Package 'RJafroc'

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Type Package

Title Analyzing Diagnostic Observer Performance Studies

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Depends R (>= 3.5.0)

Imports bbmle, binom, dplyr, ggplot2, mvtnorm, numDeriv, openxlsx,
Rcpp, stats, stringr, tools, utils

Suggests rmarkdown

LinkingTo Rcpp

Description Implements software for assessing medical imaging systems, radiologists or computer aided detection algorithms.
Models of observer performance are implemented, including the binormal model (BM), the contaminated binormal model (CBM), the
correlated contaminated binormal model (CORCBM), and the radiological search model (RSM). The software and applications are
described in a book - Chakraborty DP: Observer Performance Methods for Diagnostic Imaging - Foundations, Modeling, and
Applications with R-Based Examples. Taylor-Francis LLC; 2017 -
and its vignettes <https://dpc10ster.github.io/RJafroc/>.
Observer performance data collection paradigms are the receiver operating characteristic (ROC) and its location specific
extensions, primarily free-response ROC (FROC) and the location ROC (LROC). ROC data consists of single ratings per images.
A rating is the perceived confidence level that the image is that of a diseased patient. FROC data consists of a variable
number (including zero) of mark-
rating pairs per image, where a mark is the location of a clinically reportable suspicious region
and the rating is the corresponding confidence level that it is a real lesion. LROC data consists of a rating and a forced
localization of the most suspicious region on every image. RJafroc supersedes the Windows version of JAFROC software
V4.2.1, <http://www.devchakraborty.com>:. Package functions are organized as follows. Data file related function names are
preceded by Df, curve fitting functions by Fit, included data sets by dataset, plotting functions by

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Plot, significance testing functions by St, sample size related functions by Ss, data simulation functions
by Simulate and utility functions by Util. Implemented are figures of merit (FOMs) for quantifying performance,
functions for visualizing empirical operating characteristics: e.g., ROC, FROC, alternative FROC (AFROC) and weighted AFROC
(wAFROC) curves. Four maximum likelihood curve-
fitting algorithms are implemented: the binormal model (BM), the contaminated
binormal model (CBM), the correlated contaminated binormal model (CORCBM) and the radiological search model (RSM). Unlike the
binormal model, CBM, CORCBM and RSM predict ``proper'' ROC curves that do not cross the chance diagonal. RSM fitting additionally
yields measures of search and lesion-
classification performances. Search performance is the ability to find lesions while avoiding finding non-lesions. Lesion-
classification performance is the ability to correctly classify found lesions from found non-lesions. For fully crossed study designs significance testing of reader-
averaged FOM differences between modalities is
implemented via both Dorfman-Berbaum-Metz and the Obuchowski-
Rockette methods, including Hillis' extensions. Also implemented are
single treatment analyses, which allow comparison of performance of a group of radiologists to a specified value, or comparison
to CAD to a group of radiologists interpreting the same cases. Crossed-
modality analysis is implemented wherein there are two crossed
treatment factors and the desire is to determined performance in each treatment factor averaged over all levels of the other factor.
Sample size estimation tools are provided for ROC and FROC studies; these use estimates of the relevant variances from a pilot study
to predict required numbers of readers and cases in a pivotal study to achieve a desired power. Utility and data file manipulation
functions allow data to be read in any of the currently used input formats, including Excel, and the results of the analysis can be
viewed in text or Excel output files. The methods are illustrated with several included datasets from the author's international
collaborations. This version corrects a few bugs noticed by users and extends the Excel file input format for
greater flexibility in handling non-
crossed datasets and the sample size routines have been rewritten for ease of use.

License GPL-3

LazyData true

URL https://dpc10ster.github.io/RJafroc/

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Author Dev Chakraborty [cre, aut, cph],
    Peter Philips [aut],

Xuetong Zhai [aut],
Lucy D'Agostino McGowan [ctb],
Alejandro RodriguezRuiz [ctb]

Maintainer Dev Chakraborty `<dpc10ster@gmail.com>`

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R **topics documented:**

RJafroc-package	*RJafroc: Analyzing Diagnostic Observer Performance Studies*

Description

RJafroc implements software for assessing medical imaging systems, radiologists or computer aided detection algorithms. Models of observer performance are implemented, including the binormal model (BM), the contaminated binormal model (CBM), the correlated contaminated binormal model (CORCBM), and the radiological search model (RSM). The software and applications are described in a book - **Chakraborty DP: Observer Performance Methods for Diagnostic Imaging - Foundations, Modeling, and Applications with R-Based Examples. Taylor-Francis LLC; 2017** and its vignettes https://dpc10ster.github.io/RJafroc/. Observer performance data collection paradigms are the receiver operating characteristic (ROC) and its location specific extensions, primarily free-response ROC (FROC) and the location ROC (LROC). ROC data consists of single ratings per images. A rating is the perceived confidence level that the image is that of a diseased patient. FROC data consists of a variable number (including zero) of mark-rating pairs per image, where a mark is the location of a clinically reportable suspicious region and the rating is the corresponding confidence level that it is a real lesion. LROC data consists of a rating and a forced localization of the most suspicious region on every image. RJafroc supersedes the Windows version of **JAFROC** software V4.2.1, http://www.devchakraborty.com. Package functions are organized as follows. Data file related function names are preceded by *Df*, curve fitting functions by *Fit*, included data sets by *dataset*, plotting functions by *Plot*, significance testing functions by *St*, sample size related functions by *Ss*, data simulation functions by *Simulate* and utility functions by *Util*. Implemented are figures of merit (FOMs) for quantifying performance, functions for visualizing empirical operating characteristics: e.g., ROC, FROC, alternative FROC (AFROC) and weighted AFROC (wAFROC) curves. Four maximum likelihood curve-fitting algorithms are implemented: the binormal model (BM), the contaminated binormal model (CBM), the correlated contaminated binormal model (CORCBM) and the radiological search model (RSM). Unlike the binormal model, CBM, CORCBM and RSM predict "proper" ROC curves that do not cross the chance diagonal. RSM fitting additionally yields measures of search and lesion-classification performances. Search performance is *the ability to find lesions while avoiding finding non-lesions*. Lesion-classification performance is the ability to correctly classify found lesions from found non-lesions. For fully crossed study designs significance testing of reader-averaged FOM differences between modalities is implemented via both Dorfman-Berbaum-Metz and the Obuchowski-Rockette methods, including Hillis' extensions. Also implemented are single treatment analyses, which allow comparison of performance of a group of radiologists to a specified value, or comparison to CAD to a group of radiologists interpreting the same cases. Crossed-modality analysis is implemented wherein there are two crossed treatment factors and the desire is to determined performance in each treatment factor averaged over all levels of the other factor. Sample size estimation tools are provided for ROC and FROC studies; these use estimates of the relevant variances from a pilot study to predict required numbers of readers and cases in a pivotal study to achieve a desired power. Utility and data file manipulation functions allow data to be read in any of the currently used input formats, including Excel, and the results of the analysis can be viewed in text or Excel output files. The methods are illustrated with several included datasets from the author's international collaborations. This version corrects a few bugs noticed by users (listed in NEWS.md) and extends the Excel file input format for greater flexibility going forward in handling non-crossed datasets.

Details

Package:	RJafroc
Type:	Package
Version:	1.3.2
Date:	2020-01-13
License:	GPL-3
URL:	https://dpc10ster.github.io/RJafroc/

Abbreviations and definitions

- a: The separation or "a" parameter of the binormal model

- AFROC curve: plot of LLF (ordinate) vs. FPF, where FPF is inferred using highest rating of NL marks on **non-diseased cases**

- AFROC: alternative FROC, see Chakraborty 1989

- AFROC1 curve: plot of LLF (ordinate) vs. FPF1, where FPF1 is inferred using highest rating of NL marks on **ALL cases**

- $alpha$: The significance level α of the test of the null hypothesis of no treatment effect

- AUC: area under curve; e.g., ROC-AUC = area under ROC curve, an example of a FOM

- b: The width or "b" parameter of the conventional binormal model

- Binormal model: two unequal variance normal distributions, one at zero and one at mu, for modeling ROC ratings, $sigma$ is the std. dev. ratio of diseased to non-diseased distributions

- CAD: computer aided detection algorithm

- CBM: contaminated binormal model (CBM): two equal variance normal distributions for modeling ROC ratings, the diseased distribution is bimodal, with a peak at zero and one at μ, the integrated fraction at μ is α (not to be confused with α of NH testing)

- CI: The (1-α) confidence interval for the stated statistic

- Crossed modality: a dataset containing two modality (treatment) factors, with the levels of the two factors crossed, see paper by Thompson et al

- DBM: Dorfman-Berbaum-Metz, a significance testing method for detecting a treatment effect in MRMC studies

- DBMH: Hillis' modification of the DBM method

- ddf: Denominator degrees of freedom of appropriate F-test; the corresponding ndf is I - 1

- Empirical AUC: trapezoidal area under curve, same as the Wilcoxon statistic for ROC paradigm

- FN: false negative, a diseased case classified as non-diseased

- FOM: figure of merit, a quantitative measure of performance, performance metric

- FP: false positive, a non-diseased case classified as diseased

- FPF: number of FPs divided by number of non-diseased cases

- FROC curve: plot of LLF (ordinate) vs. NLF

- FROC: free-response ROC (a data collection paradigm where each image yields a random number, 0, 1, 2,..., of mark-rating pairs)

- FRRC: Analysis that treats readers as fixed and cases as random factors

- I: total number of modalities, indexed by i

- image/case: used interchangeably; a case can consist of several images of the same patient in the same treatment

- iMRMC: A text file format used for ROC data by FDA/CDRH researchers

- individual: A single-treatment single-reader dataset.

- Intrinsic: Used in connection with RSM; a parameter that is independent of the RSM μ parameter, but whose meaning may not be as transparent as the corresponding physical parameter

- J: number of readers, indexed by j

- JAFROC file format: A .xlsx format file, applicable to ROC, ROI, FROC and LROC paradigms

- JAFROC AUC: trapezoidal area under AFROC curve; deprecated, use AFROC AUC instead

- JAFROC: jackknife AFROC: Windows software for analyzing observer performance data: no longer updated, replaced by current package; the name is a misnomer as the jackknife is used only for significance testing; alternatively, the bootstrap could be used; what distinguishes FROC from ROC analysis is the use of the AFROC-AUC as the FOM. With this change, the DBM or the OR method can be used for significance testing

- FOM_AFROC FOM: trapezoidal area under AFROC curve; this term is obsolete; use AFROC-AUC instead

- FOM_AFROC1 FOM: trapezoidal area under AFROC1 curve; this term is obsolete; use AFROC1-AUC instead

- K: total number of cases, K = K1 + K2, indexed by k

- K1: total number of non-diseased cases, indexed by $k1$

- K2: total number of diseased cases, indexed by $k2$

- LL: lesion localization i.e., a mark that correctly locates an existing localized lesion; TP is a special case, when the proximity criterion is lax (i.e., "acceptance radius" is large)

- LLF: number of LLs divided by the total number of lesions

- LROC: location receiver operating characteristic, a data collection paradigm where each image yields a single rating and one location

- lrc/MRMC: A text file format used for ROC data by University of Iowa researchers

- mark: the location of a suspected diseased region

- maxLL: maximum number of lesions per case in dataset

- maxNL: maximum number of NL marks per case in dataset

- MRMC: multiple reader multiple case (each reader interprets each case in each treatment, i.e. fully crossed study design)

- ndf: Numerator degrees of freedom of appropriate F-test, usually number of treatments minus one

- NH: The null hypothesis that all treatment effects are zero; rejected if the p-value is smaller than α

- NL: non-lesion localization, of which FP is a special case, i.e., a mark that does not correctly locate any existing localized lesion(s)
- NLF: number of NLs divided by the total number of cases
- Operating characteristic: A plot of normalized correct decisions on diseased cases along ordinate vs. normalized incorrect decisions on non-diseased cases
- Operating point: A point on an operating characteristic, e.g., (FPF, TPF) represents an operating point on an ROC
- OR: Obuchowski-Rockette, a significance testing method for detecting a treatment effect in MRMC studies
- ORH: Hillis' modification of the OR method
- Physical parameter: Used in connection with RSM; a parameter whose meaning is more transparent than the corresponding intrinsic parameter, but which depends on the RSM μ parameter
- Proximity criterion / acceptance radius: Used in connection with FROC (or LROC data); the "nearness" criterion is used to determine if a mark is close enough to a lesion to be counted as a LL (or correct localization); otherwise it is counted as a NL (or incorrect localization)
- p-value: the probability, under the null hypothesis, that the observed treatment effects, or larger, could occur by chance
- Proper: a proper fit does not inappropriately fall below the chance diagonal, does not display a "hook" near the upper right corner
- PROPROC: Metz's binormal model based fitting of proper ROC curves
- RSM, Radiological Search Model: two unit variance normal distributions for modeling NL and LL ratings; four parameters, μ, ν', λ' and $\zeta 1$
- Rating: Confidence level assigned to a case; higher values indicate greater confidence in presence of disease; `-Inf` is allowed but `NA` is not allowed
- Reader/observer/radiologist/CAD: used interchangeably
- RJafroc: the current software
- ROC: receiver operating characteristic, a data collection paradigm where each image yields a single rating and location information is ignored
- ROC curve: plot of TPF (ordinate) vs. FPF, as threshold is varied; an example of an operating characteristic
- ROCFIT: Metz software for binormal model based fitting of ROC data
- ROI: region-of-interest (each case is divided into a number of ROIs and the reader assigns an ROC rating to each ROI)
- FRRC: Analysis that treats readers as fixed and cases as random factors
- RRFC: Analysis that treats readers as random and cases as fixed factors
- RRRC: Analysis that treats both readers and cases as random factors
- RSCORE-II: original software for binormal model based fitting of ROC data
- RSM: Radiological search model, also method for fitting a proper ROC curve to ROC data
- RSM-$\zeta 1$: Lowest reporting threshold, determines if suspicious region is actually marked
- RSM-λ: Intrinsic parameter of RSM corresponding to λ', independent of μ

- RSM-λ': Physical Poisson parameter of RSM, average number of latent NLs per case; depends on μ
- RSM-μ: separation of the unit variance distributions of RSM
- RSM-ν: Intrinsic parameter of RSM, corresponding to ν', independent of μ
- RSM-ν': binomial parameter of RSM, probability that lesion is found
- SE: sensitivity, same as TPF
- Significance testing: determining the p-value of a statistical test
- SP: specificity, same as $1 - FPF$
- Threshold: Reporting criteria: if confidence exceeds a threshold value, report case as diseased, otherwise report non-diseased
- TN: true negative, a non-diseased case classified as non-diseased
- TP: true positive, a diseased case classified as diseased
- TPF: number of TPs divided by number of diseased cases
- Treatment/modality: used interchangeably, for example, computed tomography (CT) images vs. magnetic resonance imaging (MRI) images
- wAFROC curve: plot of weighted LLF (ordinate) vs. FPF, where FPF is inferred using highest rating of NL marks on **non-diseased cases ONLY**
- wAFROC1 curve: plot of weighted LLF (ordinate) vs. FPF1, where FPF1 is inferred using highest rating of NL marks on **ALL cases**
- FOM_wAFROC FOM: weighted trapezoidal area under AFROC curve: this term is obsolete; use wAFROC-AUC instead;**this is the recommended FOM**
- FOM_wAFROC1 FOM: weighted trapezoidal area under AFROC1 curve: only use if there are zero non-diseased cases is always number of treatments minus one

Dataset

An R object either created by the user or read from an external text or Excel file. It is a `list` generally containing 8 members (9 members for crossed-modality or LROC datasets): **Note: `-Inf` is used to indicate the ratings of unmarked lesions and/or to indicate missing array items. An example of the latter would be if the maximum number of NLs in a dataset was 4, but some images had fewer than 4 NLs, in which case the corresponding "empty" positions would be filled with `-Inf`s. Do not use `NA` to denote a rating.**

Note: **"dataset" in this package always represents an `R` object with one of the following structures:**

General data structure, example `dataset02` and `dataset05`:

- `NL`: a floating-point array with dimension `c(I,J,K,maxNL)` containing the ratings of NL marks. The first K1 locations of the third index corresponds to NL marks on non-diseased cases and the remaining locations correspond to NL marks on diseased cases. The 4th dimension allows for the possibility of multiple NL marks on a case. For **FROC** datasets unavailable or missing NL ratings are assigned `-Inf`. For **ROC** datasets FP ratings are assigned to the first K1 elements of `NL[,,1:K1,1]` and the remaining K2 elements of `NL[,,(K1+1):K,1]` are set to `-Inf`. When converting from FROC to ROC data the software assigns `-Inf` to cases with no marks.

- LL: a floating-point array with dimension c(I,J,K2,maxLL) that contains the ratings of all LL marks. For ROC datasets TP ratings are assigned to LL[,,1:K2,1].
- lesionVector: a integer vector with length K2, whose elements indicate the number of lesions in each diseased case.
- lesionID: an integer array with dimension [K2, maxLL]. Its contents label lesions on diseased cases. For example, dataset05$lesionID[40,] is c(1,2,-Inf), meaning the 40th diseased case in this dataset has two lesions, labeled 1 and 2. The lesionID of an LL in the 'TP' or 'LL' worksheet must correspond to the lesionID for that case in the 'Truth' worksheet. For example, if the lesionID for the 40th diseased case in the 'TP' or 'LL' worksheet is 2, then the associated rating must correspond to the lesion labeled 2 in the 'Truth' worksheet, etc.
- lesionWeight: a floating point array with dimension c(K2,maxLL), representing the relative importance of detecting each lesion. For each case, the weights sum to unity. If zero is assigned to the Weight field in the 'Truth' worksheet, the software automatically assigns equal weighting, e.g., dataset05$lesionWeight[40,] is c(0.5,0.5), corresponding to equal weights (1/2) to each lesion on an image with two lesions.
- dataType: a character variable: "ROC", "LROC", "ROI" or "FROC".
- modalityID: a character vector of length I, which labels the modalities in the dataset.
- readerID: a character vector of length J, which labels the readers. For example, NL[1,2,,] indicates the NL-rating of the reader identified with the second label in readerID using the modality identified with the first label in modalityID.

ROI data structure, example TBA**:**

- NL: a floating-point array with dimension c(I,J,K,Q) that contains the ratings of Q quadrants for each non-diseased case (k <= K1). For k > K1, elements contain valid ratings while the rest are filled with -Infs.
- LL: a floating-point array with dimension c(I,J,K2,1) that contains the ratings of all *correct* localization (CL) marks. A -Inf indicates a case with no CL mark.
- LLIl: a floating-point array with dimension c(I,J,K2,1) that contains the ratings of all *incorrect* localization (IL) marks. A -Inf indicates a case with no IL mark.
- lesionVector: same as general case.
- lesionID: lesionID: an integer vector with length K2 containing ones.
- lesionWeight: a floating point array with dimension c(K2,1) containing ones.
- dataType: a character variable: "ROI".
- modalityID: same as general case.
- readerID: same as general case.

