

*DD-DeCaF: Bioinformatics Services for Data-Driven
Design of Cell Factories and Communities*

DD-DeCaF Workshop at DSM

Session 4: Cameo and DD-DeCaF platforms

Nikolaus Sonnenschein

niso@biosustain.dtu.dk

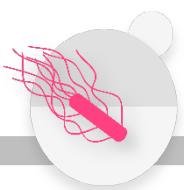
DTU



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

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

DEMO 11-Sep-2017



Download slides

<https://goo.gl/zEJg7v>



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

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

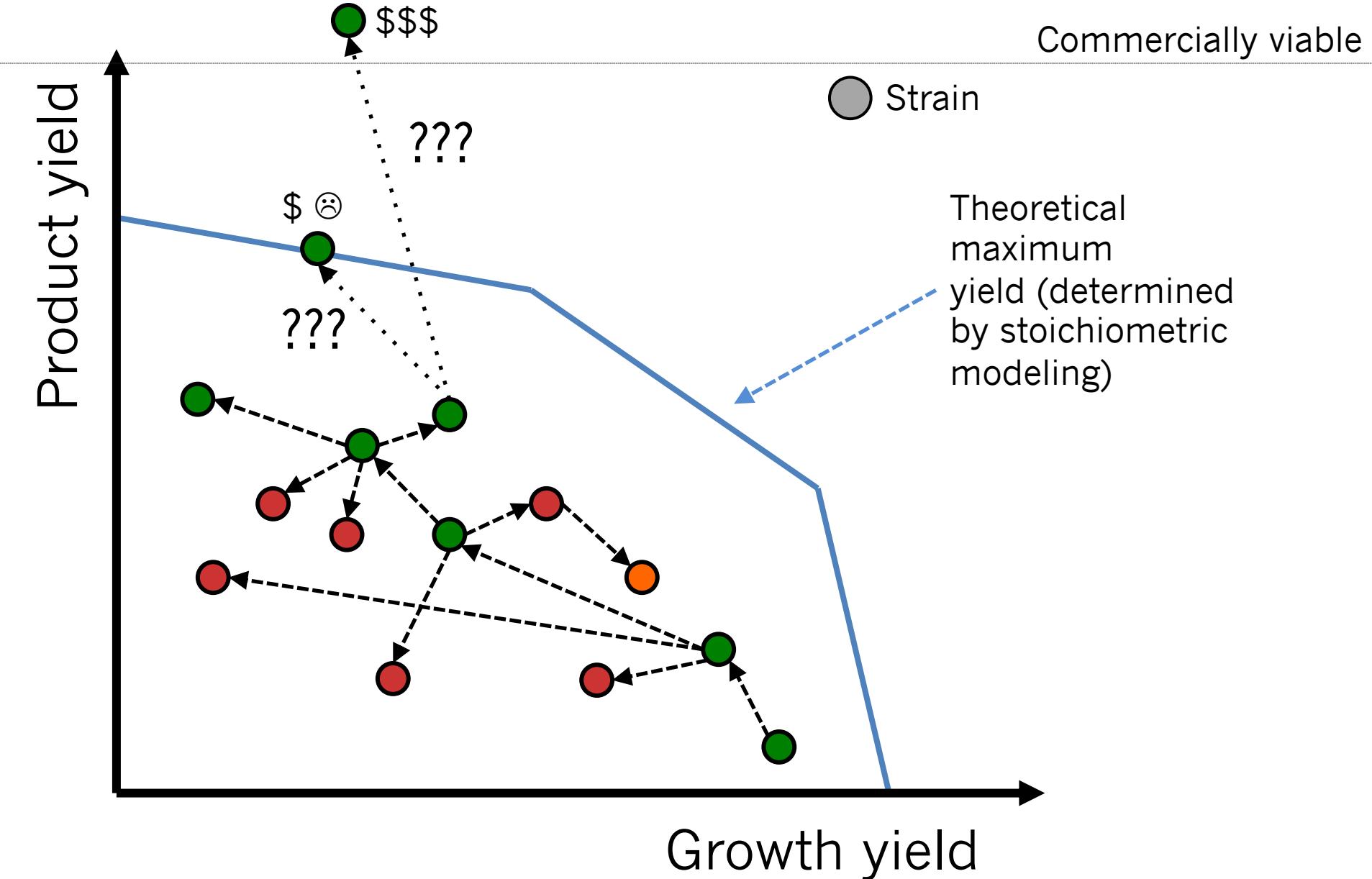
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DTU Biosustain

The Novo Nordisk Foundation Center for Biosustainability

The strain engineering problem

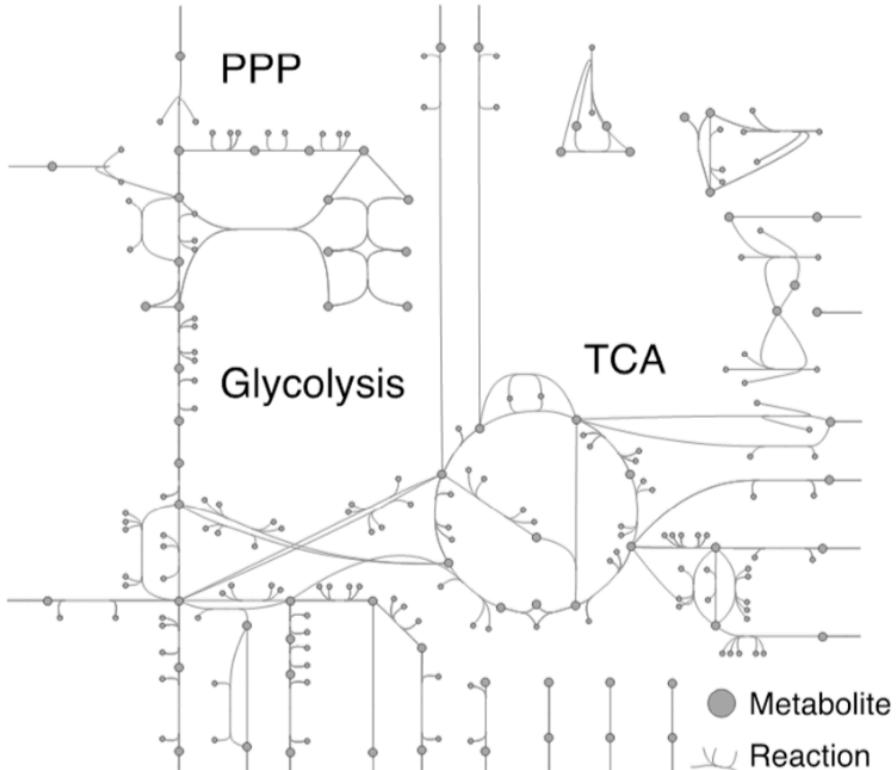


Introduction to the field

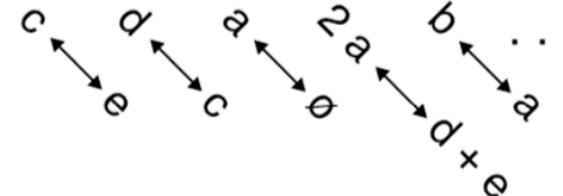
Genome-scale metabolic modeling

Math ...

a Metabolic pathway



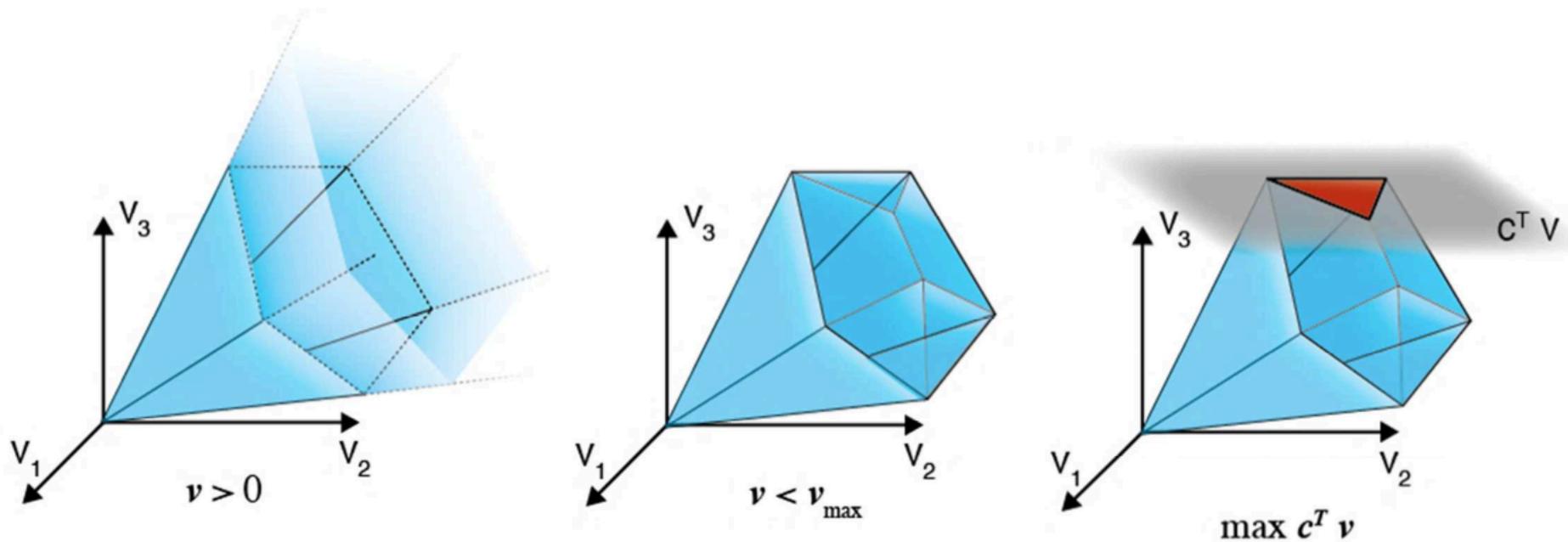
b Stoichiometric matrix



$$\frac{dx(t)}{dt} = S v = 0, \dots)$$

More math ...

- Following constraints can be superimposed
 - Mass balance: metabolite production and consumption rates are equal ($\mathbf{S} \boldsymbol{\nu} = \mathbf{0}$)
 - Thermodynamics: e.g. irreversibility of reactions
 - Flux capacities: bounds on flux e.g. nutrient uptake rates
- Optimize a biological objective (e.g. biomass production)



Hands-on session

Workshop

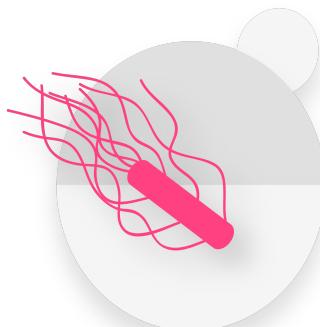


Constraint-based metabolic modeling with Python



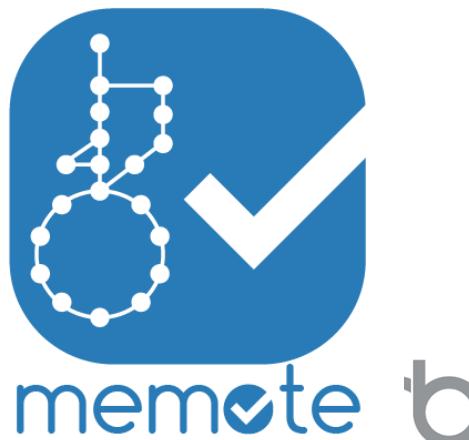
Computer-aided metabolic engineering

cameo



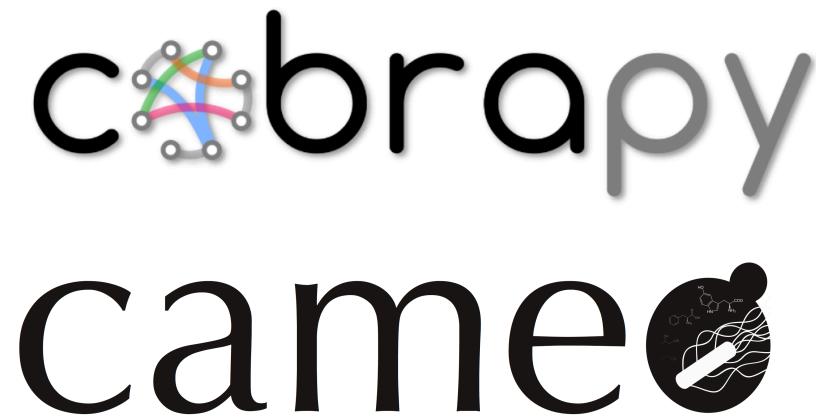
DD-DeCaF: Data-Driven Design of Cell Factories

Metabolic Model Tests



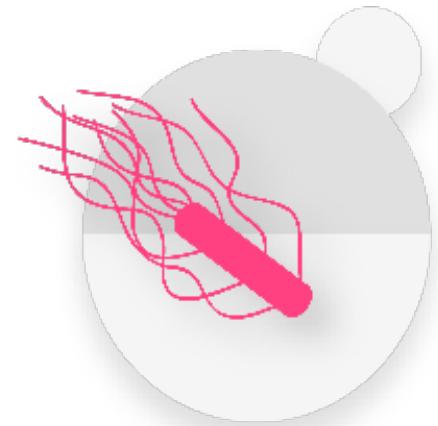
So many tools ...

