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C22: *GEAUniversal*: A Web-Based Universal Gene Expression Atlas System for Managing, Analyzing and Sharing Large-Scale RNA-Seq-Based Transcriptome Data

Tuesday, January 16, 2018

11:45 AM - 12:00 PM

📍 California

We successfully developed *GEAUniversal*, which is a Web-based Universal Gene Expression Atlas System for Managing, Analyzing and Sharing Large-scale RNA-seq-based Transcriptome Data. The system is capable of hosting data from multi-species. *GEAUniversal* was implemented using Python, Flask and MySQL. The transcriptomic data are organized in hierarchical fashion, according to species, experiments, treatments and biological samples. *GEAUniversal* provides three core functions: 1) Expression Profile Query - to query the expression levels of genes in user-defined samples. We implemented an on-the-fly data normalization algorithm to enable querying gene expressions across experiments as the RNA-seq data normalization procedure is dependent upon user-selected dataset. 2) Differential Expression (DE) Analysis - to find differentially expressed genes between two samples or treatments using DESeq2 package. The returned differentially expressed genes can be filtered, sorted, and also displayed as bar or line charts. *GEAUniversal* can further identify enriched gene ontology (GO) terms in the list of user-defined genes from previous DE analysis. This function provides valuable insights to further identifying and analyzing biological pathways of the genes of interest. 3) Gene Co-Expression Analysis - to discover genes with similar expression pattern in user selected samples. The *GEAUniversal* also integrates a suite of scripts to simplify the system installation, including metadata and transcriptomic data population. To date, the *GEAUniversal* has been successfully deployed to empower several GEA projects, for example, the Gene Expression Atlas for Cultivated Alfalfa (*Medicago sativa*) at the Diploid Level (CADL) (www.alfalfatoolbox.org/atlasCADL/) and MtSSP-Atlas: A Gene Expression Atlas for Studying the Small Signaling Peptides in *Medicago truncatula* (mtsspdb.noble.org/atlas/).

Authors

[Xinbin Dai](#)

Noble Research Institute

[Zhaohong Zhuang](#)

Noble Research Institute

[Clarissa Boschiero](#)

Noble Research Institute

[Patrick X. Zhao](#)

Noble Research Institute



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