

Single-cell transcriptomics best practices

Course description:

The goal of this course is to teach you the best practices of single-cell sequencing analysis. Encompassing the most common analysis steps from preprocessing to visualization, statistical evaluation, and more, this course equips you with the knowledge to independently analyze unimodal and multimodal single-cell sequencing data. Utilizing various tools within the Python and R ecosystems, we'll guide you through hands-on exercises in JupyterLab Notebooks, providing opportunities to apply and test your newly acquired skills. By the end of this course, you'll be well-equipped to navigate the complexities of single-cell sequencing analysis.

Topics:

- Fundamentals of single-cell sequencing analysis
- Tools recommendations for each analysis step
- Processing of single-cell data using R and Python packages
- Step-by-step analysis with visualization of the results

Methods:

Presentations, Hands-on sessions and exercises, Q&A sessions

Format:

- Mode: online course on Teams
- Duration: 4 half days (usually 1 pm – 5 pm)
- Language: English
- Participants: max. 12 persons

Requirements:

[Introduction to Python](#) and [Introduction to R](#) (or equivalent course/experience)

Dates and Application:

You can view the current dates and register for this course on [CaMS](#).