Resource Summary Report

Generated by NIF on May 15, 2025

MethPipe

RRID:SCR_005168
Type: Tool

Proper Citation

MethPipe (RRID:SCR_005168)

Resource Information

URL: http://smithlab.usc.edu/methpipe/

Proper Citation: MethPipe (RRID:SCR_005168)

Description: A computational pipeline for analyzing bisulfite sequencing data.

Abbreviations: MethPipe

Resource Type: software resource

Defining Citation: PMID:24324667

Keywords: bio.tools

Funding:

Resource Name: MethPipe

Resource ID: SCR_005168

Alternate IDs: biotools:methpipe, OMICS_00603

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

Record Creation Time: 20220129T080228+0000

Record Last Update: 20250420T014245+0000

Ratings and Alerts

No rating or validation information has been found for MethPipe.

No alerts have been found for MethPipe.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 95 mentions in open access literature.

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

Ye X, et al. (2024) Enhancer-promoter activation by the Kaposi sarcoma-associated herpesvirus episome maintenance protein LANA. Cell reports, 43(3), 113888.

Moqri M, et al. (2024) PRC2-AgeIndex as a universal biomarker of aging and rejuvenation. Nature communications, 15(1), 5956.

Murase Y, et al. (2024) In vitro reconstitution of epigenetic reprogramming in the human germ line. Nature, 631(8019), 170.

Buckley DN, et al. (2024) A comprehensive analysis of minimally differentially methylated regions common to pediatric and adult solid tumors. NPJ precision oncology, 8(1), 125.

Zhu Y, et al. (2024) DNA methylation profiling of CpG islands in trigeminal ganglion of rats with orofacial pain induced by experimental tooth movement. BMC oral health, 24(1), 1474.

Guerin LN, et al. (2024) Temporally discordant chromatin accessibility and DNA demethylation define short and long-term enhancer regulation during cell fate specification. bioRxiv : the preprint server for biology.

Chen S, et al. (2024) Cross-Species Comparative DNA Methylation Reveals Novel Insights into Complex Trait Genetics among Cattle, Sheep, and Goats. Molecular biology and evolution, 41(2).

Chalkley ML, et al. (2024) Human TSC2 Mutant Cells Exhibit Aberrations in Early Neurodevelopment Accompanied by Changes in the DNA Methylome. bioRxiv : the preprint server for biology.

Gu G, et al. (2024) Endocrine islet ?-cell subtypes with differential function are derived from biochemically distinct embryonic endocrine islet progenitors that are regulated by maternal nutrients. Research square.

Zhu S, et al. (2023) The Snapdragon Genomes Reveal the Evolutionary Dynamics of the S-Locus Supergene. Molecular biology and evolution, 40(4).

Senapati P, et al. (2023) Loss of epigenetic suppression of retrotransposons with oncogenic potential in aging mammary luminal epithelial cells. Genome research, 33(8), 1229.

Zhu W, et al. (2023) The Chromatin Remodeling Factor BrCHR39 Targets DNA Methylation to Positively Regulate Apical Dominance in Brassica rapa. Plants (Basel, Switzerland), 12(6).

Buckley DN, et al. (2023) OvaPrint-A Cell-free DNA Methylation Liquid Biopsy for the Risk Assessment of High-grade Serous Ovarian Cancer. Clinical cancer research : an official journal of the American Association for Cancer Research, 29(24), 5196.

Liu Q, et al. (2023) Genome-wide DNA methylation analysis of Astragalus and Danshen on the intervention of myofibroblast activation in idiopathic pulmonary fibrosis. BMC pulmonary medicine, 23(1), 325.

Ouni M, et al. (2023) Differences in DNA methylation of HAMP in blood cells predicts the development of type 2 diabetes. Molecular metabolism, 75, 101774.

Yuan Y, et al. (2023) Integrated analysis of methylation profiles and transcriptome of Marek's disease virus-infected chicken spleens reveal hypomethylation of CD4 and HMGB1 genes might promote Marek's disease tumorigenesis. Poultry science, 102(6), 102594.

Lin SY, et al. (2023) Novel urine cell-free DNA methylation markers for hepatocellular carcinoma. Scientific reports, 13(1), 21585.

van der Veer BK, et al. (2023) Dual functions of TET1 in germ layer lineage bifurcation distinguished by genomic context and dependence on 5-methylcytosine oxidation. Nucleic acids research, 51(11), 5469.

Kerr L, et al. (2023) Genome-wide single-molecule analysis of long-read DNA methylation reveals heterogeneous patterns at heterochromatin that reflect nucleosome organisation. PLoS genetics, 19(10), e1010958.

Zheng Y, et al. (2023) Comprehensive analyses of partially methylated domains and differentially methylated regions in esophageal cancer reveal both cell-type- and cancer-specific epigenetic regulation. Genome biology, 24(1), 193.