SCIENCE AT THE EDGE

2016 SEMINAR SERIES

Quantitative Biology Graduate Program | Gene Expression in Development and Disease

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GREAT LAKES BIOENERGY RESEARCH

"Systems Approaches to Exploring and Exploiting Microbial Metabolism"

Genome-scale networks of metabolism and regulation can be reconstructed from an organism's genome annotation. Computational models generated from these reconstructions can be used to predict microbial responses to genetic and environmental perturbations. We have recently developed new approaches to identify metabolic functions in microbes by reconciling discrepancies between model predictions and experimental results. These efforts led to the discovery of functions of enzymes and transporters in *Vibrio fischeri* and *Zymomonas mobilis*. We have used additional approaches to computationally identify genetic strategies for enhancing production of pyruvate from glucose and co-utilization of xylose from plant hydrolysates. These examples illustrate how integrating computational and experimental approaches can lead to discovery of metabolic gene functions and to novel strategies to accelerate metabolic engineering efforts.

References:

Price ND, Reed JL, and Palsson BO. Genome-scale Models of Microbial Cells: Evaluating the consequences of constraints. *Nature Reviews Microbiology*. 2:886-897 (2004).

Long MR, Ong WK, and JL Reed. Computational Methods in Metabolic Engineering for Strain Design. *Current Opinion in Biotechnology*. 34:135-141 (2015).

Reed JL, Patel TR, Chen KH, Joyce AR, Applebee MK, Herring CD, Bui OT, Knight EM, Fong SS, and Palsson BO. Systems Approach to Refining Genome Annotation. *Proc Natl Acad Sci U S A*. 103(46):17480-17484 (2006).

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