

Package ‘shinyMapR’

November 29, 2022

Title Generalized mapping of annotations from shiny taxonomy to query data.

Version 0.1

Description ADD

License GPL-3

Depends ArchR,
parallel,
data.table,
assertthat,
dplyr

Suggests knitr,
rmarkdown,
testthat

Encoding UTF-8

LazyData true

VignetteBuilder knitr

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.2

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cor	<i>Correlation based cell type mapping wrapper</i>
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Description

Correlation based cell type mapping wrapper

Usage

```
cor(...)
```

Arguments

nGenes

Value

Correlation mapping results

corrMap	<i>Correlation based mapping</i>
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Description

Correlation based mapping

Usage

```
corrMap(GEXRef, query.data)
```

Arguments

GEXRef	A reference taxonomy object.
query.data	A logCPM normalized matrix to be annotated.

Value

Correlation mapping results as a data.frame.

loadGEXRef	<i>Read in a reference data set in Allen taxonomy format</i>
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Description

Read in a reference data set in Allen taxonomy format

Usage

```
loadGEXRef(  
  refFolder = "/allen/programs/celltypes/workgroups/rnaseqanalysis/shiny/10x_seq/human_BGplus_20  
  sample_field = "sample_id",  
  nGenes = 2000,  
  hGenes = NULL,  
  sub.sample = 1000  
)
```

Arguments

refFolder	Directory containing the Shiny taxonomy.
nGenes	Number of variable genes to compute.
hGenes	User supplied variable gene vector.
sub.sample	Number of cells to keep per cluster.
sample_name_field	Field in reference taxonomy that defines the sample_id.

Value

Organized reference object ready for mapping against.

seuratMap	<i>Seurat based mapping</i>
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Description

Seurat based mapping

Usage

```
seuratMap(GEXRef, query.data, dims = 30, k.weight = 15)
```

Arguments

GEXRef	A reference taxonomy object.
query.data	A logCPM normalized matrix to be annotated.

Value

Seurat mapping results as a data.frame.

subsampleCells	<i>' Function to subsample cells</i>
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Description

' Function to subsample cells

Usage

```
subsampleCells(cluster.names, subSamp = 25, seed = 5)
```

Arguments

cluster.names	A vector of cluster names in the reference taxonomy.
subSamp	Number of cells to keep per cluster.
seed	Random seed used for subsampling.

Value

Boolean vector of cells to keep (TRUE) and cells to remove (FALSE)

taxonomy_mapping	<i>Cell type annotation and initial QC</i>
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Description

Perform initial mapping using three methods: Correlation-based, tree-based, and Seurat based, and will calculate some QC metrics.

Usage

```
taxonomy_mapping(
  GEXRef,
  query.data,
  corr.map = TRUE,
  tree.map = TRUE,
  seurat.map = TRUE,
  label.cols = c("cluster_label", "subclass_label", "class_label"),
  dims = 30,
  k.weight = 15
)
```

Arguments

GEXRef	A reference taxonomy object.
query.data	A logCPM normalized matrix to be annotated.
corr.map	Should correlation mapping be performed?
tree.map	Should tree mapping be performed?
seurat.map	Should seurat mapping be performed?
label.cols	Column names of annotations to map against
dims	Number of PCA dimensions for Seurat mapping.
k.weight	K neighborhood weight for Seurat mapping.

Value

Mapping results from all methods.

treeMap	<i>Tree based mapping</i>
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Description

Tree based mapping

Usage

```
treeMap(GEXRef, query.data)
```

Arguments

GEXRef	A reference taxonomy object.
query.data	A logCPM normalized matrix to be annotated.

Value

Tree mapping results as a data.frame.

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