

Package ‘iMRMC’

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Type Package

Title Multi-Reader, Multi-Case Analysis Methods (ROC, Agreement, and Other Metrics)

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Description Do Multi-Reader, Multi-

Case (MRMC) analyses of data from imaging studies where clinicians (readers) evaluate patient images (cases). What does this mean? ... Many imaging studies are designed so that every reader reads every case in all modalities, a fully-crossed study. In this case, the data is cross-correlated, and we consider the readers and cases to be cross-correlated random effects.

An MRMC analysis accounts for the variability and correlations from the readers and cases when estimating variances, confidence intervals, and p-values. The functions in this package can treat arbitrary study designs and studies with missing data, not just fully-crossed study designs.

The initial package analyzes the reader-average area under the receiver operating characteristic (ROC) curve with U-statistics according to Gallas, Bandos, Samuelson, and Wagner 2009 <doi:10.1080/03610920802610084>.

Additional functions analyze other endpoints with U-statistics (binary performance and score differences) following the work by Gallas, Pennello, and Myers 2007 <doi:10.1364/JOSAA.24.000B70>.

Package development and documentation is at <<https://github.com/DIDSR/iMRMC/tree/master>>.

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convertDF	<i>Convert MRMC data frames</i>
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Description

Convert MRMC data frames

Usage

```
convertDF(inDF, inDFtype, outDFtype, readers)
```

Arguments

inDF	An MRMC dataframe with reading study results in inDFtype format
inDFtype	A string indicating the format type of the input MRMC data frame
outDFtype	A string indicating the format type of the output MRMC data frame.
readers	A character array holding the column names (readerIDs) corresponding to the data from different readers

Details

MRMC data frames contain scores from readers, cases, and sometimes modalities. This packages deals with (currently) two MRMC data frame formats. These are the formats:

matrixMode For this format, each row contains all the information for a case, including the reader study result for several readers, ground truth and other information as separate columns. This mode can only hold data from one modality.

listMode For this format, each row contains the data for one observation. The columns specify the readerID, caseID, score, ground truth, and other information if there is any. This mode can hold data from multiple modalities.

Value

An MRMC dataframe with reading study results in outDFtype format

convertDFtoDesignMatrix

Convert an MRMC data frame to a design matrix

Description

Convert an MRMC data frame to a design matrix, dropping readers or cases with no observations

Usage

```
convertDFtoDesignMatrix(dfMRMC, modality = NULL, dropFlag = TRUE)
```

Arguments

dfMRMC	An MRMC data frame
modality	The score matrix depends on the modality. If more than one modality exists in the data frame, you must specify which modality to subset.
dropFlag	[logical] The default setting (TRUE) removes readers and cases that have no observations. Dropping them by default will speed up analyses. Leaving the levels (dropFlag = FALSE) is useful if you need the entire score or design matrix when comparing or doing analyses with two modalities.

Value

A matrix [nCases, nReaders] indicating which scores were reported for each reader and case

```
convertDFtoScoreMatrix
```

Convert an MRMC data frame to a score matrix

Description

Convert an MRMC data frame to a score matrix, dropping readers or cases with no observations

Usage

```
convertDFtoScoreMatrix(dfMRMC, modality = NULL, dropFlag = TRUE)
```

Arguments

dfMRMC	An MRMC data frame
modality	The score matrix depends on the modality. If more than one modality exists in the data frame, you must specify which modality to subset.
dropFlag	[logical] The default setting (TRUE) removes readers and cases that have no observations. Dropping them by default will speed up analyses. Leaving the levels (dropFlag = FALSE) is useful if you need the entire score or design matrix when comparing or doing analyses with two modalities.

Value

A matrix [nCases, nReaders] of the scores each reader reported for each case

```
createGroups
```

Assign a group label to items in a vector

Description

Assign a group label to items in a vector

Usage

```
createGroups(items, nG)
```

Arguments

items	A vector of items
nG	The number of groups

Value

A data frame containing the items and their group labels

Examples

```
x <- paste("item", 1:10, sep = "")
df <- createGroups(x, 3)
print(df)
```

createIMRMCdf	<i>Convert a data frame with all needed factors to doIMRMC formatted data frame</i>
---------------	---

