

# Package ‘diaplt’

May 8, 2026

**Type** Package

**Title** Beads Summary Plot of Ranges

**Version** 1.4.0

**Date** 2022-04-19

**Author** Shinichiro Tomizono

**Maintainer** Shinichiro Tomizono <cowares@gmail.com>

**Description** Visualize one-factor data frame.

Beads plot consists of diamonds of each factor of each data series.

A diamond indicates average and range.

Look over a data frame with many numeric columns and a factor column.

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**NeedsCompilation** no

**Repository** CRAN

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## Description

Visualize one-factor data frame. Beads plot consists of diamonds of each factor of each data series. A diamond indicates average and range. Look over a data frame with many numeric columns and a factor column.

**Details**

The DESCRIPTION file:

Package: diaplt  
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Title: Beads Summary Plot of Ranges  
Version: 1.4.0  
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Author: Shinichiro Tomizono  
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Description: Visualize one-factor data frame. Beads plot consists of diamonds of each factor of each data series. A diamond  
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Index of help topics:

beadsplot	Beads Summary Plot
diaplt-package	Beads Summary Plot of Ranges

This package contains beadsplot function.

**Author(s)**

Shinichiro Tomizono

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**References**

Beads Summary Plot of Ranges: <https://tomizonor.wordpress.com/2013/11/12/beads-plot/>

**See Also**

[beadsplot](#).

**Examples**

```
beadsplot(Species~., iris)
```

beadspplot

*Beads Summary Plot***Description**

Visualize one-factor data frame. Look over a data frame with many numeric columns and a factor column. Beads plot consists of diamonds of each factor of each data series. A diamond indicates average and range.

**Usage**

```
beadspplot(x, ...)
```

```
## Default S3 method:
```

```
beadspplot(x, index=NULL, horizontal=FALSE,
           col=NULL, sheer=NULL, shading=NA, shading.angle=NA,
           bw=0.2, lwd=1, lwd.center=lwd,
           legend=TRUE, label.factor=TRUE, label.range=TRUE,
           drift.label.factor=c(0.2,2), drift.label.range=c(0,0),
           S=min, E=mean, N=max, summary.labels=NULL,
           plot=TRUE, verbose=FALSE, ...)
```

```
## S3 method for class 'data.frame'
```

```
beadspplot(x, index=NULL, horizontal=FALSE,
           col=NULL, sheer=NULL, shading=NA, shading.angle=NA,
           bw=0.2, lwd=1, lwd.center=lwd,
           legend=TRUE, label.factor=TRUE, label.range=TRUE,
           drift.label.factor=c(0.2,2), drift.label.range=c(0,0),
           S=min, E=mean, N=max, summary.labels=NULL,
           plot=TRUE, verbose=FALSE, ...)
```

```
## S3 method for class 'numeric'
```

```
beadspplot(x, index=NULL, horizontal=FALSE,
           col=NULL, sheer=NULL, shading=NA, shading.angle=NA,
           bw=0.2, lwd=1, lwd.center=lwd,
           legend=TRUE, label.factor=TRUE, label.range=TRUE,
           drift.label.factor=c(0.2,2), drift.label.range=c(0,0),
           S=min, E=mean, N=max, summary.labels=NULL,
           plot=TRUE, verbose=FALSE, ...)
```

```
## S3 method for class 'character'
```

```
beadspplot(x, data, horizontal=FALSE,
           col=NULL, sheer=NULL, shading=NA, shading.angle=NA,
           bw=0.2, lwd=1, lwd.center=lwd,
           legend=TRUE, label.factor=TRUE, label.range=TRUE,
           drift.label.factor=c(0.2,2), drift.label.range=c(0,0),
           S=min, E=mean, N=max, summary.labels=NULL,
```

```

plot=TRUE, verbose=FALSE, ...)

## S3 method for class 'formula'
beadspot(formula, data, horizontal=FALSE,
          col=NULL, sheer=NULL, shading=NA, shading.angle=NA,
          bw=0.2, lwd=1, lwd.center=lwd,
          legend=TRUE, label.factor=TRUE, label.range=TRUE,
          drift.label.factor=c(0.2,2), drift.label.range=c(0,0),
          S=min, E=mean, N=max, summary.labels=NULL,
          plot=TRUE, verbose=FALSE, ...)

