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Applying methods from statistical physics and information theory to high-dimensional single cell omics data to establish a distribution biology framework

The aim of my PhD project is to develop a widely applicable framework tailored for the molecular characterization of single cells. Thank to single-cell techniques it is possible to analyze transcriptome, genome and the protein level at single-cell resolution. While these technical achievements are now used for characterizing cellular heterogeneity, a systematic approach interpreting and using the resulting high-dimensional data for identifying biological principles of development and pathogenesis is lacking.
We are addressing this challenge by further developing our statistical analysis framework and to complement this with a mechanistic mathematical outline based on distribution dynamics to identify critical transitions within complex systems. In order to do that we have to test different statistical methods to characterize different cell states and the transition between them.
One of possible analyzing approaches consists to exploit the statistical proprieties of random matrices to extract some solid information from the data. By combining simulations, biological constraints and mathematical approximations, we will then generate a reduced mechanistic model that emphasizes the principles of systems heterogeneity and its role in system transitions.

Summary

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