Package ‘spqnData’

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Version 1.22.0

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

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LazyData FALSE

biocViews Homo_sapiens_Data, ExpressionData, Tissue, RNASeqData

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`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 Subcutanous.

We first selected protein-coding or lincRNAs based on the supplied annotation files. Next we kept genes with a median log2(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 log2(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)
```

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