```

### Arguments

<code>x</code>	data frame, contains observation columns (for <code>beadspot.default</code> , that is, = <code>beadspot.data.frame</code> ). numeric vector, as a single observation data (for <code>beadspot.numeric</code> ). character, as a column name of factor (for <code>beadspot.character</code> ).
<code>index</code>	factor to separate rows. default (NULL) is to plot without factors. character vector, or data frame with a single column, as a factor to separate rows (for <code>beadspot.default</code> and <code>beadspot.numeric</code> ).
<code>formula</code>	formula, a model formula, eg. <code>factor ~ obs1 + obs2 + obs3</code> (for <code>beadspot.formula</code> ).
<code>data</code>	<code>data.frame</code> , contains variables in formula (for <code>beadspot.formula</code> ), or observation columns with a factor column (for <code>beadspot.character</code> ).
<code>horizontal</code>	if TRUE is given, diamond beads are plotted horizontally. default is FALSE.
<code>col</code>	character vector, as colors by factor. default is NULL to select colors automatically.
<code>sheer</code>	numeric vector of four items, as transparencies, that is, alpha levels of colors. each item must be between 0 and 1, 1 is for solid colors. items are in sequence of legend, label, border and diamond. default is NULL, same as <code>c(1, 0.9, 0.6, 0.2)</code> , legends use solid colors, labels almost solid, borders sheer, and diamonds are most sheer.
<code>shading</code>	numeric vector, as shading density to draw inside of beads. default is NA to draw automatic, usually no shadings. the density value means lines per inch. the generator depends the vector length. <b>1</b> a single value is used to all densities <b>2</b> values are generated between the pair <b>k</b> when k is number of factor levels, values are used to each level logical value TRUE has a special meaning to enable shading with automatic densities.
<code>shading.angle</code>	numeric vector, as shading angle to draw inside of beads. default is NA to draw automatic, usually no shadings. the angle value means degree of line direction to horizon. the generator depends the vector length with same manner of density.
<code>bw</code>	numeric value, as half of bead width relative to series distance, default is 0.2, is 40% width.

lwd	numeric value, as line width of bead border, default is 1. set NULL to disable border line.
lwd.center	numeric value, as line width of bead center, default is lwd, same width as border. set NULL to disable center line.
legend	logical value, to control the display of legend located at top. set FALSE to disable the legend. default is TRUE.
label.factor	logical value, to control the display of labels located at each bead. set FALSE to disable the labels. default is TRUE. character vector, as alternative labels can be also specified.
label.range	logical value, to control the display of whole range values. set FALSE to disable showing range values. default is TRUE.
drift.label.factor	numeric vector, as (value, cycle) to give small drifts to factor label location. default is c(0.2, 2), to generate 0.2, 0, 0.2, 0, ....
drift.label.range	numeric vector, as (value, cycle) to give small drifts to range label location. default is c(0, 0), to generate no drifts.
S	function, to calculate summary for bottom vertex. default is min.
E	function, to calculate summary for center diagonal. default is mean.
N	function, to calculate summary for top vertex. default is max.
summary.labels	character vector, as names of summary functions S, E and N. eg. c('Minimum', 'Mean', 'Maximum'). default is NULL, no explicit names.
plot	if FALSE is given, it disable to plot and print a summary. default is TRUE.
verbose	if TRUE is given, it print verbose debugging information. default is FALSE.
...	plot parameters and scale parameters are acceptable.

## Details

This function is designed to visualize an overview of a data frame with one factor. Such as, soil chemical components of several sites.

When you have recommended values or critical limits for upper and lower which you want to compare with the data, scale parameter arguments `scale.data.center` and `scale.data.border` can be used. Eg. setting critical values of pH, Nitrogen and Phosphorus and draw horizontal grids as these critical values.

## Value

A summary list is explicitly printed when `plot=FALSE` is given, and is invisibly returned when `plot=TRUE`.

`scaled` scaled summary of three-dimensional array (series, factors, summaries)

- series** each column of data
- factors** each index
- summaries** S/min, E/mean, N/max

	for one-dimensional vector data, series=1 is used. for one-level index=NULL, factors=1 is used.
raw	unscaled summary of three-dimensional array (series, factors, summaries) data structure is same as scaled item.
scale	scaling parameters

### Scale parameters

**scale.range** Numeric value with default=1. Width between center and border grids. NULL turns off scaling.

**scale.mean** Numeric value with default=0. Location of center grid. NULL turns off centering.

**scale.log** Logical value with default=FALSE. TRUE enables log10 scaling.

**scale.data.center** Numeric vector with default=NULL. Give center value vector from outside. See section Details and Examples.

