

Computing and Information Sciences

Fall 2019 Senior Design Project



CyFinder

Analyzing Biological Networks

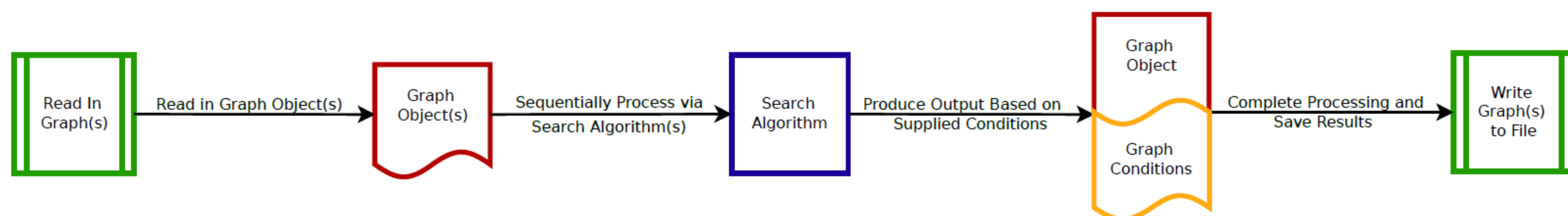
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Mentor: **Raihanul Bari Tanvir, Dr. Ananda Mohan Mondal**
Instructor/Faculty: **Dr. Masoud Sadjadi**, Florida International University



