

Technical University of Denmark



Putting computational modeling at the fingertips of bench biologists

Sonnenschein, Nikolaus; Herrgard, Markus

Publication date:
2014

Document Version
Publisher's PDF, also known as Version of record

[Link back to DTU Orbit](#)

Citation (APA):
Sonnenschein, N., & Herrgard, M. (2014). Putting computational modeling at the fingertips of bench biologists. Poster session presented at 2nd EMBO Conference on Visualizing Biological Data, Heidelberg, Germany.

DTU Library

Technical Information Center of Denmark

General rights

Copyright and moral rights for the publications made accessible in the public portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

- Users may download and print one copy of any publication from the public portal for the purpose of private study or research.
- You may not further distribute the material or use it for any profit-making activity or commercial gain
- You may freely distribute the URL identifying the publication in the public portal

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

PUTTING COMPUTATIONAL MODELING AT THE FINGERTIPS OF BENCH BIOLOGISTS

Nikolaus Sonnenschein* and Markus Herrgård

The Novo Nordisk Center for Biosustainability, Technical University of Denmark

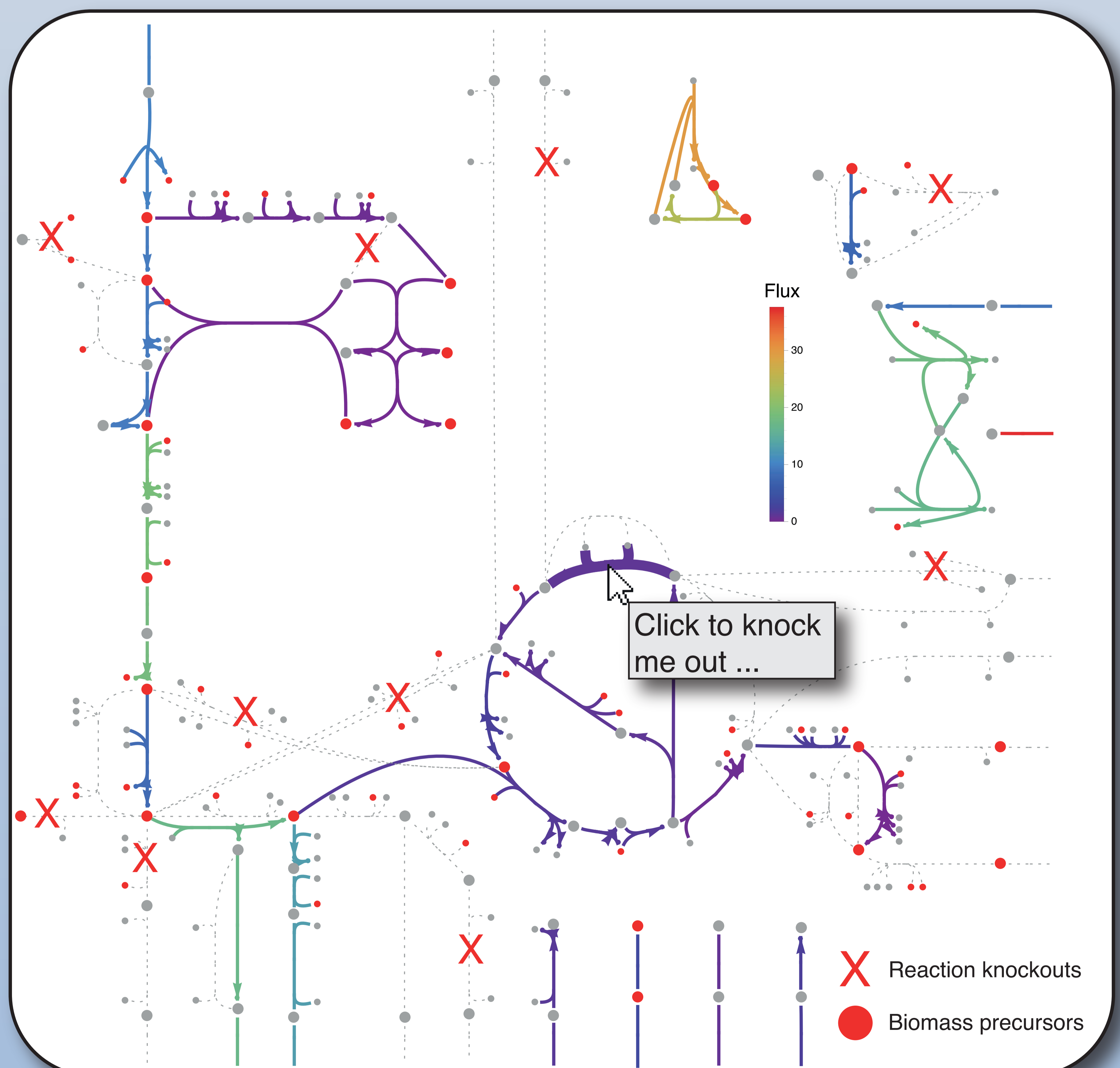
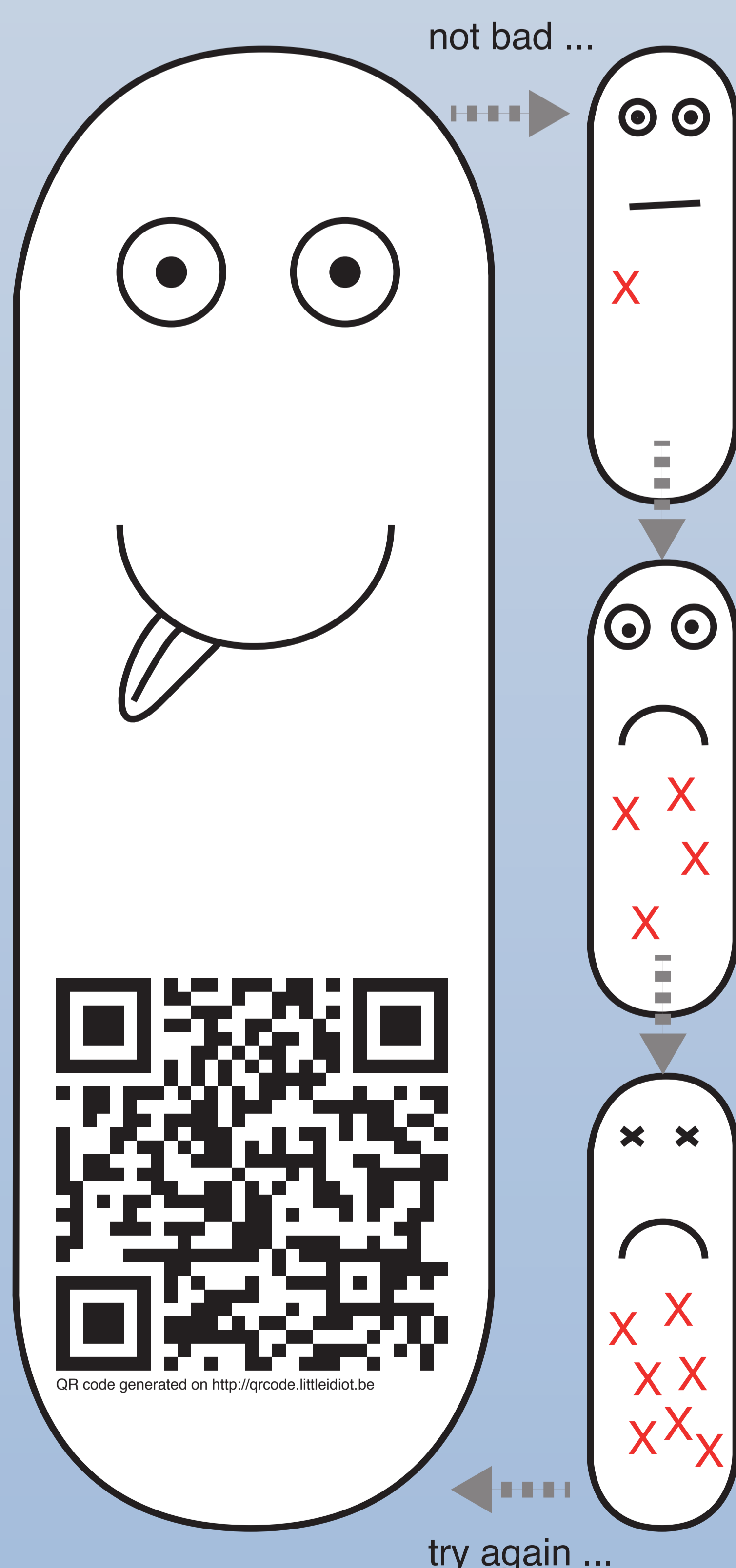
*Correspondence: niso@biosustain.dtu.dk

ABSTRACT

Communication is key in successful collaborations between theoretical and experimental life scientists. In our line of work we integrate physiological and systems-level data of cell factories with constraint-based modeling approaches to predict suitable targets for metabolic engineering. The most important step in this process is the discourse and prioritization of strategies with the people that actually implement them. Having worked with a particular host organism for many years, experimentalists can often discard strategies based on previous experience or feasibility. Counterintuitive solutions, which are often very interesting from a patenting and biological perspective, require a detailed explanation to convince experimentalists to be worthwhile pursuing. Interactive pathway visualizations have turned out to be tremendously helpful in this context. So far, we have used the high-level programming environment Mathematica and an open source metabolic modeling package (MASS Toolbox) to quickly prototype maps and other interactive widgets. In the long term, we would like to make those publicly accessible using open web technologies.

Stop reading the abstract already and checkout the live demos on the laptop next to the poster ...

Whack-A-Bug v0.1



References:

<http://sbrg.github.io/MASS-Toolbox>

<http://www.biosustain.dtu.dk/>

<http://sbrg.ucsd.edu/>

Acknowledgments:

Daniel Zielinski, Aarash Bordbar, Zachary King, Neema Jamshidi, Sirus and Bernhard Palsson at University of California, San Diego