STRUCTURAL BIOINFORMATICS

The interfacial character of antibody paratopes: analysis of antibody-antigen structures


ORIGINAL PAPERS

GENOME ANALYSIS

Application of the cghRA framework to the genomic characterization of diffuse large B-Cell Lymphoma


DIRECTION: a machine learning framework for predicting and characterizing DNA methylation and hydroxymethylation in mammalian genomes

M.Pavlovic, P.Ray, K.Pavlovic, A.Kotamarti, M.Chen and M.Q.Zhang

A multi-scenario genome-wide medical population genetics simulation framework


DNA sequence+shape kernel enables alignment-free modeling of transcription factor binding

W.Ma, L.Yang, R.Rohs and W.S.Noble

M2Align: parallel multiple sequence alignment with a multi-objective metaheuristic


DEIsoM: a hierarchical Bayesian model for identifying differentially expressed isoforms using biological replicates

H.Peng, Y.Yang, S.Zhe, J.Wang, M.Gribskov and Y.Qi

MotifHyades: expectation maximization for de novo DNA motif pair discovery on paired sequences

K.-C.Wong

APPLICATIONS NOTES

karyoploteR: an R/Bioconductor package to plot customizable genomes displaying arbitrary data

B.Gel and E.Serra

MoDMaps3D: an interactive webtool for the quantification and 3D visualization of interrelationships in a dataset of DNA sequences

K.Krasimirova and L.Kari

GfaPy: a flexible and extensible software library for handling sequence graphs in Python

G.Gonnella and S.Kurtz

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