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Heyrim Cho* (hcho1237@math.umd.edu), **Lisette de Pillis**, **Ya-Huei Kuo**, **Ami Radunskaya**, **Russell Rockne** and **Doron Levy**. *Modeling continuous levels of cell states in cancer development and drug resistance.*

Recent advances in single-cell sequencing data and high-dimensional data analysis techniques are bringing in new opportunities in modeling biological systems with continuous phenotypic structured models. In this talk, we first demonstrate that assuming continuous cell state may result in different dynamics when compared with the predictions of classical discrete models, particularly in anti-cancer drug resistance. We classify the cases when the continuum and discrete models yield different dynamical patterns in the emerging heterogeneity in response to chemotherapy, and study the maximal fitness resistance and effect of epimutations. In the second part, we develop a continuum cell state model using single-cell RNA sequencing data of hematopoietic stem cells. The trajectories of cell states in the differentiation space are abstracted as a graph, then modeled as directed and random movement on the graph with PDEs. We simulate normal and abnormal differentiation processes, that is, acute myeloid leukemia (AML) progression and predict the emergence of cells in novel intermediate states of differentiation consistent with immunophenotypic characterizations of a mouse model of AML. (Received September 17, 2018)