

# Package ‘Radviz’

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**Type** Package

**Title** Project Multidimensional Data in 2D Space

**Version** 0.7.0

**Depends** R (>= 2.15)

**Imports** graphics, stats, utils, grid, gridBase, hexbin, MASS,  
KernSmooth

**Suggests** knitr, rmarkdown, bodenmiller, colorspace

**Description** An implementation of the radviz projection in R. It enables the visualization of multidimensional data while maintaining the relation to the original dimensions. This package provides functions to create and plot radviz projections, and a number of summary plots that enable comparison and analysis. For reference see Ankerst et al. (1996) <<http://citeseer.ist.psu.edu/viewdoc/summary?doi=10.1.1.68.1811>> for original implementation, see Di Caro et al. (2010) <DOI:10.1007/978-3-642-13672-6\_13> for the original method for dimensional anchor arrangements.

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**URL** <http://github.com/yannabraham/Radviz>

**BugReports** <http://github.com/yannabraham/Radviz/issues>

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**VignetteBuilder** knitr

**NeedsCompilation** no

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## R topics documented:

bubbleRadviz . . . . .	2
contour.radviz . . . . .	3

cosine . . . . .	5
dim.radviz . . . . .	6
do.density . . . . .	6
do.hex . . . . .	7
do.L . . . . .	9
do.optim . . . . .	10
do.radviz . . . . .	11
get.optim . . . . .	12
head.radviz . . . . .	13
hexplot . . . . .	14
identify.radviz . . . . .	15
in.da . . . . .	16
is.radviz . . . . .	17
make.S . . . . .	18
plot.radviz . . . . .	19
print.radviz . . . . .	20
Radviz . . . . .	20
recenter . . . . .	21
smoothRadviz . . . . .	22
subset.radviz . . . . .	23
summary.radviz . . . . .	24
text.radviz . . . . .	25

<b>Index</b>	<b>27</b>
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bubbleRadviz	<i>A Plotting Function for the Radviz Object</i>
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---

## Description

Plots the Dimensional Anchors and projected data points in a 2D space.

## Usage

```
bubbleRadviz(x, main = NULL, label.color = "orangered4", label.size = 1,
  bubble.color = "grey", bubble.fg = "white", bubble.size = 1,
  scale = 0.5, decreasing = NA, add = FALSE)
```

## Arguments

x	a radviz object as produced by do.radviz
main	*Optional* a title to the graph, displayed on top
label.color	The color of the Dimensional Anchors (defaults to orangered4)
label.size	numeric character expansion factor for Dimensional Anchor labels; multiplied by par("cex") yields the final character size. NULL and NA are equivalent to 1.0

bubble.color	The color of the bubble, either a single color or a vector of colors (defaults to grey)
bubble.fg	The foreground color of the bubble, either a single color or a vector of colors (defaults to white)
bubble.size	the bubble size, either a single number or a vector of values (defaults to 1)
scale	A scaling factor that will be applied to bubble.size (see <a href="#">symbols</a> for details)
decreasing	How the bubbles should be sorted: either NA for no sorting, TRUE or FALSE for sorting by decreasing or increasing bubble.size respectively, or a vector specifying the bubble order (see <a href="#">symbols</a> for details)
add	Logical: if add is TRUE then only the projected points are plotted

### Details

This function allows for the projection of clusters in Radviz (for example results of the SPADE algorithm), where the cluster size is derived from the number of events that fall into a specific cluster

### Author(s)

Yann Abraham

### Examples

```
data(iris)
das <- c('Sepal.Length', 'Sepal.Width', 'Petal.Length', 'Petal.Width')
S <- make.S(das)
species <- apply(iris[,c('Sepal.Length', 'Sepal.Width', 'Petal.Length', 'Petal.Width')],
                2,
                tapply, iris$Species, median)
rv <- do.radviz(species, S)
bubbleRadviz(rv,
             bubble.color=c('red', 'green', 'blue')[seq(1, length(levels(iris$Species)))],
             bubble.size=table(iris$Species),
             decreasing=TRUE)
```

---

contour.radviz	<i>Creates a contour plot, or add a contour plot to an existing plot for a Radviz Object</i>
----------------	--

---

### Description

Plots the Dimensional Anchors and density lines for projected data points in a 2D space.