- Programming skills required
- Detailed understanding of models required



To be covered tomorrow

- No programming skills required
- No in-depth understanding of models required



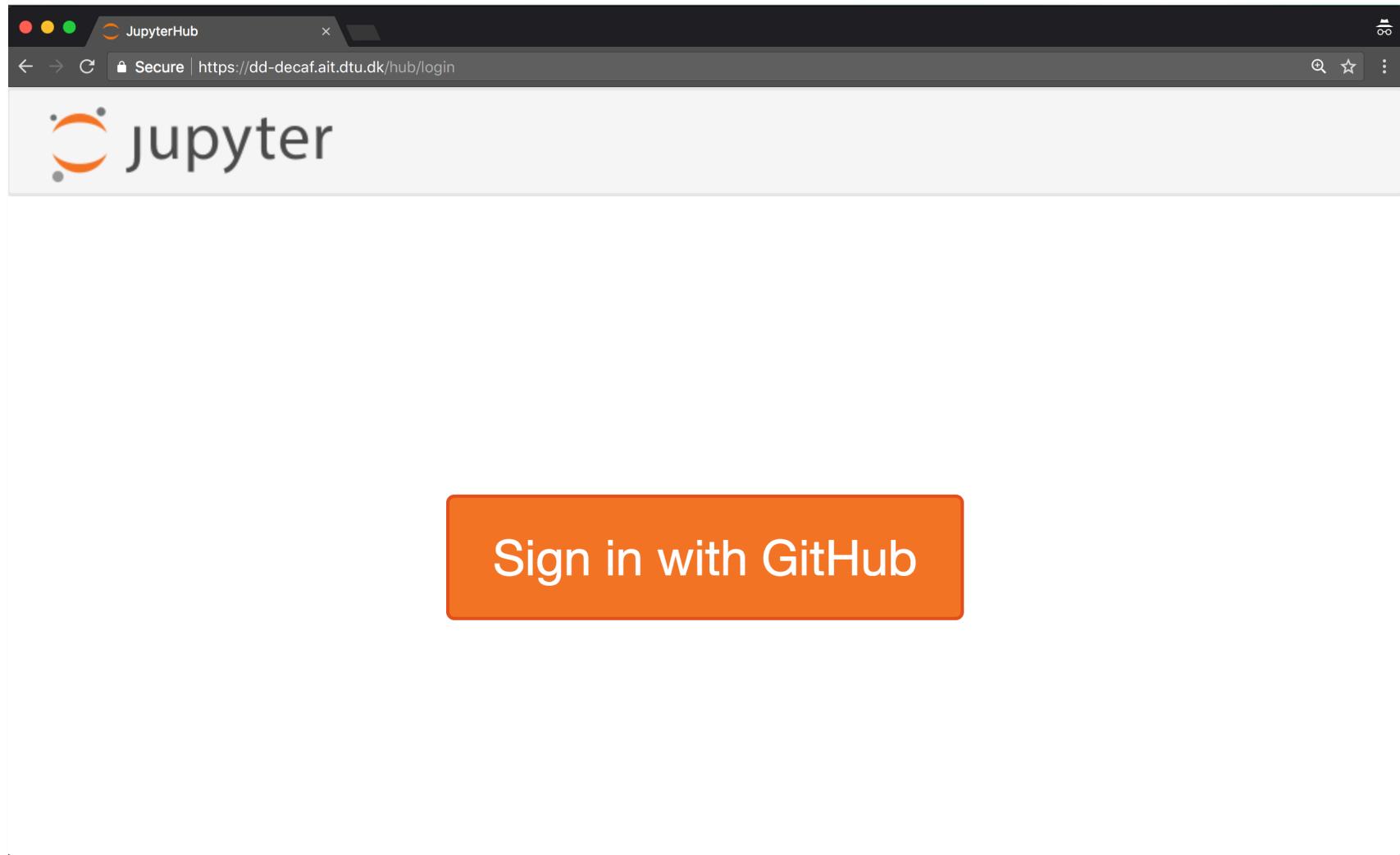
app.dd-decaf.eu

Poweruser capabilities & learning barrier

<https://dd-decaf.ait.dtu.dk/>



<https://dd-decaf.ait.dtu.dk/>



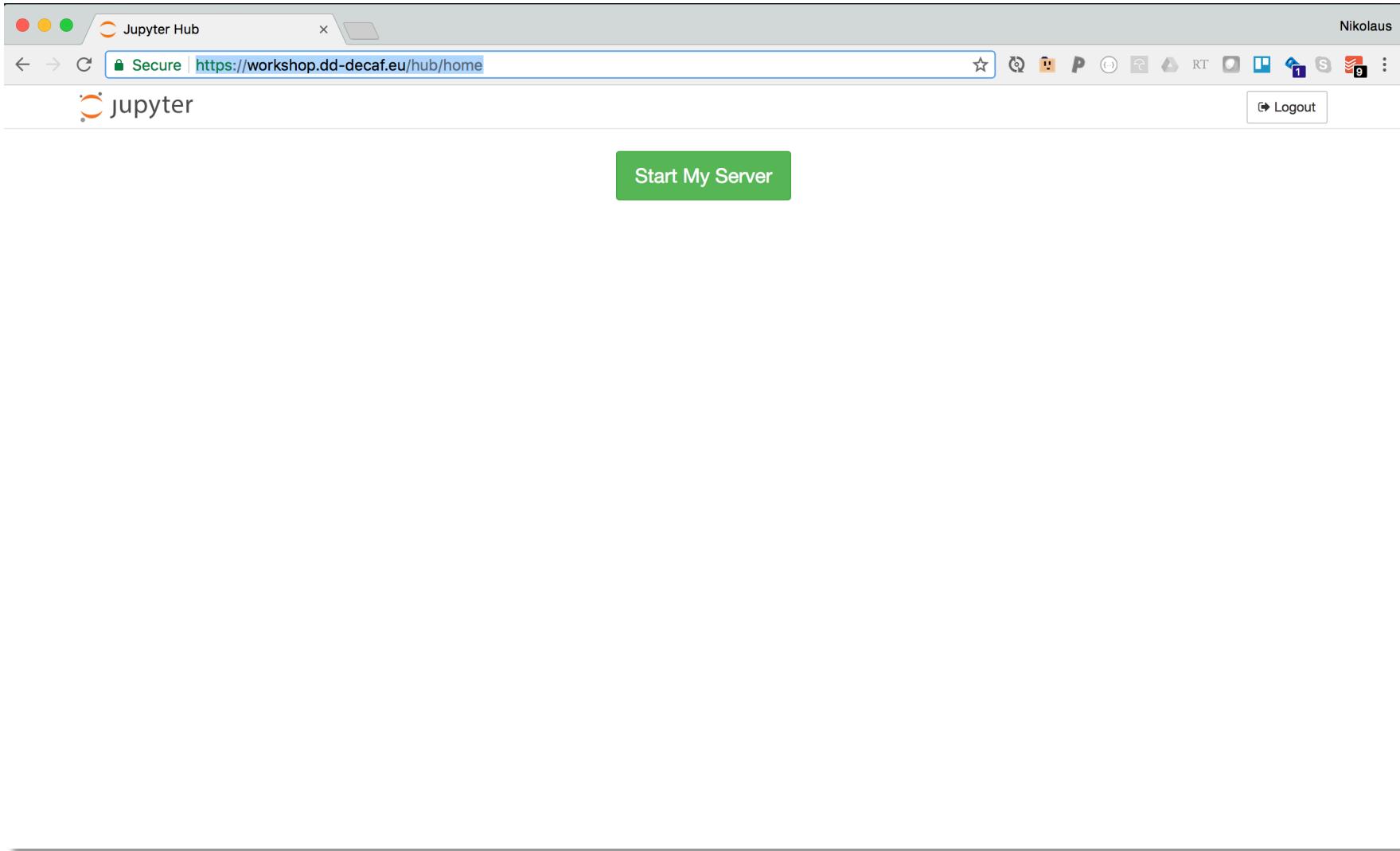
https://dd-decaf.ait.dtu.dk/

A screenshot of a web browser showing the GitHub sign-in page. The URL in the address bar is https://github.com/login?client_id=4a48c4d1c7449cb4eebf&return_to=%2Flogin%2Foauth%2Fauthorize%3Fclient_id%3D4a48c4d1c7449cb4eebf.... The page features the GitHub logo at the top, followed by a large button with a small icon. Below it, the text "Sign in to GitHub to continue to dddecaf-workshop". There are input fields for "Username or email address" and "Password", along with "Forgot password?" links. A green "Sign in" button is at the bottom. At the very bottom, there's a link "New to GitHub? Create an account." with a blue arrow pointing to it from the right. The browser window has a dark header bar with the title "Sign in to GitHub · GitHub".

Create a GitHub account if you don't have one yet (~5 min)

Terms Privacy Security Contact GitHub

<https://dd-decaf.ait.dtu.dk/>



cobrapy



models



fluxes



algorithms

<https://opencobra.github.io/cobrapy/>

Star 145 contributors 28 release v0.13.0

cobrapy is a python package that provides a simple interface to metabolic constraint-based reconstruction and analysis.

<https://dd-decaf.ait.dtu.dk/>



Get in touch: <https://gitter.im/opencobra/cobrapy>

GITTER

opencobra/cobrapy COBRApy is a package for constraint-based modeling ...

ALL CONVERSATIONS

cobrapy

Synchon Mandal

jupyter... /jupyter...

Snorre Sulheim

symen.../symen...

opencobra/memote

escher

optlang

biosustain/cameo

James Daniell

biosustain

opencobra

jupyter/notebook

potion

ADD A ROOM

I tried saving the file with MAT.jl. But when I read it from cobrapy I get an error:
`NotImplementedError: Please use HDF reader for matlab v7.3 files`

Nikolaus Sonnenschein @phantomas1234 Jun 09 08:26
Doesn't COBRA.jl support SBML?

Jorge Fernandez-de-Cossio-Diaz @cossio Jun 09 11:30
It doesn't look like it does. It can only read Matlab files, and it cannot write them

Moritz E. Beber @Midnighter Jun 10 22:29
@cossio can you send me the exported file (or any other model exported from Julia for that matter), please? I'll take a look at importing it.

Snorre Sulheim @sulheim Jun 14 10:23
Seems like this is a general problem with the different Cobra platforms. Cobratoolbox Matlab-exported models can be a hassle to load into cobrapy

Christian Diener @cdiener Jun 14 21:26
@sulheim Yeah I agree, not super surprising though. Would be a hassle to read Python pickles into matlab as well. SBML, JSON are usually much more portable.

Snorre Sulheim @sulheim Jun 15 17:18
@cdiener There can be problems when using SBML as well...

Click here to type a chat message. Supports GitHub flavoured markdown.

PEOPLE REPO INFO

ADD SEE ALL (71 PEOPLE)

ACTIVITY

pstjohn commented #728 Jun 26

silviamorins opened #729 Jun 22

gregmedlock opened #728 Jun 21

silviamorins commented #543 Jun 21

silviamorins commented #543 Jun 21

zakandrewking commented #706 Jun 20

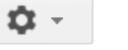
gregmedlock commented #727 Jun 20

gregmedlock commented #543 Jun 20

cb Biosustainability

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Google Search for messages  1 N

Groups NEW TOPIC C Mark all as read Filters  

My groups Shared publicly
30 of 243 topics (99+ unread)  Tags · Members · About

cobra pie Shared publicly
30 of 243 topics (99+ unread)  Tags · Members · About

This is a user support group for the ecosystem of cobrapy and escher. This is a great place to ask for "how do I" help for questions related to constraint-based modeling and metabolic maps, or to share tidbits you think may be of interest.

If you think you've found a bug, or want to discuss development issues, please post those to the relevant github instead:
cobrapy: <https://github.com/opencobra/cobrapy/>
escher: <https://github.com/zakandrewking/escher>

We're all very friendly, I promise!

Click on a group's star icon to add it to your favorites

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- cobra pie Jun 21
- COPASI User For... Jun 21
- Gurobi Optimization Jun 15
- YALMIP Jun 3
- cytoscape-helpdesk

Recent searches

- continuous integr... May 28
- docker (in gurobi)
- change variable n...
- appveyor sbml
- appveyor

Recently posted to

- cobra pie May 25
- libsbml-developm... May 24

Question on FBA (4)
By Rodrigo Colpo - 4 posts - 6 views Jun 21

cobra documentation (3)
By Jyotshana Gautam - 3 posts - 11 views Jun 21

User poll (1)
By Moritz Beber - 1 post - 5 views Jun 15

inconsistently slow optimization (1)
By Maureen Carey - 3 posts - 21 views Jun 3

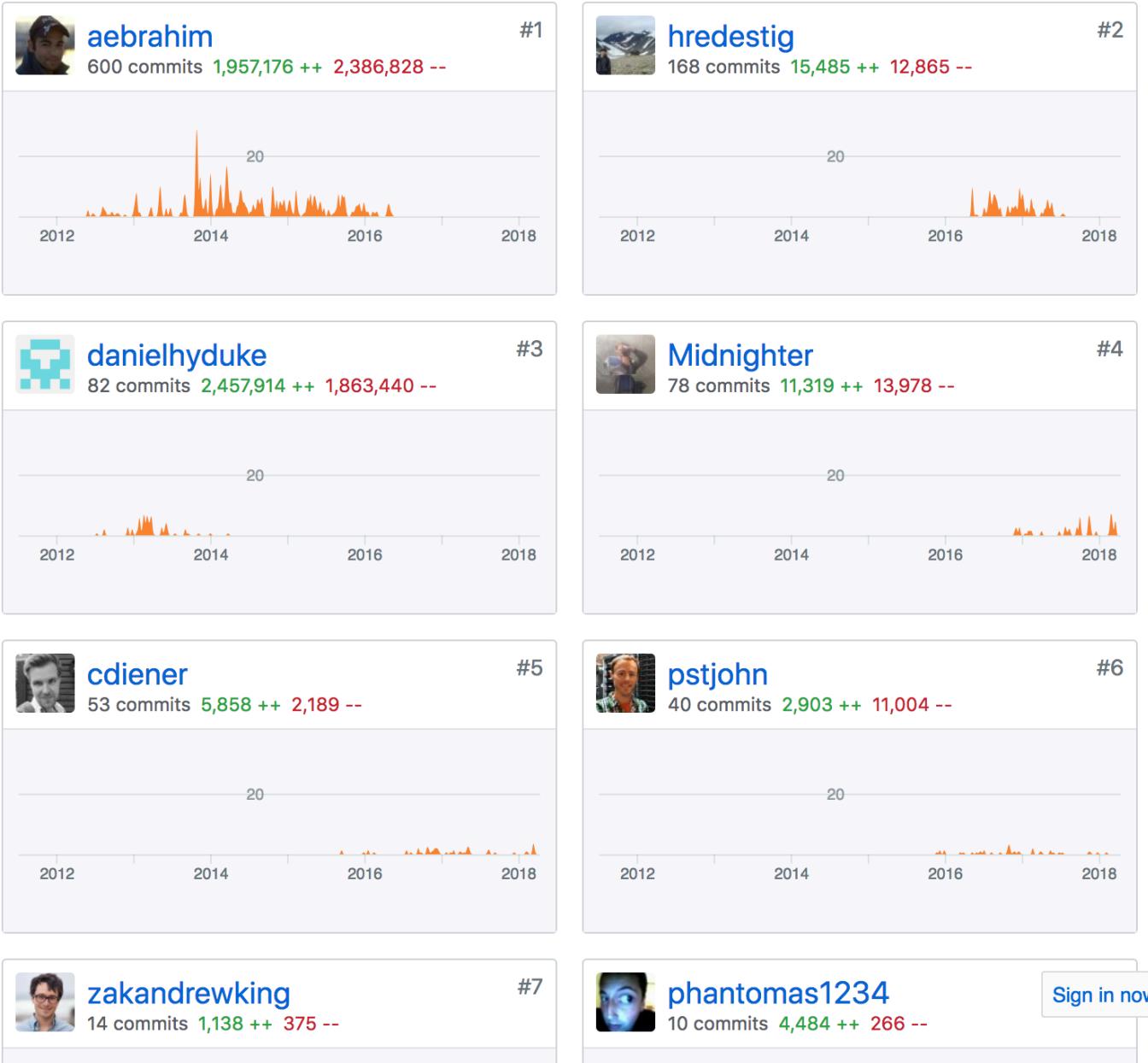
install and use Gurobi solver (6)
By Stephen Chapman - 6 posts - 56 views May 28

ANNOUNCEMENT: ROOM, geometric FBA, GSoC, User Survey (2)
By Moritz Beber - 2 posts - 12 views May 25

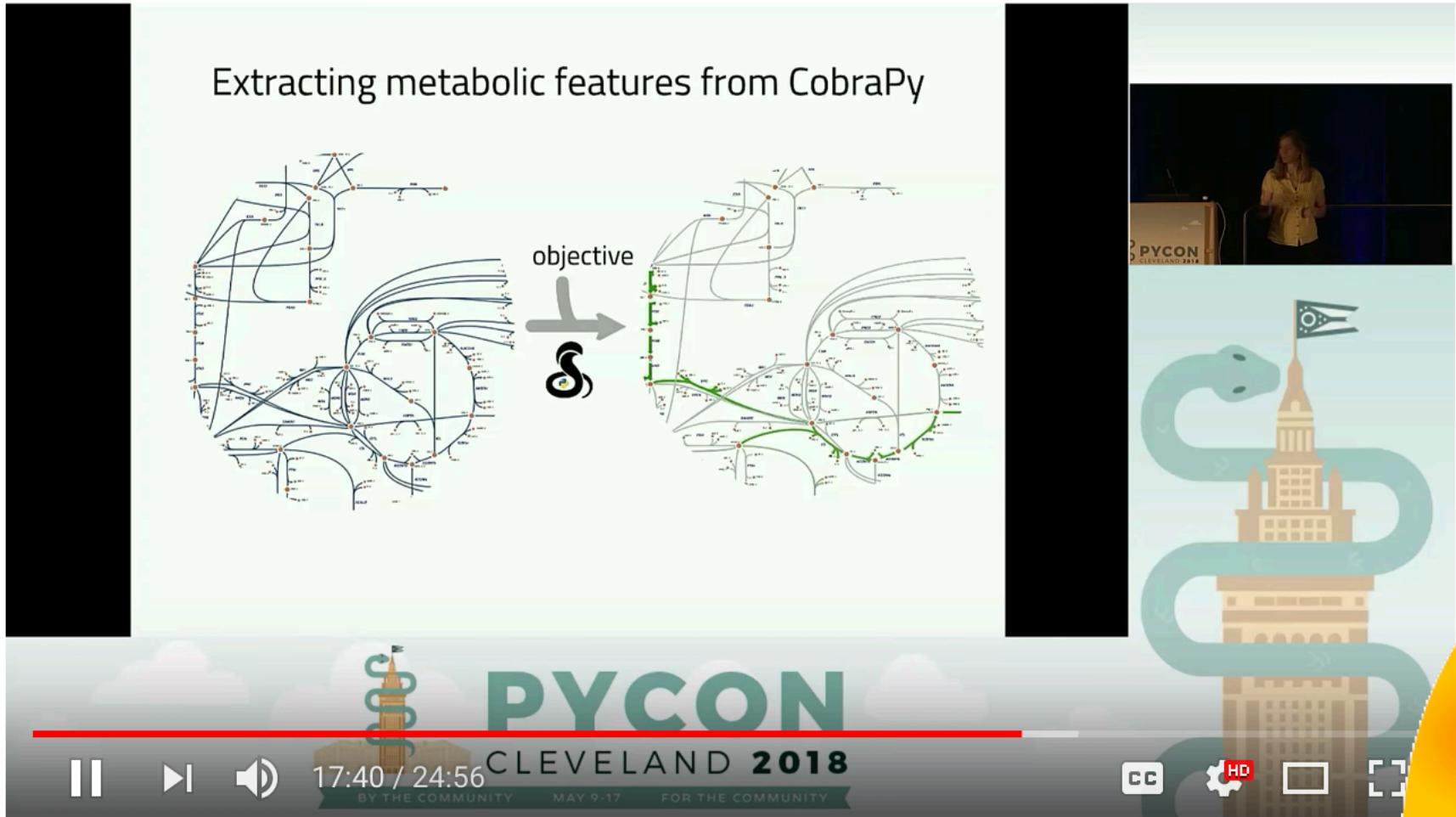
Teaching material or simple documented examples available...? (3)
By Björn Johansson - 3 posts - 28 views May 24

Conda package available for cobrapy 0.11.3 (4)
By Björn Johansson - 3 posts - 28 views May 24

- Contributions from 28 people from all around the world!

