

Swiss Institute of
Bioinformatics

Single cell transcriptomics with python

Alex Russell Lederer

Tania Wyss

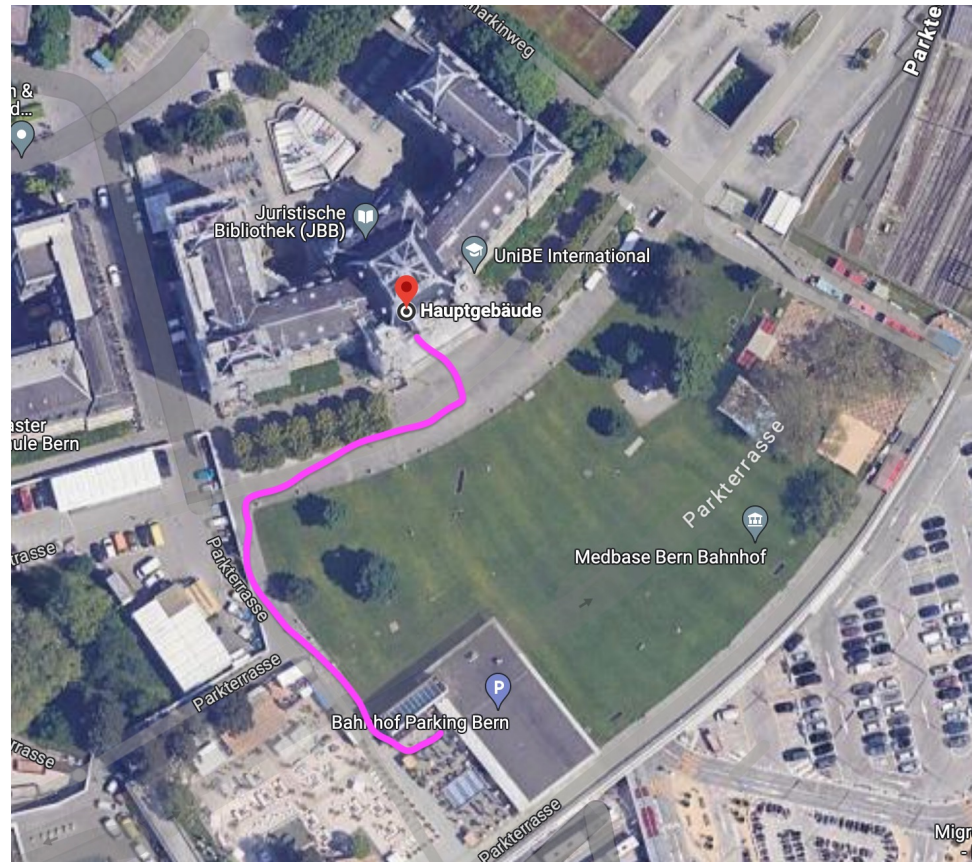
Geert van Geest

Trainers/organisers

- **Valeria di Cola:** Training coordinator at SIB
- **Alex Lederer:** PostDoc at EPFL
- **Tania Wyss:** Bioinformatician at SIB and UNIL
- **Andreia Gouvêa:** Guest speaker, Field application scientist 10x Genomics
- **Geert van Geest:** trainer at SIB/bioinformatician at IBU Bern

Social aperitive

- Social aperitive at 17:30 (not 18:30) at Grosse Schanze



Learning outcomes

- Explain the **characteristics** of the most-used **methods** to scRNA-seq data
- Perform **quality control** at different steps of the analysis
- Use **dimensionality reduction** (PCA, t-SNE, UMAP)
- Apply **best practices** for **translating** single cell transcriptomic data into **biological knowledge**

Learning experiences

- Lectures
- Quiz questions
- Exercises

Question 1-4

Communication

- Course website:

<https://sib-swiss.github.io/single-cell-python-training/>

- Google docs

Introduction round

- Your name
- What do you do?
- Why you join the course

