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**Zixuan Cang\*** (zcang@uci.edu), 401 Gabrielino Dr, Irvine, CA 92617, and **Qing Nie**. *Spatial analysis of single-cell data via optimal transport*. Preliminary report.

One of the most interesting abilities of cells in a multicellular organism is their ability to acquire and change fate. This process is controlled by many factors including the environment and communications with other cells. A recent technological breakthrough (single-cell RNA sequencing) allows us to see the expression of thousands of genes at single-cell resolution providing unprecedented information. This data makes it possible to identify the heterogeneous population of cells in a tissue and to infer cell development trajectories. However, in single-cell RNA sequencing experiments, tissues are dissected into single cells leading to loss of spatial information which is crucial to the analysis of communications among cells through space. With in situ gene expression data (usually containing only a few genes), we are able to retain some spatial information for single cells. We propose to use optimal transport theory to connect these two types of data. Based on this connection, optimal transport is applied again to reconstruct communication among single cells in space. We also infer potential intercellular regulatory relationships between genes. These new insights can shed light on mechanisms of cell fate acquisition and changes as a collaborative process. (Received September 01, 2019)