# Eigenvectors of Gene Regulatory Networks and Gene Expression Profiles

**Yuhou Zhou**
Department of Computer Science & Electrical Engineering
Jacobs University University
28201, Bremen
`yu.zhou@jacobs-university.de`

## Abstract

One of the principal steps towards an understanding of bacterial gene regulation and therefore cellular function is to quantitatively assess, how well a given gene regulatory network "explains" given gene expression data set (i.e., the activity profile of all/many genes). An interesting mathematical approach for addressing this question is to compare spectral properties of the gene regulatory network (in particular, the eigenvectors of the graph) with the activity patterns of genes (which are vectors, where each node of the network is characterized by a real number). This is the task of the present project. Gene expression data will be taken from the GEO database. The gene regulatory network will be downloaded from RegulonDB.

## 1 Introduction

## 2 Related Work

## 3 Spectral Decomposition

## 4 Network Biology

## 5 Data Source

## 6 Experiments

## 7 Discussion

## 8 Summary

## Acknowledgements

## References