Package 'Comp2ROC'

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Title Compare Two ROC Curves that Intersect

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Description Comparison of two ROC curves through the methodology proposed by Ana C. Braga.

License GPL-2

Depends R (>= 2.15.1), ROCR, boot

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R topics documented:

`Comp2ROC-package` *Comparation of Two ROC Curves that Intersect*

Description

Comaparation of ROC Curves using the methodology devoloped by Braga.

Details

Package:	Comp2ROC
Type:	Package
Version:	1.1.2
Date:	2016-05-18
License:	GPL-2

Author(s)

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References

BRAGA, A. C. AND COSTA, L. AND OLIVEIRA, P. 2011. An alternative method for global and partial comparasion of two diagnostic system based on ROC curves In Journal of Statistical Computation and Simulation.

Examples

```
# This is a simple example on how to use the package with the given dataset ZHANG (paired samples):
nameE = "Zhang"
modality1DataColumn = "modality1"
modality2DataColumn = "modality2"
data(zhang)
results = roc.curves.boot(zhang, 10, 0.05, name=nameE,
                          mod1=modality1DataColumn, mod2=modality2DataColumn)
rocboot.summary(results, "modality1", "modality2")

# This is another simple example on how to use the package with the given
# dataset CAS2015 (unpaired samples):
nameE = "CAS2015"
modality1DataColumn = "CRIBM"
modality2DataColumn = "CRIBF"
paired = FALSE
```

```
data(cas2015)
results = roc.curves.boot(cas2015, 1000, 0.05, name=nameE,
                          mod1=modality1DataColumn, mod2=modality2DataColumn, paired)
rocboot.summary(results, modality1DataColumn, modality2DataColumn)
```

`areatriangles` *Triangle Areas*

Description

This function allows to calculate the triangles area formed with two points that was next to each other and the reference point. It also allows to calculate the total area based on the previous triangles.

Usage

```
areatriangles(line.slope, line.dist1)
```

Arguments

`line.slope`	Vector with all sampling lines slope
`line.dist1`	Vector with the ROC Curves and sampling lines intersection points, the distance between this points and the reference point

Value

This function return a list with:

`auctri`	Total area
`areatri`	Vector with all triangles areas

See Also

`lineslope` `linedistance` `curvesegslope` `curvesegsloperef`

cas2015 *CAS2015 Dataset*

Description

This dataset was created by Braga, A. C. and allows the comparison of two independent samples.

Usage

```
data(cas2015)
```

Format

A data frame with a total of 800 observations on the following 2 variables and respectives status.

`mod1` CRIBM

`status1` Result1

`mod2` CRIBF

`status2` Result2

Details

The dataset contains the values of the indicator (CRIB) for 2 different groups (sex: M/F) and respective results, from 0 (alive) to 1 (deceased). These samples are unpaired, therefore presenting different statuses for each one.

Source

COELHO, S. AND BRAGA, A. C.: Performance Evaluation of Two Software for Analysis Through ROC Curves: Comp2ROC vs SPSS. Computational Science and Its Applications – ICCSA 2015; p. 144-156; Springer International Publishing., ISBN: 978-3-319-21406-1.

comp.roc.curves *Calculate distribution*

Description

This funtion calculates by bootstrapping the real distribution for the entire length set.

Usage

```
comp.roc.curves(result, ci.flag = FALSE, graph.flag = FALSE, nome)
```

Arguments

result	List of statistical measures obtaind throught rocsampling
ci.flag	Flag that indicates if the user wants to calculate the confidance intervals
graph.flag	Flag that indicates if the user wants to draw the graph
nome	Name to put on the graph

Details

In this function ci.flag and graph.flag are set FALSE by defaut

Value

boot	statistics test
p-value	p-value for one-sided
p-value2	p-value for two-sided
ci	confidance interval

See Also

rocsampling

---

comp.roc.delong *Calculate areas and stats*

Description

This function allows to calculate the areas under the curve for each curve and some statistical measures.

Usage

```
comp.roc.delong(sim1.ind, sim1.sta, sim2.ind, sim2.sta, related = TRUE)
```

Arguments

sim1.ind	Vector with the data for Curve 1
sim1.sta	Vector with the status for Curve 1
sim2.ind	Vector with the data for Curve 2
sim2.sta	Vector with the status for Curve 2
related	Boolean parameter that represents if the two modalities are related or not

Details

This function calculates the Wilcoxon Mann Whitney matrix for each modality, areas, standard deviations, variances and global correlations.

