Bioinformatics
VOLUME 27 NUMBER 24 DECEMBER 15 2011

EDITORIAL
The rise and fall of supervised machine learning techniques
L.J.Jensen and A.Bateman

ORIGINAL PAPERS

Pyicos: a versatile toolkit for the analysis of high-throughput sequencing data
S.Althammer, J.González-Vallinas, C.Ballaré, M.Beato and E.Eyras

MetaRank: a rank conversion scheme for comparative analysis of microbial community compositions
T.-Y.Wang, C.-H.Su and H.-K.Tsai

KABDOM: A new suffix array based algorithm for clustering expression data
S.Hazelhurst and Zs.Lipták

An assessment of substitution scores for protein profile-profile comparison
X.Ye, G.Wang and S.F.Altschul

KABDOM: An automatic method for CASP9 free modeling structure prediction assessment
Q.Cong, L.N.Kinch, J.Pei, S.Shi, V.N.Grishin, W.Li and N.V.Grishin

Optimized application of penalized regression methods to diverse genomic data
L.Waldron, M.Pintilie, M.-S.Tsao, F.A.Shepherd, C.Huttererower and I.Jurisica

A system-level approach for deciphering the transcriptional response to prion infection
M.Zampieri, G.Legname, D.Segrè and C.Altavilla

Cascade detection for the extraction of localized sequence features; specificity results for HIV-1 protease and structure-function results for the Schellman loop
N.E.Newell

APPLICATIONS NOTE

Pybedtools: a flexible Python library for manipulating genomic datasets and annotations
R.K.Dale, B.S.Pedersen and A.R.Quinlan

Visualization and quality assessment of de novo genome assemblies
C.Bhobe-Gregozza, L.Keller, I.Xenarios and Y.Wurm

Mapping personal functional data to personal genomes
M.Rivas-Astroza, D.Xie, X.Cao and S.Zhong

Enrich: software for analysis of protein function by enrichment and depletion of variants
D.M.Powell, C.L.Araya, W.Gerard and S.Fields

Bioinformatics
VOLUME 27 NUMBER 24 DECEMBER 15 2011
continued inside back cover
Contents continued from outside back cover

Genetics and population analysis
PoPoolation2: identifying differentiation between populations using sequencing of pooled DNA samples (Pool-Seq)
R.Kofler, R.V.Pandey and C.Schlötterer

Systems biology
BioPAX support in CellDesigner
H.Mi, A.Muruganujan, E.Demir, Y.Matsuoka, A.Funahashi, H.Kitano and P.D.Thomas

Data and text mining
BDTcomparator: a program for comparing binary classifiers
K.Fijorek, D.Fijorek, B.Wisniowska and S.Polak