

Package ‘oneSENSE’

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Type Package

Title One-Dimensional Soli-Expression by Nonlinear Stochastic Embedding (OneSENSE)

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Description A graphical user interface that facilitates the dimensional reduction method based on the t-distributed stochastic neighbor embedding (t-SNE) algorithm, for categorical analysis of mass cytometry data. With One-SENSE, measured parameters are grouped into predefined categories, and cells are projected onto a space composed of one dimension for each category. Each dimension is informative and can be annotated through the use of heatplots aligned in parallel to each axis, allowing for simultaneous visualization of two categories across a two-dimensional plot. The cellular occupancy of the resulting plots allows for direct assessment of the relationships between the categories.

Depends R (>= 3.4), webshot, shiny, shinyFiles, scatterplot3d

Imports Rtsne, plotly, gplots, grDevices, graphics, stats, utils, methods, flowCore

License GPL (>=3)

Encoding UTF-8

LazyData true

RoxygenNote 6.0.1

Suggests knitr, rmarkdown

VignetteBuilder knitr

biocViews ImmunoOncology, Software, FlowCytometry, GUI, DimensionReduction

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R topics documented:

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| | |
|---------|---|
| FCStSNE | <i>tSNE and OneSENSE algorithm for FCS data</i> |
|---------|---|

Description

tSNE and OneSENSE algorithm for FCS data

Usage

```
FCStSNE(LoaderPATH = "fcs", ceil = 5000, FNnames = "names.csv",
        OutputSuffix = "Out", DotSNE = TRUE, DoOneSENSE = TRUE, Bins = 250)
```

Arguments

| | |
|--------------|--|
| LoaderPATH | Path where FCS file is located |
| ceil | Maximum number of cells to sample from each fcs sample/file |
| FNnames | .csv file generated when markers from each category are selected |
| OutputSuffix | suffix to name output folder |
| DotSNE | boolean, if TRUE do tSNE, if FALSE skip tSNE |
| DoOneSENSE | boolean, if TRUE do OneSENSE, if FALSE skip OneSENSE |
| Bins | number of bins to put the cell data into, DEFAULT = 250 |

Value

FCS files, tSNE histograms, OneSENSE plot

Examples

```
#dir <- system.file('extdata/fcs', package='oneSENSE')
#FCStSNE(LoaderPATH=dir, FNnames=fnames) #remove hash symbol to run
```

| | |
|-----------|---|
| getCoords | <i>Get Coordinates of median position</i> |
|-----------|---|

Description

Get Coordinates of median position

Usage

```
getCoords(LoaderPATH = LoaderPATH, FFdata = FFdata)
```

Arguments

| | |
|------------|-----------------------|
| LoaderPATH | Path of fcs_out files |
| FFdata | Flow frame data |

Value

Assign global variables for access

Examples

```
#remove hash symbol to run
dir4 <- system.file('extdata/extra', package = 'oneSENSE')
file5 <- system.file('extdata/myFFdatas.rds', package = 'oneSENSE')
FFdata = readRDS(file5)
getCoords(dir4, FFdata)
```

| | |
|---------------|--------------------------------------|
| getParameters | <i>Get parameters from FCS files</i> |
|---------------|--------------------------------------|

Description

Get parameters from FCS files

Usage

```
getParameters(rawFCSdir)
```

Arguments

| | |
|-----------|----------|
| rawFCSdir | FCS path |
|-----------|----------|

Value

mid

Examples

```
#remove hash to run
dir3 <- system.file('extdata/fcs', package = 'oneSENSE')
getParameters(dir3)
```

| | |
|--------------|--|
| oneSENSE_GUI | <i>A user friendly GUI client for oneSENSE package</i> |
|--------------|--|

Description

This GUI provides an easy way for Flow Cytometry data analysis using the oneSENSE package. Main parameters for running 'oneSENSE' were integrated in this GUI, and analysis results are launched in Rstudio after submission.

Usage

```
oneSENSE_GUI()
```

Value

GUI for onesense analysis

Examples

```
if (interactive()) oneSENSE::oneSENSE_GUI()
```

| | |
|-----------------|----------------------------------|
| OneSmapperFlour | <i>Median heatmap generation</i> |
|-----------------|----------------------------------|

Description

This returns the median heatmap for each category of markers chosen. If frequency heatmap is selected in the onesense GUI, then both median and frequency heatmaps are generated as PDF files in working directory

Usage

```
OneSmapperFlour(LoaderPATH = "fcs_Out", Bins = 250, doCoords = FALSE,
doFreq = FALSE)
```

Arguments

| | |
|------------|---|
| LoaderPATH | Name of the output file containing fcs files generated from FCStSNE2.R |
| Bins | Number of bins to sort cells into corresponding heatmap |
| doCoords | a boolean that allows for frequency heatmap generation |
| doFreq | a boolean to allow for the frequency heatmap generation. TRUE to run, FALSE to not run. |

Value

PNG files of combined oneSENSE and heatplot.

Examples

```
webshot::install_phantomjs()
#fcsoutpath <- system.file('extdata/fcs_Out',package='oneSENSE')
#remove hash symbol to run
#OneSmapperFlour(LoaderPATH=fcsoutpath) #remove hash symbol to run
```

OneSmapperFreq1 *Generate Frequency Heatplot Part 1*

Description

Generate Frequency Heatplot Part 1

Usage

```
OneSmapperFreq1(LoaderPATH = "fcs_Out")
```

Arguments

LoaderPATH Path of fcs_Out files

Value

Flow Frame data for coordinate selection

Examples

```
dir1 <- system.file('extdata/fcs',package='oneSENSE')
OneSmapperFreq1(dir1) #remove hash symbol to run
```

OneSmapperFreq2 *Frequency Heatplot Generation Part 2*

Description

Frequency Heatplot Generation Part 2

Usage

```
OneSmapperFreq2(LoaderPATH = "fcs", Bins = 250, FFdata)
```

Arguments

| | |
|------------|-----------------------|
| LoaderPATH | path of fcs_Out files |
| Bins | Number of bins |
| FFdata | Flow Frame data |

Value

returns frequency heatmap

Examples

```
dir2 <- system.file('extdata/fcs_Out', package='oneSENSE')
file5 <- system.file('extdata/myFFdatas.rds', package = 'oneSENSE')
FFdata1 <- readRDS(file5)
OneSmapperFreq2(dir2, 250, FFdata1) #remove hash symbol to run
```

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