Resource Summary Report

Generated by NIF on Apr 17, 2025

omniBiomarker

RRID:SCR_005750
Type: Tool

Proper Citation

omniBiomarker (RRID:SCR_005750)

Resource Information

URL: http://omniBiomarker.bme.gatech.edu

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Description: omniBiomarker is a web-application for analysis of high-throughput -omic data. Its primary function is to identify differentially expressed biomarkers that may be used for diagnostic or prognostic clinical prediction. Currently, omniBiomarker allows users to analyze their data with many different ranking methods simultaneously using a high-performance compute cluster. The next release of omniBiomarker will automatically select the most biologically relevant ranking method based on user input regarding prior knowledge. The omniBiomarker workflow * Data: Gene Expression * Algorithms: Knowledge-Driven Gene Ranking * Differentially expressed Genes * Clinical / Biological Validation * Knowledge: NCI Thesaurus of Cancer, Cancer Gene Index * back to Algorithms

Abbreviations: omniBiomarker

Synonyms: omniBiomarker: Knowledge-Driven Biomarker Identification and Data Combination

Resource Type: data analysis service, production service resource, service resource, analysis service resource

Defining Citation: PMID:19695674

Keywords: gene, gene expression, algorithm, cancer, cancer gene, cancer gene index, biocomputing, biomarker, clinical, gene ranking

Related Condition: Cancer

Funding: Georgia Cancer Coalition ;

NCI U54CA119338;
NCI R01CA108468

Resource Name: omniBiomarker

Resource ID: SCR_005750

Alternate IDs: nlx_149210

Record Creation Time: 20220129T080232+0000

Record Last Update: 20250417T065231+0000

Ratings and Alerts

No rating or validation information has been found for omniBiomarker.

No alerts have been found for omniBiomarker.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Singh P, et al. (2020) Network-based identification of signature genes KLF6 and SPOCK1 associated with oral submucous fibrosis. Molecular and clinical oncology, 12(4), 299.

Moffitt RA, et al. (2011) caCORRECT2: Improving the accuracy and reliability of microarray data in the presence of artifacts. BMC bioinformatics, 12, 383.

Mishra A, et al. (2010) Cancer biomarkers: are we ready for the prime time? Cancers, 2(1), 190.