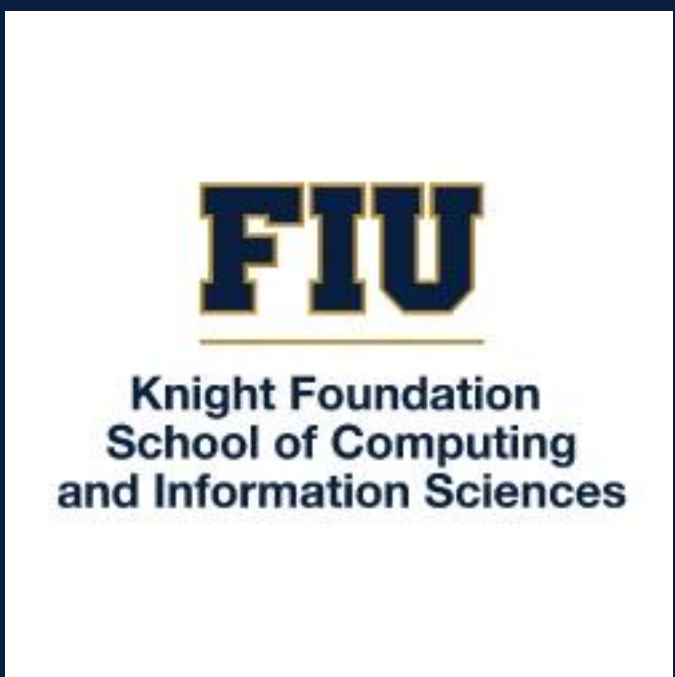




App Development for Analyzing Biological Networks

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Introduction

"App Development for Analyzing Biological Networks," delves into understanding gene and protein Interactions crucial for disease progression. The objective is to identify clique-like and bipartite-like structures in biological networks, particularly protein-protein interaction networks.

Current System

The current system facilitates the conversion of directed graphs to undirected graphs through additive or transformative approaches, allowing users to add edges between connected nodes or transform edge objects for compatibility with Cyfinder. Users can 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.

REQUIREMENTS

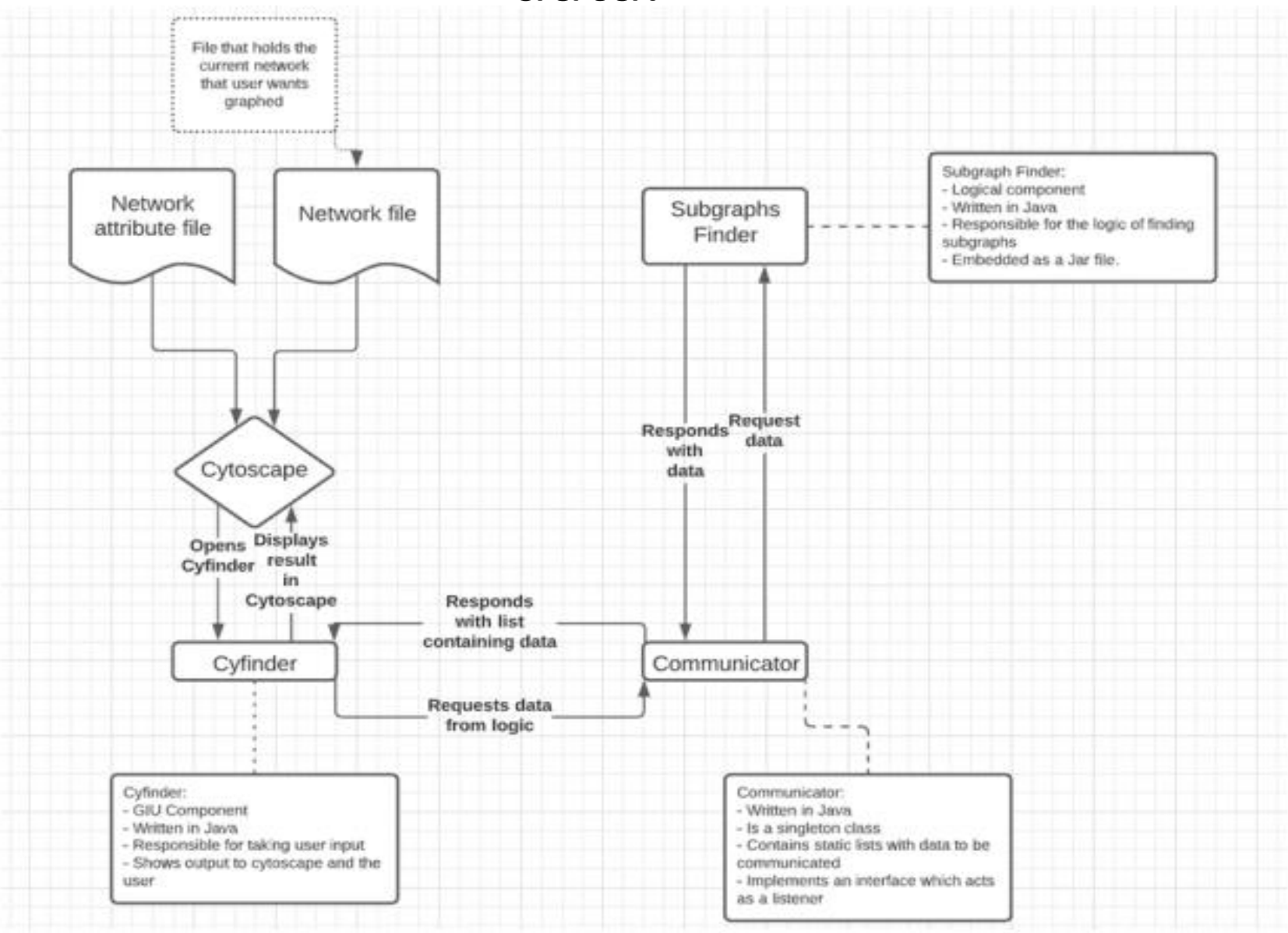
The app, CyFinder-V2, uses JAVA as the primary language for development. The architecture involves components for processing and analyzing biological network data.

PROBLEM

Deciphering complex biological networks poses a significant challenge. Existing tools often fall short in identifying key structures influencing disease initiation and progression.

SYSTEM DESIGN

The app, CyFinder-V2, employs JAVA as the primary language for development. The architecture involves components for processing and analyzing biological network data.



IMPLEMENTATION

Implementation involved developing CyFinder-V2, emphasizing features crucial for identifying key structures in biological networks. The development process addressed challenges to create a robust tool for understanding disease progression.

Solution

CyFinder-V2 proposes a solution to identify clique-like and bipartite-like structures in biological networks. This version builds upon CyFinder-V1, enhancing its capabilities for a more comprehensive analysis.

SUMMARY

The project aims to enhance the existing CyFinder-V1 app for analyzing biological networks. It focuses on unveiling clique-like and bipartite-like structures to better understand disease progression at the protein network level.

REFERENCES

- Mapping Higher-Order Network Flows in Memory and Multilayer Networks with Infomap
- The map equation, M. Rosvall* and D. Axelsson
- Previous group final deliverable

ACKNOWLEDGEMENT

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