### DISCOVERY NOTE

**Sequence analysis**

A novel domain suggests a ciliary function for *ASPM*, a brain size determining gene

C.P.Ponting

### ORIGINAL PAPER

**Genome analysis**

The UCSC Known Genes

F.Hsu, W.J.Kent, H.Clawson, R.M.Kuhn, M.Diekhans and D.Haussler

**Sequence analysis**

A deterministic motif finding algorithm with application to the human genome

L.S.Hon and A.N.Jain

A novel sensitive method for the detection of user-defined compositional bias in biological sequences

I.B.Kuznetsov and S.Hwang

**Phylogenetics**

Recco: recombination analysis using cost optimization

J.Maydt and T.Lengauer

Describing ancient horizontal gene transfers at the nucleotide and gene levels by comparative pathogenicity island genomics

F.Collyn, L.Guy, M.Marceau, M.Simonet and C.-A.HRoten

**Structural bioinformatics**

Development and validation of a consistency based multiple structure alignment algorithm

J.Ebert and D.Brutlag

Discontinuous epitope prediction based on mimotope analysis

V.Moreau, C.Granier, S.Villard, D.Laune and F.Molina

**Gene expression**

maSigPro: a method to identify significantly differential expression profiles in time-course microarray experiments

A.Conesa, M.J.Nueda, A.Ferrer and M.Talon

Algorithm to find gene expression profiles of deregulation and identify families of disease-altered genes

C.Prieto, M.J.Rivas, J.M.Sánchez, J.López-Fidalgo and J.De Las Rivas

**Rosetta error model for gene expression analysis**

L.Weng, H.Dai, Y.Zhan, Y.He, S.B.Stepaniants and D.E.Bassett

**A systematic comparison and evaluation of biclustering methods for gene expression data**


**Data and text mining**

Functional bioinformatics for *Arabidopsis thaliana*

A.Clare, A.Karwath, H.Ougham and R.D.King

**Databases and ontologies**

Adapters, shims, and glue—service interoperability for in silico experiments


### APPLICATIONS NOTE

**Genome analysis**

BioHMM: a heterogeneous hidden Markov model for segmenting array CGH data

J.C.Marioni, N.P.Thorne and S.Tavaré

**Sequence analysis**

MACGT: multi-dimensional automated clustering genotyping tool for analysis of microarray-based mini-sequencing data

D.C.Walley, B.W.Tripp, Y.C.Song, K.R.Walley and S.J.Tebbutt

**Systems biology**

WebCell: a web-based environment for kinetic modeling and dynamic simulation of cellular networks

D.-Y.Lee, C.Yun, A.Cho, B.K.Hou, S.Park and S.Y.Lee

**FANMOD: a tool for fast network motif detection**

S.Wernicke and F.Rasche

**Data and text mining**

GALGO: an R package for multivariate variable selection using genetic algorithms

V.Trevino and F.Falciani

Please visit the journal’s World Wide Web site http://bioinformatics.oxfordjournals.org