

Publication List of Jörg Stelling

Associate Professor for Computational Systems Biology

ETH Zurich, Department of Biosystems Science & Engineering, Mattenstrasse 26, 8000, CH - 4058 Basel

Secondary affiliation: ETH Zurich, Department of Computer Science, CAB J71.4, CH-8092 Zurich

T: +41-61-38-73194 or +41-44-63-27435 E: joerg.stelling@bsse.ethz.ch

F: +41-61-38-73994 or +41-44-63-21374 W: <http://www.csb.ethz.ch/>

1.1. Journals

- [1] Sunnaker, M., Zamorra-Sillero, E., Dechant, R., Ludwig, C., Busetto, A.G., Wagner, A., Stelling, J., Automatic generation of predictive dynamic models reveals nuclear phosphorylation as the key Msn2 control mechanism. *Sci Signaling*, *under revision*, 2013.
- [2] Ganter, M., Bernard, T., Moretti, S., Stelling, J., Pagni, M., MetaNetX.org: a website and repository for accessing, analyzing and manipulating metabolic networks". *Bioinformatics* (2013) [doi:10.1093/bioinformatics/btt036](https://doi.org/10.1093/bioinformatics/btt036)
- [3] Mayer, C., Dimopoulos, S., Rudolf, F., Stelling, J., Using CellX to quantify intracellular events. *Curr. Prot. Molec. Biol.*, Chapter 14: Unit 14.22, 2013.
- [4] Bacchus, W., Lang, M., Daoud El-Baba, M., Weber, W., Stelling, J., Fussenegger, M., Synthetic two-way communication between mammalian cells. *Nat. Biotechnol.*, 30(10): 991-96, 2012.
- [5] Gonnet, P., Dimopoulos, S., Widmer, L., Stelling, J., A specialized ODE integrator for efficient computation of parameter sensitivities. *BMC Syst Biol.*, 6(1): 46, 2012.
- [6] Jol, J.S., Kuemmel, A., Terzer, M., Stelling, J., Heinemann, M., System-level insights into yeast metabolism by thermodynamic analysis of elementary flux modes. *PLoS Comp Biol* 8(3):e1002415, 2012.
- [7] Buescher, J.M., Liebermeister, W., Jules, M., Uhr, M., Muntel, J., Botella, E., Hessling, B., Kleijn, R.J., Le Chat, L., Lecointe, F., Mäder, U., Nicolas, P., Piersma, S., Rügheimer, F., Becher, D., Bessieres, P., Bidnenko, E., Denham, E.L., Dervyn, E., Devine, K.M., Doherty, G., Drulhe, S., Felicori, L., Fogg, M.J., Goelzer, A., Hansen, A., Harwood, C.R., Hecker, M., Hubner, S., Hultschig, C., Jarmer, H., Klipp, E., Leduc, A., Lewis, P., Molina, F., Noirot, P., Peres, S., Pigeonneau, N., Pohl, S., Rasmussen, S., Rinn, B., Schaffer, M., Schnidder, J., Schwikowski, B., Van Dijl, J.M., Veiga, P., Walsh, S., Wilkinson, A.J., Stelling, J., Aymerich, S., Sauer, U., Global network reorganization during dynamic adaptations of *Bacillus subtilis* metabolism. *Science*, 335(6072): 1099-103, 2012.
- [8] Kaltenbach, H.-M., and Stelling, J., Modular analysis of biological networks. *Adv. Exp. Med. Biol.* 736: 3-17, 2012.
- [9] Lang, M., Rudolf, F., and Stelling, J., Use of YouScope to implement systematic microscopy protocols. *Curr. Prot. Molec. Biol.*, 14.21.1-23, 2012.
- [10] Zamorra, E., Hafner, M., Ibig, A., Stelling, J., and Wagner, A., Efficient characterization of high-dimensional parameter spaces for systems biology. *BMC Syst Biol.* 5(1):142, 2011.

