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BIOINFORBRICKLAYER

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From beginner to expert

Fabian J Theis

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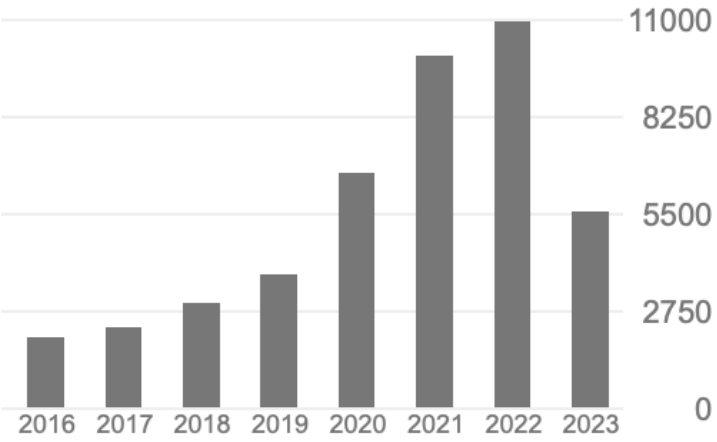

Prof. Dr. Fabian J. Theis

Professorship
Mathematical Modelling
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School
TUM School of Computation, Information and Technology

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Business card at TUMonline

ACADEMIC CAREER AND RESEARCH AREAS

Fabian Theis (b. 1976) conducts research in the field of computational biology. The main focus of his work is the application of machine learning methods to biological questions, in particular as a means of modeling cell heterogeneities on the basis of single cell analyses and also of integrating “omics” data into systems medicine approaches.

Professor Theis received PhD degrees in physics and computer science in 2002 and 2003 respectively. After working as a postdoc in Regensburg, Tokyo and Tallahassee, he took up a position as Bernstein Fellow at the Max Planck Institute for Dynamics and Self-Organization in Göttingen. He then joined the German Research Center for Environmental Health, Helmholtz Zentrum München, where he was a group leader at the Institute for Bioinformatics and Systems Biology for six years. In 2009 he was became an Associate Professor at the Chair of Applied Mathematics, TUM. Since 2013 he has been a Full Professor of biomathematics at TUM, where he holds the Chair of Mathematical Modeling of Biological Systems, and director of the Institute of Computational Biology at the Helmholtz Zentrum München.

实验室简介

ML in Single-Cell Genomics

人员构成：

Admin: 1
Postdoc: 9
PhD students: 40
Visiting scholar: 0

近五年文章：

CNS: 0
大子刊：19
小子刊：21
其他：~10

研究方向一： 单细胞数据分析方法

Single-Cell Methodologies

Single-cell technologies, such as single-cell RNA sequencing (scRNA-seq), have increased the resolution achieved in the study of cellular phenotypes, allowing measurements of thousands of different genes in thousands of individual cells. This has created an opportunity to begin understanding the dynamics of the prime biological processes undergone by cells, while requiring unique computational tools. In our lab, we develop novel and innovative computational methods for single-cell data analysis.

Scanpy

Large-scale single-cell gene expression data analysis

Wolf et al. (Genome Biology, 2018), Lücken et al. (Molecular Systems Biology, 2019)

Scanpy is a scalable toolkit for analyzing single-cell gene expression data. It includes preprocessing, visualization, clustering, pseudotime and trajectory inference, differential expression testing, and simulation of gene regulatory networks. It allows researchers to tackle the recently exploding dataset sizes without subsampling, scaling to more than one million cells.

Learn more

Helmholtz Munich | Alexander Wolf

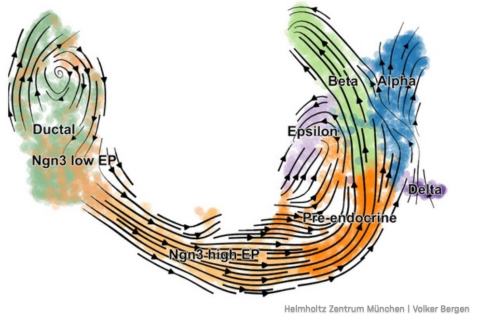
ScVelo

Generalizing RNA velocity to transient cell states through dynamical modeling

Bergen et al. (Nature Biotechnology, 2020)

scVelo is a method that generalizes RNA velocity to systems with transient cell states by solving the full transcriptional dynamics of splicing kinetics using a likelihood-based dynamical model. scVelo identifies regimes of regulatory changes, such as stages of cell fate commitment and, therein, systematically detects putative driver genes.

