

Package: ggsom (via r-universe)

September 9, 2024

Type Package

Title ggsom

Version 0.4.0

Description Tool for visualization of SOMs object.

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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

VignetteBuilder knitr

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

RoxygenNote 7.0.0

VignetteBuilder knitr

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

Repository <https://oldlipe.r-universe.dev>

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

RemoteRef HEAD

RemoteSha 15d8bc8551b93635ed4ef7e4e849a79403de3e2f

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`geom_class`*Visualization in parallelels coordinates in matrix of each attribute*

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

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

object_som	object of kohonen package
class	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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