Description

Convert a data frame with all needed factors to doIMRMC formatted data frame

Usage

```
createIMRMCdf(
  dFrame,
  keyColumns = list(readerID = "readerID", caseID = "caseID", modalityID =
    "modalityID", score = "score", truth = "truth"),
  truePositiveFactor = "cancer"
)
```

Arguments

dFrame	This data frame includes columns for readerID, caseID, modalityID, score, and truth. These columns are not expected to be named as such and other columns may exist.
keyColumns	This list identifies the column names of the data frame to be used for the analysis. list(readerID = "****", caseID = "****", modalityID = "****", score = "****", truth="****")
truePositiveFactor	The true positive label, such as "cancer" or "1"

Value

output a doIMRMC formatted data frame: rows for truth and rows for data

doIMRMC

*MIMC analysis of the area under the ROC curve***Description**

doIMRMC takes ROC data as a data frame and runs a multi-reader multi-case analysis based on U-statistics as described in the following papers Gallas2006_Acad-Radiol_v13p353 (single-modality), Gallas2008_Neural-Networks_v21p387 (multiple modalities, arbitrary study designs), Gallas2009_Commun-Stat-A-Theor_v38p2586 (framework paper).

Usage

```
doIMRMC(
  data = NULL,
  fileName = NULL,
  workDir = NULL,
  iMIMCjarFullPath = NULL,
  stripDatesForTests = FALSE
)
```

Arguments

<code>data</code>	<p>This data.frame contains the following variables:</p> <ul style="list-style-type: none"> • <code>readerID</code> Factor with levels like "reader1", "reader2", ... • <code>caseID</code> Factor with levels like "case1", "case2", ... • <code>modalityID</code> Factor with levels like "modality1", "modality2", ... • <code>score num</code> = reader score <p>Each row of this data frame corresponds to an observation. For every caseID, there must be a row corresponding to the truth observation. The readerID for a truth observation is "truth". The modalityID for a truth observation is "truth". The score for a truth observation must be either 0 (signal-absent) or 1 (signal-present).</p>
<code>fileName</code>	This character string identifies the location of an iMIMC input file. The input file is identical to data except there is a free text section to start, then a line with "BEGIN DATA:", then the data frame info.
<code>workDir</code>	This character string determines the directory where intermediate results are written. If this parameter is not set, the program writes the intermediate results to the directory specified by <code>tempdir()</code> and then deletes them.
<code>iMIMCjarFullPath</code>	This character string identifies the location of the iMIMC.jar file this jar file can be downloaded from https://github.com/DIDSR/iMIMC/releases this R program supports version iMIMC-v3p2.jar
<code>stripDatesForTests</code>	Since results include a date and time stamp, these need to be stripped out when doing the package tests. This parameter flags whether or not the dates should be stripped out.

Details

In detail, this procedure reads the name of an input file from the local file system, or takes a data frame and writes it to the local file system formatted for the iMRMC program (found at <https://github.com/DIDSR/iMRMC/releases>), it executes a java app, the iMRMC engine, which writes the results to the local files system, it reads the analysis results from the local file system, packs the analysis results into a list object, deletes the data and analysis results from the local file system, and returns the list object.

This software requires Java JDK 1.7 or higher.

The examples took too long for CRAN to accept. So here is an example:

```
# Create a sample configuration file
config <- sim.gRoeMetz.config()
# Simulate an MRMC ROC data set
dFrame.imrmc <- sim.gRoeMetz(config)
# Analyze the MRMC ROC data
result <- doIMRMC(dFrame.imrmc)
```

Value

list iMRMC outputs. The objects of this list are described in detail in the iMRMC documentation which can be found at http://didsr.github.io/iMRMC/000_iMRMC/userManualHTML/index.htm

Here is a quick summary:

