

POSTER PRESENTATION

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# An automated resource for enhanced differential analysis

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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.

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Published: 23 October 2015

## 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.

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doi:10.1186/1471-2105-16-S15-P20

Cite this article as: Wang et al.: An automated resource for enhanced differential analysis. *BMC Bioinformatics* 2015 16(Suppl 15):P20.

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