

Einladung zur Vortragsreihe *Algorithmische Bioinformatik*

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spricht über

Reconstruction and Extension of Signaling Pathways via Machine Learning

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Cellular signaling networks play a crucial role in biological processes like apoptosis or cell proliferation. Various diseases, especially cancer, are associated with dysregulated genes in specific signaling pathways. It is therefore of great importance to know, in which pathways a gene of interest is involved in. Valuable information for this purpose can be obtained from pathway databases, like KEGG. However, only a small fraction of genes is annotated with pathway information up to now. In contrast, information on contained protein domains can be obtained for a significantly higher number of genes, e.g. from the InterPro database. In the first part of my talk I address this issue by presenting a hierarchical classification model, which for a specific gene of interest can predict, in which KEGG pathways it is involved based on its protein domain signature. For signaling pathways it is even possible to forecast accurately the membership to individual pathway components.

In the second part of my talk I focus on reverse engineering of signaling networks. The advent of gene perturbation techniques, like RNA interference, has opened new perspectives for network inference methods during the last years. In combination with the measurement of downstream effects via DNA microarrays this approach can be used to gain insight into signaling pathways. Nested Effects Models (NEMs) are a probabilistic method to reverse engineer signaling cascades based on the nested structure of downstream perturbation effects. In this talk, I present an overview of this methodology with a comparison of so far proposed algorithms. As an application I present results on estimating the signaling network between 13 genes in the ER-_α pathway of human MCF-7 breast cancer cells.