Unraveling genetic networks

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If genes are the currency of life, then the whole economies are genetic networks, which include genes as well as the complex webs of interactions and interconnections between them. Genetic networks are integrally important to the proper development and functioning of an organism, just as genes are, but they tend to be far more complex and difficult to understand.

Because of their complexity, the field has been slow to unravel genetic networks, said Leon Glass, the Isadore Rosenfeld Chair in Cardiology and a professor of physiology at McGill University.

Now a special issue of the journal *CHAOS*, produced by AIP Publishing, explores new experimental and theoretical techniques for unraveling genetic networks.

"Most emphasis has been on the properties of individual genes, and mutations in individual genes have been identified that lead to diseases, such as the cystic fibrosis gene," said Glass. But the proper expression of individual genes is regulated by both environmental factors, metabolic factors and the expression of other genes in the body, he added.

"To understand these interactions," Glass said, "it is essential to consider genetic networks."

Because of the convoluted interconnectedness of gene networks, researchers have realized that they might best be understood using nonlinear dynamics—an analytical method to understand systems (such as the weather) in which simple changes can have complex, cascading and even chaotic effects.

Just such methods are the subject of the special issue of *CHAOS*. Included among the collection of articles are two papers describing powerful new methods to understand very large genetic networks and a paper combining experimental and theoretical work to unravel the genetic networks controlling development in fruit flies.

"The rapid expansion of biologic data concerning structure and dynamics of genetic networks makes it essential to develop appropriate computer and analytical methods to deal with these problems," said Glass, who was an early pioneer in the development of theoretical methods for understanding gene network models. Glass is the author of the introduction to the new issue along with James Collins, an HHMI Investigator and a bioengineering professor at Boston University and Harvard's Wyss Institute, and Réka Albert, a professor of physics and biology at Pennsylvania State University.

Understanding the functioning of genetic networks opens the door to a number of new applications in biotechnology, said Collins. Among other applications, he said, "synthetic gene networks could be used as decision-based circuits for creating programmable cells for a variety of applications including the detection and treatment of infectious diseases and complex diseases such as cancer and reprogramming the human microbiome, and as diagnostic tools for personalized medicine."

More information: The special issue of *CHAOS* can be accessed at: chaos.aip.org/resource/1/chaoeh/v23/i2?§ion=focus-issue-quantitative-approaches-to-genetic-networks&page=1