Learn more



Helmholtz Zentrum München | Volker Bergen

研究方向二：空间转录组和图像分析

Spatial Transcriptomics and Imaging

Imaging and spatial molecular profiling techniques allow us to assay morphological and molecular markers in situ. These experimental techniques provide a toolkit to investigate tissue biology at an unprecedented resolution. Computational tools are needed for the analysis of such data. We're developing analytical tools and data infrastructure for imaging and spatial molecular data, as well as modeling approaches to disentangle spatial components of cellular and tissue variation.

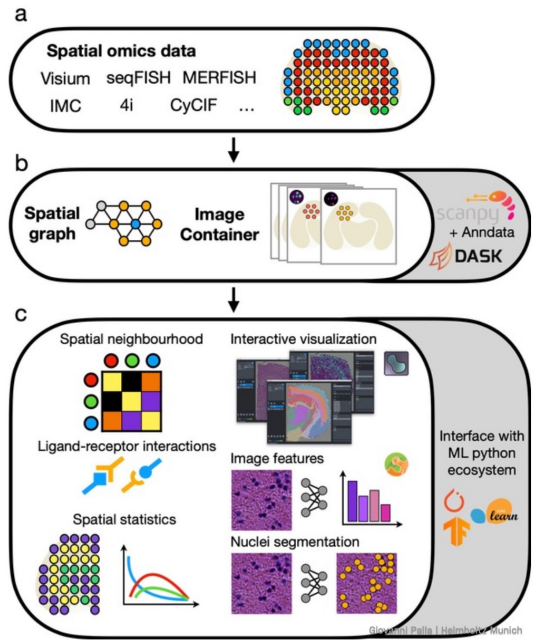
Squidpy

Spatial single-cell analysis in Python

Palla et al. (Nature Methods, 2022)

Squidpy is a tool for the analysis and visualization of spatial molecular data. It builds on top of Scanpy and anndata, from which it inherits modularity and scalability. It provides analysis tools that leverage the spatial coordinates of the data, as well as tissue images if available.

Learn more



Helmholtz Munich | Giovanni Palla

研究方向三：数据分析和基准测试

Data Analysis and Benchmarking

Organ- and body-scale cell atlases have the potential to transform our understanding of human biology. To capture the variability present in the population, these atlases must include diverse demographics such as age and ethnicity from both healthy and diseased individuals. In our lab, we utilize single-cell computational methods to build and benchmark large single-cell tissue atlasses. We also collaborate with experimental biologists on the analysis of their single-cell data.

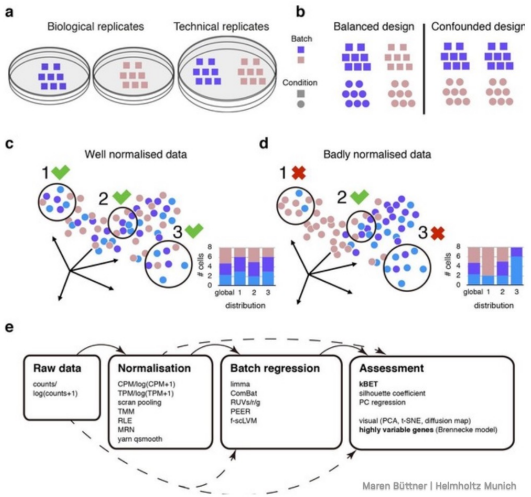
kBET

A test metric for assessing single-cell RNA-seq batch correction

Büttner et al. (Nature Methods, 2018)

kBET is a user-friendly, robust and sensitive *k*-nearest-neighbor test for the quantification of batch effects.

Learn more



Helmholtz Munich | Maren Büttner

Single-cell integration benchmark

Benchmarking atlas-level data integration in single-cell genomics

Lücken et al. (Nature Methods, 2021)

We provide a benchmark of 68 combinations of single-cell integration and preprocessing methods applied to 85 technical batches of gene expression, chromatin accessibility and simulation data from 23 publications, altogether representing >1.2 million cells distributed in 13 atlas-level integration tasks.