**Usage**

```
## S3 method for class 'radviz'
contour(x, ..., main = NULL, label.color = "orangered4",
        label.size = 1, contour.color = par("fg"), contour.size = par("lwd"),
        point.color = "lightgrey", point.shape = ".", point.size = 1, add = F,
        drawlabels = FALSE, drawpoints = FALSE)
```

**Arguments**

x	a radviz object as produced by do.radviz
...	further arguments to be passed to or from other methods
main	[Optional] a title to the graph, displayed on top
label.color	The color of the Dimensional Anchors (defaults to orangered4)
label.size	numeric character expansion factor for Dimensional Anchor labels; multiplied by par("cex") yields the final character size. NULL and NA are equivalent to 1.0
contour.color	The color of contour lines (defaults to par('fg'))
contour.size	The thickness of contour lines (defaults to par('lwd'))
point.color	The point color (defaults to black)
point.shape	The point shape (defaults to '.')
point.size	the point size (defaults to 1)
add	Logical: if add is TRUE then only the contour lines are plotted
drawlabels	Logical. Contours are labelled if TRUE
drawpoints	Logical: if TRUE then the projected points are plotted

**Details**

The density lines will be calculated before plotting, if the Radviz object does not have one yet. The `add` allows plotting of contour lines over existing data, either the one used to generate the density or a different one (for context).

**Value**

Invisibly, the Radviz object that has been used as input; useful when `do.density` has not been called before so that results can be recovered

**Author(s)**

Yann Abraham

**See Also**

[do.density](#) for details about mapping projection to density

**Examples**

```
data(iris)
das <- c('Sepal.Length', 'Sepal.Width', 'Petal.Length', 'Petal.Width')
S <- make.S(das)
rv <- do.radviz(iris,S)
rv <- do.density(rv)
contour(rv,point.shape=1,point.color=c('red','green','blue')[as.integer(iris$Species)])
```

---

cosine

*Compute the Cosine Similarity between the Columns of a Data Set*

---

**Description**

Given a dataset, compute the cosine similarity between to columns for use in optimization of Dimensional Anchors

**Usage**

```
cosine(mat)
```

**Arguments**

mat                    A matrix or data.frame

**Details**

implementation by David Ruau (see <https://gist.github.com/bobthecat/2903031> for details)

**Value**

A symmetrical matrix with as many rows as there are columns in input

**Author(s)**

Yann Abraham

David Ruau

**Examples**

```
data(iris)
das <- c('Sepal.Length', 'Sepal.Width', 'Petal.Length', 'Petal.Width')
mat <- iris[,das]
scaled <- apply(mat,2,do.L)
sim.mat <- cosine(scaled)
ncol(mat)
dim(sim.mat)
```

---

dim.radviz	<i>Dimensions of a Radviz Object</i>
------------	--------------------------------------

---

**Description**

Retrieves the dimensions of a Radviz projection

**Usage**

```
## S3 method for class 'radviz'  
dim(x)
```

**Arguments**

x                    an object of class Radviz, as returned by [do.radviz](#)

**Author(s)**

Yann Abraham

**Examples**

```
data(iris)  
das <- c('Sepal.Length', 'Sepal.Width', 'Petal.Length', 'Petal.Width')  
S <- make.S(das)  
rv <- do.radviz(iris,S)  
  
dim(rv)  
nrow(rv) # for free!
```

---

do.density	<i>Computes 2D density for contour plots of Radviz objects</i>
------------	--

---

**Description**

Computes 2D density estimate of projected data for a Radviz object, using the [kde2d](#) function from the **MASS** package

**Usage**

```
do.density(x, n = 50)
```

**Arguments**

x                    a radviz object as produced by [do.radviz](#)  
n                    Number of grid points in each direction. Can be scalar or a length-2 integer vector (see [kde2d](#) for details)

## Details

Computes a 2D density estimate of Radviz projected data and stores the results in a density slot of the Radviz object. Invalid points, if any, will be excluded.

