

# Package ‘DendSer’

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**Title** Dendrogram Seriation: Ordering for Visualisation

**Description** Re-arranges a dendrogram to optimize visualisation-based cost functions.

The methods implemented here are described in “Advances in Dendrogram Seriation for Application to Visualization”, Journal of Computational and Graphical Statistics (2015) D. Earle and C.B. Hurley <[doi:10.1080/10618600.2013.874295](https://doi.org/10.1080/10618600.2013.874295)>.

**License** GPL-2

**Encoding** UTF-8

**RoxygenNote** 7.3.3

**Imports** gclus, graphics, seriation, stats, utils

**Suggests** HSAUR2, Iyer517, RColorBrewer, mvtnorm, scagnostics, knitr, rmarkdown

**VignetteBuilder** knitr

**NeedsCompilation** yes

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cost	<i>Cost functions for DendSer Each of these functions evaluates the cost of an ordering.</i>
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**Description**

Cost functions for DendSer Each of these functions evaluates the cost of an ordering.

**Usage**

costLS(sw, o, target = seq\_along(sw), ...)

costARc(sw, o, target = nrow(sw) - 1, ...)

costED(sw, o, node, se, ...)

costPL(sw, o, ...)

costLPL(sw, o, target = (nrow(sw) - 1):1, ...)

costBAR(sw, o, target = max(2, floor(nrow(sw)/5)), ...)

**Arguments**

sw	For cost=costLS, this is a vector of object weights. Otherwise is a symmetric matrix.
o	An ordering vector.
target	Parameter used by cost function.
...	Other args.
node	The node
se	Extra info

**Value**

Result of cost

**Author(s)**

Catherine Hurley & Denise Earle

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crit2cost	<i>Cost function from seriation criterion</i>
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**Description**

Returns a cost function from seriation criterion (package seriation)

**Usage**

```
crit2cost(crit)
```

**Arguments**

`crit` One of `seriation::list_criterion_methods("dist")`

**Examples**

```
d<- dist(iris[1:20,-5])
h <- hclust(d)
DendSer(h,d,cost=function(x,o,...) seriation::criterion(as.dist(x),o,method="AR_deviations"))
DendSer(h,d,cost=crit2cost("AR_deviations")) # short version of above
DendSer(h,d,cost=crit2cost("ME"))

# use DendSer methods via seriate
# seriation::get_order(seriate(d,method="Dendser", control=list(hclust=h,cost=costARc)))
DendSer(h,d, cost=costARc)
```

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DendSer	<i>Implements dendrogram seriation</i>
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**Description**

Implements dendrogram seriation.

**Usage**

```
DendSer(
  h,
  ser_weight,
  cost = costBAR,
  node_op = NULL,
  costArg = NULL,
  maxloops = NULL,
  saveinfo = FALSE,
  direction = NULL,
  GW = NULL,
  ...
)
```

**Arguments**

<code>h</code>	An object of class <code>hclust</code>
<code>ser_weight</code>	Used by cost function to evaluate ordering. For <code>cost=costLS</code> , this is a vector of object weights. Otherwise is a dist or symmetric matrix.
<code>cost</code>	Function used to evaluate permutation. Current choices are <code>costLS</code> , <code>costPL</code> , <code>costLPL</code> , <code>costED</code> , <code>costARc</code> , <code>costBAR</code> .
<code>node_op</code>	Function used to reorder branches at a dendrogram node. DendSer picks default depending on cost function. NULL means use default depending on cost.
<code>costArg</code>	Other args for cost function.
<code>maxloops</code>	Maximum number of iterations allowed. NULL means use default depending on cost.
<code>saveinfo</code>	Logical, whether info associated with search is saved.
<code>direction</code>	Order of visiting nodes. Values are "up" or "down", for nodes in order of increasing or decreasing height. NULL means use default depending on cost.
<code>GW</code>	Logical, initial GW step or not. NULL means use default depending on cost.
<code>...</code>	Not used.

**Details**

`costED` uses the Gruvaeus and Wainer 1972 algorithm, as provided by package `gclus`.

**Value**

Numeric vector giving an optimal dendrogram order

**Author(s)**

Catherine Hurley & Denise Earle

## References

Gruvaeus, G. & Wainer, H. (1972), "Two additions to hierarchical cluster analysis", *British Journal of Mathematical and Statistical Psychology*, 25, 200-206.

