University of Basel
Department Biozentrum

SIB Swiss Institute of Bioinformatics

BIOZENTRUM
The Center for Molecular Life Sciences

Basel Computational Biology Seminar

Prof. Pierre Neveu

EMBL, Heidelberg Germany

"MorphoSeq: Complete tracing of single cell transcriptome dynamics from zygote to gastrulation in a chordate"

How the complexity of multicellular organisms arises from a fertilized egg is a fundamental question of biology. Single-cell RNA sequencing (scRNA-Seq) provided a leap forward in resolving cellular diversity and developmental trajectories. However, an in toto representation of embryonic development accounting for every single cell in space and time has not been achieved, as current approaches fail to comprehensively delineate the spatial organization and precise cellular makeup of individual embryos. Here, we reconstruct from scRNA-Seq and light sheet imaging data a canonical digital embryo that captures the genome-wide gene expression trajectory of every single cell at every cell division in all the 18 lineages up to gastrulation in the chordate P. mammillata. Using high coverage scRNA-Seq, we devised a computational framework that stratified single cells of individual embryos into cell types without prior knowledge. Moreover, we designed methods that unbiasedly infer the spatial coordinates and mother-daughter relatedness of every embryonic cell directly from their transcriptome data. Comparing high resolution datasets from individual embryos revealed both extensive reproducibility between the bilaterally symmetric embryo sides and a large degree of inter-embryonic variability. Our results demonstrate that unbiased spatiotemporal mapping of scRNA-Seq can yield the complete history of gene expression at the genome-wide level for every single cell in a developing embryo. We anticipate that the digital chordate embryo we report here will be a rich resource to mine the molecular mechanisms that instruct the patterning of entire organisms. The MorphoSeq framework of unbiased classification of cell types at various stages followed by delineating single-cell spatiotemporal transcriptome dynamics should be applicable to other developmental processes, such as early mammalian embryogenesis.

Date: **Monday, April 1st, 2019**

Time: **16:00 h**

Room: **Lounge (level 13), Klingelbergstrasse 61**
(vis-à-vis Pharmazentrum)

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