Integrated BioCAD Toolchain Enables Search for Experimentally Validated Components

Hector A. Plahar,1,2,3 Mark Forrer,1,2,4 Jacob Coble,1,2,3 William Morrell,1,2,4 Jay D. Keasling,1,3 Paul D. Adams,2,5 Hector Garcia Martin,1,3 and Nathan J. Hillson1,2,3,6* (njhillson@lbl.gov)

1Fuels Synthesis and 2Technology Divisions, DOE Joint BioEnergy Institute, Emeryville, CA; 3Biological Systems and Engineering Division, Lawrence Berkeley National Laboratory, Berkeley, CA; 4Applied Biosciences and Engineering Center, Sandia National Laboratory, Livermore, CA; 5Molecular Biophysics and Integrated Bioimaging Division, Lawrence Berkeley National Laboratory, Berkeley, CA; 6DOE Joint Genome Institute, Walnut Creek, CA.

Project Goals:

Biological computer-aided design (bioCAD) tools are gaining widespread adoption in commercial, academic, and government research settings. As more and more tools emerge, there is an increasingly urgent need to integrate them into a larger toolchain that aggregates functionality and data. Researchers at JBEI engineer plants, enzymes, and microbes to produce biofuels. To enable them to design biological systems without knowing the intricate details of the constituent components, we have integrated several of our bioCAD tools (DeviceEditor, DIVA, ICE, EDD Analytics, and EDD). The specifications of these biological components are experimentally validated to meet particular design criteria (e.g., promoters with high transcriptional levels in E. coli).

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