

Package ‘rCUR’

February 20, 2015

Type Package

Title CUR decomposition package

Version 1.3

Date 2012-03-06

Author Andras Bodor, Norbert Solymosi

Maintainer Andras Bodor <bodri.mh3@gmail.com>

Depends R (>= 2.10.0), MASS, methods, Matrix, lattice

Description Functions and objects for CUR matrix decomposition.

License GPL (>= 2)

LazyLoad yes

Repository CRAN

Date/Publication 2012-07-02 13:20:21

NeedsCompilation no

R topics documented:

rCUR-package	2
CUR	3
CURobj-class	5
getC	6
getError	7
getR	8
getU	8
leverage	9
plotLeverage	10
STTa	11
STTm	11
topLeverage	12

Index	14
--------------	-----------

rCUR-package

CUR matrix decomposition package

Description

In modern data mining tasks the user has often matrices with huge number of rows and/or columns as the base of analysis. One way of the analysis of this type of huge datasets is to reduce their dimensions. Principal component analysis (PCA) is a widely used tool for such data analysis. PCA produced singular vectors are mathematical abstractions and hardly interpretable on the field from which the data are drawn. Mahoney & Drineas (2009) proposed a method the CUR matrix decomposition what decreases the dimensions as well, but the resulting matrices are interpretable on the application area. This package contains functions and objects to help doing CUR matrix decomposition.

Details

Package: rCUR
Type: Package
Version: 1.0
Date: 2011-03-31
License: GPL (>=2)
LazyLoad: yes

Author(s)

Andras Bodor, Norbert Solymosi
Maintainer: Andras Bodor <bodri.mh3@gmail.com>

References

Mahoney M. W. and Drineas P. (2009) CUR matrix decompositions for improved data analysis. PNAS, 106(3):697-702
Andras Bodor, Istvan Csabai, Michael W Mahoney and Norbert Solymosi rCUR:an R package for CUR matrix decomposition BMC Bioinformatics 2012, 13:103 doi:10.1186/1471-2105-13-103
<http://www.cs.rpi.edu/~boutsch/files/AlgorithmCUR.m>

Examples

```
library(rCUR)
library(lattice)

data(STTm)
data(STTa)
```

```

n = 27
res = CUR(STTm, 31, n, 4)

plotLeverage(res, C=FALSE, top.n=n, xlab='Gene ID', las=1, top.col='black',
  top.pch=16, ul.col='black', ul.lty=2, col='grey')

PCA01 = prcomp(STTm, scale=TRUE)

top.idx = topLeverage(res, C=FALSE, top.n=n, sort=FALSE)
top.STTm = STTm[top.idx,]
PCA02 = prcomp(top.STTm, scale=TRUE)

t.top.STTm = t(top.STTm)
x = 1:dim(t.top.STTm)[1]
y = 1:dim(t.top.STTm)[2]

ann.tab = STTa[top.idx,]
genes = as.character(ann.tab$Gene)
genes[genes==''] = as.character(ann.tab[genes=='', 'Hs'])

op = par(mar=c(3.5, 0, 0, 5) + 0.1)
image(x, y, t.top.STTm, col=rev(gray(0:256/300)), axes=FALSE, xlab='',
  ylab='')
axis(1, at=c(10,22,31), labels=c('GIST', 'LEIO', 'SARC'), tick=FALSE,
  las=2, cex=0.6, line=-0.8)
axis(4, at=1:length(genes), labels=genes, tick=FALSE, las=1, cex=0.6,
  line=-0.8)
par(op)

PCAs = rbind(PCA01$rotation[,c(1,2)], PCA02$rotation[,c(1,2)])
group = rownames(PCAs)
pchs = ifelse(group=='GIST', 16, 0)
pchs = ifelse(group=='LEIO', 17, pchs)
pchs = ifelse(group=='SARC', 18, pchs)
PCAs = data.frame(PC1=PCAs[,1], PC2=PCAs[,2],
  lab=c(rep('all',31),rep('selected',31)), group, pchs)

xyplot(PC2 ~ PC1 | lab, data = PCAs, pch=pchs, cex=1.0, col='black',
  fill='black', key = list(space = "bottom", text = list(levels(PCAs$group))),
  points=TRUE, pch=c(16, 17, 18), fill='black', columns=3, just=1))

```

CUR

Function to perform CUR matrix decomposition

Description

By the function the CUR matrix decomposition can be done obtaining a [CURobj-class](#) object

