

# Package ‘TaxicabCA’

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**Type** Package

**Title** Taxicab Correspondence Analysis

**Version** 0.1.0

**Suggests** GA, testthat

**Imports** grDevices, graphics, stats, utils

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**Description** Computation and visualization of Taxicab Correspondence Analysis, Choulakian (2006) <doi:10.1007/s11336-004-1231-4>. Classical correspondence analysis (CA) is a statistical method to analyse 2-dimensional tables of positive numbers and is typically applied to contingency tables (Benzecri, J.-P. (1973). L'Analyse des Donnees. Volume II. L'Analyse des Correspondances. Paris, France: Dunod). Classical CA is based on the Euclidean distance. Taxicab CA is like classical CA but is based on the Taxicab or Manhattan distance. For some tables, Taxicab CA gives more informative results than classical CA.

**License** GPL (>= 2)

**LazyData** true

**RoxygenNote** 6.0.1

**NeedsCompilation** no

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## CombineCollinearRowsCols

*Removes rows and columns of zeros and optionnally, row or column duplicates*

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### Description

Removes rows and columns of zeros and optionnally, row or column duplicates

### Usage

```
CombineCollinearRowsCols(Y, rows = F, cols = F)
```

### Arguments

Y	A matrix or an object that can be coerced to a matrix
rows	Logical: Will duplicate rows be removed?
cols	Logical: Will duplicate columns be removed?

### Details

Rows and columns of zeros will be removed.

A matrix of zeros will be returned as matrix with 0 row and 0 column.

If rows 1,2,3 are combined, the name of row 1 is kept. Similarly for columns.

### Value

A matrix with rows and columns removed as requested

**Examples**

```

CombineCollinearRowsCols(matrix(1:3,nrow=3,ncol=2),cols=TRUE)

CombineCollinearRowsCols(cbind(matrix(1:3,nrow=3,ncol=2),rep(0,3)),cols=TRUE)

CombineCollinearRowsCols(cbind(matrix(1:3,nrow=3,ncol=2),rep(0,3)))

CombineCollinearRowsCols(matrix(0,nrow=3,ncol=3))

CombineCollinearRowsCols(rodent,TRUE,FALSE)

```

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ComputeLambda	<i>L1 norm of a projection</i>
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**Description**

L1 norm of a projection

**Usage**

```
ComputeLambda(uFT, pResidual)
```

**Arguments**

uFT	A vector of 0s and 1s of length nc: $(-1)^{uFT}$ is a unit vector in Linf norm
pResidual	A matrix with nc columns

**Details**

This function is for internal usage only.

**Value**

L1 norm of the pResidual x  $(-1)^{uFT}$

**Examples**

```
ComputeLambda(uFT=c(FALSE,TRUE,FALSE),pResidual=matrix(1:15,nr=5,nc=3))
```

---

CreateAllBinaries      *Create all  $2^n$  n-tuples of ab[1] and ab[2]*

---

### Description

Create all  $2^n$  n-tuples of ab[1] and ab[2]

### Usage

```
CreateAllBinaries(n = 1, ab = c(0, 1))
```

### Arguments

n	An integer > 0
ab	A vector of length 2

### Details

This function is for internal usage only.

### Value

a  $n \times 2^n$  matrix

### Examples

```
CreateAllBinaries(3,c(0,1))
```

---

JitterPosition      *Moves points that are close together*

---

### Description

Moves points that are close together

### Usage

```
JitterPosition(x, y, jitterDefault = 0.01, Near = 0.045)
```

### Arguments

x	The x-coordinates of the points
y	The y-coordinates of the points
jitterDefault	A positive number controlling the maximum jitter
Near	A positive number controlling the definition of "near"

**Details**

This function is for internal usage only.

**Value**

A list giving the new x and y coordinates, and, for each point, its number neighbours and a suggested relative size for the plotting symbol

**Examples**

```
JitterPosition(c(1:5,2,2,4,4,4),c(1:5,2,2,4,4,4))
```

---

ListToObjects

*Extract objects from a list*

---

**Description**

Extract objects from a list to the global environment

**Usage**

```
ListToObjects(L, envir = .GlobalEnv)
```

**Arguments**

L	A list
envir	The environment into which variables are created

**Details**

This function is for internal usage only.

**Value**

No return

**Examples**

```
ListToObjects(list(x=5,A="Hello",M=matrix(1:8,nr=2)),envir=.GlobalEnv)
```

---

milazzese

*Counts of archeological objects*

---

### Description

Frequency of object types across the 19 huts of the P. Milazzese settlement in north-eastern Sicily.