Value

This function returns a list with:

Z	Hanley Z calculation
pvalue	p-value for this Z
AUC	Area under curve for each modality
SE	Standard error
S	Variance for each modality
R	Correlation Coeficient

Examples

```
data(zhang)
modality1DataColumn = "modality1"
modality2DataColumn = "modality2"
data = read.manually.introduced(zhang, modality1DataColumn, TRUE,
                                modality2DataColumn, TRUE, "status", TRUE)
sim1.ind = unlist(data[1])
sim2.ind = unlist(data[2])
sim1.sta = unlist(data[3])
sim2.sta = unlist(data[4])
comp.roc.delong(sim1.ind, sim1.sta, sim2.ind, sim2.sta)
```

---

curvesegslope *Segment Slopes*

Description

This function allows to calculate the ROC curve segments slope through the points that are given by parameter.

Usage

```
curvesegslope(curve.fpr, curve.tpr)
```

Arguments

curve.fpr	False positive rate vector with all points of the given Curve
curve.tpr	True positive rate vector with all points of the given Curve

Value

This function returns a vector with all segments slopes

curvesegsloperef *Segment Slopes to Reference Point*

Description

This function allows to calculate the segments slope that connect the ROC curve segments with the reference point (1,0).

Usage

```
curvesegsloperef(curve.fpr, curve.tpr, ref.point)
```

Arguments

curve.fpr	False positive rate vector with all points of the given Curve
curve.tpr	True positive rate vector with all points of the given Curve
ref.point	Reference point where we start drawing the sample lines

Value

This function returns a vector with all segments slopes that connect the ROC curve points to the reference point.

diffareatriangles *Difference Between Area Triangles*

Description

This function allows to calculate the difference between triangles areas formed by the same sampling lines in two different ROC curves. It also allows to calculate the difference between total areas.

Usage

```
diffareatriangles(area.triangle1, area.triangle2)
```

Arguments

area.triangle1	Vector with all triangles areas of the Curve 1
area.triangle2	Vector with all triangles areas of the Curve 2

Value

This function returns a list with:

diffareas	Difference between each triangle area
diffauc	Difference between total areas

See Also

areatriangles

---

linedistance *Intersection Points*

Description

This function allows to calculate the intersection points between the ROC curve and the sampling lines. Also calculates the distance between this points and the reference point.

Usage

```
linedistance(curve.fpr, curve.tpr, curve.segslope, curve.slope, line.slope, ref.point)
```

Arguments

curve.fpr	False positive rate vector with all points of the given Curve
curve.tpr	True positive rate vector with all points of the given Curve
curve.segslope	Vector with all segments slope of the ROC curves
curve.slope	Vector with all the slope of all segments that connect the ROC curve with the reference point
line.slope	Vector with the slope of all sampling lines
ref.point	Reference point where we start drawing the sampling lines

Value

This function returns a list with:

dist	Vector with distances between the intersection points and the reference points
x	Vector with all x coordinates of intersection points
y	Vector with all y coordinates of intersection points

See Also

lineslope curvesegslope curvesegsloperef

`lineslope` *Sampling Lines Slope*

Description

This function allows to calculate the sample lines slope that were drawn beginning at the reference point.

Usage

```
lineslope(K)
```

Arguments

`K`	Number of sampling lines that we want to create

Value

This function returns a vector with all slopes of the sampling lines that we create

Examples

```
K = 100
lineslope(K)
```

`read.file` *Read data from file*

Description

This function allows to read data from a file.

Usage

```
read.file(name.file.csv, header.status = TRUE, separator = ";", decimal = ",", modality1,
testdirection1, modality2, testdirection2, status1, related = TRUE, status2 = NULL)
```

Arguments

name.file.csv	Name of the file with data. The file must be in csv or txt format
header.status	Indicates if the file has a header row
separator	Indicates what is the column separator
decimal	Indicates what is the decimal separator
modality1	Name of the column of dataframe that represents the first modality
testdirection1	Indicates the direction of the test for modality 1. If TRUE means that larger test results represent more positive test
modality2	Name of the column of dataframe that represents the second modality
testdirection2	Indicates the direction of the test for modality 2. If TRUE means that larger test results represent more positive test
status1	Name of the column of dataframe that represents the Status 1
related	Boolean parameter that represents if the two modalities are related or not
status2	Name of the column of dataframe that represents the Status 2

Details

The default column separator is ";". And the default decimal separator is ".". header.status has also a default value that is TRUE. By default, the related parameter is set to TRUE. In this case the status2 is not necessary (by default set to (NULL), because in related modalities the status is the same. Otherwise, if related is set to FALSE, its necessary to indicate the name of status2 column. In the data must be listed first all values of the distribution of negative cases (0), followed by the positive ones (1).