## Value

the Radviz object with an extra slot density containing the 2D density estimates for use with [contour.radviz](#)

## Author(s)

Yann Abraham

## See Also

[contour.radviz](#) for plotting

## Examples

```
data(iris)
das <- c('Sepal.Length', 'Sepal.Width', 'Petal.Length', 'Petal.Width')
S <- make.S(das)
rv <- do.radviz(iris,S)
rv <- do.density(rv)
contour(rv,point.shape=1,point.color=c('red','green','blue')[as.integer(iris$Species)])
```

---

do.hex

*Computes 2D hexagonal bins from a Radviz projection*

---

## Description

Computes 2D density using hexagon binning of projected data for a Radviz object, using the [hexbin](#) function from the **hexbin** package

## Usage

```
do.hex(x, n = 30, channels = NULL, colramp = function(n)
  colorRampPalette(c("yellow", "grey", "blue"))(n), ncols = 8,
  use.quantile = F, fixed = NULL)
```

## Arguments

x	a radviz object as produced by do.radviz
n	Number of bins in the grid (see <a href="#">hexbin</a> for details)
channels	[optional] if channels is not NULL, the function will compute color scales for the specified channels

colramp	[optional] function accepting an integer n as an argument and returning n colors
ncols	[optional] the number of levels used to cut each channels
use.quantile	[optional] if channels is not NULL and use.quantile is TRUE, channels will be cut into ncols+1 quantiles otherwise a fixed sequence from 0 to 1 in ncols+1 steps will be used
fixed	[optional] if channels is not NULL and fixed is TRUE, channels will be cut into length(fixed)+1 steps using the values in fixed as breaking points

### Details

The projected points will be binned into an hexagonal grid of size n. if channels is not NULL, for every channels the median intensity will be estimated over the complete grid and a color will be assigned from colramp using ncols, fixed and use.quantile; by default, channels will be split using a fixed sequence from 0 to 1 over ncols+1 levels unless use.quantile or fixed are set. Invalid points (if any) will not be used in computing the bins or the colors.

### Value

the Radviz object with an extra slot hex containing the hexbin object; if channels is not NULL an extra hexcols will be present containing the color information for every channel

### Author(s)

Yann Abraham

Dan Carr

### See Also

[hexplot](#) for plotting, [hexbin](#) for original implementation

### Examples

```
data(iris)
das <- c('Sepal.Length', 'Sepal.Width', 'Petal.Length', 'Petal.Width')
S <- make.S(das)
rv <- do.radviz(iris,S)
rv <- do.hex(rv,channels='Sepal.Length',ncols=4,use.quantile=TRUE)
summary(rv$hex)
```



---

`do.L`*Perform L-Normalization on a Vector*

---

**Description**

Standardizes all values in a vector to the unit vector  $([0,1])$  using local min and max

**Usage**

```
do.L(v, fun = range, na.rm = T)
```

**Arguments**

<code>v</code>	a vector of values
<code>fun</code>	a function that will return the minimum and maximum values to use to scale <code>v</code> ; defaults to <a href="#">range</a>
<code>na.rm</code>	Logical: should NA be removed? defaults to TRUE

**Details**

This is an alternative to performing a L normalization over the full matrix.

**Value**

A vector of values of the same length as `x`, scaled to the unit vector.

**Author(s)**

Yann Abraham

**Examples**

```
data(iris)
mat <- iris[,c('Sepal.Length', 'Sepal.Width', 'Petal.Length', 'Petal.Width')]
scaled <- apply(mat, 2, do.L)
summary(scaled) # all values are between [0,1]

scaled2 <- apply(mat, 2, do.L, fun=function(x) quantile(x, c(0.025, 0.975)))
summary(scaled2) # all values are between [0,1]

plot(scaled, scaled2,
     col=rep(seq(1, ncol(scaled)), each=nrow(scaled)),
     pch=16)
legend('topleft', legend=dimnames(scaled)[[2]], col=seq(1, ncol(scaled)), pch=16, bty='n')
```

do.optim

*Optimize the Dimensional Anchors Position using a Genetic Algorithm***Description**

Allows to compute the best arrangement of Dimensional Anchors so that visualization efficiency is maximized.

**Usage**

```
do.optim(springs, similarity, iter = 100, n = 1000, top = round(n * 0.1),
        lambda = 0.01, nlast = 5, optim = "in.da")
```

**Arguments**

springs	A matrix of 2D dimensional anchor coordinates, as returned by <a href="#">make.S</a>
similarity	A similarity matrix measuring the correlation between Dimensional Anchors
iter	The maximum number of iterations (defaults to 100)
n	The number of permutations of Dimensional Anchors to be created at each generation
top	The number of permutations to keep to create the next generation
lambda	The threshold for the optimization process
nlast	The number of generations to wait before lambda is applied
optim	The optimization function (in or rv)

**Details**

The first generation is a random sampling of all Dimensional Anchors. For every generation afterwards, only the best solutions (as specified by `top`) are kept; the solutions are normalized around the unit circle (ie  $c(1,2,3,4)$  is equivalent to  $c(4,1,2,3)$  for Radviz projection) before the next generation is created. The next generation consists of

- all unique best solutions from the previous generation (after circular normalization)
- a permutation of all previous solutions.