- `perReader` data.frame containing the performance results for each reader. Key variables of this data frame are `AUCA`, `AUCB`, `AUCAminusAUCB` and the corresponding variances, confidence intervals, degrees of freedom and p-values.
- `Ustat` data.frame containing the reader-average performance results. The analysis results are based on U-statistics and the papers listed above. Key variables of this data frame are `AUCA`, `AUCB`, `AUCAminusAUCB` and the corresponding variances, confidence intervals, degrees of freedom and p-values.
- `MLEstat` data.frame containing the reader-average performance results. The analysis results are based on V-statistics, which approximates the true distribution with the empirical distribution. The empirical distribution equals the nonparametric MLE estimate of the true distribution, which is also equivalent to the ideal bootstrap estimate. Please refer to the papers listed above. Key variables of this data frame are `AUCA`, `AUCB`, `AUCAminusAUCB` and the corresponding variances, confidence intervals, degrees of freedom and p-values.
- `ROC` list containing ROC curves There is an ROC curve for every combination of reader and modality. For every modality, there are also four average ROC curves. These are discussed in [Chen2014_Br-J-Radiol_v87p20140016](#). The diagonal average averages the reader-specific ROC curves along $y = -x + b$ for b in $(0,1)$. The horizontal average averages the reader specific ROC curves along $y = b$ for b in $(0,1)$. The vertical average averages the reader specific ROC curves along $x = b$ for b in $(0,1)$. The pooled average ignores `readerID` and pools all the scores together to create one ROC curve.
- `varDecomp` list containing different decompositions of the total variance. Please refer to [Gallas2009_Commun-Stat-A-Theor_v38p2586](#) (framework paper). The different decompositions are BCK, BDG, DBM, MS, OR.

```
extractPairedComparisonsBRBM
```

Extract between-reader between-modality pairs of scores

Description

Extract between-reader between-modality pairs of scores

Usage

```
extractPairedComparisonsBRBM(
  data0,
  modalities = c("testA", "testB"),
  keyColumns = list(readerID = "readerID", caseID = "caseID", modalityID =
    "modalityID", score = "score")
)
```

Arguments

<code>data0</code>	This data frame includes columns for readerID, caseID, modalityID, score.
<code>modalities</code>	The modalities (testA, testB) for the scores to be paired
<code>keyColumns</code>	This list identifies the column names of the data frame to be used for the analysis. <code>list(readerID = "****", caseID = "****", modalityID = "****", score = "****", truth="****")</code>

Value

A data frame of all paired observations. Each observation comes from a pair of readers evaluating a case in two modalities. The first column corresponds to one reader evaluating the case in testA. The second column corresponds to the other reader evaluating the case in testB.

```
extractPairedComparisonsWRBM
```

Extract within-reader between-modality pairs of scores

Description

Extract within-reader between-modality pairs of scores

Usage

```
extractPairedComparisonsWRBM(
  data0,
  modalities = "testA",
  keyColumns = list(readerID = "readerID", caseID = "caseID", modalityID =
    "modalityID", score = "score")
)
```


Arguments

<code>data0</code>	This data frame includes columns for readerID, caseID, modalityID, score.
<code>modalities</code>	The modalities (testA, testB) for the scores to be paired
<code>keyColumns</code>	This list identifies the column names of the data frame to be used for the analysis. <code>list(readerID = "****", caseID = "****", modalityID = "****", score = "****", truth="****")</code>

Value

A data frame of all paired observations. Each observation comes from a one reader evaluating a case in two modalities The first column corresponds to one reader evaluating the case in testA. The second column corresponds to the same reader evaluating the case in testB.

<code>getBRBM</code>	<i>Get between-reader, between-modality paired data from an MRMC data file</i>
----------------------	--

Description

Get between-reader, between-modality paired data from an MRMC data file

Usage

```
getBRBM(mcsData, modality.X, modality.Y)
```

Arguments

<code>mcsData</code>	A data frame with the following columns: readerID, caseID, modalityID, score
<code>modality.X</code>	The name of one modality
<code>modality.Y</code>	The name of one modality.

Details

If `modality.Y = modality.X`, then the data would be between-reader, within-modality (BRWM).

Value

The result of merging the `modality.X` and `modality.Y` subsets of `mcsData` by `caseID` for every pair of readers

getMRMCscore	<i>Get a score from an MRMC data frame</i>
--------------	--

Description

Get a score from an MRMC data frame

Usage

```
getMRMCscore(df, iR, iC, modality)
```

Arguments

df	An MRMC data frame
iR	The numeric index of the readerID
iC	The numeric index of the caseID
modality	The character description of the modalityID

Value

The score

getWRBM	<i>Get within-reader, between-modality paired data from an MRMC data file</i>
---------	---

Description

Get within-reader, between-modality paired data from an MRMC data file

Usage

```
getWRBM(mcsData, modality.X, modality.Y)
```

Arguments

mcsData	A data frame with the following columns: readerID, caseID, modalityID, score
modality.X	The name of one modality
modality.Y	The name of one modality. This should be different from modality.X

Value

The result of merging the modality.X and modality.Y subsets of mcsData by readerID and caseID

init.lecuyerRNG	<i>Initialize the l'Ecuyer random number generator</i>
-----------------	--

Description

See the documentation for the parallel package. If you require backwards compatibility, please run `RNGversion("3.5.0")`.

