

# Package ‘scRNAseqApp’

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**Title** A single-cell RNAseq Shiny app-package

**Version** 1.7.9

**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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**Encoding** UTF-8

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|               |                        |
|---------------|------------------------|
| APPconf-class | <i>Class "APPconf"</i> |
|---------------|------------------------|

---

### Description

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

### Usage

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

### Arguments

... Each argument in ... becomes a 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 or scATACseq.  
 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 <a href="#">Extract</a>                                      |
| drop                 | see <a href="#">drop</a>   |
| X                    | an APPconf cobject.  |
| FUN                  | function used by lapply  |
| recursive, use.names | function used by <a href="#">unlist</a>                          |

### 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)

```

---

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"),  
  markers,  
  keywords,  
  abstract  
)
```

## 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 or scMultiome.  |
| 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.  |

## 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 | <i>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.</i> |
|---------------|--|

---

**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",
  binSize = 1,
  fragmentNameMapList
)

```

**Arguments**

|           |  |
|-----------|--|
| appconf   | a list 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: |

|                     |   |
|---------------------|---|
|                     | <ul style="list-style-type: none"> <li>Seurat objects: "RNA" or "integrated" assay, default is "RNA"</li> </ul>   |
| 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. |
| 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).                   |

**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

---

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**

|                             |   |
|-----------------------------|---|
| <code>app_path</code>       | path, a directory where do you want to create the app   |
| <code>datafolder</code>     | the folder where saved the dataset for the app  |
| <code>defaultDataset</code> | default dataset for the app.  |
| <code>windowTitle</code>    | The title that should be displayed by the browser window.   |
| <code>favicon</code>        | The favicon for the page.   |
| <code>banner</code>         | The banner image.   |
| <code>footer</code>         | The footer html contents.   |
| <code>maxRequestSize</code> | Maximal upload file size. Default is 1G.  |
| <code>timeout</code>        | Timeout session (minutes) before logout if sleeping. Default to 30. 0 to disable.   |
| <code>theme</code>          | A theme.  |
| <code>use_bs_themer</code>  | logical(1). Used to determine the theme.  |
| <code>showHelpVideo</code>  | 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. |
| <code>...</code>            | 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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