

- Martins, Leonardo et al. "SCIP: a single-cell image processor toolbox". *Bioinformatics*. 2018, 34(24). 4318-4320. <https://doi.org/10.1093/bioinformatics/bty505>
- Hegele, L. A. et al. "High-Reynolds-number turbulent cavity flow using the lattice Boltzmann method". *Physical Review E*. 2018. 98(4). <https://doi.org/10.1103/PhysRevE.98.043302>
- Kartasalo, Kimmo et al. "Comparative analysis of tissue reconstruction algorithms for 3D histology". *Bioinformatics*. 2018, 34(17). 3013-3021. <https://doi.org/10.1093/bioinformatics/bty210>
- Alberucci, Alessandro et al. "Nonlinear continuous-wave optical propagation in nematic liquid crystals: Interplay between reorientational and thermal effects". *Physical Review E*. 2017. 96(1). <https://doi.org/10.1103/PhysRevE.96.012703>
- Stupnikov, Alexey et al. "SamExploreR: Exploring reproducibility and robustness of RNA-seq results based on SAM files". *Bioinformatics*. 2016, 32(21). 3345-3347. <https://doi.org/10.1093/bioinformatics/btw475>
- Palyulin, Vladimir V. et al. "Search reliability and search efficiency of combined Lévy-Brownian motion: Long relocations mingled with thorough local exploration". *Journal of Physics A: Mathematical and Theoretical*. 2016. 49(39). <https://doi.org/10.1088/1751-8113/49/39/394002>
- Luukko, P. J. J., J. Helske, ja E. Räsänen. "Introducing libeemd: a program package for performing the ensemble empirical mode decomposition". *Computational Statistics*. 2016, 31(2). 545-557. <https://doi.org/10.1007/s00180-015-0603-9>
- Häkkinen, Antti ja Andre S. Ribeiro. "Characterizing rate limiting steps in transcription from RNA production times in live cells". *Bioinformatics*. 2016, 32(9). 1346-1352. <https://doi.org/10.1093/bioinformatics/btv744>
- Aho, Vesa et al. "Diffusion through thin membranes: Modeling across scales". *Physical Review E*. 2016. 93(4). <https://doi.org/10.1103/PhysRevE.93.043309>
- Ropo, Matti et al. "First-principles data set of 45,892 isolated and cation-coordinated conformers of 20 proteinogenic amino acids". *Scientific Data*. 2016. 3. <https://doi.org/10.1038/sdata.2016.9>
- Larjo, Antti ja Harri Lähdesmäki. "Using multi-step proposal distribution for improved MCMC convergence in Bayesian network structure learning". *Eurasip Journal on Bioinformatics and Systems Biology*. 2015. 2015(1). <https://doi.org/10.1186/s13637-015-0024-7>
- Bencheikh, K. ja E. Räsänen. "Hermitian one-particle density matrix through a semiclassical gradient expansion". *Journal of Physics A: Mathematical and Theoretical*. 2015. 49(1). <https://doi.org/10.1088/1751-8113/49/1/015205>
- Mahmoudvand, Rahim, Fatemeh Alehosseini ja Paulo Canas Rodrigues. "Forecasting mortality rate by singular spectrum analysis". *REVSTAT STATISTICAL JOURNAL*. 2015, 13(3). 193-206.
- Safdari, Hadiseh et al. "Quantifying the non-ergodicity of scaled Brownian motion". *Journal of Physics A: Mathematical and Theoretical*. 2015. 48(37). <https://doi.org/10.1088/1751-8113/48/37/375002>
- Devassy, Lini et al. "Parity-time-symmetric solitons in trapped Bose-Einstein condensates and the influence of varying complex potentials: A variational approach". *Physical Review E*. 2015. 92(2). <https://doi.org/10.1103/PhysRevE.92.022914>
- Krüsemann, Henning, Aljaž Godec ja Ralf Metzler. "Ageing first passage time density in continuous time random walks and quenched energy landscapes". *Journal of Physics A: Mathematical and Theoretical*. 2015. 48(28). <https://doi.org/10.1088/1751-8113/48/28/285001>

