Package ‘missSOM’

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Title Self-Organizing Maps with Built-in Missing Data Imputation
Description The Self-Organizing Maps with Built-in Missing Data Imputation. Missing values are imputed and regularly updated during the online Kohonen algorithm. Our method can be used for data visualisation, clustering or imputation of missing data. It is an extension of the online algorithm of the 'kohonen' package. The method is described in the article "Self-Organizing Maps for Exploration of Partially Observed Data and Imputation of Missing Values" by S. Rejeb, C. Duveau, T. Rebafka (2022) <arXiv:2202.07963>.
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imputeSOM
The Self-Organizing Maps with Built-in Missing Data Imputation.

Description

imputeSOM is an extension of the online algorithm of the 'kohonen' package where missing data are imputed during the algorithm. All missing values are first imputed with initial values such as the mean of the observed variables.

Usage

```r
imputeSOM(
  data,
  grid = somgrid(),
  rlen = 100,
  alpha = c(0.05, 0.01),
  radius = quantile(nhbrdist, 2/3),
  maxNA.fraction = 1,
  keep.data = TRUE,
  dist.fcts = NULL,
  init
)
```

Arguments

data a matrix or data.frame with continuous variables containing the observations to be mapped on the grid by the kohonen algorithm, even if there are incomplete.
grid a grid for the codebook vectors: see somgrid.
rlen the number of times the complete data set will be presented to the network.
alpha learning rate, a vector of two numbers indicating the amount of change. Default is to decline linearly from 0.05 to 0.01 over rlen updates.
radius the radius of the neighbourhood, either given as a single number or a vector (start, stop). If it is given as a single number the radius will change linearly from radius to zero; as soon as the neighbourhood gets smaller than one only the winning unit will be updated. Note that the default before version 3.0 was to
run from \( r \) to \(-r\). If nothing is supplied, the default is to start with a value that covers 2/3 of all unit-to-unit distances.

- **maxNA.fraction**: the maximal fraction of values that may be NA to prevent the column to be removed.
- **keep.data**: if TRUE, return original data and mapping information. If FALSE, only return the trained map (in essence the codebook vectors).
- **dist.fcts**: distance function to be used for the data. Admissible values currently are "sumofsquares", "euclidean" and "manhattan. Default is to use "sumofsquares". 
- **init**: a matrix or data.frame corresponding to the initial values for the codebook vectors. It should have the same number of variables (columns) as the data. The number of rows corresponding to the number of units in the map.

### Value
An object of class "missSOM" with components

- **data**: Data matrix, only returned if keep.data == TRUE.
- **ximp**: Imputed data matrix.
- **unit.classif**: Winning units for data objects, only returned if keep.data == TRUE.
- **distances**: Distances of objects to their corresponding winning unit, only returned if keep.data == TRUE.
- **grid**: The grid, an object of class somgrid.
- **codes**: A list of matrices containing codebook vectors.
- **alpha, radius**: Input arguments presented to the function.
- **maxNA.fraction**: The maximal fraction of values that may be NA to prevent the column to be removed.
- **dist.fcts**: The distance function used for the data.

### See Also
somgrid, plot.missSOM, map.missSOM

### Examples
```r
data(wines)

## Data with no missing values
som.wines <- imputeSOM(scale(wines), grid = somgrid(5, 5, "hexagonal"))
summary(som.wines)
print(dim(som.wines$data))

## Data with missing values
X <- scale(wines)
missing_obs <- sample(1:nrow(wines), 10, replace = FALSE)
X[missing_obs, 1:2] <- NaN
som.wines <- imputeSOM(X, grid = somgrid(5, 5, "hexagonal"))
summary(som.wines)
```
map

Map data to a supervised or unsupervised SOM

Description

Map a data onto a trained SOM.

Usage

map(x, ...)

## S3 method for class 'missSOM'
map(x, newdata, maxNA.fraction = x$maxNA.fraction, ...)

Arguments

x an object of class missSOM.

... Currently ignored.

newdata a matrix or data.frame, equal to the data argument of the imputeSOM function.

maxNA.fraction parameters that usually will be taken from the x object, but can be supplied by the user as well. Note that it is not possible to change distance functions from the ones used in training the map. See imputeSOM for more information.

