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Brittney Hinds* (s-bhinds1@math.unl.edu). *A Game-Theoretic Approach to Protein Clustering*. Preliminary report.

Protein sequences often include multiple conserved domains. Multiple evolutionary events including duplication, loss, recombination, and divergence generate complex proteins. As a consequence of their complex evolutionary history, a large variation exists in the numbers, types, combinations, and orders of domains among member proteins from the same family, and their evolutionary history is best modeled through networks that incorporate the entire domain content of the proteins. In this talk we propose a game-theoretic approach to constructing biological networks. In this study we examine the application of that approach to classifying multidomain proteins. We applied this method to clustering several sets of simulated protein families, a real multidomain protein family, Regulator of G-Protein Signaling family, as well as entire proteomes. We compare our classification results with the results from several other existing methods, including Markov clustering, protein-domain biclustering, and phylogenetic analysis. (Received September 09, 2014)