Microarray data analysis tool to improve understanding of disease phenotype

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Technology description

Summary

Medical diagnosis of diseases often involves computational analysis of gene expression data. While useful, studying individual genes and their expression levels provides limited information. This technology presents a software tool to study system level gene expression profiles. When studied concurrently, one can identify groups of genes that would act synergistically to lead to disease phenotypes. Studied together with the biological information that one already has about the diseased state, this would provide a much better understanding of the disorder. At the same time, identification of several genes affords a possibility of drug development against any one or a subset of genes to treat the disease. Therefore, this technology may not only improve our understanding of diseases, but also provide a potential avenue for rapid drug development.

Computational analysis of gene expression data at biological module level enables identification of groups of genes and their associated pathways in diseased state.

Microarray data analysis has been limited to focusing on individual genes and the role they play in diseased phenotypes. The computational tool presented in this technology enables the study of groups of genes and their associated pathways improving our understanding of the diseased state. This computational algorithm was used to study the pathways associated with pancreatic cancer using publicly available data. Gene modules identified using this tool were validated on a different data set also derived from publicly available data. Several of the gene modules identified using this tool are normally associated with ensuring cell suicide, or apoptosis, when the cell comes under oxidative stress. Malfunctioning in this module interrupts the apoptotic mechanism and leads to cancerous tissue growth. Identification of multiple gene modules associated with this pathway underscores the usefulness of the technique.

This technology has been used to provide gene modules associated with prostate cancer from publicly available gene expression data, which was validated by independently derived data.

Publications

V. Varadan, D. Anastassiou. Inference of disease-related molecular logic from systems-based microarrays analysis. PLoS Computational Biology, Vol. 2, Issue 6, June 2006, pp. 0585-0597.

Application area

Identification of gene modules associated with disease phenotypes

Drug development target identification

Tumorigenic gene module identification

Advantages

Improves identification of gene modules as opposed to individual genes participating in diseased states

Improves understanding of genetic disorders including cancer

Based on gene expression data, a main stream lab technique that is widely available

Does not require high end computational framework for implementation

Institution

Columbia University

Inventors

Dimitris Anastassiou

联系我们

叶先生

电 话：021-65679356
手 机：13414935137
邮 箱：yeyingsheng@zf-ym.com