Single Cell Analysis to Dissect Dynamics of Cellular Heterogeneity in Health and Disease

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Cell fate commitment is the key process for understanding how a multicellular organism's genotype gives rise to phenotypic traits including disease development and progression. Recent experimental advancements in single cell RNAseq approaches allow now measuring a cell's state by its transcriptional state defined by the abundance of the versatile mRNAs.

In the lecture, I will give a brief introduction into basic molecular biology and demonstrate how we can combine live cell imaging and single cell omics approaches with mathematical analysis to identify molecular mechanisms and general characteristics of cell fate dynamics.

For this purpose we apply imaging-based approaches to toxin induced mitochondrial dysfunction to reveal potential early warning signals in Parkinson's disease und characterize underlying principles. To understand cell fate and differentiation dynamics, we derived a new correlation based measure for single cell transcriptomics time course data that allows for population classification during differentiation and validated this approach in blood cell differentiation and carcinogenesis. Furthermore, the course will further exemplify how single cell analysis and methods from non-linear time course analysis opens new routes for individualized treatments and can be used to investigate mutation specific modifications of cellular regulation.

Finally, we will have a hands-on session where we will study typical single cell RNAseq data and perform the first steps of the corresponding analysis challenges using R.
(For this part interested participants should bring their laptop with R version 3.3 or later and Monocle 2.4 installed,
see also: https://bioconductor.org/packages/release/bioc/html/monocle.html.)