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*Informatics for Identifying Complex Molecular Networks*  
(Computer Science / Engineering & Computer Science)

The National Science Foundation, Division of Biological Infrastructure, has released a program announcement (NSF 02-058) for Biological Databases and Informatics. The response target date is July, 2005. Funds from the proposed development award are intended to enhance the preliminary results supporting a full NSF proposal submission. Successful competition for this award will establish Baylor’s independent grantsmanship in the research area of bioinformatics and create stronger interdisciplinary collaborations within Baylor.

The science driving this proposed research is the increasingly critical need to explore novel strategies to store, manipulate, and analyze biological data for the study of molecular biological networks. In particular, life scientists are becoming more aware of the complex interwoven molecular structures, pathways, and processes that create emergent phenotypes from genotypes that define chordate biology. At the same time, life science researchers lack the tools that allow them to appropriately collect, collate, and identify novel and reasonable connections between previously unidentified networks. We propose to leverage advances in graph theory computing, semantic web technologies and fundamental research in phylogenetic clustering to create a data mining environment that elucidates new knowledge in a network-centric fashion. We anticipate significant advances in the creation of graph-based database storage and interoperability.