

Resource Summary Report

Generated by [kravitz2](#) on Jul 30, 2026

DMRforPairs

RRID:SCR_005702

Type: Tool

Proper Citation

DMRforPairs (RRID:SCR_005702)

Resource Information

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

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Description: Software for identifying differentially methylated regions between unique samples using array based methylation profiles. It allows researchers to compare n greater than or equal to 2 unique samples with regard to their methylation profile. The (pairwise) comparison of n unique single samples distinguishes it from other existing pipelines as these often compare groups of samples in either single CpG locus or region based analysis. DMRforPairs defines regions of interest as genomic ranges with sufficient probes located in close proximity to each other. Probes in one region are optionally annotated to the same functional class(es). Differential methylation is evaluated by comparing the methylation values within each region between individual samples and (if the difference is sufficiently large), testing this difference formally for statistical significance.

Synonyms: DMR2+, DMRforPairs: identifying Differentially Methylated Regions between unique samples using array based methylation profiles

Resource Type: software resource

Defining Citation: [PMID:24884391](#)

Keywords: standalone software, mac os x, unix/linux, windows, r, annotation, dna methylation, differential methylation, microarray, report writing, visualization, bio.tools

Availability: GNU General Public License, v2 or greater

Resource Name: DMRforPairs

Resource ID: SCR_005702

Alternate IDs: biotools:dmrforpairs, OMICS_04059

Alternate URLs: <https://bio.tools/dmrforpairs>

Record Creation Time: 20220129T080231+0000

Record Last Update: 20260725T190608+0000

Ratings and Alerts

No rating or validation information has been found for DMRforPairs.

No alerts have been found for DMRforPairs.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Patrizi S, et al. (2021) Whole-Genome Methylation Study of Congenital Lung Malformations in Children. *Frontiers in oncology*, 11, 689833.

Struijk RB, et al. (2020) Comparing genome-scale DNA methylation and CNV marks between adult human cultured ITGA6+ testicular cells and seminomas to assess in vitro genomic stability. *PloS one*, 15(3), e0230253.

Xia C, et al. (2020) Hodgkin Lymphoma Monozygotic Triplets Reveal Divergences in DNA Methylation Signatures. *Frontiers in oncology*, 10, 598872.

Rijlaarsdam MA, et al. (2015) Genome wide DNA methylation profiles provide clues to the origin and pathogenesis of germ cell tumors. *PloS one*, 10(4), e0122146.