Usage

```
CUR(A, c=dim(A)[2], r=dim(A)[1], k=NULL, sv=NULL,
     method="random", alpha=1, weighted=FALSE, beta=4,
     matrix.return=TRUE, error.return=FALSE)
```

Arguments

A	a matrix for decomposition with m rows and n columns
c	column number to be selected from matrix A. Default: all columns, in this case column selection is skipped.
r	row number to be selected from matrix A. Default: all rows, in this case row selection is skipped.
k	rank parameter with perhaps $k \ll \min(m,n)$. Default: if not supplied, singular values accounting for 80% of the sum of the singular values is selected.
sv	the singular value decomposition of A. It is the most expensive part of the computation, so it can be supplied, if already available. Default: svd is computed on the fly.
method	the method, used, to select the rows. Possible values are random the original method in [Mahoney and Drineas], rows and columns are selected randomly, with the probability of selection proportional to the leverage score exact.num.random like random, but it is guaranteed, that exactly r rows and c columns are selected top.scores the rows and columns with the highest leverage scores are returned deterministically ortho.top.scores those rows and columns are selected, where the linear combination of the leverage score and orthogonality to the subspace of previously selected items is maximal. See parameter alpha. highest.ranks rows and columns with the highest rank of leverage score for some rank parameter are selected. Every possible value is tried up to the value of k. k must be larger than 1.
alpha	if method="ortho.top.scores", the coefficient of orthogonality in the linear combination. alpha=0 is equivalent to method="top.scores". The coefficient of the leverage score is always 1. Default: 1. Should be positive.
weighted	if true, leverage scores are computed with weighting by the singular values. In this case k should be set to its default value. Not used, if method=highest.ranks. Best used whith method=top.scores. See parameter beta. Default: FALSE.
beta	if weighted=TRUE, leverage scores are computed with weighting of the singular values raised to the power of beta. Default: 4.
matrix.return	if TRUE, the matrices C, U, R are returned. If matrix.return is FALSE, U is not computed, which can be expensive, if r and c are large. Default: TRUE.
error.return	if true, the Frobenius norm of the difference between the original matrix and the CUR approximation is returned. Effective only if matrix.return is TRUE. Default: FALSE.

Value

The function produces an object of [CURobj-class](#).

References

Mahoney M. W. and Drineas P. (2009) CUR matrix decompositions for improved data analysis. PNAS, 106(3):697-702

Andras Bodor, Istvan Csabai, Michael W Mahoney and Norbert Solymosi rCUR:an R package for CUR matrix decomposition BMC Bioinformatics 2012, 13:103 doi:10.1186/1471-2105-13-103

The development was initially based on the Matlab code of Christos Boutsidis:
<http://www.cs.rpi.edu/~boutsch/files/AlgorithmCUR.m>

Examples

```
data(STTm)
CUR.results <- CUR(STTm, 31, 12, 3)
```

CURobj-class

Class "CURobj"

Description

Class for the results of CUR decomposition performed by the function [CUR](#)

Objects from the Class

Objects can be created by calls to the function [CUR](#)

Slots

C: matrix C

U: matrix U

R: matrix R

C.leverage.score: leverage scores of the columns

R.leverage.score: leverage scores of the rows

C.index: index of columns selected for C

R.index: index of rows selected for R

Error: the error of the approximation

Methods

getC retrieves the matrix C from object of CURobj-class

getU retrieves the matrix U from object of CURobj-class

getR retrieves the matrix R from object of CURobj-class

getError retrieves the error from object of CURobj-class

leverage retrieves the vector of leverage scores from object of CURobj-class

topLeverage retrieves the top elements of leverage scores from object of CURobj-class

plotLeverage plot the leverage scores of CURobj-class object

References

Mahoney M. W. and Drineas P. (2009) CUR matrix decompositions for improved data analysis. PNAS, 106(3):697-702

Andras Bodor, Istvan Csabai, Michael W Mahoney and Norbert Solymosi rCUR:an R package for CUR matrix decomposition BMC Bioinformatics 2012, 13:103 doi:10.1186/1471-2105-13-103

Examples

```
showClass("CURobj")
```

getC

Retrieve matrix C from CURobj-class

Description

Retrieve matrix C from [CURobj-class](#)

Usage

```
getC(object)
```

Arguments

object object of class [CURobj-class](#)

Value

a matrix with component C of CUR

References

Mahoney M. W. and Drineas P. (2009) CUR matrix decompositions for improved data analysis. PNAS, 106(3):697-702

Andras Bodor, Istvan Csabai, Michael W Mahoney and Norbert Solymosi rCUR:an R package for CUR matrix decomposition BMC Bioinformatics 2012, 13:103 doi:10.1186/1471-2105-13-103

Examples

```
data(STTm)
res <- CUR(STTm, 31, 12, 3)
getC(res)
```

`getError`

Retrieve the error of the approximation from CURobj-class

Description

Retrieve the error of the approximation from [CURobj-class](#)

Usage

```
getError(object)
```

Arguments

`object` object of class [CURobj-class](#)

Value

The Frobenius norm of the difference between the original matrix and the CUR approximation, or NULL, if CUR was called with `error.return=FALSE` (default).

