

Scientists develop a new computational method to uncover gene regulation

April 13 2010

(PhysOrg.com) -- Researchers from Aalto University (Finland), European Molecular Biology Laboratory Heidelberg (Germany) and the University of Manchester (UK) have developed a new computational method to identify targets of regulator genes. The method is presented in the Early Edition of *Proceedings of the National Academy of Sciences (PNAS)*.

The human [genome](#) contains instructions for making all the cells in our body. An individual cell's make up (e.g. muscle or blood) depends on how these instructions are read. This is controlled by gene regulatory mechanisms. Uncovering these mechanisms holds a key to greatly improving our understanding of biological systems.

One important [regulatory mechanism](#) is based on genes that actively promote or repress the activity of other genes. The new research addresses the problem of identifying the targets these regulator genes affect.

The new method is based on careful modelling of time series measurements of [gene activity](#). It combines a simple biochemical model of the cell with probabilistic modelling to deal with incomplete and uncertain measurements.

Dr Rattray, a senior researcher from the University of Manchester, said: "Combining biochemical and probabilistic modelling techniques as done here holds great promise for the future. Many systems we are looking at

now are too complex for purely physical models and connecting to experimental data in a principled manner is essential."

Dr Honkela, a senior research fellow from Aalto University, added: "A major contribution of our work is to show how data-driven machine learning techniques can be used to uncover physical models of cell regulation. This demonstrates how data-driven modelling can clearly benefit from the incorporation of physical modelling ideas."

More information: The original research article is available through *PNAS* early edition: A Honkela, C Girardot, EH Gustafson, Y Liu, EEM Furlong, ND Lawrence, M Rattray (2010), "Model-based method for transcription factor target identification with limited data." *Proc Natl Acad Sci USA*, www.pnas.org/cgi/doi/10.1073/pnas.0914285107

Provided by Aalto University

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