Ctc Package

Antoine Lucas

October 29, 2024

Contents

1 Overview **1**

2 Aim **1**

3 Usage **1**
3.1 Building hierarchical clustering with another software 2
3.2 Using other visualization softwares 3

4 See Also **3**

1 Overview

`Ctc` package provides several functions for conversion. Specially to export and import data from Xcluster[1] or Cluster[2] software (very used for Gene's expression analysis), and to export clusters to TreeView or Freeview visualization software.

2 Aim

- To explore clusters made by Xcluster and Cluster .
- To cluster data with Xcluster (it requires very low memory usage) and analyze the results with R. Warning: results are not exactly the same as hclust results with R.

3 Usage

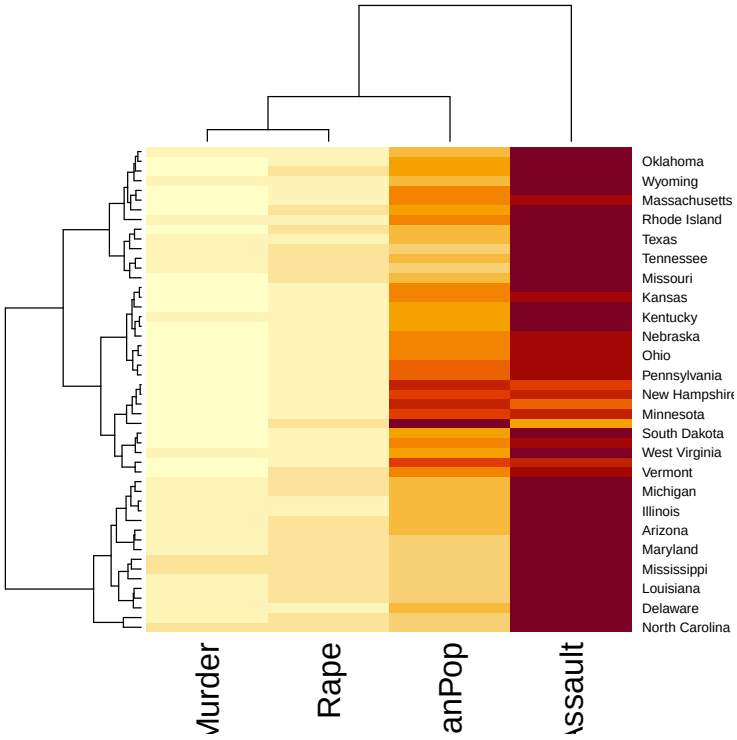
Standard way of building a hierarchical clustering with R is with this command:

```
> data(USArrests)
> h = hclust(dist(USArrests))
> plot(h)
```

Or for the "heatmap":

[1] `http://genome-www.stanford.edu/~sherlock/cluster.html`
[2] http://rana.lbl.gov/EisenSoftware.htm

```
> heatmap(as.matrix(USArrests))
```



3.1 Building hierarchical clustering with another software

We made these tools

r2xcluster Write data table to Xcluster file format

```
> library(ctc)
> 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 roughtly 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

3.2 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 = hclust(dist(USArrests))
> hc = hclust(dist(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
```

4 See Also

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

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

Ctc 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

If you want to cite amap or ctc in a publication, use :

Antoine Lucas and Sylvain Jasson, *Using amap and ctc Packages for Huge Clustering*, R News, 2006, vol 6, issue 5 pages 58-60.