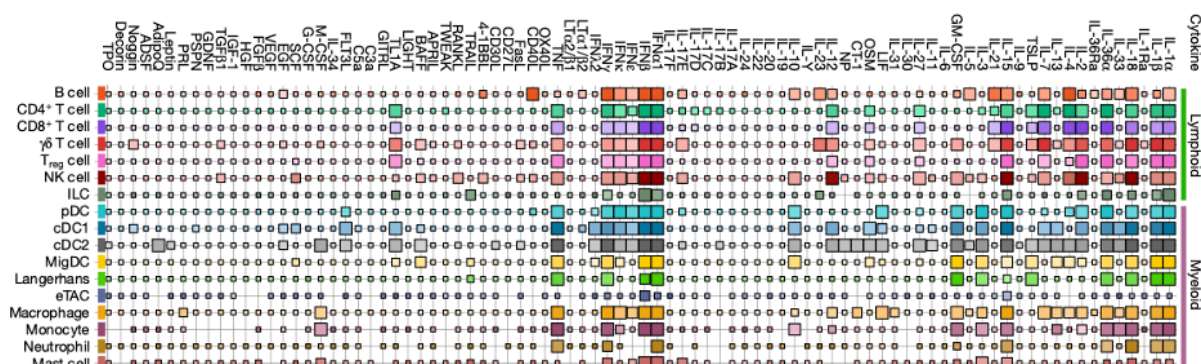


## MASTER STUDENT POSITION IN BIOLOGY

### Implementing the immune-dictionary in R/Bioconductor for single-cell annotation



DBM Bioinformatics Core Facility  
Department of Biomedicine  
Swiss Institute of Bioinformatics

**Research area** – Bioinformatics/Immunology

#### Background

Single-cell transcriptomics (scRNA-Seq) is the method of choice when studying gene regulation in heterogeneous cell populations. In the field of immunology, scRNA-Seq has helped to identify and characterize specific immune cell types and their role in the context of infection or immunization. One important regulatory signal in the communication between immune cells are cytokines. In a recent study, a comprehensive set of cytokines was tested in vivo for their transcriptional effect in all major immune cell types of mice [1]. This large-scale scRNA-Seq data set builds a unique reference for the study of gene regulation in immunological context. For example, it can be used to compare transcriptional responses, identify specific cell types and infer cytokine activity in other experimental conditions [1]. The R/Bioconductor framework offers many expert-build tools for the analysis of single cell transcriptomic data [2]. Starting from the gene expression count data, all major steps of the scRNA-Seq data analysis can be implemented in this framework. Specifically, data normalization, embedding in reduced dimensions (PCA, TSNE, UMAP), integrating different data sets or accounting for batch effects, clustering, cell annotation or differential abundance and expression analysis are all well supported [3].

#### Goal

Based on the data published in [1], build a reference atlas in R/Bioconductor to be able to use it for cell annotation and cytokine activity inference in other scRNA-Seq projects. The analysis will start from the raw sequencing data and involve all steps of scRNA-Seq analysis [3]. The student will apply and evaluate the reference atlas based on publicly available and in-house scRNA-Seq data sets. Depending on the student skills, the reference atlas will be implemented and submitted to Bioconductor as an ExperimentHub package.

#### What we offer

You will be working in close collaboration with members of the Bioinformatics core facility at the DBM (Department of Biomedicine, University of Basel). We are an international team of experts in the analysis of diverse biological data types, often at the forefront of biological research and technology. With our support, you will gain analysis skills in the dynamic fields of bioinformatics and single cell genomics.

**What you should bring:** Basic R programming skills, enthusiasm for quantitative data analysis and basic knowledge in immunology.

**Start date:** flexible

**Contact:** if you are interested in this master project, please contact [robert.ivanek@unibas.ch](mailto:robert.ivanek@unibas.ch) or [florian.geier@unibas.ch](mailto:florian.geier@unibas.ch) with details about your training and motivation for the project.

#### References

- [1] Cui, A., Huang, T., Li, S. et al. Dictionary of immune responses to cytokines at single-cell resolution. *Nature* 625, 377–384 (2024). <https://doi.org/10.1038/s41586-023-06816-9>
- [2] Amezquita, R.A., Lun, A.T.L., Becht, E. et al. Orchestrating single-cell analysis with Bioconductor. *Nat Methods* 17, 137–145 (2020). <https://doi.org/10.1038/s41592-019-0654-x>
- [3] OSCA online resource <https://bioconductor.org/books/release/OSCA/>