Package ‘spqnData’

March 28, 2024

Version  1.14.0
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 RELEASE_3_18
git_last_commit 123e5e9
git_last_commit_date 2023-10-24
Repository Bioconductor 3.18
Date/Publication 2024-03-28
Author  Yi Wang [cre, aut],
        Kasper Daniel Hansen [aut]
Maintainer Yi Wang <yiwangthu5@gmail.com>

R topics documented:

  gtx.4k ................................................................. 2

Index  3
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 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 gtxexportal.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