

Exercise 1

R comes along with a lot of sample datasets. A very popular one is called `iris`, which holds sepal and petal measurements for different iris sub-species. The dataset is directly available to you by the variable name `iris`.

- Look at the first and last few observations in the dataframe to get a first idea about the structure of the data.
- Calculate summary statistics for each of the columns.
- Calculate summary statistics for each of the sub-species separately.
(*Hint: You can use double brackets to extract an element from a list: `list_with_data[[1]]` returns the first element of the list.*)
- You can plot each column combination of a dataframe by using the `plot` function. Do this. What do you see? Can you identify patterns?

Exercise 2

Think back to the example with the fluorescence intensity at tricellular junctions from the presentation. Usually, one would not measure a single intensity value from one embryo but rather several values at different TCJ. If you view the experiment like this, what is the observational unit now? Look at the following tables. How are they wrongly formatted? What would they have to look like instead?

TCJ	Stage	Genotype	Embryo 1	Embryo 2	Embryo 3
1	14	y w	1.24	1.91	0.86
2	14	M6[W186*]	0.23	0.97	0.38
3	14	y w	0.98	1.35	0.22
⋮	⋮	⋮	⋮	⋮	⋮

Embryo	Stage	Genotype	Intensity Enrichment
1	14	y w	1.24, 1.91, 0.86, 0.55, ...
2	14	M6[W186*]	0.23, 0.97, 0.38, 1.06, ...
⋮	⋮	⋮	⋮

Embryo	Intensity Enrichment
14/yw	1.24
15/yw	0.23
15/M6[W186*]	1.92
14/M6[W186*]	1.73
⋮	⋮

*Exercise 3

This exercise is for the upcoming lecture to prepare you for the content or to sensitize you for a certain aspect.

We will see in the next lecture how we can extract specific values from vectors and lists. One way to do this is to use square brackets `[i]` or double square brackets `[[i]]` where `i` is the position of the element we'd like to extract. Create a list like below and use these two ways to extract each of the elements separately. Do you see a difference for single and double brackets? Look carefully and use `str` to analyze the result.

```
sample_list <- list(1:10, mean, list(10:1, median))
```