

## **MetaGEX: a systems biology meta-analysis toolkit and data repository with web server interface**

**Keywords:** systems – Bioconductor – meta-analysis – transcriptome analysis –

**Abstract:** The number of software resources from the Bioconductor project is expanding dramatically. In addition, public repositories such as the Gene Expression Omnibus from the US NCBI have made available vast amounts of experimental data that can be compared to new experimental results. However, the necessary computational skills to obtain these data (in their highly-structured formats) and apply the available algorithms (in the R statistical programming language) can be a daunting task requiring highly-specialized expertise. Here, we present a comprehensive resource that integrates many Bioconductor packages for data analysis and clustering to provide a comprehensive gene expression analysis within a single resource. Automated comparison across experiments is made available to permit identification of differences or commonalities between experimental results and enable hypothesis generation. Because communication between the bioinformatician and non-computational colleagues is critical, a web interface (using the Django project Python code) was implemented that supports all aspects of the implemented Bioconductor code including search and meta-analysis of GEO experiments, and comparison of private gene expression measurements to public experiments. Availability: <http://marray.cmdr.ubc.ca/metagex/>

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