

wholebrain dendrogram

load projection densities from supplemental table and try to plot a dendrogram.

load data

```
data<-read.csv(file = "~/postdoc2/DCN_tracing/m_files/anterogradetracing_round8_10/test.csv")
data<-data[,1:23]
```

```
library(ComplexHeatmap)
```

```
## Loading required package: grid
```

```
## =====
```

```
## ComplexHeatmap version 2.2.0
```

```
## Bioconductor page: http://bioconductor.org/packages/ComplexHeatmap/
```

```
## Github page: https://github.com/jokergoo/ComplexHeatmap
```

```
## Documentation: http://jokergoo.github.io/ComplexHeatmap-reference
```

```
##
```

```
## If you use it in published research, please cite:
```

```
## Gu, Z. Complex heatmaps reveal patterns and correlations in multidimensional
```

```
## genomic data. Bioinformatics 2016.
```

```
## =====
```

```
library(dendsort)
```

```
library(dendextend)
```

```
##
```

```
## -----
```

```
## Welcome to dendextend version 1.13.4
```

```
## 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
```

```
library(circlize)
```

```
## =====
```

```
## circlize version 0.4.8
```

```
## CRAN page: https://cran.r-project.org/package=circlize
```

```

## Github page: https://github.com/jokergoo/circlize
## Documentation: http://jokergoo.github.io/circlize_book/book/
##
## If you use it in published research, please cite:
## Gu, Z. circlize implements and enhances circular visualization
##   in R. Bioinformatics 2014.
## =====

library(pvclust)

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

result <- pvclust(as.matrix(data), nboot=10000, method.hclust = "complete", method.dist = function(z){as.

## 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.

pal=c('#00A651', '#EC008C', '#0072BD', '#00AEEF')
sites=as.factor(c(rep("Meda",5),rep("Medp",5),rep("Int",6),rep("Lat",7)))
levels(sites)<-c(1,2,3,4)

bars=data.frame(animal=pal[(sites)]);

dend <- (as.dendrogram(result))
dend %>% pvclust_show_signif_gradient(result, signif_type = 'au',
                                     signif_col_fun = colorRampPalette(c('white', 'black')) %>%
                                     set("nodes_pch", 19) %>%
                                     set("branches_lwd", 2) %>%
                                     plot()
colored_bars(colors = bars, dend = dend, sort_by_labels_order = TRUE, y_shift=0.02)

result %>% text

```

