

# Ctc Package

Antoine Lucas

October 28, 2009

## Contents

<b>1 Overview</b>	<b>1</b>
<b>2 Aim</b>	<b>1</b>
<b>3 Usage</b>	<b>1</b>
3.1 Building hierarchical clustering with another software . . . . .	2
3.2 Using other visualization softwares . . . . .	3
<b>4 See Also</b>	<b>3</b>

## 1 Overview

Ctc package provides several functions for conversion. Specially to export and import data from Xcluster<sup>1</sup> or Cluster<sup>2</sup> 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:

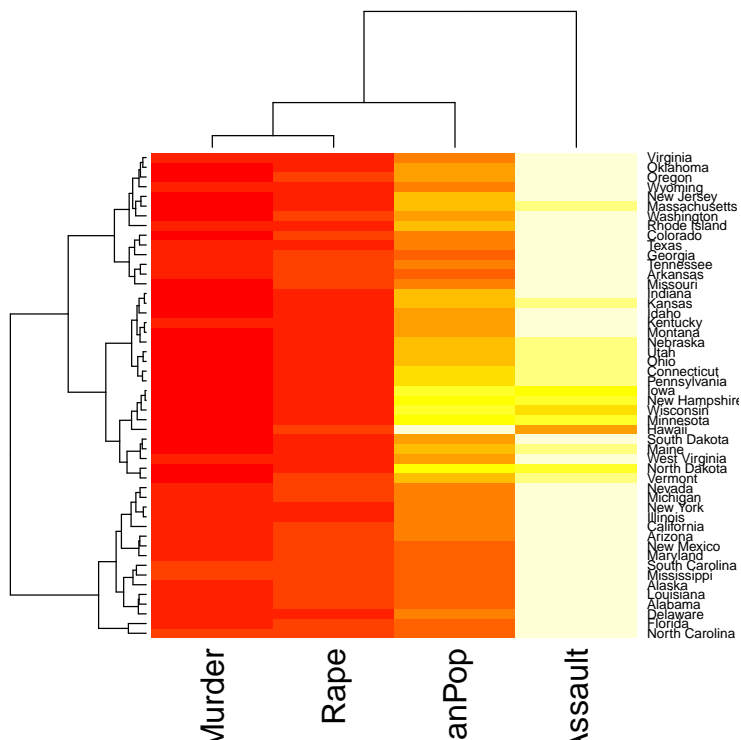
```
> data(USArrests)
> h = hclust(dist(USArrests))
> plot(h)
```

Or for the "heatmap":

---

<sup>1</sup><http://genome-www.stanford.edu/~sherlock/cluster.html>  
<sup>2</sup><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 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

## 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.