GEOMI: a tool for integrated systems biology research

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Abstract

GEOMI is a network visualisation and analysis platform that allows interactive navigation in 3D space. We have extended the functionality of GEOMI to generate integrated visualisations of transcriptomic and proteomic data, which have provided novel insights into the dynamics of the interactome.

Keywords: systems biology, software, network visualisation

1 Introduction

The emergence of high-throughput genome-scale detection methods, such as mass spectrometry and yeast two-hybrid assays, has greatly contributed to datasets enriched with novel information. Consequently, the need for scaleable techniques to integrate and interpret the vast amounts of biological data generated has become increasingly evident.

So far, visual representations have proven to be both effective and intuitive, offering contextual analysis and the ability to increase information content without complicating interpretation [1]. One such example is the visualisation of protein-protein interactions as a network of interconnecting nodes. This representation has not only consolidated our knowledge of proteins, but also provided insights into the integration and coordination of cellular function.

These representations have primarily been created in 2D space, which often results in a large number of intersecting edges, rendering the visualisation essentially uninterpretable.

2 Method and Results

GEOMI [2] is an open-source network visualisation and analysis platform originally developed at National ICT Australia (NICTA). It provides an interface that enables users to interactively navigate the network in 3D space. Functionality within GEOMI can be easily extended using customised plugins. We have adopted GEOMI for the visualisation of protein interaction networks [3]. A suite of plugins enable co-visualisation of interaction data with a range of protein characteristics. These include physicochemical properties (e.g. protein hydropathy, pI, abundance), as well as functional parameters such as gene ontology and subcellular localisation.

3 Discussion

These integrated visualisations have revealed novel insights into the organisation of the cell, further increasing our understanding of cellular dynamics:

- Contextual analysis of protein interaction networks has reinforced our current understanding of proteins and their interactions. For example, proteins that share subcellular localisation and biological function are proximal in the interaction network [3].
- Visualisation of the complexome has provided evidence for the existence of modularity, which suggests an even higher organisation of the proteome [4].
- Visualisation of methylating enzymes, demethylating enzymes and substrate proteins has established the methylation network in the yeast cell [5].
- Co-visualisation of protein interaction data with transcript data has provided insights into the mechanisms of regulatory pathways, and how function is regulated within the cell [6].

This version of GEOMI can be downloaded at:
http://www.systemsbiology.org.au

References

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