Preeti Bais, J Mol Genet Med 2014, 8:3
http://dx.doi.org/10.4172/1747-0862.S1.002

OMICS Group Conferences
Accelerating Scientific Discovery

2nd International Conference on
Genomics & Pharmacogenomics
September 08-10, 2014 DoubleTree by Hilton Hotel Raleigh-Brownstone-University, USA

"mMAP" database and metabolomics data analysis pipeline for mouse functional genomics experiments

Preeti Bais
The Jackson Laboratory for Genomic Medicine, USA

Metabolomics is a newer omics technology that can help in generating a more comprehensive view of a biological system when combined with the genomic, transcriptomic and proteomic technologies. However, the bioinformatics infrastructure to analyze and interpret metabolomics data still faces many barriers. For example, there is lack of standardization in nomenclature for metabolites, limited availability of dedicated experiment databases and the lack of metadata reporting standards hamper the reproducibility and sharing of data across researchers, and finally there are very limited automated data analysis pipelines that the researchers can use to incorporate metabolomics data into their research. We present a web based database and automated data analysis pipeline "mMAP" that addresses these issues for mass spectrometry based metabolomics experiments in mice. mMAP provides metabolomics data and the metadata along with web based automated tools that use many univariate and multivariate data analysis algorithms to generate both tabular and graphical outputs. The portal is linked with other external databases like KEGG, PubMed, LipidMaps, MouseCyc, etc. so a user can make biological interpretation and integrate the metabolomics data with other omics data by generating a list of genes and proteins associated with metabolic pathways of interest. This external database links can also be used to retrieve the Gene Ontology (GO) and Mammalian Phenotype annotations for these genes along with curated disease associations between mouse genes and their human orthologs based on data from the On-Line Mendelian Inheritance in Man (OMIM).

Biography

Preeti Bais is an Associate Scientist at the computational sciences group at the Jackson Lab's new research institute at University of Connecticut - JAX Genomics Medicine (JGM). She holds a PhD in Bioinformatics and Computational Biology. She is interested in applying metabolomics for the functional genomics analysis; human embryonic (hES) and induced pluripotent stem (IPS) cells based assays for drug toxicity screening, and cancer drug efficacy testing using orthotropic mouse models of cancer.

preetibais@hotmail.com