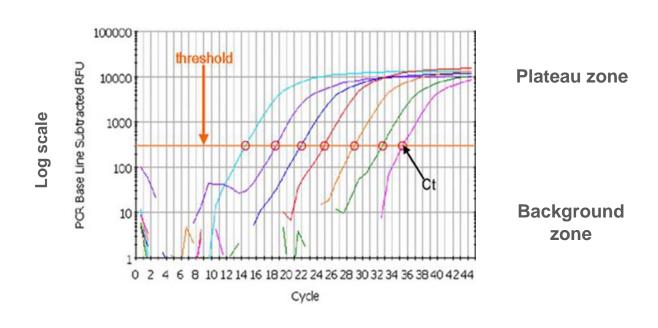
Real Time Polymerase Chain Reaction

- · Extension of the PCR technology
- Use fluorescence to measure the amount of expression at every cycle.
- Measure the number of cycles (Ct, "cycle threshold") required until the fluorescence crosses a given threshold.
- This measure is made during the exponential phase.
- The threshold is arbitrary
- Gene more expressed = lower Ct value



http://www.rt-pcr.com/

A real example



What the data looks like...

| Well | Sample | Gene | Ct |
|------|--------------|------|-------|
| A1 | WT-Treated | Α | 35 |
| A2 | WT-Treated | Α | 36.82 |
| A3 | WT-Treated | Α | 34.34 |
| A4 | WT-Untreated | Α | 34.89 |
| A5 | WT-Untreated | Α | 35.29 |
| A6 | WT-Untreated | Α | 35.65 |
| A7 | KO-Treated | Α | 34.22 |
| A8 | KO-Treated | Α | 31.94 |
| A9 | KO-Treated | Α | 35.24 |
| A10 | KO-Untreated | Α | 29.57 |
| A11 | KO-Untreated | Α | 35.79 |
| A12 | KO-Untreated | Α | 33.77 |
| ••• | | | |

| Well | Sample | Gene | Ct |
|------|--------------|------|-------|
| B1 | WT-Treated | В | 29.69 |
| B2 | WT-Treated | В | 29.14 |
| В3 | WT-Treated | В | 26.6 |
| B4 | WT-Untreated | В | 27.4 |
| B5 | WT-Untreated | В | 32.44 |
| В6 | WT-Untreated | В | 27.1 |
| В7 | KO-Treated | В | 26.03 |
| В8 | KO-Treated | В | 23.43 |
| В9 | KO-Treated | В | 27 |
| B10 | KO-Untreated | В | 26.2 |
| B11 | KO-Untreated | В | 28.21 |
| B12 | KO-Untreated | В | 24.19 |
| | | | |

Normalization

- The measured expression must be normalized for difference between samples (e.g. amount of starting material).
- This is usually done using a *reference gene* (or *standard gene*, *housekeeping gene*), which should be expressed in all cells and have the same number of copies in all cells
- · Examples of typical housekeeping genes:
 - Glyceraldehyde 3-phosphate dehydrogenase (GAPDH)
 - Beta actin
- · The assumptions are very stringent and not always satisfied...
- Common recommendations: take several (at least 3) housekeeping genes.

How to measure differential expression: the $\Delta\Delta Ct$ method

The efficiency is assumed to be perfect (100% = exact doubling at every cycle), and the efficiencies for the gene of interest and the reference should be similar.

Difference between conditions 1 and 2:

$$\Delta\Delta Ct_g = \Delta Ct_{g2} - \Delta Ct_{g1}$$

Log fold change =
$$-\Delta \Delta Ct_g = \Delta Ct_{g1} - \Delta Ct_{g2}$$

Fold change =
$$2^{-\Delta\Delta Ctg}$$

(The base is 2 because a difference of one cycle represents a doubling of the amount of the material. In comparison to other assays, the base of the logarithm is not arbitrary here)

A typical setting

Condition 1

Condition 2

| | Condit | 1011 1 | _ | | | | |
|----------------------|---------------------|--------|-------|----------------------|---------------------|------|-------|
| Biological replicate | Technical replicate | Gene | Ct | Biological replicate | Technical replicate | Gene | Ct |
| 1 | 1 | Α | 35 | 1 | 1 | Α | 29.69 |
| 1 | 2 | Α | 36.82 | 1 | 2 | Α | 29.14 |
| 1 | 3 | Α | 34.34 | 1 | 3 | Α | 26.6 |
| 2 | 1 | Α | 34.89 | 2 | 1 | Α | 27.4 |
| 2 | 2 | Α | 35.29 | 2 | 2 | Α | 32.44 |
| 2 | 3 | Α | 35.65 | 2 | 3 | Α | 27.1 |
| 3 | 1 | Α | 34.22 | 3 | 1 | Α | 26.03 |
| 3 | 2 | Α | 31.94 | 3 | 2 | Α | 23.43 |
| 3 | 3 | Α | 35.24 | 3 | 3 | Α | 27 |
| 1 | 1 | HKG | 29.57 | 1 | 1 | HKG | 26.2 |
| 1 | 2 | HKG | 35.79 | 1 | 2 | HKG | 28.21 |
| 1 | 3 | HKG | 33.77 | 1 | 3 | HKG | 24.19 |
| 2 | 1 | HKG | 29.57 | 2 | 1 | HKG | 29.69 |
| 2 | 2 | HKG | 35.79 | 2 | 2 | HKG | 29.14 |
| 2 | 3 | HKG | 33.77 | 2 | 3 | HKG | 26.6 |
| | | | | | | | |