Bioinformatics for single-cell NGS - KFO 309

Day 1: October 20th, 2022

Frankfurter Straße 98, 35392 Gießen, Veterinärklinik, Anatomie Hörsaal, 1. OG / Raum 009

9:30	Bartkuhn / Wilhelm	Welcome Note
9:45	Harald Vöhringer	The Analysis of Single Cell Data: From Prepossessing to Downstream Analysis
10:15	Leon Schulte	Decoding of the peripheral blood noncoding RNA repertoire by single cell RNA-seq
10:45		Coffee break
11:00	Gabriela Salinas	A novel single-cell RNA-sequencing approach and its applicability connecting genotype to phenotype in ageing disease
11:30	Christian Schmidl	Integrated single-cell profiling dissects cell-state-specific enhancer landscapes of human tumor-infiltrating T cells
12:00		Lunch break
13:00	Arnaud Krebs	Genome-wide quantification of transcription factor binding at single-DNA-molecule resolution
13:30	Benedikt Obermayer-Wasserscheid	Single cell genomics applications in COVID-19 and allogeneic hematopoietic stem cell transplantation
14:00		Coffee break
14:30	Florian Buettner	Pathway-driven dissection of cell-cell heterogeneity in single-cell RNA-seq data
15:00	Florian Tran	On the way from single cell phenotyping to spatial biology - lessons from studies in IBD
15:30	10x Genomics	TBA

Day 2: October 21th, 2022 Fully booked!

Heinrich-Buff-Ring 62, 35392 Gießen, Altes Chemiegebäude, EG / Raum 0024a

Time: 9:00 – 18:00

Instructors: Andreas Hoek, David Glaser, Marek Bartkuhn, Philip Lobb (10x)

On the second day of this workshop, we provide hands-on training in some of the basics bioinformatic tools to process data from single-cell NGS experiments to enable participants to go the first steps in the practical analysis of their own data.

Access to computing environment, example data and coffee will be provided.