

## **Systems engineering challenges and opportunities in computational biology**

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Systems engineering approaches are currently emerging as vital tools for deciphering the behavior of biological systems. They are depended upon for a variety of applications ranging from multiple DNA sequence alignment to effective database mining. Systems engineering contributions in biology can broadly be categorized into descriptive and predictive. Descriptive or data-driven approaches utilize statistic and information theoretic concepts to explain and/or augment the information content of genomic and proteomic data as well as measurements in the context of biological systems. Predictive approaches on the other hand rely on modeling frameworks to estimate the behavior of biological systems involved in protein structure and function, gene expression, metabolic flux distributions, genetic circuit regulation, etc. In this talk, we will first review the current state of the art and then draw analogies and contrasts with algorithmic development and applications in process systems engineering.

In the second part of the talk, we will briefly discuss examples of predictive as well as descriptive frameworks abstracted by research work in my group. Specifically, first we will see how we can model and subsequently optimize DNA recombination in the context of directed evolution experiments for protein engineering. Next we will discuss how to identify the performance limits of metabolic networks in the presence of gene additions or deletions and also infer what objective function, if any, the network is attempting to optimize under a given set of environmental conditions. Finally, we will introduce inference frameworks for identifying gene regulatory networks given DNA microarray expression data.