

Package ‘BrainSABER’

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Type Package

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Description The Allen Institute for Brain Science provides an RNA sequencing (RNA-Seq) data resource for studying transcriptional mechanisms involved in human brain development known as BrainSpan. BrainSABER is an R package that facilitates comparison of user data with the various developmental stages and brain structures found in the BrainSpan atlas by generating dynamic similarity heatmaps for the two data sets. It also provides a self-validating container for user data.

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buildAIBSARNA	<i>Function to create a SummarizedExperiment containing BrainSpan Data</i>
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Description

This function is used to build the AIBSARNA SummarizedExperiment object, and must be run prior to running any other function in **BrainSABER**. This function will download the data from <http://brainspan.org> and may take several minutes, depending on internet connection speeds.

Usage

```
buildAIBSARNA(mini = FALSE)
```

Arguments

mini	Default is FALSE. If mini=TRUE, build a miniature version of AIBSARNA that does not require internet connectivity and is suitable for example purposes only
------	---

Value

A SummarizedExperiment containing BrainSpan data, with the addition of RefSeq IDs via biomaRt

Examples

```
AIBSARNA <- buildAIBSARNA(mini = TRUE)
```

 CellScabbard

The CellScabbard class

Description

The main class used by the **BrainSABER** package to hold single cell expression data, relevant gene data, and similarity matrices. CellScabbard extends the [SummarizedExperiment::SummarizedExperiment-class] class.

Usage

```
CellScabbard(
  exprsData,
  phenoData = NULL,
  featureData = NULL,
  AIBSARNA = NULL,
  autoTrim = TRUE
)
```

Arguments

exprsData	expression data matrix for an experiment
phenoData	a data frame containing attributes of individual cells
featureData	a data frame containing attributes of features (e.g. genes)
AIBSARNA	an instance of the AIBSARNA dataset, built using the buildAIBSARNA() function
autoTrim	If TRUE (default), automatically trim user data to match AIBSARNA using the column names of AIBSARNA and featureData (or rownames of exprsData, if featureData is not supplied) which produce the most matched identifiers. Also automatically fills the relevantGenes slot, using the same column names. The column names are stored in the dataSetId and AIBSARNAid slots.

Details

This class is initialized from a matrix of gene expression values and associated metadata. Methods that operate on CellScabbard objects comprise the BrainSABER workflow.

Value

a new CellScabbard object

Fields

dataSetId A character vector of length 1, containing the column name of the user's data used to trim the data to match AIBSARNA.

AIBSARNAid A character vector of length 1, containing the column name of AIBSARNA used to trim AIBSARNA to match the user's data

relevantGenes A [SummarizedExperiment::SummarizedExperiment-class] containing a subset of data from AIBSARNA. Generated by the **BrainSABER** workflow.

similarityScores A data.frame containing similarity scores. Generated by the **BrainSABER** workflow.

similarityDFs A list containing similarity data frames with age, structure, and similarity scores sorted in decreasing order. Generated by the **BrainSABER** workflow.

similarityMatrices A [SummarizedExperiment::Assays-class] object containing similarity matrices, with identical dimensions, for each sample in phenoData. Generated by the **BrainSABER** workflow.

UNDmatrices A [SummarizedExperiment::Assays-class] object containing identical-dimension UND matrices for each sample in phenoData. Generated by the **BrainSABER** workflow.

Examples

```
# construct example data set
AIBSARNA <- buildAIBSARNA(mini = TRUE)

# get a random sample of 3 genes
totalGenes <- nrow(AIBSARNA)
gene_idx <- sample.int(totalGenes, 3)
sample_idx <- c(1,3,5)

# Subset AIBSARNA
exprs <- assay(AIBSARNA)[gene_idx, sample_idx]
fd <- rowData(AIBSARNA)[gene_idx, ]
pd <- colData(AIBSARNA)[sample_idx, ]

# construct a CellScabbard data set
myGenes <- CellScabbard(exprsData = exprs, phenoData = pd, featureData = fd,
                        AIBSARNA = AIBSARNA, autoTrim = TRUE)
```

CellScabbard-methods *Methods for the CellScabbard class*

Description

These methods operate on CellScabbard objects. They are used to access the results of the **BrainSABER** workflow stored within a CellScabbard.

