Doing More with Dendrograms: The dendextend R Package

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Abstract

The **dendextend** package extends the dendrogram objects in R.

The paper gives a detailed exposition of both the internal structure of the package and the provided user interfaces.

Keywords: Dendrogram, hclust, heirarchical clustering, visualization, tanglegram, R.

1. Introduction

1.1. The `dendrogram` object

The `dendrogram` class provides general functions for handling tree-like structures in R (R Development Core Team 2013). It is intended as a replacement for similar functions in hierarchical clustering and classification/regression trees, such that all of these can use the same engine for plotting or cutting trees.

A dendrogram object represents a tree as a nested `list` object, with various attributes.

Dendrogram has several useful methods bundled with R:

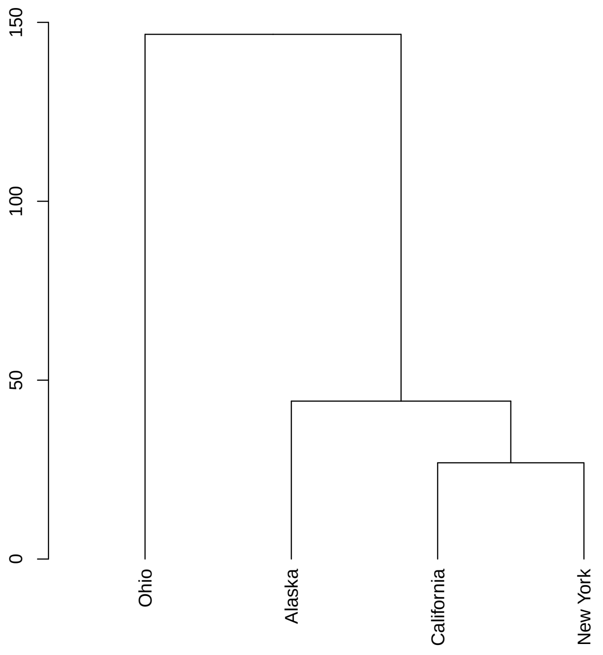
```
methods(class = "dendrogram")

##  [1] [[.dendrogram*         as.hclust.dendrogram*
##  [3] cophenetic.dendrogram* cut.dendrogram*
##  [5] head.dendrogram*       labels.dendrogram*
##  [7] labels<-.dendrogram*   merge.dendrogram*
##  [9] nleaves.dendrogram*    plot.dendrogram*
## [11] print.dendrogram*      reorder.dendrogram*
## [13] rev.dendrogram*        rotate.dendrogram*
## [15] sort.dendrogram*       str.dendrogram*
## [17] trim.dendrogram*       unroot.dendrogram*
##
##    Non-visible functions are asterisked
```

For example, let's create a dendrogram object based on an heirarchical clustering of 4 states in the U.S.:

```
# our data:
data(USArrests)
US_data <- USArrests[c(2, 5, 32, 35), ]
print(US_data)

##            Murder Assault UrbanPop Rape
## Alaska       10.0     263       48 44.5
## California    9.0     276       91 40.6
## New York     11.1     254       86 26.1
## Ohio          7.3     120       75 21.4


hc <- hclust(dist(US_data), "ave")  # create an heirarchical clustering object
dend <- as.dendrogram(hc)
```

Here are some examples for some dendrogram methods:

```
print(dend)

## 'dendrogram' with 2 branches and 4 members total, at height 146.7

labels(dend)

## [1] "Ohio"       "Alaska"     "California" "New York"

str(dend)

## --[dendrogram w/ 2 branches and 4 members at h = 147]
##   |--leaf "Ohio"
##   `--[dendrogram w/ 2 branches and 3 members at h = 44.1]
##      |--leaf "Alaska"
##      `--[dendrogram w/ 2 branches and 2 members at h = 26.9]
##         |--leaf "California"
##         `--leaf "New York"

str(dend[[2]])  # looking at one branch of the dendrogram

## --[dendrogram w/ 2 branches and 3 members at h = 44.1]
##   |--leaf "Alaska"
##   `--[dendrogram w/ 2 branches and 2 members at h = 26.9]
##      |--leaf "California"
##      `--leaf "New York"

plot(dend)
```



You might notice how the order of the items (leaves/terminal nodes) of the dendrogram is different than their order in the table. In order to re-order the rows in the data-table to have the same order as the items in the dendrogram, we can use the `order.dendrogram` function:

```
(new_order <- order.dendrogram(dend))

## [1] 4 1 2 3

# the order of the original items to have them be at the
# same order as they assume in the dendrogram
print(US_data[new_order, ])

##            Murder Assault UrbanPop Rape
## Ohio          7.3     120       75 21.4
## Alaska       10.0     263       48 44.5
## California    9.0     276       91 40.6
## New York     11.1     254       86 26.1
```