Usage

```
init.lecuyerRNG(seed = 1, stream = 2)
```

Arguments

seed	This determines the position in each stream
stream	This determines the stream

Value

Nothing

laBRBM	<i>MRMC analysis of between-reader between-modality limits of agreement</i>
--------	---

Description

The core analysis is done by `ustat11` with the identity kernel (`kernelFlag = 1`).

Usage

```
laBRBM(
  df,
  modalitiesToCompare,
  keyColumns = c("readerID", "caseID", "modalityID", "score")
)
```

Arguments

df	Data frame of observations, one per row. Columns identify random effects, fixed effects, and the observation. Namely, <ul style="list-style-type: none"> • <code>readerID</code>: The factor corresponding to the different readers in the study. The <code>readerID</code> is treated as a random effect. • <code>caseID</code>: The factor corresponding to the different cases in the study. The <code>caseID</code> is treated as a random effect.
----	--

- `modalityID`: The factor corresponding to the different modalities in the study. The `modalityID` is treated as a fixed effect.
- `score`: The score given by the reader to the case for the modality indicated.

`modalitiesToCompare`

The factors identifying the modalities to compare.

`keyColumns`

Identify the factors corresponding to the `readerID`, `caseID`, `modalityID`, and `score` (or alternative random and fixed effects).

laWRBM

MRMC analysis of within-reader between-modality limits of agreement

Description

The core analysis is done by `ustat11` with the difference kernel (`kernelFlag = 2`). This calculation can also be accomplished by `ustat11` with the identity kernel (`kernelFlag = 1`), and the code to do that is provided after the return statement so it never gets executed.

Usage

```
laWRBM(
  df,
  modalitiesToCompare,
  keyColumns = c("readerID", "caseID", "modalityID", "score")
)
```

Arguments

`df`

Data frame of observations, one per row. Columns identify random effects, fixed effects, and the observation. Namely,

- `readerID`: The factor corresponding to the different readers in the study. The `readerID` is treated as a random effect.
- `caseID`: The factor corresponding to the different cases in the study. The `caseID` is treated as a random effect.
- `modalityID`: The factor corresponding to the different modalities in the study. The `modalityID` is treated as a fixed effect.
- `score`: The score given by the reader to the case for the modality indicated.

`modalitiesToCompare`

The factors identifying the modalities to compare.

`keyColumns`

Identify the factors corresponding to the `readerID`, `caseID`, `modalityID`, and `score` (or alternative random and fixed effects).

renameCol	<i>Rename a data frame column name or a list object name</i>
-----------	--

Description

Rename a data frame column name or a list object name

Usage

```
renameCol(df, oldColName, newColName)
```

Arguments

df	A data frame
oldColName	Old column name
newColName	New column name

Value

the data frame with the updated column name

roc2binary	<i>Convert ROC data formatted for doIMRMC to TPF and FPF data formatted for doIMRMC</i>
------------	---

Description

Convert ROC data formatted for doIMRMC to TPF and FPF data formatted for doIMRMC

Usage

```
roc2binary(df.auc, threshold)
```

Arguments

df.auc	data frame of roc scores formatted for doIMRMC
threshold	The threshold for determining binary decisions

Value

a list of two data frames (df.tpf and df.fpf) both formatted for doIMRMC

 roeMetzConfigs

 roeMetzConfigs

Description

This is a data frame containing the configuration parameters used in Roe1997_Acad-Radiol_v4p298. Each row corresponds to one of the twelve configurations appearing in Table 1 of that paper in a format that can be the input to `sim.gRoeMetz`.

