

Systems biology analysis of metabolomics data for advanced metabolic engineering

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The development of a metabolomics platform workflow is hypothesis driven. The workflow is aimed at the development of a sampling and extraction methodology, targeted quantification of metabolites via LC-MS/MS, and constraint-based modeling approach using a genome-scale reconstruction to better understand and further improve metabolically engineered and adaptively evolved strains of *E. coli*. Specifically, progress in construction of a rapid sampling apparatus for batch-cultures of anaerobic and aerobic strains, selection of isotope standards for targeted analysis based upon simulations of bacterial growth, and testing of different sampling and extraction procedures will be described. Progress in the development of the computational framework to analyze metabolomics data in the context of a genome-scale reconstruction of *E. coli* to arrive at biologically meaningful conclusions will also be presented.

Biography

Douglas Taylor is currently pursuing his Ph.D. at the University of California, San Diego in Bioengineering in the Systems Biology Research Group under Professor Bernhard Palsson. Douglas Taylor earned his B.S. in biomedical engineering with a minor in material science with magna cum laude honors at the University of California, Irvine. He has published (first author, Lab on a Chip, 2010, 10, 2472-2475; second author, Lab on a Chip, 2010, 10, 1623-1626) on the topic of fabricating low-cost microfluidic devices from shrink polymers. He is interested in incorporating metabolomics data into constraint-based modeling for improved bacterial strain design.