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Statistical Comparison of Rank Lists and Molecular Profiles

Tech ID: 23010 / UC Case 2011-035-0

SUMMARY

The RRHO algorithm allows for the comparison of two gene expression signatures. Each signature is processed as a ranked list based on expression differences between two classes of samples. The signatures can be input either as raw expression data and sample and class labels, or as a pre-ranked gene list.

INNOVATION

Comparing independent high-throughput gene-expression experiments can generate hypotheses about which gene-expression programs are shared between particular biological processes. Current techniques to compare expression profiles typically involve choosing a fixed differential expression threshold to summarize results, potentially reducing sensitivity to small but concordant changes. We have developed a threshold-free algorithm called Rank-rank Hypergeometric Overlap (RRHO). This algorithm steps through two gene lists ranked by the degree of differential expression observed in two profiling experiments, successively measuring the statistical significance of the number of overlapping genes. The output is a graphical map that shows the strength, pattern and bounds of correlation between two expression profiles. The threshold-free and graphical aspects of RRHO complement other rank-based approaches such as Gene Set Enrichment Analysis (GSEA), for which RRHO is a 2D analog. Rank-rank overlap analysis is a sensitive, robust and web-accessible method for detecting and visualizing overlap trends between two complete, continuous gene-expression profiles.

APPLICATIONS

▶ Individuals interested in comparing genome-scale molecular data sets.

ADVANTAGES

▶ Fast, sensitive, and quantitative determination of the degree of overlap between two genome-scale ranked gene lists.
▶ Surveys the whole range of gene-expression changes and thus avoids missing the point of maximal overlap signal, as can occur when using fixed thresholds.
▶ In a single visualization and with minimal data pre-processing, the RRHO map indicates which of several possible overlap trends is present in expression signature comparisons and the strength of the observed trend.

STATE OF DEVELOPMENT

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PATENT STATUS

Patent Pending

RELATED MATERIALS

▶ Rank-rank hypergeometric overlap: identification of statistically significant overlap between gene-expression signatures. Nucleic Acids Research Volume 38, Issue 17:Pp. e169. - 07/01/2010

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OTHER INFORMATION

KEYWORDS

disease, rank list, GSEA, enrichment analysis, hypergeometric, statistics, comparison, gene expression, profile, hypothesis, high-throughput, concordant, overlap, correlation, data, analysis genetic profile mapping

CATEGORIZED AS

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