

## REVIEW

- Sequence analysis*  
**Bioinformatics software for biologists in the genomics era** 1713  
 S.Kumar and J.Dudley

## ORIGINAL PAPERS

- Sequence analysis*  
**A phylogenetic Gibbs sampler that yields centroid solutions for cis-regulatory site prediction** 1718  
 L.A.Newberg, W.A.Thompson, S.Conlan, T.M.Smith, L.A.McCue and C.E.Lawrence
- Fast model-based protein homology detection without alignment** 1728  
 S.Hochreiter, M.Heusel and K.Obermayer
- STOP: searching for transcription factor motifs using gene expression** 1737  
 L.Hertzberg, S.Izraeli and E.Domany
- Phylogenetics*  
**Nucleotide composition string selection in HIV-1 subtyping using whole genomes** 1744  
 X.Wu, Z.Cai, X.-F.Wan, T.Hoang, R.Goebel and G.Lin
- Structural bioinformatics*  
**Persistent voids: a new structural metric for membrane fusion** 1753  
 P.M.Kasson, A.Zomorodian, S.Park, N.Singhal, L.J.Guibas and V.S.Pande
- Assortative mixing in Protein Contact Networks and protein folding kinetics** 1760  
 G.Bagler and S.Sinha
- Gene expression*  
**Assessment of survival prediction models based on microarray data** 1768  
 M.Schumacher, H.Binder and T.Gerds
- Incorporating prior knowledge of predictors into penalized classifiers with multiple penalty terms** 1775  
 F.Tai and W.Pan
- Biological network mapping and source signal deduction** 1783  
 M.P.Brynildsen, T.-Y.Wu, S.-S.Jang and J.C.Liao
- Discovering gene expression patterns in time course microarray experiments by ANOVA-SCA** 1792  
 M.J.Nueda, A.Conesa, J.A.Westerhuis, H.C.J.Hoefsloot, A.K.Smilde, M.Talón and A.Ferrer
- Genetics and population analysis*  
**CLUMPP: a cluster matching and permutation program for dealing with label switching and multimodality in analysis of population structure** 1801  
 M.Jakobsson and N.A.Rosenberg
- Error detection in SNP data by considering the likelihood of recombinational history implied by three-site combinations** 1807  
 D.M.Toleno, P.L.Morrell and M.T.Clegg
- Databases and ontologies*  
**EuSplice: a unified resource for the analysis of splice signals and alternative splicing in eukaryotic genes** 1815  
 A.Bhasi, R.V.Pandey, S.P.Utharasamy and P.Senapathy
- Enhancing the functional annotation of PDB structures in PDBsum using key figures extracted from the literature** 1824  
 R.A.Laskowski

## APPLICATIONS NOTES

- Genome analysis*  
**ChromatinDB: a database of genome-wide histone modification patterns for *Saccharomyces cerevisiae*** 1828  
 T.R.O'Connor and J.J.Wyrick
- BioMoby web services to support clustering of co-regulated genes based on similarity of promoter configurations** 1831  
 A.Kerhornou and R.Guigó
- Sequence analysis*  
**Automated Improvement of Domain ANnotations using context analysis of domain arrangements (AIDAN)** 1834  
 F.Beaussart, J.Weiner 3rd and E.Bornberg-Bauer
- Structural bioinformatics*  
**Rapid assessment of correlated amino acids from pair-to-pair (P2P) substitution matrices** 1837  
 E.Eyal, S.Petrokovski and I.Bahar
- T-Pile—a package for thermodynamic calculations for biomolecules** 1840  
 D.Gront and A.Kolinski
- Gene expression*  
**CRCView: a web server for analyzing and visualizing microarray gene expression data using model-based clustering** 1843  
 Z.Xiang, Z.S.Qin and Y.He
- GEOQuery: a bridge between the Gene Expression Omnibus (GEO) and BioConductor** 1846  
 D.Sean and P.S.Meltzer
- Genetics and population analysis*  
**MODELER4SIMCOAL2: A user-friendly, extensible modeler of demography and linked loci for coalescent simulations** 1848  
 T.Antao, A.Beja-Pereira and G.Luikart
- Recombination-filtered genomic datasets by information maximization** 1851  
 A.E.Woerner, M.P.Cox and M.F.Hammer
- Madeline 2.0 PDE: a new program for local and web-based pedigree drawing** 1854  
 E.H.Trager, R.Khanna, A.Marrs, L.Siden, K.E.H.Branham, A.Swaroop and J.E.Richards
- Systems biology*  
**Genetdes: automatic design of transcriptional networks** 1857  
 G.Rodrigo, J.Carrera and A.Jaramillo
- Stochastic simulation GUI for biochemical networks** 1859  
 R.R.Vallabhajosyula and H.M.Sauro
- Data and text mining*  
**MutationFinder: a high-performance system for extracting point mutation mentions from text** 1862  
 J.G.Caporaso, W.A.Baumgartner, Jr, D.A.Randolph, K.B.Cohen and L.Hunter
- Databases and ontologies*  
**DoriC: a database of *oriC* regions in bacterial genomes** 1866  
 F.Gao and C.-T.Zhang
- OBO to OWL: a protégé OWL tab to read/save OBO ontologies** 1868  
 D.A.Moreira and M.A.Musen