New computational method to uncover gene regulation

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Scientists have developed a new computational model to uncover gene regulation, the key to how our body develops - and how it can go wrong.

The researchers, from The University of Manchester (UK), Aalto University (Finland) and the European Molecular Biology Laboratory Heidelberg (Germany), say the new method identifies targets of regulator genes.

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, presented in the latest edition of Proceedings of the National Academy of Sciences (*PNAS*), 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 Magnus Rattray, a senior researcher at Manchester's Faculty of

Engineering and Physical Sciences, 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 Antti Honkela, his colleague at Aalto University School of Science and Technology, 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."

Provided by University of Manchester