Usage

```
dataSetId(cs)

dataSetId(cs) <- value
```

```
AIBSARNAid(cs)
AIBSARNAid(cs) <- value
relevantGenes(cs)
relevantGenes(cs) <- value
similarityScores(cs)
similarityScores(cs) <- value
similarityDFs(cs)
similarityDFs(cs) <- value
similarityMatrices(cs)
similarityMatrices(cs) <- value
UNDMatrices(cs)
UNDMatrices(cs) <- value
```

Arguments

cs	A CellScabbard object
value	data type, any of matrix, data.frame,list, or SimpleList

Value

The contents of a slot of the CellScabbard object

Examples

```
# construct example data set
AIBSARNA <- buildAIBSARNA(mini = TRUE)

# get a random sample of 3 genes
totalGenes <- nrow(AIBSARNA)
gene_idx <- sample.int(totalGenes, 3)
sample_idx <- c(1,3,5)

# Subset AIBSARNA
exprs <- assay(AIBSARNA)[gene_idx, sample_idx]
fd <- rowData(AIBSARNA)[gene_idx, ]
pd <- colData(AIBSARNA)[sample_idx, ]

# construct a CellScabbard data set
myGenes <- CellScabbard(exprsData = exprs, phenoData = pd, featureData = fd,
```

```

                                AIBSARNA = AIBSARNA, autoTrim = TRUE)
relevantGenes(myGenes)

# the following fields will be empty as output must be assigned to
# them first
similarityScores(myGenes)
similarityMatrices(myGenes)
similarityDFs(myGenes)
UNDMatrices(myGenes)

```

getExampleVector	<i>Get an example vector for specified genes</i>
------------------	--

Description

This function returns a named example vector of gene expression values for the specified genes, taken from the 1st row of AIBSARNA, for use in demonstrating getSimScores.

Usage

```
getExampleVector(genes, AIBSARNA = NULL)
```

Arguments

genes	a character vector of HGNC-compliant gene names
AIBSARNA	an instance of the AIBSARNA dataset, built using the buildAIBSARNA() function

Value

a named character vector of gene-expression values

Examples

```

AIBSARNA <- buildAIBSARNA(mini = TRUE)
myGenes <- c("TSPAN6", "DPM1", "C1orf112")
myExampleVector <- getExampleVector(myGenes, AIBSARNA)

```

getExternalVector *getExternalVector*

Description

Get a named vector of gene expression values from a single sample in an outside SummarizedExperiment, for use in creating subsets of AIBSARNA with `getRelevantGenes` and comparison with that subset with `getSimScores`

Usage

```
getExternalVector(  
  dataSet,  
  index = 1,  
  AIBSARNA = NULL,  
  dataSetId,  
  AIBSARNAid = c("gene_id", "ensembl_gene_id", "gene_symbol", "entrez_id",  
                 "refseq_ids")  
)
```

Arguments

<code>dataSet</code>	a CellScabbard or SummarizedExperiment object
<code>index</code>	the integer index of the sample of <code>dataSet</code> to be used
<code>AIBSARNA</code>	an instance of the AIBSARNA dataset, built using the <code>buildAIBSARNA()</code> function
<code>dataSetId</code>	the name of the column of gene identifiers in <code>rowData(dataSet)</code> to be used to compare <code>dataSet</code> to AIBSARNA.
<code>AIBSARNAid</code>	the name of the column of <code>rowData(AIBSARNA)</code> that is comparable to <code>dataSetId</code> . One of "gene_id", "ensembl_gene_id", "gene_symbol", "entrez_id", "refseq_ids"

