

Package ‘QUBICdata’

December 26, 2024

Type Package

Title Data employed in the vignette of the QUBIC package

Description The data employed in the vignette of the QUBIC package. These data belong to Many Microbe Microarrays Database and STRING v10.

VignetteBuilder knitr

biocViews Escherichia_coli_Data, OrganismData, ExperimentData

Version 1.35.0

License Unlimited | file LICENSE

Depends R (>= 3.1)

Suggests knitr, rmarkdown

URL <http://github.com/zy26/QUBICdata>

BugReports <http://github.com/zy26/QUBICdata/issues>

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

git_branch devel

git_last_commit 7dfe72a

git_last_commit_date 2024-10-29

Repository Bioconductor 3.21

Date/Publication 2024-12-26

Author Yu Zhang [aut, cre],
Qin Ma [aut]

Maintainer Yu Zhang <zy26@jlu.edu.cn>

Contents

ecoli	2
ecoli.weight	2
Index	4

ecoli

E.coli

Description

Gene expression data matrix for experiments with E.coli from Many Microbe Microarrays Database (M3D).

Usage

```
data("ecoli")
```

Format

Large matrix with information about the expression levels of 4297 genes over 466 conditions.

Source

<http://m3d.mssm.edu/>

References

Faith, JJ et al. (2008) Many Microbe Microarrays Database: uniformly normalized Affymetrix compendia with structured experimental metadata. *Nucleic Acids Res.* 36 D866-70

Examples

```
data(ecoli)
## maybe str(ecoli) ; plot(ecoli) ...
```

ecoli.weight*E.coli Weight*

Description

Protein network information (scored links between proteins) for *Escherichia coli* K12 MG1655. It originates from STRING v10 and serves as example weight input for the query-based biclustering function in QUBIC.

Usage

```
data("ecoli.weight")
```

Format

Large dgcmatrix with information about the weight between proteins.

Source

<http://string-db.org/download/protein.links.v10/511145.protein.links.v10.txt.gz>

References

Szklarczyk, D et al. (2014) STRING v10: protein–protein interaction networks, integrated over the tree of life. *Nucleic Acids Res.* 43 D447–52

Examples

```
data(ecoli.weight)
## maybe str(ecoli.weight) ; plot(ecoli.weight) ...
```

Index

* datasets

ecoli, [2](#)

ecoli.weight, [2](#)

ecoli, [2](#)

ecoli.weight, [2](#)