### Usage

```
data(milazzese)
```

### Format

A data frame of frequencies with 31 rows and 19 columns

- Columns: Hut
- Rows: Object Type

### Source

Alberti, G., 2013, Making Sense of Contingency Tables in Archaeology: the Aid of Correspondence Analysis to Intra-Site Activity Areas Research, *Journal of Data Science* 11, 479-499

### Examples

```
tca(milazzese, nAxes=6, algorithm = "criss-cross")
```

---

plot.tca

*Creates a symmetric plot from a tca-class object*

---

### Description

Creates a symmetric plot from a tca-class object

### Usage

```
## S3 method for class 'tca'  
plot(x, y = NULL, axes = c(1, 2), labels.rc = c(0, 1),  
      col.rc = c("blue", "red"), pch.rc = c(16, 21, 17, 24), mass.rc = c(F,  
      F), cex.rc = c(NA, NA), jitter = c(T, F), ...)
```

**Arguments**

x	A tca-class object created by tca
y	Unused
axes	The two axes to be plotted
labels.rc	Two numbers: 0 Symbol only; 1 Label only; 2 Symbol and label
col.rc	Colors for rows and columns contributions
pch.rc	Plotting characters for rows and columns contributions
mass.rc	Logical: Will the area of plotting characters be proportional to mass
cex.rc	An overall size factor
jitter	Logical: Will close points be moved slightly?
...	Unused.

**Details**

If the number of rows is very large, labels will not be printed.

In this version, jitter is coerced.

**Value**

None

**Examples**

```
plot(tca(rodent), labels=c(0,1))
```

---

print.tca

---

*Print result of Taxicab Analysis in easily readable format*


---

**Description**

Print result of Taxicab Analysis in easily readable format

**Usage**

```
## S3 method for class 'tca'
print(x, ...)
```

**Arguments**

x	A tca tcaObject produced by the function tca
...	Unused

**Value**

An invisible list containing formatted outputs

**Examples**

```
print(tca(rodent))
```

---

RemoveRowsColumns0sAndDuplicates

*Removes rows and columns of zeros and optionnally, row or column duplicates*

---

**Description**

Removes rows and columns of zeros and optionnally, row or column duplicates

**Usage**

```
RemoveRowsColumns0sAndDuplicates(Y, rows = F, cols = F, zeros = F)
```

**Arguments**

Y	A matrix
rows	Logical Will duplicate rows be removed?
cols	Logical Will duplicate columns be removed?
zeros	Logical Will rows and columns of zeros be removed?

**Value**

A matrix with rows and columns removed as requested

**Examples**

```
RemoveRowsColumns0sAndDuplicates(matrix(1:3,nrow=3,ncol=2),cols=TRUE)
RemoveRowsColumns0sAndDuplicates(cbind(matrix(1:3,nrow=3,ncol=2),rep(0,3)),cols=TRUE)
RemoveRowsColumns0sAndDuplicates(cbind(matrix(1:3,nrow=3,ncol=2),rep(0,3)),zeros=TRUE)
RemoveRowsColumns0sAndDuplicates(matrix(0,nrow=3,ncol=3),zeros=TRUE)
```



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rodent	<i>Rodent species abundance</i>
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---

**Description**

Counts of rodents by species and site

**Usage**

```
data(rodent)
```

**Format**

A data frame of counts with 28 rows and 9 columns

- Columns: Rodent species
- Rows: Location

**Source**

Bolger et al. 1997, Response of rodents to habitat fragmentation in coastal Southern California, *Ecological Applications* 7, 552-563 (modified) via <https://www.zoology.ubc.ca/~bio501/R/workshops/workshops-multivariate-methods/>

**Examples**

```
tca(rodent, nAxes=4)
```

---

saveTCA	<i>Save tca results to a folder</i>
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---

**Description**

Save tca results to a folder

**Usage**

```
saveTCA(tcaObject, path, folder = NULL, what = c("report", "csv", "plot",  
"dataMatrix", "tcaObject"), plotAxes = matrix((1:2), nrow = 1, ncol = 2,  
byrow = T), graphicDevice = c("pdf", "postscript", "xfig", "bitmap",  
"pictex", "cairo_pdf", "cairo_ps", "svg", "png", "jpeg", "bmp", "tiff"),  
csvFormat = c("csv", "csv2"))
```

**Arguments**

tcaObject	a tca-class object created by tca
path	Location of the folder
folder	Name of the folder
what	What to save: all items specified will be saved
plotAxes	A k x 2 matrix giving pairs of axes to plot and save
graphicDevice	Format(s) of plots saved. Plots can be saved in more than one format
csvFormat	Format of csv files (North American or European)

**Value**

Figure

**Examples**

```
saveTCA(tca(rodent),path=tempdir())
```

---

SearchCrissCross	<i>Search a taxicab principal component using the criss-cross algorithm</i>
------------------	---

---

**Description**

Search a taxicab principal component using the criss-cross algorithm

**Usage**

```
SearchCrissCross(pResidual, iterationMax = 20)
```

**Arguments**

pResidual	A matrix of of non-negative numbers
iterationMax	Maximum number of iterations

**Details**

This function is for internal usage only.

