

Package ‘spqnData’

November 26, 2024

Version 1.19.0

Title Data for the spqn package

Description Bulk RNA-seq from GTEx on 4,000 randomly selected, expressed genes. Data has been processed for co-expression analysis.

Depends R (>= 4.0), SummarizedExperiment

License Artistic-2.0

LazyData FALSE

biocViews Homo_sapiens_Data, ExpressionData, Tissue, RNASeqData

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

git_branch devel

git_last_commit 672de9e

git_last_commit_date 2024-10-29

Repository Bioconductor 3.21

Date/Publication 2024-11-26

Author Yi Wang [cre, aut],
Kasper Daniel Hansen [aut]

Maintainer Yi Wang <yiwangthu5@gmail.com>

Contents

gtex.4k	2
Index	3

`gtex.4k`*Example data for the spqn package.*

Description

A random sample of 4,000 expressed genes (protein-coding or lincRNAs) from GTEx v6p. The tissue is Adipose Subcutaneous.

Usage

```
data("gtex.4k")
```

Format

An object of class SummarizedExperiment.

Details

Data is 350 samples from GTEx v6p. The tissue is Adipose Subcutaneous.

We first selected protein-coding or lincRNAs based on the supplied annotation files. Next we kept genes with a median $\log_2(\text{RPKM})$ expression greater than zero. This resulted in a data matrix with 12,267 genes of which 11,911 are protein-coding. We stored the mean expression value per gene in `rowData(gtex.4k)$ave_logrpkm`.

We next mean centered and variance scaled the expression values so all genes have zero mean and variance 1. We then removed 4 principal components from this data matrix using the `removePrincipalComponents` function from the WGCNA package.

Finally, we randomly selected 4,000 genes.

Additional information on the genes are present in the `rowData`. The type of gene (lincRNA or protein-coding) is present in the `gene_type` column. The average expression of each gene on the $\log_2(\text{RPKM})$ -scale, prior to removing principal components, are present in the `ave_logrpkm` column.

Source

Original data from gtexportal.org. A script for downloading and processing the paper is included in `scripts/gtex.Rmd`.

Examples

```
data(gtex.4k)
```

Index

* **datasets**

gtex.4k, [2](#)

gtex.4k, [2](#)