Survey of Potential Regulators in the Fog/Non-Muscle Myosin-II Pathway

Abstract

Determining proteins that are involved in signaling pathways is essential for understanding complex cellular and developmental processes. However, wet lab approaches for identifying unknown members of a pathway can be costly. Using a computational approach to identify potential regulators from known members of a pathway and previously compiled protein-protein interactome networks saves time and money, and provides potential proteins that

chosen to limit the size of the network based on proximity to known regulators prior to implementing our algorithms, thus decreasing the running time of our algorithms while hopefully increasing accuracy. Using BFS to identify maximally connected subgraphs, we identified the largest connected component

CkIIalpha	Pi3K21B	Ubi-p5E	nej	

Table				

CkIIalpha	NetB	Spn	Ubi-p63E

Table 7. Proteins Identified		

Our methods relied on a weighting scheme, which can either be evaluated by cross listing empirical data or made on an assumption of equal edge weights. Weights may be thought of as the 'distance' separating two nodes. We were not able to arrive at a system of assigned weights, such as those provided by HIPPIE or IntScore. To evaluate our assumption of uniform edge weights throughout the graph, we used EGFR as a toy data set, where assigned weights were available. By running our algorithm on the EGFR graph with assigned weights derived from empirical measures, and again on the EGFR graph where edge weights were assumed to be uniform, we found that the steiner tree and shortest paths algorithms return the same set of potential positives in both cases. In the case of the dijkstra rank algorithm, we found the comparison to have two of five top ranked nodes common to both sets, and four out of ten common in the top ten-new steiner tree. This indicates that the Dijkstra rank method is subject to greater variability in

Role of Negatives

It is important to note that both analyses were performed with non-regulators included, and the status of these nodes was not taken into consideration [illegible] algorithms. Additionally, the method for generating non-regulators should be considered when interpreting these results. Genes that were listed as likely non-regulators were involved in anom

- Shortest-paths returns a dictionary with keys of non-terminal nodes and values as sets of positives that link to that node. These values vary between nodes, and could be used as a further statistic to help characterize potential regulators in further research.

Future Directions

We believe these