

# DD-DeCaF

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

**Markus Herrgård**

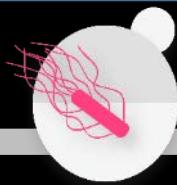
DD-DeCaF Project Coordinator

Professor MSO & Director, iLoop Translational Unit

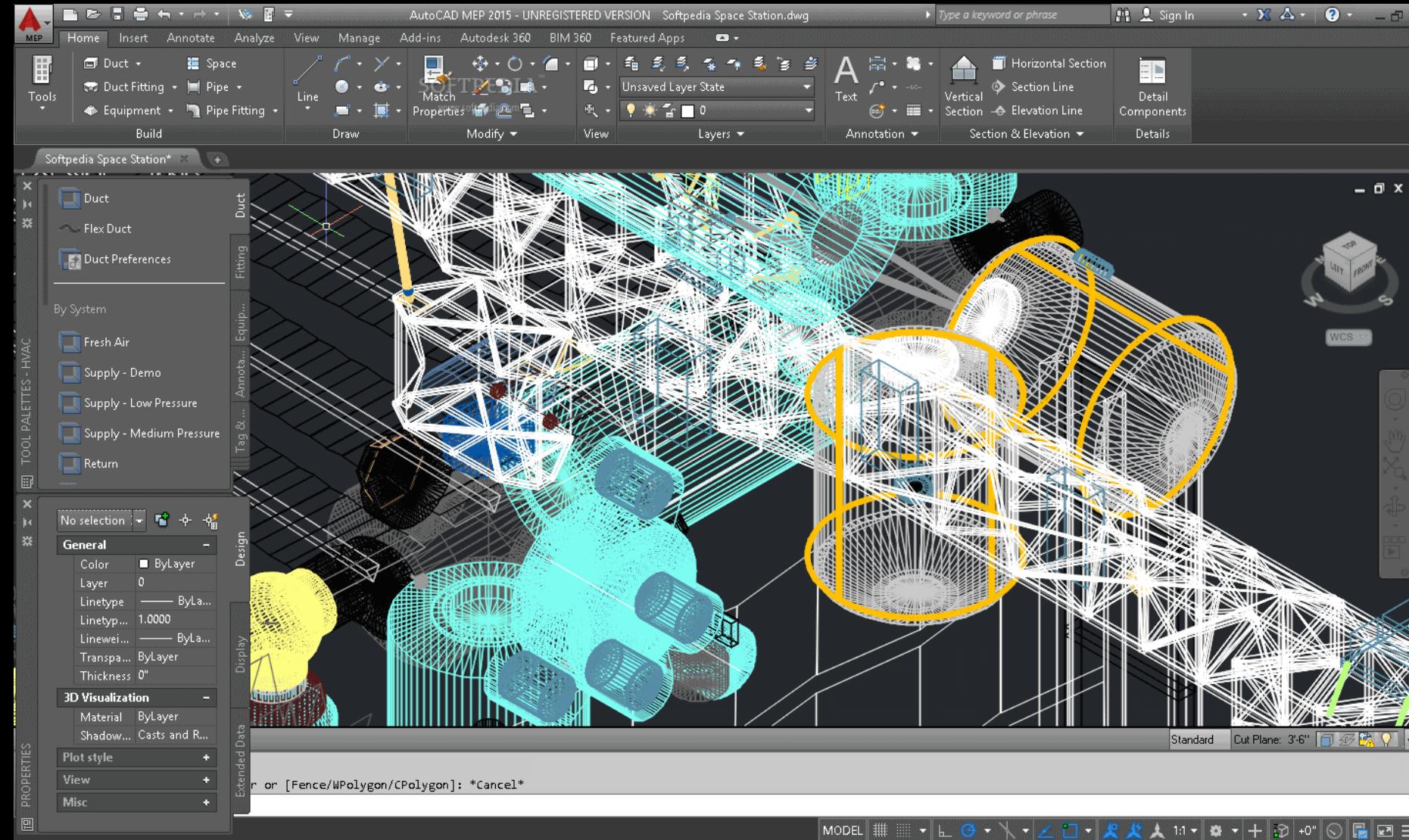
The Novo Nordisk Foundation Center for Biosustainability

