ORIGINAL PAPERS

Genome analysis

PEATH: single-individual haplotyping by a probabilistic evolutionary algorithm with toggling

QuantumClone: clonal assessment of functional mutations in cancer based on a genotype-aware method for clonal reconstruction

A rapid epistatic mixed-model association analysis by linear retransformations of genomic estimated values

Informational and linguistic analysis of large genomic sequence collections via efficient Hadoop cluster algorithms
U.Ferraro Petrillo, G.Roscigno, G.Cattaneo and R.Giancarlo

GTC: how to maintain huge genotype collections in a compressed form
A.Danek and S.Deorowicz

APARtrap: identification and quantification of alternative polyadenylation sites from RNA-seq data
C.Ye, T.Long, G.Ji, Q.Q.Li and X.Wu

Feature specific quantile normalization enables cross-platform classification of molecular subtypes using gene expression data
J.M.Franks, G.Cai and M.L.Whitfield

Gene expression

Splice Expression Variation Analysis (SEVA) for inter-tumor heterogeneity of gene isoform usage in cancer

Feature specific quantile normalization enables cross-platform classification of molecular subtypes using gene expression data
J.M.Franks, G.Cai and M.L.Whitfield

Genetics and population analysis

A distance-based approach for testing the mediation effect of the human microbiome
J.Jiang, Z.Wei and J.Chen

Discovering personalized driver mutation profiles of single samples in cancer by network control strategy

Computational drug repositioning using low-rank matrix approximation and randomized algorithms
H.Xue, M.Li, S.Xiang, Q.Lu, Yli J.J.Wang

An easy and efficient approach for testing identifiability
C.Kreutz

APPLICATIONS NOTES

Genome analysis

Toppar: an interactive browser for viewing association study results
T.Sullsfosf, R.Borsuk, N.R.Robertson, R.Mott and M.McCarthy

iPat: intelligent prediction and association tool for genomic research
C.J.Chen and Z.Zhang

VIPER: a web application for rapid expert review of variant calls
M.Wüste and M.Dugas

Haystack: systematic analysis of the variation of epigenetic states and cell-type specific regulatory elements
L.Pinello, R.Farouni and G.-C.Yuan

Sequanix: a dynamic graphical interface for Snakemake workflows
D.Desvillechabrol, R.Legendre, C.Rioualen, C.Bouchier, J.van Helden, S.Kennedy and T.Cokelaer

Primer3_masker: integrating masking of template sequence with primer design software
T.Kessasari, M.Lepamets, L.Kaplinski, K.Raine, R.Anderson and M.Remm