[Sign in now](#)

<https://youtu.be/5lYWxjSItlg>



Janet Matsen - Programming microbes using Python - PyCon 2018

927 views

25

0

SHARE

...



ALL

BY TAG

Packages

escher

by Zachary A. King

license unknown

Star 88

Tags: visualization

Escher is a web-based tool for building, viewing, and sharing visualizations of biological pathways. These 'pathway maps' are a great way to contextualize data about metabolism.

[getRepository](#)[webpage](#)

cameo

by Biosustain

license Apache-2.0

Star 57

Tags: Synthetic Biology , strain design , general modeling

optlang

by Biosustain

license Apache-2.0

Star 67

Tags: mathematical modeling , general modeling

Optlang is a Python package for solving mathematical optimization problems, i.e. maximizing or minimizing an objective function over a set of variables subject to a number of constraints. Optlang provides a common interface to a series of optimization tools, so different solver backends can be changed in a transparent way. Optlang's object-oriented API takes advantage of the symbolic math library **sympy** to allow objective functions and constraints to be easily formulated from symbolic expressions of variables

[getRepository](#)[webpage](#)

memote

by opencobra

license Apache-2.0

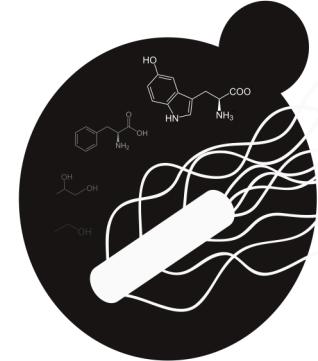
Star 28

Tags: metabolic model , metabolic reconstruction , standardization , unit-testing , cobra , sbml



Joao

Cameo

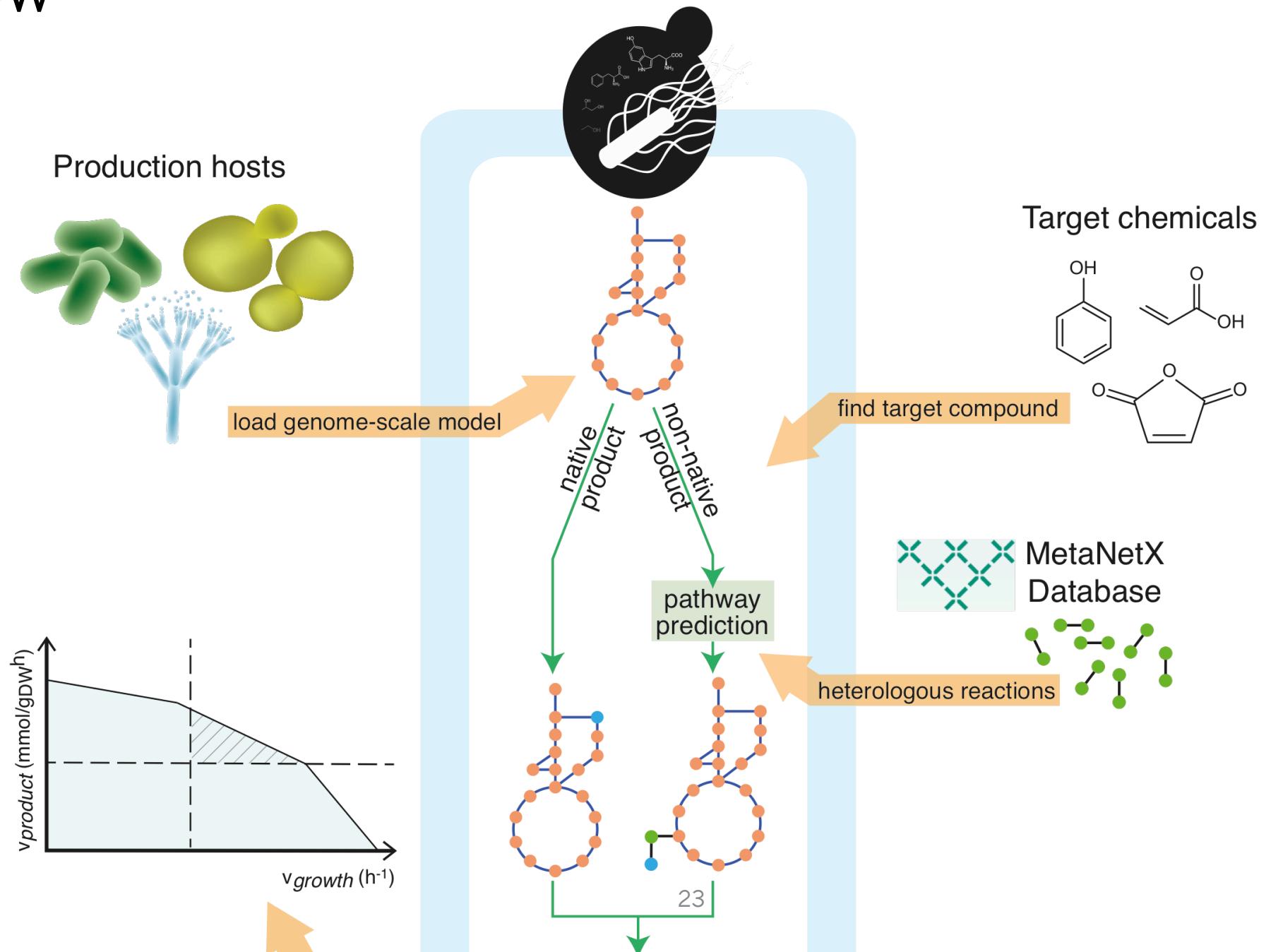


Computer Aided Metabolic Engineering
and Optimization of Cell Factories

<http://cameo.bio>

Cardoso, João G. R., Kristian Jensen, Christian Lieven, Anne Sofie Lærke Hansen, Svetlana Galkina, Moritz Beber, Emre Özdemir, Markus J. Herrgård, Henning Redestig, and Nikolaus Sonnenschein. 2018. "Cameo: A Python Library for Computer Aided Metabolic Engineering and Optimization of Cell Factories." *ACS Synthetic Biology*, April. <https://doi.org/10.1021/acssynbio.7b00423>.

