

## MPA\_09

Evaluation of methods for the reconstruction of specific models from omics data

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Recent efforts have allowed the development of genome-scale metabolic models for several organisms, including humans. These models have been used to predict cellular metabolism under the framework of constraint-based modeling. The application in health related research has spanned the issues of drug discovery, biomarker identification and targeting diseases such as cancer or Alzheimer. However, the human organism includes several cell types, each one with a different metabolic profile and functions. So, it is imperative to develop tissue-specific metabolic models. This challenge was addressed by several approaches, namely the Model-Building Algorithm, Metabolic Context specificity Assessed by Deterministic Reaction Evaluation and Task-driven Integrative Network Inference for Tissues methods. All these approaches use a generic model as a template and integrate evidences from omics data, literature and/or network analysis to infer the tissue specific metabolic model. Nevertheless, their results have not yet been adequately and critically evaluated and compared. We analysed the consistency between several omics data sources and reconstructed metabolic models of hepatocytes using different methods and distinct data sources as inputs. The results show that omics data sources have a poor overlapping and, in some cases, are contradictory. Additionally, the hepatocyte metabolic models generated are dependent on the combination of method and omics data source. Finally, we conclude that reliable methods for a priori omics data integration are required to support human cells models reconstruction.