Genome-wide statistical models of gene expression

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After a short introduction on genomics and the statistical challenges in the field, I will present three studies illustrating our research activities.

1. The interpretation of data-driven experiments in genomics often involves a search for biological categories that are enriched for the responder genes identified by the experiments. With Model-based Gene Set Analysis (MGSA), we tackle the problem by turning the question differently. Instead of searching for all significantly enriched groups, we search for a minimal set of groups that can explain the data.

2. Systems genetics with environment. We show how non-additive effects between genotype and environment can be exploited for causal inference in molecular networks. Using genome-wide perturbation assays in yeast, we experimentally demonstrate the validity of the approach.

3. Analysis of genome-wide occupancy data with bidirectional HMM. The genome has two strands with transcription going either direction depending on the location. We extended Hidden Markov Models to allow a local direction (forward or reverse) to be inferred. Applied on genome-wide occupancy data of transcription factors, we obtained a fine grain picture of transcription states in the yeast genome.

Biography: Julien Gagneur has a background in applied mathematics. His contribution includes the development of computational methods for a wide range of genomic application (metabolic and protein network, gene set enrichment, transcription) and insights into gene regulation mechanisms from genome-wide data (cis-regulatory modules, antisense expression). His lab, started in July 2012 at the gene center in Munich, focuses on computational approaches to understand mechanisms of gene regulation and their phenotypic impact from genome-wide assays.

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