

Package ‘dclust’

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Type Package

Title Divisive Hierarchical Clustering

Version 0.1.0

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Description Contains a single function dclust() for divisive hierarchical clustering based on recursive k-means partitioning ($k = 2$). Useful for clustering large datasets where computation of a $n \times n$ distance matrix is not feasible (e.g. $n > 10,000$ records). For further information see Steinbach, Karypis and Kumar (2000) <<http://glaros.dtc.umn.edu/gkhome/fetch/papers/docclusterKDDTMW00.pdf>>.

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Encoding UTF-8

LazyData true

URL <http://github.com/shaunpwilkinson/dclust>

BugReports <http://github.com/shaunpwilkinson/dclust/issues>

Imports openssl, phylogram

RoxygenNote 6.1.1

NeedsCompilation no

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Repository CRAN

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Description

This function recursively splits an $n \times p$ matrix into smaller and smaller subsets, returning a "dendrogram" object.

Usage

```
dclust(x, method = "kmeans", stand = FALSE, ...)
```

Arguments

x	a matrix
method	character string giving the partitioning algorithm to be used to split the data. Currently only "kmeans" is supported (divisive/bisecting k-means; see Steinbach et al. 2000).
stand	logical indicating whether the matrix should be standardised prior to the recursive partitioning procedure. Defaults to FALSE.
...	further arguments to be passed to splitting methods (not including centers if method = kmeans).

Details

This function creates a dendrogram by successively splitting the dataset into smaller and smaller subsets (recursive partitioning). This is a divisive, or "top-down" approach to tree-building, as opposed to agglomerative "bottom-up" methods such as neighbor joining and UPGMA. It is particularly useful for large large datasets with many records ($n > 10,000$) since the need to compute a large $n * n$ distance matrix is circumvented.

If a more accurate tree is required, users can increase the value of `nstart` passed to `kmeans` via the `...` argument. While this can increase computation time, it can improve accuracy considerably.

Value

Returns an object of class "dendrogram".

Author(s)

Shaun Wilkinson

References

Steinbach M, Karypis G, Kumar V (2000). A Comparison of Document Clustering Techniques. Proceedings of World Text Mining Conference, KDD2000, Boston.

Examples

```
## Cluster a subsample of the iris dataset
suppressWarnings(RNGversion("3.5.0"))
set.seed(999)
iris50 <- iris[sample(x = 1:150, size = 50, replace = FALSE),]
x <- as.matrix(iris50[, 1:4])
rownames(x) <- iris50[, 5]
dnd <- dclust(x, nstart = 20)
plot(dnd, horiz = TRUE, yaxt = "n")

## Color labels according to species
rectify_labels <- function(node, x){
  newlab <- factor(rownames(x))[unlist(node, use.names = FALSE)]
  attr(node, "label") <- newlab
  return(node)
}
dnd <- dendrapply(dnd, rectify_labels, x = x)

## Create a color palette as a data.frame with one row for each species
uniqspp <- as.character(unique(iris50$Species))
colormap <- data.frame(Species = uniqspp, color = rainbow(n = length(uniqspp)))
colormap[, 2] <- c("red", "blue", "green")

## Color the inner dendrogram edges
color_dendro <- function(node, colormap){
  if(is.leaf(node)){
    nodecol <- colormap$color[match(attr(node, "label"), colormap$Species)]
    attr(node, "nodePar") <- list(pch = NA, lab.col = nodecol)
    attr(node, "edgePar") <- list(col = nodecol)
  }else{
    spp <- attr(node, "label")
    dominantspp <- levels(spp)[which.max(tabulate(spp))]
    edgecol <- colormap$color[match(dominantspp, colormap$Species)]
    attr(node, "edgePar") <- list(col = edgecol)
  }
  return(node)
}
dnd <- dendrapply(dnd, color_dendro, colormap = colormap)

## Plot the dendrogram
plot(dnd, horiz = TRUE, yaxt = "n")
```

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