



CALIFORNIA STATE SCIENCE FAIR
2009 PROJECT SUMMARY

Name(s) Arjun B. Sharma	Project Number S1618
Project Title A Computational Analysis of the Topological Property of the Human Transcription Factors Protein-Protein Networks	
<p style="text-align: center;">Abstract</p> <p>Objectives/Goals Are Mammalian Transcription Regulatory Networks (TRNs) scale-free?</p> <p>Methods/Materials I got the data of Human transcriptions factors protein-protein interaction measurements generated by a Yeast Two Hybrid analysis in a text file with two columns. Then using Matlab, I applied the equations of topology analysis (see Glossary). The result of these equations was plotted using Matlab. I plotted a graph to show what would happen if several nodes were taken away from the network. In addition, also the network and an example of network hubs have been visualized using software Cytoscape.</p> <p>Results The result of the equation on the network measurements produced a discrete value for each of the three parameters. $k=7.3$; $s=3.6$; power law coefficient = -1.5. These values were compared with classical scale-free parameters, the k fit the range from 5 to 8, characteristic of a scale-free network. The s is in the range of 3 to 8, also characteristic of scale-free network. And the power law coefficient is negative, which is strong evidence that the degree fit to a power law distribution. To further test my hypothesis, I did a test similar to the tests in the literature to see if this network displayed scale-free characteristics when under attack. As shown in figure 4, when I sequentially took out hubs from the network, the average path length increased substantially, which lead to a severe decrease in productivity. My results are similar as described in the literature, so this is another strong piece of evidence pointing to the fact that this network is scale-free.</p> <p>Conclusions/Discussion After my analysis, I concluded that human transcription factors protein-protein network have a scale-free property, which means the network is dominated by hubs, proteins with more interactions than a random node. These hubs are the most important players of the network; therefore, they are important in biological pathways. All the properties of a scale-free network were shown through my experiment. The path length chart showed that all path lengths were close, unlike a random network in which the path lengths between different nodes would greatly vary. In addition, when this network was #attacked#, when nodes were taken away sequentially, the efficiency of this network drastically declined. It declined to a point to where the network became isolated clumps of nodes with no practicality.</p>	
Summary Statement I computationally analyzed with the use of MATLAB the dynamics, and topological properties of a human transcription factors network, and tested whether it exhibited scale-free properties.	
Help Received The data was provided through Dr. Timothy Ravasi at UCSD, also MATLAB was provided.	