Technical University of Denmark





# Design in Traditional Engineering Fields



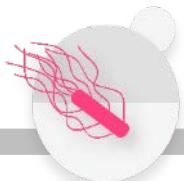


# Design in Biological Engineering

Our models are mostly qualitative and lack predictive power needed for engineering design

Omics data can help in obtaining more predictive models and enables improved design

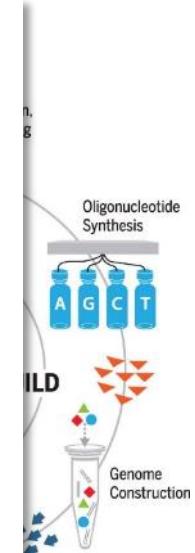




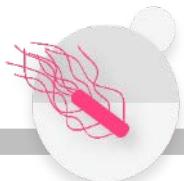
# But we can even design full bacterial genomes, right?

In the supplementary methods section for the paper:

**A. Oligonucleotide Design Software.** The oligonucleotide design software searches for a combination of parameters. These include dsDNA assembly stages, maximum fragment size, maximum number of oligos assembled per assembly stage and appended vector sequences. The software yields overlapping oligos that do not exceed 80% of the total oligo length, a size equal to half the oligo length and dsDNA fragments. In the exception of the eighth molecules which contain unique vector sequences, a unique set of vector sequences (40) are appended to the 5' and 3' ends of each resulting oligo. These appended sites are unique to each sequence. These appended sites are used for cloning or PCR amplification and insert recombination. The software exposes overlaps for subsequent assembly stages (40).

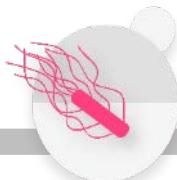


The oligonucleotide software was initially implemented as two WordPerfect macros: 1) Overlapping fragments.wcm, and 2) Oligonucleotides.wcm. The code for these macros is presented below. A streamlined version of the software is embedded in the Archetype® software package, which is commercially available through Synthetic Genomics, Inc.

