## Charité - Systems Biology of Infectious Diseases

We are a computational biology and bioinformatics research group with a focus on single-cell omics data in immunology and infectious diseases.

# Bioinformatics M. Sc. thesis

Interpretable batch effects scRNASeq

City: Berlin; Starting date (earliest): At the earliest possible; Remuneration: 0; Closing date: 26/04/26

### Tasks

Batch correction methods such as scVI, Harmony, or Seurat's anchor-based integration are essential components of single-cell analysis workflows. While these tools effectively project data from multiple batches into a shared latent space, they treat batch effects as nuisance variables to be removed without providing insight into what actually drives them. This project aims to change that: we will adapt a linear decoder variant of scVI to build a tool that not only corrects for batch effects but also allows users to interpret them, identifying associated genes and potential experimental causes. This project will allow you to gain hands-on experience with single-cell transcriptomics analysis, variational autoencoder architectures, and batch correction methodology. We are aiming to build a tool that helps researchers understand and address technical variation in their own datasets.

### Requirements

For bioinformatics students or computationally inclined biologists, biophysicists, biotechnologists etc. A previous computational biology or bioinformatics research project (e.g. B.Sc. thesis or lab rotation) is a required.

### Application

Interested individuals should send their CV, transcript of records and a short statement of motivation including a description of a previous computational project to lisa.buchauer@charite until 26th of April.

More information at https://stellenticket.de/203020/TUBS/
Offer visible until 29/04/26