

GSCN x scverse Workshop "Computational single cell genomics for stem cell biologists"

This workshop aims to equip stem cell biologists with a comprehensive introduction to computational single-cell genomics, focusing on data analysis using software from the scverse ecosystem. Designed for both beginners and advanced users, the workshop will provide hands-on experience with key tools for processing and analyzing multiple single-cell data modalities, including:

- Single-cell RNA sequencing (scRNA-seq)
- Spatial transcriptomics

Audience: Stem cell biologists (PhD students, Postdocs, Research associates) working with single-cell genomics data. Participants need to bring their own laptop.

- Beginners: first steps into single-cell data, little to no coding experience.
 - Min / max number of participants: 7 / 12
- Advanced: have already had hands-on data and some coding experience, ideally in Python.
 - Min / max number of participants: 7 / 12

The workshop duration is 1.5 days, and it will provide preliminary materials, including 1h of technical troubleshooting prior to the workshop to assist participants in setting up their programming environment and resources to enable them to begin programming in Python.

Learning objectives:

- Understand the fundamental concepts of single-cell data analysis.
- Learn best practices for preprocessing, quality control, clustering, visualization, and others using tools like scanpy, squidpy.
- Gain hands-on experience with advanced analysis techniques such as trajectory inference, batch-effect correction, cell cell communication and spatial analysis.
- Develop skills to interpret single-cell data in the context of stem cell biology.

The workshop will balance theoretical principles with interactive coding sessions, ensuring that participants at all experience levels can confidently apply scverse tools to their own single-cell datasets.



Syllabus

First day:

We will have 1h of technical troubleshooting to set up the working environments from 11:00 - 12:00.

13:00 - 13:15	Introduction
13:15 - 14:00	Common lecture on: Basic pre-processing of single-cell RNA-seq data Interpretive analysis using pydeseq2
14:00 - 15:00	Coding practice and troubleshooting session Group A (Advanced) - room: TBD Group B (Beginners) - room: TBD
15:00 - 15:30	Coffee break
15:30 - 16:15	Common lecture on: Batch correction Trajectory analysis
16:15 - 18:00	Coding practice and troubleshooting session Group A (Advanced) - room: TBD Group B (Beginners) - room: TBD

Second day:

09:00 - 10:00	Common lecture on: Ligand-receptor interactions Differential cellular abundance
10:00 - 10:30	Coffee break
10:30 - 12:00	Coding practice and troubleshooting session Group A (Advanced) - room: TBD Group B (Beginners) - room: TBD



12:00 - 13:00	Lunch
13:00 - 14:00	Common lecture on: Introduction to spatial transcriptomics Spatial data
14:00 - 15:00	Coding practice and troubleshooting session Group A (Advanced) - room: TBD Group B (Beginners) - room: TBD
15:00 - 15:30	Coffee break
15:30 - 16:30	Common lecture on: Spatially aware clustering Niche detection
16:30 - 18:00	Coding practice and troubleshooting session Group A (Advanced) - room: TBD Group B (Beginners) - room: TBD