ORIGINAL PAPERS

Genome analysis
Hierarchical hidden Markov model with application to joint analysis of ChIP-chip and ChIP-seq data
H.Choi, A.I.Nesvizhskii, D.Ghosh and Z.S.Qin 1715

SOrt-ITEMS: Sequence orthology based approach for improved taxonomic estimation of metagenomic sequences
Munirrood Haque M, T.S.Ghosh, D.Komanduri and S.S.Mande 1722

Data structures and compression algorithms for genomic sequence data
M.C.Brandon, D.C.Wallace and P.Baldi 1731

Sequence expression
ESG: extended similarity group method for automated protein function prediction
M.Chitalia, T.Kovkin, C.Park and D.Kihara 1739

Efficient computation of all perfect repeats in genomic sequences of up to half a gigabyte, with a case study on the human genome
V.Becher, A.Deymonnaz and P.Heiber 1746

Fast and accurate short read alignment with Burrows-Wheeler transform
H.Li and R.Darbin 1754

Structural bioinformatics
pGenTHREADER and pBomTHREADER: new methods for improved protein fold recognition and superfamily discrimination
A.Lobley, M.J.Sadowski and D.T.Jones 1761

Gene expression
Literature-based priors for gene regulatory networks
E.Steiert, A.Tucker, P.A.C. ‘t Hoen and M.J.Schuemie 1768

Gradient lasso for Cox proportional hazards model
I.Sohn, J.Kim, S.-H.Jung and C.Park 1775

Relating periodicity of nucleosome organization and gene regulation
J.Wan, J.Lin, D.Zack and J.Qian 1782

Seeing the forest for the trees: using the Gene Ontology to restructure hierarchical clustering
D.Dosan-Cohen, S.Kauf and A.A.Melkman 1789

Genetics and population analysis
On the inference of spatial structure from population genetics data
G.Guillot 1796

LETTERS TO THE EDITOR

Genetics and population analysis
Comment on ‘On the inference of spatial structure from population genetics data’
D.Dotan-Cohen, S.Kasif and A.A.Melkman 1802

Response to comment on ‘On the inference of spatial structure from population genetics data’
G.Guillot 1805

ORIGINAL PAPERS

Genetics and population analysis
Estimating the posterior probability that genome-wide association findings are true or false
J.Bukasir, J.L.McClay and E.J.C.G.van den Oord 1807

Systems biology
Structure discovery in PPI networks using pattern-based network decomposition
P.Bachman and Y.Lin 1814

Robust synthetic biology design: stochastic game theory approach

APPLICATIONS NOTE

Genome analysis
Rahnuma: hypergraph-based tool for metabolic pathway prediction and network comparison
A.Mithani, G.M.Preston and J.Hein 1831

baobabLUNA: the solution space of sorting by reversals
M.D.V.Braga 1833

Apollo: a community resource for genome annotation editing
E.Lee, N.Harris, M.Gibson, R.Chety and S.Lewis 1836

NTAP: for NimbleGen tiling array ChIP-chip data analysis
K.He, X.Li, J.Zhou, X.-W.Deng, H.Zhao and J.Luo 1838

rtracklayer: an R package for interfacing with genome browsers
M.Lawrence, R.Gentleman and V.Carey 1841

Sequence analysis
MetaTISA: Metagenomic Translation Initiation Site Annotator for improving gene start prediction

PESTAS: a web server for EST analysis and sequence mining

Please visit the journal’s Word Wide Web site http://bioinformatics.oxfordjournals.org

Downloaded from https://academic.oup.com/bioinformatics/issue/25/14
by guest
on 17 June 2018