Value

a named vector of gene expression values

Examples

```
miniAIBSARNA <- buildAIBSARNA(mini = TRUE)  
myGenes <- c(4.484885, 0.121902, 0.510035)  
names(myGenes) <- c("TSPAN6", "DPM1", "C1orf112")  
myGeneSet <- getRelevantGenes(myGenes, "gene_symbol", miniAIBSARNA,  
  AIBSARNAid = "gene_symbol")  
myGeneSampleVector <- getExternalVector(myGeneSet, index = 1, miniAIBSARNA,  
  dataSetId = "gene_symbol", AIBSARNAid = "gene_symbol")
```

getRelevantGenes *Get a subset of AIBSARNA using a Gene Expression Vector*

Description

This function returns a subset of the AIBSARNA dataset, containing only the genes in `data`, which may be a vector, a `SummarizedExperiment` or derivative `assay()` and `rowData()`, or a `CellScabbard`. If a vector is used, it must consist of numerical gene expression values with names comparable to one column of identifiers present in AIBSARNA. If `data` is a `CellScabbard`, results are stored in the `relevantGenes` slot of the object.

Usage

```
getRelevantGenes(
  data,
  dataSetId = NULL,
  AIBSARNA = NULL,
  AIBSARNAid = c("gene_id", "ensembl_gene_id", "gene_symbol", "entrez_id",
    "refseq_ids")
)
```

Arguments

<code>data</code>	a vector of named gene expression values, or a compatible data set
<code>dataSetId</code>	(Optional) If <code>data</code> is not a vector, the name of the column of gene identifiers in <code>rowData(dataSet)</code> to be used to compare <code>data</code> to AIBSARNA.
<code>AIBSARNA</code>	an instance of the AIBSARNA dataset, built using the <code>buildAIBSARNA()</code> function
<code>AIBSARNAid</code>	the name of the column of <code>rowData(AIBSARNA)</code> that is comparable to <code>dataSetId</code> . One of "gene_id", "ensembl_gene_id", "gene_symbol", "entrez_id", "refseq_ids"

Value

a `SummarizedExperiment` consisting of genes in `data`, sorted to match the order of the genes in `data`

Examples

```
AIBSARNA <- buildAIBSARNA(mini = TRUE)
# Example 1 - using CellScabbard class
# get a random sample of 3 genes
totalGenes <- nrow(AIBSARNA)
gene_idx <- sample.int(totalGenes, 3)
sample_idx <- c(1,3,5)
# Subset AIBSARNA
exprs <- assay(AIBSARNA)[gene_idx, sample_idx]
fd <- rowData(AIBSARNA)[gene_idx, ]
```



```

pd <- colData(AIBSARNA)[sample_idx, ]
# build a trimmed data set
myGenes <- CellScabbard(exprsData = exprs, phenoData = pd, featureData = fd,
                       AIBSARNA = AIBSARNA, autoTrim = TRUE)
relevantGenes(myGenes)

# Example 2 - manual gene selection and relevant gene extraction
myGenes <- c(4.484885, 0.121902, 0.510035)
names(myGenes) <- c("TSPAN6", "DPM1", "C1orf112")
myGeneSet <- getRelevantGenes(myGenes, AIBSARNA = AIBSARNA,
                              AIBSARNAid = "gene_symbol")

```

getSimDataFrame

Get Age, Structure Acronym, and Similarity Scores Data Frame

Description

This function takes in a CellScabbard object, or both a similarity vector or data frame as returned by `getSimScores` and a subset of AIBSARNA as returned by `getRelevantGenes`. Constructs a data.frame with columns `age`, `structure_acronym`, and either `cosine_similarity` or `euclidean_similarity`, sorted by similarity score in decreasing order. In the case of a similarity data frame, a list of data frames is returned.