Workflow



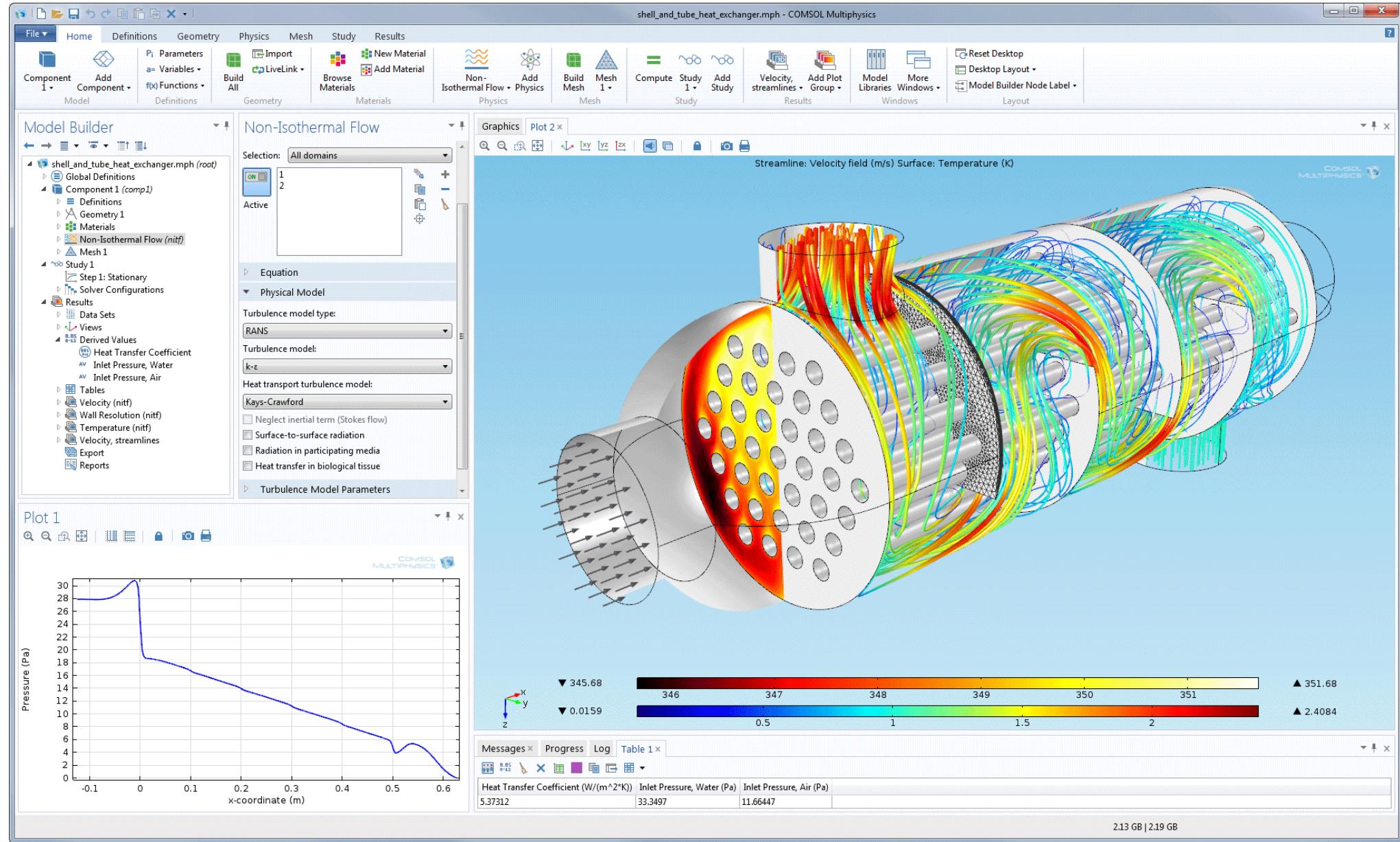
<https://dd-decaf.ait.dtu.dk/>



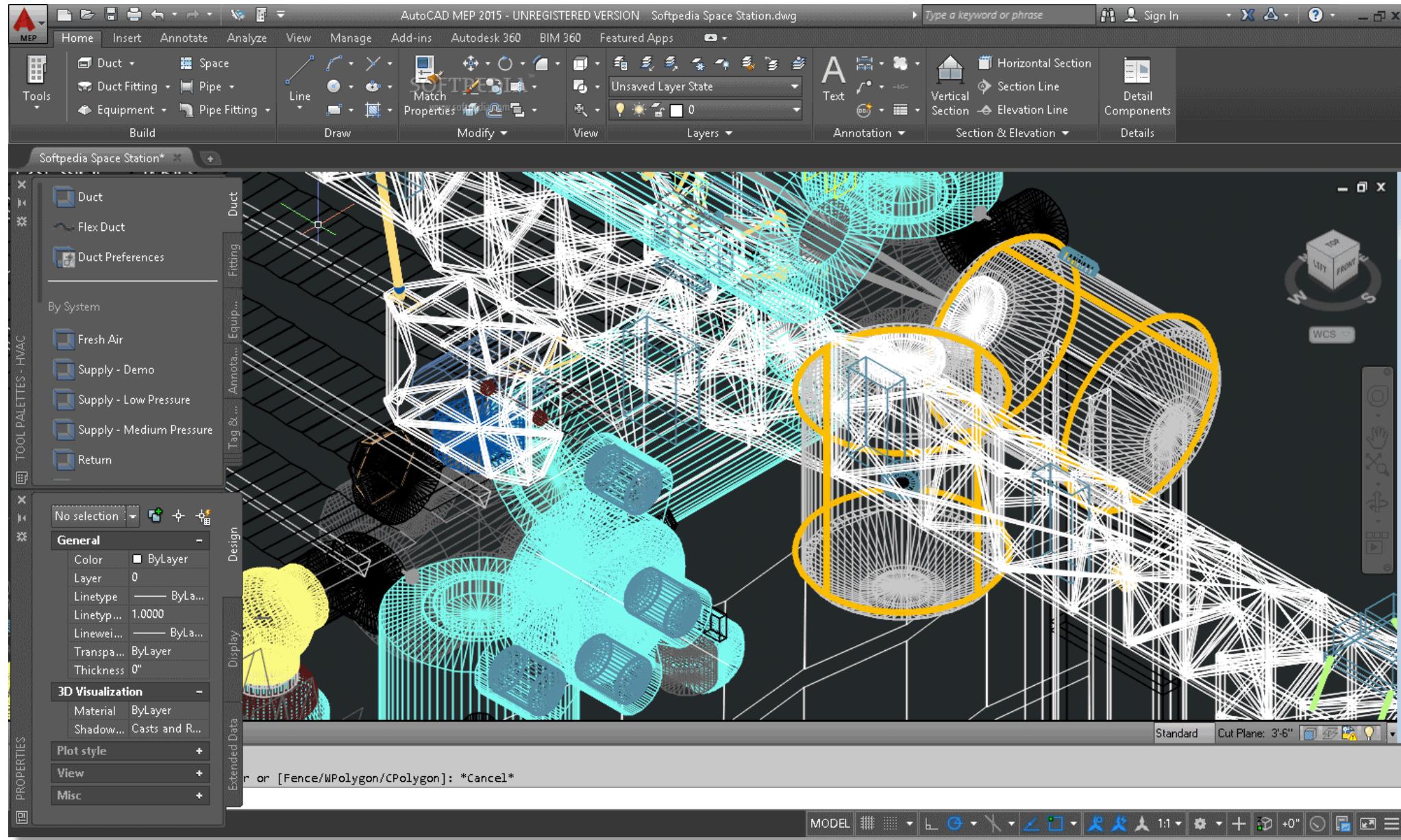
Computer aided design in biology

10 min break

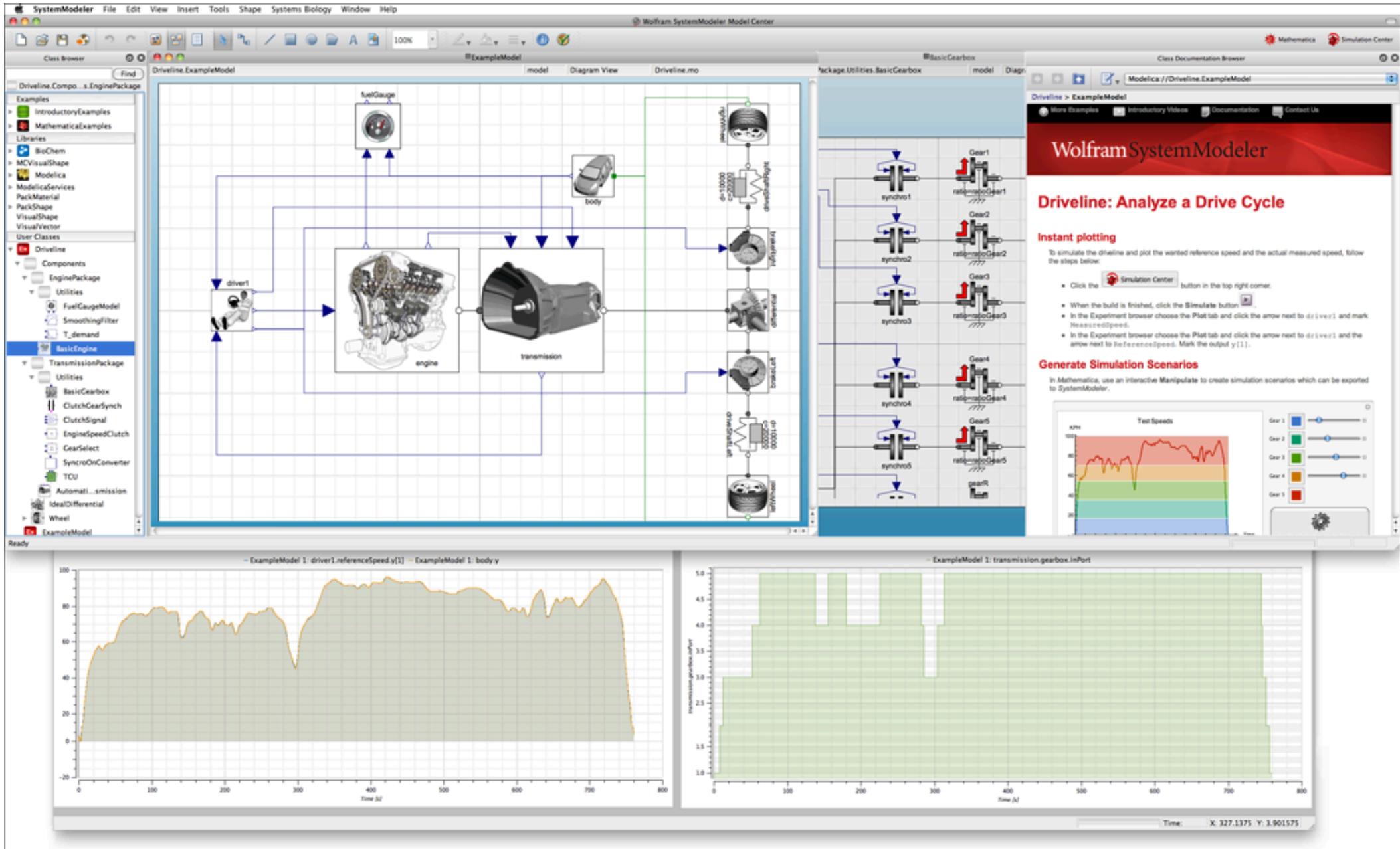
Computer aided design (CAD) in engineering



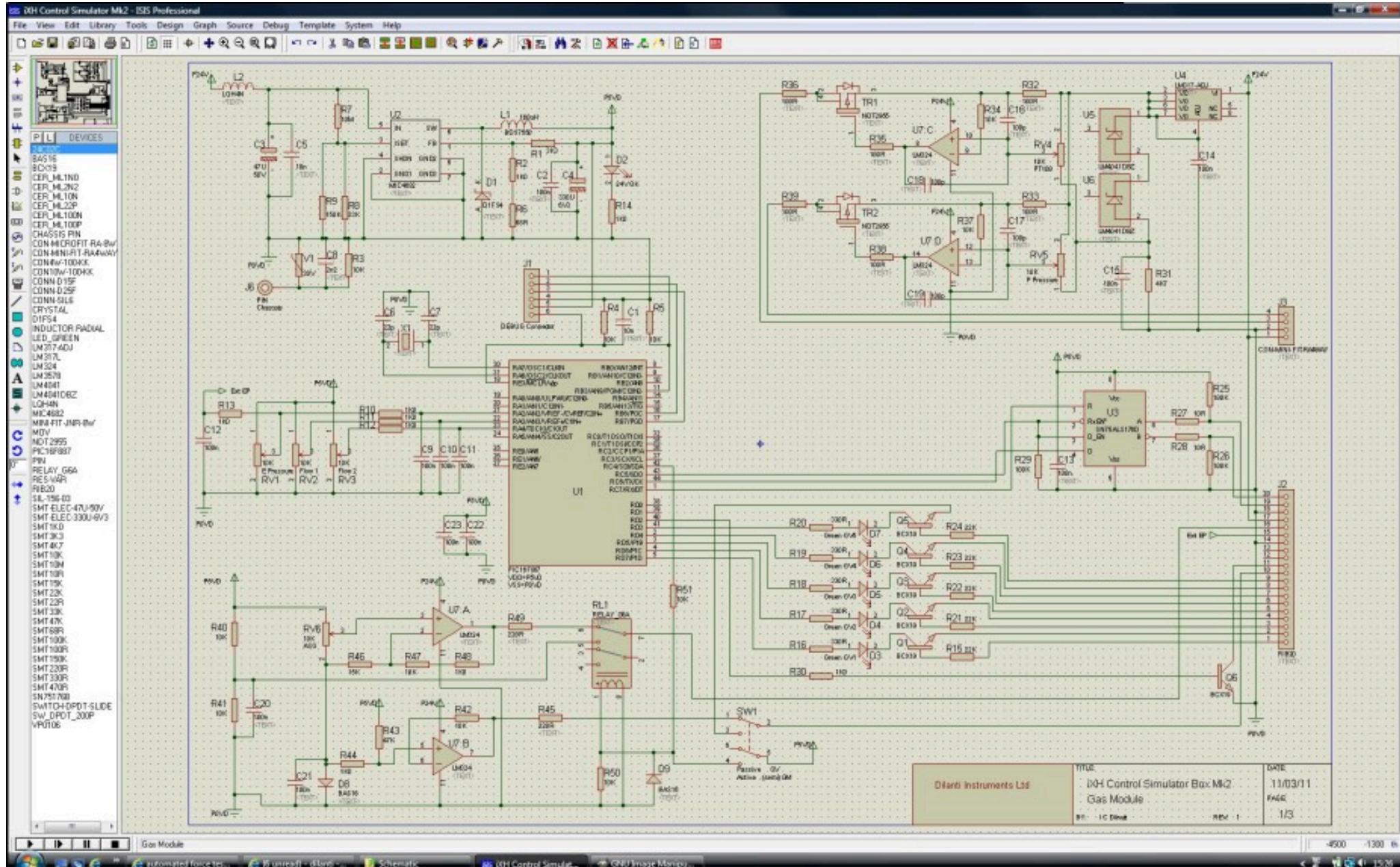
CAD in civil engineering



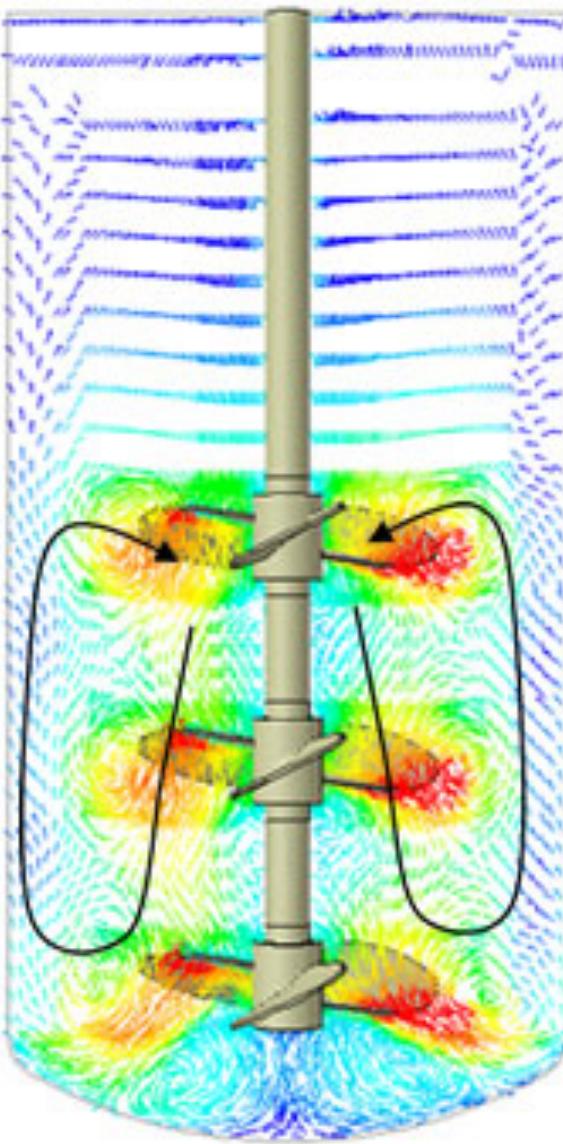
CAD in mechanical engineering



CAD in electrical engineering



CAD in chemical engineering



CAD in Synthetic Biology



GENETIC CONSTRUCTOR

CRISPRainbow Multiplex Labeling Kit

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Search

By Project By Author By Keyword

Part Libraries

- pLH-sgRNA1 Library
- pCRISPRainbow-DONOR1
- pLH-sgRNA1-boxB-MS2-PP7
- pLH-sgRNA1-boxB-MS2
- pLH-sgRNA1-PP7-boxB
- pLH-sgRNA1-MS2-PP7
- pLH-sgRNA1-2XboxB
- pLH-sgRNA1-2XPP7
- pLH-sgRNA1-2XMS2
- pLH-sgRNA1
- pHAGE-EFS-N22p-3XRFPnls
- pHAGE-EFS-PCP-3XGFPnls
- pHAGE-EFS-MCP-3XBFPnls
- pHAGE-TO-MCP-3XBFPnls
- pHAGE-TO-dCas9
- Bacterial expression plasmids
- Lentiviral plasmids
- EMMA Templates

pCRISPRainbow-DONOR1 Circular

pLH-sgRNA1-boxB-MS2-PP7 Circular

Block Information

Name: Multiple blocks selected

Description: Multiple blocks selected

Not Protected:

Source: Multiple Sources

Sequence Length: 2479 bp

Color & Symbol:

SEQUENCE GSL EDITOR

CAD in Synthetic Biology

[CRISPR Experiments ▾](#) [Projects ▾](#) [Nikolaus Sonnenschein ▾](#)

KNOCK-IN > REGION SELECTOR (i)

[Region Details](#) [Sequence Only](#)

Genome

Escherichia coli K-12 MG1655 (GCA_00000584.5) (i)

Gene (i)

pgk

Start coordinate

3071458

End coordinate

3072622

Nuclease

SpCas9

Protospacer Length

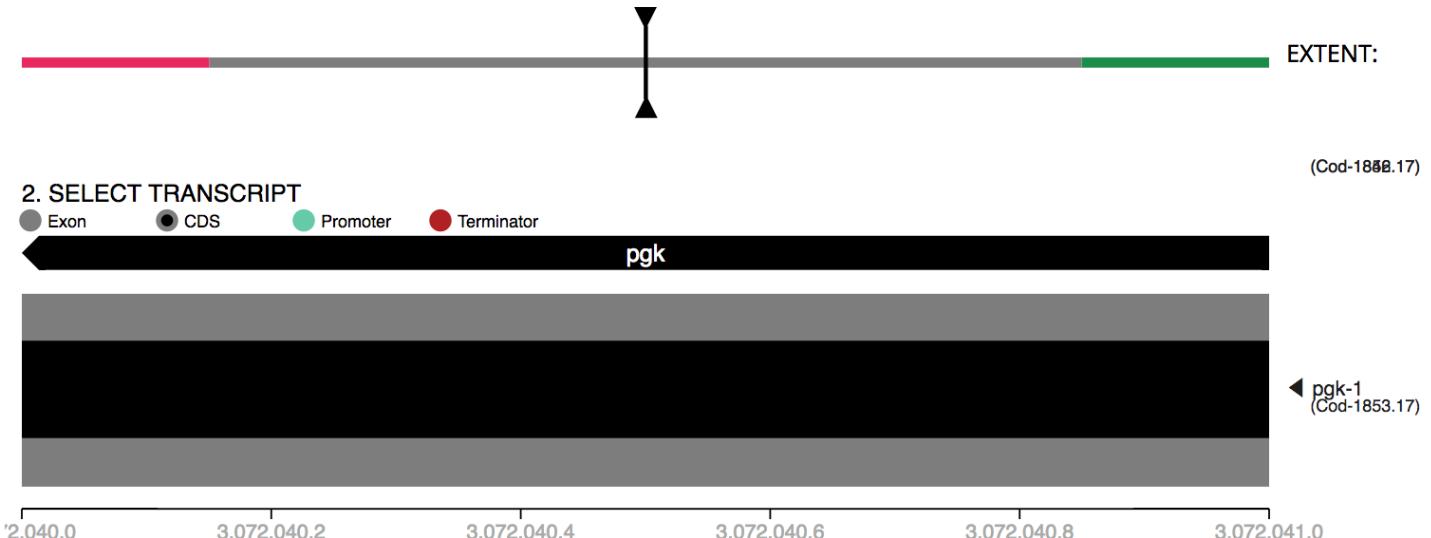
20

[Clear Form](#)

[Proceed](#)

1. DRAG TO SELECT TARGET REGION

Large and guide rich regions may cause your browser to crash. For top performance stay below 10000bp.



(i)

CAD in Synthetic Biology

Projects

- PERSONAL**
 - My First Project
Nikolaus Sonnenschein
 - My Oligos
Nikolaus Sonnenschein
 - My Sequences
Nikolaus Sonnenschein
 - SBOL
Nikolaus Sonnenschein
 - Temporary Sequences
 - iLoop HMP
Markus Herrgard (IA +4)
 - iLoop SER
Markus Herrgard (N AC +4)
 - ILOOP**
 - iLoop Team Project
Markus Herrgard (I)
 - DTU BIOSUSTAIN**
 - Benchling Schema Development Project
Benchling Support
 - iLoop Team Project
Markus Herrgard (I)

SEQUENCE MAP

pGA3K3_pLa... Untitled PREFIX_NISO1 W... PREFIX_NISO1 P... bIorg

LINEAR MAP **PLASMID** **DESIGN CRISPR X** **DESCRIPTION**

Untitled **Save** **Settings**

MfeI
acaacattgaagatgaaaggcggttcaacttagcagaccattatcaacaaaatactcca
tgttgtaacttctacccgtcaagttatcgatcgctggtaatagggtttatgaggt
GFP (E0040) no stop

BtgZI
attggcgatggccctgtcctttaccagacaaccattacctgtccacacaatctgc
taaccgttaccggacaggaaaatggtctgttggtaatggacagggtgttagacg
GFP (E0040) no stop

BstBI **BsaI** **DrdI**
ccttcgaaatccaaacggaaaagagagaccatggccctttgagttttaa
ggaaagcttctagggttctttctctgttggtaatggacaggaaactcaaaccatt
GFP (E0040) no stop

BseYI **A1wNI**
PvuII **BamHI**
cagctgtggattacacatggcatggatgaactatacaaaaggatccaaacagggtt
gtcgacgaccataatgttacccatgttataatgtttccatgggttgcacaa

GFP (E0040) no stop

BASES 3547 **START 60** **END 894** **LENGTH 835** **GC 38.56%** **MELTING TEMP 75.0 °C**

Target **60** **894** **+ Settings**

Region

Start	End	Annotations	Genome Region
<input type="checkbox"/> 18	47		No region set (edit, delete)
<input checked="" type="checkbox"/> 60	894	R0011 (pLac), stem loop terminator, pGA prefix (bglBrick...)	No region set (edit, delete)

You don't have a genome region set above, so scores may not match other sites such as [crispr.mit.edu](#). Benchling uses the genome region to locate your target region and to ignore potential off-target sites in that part of the genome.

