

- 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*. 82(2):193-207. <https://doi.org/10.1080/00949655.2011.615839>
- 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*. 48(28). <https://doi.org/10.1088/1751-8113/48/28/285001>
- Safdari H, Chechkin AV, Jafari GR, Metzler R. 2015. Aging scaled Brownian motion. *Physical Review E*. 91(4). <https://doi.org/10.1103/PhysRevE.91.042107>
- Rodrigues PC, Monteiro A, Lourenço VM. 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>
- 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*. 54(1):20-44. <https://doi.org/10.1002/bimj.201000107>
- 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*. 27(11):1473-1480. <https://doi.org/10.1093/bioinformatics/btr183>
- Häkkinen A, Ribeiro AS. 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>
- 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>
- Kartasalo K, Latonen L, Vihinen J, Visakorpi T, Nykter M, Ruusuvoori P. 2018. Comparative analysis of tissue reconstruction algorithms for 3D histology. *Bioinformatics*. 34(17):3013-3021. <https://doi.org/10.1093/bioinformatics/bty210>
- Blavatska V, Metzler R. 2015. Conformational properties of complex polymers: Rosette versus star-like structures. *Journal of Physics A: Mathematical and Theoretical*. 48(13). <https://doi.org/10.1088/1751-8113/48/13/135001>
- 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*. 93(4). <https://doi.org/10.1103/PhysRevE.93.043309>
- Potapov I, Volkov E, Kuznetsov A. 2011. Dynamics of coupled repressilators: The role of mRNA kinetics and transcription cooperativity. *Physical Review E*. 83(3). <https://doi.org/10.1103/PhysRevE.83.031901>
- Subramaniam NP, Hyttinen J. 2015. Dynamics of intracranial electroencephalographic recordings from epilepsy patients using univariate and bivariate recurrence networks. *Physical Review E*. 91(2). <https://doi.org/10.1103/PhysRevE.91.022927>
- 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*. 2015(5). <https://doi.org/10.1088/1742-5468/2015/05/P05010>
- Häkkinen A, Ribeiro AS. 2015. Estimation of GFP-tagged RNA numbers from temporal fluorescence intensity data. *Bioinformatics*. 31(1):69-75. <https://doi.org/10.1093/bioinformatics/btu592>

Emmert-Streib F. 2010. Exploratory analysis of spatiotemporal patterns of cellular automata by clustering compressibility. *Physical Review E*. 81(2). <https://doi.org/10.1103/PhysRevE.81.026103>

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>

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. <https://doi.org/10.1038/sdata.2016.9>

Mahmoudvand R, Alehosseini F, Rodrigues PC. 2015. Forecasting mortality rate by singular spectrum analysis. *REVSTAT STATISTICAL JOURNAL*. 13(3):193-206.

Peltonen J, Kaski S. 2011. Generative modeling for maximizing precision and recall in information visualization. *Journal of Machine Learning Research*. 15:579-587.

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>

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>

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

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*. 98(4). <https://doi.org/10.1103/PhysRevE.98.043302>

Peltonen J, Lin Z. 2013. Information retrieval perspective to meta-visualization. *Journal of Machine Learning Research*. 29:165-180.

Luukko PJJ, 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>

Mattila KK, Hegele LA, Philippi PC. 2015. Investigation of an entropic stabilizer for the lattice-Boltzmann method. *Physical Review E*. 91(6). <https://doi.org/10.1103/PhysRevE.91.063010>

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>

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*. 96(1). <https://doi.org/10.1103/PhysRevE.96.012703>

Godec A, Metzler R. 2015. Optimization and universality of Brownian search in a basic model of quenched heterogeneous media. *Physical Review E*. 91(5). <https://doi.org/10.1103/PhysRevE.91.052134>

- 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*. 92(2). <https://doi.org/10.1103/PhysRevE.92.022914>
- 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*. 48(37). <https://doi.org/10.1088/1751-8113/48/37/375002>
- Assanto G, Marchant TR, Minzoni AA, Smyth NF. 2011. Reorientational versus Kerr dark and gray solitary waves using modulation theory. *Physical Review E*. 84(6). <https://doi.org/10.1103/PhysRevE.84.066602>
- 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. <https://doi.org/10.1093/bioinformatics/btq259>
- 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*. 32(21):3345-3347. <https://doi.org/10.1093/bioinformatics/btw475>
- Martins L, Neeli-Venkata R, Oliveira SMD, Häkkinen A, Ribeiro AS, Fonseca JM. 2018. SCIP: a single-cell image processor toolbox. *Bioinformatics*. 34(24):4318-4320. <https://doi.org/10.1093/bioinformatics/bty505>
- 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*. 49(39). <https://doi.org/10.1088/1751-8113/49/39/394002>
- Godec A, Metzler R. 2015. Signal focusing through active transport. *Physical Review E*. 92(1). <https://doi.org/10.1103/PhysRevE.92.010701>
- Rodrigues PC, Moreira EE, Jesus VM, Mexia JT. 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>
- Glazko GV, 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>
- 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). <https://doi.org/10.1186/s13637-015-0024-7>
- 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>