Abstract

Deciphering gene regulation and its mode of function is one of the major challenges in systems biology. Many different factors impact gene regulation and many studies have been carried out to elucidate what triggers genetic transcription and how different genes impact each other. In the last decade it has been shown that epigenetic modifications have a major impact on gene regulation. New sequencing technologies have become available which allow analysis of complex relations in the living cell.
The innovations of RNA-seq and ChIP-seq made it feasible to perform whole genome sequencing for detection of novel splicing, quantification of transcriptional activity, detection of transcription factor binding sites and analysis of histone modifications. Integration of different *-omics* datasets is a promising approach to gain deeper insights in gene regulation.

In this thesis RNA-seq data and ChIP-seq data for *Saccharomyces cerevisiae* were analyzed. Clustering of the histone modification patterns was performed and a relation between histone modifications and their impact on expression was analyzed. The adaption of a genetic regulatory network reconstruction algorithm was evaluated and different approaches for integrative analysis were performed.
For a set of histone modifications a strong impact on gene expression could be established, as well as that rather combinations of modifications are responsible for regulation of gene expression than a single modification alone, i.e. that H3K9ac, H4K5ac, and H3K14ac act together in gene activation while H3K36me3 regulates the impact which H3K9ac, H4K5ac, and H3K14ac have on gene regulation.

Furthermore the use of the ARACNE algorithm on datasets other than gene expression data is discussed, and its mode of function is explained in detail. The different approaches for deduction of histone modifications impact on gene regulation which were used in this thesis are discussed in detail.