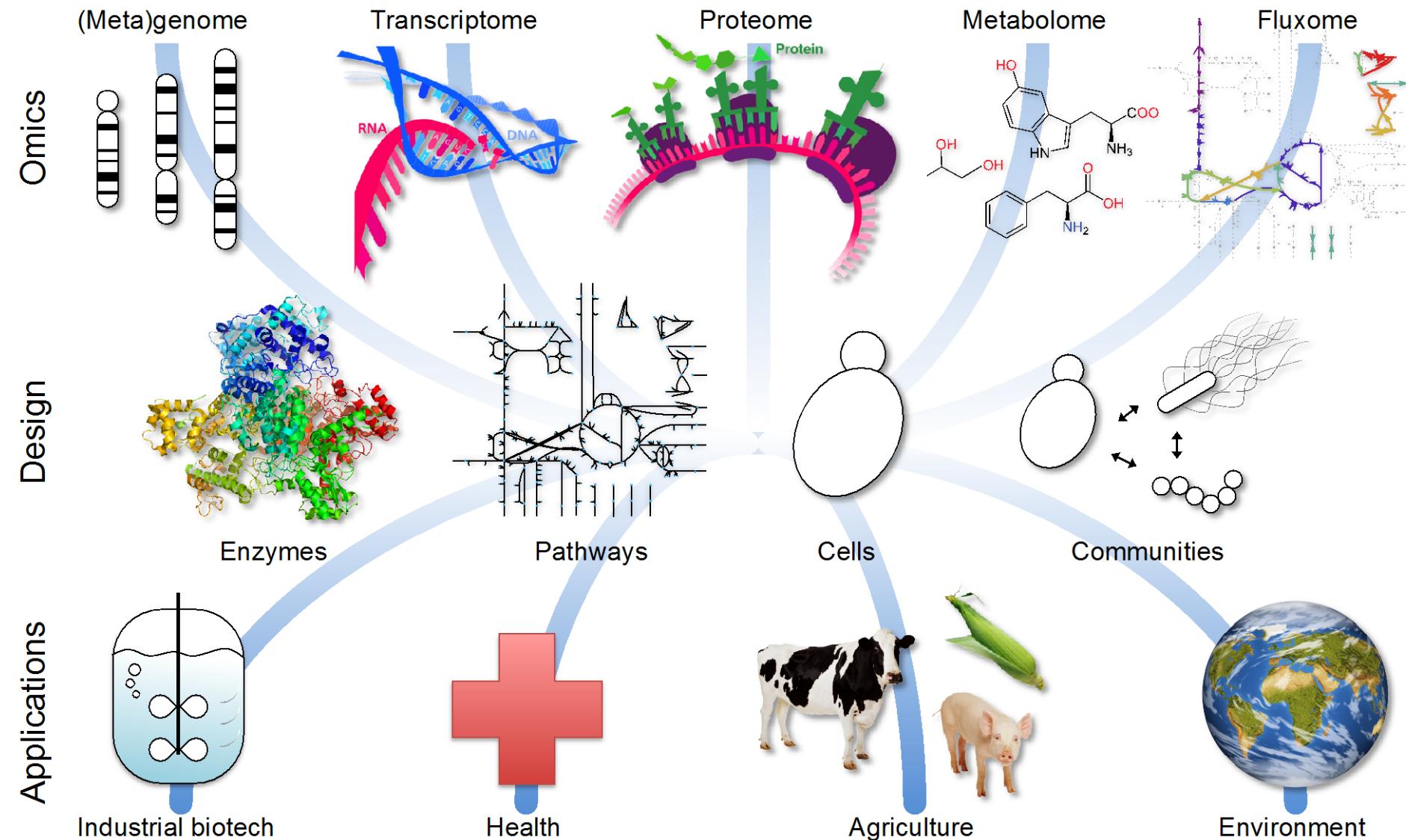


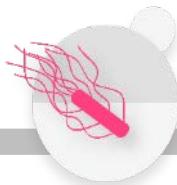
# Design complexity

Level	Length	Number of choices	Unit	Design space
DNA	50	4	Base pair	$10^{30}$
Protein	300	20	Amino acid	$10^{390}$
<i>Pathway</i>	<b>15</b>	<b>5</b>	<i>Part</i>	<b><math>10^6</math></b>
<i>Organism</i>	<b>1000</b>	<b>3</b>	<i>Gene</i>	<b><math>10^9</math></b>
<i>Community</i>	<b>3</b>	<b>50</b>	<i>Organism</i>	<b><math>10^{23}</math></b>
Process	10	5	Unit operation	$10^5$
Industry	1	10000	Chemical product	10000



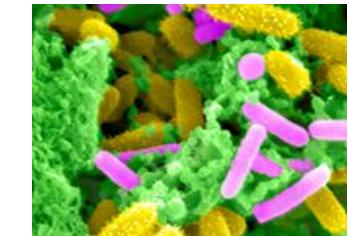
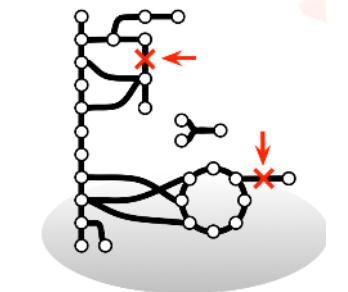
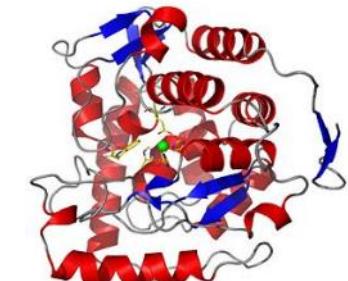
# Concept: From data through design to biotech products

