

Master project on single cell transcriptomics



We are looking for a highly motivated and ambitious bioinformatics student to carry out a Master thesis project focused on characterizing the unique molecular features of endothelial cells in different organs.

The group of Taija Mäkinen at Uppsala University studies fundamental mechanisms of tissue morphogenesis and disease in the vascular system. The aim is to understand how endothelial cells lining blood and lymphatic vessels communicate with the tissue environment to co-ordinate morphogenesis and functional specialization of the vasculature, but also how regulators of developmental (lymph)angiogenesis impact on genetic human diseases such as vascular malformations. For more details about the group's research please see: <http://www.makinenlab.com/>

The bioinformatics Master thesis project will help uncovering the mechanisms of organ-specific lymphatic vessel development and functional specialization by analyzing pre-processed single cell RNA sequencing (scRNA-seq) data available in the lab. From these analyses the student will assist in identifying new markers of specific endothelial cell subtypes and targets for further functional characterization. The student will use existing computational pipelines and algorithms (e.g. R package *Seurat*) to analyze data sets and generate reports as well as write codes to fit individual biological questions in collaboration with the lab team. Therefore, the student will need to be able to work with Unix, R or Python and be familiar with the Uppsala University's UPPMAX service.

To apply, please send your CV (including personal data and account of your previous education), together with a short description of yourself, name(s) of 1-2 reference(s), and the motivation to join the group to: taija.makinen@igp.uu.se