Analysis of mRNA data of patients with atherosclerosis[1]

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Abstract

1 Introduction

2 Weighted Gene Co-Expression Network Analysis

Weighted gene co-expression network analysis is a systems biology method for describing the correlation patterns among genes across microarray samples. Weighted correlation network analysis (WGCNA) can be used for finding clusters (modules) of highly correlated genes, for summarizing such clusters using the module eigengene or an intramodular hub gene, for relating modules to one another and to external sample traits (using eigengene network methodology), and for calculating module membership measures [2].

2.1 Selection of power

2.2 Module Detection

2.3 Interconnectivity analysis

3 Survival Analysis

Survival analysis examines and models the time it takes for events to occur and it typically examines the relationship of the survival distribution to covariates [4]. One application of survival analysis that will be focused on is Cox Model.

3.1 Cox Model

Cox model, also known as Cox proportional hazards model, is an example to survival models that are used in survival analysis of patient data.

4 Regression

This section describes regression models used for further analysis of mRNA data of patients. Regression models were used in order to compute how essential are given set of attributes (i.e., if patient is smoking or not, blood pressure level, level of diabetes etc.).

4.1 Logistic regression

Logistic regression is a type of probabilistic statistical classification model

5 Experiments

5.1 Setup of experiments

5.2 Results

6 Conclusion

7 Future Work

References

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[3] Storey JD and Tibshirani R. , "Statistical significance for genome-wide experiments". *Proceedings of the National Academy of Sciences", 100: 9440-9445.*

[4] John Fox, "Cox Proportional-Hazards Regression for Survival Data", *Appendix to An R and S-PLUS Companion to Applied Regression*

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