

FAKULTÄT MEDIZIN Institut für Funktionelle Genomik Lehrstuhl für Statistische Bioinformatik

## Regensburg Lectures in Medical Bioinformatics

"How cancer remodels the structure of cellular networks"

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## <u>Abstract</u>

We tend to think of complex phenotypes, including disease, as being characterized by the expression of specific genes. However, we are increasingly recognizing that different phenotypes, and the gene expression profiles associated with them, are driven by distinct gene regulatory networks. Fully characterizing these phenotypes requires that we understand how regulatory networks differ between biological states, and how these structural changes can influence function. Using cancer as a model, I will present two ways in which the local and global structure of cellular networks is reorganized by disease. First, I will show that we can prioritize master regulators of cancer by computing their degree centrality in transcriptional networks and protein interaction networks. Second, I will introduce ALPACA, an algorithm for finding the biggest changes in modular structure between two transcriptional networks derived from different disease states. When applied to the analysis of ovarian tumors, this method allows us to detect both known and unexpected pathways associated with poor prognosis in ovarian cancer. Finally, I will present some initial work on relating networks in cancer cells to drug response.

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Host: Prof. Dr. Rainer Spang