ORIGINAL ARTICLES

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

Sequence analysis
Simultaneous alignment and clustering of peptide data using a Gibbs sampling approach
M.Andreatta, O.Lund and M.Nielsen
STAR: ultrafast universal RNA-seq aligner
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.Li
DLocalMotif: a discriminative approach for discovering local motifs in protein sequences
A.M.Mehdi, M.S.B.Sehgal, B.Kobe, T.L.Bailey and M.Boden

Structural bioinformatics
Towards the development of standardized methods for comparison, ranking and evaluation of structure alignments
A.W.Slater, J.I.Castellanos, M.J.Sippl and F.Melo
MP-T: improving membrane protein alignment for structure prediction
J.R.Hill and C.M.Deane
MycPermCheck: the Mycobacterium tuberculosis permeability prediction tool for small molecules
B.Merget, D.Zilian, T.Müller and C.A.Sotriffer
LOGICOIL—multi-state prediction of coiled-coil oligomeric state
T.L.Vincent, P.J.Green and D.N.Woolfson

Gene expression
RIP-chip enrichment analysis
F.Erhardt, L.Dölken and R.Zimmer

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

Systems biology
Human protein–protein interaction prediction by a novel sequence-based co-evolution method: co-evolutionary divergence
C.Hsin Liu, K.-C.Li and S.Yuan
Pathway hunting by random survival forests
X.Chen and H.Ishwaran
NARROMI: a noise and redundancy reduction technique improves accuracy of gene regulatory network inference

APPLICATIONS NOTES

Genome analysis
MetaGeneTack: ab initio detection of frameshifts in metagenomic sequences
S.Tang, I.Antonov and M.Borodovsky

Sequence analysis
Dragon TIS Spotter: an Arabidopsis-derived predictor of translation initiation sites in plants
A.Magana-Mora, H.Ashoor, B.R.Jankovic, A.Kamal, K.Awara, R.Chowdhary, J.A.C.Archer and V.B.Bajic

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

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

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

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