Fault tolerance of information processing in gene networks

Unite and conquer
Univariate and multivariate approaches for finding differentially expressed gene sets

Exploratory analysis of spatiotemporal patterns of cellular automata by clustering compressibility

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

Generative modeling for maximizing precision and recall in information visualization

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

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

Reorientational versus Kerr dark and gray solitary waves using modulation theory

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

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

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

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

Information retrieval perspective to meta-visualization

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

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

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

Majorization-minimization for manifold embedding

Estimation of GFP-tagged RNA numbers from temporal fluorescence intensity data

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

Aging scaled Brownian motion

Conformational properties of complex polymers
Rosette versus star-like structures

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

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

Investigation of an entropic stabilizer for the lattice-Boltzmann method

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

Signal focusing through active transport

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

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

Forecasting mortality rate by singular spectrum analysis

Hermitian one-particle density matrix through a semiclassical gradient expansion

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

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

Diffusion through thin membranes
Modeling across scales

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

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

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

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

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

Comparative analysis of tissue reconstruction algorithms for 3D histology

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

SCIP
a single-cell image processor toolbox

Performance of Variable Partial Factor approach in a slope design