References

Mahoney M. W. and Drineas P. (2009) CUR matrix decompositions for improved data analysis. PNAS, 106(3):697-702

Andras Bodor, Istvan Csabai, Michael W Mahoney and Norbert Solymosi rCUR:an R package for CUR matrix decomposition BMC Bioinformatics 2012, 13:103 doi:10.1186/1471-2105-13-103

Examples

```
data(STTm)
res <- CUR(STTm, 31, 12, 3, error.return=TRUE)
getError(res)
```

getR	<i>Retrieve matrix R from CURobj-class</i>
------	--

Description

Retrieve matrix R from [CURobj-class](#)

Usage

```
getR(object)
```

Arguments

object object of class [CURobj-class](#)

Value

a matrix with component R of CUR

References

Mahoney M. W. and Drineas P. (2009) CUR matrix decompositions for improved data analysis. PNAS, 106(3):697-702

Andras Bodor, Istvan Csabai, Michael W Mahoney and Norbert Solymosi rCUR:an R package for CUR matrix decomposition BMC Bioinformatics 2012, 13:103 doi:10.1186/1471-2105-13-103

Examples

```
data(STTm)
res <- CUR(STTm, 31, 12, 3)
getR(res)
```

getU	<i>Retrieve matrix U from CURobj-class</i>
------	--

Description

Retrieve matrix U from [CURobj-class](#)

Usage

```
getU(object)
```

Arguments

object object of class [CURobj-class](#)

Value

a matrix with component U of CUR

References

Mahoney M. W. and Drineas P. (2009) CUR matrix decompositions for improved data analysis. PNAS, 106(3):697-702

Andras Bodor, Istvan Csabai, Michael W Mahoney and Norbert Solymosi rCUR:an R package for CUR matrix decomposition BMC Bioinformatics 2012, 13:103 doi:10.1186/1471-2105-13-103

Examples

```
data(STTm)
res <- CUR(STTm, 31, 12, 3)
getU(res)
```

leverage

Retrieve leverage scores from CURobj-class

Description

Retrieve leverage scores from [CURobj-class](#)

Usage

```
leverage(object, C = TRUE)
```

Arguments

object	object of class CURobj-class
C	logical, if it is TRUE, then the obtained leverage scores belongs to columns, if FALSE, then to rows

Value

the function returns a numerical vector of leverage scores

References

Mahoney M. W. and Drineas P. (2009) CUR matrix decompositions for improved data analysis. PNAS, 106(3):697-702

Andras Bodor, Istvan Csabai, Michael W Mahoney and Norbert Solymosi rCUR:an R package for CUR matrix decomposition BMC Bioinformatics 2012, 13:103 doi:10.1186/1471-2105-13-103

Examples

```
data(STTm)
res <- CUR(STTm, 31, 12, 3)
leverage(res, C=TRUE)
```

plotLeverage *Function to plot leverage scores*

Description

Function to plot the individual values and uniform level of leverage scores. The most influential features may be highlighted.

Usage

```
plotLeverage(x, C=TRUE, mplr=1000, top.n=100,  
             top.col='red', top.pch=16, ul.col='red', ul.lty=2, ...)
```

Arguments

x	object of class CURobj-class
C	logical, if it is TRUE, then calculated the rank for the leverage scores belongs to columns, if FALSE, then to rows
mplr	multiplier of leverage scores
top.n	number of highlighting items from top of leverage score list
top.col	color of highlighting points
top.pch	pch of highlighting points, see <code>par()</code>
ul.col	color of the line of leverage score uniform level
ul.lty	line type of leverage score uniform level
...	further graphical parameters of function <code>plot()</code>

References

Mahoney M. W. and Drineas P. (2009) CUR matrix decompositions for improved data analysis. PNAS, 106(3):697-702

Andras Bodor, Istvan Csabai, Michael W Mahoney and Norbert Solymosi rCUR:an R package for CUR matrix decomposition BMC Bioinformatics 2012, 13:103 doi:10.1186/1471-2105-13-103

Examples

```
data(STTm)  
res <- CUR(STTm, 31, 12, 3)  
plotLeverage(res, C=FALSE, top.n=10, las=1)
```

STTa

Annotation data.frame of soft tissue tumour gene expression dataset

Description

Annotation data for STTm soft tissue tumour gene expression dataset

Format

A data frame with 5520 observations on the following 4 variables.

