Limitations of Model-Based Experimental Design in Systems Biology ANDREW WHITE, MARK TRANSTRUM, Brigham Young Univ - Provo
— Mathematical models can help us understand complex biological systems such as gene regulatory networks and signaling pathways. These models can include hundreds of unknown parameters. Data fitting typically leads to huge uncertainties in the inferred parameter values, a phenomenon known as sloppiness. It has been suggested that model-based experimental design can help overcome this challenge. However, models of complex systems, such as those in biology, never account for all of the system's details. Contriving experiments to make previously irrelevant model details become more important may result in the model no longer being able to fit all the data. If such is the case, it will require a change in the model itself. We test this by considering two models of a cell-signaling process, each of varying complexity. Performing experimental design guided by the simple model but using the complex model as a surrogate for the actual system, we hope to determine the limits of model-based experimental design for accurate parameter inference.

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