

MEETING ABSTRACT

Open Access

Comparative studies of high-throughput biological graphs

Jonathan Reyles^{1*}, Charles Phillips²

From 10th Annual UT-ORNL-KBRIN Bioinformatics Summit 2011
Memphis, TN, USA. 1-3 April 2011

Background

The exponential growth of biological data has given rise to new and difficult challenges. Because large data is often dealt with, it is inefficient to infer from each individual characteristics of a given dataset. Bioinformaticists are developing quantitative techniques to analyze and interpret key data properties. Graph algorithms can provide powerful and intuitive insight on such properties [1]. Using this approach, we collect biological data from transcriptomic and protein-protein interaction (PPI) sources. These data can be represented as a correlation matrix, where the rows are the vertices and the columns are the edges. We will analyze these graphs, and describe their differing structural characteristics.

Materials and methods

We are using a high throughput method for graphical exploration of genomic and proteomic data. Experimental datasets are extracted from the public databases Biomart and Gene Expression Omnibus (GEO) [2,3]. R [4] and MATLAB are used to develop algorithms that compute and compare various structural characteristics. We specifically developed an in-house script used to output essential histograms and unweighted/weighted edges. We are currently developing protocols to analyze the comparison of transcriptomes and PPI sources.

Acknowledgements

We express gratitude towards Jay Snoddy and Michael Langston for the ideas that led us to pursue this bioinformatics investigation.

* Correspondence: jreyles@utk.edu

¹Graduate School of Genome Science & Technology, UT-ORNL, Oak Ridge, TN, 37830, USA

Full list of author information is available at the end of the article

Author details

¹Graduate School of Genome Science & Technology, UT-ORNL, Oak Ridge, TN, 37830, USA. ²Department of Electrical Engineering and Computer Science, University of Tennessee, Knoxville, Knoxville, TN, 37996, USA.

Published: 5 August 2011

References

1. Tor-Kristian Jensen AL, Komorowski J, Hovig E: A literature network of human genes for high-throughput analysis of gene expression. *Nature Genetics* 2001, **28**:21-28.
2. Smedley D, Haider S, Ballester B, Holland R, London D, Thorisson G, Kasprzyk A: BioMart – biological queries made easy. *BMC Genomics* 2009, **10**:22.
3. Barrett TD, Wilhite SE, Ledoux P, Rudnev D, Evangelista C, Kim IF, Soboleva A, Tomashevsky M, Marshall KA, Phillippy KH, Sherman PM, Muetterter RN, Edgar R: NCBI GEO: archive for high-throughput functional genomic data. *Nucleic Acids Res* 2009, **37**:D5-15.
4. Development Core Team: R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria.

doi:10.1186/1471-2105-12-S7-A12

Cite this article as: Reyles and Phillips: Comparative studies of high-throughput biological graphs. *BMC Bioinformatics* 2011 **12**(Suppl 7):A12.

Submit your next manuscript to BioMed Central and take full advantage of:

- Convenient online submission
- Thorough peer review
- No space constraints or color figure charges
- Immediate publication on acceptance
- Inclusion in PubMed, CAS, Scopus and Google Scholar
- Research which is freely available for redistribution

Submit your manuscript at
www.biomedcentral.com/submit

BioMed Central