# Using MetRxn for metabolic model reconstruction, flux elucidation and redesign

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**Project Goals: This project aims to organize and disseminate standardized metabolite and reaction information to improve metabolic modeling by accurately describing reaction stoichiometry, directionality, atom mapping from reactants to products, and gene to protein to reaction relations. This resource is deployed for microbial, multi-tissue and multi-organism metabolic model reconstruction, metabolic flux elucidation using labeled substrates (MFA) and computational strain design.**

MetRxn is a standardized non-redundant searchable collection of published metabolic models and databases from a wide variety of organisms. The current MetRxn 2.0 update includes recently published metabolic data for a total of 112 metabolic models and 8 metabolic databases. The number of distinct reactions that have been mapped is greater than 20,000 and MetRxn contains tools that allow users to download atom mapping data for each reaction. In this talk, we will elaborate on new features of MetRxn 2.0 (http://www.metrxn.che.psu.edu/) including atom mapping information across all reactions and enhanced integration with other databases. We will describe how this resource can impact genome-scale metabolic model reconstruction by providing curated reaction and metabolite content. Progress towards the development of a multi-tissue metabolic model for maize, rapid generation of cyanobacterial models and metabolic modeling of microbial communities will be briefly highlighted. Reaction atom transition information in MetRxn can rapidly be leveraged to create genome-scale atom mapping models. Efforts towards resolving metabolic fluxes at a genome-scale and computational challenges with current flux elucidation tools will be described and the impact on flux elucidation fidelity will be quantified.

Existing computational strain design approaches relying solely on stoichiometry and rudimentary constraint-based regulation overlook the effect of metabolite concentrations and substrate-level enzyme regulation while identifying metabolic interventions. This may lead to suggested interventions that cannot be implemented. To remedy this, we developed the k-OptForce procedure which integrates all available kinetic descriptions of metabolic reactions with stoichiometric models to sharpen the prediction of intervention strategies for improving the bio-production of a chemical of interest. In addition, we have used the Ensemble Modeling (EM) procedure for constructing kinetic models of core *E. coli* metabolism consistent with available measurements (metabolomic & fluxomic).

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