Value

A list with elements

unit.classif a vector of units that are closest to the objects in the data.

dists distances of the objects to the closest units. Distance measures are the same ones used in training the map.

See Also

imputeSOM

print(dim(som.wines$ximp))
print(sum(is.na(som.wines$ximp)))
Examples

data(wines)
set.seed(7)

training <- sample(nrow(wines), 150)
Xtraining <- scale(wines[training, ])
somnet <- imputeSOM(Xtraining, somgrid(5, 5, "hexagonal"))

map(somnet, scale(wines[-training, ],
   center=attr(Xtraining, "scaled:center"),
   scale=attr(Xtraining, "scaled:scale")))

missSOM  missSOM

Description

The Self-Organizing Maps with Built-in Missing Data Imputation. Missing values are imputed and regularly updated during the online Kohonen algorithm. Our method can be used for data visualisation, clustering or imputation of missing data. It is an extension of the online algorithm of the kohonen package.

Details

Self-Organizing Maps with Built-in Missing Data Imputation

Author(s)

you <youremail>

nir  Title Near-infrared data with temperature effects

Description

A data object containing near-infrared spectra of ternary mixtures of ethanol, water and iso-propanol, measured at five different temperatures (30, 40, ..., 70 degrees Centigrade).

Author(s)

My Name <blahblah@roxygen.org>

References

object.distances

Calculate distances between object vectors in a SOM

Description

This function calculates the distance between objects using the distance functions, weights and other attributes of a trained SOM. This function is used in the calculation of the U matrix in function plot.missSOM using the type = "dist.neighbours" argument.

Usage

object.distances(kohobj, type = c("data", "ximp", "codes"))

Arguments

kohobj
An object of class missSOM.

type
Whether to calculate distances between the data objects, or the codebook vectors.

Value

An object of class dist, which can be directly fed into (e.g.) a hierarchical clustering.

See Also

unit.distances, imputeSOM

Examples

data(wines)

## Data with no missing values
set.seed(7)
sommap <- imputeSOM(scale(wines), grid = somgrid(6, 4, "hexagonal"))
obj.dists <- object.distances(sommap, type = "data")
code.dists <- object.distances(sommap, type = "codes")

## Data with missing values
X <- scale(wines)
X[1:5, 1] <- NaN
sommap <- imputeSOM(X, grid = somgrid(6, 4, "hexagonal"))
obj.dists <- object.distances(sommap, type = "ximp")
code.dists <- object.distances(sommap, type = "codes")
**plot.missSOM**  
*Plot missSOM object*

**Description**

Plot objects of class missSOM. Several types of plots are supported.

**Usage**

```r
# S3 method for class 'missSOM'
plot(
  x,  
  type = c("codes", "changes", "counts", "dist.neighbours", "mapping", "property", 
    "quality"),
  classif = NULL,
  labels = NULL,
  pchs = NULL,
  main = NULL,
  palette.name = NULL,
  ncolors,
  bgcol = NULL,
  zlim = NULL,
  heatkey = TRUE,
  property,
  codeRendering = NULL,
  keepMargins = FALSE,
  heatkeywidth = 0.2,
  shape = c("round", "straight"),
  border = "black",
  na.color = "gray",
  ...
)

add.cluster.boundaries(x, clustering, lwd = 5, ...)

# S3 method for class 'missSOM'
identify(x, ...)
```

**Arguments**

- **x** missSOM object.
- **type** type of plot. (Wow!)
- **classif** classification object or vector of unit numbers. Only needed if type equals "mapping" and "counts".
- **labels** labels to plot when type equals "mapping".
- **pchs** symbols to plot when type equals "mapping".
main

title of the plot.

palette.name

colors to use as unit background for "codes", "counts", "prediction", "property", and "quality" plotting types.

ncolors

number of colors to use for the unit backgrounds. Default is 20 for continuous data.

bgcol

optional argument to colour the unit backgrounds for the "mapping" and "codes" plotting type. Defaults to "gray" and "transparent" in both types, respectively.

zlim

optional range for color coding of unit backgrounds.

heatkey

whether or not to generate a heatkey at the left side of the plot in the "property" and "counts" plotting types.

property

values to use with the "property" plotting type.