SAVE **ASSEMBLE** 0 1-8 of 8 **Prev** **Next**

selected

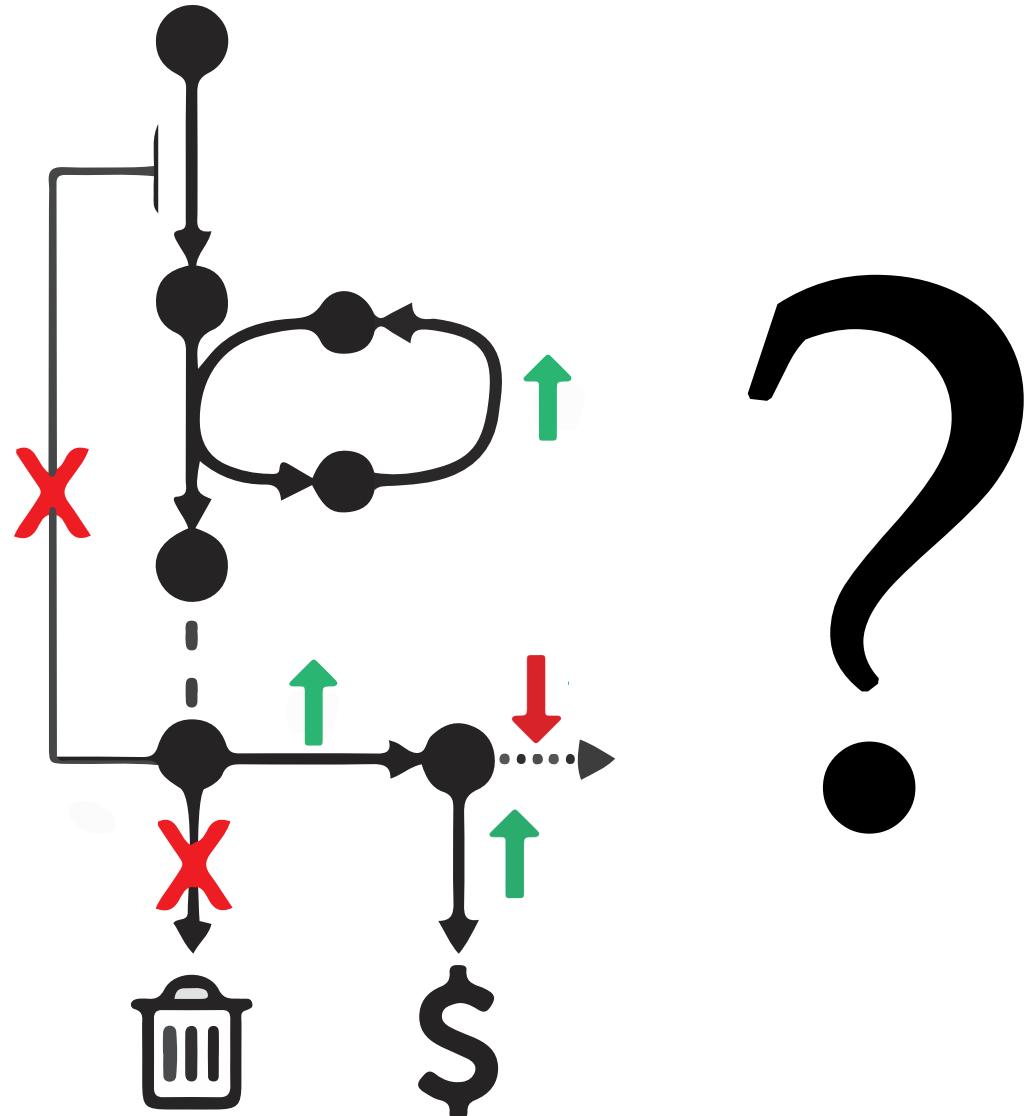
Position	Strand	Sequence	PAM	On-Tar Score
<input type="checkbox"/> 123	-	agatctccgcagcaggaaatt ccagaaaa	11.1	

ASSEMBLY WIZARD ▾ **SPLIT WORKSPACE**

? **crb**

Center for Biosustainability

CAD in metabolic engineering?



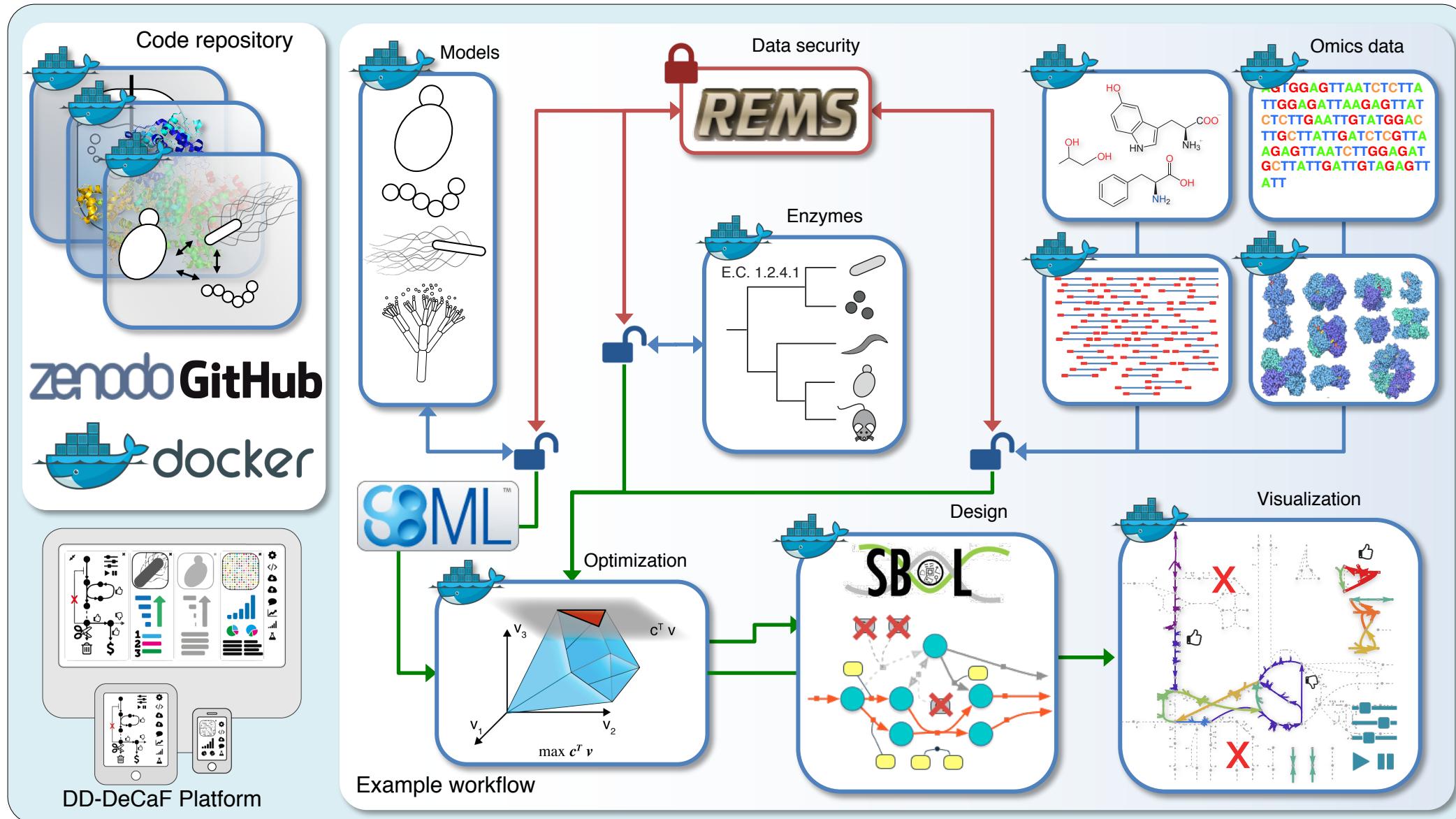
Data-Driven Design of Cell Factories and Communities



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

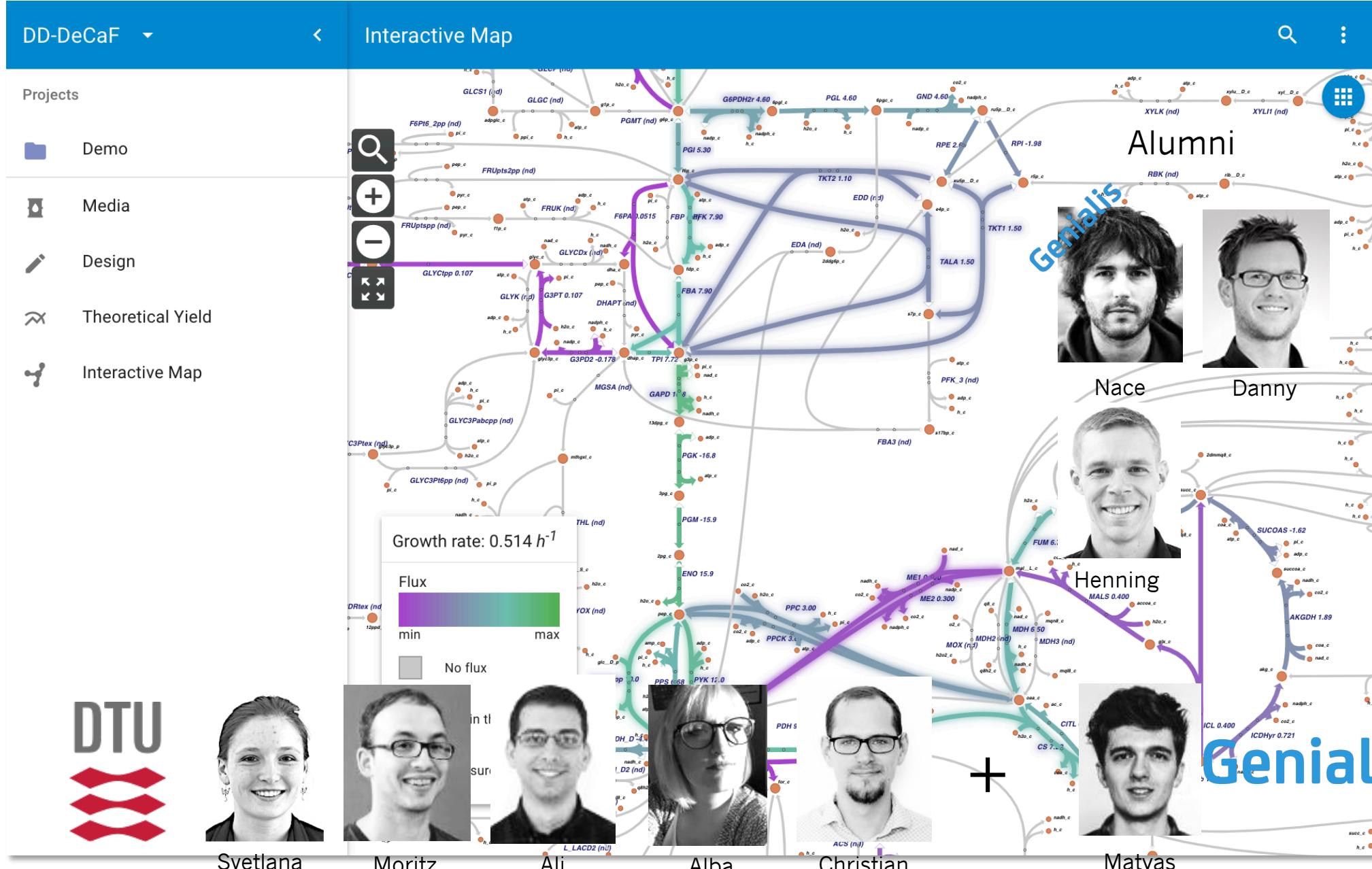
<http://dd-decaf.eu/>

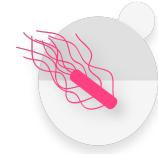
Modular architecture of dockerized microservices





Platform demo





DD-DeCaF ▾

Home

Projects

- Demo
- Media
- Design
- Theoretical Yield
- Interactive Map

Getting started

- [Login \(optional\)](#)
- [Interactive cell factory design and omics data integration](#)
- [Computational cell factory design](#)
- [Assessing the capabilities of cell factories](#)
- [Uploading data](#)

Welcome to our cell factory design and analysis platform! We develop the platform as part of the [DD-DeCaF](#) project with the goal to put model-guided and data-driven design into practice in industrial biotechnology. The platform will enable the following key technologies:

- Metagenomics-enabled design of novel enzymes and biochemical pathways.
- Omics data-driven design of cell factories for the production of chemicals and proteins.
- Analysis and design of microbial communities relevant to human health, industrial biotechnology and agriculture.

With this interactive web application, we target primarily non-expert users that have a need to analyze omics data and compute strains designs. An advance programming interface is provided for expert users ([API docs](#)) enabling them deviate from the default workflows and perform custom analyses.

The platform is currently in **beta** and tested primarily with Google Chrome. If you'd like to stay up-to-date with new releases, please [subscribe](#) to our quarterly newsletter. We will be eternally grateful for feedback in case you miss features or you encountered a problem (for now please drop us a message at niso@biosustain.dtu.dk).

The following sections provide an overview of what you can currently do on platform. Have fun!

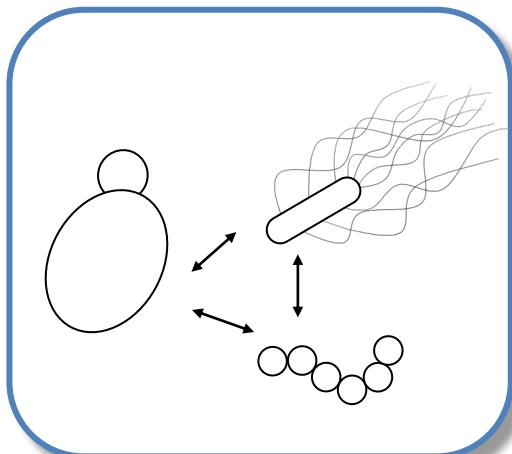
Login (optional)

You can log in [here](#) or by navigating to the menu in the upper right-hand corner. We support sign-on through a number of social media platforms. Alternatively, you can [contact](#) us for an account.

