Computer-Aided Engineering for Inference of Genetic Regulatory Networks Using Data from DNA Microarrays

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Abstract. Biological research topics gradually shift from structural genomics into functional genomics. DNA microarrays have been used to generate abundant data for exploring functions and interactions among genes. We propose a reverse-engineering strategy to predict the interactions between genes within a genetic network. Our inputs are perturbation matrices experimentally obtained from DNA microarrays. First, we make some assumptions for the interactions in the network. The proposed network is represented as a directed graph. After that, we enumerate all possible network models according to the assumptions. And then, some candidate models are obtained, resulted from calculated perturbation matrices out of computational simulation. The network involves in not only the transcription level but also the nucleotide/protein interactions in general. To justify this method, we take a well-known genetic regulatory network in yeast Saccharomyces cerevisia for a test. The result shows that one of the candidate models can generate an identical perturbation matrix as that from the yeast's DNA microarrays, experimentally determined by others. In conclusion, our method is useful and feasible for determining probable interactions within biological networks

Keywords: Reverse engineering, genetic regulatory network, DNA microarray

References

[1] E.J. Chikofsky and J.H. Cross, "Reverse engineering and design recovery: A taxonomy," *IEEE Software*, Vol. 7, No. 1, pp. 13-17, 1990.

[2] D. Lee, "Reverse Engineering of Communication Protocols," *Proceedings of International Conference on Network Protocols*, pp.218-216, 1993.

[3] K. Saleh, R. Probert, K. Al-Saqabi, "Recovery of CFSM-based Protocol and Service Design from Protocol Execution Traces," *Information and Software Technology*, Vol. 41, No. 11-12, pp. 839-852, 1999.

[4] I. Baxter and M. Mehlich, "Reverse Engineering is Reverse Forward Engineering," *Science of Computer Programming*, Vol. 36, pp. 131-147, 2000.

[5] K. Saleh and A. Boujarwah, "Communications Software Reverse Engineering: a Semi-Automatic Approach," *Information and Software Technology*, Vol. 38, No. 6, pp. 379-390, 1996.

[6] R. Chiang, T. Barron, A. Storey, "A Framework for the Design and Evaluation of Reverse Engineering Methods for Relational Databases," *Data & Knowledge Engineering*. Vol. 21, No. 1, pp. 57-77, 1996.

[7] T. Varady, R. Martin, J. Cox, "Reverse Engineering of Geometric Models-An Introduction," *Computer-Aided Design*,

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Vol. 29, No. 4, pp. 255-268, 1997.

[8] T. Chen, V. Filkov, S. Skiena, "Identifying Genetic Regulatory Networks from Experimental Data," *Proceedings of RECOMB'99*, 1999.

[9] T. Ideker, V. Thorsson, J.A. Ranish, R. Christmas,J. Buhler, J.K. Eng, R. Bumgarner, D.R. Goodlett, R. Aebersold, L. Hood, "Integrated Genomic and Proteomic Analyses of a Systematically Perturbed Metabolic Network," *Science* Vol. 292, No. 5518, pp. 929-933, 2001.

[10] R.W. We, T. Wang, L. Bedzyk, K.M. Croker, "Applications of DNA Microarrays in Microbial systems," *Journal of Microbiological Methods*, Vol. 47, No. 3, pp. 257-272, 2001.

[11] A.J. Hartemink, D.K. Gifford, T.S. Jaakkola, R.A. Young, "Using Graphical Models and Genomic Expression Data to Statistically Validate Models of Genetic Regulatory Networks," *Pacific Symposium on Biocomputing'01*, Vol. 6, pp. 422-433., 2001.