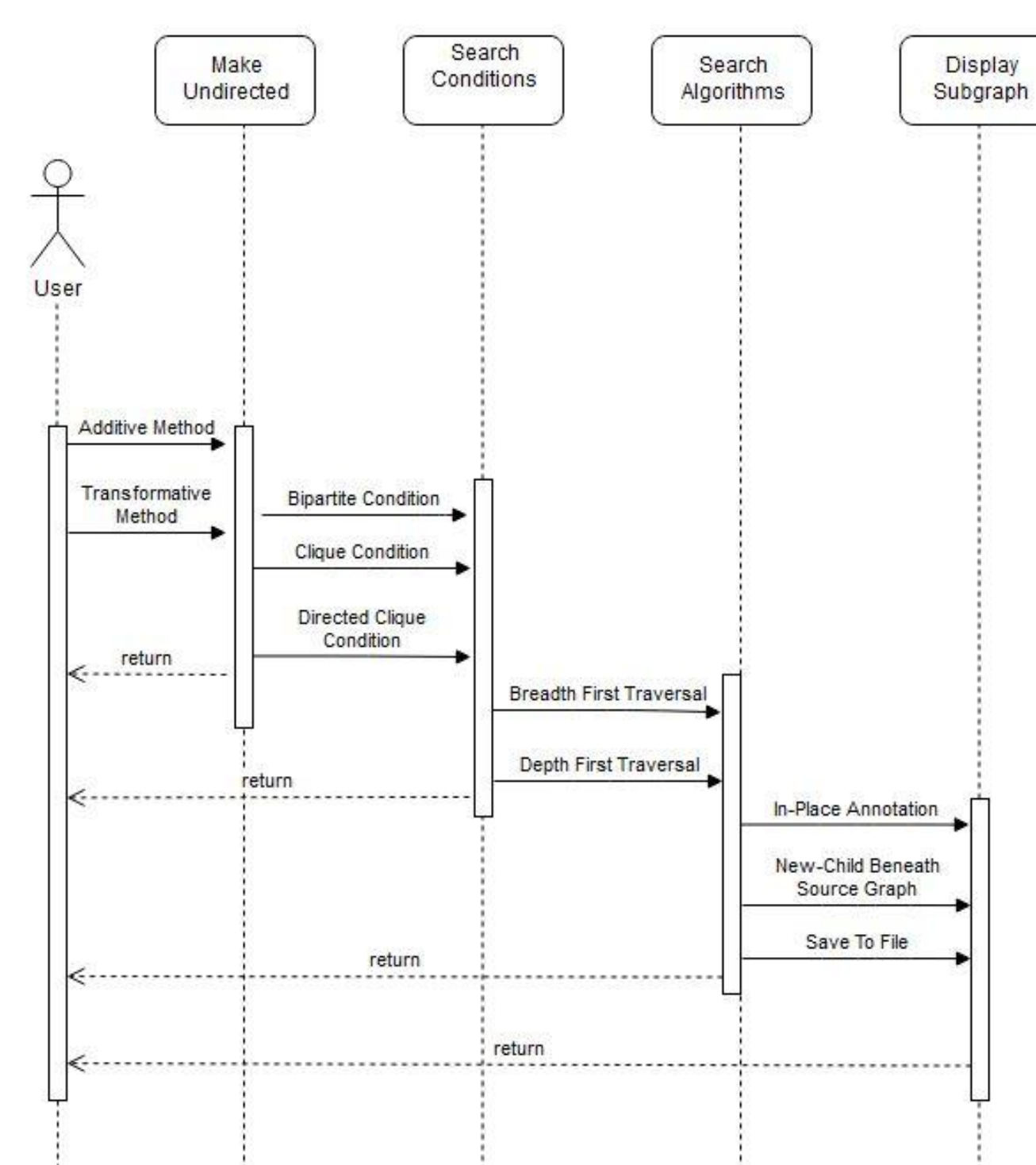
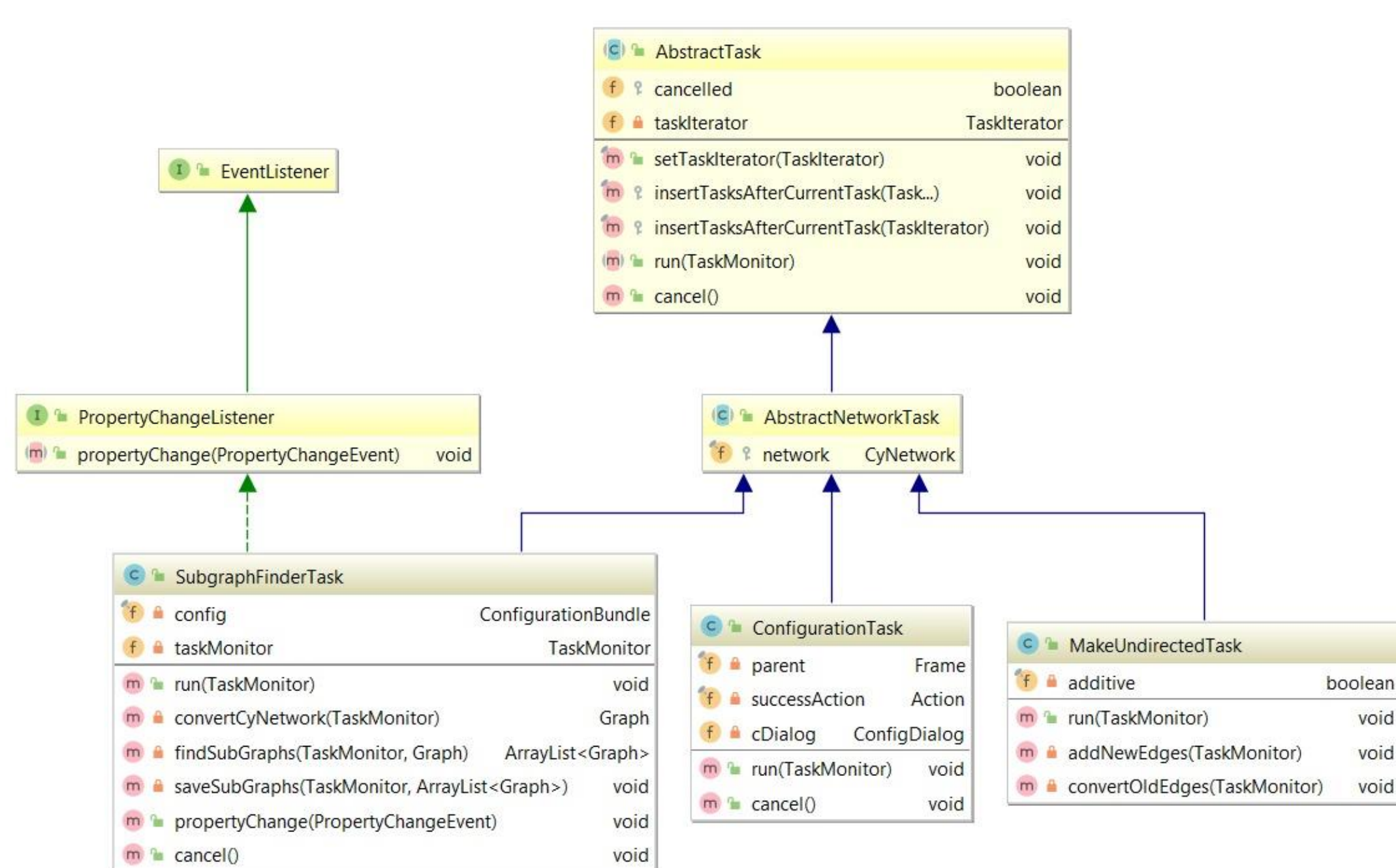
Problem

The main objective of this project is to develop an app for the software Cytoscape. This app can then be used to identify clique-like and bipartite-like structures from a biological network and display the results as subgraphs. These subgraphs can be used to represent disease progression on a protein network level. There is currently no app for Cytoscape that provides this feature.

