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**UNIVERSITÄT
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SEIT 1386

Tea, Coffee, Cake and TDA

Persistent Homology for Detecting the Topology of Single-Cell Data

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Single-cell RNA-sequencing records the expression values of thousands of genes in individual cells, making the study of cell functionality and development possible at high resolution. To understand the structure of single-cell data on a global level, topological descriptors, such as the presence of loops or voids in the data, are useful. For instance, loops might challenge the assumption of hierarchical cell development or be indicative of missing data in datasets of fully differentiated cells. The established computational tool for detecting the topology of point clouds is persistent homology. However, single-cell data is high-dimensional and notoriously noisy. We show that in high dimensionality traditional persistent homology becomes very sensitive to noise and fails to detect the correct topology. The same holds true for existing refinements of persistent homology. As a remedy, we find that spectral distances, such as diffusion distance and effective resistance, allow persistent homology to detect the correct topology even in the presence of high-dimensional noise. In particular, persistent homology with spectral distances can robustly detect the correct topology of single-cell data.

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Seminarraum Statistik, 2/104, Mathematikon, INF 205

After the talk, we invite everyone to stay for discussions as well as for tea, coffee and cake.