In order to see what our dendrogram (`list`) object includes, we need to use the `unclass` function, which will strip away the class atrribute and will allow us to print the list as is, without going through the `print.dendrorgam` method. We can see how each node in the dendrogram/list object has the following (self explaining) attributes:

```
unclass(dend)

## [[1]]
## [1] 4
## attr(,"members")
## [1] 1
## attr(,"height")
## [1] 0
## attr(,"label")
## [1] "Ohio"
## attr(,"leaf")
## [1] TRUE
##
## [[2]]
## [[2]][[1]]
## [1] 1
## attr(,"members")
## [1] 1
## attr(,"height")
## [1] 0
## attr(,"label")
## [1] "Alaska"
## attr(,"leaf")
## [1] TRUE
##
## [[2]][[2]]
## [[2]][[2]][[1]]
## [1] 2
## attr(,"label")
## [1] "California"
## attr(,"members")
## [1] 1
## attr(,"height")
## [1] 0
## attr(,"leaf")
## [1] TRUE
##
## [[2]][[2]][[2]]
## [1] 3
## attr(,"label")
## [1] "New York"
## attr(,"members")
## [1] 1
## attr(,"height")
## [1] 0
## attr(,"leaf")
## [1] TRUE
##
## attr(,"members")
## [1] 2
## attr(,"midpoint")
## [1] 0.5
## attr(,"height")
## [1] 26.9
##
## attr(,"members")
## [1] 3
## attr(,"midpoint")
## [1] 0.75
## attr(,"height")
## [1] 44.14
##
## attr(,"members")
## [1] 4
## attr(,"midpoint")
## [1] 0.875
## attr(,"height")
## [1] 146.7
```

Also, terminal nodes also has the ”leaf” attribute (set to TRUE).

```
names(attributes(dend)[-4])

## [1] "members"  "midpoint" "height"
```

A very important function is `dendrapply`. It applies some function recursively to each node of a dendrogram. It is often used for adjusting attributes of the object, or extracting something from it.

One current ”feature” with this function is that just sending a dendrogram through it will return it with each of its nodes becoming of class ”dendrogram”. For example:

```
# dendrapply(dend, unclass) # in case the
itself <- function(x) x
dend_from_dendrapply <- dendrapply(dend, itself)

# here we must first use unclass since '[[]]' inherits its
# class to the output:
class(unclass(dend)[[2]])

## [1] "list"

class(unclass(dend_from_dendrapply)[[2]])
```

```
## [1] "dendrogram"
```

1.2. Motivation for creating `dendextend`

The `dendrogram` object has several **advantages**:

1. `dendrogram` objects are simply list R objects. This makes their structure very simple to understand by R users.
2. `dendrogram` objects has various methods and functions for using them in R.
3. `dendrogram` objects are relatively simple to manipulte and extend.
4. Other tree objects (such as *hclust*, and objects from the *ape* package) include an *as.dendrogram* method for converting their objects into a dendrogram.

However, even with all of its advantages, the `dendrogram` class in R still lacks various basic features.

The `dendextend` package aims at filling some gaps in base R, by extending the available functions for dendrogram manipulation, statistical analysis, and visualization.

This vignettes Provides a step-by-step description of the functionality provided by the `dendextend` package.

1.3. Installing `dendextend`

To install the stable version from CRAN use:

```
install.packages("dendextend")  # not yet available from CRAN
```

To install the GitHub version use:

```
if (!require("devtools")) install.packages("devtools")
require("devtools")
install_github("dendextend", "talgalili")
```

2. Labels extraction and assignment

2.1. labels in base R

In base R, the `labels` function is intended to find/extract a suitable set of labels from an object for use in printing or plotting, for example. By default, it uses the `names` and `dimnames` functions.

What base R `labels` function is mising is assignment. In the next few examples we will go through different examples of what the `dendextend` package offers for various objects.

Credit: These assignment functions were originally written by Gavin Simpson (in a post on (stackoverflow)), and adopted/adjusted to this package by Tal Galili.

2.2. labels for vectors and matrixes

In base R, for vectors, labels gives the `names` of the object. And if these are missing, then `labels` will give the vector itself as a character vector:

```
x <- 1:3
names(x)  # this vector has no names

## NULL

labels(x)  # this vector has no labels

## [1] "1" "2" "3"
```

Assignment to names is available in base R and works as follows:

```
x <- 1:3
names(x) <- letters[1:3]  # assignment for names is in base R
# both names and labels will give the same result:
names(x)

## [1] "a" "b" "c"

labels(x)

## [1] "a" "b" "c"
```

The new labels assignment function will allow a user to change the labels of the vector just as if it was ”names”:

```
x <- 1:3
labels(x) <- letters[1:3]
names(x)

## [1] "a" "b" "c"

labels(x)

## [1] "a" "b" "c"
```

Labels assignment are also available for matrixes.

2.3. labels for dendrogram objects

2.4. labels for hclust objects

2.5. labels assignment and recycling

3. Summary

The **dendextend** package presented in this paper greatly extends the available functionality of the dendrogram objects in R.

References

R Development Core Team (2013). *R: A Language and Environment for Statistical Computing*. R Foundation for Statistical Computing, Vienna, Austria. ISBN 3-900051-07-0, URL http://www.R-project.org/.

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