The vector uMax is normalize to  $uMax[1] = 1$

**Value**

A list: L1Max = maximum L1 norm; uMax = Linf unit vector giving the maximum L1 norm

**Examples**

```
SearchCrissCross(matrix(-3:8,nrow=4,ncol=3))
```

---

SearchExhaustive	<i>Search a taxicab principal component via exhaustive search</i>
------------------	---

---

**Description**

Search a taxicab principal component via exhaustive search

**Usage**

```
SearchExhaustive(pResidual)
```

**Arguments**

pResidual      A matrix of of non-negative numbers

**Details**

This function is for internal usage only.

The vector uMax is normalize to  $uMax[1] = 1$

**Value**

A list: L1Max = maximum L1 norm; uMax = Linf unit vector giving the maximum L1 norm

**Examples**

```
SearchExhaustive(matrix(-3:8,nrow=4,ncol=3))
```

---

SearchGeneticAlgoritm	<i>Search a taxicab principal component using the genetic algorithm</i>
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---

**Description**

Search a taxicab principal component using the genetic algorithm

**Usage**

```
SearchGeneticAlgoritm(pResidual)
```

**Arguments**

pResidual      A matrix of of non-negative numbers

**Details**

This function is for internal usage only.

The vector uMax is normalize to  $uMax[1] = 1$

**Value**

A list: L1Max = maximum L1 norm; uMax = Linf unit vector giving the maximum L1 norm

**Examples**

```
SearchGeneticAlgorithm(matrix(-3:8,nrow=4,ncol=3))
```

---

summary.tca

*Summary of the Taxicab analysis*

---

**Description**

Summary of the Taxicab analysis

**Usage**

```
## S3 method for class 'tca'  
summary(object, ...)
```

**Arguments**

object	A tca tcaObject produced by the function tca
...	Unused

**Details**

Shows the unstandardized dispersion values

**Value**

A list

**Examples**

```
summary(tca(rodent))
```

---

tca	<i>Taxicab Correspondance analysis</i>
-----	--

---

**Description**

Computes the Taxicab correspondance analysis of a matrix of non-negative numbers

**Usage**

```
tca(Y, nAxes = 2, dataName = NULL, combineCollinearRows = c(F, T),
    combineCollinearCols = c(F, T), algorithm = c("exhaustive", "criss-cross",
    "genetic"), returnInputMatrix = c(T, F), verbose = (nAxes > 2),
    exhaustiveAlgorithmMaxnCol = 20, L1MaxDeltaMax = 10^-10)
```

**Arguments**

Y	A m x n matrix of non-negative numbers. If Y is not a matrix, the 'as.matrix' transformation will be attempted. Missing values are not allowed.
nAxes	Number of axes to compute
dataName	A name to be used to identify the outputs in 'plot' and 'saveTCA' ()
combineCollinearRows	Should collinear rows be combined?
combineCollinearCols	Should collinear columns be combined?
algorithm	Algorithm requested - may be abbreviated to first two letters
returnInputMatrix	Will the input matrix be returned
verbose	Report progress (default) or not
exhaustiveAlgorithmMaxnCol	Maximum size for exhaustive search
L1MaxDeltaMax	Change of L1 norm acceptable for convergence in iterative searches

**Details**

Computations are carried out on the transposed matrix if  $nrow(Y) < ncol(Y)$ . In the following, we assume that  $nrow(Y) \geq ncol(Y)$

Row and column names will be created if necessary.

Zeros rows and columns are removed.

If  $ncol(Y) \leq exhaustiveAlgorithmMaxnCol$  the exhaustive algorithm used unless otherwise specified.

If  $ncol(Y) > exhaustiveAlgorithmMaxnCol$  the genetic algorithm used unless otherwise specified.

Algorithm = exhaustive is overridden if  $ncol(Y) > exhaustiveAlgorithmMaxnCol$ .

For `ncol(Y) <= exhaustiveAlgorithmMaxnCol`, the user may want to specify `algorithm = genetic` if `nrow(Y)` is very large, since exhaustive computation may be slow.

If `ncol(Y) <= exhaustiveAlgorithmMaxnCol` the genetic algorithm is used unless otherwise specified.

(`ncol(Y) = 20` appears to be the maximum practical on 2017 vintage Intel-based desktops).

### Value

A list with class `'tca'` containing the following components:

<code>dispersion</code>	A <code>nAxes</code> -length vector of matrix of column contributions
<code>rowScores</code>	A <code>m x nAxes</code> matrix of column contributions
<code>colScores</code>	A <code>nAxes x n</code> matrix of row contributions
<code>rowMass</code>	Row weights: <code>apply(Y,1,sum)/sum(Y)</code>
<code>colMass</code>	Column weights: <code>apply(Y,2,sum)/sum(Y)</code>
<code>dataName</code>	A name to be used to identify the output in <code>'plot'</code> and <code>'save'</code>
<code>algorithm</code>	Algorithm used (may be different from the algorithm requested)
<code>dataMatrixTotal</code>	Sum of the input matrix entries
<code>dataMatrix</code>	The matrix used in the computation
<code>rowColCombined</code>	A list describing removed or combined rows and columns, if any

### Examples

```
tca(rodent,nAxes=4)
tca(rodent,nAxes=4,combineCollinearRows=c(TRUE,FALSE))
```

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