Publications

Software

J. Starruß, W. de Back, L. Brusch and A. Deutsch.
Morpheus: a user-friendly modeling environment for multiscale and multicellular systems biology.
Bioinformatics, 30(9):1331-1332, 2014.
Please use this reference when citing the software.

Research papers

Meyer, K., Ostrenko, O., Bourantas, G., Morales-Navarrete, H., Porat-Shliom, N., Segovia-Miranda, F., Nonaka, H., Ghaemi, A., Verbavatz, J.M., Brusch, L. and Sbalzarini, I., Kalaidzidis, Y., Weigert, R., Zerial M.
A Predictive 3D Multi-Scale Model of Biliary Fluid Dynamics in the Liver Lobule. *Cell Systems*, 2017.

O. Parvu and D. Gilbert.
A novel method to verify multilevel computational models of biological systems using multiscale spatio-temporal meta model checking.
PLoS ONE, 11(5): e0154847, 2016.

M. Herberg, T. Zerjatke, W. de Back, I. Glauche and I. Roeder.
Image-based quantification and mathematical modeling of spatial heterogeneity in ESC colonies.
Cytometry: Part A, 2015.

O. Parvu and D. Gilbert.
Automatic validation of computational models using pseudo-3D spatio-temporal model checking.
BMC Systems Biology, 8:124, 2014.

A. Köhn-Luque, W. de Back, Y. Yamaguchi, K. Yoshimura, M. A. Herrero and T. Miura.
Dynamics of VEGF matrix-retention in vascular network patterning.
Physical Biology, 10:066007, 2013.

W. de Back, R. Zimm, L. Brusch
Transdifferentiation of pancreatic cells by loss of contact-mediated signaling.
BMC Systems Biology, 7:77, 2013.

W. de Back, J. X. Zhou, L. Brusch
On the role of lateral stabilization during early patterning in the pancreas.
Journal of the Royal Society Interface 10(79):20120766, 2012.

A. Köhn-Luque, W. de Back, J. Starruß, A. Mattiotti, A. Deutsch, J. M. Pérez-Pomares, M. A. Herrero
Early embryonic vascular patterning by matrix-mediated paracrine signalling.
PLoS ONE 6(9):e24175, 2011.

J. Starruß, T. Bley, L. Søgaard-Andersen, A. Deutsch
A new mechanism for collective migration in Myxococcus xanthus.
Journal of Statistical Physics, 128, 269-286, 2007.

Also cited in

Appleton, E., Madsen, C., Roehner, N. and Densmore, D.,
Design Automation in Synthetic Biology. *Cold Spring Harbor Perspectives in Biology*, 2017.

Cytowski, M., Szymańska, Z., Umiński, P., Andrejczuk, G. and Raszkowski, K.
Implementation of an Agent-Based Parallel Tissue Modelling Framework for the Intel MIC Architecture. *Scientific Programming*, 2017.

P. Macklin, H. Frieboes, J. Sparks, A. Ghaffarizadeh, S. Friedman, E. Juarez, E. Jonckheere, S. Mumenthaler
Progress Towards Computational 3-D Multicellular Systems Biology
In: *Systems Biology of Tumor Microenvironment* (edited by: K. Rejniak), 2016.

J. S. Yu, N. Bagheri. Multi-class and multi-scale models of complex biological phenomena *Current Opinion in Biotechnology*, 39:167–173, 2016.
O. Chara, E. Tanaka, L. Brusch. Mathematical Modeling of Regenerative Processes. In: *Current Topics in Developmental Biology*: Mechanisms of Regeneration (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. *Proteomics*, 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. *Progress in biophysics and molecular biology*, 2014.
S. Kang, S. Kahan, J. McDermott, N. Flann and I. Shmulevich. Biocellion: accelerating computer simulation of multicellular biological system models. *Bioinformatics* 30(2):3101-3108, 2014.

Education

Morpheus was used in the following courses:

GSCN workshop on Computational Stem Cell Biology 1-2 December 2014.
DIGS-BB course on Spatio-temporal Pattern Formation in Cells and Tissues Autumn 2012 and 2013.
ECMI modeling week European Summer School in Industrial Mathematics and Modelling Week (ESSIM2012) August 12-22, 2012. Described in this paper: F. Rost, A. Quintero, M. Myllykoski, A. Igolkina, A. Rohde O'Sullivan Freltoft, N. Dixit Morphogenesis and Dynamics of Multicellular Systems ECMI Newsletter, 52, October 2012.

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, J. Starruß, L. Brusch, A. Deutsch, Morpheus: Computational modeling for stem cell biologists, 3rd International Conference of the German Stem Cell Network (**GSCN 2015**), Franktfurt am Main, Germany, September 2015 (talk)
W. de Back, Spatial multiscale computational systems biology, Schloss **Dagstuhl** - Leibniz-Zentrum für Informatik, Germany, November 2014 (talk)
W. de Back, A. Köhn-Luque, A. Deutsch, Morpheus: a user-friendly modeling environment for multicellular systems, Joint Annual Meeting of the Japanese Society for Mathematical Biology and the Society for Mathematical Biology (**JSMB/SMB**), Osaka, Japan, 2014. (abstract) (talk)

W. de Back, J. Starruß, L. Brusch, A. Deutsch, Morpheus: a User-friendly Modeling Environment for Multiscale and Multicellular Systems Biology, 5th Conference on Systems Biology of Mammalian Cells (**SBMC**), Berlin, Germany, 2014. (poster)
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)
A. Köhn-Luque Morpheus: a simulation environment for multicellular and multiscale systems biology, High Performance Computing Center, Kyoto University, Japan, 2012. (talk)
W. de Back, J. Starruß, A. Deutsch, Morpheus: a novel modeling environment for multicellular systems biology, **BIOTEC** Forum: Bioinformatics and Computational Biology, Dresden, 2012. (poster)
W. de Back, J. Starruß, A. Deutsch, Morpheus: modeling environment for multicellular systems biology, 4th Conference on Systems Biology of Mammalian Cells (**SBMC**), Leipzig, 2012. (poster)
W. de Back, J. Starruß, A. Deutsch, Morpheus: a Modeling Environment for Multiscale Morphodynamics, 12th International Conference on Systems Biology (**ICSB**), Heidelberg/Mannheim, 2011. (poster)
W. de Back, A. Deutsch, Morpheus: Modeling and Simulation in Multicellular System Biology, 1st Sino-German Workshop on Simulation, Changsha, China, 2011. (talk)
W. de Back, J. Starruß, Multiscale Modeling of Morphodynamic Systems, 3rd Conference on Systems Biology of Mammalian Cells (**SBMC**), Freiburg, 2010. (poster)
W. de Back, J. Starruß, Multiscale Modeling of Morphodynamic Systems, 4th **CRTD** Summer conference on Regenerative Medicine, Dresden, 2010. (poster)
W. de Back, J. Starruß, Middle-out Modeling of Multiscale Morphodynamics, 12th International Conference on the Synthesis and Simulation of Living Systems (**ALIFE XII**), Odense, Denmark, 2010. In: H. Fellermann et al. (Eds.) Proceedings of the Twelfth International Conference on Artificial Life (Alife XII), MIT Press, Cambridge, MA., 2010. (talk)
W. de Back, J. Starruß, Multiscale Modeling of Morphodynamic Systems, EMBO Workshop in System Biology of Development, Ascona, Switzerland, 2010. (**EMBO Poster award**)

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