

Package ‘multiWGCNAdata’

December 4, 2025

Type Package

Title Data Package for multiWGCNA

Version 1.8.0

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 BiocStyle, knitr, multiWGCNA, rmarkdown, SummarizedExperiment

RoxygenNote 7.2.3

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

git_branch RELEASE_3_22

git_last_commit 42ab777

git_last_commit_date 2025-10-29

Repository Bioconductor 3.22

Date/Publication 2025-12-04

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

Maintainer Dario Tommasini <dtommasini0@gmail.com>

Contents

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**

multiWGCNAdat-package, [2](#)

multiWGCNAdat

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

multiWGCNAdat-package, [2](#)