Package: GSE142512 (via r-universe)

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Type Package

Title GSE142512 DNA Methylation ExperimentHub Data

Version 0.99.0

Date 2026-07-06

Description Provides ExperimentHub access to processed DNA methylation resources derived from GEO accession GSE142512. The resources contain Illumina HumanMethylation450 and Infinium MethylationEPIC data represented as RangedSummarizedExperiment objects with beta, M, and CN assays, hg19 genomic ranges, and sample phenotype metadata.

URL `https://github.com/paulYRP/GSE142512`

BugReports `https://github.com/paulYRP/GSE142512/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/GSE142512

RemoteRef HEAD

RemoteSha 8a5d7dfbe2e82f8b430531e478c69ec20756bc35

Contents

`GSE142512-package` *GSE142512 methylation data in ExperimentHub*

Description

The **GSE142512** package provides ExperimentHub access to processed DNA methylation resources derived from GEO accession GSE142512.

Details

The hosted resources are `RangedSummarizedExperiment` objects created from Illumina HumanMethylation450 and Infinium MethylationEPIC `GenomicRatioSet` objects. They contain beta, M, and CN assays with hg19 genomic ranges and sample-level phenotype metadata.

The resources are hosted on Zenodo at `https://zenodo.org/records/21198533` and are registered for access through **ExperimentHub**.

See `browseVignettes("GSE142512")` for usage examples.

See Also

`https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE142512`

`GSE142512` *Load GSE142512 ExperimentHub resources*

Description

Convenience helpers for loading processed GSE142512 DNA methylation resources from **ExperimentHub**.

Usage

```
GSE142512(platform = c("450K", "EPIC"), metadata = FALSE)

GSE142512_GPL13534_450K(metadata = FALSE)

GSE142512_GPL21145_EPIC(metadata = FALSE)
```

Arguments

`platform`	`character(1)`. Platform to load. Use `"450K"` for the GPL13534 Illumina HumanMethylation450 resource or `"EPIC"` for the GPL21145 Infinium MethylationEPIC resource.
`metadata`	`logical(1)`. If `TRUE`, return ExperimentHub metadata for the matching resource. If `FALSE`, load the matching resource.

Details

The package registers two ExperimentHub resources: `GSE142512_GPL13534_450K` and `GSE142512_GPL21145_EPIC`. Each resource contains beta, M, and CN assays with hg19 genomic ranges and sample-level phenotype metadata.

The resource-title accessors are generated from ‘`inst/extdata/metadata.csv`’ when the package is loaded.

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 = "GSE142512")
metadata <- utils::read.csv(metadata_file, stringsAsFactors = FALSE)
metadata[, c("Title", "Genome", "RDataClass")]

if (interactive()) {
    library(GSE142512)
    GSE142512(platform = "450K", metadata = TRUE)
    se450k <- GSE142512(platform = "450K")
    seEPIC <- GSE142512(platform = "EPIC")
    se450k
    seEPIC
}
```

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