



Fall 2008 CIS Colloquium Series

Functions of Intrinsically Disordered Proteins and Relationship with Human Disease Network

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Abstract: About 10 years ago we developed the first prediction based method to show that thousands of proteins lack fixed structure or are disordered (or unfolded) under physiological conditions. In this talk we will first briefly present the initial and our more recent predictor rated as the best model in disorder category at the seventh critical assessment of structure prediction experiments (CASP7). Next, we will describe how we used this predictor to provide a leap jump in answering a challenging question of understanding relationship between protein disorder and protein function by discovering that 238 Swiss-Prot functional categories are strongly positively correlated with predicted long intrinsically disordered regions. We will also describe a text mining method that can help further characterizations by identifying PubMed publications with relevant protein-disorder related experimental evidence. Motivated by observed strong correlation between intrinsic disorder and molecular functions known to be involved in cancer, we performed a large scale analysis of intrinsic disorder in genes implicated in Human Disease Network. We found significant differences in disorder content distributions for genes related to 20 human disease classes. Prediction of Molecular Recognition Features (MoRFs) suggests that intrinsic disorder in disease genes is mainly involved in protein-protein interactions. Genes related to several classes of diseases were found to have significantly higher occurrence of alternative splicing (AS), and given that we found AS regions to be highly disordered, we conclude that intrinsic disorder, together with AS, likely plays an important role in these classes of diseases.

Bio: Zoran Obradovic's research interests focus on developing data mining and statistical learning methods for knowledge discovery at large databases. He has authored about 200 articles addressing data analysis challenges in bioinformatics, medical informatics and other domains. For example, Obradovic co-authored a number of "first of" informatics studies on protein disorder providing strong support for a hypothesis that intrinsic protein disorder lies at the basis of signaling, regulation, and control. He also served as the team leader for the best predictor in protein disorder category at the fifth, the sixth and the seventh Critical Assessments of Structure Prediction experiments (CASP). Obradovic is currently journal editorial board member at seven journals. He was track chair at seven and program committee member at about 40 informatics conferences.

Location: 4th Floor Conference Room (Wachman 447)

Time: 3-4pm, Wednesday, September 17, 2008

Refreshments will be served!