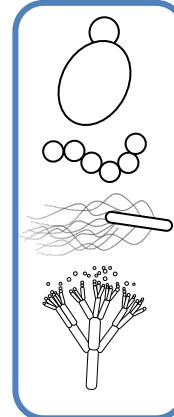


Next steps

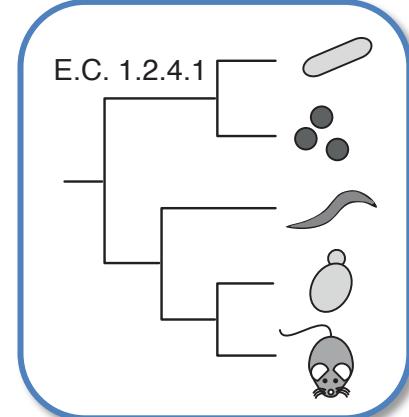
- Run complete strain design workflows
- Bring your own models
- Mine (meta)genomic data for enzymes
- Support more types of omics data
- Add community modeling



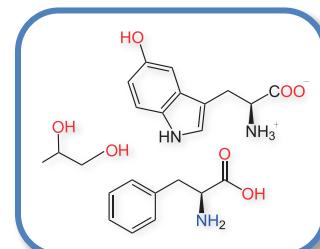
Models



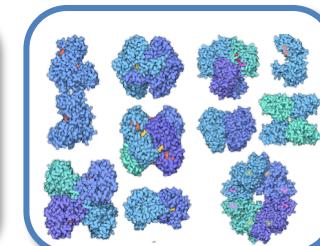
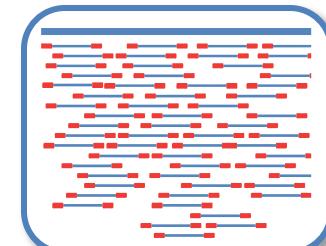
Enzymes



Omics data



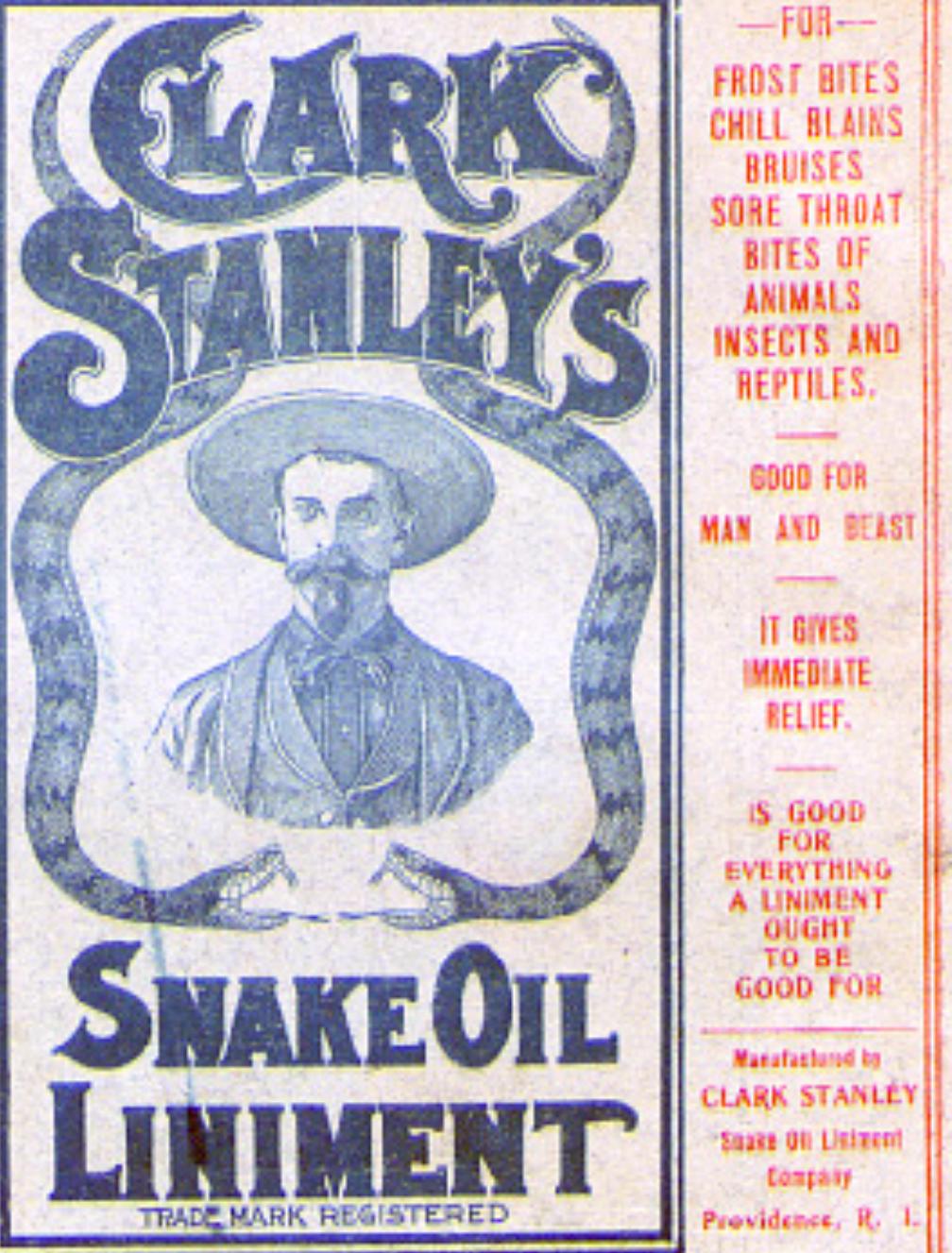
AGTGGAGTTAACCTCTTATTGG
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TTGTATGGACTTGCTTATTGAT
CTCGTTAAGAGTTAACCTTGGA
GATGCTTATTGATTGTAGAGTT
ATT



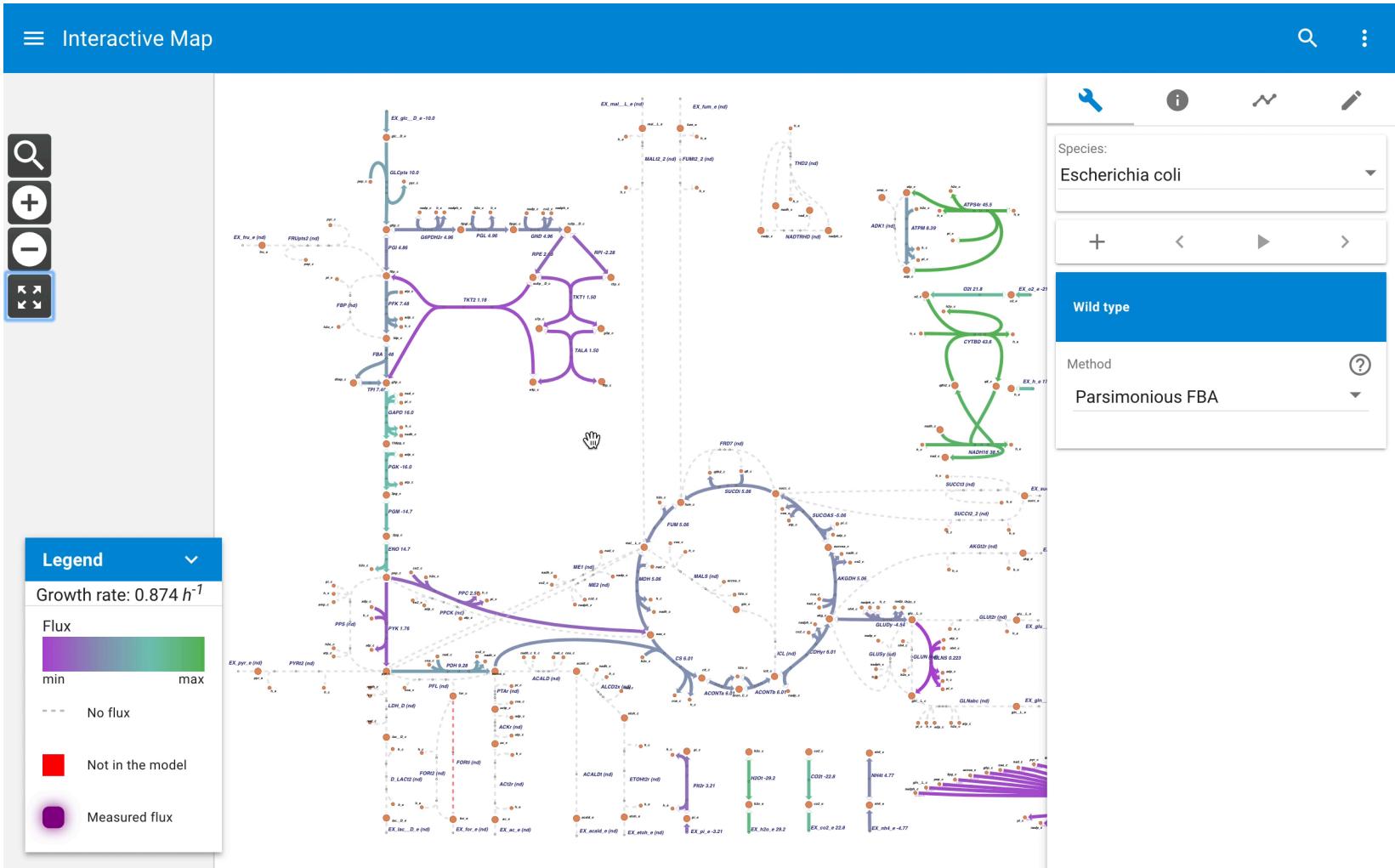
SNAKE
OIL
LINIMENT

THE
STRONGEST AND
BEST LINIMENT
KNOWN FOR PAIN
AND LAMENESS.

USED EXTERNAL
ONLY—
FOR
RHEUMATISM
NEURALGIA
SCIATICA
LAME BACK
LUMBAGO
CONTRACTED
CORDS
TOOTHACHE
SPRAINS
SWELLINGS
ETC.



How do we avoid misleading our users?





