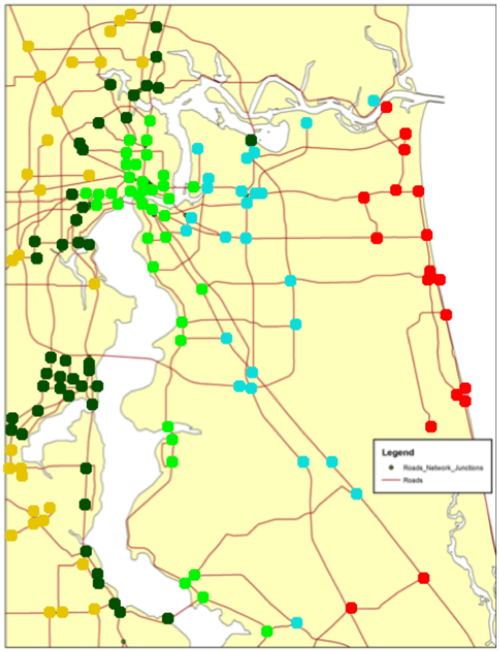
NDSU Engineering Grand Challenge Project Examples

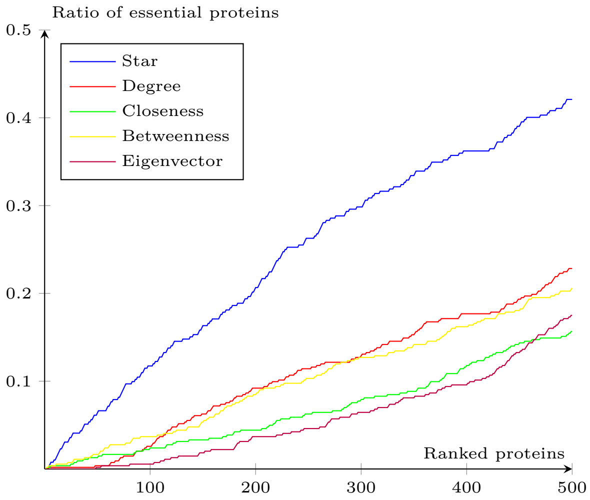
Nuclear Material Detection

Operations research and mathematical programming can help towards preventing nuclear attacks through the proper installation of radioactive material detection equipment in entry points and hubs. Assuming that radioactive material that are illegally entered into a country are prone to be used to attack densely populated areas, installing such detection technology in busy hubs can deter such practices. Ideally such detection schemes would be affordable (and the budget for them to be acquired, properly installed, and maintained would be available), but this is rarely ever the case. Thus, we once more are looking at a way of identifying the best locations for their installation, such that we ensure a high rate of detection and deterring, along with allocating funds appropriately. Join us to investigate where to locate our detection equipment, how to sample entries reliably, and how to route resources effectively.



Which proteins are *more* important?

Complex network theory has been a paradigm-shifting force in many disciplines. One such discipline is *computational biology*: with the use of network analysis, researchers are now enabled with novel tools to detect protein complexes, analyze protein essentiality, and predict protein functionality. To do that, the first step is to create a *protein-protein interaction network* (PPIN) based on the discovered interactions of various proteins. PPINs are mathematical constructs where each protein is represented as a vertex, with two vertices being connected by an edge whenever the two proteins interact. A fundamental question in the analysis of PPINs is whether there exist proteins that significantly affect the functionality of a cell. A protein is said to be essential or lethal when, if absent, it causes the biological cell to die or be unable to reproduce properly. The study of essential proteins was and still is performed experimentally; however, those experiments tend to be expensive, both resource- and time-wise. Our research question, then, can be summarized to the following: *Does there exist a network topology metric that captures the importance of a single protein in the grand scheme of the proteome?*



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