

Package ‘ggsom’

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Type Package

Title New Data Visualisations for SOMs Cluster

Version 0.2.1

Description Contains parallel coordinate and attribute mapping visualisations for cluster data.

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LazyData true

Encoding UTF-8

Depends R (>= 3.3.0)

Imports tidyverse, kohonen, ggthemes, ggplot2, dplyr, tidyr

Suggests RCurl, knitr, rmarkdown, testthat

URL <https://github.com/oldlipe/ggsom>

RoxygenNote 6.1.0

VignetteBuilder knitr

Collate 'utils.R' 'aes_som.R' 'ggsom.R' 'ggsom_line.R' 'ggsom_rect.R'
'ggsom_ribbon.R' 'zzz.R'

NeedsCompilation no

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aes_color	<i>aes_color</i>
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Description

Function that return the base plot with or without color

Usage

```
aes_color(color, aes_som)
```

Arguments

color	Boolean type to adding color on plot
aes_som	Function aes_som for input data on plot

Value

Base plot

aes_som	<i>aes_som</i>
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Description

aesthetics data of som object

Usage

```
aes_som(model_som, ...)
```

Arguments

model_som	object of self-organising maps (SOMs) package
...	cutree_value division number of clusters

Value

Model data that is used in plots

`ggsom`*ggsom plots*

Description

The goal of this packages is to improve plots of kohonen package

`ggsom_line`*ggsom_line*

Description

Visualization that is contains amount of neuron per grid with color based on classes

Usage

```
ggsom_line(aes_som, color)
```

Arguments

<code>aes_som</code>	Function <code>aes_som</code> for input data on plot
<code>color</code>	Boolean to change color of the edges

Value

ggplot visualization

Examples

```
library(ggthemes)
library(ggsom)
library(ggplot2)
library(kohonen)

iris_som <- som(scale(iris[1:4]), grid = somgrid(6, 4, 'rectangular'))

ggsom_line(aes_som(iris_som), TRUE)
```

ggsom_rect	<i>Cluster plot using geom rect with color</i>
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Description

Cluster plot using geom rect with color

Usage

```
ggsom_rect(aes_som, text = TRUE)
```

Arguments

aes_som	Function aes_som for input data on plot
text	Boolean type to visualize numbers of neurons per grid

Value

ggplot visualization

Examples

```
library(ggthemes)
library(ggsom)
library(ggplot2)
library(kohonen)

iris_som <- som(scale(iris[1:4]), grid = somgrid(6, 4, 'rectangular'))

ggsom_rect(aes_som(iris_som, cutree_value=3), TRUE)
```

ggsom_ribbon	<i>ggsom_ribbon</i>
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Description

Cluster plot using geom ribbon with color

Usage

```
ggsom_ribbon(aes_som, color)
```

Arguments

aes_som Function aes_som for input data on plot
color Boolean type to add color on plot

Value

ggplot visualization

Examples

```
library(ggthemes)
library(ggsom)
library(ggplot2)
library(kohonen)

iris_som <- som(scale(iris[1:4]), grid = somgrid(6, 4, 'rectangular'))

ggsom_ribbon(aes_som(iris_som, cutree_value=3), FALSE)
```

is.cluster *Check if the parameter has a cluster column*

Description

Check if the parameter has a cluster column

Usage

```
is.cluster(x)
```

Arguments

x Dataframe

Value

TRUE if cluster in data frame otherwise FALSE

is.kohonen	<i>Check if the object is inherits of kohonen</i>
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Description

Check if the object is inherits of kohonen

Usage

```
is.kohonen(x)
```

Arguments

x	Dataframe This is used by aes_som to simplify comparison between objects
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Value

if object inherits kohonen class return TRUE otherwise stop

sum_unit_class	<i>sum_unit_class</i>
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Description

Sum of each grid the neuron

Usage

```
sum_unit_class(model_som_values)
```

Arguments

model_som_values	Model of values that is generate in generate.model.result
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Value

Sum of amount neurons per grid

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