Details

The columns of this data frame are as follows

- Experiment labels and size
 - `modalityID.A`: [chr] label modality A
 - `modalityID.B`: [chr] label modality B
 - `nR`: [num] number of readers
 - `nC.neg`: [num] number of signal-absent cases
 - `nC.pos`: [num] number of signal-present cases
- There are six fixed effects:
 - `mu.neg`: [num] signal-absent (neg, global mean)
 - `mu.pos`: [num] signal-present (pos, global mean)
 - `mu.Aneg`: [num] modality A signal-absent (Aneg, modality effect)
 - `mu.Bneg`: [num] modality B signal-absent (Bneg, modality effect)
 - `mu.Apos`: [num] modality A signal-present (Apos, modality effect)
 - `mu.Bpos`: [num] modality B signal-present (Bpos, modality effect)
- There are six random effects that are independent of modality
 - `var_r.neg`: [num] variance of random reader effect
 - `var_c.neg`: [num] variance of random case effect
 - `var_rc.neg`: [num] variance of random reader by case effect
 - `var_r.pos`: [num] variance of random reader effect
 - `var_c.pos`: [num] variance of random case effect
 - `var_rc.pos`: [num] variance of random reader by case effect
- There are six random effects that are specific to modality A
 - `var_r.Aneg`: [num] variance of random reader effect
 - `var_c.Aneg`: [num] variance of random case effect
 - `var_rc.Aneg`: [num] variance of random reader by case effect
 - `var_r.Apos`: [num] variance of random reader effect
 - `var_c.Apos`: [num] variance of random case effect
 - `var_rc.Apos`: [num] variance of random reader by case effect
- There are six random effects that are specific to modality B

- var_r.Bneg: [num] variance of random reader effect
- var_c.Bneg: [num] variance of random case effect
- var_rc.Bneg: [num] variance of random reader by case effect
- var_r.Bpos: [num] variance of random reader effect
- var_c.Bpos: [num] variance of random case effect
- var_rc.Bpos: [num] variance of random reader by case effect

sim.gRoeMetz	<i>Simulate an MRMC data set of an ROC experiment comparing two modalities</i>
--------------	--

Description

This procedure simulates an MRMC data set of an ROC experiment comparing two modalities. It is based on Gallas2014_J-Med-Img_v1p031006, which generalizes of the model in Roe1997_Acad-Radiol_v4p298 and Roe1997_Acad-Radiol_v4p587. Specifically, it allows the variance components to depend on the truth and the modality. For the simpler Roe and Metz model, you can enter the smaller set of parameters into sim.gRoeMetz.config and get back the larger set of parameters and then used with this function.

Usage

```
sim.gRoeMetz(config)
```

Arguments

- | | |
|--------|--|
| config | <p>[list] of simulation parameters:</p> <ul style="list-style-type: none"> • Experiment labels and size <ul style="list-style-type: none"> - modalityID.A: [chr] label modality A - modalityID.B: [chr] label modality B - nR: [num] number of readers - nC.neg: [num] number of signal-absent cases - nC.pos: [num] number of signal-present cases • There are six fixed effects: <ul style="list-style-type: none"> - mu.neg: [num] signal-absent (neg, global mean) - mu.pos: [num] signal-present (pos, global mean) - mu.Aneg: [num] modality A signal-absent (Aneg, modality effect) - mu.Bneg: [num] modality B signal-absent (Bneg, modality effect) - mu.Apos: [num] modality A signal-present (Apos, modality effect) - mu.Bpos: [num] modality B signal-present (Bpos, modality effect) • There are six random effects that are independent of modality <ul style="list-style-type: none"> - var_r.neg: [num] variance of random reader effect - var_c.neg: [num] variance of random case effect - var_rc.neg: [num] variance of random reader by case effect |
|--------|--|

- var_r.pos: [num] variance of random reader effect
- var_c.pos: [num] variance of random case effect
- var_rc.pos: [num] variance of random reader by case effect
- There are six random effects that are specific to modality A
 - var_r.Aneg: [num] variance of random reader effect
 - var_c.Aneg: [num] variance of random case effect
 - var_rc.Aneg: [num] variance of random reader by case effect
 - var_r.Apos: [num] variance of random reader effect
 - var_c.Apos: [num] variance of random case effect
 - var_rc.Apos: [num] variance of random reader by case effect
- There are six random effects that are specific to modality B
 - var_r.Bneg: [num] variance of random reader effect
 - var_c.Bneg: [num] variance of random case effect
 - var_rc.Bneg: [num] variance of random reader by case effect
 - var_r.Bpos: [num] variance of random reader effect
 - var_c.Bpos: [num] variance of random case effect
 - var_rc.Bpos: [num] variance of random reader by case effect

