

Publications

Research papers

<p>Meyer, K., Ostrenko, O., Bourantas, G., Morales-Navarrete, H., Porat-Shliom, N., Segovia-Miranda, F., Nonaka, H., Ghaemi, A., Verbavatz, J.M., Bruschi, L. and Sbalzarini, I., Kalaidzidis, Y., Weigert, R., Zerial M.</p> <p>A Predictive 3D Multi-Scale Model of Biliary Fluid Dynamics in the Liver Lobule. <i>Cell Systems</i> 4 (3), 277–290, 2017.</p>
<p>K.B. Hoffmann, A. Voss-Böhme, J.C. Rink, L. Bruschi.</p> <p>A dynamically diluted alignment model reveals the impact of cell turnover on the plasticity of tissue polarity patterns. <i>Journal of the Royal Society Interface</i> 14 (135), 20170466, 2017.</p>
<p>O. Ostrenko, P. Incardona, R. Ramaswamy, L. Bruschi, I.F. Sbalzarini.</p> <p>pSSAlib: The partial-propensity stochastic chemical network simulator. <i>PLoS Computational Biology</i> 13(12), e1005865, 2017.</p>
<p>O. Parvu and D. Gilbert.</p> <p>A novel method to verify multilevel computational models of biological systems using multiscale spatio-temporal meta model checking. <i>PLoS ONE</i>, 11(5): e0154847, 2016.</p>
<p>M. Herberg, T. Zerjatke, W. de Back, I. Glauche and I. Roeder.</p> <p>Image-based quantification and mathematical modeling of spatial heterogeneity in ESC colonies. <i>Cytometry: Part A</i>, 2015.</p>
<p>O. Parvu and D. Gilbert.</p> <p>Automatic validation of computational models using pseudo-3D spatio-temporal model checking. <i>BMC Systems Biology</i>, 8:124, 2014.</p>
<p>A. Köhn-Luque, W. de Back, Y. Yamaguchi, K. Yoshimura, M. A. Herrero and T. Miura.</p> <p>Dynamics of VEGF matrix-retention in vascular network patterning. <i>Physical Biology</i>, 10:066007, 2013.</p>
<p>W. de Back, R. Zimm, L. Bruschi</p> <p>Transdifferentiation of pancreatic cells by loss of contact-mediated signaling. <i>BMC Systems Biology</i>, 7:77, 2013.</p>
<p>W. de Back, J. X. Zhou, L. Bruschi</p> <p>On the role of lateral stabilization during early patterning in the pancreas. <i>Journal of the Royal Society Interface</i> 10(79):20120766, 2012.</p>
<p>A. Köhn-Luque, W. de Back, J. Starruß, A. Mattiotti, A. Deutsch, J. M. Pérez-Pomares, M. A. Herrero</p> <p>Early embryonic vascular patterning by matrix-mediated paracrine signalling. <i>PLoS ONE</i> 6(9):e24175, 2011.</p>
<p>J. Starruß, T. Bley, L. Søgaard-Andersen, A. Deutsch</p> <p>A new mechanism for collective migration in <i>Myxococcus xanthus</i>. <i>Journal of Statistical Physics</i>, 128, 269-286, 2007.</p>

Also cited in

<p>Appleton, E., Madsen, C., Roehner, N. and Densmore, D.,</p> <p>Design Automation in Synthetic Biology. <i>Cold Spring Harbor Perspectives in Biology</i>, 2017.</p>
<p>Cytowski, M., Szymańska, Z., Umiński, P., Andrejczuk, G. and Raszkowski, K.</p> <p>Implementation of an Agent-Based Parallel Tissue Modelling Framework for the Intel MIC Architecture. <i>Scientific Programming</i>, 2017.</p>
<p>P. Macklin, H. Frieboes, J. Sparks, A. Ghaffarizadeh, S. Friedman, E. Juarez, E. Jonckheere, S. Mumenthaler</p> <p>Progress Towards Computational 3-D Multicellular Systems Biology In: <i>Systems Biology of Tumor Microenvironment</i> (edited by: K. Rejniak), 2016.</p>

J. S. Yu, N. Bagheri. Multi-class and multi-scale models of complex biological phenomena <i>Current Opinion in Biotechnology</i> , 39:167-173, 2016.
O. Chara, E. Tanaka, L. Brusch. Mathematical Modeling of Regenerative Processes . In: <i>Current Topics in Developmental Biology: Mechanisms of Regeneration</i> (edited by: B. Galliot) Volume 108, 2014.
S.J. Parker, K. Raedschelders and J. E. Van Eyk. Emerging proteomic technologies for elucidating context-dependent cellular signaling events: A big challenge of tiny proportions . <i>Proteomics</i> , 2014.
L.A. D'Alessandro, S. Hoehme, A. Henney, D. Drasdo and U. Klingmüller. Unraveling liver complexity from molecular to organ level: Challenges and perspectives . <i>Progress in biophysics and molecular biology</i> , 2014.
S. Kang, S. Kahan, J. McDermott, N. Flann and I. Shmulevich. Biocellion: accelerating computer simulation of multicellular biological system models . <i>Bioinformatics</i> 30(2):3101-3108, 2014.

Beyond this selection, 44 sources have so far cited our paper in total (as of Dec. 2017).

Conferences

Talks and poster presentations at the following conferences and workshops:

W. de Back, Morpheus 2: Modeling and simulation platform for multicellular systems biology. And MorpheusML: declarative markup language for multicellular systems biology, Workshop "Towards a unified framework for benchmarking multi-cellular models and simulation software" (organized D. Drasdo and S. Hoehme et al., Leipzig, March 2016 (invited talks)
W. de Back, Spatial multiscale computational systems biology , Schloss Dagstuhl - Leibniz-Zentrum für Informatik, Germany, November 2014 (talk)
L. Brusch, W. de Back, J. Starruß, A. Deutsch, Morpheus: a User-friendly Modeling Environment for Multiscale and Multicellular Systems Biology, Symposium on "Executable cell biology for tissue engineering and regenerative medicine", TERMIS-EU , Genova, Italy, 2014. (abstract) (talk)
W. de Back, Integrative modeling in developmental systems biology, Institute for Medical Informatics and Biometry, Medical Faculty „Carl Gustav Carus“, Technische Universität Dresden, 2013. (talk)
W. de Back, A. Deutsch, Morpheus: Modeling and Simulation in Multicellular System Biology, 1st Sino-German Workshop on Simulation, Changsha, China, 2011. (talk)

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