

Martins, L, Neeli-Venkata, R, Oliveira, SMD, Häkkinen, A, Ribeiro, AS & Fonseca, JM 2018, 'SCIP: a single-cell image processor toolbox', *Bioinformatics*, Vuosikerta. 34, Nro 24, Sivut 4318-4320. <https://doi.org/10.1093/bioinformatics/bty505>

Hegele, LA, Scagliarini, A, Sbragaglia, M, Mattila, KK, Philippi, PC, Puleri, DF, Gounley, J & Randles, A 2018, 'High-Reynolds-number turbulent cavity flow using the lattice Boltzmann method', *Physical Review E*, Vuosikerta. 98, Nro 4, 043302. <https://doi.org/10.1103/PhysRevE.98.043302>

Kartasalo, K, Latonen, L, Vihinen, J, Visakorpi, T, Nykter, M & Ruusuvuori, P 2018, 'Comparative analysis of tissue reconstruction algorithms for 3D histology', *Bioinformatics*, Vuosikerta. 34, Nro 17, Sivut 3013-3021. <https://doi.org/10.1093/bioinformatics/bty210>

Alberucci, A, Laudyn, UA, Piccardi, A, Kwasny, M, Klus, B, Karpierz, MA & Assanto, G 2017, 'Nonlinear continuous-wave optical propagation in nematic liquid crystals: Interplay between reorientational and thermal effects', *Physical Review E*, Vuosikerta. 96, Nro 1, 012703. <https://doi.org/10.1103/PhysRevE.96.012703>

Stupnikov, A, Tripathi, S, De Matos Simoes, R, McArt, D, Salto-Tellez, M, Glazko, G, Dehmer, M & Emmert-Streib, F 2016, 'SamExploreR: Exploring reproducibility and robustness of RNA-seq results based on SAM files', *Bioinformatics*, Vuosikerta. 32, Nro 21, Sivut 3345-3347. <https://doi.org/10.1093/bioinformatics/btw475>

Palyulin, VV, Chechkin, AV, Klages, R & Metzler, R 2016, 'Search reliability and search efficiency of combined Lévy-Brownian motion: Long relocations mingled with thorough local exploration', *Journal of Physics A: Mathematical and Theoretical*, Vuosikerta. 49, Nro 39, 394002. <https://doi.org/10.1088/1751-8113/49/39/394002>

Luukko, PJJ, Helske, J & Räsänen, E 2016, 'Introducing libeemd: a program package for performing the ensemble empirical mode decomposition', *Computational Statistics*, Vuosikerta. 31, Nro 2, Sivut 545-557. <https://doi.org/10.1007/s00180-015-0603-9>

Häkkinen, A & Ribeiro, AS 2016, 'Characterizing rate limiting steps in transcription from RNA production times in live cells', *Bioinformatics*, Vuosikerta. 32, Nro 9, Sivut 1346-1352. <https://doi.org/10.1093/bioinformatics/btv744>

Aho, V, Mattila, K, Kühn, T, Kekäläinen, P, Pulkkinen, O, Minussi, RB, Vihinen-Ranta, M & Timonen, J 2016, 'Diffusion through thin membranes: Modeling across scales', *Physical Review E*, Vuosikerta. 93, Nro 4, 043309. <https://doi.org/10.1103/PhysRevE.93.043309>

Ropo, M, Schneider, M, Baldauf, C & Blum, V 2016, 'First-principles data set of 45,892 isolated and cation-coordinated conformers of 20 proteinogenic amino acids', *Scientific Data*, Vuosikerta. 3, 160009. <https://doi.org/10.1038/sdata.2016.9>

Larjo, A & Lähdesmäki, H 2015, 'Using multi-step proposal distribution for improved MCMC convergence in Bayesian network structure learning', *Eurasip Journal on Bioinformatics and Systems Biology*, Vuosikerta. 2015, Nro 1, 6. <https://doi.org/10.1186/s13637-015-0024-7>

Bencheikh, K & Räsänen, E 2015, 'Hermitian one-particle density matrix through a semiclassical gradient expansion', *Journal of Physics A: Mathematical and Theoretical*, Vuosikerta. 49, Nro 1, 015205. <https://doi.org/10.1088/1751-8113/49/1/015205>

Mahmoudvand, R, Alehosseini, F & Rodrigues, PC 2015, 'Forecasting mortality rate by singular spectrum analysis', *REVSTAT STATISTICAL JOURNAL*, Vuosikerta. 13, Nro 3, Sivut 193-206.

