Resource Summary Report

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COHCAP

RRID:SCR_006499
Type: Tool

Proper Citation

COHCAP (RRID:SCR_006499)

Resource Information

URL: http://sourceforge.net/projects/cohcap/

Proper Citation: COHCAP (RRID:SCR_006499)

Description: An algorithm to analyze single-nucleotide resolution methylation data (Illumina 450k methylation array, targeted BS-Seq, etc.). It provides QC metrics, differential methylation for CpG Sites, differential methylation for CpG Islands, integration with gene expression data, and visualization of methylation values.

Abbreviations: COHCAP

Synonyms: City of Hope CpG Island Analysis Pipeline, COHCAP - City of Hope CpG Island Analysis Pipeline

Resource Type: software resource

Defining Citation: PMID:23598999

Keywords: java, perl, s/r, java swing, bio.tools

Funding:

Availability: Acknowledgement requested, Attribution Assurance License

Resource Name: COHCAP

Resource ID: SCR_006499

Alternate IDs: biotools:cohcap, OMICS_00595

Alternate URLs: https://bio.tools/cohcap

Record Creation Time: 20220129T080236+0000

Record Last Update: 20250410T065439+0000

Ratings and Alerts

No rating or validation information has been found for COHCAP.

No alerts have been found for COHCAP.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 18 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Sun JX, et al. (2024) Upregulation of GPR133 expression impaired the phagocytosis of macrophages in recurrent spontaneous miscarriage. Epigenetics, 19(1), 2337087.

Elhai M, et al. (2023) The long non-coding RNA HOTAIR contributes to joint-specific gene expression in rheumatoid arthritis. Nature communications, 14(1), 8172.

Zhang W, et al. (2022) Epigenetic study of early breast cancer (EBC) based on DNA methylation and gene integration analysis. Scientific reports, 12(1), 1989.

Wang G, et al. (2022) Uncovering potential genes in colorectal cancer based on integrated and DNA methylation analysis in the gene expression omnibus database. BMC cancer, 22(1), 138.

Xu Y, et al. (2021) Epigenetic Study of Esophageal Carcinoma Based on Methylation, Gene Integration and Weighted Correlation Network Analysis. OncoTargets and therapy, 14, 3133.

Ren J, et al. (2020) Identification of Methylated Gene Biomarkers in Patients with Alzheimer's Disease Based on Machine Learning. BioMed research international, 2020, 8348147.

Tini G, et al. (2020) DNA methylation during human adipogenesis and the impact of fructose. Genes & nutrition, 15(1), 21.

Sun XJ, et al. (2018) An integrated analysis of genome-wide DNA methylation and gene expression data in hepatocellular carcinoma. FEBS open bio, 8(7), 1093.

Huang J, et al. (2018) Use of methylation profiling to identify significant differentially methylated genes in bone marrow mesenchymal stromal cells from acute myeloid leukemia. International journal of molecular medicine, 41(2), 679.

Gerhard GS, et al. (2018) Differentially methylated loci in NAFLD cirrhosis are associated with key signaling pathways. Clinical epigenetics, 10(1), 93.

Wang Y, et al. (2018) Identification of methylated genes and miRNA signatures in nasopharyngeal carcinoma by bioinformatics analysis. Molecular medicine reports, 17(4), 4909.

Men C, et al. (2017) Identification of DNA methylation associated gene signatures in endometrial cancer via integrated analysis of DNA methylation and gene expression systematically. Journal of gynecologic oncology, 28(6), e83.

Yang Y, et al. (2017) Identification of regulatory role of DNA methylation in colon cancer gene expression via systematic bioinformatics analysis. Medicine, 96(47), e8487.

Frank-Bertoncelj M, et al. (2017) Epigenetically-driven anatomical diversity of synovial fibroblasts guides joint-specific fibroblast functions. Nature communications, 8, 14852.

Hui L, et al. (2017) Identification of potentially critical differentially methylated genes in nasopharyngeal carcinoma: A comprehensive analysis of methylation profiling and gene expression profiling. Oncology letters, 14(6), 7171.

Geoghegan F, et al. (2017) Bioenergetics of acquired cisplatin resistant H1299 non-small cell lung cancer and P31 mesothelioma cells. Oncotarget, 8(55), 94711.

Hua Y, et al. (2017) Abnormal expression of mRNA, microRNA alteration and aberrant DNA methylation patterns in rectal adenocarcinoma. PloS one, 12(3), e0174461.

Gevaert O, et al. (2015) Pancancer analysis of DNA methylation-driven genes using MethylMix. Genome biology, 16(1), 17.