IMPROVER CHALLENGE SPECIAL ISSUE; SPECIES TRANSLATION CHALLENGE

Editorial
Where are we at regarding species translation? A review of the sbv IMPROVER challenge
J.Hoeng, M.C.Petitsch, P.Meyer and I.Jurisica

Systems biology
Inter-species prediction of protein phosphorylation in the sbv IMPROVER species translation challenge
Predicting protein phosphorylation from gene expression: top methods from the IMPROVER Species Translation Challenge

Understanding the limits of animal models as predictors of human biology: lessons learned from the sbv IMPROVER Species Translation Challenge

A crowd-sourcing approach for the construction of species-specific cell signaling networks

Gene expression
Inter-species inference of gene set enrichment in lung epithelial cells from proteomic and large transcriptomic datasets
S.Hormoz, G.Bhanot, M.Biehl, E.Bilal, P.Meyer, R.Norel, K.Rhrissorrakrai and A.Dayarian
Inter-species pathway perturbation prediction via data-driven detection of functional homology

ORIGINAL PAPERS

Genome analysis
E-MEM: efficient computation of maximal exact matches for very large genomes
N.Khiste and L.Ilie

Sequence analysis
Accurate estimation of haplotype frequency from pooled sequencing data and cost-effective identification of rare haplotype carriers by overlapping pool sequencing
C.-C.Cao and X.Sun

FuncPatch: a web server for the fast Bayesian inference of conserved functional patches in protein 3D structures
Y.-F.Huang and G.B.Golding
An efficient algorithm for the blocked pattern matching problem
F.Deng, L.Wang and X.Liu

Structural bioinformatics
LIGSIFT: an open-source tool for ligand structural alignment and virtual screening
A.Roy and J.Skolnick

Gene expression
Statistical significance of variables driving systematic variation in high-dimensional data
N.C.Chung and J.D.Storey

DIANA—algorithmic improvements for analysis of data-independent acquisition MS data

APPLICATIONS NOTES

Genome analysis
A5-miseq: an updated pipeline to assemble microbial genomes from Illumina MiSeq data
D.Coll, G.Jospin and A.E.Darling
minicMe: a web server for prediction and analysis of host-like proteins in microbial pathogens
P.Petrenko and A.C.Doxey

Sequence analysis
piPipes: a set of pipelines for piRNA and transposon analysis via small RNA-seq, RNA-seq, degradome- and CAGE-seq, ChIP-seq and genomic DNA sequencing
B.W.Han, W.Wang, P.D.Zamore and Z.Weng
miRseqViewer: multi-panel visualization of sequence, structure and expression for analysis of microRNA sequencing data
I.Jiang, H.Chang, Y.Jun, S.Park, J.O.Yang, B.Lee, W.Kim, V.N.Kim and S.Lee
Simple, rapid and accurate genotyping-by-sequencing from aligned whole genomes with ArrayMaker
C.E.Willet, B.Haase, M.A.Charleston and C.M.Wade

Genetics and population analysis
Seed: a user-friendly tool for exploring and visualizing microbial community data
D.Beck, C.Dennis and J.A.Foster

Systems biology
SYSBIONS: nested sampling for systems biology models
R.Johnson, P.Kirk and M.P.H.Stumpf
flowDensity: reproducing manual gating of flow cytometry data by automated density-based cell population identification
M.Malek, M.J.Taghiyar, L.Chong, G.Finak, R.Gottardo and R.R.Brinkman

DOSE: an R/Bioconductor package for disease ontology semantic enrichment analysis
G.Yu, L.-G.Wang, G.-R.Yan and Q.-Y.He

MOST: a software environment for constraint-based metabolic modeling and strain design
J.J.Kelley, A.Lane, X.Li, B.Mutthoju, S.Maor, D.Egen and D.S.Lun

LETTER TO THE EDITOR

Structural bioinformatics
Comment on ‘protein–protein binding affinity prediction from amino acid sequence’
I.H.Moal and J.Fernández-Recio

Please visit the journal’s World Wide Web site http://bioinformatics.oxfordjournals.org
MESSAGE FROM THE ISCB
Message from the ISCB: ISCB Ebola award for important future research on the computational biology of Ebola virus
P.D.Karp, B.Berger, D.Kovats, T.Lengauer, M.Linial, P.Sabeti, W.Hide and B.Rost

CORRIGENDUM

ERRATUM