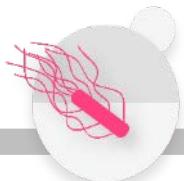




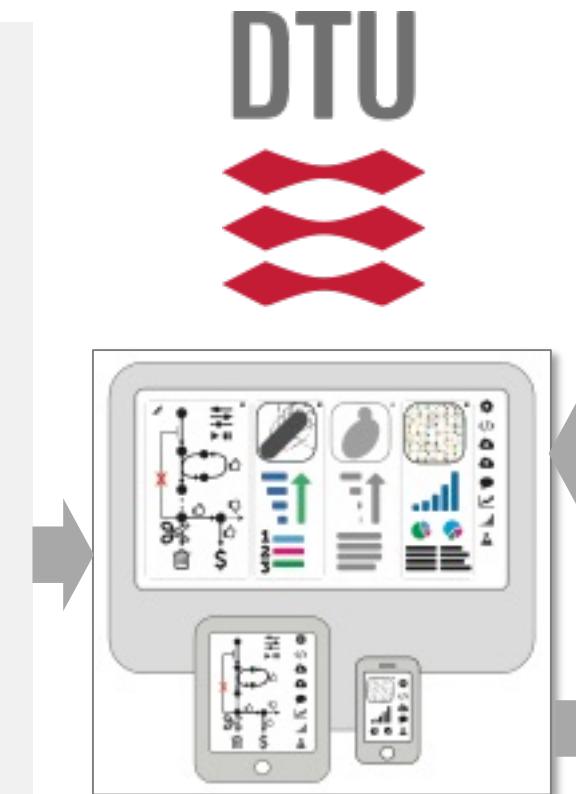
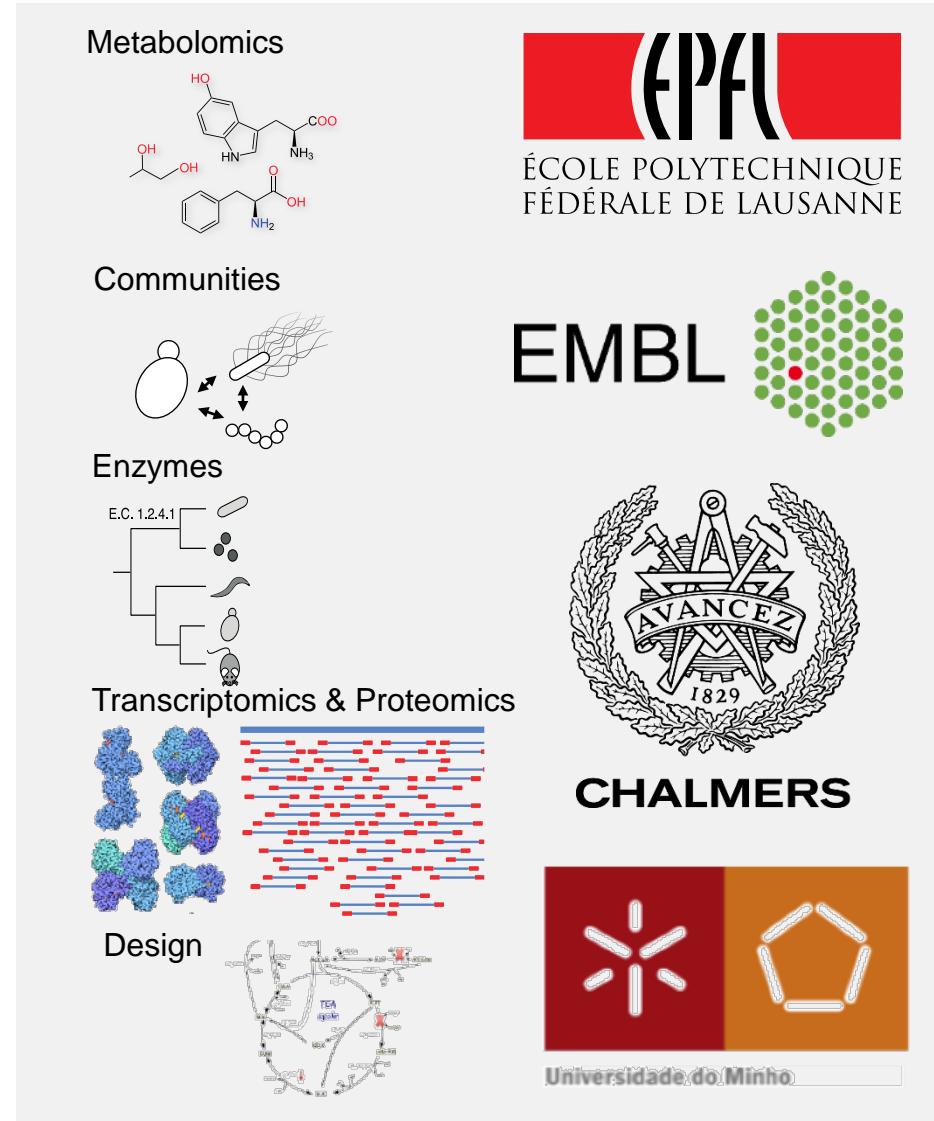
# Application areas