-
- [11] Marchisio, M. and Stelling, J., Automatic design of digital synthetic gene circuits. *PLoS Comp. Biol.*, *PLoS Comput Biol* 7(2): e1001083, 2011.
 - [12] Mirsky, H.P., Taylor, S.R., Harvey, R.A., Stelling, J., and Doyle FJ., Distribution-based sensitivity metric for highly variable biochemical systems. *IET Syst Biol.* 5(1):50, 2011.
 - [13] Lang, M., Marquez-Lago, T., Stelling, J., and Waldherr, S., Autonomous synchronization of chemically coupled oscillators. *Bull. Math. Biol.*, DOI: 10.1007/s11538-011-9642-8.
 - [14] Susaki, E., Stelling, J., and Ueda, H. Challenges in synthetically designing mammalian circadian clocks. *Curr Opin Biotechnol.* 21(4):556-65, 2010.
 - [15] Kemmer, C., Gitzinger, M., Daoud-El Baba, M., Djonov. V., Stelling, J., and Fussenegger, M. Self-sufficient control of urate homeostasis in mice by a synthetic circuit. *Nat Biotechnol.* 28(4): 355-60, 2010.
 - [16] Marquez-Lago, T. and Stelling, J., Counter-intuitive stochastic behavior of simple gene circuits with negative feedback. *Biophys. J.* 98(9): 1742-50, 2010.
 - [17] Tigges, M., Denervaud, N., Greber, D., Stelling, J., and Fussenegger, M., A synthetic low-frequency mammalian oscillator. *Nucleic Acid Res.* 38(9): 2702-11, 2010.
 - [18] Kaltenbach, H.M., Dimopoulos, S. and Stelling J., Systems analysis of cellular networks under uncertainty. *FEBS Lett.* 583(24): 3923-30, 2009.
 - [19] Marchisio, M. and Stelling, J., Computational design tools for synthetic biology. *Curr. Opin. Biotechnol.* 20(4): 479-85, 2009.
 - [20] Terzer, M., Maynard, N.D., Covert, M.W. and Stelling, J., Genome-scale metabolic networks. *Wiley Interdisc. Rev. Systems Biol.*, <http://dx.doi.org/10.1002/wsbm.37>, 2009.
 - [21] Mueller, D. and Stelling, J., Precise regulation of gene expression dynamics favors complex promoter architectures. *PLoS Comput. Biol.* 5(1): e1000279, 2009.
 - [22] Tigges, M., Marquez-Lago, T., Stelling, J. and Fussenegger, M., A tunable synthetic mammalian oscillator. *Nature* 457: 309-312, 2009.
 - [23] Stelling, J. and Kholodenko, B., Signaling cascades as cellular devices for spatial computations. *J. Math. Biol.* 58: 35-55, 2009.
 - [24] Marchisio, M. and Stelling, J., Computational design of synthetic gene circuits with composable parts. *Bioinformatics* 24: 1903-1910, 2008.
 - [25] Terzer, M. and Stelling, J., Large scale computation of elementary flux modes with bit pattern trees. *Bioinformatics* 24: 2229-2235, 2008.
 - [26] Bagheri, N., Stelling, J. and Doyle III, F.J., Circadian phase resetting via single & multiple control targets. *PLoS Comput. Biol.* 4: e1000104, 2008.
 - [27] Conradi, C., Flockerzi, D., Raisch, J. and Stelling, J., Subnetwork analysis reveals dynamic features of complex (bio)chemical networks. *Proc Natl Acad Sci U S A* 104: 19175-19180, 2007.
 - [28] Kuepfer, L., Peter, M., Sauer, U. and Stelling, J., Ensemble modeling for analysis of cell signaling dynamics. *Nat. Biotechnol.* 25: 1001-1006, 2007.

