



MASTER STUDENT POSITION IN BIOINFORMATICS

Measuring the gene expression of single cells through sequencing (scRNA-Seq) has become a routine method in many labs to study biological systems. However, after generating scRNA-Seq datasets, it is still often challenging to characterize cells based on their gene expression profile, for example identify their cell type of origin, or associate them with a differentiation state. There are different tools developed by the bioinformatic community that perform unbiased cell type annotation, such as SingleR. These tools are based on the comparison to reference transcriptomic datasets of pure cell types. There exist databases providing collections of reference samples, such as Immgen or Haemosphere, especially useful for the annotation of immune cell types. Still, these databases are limited and not regularly updated. At the DBM Bioinformatics Core Facility we collected additional published datasets to annotate scRNA-Seq datasets generated at the institute, which proves to be a bottleneck in the analysis process. We reasoned that creating a reference collection of all the publicly available datasets used so far would be useful not only in our daily work, but also for the genomics and bioinformatics community, which faces a similar problem. The collection grows and needs to be properly organized in the form of an approachable database. We would like to offer the development of this database and the tools required for an easy use during the analysis workflows as a master project for students learning bioinformatics, computational biology or computer science.

Required skills

Basics of R programming and bash/shell scripting

We provide

The project will be supervised by experienced bioinformaticians working at the facility. The student will become a member of the facility team learning about a variety of projects taking place at the institute. We will support the student to publish the developed database.

Contact

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