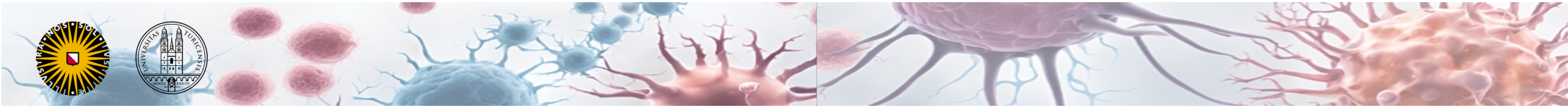


# R challenge Week 6

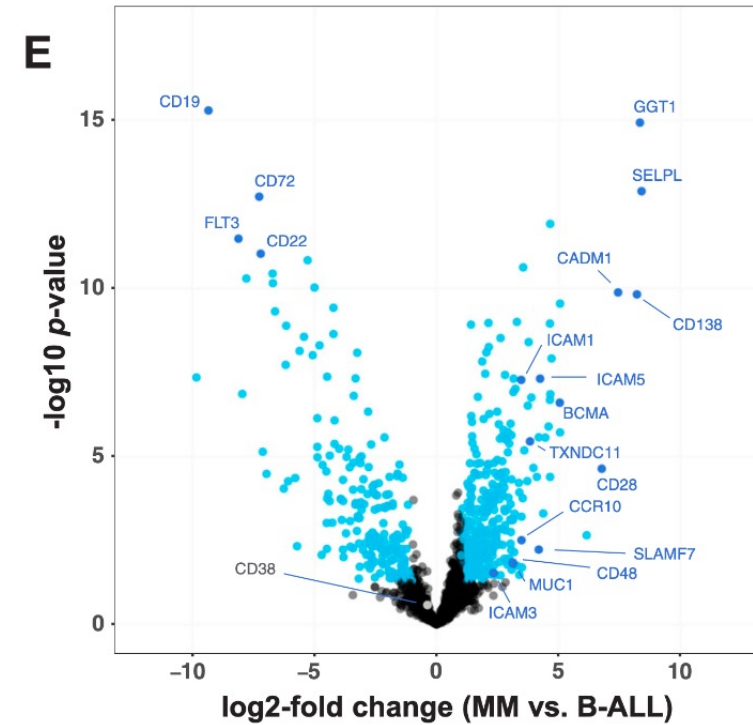
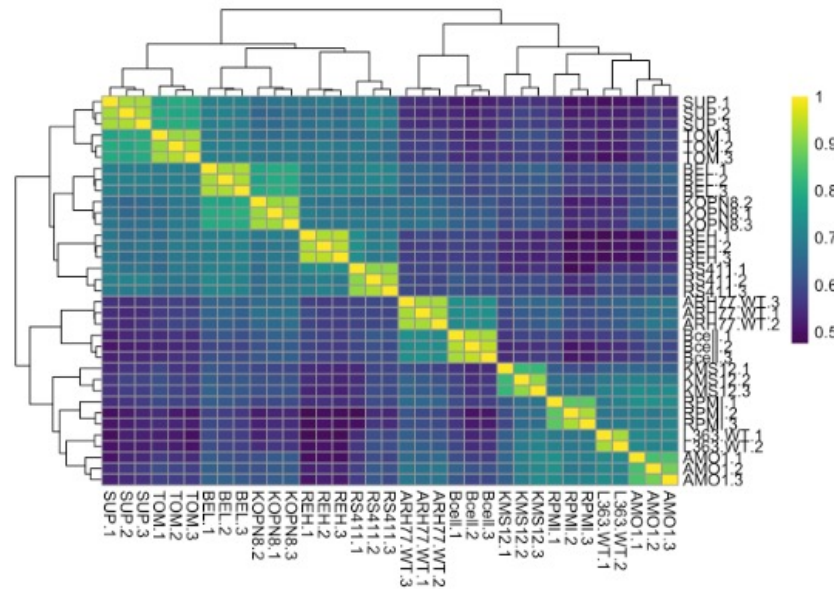
@ Jonas Grossmann

