Finding New Order in Biological Functions from the Network Structure of Gene Annotations

Michelle Girvan*, University of Maryland

Abstract
The Gene Ontology (GO) provides a controlled vocabulary of terms for describing gene functions and specifies how these functional terms are related to each other. Biologists can then submit annotations connecting genes to the appropriate functional terms. We propose a method for using the network structure of gene-term annotations associated with GO to establish an alternate natural grouping of biological functions which is very different from the conceptual hierarchical structure that relates functional terms in the ontology. Unlike the GO hierarchy, which is specifically species neutral, our method captures variation in functional organization across species. As a result, it can provide insights into the evolution of function. Further, grouping terms by our alternate scheme provides a new framework with which to describe and predict the functions of experimentally identified groups of genes. To demonstrate this, we examine a set of gene signatures for cancer and find enrichment with respect to the groups of terms identified through our alternate approach on par with enrichment with respect to branches of the GO hierarchy.

Keywords: Gene ontology, Gene functioning annotations in new network structure.

* Presenting author