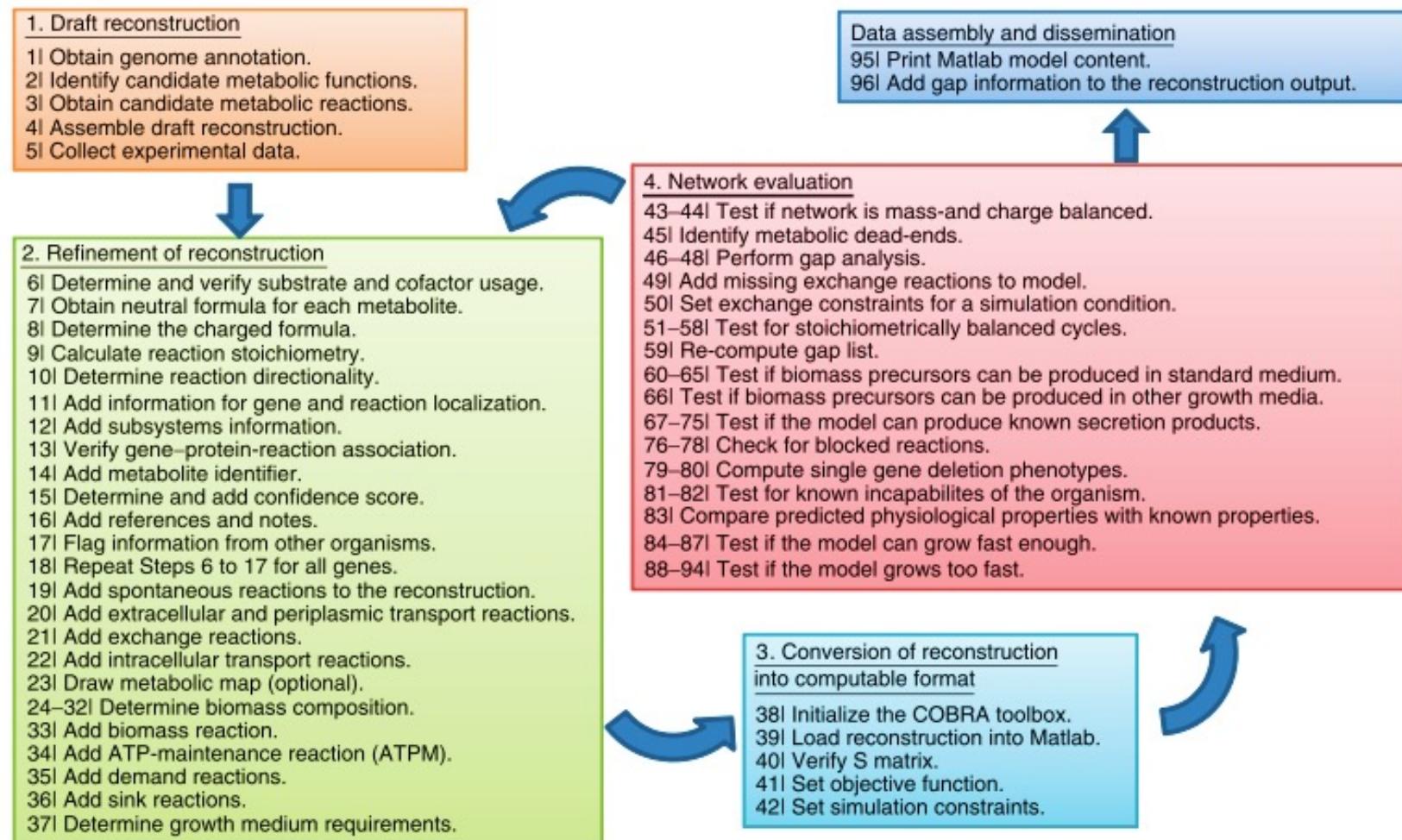
Moritz



Christian



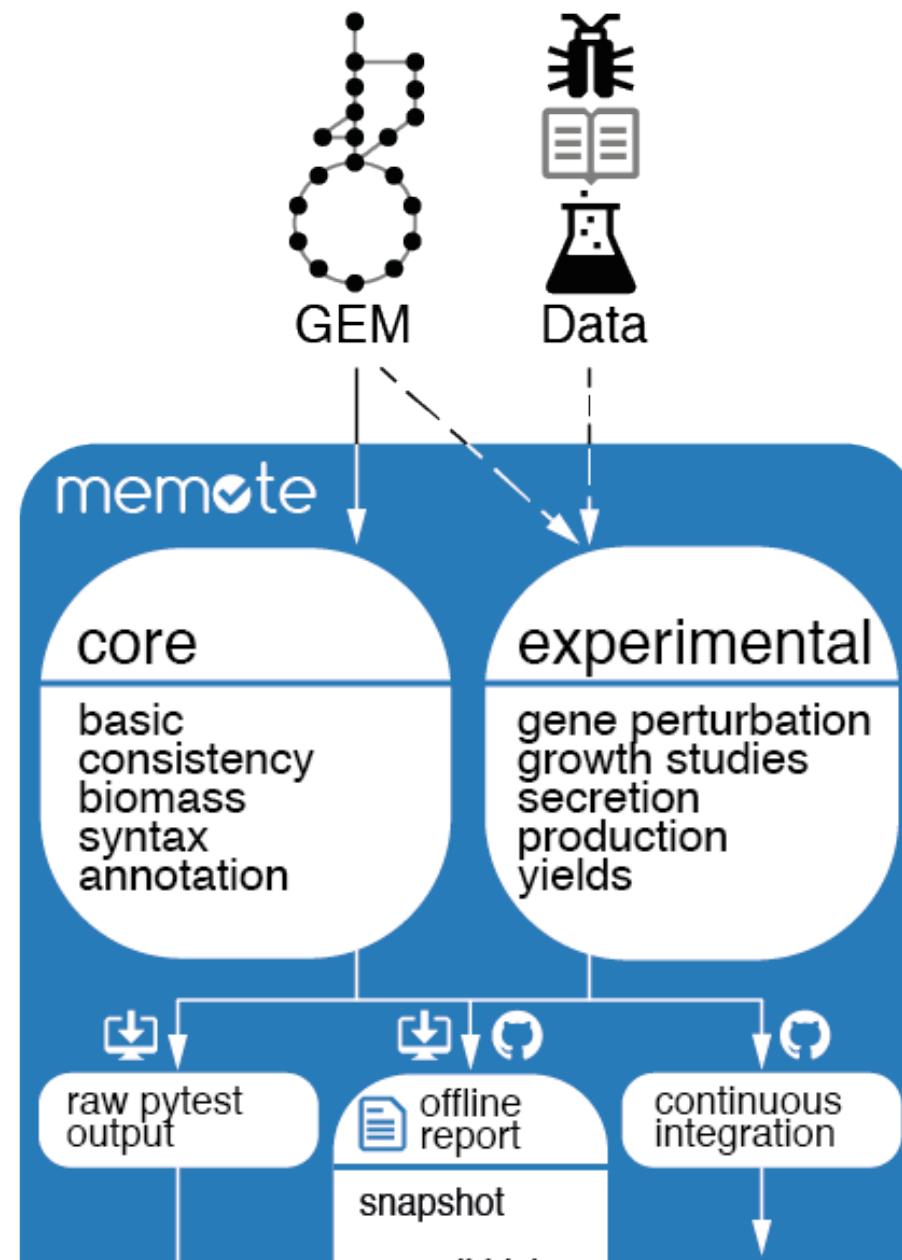
memote - metabolic model tests

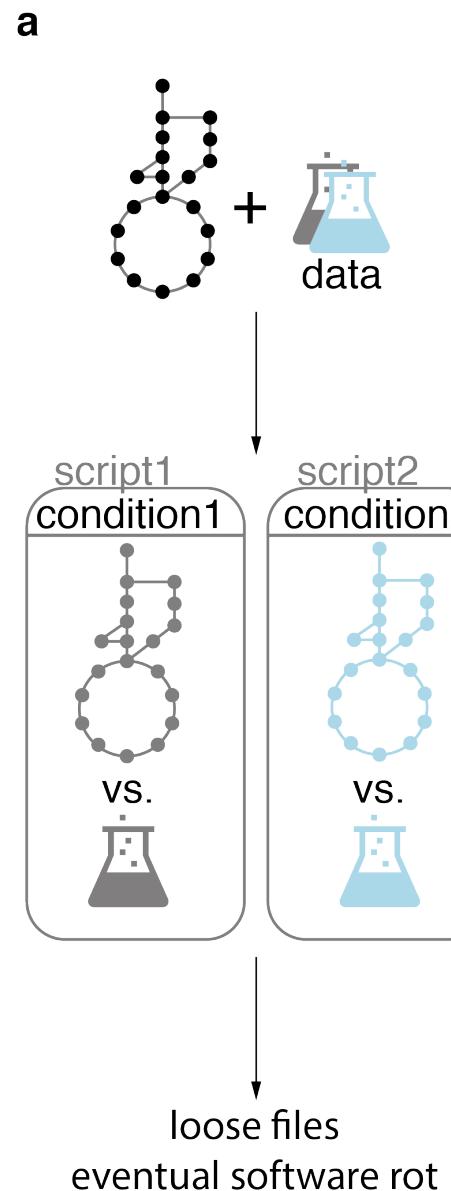


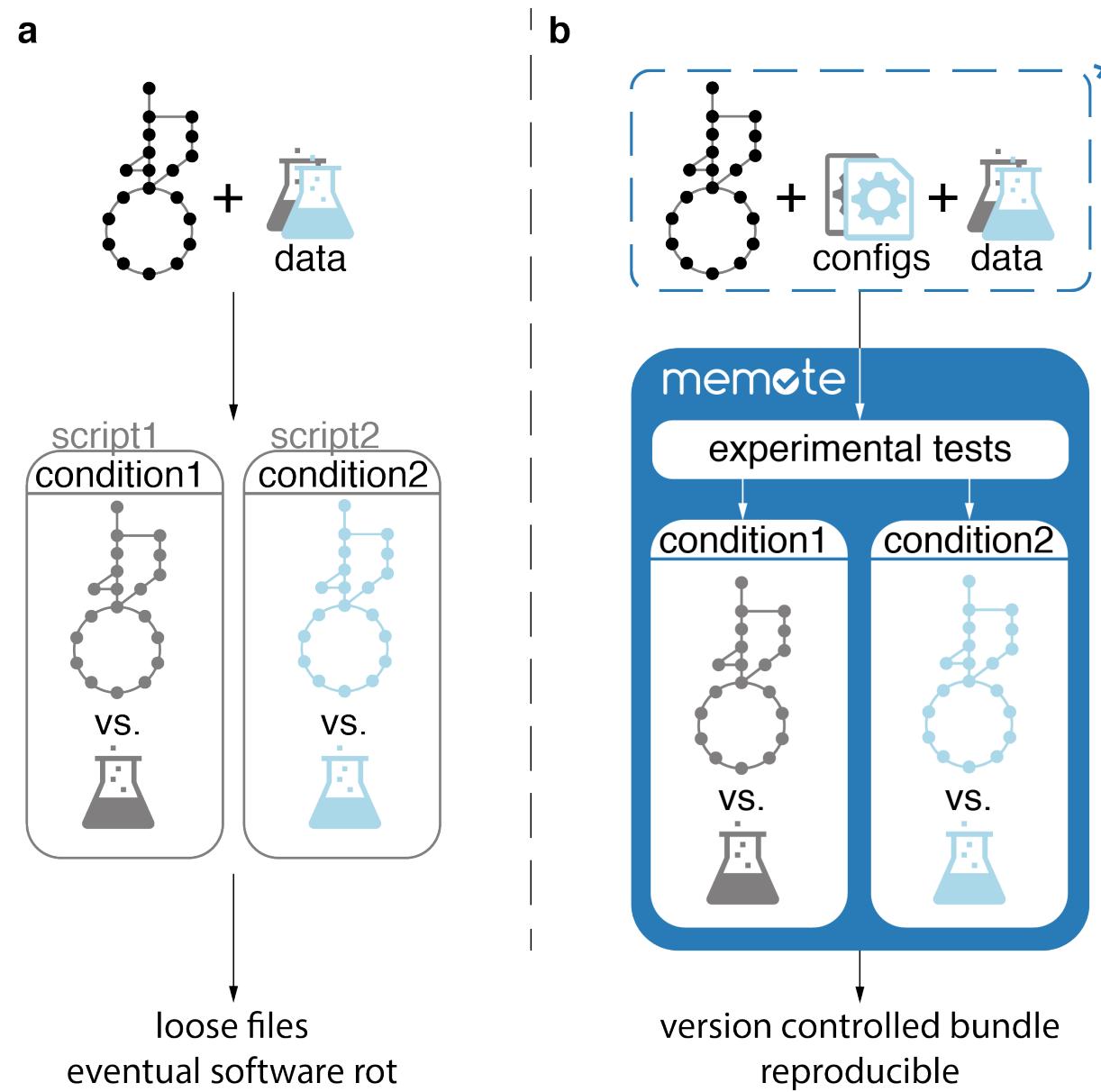
Thiele, I., & Palsson, B. Ø. (2010, January). A protocol for generating a high-quality genome-scale metabolic reconstruction. *Nature protocols*. Nature Publishing Group. <http://doi.org/10.1038/nprot.2009.203>

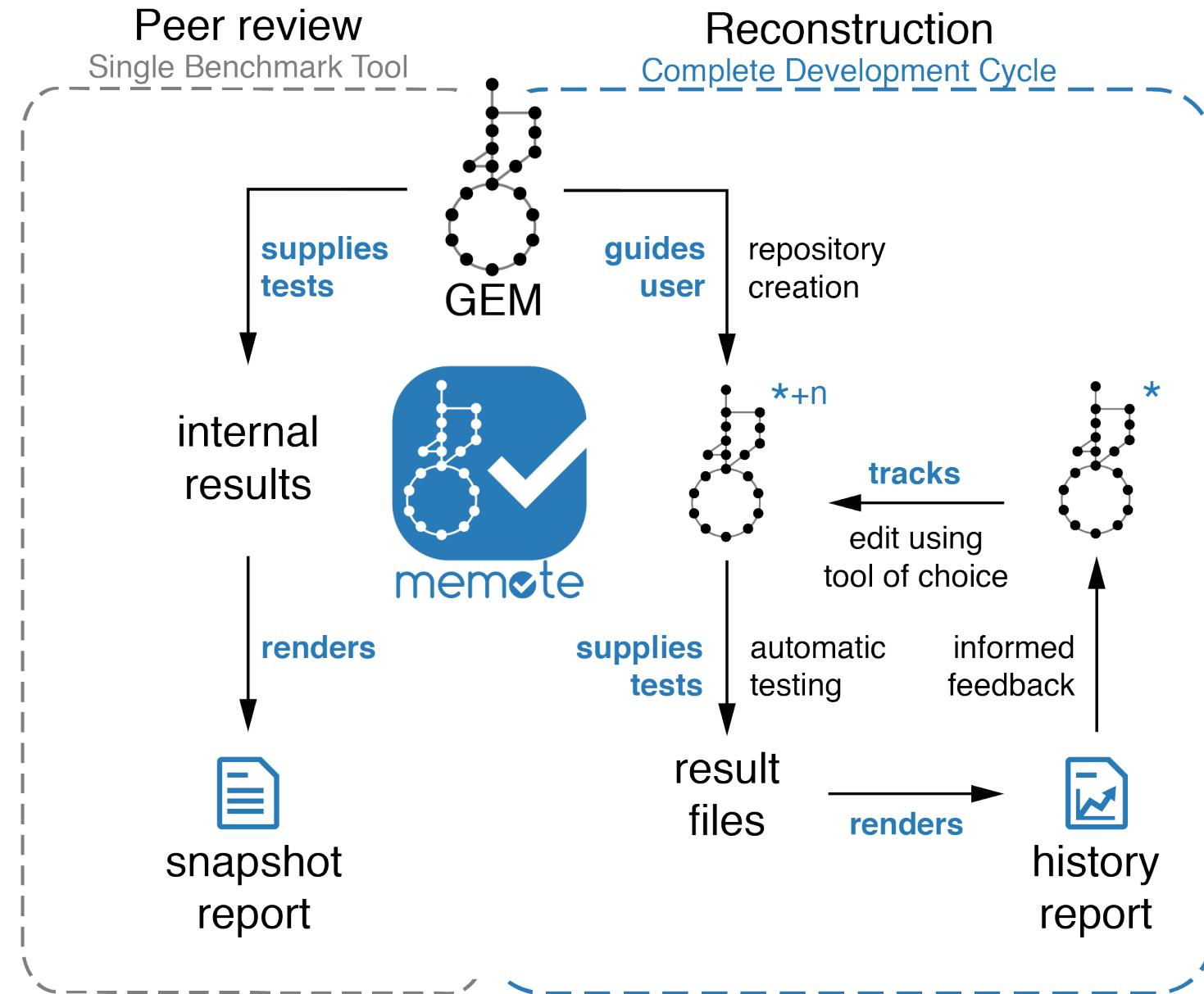
- “A lack of rigor in applying established reconstruction protocols is another factor [...].”
- [...] the notions of ‘quality’ and ‘completeness’ of a metabolic network reconstruction are not well defined

Monk, J., Nogales, J., & Palsson, B. O. (2014). Optimizing genome-scale network reconstructions. *Nature Biotechnology*, 32(5), 447–452. <http://doi.org/10.1038/nbt.2870>











New Results

Memote: A community-driven effort towards a standardized genome-scale metabolic model test suite

✉ Christian Lieven,  Moritz Emanuel Beber, Brett G. Olivier,  Frank T. Bergmann,  Parizad Babaei,  Jennifer A. Bartell,  Lars M. Blank,  Siddharth Chauhan,  Kevin Correia,  Christian Diener,  Andreas Dräger,  Birgitta Elisabeth Ebert,  Janaka N. Edirisinghe,  Ronan M. T. Fleming,  Beatriz Garcia-Jimenez,  Wout van Helvoirt,  Christopher Henry,  Henning Hermjakob,  Markus J. Herrgard,  Hyun Uk Kim,  Zachary King,  Jasper Jan Koehorst,  Steffen Klamt,  Edda Klipp,  Meiyappan Lakshmanan,  Nicolas Le Novere,  Dong-Yup Lee,  Sang Yup Lee,  Sunjae Lee,  Nathan E. Lewis,  Hongwu Ma,  Daniel Machado,  Radhakrishnan Mahadevan,  Paulo Maia,  Adil Mardinoglu,  Greg L. Medlock,  Jonathan Monk,  Jens Nielsen,  Lars K. Nielsen,  Juan Nogales,  Intawat Nookaew,  Osbaldo Resendis,  Bernhard Palsson,  Jason A. Papin,  Kiran Raosaheb Patil,  Nathan D. Price,  Anne Richelle,  Isabel Rocha,  Peter Schaap,  Rahuman S. Malik Sheriff,  Saeed Shoiae,  Nikolaus Sonnenschein,  Bas Teusink,  Paulo Vilaca,  Jon Olav Vik,  Judith A. Wodke,  Joana C. Xavier,  Qianqian Yuan,  Maksim Zakhartsev,  Cheng Zhang

doi: <https://doi.org/10.1101/350991>

COBRA 2018

5th Conference on Constraint-Based Reconstruction and Analysis (COBRA 2018)

<https://goo.gl/QTXqMt>



Featured Speakers



Vassily Hatzimanikatis

Dr. Vassily Hatzimanikatis is currently Associate Professor of Chemical Engineering and Bioengineering at Ecole Polytechnique Federale de Lausanne (EPFL), in Lausanne, Switzerland. Dr. Hatzimanikatis is also Editor-in-Chief of Metabolic Engineering Communication, and associate editor of the journals Metabolic Engineering, Biotechnology & Bioengineering and Integrative Biology, and Senior Editor of Biotechnology Journal. [Read more →](#)



Nathan E. Lewis

Dr. Lewis is an Assistant Professor of Pediatrics and Bioengineering at the University of California, San Diego. Dr. Lewis' lab focuses heavily on the use of systems biology and genome editing techniques to map out and engineer the cell pathways controlling mammalian cell growth, protein synthesis, and protein glycosylation. [Read more →](#)



Christian Lieven

Christian Lieven is currently finishing his PhD in Bioengineering. During his PhD in the Design group of the iLoop Core, a translational research unit focused on microbial cell factory engineering at the Center for Biosustainability, Christian has been working on the EFPro2 project: in collaboration with other researchers from the University of Southern Denmark, Aarhus University, Vestjyllands Andel and Unibio A/S he reconstructed a genome-scale metabolic model for the methanotroph *Methylococcus capsulatus*. Christian is interested in emerging technologies to harness the potential of C1 feedstocks, software development, and the standardization and maintenance of genome-scale metabolic reconstructions. [Read more →](#)



Costas D. Maranas

Dr. Costas D. Maranas (b. 1967) is the Donald B. Broughton Professor in the Department of Chemical Engineering at The Pennsylvania State University. The C. Maranas group develops and deploys computational framework informed by systems engineering and mathematical optimization to understand, analyze and redesign metabolism and proteins. [Read more →](#)



Jens Nielsen

In 2008, Jens Nielsen was recruited as Professor and Director to Chalmers University of Technology, Sweden, where he is currently directing a research group of more than 50 people. At Chalmers he established the Area of Advance Life Science Engineering, a cross departmental strategic research initiative and was founding Head of the Department of Biology and Biological Engineering, which now encompass more than 170 people. [Read more →](#)

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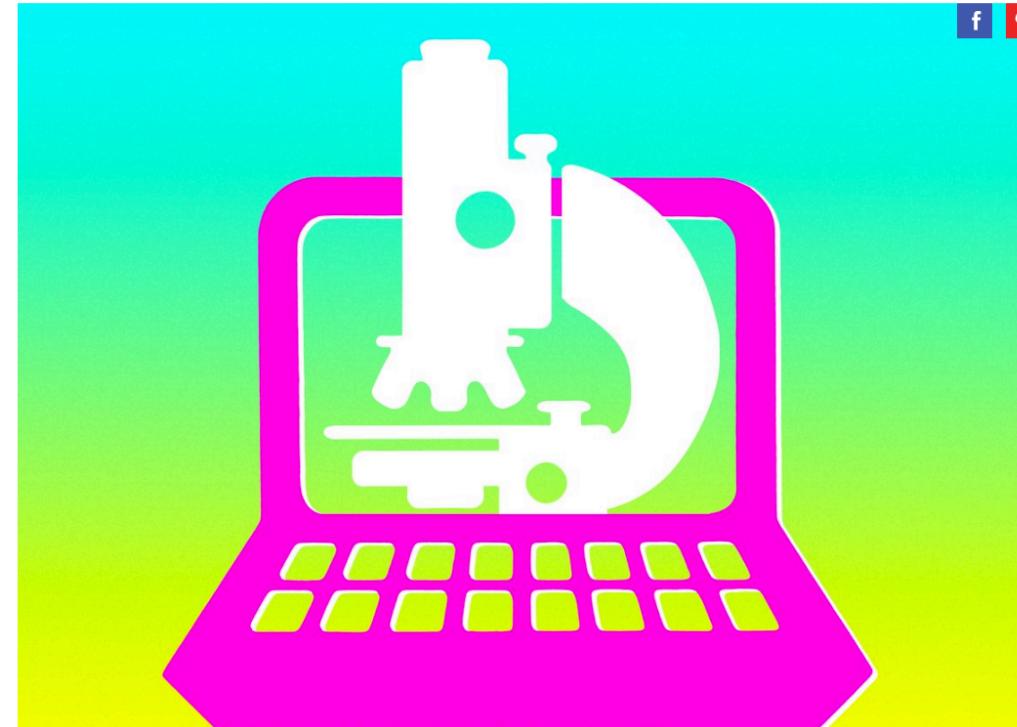
 TWEET

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7

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EMILY DREYFUSS SCIENCE 03.10.17 12:00 PM

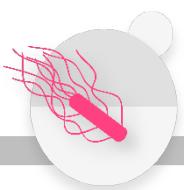
WANT TO MAKE IT AS A BIOLOGIST? BETTER LEARN TO CODE



