

Amap Package

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1 Overview

Amap package includes standard hierarchical clustering and k-means. We optimize implementation (with a parallelized hierarchical clustering) and allow the possibility of using different distances like Eulidean or Spearman (rank-based metric).

We implement a principal component analysis (with robust methods).

We provide several functions for conversion. Specially to import data from Xcluster¹ or Cluster² software (very used for Gene's expression analysis), and to export clusters to TreeView or Freeview visualization software.

2 Usage

2.1 Clustering

The standard way of building a hierarchical clustering:

```
> library(amap)
```

```
Loading required package: Biobase
```

```
Welcome to Bioconductor
```

```
Vignettes contain introductory material.
```

¹<http://genome-www.stanford.edu/~sherlock/cluster.html>

²<http://rana.lbl.gov/EisenSoftware.htm>

To view, simply type 'openVignette()' or start with 'help(Biobase)'.
For details on reading vignettes, see the openVignette help page.

```
> data(USArrests)
> h = hcluster(USArrests)
> plot(h)
```

Or for the “heatmap”:

```
> heatmap(as.matrix(USArrests), hclustfun = hcluster, distfun = function(u) {
+   u
+ })
```

On a multiprocessor computer:

```
> h = hclusterpar(USArrests, nbproc = 4)
```

The K-means clustering:

```
> Kmeans(USArrests, centers = 3, method = "correlation")
```

2.2 Robust tools

A robust variance computation:

```
> data(lubisch)
> lubisch <- lubisch[, -c(1, 8)]
> varrob(scale(lubisch), h = 1)
```

A robust principal component analysis:

```
> p <- acpgen(lubisch, h1 = 1, h2 = 1/sqrt(2))
> plot(p)
```

Another robust pca:

```
> p <- acprob(lubisch, h = 4)
> plot(p)
```

2.3 Building hierarchical clustering with another software

We made these tools

r2xcluster Write data table to Xcluster file format

```
> r2xcluster(USArrests, file = "USArrests_xcluster.txt")
```

r2cluster Write data table to Cluster file format

```
> r2cluster(USArrests, file = "USArrests_xcluster.txt")
```

xcluster Hierarchical clustering (need Xcluster tool by Gavin Sherlock)

```
> h.xcl=xcluster(USArrests)
> plot(h.xcl)
```

It is roughly the same as

```
> r2xcluster(USArrests,file='USArrests_xcluster.txt')
> system('Xcluster -f USArrests_xcluster.txt -e 0 -p 0 -s 0 -l 0')
> h.xcl=xcluster2r('USArrests_xcluster.gtr',labels=TRUE)
```

xcluster2r Importing Xcluster/Cluster output

2.4 Using other visualization softwares

We now consider that we have an object of the type produced by 'hclust' (or a hierarchical cluster imported with previous functions) like:

```
> hr = hcluster(USArrests)
> hc = hcluster(t(USArrests))
```

hc2Newick Export hclust objects to Newick format files

```
> write(hc2Newick(hr), file = "hclust.newick")
```

r2gtr,r2atr,r2cdt Export hclust objects to Freeview or Treeview visualization softwares

```
> r2atr(hc, file = "cluster.atr")
> r2gtr(hr, file = "cluster.gtr")
> r2cdt(hr, hc, USArrests, file = "cluster.cdt")
```

hclust2treeview Clustering and Export hclust objects to Freeview or Treeview visualization softwares

```
> hclust2treeview(USArrests, file = "cluster.cdt")
```

```
[1] 1
```

3 See Also

Theses examples can be tested with command `demo(amap)`.

All functions has got man pages, try `help.start()`.

Robust tools has been published: [2] and [1].

Amap aims to interact with other softwares, some of them:

xcluster made by Gavin Scherlock, <http://genome-www.stanford.edu/~sherlock/cluster.html>

Cluster, Treeview made by Michael Eisen, <http://rana.lbl.gov/EisenSoftware.htm>

Freeview made by Marco Kavcic and Blaz Zupan, <http://magix.fri.uni-lj.si/freeview>

References

- [1] H. Caussinus, M. Fekri, S. Hakam, and A. Ruiz-Gazen. A monitoring display of multivariate outliers. *Computational Statistics and Data Analysis*, 44:237–252, October 2003.
- [2] H. Caussinus, S. Hakam, and A. Ruiz-Gazen. Projections révélatrices contrôlées. recherche d’individus atypiques. *Revue de Statistique Appliquée*, 50(4), 2002.