Approaches to acquire and analyze single cell RNA-seq data 2nd Meeting Single Cell Center Heidelberg (SCC HD)

https://single-cell-center-hd.de

June 7, 2018 14-17:30, Bioquant, SR 41, ground floor

Organizers: Eileen Furlong, Karsten Rippe, Josephine Bageritz, Charles Girardot

Venue: Bioquant Center, Im Neuenheimer Feld 267, for directions see:

http://malone.bioquant.uni-heidelberg.de/contact/Campus_Heidelberg_BQ.jpg

Please send an e-mail to Sofie Steinfest (s.steinfest@dkfz.de) if you want to attend.

14:00-14:15	issues
14:15-15:30	Session I (15 min talks + 10 min discussion), chair Karsten
14:15-14:40	Philipp Mallm: What you ever wanted to know about single cell RNA-seq experiments
14:40-15:05	Bernd Klaus : An overview of computational methods for the analysis of scRNA-seq data.
15:05-15:30	Josephine Bageritz: Some insights into the drop-seq technology
15:30-16:00	Coffee break with informal discussions
16:00-17:15	Session II (15 min talks + 10 min discussion), chair Eileen
16:00-16:25	Britta Velten : Single cell, multiple assays: disentangling cell-to-cell heterogeneity across molecular layers using multi-omics factor analysis
16:25-16:50	Simon Anders: Interactive visualization tools for single cell transcriptomics
16:50-17:15	Lars Velten: Stories of blood and bone, one cell at a time
17:15-17:30	Wrap up, format/topics of next meetings on Sep 20 and Dec 13, 2018.

Discussion with beer & pizza