EDITORIAL

ORIGINAL PAPERS

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Analysis of differentially-regulated genes within a regulatory network by GPS genome navigation
I.Zwir, H.Huang and E.A.Groisman

A comparison study: applying segmentation to array CGH data for downstream analyses
H.Willenbrock and J.Fridlyand

Sequence analysis

Design of long oligonucleotide probes for functional gene detection in a microbial community

Prediction of the coupling specificity of GPCRs to four families of G-proteins using hidden Markov models and artificial neural networks
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Calibrating E-values for hidden Markov models using reverse-sequence null models
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Using information theory to search for co-evolving residues in proteins
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Optimal word sizes for dissimilarity measures and estimation of the degree of dissimilarity between DNA sequences
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Structural bioinformatics

ChemDB: a public database of small molecules and related chemoinformatics resources
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Energy landscape of k-point mutants of an RNA molecule
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Gene expression

Classification of microarrays to nearest centroids
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DNA microarray data imputation and significance analysis of differential expression
R.Jönsten, H.-Y.Wang, W.J.Welsh and M.Ouyang

Oligonucleotide arrays: information from replication and spatial structure
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RSIR: regularized sliced inverse regression for motif discovery
W.Zhong, P.Zeng, P.Ma, J.S.Liu and Y.Zhu

Systems biology

Functional stoichiometric analysis of metabolic networks
R.Urbanczik and C.Wagner

Databases and ontologies

SNPselector: a web tool for selecting SNPs for genetic association studies

APPLICATIONS NOTE

Genome analysis

Virtual Footprint and PRODORIC: an integrative framework for regulon prediction in prokaryotes

Sequence analysis

BADASP: predicting functional specificity in protein families using ancestral sequences
R.J.Edwards and D.C.Shields

Gene expression

MILVA: An interactive tool for the exploration of multidimensional microarray data
D.D’Alimonte, D.Lowe, I.T.Nabney, V.Mersinias and C.P.Smith

Doelan: a solution for quality control monitoring of microarray production
L.Jourdren and S.L.Crom

Data and text mining

METIS: multiple extraction techniques for informative sentences

ERRATUM

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