The Novo Nordisk Foundation Center for Biosustainability
Kogle Allé 6, DK-2970 Hørsholm
Denmark
+45 217 989 22
niso@biosustain.dtu.dk
www.nikosonnensche.in
nikosonnenschein
phantomas1234
phantomas1234
orcid: 0000-0002-7581-4936

Nikolaus Sonnenschein

Ph.D.

Research Interests

Various aspects of computational systems and synthetic biology, in particular models of metabolism, eukaryotic and prokaryotic gene regulation, dynamics on networks, analysis of high-throughput data, kinetic modeling of biological processes, *in silico* cell factory design, and scientific software development.

Education

January 2011 ***Ph.D.* in Bioinformatics**, *Jacobs University Bremen*, Germany, with special distinction.

July 2007 ***Diplom* in Biology (equivalent to M.Sc.)**, *Technical University of Darmstadt*, Germany, with distinction (overall grade: 1.0, very good).

May 2004 ***Vordiplom* in Biology (equivalent to B.Sc.)**, *Technical University of Darmstadt*, Germany.

Professional Experience

since August 2013 **Research Scientist**, *The Novo Nordisk Foundation Center for Biosustainability, DTU*, Denmark.
Modeling work for cell factory engineering projects run in the iLoop Core Unit. Software development of cameo, a Python package for *in silico* cell factory design (see also Scientific Software). Supervision of three PhD students working on interpreting genetic variation in the context of metabolic models, a genome-scale metabolic reconstruction of *Methylococcus capsulatus*, and a kinetic model of *Escherichia coli* central carbon metabolism. Furthermore, supervision of one postdoc working on dedicated strain engineering projects in the iLoop project.

March 2011 – July 2013 **Postdoctoral Researcher**, *University of California, San Diego*, USA.
Development of the next-generation modeling environment for kinetic modeling of metabolic systems (MASS toolbox; see also Scientific Software). Involved in the construction of genome-scale kinetic models of the human erythrocyte and central carbon metabolism of *E. coli*. Detailed enzyme module reconstructions from bibliomic data and calibration using derivative based and derivative free optimization techniques.

September 2007 – January 2011
PhD Student, *Jacobs University Bremen*, Germany.
Combination of constraint-based modeling techniques and graph theoretical methods for the following purposes: (1) Topological classification of medium-dependent essentiality, (2) integration of gene-expression data with metabolic reconstructions of *E. coli* and the human, and (3) the analysis of metabolite correlation networks. Application of point-process statistics to the transcriptional regulatory network and spatial gene organization of *E. coli*.

August 2006 – July 2007
Diploma Student, *Technical University of Darmstadt*, Germany.
Correlation study of perturbed metabolic systems, comparing flux balance analysis and cellular automata dynamics.

October 2005 – July 2006
Research Assistant, *Technical University of Darmstadt*, Germany.
Topological reasons for dynamical stability. Implementation of systems of linear ODEs and cellular automata dynamics on random network topologies.

February 2005 – June 2006
Student Assistant, *Berlin-Brandenburg Academy of Sciences and Humanities*, Germany.
Help with planning the curriculum of a new biophysics study program in the biology department of the Technical University of Darmstadt.

July 2005 – August 2005
Internship, *Max-Planck Institute for Brain Research*, Frankfurt, Germany.
Cell migrations in the Rhombencephalon. *In situ* hybridization study of genes expressed during early mouse brain development.

Publications

Full publication list also available at scholar.google.com/citations?user=8RqKcm0AAAAJ.

Articles

[1] A. Bordbar, D. McCloskey, D. C. Zielinski, **N. Sonnenschein**, N. Jamshidi, and B. Ø. Palsson. "Personalized Whole-Cell Kinetic Models of Metabolism for Discovery in Genomics and Pharmacodynamics". In: *Cell Systems* 1.4 (Oct. 2015), pp. 283–292. ISSN: 24054712. DOI: 10.1016/j.cels.2015.10.003.

[2] J. G. R. Cardoso, M. R. Andersen, M. J. Herrgard, and **N. Sonnenschein**. "Analysis of genetic variation and potential applications in genome-scale metabolic modeling." In: *Frontiers in bioengineering and biotechnology* 3 (2015), p. 13. DOI: 10.3389/fbioe.2015.00013.

[3] A. Ebrahim, E. Almaas, E. Bauer, A. Bordbar, A. P. Burgard, R. L. Chang, A. Dräger, I. Famili, A. M. Feist, R. M. Fleming, S. S. Fong, V. Hatzimanikatis, M. J. Herrgard, A. Holder, M. Hucka, D. Hyduke, N. Jamshidi, S. Y. Lee, N. Le Novere, J. A. Lerman, N. E. Lewis, D. Ma, R. Mahadevan, C. Maranas, H. Nagarajan, A. Navid, J. Nielsen, L. K. Nielsen, J. Nogales, A. Noronha, C. Pal, B. Ø. Palsson, J. A. Papin, K. R. Patil, N. D. Price, J. L. Reed, M. Saunders, R. S. Senger, **N. Sonnenschein**, Y. Sun, and I. Thiele. "Do genome-scale models need exact solvers or clearer standards?" In: *Molecular Systems Biology* 11.10 (Oct. 2015), pp. 831–831. ISSN: 1744-4292. DOI: 10.15252/msb.20156157.

