



A study to identify interactions between transcription factors and non-housekeeping genes to determine expression regulation of cancer genes.

Amitava Karmaker, Kihoon Yoon, Stephen Kwek

Department of Computer Science

University of Texas at San Antonio



Overview

- The expression of non-housekeeping genes are predominantly regulated by transcription factors.
- To study gene expressions in normal and cancer cell types, microarray technology has been widely used.
- we perform a systematic study to determine which genes are regulated by which transcription factors and whether an over/under-expressed gene is caused by changes in expression levels of its regulatory transcription factors.



Preliminary Results

- The dataset we used consists of 26,260 unique genes for 115 normal tissue samples from 35 different tissues.
- We construct a family of subsets of genes that are co-expressed in a specific tissue or a group of tissues that exhibit similar function.
- We also found several groups of transcription factors that may act collectively as co-factors in gene regulation.



Discussion

- We are currently investigating the correlations among certain disease (cancer, diabetes etc.) genes and corresponding transcription factors.
- We believe our approach will help predict behavior of disease related genes and provide better insight to recognize gene regulation network.