

Inferring cell dynamics by learning curves valued in the Wasserstein space

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We tackle the “trajectory inference” which problem arises when one tries to study biological processes with new experimental technologies like single cell RNA sequencing and is interested in the evolution of cell states over time. Indeed these technologies provide high dimensional measurements of cell states, but they are destructive thus cannot track the trajectories of the cells over time.

We rephrase this problem as learning a curve valued in the space of probability distributions (a.k.a. Wasserstein space) and we explain how optimal transport, a mathematical theory which enables to compare probability distributions and compute couplings between random variables, can be used to solve this problem and reconstruct the temporal couplings as well as the trajectories and the fates of the cells. This method was tested on synthetic and real data, in particular to study differentiation of cells in developmental biology. We will also mention some of the theoretical challenges linked to this problem.

Joint work with: Stephen Zhang, Young-Heon Kim and Geoff Schiebinger.

References

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