

REVIEW

Databases and ontologies

- Enrichment or depletion of a GO category within a class of genes: which test?** 401
I.Rivals, L.Personnaz, L.Taing and M.-C.Potier

ORIGINAL PAPERS

Genome analysis

- Accurate automated clustering of two-dimensional data for single-nucleotide polymorphism genotyping by a combination of clustering methods: evaluation by large-scale real data** 408
S.Takitoh, S.Fujii, Y.Mase, J.Takasaki, T.Yamazaki, Y.Ohnishi, M.Yanagisawa, Y.Nakamura and N.Kamatani

Sequence analysis

- In search of the small ones: improved prediction of short exons in vertebrates, plants, fungi and protists** 414
Y.Saeyns, P.Rouzé and Y.Van de Peer

Structural bioinformatics

- Inherent limitations in protein-protein docking procedures** 421
N.Kowalsman and M.Eisenstein

- ADP_EM: fast exhaustive multi-resolution docking for high-throughput coverage** 427
J.I.Garzón, J.Kovacs, R.Abagyan and P.Chacón

- Robust prediction of consensus secondary structures using averaged base pairing probability matrices** 434
H.Kiryu, T.Kin and K.Asai

Gene expression

- Causality and pathway search in microarray time series experiment** 442
N.D.Mukhopadhyay and S.Chatterjee

- Markers improve clustering of CGH data** 450
J.Liu, S.Ranka and T.Kahveci

- Segmentation and intensity estimation of microarray images using a gamma-t mixture model** 458
J.Baek, Y.S.Son and G.J.McLachlan

- Clustering threshold gradient descent regularization: with applications to microarray studies** 466
S.Ma and J.Huang

- The discovery of transcriptional modules by a two-stage matrix decomposition approach** 473
H.Li, Y.Sun and M.Zhan

Systems biology

- Parameter estimation using Simulated Annealing for S-system models of biochemical networks** 480
O.R.Gonzalez, C.Küper, K.Jung, P.C.Naval,Jr and E.Mendoza

Data and text mining

- Oligonucleotide microarray identification of *Bacillus anthracis* strains using support vector machines** 487
M.Doran, D.S.Raicu, J.D.Furst, R.Settimi, M.Schipma and D.P.Chandler

APPLICATIONS NOTES

Genome analysis

- MotifScorer: using a compendium of microarrays to identify regulatory motifs** 493
M.Brilli, R.Fani and P.Lió

- Visualization of genomic aberrations using Affymetrix SNP arrays** 496
A.Müller, K.Holzmann and H.A.Kestler

- AutoGRAPH: an interactive web server for automating and visualizing comparative genome maps** 498
T.Derrien, C.André, F.Galibert and C.Hitte

- Assembling millions of short DNA sequences using SSAKE** 500
R.L.Warren, G.G.Sutton, S.J.M.Jones and R.A.Holt

Sequence analysis

- Mclip: motif detection based on cliques of gapped local profile-to-profile alignments** 502
T.Frickey and G.Weiller

- AllerTool: a web server for predicting allergenicity and allergic cross-reactivity in proteins** 504
Z.H.Zhang, J.L.Y.Koh, G.L.Zhang, K.H.Choo, M.T.Tammi and J.C.Tong

Phylogenetics

- cBrother: relaxing parental tree assumptions for Bayesian recombination detection** 507
F.Fang, J.Ding, V.N.Minin, M.A.Suchard and K.S.Dorman

- The automation of Nested Clade Phylogeographic Analysis** 509
M.Panchal

- URec: a system for unrooted reconciliation** 511
P.Górecki and J.Tiuryn

Structural bioinformatics

- QSCOP—SCOP quantified by structural relationships** 513
S.J.Suhrer, M.Wiederstein and M.J.Sippl

- MinSet: a general approach to derive maximally representative database subsets by using fragment dictionaries and its application to the SCOP database** 515
A.Pandini, L.Bonati, F.Fraternali and J.Kleinjung

Genetics and population analysis

- Exploiting large scale computing to construct high resolution linkage disequilibrium maps of the human genome** 517
W.Lau, T.-Y.Kuo, W.Tapper, S.Cox and A.Collins

- msHOT: modifying Hudson's ms simulator to incorporate crossover and gene conversion hotspots** 520
G.Hellenthal and M.Stephens

- GGtools: analysis of genetics of gene expression in bioconductor** 522
V.J.Carey, M.Morgan, S.Falcon, R.Lazarus and R.Gentleman

Systems biology

- OmicBrowse: a browser of multidimensional omics annotations** 524
T.Toyoda, Y.Mochizuki, K.Player, N.Heida, Norio Kobayashi and Y.Sakaki