BMC Bioinformatics

POSTER PRESENTATION

Open Access

An automated resource for enhanced differential analysis

Kai Wang[1], Charles A Phillips[1], Arnold M Saxton[2], Michael A Langston[1*]

From 14th Annual UT-KBRIN Bioinformatics Summit 2015
Buchanan, TN, USA. 20-22 March 2015

Background

Differential Shannon entropy (DSE) and differential coefficient of variation (DCV) have proven to be effective complements to differential expression (DE) in the analysis of gene co-expression data[1]. Because DSE and DCV measure difference in variability, rather than mere difference in magnitude, they can often identify significant changes in gene activity not reflected in mere mean expression level.

Materials and methods

Thus, we have devised a general purpose, easy-to-use R package to calculate DSE and DCV. Dubbed *Entropy Explorer*, this package operates on two numeric matrices with identically labeled rows, such as case/control transcriptomic data. All functionality has been wrapped into one routine. With a single procedure call a user may select a metric, whether to display that metric, its raw and adjusted p-value, or both, whether to sort by metric or raw or adjusted p-value, and how many of the most highly ranked results to display.

Authors' details

[1]Department of Electrical Engineering and Computer Science, University of Tennessee, Knoxville, TN 37996-2250, USA. [2]Department of Animal Science, University of Tennessee Institute of Agriculture, Knoxville, TN 37996-4574, USA.

Reference

1.   Wang K, Phillips CA, Rogers GL, Barrenas F, Benson M, Langston MA:
     Differential Shannon Entropy and Differential Coefficient of Variation:
     Alternatives and Augmentations to Differential Expression in the Search
     for Disease-Related Genes. *International Journal of Computational Biology*
     and Drug Design 2014, 183-194.

* Correspondence: langston@tennessee.edu
[1]Department of Electrical Engineering and Computer Science, University of Tennessee, Knoxville, TN 37996-2250, USA
Full list of author information is available at the end of the article