LROC data structure, example datasetCadLroc**:**

- NL: a floating-point array with dimension c(I,J,K,1) that contains the ratings of FP marks. For the third index, the first K1 elements contain valid ratings while the rest are filled with -Infs.
- LLCl: a floating-point array with dimension c(I,J,K2,1) that contains the ratings of all *correct* localization (CL) marks. A -Inf indicates a case with no CL mark.
- LLIl: a floating-point array with dimension c(I,J,K2,1) that contains the ratings of all *incorrect* localization (IL) marks. A -Inf indicates a case with no IL mark.
- lesionVector: same as general case.

- lesionID: lesionID: an integer vector with length K2 containing ones.
- lesionWeight: a floating point array with dimension c(K2,1) containing ones.
- dataType: a character variable: "LROC".
- modalityID: same as general case.
- readerID: same as general case.

Crossed modality data structure, example datasetCrossedModality**:**

- NL: a floating-point array with dimension c(I1,I2,J,K,maxNL) that contains the ratings of NL marks. Note the existence of two modality indices.
- LL: a floating-point array with dimension c(I1,I2,J,K2,maxLL)that contains the ratings of all LL marks. Note the existence of two modality indices.
- lesionVector: same as general case.
- lesionID: same as general case.
- lesionWeight: same as general case.
- dataType: a character variable: "ROC" or "FROC".
- modalityID1: same as general case, corresponding to first modality factor.
- modalityID2: same as general case, corresponding to second modality factor.
- readerID: same as general case.

Data file format: The package reads JAFROC, MRMC (ROC data only) and iMRMC (ROC data only) data files. The data can be imported by using the function DfReadDataFile.

- **JAFROC data file format** The JAFROC data file is an Excel file containing three worksheets (*.xls and *.xlsx are supported): (1) the 'Truth' worksheet, (2) the 'TP' or 'LL' worksheet and (3) the 'FP' or 'NL' worksheet. Except for the 'Truth' worksheet, where each case must occur at least once, the number of rows in the other worksheets is variable.

  1. 'Truth' worksheet consists of
     - 'CaseID', an integer field uniquely labeling the cases (images). It must occur at least once for each case, and since a case may have multiple lesions, it can occur multiple times, once for each lesion.
     - 'LesionID', an integer field uniquely labeling the lesions in each case. This field is zero for non-diseased cases.
     - 'Weight', a floating-point field, which is the relative importance of detecting each lesion. This field is zero for non-diseased cases and for equally weighted lesions; otherwise the weights must sum to unity for each case. Unless a weighted figure of merit is selected, this field is irrelevant.

  2. 'TP' worksheet consists of
     - 'ReaderID', a character field uniquely labeling the readers (radiologists).
     - 'ModalityID', a character field uniquely labeling the modalities.
     - 'CaseID', see 'Truth' worksheet. A non-diseased case in this field will generate an error.
     - 'LesionID', see 'Truth' worksheet. An entry in this field that does not appear in the 'Truth' worksheet will generate an error. It is the user's responsibility to ensure that the entries in the 'Truth' and 'TP' worksheets correspond to the same physical lesions.
     - 'TP_Rating', a positive floating-point field denoting the rating assigned to a particular lesion-localization mark, with higher numbers represent greater confidence that the location is actually a lesion.

3. 'FP' worksheet consists of
   - 'ReaderID', see 'TP' worksheet.
   - 'ModalityID', see 'TP' worksheet.
   - 'CaseID', see 'TP' worksheet.
   - 'FP_Rating', a positive floating-point field denoting the rating assigned to a particular non-lesion-localization mark, with higher numbers represent greater confidence that the location is actually a lesion.

- **MRMC data file format / LABMRMC format**
  - *Input format for MRMC.* This format is described in the Medical Image Perception Laboratory website, currently <http://perception.radiology.uiowa.edu/>.
  - *LABMRMC data format.* The data file includes following parts. The file must be saved as plain text file with *.lrc extension. All items in the file are separated by one or more blank spaces.
    1. The first line is a free text description of the file.
    2. The second line is the name or ID of the first reader.
    3. The third line has the names or IDs of all the modalities. Each name or ID must be enclosed by double quotes(" ").
    4. The fourth line must have the letter (l or s) or word (large or small) for each modality. The letter or word indicates that smaller or larger ratings represent stronger confidence of presence of disease.
    5. The following lines contain the ratings in all modalities, separated by spaces or tabs, of the non-diseased cases, one case per line. The cases must appear in the same order for all readers. Missing value is not allowed.
    6. After the last non-diseased case insert a line containing the asterisk (*) symbol.
    7. Repeat steps 5 and 6 for the diseased cases.
    8. Repeat steps 2, 5, 6 and 7 for the remaining readers.
    9. The last line of the data file must be a pound symbol (#).

  iMRMC data format This is described in the iMRMC website, currently <https://code.google.com/p/imrmc/>.

Df: Datafile Related Functions

- `Df2RJafrocDataset`: Convert a ratings array to a dataset object.
- `DfBinDataset`: Return a binned dataset.
- `DfCreateCorCbmDataset`:Create paired dataset for testing FitCorCbmRoc.
- `DfExtractDataset`: Extract a subset of modalities and readers from a dataset.
- `DfFroc2Afroc`: Convert an FROC dataset to an AFROC dataset.
- `DfFroc2Roc`: Convert an FROC dataset to a highest rating inferred ROC dataset.
- `DfLroc2Roc`: Convert an LROC dataset to a highest rating inferred ROC dataset.
- `DfLroc2Froc`: Simulates an "AUC-equivalent" FROC dataset from a supplied LROC dataset.
- `DfFroc2Lroc`: Simulates an "AUC-equivalent" LROC dataset from a supplied FROC dataset.
- `DfReadCrossedModalities`: Read a crossed-modalities data file.
- `DfReadDataFile`: Read a general data file.

- `DfReadLrocDataFile`: Read a LROC data file.

- `DfSaveDataFile`: Save ROC data file in a different format.

- `DfExtractCorCbmDataset`: Extract two arms of a pairing from an MRMC ROC dataset suitable for using FitCorCbmRoc.

Fitting Functions

- `FitBinormalRoc`: Fit the binormal model to ROC data (R equivalent of ROCFIT or RSCORE).

- `FitCbmRoc`: Fit the contaminated binormal model (CBM) to ROC data.

- `FitRsmRoc`: Fit the radiological search model (RSM) to ROC data.

- `FitCorCbmRoc`: Fit the correlated contaminated binormal model (CORCBM) to paired ROC data.

- `FitRsmRoc`: Fit the radiological search model (RSM) to ROC data.

Plotting Functions

- `PlotBinormalFit`: Plot binormal-predicted ROC curve with provided BM parameters.

- `PlotEmpiricalOperatingCharacteristics`: Plot empirical operating characteristics for specified dataset.

- `PlotRsmOperatingCharacteristics`: Plot RSM-fitted ROC curves.

Simulation Functions

- `SimulateFrocDataset`: Simulates an uncorrelated FROC dataset using the RSM.

- `SimulateRocDataset`: Simulates an uncorrelated binormal model ROC dataset.

- `SimulateCorCbmDataset`: Simulates an uncorrelated binormal model ROC dataset.

- `SimulateLrocDataset`: Simulates an uncorrelated LROC dataset.

Sample size Functions

- `SsPowerGivenJK`: Calculate statistical power given numbers of readers J and cases K.

- `SsPowerTable`: Generate a power table.

- `SsSampleSizeKGivenJ`: Calculate number of cases K, for specified number of readers J, to achieve desired power for an ROC study.

Significance Testing Functions

- `StSignificanceTesting`: Perform significance testing, DBM or OR.

- `StSignificanceTestingCadVsRadiologists`: Perform significance testing, CAD vs. radiologists.

- `StSignificanceTestingCrossedModalities`: Perform significance testing using crossed modalities analysis.

- `StSignificanceTestingSingleFixedFactor`: Perform significance testing for single fixed factor analysis.

Miscellaneous and Utility Functions

- `Compare3ProperRocFits`: Compare three proper-ROC curve fitting models.
- `UtilAucBinormal`: Binormal model AUC function.
- `UtilAucCBM`: CBM AUC function.
- `UtilAucPROPROC`: PROPROC AUC function.
- `UtilAucsRSM`: RSM ROC/AFROC AUC calculator.
- `UtilFigureOfMerit`: Calculate empirical figures of merit (FOMs) for specified dataset.
- `UtilIntrinsic2PhysicalRSM`: Convert from intrinsic to physical RSM parameters.
- `UtilLesionDistr`: Calculates the lesion distribution matrix.
- `UtilLesionWeightsDistr`: Calculates the lesion weights matrix.
- `UtilMeanSquares`: Calculates the mean squares used in the DBMH and ORH methods.
- `UtilOutputReport`: Generate a formatted report file.
- `UtilPhysical2IntrinsicRSM`: Convert from physical to intrinsic RSM parameters.
- `UtilPseudoValues`: Return jackknife pseudovalues.
- `UtilVarComponentsDBM`: Utility for Dorfman-Berbaum-Metz variance components.
- `UtilVarComponentsOR`: Utility for Obuchowski-Rockette variance components.

Author(s)

- Creator: Dev Chakraborty <dpc10ster@gmail.com>.
- Creator: Xuetong Zhai <xuetong.zhai@gmail.com>.
- Contributor: Lucy D'Agostino McGowan <ld.mcgowan@vanderbilt.edu>.
- Contributor: Alejandro RodriguezRuiz <Alejandro.RodriguezRuiz@radboudumc.nl>.

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Basics of ROC

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ChisqrGoodnessOfFit	*Compute the chisquare goodness of fit statistic for ROC fitting model*

Description

Compute the chisquare goodness of fit statistic for specified ROC data fitting model

Usage

```
ChisqrGoodnessOfFit(fpCounts, tpCounts, parameters, model, lesDistr)
```

Arguments

fpCounts	The FP counts table
tpCounts	The TP counts table
parameters	The parameters of the model including cutoffs, see details
model	The fitting model: "BINORMAL", "CBM" or "RSM
lesDistr	The lesion distribution matrix; not needed for "BINORMAL" or "CBM" models. Array [1:maxLL,1:2]. The probability mass function of the lesion distribution for diseased cases. The first column contains the actual numbers of lesions per case. The second column contains the fraction of diseased cases with the number of lesions specified in the first column. The second column must sum to unity.

Details

For model = "BINORMAL" the parameters are c(a,b,zetas). For model = "CBM" the parameters are c(mu,alpha,zetas). For model = "RSM" the parameters are c(mu,lambdaP,nuP,zetas).

Value

The return value is a list with the following elements:

chisq	The chi-square statistic
pVal	The p-value of the fit
df	The degrees of freedom

Compare3ProperRocFits   *Compare three proper-ROC curve fitting models*

Description

Applies the Radiological Search Model (RSM) and the Contaminated Binormal Model (CBM) ROC-curve fitting methods to 14 datasets and compares the fits to Proper ROC (PROPROC) fits obtained using Windows software downloaded from the Univ. of Iowa ROC website ca. June 2017.

Usage

```
Compare3ProperRocFits(
  startIndx = 1,
  endIndx = 14,
  showPlot = FALSE,
  saveProprocLrcFile = FALSE,
  reAnalyze = FALSE
)
```

Arguments

startIndx	An integer in the range 1 to 14.
endIndx	An integer in the range 1 to 14, greater than or equal to `startIndx`.
showPlot	If TRUE the three plots are shown along with 95 percent confidence intervals on the lowest and uppermost operating points. The default is FALSE.
saveProprocLrcFile	
	If TRUE the binned datasets are saved for subsequent analysis using other ROC software, e.g., Windows DBM-MRMC. The default is FALSE.
reAnalyze	If TRUE the data is reanalyzed. The default is FALSE in which case the previously saved results are used.

Details

allDatasetsResults is a list-array of length (`endIndx - startIndx + 1`), where each element of the list-array is a list with 10 elements.

- allDatasetsResults[[1]][[1]]parameters of treatment 1 reader 1 in dataset `startIndx`
- allDatasetsResults[[1]][[2]]parameters of treatment 1 reader 2 in dataset `startIndx`
- allDatasetsResults[[1]][[IJ]]parameters of treatment I reader J in dataset `startIndx`
- allDatasetsResults[[2]][[1]]parameters of treatment 1 reader 1 in dataset `startIndx+1`
- allDatasetsResults[[2]][[2]]parameters of treatment 1 reader 2 in dataset `startIndx+1`
- allDatasetsResults[[2]][[IJ]]parameters of treatment I reader J in dataset `startIndx+1`
- allBinnedDatasets[[1]]binned ROC dataset corresponding to dataset `startIndx`
- allDatasetsResults[[2]][[IJ]]binned ROC dataset corresponding to dataset `startIndx+1`

A specific member, e.g., `allDatasetsResults[[1]][[1]]`, has the following structure:

- `retRsm` The RSM parameters following the output structure of `FitRsmRoc`
- `retCbm` The CBM parameters following the output structure of `FitCbmRoc`
- `lesDistr` The lesion distribution matrix
- `c1` The c-parameter of PROPROC
- `da` The d_sub_a parameter of PROPROC
- `aucProp` The PROPROC AUC
- `I` The number of treatments
- `J` The number of readers
- `K1` The number of non-diseased cases
- `K2` The number of diseased cases

The PROPROC parameters were obtained by running Windows software OR DBM-MRMC 2.50 (Sept. 04, 2014, Build 4) with **PROPROC** and **area** selected. The RSM and CBM fits are implemented in this package. Chapter 19 of the author's book has further details. If `saveProprocLrcFile` is TRUE, the `.lrc` files will be written to the `inst-MRMCRuns` directory, to appropriate subdirectory, **overwriting** any existing files.

Value

The returned value is a list of 2: `allDatasetsResults` containing the fitting results and `allBinnedDatasets` containing the binned datasets used in the fitting. See details.

References

Chakraborty DP (2017) *Observer Performance Methods for Diagnostic Imaging - Foundations, Modeling, and Applications with R-Based Examples*, CRC Press, Boca Raton, FL. https://www.crcpress.com/Observer-Performance-Methods-for-Diagnostic-Imaging-Foundations-Modeling/Chakraborty/p/book/9781482214840

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Dorfman DD, Berbaum KS, 2000 A contaminated binormal model for ROC data: Part II. A formal model Acad Radiol **7**, 427–437.

Examples

```
ret <- Compare3ProperRocFits(1,1) # analyze first two datasets

## Not run:
## takes longer than 5 sec on OSX
ret <- Compare3ProperRocFits(1,2,reAnalyze = TRUE) # analyze first two datasets
x <- ret$allDatasetsResults
str(x[[1]][[1]]) # parameters for dataset 1 trt 1 and rdr 1
str(x[[1]][[2]]) # parameters for dataset 1 trt 1 and rdr 2
str(x[[1]][[10]])# parameters for dataset 1 trt 2 and rdr 5
str(x[[2]][[1]]) # parameters for dataset 2 trt 1 and rdr 1
```

```
str(x[[2]][[2]]) # parameters for dataset 2 trt 1 and rdr 2
str(x[[2]][[10]])# parameters for dataset 2 trt 2 and rdr 5

## End(Not run)

## Not run:
## these examples will cause errors;
##these are intended to illustrate the structure of the functions return object
str(x[[1]][[11]])# error
str(x[[3]][[1]]) # error

## End(Not run)
```

---

dataset01   *TONY FROC dataset*

Description

This is referred to in the book as the "TONY" dataset. It consists of 185 cases, 89 of which are diseased, interpreted in two treatments ("BT" = breast tomosynthesis and "DM" = digital mammography) by five radiologists using the FROC paradigm. The diseased cases had at most two cancers (lesions) per case while the maximum number of non-lesion localizations (NLs) per case, over the entire dataset, was 3. The example below displays the wAFROC plot for the first treatment and first reader.

Usage

```
dataset01
```

Format

A list with 8 elements:

- NL Ratings array [1:2, 1:5, 1:185, 1:3], of non-lesion localizations, NLs
- LL Ratings array [1:2, 1:5, 1:89, 1:2], of lesion localizations, LLs
- lesionVector array [1:89], number of lesions per diseased case
- lesionID array [1:89, 1:2], labels of lesions on diseased cases
- lesionWeight array [1:89, 1:2], weights (or clinical importance) of lesions
- dataType "FROC", the data type
- modalityID [1:2] "BT" "DM", treatment labels
- readerID [1:5] "1" "2" "3" "4" ..., reader labels

References

Chakraborty DP, Svahn T (2011) Estimating the parameters of a model of visual search from ROC data: an alternate method for fitting proper ROC curves. PROC SPIE 7966.

Examples

```
str(dataset01)
PlotEmpiricalOperatingCharacteristics(dataset = dataset01, opChType = "wAFROC")$Plot
```

---

dataset02   *Van Dyke ROC dataset*

Description

This is referred to in the book as the "VD" dataset. It consists of 114 cases, 45 of which are diseased, interpreted in two treatments ("0" = single spin echo MRI, "1" = cine-MRI) by five radiologists using the ROC paradigm. Each diseased cases had an aortic dissection; the ROC paradigm generates one rating per case. Often referred to in the ROC literature as the Van Dyke dataset, which, along with the Franken dataset, has been widely used to illustrate advances in ROC methodology. The example below displays the ROC plot for the first treatment and first reader.

Usage

```
dataset02
```

Format

A list with 8 elements:

- NL Ratings array [1:2, 1:5, 1:114, 1], of false positives, FPs
- LL Ratings array [1:2, 1:5, 1:45, 1], of true positives, TPs
- lesionVector array [1:45], number of lesions per diseased case, all set to 1
- lesionID array [1:45, 1], labels of lesions on diseased cases, all set to 1
- lesionWeight array [1:45, 1], weights (or clinical importance) of lesions, all set to 1
- dataType "ROC", the data type
- modalityID [1:2] "0" "1", treatment labels
- readerID [1:5] "0" "1" "2" ..., reader labels

References

Van Dyke CW, et al. Cine MRI in the diagnosis of thoracic aortic dissection. 79th RSNA Meetings. 1993.

Examples

```
str(dataset02)
PlotEmpiricalOperatingCharacteristics(dataset = dataset02, opChType = "ROC")$Plot
```

---

dataset03 *Franken ROC dataset*

Description

This is referred to in the book as the "FR" dataset. It consists of 100 cases, 67 of which are diseased, interpreted in two treatments, "0" = conventional film radiographs, "1" = digitized images viewed on monitors, by four radiologists using the ROC paradigm. Often referred to in the ROC literature as the Franken-dataset, which, along the the Van Dyke dataset, has been widely used to illustrate advances in ROC methodology.