Usage

```

getSimDataFrame(
  data = NULL,
  sim_score = NULL,
  relevantGenes = NULL,
  similarity_method = "cosine"
)

```

Arguments

<code>data</code>	a CellScabbard object with non-empty <code>relevantGenes</code> and <code>similarityScores</code> slots, or a SummarizedExperiment created using the <code>getRelevantGenes()</code> function
<code>sim_score</code>	a vector or data frame of similarity scores
<code>relevantGenes</code>	a SummarizedExperiment object created using the <code>getRelevantGenes()</code> function
<code>similarity_method</code>	currently supported similarity methods are "cosine" and "euclidean", defaults to "cosine"

Value

a three-column data.frame or list of data frames

Examples

```

AIBSARNA <- buildAIBSARNA(mini = TRUE)
# Example 1 - using CellScabbard class
# get a random sample of 3 genes
totalGenes <- nrow(AIBSARNA)
gene_idx <- sample.int(totalGenes, 3)
sample_idx <- c(1,3,5)
# Subset AIBSARNA
exprs <- assay(AIBSARNA)[gene_idx, sample_idx]
fd <- rowData(AIBSARNA)[gene_idx, ]
pd <- colData(AIBSARNA)[sample_idx, ]
# build a trimmed data set
myGenes <- CellScabbard(exprsData = exprs, phenoData = pd, featureData = fd,
                        AIBSARNA = AIBSARNA, autoTrim = TRUE)
# cosine similarity method
similarityScores(myGenes) <- getSimScores(data = myGenes,
                                           similarity_method = "cosine")
similarityDFs(myGenes) <- getSimDataFrame(data = myGenes,
                                          similarity_method = "cosine")
similarityDFs(myGenes)
# euclidean similarity method
similarityScores(myGenes) <- getSimScores(data = myGenes,
                                           similarity_method = "euclidean")
similarityDFs(myGenes) <- getSimDataFrame(data = myGenes,
                                          similarity_method = "euclidean")
similarityDFs(myGenes)

# Example 2 - manual gene selection and relevant gene extraction
myGenes <- c(4.484885, 0.121902, 0.510035)
names(myGenes) <- c("TSPAN6", "DPM1", "C1orf112")
myGeneSet <- getRelevantGenes(myGenes, AIBSARNA = AIBSARNA,
                              AIBSARNAid = "gene_symbol")
myCosScore <- getSimScores(myGenes, relevantGenes = myGeneSet,
                           similarity_method = "cosine")
myEucScore <- getSimScores(myGenes, relevantGenes = myGeneSet,
                           similarity_method = "euclidean")
myCosineDF <- getSimDataFrame(sim_score = myCosScore,
                              relevantGenes = myGeneSet,
                              similarity_method = "cosine")
myEuclideanDF <- getSimDataFrame(sim_score = myEucScore,
                                 relevantGenes = myGeneSet,
                                 similarity_method = "euclidean")

```

getSimMatrix

Get Age, Structure Acronym, and Similarity Score Matrix

Description

This function takes a similarity vector or data frame as returned by `getSimScores` and either a `CellScabbard` object or a subset of `AIBSARNA` as returned by `getRelevantGenes`. Returns a

numeric matrix or list of matrices of similarity scores with rows labeled by age, and columns labeled by structure_acronym.

Usage

```
getSimMatrix(data = NULL, sim_score = NULL, relevantGenes = NULL)
```

Arguments

`data` a CellScabbard object with non-empty relevantGenes slot
`sim_score` a vector or data frame of similarity scores
`relevantGenes` a SummarizedExperiment created using the `getRelevantGenes()` function

