

Resource Summary Report

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MethylAid

RRID:SCR_002659

Type: Tool

Proper Citation

MethylAid (RRID:SCR_002659)

Resource Information

URL: <http://www.bioconductor.org/packages/devel/bioc/html/MethylAid.html>

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Description: Software for visual and interactive quality control of large Illumina 450k data sets. Bad quality samples are detected using sample-dependent and sample-independent controls present on the array and user adjustable thresholds. In depth exploration of bad quality samples can be performed using several interactive diagnostic plots of the quality control probes present on the array. Furthermore, the impact of any batch effect provided by the user can be explored.

Synonyms: MethylAid - Visual and interactive quality control of large Illumina 450k data sets, MethylAid: Visual and interactive quality control of large Illumina 450k data sets

Resource Type: software resource

Defining Citation: [PMID:25147358](#)

Keywords: software package, illumina, mac os x, unix/linux, windows, r, dna methylation, gui, methylation array, microarray, quality control, two channel, visualization, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: MethylAid

Resource ID: SCR_002659

Alternate IDs: biotools:methylaid, OMICS_05457

Alternate URLs: <http://www.bioconductor.org/packages/release/bioc/html/MethylAid.html>, <http://shiny.bioexp.nl/MethylAid/>, <https://bio.tools/methylaid>

License: GNU General Public License, v2 or greater

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Ratings and Alerts

No rating or validation information has been found for MethylAid.

No alerts have been found for MethylAid.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 68 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Rasmussen CPV, et al. (2026) Differential DNA Methylation of the Serotonin Receptor Signaling and Glutamatergic Synapse Pathways in Adult Twins Born Preterm. *Genes*, 17(6).

Lauffer P, et al. (2026) Multi-omics investigation of thyroid development and dysfunction in down syndrome. *Human molecular genetics*, 35(4).

Zhang X, et al. (2026) Genetic impacts on within-pair DNA methylation variance in monozygotic twins capture gene-environment interactions and cell-type effects. *Genome biology*, 27(1).

Sinke L, et al. (2025) Tissue-specific methylomic responses to a lifestyle intervention in older adults associate with metabolic and physiological health improvements. *Aging cell*, 24(4), e14431.

Hagenbeek FA, et al. (2025) Intergenerational transmission of complex traits and the offspring methylome. *Molecular psychiatry*, 30(7), 3338.

Taryma-Le?niak O, et al. (2025) Changes of methylation at enhancers appear to be essential for HIV infection progression. *Clinical epigenetics*, 17(1), 104.

Kou M, et al. (2025) Epigenetic Age Acceleration and Cardiometabolic Biomarkers in Response to Weight-Loss Dietary Interventions Among Obese Individuals: The MACRO Trial. *Aging cell*, 24(11), e70224.

Ensink JBM, et al. (2024) Distinct saliva DNA methylation profiles in relation to treatment outcome in youth with posttraumatic stress disorder. *Translational psychiatry*, 14(1), 309.

van Toledo DE, et al. (2024) Aberrant PRDM2 methylation as an early event in serrated lesions destined to evolve into microsatellite-unstable colorectal cancers. *The journal of*

pathology. Clinical research, 10(2), e348.

Todtenhaupt P, et al. (2024) Twisting the theory on the origin of human umbilical cord coiling featuring monozygotic twins. Life science alliance, 7(8).

Risha MA, et al. (2024) Epigenetic training of human bronchial epithelium cells by repeated rhinovirus infections. Allergy, 79(12), 3385.

Lange de Luna J, et al. (2024) Epigenome-wide association study of dietary fatty acid intake. Clinical epigenetics, 16(1), 29.

Demirkan A, et al. (2024) Linking the gut microbiome to host DNA methylation by a discovery and replication epigenome-wide association study. BMC genomics, 25(1), 1224.

Bloks NGC, et al. (2024) Hyper-physiologic mechanical cues, as an osteoarthritis disease-relevant environmental perturbation, cause a critical shift in set points of methylation at transcriptionally active CpG sites in neo-cartilage organoids. Clinical epigenetics, 16(1), 64.

Hajmoussa G, et al. (2024) The role of DNA methylation in chondrogenesis of human iPSCs as a stable marker of cartilage quality. Clinical epigenetics, 16(1), 141.

Reho P, et al. (2024) Differential methylation analysis in neuropathologically confirmed dementia with Lewy bodies. Communications biology, 7(1), 35.

Robinson O, et al. (2023) Associations of four biological age markers with child development: A multi-omic analysis in the European HELIX cohort. eLife, 12.

Costeira R, et al. (2023) Metabolomic biomarkers of habitual B vitamin intakes unveil novel differentially methylated positions in the human epigenome. Clinical epigenetics, 15(1), 166.

van Dongen J, et al. (2023) Effects of smoking on genome-wide DNA methylation profiles: A study of discordant and concordant monozygotic twin pairs. eLife, 12.

Stols-Gonçalves D, et al. (2023) Faecal Microbiota transplantation affects liver DNA methylation in Non-alcoholic fatty liver disease: a multi-omics approach. Gut microbes, 15(1), 2223330.