Usage

```
dataset03
```

Format

A list with 8 elements:

- NL Ratings array [1:2, 1:4, 1:100, 1], of false positives, FPs
- LL Ratings array [1:2, 1:4, 1:67, 1], of true positives, TPs
- lesionVector array [1:67], number of lesions per diseased case, all set to 1
- lesionID array [1:67, 1], labels of lesions on diseased cases, all set to 1
- lesionWeight array [1:67, 1], weights (or clinical importance) of lesions, all set to 1
- dataType "ROC", the data type
- modalityID [1:2] "TREAT1" "TREAT2", the treatment labels
- readerID [1:4] "READER_1" "READER_2" "READER_3" "READER_4", the reader labels

References

Franken EA, et al. Evaluation of a Digital Workstation for Interpreting Neonatal Examinations: A Receiver Operating Characteristic Study. Investigative Radiology. 1992;27(9):732-737.

Examples

```
str(dataset03)
PlotEmpiricalOperatingCharacteristics(dataset = dataset03, opChType = "ROC")$Plot
```

---

dataset04   *Federica Zanca FROC dataset*

Description

This is referred to in the book as the "FED" dataset. It consists of 200 mammograms, 100 of which
contained one to 3 simulated microcalcifications, interpreted in five treatments (basically different
image processing algorithms), by four radiologists using the FROC paradigm and a 5-point rating
scale. The maximum number of NLs per case, over the entire dataset was 7 and the dataset contained
at least one diseased mammogram with 3 lesions.

Usage

```
dataset04
```

Format

A list with 8 elements:

- `NL` Ratings array [1:5, 1:4, 1:200, 1:7], of non-lesion localizations, NLs

- `LL` Ratings array [1:5, 1:4, 1:100, 1:3], of lesion localizations, LLs

- `lesionVector` array [1:100], number of lesions per diseased case

- `lesionID` array [1:100, 1:3], labels of lesions on diseased cases, all set to 1

- `lesionWeight` array [1:100, 1:3] weights (or clinical importance) of lesions, all set to 1

- `dataType` "FROC", the data type

- `modalityID` [1:5] "1" "2" ... treatment labels

- `readerID` [1:4] "1" "3" "4" "5" reader labels

References

Zanca F et al. Evaluation of clinical image processing algorithms used in digital mammography.
Medical Physics. 2009;36(3):765-775.

Examples

```
str(dataset04)
PlotEmpiricalOperatingCharacteristics(dataset = dataset04, opChType = "wAFROC")$Plot
```

---

dataset05   *John Thompson FROC dataset*

Description

This is referred to in the book as the "JT" dataset. It consists of 92 cases, 47 of which are diseased, interpreted in two treatments ("1" = CT images acquired for attenuation correction, "2" = diagnostic CT images), by nine radiographers using the FROC paradigm. Each case was a slice of an anthropomorphic phantom 47 with inserted nodular lesions (max 3 per slice). The maximum number of NLs per case, over the entire dataset was 7.

Usage

```
dataset05
```

Format

A list with 8 elements:

- NL Ratings array [1:2, 1:9, 1:92, 1:7], of non-lesion localizations, NLs

- LL Ratings array [1:2, 1:9, 1:47, 1:3, of lesion localizations, LLs

- lesionVector array [1:47], number of lesions per diseased case

- lesionID array [1:47, 1:3], labels of lesions on diseased cases, all set to 1

- lesionWeight array [1:67, 1] weights (or clinical importance) of lesions, all set to 1

- dataType "FROC", the data type

- modalityID [1:2] "1" "2", treatment labels

- readerID [1:4] "1" "2" "3" "4", reader labels

References

Thompson JD et al. Effect of reconstruction methods and x-ray tube current-time product on nodule detection in an anthropomorphic thorax phantom: a crossed-treatment JAFROC observer study. Medical Physics. 2016;43(3):1265-1274.

Examples

```
str(dataset05)
PlotEmpiricalOperatingCharacteristics(dataset = dataset05, opChType = "wAFROC")$Plot
```

---

dataset06   *Magnus FROC dataset*

Description

This is referred to in the book as the "MAG" dataset (after Magnus Bath, who conducted the JAFROC analysis). It consists of 100 cases, 69 of which are diseased, interpreted in two treatments ("1" = conventional chest, "1" = chest tomosynthesis) by four radiologists using the FROC paradigm.

Usage

```
dataset06
```

Format

A list with 8 elements:

- NL Ratings array [1:2, 1:4, 1:89, 1:17], of non-lesion localizations, NLs
- LL Ratings array [1:2, 1:4, 1:42, 1:15], of lesion localizations, LLs
- lesionVector array [1:42], number of lesions per diseased case
- lesionID array [1:42, 1:15], labels of lesions on diseased cases, all set to 1
- lesionWeight array [1:42, 1:15] weights (or clinical importance) of lesions, all set to 1
- dataType "FROC", the data type
- modalityID [1:2] "1" "2", treatment labels
- readerID [1:4] "1" "2" ..., reader labels

References

Vikgren J et al. Comparison of Chest Tomosynthesis and Chest Radiography for Detection of Pulmonary Nodules: Human Observer Study of Clinical Cases. Radiology. 2008;249(3):1034-1041.

Examples

```
str(dataset06)
PlotEmpiricalOperatingCharacteristics(dataset = dataset06, opChType = "wAFROC")$Plot
```

---

dataset07   *Lucy Warren FROC dataset*

Description

This is referred to in the book as the "OPT" dataset (for OptiMam). It consists of 162 cases, 81 of which are diseased, interpreted in five treatments (see reference, basically different ways of acquiring the images) by seven radiologists using the FROC paradigm.

Usage

```
dataset07
```

Format

A list with 8 elements:

- NL Ratings array [1:5, 1:7, 1:162, 1:4], of non-lesion localizations, NLs

- LL Ratings array [1:5, 1:7, 1:81, 1:3], of lesion localizations, LLs

- lesionVector array [1:81], number of lesions per diseased case, all set to 1

- lesionID array [1:81, 1:3], labels of lesions on diseased cases, all set to 1

- lesionWeight array [1:81, 1:3] weights (or clinical importance) of lesions, all set to 1

- dataType "FROC", the data type

- modalityID [1:5] "1" "2", ..., treatment labels

- readerID [1:7] "1" "2" ..., reader labels

References

Warren LM, Mackenzie A, Cooke J, et al. Effect of image quality on calcification detection in digital mammography. Medical Physics. 2012;39(6):3202-3213.

Examples

```
str(dataset07)
PlotEmpiricalOperatingCharacteristics(dataset = dataset07, opChType = "wAFROC")$Plot
```

---

dataset08   *Monica Penedo ROC dataset*

Description

This is referred to in the book as the "PEN" dataset. It consists of 112 cases, 64 of which are diseased, interpreted in five treatments (basically different image compression algorithms) by five radiologists using the FROC paradigm (the inferred ROC dataset is included; the original FROC data is lost).

Usage

```
dataset08
```

Format

A list with 8 elements:

- `NL` Ratings array [1:5, 1:5, 1:112, 1], of false positives, FPs

- `LL` Ratings array [1:5, 1:5, 1:64, 1], of true positives, TPs

- `lesionVector` array [1:64], number of lesions per diseased case, all set to 1

- `lesionID` array [1:64, 1], labels of lesions on diseased cases, all set to 1

- `lesionWeight` array [1:64, 1], weights (or clinical importance) of lesions, all set to 1

- `dataType` "ROC", the data type

- `modalityID` [1:5] "0" "1", treatment labels

- `readerID` [1:5] "0" "1" "2" ..., reader labels

References

Penedo et al. Free-Response Receiver Operating Characteristic Evaluation of Lossy JPEG2000 and Object-based Set Partitioning in Hierarchical Trees Compression of Digitized Mammograms. Radiology. 2005;237(2):450-457.

Examples

```
str(dataset08)
PlotEmpiricalOperatingCharacteristics(dataset = dataset08, opChType = "ROC")$Plot
```

---

dataset09   *Nico Karssemeijer ROC dataset (CAD vs. radiologists)*

Description

This is referred to in the book as the "NICO" dataset. It consists of 200 mammograms, 80 of which contain one malignant mass, interpreted by a CAD system and nine radiologists using the LROC paradigm. The first reader is CAD. The highest rating method was used to convert this to an ROC dataset. The original LROC data is datasetCadLroc. Analyzing this **one-treatment** data requires methods described in the book, specifically, the function StSignificanceTestingSingleFixedFactor analyzes such datasets.

Usage

```
dataset09
```

Format

A list with 8 elements:

- NL Ratings array [1, 1:10, 1:200, 1], of false positives, FPs
- LL Ratings array [1, 1:10, 1:80, 1], of true positives, TPs
- lesionVector array [1:80], number of lesions per diseased case, all set to 1
- lesionID array [1:80, 1], labels of lesions on diseased cases, all set to 1
- lesionWeight array [1:80, 1], weights (or clinical importance) of lesions, all set to 1
- dataType "ROC", the data type
- modalityID [1] "1" treatment label
- readerID [1:10] "1" "2" ..., reader labels

References

Hupse R et al. Standalone computer-aided detection compared to radiologists' performance for the detection of mammographic masses. Eur Radiol. 2013;23(1):93-100.

Examples

```
str(dataset09)
PlotEmpiricalOperatingCharacteristics(dataset = dataset09, rdrs = 1:10, opChType = "ROC")$Plot
```

---

dataset10   *Marc Ruschin ROC dataset*

Description

This is referred to in the book as the "RUS" dataset. It consists of 90 cases, 40 of which are diseased, the images were acquired at three dose levels, which can be regarded as treatments. "0" = conventional film radiographs, "1" = digitized images viewed on monitors, Eight radiologists interpreted the cases using the FROC paradigm. These have been reduced to ROC data by using the highest ratings (the original FROC data is lost).

Usage

```
dataset10
```

Format

A list with 8 elements:

- `NL` Ratings array [1:3, 1:8, 1:90, 1], of false positives, FPs
- `LL` Ratings array [1:3, 1:8, 1:40, 1], of true positives, TPs
- `lesionVector` array [1:40], number of lesions per diseased case, all set to 1
- `lesionID` array [1:40, 1], labels of lesions on diseased cases, all set to 1
- `lesionWeight` array [1:40, 1], weights (or clinical importance) of lesions, all set to 1
- `dataType` "ROC", the data type
- `modalityID` [1:3] "1" "2" "3", treatment labels
- `readerID` [1:8] "1" "2" ..., reader labels

References

Ruschin M, et al. Dose dependence of mass and microcalcification detection in digital mammography: free response human observer studies. Med Phys. 2007;34:400 - 407.

Examples

```
str(dataset10)
PlotEmpiricalOperatingCharacteristics(dataset = dataset10, opChType = "ROC")$Plot
```

---

dataset11   *Dobbins 1 FROC dataset*

Description

This is referred to in the book as the "DOB1" dataset. Dobbins et al conducted a multi-institutional, MRMC study to compare the performance of digital tomosynthesis (GE's VolumeRad device), dual-energy (DE) imaging, and conventional chest radiography for pulmonary nodule detection and management. All study images were obtained with a flat-panel detector developed by GE. The case set consisted of 158 subjects, of which 43 were non-diseased and the rest had 1 - 20 pulmonary nodules independently verified, using with CT images, by 3 experts who did not participate in the observer study. The study used FROC paradigm data collection. There are 4 treatments labeled 1 - 4 (conventional chest x-ray, CXR, CXR augmented with dual-energy (CXR+DE), VolumeRad digital tomosynthesis images and VolumeRad augmented with DE (VolumeRad+DE).

Usage

```
dataset11
```

Format

A list with 8 elements:

- `NL` Ratings array [1:4, 1:5, 1:158, 1:4], of non-lesion localizations, NLs
- `LL` Ratings array [1:4, 1:5, 1:115, 1:20], of lesion localizations, LLs
- `lesionVector` array [1:115], number of lesions per diseased case
- `lesionID` array [1:115, 20], labels of lesions on diseased cases, all set to 1
- `lesionWeight` array [1:115, 20] weights (or clinical importance) of lesions, all set to 1
- `dataType` "FROC", the data type
- `modalityID` [1:4] "1" "2" ..., treatment labels
- `readerID` [1:5] "1" "2" ..., reader labels

References

Dobbins III JT et al. Multi-Institutional Evaluation of Digital Tomosynthesis, Dual-Energy Radiography, and Conventional Chest Radiography for the Detection and Management of Pulmonary Nodules. Radiology. 2016;282(1):236-250.

Examples

```
str(dataset11)
```

---

dataset12   *Dobbins 2 ROC dataset*

Description

This is referred to in the code as the "DOB2" dataset. It contains actionability ratings, i.e., do you recommend further follow up on the patient, one a 1 (definitely not) to 5 (definitely yes), effectively an ROC dataset using a 5-point rating scale.

Usage

```
dataset12
```

Format

A list with 8 elements:

- `NL` Ratings array [1:4, 1:5, 1:152, 1], of false positives, FPs

- `LL` Ratings array [1:4, 1:5, 1:88, 1], of true positives, TPs

- `lesionVector` array [1:88], number of lesions per diseased case, all set to 1

- `lesionID` array [1:88, 1], labels of lesions on diseased cases, all set to 1

- `lesionWeight` array [1:88, 1], weights (or clinical importance) of lesions, all set to 1

- `dataType` "ROC", the data type

- `modalityID` [1:2] "0" "1", treatment labels

- `readerID` [1:4] "0" "1" "2" ..., reader labels

References

Dobbins III JT et al. Multi-Institutional Evaluation of Digital Tomosynthesis, Dual-Energy Radiography, and Conventional Chest Radiography for the Detection and Management of Pulmonary Nodules. Radiology. 2016;282(1):236-250.

Examples

```
str(dataset11)
```

---

dataset13 *Dobbins 3 FROC dataset*

Description

This is referred to in the code as the "DOB3" dataset. This is a subset of DOB1 which includes data for lesions not-visible on CXR, but visible to truth panel on all treatments.

Usage

```
dataset13
```

Format

A list with 8 elements:

- NL Ratings array [1:4, 1:5, 1:158, 1:4], of non-lesion localizations, NLs

- LL Ratings array [1:4, 1:5, 1:106, 1:15], of lesion localizations, LLs

- lesionVector array [1:106], number of lesions per diseased case, all set to 1

- lesionID array [1:106, 15], labels of lesions on diseased cases, all set to 1

- lesionWeight array [1:106, 15] weights (or clinical importance) of lesions, all set to 1

- dataType "FROC", the data type

- modalityID [1:4] "1" "2" ..., treatment labels

- readerID [1:5] "1" "2" ..., reader labels

References

Dobbins III JT et al. Multi-Institutional Evaluation of Digital Tomosynthesis, Dual-Energy Radiography, and Conventional Chest Radiography for the Detection and Management of Pulmonary Nodules. Radiology. 2016;282(1):236-250.

Examples

```
str(dataset13)
```

---

dataset14   *Federica Zanca real (as opposed to inferred) ROC dataset*

Description

This is referred to in the book as the "FZR" dataset. It is a real ROC study, conducted on the same images and using the same radiologists, on treatments "4" and "5" of dataset04. This was compared to highest rating inferred ROC data from dataset04 to conclude, erroneously, that the highest rating assumption is invalid. See book Section 13.6.2.

Usage

```
dataset14
```

Format

A list with 8 elements:

- NL Ratings array [1:2, 1:4, 1:200, 1], of false positives, FPs

- LL Ratings array [1:2, 1:4, 1:100, 1], of true positives, TPs

- lesionVector array [1:100], number of lesions per diseased case, all set to 1

- lesionID array [1:100, 1], labels of lesions on diseased cases, all set to 1

- lesionWeight array [1:100, 1], weights (or clinical importance) of lesions, all set to 1

- dataType "ROC", the data type

- modalityID [1:2] "1" "2", treatment labels

- readerID [1:4] "1" "2" ..., reader labels

References

Zanca F, Hillis SL, Claus F, et al (2012) Correlation of free-response and receiver-operating-characteristic area-under-the-curve estimates: Results from independently conducted FROC/ROC studies in mammography. Med Phys. 39(10):5917-5929.

Examples

```
str(dataset14)
```

datasetBinned123   *Binned dataset suitable for checking* FitCorCbmRoc*; seed = 123*

Description

A binned dataset suitable for analysis by FitCorCbmRoc. It was generated by DfCreateCorCbm-Dataset by setting the seed variable to 123. Note the formatting of the data as a single treatment two reader dataset, even though the actual pairing might be different, see FitCorCbmRoc. The dataset is intentionally large so as to demonstrate the asymptotic convergence of ML estimates, produced by FitCorCbmRoc, to the population values. The data was generated by the following argument values to DfCreateCorCbmDataset: seed = 123, K1 = 5000, K2 = 5000, desiredNumBins = 5, muX = 1.5, muY = 3, alphaX = 0.4, alphaY = 0.7, rhoNor = 0.3, rhoAbn2 = 0.8.

Usage

```
datasetBinned123
```

Format

A list with 8 elements:

- NL Ratings array [1, 1:2, 1:10000, 1], of non-lesion localizations, NLs

- LL Ratings array [1, 1:2, 1:5000, 1], of lesion localizations, LLs

- lesionVector array [1:5000], number of lesions per diseased case, all set to one

- lesionID array [1:5000, 1], lesions labels on diseased cases, all set to one

- lesionWeight array [1:5000, 1], weights, all set to one

- dataType "ROC", the data type

- modalityID "1", treatment label

- readerID [1:2] "1" "2", reader labels

References

Zhai X, Chakraborty DP (2017). A bivariate contaminated binormal model for robust fitting of proper ROC curves to a pair of correlated, possibly degenerate, ROC datasets. Medical Physics. 44(6):2207–2222.

Examples

```
str(datasetBinned123)
```

datasetBinned124   *Binned dataset suitable for checking* FitCorCbmRoc; *seed = 124*

Description

A binned dataset suitable for analysis by FitCorCbmRoc. It was generated by DfCreateCorCbmDataset by setting the seed variable to 124. Otherwise similar to datasetBinned123.

Usage

```
datasetBinned124
```

Format

A list with 8 elements:

- NL Ratings array [1, 1:2, 1:10000, 1], of non-lesion localizations, NLs

- LL Ratings array [1, 1:2, 1:5000, 1], of lesion localizations, LLs

- lesionVector array [1:5000], number of lesions per diseased case, all set to one

- lesionID array [1:5000, 1], lesions labels on diseased cases, all set to one

- lesionWeight array [1:5000, 1], weights, all set to one

- dataType "ROC", the data type

- modalityID "1", treatment label

- readerID [1:2] "1" "2", reader labels

References

Zhai X, Chakraborty DP (2017). A bivariate contaminated binormal model for robust fitting of proper ROC curves to a pair of correlated, possibly degenerate, ROC datasets. Medical Physics. 44(6):2207–2222.

Examples

```
str(datasetBinned124)
```

datasetBinned125   *Binned dataset suitable for checking* FitCorCbmRoc*; seed = 125*

Description

A binned dataset suitable for analysis by FitCorCbmRoc. It was generated by DfCreateCorCbmDataset by setting the seed variable to 125. Otherwise similar to datasetBinned123.

