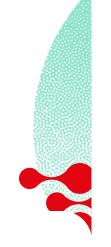
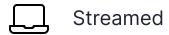
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Single-Cell Transcriptomics with R









Cancellation deadline: 16 February 2021

Rachel Jeitziner and Tania Wyss

Omics data analysis

Intermediate

Academic: 180 CHF For-profit: 900 CHF





Applications are closed because the course is full with a long waiting list or has just passed. Sign up to receive notification when a new course is scheduled.



Next course(s): 15 - 17 JUN 2021 ☐ Streamed O Bern 08 - 10 NOV 2021 28 FEB - 02 MAR 2022 □ Streamed 04 - 06 JUL 2022 Bern O Bern 14 - 16 NOV 2022 06 - 08 MAR 2023 ☐ Streamed 03 - 05 JUL 2023 Bern 13 - 15 NOV 2023 Bern O Bern 18 - 20 MAR 2024 29 - 31 OCT 2024 Bellinzona 18 - 20 MAR 2025 Bern 02 - 04 JUL 2025 Zürich





12 - 14 NOV 2025



The course is now full with a long waiting list. If you do not want to miss your chance to be part of the next session and remain informed about all training activities at SIB, we highly recommend you to keep an eye on our list of upcoming events and subscribe to our courses mailing list here (if not yet done). Thank you for your understanding.

Overview

In contrast to the Bulk RNA sequencing used to quantify the abundance of gene and transcript expression at a whole population level, single-cell RNA sequencing (scRNAseq) allows researchers to study gene expression profile at a single cell resolution while enabling the discovery of tissue specific subpopulations and markers. For example, contrasting different sample conditions i.e. disease vs. normal using scRNAseq can help identify sub-cellular differential behaviours and thus target specific gene markers. This 3-day course will cover the main technologies as well as the main aspects to consider when designing a scRNAseq experiment, including a hands-on practical data analysis session applied to droplet-based methods.

Audience





skills to analyse scRNA-seq gene expression data.

Learning objectives

At the end of the course, participants will be able to:

- distinguish advantages and pitfalls of scRNAseq
- design their own scRNA-seq experiment
- apply a downstream analysis using R

Knowledge / competencies prerequired (Mandatory)

Participants should already have a basic knowledge in Next Generation Sequencing (NGS) techniques, or have already followed the "NGS - Quality control, Alignment, Visualisation". Knowledge in RNA sequencing is a plus. A basic knowledge of the R statistical software is required. Test your R skills with the quiz here, before registering.

Technical requirements

Attendees should bring a Wi-Fi enabled laptop. An online R and RStudio environment will be provided, but attendees who wish to run the practicals on their own laptop should install <u>R</u> and <u>RStudio</u>, as well as





Program

First day

Introduction to scRNAseq:

- Technologies
- Experimental design
- R versus GUI-based tools

Quality control

- Dropouts Doublets
- Doublet removal using simulation
- Ribosomal / mitochondrial RNAs
- Cell cycling

Normalization and scalability

- Feature selection
- Log scaling
- Confounding factors removal

Second day

Dimensionality reduction and cell type clustering

PCA





- Clustering methods (Hierarchical, K-means and Graph-based)
- Data integration of complex experimental designs

Cell type identification and marker identification

Methods and applications

Differential expression analysis

Methods overview

Third day

Differential expression analysis - continued

- DE between clusters
- DE between samples (involving data integration)
- Gene set enrichment analysis

Pseudotime analysis

Methods and applications

Application

**The course is now full with a long waiting list. **

The registration fees for academics are **180 CHF** and **900 CHF** for forprofit companies.





You will be informed by email of your registration confirmation. Upon reception of the confirmation email, participants will be asked to confirm attendance by paying the fees within 5 days.

Applications will close once the places will be filled. Deadline for registration and free-of-charge cancellation is set to **16/02/2021**. Cancellation after this date will not be reimbursed. Please note that participation in SIB courses is subject to our <u>general conditions</u>.

Venue and Time

This course will be streamed.

It will start at 9:00 and end around 17:00.

Precise information will be provided to the participants in due time.

Additional information

Coordination: Patricia Palagi

We will recommend 0.75 ECTS credits for this course (given a passed exam at the end of the course).

You are welcome to register to the SIB courses mailing list to be informed of all future courses and workshops, as well as all important deadlines using the form <u>here</u>.

Please note that participation in SIB courses is subject to our general





SIB abides by the <u>ELIXIR Code of Conduct</u>. Participants of SIB courses are also required to abide by the same code.

For more information, please contact training@sib.swiss.

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