Value

a numeric matrix of similarity scores, or a list of matrices

Examples

```
AIBSARNA <- buildAIBSARNA(mini = TRUE)
# Example 1 - using CellScabbard class
# get a random sample of 3 genes
totalGenes <- nrow(AIBSARNA)
gene_idx <- sample.int(totalGenes, 3)
sample_idx <- c(1,3,5)
# Subset AIBSARNA
exprs <- assay(AIBSARNA)[gene_idx, sample_idx]
fd <- rowData(AIBSARNA)[gene_idx, ]
pd <- colData(AIBSARNA)[sample_idx, ]
# build a trimmed data set
myGenes <- CellScabbard(exprsData = exprs, phenoData = pd, featureData = fd,
  AIBSARNA = AIBSARNA, autoTrim = TRUE)
similarityScores(myGenes) <- getSimScores(data = myGenes,
  similarity_method = "cosine")
similarityMatrices(myGenes) <- getSimMatrix(data = myGenes)
similarityMatrices(myGenes)
similarityScores(myGenes) <- getSimScores(data = myGenes,
  similarity_method = "euclidean")
similarityMatrices(myGenes) <- getSimMatrix(data = myGenes)
similarityMatrices(myGenes)

# Example 2 - manual gene selection and relevant gene extraction
myGenes <- c(4.484885, 0.121902, 0.510035)
names(myGenes) <- c("TSPAN6", "DPM1", "C1orf112")
myGeneSet <- getRelevantGenes(myGenes, AIBSARNA = AIBSARNA,
  AIBSARNAid = "gene_symbol")
myCosScore <- getSimScores(myGenes, myGeneSet, similarity_method = "cosine")
myEucScore <- getSimScores(myGenes, myGeneSet,
  similarity_method = "euclidean")
myCosineMatrix <- getSimMatrix(sim_score = myCosScore,
  relevantGenes = myGeneSet)
```

```
myEuclideanMatrix <- getSimMatrix(sim_score = myEucScore,
                                  relevantGenes = myGeneSet)
```

getSimScores

Get Similarity Scoring for a Gene Expression Vector

Description

This function computes the similarity score of a gene expression vector returned by `getExternalVector` or a trimmed data set returned by `getTrimmedExternalSet`, compared to a subset of AIBSARNA, obtained by `getRelevantGenes`.

Usage

```
getSimScores(data, relevantGenes = NULL, similarity_method = "cosine")
```

Arguments

<code>data</code>	a named vector of gene expression values returned by <code>getExternalVector</code> , a <code>SummarizedExperiment</code> returned by <code>getTrimmedExternalSet</code> , or a <code>CellScabbard</code> object.
<code>relevantGenes</code>	a <code>SummarizedExperiment</code> object created using the <code>getRelevantGenes()</code> function
<code>similarity_method</code>	currently supported similarity methods are "cosine" and "euclidean", defaults to "cosine"

Value

If `data` is a vector, returns a vector of similarity scores for each sample in `relevantGenes`. If `data` is a `SummarizedExperiment`, returns a data frame, with columns containing the similarity scores for and named after each sample in `data`, and rows named after each sample in `relevantGenes`. If `data` is a `CellScabbard`, the results will be stored in its `similarityScores` slot.

Examples

```
AIBSARNA <- buildAIBSARNA(mini = TRUE)
# Example 1 - using CellScabbard class
# get a random sample of 3 genes
totalGenes <- nrow(AIBSARNA)
gene_idx <- sample.int(totalGenes, 3)
sample_idx <- c(1,3,5)
# Subset AIBSARNA
exprs <- assay(AIBSARNA)[gene_idx, sample_idx]
fd <- rowData(AIBSARNA)[gene_idx, ]
pd <- colData(AIBSARNA)[sample_idx, ]
# build a trimmed data set
myGenes <- CellScabbard(exprsData = exprs, phenoData = pd, featureData = fd,
```

```

AIBSARNA = AIBSARNA, autoTrim = TRUE)
similarityScores(myGenes) <- getSimScores(data = myGenes,
                                           similarity_method = "cosine")

similarityScores(myGenes)
similarityScores(myGenes) <- getSimScores(data = myGenes,
                                           similarity_method = "euclidean")

similarityScores(myGenes)

# Example 2 - manual gene selection and relevant gene extraction
myGenes <- c(4.484885, 0.121902, 0.510035)
names(myGenes) <- c("TSPAN6", "DPM1", "C1orf112")
myGeneSet <- getRelevantGenes(myGenes, AIBSARNA = AIBSARNA,
                              AIBSARNAid = "gene_symbol")
CosScores <- getSimScores(myGenes, myGeneSet,
                          similarity_method = "cosine")
EucScores <- getSimScores(myGenes, myGeneSet,
                          similarity_method = "euclidean")

```

getTrimmedExternalSet *Get a trimmed version of an external data set*

Description

Returns a SummarizedExperiment that is a subset of dataSet containing only genes that are present in AIBSARNA, for use in getSimScores or getUNDMatrix.

