April 30, 2015

Dominic: Future Direction

* Use of Bayesian Network approach to find the relationship between cliques found by Prayas
* Dominic talked about odds, Bayes factor.

**September 4, 2015:** BIBM Paper

Algortihm

* Work with only one subnetwork
* Start with a subnetwork
* Find the missing PPIs based on kernel values **greater than the average kernel values of existing PPIs(threshold)**
* Find the updated network by adding the missing PPIs
* Find the kernel values for the updated network
* Concern: 🡪 by repeated iteration, we might end up in a situation that the final network will have all possible PPIs. **My answer to this is NO.**

**September 20, 2015**

For the networks (N\_500 through N\_950) how many of the discovered (missing) PPIs were in the original network biomarker? By discovered PPIs we mean sum of all the missing PPIs found in different iterations. Original Network is the network with 84 proteins.

Deliverable: A table Like

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Network | # Protein | # Existing PPI | Discovered PPIs | |
| Total # | # exist in original network |
| N\_500 | 83 | 610 | 38 | 14 |
| N\_600 | 82 | 540 | 32 | 10 |
| N\_700 | 77 | 468 | 16 | 5 |
| N\_800 | 73 | 346 | 14 | 7 |
| N\_900 | 68 | 240 | 17 | 13 |
| N\_950 | 61 | 183 | 11 | 8 |
|  |  |  |  |  |