- Godec, Aljaž ja Ralf Metzler. "Signal focusing through active transport". *Physical Review E*. 2015. 92(1). <https://doi.org/10.1103/PhysRevE.92.010701>
- Rodrigues, Paulo C., Andreia Monteiro ja Vanda M. Lourenço. "A robust AMMI model for the analysis of genotype-by-environment data". *Bioinformatics*. 2015, 32(1). 58-66. <https://doi.org/10.1093/bioinformatics/btv533>
- Mattila, Keijo K., Luiz A. Hegele ja Paulo C. Philippi. "Investigation of an entropic stabilizer for the lattice-Boltzmann method". *Physical Review E*. 2015. 91(6). <https://doi.org/10.1103/PhysRevE.91.063010>
- Godec, Aljaž ja Ralf Metzler. "Optimization and universality of Brownian search in a basic model of quenched heterogeneous media". *Physical Review E*. 2015. 91(5). <https://doi.org/10.1103/PhysRevE.91.052134>
- Cherstvy, Andrey G. ja Ralf Metzler. "Ergodicity breaking, ageing, and confinement in generalized diffusion processes with position and time dependent diffusivity". *Journal of Statistical Mechanics: Theory and Experiment*. 2015. 2015(5). <https://doi.org/10.1088/1742-5468/2015/05/P05010>
- Safdari, Hadiseh et al. "Aging scaled Brownian motion". *Physical Review E*. 2015. 91(4). <https://doi.org/10.1103/PhysRevE.91.042107>
- Blavatska, V. ja R. Metzler. "Conformational properties of complex polymers: Rosette versus star-like structures". *Journal of Physics A: Mathematical and Theoretical*. 2015. 48(13). <https://doi.org/10.1088/1751-8113/48/13/135001>
- Subramaniam, Narayan Puthanmadam ja Jari Hyttinen. "Dynamics of intracranial electroencephalographic recordings from epilepsy patients using univariate and bivariate recurrence networks". *Physical Review E*. 2015. 91(2). <https://doi.org/10.1103/PhysRevE.91.022927>
- Häkkinen, Antti ja Andre S. Ribeiro. "Estimation of GFP-tagged RNA numbers from temporal fluorescence intensity data". *Bioinformatics*. 2015, 31(1). 69-75. <https://doi.org/10.1093/bioinformatics/btu592>
- Yang, Zhirong, Jaakko Peltonen ja Samuel Kaski. "Majorization-minimization for manifold embedding". *Journal of Machine Learning Research*. 2015, 38. 1088-1097.
- Tripathi, Shailesh, Matthias Dehmer, ja Frank Emmert-Streib. "NetBioV: An R package for visualizing large network data in biology and medicine". *Bioinformatics*. 2014, 30(19). 2834-2836. <https://doi.org/10.1093/bioinformatics/btu384>
- Rahmatallah, Yasir, Frank Emmert-Streib ja Galina Glazko. "Gene Sets Net Correlations Analysis (GSNCA): A multivariate differential coexpression test for gene sets". *Bioinformatics*. 2014, 30(3). 360-368. <https://doi.org/10.1093/bioinformatics/btt687>
- Rodrigues, Paulo C. et al. "Structured orthogonal families of one and two strata prime basis factorial models". *Statistical Papers*. 2014, 55(3). 603-614. <https://doi.org/10.1007/s00362-013-0507-0>
- Peltonen, Jaakko ja Ziyuan Lin. "Information retrieval perspective to meta-visualization". *Journal of Machine Learning Research*. 2013, 29. 165-180.
- Rahmatallah, Y., F. Emmert-Streib ja G. Glazko. "Gene set analysis for self-contained tests: Complex null and specific alternative hypotheses". *Bioinformatics*. 2012, 28(23). 3073-3080. <https://doi.org/10.1093/bioinformatics/bts579>
- Pereira, Dulce G. et al. "A comparison between joint regression analysis and the AMMI model: A case study with barley". *JOURNAL OF STATISTICAL COMPUTATION AND SIMULATION*. 2012, 82(2). 193-207. <https://doi.org/10.1080/00949655.2011.615839>

- Wu, Grace Hui Min et al. "A stochastic model for survival of early prostate cancer with adjustments for leadtime, length bias, and over-detection". *Biometrical Journal*. 2012, 54(1). 20-44. <https://doi.org/10.1002/bimj.201000107>
- Pearlman, Alexander et al. "Clustering-based method for developing a genomic copy number alteration signature for predicting the metastatic potential of prostate cancer". *JOURNAL OF PROBABILITY AND STATISTICS*. 2012. <https://doi.org/10.1155/2012/873570>
- Assanto, Gaetano et al. "Reorientational versus Kerr dark and gray solitary waves using modulation theory". *Physical Review E*. 2011. 84(6). <https://doi.org/10.1103/PhysRevE.84.066602>
- Yu, Guoqiang et al. "BACOM: In silico detection of genomic deletion types and correction of normal cell contamination in copy number data". *Bioinformatics*. 2011, 27(11). 1473-1480. <https://doi.org/10.1093/bioinformatics/btr183>
- Potapov, I., E. Volkov ja A. Kuznetsov. "Dynamics of coupled repressilators: The role of mRNA kinetics and transcription cooperativity". *Physical Review E*. 2011. 83(3). <https://doi.org/10.1103/PhysRevE.83.031901>
- Peltonen, Jaakko ja Samuel Kaski. "Generative modeling for maximizing precision and recall in information visualization". *Journal of Machine Learning Research*. 2011, 15. 579-587.
- Altay, Gökmen ja Frank Emmert-Streib. "Revealing differences in gene network inference algorithms on the network level by ensemble methods". *Bioinformatics*. 2010, 26(14). 1738-1744. <https://doi.org/10.1093/bioinformatics/btq259>
- Emmert-Streib, Frank. "Exploratory analysis of spatiotemporal patterns of cellular automata by clustering compressibility". *Physical Review E*. 2010. 81(2). <https://doi.org/10.1103/PhysRevE.81.026103>
- Glazko, Galina V. ja Frank Emmert-Streib. "Unite and conquer: Univariate and multivariate approaches for finding differentially expressed gene sets". *Bioinformatics*. 2009, 25(18). 2348-2354. <https://doi.org/10.1093/bioinformatics/btp406>
- Emmert-Streib, Frank ja Matthias Dehmer. "Fault tolerance of information processing in gene networks". *Physica A: Statistical Mechanics and Its Applications*. 2009, 388(4). 541-548. <https://doi.org/10.1016/j.physa.2008.10.032>
- Knuuti, Mika ja Tim Länsivaara "Performance of Variable Partial Factor approach in a slope design". *13th International Conference on Applications of Statistics and Probability in Civil Engineering(ICASP13), Seoul, South Korea, May 26-30, 2019*. 2019. <https://doi.org/10.22725/ICASP13.475>