

- Martins, L., Neeli-Venkata, R., Oliveira, S. M. D., Häkkinen, A., Ribeiro, A. S., & Fonseca, J. M. (2018). SCIP: a single-cell image processor toolbox. *Bioinformatics*, *34*(24), 4318-4320. <https://doi.org/10.1093/bioinformatics/bty505>
- Hegele, L. A., Scagliarini, A., Sbragaglia, M., Mattila, K. K., Philippi, P. C., Puleri, D. F., ... Randles, A. (2018). High-Reynolds-number turbulent cavity flow using the lattice Boltzmann method. *Physical Review E*, *98*(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*, *34*(17), 3013-3021. <https://doi.org/10.1093/bioinformatics/bty210>
- Alberucci, A., Laudyn, U. A., Piccardi, A., Kwasny, M., Klus, B., Karpierz, M. A., & Assanto, G. (2017). Nonlinear continuous-wave optical propagation in nematic liquid crystals: Interplay between reorientational and thermal effects. *Physical Review E*, *96*(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., ... Emmert-Streib, F. (2016). SamExploreR: Exploring reproducibility and robustness of RNA-seq results based on SAM files. *Bioinformatics*, *32*(21), 3345-3347. <https://doi.org/10.1093/bioinformatics/btw475>
- Palyulin, V. V., Chechkin, A. V., 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*, *49*(39), [394002]. <https://doi.org/10.1088/1751-8113/49/39/394002>
- Luukko, P. J. J., Helske, J., & Räsänen, E. (2016). Introducing libeemd: a program package for performing the ensemble empirical mode decomposition. *Computational Statistics*, *31*(2), 545-557. <https://doi.org/10.1007/s00180-015-0603-9>
- Häkkinen, A., & Ribeiro, A. S. (2016). Characterizing rate limiting steps in transcription from RNA production times in live cells. *Bioinformatics*, *32*(9), 1346-1352. <https://doi.org/10.1093/bioinformatics/btv744>
- Aho, V., Mattila, K., Kühn, T., Kekäläinen, P., Pulkkinen, O., Minussi, R. B., ... Timonen, J. (2016). Diffusion through thin membranes: Modeling across scales. *Physical Review E*, *93*(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*, *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*, *2015*(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*, *49*(1), [015205]. <https://doi.org/10.1088/1751-8113/49/1/015205>
- Mahmoudvand, R., Alehosseini, F., & Rodrigues, P. C. (2015). Forecasting mortality rate by singular spectrum analysis. *REVSTAT STATISTICAL JOURNAL*, *13*(3), 193-206.
- Safdari, H., Cherstvy, A. G., Chechkin, A. V., Thiel, F., Sokolov, I. M., & Metzler, R. (2015). Quantifying the non-ergodicity of scaled Brownian motion. *Journal of Physics A: Mathematical and Theoretical*, *48*(37), [375002]. <https://doi.org/10.1088/1751-8113/48/37/375002>
- Devassy, L., Jisha, C. P., Alberucci, A., & Kuriakose, V. C. (2015). Parity-time-symmetric solitons in trapped Bose-Einstein condensates and the influence of varying complex potentials: A variational approach. *Physical Review E*, *92*(2), [022914]. <https://doi.org/10.1103/PhysRevE.92.022914>

