Resource Summary Report

Generated by NIF on Apr 29, 2025

methyAnalysis

RRID:SCR_001290
Type: Tool

Proper Citation

methyAnalysis (RRID:SCR_001290)

Resource Information

URL: http://www.bioconductor.org/packages/release/bioc/html/methyAnalysis.html

Proper Citation: methyAnalysis (RRID:SCR_001290)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 23,2022. Software package for DNA methylation data analysis and visualization. A new class is defined to keep the chromosome location information together with the data. The current version of the package mainly focuses on analyzing the Illumina Infinium methylation array data, but most methods can be generalized to other methylation array or sequencing data.

Abbreviations: methyAnalysis

Synonyms: methyAnalysis - DNA methylation data analysis and visualization

Resource Type: software resource

Defining Citation: PMID:21159174

Keywords: dna methylation, microarray, visualization

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: methyAnalysis

Resource ID: SCR_001290

Alternate IDs: OMICS_02046

Record Creation Time: 20220129T080206+0000

Record Last Update: 20250420T014025+0000

Ratings and Alerts

No rating or validation information has been found for methyAnalysis.

No alerts have been found for methyAnalysis.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

McKinney BC, et al. (2019) DNA methylation in the human frontal cortex reveals a putative mechanism for age-by-disease interactions. Translational psychiatry, 9(1), 39.

Kan S, et al. (2019) DNA methylation profiling identifies potentially significant epigenetically-regulated genes in glioblastoma multiforme. Oncology letters, 18(2), 1679.

Janssens S, et al. (2018) Zika Virus Alters DNA Methylation of Neural Genes in an Organoid Model of the Developing Human Brain. mSystems, 3(1).

Daemen A, et al. (2018) HER2 is not a cancer subtype but rather a pan-cancer event and is highly enriched in AR-driven breast tumors. Breast cancer research : BCR, 20(1), 8.

Xu J, et al. (2017) An integrative analysis of DNA methylation in osteosarcoma. Journal of bone oncology, 9, 34.

Zhang K, et al. (2017) Screening of candidate key genes associated with human osteosarcoma using bioinformatics analysis. Oncology letters, 14(3), 2887.

Khuc E, et al. (2017) Comprehensive characterization of DNA methylation changes in Fuchs endothelial corneal dystrophy. PloS one, 12(4), e0175112.

Li D, et al. (2015) An evaluation of statistical methods for DNA methylation microarray data analysis. BMC bioinformatics, 16, 217.

Assenov Y, et al. (2014) Comprehensive analysis of DNA methylation data with RnBeads. Nature methods, 11(11), 1138.