-
- [29] Terzer, M., Jovanovic, M., Choutko, A., Nikolayeva, O., Korn, A., Brockhoff, D., Zürcher, F., Friedmann, M., Schütz, R., Zitzler, E., Stelling, J. and Panke, S., Design of a biological half adder. *IET Systems Biol.* 1: 53-58, 2007.
 - [30] Bagheri, N., Stelling, J. and Doyle III, F.J., Circadian phase entrainment via nonlinear model predictive control. *Int J Robust Nonlinear Control* 17: 1555-1571, 2007.
 - [31] Stelling, J., Understandable complexity. *Science STKE*: pe9, 2007.
 - [32] Weber, W., Stelling, J., Rinnann, M., Keller, B., Daoud-El Baba, M., Weber, C.C., Aubel, D. and Fussenegger, M., A synthetic time-delay circuit in mammalian cells and mice. *Proc. Natl. Acad. Sci. USA* 104: 2643-2648, 2007.
 - [33] Bagheri, N., Stelling, J. and Doyle III, F.J., Quantitative performance metrics for robustness in circadian rhythms. *Bioinformatics* 23: 358-64, 2007.
 - [34] Anders, A., Hager, K., Lilie, H., Kapp, L., Stelling, J., Gilles, E.D. and Breunig, K., The galactose switch in *Kluyveromyces lactis* depends on nuclear competition between Gal4 and Gal1 for Gal80 binding. *J Biol Chem* 281: 29337-48, 2006.
 - [35] Doyle III, F.J. and Stelling, J., Systems interface biology. *J. R. Soc. Interface* 3: 603-616, 2006.
 - [36] Zak, D.E., Stelling, J. and Doyle III, F.J., Sensitivity analysis of oscillatory (bio)chemical systems. *Comp. Chem. Eng.* 29: 663-673, 2005.
 - [37] Stelling, J., Mathematical models in microbial systems biology. *Curr. Opin. Microbiol.* 7(5): 513-518, 2004.
 - [38] Stelling, J., Sauer, U., Szallasi, Z., Doyle III, F.J. and Doyle J., Robustness of cellular functions. *Cell* 118: 675-685, 2004.
 - [39] Stelling, J., Gilles, E.D. and Doyle III, F.J., Robustness properties of circadian clock architectures. *Proc. Natl. Acad. Sci. USA* 101(36): 13210-13215, 2004.
 - [40] Stelling, J. and Gilles, E.D., Mathematical modeling of complex regulatory networks. *IEEE Trans. NanoBioSci.* 3(3): 172-179, 2004.
 - [41] Papin, J., Stelling, J., Price, N., Klamt, S., Schuster, S. and Palsson, B.O., Comparison of network-based pathway analysis methods. *Trends Biotechnol.* 22(8): 400-405, 2004.
 - [42] Hucka, M., Finney, A., Sauro, H., Bolouri, H., Doyle, J., Kitano, H., Arkin, A., Bornstein, B., Bray, D., Cornish-Bowden, A., Cuellar, A., Dronov, S., Gilles, E. D., Ginkel, M., Gor, V., Goryanin, I., Hedley, W., Hodgman, T., Hofmeyr, J., Hunter, P., Juty, N., Kasberger, J., Kremling, A., Kummer, U., Le Novere, N., Loew, L., Lucio, D., Mendes, P., Minch, E., Mjolsness, E., Nakayama, Y., Nelson, M., Nielsen, P., Sakurada, T., Schaff, J., Shapiro, B., Shimizu, T., Spence, H., Stelling, J., Takahashi, K., Tomita, M., Wagner, J., and Wang, J., The Systems Biology Markup Language (SBML): a medium for representation and exchange of biochemical network models. *Bioinformatics* 19(4): 524-531, 2003.
 - [43] Klamt, S., Stelling, J., Ginkel, M. and Gilles, E.D., *FluxAnalyzer*: Exploring structure, pathways and flux distributions in metabolic networks on interactive flux maps. *Bioinformatics* 19 (2): 261-269, 2003.

-
- [44] Klamt, S. and Stelling, J., Two approaches for metabolic pathway analysis? *Trends Biotechnol.* 21(2): 64-69, 2003.
 - [45] Stelling, J., Klamt, S., Bettenbrock, K., Schuster, S. and Gilles, E.D., Metabolic network structure determines key aspects of functionality and regulation. *Nature* 420: 190-193, 2002.
 - [46] Klamt, S. and Stelling, J., Combinatorial complexity of pathway analysis in metabolic networks. *Mol. Biol. Rep.* 29 (1-2): 233-236, 2002.
 - [47] Desbrosses, G., Stelling, J. and Renaudin J., Dephosphorylation activates the purified plasma membrane (H^+)-ATPase. Possible function of phosphothreonine residues in a mechanism not involving the regulatory C-terminal domain of the enzyme. *Eur. J. Biochem.* 251: 496-503, 1998.
 - [48] Posten, C., Schröder, M., Stelling, J. and Hecht, V., Bestimmung von Substrat-inhibierten Zuständen zur Validierung von Modellen zum Schadstoffabbau. *Automatisierungstechnik* 46(8): 381-385, 1998.

