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**UNIVERSITÄT
HEIDELBERG**
ZUKUNFT
SEIT 1386

STRUCTURES JOUR FIXE

SIMON ANDERS

BioQuant & ZMBH, Uni Heidelberg

“Mathematical Methods for Single-
cell Transcriptomics”

June 3, 2022 1:30 PM

**HYBRID: Great lecture hall in Philosophenweg 12 and
Zoom. Meeting ID: 935 6549 3662, Code: 928036
Contact: office@structures.uni-heidelberg.de**



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ABSTRACT

Over the last twenty years, DNA sequencing technology has transformed biology, by providing an easy means to get Gigabytes of data from a single sample. Naturally, making use of this data has required the development of sophisticated mathematical and algorithmic methods.

In my talk, I will discuss one of the currently most exciting new technological developments in this area: single-cell transcriptomics.

Here, sequencing is used to characterize, for thousands of cells in parallel, which genes are expressed (i.e., active) at which strength in each cell. This allows us to understand how the cells in a tissue, comprising cells of many different types, work together to carry out their functions or react to challenges, or how this breaks down in disease.

When analysing such data, we extensively use ideas from linear algebra:

We consider each cell as a vector in a so-called "feature space", spanned by the organism's genes, where we establish a metric to judge how similar any two cells are in their type and state. Often, we wish to study a dynamic process, for example, stem cells developing into finally differentiated cells. To understand this, we assume that the cells' trajectories map out a sub-manifold in feature space, which we want to characterize. To address such challenges, bioinformaticians have drawn on ideas from all over the full range of applied mathematics.

I will give an overview of single-cell data analysis, describing the mathematical details of a few typical approaches, in order to give an impression what kind of mathematics is used in omics data analysis, and what kind of challenges molecular biology offers to the mathematical research community.

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