Details

The simulation is a linear model with six fixed effects related to modality and truth and 18 normally distributed independent random effects for readers, cases, and the interaction between the two. Here is the linear model:

$$L.mrct = \mu.t + \mu.mt + \text{reader.rt} + \text{case.ct} + \text{readerXcase.rct} + \text{modalityXreader.mrt} + \text{modalityXcase.mct} + \text{modalityXreaderXcase.mrct}$$

- m=modality (levels: A and b)
- t=truth (levels: neg and Pos)
- $\mu.t$ is the global mean for t=neg and t=pos cases
- $\mu.mt$ is the modality specific fixed effects for t=neg and t=pos cases
- the remaining terms are the random effects: all independent normal random variables

Value

dFrame.imrmc [data.frame] with $(nC.neg + nC.pos) \cdot (nR+1)$ rows including

- readerID: [Factor] w/ nR levels "reader1", "reader2", ...
- caseID: [Factor] w/ nC levels "case1", "case2", ...
- modalityID: [Factor] w/ 1 level config\$modalityID
- score: [num] reader score

Note that the first $nC.neg + nC.pos$ rows specify the truth labels for each case. For these rows, the readerID must be "truth" and the score must be 0 for negative cases and 1 for positive cases.

sim.gRoeMetz.config *Create a configuration object for the sim.gRoeMetz program*

Description

This function creates a configuration object for the Roe & Metz simulation model to be used as input for the sim.gRoeMetz program. The default model returned when there are no arguments given to the function is the "HH" model from Roe1987_Acad-Radiol_v4p298. Following that paper, The user can specify three parameters related to experiment size (nR, nC.neg, nC.pos) and five parameters parameters specifying a linear model that does not depend on modality or truth (mu.neg, mu.pos, var_r, var_c, var_rc).

Usage

```
sim.gRoeMetz.config(
  nR = 5,
  nC.neg = 40,
  nC.pos = 40,
  mu.neg = 0,
  mu.pos = 1,
  var_r = 0.03,
  var_c = 0.3,
  var_rc = 0.2
)
```

Arguments

nR	Number of readers (default = 5)
nC.neg	Number of signal-absent cases (default = 25)
nC.pos	Number of signal-present cases (default = 25)
mu.neg	Mean fixed effect of signal-absent distribution (default = 0.0) Modality specific parameters are set to zero: mu.Aneg = mu.Bneg = 0
mu.pos	Mean fixed effect of signal-present distribution (default = 1.0) Modality specific parameters are set to zero: mu.Apos = mu.Bpos = 0
var_r	Variance of reader random effect (default = 0.03) var_r.neg = var_r.pos = var_r.Aneg = var_r.Apos = var_r.Bneg = var_r.Bpos = var_r
var_c	Variance of case random effect (default = 0.30) var_c.neg = var_c.pos = var_c.Aneg = var_c.Apos = var_c.Bneg = var_c.Bpos = var_c
var_rc	Variance of reader.by.case random effect (default = 0.20) var_rc.neg = var_rc.pos = var_rc.Aneg = var_rc.Apos = var_rc.Bneg = var_rc.Bpos = var_rc

Details

If no arguments, this function returns a default simulation configuration for `sim.gRoeMetz`

Value

`config` [list] Refer to the `sim.gRoeMetz` input variable

simMRMC

Simulate an MRMC data set

Description

This program simulates observations from one set of readers scoring one set of cases. It produces one modality and one truth state of ROC data following Roe1997_Acad-Radiol_v4p298 and Roe1997_Acad-Radiol_v4p587. In order to produce an entire ROC data set, please use `sim.gRoeMetz`.