1.2. Proceedings (peer-reviewed)

- [49] Otero-Muras, I., Yordanov, P., Stelling, J., Advances in chemical reaction network theory for the identification of kinetic models. *Proc. SYSID 16th IFAC Symposium on Systems Identification*, 2012.
- [50] Kaltenbach, M., Constantinescu, S., Feigelman, J., and Stelling, J., Graph-based decomposition of biochemical reaction networks into monotone subsystems. *Proc. WABI 2011; Lecture Notes in Computer Science* 6833: 139-150, 2011.
- [51] Uhr, M., Villaverde, A.F., Egea, J.A, Banga, J., and Stelling, J., Inference of transcriptional control design of metabolic networks. *Proc. IFAC World Congress 2011*, 10448-53, 2011.
- [52] Mirsky, H., Stelling, J., and Doyle III, F.J., Concentrated fragilities and noise resistance in the mammalian circadian clock. *Proc. FOSBE 2009, under revision*.
- [53] Terzer, M. and Stelling, J., Parallel extreme ray and pathway computation, *Proc. PPAM 2009 Conference, Wroclaw, Poland; Lecture Notes Computer Science* 6068: 300-309, 2010.
- [54] Uhr, M., Kaltenbach, H.-M., Conradi, C. and Stelling, J., Analysis of degenerate chemical reaction networks. *3rd Intl. Symposium on Positive Systems: Theory and Applications 2009 (POSTA 2009), LNCIS* 389: 163-171, 2009.
- [55] Marchisio, M.A. and Stelling, J., Synthetic gene network computational design. *Proc. IEEE International Symposium Circuits and Systems (ISCAS) 2009*, pages 309-312, 2009.
- [56] Uhr, M. and Stelling, J., Structural sensitivity analysis of metabolic networks. *Proc. IFAC World Congress 2008* (6 pages).
- [57] Ibig, A. and Stelling, J., Robustness of minimal biochemical oscillators, *Proc. 3rd Int. Symposium Communications, Control and Signal Processing*, pages 148-153, 2008.
- [58] Terzer, M. and Stelling, J., Accelerating the computation of elementary modes using pattern trees. *Lecture Notes Bioinformatics* 4175: 333-43, 2006.

- [59] Bagheri, N., Taylor, S., Stelling, J. and Doyle III, F.J., A finite differences approach to phase-based sensitivity analysis of biological oscillators. *Proc. FOSBE 2005, Santa Barbara / CA*, pages 93-98, 2005.
- [60] Stelling, J. and Gilles, E.D., Perturbations are key to quantitative identification of a complex subsystem in yeast cell cycle control. *Proc. FOSBE 2005, Santa Barbara / CA*, pages 111-114, 2005.
- [61] Doyle III, F.J. and Stelling, J., Robust performance in biophysical networks. *16th IFAC World Congress, Prague 2005*, paper ID 03497 (6 pages).
- [62] Bagheri, N., Stelling, J. and Doyle III, F.J., Optimal phase-tracking of the nonlinear circadian oscillator. *Proc. 24th American Control Conference, Portland*, pages 3235-3240, 2005.
- [63] Stelling, J., Hierarchies and modularity in metabolic networks. In Gauges R. et al., editors, *Proc. 3rd Workshop on Computation of Biochemical Pathways and Genetic Networks, Heidelberg, Germany*, pages 11-16. Logos Verlag, Berlin, 2003.
- [64] Schuster, S., Klamt, S. and Stelling, J., Making predictions about robustness and flexibility from metabolic network structure. In Mewes, H.-W., Henn, V., Frishman, D. and Kramer, S., editors, *Proc. German Conf. Bioinformatics 2003*, Munich, pages 129-134. belleville Verlag Michael Farin, 2003.
- [65] Stelling, J. and Gilles, E.D., Robustness vs. identifiability of regulatory modules? The case of mitotic control in budding yeast cell cycle regulation. In *Proc. 2nd International Conference on Systems Biology*, Pasadena, USA, pages 181–190, 2001.
- [66] Conradi, C., Stelling, J. and Raisch, J., Structure discrimination of continuous models for (bio)chemical reaction networks via finite state machines. In *Proc. IEEE / ISIC 2001*, Mexico City, Mexico, pages 138–143, 2001.
- [67] Stelling, J., Kremling, A. and Gilles, E.D., Towards a Virtual Biological Laboratory. In *Proc. 1st International Conference on Systems Biology*, Tokyo, Japan, pages 29–38, 2000.
- [68] Stelling, J. and Gilles, E.D., Modular mathematical modeling of complex regulatory networks: Application to cell cycle regulation in *Saccharomyces cerevisiae*. In H. Brunner, editor, *Proc. 4th International Congress in Biochemical Engineering*, Stuttgart, Germany, pages 43–47. Fraunhofer IRB Verlag, 2000.
- [69] Posten, C., Schröder, M., Stelling, J. and Hecht, V., Control of substrate inhibited steady states for model validation. In *Proc. 13th IFAC World Congress*, San Francisco, USA, Volume N, pages 467-472, 1996.

