

A comparison between joint regression analysis and the AMMI model
A case study with barley

Ageing first passage time density in continuous time random walks and quenched energy landscapes

Aging scaled Brownian motion

A robust AMMI model for the analysis of genotype-by-environment data

A stochastic model for survival of early prostate cancer with adjustments for leadtime, length bias, and over-detection

BACOM

In silico detection of genomic deletion types and correction of normal cell contamination in copy number data

Characterizing rate limiting steps in transcription from RNA production times in live cells

Clustering-based method for developing a genomic copy number alteration signature for predicting the metastatic potential of prostate cancer

Comparative analysis of tissue reconstruction algorithms for 3D histology

Conformational properties of complex polymers
Rosette versus star-like structures

Diffusion through thin membranes
Modeling across scales

Dynamics of coupled repressilators
The role of mRNA kinetics and transcription cooperativity

Dynamics of intracranial electroencephalographic recordings from epilepsy patients using univariate and bivariate recurrence networks

Ergodicity breaking, ageing, and confinement in generalized diffusion processes with position and time dependent diffusivity

Estimation of GFP-tagged RNA numbers from temporal fluorescence intensity data
Julkaisun otsikon käännös: : Estimation of GFP-tagged RNA numbers from temporal fluorescence intensity data

Exploratory analysis of spatiotemporal patterns of cellular automata by clustering compressibility

Fault tolerance of information processing in gene networks

First-principles data set of 45,892 isolated and cation-coordinated conformers of 20 proteinogenic amino acids

Forecasting mortality rate by singular spectrum analysis

Generative modeling for maximizing precision and recall in information visualization

Gene set analysis for self-contained tests
Complex null and specific alternative hypotheses

Gene Sets Net Correlations Analysis (GSNCA)
A multivariate differential coexpression test for gene sets

Hermitian one-particle density matrix through a semiclassical gradient expansion

High-Reynolds-number turbulent cavity flow using the lattice Boltzmann method

Information retrieval perspective to meta-visualization

Introducing libeemd
a program package for performing the ensemble empirical mode decomposition

Investigation of an entropic stabilizer for the lattice-Boltzmann method

Majorization-minimization for manifold embedding

NetBioV
An R package for visualizing large network data in biology and medicine

Nonlinear continuous-wave optical propagation in nematic liquid crystals
Interplay between reorientational and thermal effects

Optimization and universality of Brownian search in a basic model of quenched heterogeneous media

Parity-time-symmetric solitons in trapped Bose-Einstein condensates and the influence of varying complex potentials
A variational approach

Quantifying the non-ergodicity of scaled Brownian motion

Reorientational versus Kerr dark and gray solitary waves using modulation theory

Revealing differences in gene network inference algorithms on the network level by ensemble methods

SamExploreR
Exploring reproducibility and robustness of RNA-seq results based on SAM files

SCIP
a single-cell image processor toolbox

Search reliability and search efficiency of combined Lévy-Brownian motion
Long relocations mingled with thorough local exploration

Signal focusing through active transport

Structured orthogonal families of one and two strata prime basis factorial models

Unite and conquer

Univariate and multivariate approaches for finding differentially expressed gene sets

Using multi-step proposal distribution for improved MCMC convergence in Bayesian network structure learning

Performance of Variable Partial Factor approach in a slope design