

# Package ‘oneSENSE’

November 13, 2023

**Type** Package

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

**Version** 1.25.0

**Date** 2017-07-10

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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

**git\_url** <https://git.bioconductor.org/packages/oneSENSE>

**git\_branch** devel  
**git\_last\_commit** 7eb26a5  
**git\_last\_commit\_date** 2023-10-24  
**Date/Publication** 2023-11-13

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FCStSNE	<i>tSNE and OneSENSE algorithm for FCS data</i>
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### 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
```

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getCoords	<i>Get Coordinates of median position</i>
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**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)
```

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getParameters	<i>Get parameters from FCS files</i>
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**Description**

Get parameters from FCS files

**Usage**

```
getParameters(rawFCSdir)
```

**Arguments**

rawFCSdir	FCS path
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**Value**

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**Examples**

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

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oneSENSE_GUI	<i>A user friendly GUI client for oneSENSE package</i>
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**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()
```

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OneSmapperFlour	<i>Median heatmap generation</i>
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**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
```

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OneSmapperFreq1      *Generate Frequency Heatplot Part 1*

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**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*

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**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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