System Design



Object Design



Summary

CyFinder has been worked on over the last few years and has had many features added. Currently this plugin can detect bipartite and clique subgraphs using BFS and DFS for the searching algorithm. In addition, this plugin now provides what group the nodes in the bipartite subgraphs belong to. This grouping attribute allows the user to display the nodes side by side for better visualization. Future features that can be added, are displaying the largest complete subgraphs within a bipartite subgraph and allowing the user more sorting options.

Verification

Since the CyFinder app had to be tested through Cytoscape, all of the testing for our code was done manually.

Current System

- The CyFinder plugin must first be installed in the Cytoscape application before it can be used.
- The data to be used must then be imported into Cytoscape for use with CyFinder.
- Data imported must be set as undirected before any subgraphs can be found using the additive method or transformative method available in CyFinder.
- Once data has been pre-processed, bipartite and clique subgraphs can then be found after selecting the type of search algorithm to use and the specified option for display.

Requirements

To run CyFinder:

- The latest version of Cytoscape (3.7.2) must first be installed.
- The CyFinder app should be installed through the Cytoscape App Manager.
- The data inputted must be in the .csv or .txt file format.
- Data must then be pre-processed using one of the options available in the "Make Undirected" tab in CyFinder.
- Subgraph Finder needs to be opened then the search condition and a search algorithm must be selected to display subgraphs.

Implementation

- Java
 - Main language used to create CyFinder
- Maven
 - Combined the logic with the GUI to generate JAR
- Apache Ant
 - Responsible for building the project that contains the logic of CyFinder
- Cytoscape API
 - Necessary tools needed to implement Cytoscape features for CyFinder

