



生物信息学研究中心

Center of Bioinformatics

学术报告

题目 : A Systems Biology Approach for Studying Gene Function and Pathway through Mining Functional Genomic Data

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时间 : 5月31日(星期三)下午3:00

地点 : 思源楼712室

摘要 : We have developed a number of computational approaches to infer gene function and pathway through utilizing various functional genomic data, including protein-protein interactions, protein complexes, microarray data, and genomic sequences. We quantify the relationship between functional similarity in the Gene Ontology biological process and functional data, and coded the relationship into a "functional linkage graph", where each node represents one gene and the weight of each edge is characterized by the Bayesian probability of function similarity between the two connected genes. We utilized the graph to predict gene function and signaling pathways in yeast and Arabidopsis. We also analyzed Arabidopsis tiling array data to predict anti-sense gene silencing and validated the prediction using EST data. Some anti-sense predictions were confirmed through RT-PCR.