Usage

```
datasetBinned125
```

Format

A list with 8 elements:

- NL Ratings array [1, 1:2, 1:10000, 1], of non-lesion localizations, NLs

- LL Ratings array [1, 1:2, 1:5000, 1], of lesion localizations, LLs

- lesionVector array [1:5000], number of lesions per diseased case, all set to one

- lesionID array [1:5000, 1], lesions labels on diseased cases, all set to one

- lesionWeight array [1:5000, 1], weights, all set to one

- dataType "ROC", the data type

- modalityID "1", treatment label

- readerID [1:2] "1" "2", reader labels

References

Zhai X, Chakraborty DP (2017). A bivariate contaminated binormal model for robust fitting of proper ROC curves to a pair of correlated, possibly degenerate, ROC datasets. Medical Physics. 44(6):2207–2222.

Examples

```
str(datasetBinned125)
```

---

datasetCadLroc   *Nico Karssemeijer LROC dataset (CAD vs. radiologists)*

Description

This is the actual LROC data corresponding to dataset09, which was the inferred ROC data. Note that the LL field is split into two, LLCl, representing true positives where the lesions were correctly localized, and LLIl, representing true positives where the lesions were incorrectly localized. The first reader is CAD and the remaining readers are radiologists. The function StSignificanceTestingSingleFixedFactor analyzes such datasets.

Usage

    datasetCadLroc

Format

A list with 9 elements:

- NL Ratings array [1, 1:10, 1:200, 1], of false positives, FPs
- LLCl Ratings array [1, 1:10, 1:80, 1], of true positives with correct localization, TPCls
- LLIl Ratings array [1, 1:10, 1:80, 1], of true positives with incorrect localization, TPIls
- lesionVector array [1:80], number of lesions per diseased case, all set to 1
- lesionID array [1:80, 1], labels of lesions on diseased cases, all set to 1
- lesionWeight array [1:80, 1], weights (or clinical importance) of lesions, all set to 1
- dataType "LROC", the data type
- modalityID [1:2] "0" "1", treatment labels
- readerID [1:10] "1" "2" ..., reader labels

References

Hupse R et al. Standalone computer-aided detection compared to radiologists' performance for the detection of mammographic masses. Eur Radiol. 2013;23(1):93-100.

Examples

    str(datasetCadLroc)

datasetCadSimuFroc   *Simulated FROC CAD vs. RAD dataset*

Description

Simulated FROC CAD vs. RAD dataset suitable for checking code. It was generated from dataset-CadLroc using SimulateFrocFromLrocData.R.

Usage

```
datasetCadSimuFroc
```

Format

A list with 8 elements:

- NL Ratings array [1, 1:10, 1:200, 1], of non-lesion localizations, NLs
- LL Ratings array [1, 1:10, 1:80, 1], of lesion localizations, LLs
- lesionVector array [1:80], number of lesions per diseased case, all set to one
- lesionID array [1:80, 1], lesions labels on diseased cases, all set to one
- lesionWeight array [1:80, 1], weights, all set to one
- dataType "FROC", the data type
- modalityID "1", treatment label
- readerID [1:10] "1" "2", reader labels

Examples

```
str(datasetCadSimuFroc)
```

datasetCrossedModality

                 John Thompson crossed treatment FROC dataset

Description

This is a crossed treatment dataset, see book Section 18.5. There are two treatment factors. The first treatment factor modalityID1 can be "F" or "I", which represent two CT reconstruction algorithms. The second treatment factor modalityID2 can be "20" "40" "60" "80", which represent the mAs values of the image acquisition. The factors are fully crossed. The function StSignificanceTestingCrossedModalities analyzes such datasets.

Usage

```
datasetCrossedModality
```

Format

A list with 9 elements:

- `NL` Ratings array [1:2, 1:4, 1:11, 1:68, 1:5], of non-lesion localizations, NLs

- `LL` Ratings array [1:2, 1:4, 1:11, 1:34, 1:3], of lesion localizations, LLs

- `lesionVector` array [1:34], number of lesions per diseased case, all set to 1

- `lesionID` array [1:34, 3], labels of lesions on diseased cases, all set to 1

- `lesionWeight` array [1:34, 3] weights (or clinical importance) of lesions, all set to 1

- `dataType` "FROC", the data type

- `modalityID1` [1:2] "F" "I", treatment labels

- `modalityID2` [1:4] "20" "40" "60" "80", treatment labels

- `readerID` [1:11] "1" "10" "11" ..., reader labels

References

Thompson JD, Chakraborty DP, Szczepura K, et al. (2016) Effect of reconstruction methods and x-ray tube current-time product on nodule detection in an anthropomorphic thorax phantom: a crossed-treatment JAFROC observer study. Medical Physics. 43(3):1265-1274.

Examples

```
str(datasetCrossedModality)
```

---

datasetDegenerate   *Simulated degenerate ROC dataset (for testing purposes)*

Description

A simulated degenerated dataset. A degenerate dataset is defined as one with no interior operating points on the ROC plot. Such data tend to be observed with expert level radiologists. This dataset is used to illustrate the robustness of two fitting models, namely CBM and RSM. The widely used binormal model and PROPROC fail on such datasets.

Usage

```
datasetDegenerate
```

Format

A list with 8 elements:

- `NL` Ratings array [1, 1, 1:15, 1], of false positives, FPs
- `LL` Ratings array [1, 1, 1:10, 1], of true positives, TPs
- `lesionVector` array [1:10], number of lesions per diseased case, all set to 1
- `lesionID` array [1:10, 1], labels of lesions on diseased cases, all set to 1
- `lesionWeight` array [1:10, 1], weights (or clinical importance) of lesions, all set to 1
- `dataType` "ROC", the data type
- `modalityID` "1", treatment label
- `readerID` "1", reader label

Examples

```
str(datasetDegenerate)
```

---

datasetROI   *Simulated ROI dataset*

Description

Simulated ROI dataset: assumed are 4 ROIs per case, 5 readers, 50 non-dieased and 40 diseased cases.

Usage

```
datasetROI
```

Format

A list with 9 elements:

- `NL` Ratings array [1:2, 1:5, 1:90, 1:4], of non-lesion localizations, NLs
- `LL` Ratings array [1:2, 1:5, 1:40, 1:4], of lesion localizations, LLs
- `lesionVector` array [1:40], number of lesions per diseased case, varies between 1 and 4
- `lesionID` array [1:40, 1:4], labels of lesions on diseased cases
- `lesionWeight` array [1:40, 1:4] weights (or clinical importance) of lesions, set to 1 divided by number of lesions in the case
- `dataType` "ROI", the data type
- `modalityID1` [1:2] "1" "2", treatment labels
- `readerID` [1:5] "1" "2" "3" "4" "5", reader labels

Examples

```
str(datasetROI)
```

Df2RJafrocDataset   *Convert ratings arrays to an RJafroc dataset*

Description

Converts ratings arrays, ROC or FROC, *not LROC*, to an **RJafroc** dataset, thereby allowing the user to leverage the file I/O, plotting and analyses capabilities of **RJafroc**.

Usage

```
Df2RJafrocDataset(NL, LL, ...)
```

Arguments

NL   Non-lesion localizations array (or FP array for ROC data).

LL   Lesion localizations array (or TP array for ROC data).

...   Other elements of **RJafroc** dataset that may, depending on the context, need to
                be specified. lesionVector **must** be specified if an FROC dataset is to be re-
                turned. It is a K2-length array specifying the numbers of lesions in each diseased
                case in the dataset.

Details

The function "senses" the data type (ROC or FROC) from the the absence or presence of lesionVector. ROC data can be NL[1:K1] and LL[1:K2] or NL[1:I,1:J,1:K1] and LL[1:I,1:J,1:K2]. FROC data can be NL[1:K1,1:maxNL] and LL[1:K2,1:maxLL] or NL[1:I,1:J,1:K1,1:maxNL] and LL[1:I,1:J,1:K2,1:maxLL]. Here maxNL/maxLL = maximum numbers of NLs/LLs, per case, over entire dataset. Equal weights are assigned to every lesion (FROC data). Consecutive characters/integers starting from "1" are assigned to lesionID, modalityID and readerID.

Value

A dataset with the structure described in RJafroc-package.

Examples

```
set.seed(1)
NL <- rnorm(5)
LL <- rnorm(7)*1.5 + 2
dataset <- Df2RJafrocDataset(NL, LL) # an ROC dataset

I <- 2;J <- 3;set.seed(1)
```

```
K1 <- 25;K2 <- 35
z1 <- array(dim = c(I, J, K1))
z2 <- array(dim = c(I, J, K2))
mu <- 2;sigma <- 1.5
for (i in 1:I) {
 for (j in 1:J) {
   z1[i,j,1:K1] <- rnorm(K1)
   z2[i,j,] <- rnorm(K2) * sigma + mu
 }
}
dataset <- Df2RJafrocDataset(z1, z2) ## note lesionVector consists of 1s; i.e., an ROC dataset

set.seed(1)
mu <- 1;lambda <- 1;nu <- 1; zeta1 <- 0
K1 <- 5;K2 <- 7
Lmax <- 2;Lk2 <- floor(runif(K2, 1, Lmax + 1))
frocDataRaw <- SimulateFrocDataset(mu, lambda, nu, zeta1, I = 1, J = 1, K1, K2,
lesionVector = Lk2)
NL <- drop(frocDataRaw$NL)
LL <- drop(frocDataRaw$LL)
dataset <- Df2RJafrocDataset(NL, LL, lesionVector = Lk2)
## note lesionVector is not all 1s, signalling an FROC dataset

## Simulate FROC dataset, convert to dataset object, display ROC, FROC and AFROC curves
I <- 2;J <- 3;set.seed(1)
K1 <- 25;K2 <- 35
mu <- 1;nuP <- 0.8;lambdaP <- 1;zeta1 <- 0
lambda <- UtilPhysical2IntrinsicRSM(mu,lambdaP,nuP)$lambda
nu <- UtilPhysical2IntrinsicRSM(mu,lambdaP,nuP)$nu
Lmax <- 2;Lk2 <- floor(runif(K2, 1, Lmax + 1))
z1 <- array(-Inf,dim = c(I,J,K1+K2,40))
z2 <- array(-Inf,dim = c(I,J,K2,40))
dimNL <- array(dim=c(I,J,2))
## the last value (2) accommodates case and location indices
dimLL <- array(dim=c(I,J,2))
for (i in 1:I) {
  for (j in 1:J) {
    frocDataRaw <- SimulateFrocDataset(mu, lambda, nu, zeta1, I = 1,
    J = 1, K1, K2, lesionVector = Lk2)
    dimNL[i,j,] <- dim(drop(frocDataRaw$NL))
    dimLL[i,j,] <- dim(drop(frocDataRaw$LL))
    z1[i,j,,1:dimNL[i,j,2]] <- drop(frocDataRaw$NL) # drop the excess location indices
    z2[i,j,,1:dimLL[i,j,2]] <- drop(frocDataRaw$LL)
  }
}
z1 <- z1[,,,1:max(dimNL[,,2])]
z2 <- z2[,,,1:max(dimLL[,,2])]

dataset <- Df2RJafrocDataset(z1, z2, lesionVector = Lk2)

retPlot <- PlotEmpiricalOperatingCharacteristics(dataset,
trts = seq(1,I), rdrs = seq(1,J), opChType = "ROC")
print(retPlot$Plot)
```

```
retPlot <- PlotEmpiricalOperatingCharacteristics(dataset,
trts = seq(1,I), rdrs = seq(1,J), opChType = "FROC")
print(retPlot$Plot)

retPlot <- PlotEmpiricalOperatingCharacteristics(dataset,
trts = seq(1,I), rdrs = seq(1,J), opChType = "AFROC")
print(retPlot$Plot)
```

DfBinDataset   *Returns a binned dataset*

Description

Bins continuous (i.e. floating point) or quasi-continuous (e.g. integers 0-100) ratings in a dataset
and returns the corresponding binned dataset in which the ratings are integers 1, 2,...., with higher
values representing greater confidence in presence of disease

Usage

```
DfBinDataset(dataset, desiredNumBins = 7, opChType)
```

Arguments

dataset   The dataset to be binned, with structure as in [RJafroc-package](#).

desiredNumBins   The desired number of bins. The default is 7.

opChType   The operating characteristic relevant to the binning operation: "ROC", "FROC",
                 "AFROC", or "wAFROC".

Details

For small datasets the number of bins may be smaller than desiredNumBins. **The algorithm needs
to know the type of operating characteristic relevant to the binning operation.** For ROC the
bins are FP and TP counts, for FROC the bins are NL and LL counts, for AFROC the bins are FP
and LL counts, and for wAFROC the bins are FP and wLL counts. Binning is generally employed
prior to fitting a statistical model, e.g., maximum likelihood, to the data. This version chooses ctffs
so as to maximize empirical AUC (this yields a unique choice of ctffs which gives the reader the
maximum deserved credit).

Value

The binned dataset

References

Miller GA (1956) The Magical Number Seven, Plus or Minus Two: Some limits on our capacity for processing information, The Psychological Review 63, 81-97

Chakraborty DP (2017) *Observer Performance Methods for Diagnostic Imaging - Foundations, Modeling, and Applications with R-Based Examples*, CRC Press, Boca Raton, FL. https://www.crcpress.com/Observer-Performance-Methods-for-Diagnostic-Imaging-Foundations-Modeling/Chakraborty/p/book/9781482214840

Examples

```
binned <- DfBinDataset(dataset05, opChType = "ROC")
PlotEmpiricalOperatingCharacteristics(dataset05,
trts= c(1,2), rdrs = seq(1,9), opChType = "ROC")$Plot
PlotEmpiricalOperatingCharacteristics(binned, trts= c(1,2),
rdrs = seq(1,9), opChType = "ROC")$Plot

binned <- DfBinDataset(dataset05, opChType = "AFROC")
PlotEmpiricalOperatingCharacteristics(dataset05,
trts= c(1,2), rdrs = seq(1,9), opChType = "AFROC")$Plot
PlotEmpiricalOperatingCharacteristics(binned, trts= c(1,2),
rdrs = seq(1,9), opChType = "AFROC")$Plot


## Not run:
## takes longer than 5 sec on OSX
library(ggplot2)
dataset <- SimulateRocDataset(K1 = 5000, K2 = 7000, a = 1, b = 0.5, seed = 123)
datasetB <- DfBinDataset(dataset, desiredNumBins = 7, opChType = "ROC")
fomOrg <- as.matrix(UtilFigureOfMerit(dataset, FOM = "Wilcoxon"), nrow = 2, ncol = 9)
print(fomOrg)
fomBinned <- as.matrix(UtilFigureOfMerit(datasetB, FOM = "Wilcoxon"), nrow = 2, ncol = 9)
print(fomOrg)
cat("fomOrg = ", mean(fomOrg), "\n")
cat("fomBinned = ", mean(fomBinned), "\n")
x <- PlotEmpiricalOperatingCharacteristics(dataset, opChType = "ROC")$Plot
y <- PlotEmpiricalOperatingCharacteristics(datasetB, opChType = "ROC")$Points
fpf <- y$genAbscissa[-1];fpf <- fpf[-length(fpf)]
tpf <- y$genOrdinate[-1];tpf <- tpf[-length(tpf)]
plotOpPnts <- rbind(data.frame(fpf = fpf, tpf = tpf))
x <- x + geom_point(data = plotOpPnts, aes(x = fpf, y = tpf), size = 4)
print(x)
xx <- PlotEmpiricalOperatingCharacteristics(datasetB, opChType = "ROC")
print(xx$Points)

## End(Not run)
```

DfCreateCorCbmDataset   *Create paired dataset for testing* FitCorCbmRoc

Description

The paired dataset is generated using bivariate sampling; details are in referenced publication

Usage

```
DfCreateCorCbmDataset(
  seed = 123,
  K1 = 50,
  K2 = 50,
  desiredNumBins = 5,
  muX = 1.5,
  muY = 3,
  alphaX = 0.4,
  alphaY = 0.7,
  rhoNor = 0.3,
  rhoAbn2 = 0.8
)
```

Arguments

seed	The seed variable, default is 123; set to NULL for truly random seed
K1	The number of non-diseased cases, default is 50
K2	The number of diseased cases, default is 50
desiredNumBins	The desired number of bins; default is 5
muX	The CBM μ parameter in condition X
muY	The CBM μ parameter in condition Y
alphaX	The CBM α parameter in condition X
alphaY	The CBM 'alpha' parameter in condition Y
rhoNor	The correlation of non-diseased case z-samples
rhoAbn2	The correlation of diseased case z-samples, when disease is visible in both conditions

Details

The ROC data is bined to 5 bins in each condition.

Value

The return value is the desired dataset, suitable for testing FitCorCbmRoc.

References

Zhai X, Chakraborty DP (2017) A bivariate contaminated binormal model for robust fitting of proper ROC curves to a pair of correlated, possibly degenerate, ROC datasets. Medical Physics. 44(6):2207–2222.

Examples

```
## seed <- 1
## this gives unequal numbers of bins in X and Y conditions for 50/50 dataset
dataset <- DfCreateCorCbmDataset()

## Not run:
## this takes very long time!! used to show asymptotic convergence of ML estimates
dataset <- DfCreateCorCbmDataset(K1 = 5000, K2 = 5000)

## End(Not run)
```

DfExtractCorCbmDataset

Extract two arms of a pairing from an MRMC ROC dataset

Description

Extract a paired dataset from a larger dataset. The pairing could be two readers in the same treatment, or different readers in different treatments, or the same reader in different treatments. If necessary The data is binned to 5 bins in each condition.

Usage

```
DfExtractCorCbmDataset(dataset, trts = 1, rdrs = 1)
```

Arguments

dataset	The original dataset from which the pairing is to be extracted
trts	A vector, maximum length 2, contains the indices of the treatment or treatments to be extracted
rdrs	A vector, maximum length 2, contains the indices of the reader or readers to be extracted

Details

The desired pairing is contained in the vectors `trts` and `rdrs`. If either has length one, the other must have length two and the pairing is implicit. If both are length two, then the pairing is that implied by the first treatement and the second reader, which is one arm, and the other arm is that implied by the second treatment paired with the first reader. Using this method any allowed pairing can be extracted and analyzed by `FitCorCbmRoc`. The utility of this software is in designing a ratings simulator that is statistically matched to a real dataset.