Usage

```
simMRMC(simMRMC.config)
```

Arguments

`simMRMC.config` [list] of simulation parameters:

- `modalityID` [chr] label modalityID
- `readerIDs` [factor] the ID of each reader
- `caseIDs` [factor] the ID of each case
- `mu` [num] mean
- `var_r` [num] variance of random reader effect
- `var_c` [num] variance of random case effect
- `var_rc` [num] variance of random reader by case effect

Details

The simulation is a linear model with one fixed effect and three normally distributed independent random effects corresponding to readers, cases, and an interaction between the two.

$$L.rc = \mu + \text{readerEffect.r} + \text{caseEffect.c} + \text{readerXcaseEffect.rc}$$
Value

`L` [data.frame] with `nC*nR` rows of 4 variables

- `L$modalityID` [factor] determined by input `modalityID`
- `L$readerID` [factor] determined by input `readerIDs`
- `L$caseID` [factor] determined by input `caseIDs`
- `L$score` [num] $R.r + C.c + RC.rc$

- $r = 1, 2, \dots, nR$
- $c = 1, 2, \dots, nC$
- $R.r \sim N(0, \text{var}_r)$
- $C.c \sim N(0, \text{var}_c)$
- $RC.rc \sim N(0, \text{var}_{rc})$

simRoeMetz.example *Simulates a sample MRMC ROC experiment*

Description

Simulates a sample MRMC ROC experiment

Usage

simRoeMetz.example()

Value

dFrame.imrmc [data.frame] Please refer to the description of the simRoeMetz return variable

successDFtoROCdf *Convert an MRMC data frame of successes to one formatted for doIM-RMC*

Description

Convert an MRMC data frame of successes to one formatted for doIMRMC

Usage

successDFtoROCdf(df)

Arguments

df Each row contains a success observation for one reader evaluating one case

Value

data frame ready for doIMRMC

undoIMRMCdf	<i>Convert a doIMRMC formatted data frame to a standard data frame with all factors.</i>
-------------	--

Description

Convert a doIMRMC formatted data frame to a standard data frame with all factors.

Usage

```
undoIMRMCdf(df.MRMC)
```

Arguments

df.MRMC	This data frame includes columns for readerID, caseID, modalityID, score. Each row is a reader x case x modality observation from the study. In addition to observations from the study, this data frame requires rows specifying the truth for each caseID. For truth specifications, the readerID needs to equal "truth" or "-1", modalityID can be anything ("truth" is a good choice), and score should be 0 for signal-absent normal case, 1 for signal-present disease case.
---------	--

Details

Delete rows specifying truth and put the truth information on every row.

Value

output a data frame with columns readerID, caseID, modalityID, score, truth

uStat11	<i>Analysis of U-statistics degree 1,1</i>
---------	--

Description

These two functions calculate the mean and variance of a user-specified U-statistic kernel, which is a function of cross-correlated scores.

The motivation for this analysis is data collected in imaging studies where multiple readers read multiple cases in different modes or modalities. The goal is to evaluate the variance of a reader- and case-averaged endpoint, accounting for cross-correlated data arising from two random effects: the random reader skill and the random case difficulty. This analysis is sometimes referred to as an MRMC analysis. Of course, the random effects can be from sources other than readers and cases.

Usage

```

uStat11.jointD(
  df.input,
  modalitiesToCompare,
  kernelFlag = 1,
  keyColumns = c("readerID", "caseID", "modalityID", "score")
)

uStat11.conditionalD(
  df.input,
  modalitiesToCompare,
  kernelFlag = 1,
  keyColumns = c("readerID", "caseID", "modalityID", "score")
)

```

Arguments

<code>df.input</code>	Data frame of observations, one per row. Columns identify random effects, fixed effects, and the observation. Namely, <ul style="list-style-type: none"> • <code>readerID</code>: The factor corresponding to the different readers in the study. The <code>readerID</code> is treated as a random effect. • <code>caseID</code>: The factor corresponding to the different cases in the study. The <code>caseID</code> is treated as a random effect. • <code>modalityID</code>: The factor corresponding to the different modalities in the study. The <code>modalityID</code> is treated as a fixed effect. • <code>score</code>: The score given by the reader to the case for the modality indicated.
<code>modalitiesToCompare</code>	The factors identifying the modalities to compare.
<code>kernelFlag</code>	This determines the kernel function <ul style="list-style-type: none"> • <code>kernelFlag = 1</code> == identity kernel: requires two modalities: A,B. • <code>kernelFlag = 2</code> == kernel of the difference in modalities: requires four modalities: A,B,C,D.
<code>keyColumns</code>	Identify the factors corresponding to the <code>readerID</code> , <code>caseID</code> , <code>modalityID</code> , and <code>score</code> (or alternative random and fixed effects).

