Package 'scRNAseqApp'

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Title A single-cell RNAseq Shiny app-package

Version 1.11.26

Description The scRNAseqApp is a Shiny app package designed for interactive visualization of single-cell data. It is an enhanced version derived from the ShinyCell, repackaged to accommodate multiple datasets.
The app enables users to visualize data containing various types of information simultaneously, facilitating comprehensive analysis.
Additionally, it includes a user management system to regulate database accessibility for different users.

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Contents

`APPconf-class` *Class* `"APPconf"`

Description

An object of class `"APPconf"` represents the metadata for a dataset.

Usage

```
APPconf(...)
```

Arguments

`...`	Each argument in ... becomes an slot in the new `"APPconf"`-class.

Value

A APPconf object.

Slots

`title` character(1). Title of the data

`id` character(1). Folder name of the data

`species` character(1). species

`ref` Reference information in a list with element bib, doi, pmid and entry. Entry must be an object of bibentry

`type` character(1). Type of the data, scRNAseq, scATACseq, scMultiome or spatial.

`markers` list. A list of data.frame represents cell markers.

`keywords` character. A vector of characters represents the keywords of the study.

`groupCol` character. The key group column name to separate the cells.

Examples

```
appconf <- readRDS(system.file("extdata", "data",
    "pbmc_small", "appconf.rds", package="scRNAseqApp"))
appconf
```

APPconf-methods *The methods for APPconf-class*

Description

The assessment and replacement methods for APPconf-class

Usage

```
## S4 method for signature 'APPconf'
show(object)

## S4 method for signature 'APPconf'
x$name

## S4 replacement method for signature 'APPconf'
x$name <- value

## S4 method for signature 'APPconf,ANY,ANY'
x[[i, j, ..., exact = TRUE]]

## S4 replacement method for signature 'APPconf,ANY,ANY,ANY'
x[[i, j, ...]] <- value

## S4 method for signature 'APPconf,ANY,ANY,ANY'
x[i, j, ..., drop = TRUE]

## S4 method for signature 'APPconf'
as.list(x, ...)

## S4 method for signature 'APPconf'
as.character(x, ...)

## S4 method for signature 'APPconf'
markers(x)

## S4 method for signature 'APPconf'
lapply(X, FUN, ...)

## S4 method for signature 'APPconf'
unlist(x, recursive = TRUE, use.names = TRUE)
```

Arguments

object	an object of APPconf
x	APPconf object.

name	A literal character string or a name (possibly backtick quoted).
value	value to replace.
i, j	indices specifying elements to extract or replace.
...	Named or unnamed arguments to form a signature.
exact	see Extract
drop	see drop
X	an APPconf object.
FUN	function used by lapply
recursive, use.names	function used by unlist

Value

A named character vector.

Examples

```
appconf <- readRDS(system.file("extdata", "data",
    "pbmc_small", "appconf.rds", package="scRNAseqApp"))
appconf
appconf$title
appconf[["title"]]
as.list(appconf)
as.character(appconf)
markers(appconf)
lapply(appconf, print)
unlist(appconf)
```

---

availableThemes *Available themes of color sets*

Description

The color themes inspired by modern web design palettes

Usage

```
availableThemes(output = "name")
```

Arguments

output	The theme names or 'name' to print all available themes.

Value

A palette.

Examples

```
availableThemes()
```

createAppConfig *Create a metadata to describe the dataset*

Description

The function will return a APPconf object which contain the reference, keywords for the dataset.

Usage

```
createAppConfig(
  title,
  destinationFolder,
  species,
  doi,
  pmid,
  bibentry,
  datatype = c("scRNAseq", "scATACseq", "scMultiome", "spatial"),
  markers,
  keywords,
  abstract,
  email
)
```

Arguments

title	The title of the dataset
destinationFolder	The destination folder name of the dataset without the root folder of the datasets. The data will be saved as appdataFolder/destinationFolder
species	The species of the dataset
doi, pmid	The DOI or PMID of the reference
bibentry	An object of bibentry
datatype	character(1). Type of the data, scRNAseq, scATACseq, scMultiome or spatial.
markers	A list of data.frame with gene symbols as rownames or a character vector.
keywords	The keywords for the dataset. For example the condition, cell type, tissue information The keywords will be used for whole database search
abstract	The abstract of the reference.
email	The request e-mail address to retrieve the doi or pmid.

Value

An object of APPconf object

Examples

```
if(interactive()){
    config <- createAppConfig(
        title="pbmc_small",
        destinationFolder = "pbmc_small",
```

```
        species = "Homo sapiens",
        doi="10.1038/nbt.3192",
        datatype = "scRNAseq")
}
```

`createDataSet` *Create a dataset Create a dataset from a Seurat object. The function will try to find the markers in the Misc data named as 'markers'. The misc data should be output of function* `FindAllMarkers`.

Description

Create a dataset Create a dataset from a Seurat object. The function will try to find the markers in the Misc data named as 'markers'. The misc data should be output of function `FindAllMarkers`.

