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http://bioinformatics.udel.edu/seminars

MONDAY, December 1, 2014
3:30pm
DBI Room 102

WebGIVI: A Website Visualization of Gene and *i*Term
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http://bigbird.anr.udel.edu/~sunliang/project_web/index.php

ABSTRACT: The challenge of high throughput transcriptome studies is to present the data to researchers in an interpretable format. In many cases, the outputs of such studies are gene lists which are then examined for enriched biological concepts. One approach is to associate genes and informative terms (iTerm) that are obtained from the biomedical literature using eGIFT. However, examining large lists of *iTerm* and gene pairs is a challenge. We have developed WebGIVI, a user-friendly web interface (http://raven.anr.udel.edu/~sunliang/webgivi/index.php), which was built via Cytoscape and Data Driven Document (d3.js) JavaScript library and can be used to visualize gene and *i*Term pairs. WebGIVI can accept EntrezGene list that will be used to retrieve a gene symbol and *iTerm* list. This list can be resubmitted to visualize the gene-*i*Term pairs using Cytoscape, BioLayout or Concept Map methods. A variety of visualization layout methods are available in WebGIV including force directed, tree and circle. Visualized Graph on the website can also be saved as PNG format.

VIROME and MgOl: Optimizing Functionality by Leveraging Metadata
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ABSTRACT: Metadata collected to capture sample and environmental descriptors are crucial in interpreting the information gleaned from metagenomic sequencing as it is the environmental context of a sample that gives value to the sequence-based results. Comprehensive metadata allows the investigator to test hypotheses using evolutionary or ecological genomic approaches, to group, sort, and search by similar sources or environments, and to accurately describe the massive data volumes generated through metagenome or metatranscriptome sequencing. The VIROME (Viral Informatics Resource for Metagenomic Exploration) pipeline was developed to provide functional, taxonomic, and environmental homology evidence for viral sequences, and to provide visualization capabilities and useful binning and comparison tools. VIROME takes advantage of environmental and viral-centric databases, making accurate environmental metadata essential to optimizing the tool's capabilities. Metadata, including environment descriptors, plays an even larger role in viral metagenome analysis since the majority of sequences will only find a homolog in previously studied metagenomes. This project evaluates the environmental metadata captured in VIROME and its associated environmental database, MgOl (Metagenomes OnLine), against applicable standards for metadata. Improvements are designed and implemented to 1) retrofit the current VIROME and MgOl databases to better reflect metadata standards, 2) implement a new VIROME submitter interface to collect compliant metadata for future submissions, and 3) design ways to better leverage metadata in VIROME and MgOl. Potential impacts of this project include increased visibility of the VIROME tool due to adoption of standard environmental description ontologies, increased collaboration with other resources also using detailed and standard metadata, and potential user preference for VIROME as a viral metagenome exploration tool.