

Package ‘ggsom’

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Type Package

Title New Data Visualisations for SOMs Networks

Version 0.4.0

Description

The aim of this package is to offer more variability of graphics based on the self-organizing maps.

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LazyData true

Encoding UTF-8

Depends R (>= 3.4.0)

Imports dplyr, magrittr, tidyr, ggplot2, kohonen, assertthat,
data.table, entropy, tibble

Suggests devtools, knitr, rmarkdown

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

RoxygenNote 7.0.0

Collate 'ggsom.R' 'ggsom_aes.R' 'ggsom_entropy.R' 'ggsom_plot.R'
'ggsom_utils.R' 'zzz.R'

NeedsCompilation no

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geom_class	<i>Visualization in parallelels coordinates in matrix of each attribute</i>
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Description

Visualization of the classes corresponding to each neuron of the SOM

Usage

```
geom_class(object_som, class = NULL, x_o = 3, y_o = 5.5, x_e = 3, y_e = 6.3)
```

Arguments

object_som	object of Kohonen package
class	categorical vector corresponding to the class of the dataset
x_o	x-axis to map the number of observations of each neuron
y_o	y-axis to map the number of observations of each neuron
x_e	x-axis to map the entropy of each neuron
y_e	y-axis to map the entropy of each neuron

Value

ggplot2 object

Author(s)

Felipe Carvalho, <lipecaso@gmail.com>

References

‘ggplot2’ package (<https://CRAN.R-project.org/package=ggplot2>)

Examples

```
# Creating SOM object
iris_som <- kohonen::som(X = as.matrix(iris[1:4]),
                        grid = kohonen::somgrid(xdim = 5,
                                                ydim = 5,
                                                neighbourhood.fct = "gaussian",
                                                topo = "rectangular"),
                        rlen = 100)

# Creating ggsom class plot
geom_class(iris_som, class = iris$Species,
           x_o = 1, y_o = 6,
           x_e = 1.1, y_e = 7.4)
```

`ggsom`*ggsom*

Description

The aim of this package is to offer more variability of graphics based on the self-organizing maps

`ggsom_aes`*kohonen package object modeling*

Description

Function to map each SOM neuron with its corresponding class

Usage

```
ggsom_aes(object_som, class)
```

Arguments

<code>object_som</code>	object of kohonen package
<code>class</code>	categorical vector corresponding to the class of the dataset

Value

data.table model used in visualizations

Author(s)

Felipe Carvalho, <lipecaso@gmail.com>

References

‘Kohonen’ package (<https://CRAN.R-project.org/package=kohonen>)

`ggsom_entropy`*Function to obtain the purity of each neuron in the SOM network*

Description

Entropy calculation using the maximum likelihood method

Usage

```
ggsom_entropy(ggsom_aes)
```

Arguments

`ggsom_aes` kohonen package object modeling

Value

Data set with the purity attribute added in Tibble

Author(s)

Felipe Carvalho, <felipe.carvalho@inpe.br>

`is.kohonen`*verifies that the object inherits kohonen object*

Description

if object inherits kohonen class return TRUE otherwise FALSE

Usage

```
is.kohonen(object_som)
```

Arguments

`object_som` object of Kohonen package

Value

Boolean value

Author(s)

Felipe Carvalho, <lipecaso@gmail.com>

References

‘Kohonen’ package (<https://CRAN.R-project.org/package=kohonen>)

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