[4] Z. A. King, A. Dräger, A. Ebrahim, **N. Sonnenschein**, N. E. Lewis, and B. Ø. Palsson. "Escher: A Web Application for Building, Sharing, and Embedding Data-Rich Visualizations of Biological Pathways." In: *PLoS computational biology* 11.8 (2015), e1004321. DOI: 10.1371/journal.pcbi.1004321.

[5] D. Machado, K. H. Zhuang, **N. Sonnenschein**, and M. J. Herrgard. "Editorial: Current Challenges in Modeling Cellular Metabolism". In: *Frontiers in bioengineering and biotechnology* 3 (2015), p. 107. DOI: 10.3389/fcell.2015.00017.

[6] K. R. Kildegaard, B. M. Hallström, T. H. Blicher, **N. Sonnenschein**, N. B. Jensen, S. Sherstyk, S. J. Harrison, J. Maury, M. J. Herrgard, A. S. Juncker, J. Forster, J. Nielsen, and I. Borodina. "Evolution reveals a glutathione-dependent mechanism of 3-hydroxypropionic acid tolerance." In: *Metabolic engineering* 26C (2014), pp. 57–66. DOI: 10.1016/j.ymben.2014.09.004.

[7] I. Thiele, N. Swainston, R. M. T. Fleming, A. Hoppe, S. Sahoo, M. K. Aurich, H. Haraldsdottir, M. L. Mo, O. Rolfsson, M. D. Stobbe, S. G. Thorleifsson, R. Agren, C. Bölling, S. Bordel, A. K. Chavali, P. Dobson, W. B. Dunn, L. Endler, D. Hala, M. Hucka, D. Hull, D. Jameson, N. Jamshidi, J. J. Jonsson, N. Juty, S. Keating, I. Nookaew, N. Le Novère, N. Malys, A. Mazein, J. A. Papin, N. D. Price, E. Selkov, M. I. Sigurdsson, E. Simeonidis, **N. Sonnenschein**, K. Smallbone, A. Sorokin, J. H. G. M. van Beek, D. Weichart, I. Goryanin, J. Nielsen, H. V. Westerhoff, D. B. Kell, P. Mendes, and B. Ø. Palsson. "A community-driven global reconstruction of human metabolism." In: *Nature biotechnology* 31.5 (2013), pp. 419–425. DOI: 10.1038/nbt.2488.

[8] M. E. Beber, C. Fretter, S. Jain, **N. Sonnenschein**, M. Müller-Hannemann, and M.-T. Hütt. "Artefacts in statistical analyses of network motifs: general framework and application to metabolic networks." In: *Journal of the Royal Society, Interface / the Royal Society* 9.77 (2012), pp. 3426–3435. DOI: 10.1098/rsif.2012.0490.

[9] **N. Sonnenschein**, J. F. Golib Dzib, A. Lesne, S. Eilebrecht, S. Boulkroun, M.-C. Zennaro, A. Benecke, and M.-T. Hütt. "A Network Perspective on Metabolic Inconsistency." In: *BMC systems biology* 6.1 (2012), p. 41. DOI: 10.1186/1752-0509-6-41.

[10] **N. Sonnenschein**, C. Marr, and M.-T. Hütt. "A topological characterization of medium-dependent essential metabolic reactions." In: *Metabolites* 2.3 (2012), pp. 632–647. DOI: 10.3390/metabo2030632.

[11] **N. Sonnenschein**, M. Geertz, G. Muskhelishvili, and M.-T. Hütt. "Analog regulation of metabolic demand". In: *BMC Systems Biology* 5.1 (2011), p. 40. ISSN: 1752-0509. DOI: 10.1186/1752-0509-5-40.

[12] **N. Sonnenschein**, M.-T. Hütt, H. Stoyan, and D. Stoyan. "Ranges of control in the transcriptional regulation of *Escherichia coli*." In: *BMC systems biology* 3 (2009), p. 119. DOI: 10.1186/1752-0509-3-119.

Book chapters

[13] B. Bergdahl, **N. Sonnenschein**, D. Machado, M. Herrgård, and J. Forster. "Genome-Scale Models - Fundamental Bioengineering". In: *Fundamental Bioengineering*. Wiley-VCH Verlag GmbH & Co. KGaA, 2015, pp. 143–182. ISBN: 9783527697441. DOI: 10.1002/9783527697441.ch06.

