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Evolutionary Rate in the Protein Interaction Network

In Fraser’s paper he discussed the importance of the organization of the protein interaction network in the yeast *Saccharomyces cerevisiae* and its effect on the evolution of the proteins that compose it. To support this data, he compiled a list of 3541 interactions between 2445 different yeast proteins. He found that there is a negative correlation between the connectivity of the proteins in the network to their rate of evolution. He demonstrated this data in Figure 1 showing the linear regression of the number of protein-protein interactions as estimated by the evolutionary distance (K). He showed the correlation between a protein’s number of interactors and its effect on organismal fitness, which will affect the rate of evolution. Fraser argued that proteins with more interactors evolved more slowly due to a greater proportion of the protein being directly involved in its function. He tested this as well as the hypothesis of the number of interactors being correlated with its effect on organismal fitness in Figure 2. He rejected the seconded hypothesis due to the effect of protein interactions on evolutionary rate not being mediated by protein fitness effect. Fraser made the prediction that interacting proteins evolve at similar rates due to co evolution. He demonstrated this in Figure 3 by calculating ΔK (the difference between the evolutionary distances separating the yeast proteins from their orthologs in the nematode). Fraser found that interacting proteins had similar effects on organismal fitness, but this only contributed slightly to the correlation between their evolutionary rates.