

Metabolic model and data-driven exploration linking genotypes to phenotypes

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Introduction

Current bioinformatics trends show a shift toward understanding an organism as a functional, metabolic entity rather than only through the lens of its genetic landscape.

Due to data complexity of genome annotation and phenotypic results it is difficult to evaluate an organism in the context of its genome coupled with its metabolism.

Functional genomic studies are supplemented by in silico genome-scale metabolic models to explore the metabolism of an organism using Flux-Balance Analysis (FBA).

Based on the organism's metabolicassociated genes, these models allow the exploration of metabolic flux through an entire metabolic network.



Methods

Funding

Genomics



annotated using the RAST platform.

Figure 2. Phylogenetic tree of Vibrio samples. The average nucleotide identity was calculated between the 10 genomes. **Organism names** were identified by RAST.



Metabolic Models







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genomic contexts

GitHub: http://linsalrob.github.io/PyFBA PyPI: https://pypi.python.org/pypi/PyFBA

http://edwards.sdsu.edu/pmanalyzer





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Next Steps

Data visualizations to explore the FBA results in the context of genomics, such as network-visualization software (e.g., Cytoscape)

Develop quantitative metrics that help explain phenotypic responses in

Identify sources within models responsible for biomass flux diversity

References

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