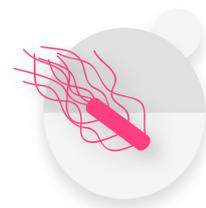


DD-DeCaF



Bioinformatics Services for Data-Driven Design of Cell Factories and Communities

Concept and approach

DD-DeCaF brings together leading academic partners from five European universities with five innovative European companies to address the challenge of building a comprehensive design tool. The academic partners will develop cutting edge methods to design cell factories and communities for biotechnological applications. Three innovative SMEs will convert these advanced methods to software tools. These tools will be tested and applied to real world cell factory development projects by end-user partners.

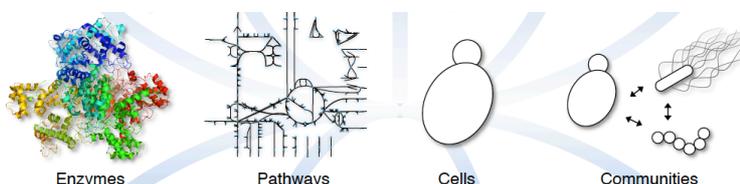
Horizon 2020

This project has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 686070.



What is DD-DeCaF?

The European Commission has awarded a four-year collaborative project on data-driven design of cells and microbial communities for applications ranging from human health to sustainable production of chemicals. With advances in synthetic biology genomes can now be edited at unprecedented speed allowing making multiple changes in the same genome at the same time. This increases the need for computational tools to design cells and communities of cells analogous to the tools used in Computer Aided Design of cars, buildings and other man-made objects. In biotechnology these design tools need to be able to use existing large-scale databases to discover new parts and place them in the functioning context of the cell. The tools need to be easily accessible and provide an intuitive visual map of the cell to the biotechnologists working in the lab on building better cell factories and communities.



Publications

In 2016 four articles were published as part of the DD-DeCaF project:

- Huerta-Cepas J. *et al*, Fast genome-wide functional annotation through orthology assignment by eggNOG-mapper, bioRxiv, 2016
- Machado D. *et al*, Stoichiometric Representation of Gene-Protein-Reaction Associations Leverages Constraint-Based Analysis from Reaction to Gene-Level Phenotype Prediction, PLoS Comp Biol, 2016
- Jensen K. *et al*, Optlang - An algebraic modeling language for mathematical optimization, The Journal of Open Source Software, 2016
- Xavier J. *et al*, Integration of Biomass Formulations of Genome-Scale Metabolic Models with Experimental Data Reveals Universally Essential Cofactors in Prokaryotes, Metabolic Engineering, 2016

Meetings

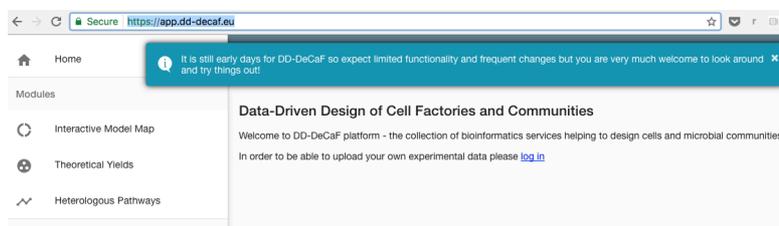
The official kick-off meeting was held in Brussels on 7-8 March 2016 at creoDK and hosted by the project coordinator DTU. Mr Ioannis Vouldis, project officer of the European Commission, was also present where he presented an introduction to Horizon2020 and its best practices.

The second consortium meeting was held in Heidelberg on 26-27 September 2016 at EMBL. All the consortium partners were present to discuss the latest project developments, initial results and next developments.

The next consortium meeting will be held at Lyngby (Denmark) on 11-12 May 2017 and hosted by DTU.

Platform is now live!

A minimal version of the platform is already available at app.dd-decaf.eu to promote the early adoption of the framework and collect feedback from potential users. Try it now!



First workshop in September

The first workshop will take place in Delft in September 2017, hosted by DSM, and it is being designed to address an audience composed by both students and industry. A brief introduction to modeling and simulation methods will be provided, an overview of DD-DeCaF platform and current status, and other resources developed by the consortium will be presented. More information to come soon!

Resources

Github

Follow the latest code developments in our Github repository. github.com/dd-decaf

Webcasts on Youtube

The first webcast is now available in the [Youtube channel](#) of the project, presenting the component for pathway visualization that is already available in the beta version of the platform.



For update information please visit the project website and follow us on twitter.

Consortium

