

## DISCOVERY NOTE

*Systems biology*

**Biological pathway kinetic rate constants are scale-invariant**  
S.Grandison and R.J.Morris

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## ORIGINAL PAPERS

*Genome analysis*

**A machine-learning approach to combined evidence validation of genome assemblies**

J.-H.Choi, S.Kim, H.Tang, J.Andrews, D.G.Gilbert and J.K.Colbourne

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**A segmental maximum a posteriori approach to genome-wide copy number profiling**

R.Andersson, C.E.G.Bruder, A.Piotrowski, U.Menzel, H.Nord, J.Sandgren, T.R.Hvidsten, T.D.de Ståhl, J.P.Dumanski and J.Komorowski

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**Estimation and assessment of raw copy numbers at the single locus level**

H.Bengtsson, R.Irizarry, B.Carvalho and T.P.Speed

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**ITALICS: an algorithm for normalization and DNA copy number calling for Affymetrix SNP arrays**

G.Rigaill, P.Hupé, A.Almeida, P.La Rosa, J.-P.Meyniel, C.Decraene and E.Barillot

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*Sequence analysis*

**Prediction of zinc-binding sites in proteins from sequence**

N.Shu, T.Zhou and S.Hovmöller

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**SVM-HUSTLE—an iterative semi-supervised machine learning approach for pairwise protein remote homology detection**

A.R.Shah, C.S.Oehmen and B.-J.Webb-Robertson

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**Compressed indexing and local alignment of DNA**

T.W.Lam, W.K.Sung, S.L.Tam, C.K.Wong and S.M.Yiu

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**ConFunc—functional annotation in the twilight zone**

M.N.Wass and M.J.E.Sternberg

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**De novo identification of highly diverged protein repeats by probabilistic consistency**

A.Biegert and J.Söding

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**Prediction of neuropeptide cleavage sites in insects**

B.R.Southey, J.V.Sweedler and S.L.Rodriguez-Zas

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*Phylogenetics*

**Inferring horizontal transfers in the presence of rearrangements by the minimum evolution criterion**

H.Birin, Z.Gal-Or, I.Elias and T.Tuller

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*Systems biology*

**Bayesian ranking of biochemical system models**

V.Vyshemirsky and M.A.Girolami

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**Flexible informatics for linking experimental data to mathematical models via *DataRail***

J.Saez-Rodriguez, A.Goldsipe, J.Muhlich, L.G.Alexopoulos, B.Millard, D.A.Lauffenburger and P.K.Sorger

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**Complexity reduction of biochemical rate expressions**

H.Schmidt, M.F.Madsen, S.Danø and G.Cedersund

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*Data and text mining*

**Effect of spatial distribution of T-Cells and HIV load on HIV progression**

F.M.Graziano, S.Y.Kettoola, J.M.Munshower, J.T.Stapleton and G.J.Towfic

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## APPLICATIONS NOTES

*Genome analysis*

**GenomeVx: simple web-based creation of editable circular chromosome maps**

G.C.Conant and K.H.Wolfe

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**Prophinder: a computational tool for prophage prediction in prokaryotic genomes**

G.Lima-Mendez, J.Van Helden, A.Toussaint and R.Leplae

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*Sequence analysis*

**TaxonGap: a visualization tool for intra- and inter-species variation among individual biomarkers**

B.Slabbinck, P.Dawyndt, M.Martens, P.De Vos and B.De Baets

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*Phylogenetics*

**Interactive visualization software for exploring phylogenetic trees and clades**

M.Derthick

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*Structural bioinformatics*

**A discrete view on fold space**

M.J.Sippl, S.J.Suhrer, M.Gruber and M.Wiederstein

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**On distance and similarity in fold space**

M.J.Sippl

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*Gene expression*

**Model-based Bayesian clustering (MBBC)**

Y.Joo, J.G.Booth, Y.Namkoong and G.Casella

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*Systems biology*

**BiNoM: a Cytoscape plugin for manipulating and analyzing biological networks**

A.Zinovyev, E.Viara, L.Calzone and E.Barillot

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**Using flowViz to visualize flow cytometry data**

D.Sarkar, N.L.Meur and R.Gentleman

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**LibSBML: an API Library for SBML**

B.J.Bornstein, S.M.Keating, A.Jouraku and M.Hucka

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*Data and text mining*

**OutlierD: an R package for outlier detection using quantile regression on mass spectrometry data**

H.Cho, Y.-j.Kim, H.J.Jung, S.-W.Lee and J.W.Lee

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*Database and ontologies*

**ONTO-PERL: An API for supporting the development and analysis of bio-ontologies**

E.Antezana, M.Egaña, B.De Baets, M.Kuiper and V.Mironov

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