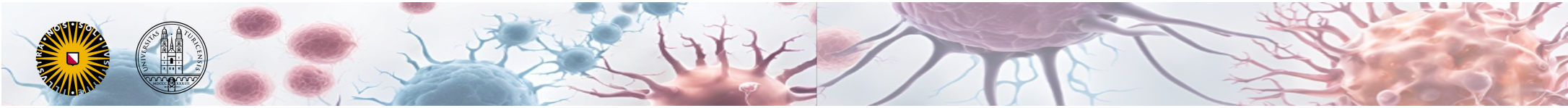


# What is it all about

- Reproduce the Volcano plot (Fig 1E)
- Generate some QC plots

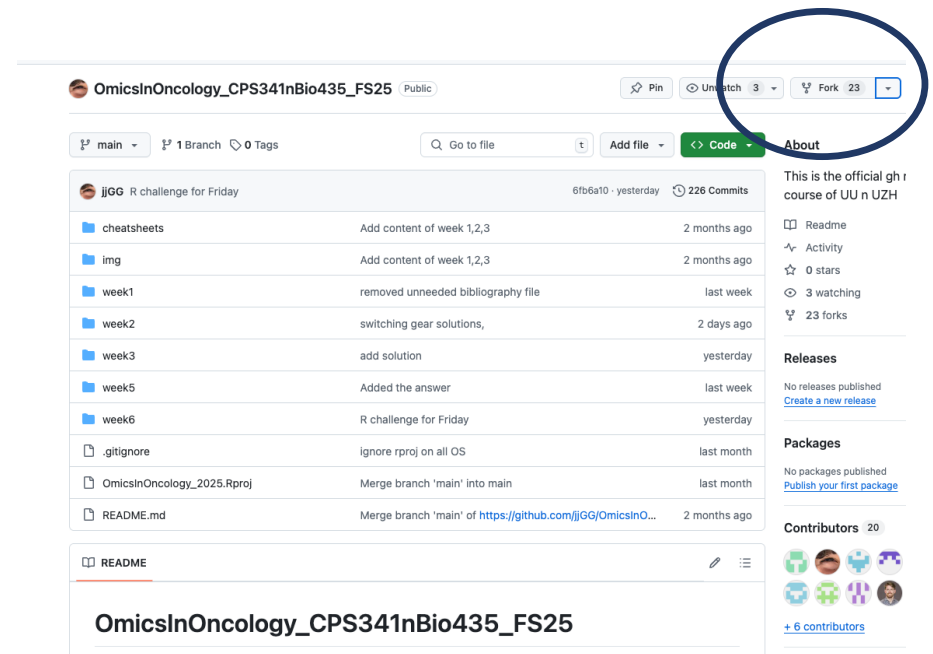
A Correlation-Heatmap

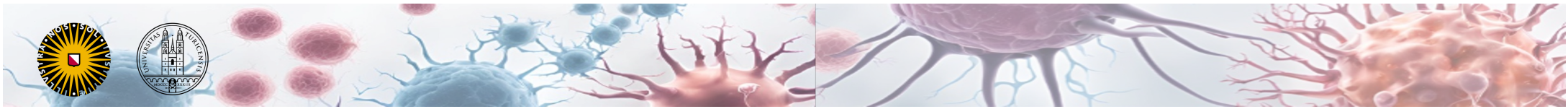




# How to do it:

- Synchronize or re-fork our gh repos to your gh-account
  - > either one person per groups forks and everyone else clones it from there and contributes back
  - > alternatively everyone forks from jjGG
  - > I expect one PR per group in the end
- Connect your Rstudio to it
- Work in your coding groups
- Use the coding channels to support each other
- Teachers solution will be available in the evening





# In the week 6 folder

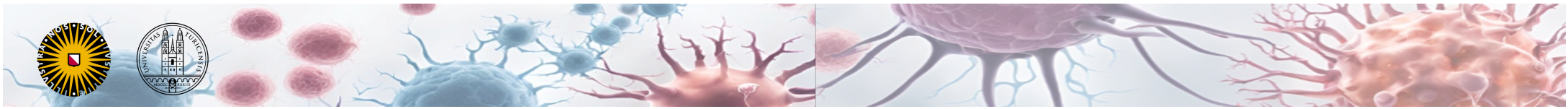
- You find:
  - pdf -> the paper again
  - xlsx -> Supp Mat
  - COILbiobibliography.bib  
→ the reference in html
  - MarkerProteinsPOIs.txt  
→ what proteins to label
  - \_minimal.Rmd
  - \_partOfItDone.Rmd  
→ template to start either  
from the very scratch  
or with some more help (part of it done)

OmicsInOncology\_CPS341nBio435\_FS25 / week6 /

 jjGG R challenge for Friday

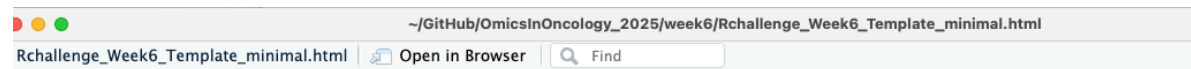
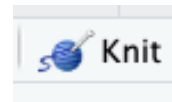
Name	Last commit message
..	
img	R challenge for Friday
41467_2022_31810_MOESM3_ESM.xlsx	R challenge for Friday
COILbibliography.bib	R challenge for Friday
MarkerProteinsPOIs.txt	R challenge for Friday
Rchallenge_Week6_Template_minimal.Rmd	R challenge for Friday
Rchallenge_Week6_Template_partOfItDone.Rmd	R challenge for Friday
s41467-022-31810-6.pdf	R challenge for Friday





