

# Package ‘missSOM’

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**Version** 1.0.1

**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) <[doi:10.48550/arXiv.2202.07963](https://doi.org/10.48550/arXiv.2202.07963)>.

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 imputeSOM

*The Self-Organizing Maps with Built-in Missing Data Imputation.*


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## 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

```
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 radius to -radius. 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

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

```

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map

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*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 <a href="#">imputeSOM</a> 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](#)

**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")))
```

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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 <youemail>

---

nir

*Title Near-infrared data with temperature effects*

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**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**

F. Wulfert , W.Th. Kok, A.K. Smilde: Anal. Chem. 1998, 1761-1767

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object.distances	<i>Calculate distances between object vectors in a SOM</i>
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---

### 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 <code>missSOM</code> .
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	<i>Plot missSOM object</i>
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---

### Description

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

### Usage

```
## 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 <code>identify</code> 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 "pchs" 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"))
```

```

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)

```

---

somgrid

*SOM-grid related functions*


---

### Description

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

```

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

unit.distances(grid, toroidal)

```

### Arguments

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

### 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, ...)

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

```

**Arguments**

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

**Value**

No return a value.

**See Also**[imputeSOM](#)**Examples**

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

---

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](#)

**Examples**

```

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))

```

wines

*Wine data***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**

M. Forina, C. Armanino, M. Castino and M. Ubigli. *Vitis*, 25:189-201 (1986)

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>

**References**

P. Spellman et al., Mol. Biol. Cell 9, 3273-3297 (1998)

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