

ORIGINAL PAPERS

Sequence analysis

Identifying sequence regions undergoing conformational change via predicted continuum secondary structure 1809
M.Bodén and T.L.Bailey

Evolutionary simulations to detect functional lineage-specific genes 1815
I.Dupanloup and H.Kaessmann

Structural bioinformatics

INFO-RNA—a fast approach to inverse RNA folding 1823
A.Busch and R.Backofen

Application of the multiensemble sampling to the equilibrium folding of proteins 1832
H.S.Son, S.-Y.Kim, J.Lee and K.-K.Han

Developing a move-set for protein model refinement 1838
M.N.Offman, P.W.Fitzjohn and P.A.Bates

Imprint of evolutionary conservation and protein structure variation on the binding function of protein tyrosine kinases 1846
G.M.Verkhivker

Gene expression

Independent component analysis-based penalized discriminant method for tumor classification using gene expression data 1855
D.-S.Huang and C.-H.Zheng

Scanning microarrays at multiple intensities enhances discovery of differentially expressed genes 1863
D.S.Skibbe, X.Wang, X.Zhao, L.A.Borsuk, D.Nettleton and P.S.Schnable

Systems biology

Protein classification using probabilistic chain graphs and the Gene Ontology structure 1871
S.Carroll and V.Pavlovic

A model diagram layout extension for SBML 1879
R.Gauges, U.Rost, S.Sahle and K.Wegner

Transcriptome network component analysis with limited microarray data 1886
S.J.Galbraith, L.M.Tran and J.C.Liao

Spatial stochastic modelling of the phosphoenolpyruvate-dependent phosphotransferase (PTS) pathway in *Escherichia coli* 1895
J.Vidal Rodríguez, J.A.Kaandorp, M.Dobrzyński and J.G.Blom

Data and text mining

A suite of algorithms for the comprehensive analysis of complex protein mixtures using high-resolution LC-MS 1902
M.Bellew, M.Coram, M.Fitzgibbon, M.Igra, T.Randolph, P.Wang, D.May, J.Eng, R.Fang, C.Lin, J.Chen, D.Goodlett, J.Whiteaker, A.Paulovich and M.McIntosh

Databases and ontologies

caGrid: design and implementation of the core architecture of the cancer biomedical informatics grid 1910
J.Saltz, S.Oster, S.Hastings, S.Langella, T.Kurc, W.Sanchez, M.Kher, A.Manisundaram, K.Shanbhag and P.Covitz

APPLICATIONS NOTE

Genome analysis

tuple_plot: Fast pairwise nucleotide sequence comparison with noise suppression 1917
K.Szafranski, N.Jahn and M.Platzer

ACE-it: a tool for genome-wide integration of gene dosage and RNA expression data 1919
W.N.van Wieringen, J.A.M.Belien, S.J.Vosse, E.M.Achame and B.Ylstra

Phylogenetics

NETGEN: generating phylogenetic networks with diploid hybrids 1921
M.M.Morin and B.M.E.Moret

Gene expression

Comparative gene marker selection suite 1924
J.Gould, G.Getz, S.Monti, M.Reich and J.P.Mesirov

Genetics and population analysis

JADE: a distributed Java application for deleterious genomic mutation (DGM) estimation 1926
J.-L.Li, M.-X.Li, Y.-F.Guo, H.-Y.Deng and H.-W.Deng

SNPStats: a web tool for the analysis of association studies 1928
X.Solé, E.Guinó, J.Valls, R.Iniesta and V.Moreno

Systems biology

Metatool 5.0: fast and flexible elementary modes analysis 1930
A.von Kamp and S.Schuster