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PREDAVANJE

Uncertainty Reduction in Gene Expression Data Analysis

(Smanjenje neizvesnosti u analizi genomskih podataka)

Predavač

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Abstract:

The traditional approach to molecular biology consists of studying a small number of genes or proteins that are related to a single biochemical process or pathway. A major paradigm shift recently occurred with the introduction of gene-expression microarrays that measure the expression levels of thousands of genes at once. These comprehensive snapshots of gene activity can be used to investigate metabolic pathways, identify drug targets, and improve disease diagnosis. However, the sheer amount of data obtained using the high throughput microarray experiments, and the complexity of the existing relevant biological knowledge is beyond the scope of manual analysis. Thus, the bioinformatics algorithms that help analyse such data are a very valuable tool for biomedical science. In this talk we propose several prior knowledge based methods for reducing uncertainty in gene expression data analysis. The proposed methods are illustrated with case studies related to cancer survival prediction and biomarker candidates selection.

About speaker:

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 signalling, 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. Last year Obradovic co-chaired 39th Symposium on the Interface of Statistics, Computing Science and Applications, ACM First International Workshop on Text Mining in Bioinformatics, and IEEE International Conference on Bioinformatics and Biomedicine. Currently he serves as the steering committee member of 2008 IEEE International Conference on Bioinformatics and Biomedicine and is the program chair of 2009 SIAM International Conference on Data Mining.

For more details see www.ist.temple.edu/~zoran

Branimir Reljin, Senior Member IEEE, IEEE SCG CAS-SP Chair