**DISCOVERY NOTE**

**Sequence analysis**

In silico analysis of promoter regions from cold-induced genes in rice (*Oryza sativa* L.) and *Arabidopsis thaliana* reveals the importance of combinatorial control.

A. Lindlöf, M. Bräutigam, A. Chawade, O. Olsson and B. Olsson

**ORIGINAL PAPERS**

**Genome analysis**

Automatic identification of species-specific repetitive DNA sequences and their utilization for detecting microbial organisms

T. Koressaar, K. Jõers and M. Remm

**Sequence analysis**

Reduced amino acid alphabets exhibit an improved sensitivity and selectivity in fold assignment

E. L. Peterson, J. Kondev, J. A. Theriot and R. Phillips

CloudBurst: highly sensitive read mapping with MapReduce

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Phylogenetics

Many-core algorithms for statistical phylogenetics

M. A. Suchard and A. Rambaut

Genetics and population analysis

A web application to perform linkage disequilibrium and linkage analyses on a computational grid

J. Hernández-Sánchez, J. A. Brunehelc and S. Vast

**Data and text mining**

Integrating shotgun proteomics and mRNA expression data to improve protein identification

S. R. Ramavath, C. Vogel, J. T. Prince, R. Wang, Z. Li, L. O. Penhaligon, M. Myers, E. M. Marcotte and D. J. Minziner

KiPar, a tool for systematic information retrieval regarding parameters for kinetic modelling of yeast metabolic pathways

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MeSH Up: effective MeSH text classification for improved document retrieval

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**APPLICATIONS NOTE**

**Genome analysis**

CNVVdb: a database of copy number variations across vertebrate genomes

F. C. Chen, Y. Z. Chen and T. J. Chuang

**Sequence analysis**

Biopython: freely available Python tools for computational molecular biology and bioinformatics


ProbeMatch: rapid alignment of oligonucleotides to genome allowing both gaps and mismatches


**Structural bioinformatics**

Evolutionary Trace Annotation Server: automated enzyme function prediction in protein structures using 3D templates

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PseudoViewer3: generating planar drawings of large-scale RNA structures with pseudoknots
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