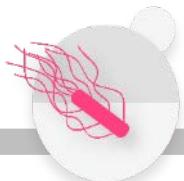
- 1. Design of novel enzymes and biochemical pathways by mining large-scale metagenomic data**
- 2. Design of cell factories for chemical and protein production** by integrating multiple omics data types using next generation genome-scale models
- 3. Design and analysis of microbial communities** in industrial, health and environmental applications by building community-scale models based on metagenomic data



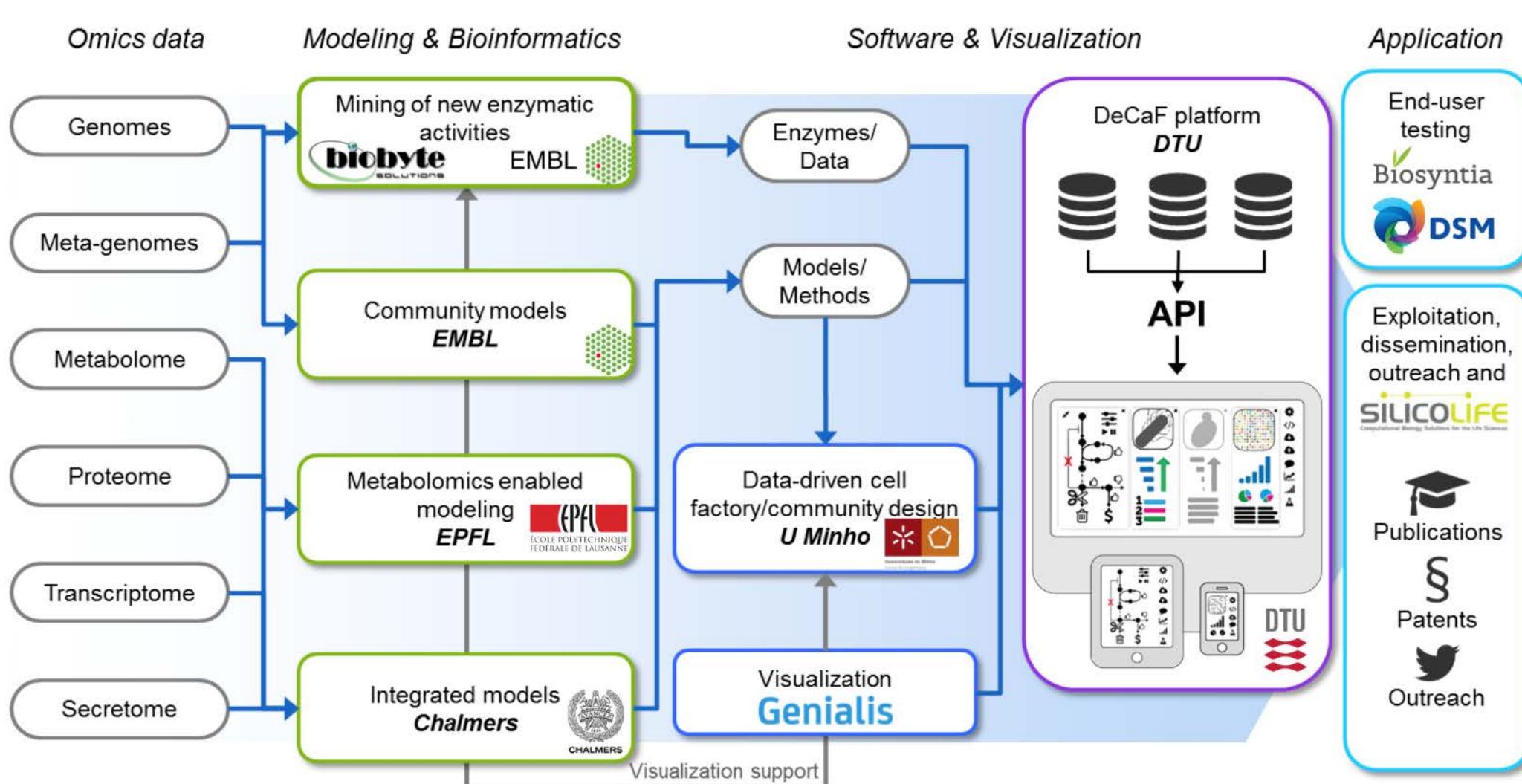


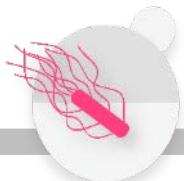
# Consortium





# Work plan





# Tools & databases associated with the project

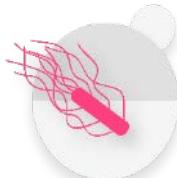


eggNOG-mapper

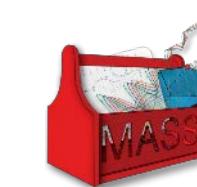
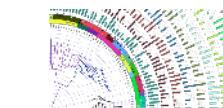
NGLess