Briefly, for every Dimensional Anchor position the previous generation is sampled to give a mixture of identical and slightly shifted (mutated) solutions. The algorithm will stop when the maximum number of iterations (as defined by `iter`) is reached, or when a number of generations (defined by `nlast`) as not improved over the best solution by more than a given threshold (specified by `lambda`).

**Value**

a list containing 3 sets of values:

- `perfs` the list of the best performances by generation
- `best` the best performing arrangement by generation
- `last` the top performing arrangements of the last generation

**Author(s)**

Yann Abraham

**Examples**

```

data(iris)
das <- c('Sepal.Length', 'Sepal.Width', 'Petal.Length', 'Petal.Width')
S <- make.S(das)
scaled <- apply(iris[,das],2,do.L)
rv <- do.radviz(scaled,S)
plot(rv,main='Iris Columns',
      point.shape=1,
      point.color=c('red','green','blue')[as.integer(iris$Species)])
sim.mat <- cosine(scaled)
in.da(S,sim.mat) # the starting value
new <- do.optim(S,sim.mat,iter=10,n=100)
new.S <- make.S(get.optim(new))
new.rv <- do.radviz(scaled,new.S)
plot(new.rv,main='Optimized columns',
      point.shape=1,
      point.color=c('red','green','blue')[as.integer(iris$Species)])

```

do.radviz

---

*Projects a Matrix or a Data Frame to a 2D space defined by Dimensional Anchors*

---

**Description**

do.radviz will return a projection of a multidimensional dataset onto a 2D space defined by dimensional anchors that have been projected on the unit circle using [make.S](#)

**Usage**

```
do.radviz(x, springs)
```

**Arguments**

x	a data.frame or matrix to be projected, with column names matching row names in springs
springs	A matrix of 2D dimensional anchor coordinates, as returned by <a href="#">make.S</a>

**Details**

The function expects that at least some of the column names in df will be matched by row names in springs

**Value**

An object of class `radviz` with the following slots:

- `data` the original data (`x`)
- `springs` the original springs
- `projected` the projection of `x` on `springs`, a matrix of 2D coordinates for every line in `df`
- `valid` a logical vector

**Author(s)**

Yann Abraham

**Examples**

```
# the first example generates a simple Radviz object
data(iris)
das <- c('Sepal.Length', 'Sepal.Width', 'Petal.Length', 'Petal.Width')
S <- make.S(das)
rv <- do.radviz(iris,S)
summary(rv)

# in case a point cannot be projected, a warning will be raise
iris0 <- rbind(iris,c(rep(0,length(das)),NA))
rv0 <- do.radviz(iris0,S)

# to find out how many points could not be projected:
with(rv0,sum(!valid))

# to find which points where invalid in the data
with(rv0,which(!valid))

# to review the original data points
with(rv0,subset(data,!valid))
```

---

get.optim

*Get the Result of the Optimization Operation*

---

**Description**

Once the order of anchors has been optimized using `do.optim` this function can be used to recover the optimized anchors or any intermediate step

**Usage**

```
get.optim(opt, n = NULL)
```

**Arguments**

opt	the result of the optimization operation performed by <a href="#">do.optim</a>
n	the optimized order of anchors to return; defaults to NULL, which returns the best identified combination

**Value**

a character vector of the anchor names, ordered as in the  $n^{\text{th}}$  step of the optimization

**Author(s)**

Yann Abraham

**Examples**

```
#' data(iris)
das <- c('Sepal.Length', 'Sepal.Width', 'Petal.Length', 'Petal.Width')
S <- make.S(das)
scaled <- apply(iris[,das],2,do.L)
rv <- do.radviz(scaled,S)
plot(rv,main='Iris Columns',
      point.shape=1,
      point.color=c('red', 'green', 'blue')[as.integer(iris$Species)])
sim.mat <- cosine(scaled)
in.da(S,sim.mat) # the starting value
new <- do.optim(S,sim.mat,iter=10,n=100)
get.optim(new) # the optimal order
get.optim(new,2) # the second step of the optimization
```

---

head.radviz

*Radviz Object Summary, head, Print, Subset Methods*

---

**Description**

Provides helper function to deal with Radviz objects

**Usage**

```
## S3 method for class 'radviz'
head(x, n = 6, ...)
```

**Arguments**

x	an object of class Radviz, as returned by <a href="#">do.radviz</a>
n	the number of lines from each slots in the Radviz object to display (defaults to 6)
...	further arguments to be passed to or from other methods

**Details**

head.radviz shows the first n lines of the radviz data object.

