Using systems engineering tools to elucidate and redesign biological networks

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Abstract:
Metabolism is defined as the full complement of chemical transformations in living systems. In this talk, we will discuss how we can speed up the process of building and correcting organism-specific metabolic models (both stoichiometric and kinetic) using the recently developed MetRxn knowledgebase of curated reaction, metabolite and atom mapping content. We will describe how metabolite and reaction information can be leveraged for identifying thermodynamically feasible, carbon and energy efficient, overall conversion stoichiometries from a substrate to a target product by globally assessing all possible co-reactant/products combinations (optStoic). In addition, we will discuss how global reaction atom mapping information can be used to perform metabolic flux elucidation at a genome-scale revealing how the assumptions implied by core metabolic models may propagate in the inference of internal metabolic fluxes. Finally, we will highlight ongoing efforts that make use of multiple flux datasets of deletion mutants to robustly parameterize kinetic models that approach genome-scale for E. coli and other microbes.

Bio:
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