

A Systems Biology Approach for Identifying Drug Targets

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BACKGROUND

Bayesian networks are a popular class of graphical probabilistic models based on Bayes theorem. Bayesian networks represent a joint probability distribution over a set of variables. Once known, this joint distribution may be used to compute the probabilities of any configuration of the variables. Bayesian networks have been increasingly applied to various computation applications, such as computational biology and computer vision. The commonly used approach of modeling network behavior employs ordinary or partial differential equations (ODE or PDE), but this approach is limited to analyzing relatively small networks (10-20 nodes), as ODE or PDE approaches may consider only local effects in the network. There is need to overcome this limitation and provide a systematic way, based on biological networks, to evaluate the effects of inhibiting multiple drug targets on treating a disease.

TECHNOLOGY DESCRIPTION

Scientists at UC San Diego have developed a method to identify drug targets using a systems biology approach. Given a network that regulates a disease, the method can predict the effects of inhibiting a set of genes on the marker genes of the disease. For example, if two marker genes are up-regulated in a disease, the method can identify inhibition of genes that can reduce the expression of the two marker genes to normal levels. Therefore, the invention provides a systematic way to evaluate the effects of inhibiting multiple drug targets for treating diseases. Such effects cannot easily be identified using traditional molecular biology approaches.

PATENT STATUS

Country	Type	Number	Dated	Case
United States Of America	Issued Patent	9,076,104	07/07/2015	2009-054

ADDITIONAL TECHNOLOGIES BY THESE INVENTORS

- [Quantitative Peptide Microarray Technology](#)

CONTACT

University of California, San Diego
Office of Innovation and Commercialization
innovation@ucsd.edu
tel: 858.534.5815.



INVENTORS

- Wang, Wei

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