Safdari, H, Cherstvy, AG, Chechkin, AV, Thiel, F, Sokolov, IM & Metzler, R 2015, 'Quantifying the non-ergodicity of scaled Brownian motion', *Journal of Physics A: Mathematical and Theoretical*, Vuosikerta. 48, Nro 37, 375002. <https://doi.org/10.1088/1751-8113/48/37/375002>

- Devassy, L, Jisha, CP, Alberucci, A & Kuriakose, VC 2015, 'Parity-time-symmetric solitons in trapped Bose-Einstein condensates and the influence of varying complex potentials: A variational approach', *Physical Review E*, Vuosikerta. 92, Nro 2, 022914. <https://doi.org/10.1103/PhysRevE.92.022914>
- Krüsemann, H, Godec, A & Metzler, R 2015, 'Ageing first passage time density in continuous time random walks and quenched energy landscapes', *Journal of Physics A: Mathematical and Theoretical*, Vuosikerta. 48, Nro 28, 285001. <https://doi.org/10.1088/1751-8113/48/28/285001>
- Godec, A & Metzler, R 2015, 'Signal focusing through active transport', *Physical Review E*, Vuosikerta. 92, Nro 1, 010701. <https://doi.org/10.1103/PhysRevE.92.010701>
- Rodrigues, PC, Monteiro, A & Lourenço, VM 2015, 'A robust AMMI model for the analysis of genotype-by-environment data', *Bioinformatics*, Vuosikerta. 32, Nro 1, Sivut 58-66. <https://doi.org/10.1093/bioinformatics/btv533>
- Mattila, KK, Hegele, LA & Philippi, PC 2015, 'Investigation of an entropic stabilizer for the lattice-Boltzmann method', *Physical Review E*, Vuosikerta. 91, Nro 6, 063010. <https://doi.org/10.1103/PhysRevE.91.063010>
- Godec, A & Metzler, R 2015, 'Optimization and universality of Brownian search in a basic model of quenched heterogeneous media', *Physical Review E*, Vuosikerta. 91, Nro 5, 052134. <https://doi.org/10.1103/PhysRevE.91.052134>
- Cherstvy, AG & Metzler, R 2015, 'Ergodicity breaking, ageing, and confinement in generalized diffusion processes with position and time dependent diffusivity', *Journal of Statistical Mechanics: Theory and Experiment*, Vuosikerta. 2015, Nro 5, P05010. <https://doi.org/10.1088/1742-5468/2015/05/P05010>
- Safdari, H, Chechkin, AV, Jafari, GR & Metzler, R 2015, 'Aging scaled Brownian motion', *Physical Review E*, Vuosikerta. 91, Nro 4, 042107. <https://doi.org/10.1103/PhysRevE.91.042107>
- Blavatska, V & Metzler, R 2015, 'Conformational properties of complex polymers: Rosette versus star-like structures', *Journal of Physics A: Mathematical and Theoretical*, Vuosikerta. 48, Nro 13, 135001. <https://doi.org/10.1088/1751-8113/48/13/135001>
- Subramaniam, NP & Hyttinen, J 2015, 'Dynamics of intracranial electroencephalographic recordings from epilepsy patients using univariate and bivariate recurrence networks', *Physical Review E*, Vuosikerta. 91, Nro 2, 022927. <https://doi.org/10.1103/PhysRevE.91.022927>
- Häkkinen, A & Ribeiro, AS 2015, 'Estimation of GFP-tagged RNA numbers from temporal fluorescence intensity data', *Bioinformatics*, Vuosikerta. 31, Nro 1, Sivut 69-75. <https://doi.org/10.1093/bioinformatics/btu592>
- Yang, Z, Peltonen, J & Kaski, S 2015, 'Majorization-minimization for manifold embedding', *Journal of Machine Learning Research*, Vuosikerta. 38, Sivut 1088-1097.
- Tripathi, S, Dehmer, M & Emmert-Streib, F 2014, 'NetBioV: An R package for visualizing large network data in biology and medicine', *Bioinformatics*, Vuosikerta. 30, Nro 19, Sivut 2834-2836. <https://doi.org/10.1093/bioinformatics/btu384>
- Rahmatallah, Y, Emmert-Streib, F & Glazko, G 2014, 'Gene Sets Net Correlations Analysis (GSNCA): A multivariate differential coexpression test for gene sets', *Bioinformatics*, Vuosikerta. 30, Nro 3, Sivut 360-368. <https://doi.org/10.1093/bioinformatics/btt687>
- Rodrigues, PC, Moreira, EE, Jesus, VM & Mexia, JT 2014, 'Structured orthogonal families of one and two strata prime basis factorial models', *Statistical Papers*, Vuosikerta. 55, Nro 3, Sivut 603-614. <https://doi.org/10.1007/s00362-013-0507-0>

