

ORIGINAL PAPERS

Genome analysis

Improved peak detection in mass spectrum by incorporating continuous wavelet transform-based pattern matching 2059
P.Du, W.A.Kibbe and S.M.Lin

VAMP: Visualization and analysis of array-CGH, transcriptome and other molecular profiles 2066
P.La Rosa, E.Viara, P.Hupé, G.Pierron, S.Liva, P.Neuvial, I.Brito, S.Lair, N.Servant, N.Robine, E.Manié, C.Brennetot, L.Janoueix-Lerosey, V.Raynal, N.Gruel, C.Rouveirol, N.Stransky, M.-H.Stern, O.Delattre, A.Aurias, F.Radvanyi and E.Barillot

Searching RNA motifs and their intermolecular contacts with constraint networks 2074
P.Thébault, S.de Givry, T.Schiex and C.Gaspin

Sequence analysis

An initial strategy for comparing proteins at the domain architecture level 2081
K.Lin, L.Zhu and D.-Y.Zhang

Structural bioinformatics

An iterative refinement algorithm for consistency based multiple structural alignment methods 2087
Y.Chen and G.M.Crippen

Intramolecular surface contacts contain information about protein-protein interface regions 2094
S.J.de Vries and A.M.J.J.Bonvin

Mutagenic probability estimation of chemical compounds by a novel molecular electrophilicity vector and support vector machine 2099
M.Zheng, Z.Liu, C.Xue, W.Zhu, K.Chen, X.Luo and H.Jiang

Gene expression

Probe-level measurement error improves accuracy in detecting differential gene expression 2107
X.Liu, M.Milo, N.D.Lawrence and M.Rattray

Detecting potential labeling errors in microarrays by data perturbation 2114
A.Malossini, E.Blanzieri and R.T.Ng

Genetics and population analysis

A whole genome long-range haplotype (WGLRH) test for detecting imprints of positive selection in human populations 2122
C.Zhang, D.K.Bailey, T.Awad, G.Liu, G.Xing, M.Cao, V.Valmeekam, J.Retief, H.Matsuzaki, M.Taub, M.Seielstad and G.C.Kennedy

Systems biology

Inferring gene regulatory networks from time series data using the minimum description length principle 2129
W.Zhao, E.Serpedin and E.R.Dougherty

Data and text mining

Substring selection for biomedical document classification 2136
B.Han, Z.Obradovic, Z.-Z.Hu, C.H.Wu and S.Vucetic

Constructing biological networks through combined literature mining and microarray analysis: a LMMA approach 2143
S.Li, L.Wu and Z.Zhang

Combination of text-mining algorithms increases the performance 2151
R.Malik, L.Franke and A.Siebes

APPLICATIONS NOTE

Sequence analysis

Branch and bound computation of exact p-values 2158
G.Bejerano

Cleaver: software for identifying taxon specific restriction endonuclease recognition sites 2160
S.N.Jarman

Phylogenetics

SeqVis: Visualization of compositional heterogeneity in large alignments of nucleotides 2162
J.W.K.Ho, C.E.Adams, J.B.Lew, T.J.Matthews, C.C.Ng, A.Shahabi-Sirjani, L.H.Tan, Y.Zhao, S.Easteal, S.R.Wilson and L.S.Jermin

Structural bioinformatics

MAGOS: multiple alignment and modelling server 2164
N.Garnier, A.Friedrich, R.Bolze, E.Bettler, L.Moulinier, C.Geourjon, J.D.Thompson, G.Deléage and O.Poch

VISTAL—a new 2D visualization tool of protein 3D structural alignments 2166
R.Kolodny and B.Honig

Ribostral: an RNA 3D alignment analyzer and viewer based on basepair isostericities 2168
A.Mokdad and N.B.Leontis

THESEUS: maximum likelihood superpositioning and analysis of macromolecular structures 2171
D.L.Theobald and D.S.Wuttke

Genetics and population analysis

Parallel multifactor dimensionality reduction: a tool for the large-scale analysis of gene-gene interactions 2173
W.S.Bush, S.M.Dudek and M.D.Ritchie

Systems biology

NetAlign: a web-based tool for comparison of protein interaction networks 2175
Z.Liang, M.Xu, M.Teng and L.Niu

GenePro: a cytoscape plug-in for advanced visualization and analysis of interaction networks 2178
J.Vlasblom, S.Wu, S.Pu, M.Superina, G.Liu, C.Orsi and S.J.Wodak

Databases and ontologies

ZooDDD: a cross-species database for digital differential display analysis 2180
Y.-C.Chen, C.-D.Hsiao, W.-D.Lin, C.-M.Hu, P.-P.Hwang and J.-M.Ho

SNPeffect v2.0: a new step in investigating the molecular phenotypic effects of human non-synonymous SNPs 2183
J.Reumers, S.Maurer-Stroh, J.Schymkowitz and F.Rousseau