codeRendering

How to show the codes. Possible choices: "segments", "stars" and "lines".

keepMargins

if FALSE (the default), restore the original graphical parameters after plotting the kohonen map. If TRUE, one retains the map coordinate system so that one can add symbols to the plot, or map unit numbers using the identify function.

heatkeywidth

width of the colour key; the default of 0.2 should work in most cases but in some cases, e.g. when plotting multiple figures, it may need to be adjusted.

shape

kind shape to be drawn: "round" (circle) or "straight". Choosing "straight" produces a map of squares when the grid is "rectangular", and produces a map of hexagons when the grid is "hexagonal".

border

color of the shape’s border.

na.color

background color matching NA - default "gray".

...

other graphical parameters.

clustering

cluster labels of the map units.

lwd

other graphical parameters.

Details

Several different types of plots are supported:

"changes" shows the mean distance to the closest codebook vector during training.

"codes" shows the codebook vectors.

"counts" shows the number of objects mapped to the individual units. Empty units are depicted in gray.

"dist.neighbours" shows the sum of the distances to all immediate neighbours. This kind of visualisation is also known as a U-matrix plot. Units near a class boundary can be expected to have higher average distances to their neighbours.

"mapping" shows where objects are mapped. It needs the "classif" argument, and a "labels" or "pch" argument.

"property" properties of each unit can be calculated and shown in colour code. It can be used to visualise the similarity of one particular object to all units in the map, to show the mean similarity of all units and the objects mapped to them, etcetera. The parameter property contains the numerical values. See examples below.
"quality" shows the mean distance of objects mapped to a unit to the codebook vector of that unit. The smaller the distances, the better the objects are represented by the codebook vectors.

Function `identify.missSOM` shows the number of a unit that is clicked on with the mouse. The tolerance is calculated from the ratio of the plotting region and the user coordinates, so clicking at any place within a unit should work.

Function `add.cluster.boundaries` will add to an existing plot of a map thick lines, visualizing which units would be clustered together. In toroidal maps, boundaries at the edges will only be shown on the top and right sides to avoid double boundaries.

Value

Several types of plots return useful values (invisibly): the "counts", "dist.neighbours", and "quality" return vectors corresponding to the information visualized in the plot (unit background colours and heatkey).

See Also

imputeSOM

Examples

data(wines)
set.seed(7)
SOM.map <- imputeSOM(scale(wines), grid = somgrid(5, 5, "hexagonal"), rlen=100)
plot(SOM.map, type="changes")
counts <- plot(SOM.map, type="counts", shape = "straight")
## show both sets of codebook vectors in the map
plot(SOM.map, type="codes", main = c("Codes X"))
oldpar <- par(mfrow = c(1,2))
similarities <- plot(SOM.map, type="quality", palette.name = terrain.colors)
plot(SOM.map, type="mapping",
     labels = as.integer(vintages), col = as.integer(vintages),
     main = "mapping plot")
par(oldpar)

## Show 'component planes'
set.seed(7)
sommap <- imputeSOM(scale(wines), grid = somgrid(6, 4, "hexagonal"))
plot(sommap, type = "property", property = sommap$codes[,1],
     main = colnames(sommap$codes)[1])

## Show the U matrix
Umat <- plot(sommap, type="dist.neighbours", main = "SOM neighbour distances")
## use hierarchical clustering to cluster the codebook vectors
som.hc <- cutree(hclust(object.distances(sommap, "codes")), 5)
add.cluster.boundaries(sommap, som.hc)

## and the same for rectangular maps
set.seed(7)
sommap <- imputeSOM(scale(wines), grid = somgrid(6, 4, "rectangular"))
Function somgrid (modified from the version in the class package) sets up a grid of units, of a specified size and topology. Distances between grid units are calculated by function unit.distances.

### Usage

```r
somgrid(
  xdim = 8,
  ydim = 6,
  topo = c("rectangular", "hexagonal"),
  neighbourhood.fct = c("bubble", "gaussian"),
  toroidal = FALSE
)
```

```r
unit.distances(grid, toroidal)
```

### Arguments

- `xdim`: dimensions of the grid.
- `ydim`: dimensions of the grid.
- `topo`: choose between a hexagonal or rectangular topology.
- `neighbourhood.fct`: choose between bubble and gaussian neighbourhoods when training a SOM.
- `toroidal`: logical, whether the grid is toroidal or not. If not provided to the `unit.distances` function, the information in the `grid` object will be used.
- `grid`: an object of class `somgrid`.

