DISTINGUISHED LECTURE in BIOLOGICAL ENGINEERING

“Single-Cell Gene Regulatory Networks”

Monday, July 3, 2017 – 12h15
EPFL – room SV1717

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host: Prof. Bart Deplancke

Abstract:
Single-cell transcriptomics and single-cell epigenomics allow building cell atlases of any given tissue and infer the dynamics of cellular state transitions during developmental or disease trajectories.

In the first part of my talk I will describe a single-cell atlas of the ageing Drosophila brain, for which we profiled more than 30,000 single cells with Drop-seq and 10X Chromium. Using a new bioinformatics method we developed, called SCENIC (Single Cell rEgulatory Network Inference and Clustering), we identified transcription factors, networks, and cell states of glutamatergic, cholinergic, gabaergic, dopaminergic, and mushroom body neurons, as well as various glial cell types including astrocytes and perineural glia.

In the second part of my talk I will describe a single-cell ATAC-seq data set we generated in the Drosophila eye imaginal disc. Using another new bioinformatics method, called cisTopic, we overcome the sparsity of these data, identifying relevant regulatory programs and stable cell states in the normal tissue, as well as in a Drosophila tumour model. Altogether, I will discuss various examples and computational methods to trace genomic regulatory programs at single-cell resolution.

Sandwiches will be served

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