Amap Package

Antoine Lucas

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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 robusts methods).

2 Usage

2.1 Clustering

The standard way of building a hierarchical clustering:

- > library(amap)
 > data(USArrests)
 > h = hcluster(USArrests)
- > n = ncluster(USArrests,
- > plot(h)

Or for the "heatmap":

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

On a multiprocessor computer:

> h = hcluster(USArrests,nbproc=4)

The K-means clustering:

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

2.2 Robust tools

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A robust variance computation:
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> 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)
```

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].

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.