<https://goo.gl/NRcW2U>



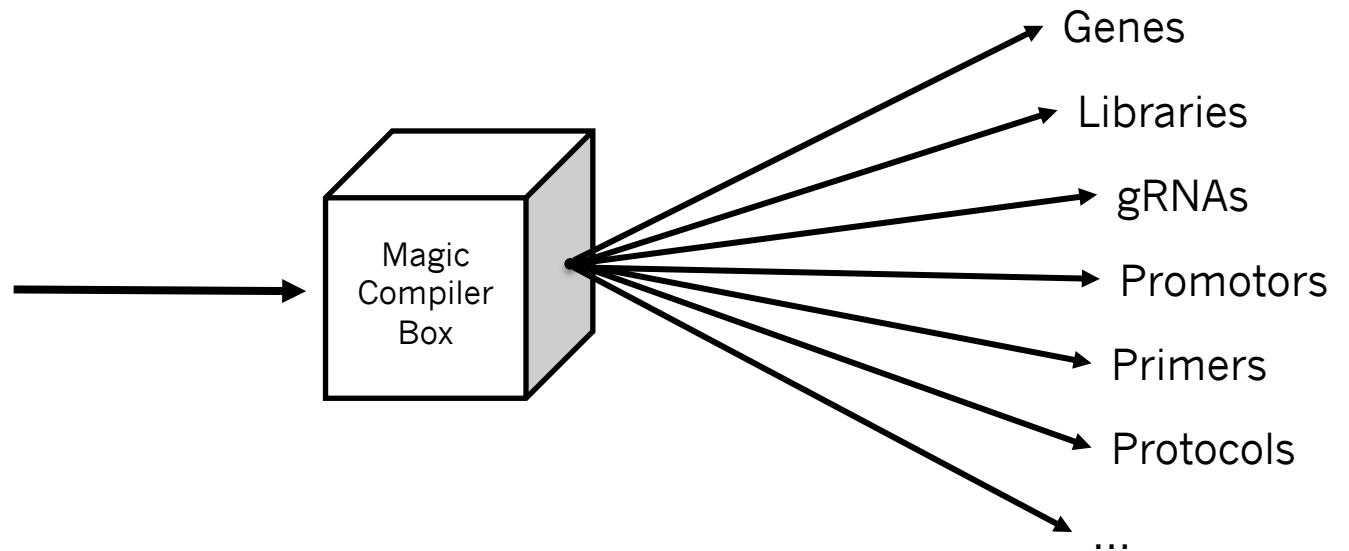
software carpentry + Computational cell
factory engineering course at DTU Biosustain
Open to everyone (including industry)
10–14 September, registration => goo.gl/W7Tdve



The future ...

High-level strain design

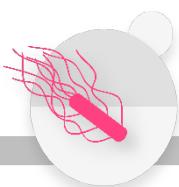
“Delete native genes A, B, C, and D. Add foreign genes X, Y, Z. Increase flux through reaction F by twofold while reducing flux through reaction G by threefold. Remove product inhibition in pathway Q ...”



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

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

DEMO 11-Sep-2017



Import into Genetic Constructor (by Autodesk)

AUTODESK. LIFE SCIENCES

GENETIC CONSTRUCTOR

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Search By Project By Author By Keyword

Part Libraries

CRISPRainbow Multiplex Labeling Kit

Add to my projects... Project Saved

Block Information

Name: Multiple blocks selected

Description: Multiple blocks selected

Not Protected

Source: Multiple Sources

Sequence Length: 2479 bp

Color & Symbol: Green circle

pCRISPRainbow-DONOR1 Circular

pLH-sgRNA1-boxB-MS2-PP7 Circular

Strain designs

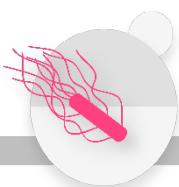
SEQUENCE GSL EDITOR



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

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

DEMO 11-Sep-2017

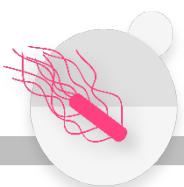


Export Genotype Specification Language (GSL)

The screenshot shows the Autodesk Life Sciences Genetic Constructor interface. On the left, a sidebar lists various project categories like 'The Commons' and 'By Project'. The main workspace displays two circular constructs: 'pCRISPRainbow-DONOR1' and 'pLH-sgRNA1-boxB-MS2-PP7'. Each construct is shown as a sequence of DNA elements with restriction sites and promoters. The right side of the interface contains a 'Block Information' panel with details such as 'Name: Multiple blocks selected', 'Description: Multiple blocks selected', 'Sequence Length: 2479 bp', and a color swatch. At the bottom, a 'SEQUENCE' tab shows the corresponding Genotype Specification Language (GSL) code:

```
1 // First construct derives all elements from BY4741 genome
2 #refgenome BY4741
3 #name BY4741_construct
4 uHO ; pADH1 ; gERG10 ; ### ; dHO
5
6 // Second construct only derives ERG10 from S288C while the rest
// come from BY4741
7 #name BY4741_construct_with_S288C_erg10
8 uHO ; pADH1 ; gERG10 {#refgenome S288C} ; ### ; dHO
```

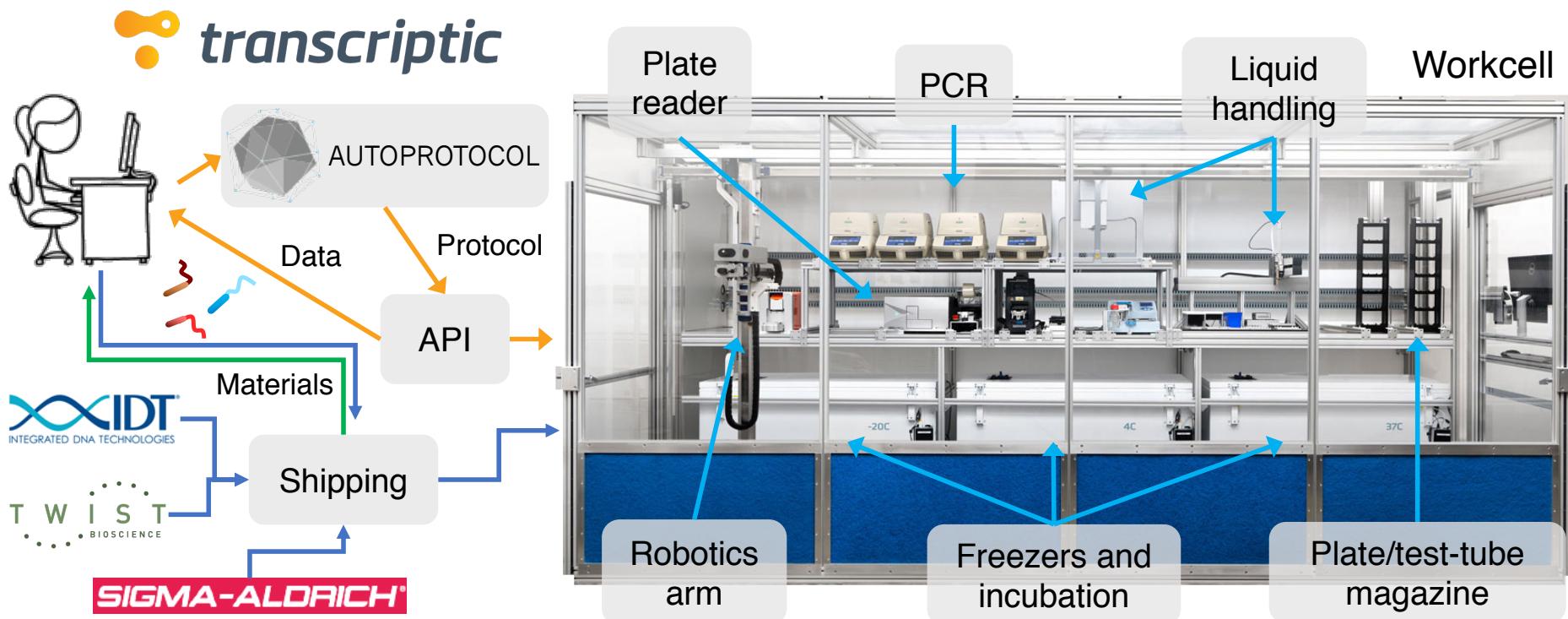
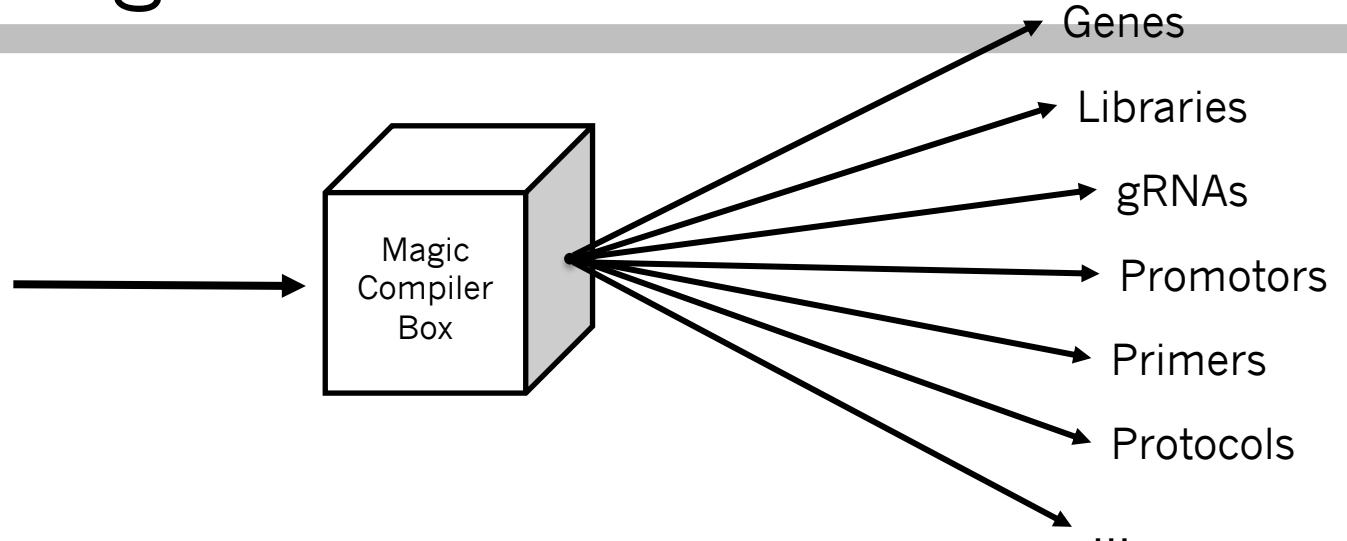
Genotype Specification Language (GSL)

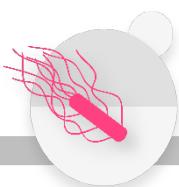


Automate all the things

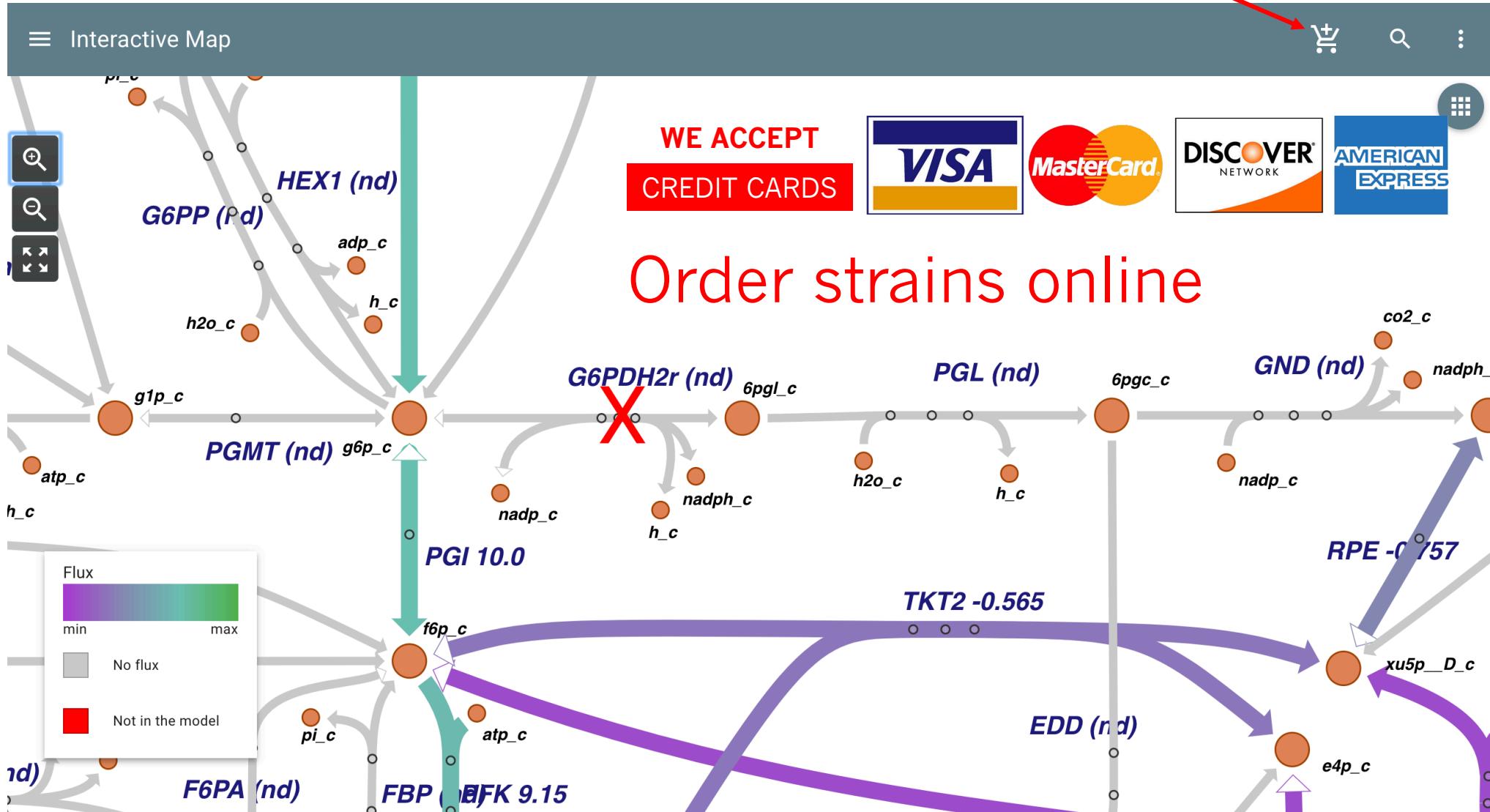
High-level strain design

"Delete native genes A, B, C, and D. Add foreign genes X, Y, Z. Increase flux through reaction F by twofold while reducing flux through reaction G by threefold. Remove product inhibition in pathway Q ..."





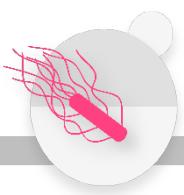
Order button



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





Practical part

- Gentle introduction to Python + Jupyter notebooks (5 min)
- Cobrapy
 - <https://github.com/DD-DeCaF/tutorials/blob/master/cobrapy-01-getting-started.ipynb> (15 min)
 - <https://github.com/DD-DeCaF/tutorials/blob/master/cobrapy-02-genome-scale-metabolic-models.ipynb> (10 min)
 - <https://biosustain.github.io/cell-factory-design-course/08-Theoretical-maximum-yields/> (15 min)
- Cameo
 - <https://github.com/DD-DeCaF/tutorials/blob/master/cameo-01-predict-heterologous-pathways.ipynb> (30 min)
 - <https://github.com/DD-DeCaF/tutorials/blob/master/cameo-02-generating-gene-knockout-strategies.ipynb> (30 min OptGene example)
- DD-DeCaF
 - <https://app.dd-decaf.eu>



Acknowledgements



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Get in touch with us via:
<http://dd-decaf.eu/>
[@ddddecaf](https://twitter.com/ddddecaf) (Twitter)



ESCHER
Build, share, and embed visualizations of biological pathways.

Zachary King (UCSD)

The ESCHER logo features the word "ESCHER" in a large, bold, serif font. To the left of the text is a small icon depicting a stylized biological pathway with red and purple nodes and connecting lines. Below the main text, a smaller box contains a portrait photo of Zachary King and the text "Zachary King (UCSD)".

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