## See Also

[dser](#)

## Examples

```
d<- dist(iris[,-5])
h <- hclust(d,method="average")
ob<- DendSer(h,d)
opl<- DendSer(h,d,cost=costPL)
plotAsColor(d,ob)

w <- rowSums(iris[,-5])
ow <- DendSer(h,w,cost=costLS) # arranges cases by size, within hclust
stars(iris[ow,-5],labels=NULL, col.stars=cutree(h,3)[ow]) # and color by cluster
#stars(iris[ow,-5],labels=NULL, col.stars=iris[ow,5]) # or by species
```

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dser

*Implements dendrogram seriation. Interface to DendSer.*

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## Description

Implements dendrogram seriation. Interface to DendSer.

## Usage

```
dser(x, ser_weight, cost = costBAR, ...)

## S3 method for class 'data.frame'
dser(x, ser_weight, cost = costBAR, ...)

## S3 method for class 'matrix'
dser(x, ser_weight, cost = costBAR, scale = TRUE, dmethod = "euclidean", ...)

## S3 method for class 'dist'
dser(x, ser_weight, cost = costBAR, hmethod = "average", ...)

## S3 method for class 'hclust'
dser(x, ser_weight, cost = costBAR, ...)
```

**Arguments**

<code>x</code>	Used to select method.
<code>ser_weight</code>	Serialiation weights. For <code>cost=costLS</code> , defaults to first column of matrix <code>x</code> , otherwise to symmetric matrix version of <code>dist d</code> .
<code>cost</code>	Current choices are <code>costLS</code> , <code>costPL</code> , <code>costLPL</code> , <code>costED</code> , <code>costARc</code> , <code>costBAR</code> .
<code>...</code>	Other args
<code>scale</code>	Logical value, controls whether matrix <code>x</code> should be scaled prior to forming <code>dist</code> .
<code>dmethod</code>	Method of <code>dist</code> calculation. See function <code>dist</code> .
<code>hmethod</code>	Method of <code>hclust</code> calculation. See function <code>hclust</code> .

**Details**

When `x` is a matrix or `data.drame`, forms a `dist` of rows using function `dist` with `method = dmethod`.  
 When `x` is a `dist`, forms a `hclust` with `method = hmethod` which is then reordered.

**Value**

Numeric vector giving an optimal dendrogram order

**Methods (by class)**

- `dser(data.frame)`: `dser` method
- `dser(matrix)`: `dser` method
- `dser(dist)`: `dser` method
- `dser(hclust)`: `dser` method

**Author(s)**

Catherine Hurley & Denise Earle

**Examples**

```

iriss <- scale(iris[,-5])
plotAsColor(iriss,order.row=dser(iriss))

w <- prcomp(iris[,-5],scale=TRUE)$x[,1]
h<- hclust(dist(iriss))
h$order <- ow <- dser(h,w,cost=costLS) # arranges cases along first PC, within dendrogram

# compare re-ordered dendrogram to PC scores, w
dev.new(width=10,height=5)
par(mar=c(0,2,1,1))
layout(matrix(1:2, nrow = 2), heights = c(4,1.5) )

```

```

par(cex=.7)
plot(h,main="",xlab="",hang=-1,labels=FALSE)
u <- par("usr")
par(mar=c(1,2,0,1))

plot.new()
par(usr=c(u[1:2],min(w),max(w)))

x<- 1:length(w)
rect(x-.5,0,x+.5,w[ow],col=cutree(h,3)[ow]+1)

```

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plotAsColor

*Function that plots a matrix as a color image*


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### Description

Function that plots a matrix as a color image, in matrix order.

### Usage

```

plotAsColor(
  m,
  order = NULL,
  order.col = order,
  order.row = order,
  rank = FALSE,
  border.color = "grey70",
  labels = FALSE,
  x = 1:ncol(d),
  y = 1:nrow(d),
  ...
)

```

### Arguments

m	Numeric matrix.
order	Default order used for rows and columns.
order.col	Column order.
order.row	Row order
rank	Logical, whether matrix m should be converted to ranks or not.
border.color	Color of border. Null for no border.
labels	If TRUE, add labels obtained from m.
x	X coordinates, passed to image.
y	Y coordinates, passed to image.
...	passed to image.

**See Also**

See Also as [image](#).

**Examples**

```
d<- dist(scale(iris[,-5]))  
plotAsColor(d,dser(d,hmethod="average"))
```

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