### Value

Function `somgrid` returns an object of class "somgrid", with elements `pts`, and the input arguments to the function.

Function `unit.distances` returns a (symmetrical) matrix containing distances. When `grid$n.hood` equals "circular", Euclidean distances are used; for `grid$n.hood` is "square" maximum distances. For toroidal maps (joined at the edges) distances are calculated for the shortest path.
Examples

mygrid <- somgrid(5, 5, "hexagonal")
fakesom <- list(grid = mygrid)
class(fakesom) <- "missSOM"

oldpar <- par(mfrow = c(2,1))
dists <- unit.distances(mygrid)
plot(fakesom, type="property", property = dists[1,],
     main="Distances to unit 1", zlim=c(0,6),
     palette = rainbow, ncolors = 7)
dists <- unit.distances(mygrid, toroidal=TRUE)
plot(fakesom, type="property", property = dists[1,],
     main="Distances to unit 1 (toroidal)", zlim=c(0,6),
     palette = rainbow, ncolors = 7)
par(oldpar)

summary.missSOM

Summary and print methods for missSOM objects

Description

Summary and print methods for missSOM objects. The print method shows the dimensions and the topology of the map; if information on the training data is included, the summary method additionally prints information on the size of the data, the distance functions used, and the mean distance of an object to its closest codebookvector, which is an indication of the quality of the mapping.

Usage

## S3 method for class 'missSOM'
summary(object, ...)
## S3 method for class 'missSOM'
print(x, ...)

Arguments

  object    a missSOM object
  ...       Not used.
  x         a kohonen object

Value

No return a value.
tricolor

Provides smooth unit colors for SOMs

Description

Function provides colour values for SOM units in such a way that the colour changes smoothly in every direction.

Usage

tricolor(grid, phis = c(0, 2 * pi/3, 4 * pi/3), offset = 0)

Arguments

- **grid**: An object of class somgrid, such as the grid element in a kohonen object.
- **phis**: A vector of three rotation angles. Values for red, green and blue are given by the y-coordinate of the units after rotation with these three angles, respectively. The default corresponds to (approximate) red colour of the middle unit in the top row, and pure green and blue colours in the bottom left and right units, respectively. In case of a triangular map, the top unit is pure red.
- **offset**: Defines the minimal value in the RGB colour definition (default is 0). By supplying a value in the range [0, .9], pastel-like colours are provided.

Value

Returns a matrix with three columns corresponding to red, green and blue. This can be used in the rgb function to provide colours for the units.

See Also

- plot.missSOM
### wines

#### Examples

```r
data(wines)
som.wines <- imputeSOM(wines, grid = somgrid(5, 5, "hexagonal"))

colour1 <- tricolor(som.wines$grid)
plot(som.wines, "mapping", bg = rgb(colour1))
colour2 <- tricolor(som.wines$grid, phi = c(pi/6, 0, -pi/6))
plot(som.wines, "mapping", bg = rgb(colour2))
colour3 <- tricolor(som.wines$grid, phi = c(pi/6, 0, -pi/6), offset = .5)
plot(som.wines, "mapping", bg = rgb(colour3))
```

---

#### Description

A data frame containing 177 rows and thirteen columns; object vintages contains the class labels. These data are the results of chemical analyses of wines grown in the same region in Italy (Piedmont) but derived from three different cultivars: Nebbiolo, Barberas and Grignolino grapes. The wine from the Nebbiolo grape is called Barolo. The data contain the quantities of several constituents found in each of the three types of wines, as well as some spectroscopic variables.

#### Author(s)

My Name <blahblah@roxygen.org>

#### Source

http://kdd.ics.uci.edu

#### References


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### yeast

#### Title Yeast cell-cycle data

#### Description

Microarray cell-cycle data for 800 yeast genes, arrested with six different methods, arranged in a list. Additional class information is present as well.

#### Author(s)

My Name <blahblah@roxygen.org>
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