optlang

cameo

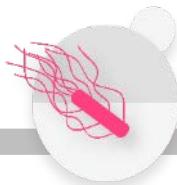


DD-DeCaF

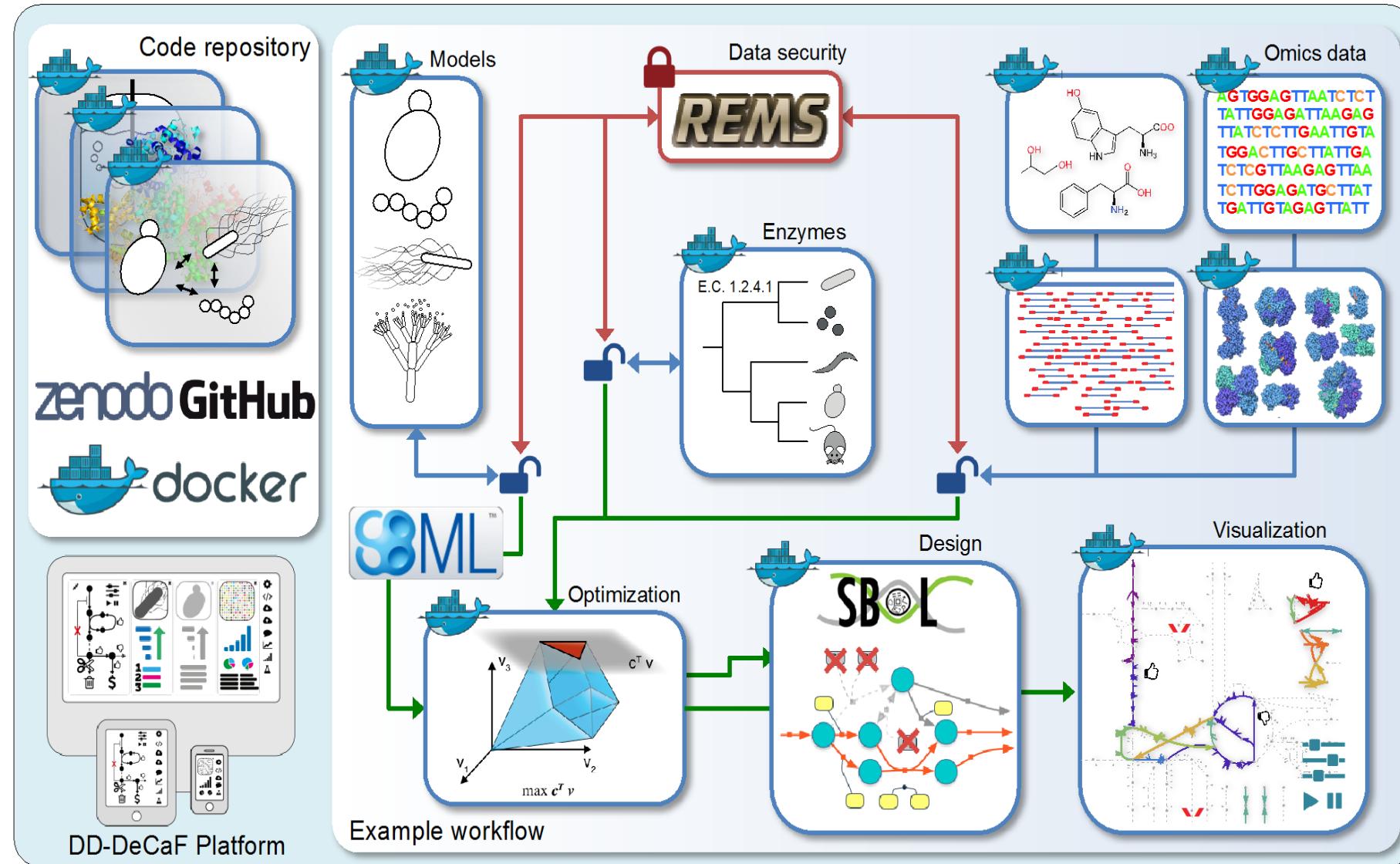


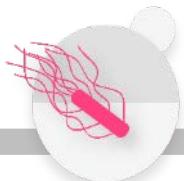
iTOL





# Platform architecture: Modular