**Author(s)**

Yann Abraham

**Examples**

```
data(iris)
das <- c('Sepal.Length', 'Sepal.Width', 'Petal.Length', 'Petal.Width')
S <- make.S(das)
rv <- do.radviz(iris,S)

head(rv)
```

---

hexplot

*A smoothScatter function for Radviz objects*

---

**Description**

Plots the Dimensional Anchors and a smoothed color density representation of projected data points in a 2D space.

**Usage**

```
hexplot(x, main = NULL, label.color = "orangered4", label.size = 1,
        mincnt = 0, color = NULL, style = "constant.col")
```

**Arguments**

x	a radviz object as produced by do.radviz
main	[Optional] a title to the graph, displayed on top
label.color	The color of the Dimensional Anchors (defaults to orangered4)
label.size	numeric character expansion factor for Dimensional Anchor labels multiplied by par("cex") yields the final character size. NULL and NA are equivalent to 1.0
mincnt	numeric; cells with counts smaller than mincnt are not shown (see <a href="#">grid.hexagons</a> for details)
color	if color is not NULL and corresponds to one of the channels in the hexcols slot of the Radviz object, cells will be colored using colors in the hexcols slot
style	character string specifying the type of plotting (see <a href="#">grid.hexagons</a> for details)

**Value**

Plots the result of a [do.hex](#) function

**Author(s)**

Yann Abraham  
Dan Carr  
Nicholas Lewin-Koh

**See Also**

[grid.hexagons](#) and [hexbin](#) for original implementation

**Examples**

```
data(iris)
das <- c('Sepal.Length', 'Sepal.Width', 'Petal.Length', 'Petal.Width')
S <- make.S(das)
rv <- do.radviz(iris, S)
rv <- do.hex(rv, channels='Sepal.Length', ncols=4, use.quantile=TRUE)
hexplot(rv, color='Sepal.Length')
```

---

identify.radviz

*Identify a Point in a Radviz Projection*

---

**Description**

Use this function to get the index of a point in a Radviz projection

**Usage**

```
## S3 method for class 'radviz'
identify(x, ..., n = 1)
```

**Arguments**

x	a radviz object as produced by <a href="#">do.radviz</a>
...	further arguments to be passed to or from other methods
n	the number of points to identify, defaults to 1

**Details**

The function will use the row names of the data variable in the rv object for labeling the plot

**Value**

an integer vector containing the indices of the identified points, in the order they were identified.

**Author(s)**

Yann Abraham

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

```
data(iris)
das <- c('Sepal.Length', 'Sepal.Width', 'Petal.Length', 'Petal.Width')
S <- make.S(das)
rv <- do.radviz(iris,S)
plot(rv,point.shape=1,point.color=c('red','green','blue')[as.integer(iris$Species)])
identify(rv)
```

---

in.da

*Optimization functions for Dimensional Anchors in Radviz*

---

**Description**

Visual efficiency of Radviz plots depends heavily on the correct arrangement of Dimensional Anchors. These functions implement the optimization strategies described in [Di Caro et al 2012](#)

**Usage**

```
in.da(springs, similarity)
rv.da(springs, similarity)
```

**Arguments**

springs	A matrix of 2D dimensional anchor coordinates, as returned by <a href="#">make.S</a>
similarity	A similarity matrix measuring the correlation between Dimensional Anchors

**Details**

Following the recommendation of de cario et al. we used a cosine function to calculate the similarity between Dimensional Anchors (see [cosine](#) for details). The in.da function implements the independent similarity measure, where the value increases as the Radviz projection improves. The rv.da function implements the radviz-dependent similarity measure, where the value decreases as the Radviz projection improves.

