# Introduction to R
# for data analysis

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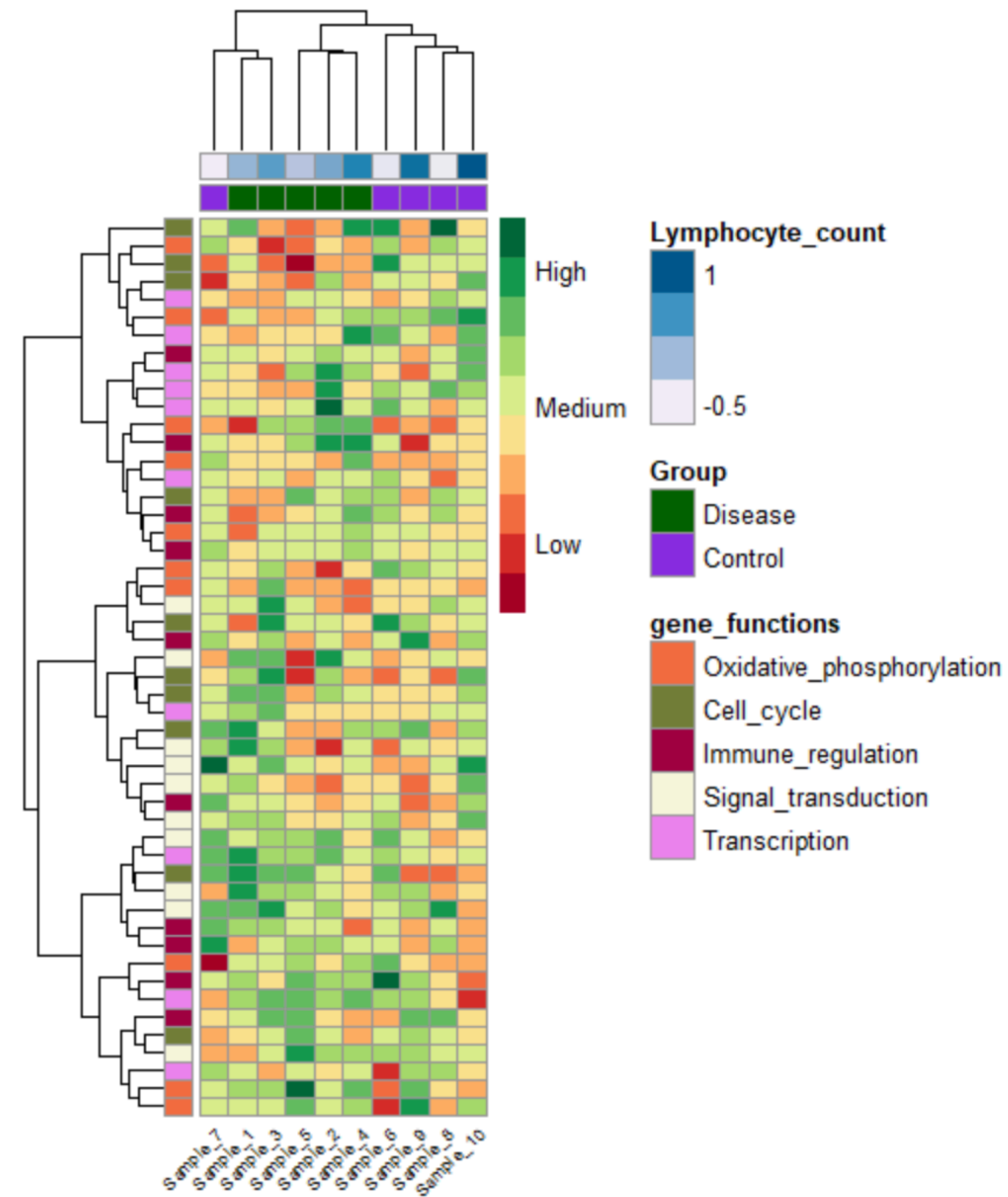ZUKUNFT
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# R for single-cell analysis

# R for ~~single-cell~~ analysis
## data



**How do we get to this plots?**

**What can we learn from it?**

# Content

**Day 1 : the basics**

1. first steps in R

2. reading data frames

3. cleanup

4. simple plots

5. statistical tests

**Day 2 : simple scRNA-seq workflow**

1. Building Seurat objects

2. QC

3. Feature selection

4. Dimension reduction

5. UMAP plots

6. Diffusion models

# Welcome!

- What to **expect** from this course:
  - getting familiar with **R data types**, and basic manipulation
  - learning how to handle **data tables**
  - making **simple plots**
  - performing **simple statistical tests**
  - learning how to organize **reproducible analysis**
  - getting a glimpse into an analysis workflow for **single-cell RNA-seq**

  ### = *talking without shame to your favorite bioinformatician!*

- What **not to expect** from this course:
  - being able to perform sophisticated analysis
  - being able to program in R
  - being able to perform a full analysis of single-cell RNA-seq

# How the course is organized

- Focus on **hands-on experience**!!

- Typical sequence (for each chapter)
  1. some introductory slides on important concepts
  2. hands-on work on small exercises
  3. some more advanced exercises at the end of chapter
  4. Common debrief at the end of each chapter

https://www.hdsu.org/r4sc2024/

# Schedule

- Morning session: 9am → 12am

- Afternoon session: 2pm → 5pm

- Break at 10h30 and 3.30pm