microservices



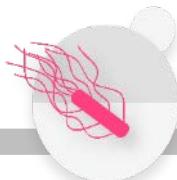


# Three key ideas of the project

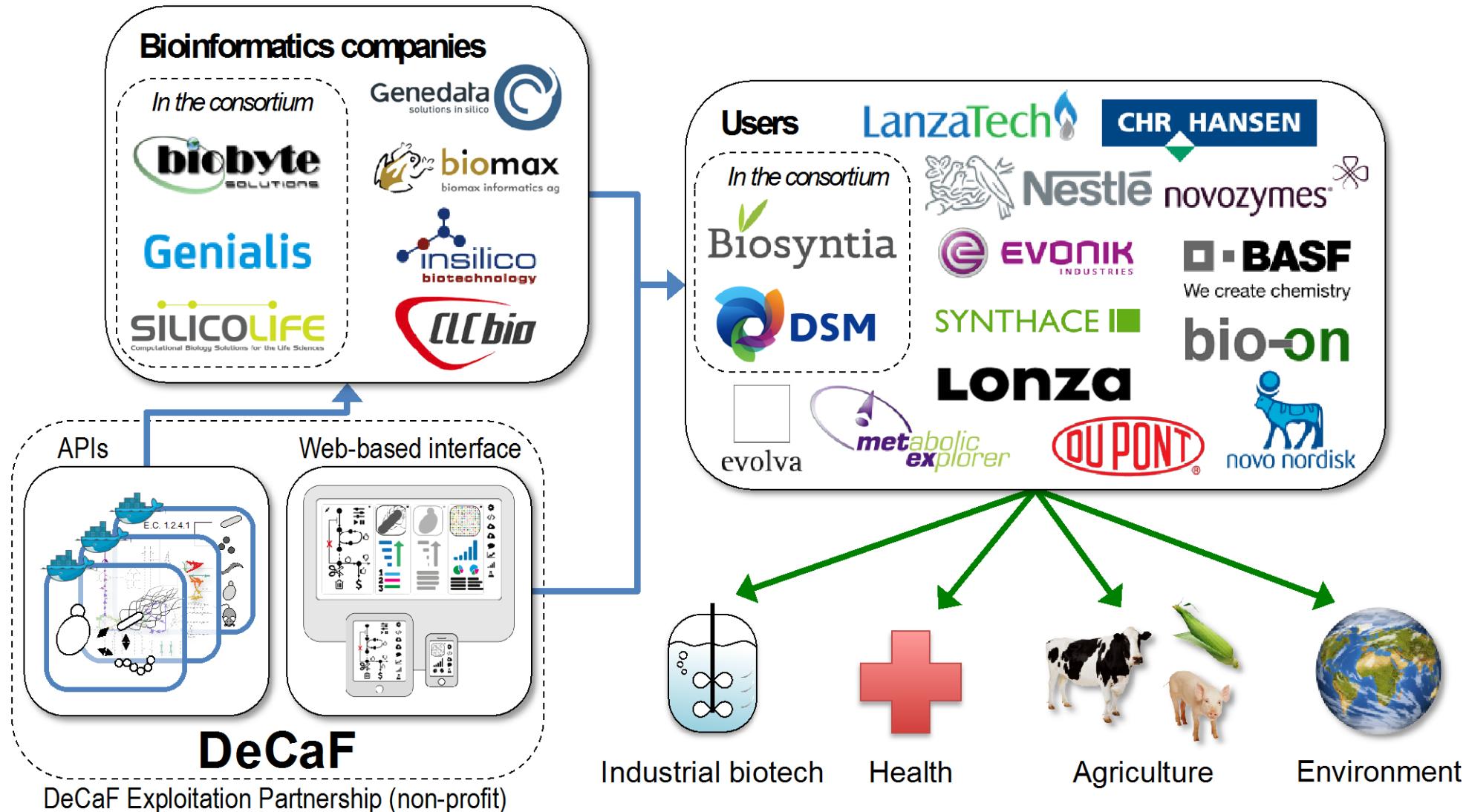
Use of genome-scale models as the scaffolds to integrate diverse data types

