

Package ‘multiWGCNAdata’

April 16, 2024

Type Package

Title Data Package for multiWGCNA

Version 1.0.0

biocViews ExperimentHub, ExpressionData, Homo_sapiens_Data,
Mus_musculus_Data, RNASeqData, MicroarrayData

Description Stores expression profiling data from experiments compatible with the multiWGCNA R package. This includes human postmortem microarray data from patients and controls (GSE28521), astrocyte Ribotag RNA-seq data from EAE and wildtype mice (GSE100329), and mouse RNA-seq data from tau pathology (rTg4510) and wildtype control mice (GSE125957). These data can be accessed using the ExperimentHub workflow (see multiWGCNA vignettes).

License Artistic-2.0

VignetteBuilder knitr

Encoding UTF-8

LazyData false

Depends ExperimentHub

Imports utils

Suggests knitr, multiWGCNA, rmarkdown, SummarizedExperiment

RoxygenNote 7.2.3

git_url <https://git.bioconductor.org/packages/multiWGCNAdata>

git_branch RELEASE_3_18

git_last_commit 106183b

git_last_commit_date 2023-10-24

Repository Bioconductor 3.18

Date/Publication 2024-04-16

Author Dario Tommasini [aut, cre] (<<https://orcid.org/0000-0002-1214-6547>>)

Maintainer Dario Tommasini <dtommasini@gmail.com>

R topics documented:

multiWGCNAdata-package 2

Index 3

multiWGCNAdata-package

multiWGCNAdata available as R objects

Description

Stores expression profiling data from experiments compatible with the multiWGCNA R package. This includes human postmortem microarray data from patients and controls (GSE28521), astrocyte Ribotag RNA-seq data from EAE and wildtype mice (GSE100329), and mouse RNA-seq data from tau pathology (rTg4510) and wildtype control mice (GSE125957). These data have been parsed into list objects and are available in the ExperimentHub.

Details

See the vignette for examples of using these data in analyses.

`browseVignettes("multiWGCNAdata")`

Details of how these data were created are in the scripts/ directory of the source package.

Value

NA

Examples

```
library(ExperimentHub)
eh = ExperimentHub()
eh_query = query(eh, c("multiWGCNAdata"))
astrocyte_se = eh_query[["EH8223"]]
astrocyte_se
```

Index

* **utilities**

multiWGCNAdata-package, [2](#)

multiWGCNAdata

(multiWGCNAdata-package), [2](#)

multiWGCNAdata-package, [2](#)