

Abstract Submitted
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Towards a principled way of making kinetic models from data¹
STEVE PRESSE, UCSF — Kinetic model extraction from noisy data is the basic route to mechanistic insight in biology. I will show how the tools of Maximum Caliber (the dynamical analog of Maximum Entropy) can be used to infer -and not fit- models in a way which is driven by the structure and limitations of the data. For instance, the typical output of an experiment in systems biology is the stochastic expression of one reporter gene. Master equations used to model the regulatory process underlying the stochastic gene expression require knowledge of a circuit topology and rates. However rates and topology are often fit as these are rarely all independently determinable from the limited data. Our goal is to build a kinetic model from the data available with no adjustable parameter using the tools of Maximum Caliber. We apply our method to infer the statistics of rare stochastic switching events in the genetic toggle switch from fluctuations on shorter measurable timescales. In addition, we discuss how these tools can be used to infer kinetic models from real single molecule data drawn from anomalous folding kinetics of phosphoglycerate kinase and RNA hairpin zipping-unzipping time traces.

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