How to customise a `pvclust` plot

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2021-06-21

Package `dendextend` can be used to enhance many dendrogram/clustering packages including `pvclust`.

Check this post: http://www.sthda.com/english/wiki/beautiful-dendrogram-visualizations-in-r-5-must-known-methods-unsupervised-machine-learning

Required packages

```
# install.packages(c("pvclust", "dendextend"))
require(dplyr)
```

```
## Loading required package: dplyr
```

```
##
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
require(pvclust)
```

```
## Loading required package: pvclust
```

```
require(dendextend)
```

```
## Loading required package: dendextend
```

```
## Registered S3 method overwritten by 'dendextend':
##   method        from
##   text.pvclust pvclust
```

```
##
## ---------------------
## Welcome to dendextend version 1.15.1
## Type citation('dendextend') for how to cite the package.
##
## Type browseVignettes(package = 'dendextend') for the package vignette.
## The github page is: https://github.com/talgalili/dendextend/
##
## Suggestions and bug-reports can be submitted at: https://github.com/talgalili/dendextend/issues
## Or contact: <tal.galili@gmail.com>
##
##   To suppress this message use:  suppressPackageStartupMessages(library(dendextend))
```

```
## ---------------------
##
## Attaching package: 'dendextend'

## The following object is masked from 'package:stats':
##
##     cutree
```

Reproducible data

Load existing dataset and run the `pvclust` function:

```
data(lung)
set.seed(1234)
result <- pvclust(lung[1:100, 1:10], method.dist="cor",
                  method.hclust="average", nboot=10)
```

```
## Bootstrap (r = 0.5)... Done.
## Bootstrap (r = 0.6)... Done.
## Bootstrap (r = 0.7)... Done.
## Bootstrap (r = 0.8)... Done.
## Bootstrap (r = 0.9)... Done.
## Bootstrap (r = 1.0)... Done.
## Bootstrap (r = 1.1)... Done.
## Bootstrap (r = 1.2)... Done.
## Bootstrap (r = 1.3)... Done.
## Bootstrap (r = 1.4)... Done.
```
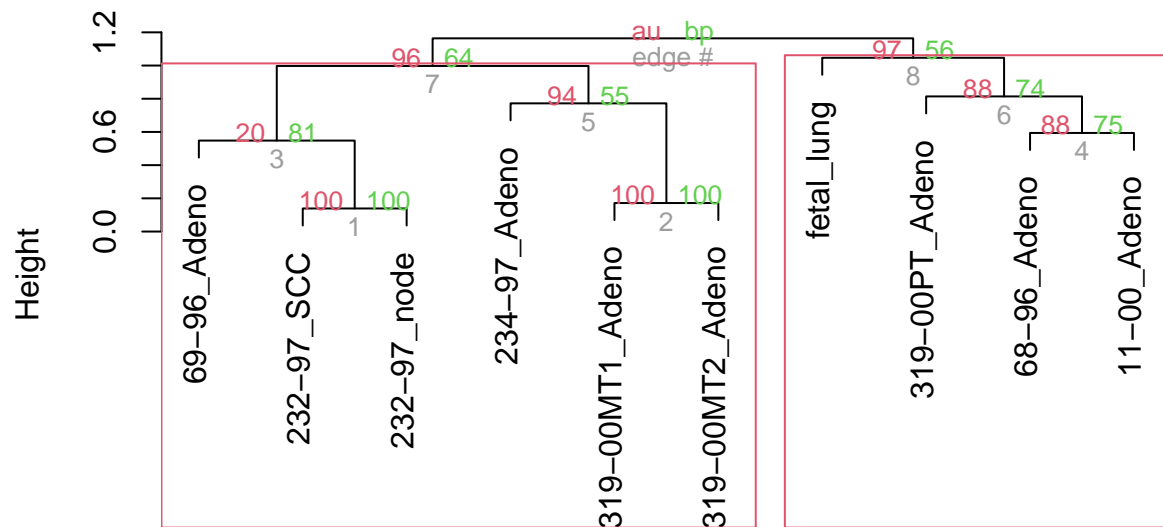
We will also need a vector for the colors, for example:

```
color_values <- rep(c("wheat", "peru","brown"),c(4,3,3))
```

Check the default plot of the result

```
plot(result)
pvrect(result)
```

Cluster dendrogram with p–values (%)

