

Package: methylationArrayAnalysis (via r-universe)

October 13, 2026

Title A cross-package Bioconductor workflow for analysing methylation array data

Version 1.36.1

Description Methylation in the human genome is known to be associated with development and disease. The Illumina Infinium methylation arrays are by far the most common way to interrogate methylation across the human genome. This Bioconductor workflow uses multiple packages for the analysis of methylation array data. Specifically, we demonstrate the steps involved in a typical differential methylation analysis pipeline including: quality control, filtering, normalization, data exploration and statistical testing for probe-wise differential methylation. We further outline other analyses such as differential methylation of regions, differential variability analysis, estimating cell type composition and gene ontology testing. Finally, we provide some examples of how to visualise methylation array data.

Depends R (>= 3.3.0), knitr, rmarkdown, BiocStyle, limma, minfi, IlluminaHumanMethylation450kanno.ilmn12.hg19, IlluminaHumanMethylation450kmanifest, RColorBrewer, missMethyl, matrixStats, minfiData, Gviz, DMRcate, stringr, FlowSorted.Blood.450k

License Artistic-2.0

Encoding UTF-8

LazyData true

VignetteBuilder knitr

biocViews Workflow, EpigeneticsWorkflow

NeedsCompilation no

Author Jovana Maksimovic [aut, cre]

Maintainer Jovana Maksimovic <jovana.maksimovic@petermac.org>

RoxygenNote 7.3.3

Config/pak/sysreqs cmake make libbz2-dev libicu-dev libjpeg-dev liblzma-dev libpng-dev libuv1-dev libxml2-dev libssl-dev libx11-dev xz-utils zlib1g-dev

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