Package: GSE142512 (via r-universe)

November 1, 2026

Type Package

Title 450K and EPIC Methylation ExperimentHub Data from GEO

Version 0.99.2

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, testthat (>= 3.0.0)

VignetteBuilder knitr

Config/testthat/edition 3

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://bioc.r-universe.dev

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RemoteUrl https://github.com/bioc/GSE142512

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Contents

GSE142512-package 2
GSE142512 2

Index **4**

`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
}
```

Index

∗ **datasets**
GSE142512, 2
GSE142512-package, 2

ExperimentHub, *3*

GSE142512, 2
GSE142512-package, 2
GSE142512_GPL13534_450K *(*GSE142512*)*, 2
GSE142512_GPL21145_EPIC *(*GSE142512*)*, 2

listResources, *3*
loadResources, *3*