- Peltonen, J & Lin, Z 2013, 'Information retrieval perspective to meta-visualization', *Journal of Machine Learning Research*, Vuosikerta. 29, Sivut 165-180.
- Rahmatallah, Y, Emmert-Streib, F & Glazko, G 2012, 'Gene set analysis for self-contained tests: Complex null and specific alternative hypotheses', *Bioinformatics*, Vuosikerta. 28, Nro 23, Sivut 3073-3080.  
<https://doi.org/10.1093/bioinformatics/bts579>
- Pereira, DG, Rodrigues, PC, Mejza, S & Mexia, JT 2012, 'A comparison between joint regression analysis and the AMMI model: A case study with barley', *JOURNAL OF STATISTICAL COMPUTATION AND SIMULATION*, Vuosikerta. 82, Nro 2, Sivut 193-207. <https://doi.org/10.1080/00949655.2011.615839>
- Wu, GHM, Auvinen, A, Yen, AMF, Hakama, M, Walter, SD & Chen, HH 2012, 'A stochastic model for survival of early prostate cancer with adjustments for leadtime, length bias, and over-detection', *Biometrical Journal*, Vuosikerta. 54, Nro 1, Sivut 20-44. <https://doi.org/10.1002/bimj.201000107>
- Pearlman, A, Campbell, C, Brooks, E, Genshaft, A, Shajahan, S, Ittman, M, Bova, GS, Melamed, J, Holcomb, I, Schneider, RJ & Ostrer, H 2012, 'Clustering-based method for developing a genomic copy number alteration signature for predicting the metastatic potential of prostate cancer', *JOURNAL OF PROBABILITY AND STATISTICS*.  
<https://doi.org/10.1155/2012/873570>
- Assanto, G, Marchant, TR, Minzoni, AA & Smyth, NF 2011, 'Reorientational versus Kerr dark and gray solitary waves using modulation theory', *Physical Review E*, Vuosikerta. 84, Nro 6, 066602. <https://doi.org/10.1103/PhysRevE.84.066602>
- Yu, G, Zhang, B, Bova, GS, Xu, J, Shih, IM & Wang, Y 2011, 'BACOM: In silico detection of genomic deletion types and correction of normal cell contamination in copy number data', *Bioinformatics*, Vuosikerta. 27, Nro 11, btr183, Sivut 1473-1480. <https://doi.org/10.1093/bioinformatics/btr183>
- Potapov, I, Volkov, E & Kuznetsov, A 2011, 'Dynamics of coupled repressilators: The role of mRNA kinetics and transcription cooperativity', *Physical Review E*, Vuosikerta. 83, Nro 3, 031901.  
<https://doi.org/10.1103/PhysRevE.83.031901>
- Peltonen, J & Kaski, S 2011, 'Generative modeling for maximizing precision and recall in information visualization', *Journal of Machine Learning Research*, Vuosikerta. 15, Sivut 579-587.
- Altay, G & Emmert-Streib, F 2010, 'Revealing differences in gene network inference algorithms on the network level by ensemble methods', *Bioinformatics*, Vuosikerta. 26, Nro 14, btq259, Sivut 1738-1744.  
<https://doi.org/10.1093/bioinformatics/btq259>
- Emmert-Streib, F 2010, 'Exploratory analysis of spatiotemporal patterns of cellular automata by clustering compressibility', *Physical Review E*, Vuosikerta. 81, Nro 2, 026103. <https://doi.org/10.1103/PhysRevE.81.026103>
- Glazko, GV & Emmert-Streib, F 2009, 'Unite and conquer: Univariate and multivariate approaches for finding differentially expressed gene sets', *Bioinformatics*, Vuosikerta. 25, Nro 18, Sivut 2348-2354.  
<https://doi.org/10.1093/bioinformatics/btp406>
- Emmert-Streib, F & Dehmer, M 2009, 'Fault tolerance of information processing in gene networks', *Physica A: Statistical Mechanics and Its Applications*, Vuosikerta. 388, Nro 4, Sivut 541-548. <https://doi.org/10.1016/j.physa.2008.10.032>
- Knuuti, M & Lämsivaara, T 2019, Performance of Variable Partial Factor approach in a slope design. julkaisussa *13th International Conference on Applications of Statistics and Probability in Civil Engineering(ICASP13)*, Seoul, South Korea, May 26-30, 2019., Seoul, Etelä-Korea, 26/05/19. <https://doi.org/10.22725/ICASP13.475>