ID identification number of gene

Gene gene symbol

Hs UniGene ID

Descr function description of transcriptum of gene

Source

The original, full dataset is downloadable from the Gene Expression Omnibus database (GSE3443) and from Stanford Microarray Database (<http://smd.stanford.edu>).

References

Nielsen T. et al. (2002) Molecular characterisation of soft tissue tumours: A gene expression study. *Lancet* 359:1301-1307.

Mahoney M. W. and Drineas P. (2009) CUR matrix decompositions for improved data analysis. *PNAS*, 106(3):697-702

Andras Bodor, Istvan Csabai, Michael W Mahoney and Norbert Solymosi rCUR:an R package for CUR matrix decomposition *BMC Bioinformatics* 2012, 13:103 doi:10.1186/1471-2105-13-103

Examples

```
data(STTa)
```

STTm

Soft tissue tumour dataset

Description

STTm is a matrix containing a subset of the soft tissue tumour gene expression study dataset published by Nielsen et al. (2002). The matrix constructed from 31 columns and 5520 rows, samples and genes respectively. Samples came from three different tumour types: gastrointestinal stromal tumor (GIST), leiomyosarcoma (LEIO) and synovial sarcoma (SARC).

Source

The original, full dataset is downloadable from the Gene Expression Omnibus database (GSE3443) and from Stanford Microarray Database (<http://smd.stanford.edu>).

References

Nielsen T. et al. (2002) Molecular characterisation of soft tissue tumours: A gene expression study. *Lancet* 359:1301-1307.

Mahoney M. W. and Drineas P. (2009) CUR matrix decompositions for improved data analysis. *PNAS*, 106(3):697-702

Andras Bodor, Istvan Csabai, Michael W Mahoney and Norbert Solymosi rCUR:an R package for CUR matrix decomposition *BMC Bioinformatics* 2012, 13:103 doi:10.1186/1471-2105-13-103

Examples

```
data(STTm)
```

topLeverage	<i>Function to obtain indexes of the most influential features due to leverage score</i>
-------------	--

Description

The function sort the features (rows or columns) based on their influence (leverage score) and list out the indexes of the top valued items

Usage

```
topLeverage(object, C=TRUE, top.n=100, sort=TRUE)
```

Arguments

object	object of class CURobj-class
C	logical, if it is TRUE, then calculated the rank for the leverage scores belongs to columns, if FALSE, then to rows
top.n	number of indexes to list
sort	logical, if TRUE the indexes are sorted increasing

Value

The function returns a numerical vector of indexes of the most influential features

References

Mahoney M. W. and Drineas P. (2009) CUR matrix decompositions for improved data analysis. PNAS, 106(3):697-702

Andras Bodor, Istvan Csabai, Michael W Mahoney and Norbert Solymosi rCUR:an R package for CUR matrix decomposition BMC Bioinformatics 2012, 13:103 doi:10.1186/1471-2105-13-103

Examples

```
data(STTm)
res <- CUR(STTm, 3, 31, 12)
topLeverage(res, top.n=10)
```

Index

*Topic **classes**

CURobj-class, 5

*Topic **datasets**

STTa, 11

STTm, 11

*Topic **prcomp**

CUR, 3

rCUR-package, 2

*Topic **svd**

CUR, 3

rCUR-package, 2

CUR, 3, 5

CURobj-class, 3, 5, 5, 6–10, 12

getC, 6, 6

getC, CURobj-method (CURobj-class), 5

getError, 6, 7

getError, CURobj-method (CURobj-class), 5

getR, 6, 8

getR, CURobj-method (CURobj-class), 5

getU, 6, 8

getU, CURobj-method (CURobj-class), 5

leverage, 6, 9

leverage, CURobj-method (CURobj-class), 5

plotLeverage, 6, 10

plotLeverage, CURobj-method
(CURobj-class), 5

rCUR (rCUR-package), 2

rCUR-package, 2

STTa, 11

STTm, 11

topLeverage, 6, 12

topLeverage, CURobj-method
(CURobj-class), 5