Value

A new dataset in which the number of treatments is one and the number of readers is two

Examples

```
## Extract the paired data corresponding to the second and third readers in the first treatment
##from the include ROC dataset
dataset11_23 <- DfExtractCorCbmDataset(dataset05, trts = 1, rdrs = c(2,3))

## Extract the paired data corresponding to the third reader in the first and second treatments
dataset12_33 <- DfExtractCorCbmDataset(dataset05, trts = c(1,2), rdrs = 3)

## Extract the data corresponding to the first reader in the first
## treatment paired with the data
## from the third reader in the second treatment
## (the indices are at different positions in the respective arrays)
dataset12_13 <- DfExtractCorCbmDataset(dataset05,
trts = c(1,2), rdrs = c(1,3))
```

DfExtractDataset   *Extract a subset of treatments and readers from a dataset*

Description

Extract a dataset consisting of a subset of treatments/readers from a larger dataset

Usage

```
DfExtractDataset(dataset, trts, rdrs)
```

Arguments

dataset	The original dataset from which the subset is to be extracted; can be ROC, FROC or LROC
trts	A vector contains the indices of the treatments to be extracted. **If this parameter is not supplied, all treatments are extracted.**
rdrs	A vector contains the indices of the readers to be extracted. **If this parameter is not supplied, all readers are extracted.**

Details

Note that trts and rdrs are the vectors of **indices** not **IDs**. For example, if the ID of the first reader is "0", the corresponding value in trts should be **1** not **0**.

Value

A new dataset containing only the specified treatments and readers that were extracted from the original dataset

Examples

```
## Extract the data corresponding to the second reader in the
## first treatment from an included ROC dataset
dataset1_2 <- DfExtractDataset(dataset05, trts = 1, rdrs = 2)

## Extract the data of the first and third reader in all
## treatment from the included ROC dataset
datasetA_123 <- DfExtractDataset(dataset05, rdrs = c(1, 3))
```

DfFroc2Afroc   *Convert an FROC dataset to an AFROC dataset*

Description

Converts an FROC dataset to a AFROC dataset, where only the highest rated mark on each non-diseased case is counted and all lesion localizations are counted

Usage

```
DfFroc2Afroc(dataset)
```

Arguments

dataset   The dataset to be converted, `RJafroc-package`.

Details

The first list member of the AFROC dataset is NL, whose third dimension has length (K1 + K2), the total number of cases. The ratings of cases (K1 + 1) through (K1 + K2) are -Inf. **In an AFROC dataset FPs are only possible on non-diseased cases.** The second member of the list is LL. Its third dimension has length K2, the total number of diseased cases. This is because LLs are only possible on diseased cases. The structure is shown below:

- NL Ratings array [1:I, 1:J, 1:(K1+K2), 1:maxNL], of non-lesion localizations, NLs
- LL Ratings array [1:I, 1:J, 1:K2, 1:maxLL], of lesion localizations, LLs
- lesionVector array [1:K2], number of lesions per diseased case
- lesionID array [1:K2, 1:maxLL], labels of lesions on diseased cases
- lesionWeight array [1:K2, 1:maxLL], weights (or clinical importances) of lesions
- dataType "FROC", the data type
- modalityID [1:I] inherited modality labels
- readerID [1:J] inherited reader labels

Value

An AFROC dataset

Examples

```
afrocDataSet <- DfFroc2Afroc(dataset05)
p <- PlotEmpiricalOperatingCharacteristics(afrocDataSet, trts = 1, rdrs = 1, opChType = "wAFROC")
print(p$Plot)
str(afrocDataSet)
```

DfFroc2Lroc   *Simulates an "AUC-equivalent" LROC dataset from an FROC dataset*

Description

Simulates a multiple-treatment multiple-reader "AUC-equivalent" LROC dataset from a supplied
FROC dataset.

Usage

```
DfFroc2Lroc(dataset)
```

Arguments

dataset   The FROC dataset to be converted to LROC.

Details

The FROC paradigm can have 0 or more marks per case. However, LROC is restricted to **exactly
one mark per case**. For the NL array of the LROC data, for non-disesed cases, the **highest** rating
of the FROC marks, or -Inf if there are no marks, is copied to case index k1 = 1 to k1 = K1 of the
LROC dataset. For each diseased case, if the max LL rating exceeds the max NL rating, then the
max LL rating is copied to the LLCl array, otherwise the max NL rating is copied to the LLIl array.
The max NL rating on each diseased case is then set to -Inf (since the LROC paradigm only allows
one mark. The equivalent FROC dataset has the same HrAuc as the original LROC dataset. See
example. The main use of this function is to test the Significance testing functions using MRMC
LROC datasets, which I currently don't have.

Value

The equivalent LROC dataset

Examples

```
lrocDataset <- DfFroc2Lroc(dataset05)
frocHrAuc <- UtilFigureOfMerit(dataset05, FOM = "HrAuc")
lrocWilcoxonAuc <- UtilFigureOfMerit(lrocDataset, FOM = "Wilcoxon")
```

DfFroc2Roc

Convert an FROC dataset to an ROC dataset

Description

Convert an FROC dataset to a highest rating inferred ROC dataset

Usage

```
DfFroc2Roc(dataset)
```

Arguments

dataset   The FROC dataset to be converted, `RJafroc-package`.

Details

The first member of the ROC dataset is NL, whose 3rd dimension has length (K1 + K2), the total number of cases. Ratings of cases (K1 + 1) through (K1 + K2) are -Inf. **This is because in an ROC dataset FPs are only possible on non-diseased cases.** The second member of the list is LL. Its 3rd dimension has length K2, the number of diseased cases. **This is because TPs are only possible on diseased cases**. For each case the inferred ROC rating is the highest of all FROC ratings on that case. If a case has no marks, a **finite ROC rating, guaranteed to be smaller than the rating on any marked case**, is assigned to it. The dataset structure is shown below:

- NL Ratings array [1:I, 1:J, 1:(K1+K2), 1], of false positives, FPs
- LL Ratings array [1:I, 1:J, 1:K2, 1], of true positives, TPs
- lesionVector array [1:K2], number of lesions per diseased case
- lesionID array [1:K2, 1], labels of lesions on diseased cases
- lesionWeight array [1:K2, 1], weights (or clinical importances) of lesions
- dataType "ROC", the data type
- modalityID [1:I] inherited modality labels
- readerID [1:J] inherited reader labels

Value

An ROC dataset with **finite ratings** in NL[,,1:K1,1] and LL[,,1:K2,1].

Examples

```
rocDataSet <- DfFroc2Roc(dataset05)
p <- PlotEmpiricalOperatingCharacteristics(rocDataSet, trts = 1, rdrs = 1, opChType = "ROC")
print(p$Plot)
str(rocDataSet)

## in the following example, because of the smaller number of cases,
```

```
## it is easy to see the process at work:
set.seed(1);K1 <- 3;K2 <- 5
mu <- 1;nuP <- 0.5;lambdaP <- 2;zeta1 <- 0
lambda <- UtilPhysical2IntrinsicRSM(mu,lambdaP,nuP)$lambda
nu <- UtilPhysical2IntrinsicRSM(mu,lambdaP,nuP)$nu
Lmax <- 2;Lk2 <- floor(runif(K2, 1, Lmax + 1))
frocDataRaw <- SimulateFrocDataset(mu, lambda, nu, zeta1, I = 1, J = 1,
K1, K2, lesionVector = Lk2)
hrData <- DfFroc2Roc(frocDataRaw)
print("frocDataRaw$NL[1,1,,] = ");print(frocDataRaw$NL[1,1,,])
print("hrData$NL[1,1,1:K1,] = ");print(hrData$NL[1,1,1:K1,])
print("frocDataRaw$LL[1,1,,] = ");print(frocDataRaw$LL[1,1,,])
print("hrData$LL[1,1,,] = ");print(hrData$LL[1,1,,])
## following is the output
## [1] "frocDataRaw$NL[1,1,,] = "
##      [,1]      [,2]       [,3] [,4]
## [1,] 2.4046534 0.7635935      -Inf -Inf
## [2,]      -Inf      -Inf      -Inf -Inf
## [3,] 0.2522234      -Inf      -Inf -Inf
## [4,] 0.4356833      -Inf      -Inf -Inf
## [5,]      -Inf      -Inf      -Inf -Inf
## [6,]      -Inf      -Inf      -Inf -Inf
## [7,]      -Inf      -Inf      -Inf -Inf
## [8,] 0.8041895 0.3773956 0.1333364 -Inf
## > print("hrData$NL[1,1,1:K1,] = ");print(hrData$NL[1,1,1:K1,])
## [1] "hrData$NL[1,1,1:K1,] = "
## [1] 2.4046534      -Inf 0.2522234
## > print("frocDataRaw$LL[1,1,,] = ");print(frocDataRaw$LL[1,1,,])
## [1] "frocDataRaw$LL[1,1,,] = "
## [,1] [,2]
## [1,]      -Inf -Inf
## [2,] 1.5036080 -Inf
## [3,] 0.8442045 -Inf
## [4,] 1.0467262 -Inf
## [5,]      -Inf -Inf
## > print("hrData$LL[1,1,,] = ");print(hrData$LL[1,1,,])
## [1] "hrData$LL[1,1,,] = "
## [1] 0.4356833 1.5036080 0.8442045 1.0467262 0.8041895
## Note that rating of the first and the last diseased case came from NL marks
```

DfLroc2Froc   *Simulates an "AUC-equivalent" FROC dataset from an LROC dataset*

Description

Simulates a multiple-treatment multiple-reader "AUC-equivalent" FROC dataset from a supplied LROC dataset, e.g., datasetCadLroc.

Usage

```
DfLroc2Froc(dataset)
```

Arguments

dataset   The LROC dataset to be converted to FROC.

Details

The LROC paradigm always yields a single mark per case. Therefore the equivalent FROC will also have only one mark per case. The NL arrays of the two datasets are identical. The LL array is created by copying the LLCl array of the LROC dataset to the LL array of the FROC dataset, from diseased case index $k2 = 1$ to $k2 = K2$. Additionally, the LLIl array of the LROC dataset is copied to the NL array of the FROC dataset, starting at case index $k1 = K1+1$ to $k1 = K1+K2$. Any zero ratings are replace by -Infs. The equivalent FROC dataset has the same HrAuc as the original LROC dataset. See example. The main use of this function is to test the CAD significance testing functions using CAD FROC datasets, which I currently don't have.

Value

The equivalent FROC dataset

Examples

```
frocDataset <- DfLroc2Froc(datasetCadLroc)
lrocAuc <- UtilFigureOfMerit(datasetCadLroc, FOM = "Wilcoxon")
frocHrAuc <- UtilFigureOfMerit(frocDataset, FOM = "HrAuc")
```

DfLroc2Roc   *Convert an LROC dataset to a ROC dataset*

Description

Converts an LROC dataset to an ROC dataset

Usage

```
DfLroc2Roc(dataset)
```

Arguments

dataset   The **LROC** dataset to be converted.

Details

For the diseased cases one takes the maximum rating on each diseased case, which could be a LLCl ("true positive" correct localization) or a LLIl ("true positive" incorrect localization) rating, whichever has the higher rating. For non-diseased cases the NL arrays are identical.

Value

An ROC dataset

Examples

```
str(datasetCadLroc)
rocDataSet <- DfLroc2Roc(datasetCadLroc)
str(rocDataSet)
```

DfReadCrossedModalities

Read a crossed-treatment data file

Description

Read an crossed-treatment data file, in which the two treatment factors are crossed

Usage

```
DfReadCrossedModalities(fileName, sequentialNames = FALSE)
```

Arguments

fileName   A string specifying the name of the file that contains the dataset, which must be an extended-JAFROC format data file containing an additional treatment factor.

sequentialNames

If `TRUE`, consecutive integers (starting from 1) will be used as the treatment and reader IDs. Otherwise, treatment and reader IDs in the original data file will be used. The default is `FALSE`.

Details

The data format is similar to the JAFROC format (see RJafroc-package). The notable difference is that there are two treatment factors. A sample crossed treatment file "CrossedModalitiesData.xlsx" is in the `inst\extdata` subdirectory of RJafroc.

Value

A dataset with the specified structure, similar to a standard **RJafroc**(see RJafroc-package). Because of the extra treatment factor, NL and LL are each five dimensional arrays. There are also two treatment IDS: modalityID1 and modalityID2.

References

Thompson JD, Chakraborty DP, Szczepura K, et al. (2016) Effect of reconstruction methods and x-ray tube current-time product on nodule detection in an anthropomorphic thorax phantom: a crossed-treatment JAFROC observer study. Medical Physics. 43(3):1265-1274.

Chakraborty DP (2017) *Observer Performance Methods for Diagnostic Imaging - Foundations, Modeling, and Applications with R-Based Examples*, CRC Press, Boca Raton, FL. https://www.crcpress.com/Observer-Performance-Methods-for-Diagnostic-Imaging-Foundations-Modeling/Chakraborty/p/book/9781482214840

Examples

```
crossedFileName <- system.file("extdata",
    "CrossedModalitiesData.xlsx", package = "RJafroc", mustWork = TRUE)
crossedData <- DfReadCrossedModalities(crossedFileName)
str(crossedData)
```

DfReadDataFile   *Read a data file*

Description

Read a disk file and create a dataset object from it.

Usage

```
DfReadDataFile(
  fileName,
  format = "JAFROC",
  newExcelFileFormat = FALSE,
  delimiter = ",",
  sequentialNames = FALSE
)
```

Arguments

fileName   A string specifying the name of the file. The file-extension must match the format specified below

format   A string specifying the format of the data in the file. It can be "JAFROC" (the default), "MRMC" or "iMRMC". For "MRMC" the format is determined by the data file extension as specified in http://perception.radiology.uiowa.edu/, i.e., .csv or .txt or .lrc. For file extension .imrmc the format is described in https://code.google.com/p/imrmc/.

newExcelFileFormat

> This argument only applies to the "JAFROC" format. The default is FALSE. if TRUE the function accommodates 3 additional columns in the Truth worksheet. If FALSE, the original function, as in version 1.2.0 is used, and the three extra columns, if present, throws an error.

delimiter   The string delimiter to be used for the "MRMC" format ("," is the default), see <http://perception.radiology.uiowa.edu/>. This parameter is not used when reading "JAFROC" or "iMRMC" data files.

sequentialNames

> A logical variable: if TRUE, consecutive integers (starting from 1) will be used as the treatment and reader IDs (i.e., names). Otherwise, treatment and reader IDs in the original data file will be used.

Value

A dataset with the structure specified in RJafroc-package.

Examples

```
fileName <- system.file("extdata", "toyFiles/ROC/rocCr.xlsx",
package = "RJafroc", mustWork = TRUE)
x <- DfReadDataFile(fileName, newExcelFileFormat = TRUE)


{
fileName <- system.file("extdata", "toyFiles/FROC/frocCr.xlsx",
package = "RJafroc", mustWork = TRUE)
x <- DfReadDataFile(fileName, newExcelFileFormat = TRUE)
}


fileName <- system.file("extdata", "RocData.xlsx",
package = "RJafroc", mustWork = TRUE)
RocDataXlsx <- DfReadDataFile(fileName)

fileName <- system.file("extdata", "RocData.csv",
package = "RJafroc", mustWork = TRUE)
RocDataCsv<- DfReadDataFile(fileName, format = "MRMC")

fileName <- system.file("extdata", "RocData.imrmc",
package = "RJafroc", mustWork = TRUE)
RocDataImrmc<- DfReadDataFile(fileName, format = "iMRMC")

fileName <- system.file("extdata", "FrocData.xlsx",
package = "RJafroc", mustWork = TRUE)
FrocDataXlsx <- DfReadDataFile(fileName, sequentialNames = TRUE)
```

`DfReadLrocDataFile`   *Read a LROC data file*

Description

Read the Hupse-Karssemeijer LROC data file, a study comparing standalone performance of breast CAD vs. radiologists; the study actually included radiologists and residents; the following usage includes only the radiologists

Usage

```
DfReadLrocDataFile(RADIOLOGISTS = TRUE)
```

Arguments

RADIOLOGISTS   Logical; if TRUE, the default, only radiologists are analyzed otherwise all readers are analyzed

Details

The data format is similar to the JAFROC format (see [`RJafroc-package`](RJafroc-package)) with the **crucial difference** that there are two types of LL (TP) events: those representing correct localizations and those representing incorrect localizations. Also, every diseased case has one lesion and NLs are not possible on diseased cases. J is one plus the number of readers. The first treatment is CAD, followed by the readers.

The return value is a list with the following elements:

- `NL` [1, 1:J, 1:K1, 1] array containing the FP ratings
- `LLCl` [1, 1:J, 1:K2, 1] array containing the TP correct localization ratings
- `LLIl` [1, 1:J, 1:K2, 1] array containing the TP incorrect localization ratings
- `lesionVector` array [1:K2], as in standard JAFROC/ROC format dataset, ones
- `lesionID` array [1:K2], as in standard JAFROC/ROC format dataset, ones
- `lesionWeight` array [1:K2], weights (or clinical importances) of lesions
- `dataType` "LROC", the data type
- `modalityID` [1:I], treatment labels
- `readerID` [1:J], reader labels

Value

The **LROC** dataset.

References

Hupse R, Samulski M, Lobbes M, et al. Standalone computer-aided detection compared to radiologists' performance for the detection of mammographic masses. Eur Radiol 2013.

Chakraborty DP (2017) *Observer Performance Methods for Diagnostic Imaging - Foundations, Modeling, and Applications with R-Based Examples*, CRC Press, Boca Raton, FL. `https://www.crcpress.com/Observer-Performance-Methods-for-Diagnostic-Imaging-Foundations-Modeling/Chakraborty/p/book/9781482214840`

Examples

```
radData <- DfReadLrocDataFile()
str(radData)
allData <- DfReadLrocDataFile(FALSE)
str(allData)
```

DfSaveDataFile   *Save ROC data file in a different format*

Description

Save ROC data file in a different format so it can be analyzed with alternate software

Usage

```
DfSaveDataFile(
  dataset,
  fileName,
  format = "JAFROC",
  dataDescription = paste0(deparse(substitute(dataset)), " Data File")
)
```

Arguments

dataset	The dataset to be saved in the specified format, see RJafroc-package.
fileName	The file name of the output data file. The extension of the data file must match the corresponding format, see RJafroc-package
format	The format of the data file, which can be "JAFROC", "MRMC" or "iMRMC", see RJafroc-package.
dataDescription	
	An optional string variable describing the data file, the default value is the variable name of dataset The description appears on the first line of *.lrc or *imrmc data file. This parameter is not used when saving dataset in other formats.

Examples

```
DfSaveDataFile(dataset = dataset05,
    fileName = "rocData2.xlsx", format = "JAFROC")
DfSaveDataFile(dataset = dataset02,
    fileName = "rocData2.csv", format = "MRMC")
DfSaveDataFile(dataset = dataset02,
    fileName = "rocData2.lrc", format = "MRMC",
    dataDescription = "ExampleROCdata1")
DfSaveDataFile(dataset = dataset02,
    fileName = "rocData2.txt", format = "MRMC",
    dataDescription = "ExampleROCdata2")
DfSaveDataFile(dataset = dataset02,
    fileName = "dataset05.imrmc", format = "iMRMC",
    dataDescription = "ExampleROCdata3")
```

FitBinormalRoc	*Fit the binormal model to selected treatment and reader in an ROC dataset*

Description

Fit the binormal model-predicted ROC curve for a dataset. This is the R equivalent of ROCFIT or RSCORE

Usage

```
FitBinormalRoc(dataset, trt = 1, rdr = 1)
```

Arguments

dataset	The ROC dataset
trt	The desired treatment, default is 1
rdr	The desired reader, default is 1

Details

In the binormal model ratings (more accurately the latent decision variables) from diseased cases are sampled from $N(a, 1)$ while ratings for non-diseased cases are sampled from $N(0, b^2)$. To avoid clutter error bars are only shown for the lowest and uppermost operating points. An FROC dataset is internally converted to a highest rating inferred ROC dataset. To many bins containing zero counts will cause the algorithm to fail; so be sure to bin the data appropriately to fewer bins, where each bin has at least one count.