**scale.data.border** Numeric matrix with default=NULL. Give border value matrix from outside. See section Details and Examples.

**scale.grid.center** Character value with default=NA. Color of center grid. NULL turns off drawing the grid.

**scale.grid.border** Character value with default=NA. Color of border grids. NULL turns off drawing the grids.

**cex.axis** Numeric value with default=1. Font size of grid label.

### Author(s)

Shinichiro Tomizono

### References

Beads Summary Plot of Ranges: <https://tomizonor.wordpress.com/2013/11/12/beads-plot/>

### See Also

[range](#), [min](#), [max](#), [mean](#).

### Examples

```
# iris data, by Species
beadsplot(Species~., iris)
beadsplot('Species', iris)
beadsplot(iris[1:4], iris[5])
beadsplot(iris[1:4], iris[,5])

# iris data, Petal.Length by Species
beadsplot(iris[, 'Petal.Length'], iris[, 'Species'], drift.label.factor=-0.2)

# horizontal
beadsplot(Species~., iris, horizontal=TRUE)
```

```

# color, sheer and shading
beadspot(Species~., iris,
          col=c('tomato1','tomato4','tomato3'), sheer=c(1,0.3,0.6,0.05))
beadspot(Species~., iris, bw=0.5, label.factor=FALSE,
          sheer=c(1,0.9,0.6,0.4), lwd=NULL)
beadspot(Species~., iris, shading=c(3,5))

# labels
beadspot(Species~., iris, label.factor=FALSE)
beadspot(Species~., iris, label.factor=c('a','b','c'),
          drift.label.factor=0.05)
beadspot(Species~., iris, legend=FALSE)

# scale grids
## disable grids
beadspot(Species~., iris, scale.grid.center=FALSE, scale.grid.border=FALSE)
## color grids
beadspot(Species~., iris, scale.grid.center='red', scale.grid.border='tan')

# scaling
beadspot(Species~., iris, scale.range=50, scale.mean=50)
## no centering by mean
beadspot(Species~., iris, scale.mean=NULL)
## plot raw values
beadspot(Species~., iris, scale.range=NULL, scale.mean=NULL)
beadspot(Species~., iris, scale.range=NULL, scale.mean=NULL, scale.log=TRUE)
## custom value scaling

### critical matrix as ranges of versicolor,
###   in sequence of Sep.Len, Sep.Wid, Pet.Len, Pet.Wid
criticals <- matrix(c(4.9,7.0, 2.0,3.4, 3.0,5.1, 1.0,1.8), nrow=2, ncol=4)
beadspot(Species~., iris, scale.data.border=criticals)

### recommend vector as mean of versicolor, in sequence of
###   S.Len, S.Wid, P.Len, P.Wid
recommend <- c(5.936, 2.770, 4.260, 1.326)
beadspot(Species~., iris, scale.data.border=criticals, scale.data.center=recommend)
### when both of center and border is specified,
### center is dominance, border is adjusted to indicate
### the width between lower and upper grids.
### in this case, criticals can be simplified as follows,
### criticals <- matrix(c(0,2.1, 0,1.4, 0,2.1, 0,0.8), nrow=2, ncol=4)
### because differences each are used.

### recommend vector as mean of setosa, in sequence of
###   S.Len, S.Wid, P.Len, P.Wid
recommend2 <- c(5.006, 3.428, 1.462, 0.246)
beadspot(Species~., iris, scale.data.border=criticals, scale.data.center=recommend2)
### center grid is on setosa mean,
### lower and upper grids indicate versicolor range width.

beadspot(Species~., iris, scale.data.center=recommend2)
### center grid is on setosa mean,

```

```
### lower and upper grids indicate whole range width.  
  
# using median and IQR  
q1 <- function(x) fivenum(x)[2]  
q3 <- function(x) fivenum(x)[4]  
q2 <- median  
beadsplot(Species~., iris, S=q1, E=q2, N=q3)  
  
# graphic parameters  
beadsplot(Species~., iris, cex=0.7, cex.axis=0.7)  
  
# print summary  
beadsplot(Species~., iris, plot=FALSE)
```

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