

Computational Inference of Regulatory Pathways in Microbes

An application to phosphorus assimilation pathways in *Synechococcus* WH8102

Z. Su¹, P. Dam¹, X. Chen², V. Olman¹, T. Jiang², B. Palenik³ and Y. Xu¹

¹Protein Informatics Group, Divisions of Life Sciences and Computer Sciences & Mathematics, Oak Ridge National Laboratory, ²Department of Computer Science and Engineering, Univ. of California at Riverside, and ³Scripps Institute of Oceanography, University of California at San Diego

Abstract

We present a computational protocol for inference of regulatory and signaling pathways in a microbial cell, through mining “high-throughput” biological data of various types, literature search, and computer-assisted human inference. This protocol consists of four key components: (a) construction of template pathways for microbial genomes related to the target genome, which have either been thoroughly studied or had a significant amount of relevant experimental data, (b) inference of target pathways for the target genome, by combining the template pathway

*models and target genome-specific information, (c) assignment of genes of the target genome to each individual functional roles in the pathway model, and (d) validation and refinement of the pathway models using pathway-specific experimental data or other information. To demonstrate the effectiveness of this procedure, we have applied this computational protocol to the construction of the phosphorus assimilation pathways in *Synechococcus* WH8102. In this paper, we present a model of the core component of this pathway and provide our justification in support of the predicted model.*