Value

The returned value is a list with the following elements:

a	The mean of the diseased distribution; the non-diseased distribution is assumed to have zero mean
b	The standard deviation of the non-diseased distribution. The diseased distribution is assumed to have unit standard deviation
zetas	The binormal model cutoffs, zetas or thresholds
AUC	The binormal model fitted ROC-AUC
StdAUC	The standard deviation of AUC
NLLIni	The initial value of negative LL
NLLFin	The final value of negative LL
ChisqrFitStats	The chisquare goodness of fit results
covMat	The covariance matrix of the parameters
fittedPlot	A **ggplot2** object containing the fitted operating characteristic along with the empirical operating points. Use `print()` to display the object

References

Dorfman DD, Alf E (1969) Maximum-Likelihood Estimation of Parameters of Signal-Detection Theory and Determination of Confidence Intervals - Rating-Method Data, Journal of Mathematical Psychology 6, 487-496.

Grey D, Morgan B (1972) Some aspects of ROC curve-fitting: normal and logistic models. Journal of Mathematical Psychology 9, 128-139.

Examples

```
## Test with an included ROC dataset
retFit <- FitBinormalRoc(dataset02);print(retFit$fittedPlot)


## Test with an included FROC dataset; it needs to be binned
## as there are more than 5 discrete ratings levels
binned <- DfBinDataset(dataset05, desiredNumBins = 5, opChType = "ROC")
retFit <- FitBinormalRoc(binned);print(retFit$fittedPlot)


## Test with single interior point data
fp <- c(rep(1,7), rep(2, 3))
tp <- c(rep(1,5), rep(2, 5))
dataset <- Df2RJafrocDataset(fp, tp)
retFit <- FitBinormalRoc(dataset);print(retFit$fittedPlot)

## Test with two interior data points
fp <- c(rep(1,7), rep(2, 5), rep(3, 3))
tp <- c(rep(1,3), rep(2, 5), rep(3, 7))
```

```
dataset <- Df2RJafrocDataset(fp, tp)
retFit <- FitBinormalRoc(dataset);print(retFit$fittedPlot)

## Test with TONY data for which chisqr can be calculated
ds <- DfFroc2Roc(dataset01)
retFit <- FitBinormalRoc(ds, 2, 3);print(retFit$fittedPlot)
retFit$ChisqrFitStats

## Test with included degenerate ROC data
retFit <- FitBinormalRoc(datasetDegenerate);print(retFit$fittedPlot)
```

FitCbmRoc	*Fit the contaminated binormal model (CBM) to selected treatment and reader in an ROC dataset*

Description

Fit the CBM-predicted ROC curve for specified treatment and reader

Usage

```
FitCbmRoc(dataset, trt = 1, rdr = 1)
```

Arguments

dataset	The dataset containing the data
trt	The desired treatment, default is 1
rdr	The desired reader, default is 1

Details

In CBM ratings from diseased cases are sampled from a mixture distribution: (1) with integrated area $alpha$ distributed $N(\text{mu}1)$ and (2) from a distribution with integrated area $1 - alpha$ distributed $N(0, 1)$. Ratings for non-diseased cases are sampled from $N(0, 1)$. The ChisqrFitStats consists of a list containing the chi-square value, the p-value and the degrees of freedom.

Value

The return value is a list with the following elements:

mu	The mean of the visible diseased distribution (the non-diseased) has zero mean
alpha	The proportion of diseased cases where the disease is visible
zetas	The cutoffs, zetas or thresholds

AUC	The AUC of the fitted ROC curve
StdAUC	The standard deviation of AUC
NLLIni	The initial value of negative LL
NLLFin	The final value of negative LL
ChisqrFitStats	The chisqare goodness of fit results
covMat	The covariance matrix of the parameters
fittedPlot	A **ggplot2** object containing the fitted operating characteristic along with the empirical operating points. Use print() to display the object

Note

This algorithm is more robust than the binormal model.

References

Dorfman DD, Berbaum KS (2000) A contaminated binormal model for ROC data: Part II. A formal model, Acad Radiol, 7:6, 427–437.

Examples

```
## Not run:
## CPU time 8.7 sec on Ubuntu (#13)
## Test with included ROC data
retFit <- FitCbmRoc(dataset02);print(retFit$fittedPlot)

## Test with included degenerate ROC data (yes! CBM can fit such data)
retFit <- FitCbmRoc(datasetDegenerate);print(retFit$fittedPlot)

## Test with single interior point data
fp <- c(rep(1,7), rep(2, 3))
tp <- c(rep(1,5), rep(2, 5))
dataset <- Df2RJafrocDataset(fp, tp)
retFit <- FitCbmRoc(dataset);print(retFit$fittedPlot)

## Test with two interior data points
fp <- c(rep(1,7), rep(2, 5), rep(3, 3))
tp <- c(rep(1,3), rep(2, 5), rep(3, 7))
dataset <- Df2RJafrocDataset(fp, tp)
retFit <- FitCbmRo
c(dataset);print(retFit$fittedPlot)

## Test with included ROC data (some bins have zero counts)
retFit <- FitCbmRoc(dataset02, 2, 1);print(retFit$fittedPlot)

## Test with TONY data for which chisqr can be calculated
ds <- DfFroc2Roc(dataset01)
retFit <- FitCbmRoc(ds, 2, 3);print(retFit$fittedPlot)
retFit$ChisqrFitStats
```

```
## End(Not run)
```

FitCorCbmRoc   *Fit CORCBM to a paired ROC dataset*

Description

Fit the Correlated Contaminated Binormal Model (CORCBM) to a paired ROC dataset. The **ROC** dataset has to be formatted as a **single treatment**, **two-reader** dataset, even though the actual pairing may be different, see details.

Usage

```
FitCorCbmRoc(dataset)
```

Arguments

dataset   A **paired ROC** dataset

Details

The conditions (X, Y) can be two readers interpreting images in the same treatment, the same reader interpreting images in different treatments, or different readers interpreting images in 2 different treatments. Function `DfExtractCorCbmDataset` can be used to construct a dataset suitable for `FitCorCbmRoc`. With reference to the returned values, and assuming R bins in condition X and L bins in conditon Y, FPCounts is the R x L matrix containing the counts for non-diseased cases, TPCounts is the R x L matrix containing the counts for diseased cases; muX,muY,alphaX,alphaY,rhoNor,rhoAbn2 are the CORCBM parameters; aucX,aucX are the AUCs in the two conditions; stdAucX,stdAucY are the corresponding standard errors;stdErr contains the standard errors of the parameters of the model; areaStat, areaPval,covMat are the area-statistic, the p-value and the covariance matrix of the parameters. If a parameter approaches a limit, e.g., rhoNor = 0.9999, it is held constant at near the limiting value and the covariance matrix has one less dimension (along each edge) for each parameter that is held constant. The indices of the parameters held fixed are in `fitCorCbmRet$fixParam`.

Value

The return value is a list containing three objects:

fitCorCbmRet	list(FPCounts,TPCounts, muX,muY,alphaX,alphaY,rhoNor, rhoAbn2,zetaX,zetaY,covMat,fixParam)
stats	list(aucX,aucX,stdAucX, stdAucY,stdErr,areaStat,areaPval)
fittedPlot	The fitted plot with operating points, error bars, for both conditions

References

Zhai X, Chakraborty DP (2017) A bivariate contaminated binormal model for robust fitting of proper ROC curves to a pair of correlated, possibly degenerate, ROC datasets. Medical Physics. 44(6):2207–2222.

FitRsmRoc *Fit the radiological search model (RSM) to an ROC dataset*

Description

Fit an RSM-predicted ROC curve to a **binned single-modality single-treatment ROC dataset**

Usage

```
FitRsmRoc(binnedRocData, lesDistr, trt = 1, rdr = 1)
```

Arguments

binnedRocData	The **binned ROC** dataset containing the data
lesDistr	Array [1:maxLL,1:2]. The probability mass function of the lesion distribution for diseased cases. The first column contains the actual numbers of lesions per case. The second column contains the fraction of diseased cases with the number of lesions specified in the first column. The second column must sum to unity.
trt	The selected treatment, default is 1
rdr	The selected reader, default is 1

Details

If dataset is FROC, first convert it to ROC, using `DfFroc2Roc`. MLE ROC algorithms require binned datasets. Use `DfBinDataset` to perform the binning prior to calling this function. In the RSM: (1) The (random) number of latent NLs per case is Poisson distributed with mean parameter lambdaP, and the corresponding ratings are sampled from $N(0,1)$. The (2) The (random) number of latent LLs per diseased case is binomial distributed with success probability nuP and trial size equal to the number of lesions in the case, and the corresponding ratings are sampled from N(mu,1). (3) A latent NL or LL is actually marked if its rating exceeds the lowest threshold zeta1. To avoid clutter error bars are only shown for the lowest and uppermost operating points. Because of the extra parameter, and the requirement to have five counts, the chi-square statistic often cannot be calculated.

Value

The return value is a list with the following elements:

mu	The mean of the diseased distribution relative to the non-diseased one
lambdP	The Poisson parameter describing the distribution of latent NLs per case
nuP	The binomial success probability describing the distribution of latent LLs per diseased case
zetas	The RSM cutoffs, zetas or thresholds
AUC	The RSM fitted ROC-AUC
StdAUC	The standard deviation of AUC

NLLIni	The initial value of negative LL
NLLFin	The final value of negative LL
ChisqrFitStats	The chisquare goodness of fit results
covMat	The covariance matrix of the parameters
fittedPlot	A **ggplot2** object containing the fitted operating characteristic along with the empirical operating points. Use print to display the object

References

Chakraborty DP (2006) A search model and figure of merit for observer data acquired according to the free-response paradigm. Phys Med Biol 51, 3449-3462.

Chakraborty DP (2006) ROC Curves predicted by a model of visual search. Phys Med Biol 51, 3463–3482.

Chakraborty DP (2017) *Observer Performance Methods for Diagnostic Imaging - Foundations, Modeling, and Applications with R-Based Examples*, CRC Press, Boca Raton, FL. https://www.crcpress.com/Observer-Performance-Methods-for-Diagnostic-Imaging-Foundations-Modeling/Chakraborty/p/book/9781482214840

Examples

```
## Test with included ROC data (some bins have zero counts)
lesDistr <- UtilLesionDistr(dataset02)
retFit <- FitRsmRoc(dataset02, lesDistr)
print(retFit$fittedPlot)

## Test with included degenerate ROC data
lesDistr <- UtilLesionDistr(datasetDegenerate)
retFit <- FitRsmRoc(datasetDegenerate, lesDistr);print(retFit$fittedPlot)

## Test with single interior point data
fp <- c(rep(1,7), rep(2, 3))
tp <- c(rep(1,5), rep(2, 5))
binnedRocData <- Df2RJafrocDataset(fp, tp)
lesDistr <- UtilLesionDistr(binnedRocData)
retFit <- FitRsmRoc(binnedRocData, lesDistr);print(retFit$fittedPlot)

## Test with two interior data points
fp <- c(rep(1,7), rep(2, 5), rep(3, 3))
tp <- c(rep(1,3), rep(2, 5), rep(3, 7))
binnedRocData <- Df2RJafrocDataset(fp, tp)
lesDistr <- UtilLesionDistr(binnedRocData)
retFit <- FitRsmRoc(binnedRocData, lesDistr);print(retFit$fittedPlot)


## Test with three interior data points
fp <- c(rep(1,12), rep(2, 5), rep(3, 3), rep(4, 5)) #25
tp <- c(rep(1,3), rep(2, 5), rep(3, 7), rep(4, 10)) #25
binnedRocData <- Df2RJafrocDataset(fp, tp)
lesDistr <- UtilLesionDistr(binnedRocData)
```

```
retFit <- FitRsmRoc(binnedRocData, lesDistr);print(retFit$fittedPlot)

## test for TONY data, i = 2 and j = 3; only case permitting chisqure calculation
lesDistr <- UtilLesionDistr(dataset01)
rocData <- DfFroc2Roc(dataset01)
retFit <- FitRsmRoc(rocData, lesDistr, trt = 2, rdr = 3)
print(retFit$fittedPlot)
retFit$ChisqrFitStats
```

PlotBinormalFit   *Plot binormal fit*

Description

Plot the binormal-predicted ROC curve with provided parameters

Usage

```
PlotBinormalFit(a, b)
```

Arguments

a	vector: the mean(s) of the diseased distribution(s).
b	vector: the standard deviations(s) of the diseased distribution(s).

Details

a and b must have the same length. The predicted ROC curve for each a and b pair will be plotted.

Value

A **ggplot2** object of the plotted ROC curve(s) are returned. Use print function to display the saved object.

Examples

```
binormalPlot <- PlotBinormalFit(c(1, 2), c(0.5, 0.5))
print(binormalPlot)
```

`PlotCbmFit` *Plot CBM fitted curve*

Description

Plot the CBM-predicted ROC curve with provided CBM parameters

Usage

```
PlotCbmFit(mu, alpha)
```

Arguments

mu	vector: the mean(s) of the z-samples of the diseased distribution(s) where the disease is visible
alpha	vector: the proportion(s) of the diseased distribution(s) where the disease is visible

Details

mu and `alpha` must have equal length. The predicted ROC curve for each `mu` and `alpha` pair will be plotted.

Value

A **ggplot2** object of the plotted ROC curve(s)

References

Dorfman DD, Berbaum KS (2000) A contaminated binormal model for ROC data: Part II. A formal model, Acad Radiol 7, 427–437.

Examples

```
cbmPlot <- PlotCbmFit(c(1, 2), c(0.5, 0.5))
print(cbmPlot)
```

PlotEmpiricalOperatingCharacteristics

Plot empirical operating characteristics, ROC, FROC or LROC

Description

Plot empirical operating characteristics (operating points connected by straight lines) for specified modalities and readers, or, if desired, plots (no operating points) averaged over specified modalities and / or readers.

Usage

```
PlotEmpiricalOperatingCharacteristics(
  dataset,
  trts = 1,
  rdrs = 1,
  opChType,
  legend.position = c(0.8, 0.2)
)
```

Arguments

dataset	Dataset object.
trts	List or vector: **integer** indices of modalities to be plotted. Default is 1.
rdrs	List or vector: **integer** indices of readers to be plotted. Default is 1.
opChType	Type of operating characteristic to be plotted: ″ROC″, ″FROC″, ″AFROC″, ″wAFROC″, ″AFROC1″, ″wAFROC1″, or ″LROC″.
legend.position	
	Where to position the legend. The default is c(0.8, 0.2), i.e., 0.8 rightward and 0.2 upward (the plot is a unit square).

Details

The trts and rdrs are vectors or lists of **integer** indices, not the corresponding **string** IDs. For example, if the string ID of the first reader is "0", the value in rdrs should be **1** not **0**. The legend will display the string IDs.

If both of trts and rdrs are vectors, all combinations of modalities and readers are plotted. See Example 1.

If both trts and rdrs are lists, they must have the same length. Only the combination of modality and reader at the same position in their respective lists are plotted. If some elements of the modalities and / or readers lists are vectors, the average operating characteristic over the implied modalities and / or readers are plotted. See Example 2.

For LROC datasets, opChType can be "ROC" or "LROC".

Value

A **ggplot2** object containing the operating characteristic plot(s) and a data frame containing the points defining the operating characteristics.

Plot   **ggplot2** object. For continuous or averaged data, operating characteristics curves are plotted **without** showing operating points. For binned (individual) data, both operating points and connecting lines are shown. To avoid clutter, if there are more than 20 operating points, they are not shown.

Points   Data frame with four columns: abscissa, ordinate, class (which codes modality and reader) and type, which can be "individual", "continuous", i.e., more than 20 operating points, or "rdrAveraged".

Examples

```
## Example 1
## Plot individual empirical ROC plots for all combinations of modalities
## 1 and 2 and readers 1, 2 and 3. Six operating characteristics are plotted.

ret <- PlotEmpiricalOperatingCharacteristics(dataset =
dataset02, trts = c(1:2), rdrs = c(1:3), opChType = "ROC")
print(ret$Plot)


## Example 2
## Empirical ROC, FROC, AFROC and wAFROC plots. Each plot consists of
## three sub-plots (see Example 3 for correspondences between indices and
## string identifiers for modalities and readers):
## (1) sub-plot, with operating points, for the 1st modality (string ID "1") and the 2nd
## reader (string ID "3"), labeled M:1 R:3
## (2) sub-plot, no operating points, for the 2nd modality (string ID "2") AVERAGED
## over the 2nd and 3rd readers (string IDs "3" and "4"), labeled M:2  R: 3 4
## (3) sub-plot, no operating points, AVERAGED over the first two modalities
## (string IDs "1" and "2") AND over the 1st, 2nd and 3rd readers
## (string IDs "1", "3" and "4"), labeled M: 1 2  R: 1  3 4

plotT <- list(1, 2, c(1:2))
plotR <- list(2, c(2:3), c(1:3))
ret <- PlotEmpiricalOperatingCharacteristics(dataset = dataset04,
   trts = plotT, rdrs = plotR, opChType = "ROC")
print(ret$Plot)

ret <- PlotEmpiricalOperatingCharacteristics(dataset = dataset04, trts = plotT,
   rdrs = plotR, opChType = "FROC")
print(ret$Plot)

ret <- PlotEmpiricalOperatingCharacteristics(dataset = dataset04, trts = plotT,
   rdrs = plotR, opChType = "AFROC")
print(ret$Plot)

ret <- PlotEmpiricalOperatingCharacteristics(dataset = dataset04, trts = plotT,
   rdrs = plotR, opChType = "wAFROC")
print(ret$Plot)
```

```
##Example 3
## Correspondences between indices and string identifiers for modalities and
## readers in this dataset. Apparently reader "2" did not complete the study.

str(dataset04)

## List of 8
## NL          : num [1:5, 1:4, 1:200, 1:7] -Inf -Inf 1 -Inf -Inf ...
## LL          : num [1:5, 1:4, 1:100, 1:3] 4 5 4 5 4 3 5 4 4 3 ...
## $ lesionVector  : int [1:100] 1 1 1 1 1 1 1 1 1 1 ...
## $ lesionID    : num [1:100, 1:3] 1 1 1 1 1 1 1 1 1 1 ...
## $ lesionWeight: num [1:100, 1:3] 1 1 1 1 1 1 1 1 1 1 ...
## $ dataType    : chr "FROC"
## $ modalityID  : chr [1:5] "1" "2" "3" "4" "5"
## $ readerID    : chr [1:4] "1" "3" "4" "5"
```

PlotRsmOperatingCharacteristics

RSM predicted operating characteristics, ROC pdfs and different FOMs possible with FROC data

Description

Visualize predicted ROCs, AFROCs, wAFROCs, FROCs and pdfs (probability density functions of highest ratings, for non-diseased and diseased cases), for up to 2 sets of search model parameters. This function is useful as an instructional tool towards understanding the RSM.

