Genome analysis
Using combined evidence from replicates to evaluate ChIP-seq peaks
V. Jalili, M. Matteucci, M. Masseroli and M.J. Morelli
Sequence analysis
Data-dependent bucketing improves reference-free compression of sequencing reads
R. Patro and C. Kingsford
Polyester: simulating RNA-seq datasets with differential transcript expression
A.C. Frazee, A.E. Jaffe, B. Langmead and J.T. Leek
RV2D: a ultra-sensitive variant detection model for low-depth heterogeneous next-generation sequencing data
V.Ha, F. Zhang and R. Kuffner
Phylogenetics
Phylesystem: a git-based data store for community-curated phylogenetic estimates
Structural bioinformatics
DockStar: a novel ILP-based integrative method for structural modeling of multimolecular protein complexes
N. Amir, D. O’Sheen and H.J. Wolfson
Automated band annotation for RNA structure probing experiments with numerous capillary electrophoresis profiles
S. Lee, H. Kim, S. Tian, T. Lee, S. Yoon and R. Das
INPS: predicting the impact of non-synonymous variations on protein stability from sequence
P. Frisellii, P.L. Martelli, C. Savojardo and R. Casadio
Gene expression
Inferring data-specific micro-RNA function through the joint ranking of micro-RNA and pathways from matched micro-RNA and gene expression data
E. Patrick, M. Buckley, S. Mullier, D.M. Lin and J.V. I. Young
APPLICATIONS NOTES
CiVi: circular genome visualization with unique features to analyze sequence elements
L. Overmars, S.A.F. T. van Hijum, R.J. Siezen and C. Francke
IonGap: integrative bacterial genome analysis for Ion Torrent sequence data
Interactive analysis of large cancer copy number studies with Copy Number Explorer
S. Newman
kSNP3.0: SNP detection and phylogenetic analysis of genomes without genome alignment or reference genome
S.N. Daoistar, T. Tatsuk and B.A. Hall
Identification of C2H2-ZF binding preferences from ChIP-seq data using RCADE
H.S.Najafabadi, M.Albu and T.R.Hughes

Tax4Fun: predicting functional profiles from metagenomic 16S rRNA data
K.P.Aßhauer, B.Wemheuer, R.Daniel and P.Meinicke

BFC: correcting Illumina sequencing errors
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Phylogenetics

pez: phylogenetics for the environmental sciences

Structural bioinformatics

iFoldRNA v2: folding RNA with constraints
A.Krokhotin, K.Houlihan and N.V.Dokholyan

PDBest: a user-friendly platform for manipulating and enhancing protein structures

MemGen: a general web server for the setup of lipid membrane simulation systems
C.J.Knight and J.S.Hub

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chipPCR: an R package to pre-process raw data of amplification curves
S.Rödiger, M.Burdukiewicz and P.Schierack

Systems biology

ms-data-core-api: an open-source, metadata-oriented library for computational proteomics

Gener: a minimal programming module for chemical controllers based on DNA strand displacement
O.Kahramanog˘ulları and L.Cardelli

Data and text mining

phylogeo: an R package for geographic analysis and visualization of microbiome data
Z.Charlop-Powers and S.F.Brady

GOplot: an R package for visually combining expression data with functional analysis
W.Walter, F.Sánchez-Cabo and M.Ricote

Databases and ontologies

HTT-DB: Horizontally transferred transposable elements database
B.R.Dotto, E.L.Carvalho, A.F.Silva, L.F.Duarte Silva, P.M.Pinto, M.F.Ortiz and G.L.Wallau

Bioimage informatics

‘Flatten plus’: a recent implementation in WSxM for biological research
A.Gimeno, P.Ares, I.Horcas, A.Gil, J.M.Gómez-Rodríguez, J.Colchero and J.Gómez-Herrero