**Value**

A measure of the efficiency of the Radviz projection of the similarity matrix onto a set of springs

**Author(s)**

Yann Abraham



## Examples

```
data(iris)
das <- c('Sepal.Length', 'Sepal.Width', 'Petal.Length', 'Petal.Width')
S <- make.S(das)
scaled <- apply(iris[,das],2,do.L)
sim.mat <- cosine(scaled)
in.da(S,sim.mat) # increases with better projections
rv.da(S,sim.mat) # decreases with better projections
```

---

is.radviz

*Test if the object is a Radviz object*

---

## Description

The function will return TRUE if the object is a Radviz object

## Usage

```
is.radviz(x)
```

## Arguments

x                    an object of class Radviz, as returned by [do.radviz](#)

## Author(s)

Yann Abraham

## Examples

```
data(iris)
das <- c('Sepal.Length', 'Sepal.Width', 'Petal.Length', 'Petal.Width')
S <- make.S(das)
rv <- do.radviz(iris,S)

is.radviz(rv) # should be true
```

---

`make.S`*Define Dimensional Anchors around the Unit Circle*

---

## Description

`make.S` will return xy coordinates for n dimensional anchors equally spaced around the unit circle

## Usage

```
make.S(x)
```

## Arguments

`x` a vector of dimensional anchors or the number of anchors to put on the circle

## Details

If `x` is a vector, values will be used to set the row names of the matrix.

## Value

A matrix with 2 columns (x and y coordinates of dimensional anchors) and 1 line per dimensional anchor (so called springs). If `x` is a vector, the row names of the matrix will be set to the syntactically correct version of values in the vector (through a call to [make.names](#)). Please note that some functions expect to match column names of data to row names of the spring matrix.

## Author(s)

Yann Abraham

## Examples

```
data(iris)
das <- c('Sepal.Length', 'Sepal.Width', 'Petal.Length', 'Petal.Width')
make.S(length(das)) # without row names
make.S(das) # with row names
```

---

plot.radviz                      *A Plotting Function for the Radviz Object*

---

### Description

Plots the Dimensional Anchors and projected data points in a 2D space.

### Usage

```
## S3 method for class 'radviz'
plot(x, main = NULL, label.color = "orangered4",
     label.size = 1, point.color = "black", point.shape = ".",
     point.size = 1, add = FALSE, anchors.only = FALSE, ...)
```

### Arguments

x	a radviz object as produced by <a href="#">do.radviz</a>
main	[Optional] a title to the graph, displayed on top
label.color	The color of the Dimensional Anchors (defaults to orangered4)
label.size	numeric character expansion factor for Dimensional Anchor labels; multiplied by par("cex") yields the final character size. NULL and NA are equivalent to 1.0
point.color	The point color (defaults to black)
point.shape	The point shape (defaults to '.')
point.size	The point size (defaults to 1)
add	Logical: if add is TRUE then only the projected points are plotted
anchors.only	plot only the anchors so that other plots can be freely overlaid
...	further arguments to be passed to or from other methods

### Details

The add option allows plotting of additional data such as cluster centers onto an existing plot.

### Author(s)

Yann Abraham

### Examples

```
data(iris)
das <- c('Sepal.Length', 'Sepal.Width', 'Petal.Length', 'Petal.Width')
S <- make.S(das)
rv <- do.radviz(iris,S)
plot(rv,point.shape=1,point.color=c('red','green','blue')[as.integer(iris$Species)])
```

---

`print.radviz`                      *Print Radviz Object*

---

### Description

Prints the first few lines of the data used to generate a Radviz projection

### Usage

```
## S3 method for class 'radviz'  
print(x, n = 6, ...)
```

### Arguments

`x`                      an object of class Radviz, as returned by [do.radviz](#)

`n`                      the number of lines from each slots in the Radviz object to display (defaults to 6)

`...`                    further arguments to be passed to or from other methods

### Author(s)

Yann Abraham

### Examples

```
data(iris)  
das <- c('Sepal.Length', 'Sepal.Width', 'Petal.Length', 'Petal.Width')  
S <- make.S(das)  
rv <- do.radviz(iris, S)  
  
print(rv)
```

---

Radviz                              *Radviz Projection of Multidimensional Data*

---

### Description

Radviz uses Dimensional Anchors and the spring paradigm to project a multidimensional space in 2D. This allows for the quick visualization of large and complex datasets.

