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From gene expressions to genetic networks

MAREK CIEPLAK, Institute of Physics, Polish Academy of Sciences

A method based on the principle of entropy maximization is used to identify the gene interaction network with the highest probability of giving rise to experimentally observed transcript profiles [1]. In its simplest form, the method yields the pairwise gene interaction network, but it can also be extended to deduce higher order correlations. Analysis of microarray data from genes in Saccharomyces cerevisiae chemostat cultures exhibiting energy metabollic oscillations identifies a gene interaction network that reflects the intracellular communication pathways. These pathways adjust cellular metabolic activity and cell division to the limiting nutrient conditions that trigger metabolic oscillations. The success of the present approach in extracting meaningful genetic connections suggests that the maximum entropy principle is a useful concept for understanding living systems, as it is for other complex, nonequilibrium systems. The time-dependent behavior of the genetic network is found to involve only a few fundamental modes [2,3].

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