Bioinformatics

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ORIGINAL PAPERS

GenoMetric Query Language: a novel approach to large-scale genomic data management

A novel statistical method for quantitative comparison of multiple ChIP-seq datasets
L.Chen, C.Wang, Z.S.Qin and H.Wu

Sequence analysis

Analysis of nanopore data using hidden Markov models
J.Schreiber and K.Karplus

Methods for the detection and assembly of novel sequence in high-throughput sequencing data
M.Kollberg, L.Ruchenbecker and K.Reinert

Starcode: sequence clustering based on all-pairs search
E.Zilla, A.Ross and G.J.Filion

Reference-based compression of short-read sequences using path encoding
C.Kingstard and R.Patrus

Comparative study of the effectiveness and limitations of current methods for detecting sequence conservation
W.Mao, C.Kaya, A.Dutta, A.Horovitz and I.Bahar

Structure prediction

mFASD: a structure-based algorithm for discriminating different types of metal-binding sites
W.He, Z.Liang, M.Teng and L.Niu

Evolutionary profiles improve protein-protein interaction prediction from sequence
T.Hamp and B.Rest

MESMER: minimal ensemble solutions to multiple experimental restraints
E.C.Ihms and M.P.Foster

Mobility-based prediction of hydration structures of protein surfaces
N.Jeszeni , I.Horváth, M.Bálint, D.van der Spoel and C.Hetényi

Extending P400 site-of-metabolism models with region-resolution data
J.M.Zaretzki, M.R.Browning, T.B.Hughes and S.J.Swamidass

Identification of cell types from single-cell transcriptomes using a novel clustering method
C.Xu and Z.Su

Genetics and population analysis

Application of clinical text data for phenotype-wide association studies (PhenWAS)
S.J.Hebbring, M.Rastegar-Mojarrad, Z.Ye, J.Mayer, C.Jacobson and S.Lin

Systems biology

A multiobjective memetic algorithm for PPI network alignment
C.Clark and J.Kalita

Incorporating peak grouping information for alignment of multiple liquid chromatography-mass spectrometry datasets
J.Wandy, R.Daly, R.Brettling and S.Rogers

Large-scale exploration and analysis of drug combinations

Discriminating precursors of common fragments for large-scale metabolite profiling by triple quadrupole mass spectrometry
I.Nikolsky, G.Siuzdak and G.J.Patti

Bioimage informatics

Characterizing spatial distributions of astrocytes in the mammalian retina

APPLICATIONS NOTES

Sambamba: fast processing of NGS alignment formats
A.Tarasov, A.J.Vilella, E.Cuppen, I.J.Nijman and P.Prins