Discovery of key regulatory genes in multi-layered biological graphs

Master 2 Intership,
Dyliss team, Irisa / Inria Rennes-Bretagne Atlantique
Collaboration with UMR Pégase, INRA & Agrocampus

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1 Context

Biological processes and their regulation result from complex interactions between various biological entities. The structure of these biological systems can be classically modeled by a graph (or network).

However, biological entities involved in biological processes and their regulation can be of different nature (a gene, a protein, a metabolite ...), or come from a more or less reliable data source (different databases, or different identification techniques), and modeling as a multi-layer graph might be more appropriate [1,2,4,5]. For example, a recent study has shown that the modular structure of protein-protein interaction networks was more effectively demonstrated by analyzes based on the multi-layer model [3], compared with analyzes aggregating all sources into a unified graph.

2 Subject proposal

The subject is not fixed; we are open to suggestions and the subject can evolve if the student has interesting ideas.

We propose to study metabolic networks using a multi-layer model. The objective of the internship is to determine whether the search for key regulators of metabolic pathways is more efficient on a multilayer network or on a unified monolayer network.

Two types of multi-layer networks can be envisaged:

1. Each layer represents a different databank. While public databases aggregate a large part of the knowledge of biological networks, many genes and regulatory mechanisms remain poorly studied. In this case, less validated data sources produced with high throughput technologies, for example, could complement reliable

reference sources. We are therefore considering multi-layer modeling to differentiate interactions from reliable sources to those from less stringent banks.

2. Each layer is focused on a biological entity nature: a layer for interactions between metabolites (metabolic network), a layer for regulatory interactions between genes (genetic networks) ...

A framework dedicated to the analysis of biological networks has been initiated in the team. The student will contribute to the extension of this framework for multilayer graphs. Based on a list of dis-regultaed genes, he or she will design scoring algorirthms to highlight key regulators whose alteration would explain the dis-regulation of the input genes. He or she will compare the results on the multilayer graphs with the results on a "unified graph", as described in `Key Regulatory Finder`, a tool jointly developed by the Dyliss team (IRISA) and Pegase (INRA).

3 Prerequisite, Keywords

Prerequisite: no knowledge of biology is required to complete the project, but interest in biological issues would be appreciated.

Keywords: biological graphs, oriented multi-layered graphs, algorithm on graphs, random walk with restart, object oriented Python development, search for regulators.

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4 References and reviews

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