Testing the assumption of optimality in genome-scale metabolic models and using them to predict multi-species growth in space and time

Friday, January 25, 2013, 10:30 – 11:30 AM
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The most powerful framework currently available for predicting metabolism from annotated genomes (i.e., flux balance analysis, or FBA) takes advantage of the assumption of evolutionary optimality to make a prediction from an under-determined space of feasible steady-states a cell could adopt. This assumption of FBA is rooted upon the idea that selection drives metabolic changes toward criteria such as maximal yield of biomass per substrate utilized. We directly tested whether the metabolism of experimentally-evolved populations actually achieves or at least moves toward these predictions. Furthermore, I will discuss how FBA can generate testable predictions regarding the growth of multi-species communities in space and time.