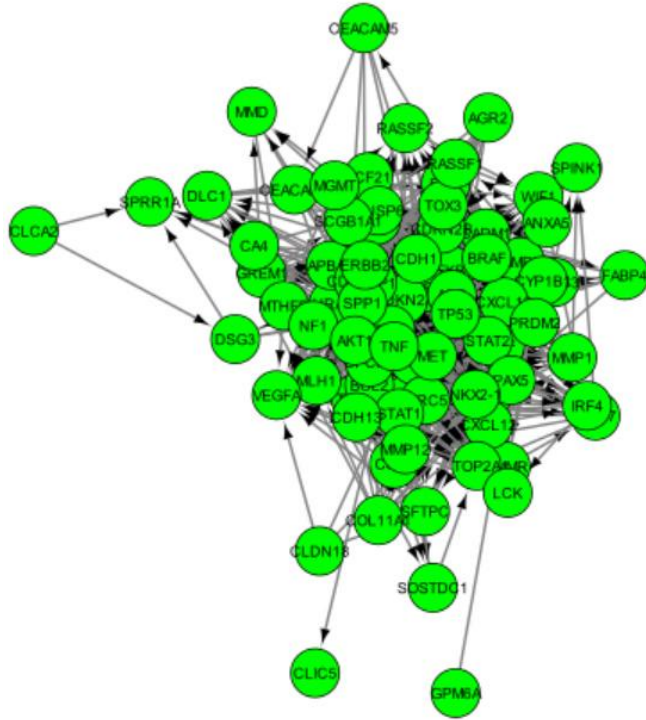
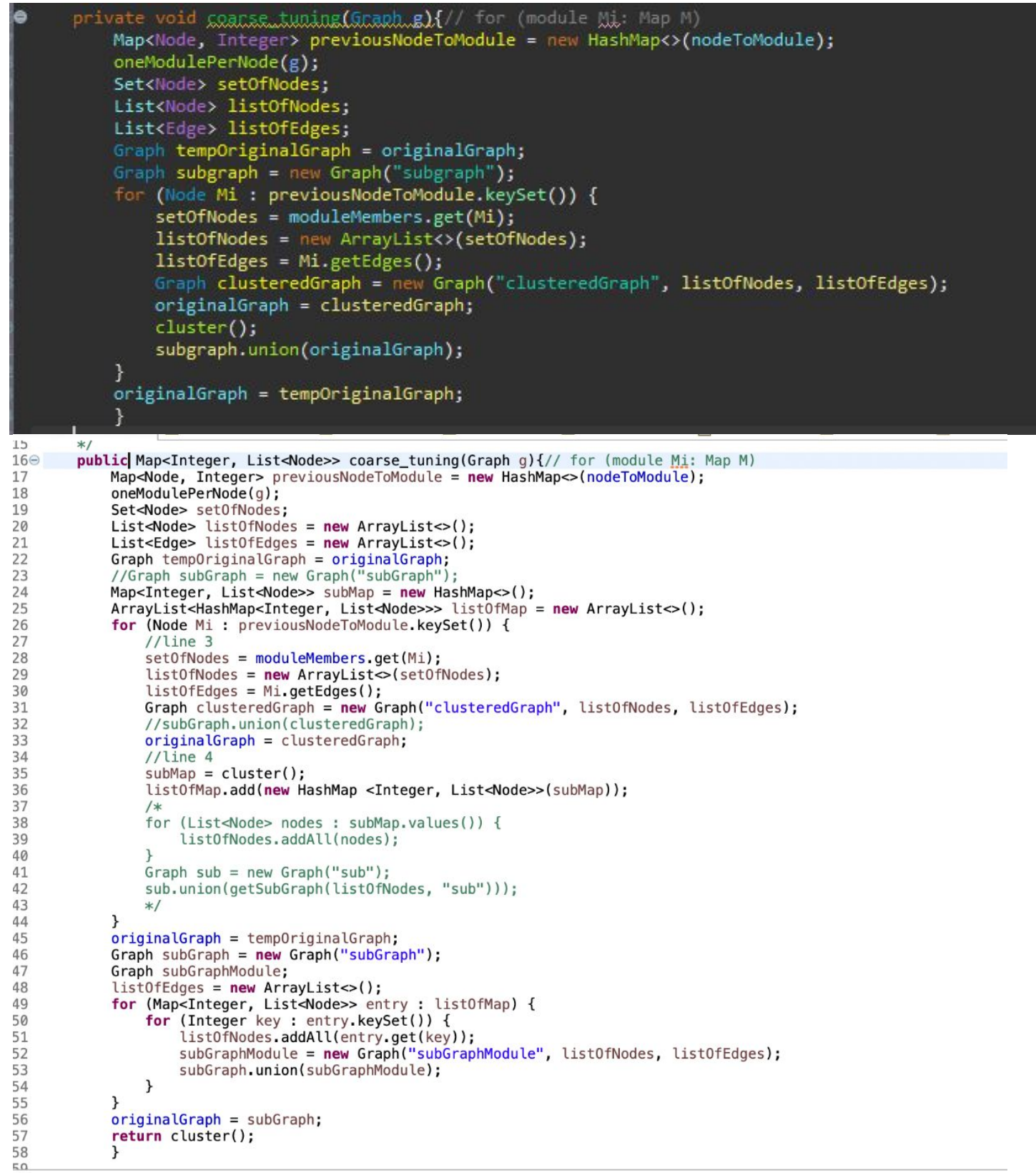


