Mathematical Biology Seminar

Monday, March 18, 2024

3 pm MDT - 457 CAB (virtual)

Join Zoom Meeting

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Meeting ID: 984 9769 5684
Passcode: 32123

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Identifiability for PDE models of fluorescence microscopy experiments

The dynamics of intracellular proteins is key to many cellular functions. One of the most versatile experimental techniques for probing protein dynamics in living cells is FRAP (fluorescence recovery after photobleaching). This experiment generates time-series data that average out spatial information about diffusion, transport, and binding dynamics of proteins. Partial differential equations (PDE) models provide the appropriate framework to model the fluorescence dynamics and to infer parameters such as diffusion coefficients or reaction rates. However, it is not known whether these parameters can be identified based on the spatially-averaged data available from FRAP experiments. We recently investigated limitations of known methods in assessing parameter identifiability for PDE models and proposed methods for learning parameter combinations based on re-parametrization and profile likelihoods analysis. In this work, we are particularly motivated by the study of dynamic RNA binding proteins in the development of frog egg cells.