Robin Levy

Bio 320

January 18, 2012

Summary to Evolutionary Rate in the Protein Interaction Network article

This study is trying to show that the evolutionary rate of proteins is not correlated with well-conserved proteins. Through analyzing multiple proteins and their interactions and their relations to the rate of protein evolution, the researchers were able to find and compare their data to try to prove their alternative hypothesis. In figure 2, it is showing a model for the alternative hypothesis. It shows that random effects, protein fitness effects, and protein interactions have an effect on Evolutionary rate, and that the effect of protein interactions is correlated with protein fitness which is in turn correlated with evolutionary rate. From the results that the researchers got form comparing parametric and nonparametric partial correlations, they concluded that there is no relation between fitness and evolutionary rate. The scientists then went on to investigate the similarity in evolutionary rates between interacting proteins hypothesizing that it is due to the similarity in the protein’s fitness effects. They wanted to see if interacting proteins even have similar effects on organism fitness. From their comparison in figure 3b, it shows from the extremely low p-value, p < 10-5, that interacting proteins indeed have similar effects on organism fitness. Figure 3c is a model to show that correlations between protein fitness effects on interacting proteins contributes very little to the correlation with protein’s evolutionary rate. Thus further proving that fitness has nothing to do with the correlation between protein interaction and evolutionary rate. They had another alternative hypothesis stating that interacting proteins may evolve at similar rates because they have a similar number of interactionss. This thought was formed when the results of figure 1 were analyzed. It shows that the number of interactions influences the rate f evolution. This hypothesis was rejected when it was found out that proteins that interact do not have similar numbers of interactions through the p- value, p = 0.26. In the end, they concluded that the co-evolution of interacting proteins may have an effect on the observed similarity in evolutionary rates.