

THE MATHEMATICS OF BIOMOLECULAR ENGINEERING



Abstract:

Biological engineering is emerging from biology, as a distinct discipline based on quantification. This quantification of biological phenomena is necessary to rationalize engineering efforts away from the traditional description-based paradigm of biological sciences.



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Mathematics helped **chemical engineering** in the 1950s to develop its unique, successful identity. In a similar way, mathematical theories that reduce biological knowledge are becoming a sine qua non for progress in **biological engineering**.

Although the principles of thermodynamics and kinetics apply to biological systems, these systems differ from industrial-scale chemical systems in a fundamental way: they are far from the thermodynamic limit. This hinders the application of mathematics developed by chemical engineers to model kinetic and thermodynamic processes in living organisms.

For example, there are networks of biomolecular interactions (e.g. gene regulatory networks) whose kinetic behavior is key for emerging phenotypes. Models of these interactions are important for rationalizing genetic engineering of sequences that lead to desired phenotypes. Using deterministic, ordinary differential equations for simulating the reaction kinetics assumes the absence of thermal, stochastic noise in biomolecular systems. This can indeed be distinctly false.

We will explore the limitations of traditional mathematical frameworks and we will discuss emerging models that account for the distinct nature of biological organisms. We will detail the multiscale algorithms we developed to properly capture biological complexity from the molecular to the system level. We will describe how these models are being used in engineering novel gene regulatory networks.