



# Introduction to R for data analysis

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IRTG Course - June 2021



Medizinische Fakultät Heidelberg

# Content



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## 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. count matrices

2. Seurat objects

3. QC

4. Feature selection

5. Dimension reduction

6. UMAP plots

# Welcome!



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- 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



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- 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
- **2 groups** (see Google Sheet)
  - Group 1 → Carlos
  - Group 2 → Carl

*Document your progress in the Google Sheet*

*Contact us through Discord in case of problems (text/ audio channel, screen sharing)*

# Schedule



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- Morning session: 10h → 12h30
- Afternoon session: 13h30 → 17h30
- Break from 15 → 15h30