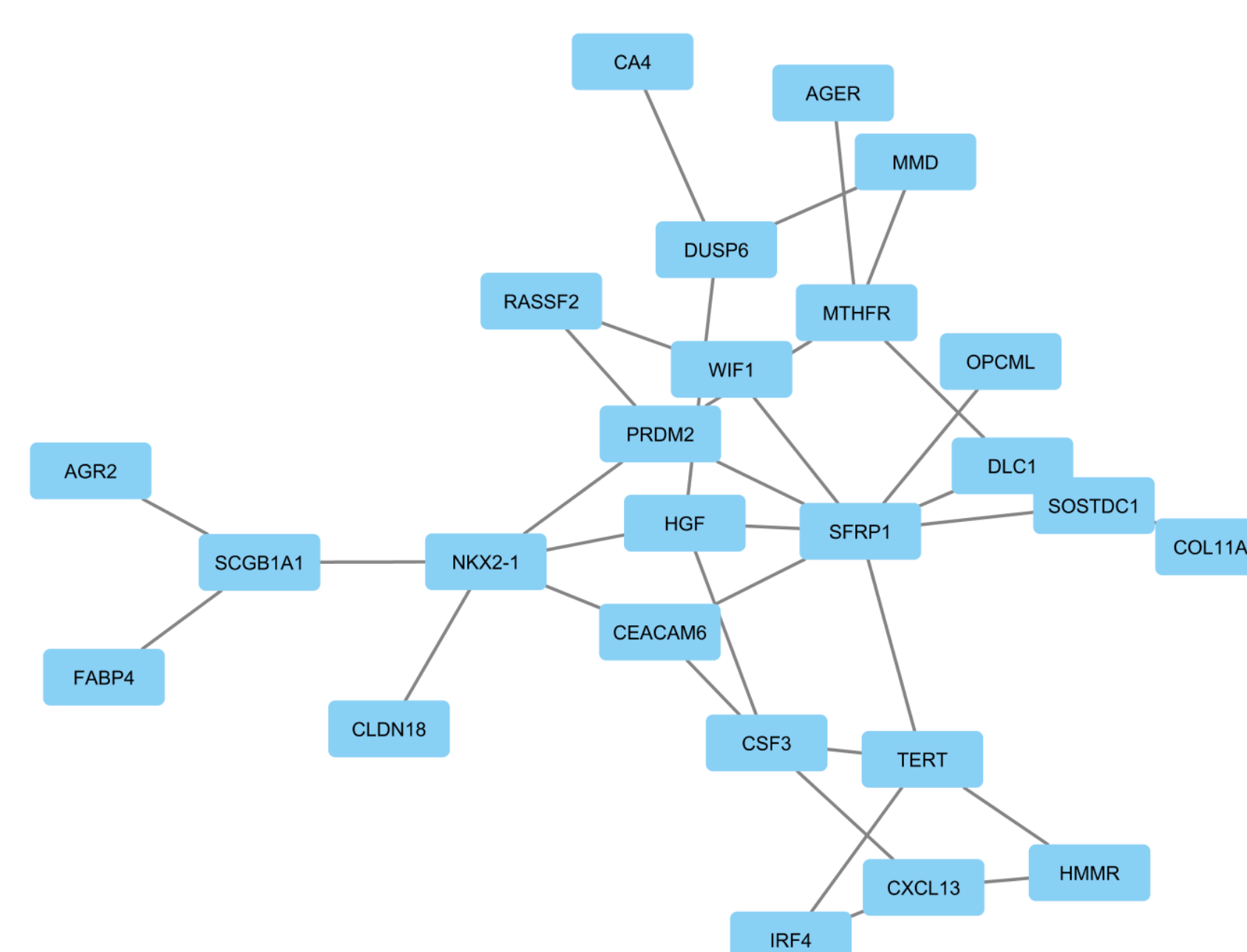
Contributions

I contributed to this project by:

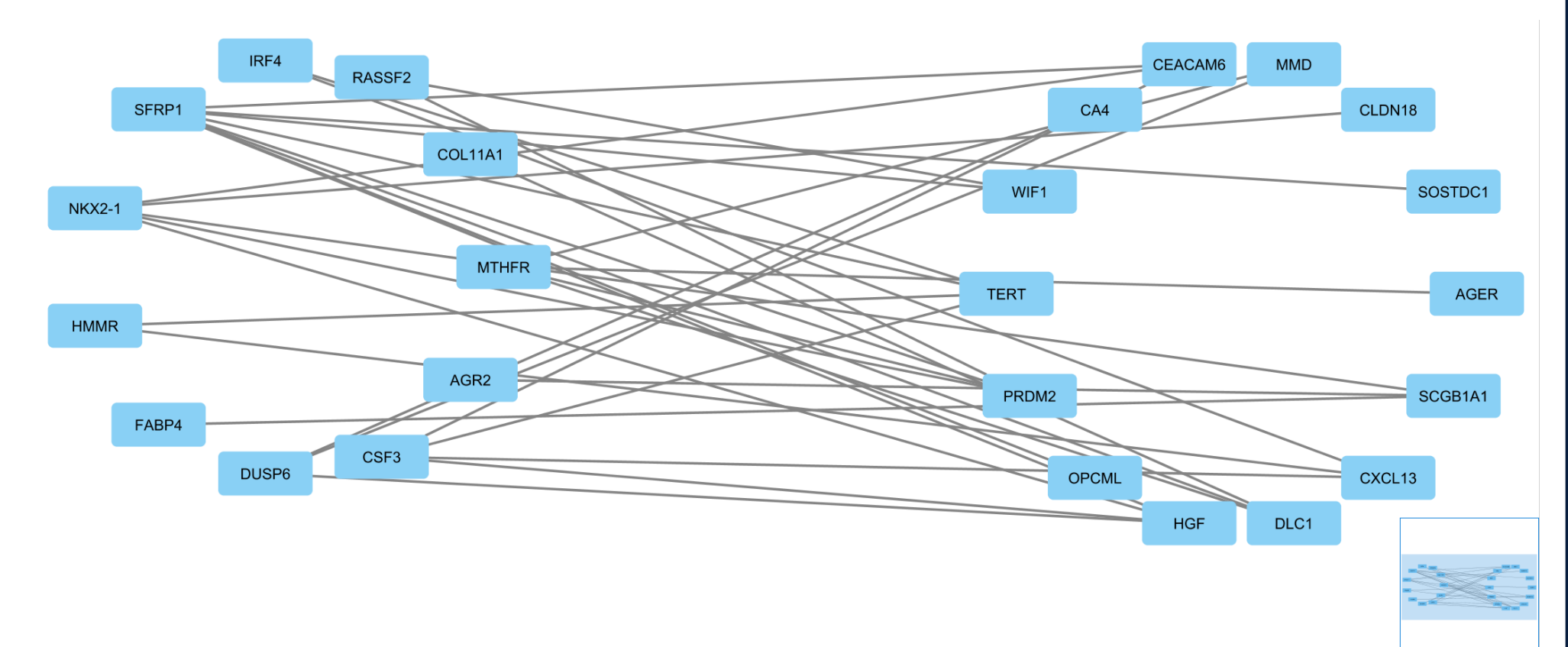
- Creating a component that checks for bipartite condition using the breadth first search algorithm.
- Providing an easier way to group and display subgraphs through Cytoscape.
- Implementing a component for parsing, purging, and handling Cytoscape data
- Integrating the CyFinder app and subgraph finder module

Screenshots

Subgraph before:



After applying the bipartite grouping feature:



Acknowledgement

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