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.Holtgrewe, L.Kuchenbecker and K.Reinert

Starcode: sequence clustering based on all-pairs search
E.Zorita, R.Cuscó and G.J.Filion

Reference-based compression of short-read sequences using path encoding
C.Kingsford and R.Patro

Comparative study of the effectiveness and limitations of current methods for detecting sequence coevolution
W.He, Z.Liang, M.Teng and L.Niu

mFASD: a structure-based algorithm for discriminating different types of metal-binding sites

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.Jeszenész, I.Horváth, M.Bálint, D.van der Spoel and C.Hetényi

Extending P450 site-of-metabolism models with region-resolution data

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

APPLICATIONS NOTES

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