University of Basel
Department Biozentrum

SIB
Swiss Institute of Bioinformatics

BIOZENTRUM
The Center for Molecular Life Sciences

Basel Computational Biology Seminar

21563 Current research in Bioinformatics II

Prof. David Suter

Gene regulation & Cell identity
EPFL, Lausanne, Switzerland

Reuniting cell families through gene expression memory

Assigning single cell transcriptomes to cellular lineage trees has transformed our understanding of differentiation during development, regeneration, and disease. However, lineage identification is technically demanding and most single cell (sc) RNA-seq datasets are devoid of lineage information. In this talk I will describe Gene Expression Memory-based Lineage Inference (GEMLI), a computational tool allowing to robustly determine cell lineages solely from scRNA-seq datasets. GEMLI allows to study heritable gene expression, to discriminate symmetric and asymmetric cell fate decisions and to reconstruct individual multicellular structures from pooled scRNA-seq datasets. In human breast cancer biopsies, GEMLI revealed previously unknown gene expression changes at the onset of cancer invasiveness. The universal applicability of GEMLI allows studying the role of cell lineage trees in a wide range of physiological and pathological contexts. GEMLI is available as an R package on GitHub (https://github.com/UPSUTER/GEMLI).

Date: Monday, April 8, 2024

Time: 16:15 h – 17:15h

Location: Biozentrum, 02.073

Contact: Daan de Groot (daan.degroot@unibas.ch)