Usage

```
PlotRsmOperatingCharacteristics(
  mu,
  lambda,
  nu,
  lesDistr,
  lesWghtDistr,
  OpChType = "ALL",
  legendPosition = c(1, 0),
  legendDirection = "horizontal",
  legendJustification = c(0, 1),
  nlfRange = NULL,
  llfRange = NULL,
  nlfAlpha = NULL,
  myNegInf = -3
)
```

Arguments

mu	Array, max length 2. The mean(s) of the Gaussian distribution(s) for the ratings of latent LLs (continuous ratings of lesions that are found by the observer's search mechanism)
lambda	Array, max length 2. The Poisson distribution *intrinsic* parameter(s), which model the random numbers of latent NLs (suspicious regions that do not correspond to actual lesions) per case, for up to two treatments. The corresponding *physical* parameters are lambda/mu. Two conversion functions are provided: UtilIntrinsic2PhysicalRSM and UtilPhysical2IntrinsicRSM.
nu	Array, max length 2. The binomial distribution success probability *intrinsic* parameters, which model the random numbers of latent LLs (suspicious regions that correspond to actual lesions) per diseased case for up to two treatments; the corresponding *physical* parameter is 1 -exp(nu*mu), the success probability of the binomial distribution(s).
lesDistr	Array [1:maxLL,1:2]. The probability mass function of the lesion distribution for diseased cases. The first column contains the actual numbers of lesions per case. The second column contains the fraction of diseased cases with the number of lesions specified in the first column. The second column must sum to unity. See UtilLesionDistr.
lesWghtDistr	The lesion weights distribution, an [1:maxLL,1:maxLL] array. The probability mass function of the lesion weights for diseased cases. maxLL is the maximum number of lesions in the dataset. The 1st row contains the weight of the lesion on cases with one lesion only, necessarily 1, assuming the dataset has cases with only one lesion; the remaining elements of the row are -Inf. The 2nd row contains the weights of the 2 lesions on cases with 2 lesions only, the remaining elements of the row, if any, are -Inf, assuming the dataset has cases with two lesion. Excluding the -Inf, each row must sum to 1. The default is equal weighting, e.g., weights are 1/3, 1/3, 1/3 on row 3, assuming the dataset has cases with three lesions. This parameter is not to be confused with the lesionWeight list member in an FROC dataset which enumerates the weights of lesions on individual cases. See UtilLesionWeightsDistr.
OpChType	The type of operating characteristic desired: can be "ROC", "AFROC", "wAFROC", "FROC" or "pdfs" or "ALL". The default is "ALL".
legendPosition	The positioning of the legend: "right", "left", "top" or "bottom". Use "none" to suppress the legend.
legendDirection	Allows control on the direction of the legend; "horizontal", the default, or "vertical"
legendJustification	Where to position the legend, default is bottom right corner c(0,1)
nlfRange	**This applies to FROC plot only**. The x-axis range, e.g., c(0,2), for FROC plot. Default is "NULL", which means the maximum NLF range, as determined by the data.
llfRange	**This applies to FROC plot only**. The y-axis range, e.g., c(0,1), for FROC plot. Default is "NULL", which means the maximum LLF range, as determined by the data.

nlfAlpha   Upper limit of the integrated area under the FROC plot. Default is "NULL", which
                  means the maximum NLF range is used (i.e., lambda/mu). Attempt to integrate
                  outside the maximum NLF will generate an error.

myNegInf   How close one approaches the end-point; the default is -3. This is used in the
                  code to demonstrate continuity of the slope of the ROC at the end point; Online
                  Appendix 17.H.3

Details

RSM is the Radiological Search Model described in the book.

Value

A list of elements containing five **ggplot2** objects (ROCPlot, AFROCPlot wAFROCPlot, FROC-
Plot and PDFPlot) and two area measures (each of which can have up to two elements), the area
under the search model predicted ROC curves in up to two treatments, the area under the search
model predicted AFROC curves in up to two treatments, the area under the search model predicted
wAFROC curves in up to two treatments, the area under the search model predicted FROC curves
in up to two treatments.

- ROCPlot The predicted ROC plots
- AFROCPlot The predicted AFROC plots
- wAFROCPlot The predicted wAFROC plots
- FROCPlot The predicted FROC plots
- PDFPlot The predicted pdf plots
- aucROC The predicted ROC AUCs
- aucAFROC The predicted AFROC AUCs
- aucwAFROC The predicted wAFROC AUCs
- aucFROC The predicted FROC AUCs

Note

For lesDistr, the sum over the second column must equal one. If all cases contain same number
of lesions, simply supply this number instead of the matrix. If the argument is missing, the default
value of one lesion per diseased case is used.

In lesWghtDistr, the sum over each row (excluding -Inf) must be one. The value -Inf should
be assigned if the corresponding lesion does not exist. Equal lesion weighting is applied if this
argument is missing.

For example, if the maximum number of distinct lesion configurations per case is 3 (e.g., 1, 2
and 4, implying there are no cases with 3 lesions), the first column of lesDistr will be c(1,2,4).
The second column might be c(0.8, 0.15, 0.05), which sums to one, meaning 80% of cases have
only one lesion, 15% have two lesions and 5% have three lesions. The lesWghtDistr matrix will
be [1:3,1:4], where each row will sum to one (excluding the first entry and excluding negative
infinities).

References

Chakraborty DP (2006) A search model and figure of merit for observer data acquired according to the free-response paradigm, Phys Med Biol 51, 3449-3462.

Chakraborty DP (2006) ROC Curves predicted by a model of visual search, Phys Med Biol 51, 3463–3482.

Chakraborty, DP, Yoon, HJ (2008) Operating characteristics predicted by models for diagnostic tasks involving lesion localization, Med Phys, 35:2, 435.

Chakraborty DP (2017) *Observer Performance Methods for Diagnostic Imaging - Foundations, Modeling, and Applications with R-Based Examples* (CRC Press, Boca Raton, FL). https://www.crcpress.com/Observer-Performance-Methods-for-Diagnostic-Imaging-Foundations-Modeling/Chakraborty/p/book/9781482214840

Examples

```
## Following example is for mu = 2, lambda = 1, nu = 0.6, in one treatment and
## mu = 3, lambda = 1.5, nu = 0.8, in the other treatment. 20% of the diseased
## cases have a single lesion, 40% have two lesions, 10% have 3 lesions,
## and 30% have 4 lesions.
lesDistr <- rbind(c(1, 0.2), c(2, 0.4), c(3, 0.1), c(4, 0.3))

## On cases with one lesion the weights are 1, on cases with 2 lesions the weights
## are 0.4 and 0.6, on cases with three lesions the weights are 0.2, 0.3 and 0.5, and
## on cases with 4 lesions the weights are 0.3, 0.4, 0.2 and 0.1:
lesWghtDistr <- rbind(c(1, 1.0, -Inf, -Inf, -Inf),
                      c(2, 0.4,  0.6, -Inf, -Inf),
                      c(3, 0.2,  0.3,  0.5, -Inf),
                      c(4, 0.3,  0.4, 0.2,  0.1))
ret <- PlotRsmOperatingCharacteristics(mu = c(2, 3), lambda = c(1, 1.5), nu = c(0.6, 0.8),
   lesDistr = lesDistr, lesWghtDistr = lesWghtDistr,
   legendPosition = "bottom", nlfRange = c(0, 1), llfRange = c(0, 1))
   print(ret$ROCPlot)
   print(ret$AFROCPlot)
   print(ret$wAFROCPlot)
   print(ret$FROCPlot)
## the FROC plot ends at NLF = 0.5 because for both treatments the physical lambdas are 0.5.
```

SimulateCorCbmDataset   *Simulate paired binned data for testing FitCorCbmRoc*

Description

Simulates single treatment 2-reader binned ROC dataset, simulated according to the CORCBM model, for the purpose of testing the fitting program `FitCorCbmRoc`.

Usage

```
SimulateCorCbmDataset(
  seed = 123,
  K1 = 50,
  K2 = 50,
  desiredNumBins = 5,
  muX = 1.5,
  muY = 3,
  alphaX = 0.4,
  alphaY = 0.7,
  rhoNor = 0.3,
  rhoAbn2 = 0.8
)
```

Arguments

seed	The seed variable, default is 123; set to NULL for truly random seed
K1	The number of non-diseased cases, default is 50
K2	The number of diseased cases, default is 50
desiredNumBins	The desired number of bins; default is 5
muX	The CBM mu parameter in condition X
muY	The CBM mu parameter in condition Y
alphaX	The CBM alpha parameter in condition X
alphaY	The CBM alpha parameter in condition Y
rhoNor	The correlation of non-diseased case z-samples
rhoAbn2	The correlation of diseased case z-samples, when disease is visible in both conditions

Details

X and Y refer to the two arms of the pairing. muX and alphaX refer to the univariate CBM parameters in condition X, rhoNor is the correlation of ratings of non-diseased cases and rhoAbn2 is the correlation of ratings of diseased cases when disease is visible in both conditions. The ROC data is bined to 5 bins in each condition. See referenced publication.

Value

The return value is the desired dataset, suitable for testing FitCorCbmRoc

References

Zhai X, Chakraborty DP (2017) A bivariate contaminated binormal model for robust fitting of proper ROC curves to a pair of correlated, possibly degenerate, ROC datasets. Medical Physics. 44(6):2207–2222.

Examples

```
dataset <- SimulateCorCbmDataset()

## Not run:
## this takes very long
dataset <- SimulateCorCbmDataset(K1 = 5000, K2 = 5000)


## End(Not run)
```

SimulateFrocDataset   *Simulates an MRMC uncorrelated FROC dataset using the RSM*

Description

Simulates an uncorrelated MRMC FROC dataset for specified numbers of readers and treatments

Usage

```
SimulateFrocDataset(mu, lambda, nu, zeta1, I, J, K1, K2, lesionVector)
```

Arguments

mu	The intrinsic mu parameter of the RSM
lambda	The intrinsic lambda parameter of the RSM (not the physical parameter)
nu	The intrinsic nu parameter of the RSM (not the physical parameter)
zeta1	The lowest reporting threshold
I	The number of treatments
J	The number of readers
K1	The number of non-diseased cases
K2	The number of diseased cases
lesionVector	A K2 length array containing the numbers of lesions per diseased case

Details

See book chapters on the Radiological Search Model (RSM) for details. In this code correlations between ratings on the same case are assumed to be zero.

Value

The return value is an FROC dataset.

References

Chakraborty DP (2017) *Observer Performance Methods for Diagnostic Imaging - Foundations, Modeling, and Applications with R-Based Examples*, CRC Press, Boca Raton, FL. https://www.crcpress.com/Observer-Performance-Methods-for-Diagnostic-Imaging-Foundations-Modeling/Chakraborty/p/book/9781482214840

Examples

```
set.seed(1)
K1 <- 5;K2 <- 7;
maxLL <- 2;lesionVector <- floor(runif(K2, 1, maxLL + 1))
mu <- 1;lambda <- 1;nu <- 1 ;zeta1 <- -1
I <- 2; J <- 5

frocDataRaw <- SimulateFrocDataset(
  mu = mu, lambda = lambda, nu = nu, zeta1 = zeta1,
  I = I, J = J, K1 = K1, K2 = K2, lesionVector = lesionVector )

## plot the data
ret <- PlotEmpiricalOperatingCharacteristics(frocDataRaw, opChType = "FROC")
print(ret$Plot)
```

SimulateLrocDataset   *Simulates an uncorrelated FLROC FrocDataset using the RSM*

Description

Simulates an uncorrelated LROC dataset for specified numbers of readers and treatments

Usage

```
SimulateLrocDataset(mu, lambda, nu, zeta1, I, J, K1, K2, lesionVector)
```

Arguments

mu	The intrinsic mu parameter of the RSM
lambda	The intrinsic lambda parameter of the RSM (not the physical parameter)
nu	The intrinsic nu parameter of the RSM (not the physical parameter)
zeta1	The lowest reporting threshold
I	The number of treatments
J	The number of readers
K1	The number of non-diseased cases
K2	The number of diseased cases
lesionVector	A K2 length array containing the numbers of lesions per diseased case

Details

See book chapters on the Radiological Search Model (RSM) for details. The spproach is to first simulate an FROC dataset and then convert it to an Lroc dataset. The correlations between FROC ratings on the same case are assumed to be zero.

Value

The return value is an LROC dataset.

References

Chakraborty DP (2017) *Observer Performance Methods for Diagnostic Imaging - Foundations, Modeling, and Applications with R-Based Examples*, CRC Press, Boca Raton, FL. `https://www.crcpress.com/Observer-Performance-Methods-for-Diagnostic-Imaging-Foundations-Modeling/Chakraborty/p/book/9781482214840`

Examples

```
set.seed(1)
K1 <- 5
K2 <- 5
mu <- 2
lambda <- 1
lesionVector <- rep(1, 5)
nu <- 0.8
zeta1 <- -3
frocData <- SimulateFrocDataset(mu, lambda, nu, zeta1, I = 2, J = 5, K1, K2, lesionVector)
lrocData <- DfFroc2Lroc(frocData)
```

SimulateRocDataset   *Simulates a binormal model ROC dataset*

Description

Simulates a binormal model ROC dataset for a single treatment and reader

Usage

```
SimulateRocDataset(K1, K2, a, b, seed = NULL)
```

Arguments

K1	The number of non-diseased cases
K2	The number of diseased cases
a	The a parameter of the binormal model
b	The b parameter of the binormal model
seed	The initial seed, default is NULL

Details

See book Chapter 6 for details

Value

An ROC dataset

References

Chakraborty DP (2017) *Observer Performance Methods for Diagnostic Imaging - Foundations, Modeling, and Applications with R-Based Examples*, CRC Press, Boca Raton, FL. `https://www.crcpress.com/Observer-Performance-Methods-for-Diagnostic-Imaging-Foundations-Modeling/Chakraborty/p/book/9781482214840`

Examples

```
K1 <- 5;K2 <- 7;
a <- 1.5;b <- 0.5

rocDataRaw <- SimulateRocDataset(K1 = K1, K2 = K2,
  a = a, b = b)

## plot the data
ret <- PlotEmpiricalOperatingCharacteristics(rocDataRaw, trts= 1, rdrs = 1, opChType = "ROC")
print(ret$Plot)
```

SsFrocNhRsmModel   *RSM fitted model for FROC sample size*

Description

RSM fitted model for FROC sample size

Usage

```
SsFrocNhRsmModel(dataset, lesionPmf)
```

Arguments

dataset   The **pilot** dataset object representing a NH ROC (or FROC) dataset.

lesionPmf   An array containing the probability mass function of number of lesions per diseased case in the proposed **pivotal FROC** study.

Details

If dataset is FROC, it is converted to an ROC dataset. The search model is used to fit each treatment-reader combination in the pilot dataset. The median value for each parameter is computed and are returned by the function (3 vaalues). These are used to compute predicted wAFROC and ROC FOMS over a range of values of deltaMu, which are fitted by a straight line constrained to pass throught the origin. The scaleFactor (scaling factor) and R2 are returned. The scaling factor is the value by which the ROC effect size must be multiplied to get the wAFROC effect size. Also returned are the lesDist and lesWghtDist arrays, which are needed for computing FOMs. See 2nd FROC SS vignette. Equally weighted lesions is assumed.

Value

A list containing:

- `muMed`, the median mu parameter of the NH model.

- `lambdaMed`, the median lambda parameter of the NH model.

- `nuMed`, the median nu parameter of the NH model.

- `lesDistr`, the lesion distribution array.

- `lesWghtDistr`, the lesion weight distribution array.

- `scaleFactor`, the scaling factor that multiplies the ROC effect size to get wAFROC effect size.

- `R2`, the R2 of the fit.

Examples

```
SsFrocNhRsmModel(dataset02, c(0.7, 0.2, 0.1))
## the next one should match the vignette
SsFrocNhRsmModel(DfExtractDataset(dataset04, trts = c(1,2)), c(0.69, 0.2, 0.11))
```

SsPowerGivenJK   *Statistical power for specified numbers of readers and cases*

Description

Calculate the statistical power for specified numbers of readers J, cases K, analysis method and DBM or OR variances components

Usage

```
SsPowerGivenJK(
  dataset,
  ...,
  FOM,
  FPFValue = 0.2,
  J,
  K,
  effectSize = NULL,
  method = "DBMH",
  option = "ALL",
  alpha = 0.05
)
```

Arguments

dataset	The **pilot** dataset. If set to NULL then variance components must be supplied.
...	Optional variance components, varYTR, varYTC and varYEps. These are needed if dataset is not supplied.
FOM	The figure of merit
FPFValue	Only needed for LROC data **and** FOM = "PCL" or "ALROC"; where to evaluate a partial curve based figure of merit. The default is 0.2.
J	The number of readers in the pivotal study.
K	The number of cases in the pivotal study.
effectSize	The effect size to be used in the **pivotal** study. Default is NULL, which uses the observed effect size in the pilot dataset. Must be supplied if dataset is set to NULL and variance components are supplied.
method	"DBMH" (the default) or "ORH".
option	Desired generalization, "RRRC", "FRRC", "RRFC" or "ALL" (the default).
alpha	The significance level, default is 0.05.

Details

The default `effectSize` uses the observed effect size in the pilot study. A numeric value over-rides the default value. This argument must be supplied if dataset = NULL and variance compenents (the ... arguments) are supplied.

Value

The expected statistical power.

References

Hillis SL, Obuchowski NA, Berbaum KS (2011). Power Estimation for Multireader ROC Methods: An Updated and Unified Approach. Acad Radiol, 18, 129–142.

Hillis SL, Obuchowski NA, Schartz KM, Berbaum KS (2005). A comparison of the Dorfman-Berbaum-Metz and Obuchowski-Rockette methods for receiver operating characteristic (ROC) data. Statistics in Medicine, 24(10), 1579–607.

