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Mathurin Dorel, Eric Viara, Emmanuel Barillot, Andrei Zinovyev, Inna Kuperstein (2017 Apr 18)

NaviCom: a web application to create interactive molecular network portraits using multi-level omics data.

Database : the journal of biological databases and curation : DOI : 10.1093/database/bax026

Résumé

Human diseases such as cancer are routinely characterized by high-throughput molecular technologies, and multi-level omics data are accumulated in public databases at increasing rate. Retrieval and visualization of these data in the context of molecular network maps can provide insights into the pattern of regulation of molecular functions reflected by an omics profile. In order to make this task easy, we developed NaviCom, a Python package and web platform for visualization of multi-level omics data on top of biological network maps. NaviCom is bridging the gap between cBioPortal, the most used resource of large-scale cancer omics data and NaviCell, a data visualization web service that contains several molecular network map collections. NaviCom proposes several standardized modes of data display on top of molecular network maps, allowing addressing specific biological questions. We illustrate how users can easily create interactive network-based cancer molecular portraits via NaviCom web interface using the maps of Atlas of Cancer Signalling Network (ACSN) and other maps. Analysis of these molecular portraits can help in formulating a scientific hypothesis on the molecular mechanisms deregulated in the studied disease.

Laura Cantini, Michele Caselle, Antoine Forget, Andrei Zinovyev, Emmanuel Barillot, Loredana Martignetti (2017 Apr 15)

A review of computational approaches detecting microRNAs involved in cancer.

Frontiers in bioscience (Landmark edition) : 1774-1791

Résumé

MicroRNAs (miRNAs) are small non-coding RNAs playing an essential role in gene expression regulation. Multiple studies have demonstrated that miRNAs are dysregulated in cancer initiation and progression, pointing out their potential as biomarkers for diagnosis, prognosis and response to treatment. With the introduction of high-throughput technologies several computational approaches have been proposed to identify cancer-associated miRNAs. Here, we present a systematic and comprehensive overview of the current knowledge concerning the computational detection of miRNAs involved in tumor onset and subtyping, with possible theranostic employment. An overview of the state of art in this field is thus proposed with the aim of supporting researchers, especially experimentalists and pathologists, in choosing the optimal approach for their case of study.

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Identification of 12 new susceptibility loci for different histotypes of epithelial

ovarian cancer.
Nature genetics : DOI : 10.1038/ng.3826

Résumé

To identify common alleles associated with different histotypes of epithelial ovarian cancer (EOC), we pooled data from multiple genome-wide genotyping projects totaling 25,509 EOC cases and 40,941 controls. We identified nine new susceptibility loci for different EOC histotypes: six for serous EOC histotypes (3q28, 4q32.3, 8q21.11, 10q24.33, 18q11.2 and 22q12.1), two for mucinous EOC (3q22.3 and 9q31.1) and one for endometrioid EOC (5q12.3). We then performed meta-analysis on the results for high-grade serous ovarian cancer with the results from analysis of 31,448 BRCA1 and BRCA2 mutation carriers, including 3,887 mutation carriers with EOC. This identified three additional susceptibility loci at 2q13, 8q24.1 and 12q24.31. Integrated analyses of genes and regulatory biofeatures at each locus predicted candidate susceptibility genes, including OBFC1, a new candidate susceptibility gene for low-grade and borderline serous EOC.

Haitham Ashoor, Caroline Louis-Brennetot, Isabelle Janoueix-Lerosey, Vladimir B Bajic, Valentina Boeva (2017 Jan 6)
HMCan-diff: a method to detect changes in histone modifications in cells with different genetic characteristics.
Nucleic acids research : DOI : gkw1319

Résumé

Comparing histone modification profiles between cancer and normal states, or across different tumor samples, can provide insights into understanding cancer initiation, progression and response to therapy. ChIP-seq histone modification data of cancer samples are distorted by copy number variation innate to any cancer cell. We present HMCan-diff, the first method designed to analyze ChIP-seq data to detect changes in histone modifications between two cancer samples of different genetic backgrounds, or between a cancer sample and a normal control. HMCan-diff explicitly corrects for copy number bias, and for other biases in the ChIP-seq data, which significantly improves prediction accuracy compared to methods that do not consider such corrections. On in silico simulated ChIP-seq data generated using genomes with differences in copy number profiles, HMCan-diff shows a much better performance compared to other methods that have no correction for copy number bias. Additionally, we benchmarked HMCan-diff on four experimental datasets, characterizing two histone marks in two different scenarios. We correlated changes in histone modifications between a cancer and a normal control sample with changes in gene expression. On all experimental datasets, HMCan-diff demonstrated better performance compared to the other methods.

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A N Gorban, E M Mirkes, A Zinovyev (2016 Sep 19)

Piece-wise quadratic approximations of arbitrary error functions for fast and robust machine learning.

Neural networks : the official journal of the International Neural Network Society : 28-38 : DOI : S0893-6080(16)30111-3

Résumé

Most of machine learning approaches have stemmed from the application of minimizing the mean squared distance principle, based on the computationally efficient quadratic optimization methods. However, when faced with high-dimensional and noisy data, the quadratic error functionals demonstrated many weaknesses including high sensitivity to contaminating factors and dimensionality curse. Therefore, a lot of recent applications in machine learning exploited properties of non-quadratic error functionals based on L1 norm or even sub-linear potentials corresponding to quasinorms Lp (0