## Examples

```
data(iris)
das <- c('Sepal.Length', 'Sepal.Width', 'Petal.Length', 'Petal.Width')
S <- make.S(das)
rv <- do.radviz(iris, S)
plot(rv, point.shape=1, point.color=c('red', 'green', 'blue')[as.integer(iris$Species)])
```

---

recenter

*Rotate Dimensional Anchors around the Unit Circle*

---

## Description

recenter will rotate the order of the dimensional anchors around the circle, to put a channel of reference to the top of the display.

## Usage

```
recenter(springs, newc)
```

## Arguments

springs	a spring object as created by <a href="#">make.S</a>
newc	a string specifying which dimensional anchor should be placed on top of the unit circle

## Value

a spring object with rotated labels

## Author(s)

Yann Abraham

## Examples

```
data(iris)
das <- c('Sepal.Length', 'Sepal.Width', 'Petal.Length', 'Petal.Width')
iris.S <- make.S(das)
iris.S
recenter(iris.S, 'Petal.Length')
```

---

smoothRadviz

*A smoothScatter function for Radviz objects*


---

## Description

Plots the Dimensional Anchors and a smoothed color density representation of projected data points in a 2D space.

## Usage

```
smoothRadviz(x, main = NULL, label.color = "orangered4", label.size = 1,
             smooth.color = colorRampPalette(c("white", blues9)),
             transformation = function(x) x^0.25, nbin = 128, nrpoints = 100,
             bandwidth)
```

## Arguments

x	a radviz object as produced by <a href="#">do.radviz</a>
main	[Optional] a title to the graph, displayed on top
label.color	The color of the Dimensional Anchors (defaults to orangered4)
label.size	numeric character expansion factor for Dimensional Anchor labels; multiplied by <code>par("cex")</code> yields the final character size. NULL and NA are equivalent to 1.0
smooth.color	function accepting an integer n as an argument and returning n colors (see <a href="#">smoothScatter</a> for details)
transformation	function mapping the density scale to the color scale
nbin	numeric vector of length one (for both directions) or two (for x and y separately) specifying the number of equally spaced grid points for the density estimation; directly used as <code>gridsize</code> in <a href="#">bkde2D</a> (see <a href="#">smoothScatter</a> for details)
nrpoints	number of points to be superimposed on the density image (see <a href="#">smoothScatter</a> for details)
bandwidth	numeric vector (length 1 or 2) of smoothing bandwidth(s). If missing, a more or less useful default is used. <code>bandwidth</code> is subsequently passed to function <a href="#">bkde2D</a> (see <a href="#">smoothScatter</a> for details)

## Details

The add allows plotting of additional data such as cluster centers onto an existing plot.

## Author(s)

Yann Abraham  
 Florian Hahne

**See Also**

[smoothScatter](#) for original implementation

**Examples**

```
data(iris)
das <- c('Sepal.Length', 'Sepal.Width', 'Petal.Length', 'Petal.Width')
S <- make.S(das)
rv <- do.radviz(iris,S)
smoothRadviz(rv)
```

---

subset.radviz	<i>Title</i>
---------------	--------------

---

**Description**

Title

**Usage**

```
## S3 method for class 'radviz'
subset(x, i, ...)
```

**Arguments**

x	a radviz object
i	A logical or indices vector of the same length as the original data used to create the Radviz object, that is used to subset each slots
...	further arguments to be passed to or from other methods

**Value**

a new Radviz object containing only rows specified in i. Any density or hexbin analysis is dropped

**Author(s)**

Yann Abraham

**Examples**

```
# create a radviz object
data(iris)
das <- c('Sepal.Length', 'Sepal.Width', 'Petal.Length', 'Petal.Width')
S <- make.S(das)
rv <- do.radviz(iris,S)

# subset rv
```

```
srv <- subset(rv,iris$Species=='setosa')
summary(srv)
sum(iris$Species=='setosa') # 50 objects in srv corresponding to setosa values
```

---

summary.radviz      *Radviz Summary*

---

### Description

Provides a summary for Radviz objects

### Usage

```
## S3 method for class 'radviz'
summary(object, n = 6, ...)
```

### Arguments

object	an object of class Radviz, as returned by <a href="#">do.radviz</a>
n	the number of lines from each slots in the Radviz object to display (defaults to 6)
...	further arguments to be passed to or from other methods