Value

This functions returns a list with the following data:

sim1.ind	Vector with the data for Curve 1
sim2.ind	Vector with the data for Curve 2
sim1.sta	Vector with the status for Curve 1
sim2.sta	Vector with the status for Curve 2

See Also

read.manually.introduced

Examples

```
# This is a simple example how to read a file:

data.filename = "zhang.csv"
modality1DataColumn = "modality1"
modality2DataColumn = "modality2"
modality2StatusHeader = "status"  # if different from modality1's header
                                  # (a.k.a they are independent)
zhang = read.file(data.filename, TRUE, ";", ".", modality1, TRUE, modality2, TRUE, "status")
```

`read.manually.introduced` *Read data manually introduced*

Description

This function allows to read the testing data.

Usage

```
read.manually.introduced(dat, modality1, testdirection1, modality2,
testdirection2, status1, related = TRUE, status2 = NULL)
```

Arguments

`dat`	Dataframe of data to anlyse
`modality1`	Name of the column of dataframe that represents the first modality
`testdirection1`	Indicates the direction of the test for modality 1. If `TRUE` means that larger test results represent more positive test
`modality2`	Name of the column of dataframe that represents the second modality
`testdirection2`	Indicates the direction of the test for modality 2. If `TRUE` means that larger test results represent more positive test
`status1`	Name of the column of dataframe that represents the Status 1
`related`	Boolean parameter that represents if the two modalities are related or not
`status2`	Name of the column of dataframe that represents the Status 2

Details

By default, the related parameter is set to `TRUE`. In this case the `status2` is not necessary (by default set to `(NULL)`, because in related modalities the status is the same. Otherwise, if related is set to `FALSE`, its necessary to indicate the name of `status2` column. In the data must be listed first all values of the distribution of negative cases (0), followed by the positive ones (1).

Value

This functions returns a list with the following data:

`sim1.ind`	Vector with the data for Curve 1
`sim2.ind`	Vector with the data for Curve 2
`sim1.sta`	Vector with the status for Curve 1
`sim2.sta`	Vector with the status for Curve 2

Examples

```
data(zhang)
moda1 = "modality1"
moda2 = "modality2"
data = read.manually.introduced(zhang, moda1, TRUE, moda2, TRUE, "status", TRUE)
```

`roc.curves.boot` *Compare curves*

Description

This is the function which control the whole package.This uses all functions except the reading ones and `rocboot.summary` and `save.file.summary`.

Usage

```
roc.curves.boot(data, nb = 1000, alfa = 0.05, name, mod1, mod2, paired)
```

Arguments

`data`	Data obtained throught `read.file` or `read.manually.introduced`
`nb`	Number of permutations
`alfa`	Confidance level for parametric methods
`name`	Name too show in graphs
`mod1`	Name of Modality 1
`mod2`	Name of Modality 2
`paired`	Boolean parameter that represents if the two modalities are related or not

Value

This function returns a list with:

`Area1`	Area of Curve 1
`SE1`	Standard error of Curve 1
`Area2`	Area of Curve 2
`SE2`	Standard error of Curve 2
`CorrCoef`	Correlation Coeficient
`diff`	Difference Between Areas (TS)
`zstats`	Z Statistic
`pvalue1`	p-value of Z Statistics
`TrapArea1`	Area of curve 1 using the Trapezoidal rule

TrapArea2	Area of curve 2 using the Trapezoidal rule
bootpvalue	p-value of bootstrapping
nCross	Number of Crossings
ICLB1	Confidance Interval: Lower Bound for Curve 1
ICUB1	Confidance Interval: Upper Bound for Curve 1
ICLB2	Confidance Interval: Lower Bound for Curve 2
ICUB2	Confidance Interval: Upper Bound for Curve 2
ICLBDiff	Confidance Interval: Lower Bound for Difference between areas
ICUBDiff	Confidance Interval: Upper Bound for Difference between areas

Examples

```
data(zhang)
nameE = "new_Zhang"
modality1DataColumn = "modality1"
modality2DataColumn = "modality2"
data = read.manually.introduced(zhang, moda1, TRUE, moda2, TRUE, "status", TRUE)
results = roc.curves.boot(zhang, 1000, 0.05, name=nameE,
                          mod1=modality1DataColumn, mod2=modality2DataColumn)
```

---

roc.curves.plot *Plot ROC curves*

Description

This function allows to plot the two roc curves in comparasion.

