Quantitative metabolic modeling at the Joint BioEnergy Institute (JBEI)

Héctor García Martín,[1,2,3]* (hgmartin@lbl.gov), David Ando,[1,2] Zak Costello,[1,2,3] Tyler Backman,[1,2,3] Jennifer Gin,[1,2] Jason Brice,[1,2] Christopher Beitel,[1,2] William Morrell,[1,4] Garrett Birkel,[1,2] Teresa Lopez,[1,2] Mark Forrer,[1,4] Nathan Hillson,[1,2,3] Christopher Petzold,[1,2,3]

[1]DOE Joint BioEnergy Institute, Emeryville, CA; [2]Lawrence Berkeley National Laboratory, Berkeley, CA; [3]DOE Agile BioFoundry, Emeryville, CA; [4]Biotechnology and Bioengineering and Biomass science and Conversion Department, Sandia National Laboratory, Livermore, CA

https://www.jbei.org

Project Goals:

The Quantitative Metabolic Modeling (QMM) directorate at the Fuels Synthesis Division is devoted to developing models of metabolism which are both quantitative and predictive, in order to improve biofuel production in a rationally directed fashion. Here, we present our work in three different thrusts: machine learning modeling, mechanistic modeling, and software development. Machine learning modeling is used to systematically improve biofuel production without a detailed understanding of pathway dynamics and, separately, is combined with kinetic modeling in order to predict time-dependent metabolomic data from measured protein levels. Mechanistic models involving ^{13}C Metabolic Flux Analysis for genome-scale models are used to produce actionable items for metabolic engineering that have improved fatty acid production by 70%. All these methods are supported by a suite of software tools that improve productivity: the Experiment Data Depot (EDD) stores data and metadata for a variety metabolic engineering experiments. EDD allows easy visualization of these data and its access in a standardized manner for use with modelling approaches. Arrowland (https://public-arrowland.jbei.org/) provides an intuitive and interactive tool to explore -omics data and make predictions on possible metabolic engineering approaches. The JBEI QMM library is a python open source library that provides the tools for all the aforementioned capabilities.

This work was part of the DOE Joint BioEnergy Institute (http:// www.jbei.org) supported by the U. S. Department of Energy, Office of Science, Office of Biological and Environmental Research, and was part of the Agile BioFoundry (http://agilebiofoundry.org) supported by the U.S. Department of Energy, Energy Efficiency and Renewable Energy, Bioenergy Technologies Office, through contract DE-AC02-05CH11231 between Lawrence Berkeley National Laboratory and the U. S. Department of Energy.