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**Adam L. MacLean\***, [macleana@usc.edu](mailto:macleana@usc.edu), CA 90089. *Inference of stem cell fate and gene regulatory dynamics from single-cell data.*

Since single-cell RNA sequencing technologies have become widespread, great efforts have been made to develop appropriate computational methods to learn biological features from high dimensional datasets. Despite advances in many areas, such as cell clustering and trajectory inference, major gaps remain. We address two such gaps: how to infer cell-cell communication networks, and how to combine dynamical models with data-derived cell states. A prerequisite to such integration is a sufficient description of the cell states and their interactions: to accomplish this we introduce a method to learn cell states by nonnegative matrix factorization (SoptSC). We go on to infer cell-cell communication networks directly from data. Coupled to the inferred cell lineage relationships, SoptSC predicts both known and novel regulatory interactions. Finally, we describe how dynamical signaling models can be derived from data, and how their parameters can be identified via Bayesian inference, with application to hematopoiesis. (Received February 18, 2020)