JBEI Computational Biology Core

Dylan Chivian[1,2,3*], Greg D. Friedland[1,2,4], John T. Bates[1,2,3], Paramvir S. Dehal[2,3], Marcin P. Joachimiak[2,3], Keith Keller[2,3], Morgan N. Price[2,3], Jason K. Baumohl[2,3], Adam P. Arkin[1,2,3,5*] Presenting (DCChivian@lbl.gov); [1]DOE Joint BioEnergy Institute, Berkeley, CA, 94720; [2]Virtual Institute for Microbial Stress and Survival, Berkeley, CA 94720; [3]Lawrence Berkeley National Laboratory, Berkeley, CA, 94720; [4]Sandia National Laboratory, Livermore, CA, 94551; [5]University of California, Berkeley, CA, 94720

The Computational Biology Core Group in the Technology Division of the Joint BioEnergy Institute (JBEI) is responsible for data integration and comparative, evolutionary, and functional genomic analysis for the purpose of engineering microbes for biofuel production. Leveraging the VIMSS MicrobesOnline web resource (http://www.microbesonline.org) for comparative and evolutionary genomics and analysis of microarray, proteomic, and metabolomic data sets, we are extending the supported microorganisms to include bioenergy-relevant fungi and algae as well as integrating capabilities to allow for pursuit of questions specific to bioenergy challenges.

Computational analysis and biological engineering requires an understanding of the biology at several scales. The efforts of the Computational Biology Core are therefore geared towards creating tools to facilitate our research at the level of components, systems, cells, and communities. For example, biological degradation of plant cells walls is accomplished by enzymes containing multiple domains that in combination confer specificity and activity. We are studying the combinations nature has employed to allow for making our own combinations. At the atomic scale, we are computationally designing the structures of proteins for increased stability under industrial conditions. At the system level, we are working to discover metabolic pathways for biofuel production as well as the genetic factors involved in tolerance to harsh biomass pretreatment conditions and resistance to biofuel toxicity. To aid efforts in synthetic pathway engineering, we are building a framework for analyzing functional data in a metabolic network context. At the cellular level, we are using evolutionary studies with phenotype data and genetic analysis to engineer cell lines that are better suited to industrial conditions or have superior yields of the desired biofuel. Finally, at the community level, discovery of genes from environmental samples will expand the repertoire of enzymes we can engineer for biomass degradation under varying conditions. Our approach is to analyze the environmental genomic data in a phylogenetic context to allow for a higher-resolution annotation of the role of each enzyme, as well as to obtain an evolutionary picture of the key functional genes and organisms in each ecosystem.

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, through contract DE-AC02-05CH11231 between Lawrence Berkeley National Laboratory and the U.S. Department of Energy.

DISCLAIMER

This document was prepared as an account of work sponsored by the United States Government. While this document is believed to contain correct information, neither the United States Government nor any agency thereof, nor the Regents of the University of California, nor any of their employees, makes any warranty, express or implied, or assumes any legal responsibility for the accuracy, completeness, or usefulness of any information, apparatus, product, or process disclosed, or represents that its use would not infringe privately owned rights. Reference herein to any specific commercial product, process, or service by its trade name, trademark, manufacturer, or otherwise, does not necessarily constitute or imply its endorsement, recommendation, or favoring by the United States Government or any agency thereof, or the Regents of the University of California. The views and opinions of authors expressed herein do not necessarily state or reflect those of the United States Government or any agency thereof or the Regents of the University of California.