Package: GSE280465 (via r-universe)

July 5, 2026

Type Package

Title GSE280465 EPICv2 Methylation ExperimentHub Data

Version 0.99.0

Date 2026-07-05

Description Provides ExperimentHub access to a processed DNA methylation resource derived from GEO accession GSE280465. The resource contains adult Illumina Infinium MethylationEPIC version 2 data from 163 samples across four tissue types, represented as a RangedSummarizedExperiment with beta, M, and CN assays, hg38 genomic ranges, and sample phenotype metadata.

URL `https://github.com/paulYRP/GSE280465`

BugReports `https://github.com/paulYRP/GSE280465/issues`

License Artistic-2.0

Depends R (>= 4.4.0)

Imports ExperimentHub, utils

Suggests BiocStyle, ExperimentHubData, knitr, rmarkdown, SummarizedExperiment

VignetteBuilder knitr

biocViews ExperimentData, ExperimentHub, GEO, Homo_sapiens_Data, MethylationArrayData, MicroarrayData, Tissue

Encoding UTF-8

NeedsCompilation no

Config/pak/sysreqs libicu-dev libpng-dev libssl-dev zlib1g-dev

Repository https://biocstaging.r-universe.dev

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RemoteUrl https://github.com/BiocStaging/GSE280465

RemoteRef HEAD

RemoteSha bc2525611884fc38bdc1787f70f1fb6d4b747298

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`GSE280465-package` *GSE280465 EPICv2 methylation data in ExperimentHub*

Description

The **GSE280465** package provides ExperimentHub access to a processed adult DNA methylation resource derived from GEO accession GSE280465.

Details

The hosted resource is a `RangedSummarizedExperiment` created from an Illumina Infinium MethylationEPIC version 2 `GenomicRatioSet`. It contains beta, M, and CN assays for 163 adult samples from 47 individuals across buccal, saliva, dried blood spot, and peripheral blood mononuclear cell tissues.

The resource is hosted on Zenodo at `https://zenodo.org/records/21200586` and is registered for access through **ExperimentHub**.

See `browseVignettes("GSE280465")` for a usage example.

See Also

`https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE280465`

`GSE280465` *Load the GSE280465 ExperimentHub resource*

Description

Convenience helper for loading the GSE280465 EPICv2 adult cross-tissue DNA methylation resource from **ExperimentHub**.

Usage

```
GSE280465(metadata = FALSE, filterBy = "GSE280465_GPL33022_EPICv2")

GSE280465_GPL33022_EPICv2(metadata = FALSE)
```

Arguments

`metadata`	`logical(1)`. If `TRUE`, return ExperimentHub metadata for the matching resource. If `FALSE`, load the matching resource.
`filterBy`	`character(1)`. Resource title used to filter the **ExperimentHub** entries for this package.

Details

The resource is registered as `GSE280465_GPL33022_EPICv2` in **ExperimentHub**. It contains beta, M, and CN assays with hg38 genomic ranges and sample-level phenotype metadata.

The `GSE280465_GPL33022_EPICv2()` function is the resource-title accessor generated from ‘`inst/extdata/metadata.csv`’ when the package is loaded. It returns the same hosted resource as `GSE280465()`.

Value

When `metadata = FALSE`, a `RangedSummarizedExperiment`. When `metadata = TRUE`, the matching ExperimentHub metadata.

See Also

`ExperimentHub`, `listResources`, `loadResources`

Examples

```
metadata_file <- system.file("extdata", "metadata.csv", package = "GSE280465")
metadata <- utils::read.csv(metadata_file, stringsAsFactors = FALSE)
metadata[, c("Title", "Genome", "RDataClass")]

if (interactive()) {
    library(GSE280465)
    GSE280465(metadata = TRUE)
    se <- GSE280465()
    se
    se <- GSE280465_GPL33022_EPICv2()
}
```

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