



STRUCTURES
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EXCELLENCE



**UNIVERSITÄT
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Tea, Coffee, Cake and TDA

Cohomology classes in the RNA transcriptome

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Single-cell sequencing data consists of a point cloud where the points are cells, with coordinates RNA expression levels in each gene. Since the tissue is destroyed by the sequencing procedure, the dynamics of gene expression must be inferred from the structure and geometry of the point cloud. In this talk, we will build a biological interpretation of the one-dimensional cohomology classes in hallmark gene subsets as models for transient biological processes. Such processes include the cell-cycle, but more generally model homeostatic negative feedback loops. Our procedure uses persistent cohomology to identify features, and integration of differential forms to estimate the cascade of genes associated with the underlying dynamics of gene expression.

27 June 2024, 2pm

Konferenzraum 05/104, Mathematikon, INF 205

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