Usage

```
createDataSet(
  appconf,
  seu,
  config,
  contrast,
  assayName,
  gexSlot = c("data", "scale.data", "counts"),
  atacAssayName,
  atacSlot = c("data", "scale.data", "counts"),
  LOCKER = FALSE,
  datafolder = "data",
  default.symbol = "rownames",
  theme = "Paired",
  binSize = 1,
  fragmentNameMapList,
  fov = NULL,
  boundaries = NULL,
  molecules = NULL
)
```

Arguments

`appconf`	a APPconf object represent the information about the dataset
`seu`	a Seurat object
`config`	config file for makeShinyFiles
`contrast`	The contrast group
`assayName`	assay in single-cell data object to use for plotting gene expression, which must match one of the following: • Seurat objects: "RNA" or "integrated" assay, default is "RNA"
`gexSlot`	layer in single-cell assay to plot. Default is to use the "data" layer
`atacAssayName`	assay in single-cell data object to use for plotting open chromatin.
`atacSlot`	layer in single-cell atac assay to plot. Default is to use the "data" layer

LOCKER	Set locker if the file is required login
datafolder	app data folder
default.symbol	character(1L) specifying the default rownames to be used. If use default, the gene symbols will be the row names of the assay. If one column name of the meta.feature of the assay is supplied, the function will try to extract the symbols from the meta.feature slot of the assay.
theme	color theme. default is "Paired" from ColorBrewer palettes.
binSize	number of bps for each bin for ATAC fragment coverage. Used to reduce the file size of bigwig.
fragmentNameMapList	list of named character vector. The name map list must be the same order as the fragment list in the object. For each element of the list, the names of the vector are the name of the fragment and the vector contains the cell names (column names of the assay). You can try extractFragmentNameMapList.
fov	Name of FOV (field of view).
boundaries	The container name of segmentation coordinates.
molecules	The container name of molecules coordinates.

Value

The updated Seurat object.

Examples

```
library(Seurat)
if(interactive()){
    appconf <- createAppConfig(
        title="pbmc_small",
        destinationFolder = "pbmc_small",
        species = "Homo sapiens",
        doi="10.1038/nbt.3192",
        datatype = "scRNAseq")
    createDataSet(appconf, pbmc_small, datafolder=tempdir())
}
```

---

createSeuFromCellRanger

load data from cellRanger

Description

load data from cellRanger

Usage

```
createSeuFromCellRanger(outsFolder)
```

Arguments

outsFolder	the outs folder of cellRanger

Value

An SeuratObject

`createSeuFromMatrix` *load data from a count matrix*

Description

load data from a count matrix

Usage

```
createSeuFromMatrix(matrix, meta, genes, cluster, ...)
```

Arguments

`matrix`	count matrix
`meta`	cell-level meta data
`genes`	character. gene names, will be the rownames of the matrix
`cluster`	the cluster coordinates
`...`	The parameter passed to read.delim when read cluster file.

Value

An SeuratObject

`extractFragmentNameMapList`
Extract fragment name map

Description

Try to extract cell name information. It will be used to map the fragment cell name to the object cell name.

Usage

```
extractFragmentNameMapList(obj, atacAssayName)
```

Arguments

`obj`	input single-cell object for Seurat (v3+)
`atacAssayName`	assay in single-cell data object to use for plotting open chromatin.

Value

A list of fragment name map.

Examples

```
library(Seurat)
#library(Signac)
#fnm <- extractFragmentNameMapList(atac_small, 'peaks')
```

`scInit` *Create a scRNAseqApp project*

Description

To run scRNAseqApp, you need to first create a directory which contains the required files.

Usage

```
scInit(
  app_path = getwd(),
  root = "admin",
  password = "scRNAseqApp",
  datafolder = "data",
  overwrite = FALSE,
  app_title = "scRNAseq Database",
  app_description =
    "This database is a collection of\n        single cell RNA-seq data.",
  passphrase = NULL
)
```

Arguments

`app_path`	path, a directory where do you want to create the app
`root`	character(1), the user name for administrator
`password`	character(1), the password for administrator
`datafolder`	the folder where saved the dataset for the app
`overwrite`	logical(1), overwrite the `app_path` if there is a project.
`app_title, app_description`	character(1). The title and description of the home page.
`passphrase`	A password to protect the data inside the database.

Value

no returns. This function will copy files to `app_path`

Examples

```
if(interactive()){
    scInit()
}
```

scRNAseqApp *scRNAseqApp main function*

Description

create a scRNAseqApp once the initialization is done.

Usage

```
scRNAseqApp(
  app_path = getwd(),
  datafolder = "data",
  defaultDataset = "pbmc_small",
  windowTitle = "scRNAseq/scATACseq database",
  favicon = system.file("assets", "img", "favicon.ico", package = "scRNAseqApp"),
  banner = system.file("assets", "img", "banner.png", package = "scRNAseqApp"),
  footer = tagList(HTML("&copy;"), "2024 -", format(Sys.Date(), "%Y"),
    "jianhong@morgridge"),
  maxRequestSize = 1073741824,
  timeout = 30,
  theme = bs_theme(bootswatch = "lumen"),
  use_bs_themer = FALSE,
  showHelpVideo = FALSE,
  ...
)
```

Arguments

app_path	path, a directory where do you want to create the app
datafolder	the folder where saved the dataset for the app
defaultDataset	default dataset for the app.
windowTitle	The title that should be displayed by the browser window.
favicon	The favicon for the page.
banner	The banner image.
footer	The footer html contents.
maxRequestSize	Maximal upload file size. Default is 1G.
timeout	Timeout session (minutes) before logout if sleeping. Default to 30. 0 to disable.
theme	A theme.
use_bs_themer	logical(1). Used to determine the theme.
showHelpVideo	logical(1) or character(1). Show help videos in homepage or not. If an url is provided, the url will be embedded as a iframe element.
...	parameters can be passed to shinyApp except ui and server.

Value

An object that represents the app.

Examples

```
if(interactive()){
    app_path=tempdir()
    scInit(app_path=app_path)
    setwd(app_path)
    scRNAseqApp()
}
```

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