Abstract Submitted
for the SES11 Meeting of
The American Physical Society

Utilizing protein networks to determine novel annotations KENNETH SHIAO, JERRY FENG, TINA DOAN, ANDREY GORIN — Proteins are a key element of life because they are involved in every metabolic process, yet a majority of proteins remain unannotated. Current chemical and physical annotation methods are inaccurate, inefficient, or expensive. Without proper annotation, understanding of organisms' metabolic pathways is limited. Based on the hypothesis that proteins with similar primary structures have similar characteristics, we theorize that a method for protein annotation can be developed using protein networking, which was previously thought to be useful in determining the evolutionary paths of proteins. A large, diverse database of proteins is used to connect protein fragments by using a preset identity threshold. With this method, unknown proteins are connected to known ones. By observing the number of links to proteins with annotated functions, a likely annotation candidate will be reached. This procedure can potentially facilitate the process of finding more accurate annotations. We have used and validated this approach to annotate putative uncharacterized proteins. Results will be presented at the conference.

Kenneth Shiao

Date submitted: 06 Oct 2011 Electronic form version 1.4