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.Luind and M.Nielsen

STAR: ultrastar 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 I.U.

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

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.Walter, P.J.Green and D.N.Woolfson

Gene expression
F.Searcher, J.Dtien and K.Zimmer

APPLICATIONS NOTES

MetaGeneTack: ab initio detection of frameshifts in metagenomic sequences
S.Tang, J.Akotonye and M.Borodovsky

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

PBSIM: PacBio reads simulator—toward accurate genome assembly
Y.Oho, K.Arai and M.Hamada

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

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

Introducing Drugster: a comprehensive and fully integrated drug design, lead and structure-optimization toolkit
D.Vlachakis, D.Tsagrasoulis, V.Megalooikonomou and S.Kossida