Details

`uStat11.conditionalD` is identical to `uStat11.jointD` when the study is fully-crossed: when every reader reads all the cases in both modalities. For arbitrary study designs the two functions differ according to how the components of variance are estimated.

- `uStat11.conditionalD` follows Gallas2007_J-Opt-Soc-Am-A_v24pB70 <doi:10.1364/JOSAA.24.000B70> and estimates the components of variance (which isolate combinations of different random effects) with nested conditional means.
- `uStat11.jointD` is analogous to the method in Gallas2008_Neural-Networks_v21p387 <doi:10.1016/j.neunet.2007.12> and estimates the components of variance (which isolate combinations of different random effects) with a joint distribution over all the observations giving equal weight to each one.

Both functions yield unbiased variance estimates. Our simulations find that `uStat11.conditionalD` is statistically more efficient than `uStat11.jointD` (its variance estimate is more precise), but it is slower.

Please refer to the `tests/testthat` folder of the package for examples using these functions.

Value

This function calculates the mean and variance of the indicated U-statistic kernel, which is a function of the scores. For the identity kernel, we simply return the mean and variance of the scores.

The function returns a list of outputs. Many of these outputs have three elements.

- If `kernelFlag = 1` == identity kernel, the first element corresponds to the mean score of modality A, the second corresponds to mean score of modality B, and the third corresponds to the mean of the difference in scores from modality A and B.
- If `kernelFlag = 2` == difference kernel, the first element corresponds to the mean difference in scores from modalities A and B, the second element corresponds to the mean difference in scores from modalities C and D, and the third elements corresponds to the difference of the just-mentioned differences.

There are 16 outputs:

- `mean`: See description above.
- `var`: The variance of the mean.
- `var.1obs`: The variance of one reader-case-modality observation.
- `meanPerR` The reader-specific means.
- `nR` The number of readers in the study.
- `nC` The number of cases in the study.
- `nCperR` The number of cases evaluated by each reader for each modality.
- `moments` The second order moments of the problem.
- `coeff` The coefficients corresponding to the second-order moments such that the scalar product between the moments and coefficients yields the variance.
- `kernel.A` A matrix showing the kernel evaluated for each combination of each reader and case for modality A (or AB).
- `design.A` A matrix showing the what data exists for each combination of each reader and case for modality A (or AB).
- `kernel.B` A matrix showing the kernel evaluated for each combination of each reader and case for modality B (or CD).
- `design.B` A matrix showing the what data exists for each combination of each reader and case for modality B (or CD).

Examples

```
# Create an MRMC data frame
# Refer to Gallas2014_J-Med-Img_v1p031006
simRoeMetz.config <- sim.gRoeMetz.config()
```

```

# Simulate data
df.MRMC <- sim.gRoeMetz(simRoeMetz.config)

# Reformat data
df <- undoIMRMCdf(df.MRMC)

# Grab part of the data
df <- droplevels(df[grepl("pos", df$caseID), ])

#### uStat11.jointD.identity ####
# Calculate the reader- and case-averaged difference in scores from testA and testB
# (kernelFlag = 1 specifies the U-statistics kernel to be the identity)
result.jointD.identity <- uStat11.jointD(
  df,
  kernelFlag = 1,
  keyColumns = c("readerID", "caseID", "modalityID", "score"),
  modalitiesToCompare = c("testA", "testB"))

cat("\n")
cat("uStat11.jointD.identity \n")
print(result.jointD.identity[1:2])

```

uStat11.diff

Create the kernel and design matrices for uStat11

Description

The kernel is the difference kernel

Usage

```

uStat11.diff(
  df.input,
  modalitiesToCompare,
  keyColumns = c("readerID", "caseID", "modalityID", "score")
)

```

Arguments

df.input	Data frame of observations, one per row. Columns also identify random and fixed effects.
modalitiesToCompare	The factors identifying the modalities to compare
keyColumns	The required columns

uStat11.identity *Create the kernel and design matrices for uStat11*

Description

The kernel is the identity kernel

Usage

```
uStat11.identity(  
  df.input,  
  modalitiesToCompare,  
  keyColumns = c("readerID", "caseID", "modalityID", "score")  
)
```

Arguments

df.input	Data frame of observations, one per row. Columns also identify random and fixed effects.
modalitiesToCompare	The factors identifying the modalities to compare
keyColumns	The required columns

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