

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
Suggests knitr,
rmarkdown,
testthat
Encoding UTF-8
LazyData true
VignetteBuilder knitr
Roxygen list(markdown = TRUE)
RoxygenNote 7.1.2

R topics documented:

corrMap	1
loadGEXRef	2
seuratMap	3
taxonomy_mapping	3
treeMap	4
Index	5

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,
  sample_id = "sample_id",
  nGenes = 2000,
  hGenes = NULL,
  sub.sample = 1000
)
```

Arguments

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

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.

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.

Index

corrMap, [1](#)

loadGEXRef, [2](#)

seuratMap, [3](#)

taxonomy_mapping, [3](#)

treeMap, [4](#)