- Krüseemann, 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*, *48*(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*, *92*(1), [010701]. <https://doi.org/10.1103/PhysRevE.92.010701>
- Rodrigues, P. C., Monteiro, A., & Lourenço, V. M. (2015). A robust AMMI model for the analysis of genotype-by-environment data. *Bioinformatics*, *32*(1), 58-66. <https://doi.org/10.1093/bioinformatics/btv533>
- Mattila, K. K., Hegele, L. A., & Philippi, P. C. (2015). Investigation of an entropic stabilizer for the lattice-Boltzmann method. *Physical Review E*, *91*(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*, *91*(5), [052134]. <https://doi.org/10.1103/PhysRevE.91.052134>
- Cherstvy, A. G., & 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*, *2015*(5), [P05010]. <https://doi.org/10.1088/1742-5468/2015/05/P05010>
- Safdari, H., Chechkin, A. V., Jafari, G. R., & Metzler, R. (2015). Aging scaled Brownian motion. *Physical Review E*, *91*(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*, *48*(13), [135001]. <https://doi.org/10.1088/1751-8113/48/13/135001>
- Subramaniam, N. P., & Hyttinen, J. (2015). Dynamics of intracranial electroencephalographic recordings from epilepsy patients using univariate and bivariate recurrence networks. *Physical Review E*, *91*(2), [022927]. <https://doi.org/10.1103/PhysRevE.91.022927>
- Häkkinen, A., & Ribeiro, A. S. (2015). Estimation of GFP-tagged RNA numbers from temporal fluorescence intensity data. *Bioinformatics*, *31*(1), 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*, *38*, 1088-1097.
- Tripathi, S., Dehmer, M., & Emmert-Streib, F. (2014). NetBioV: An R package for visualizing large network data in biology and medicine. *Bioinformatics*, *30*(19), 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*, *30*(3), 360-368. <https://doi.org/10.1093/bioinformatics/btt687>
- Rodrigues, P. C., Moreira, E. E., Jesus, V. M., & Mexia, J. T. (2014). Structured orthogonal families of one and two strata prime basis factorial models. *Statistical Papers*, *55*(3), 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*, *29*, 165-180.
- Rahmatallah, Y., Emmert-Streib, F., & Glazko, G. (2012). Gene set analysis for self-contained tests: Complex null and specific alternative hypotheses. *Bioinformatics*, *28*(23), 3073-3080. <https://doi.org/10.1093/bioinformatics/bts579>

Pereira, D. G., Rodrigues, P. C., Mejza, S., & Mexia, J. T. (2012). A comparison between joint regression analysis and the AMMI model: A case study with barley. *JOURNAL OF STATISTICAL COMPUTATION AND SIMULATION*, *82*(2), 193-207. <https://doi.org/10.1080/00949655.2011.615839>

Wu, G. H. M., Auvinen, A., Yen, A. M. F., Hakama, M., Walter, S. D., & Chen, H. H. (2012). A stochastic model for survival of early prostate cancer with adjustments for leadtime, length bias, and over-detection. *Biometrical Journal*, *54*(1), 20-44. <https://doi.org/10.1002/bimj.201000107>

Pearlman, A., Campbell, C., Brooks, E., Genshaft, A., Shajahan, S., Ittman, M., ... 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*, [873570]. <https://doi.org/10.1155/2012/873570>

Assanto, G., Marchant, T. R., Minzoni, A. A., & Smyth, N. F. (2011). Reorientational versus Kerr dark and gray solitary waves using modulation theory. *Physical Review E*, *84*(6), [066602]. <https://doi.org/10.1103/PhysRevE.84.066602>

Yu, G., Zhang, B., Bova, G. S., Xu, J., Shih, I. M., & Wang, Y. (2011). BACOM: In silico detection of genomic deletion types and correction of normal cell contamination in copy number data. *Bioinformatics*, *27*(11), 1473-1480. [btr183]. <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*, *83*(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*, *15*, 579-587.

Altay, G., & Emmert-Streib, F. (2010). Revealing differences in gene network inference algorithms on the network level by ensemble methods. *Bioinformatics*, *26*(14), 1738-1744. [btq259]. <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*, *81*(2), [026103]. <https://doi.org/10.1103/PhysRevE.81.026103>

Glazko, G. V., & Emmert-Streib, F. (2009). Unite and conquer: Univariate and multivariate approaches for finding differentially expressed gene sets. *Bioinformatics*, *25*(18), 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*, *388*(4), 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. teoksessa *13th International Conference on Applications of Statistics and Probability in Civil Engineering(ICASP13)*, Seoul, South Korea, May 26-30, 2019 <https://doi.org/10.22725/ICASP13.475>