

Pantograph: A template-based method for genome-scale metabolic model reconstruction

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Resumen

Genome-scale metabolic models are a powerful tool to study the inner workings of biological systems and to guide applications. The advent of cheap sequencing has brought the opportunity to create metabolic maps of biotechnologically interesting organisms. While this drives the development of new methods and automatic tools, network reconstruction remains a time-consuming process where extensive manual curation is required. This curation introduces specific knowledge about the modeled organism, either explicitly in the form of molecular processes, or indirectly in the form of annotations of the model elements. Paradoxically, this knowledge is usually lost when reconstruction of a different organism is started. We introduce the Pantograph method for metabolic model reconstruction. This method combines a template reaction knowledge base, orthology mappings between two organisms, and experimental phenotypic evidence, to build a genome-scale metabolic model for a target organism. Our method infers implicit knowledge from annotations in the template, and rewrites these inferences to include them in the resulting model of the target organism. The generated model is well suited for manual curation. Scripts for evaluating the model with respect to experimental data are automatically generated, to aid curators in iterative improvement. We present an implementation of the Pantograph method, as a toolbox for genome-scale model reconstruction, curation and validation. This open source package can be obtained from: pathtastic.gforge.inria.fr.

Palabras clave

Palabras clave de autor: [Metabolic modeling](#); [genome-scale reconstruction](#); [model validation](#)

KeyWords Plus: [YEAST YARROWIA-LIPOLYTICA](#); [SYSTEMS BIOLOGY](#); [NETWORK](#)

[RECONSTRUCTION](#); [BIOCHEMICAL](#)

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