Usage

```
roc.curves.plot(sim1.curve, sim2.curve, mod1, mod2)
```

Arguments

sim1.curve	Curve 1 created using the function performance.
sim2.curve	Curve 2 created using the function performance.
mod1	Name of Modality 1
mod2	Name of Modality 2

See Also

read.file read.manually.introduced

Examples

```
data(zhang)
moda1 = "modality1"
moda2 = "modality2"
data = read.manually.introduced(zhang, moda1, TRUE, moda2, TRUE, "status", TRUE)

sim1.ind = unlist(data[1])
sim2.ind = unlist(data[2])
sim1.sta = unlist(data[3])
sim2.sta = unlist(data[4])

sim1.pred = prediction(sim1.ind, sim1.sta)
sim2.pred = prediction(sim2.ind, sim2.sta)

sim1.curve = performance(sim1.pred, "tpr", "fpr")
sim2.curve = performance(sim2.pred, "tpr", "fpr")

roc.curves.plot(sim1.curve, sim2.curve, mod1=moda1, mod2=moda2)
```

---

rocboot.summary *Summary of Comparation*

Description

This function allows to see the information obtained throught function `roc.curve.boot`.

Usage

```
rocboot.summary(result, mod1, mod2)
```

Arguments

`result`	List of statistical measures obtaind throught `roc.curves.boot`
mod1	Name of the column of dataframe that represents the first modality
mod2	Name of the column of dataframe that represents the second modality

See Also

`save.file.summary`

Examples

```
data(zhang)
moda1 = "modality1"
moda2 = "modality2"
```

```
nameE = "new_Zhang"
data = read.manually.introduced(zhang, moda1, TRUE, moda2, TRUE, "status", TRUE)
results = roc.curves.boot(data, name=nameE, mod1=moda1, mod2=moda2)
rocboot.summary(results, moda1, moda2)
```

`rocsampling` *ROC Sampling*

Description

This function allows to calculate some statistical measures like extension and location.

Usage

```
rocsampling(curve1.fpr, curve1.tpr, curve2.fpr, curve2.tpr, K = 100)
```

Arguments

`curve1.fpr`	False positive rate vector with all points of the Curve 1
`curve1.tpr`	True positive rate vector with all points of the Curve 1
`curve2.fpr`	False positive rate vector with all points of the Curve 2
`curve2.tpr`	True positive rate vector with all points of the Curve 2
`K`	Number of sampling lines

Details

This function uses functions like `areatriangles`, `curvesegslope`, `curvesegsloperef`, `diffareatriangles`, `linedistance` and `lineslope` to `calculate` that measures. By default the number of sampling lines is 100, beacause it was proved by Braga that it was the optimal number.

Value

This funcion returns a list with the following components:

`AUC1`	Total Area of Curve 1 (using triangles)
`AUC2`	Total Area of Curve 2 (using triangles)
`propc1`	Proportion of Curve1
`propc2`	Proportion of Curve2
`propties`	Proportion of ties
`locc1`	Location of Curve 1
`locc2`	Location of Curve 2
`locties`	Location of Ties
`K`	Number of sampling lines

lineslope	Slopes of sampling lines
diffareas	Difference of area of triangles
dist1	Distance of the intersection points of Curve 1 to reference point
dist2	Distance of the intersection points of Curve 2 to reference point

See Also

areatriangles curvesegslope curvesegsloperef diffareatriangles linedistance lineslope

---

rocsampling.summary *Summary of ROC Sampling*

Description

This function allows to see with a simple interface the results obtained in rocsampling.

Usage

```
rocsampling.summary(result, mod1, mod2)
```

Arguments

result	List with results obtained throught the use of rocsampling
mod1	Name of the column of dataframe that represents the first modality
mod2	Name of the column of dataframe that represents the second modality

See Also

rocsampling

---

save.file.summary *Save File*

Description

This functions allow to save the information on a file.

Usage

```
save.file.summary(result, name, app = TRUE, mod1, mod2)
```

Arguments

result	List of statistical measures obtaind throught roc.curves.boot
name	File name
app	Indicates if the user wants to append information on the same file
mod1	Name of the column of dataframe that represents the first modality
mod2	Name of the column of dataframe that represents the second modality

Details

The user don't need to fill the app parameter, because by default it was set to TRUE. This parameter allow the user to choose if he wants the results of differents performances in the same file, or each time that he starts a new performance the file will be new.

Value

This functions saves on the file with name name the performance parameters of the test.

Examples

```
# If the user wants to append the results
save.file.summary(results, nameE, mod1=moda1, mod2=moda2)

# If the user does not want to append the results
save.file.summary(results, nameE, app=FALSE, moda1, moda2)
```

---

zhang *Zhang Dataset*

Description

This dataset was created by Zhang and we use it as example on our package

Usage

```
data(zhang)
```

Format

A data frame with 2410 observations on the following 3 variables.

mod1 modality 1

status status

mod2 modality 2

Details

This modalities are related to each other, so they have the same status

Source

ZHANG, D. AND ZHOU, X.AND FREEMAN, D. AND FREEMAN, J. 2002. A nonparametric method for the comparison of partial areas under ROC curves and its application to large health care data sets In Stat. Med., Vol. 21 N. 5 701-715.

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