KFCIS Fall 2024 Capstone Project: App Development for Analyzing Biological Networks/CyFinder

Students: Tyler Uwate, Valeria Garcia, William Lopez, Leonardo Villa, Oscar Alvarez, Sushmita Karre

Introduction	Problem	Summary
Cytoscape is a bioinformatics software project that analyzes biological networks, such as cancer, and generates graphs of them. CyFinder is a plugin that adds clustering algorithms for early disease detection. Subgraph Finder develops and implements the algorithms (or rather is the algorithms) CyFinder uses to accomplish this goal.	In the current implementation of the research papers and general design, some of the algorithms have already been implemented by previous senior project/capstone teams, but not all have been linked together as needed or even been coded in and of themselves. So accordingly, the system needs to add more of what is needed in the “roadmap” of sorts.	CyFinder is a plugin/extension designed to add clustering algorithms (for early disease detection) in the CytoScape program, and this group worked on it to further its completion.
Current System	Solution	Implementation
In the current (and future) system implementation, this is a CytoScape plugin that generates network views of directed and undirected graphs, and allows users to set search conditions, algorithms, and so on.	The problem has already been laid out. So accordingly, the solution is the implement the algorithms for the subgraph generators present in the research papers (helpfully denoted by our predecessor group), continue and/or optimize any already existing code that is working towards implementation, and link the algorithms (or enable one to call another) where appropriate.	Creating a new graph and storing the original graph in a temporary variable in order to use the graph to cluster later Then, we implemented course-tuning for graph generation, creating subgraphs and clustering them based on submodules that have been moved into new or neighboring modules.
		
System Design	Requirements	References
This is a modification of the current plugin to link existing algorithms together by -Integrating the fine-tuning algorithm -Coarse tuning, by moving submodules from existing modules into new or neighboring modules, before clutering like in the previous step, but with each submodules free to move between the modules.	-Java 11.0 -Apache Ant -Maven -CytoScape 3.9.1	- Edler D, Bohlin L, Rosvall M. Mapping Higher-Order Network Flows in Memory and Multilayer Networks with Infomap. Algorithms. 2017; 10(4):112. https://doi.org/10.3390/a10040112 - Rosvall, M., Axelsson, D. & Bergstrom, C. The map equation. Eur. Phys. J. Spec. Top. 178, 13–23 (2009). https://doi.org/10.1140/epjst/e2010-01179-1 - Edler, D., Holmgren, A., & Rosvall, M. (n.d.). Simplify and highlight important structures in complex networks. MapEquation. Retrieved April 17, 2023, from https://www.mapequation.org/