**ORIGINAL ARTICLES**

- **Binary Interval Search: a scalable algorithm for counting interval intersections**
  R.M. Layer, K. Skadron, G. Robins, I.M. Hall and A.R. Quinlan

- **Simultaneous alignment and clustering of peptide data using a Gibbs sampling approach**
  M. Andreatta, D. Lund and M. Nielsen

**GENOME ANALYSIS**

- **STAR: ultrafast universal RNA-seq aligner**

**SEQUENCE ANALYSIS**

- **A hidden Markov model to identify combinatorial epigenetic regulation patterns for estrogen receptor α target genes**
  R. Bonneville and V.X. Jin

- **Rare variant discovery and calling by sequencing pooled samples with overlaps**
  W. Wang, X. Yin, Y. Soo Pyon, M. Hayes and J.U.

- **DLCalMotif: a discriminative approach for discovering local motifs in protein sequences**
  A.M. Mehdī, M.S.B. Sehgal, B. Kobe, T.L. Bailey and M. Bodén

**APPLICATIONS NOTES**

- **MetaGeneTack: ab initio detection of frameshifts in metagenomic sequences**
  S. Tang, J. Ackerley and M. Borosovski

- **MGAviewer: a desktop visualization tool for analysis of metagenomics alignment data**
  Z. Zhu, B. Niu, J. Chen, S. Wu, S. Sun and W.Li

- **PriVar: a toolkit for prioritizing SNVs and indels from next-generation sequencing data**
  L. Zhang, J. Zhang, J. Yang, D. Ying, Y. Lung, L. and W. Yang

**STRUCTURAL BIOINFORMATICS**

- **Towards the development of standardized methods for comparison, ranking and evaluation of structure alignments**
  A.W. Slater, G. Castelain, M.J. Eppol and F. Melo

- **MP-T: improving membrane protein alignment for structure prediction**
  J.R. Hill and C.M. Deane

- **LOGICOIL—multi-state prediction of coiled-coil oligomeric state**
  T.L. Vincent, F.J. Green and D.N. Woolfson

**GENE EXPRESSION**

- **Genotype calling and phasing using next-generation sequencing reads and a haplotype scaffold**
  A. Menelaou and J. Marchini

**SYSTEMS BIOLOGY**

- **NARROMI: a noise and redundancy reduction technique improves accuracy of gene regulatory network inference**

**DATABASES**

- **Introducing Drugster: a comprehensive and fully integrated drug design, lead and structure-optimization toolkit**
  D. Vlachakis, D. Tsagrasoulis, V. Megaleisokonomou and S. Kossida
Contents continued from outside back cover

Gene expression

AffyRNAdegradation: control and correction of RNA quality effects in GeneChip expression data
M.Fasold and H.Binder

DvD: An R/Cytoscape pipeline for drug repurposing using public repositories of gene expression data
C.Pacini, F.Iorio, E.Gonçalves, M.Iskar, T.Klabunde,
P.Bork and J.Saez-Rodriguez

Genetics and population analysis

BlueSNP: R package for highly scalable genome-wide association studies using Hadoop clusters
H.Huang, S.Tata and R.J.Prill

Systems biology

XiP: a computational environment to create, extend and share workflows
M.Nagasaki, A.Fujita, Y.Sekiya, A.Saito, E.Ikeda,
C.Li and S.Miyano

SPSens: a software package for stochastic parameter sensitivity analysis of biochemical reaction networks
P.W.Sheppard, M.Rathinam and M.Khammash

13CFLUX2—high-performance software suite for 13C-metabolic flux analysis
M.Weitzel, K.Nöh, T.Dalman, S.Niedenführ, B.Stute and W.Wiechert

Databases and ontologies

ADAM: automated data management for research datasets
M.Woodbridge, C.D.Tomlinson and S.A.Butcher