Google-style ranking used to describe gene connectivity

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Using the technique known as "Gene Rank" (GR), Dartmouth's Norris Cotton Cancer Center investigator Eugene Demidenko, PhD, captured and described a new characterization of gene connectivity in "Microarray Enriched Gene Rank," published in *BioData Mining*. The effective computer algorithm can be used to compare tissues across or within organisms at great speed with a simple laptop computer.

"This paper introduces a new bioinformatics concept called Gene Rank (GR)," explained Demidenko. "GR is computed based on gene expression data and reflects how well a particular gene is connected to other genes. Our GR is built along the lines of PageRank used by Google to rank and display web pages upon key word search."

As a new scientific concept, GR looks at genetic networks from a different angle that may lead to new biological insights and formulation of new scientific hypothesis with important clinical applications. Many other studies in bioinformatics have tested their concepts using computer simulation. Demidenko tested GR on various de novo studies, resulting in plausible biological findings. For example, one series tested the complexity of genes in four stages of the development of rice, showing that it gradually increased over time. A subsequent test of Drosophila flies showed their genes to be more complex than rice, but less complex than human genes. These are expected findings, and meeting biological expectations is respected validation of concept.

Demidenko applied the GR concept to several cancer-related gene expression data sets, and discovered that disconnected genes in tumors are cancer associated. "It's a provocative statement, but we can say that cancer genes are lonely killers," said Demidenko. Further investigation revealed that GR of the same gene changes during cancer development, and that this can be used for disease prognosis as well as early cancer detection.

"The devised computer algorithm allows the computation of GR for 50 thousand genes and 500 samples within just a few minutes on a personal computer," said Demidenko. "Our GR can be used by researchers on a daily basis to investigate and characterize the dynamic complexity of living bodies. In particular, this will be helpful to characterize malignant tumors."

Future work for Demidenko includes applying the new GR to other data sets to determine how gene connectivity changes in the course of a tumor's development, and how gene connectivity varies across tumors.

More information: *BioData Mining*, www.biodatamining.org/content/8/1/2

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