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Publication date:
2014

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

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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.

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PUTTING COMPUTATIONAL MODELING AT THE FINGERTIPS OF BENCH BIOLOGISTS

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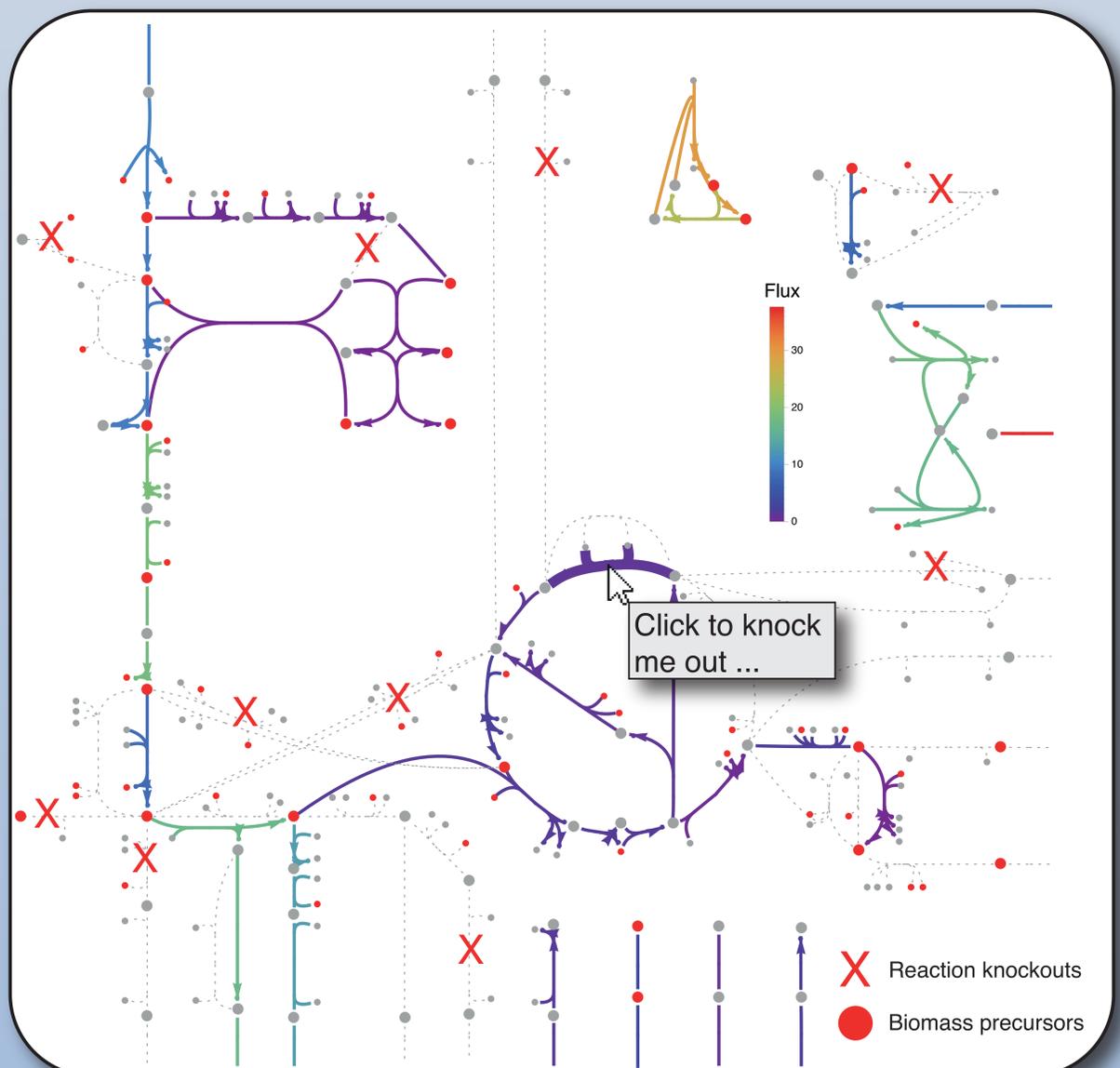
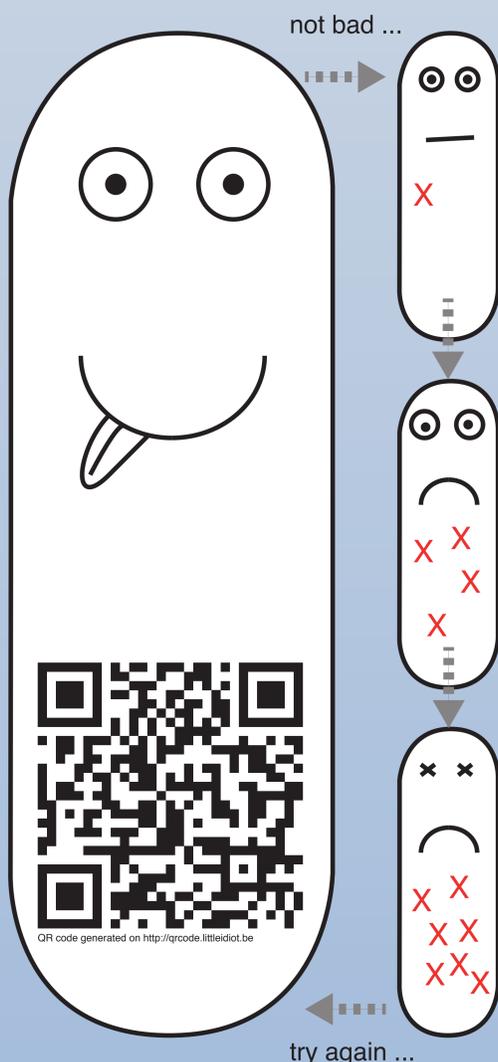
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ABSTRACT

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