

App Development for Analyzing Biological Networks

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Introduction

"App Development for Analyzing Biological Networks" seeks to understand the interactions of proteins and genes within biological networks. The program aims to identify patterns in the data and its relation to diseases.

Current System

The current system allows users to specify search conditions (bi-partite, clique, or directed clique), choose search algorithms (Breadth or Depth First Search), determine graph ordering criteria, and customize subgraph saving options. Users can also choose the community detection approach applied to their data. One of these approaches is *infomap* algorithm.

Summary

The program for analyzing biological networks (Cyfinder) is improved by adding algorithms that execute in sequence within the Infomap feature. This furthers intricate detection of connections and subnetworks within the data making infomap a more robust detection tool.

Problem

Cyfinder uses a version of Infomap that is not fully developed. Infomap consists of a series of algorithms applied sequentially to detect the biological networks and subnetworks found in the given data set. Infomap must be more robust to be able to detect more complex connections.

Solution

Further develop infomap so that, having a more complex structure, it can better detect connections within the network. Our team integrated a new series of algorithms to Infomap to execute in sequence along with the ones Infomap already utilizes for detection.

Implementation

Developed Fine tuning and Coarse tuning algorithms to execute within infomap alongside cluster algorithm. These algorithms allow Infomap to find connections within the subnetworks of the data and improve its performance by expanding its capabilities.

References

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