

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

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Sort-ITEMS: Sequence orthology based approach for improved taxonomic estimation of metagenomic sequences

Monzoorul Haque M, T.S.Ghosh, D.Komanduri and S.S.Mande

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Data structures and compression algorithms for genomic sequence data

M.C.Brandon, D.C.Wallace and P.Baldi

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*Sequence analysis***ESG: extended similarity group method for automated protein function prediction**

M.Chitale, T.Hawkins, C.Park and D.Kihara

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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

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Fast and accurate short read alignment with Burrows-Wheeler transform

H.Li and R.Durbin

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*Structural bioinformatics***pGenTHREADER and pDomTHREADER: new methods for improved protein fold recognition and superfamily discrimination**

A.Lobley, M.I.Sadowski and D.T.Jones

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*Gene expression***Literature-based priors for gene regulatory networks**

E.Steele, A.Tucker, P.A.C. 't Hoen and M.J.Schuemie

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Gradient lasso for Cox proportional hazards model

I.Sohn, J.Kim, S.-H.Jung and C.Park

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Relating periodicity of nucleosome organization and gene regulation

J.Wan, J.Lin, D.J.Zack and J.Qian

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Seeing the forest for the trees: using the Gene Ontology to restructure hierarchical clustering

D.Dotan-Cohen, S.Kasif and A.A.Melkman

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*Genetics and population analysis***On the inference of spatial structure from population genetics data**

G.Guillot

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Response to comment on 'On the inference of spatial structure from population genetics data'

G.Guillot

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ORIGINAL PAPERS

*Genetics and population analysis***Estimating the posterior probability that genome-wide association findings are true or false**

J.Bukszár, J.L.McClay and E.J.C.G.van den Oord

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*Systems biology***Structure discovery in PPI networks using pattern-based network decomposition**

P.Bachman and Y.Liu

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Robust synthetic biology design: stochastic game theory approach

B.-S.Chen, C.-H.Chang and H.-C.Lee

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APPLICATIONS NOTE

*Genome analysis***Rahnuma: hypergraph-based tool for metabolic pathway prediction and network comparison**

A.Mithani, G.M.Preston and J.Hein

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baobabLUNA: the solution space of sorting by reversals

M.D.V.Braga

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Apollo: a community resource for genome annotation editing

E.Lee, N.Harris, M.Gibson, R.Chetty and S.Lewis

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NTAP: for NimbleGen tiling array ChIP-chip data analysis

K.He, X.Li, J.Zhou, X.-W.Deng, H.Zhao and J.Luo

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rtracklayer: an R package for interfacing with genome browsers

M.Lawrence, R.Gentleman and V.Carey

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*Sequence analysis***MetaTISA: Metagenomic Translation Initiation Site**

Annotator for improving gene start prediction

G.-Q.Hu, J.-T.Guo, Y.-C.Liu and H.Zhu

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PESTAS: a web server for EST analysis and sequence mining

S.-H.Nam, D.-W.Kim, T.-S.Jung, Y.-S.Choi, D.-W.Kim, H.-S.Choi, S.-H.Choi and H.-S.Park

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LETTERS TO THE EDITOR

*Genetics and population analysis***Comment on 'On the inference of spatial structure from population genetics data'**

E.Durand, C.Chen and O.François

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