








Gazing into the Metaverse: Automated contextualization of metabolic data

This manuscript was automatically generated on February 10, 2020.

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Abstract

Metabolism is a complex network of perturbations to essential chemical and enzymatic reactions; however, the past century has seen a largely reductionist approach to understanding this system. While previously this approach was necessary due to technological limitations, current computer age technological advances allow us to survey, model, and explore the biological details of individual cells and populations of cells. Yet, our ability to contextualize and extract the full extent of these enormous datasets continues to lag and often results in focusing on only a handful of entities from a dataset. We therefore created Metaboverse, a multi-omic computational analysis framework and application for the automated extraction of regulatory events from user multi-omic data within the metabolic network and interactive visualization of the data. This framework will revolutionize our ability to more holistically understand temporal metabolic shifts and gene-metabolite intra-cooperativity, as well as ensure we obtain the maximum amount of information from our data. Metaboverse is freely available under a GPL-3.0 license at <https://github.com/Metaboverse/>.

Introduction

Results

Discussion

Methods

Results

References
