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Integrative Approach for the Analysis and Visualization of Static or Dynamic Omic Data, Including Genomic, Proteomic, Gene Expression, and Metabolic Data

Tech ID: 25209 / UC Case 2011-813-0

BRIEF DESCRIPTION

The technology is a method for analysis and mapping of a broad range of omic data. It features maps and visualizes interactions between omic data, such as how the circadian metabolome, transcriptome, and proteome operate in concert. With this technology, users can use non-public and public data, per tissue/organ data and data across multiple conditions.

FULL DESCRIPTION

This invention is a system that can create an integrated map of different types of omic data using both non-public data and public data from literature or databases. The system can build interaction networks between static and dynamic data, per tissues/organ data, and data across multiple conditions, making inferences about and visualizing such interactions, including time varying behavior under different conditions, development, etc.

The system is applicable to a range of biological processes, and a prototype called "CircadiOmics" has already been developed for the circadian cycle to better understand how circadian metabolome functions on the backdrop of already known oscillating events and metabolic activities within the liver. "CircadiOmics" integrates metabolic pathway and reaction information, known oscillating gene expression and periodicity information previously reported high-resolution DNA microarrays, protein-protein interactions from multiple protein-protein interaction databases and putative transcription factor-enzyme relationships, along with the metabolomics profile for wild-type and Clock^{-/-} mouse samples.

Metabolite identification is a critical aspect of understanding the chemical processes of cells. In the past, metabolite identities were studied in depth individually, as they pertained to metabolic pathways and circadian gene transcription. This individualized approach limits exploration and mapping of metabolites that relate to both metabolism and circadian rhythm and lacks the high throughput analysis needed to determine where interfaces between the two areas exist. This invention makes possible high-throughput mapping of the entire metabolome and analysis and visualization of its complex relationship to the proteome, the transcriptome, and also pathways and gene regulation.

SUGGESTED USES

ADVANTAGES

- » A comprehensive map detailing hundreds of metabolites superimposed within networks of supporting enzymes and transcription factors has been realized.

STATE OF DEVELOPMENT

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OTHER INFORMATION

CATEGORIZED AS

- » **Biotechnology**
 - » Bioinformatics
- » **Computer**
 - » Software
- » **Engineering**
 - » Engineering
- » **Research Tools**
 - » Animal Models
 - » Bioinformatics
 - » Cell Lines
 - » Other

A prototype has been created for the circadian rhythm in liver cells. Prototype is available through the Circadiomics website.

RELATED CASES

2011-813-0

PUBLICATIONS

<http://www.igb.uci.edu/~pfbaldi/?page=publications>

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