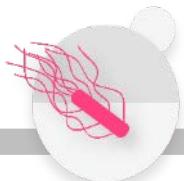
Use of microservices to integrate diverse databases, tools and methods

Direct involvement of end-user partners as part of the project

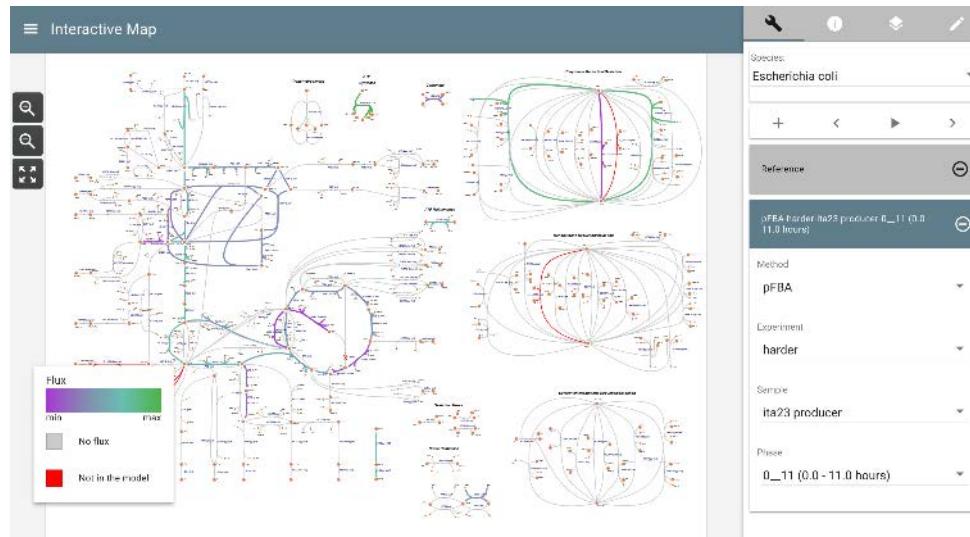


# Exploitation model

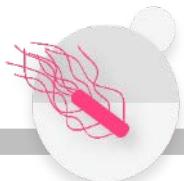




# Following the DD-DeCaF project



**Website:** <http://dd-decaf.eu/>  
**App:** <https://app.dd-decaf.eu>  
**Twitter:** [@dddecaf](https://twitter.com/dddecaf)  
**Youtube channel:** [https://www.youtube.com/channel/UCg\\_EU0w-OI2YhMm94wUq-Jw](https://www.youtube.com/channel/UCg_EU0w-OI2YhMm94wUq-Jw)



# Acknowledgements



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Manager



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