1.3. Books and Book Chapters

- [70] Szallasi, Z., Stelling, J. and Periwal, V., editors, *System modeling in cellular biology: From concepts to nuts and bolts*, MIT Press, Cambridge / Massachusetts, 2006.
- [71] Stelling, J., Systems analysis of robustness in cellular networks. (*Forschungsberichte aus dem Max-Planck-Institut für Dynamik komplexer technischer Systeme*, Vol. 8) Shaker Verlag, Aachen, 2004.

- [72] Mirsky, H., Stelling, J., Gunawan, R., Bagheri, N., Taylor, S.R., Kwei, E., Shoemaker, J.E., and Doyle, F.J., III. Automatic control in systems biology. In Nof, S.Y., editor, Springer *Handbook of Automation*, pages 1335-60, 2009.
- [73] Stelling, J., Sauer, U., Doyle III, F.J. and Doyle, J., Complexity and robustness of cellular systems. In Z. Szallasi et al., editors, pages 19-40, MIT Press, 2006.
- [74] Szallasi, Z., Periwal, V. and Stelling, J., On modules and modularity. In Z. Szallasi et al., editors, pages 41-50, MIT Press, 2006.
- [75] Klamt, S. and Stelling, J., Stoichiometric and constraint-based modeling. In Z. Szallasi et al., editors, pages 73-96, MIT Press, 2006.
- [76] Kremling, A., Stelling, J., Bettenbrock, K., Fischer, S. and Gilles, E.D., Metabolic networks: Biology meets Engineering. In L. Alberghina and H.V. Westerhoff, editors, *Systems Biology: Definitions and Perspectives*, pages 214-234, Springer Verlag, 2005.
- [77] Stelling, J., Kremling, A., Ginkel, M., Bettenbrock, K. and Gilles, E.D., Towards a Virtual Biological Laboratory. In H. Kitano, editor, *Foundations of Systems Biology*, pages 189–212. MIT Press, Cambridge / Massachusetts, 2001.
- [78] Stelling, J., Biener, R., Haas, J., Oswald, G., Schuller, D., Noé, W. and Gilles, E.D., Modeling of glycoprotein production by Chinese Hamster Ovary cells for process monitoring and control. In Mertens, O.-W., Perrin, P. and Griffiths, B., editors, *Animal Cell Technology: New developments - new applications*, pages 359-362. Kluwer Academic Publishers, 1998.

1.4. Reports

- [79] European Commission / Directorate General for Research, Synthetic Biology: Applying Engineering to Biology (NEST High-level expert group report: Serrano, L., Vancompernolle, K., Ball, P., Benenson, Y., Holliger, P., Panke, S., Rettberg, R., Stelling, J. and Weiss, R.), EUR 21796, 2005.