In Preparation

[14] J. G. R. Cardoso, K. Jensen, E. Özdemir, M. J. Herrgård, and **N. Sonnenschein**. *Cameo: A Python Library for Computer Aided Metabolic Engineering and Optmiziation of Cell Factories. in preparation.*

[15] **N. Sonnenschein**, A. Sastry, D. Zielinski, S. P. James de Bree, A. Thomas, A. Bordbar, N. Jamshidi, and B. Ø. Palsson. *The MASS Toolbox: Accessible dynamic modeling. revised manuscript will be submitted soon.*

Oral Conferences Contributions

7th Copenhagen Bioscience Conference — Novo Nordisk Foundation, Hillerørd, Denmark, May 2015, Chairman of "Modeling" session. Speakers: Bernhard Palsson (University of California, San Diego), Nathan Price (Institute for Systems Biology), and Hector Garcia Martin (Joint BioEnergy Institute)

COBRA — Charlottesville, Virginia, USA, May 2014, Invited talk: *Putting constraint-based modeling at the fingertips of bench biologists*, N. Sonnenschein and M. Herrgård

Winter q-bio Meeting — Waikiki, Hawaii, USA, February 2013, Contributed talk: *Dynamic modeling for the masses: the MASS toolbox*, N. Sonnenschein, D.C. Zielinski, A. Bordbar, N. Jamshidi, B.Ø. Palsson,

A complex systems view on production and distribution networks — Organized by *Volkswagen Stiftung*, Berlin, Germany, April 2009, Contributed talk: *A Network Perspective on Metabolic Inconsistency*, N. Sonnenschein, J.F. Golib Dzib, S. Boulkroun, A. Lesne, M.-C. Zennaro, A. Benecke, and M.-T. Hütt

Grants and Fellowships

Ongoing

2016 – 2020 — H2020: New bioinformatics approaches in service of biotechnology (BIOTEC-2-2015), co-written application, role of scientific deputy in the consortium.

Past

2007 – 2011 — PhD fellowship awarded by Jacobs University Bremen, Germany.

May 2009 — Travel stipend, German Academic Exchange Service (DAAD), awarded to attend Systems Biology Short Course & Human Reconstruction Jamboree, Center of Systems Biology, Reykjavik, June 2009.

Teaching Experience

2012 – 2013, annually — *BENG 123, Systems Biology and Bioengineering*, University of California, San Diego, undergraduate level, instructor

2010, occasionally — *Bioinformatics and Computational Biology I*, Jacobs University Bremen, graduate level, substitute lecturer

2007 – 2010, annually — *Advanced Bioinformatics Laboratory Course III: Genomics and Elementary Systems Biology*, Jacobs University Bremen, graduate level, substitute lecturer

Scientific Software

MASS toolbox
opencobra.github.io/MASS-toolbox

The Mass-Action Stoichiometric Simulation (MASS) toolbox is a modeling software package that focuses on the construction and analysis of kinetic and constraint-based models of biochemical reactions systems. It has been developed in the group of Bernhard Palsson at the University of California, San Diego. It is licensed under BSD open source license. A publication will be re-submitted soon (see Publications).

Cameo
cameo.bio

A python package for computer aided metabolic engineering and optimization of cell factories. Cameo is a high-level python library developed to aid the strain design process in metabolic engineering projects. The library provides a modular framework of simulation methods, strain design methods, and access to models, that targets developers that want custom analysis workflows. Furthermore, it exposes a high-level API to users that simply want to compute promising strain designs. It is licensed under Apache License (v2.0) open source license. A publication is in preparation (see Publications).

optlang
biosustain.github.io/optlang

Optlang provides a common interface to a series of optimization software and relies on the popular symbolic mathematics package sympy for problem formulation (constraints, objectives, variables, etc.). Optlang is also used in cameo to solve optimization problems encountered in genome-scale metabolic modeling. It is licensed under Apache License (v2.0) open source license.

Driven
driven.bio

Driven provides state-of-the-art methods to analyze omics data using constraint-based models. It is a project by one of my PhD students and is currently under active development. It is licensed under Apache License (v2.0) open source license.

Editorial and Peer Review Duties

Peer review

Reviewer for *BMC Evolutionary Biology*, *BMC Systems Biology*, *Physical Review E*, *Biotechnology and Bioengineering*, *Bioinformatics*, and *Scientific Reports*. Verified peer review record available at publons.com/author/643329.

Editor

Editor for *EPJ Nonlinear Biomedical Physics* (since 2013) and guest editor for *Frontiers in Bioengineering* research topic *Current challenges in modeling cellular metabolism*.

Technical skills

Programming languages

Mathematica, Python, R, C, Matlab, C++, Javascript

Version control

GIT, SVN, Github, Bitbucket

Databases

MySQL, SQLite, HDF5, pytables

Systems

Apple OS X, Linux, BSD, and other UNIX variants, Microsoft Windows

Bioinformatics	BLAST, Biopython, KEGG API, Pathway Tools, SBML, libSBML	Chemoinformatics	Open Babel, ChemAxon Marvin (Java API and command-line tools), SMILES, InChI, SMARTS, ChEBI API
Modeling tools	cobrapy, cameo, driven, COBRA Toolbox, Copasi, CellDesigner, SBW	Optimization	CPLEX, Gurobi, GLPK, GAMS, NEOS optimization server, inspyred

Languages

German	Native speaker	English	Fluent
Greek	Fluent	Danish	Basic