# In RStudio

- Start w/ knitting the template
- Have a read
- Find the junks where to put some "code"



## Get more experience with R

Group XX

13 March, 2025

## Introduction

```

```{r readInData, echo=FALSE, include=TRUE}
# read in the data and put it into an object (e.g. dat) have a look at the head of the data

print("here we look into head of the data")
```

```{r reshapeData, echo=FALSE, include=TRUE}
# ideally you reshape the data into another object by selecting only necessary columns
# maybe also rename the columns to make it easier to work with

# rename columns
```

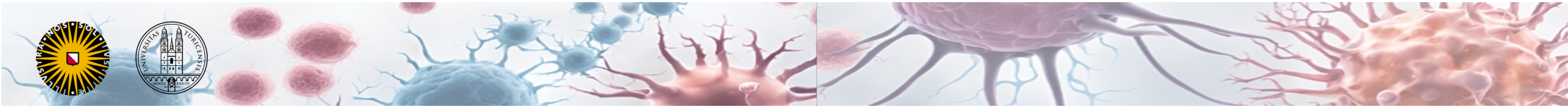
```

ice a volcano plot from an article using the provided supplementary data and t  
 . Basically, in the same article, the authors also provide a matrix with the expre  
 cells. We will try to visualize this matrix as a heatmap, a correlation heatmap o  
**cells suggests potential immunotherapeutic strategies and protein mark**

a cells suggests potential immunotherapeutic strategies and protein markers o  
 restigation of the surface proteome, or surfaceome, of multiple myeloma cells.  
 nces the interaction between tumor cells and their microenvironment, making i  
 tanding drug resistance mechanisms (Ferguson et al. 2022).

teomics to systematically characterize the myeloma surfaceome under various  
 sponse to acute drug treatments. This methodology allowed for a detailed exa  
 apy. The findings from this study include the establishment of a scoring system  
 potential therapeutic value (Ferguson et al. 2022).

dy is the identification of CCR10 as a promising target for immunotherapeutic i  
 among malignant plasma cells, suggesting that therapies targeting this marke  
 ction for developing new immunotherapies aimed specifically at overcoming th



## Goal 2:

- Try to come up at least with the protein heatmap
- And ONE QC plot

## Goal 2: Try to visualize the expression matrix as a heatmap and make some QC plots

The authors of the article also provide a matrix with the expression of the proteins in the surfaceome of multiple myeloma cells. Please also remember the QC-plots from week 3. We will try to visualize this matrix as a heatmap and do some more QC plots such as correlation heatmap or a PCA/MDS plot.

```
# Do you find a pattern that matches all the columns that you want? There is a regex pattern that matches the columns of interest
```

First some reshaping is necessary again.

A heatmap with clustering

A Correlation-Heatmap

Some QC plots like in week 3

First again some reshaping

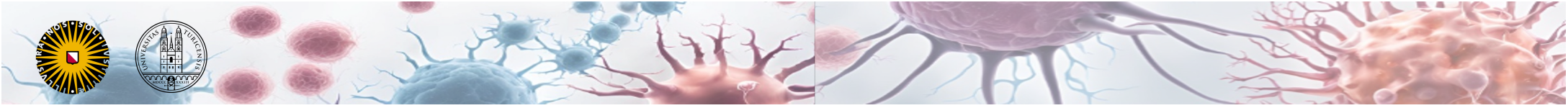
Here we take the recipe from week 3 and apply it to the data we have here. Important here is that the **protein names** are redundant that causes problems. Therefore we take the Uniprot\_ID instead of the protein names to generate the SummarizedExperiment object.

PCA and MDS plots like in Week 3

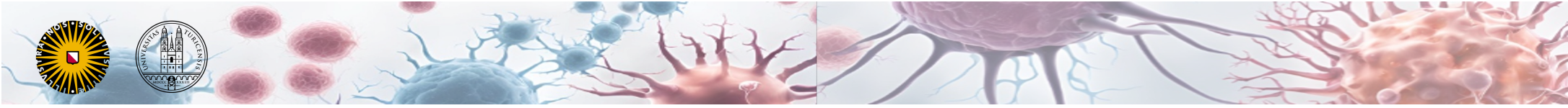
```
# Do PCA
```

Correlation plot like in week 3

```
# Pearson correlation plot
```



How does the endproduct look like?



## What to do if you «struggle»?

- Try to help each other in your coding groups
- Formulate good questions to ask AI for help  
e.g: "some R fun?", "here my data.. *Give the first few lines of your data* how can I do .. ", or .. "Looks good but I want this and that..".
- Call the teachers for help ;).. -> we will also "visit your channel" from time to time..