Reconstruction and Comparative Analysis of Transcriptional Networks of *Shewanella oneidensis*

Andrea M. Rocha
University of South Florida
Research Alliance in Math and Science
Computer Science and Mathematics Division, Oak Ridge National Laboratory
Mentor: Dr. Nagiza Samatova

http://computing.ornl.gov/Internships/rams/rams08/abstracts/a_rocha.pdf

Abstract

Application of systems-based models in microbial studies is important to understanding cellular networks and transcriptional regulatory interactions in potentially important microorganisms. Predictions of microbial cellular response to environmental perturbations is critical to developing and implementing bioremediation strategies. This study evaluated the use of a newly developed system-model, cMonkey, for predicting transcriptional gene responses in *Shewanella oneidensis* MR-1. Transcriptional regulatory networks were constructed using upstream annotated genome sequences for 162 transcriptional genes, available micro-array data by the *Shewanella* Federation, and identified association networks for *S. oneidensis.* Results from this study will not only evaluate the value of systems-based models in predicting regulatory responses, but will also be used to generate specific hypothesis regarding growth rates of *Shewanella* in natural sediments.

Systems-based Models

- Important in understanding cellular networks of microorganisms
- Predict microbial cellular response to environmental perturbations

Research Objectives

- Reconstruct results from previous studies to validate understanding of programs
- Evaluate the cMonkey and Context Likelihood of Relatedness algorithm in predicting transcriptional gene responses in *S. oneidensis* MR-1
- Identify potential microbial cellular response to environmental perturbations

Methods

M³D (Many Microbes Microarray) Database/ Shewanella Knowledgebase

Compendium: S. oneidensis Build 2

Genes: 162 transcriptional regulatory genes

Experiments: 207 Experiments

Environmental Perturbations: Electron donors/acceptors, temperature, pH, oxygen, light, and salinity

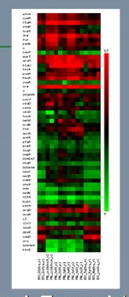


Figure 1. Transcriptional gene expression

cMonkey Algorithm

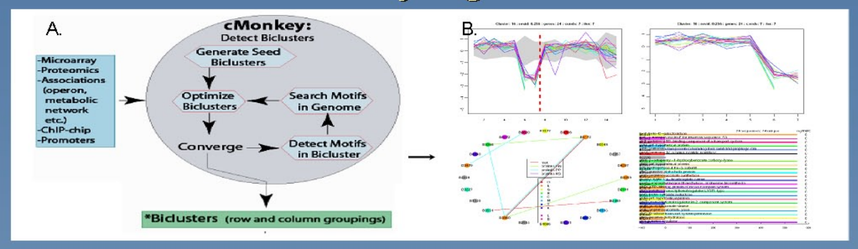


Figure 2. (A.) Overview of the cMonkey algorithm. Image by N. S. Baliga (2007); (B) Replication of expression ratios (top), network associations (bottom left), and upstream positions of motifs (bottom right) for biculsters (Bonneau et al. 2006)

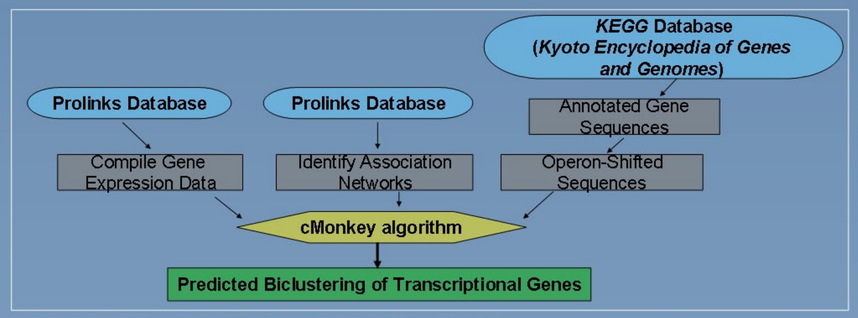


Figure 3. Integrative approach for the cMonkey algorithm.

CLR Algorithm

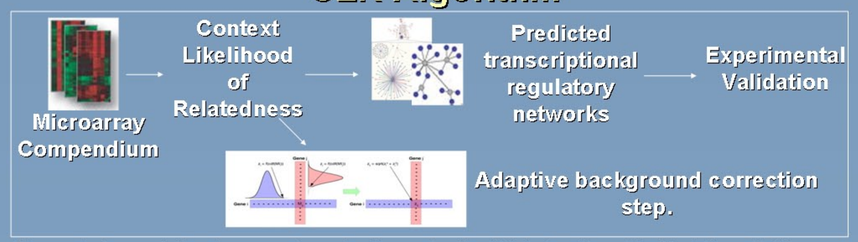


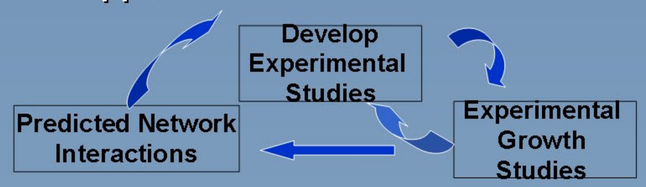
Figure 4. Computational approach and schema for the CLR algorithm. Modified from Faith et. al. (2007)

Expected Results

- Biclustering of transcriptional regulatory genes should identify co-regulated gene clusters for *S. oneidensis*
- Correlation of gene biclusters with varying experimental conditions should identify potential microbial response to environmental perturbations

Future Research

- Integrate cMonkey data into the Inferelator algorithm
- Compare use of the CLR algorithm (Context Likelihood of Relatedness) in predicting transcriptional regulatory genes to cMonkey
- Future application:



References

- Faith, J.J. B. Hayete, J. T. Thaden, I. Mogno, J. Wierzbowski, G. Cottarel, S. Kassif, J. J. Collins, and T. Gardner. Large scale mapping and validation of *Escherichia coli* transcriptional regulation from a compendium of expression profiles. *PLoS Biology* 5:e8
- Reiss, D. J., N. Baliga, and R. Bonneau. 2006. Integrated biclustering of heterogeneous genome-wide datasets for the interface of global regulatory networks. *BMC Bioinformatics* 7:280

The Research Alliance in Math and Science program is sponsored by the Office of Advanced Scientific Computing Research, U.S. Department of Energy. The work was performed at the Oak Ridge National Laboratory which is managed by UT-Battelle, LLC under Contract No. De-AC05-00OR22725. This work has been authored by a contractor of the U.S. Government, accordingly, the U.S. Government retains a nonexclusive, royalty-free license to publish or reproduce the published form of this contribution, or allow others to do so, for U.S. Government purposes.

I would like to thank Dr. Nagiza Samatova for the opportunity to work on this project. Also, I would like to thank Dr. Peter Stroot and Mr. Bernard Batson for their continued support. Finally, special thanks go to Debbie McCoy, who made provisions for this research experience.