**LETTER TO THE EDITOR**

*Data and text mining*

*Do you do text?*

C.Blaschke, A.Yeh, E.Camon, M.Colosimo, R.Apweiler, L.Hirschman and A.Valencia

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**DISCOVERY NOTE**

*Structural bioinformatics*

*An attempt to define allergen-specific molecular surface features: a bioinformatic approach*

R.Furmonaviciene, B.J.Sutton, F.Glaser, C.A.Laughton, N.Jones, H.F.Sewell and F.Shakib

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**ORIGINAL PAPERS**

*Genome analysis*

*Syntons, metabolons and interactons: an exact graph-theoretical approach for exploring neighbourhood between genomic and functional data*

F.Boyer, A.Morgat, L.Labarre, J.Pothier and A.Viari

*Sequence analysis*

*Discovering hidden viral piracy*

E.Kim and Y.Kliger

*Discrimination of outer membrane proteins using support vector machines*

K.-J.Park, M.M.Gromiha, P.Horton and M.Suwa

*Structural bioinformatics*

*Bioinformatics analyses of circular dichroism protein reference databases*

R.W.Janes

*Profile-based direct kernels for remote homology detection and fold recognition*

H.Rangwala and G.Karypis

*Pecons5: combining consensus, structural evaluation and fold recognition scores*

B.Wallner and A.Elofsson

*Gene expression*

*Noise and rank-dependent geometrical filter improves sensitivity of highly specific discovery by microarrays*

H.M.Fathallah-Shaykh

*Sample size determination for the false discovery rate*

S.Pounds and C.Cheng

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The influence of missing value imputation on detection of differentially expressed genes from microarray data


A note on using permutation-based false discovery rate estimates to compare different analysis methods for microarray data

Y.Xie, W.Pan and A.B.Khodursky

Improved approach for proteochemometrics modeling: application to organic compound—amine G protein-coupled receptor interactions

M.Lapinsh, P.Prusis, S.Uhlen and J.E.S.Wikberg

Mapping PDB chains to UniProtKB entries

A.C.R.Martin

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**APPLICATIONS NOTE**

*Genome analysis*

*GARSA: genomic analysis resources for sequence annotation*


*Sequence analysis*

*CREDO: a web-based tool for computational detection of conserved sequence motifs in noncoding sequences*

T.Hindemitt and K.F.X.Mayer

*Genetics and population analysis*

*OxfordGrid: a web interface for pairwise comparative map views*

H.Yang and A.R.Gingle

*HapSim: a simulation tool for generating haplotype data with pre-specified allele frequencies and LD coefficients*

G.Montana

*Databases and ontologies*

*ATID: a web-oriented database for collection of publicly available alternative translational initiation events*

J.Cai, J.Zhang, Y.Huang and Y.Li

*MACiE: a database of enzyme reaction mechanisms*


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