Height

1.2 0.6 0.0

au bp
edge #

96 64
7

97 56
8

20 81
3

94 55
5

88 74
6

100 100
1

100 100
2

88 75
4

69-96_Adeno
232-97_SCC
232-97_node
234-97_Adeno
319-00MT1_Adeno
319-00MT2_Adeno
fetal_lung
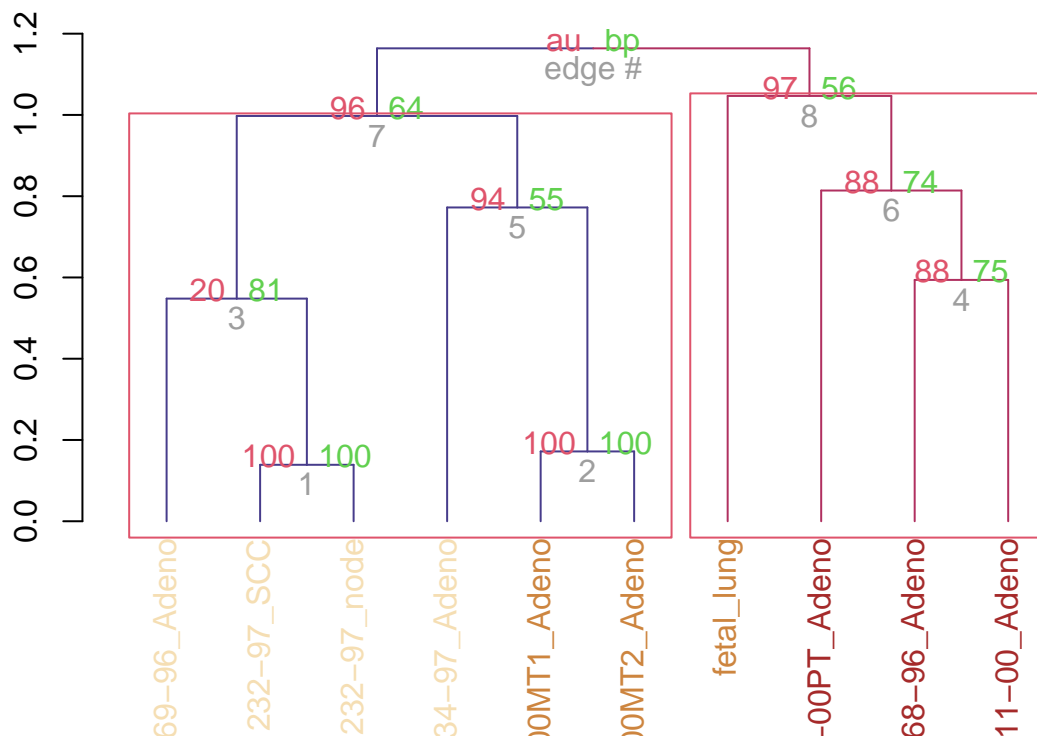319-00PT_Adeno
68-96_Adeno
11-00_Adeno

Distance: correlation
Cluster method: average

Solution

Customised plot :

```
result %>% as.dendrogram %>%
  set("branches_k_color", k = 2, value = c("slateblue4", "maroon")) %>%
  set("labels_colors", value = color_values ) %>%
  plot
result %>% text
result %>% pvrect
```

Debugging info

Check the R session info:

```
sessionInfo()
```

```
## R version 4.1.0 (2021-05-18)
## Platform: x86_64-apple-darwin17.0 (64-bit)
## Running under: macOS Big Sur 10.16
##
## Matrix products: default
## BLAS:    /Library/Frameworks/R.framework/Versions/4.1/Resources/lib/libRblas.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.1/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en_AU.UTF-8/en_AU.UTF-8/en_AU.UTF-8/C/en_AU.UTF-8/en_AU.UTF-8
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
## [1] dendextend_1.15.1 pvclust_2.2-0     dplyr_1.0.7
##
## loaded via a namespace (and not attached):
##  [1] highr_0.9        pillar_1.6.2      compiler_4.1.0    viridis_0.6.1
##  [5] tools_4.1.0      digest_0.6.27     evaluate_0.14     lifecycle_1.0.0
##  [9] tibble_3.1.3     gtable_0.3.0      viridisLite_0.4.0 pkgconfig_2.0.3
```

```
## [13] rlang_0.4.11      DBI_1.1.1        yaml_2.2.1         xfun_0.24
## [17] gridExtra_2.3     stringr_1.4.0    knitr_1.33         generics_0.1.0
## [21] vctrs_0.3.8       grid_4.1.0       tidyselect_1.1.1  glue_1.4.2
## [25] R6_2.5.0          fansi_0.5.0      rmarkdown_2.9     purrr_0.3.4
## [29] ggplot2_3.3.5     magrittr_2.0.1   scales_1.1.1      ellipsis_0.3.2
## [33] htmltools_0.5.1.1 assertthat_0.2.1 colorspace_2.0-2 utf8_1.2.2
## [37] stringi_1.7.3     munsell_0.5.0    crayon_1.4.1
```