1137-92-216   **Ami Radunskaya*** (`aer04747@pomona.edu`). *What's next in biomathematics? Describing the dynamics of a disease using networks.*

How can we use mathematics to understand disease progression? Traditional ODE models can be validated using time-series data from experiments. However, in trying to understand the evolution of a disease at the cellular level, we often lack this time-series data. Instead, we are presented with data from two states: 'healthy' and 'diseased', and we'd like to know what has changed. How can we reconstruct the dynamics of the disease from a small number of time points, typically with small sample sizes of high-dimensional data? In this talk, I will describe an approach to this problem that uses network complexity metrics and transcription data. I will describe how information from several sources can be used to identify key players in the development of the disease, as well as the beginnings of a theoretical framework that will give us confidence in the results that we obtain from this method.

Progress in biomathematics requires collaboration across disciplinary boundaries. Many challenges remain in using high-dimensional data to inform the dynamical progression of a disease; I look forward to a productive discussion.

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