

Preliminary project direction of Group 3

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2022-04-07

The Dataset

The original data comes from 236 RNA-seq synovial biopsy samples from the papers of Walsh et al. and Guo et al. as provided by Platzer et al. [1-3].

Links to datasets

Raw data article 1

Raw data article 2

A rough workflow

Following tidying and wrangling of the raw data, a PCA, boxplot and heatmap of the gene-expression data will be done for each of the patient groups.

Libraries

Some of the libraries we expect to use are the following: ggplot2, tidyr, patchwork, dplyr, broom, purrr, tibble.

Aim

Our aim is to profile these based on the transcriptomic analysis. A biological analysis and conclusion will follow.

References

- [1]Walsh, Alice M., et al. "Triple DMARD treatment in early rheumatoid arthritis modulates synovial T cell activation and plasmablast/plasma cell differentiation pathways." PLoS One 12.9 (2017): e0183928.
- [2]Guo, Yanxia, et al. "CD40L-dependent pathway is active at various stages of rheumatoid arthritis disease progression." The Journal of Immunology 198.11 (2017): 4490-4501.
- [3]Platzer, Alexander, et al. "Analysis of gene expression in rheumatoid arthritis and related conditions offers insights into sex-bias, gene biotypes and co-expression patterns." PloS one 14.7 (2019): e0219698.