MASTER'S THESIS

Inferring regulatory subnetworks through the analysis of genome-wide expression profiles

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ABSTRACT

Transcription factors (TFs) are a diverse family of proteins that function by binding onto DNA, often as part of multi-unit protein complexes. Once bound, they can promote or inhibit the binding of RNA polymerase, thus regulating the genes' expression rates. In this way, TF control a multitude of constitutive, cell-specific, developmental, proliferative or homeostatic processes in the cells of all known organisms. Due to their central role in gene regulation a considerable number of human diseases have been associated with TF function, including metabolic, autoimmune disorders and cancer. Despite the progress over the last years, towards the identification of TFs' gene targets, either with experimental or *in silico* approaches, we are still far from reconstructing the hierarchy of transcriptional regulators from genome-wide data. In this work we are trying to overcome the existing limitations for the reconstruction and study of regulatory networks of TF-interaction and their subsequent use in enriching our understanding of key biological processes. Furthermore we are combining our approach with state of the art functional enrichment analyses in order to create a tool that will prioritize transcriptional and functional characteristics of a genome-wide expression experiment.

SUBJECT AREA: Bioinformatics

KEYWORDS: Transcription factors, regulatory networks, functional analysis, genome-wide expression analysis