Usage

```

getTrimmedExternalSet(
  dataSet,
  dataSetId = "gene_symbol",
  AIBSARNA = NULL,
  AIBSARNAid = c("gene_id", "ensembl_gene_id", "gene_symbol", "entrez_id",
                 "refseq_ids")
)

```

Arguments

dataSet	a CellScabbard or SummarizedExperiment object
dataSetId	the name of the column of gene identifiers in rowData(dataSet) to be used to compare dataSet to AIBSARNA.
AIBSARNA	an instance of the AIBSARNA dataset, built using the buildAIBSARNA() function
AIBSARNAid	the name of the column of rowData(AIBSARNA) that is comparable to dataSetId. One of "gene_id", "ensembl_gene_id", "gene_symbol", "entrez_id", "refseq_ids"

Value

a SummarizedExperiment object containing trimmed data set

Examples

```

AIBSARNA <- buildAIBSARNA(mini = TRUE)
# Example 1 - using CellScabbard class
# get a random sample of 3 genes
totalGenes <- nrow(AIBSARNA)
gene_idx <- sample.int(totalGenes, 3)
sample_idx <- c(1,3,5)
# Subset AIBSARNA
exprs <- assay(AIBSARNA)[gene_idx, sample_idx]
fd <- rowData(AIBSARNA)[gene_idx, ]
pd <- colData(AIBSARNA)[sample_idx, ]
# build a trimmed data set
myGenes <- CellScabbard(exprsData = exprs, phenoData = pd, featureData = fd,
                        AIBSARNA = AIBSARNA, autoTrim = TRUE)
# use the appropriate id's to extract the trimmed gene set from the data
dataSetId = dataSetId(myGenes)
AIBSARNAid = AIBSARNAid(myGenes)
myTrimmedGeneSet <- getTrimmedExternalSet(myGenes,
                                           dataSetId = dataSetId, AIBSARNA, AIBSARNAid = AIBSARNAid)

# Example 2 - manual gene selection and relevant gene extraction
myGenes <- c(4.484885, 0.121902, 0.510035)
names(myGenes) <- c("TSPAN6", "DPM1", "C1orf112")
myGeneSet <- getRelevantGenes(myGenes, AIBSARNA = AIBSARNA,
                              AIBSARNAid = "gene_symbol")
myTrimmedGeneSet <- getTrimmedExternalSet(myGeneSet,
                                           dataSetId = "gene_symbol", AIBSARNA, AIBSARNAid = "gene_symbol")

```

getUNDmatrix

getUNDmatrix

Description

This function returns a matrix showing whether gene expression values in `dataSet` are up-regulated, down-regulated, or normal. `method = "discrete"` will function on any `CellScabbard` object, while `method = "log2FC"` requires a trimmed data set as returned by `getTrimmedExternalSet` and a matching subset of `AIBSARNA` as returned by `getRelevantGenes`. Results are stored in the 'UNDmatrices' slot of the `dataSet` if it's a `CellScabbard` object.

Usage

```

getUNDmatrix(
  dataSet,
  relevantGenes = NULL,
  method = c("discrete", "log2FC"),
  up_threshold = 0.5,
  down_threshold = -0.5,
  matrix_type = c("num", "char")
)

```



```
myTrimmedGeneSet <- getTrimmedExternalSet(myGeneSet,  
  dataSetId = "gene_symbol", AIBSARNA, AIBSARNAid = "gene_symbol")  
myUNDnumericalMatrix <- getUNDMatrix(myTrimmedGeneSet, method = "discrete",  
  up_threshold = 3, down_threshold = 1, matrix_type = "num")  
myUNDcharacterMatrix <- getUNDMatrix(myTrimmedGeneSet, myGeneSet,  
  method = "log2FC",  
  up_threshold = 3, down_threshold = 1, matrix_type = "char")
```


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