Resource Summary Report

Generated by SPARC SAWG on Sep 18, 2026

EpiDISH R package

RRID:SCR_018004
Type: Tool

Proper Citation

EpiDISH R package (RRID:SCR_018004)

Resource Information

URL: https://bioconductor.org/packages/EpiDISH/

Proper Citation: EpiDISH R package (RRID:SCR_018004)

Description: Software R package provides tools to infer proportions of priori known cell-types present in sample representing mixture of such cell-types. Comparison of reference based algorithms for correcting cell-type heterogeneity in Epigenome-Wide Association Studies.

Abbreviations: EpiDISH

Synonyms: Epigenetic Dissection of Intra-Sample Heterogeneity

Resource Type: software resource, software toolkit

Defining Citation: PMID:28193155

Keywords: Epigenetic, sample heterogeneity, reference, algorithm, correcting, cell type, bio.tools

Funding: Chinese Academy of Sciences ;
EU-FP7 ;
Max-Planck Society ;
NSFC 31571359;
Royal Society Newton Advanced Fellowship ;
Shanghai Institute for Biological Sciences

Availability: Free, Available for download, Freely available

Resource Name: EpiDISH R package

Resource ID: SCR_018004

Alternate IDs: biotools:epidish

Alternate URLs: https://github.com/sjczheng/EpiDISH, https://bio.tools/epidish

Record Creation Time: 20220129T080338+0000

Record Last Update: 20260912T200255+0000

Ratings and Alerts

No rating or validation information has been found for EpiDISH R package.

No alerts have been found for EpiDISH R package.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Campbell KA, et al. (2026) Epigenetic Responses to Abusive versus Accidental Injuries in Children: A Cross-sectional Epigenome Wide Association Meta-analysis. medRxiv : the preprint server for health sciences.

Shan J, et al. (2026) Lifestyle factors and DNA methylation-based aging clocks: cross-sectional and longitudinal associations in the Singapore diet and healthy aging cohort. The journal of prevention of Alzheimer's disease, 13(4), 100522.

Schallen KP, et al. (2026) Non-ablative fractional laser 1940-nm treatment modulates epigenetic signatures associated with skin aging in a split-face investigation. Scientific reports, 16(1).

Guo X, et al. (2026) Guidelines on optimizing DNA methylation reference panels for cell-type deconvolution. Communications biology, 9(1).

Zeng Z, et al. (2026) Red Blood Cells Internalize Extracellular DNA via Apoptotic Bodies with Clinical Relevance to Cancer Patients. Advanced science (Weinheim, Baden-Wurttemberg, Germany), e11408.

Herzog CMS, et al. (2025) Systems epigenetic approach towards non-invasive breast cancer detection. Nature communications, 16(1), 3082.

Martínez-López J, et al. (2025) A Strong Dysregulated Myeloid Component in the Epigenetic Landscape of Systemic Sclerosis: An Integrated DNA Methylome and Transcriptome Analysis. Arthritis & rheumatology (Hoboken, N.J.), 77(4), 439.

Lemaire M, et al. (2025) Meta-analysis examining fetal sex-specific placental DNA methylation intensities and estimated cell composition post IVF. Molecular human

reproduction, 31(3).

Guo X, et al. (2025) Epigenetic clocks and inflammaging: pitfalls caused by ignoring cell-type heterogeneity. GeroScience, 47(3), 2707.

Meng G, et al. (2023) A comprehensive assessment of cell type-specific differential expression methods in bulk data. Briefings in bioinformatics, 24(1).

Galkin F, et al. (2021) Adapting Blood DNA Methylation Aging Clocks for Use in Saliva Samples With Cell-type Deconvolution. Frontiers in aging, 2, 697254.

Lapsley CR, et al. (2020) Methylome profiling of young adults with depression supports a link with immune response and psoriasis. Clinical epigenetics, 12(1), 85.

You C, et al. (2020) A cell-type deconvolution meta-analysis of whole blood EWAS reveals lineage-specific smoking-associated DNA methylation changes. Nature communications, 11(1), 4779.

Zheng SC, et al. (2018) Identification of differentially methylated cell types in epigenome-wide association studies. Nature methods, 15(12), 1059.