### Author(s)

Yann Abraham

### Examples

```
data(iris)
das <- c('Sepal.Length', 'Sepal.Width', 'Petal.Length', 'Petal.Width')
S <- make.S(das)
rv <- do.radviz(iris,S)

summary(rv)
```



---

text.radviz

*Text annotations for for the Radviz Plots*


---

## Description

Text draws the strings given in the vector labels at the coordinates given by the radviz projection

## Usage

```
## S3 method for class 'radviz'
text(x, ..., main = NULL, label.color = "orangered4",
      label.size = 1, labels = NULL, adj = NULL, pos = NULL, offset = 0.5,
      vfont = NULL, cex = 1, col = NULL, font = NULL, add = TRUE)
```

## Arguments

x	a radviz object as produced by do.radviz
...	further arguments to be passed to or from other methods
main	[Optional] a title to the graph, displayed on top if add is TRUE
label.color	[Optional] The color of the Dimensional Anchors if add is TRUE (defaults to orangered4)
label.size	[Optional] numeric character expansion factor for Dimensional Anchor labels if add is TRUE; multiplied by par("cex") yields the final character size. NULL and NA are equivalent to 1.0
labels	a character vector specifying the text to be written. An attempt is made to coerce other language objects (names and calls) to characters using <a href="#">as.graphicsAnnot</a> . If labels is longer than x and y, the coordinates are recycled to the length of labels.
adj	one or two values in [0, 1] which specify the x (and optionally y) adjustment of the labels. On most devices values outside that interval will also work.
pos	a position specifier for the text. If specified this overrides any adj value given. Values of 1, 2, 3 and 4, respectively indicate positions below, to the left of, above and to the right of the specified coordinates.
offset	when pos is specified, this value gives the offset of the label from the specified coordinate in fractions of a character width.
vfont	NULL for the current font family, or a character vector of length 2 for Hershey vector fonts. The first element of the vector selects a typeface and the second element selects a style. Ignored if labels is an expression.
cex	numeric character expansion factor; multiplied by par("cex") yields the final character size. NULL and NA are equivalent to 1.0.
col, font	the color and (if vfont = NULL) font to be used, possibly vectors. These default to the values of the global <a href="#">graphical parameters</a> in par().
add	Logical: if add is TRUE then only the projected points are plotted

**Author(s)**

Yann Abraham

**Examples**

```
data(iris)
das <- c('Sepal.Length', 'Sepal.Width', 'Petal.Length', 'Petal.Width')
S <- make.S(das)
rv <- do.radviz(iris,S)
plot(rv,point.shape=1,point.color='grey')
med.iris <- split(iris,iris$Species)
med.iris <- lapply(med.iris,function(df) {
  spc <- unique(df$Species)
  df <- df[,names(df)!='Species']
  df <- apply(df,2,median)
  df <- data.frame(t(df))
  df$Species <- spc
  return(df)
})
med.iris <- do.call('rbind',med.iris)
med.rv <- do.radviz(med.iris,S)
text(med.rv,labels=med.iris$Species,col=c('red','green','blue')[as.integer(med.iris$Species)])
```

# Index

- \*Topic **cluster**
  - bubbleRadviz, 2
- \*Topic **hplot**
  - bubbleRadviz, 2
  - contour.radviz, 3
- \*Topic **multivariate**
  - bubbleRadviz, 2
  - contour.radviz, 3
- as.graphicsAnnot, 25
- bkde2D, 22
- bubbleRadviz, 2
- contour.radviz, 3, 7
- cosine, 5, 16
- dim.radviz, 6
- do.density, 4, 6
- do.hex, 7, 14
- do.L, 9
- do.optim, 10, 12, 13
- do.radviz, 6, 11, 13, 15, 17, 19, 20, 22, 24
- get.optim, 12
- graphical parameters, 25
- grid.hexagons, 14, 15
- head.radviz, 13
- hexbin, 7, 8, 15
- hexplot, 8, 14
- identify, 16
- identify.radviz, 15
- in.da, 16
- is.radviz, 17
- kde2d, 6
- make.names, 18
- make.S, 10, 11, 16, 18, 21
- par, 25
- plot.radviz, 19
- print.radviz, 20
- Radviz, 20
- Radviz-package (Radviz), 20
- range, 9
- recenter, 21
- rv.da (in.da), 16
- smoothRadviz, 22
- smoothScatter, 22, 23
- subset.radviz, 23
- summary.radviz, 24
- symbols, 3
- text.radviz, 25