

Simulation Studies for the Identification of Genetic Networks from cDNA Array and Regulatory Activity Data

Daniel E. Zak
Daniel Baugh Institute
Thomas Jefferson University
Philadelphia, PA 19107
Department of Chemical
Engineering
University of Delaware
Newark, DE 19716
zak@che.udel.edu

Francis J. Doyle III
Department of Chemical
Engineering
University of Delaware
Newark, DE 19716
doyle@che.udel.edu

Gregory E. Gonye
Daniel Baugh Institute
Department of Pathology,
Anatomy and Cell Biology
Thomas Jefferson University
1020 Locust Street
Philadelphia, PA 19107
gregory.gonye@mail.tju.edu

ABSTRACT

A model genetic regulatory network for the evaluation of genetic regulatory network identification methods is described. This model is novel in comparison to models of previously published studies [3] for its mechanistic basis and its relatively large (10 gene) scale. The model is used to evaluate several simple techniques from the literature for identifying genetic regulatory networks from high throughput data sets. Even though simple models derived using cDNA array data alone [1][2][3] are found to fit the data very well, their applicability for determining network architecture is questionable. A method that combines cDNA array data, regulatory activity data, and genomic information is, of the methods considered, most promising for the identification of genetic network architecture.

ADDITIONAL AUTHORS

James S. Schwaber, Daniel Baugh Institute for Functional Genomics and Computational Biology, Department of Pathology, Anatomy, and Cell Biology, Thomas Jefferson University, email address: james.schwaber@mail.tju.edu

REFERENCES

- [1] P. D'Haeseleer, X. Wen, S. Fuhrman, and R. Somogyi. Linear modeling of mrna expression levels during cns development and injury. *Pacific Symposium on Biocomputing*, 4:41–45, 1999.
- [2] D. C. Weaver, C. T. Workman, and G. D. Stormo. Modeling regulatory networks with weight matrices. *Pacific Symposium on Biocomputing*, 4:102–111, 1999.
- [3] L. F. Wessels, E. P. V. Someren, and M. J. Reinders. A comparison of genetic network models. *Pacific Symposium on Biocomputing*, 6:508–519, 2001.