

Systems Biology approaches to drug discovery and gene function

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One of the grand challenges in the future of genomics research is the need to develop computational and experimental methods to detect gene-gene and gene-environment interactions for identifying the genetic contributions to disease and drug response. Scientists have been successful in cataloguing genes through genome sequencing projects, and we can now generate vast quantities of gene expression data using microarrays. However, the biology community has had far less success in understanding how genes and proteins are connected and operate within networks. When a cell is perturbed (whether by a drug or in a disease state), it is important to understand how it will respond in terms of gene expression and protein interactions.

A large volume of current research aims at understanding the regulatory connections in a given genetic network. Recent efforts to define the components and organization of genetic networks include experimental and computational methods to identify putative gene, protein and metabolite interactions, global structural properties, and regulatory modules and characteristic. The objective of the presentation is to illustrate how combined experimental and computational approaches can be used to infer the genetic network in which a particular gene of interest is embedded in order to understand its function and regulation. During the presentation the use of this approach in drug discovery will also be illustrated.