Chakraborty DP (2017) *Observer Performance Methods for Diagnostic Imaging - Foundations, Modeling, and Applications with R-Based Examples*, CRC Press, Boca Raton, FL. https://www.crcpress.com/Observer-Performance-Methods-for-Diagnostic-Imaging-Foundations-Modeling/Chakraborty/p/book/9781482214840

Examples

```
## the following two should give identical results
SsPowerGivenJK(dataset02, FOM = "Wilcoxon", effectSize = 0.05, J = 6, K = 251, method = "DBMH")
a <- UtilVarComponentsDBM(dataset02, FOM = "Wilcoxon")$varComp
SsPowerGivenJK(dataset = NULL, J = 6, K = 251, effectSize = 0.05, method = "DBMH",
                   list(varYTR = a$varTR, varYTC = a$varTC, varYEps = a$varErr))

## the following two should give identical results
SsPowerGivenJK(dataset02, FOM = "Wilcoxon", effectSize = 0.05, J = 6, K = 251, method = "ORH")
a <- UtilVarComponentsOR(dataset02, FOM = "Wilcoxon")$varComp
KStar <- length(dataset02$NL[1,1,,1])
SsPowerGivenJK(dataset = NULL, effectSize = 0.05, J = 6, K = 251, method = "ORH",
   list(KStar = KStar, varTR = a$varTR, cov1 = a$cov1, cov2 = a$cov2,
   cov3 = a$cov3, varEps = a$var))
```

SsPowerGivenJKDbmVarComp

Power given J, K and Dorfman-Berbaum-Metz variance components

---

Description

Power given J, K and Dorfman-Berbaum-Metz variance components

Usage

```
SsPowerGivenJKDbmVarComp(
  J,
  K,
  effectSize,
  varYTR,
  varYTC,
  varYEps,
  alpha = 0.05,
  option
)
```

Arguments

J	The number of readers
K	The number of cases
effectSize	The effect size
varYTR	The treatment-reader DBM variance component
varYTC	The treatment-case DBM variance component
varYEps	The error-term DBM variance component
alpha	The size of the test (default = 0.05)
option	The desired generalization ("RRRC", "FRRC", "RRFC", "ALL")

Details

The variance components are obtained using [StSignificanceTesting](#) with `method = "DBMH"`.

Value

A list object containing the estimated power and associated statistics for each desired generalization.

Examples

```
VarComp <- StSignificanceTesting(dataset02, FOM = "Wilcoxon", method = "DBMH",
   option = "RRRC")$varComp
varYTR <- VarComp$varTR
varYTC <- VarComp$varTC
varYEps <- VarComp$varErr
ret <- SsPowerGivenJKDbmVarComp (J = 5, K = 100, effectSize = 0.05, varYTR,
   varYTC, varYEps, option = "RRRC")
cat("RRRC power = ", ret$powerRRRC)
```

SsPowerGivenJKOrVarComp

Power given J, K and Obuchowski-Rockette variance components

Description

Power given J, K and Obuchowski-Rockette variance components

Usage

```
SsPowerGivenJKOrVarComp(
  J,
  K,
  KStar,
  effectSize,
  varTR,
```

```
    cov1,
    cov2,
    cov3,
    varEps,
    alpha = 0.05,
    option
)
```

Arguments

J	The number of readers in the **pivotal** study
K	The number of cases in the **pivotal** study
KStar	The number of cases in the **pilot** study
effectSize	The effect size
varTR	The treatment-reader OR variance component
cov1	The OR cov1 covariance
cov2	The OR cov2 covariance
cov3	The OR cov3 covariance
varEps	The OR pure variance term
alpha	The size of the test (default = 0.05)
option	The desired generalization ("RRRC", "FRRC", "RRFC", "ALL")

Details

The variance components are obtained using StSignificanceTesting with method = "ORH".

Value

A list object containing the estimated power and associated statistics for each desired generalization.

Examples

```
dataset <- dataset02 ## the pilot study
KStar <- length(dataset$NL[1,1,,1])
VarComp <- StSignificanceTesting(dataset, FOM = "Wilcoxon", method = "ORH", option = "RRRC")$varComp
varTR <- VarComp$varTR
cov1 <- VarComp$cov1
cov2 <- VarComp$cov2
cov3 <- VarComp$cov3
varEps <- VarComp$var
ret <- SsPowerGivenJKOrVarComp (J = 5, K = 100, KStar = KStar,
    effectSize = 0.05, varTR, cov1, cov2, cov3, varEps, option = "RRRC")

cat("RRRC power = ", ret$powerRRRC)
```

SsPowerTable   *Generate a power table*

Description

Generate combinations of numbers of readers J and numbers of cases K for desired power and specified generalization(s)

Usage

```
SsPowerTable(
  dataset,
  FOM,
  effectSize = NULL,
  alpha = 0.05,
  desiredPower = 0.8,
  method = "DBMH",
  option = "ALL"
)
```

Arguments

dataset	The **pilot** ROC dataset to be used to extrapolate to the **pivotal** study.
FOM	The figure of merit.
effectSize	The effect size to be used in the **pivotal** study, default value is NULL. See Details.
alpha	The The size of the test, default is 0.05.
desiredPower	The desired statistical power, default is 0.8.
method	Analysis method, "DBMH" or "ORH", the default is "DBMH".
option	Desired generalization, "RRRC", "FRRC", "RRFC" or "ALL" (the default).

Details

The default effectSize uses the observed effect size in the pilot study. A numeric value over-rides the default value.

Value

A list containing up to 3 (depending on options) dataframes. Each dataframe contains 3 arrays:

numReaders	The numbers of readers in the pivotal study.
numCases	The numbers of cases in the pivotal study.
power	The estimated statistical powers.

Note

The procedure is valid for ROC studies only; for FROC studies see Online Appendix Chapter 19.

Examples

```
## Examples with CPU or elapsed time > 5s
##              user    system elapsed
## SsPowerTable 20.033  0.037  20.077

## Example of sample size calculation with DBM method
SsPowerTable(dataset02, FOM = "Wilcoxon", method = "DBMH")

## Example of sample size calculation with OR method
SsPowerTable(dataset02, FOM = "Wilcoxon", method = "ORH")
```

SsSampleSizeKGivenJ   *Number of cases, for specified number of readers, to achieve desired*
                          power

Description

Number of cases to achieve the desired power, for specified number of readers J, and specified
DBMH or ORH analysis method

Usage

```
SsSampleSizeKGivenJ(
  dataset,
  ...,
  J,
  FOM,
  effectSize = NULL,
  method = "DBMH",
  alpha = 0.05,
  desiredPower = 0.8,
  option = "ALL"
)
```

Arguments

dataset	The **pilot** dataset. If set to NULL then variance components must be supplied.
...	Optional variance components, varYTR, varYTC and varYEps. These are needed if dataset is not supplied.
J	The number of readers in the **pivotal** study.
FOM	The figure of merit. Not needed if variance components are supplied.
effectSize	The effect size to be used in the **pivotal** study. Default is NULL. Must be supplied if dataset is set to NULL and variance components are supplied.

method	"DBMH" (default) or "ORH".
alpha	The significance level of the study, default is 0.05.
desiredPower	The desired statistical power, default is 0.8.
option	Desired generalization, "RRRC", "FRRC", "RRFC" or "ALL" (the default).

Details

`effectSize` = NULL uses the **observed** effect size in the pilot study. A numeric value over-rides the default value. This argument must be supplied if dataset = NULL and variance compenents (the optional ... arguments) are supplied.

Value

A list of two elements:

| K | The minimum number of cases K in the pivotal study to just achieve the desired statistical power. This is calculated for each value of option. |
| power | The predicted statistical power. |

References

Hillis SL, Obuchowski NA, Berbaum KS (2011) Power Estimation for Multireader ROC Methods: An Updated and Unified Approach, Acad Radiol, 18, 129–142.

Hillis SL, Obuchowski NA, Schartz KM, Berbaum KS (2005) A comparison of the Dorfman-Berbaum-Metz and Obuchowski-Rockette methods for receiver operating characteristic (ROC) data, Statistics in Medicine, 24:10, 1579–607.

Examples

```
## the following two should give identical results
SsSampleSizeKGivenJ(dataset02, FOM = "Wilcoxon", effectSize = 0.05, J = 6, method = "DBMH")
a <- UtilVarComponentsDBM(dataset02, FOM = "Wilcoxon")$varComp
SsSampleSizeKGivenJ(dataset = NULL, J = 6, effectSize = 0.05, method = "DBMH",
   list(varYTR = a$varTR, varYTC = a$varTC, varYEps = a$varErr))



## the following two should give identical results
SsSampleSizeKGivenJ(dataset02, FOM = "Wilcoxon", effectSize = 0.05, J = 6, method = "ORH")
a <- UtilVarComponentsOR(dataset02, FOM = "Wilcoxon")$varComp
KStar <- length(dataset02$NL[1,1,,1])
SsSampleSizeKGivenJ(dataset = NULL, J = 6, effectSize = 0.05, method = "ORH",
   list(KStar = KStar, varTR = a$varTR, cov1 = a$cov1, cov2 = a$cov2,
   cov3 = a$cov3, varEps = a$var))

for (J in 6:10) {
 ret <- SsSampleSizeKGivenJ(dataset02, FOM = "Wilcoxon", J = J, option = "RRRC")
 message("# of readers = ", J, " estimated # of cases = ", ret$K,
 ", predicted power = ", signif(ret$powerRRRC,3), "\n")
}
```

StSignificanceTesting   *Perform DBM or OR significance testing*

Description

Performs Dorfman-Berbaum-Metz (DBM) or Obuchowski-Rockette (OR) significance testing (with Hillis' improvements), for specified dataset; significance testing refers to analysis designed to assign a P-value, and other statistics, for rejecting the null hypothesis (NH) that the reader-averaged figure of merit (FOM) difference between treatments is zero. The results of the analysis are better visualized in the text or Excel-formatted files produced by `UtilOutputReport`.

Usage

```
StSignificanceTesting(
  dataset,
  FOM,
  FPFValue = 0.2,
  alpha = 0.05,
  method = "DBMH",
  covEstMethod = "Jackknife",
  nBoots = 200,
  option = "ALL",
  tempOrgCode = FALSE
)
```

Arguments

dataset	The dataset to be analyzed, see `RJafroc-package`. **Must have two or more treatments and two or more readers.**
FOM	The figure of merit, see `UtilFigureOfMerit`
FPFValue	Only needed for LROC data **and** FOM = "PCL" or "ALROC"; where to evaluate a partial curve based figure of merit. The default is 0.2.
alpha	The significance level of the test of the null hypothesis that all treatment effects are zero; the default is 0.05
method	The significance testing method to be used. There are two options: "DBMH" (the default) or "ORH", representing the Dorfman-Berbaum-Metz and the Obuchowski-Rockette significance testing methods, respectively.
covEstMethod	The covariance matrix estimation method in ORH analysis (for method = "DBMH" the jackknife is always used).

- "Jackknife", the default,
- "Bootstrap", in which case nBoots (above) is relevant
- "DeLong"; requires FOM = "Wilcoxon", otherwise an error results.

nBoots	The number of bootstraps (defaults to 200), relevant only if `covEstMethod = "Bootstrap"` and `method = "ORH"`
option	Determines which factors are regarded as random vs. fixed:

- `"RRRC"` = random-reader random case,
- `"FRRC"` = fixed-reader random case,
- `"RRFC"` = random-reader fixed case,
- `"ALL"` = outputs the results of `"RRRC"`, `"FRRC"` and `"RRFC"` analyses

tempOrgCode,	default FALSE; if TRUE, then code from version 0.0.1 of RJafroc is used (see RJafroc_0.0.1.tar). This is intended to check against errors that crept in subsequent to the original version as I attempted to improve the organization of the code and the output. As implicit in the name of this temporary flag, it will eventually be removed.

Value

For `method = "DBMH"` the returned list has 15 members:

fomArray	Figure of merit array: see return of [UtilFigureOfMerit](#)
anovaY	ANOVA table of the pseudovalues, over all treatments
anovaYi	ANOVA table of the pseudovalues, for each treatment
varComp	The variance components of the DBM pseudovalue mode; 6 values, in the following order: varR, varC, varTR, varTC, varRC and varErr
FTestStatsRRRC	Results of the F-test for RRRC **random reader random case** analysis; contains the following items: fRRRC - the value of the F-statistic, ndfRRRC - the numerator degrees of freedom, ddfRRRC - the denominator degrees of freedom and pRRRC - the pvalue
ciDiffTrtRRRC	For RRRC analysis, the confidence intervals and related statistics for the FOM differences between pairs of treatments
ciAvgRdrEachTrtRRRC	
	For RRRC analysis, the confidence intervals and related test statistics for rdr. avg. FOM in each treatment
FTestStatsFRRC	As for FTestStatsRRRC except that this is for **fixed-reader random-case** (FRRC) analysis
ciDiffTrtFRRC	For FRRC analysis, the confidence intervals and related test statistics for the FOM differences between pairs of treatments
ciAvgRdrEachTrtFRRC	
	For FRRC analysis, the confidence intervals and related tests for rdr. avg. FOM in each treatment
msAnovaEachRdrFRRC	
	The mean squares table of the ANOVA of the pseudovalues for each reader (based on data for the specified reader)
ciDiffTrtEachRdrFRRC	
	The confidence intervals and related tests of the FOM differences between pairs of treatments for each reader

FTestStatsRRFC   As for `FTestStatsRRRC` except that this is for **random-reader fixed-case** (RRFC) analysis

ciDiffTrtRRFC   For RRFC analysis, the confidence intervals and related test statistics for the FOM differences between pairs of treatments

ciAvgRdrEachTrtRRFC

      For RRFC analysis, the confidence intervals and related tests for reader averaged FOM in each treatment

For method = "ORH" the return list has 14 members:

fomArray   Figure of merit array: see return of UtilFigureOfMerit

meanSquares   List with 3 members: msT, msR, msTR

varComp   The variance components of the OR figure of merit model; 6 values, listed in the following order: varR, varTR, cov1, cov2, cov3 and var

FTestStatsRRRC   Results of the F-test for RRRC **random reader random case** analysis; contains the following items: fRRRC - the value of the F-statistic, ndfRRRC - the numerator degrees of freedom, ddfRRRC - the denominator degrees of freedom and pRRRC - the pvalue

ciDiffTrtRRRC   Same as in DBMH method

ciAvgRdrEachTrtRRRC

      Same as in DBMH method

FTestStatsFRRC   Same as `FTestStatsRRRC`, but now treating reader as a fixed effect

ciDiffTrtFRRC   Same as in DBMH method

ciAvgRdrEachTrtFRRC

      Same as in DBMH method

ciDiffTrtEachRdrFRRC

      Same as in DBMH method

varCovEachRdr   Var and Cov1 estimates for each reader

FTestStatsRRFC   Same as `FTestStatsRRRC`, but now treating case as a fixed effect

ciDiffTrtRRFC   Same as in DBMH method

ciAvgRdrEachTrtRRFC

      Same as in DBMH method

References

Dorfman DD, Berbaum KS, Metz CE (1992) ROC characteristic rating analysis: Generalization to the Population of Readers and Patients with the Jackknife method, Invest. Radiol. 27, 723-731.

Obuchowski NA, Rockette HE (1995) Hypothesis Testing of the Diagnostic Accuracy for Multiple Diagnostic Tests: An ANOVA Approach with Dependent Observations, Communications in Statistics: Simulation and Computation 24, 285-308.

Hillis SL (2014) A marginal-mean ANOVA approach for analyzing multireader multicase radiological imaging data, Statistics in medicine 33, 330-360.

Chakraborty DP (2017) *Observer Performance Methods for Diagnostic Imaging - Foundations, Modeling, and Applications with R-Based Examples*, CRC Press, Boca Raton, FL. https://www.crcpress.com/Observer-Performance-Methods-for-Diagnostic-Imaging-Foundations-Modeling/Chakraborty/p/book/9781482214840

Examples

```
StSignificanceTesting(dataset02,FOM = "Wilcoxon", method = "DBMH")
StSignificanceTesting(dataset02,FOM = "Wilcoxon", method = "ORH")


StSignificanceTesting(dataset05, FOM = "wAFROC")
StSignificanceTesting(dataset05, FOM = "HrAuc", method = "DBMH")
StSignificanceTesting(dataset05, FOM = "SongA1", method = "DBMH")
StSignificanceTesting(dataset05, FOM = "SongA2", method = "DBMH")
StSignificanceTesting(dataset05, FOM = "FOM_wAFROC1", method = "DBMH")
StSignificanceTesting(dataset05, FOM = "FOM_AFROC1", method = "DBMH")
StSignificanceTesting(dataset05, FOM = "FOM_AFROC", method = "DBMH")
```

StSignificanceTestingCadVsRadiologists

Significance testing: standalone CAD vs. radiologists

Description

Comparing standalone CAD vs. a group of radiologists interpreting the same cases; (ideally) **standalone CAD** means that all the **designer-level** mark-rating pairs provided by the CAD algorithm are available, not just the one or two marks usually displayed to the radiologist. At the very minimum, location-level information, such as in the LROC paradigm, should be used. Ideally the FROC paradigm should be used. A severe statistical power penalty is paid if one uses the ROC paradigm. Details of the method are in a pdf file that will be uploaded to GitHub and in my 2017 book.

Usage

```
StSignificanceTestingCadVsRadiologists(
  dataset,
  FOM,
  FPFValue = 0.2,
  method = "1T-RRRC",
  alpha = 0.05,
  plots = FALSE
)
```

Arguments

dataset	**The dataset to be analzed; must be single-treatment multiple-readers, where the first reader is CAD.**
FOM	The desired FOM; for ROC data it must be "Wilcoxon", for FROC data it can be any valid FOM, e.g., "HrAuc", "wAFROC", etc; for LROC data it must be "Wilcoxon", or "PCL" or "ALROC".

FPFValue   Only needed for `LROC` data **and** FOM = "PCL" or "ALROC"; where to evaluate
                    a partial curve based figure of merit. The default is 0.2.

method   The desired analysis: "1T-RRFC","1T-RRRC" (the default) or "2T-RRRC", see
                    manuscript for details. **Note: method "2T-RRRC" is not implemented for
                    non-LROC data. It is an obsolete method, included here only to show that
                    it gives identical summary statistics, e.g., p-value, as "1T-RRRC".**

alpha   Significance level of the test, defaults to 0.05.

plots   Flag, default is FALSE, i.e., a plot is not displayed. If TRUE, it displays the
                    appropriate operating characteristic for all readers and CAD.

Details

- **PCL** is the probability of a correct localization.
- The LROC is the plot of PCL (ordinate) vs. FPF.
- For LROC data, FOM = "PCL" means the interpolated PCL value at the specified `FPFValue`.
- For FOM = "ALROC" the trapezoidal area under the LROC from FPF = 0 to FPF = `FPFValue` is used.
- If method = "1T-RRRC" the first **reader** is assumed to be CAD.
- If method = "2T-RRRC" the first **treatment** is assumed to be CAD.
- The NH is that the FOM of CAD equals the average of the readers.
- The method = "1T-RRRC" analysis uses an adaptation of the single-treatment multiple-reader Obuchowski Rockette (OR) model described in a paper by Hillis (2007), section 5.3. It is characterized by 3 parameters `VarR`, `Var` and `Cov2`, where the latter two are estimated using the jackknife.
- For method = "2T-RRRC" the analysis replicates the CAD data as many times as necessary so as to form one "treatment" of an MRMC pairing, the other "treatment" being the radiologists. Then standard ORH analysis is applied. The method is described in Kooi et al. It gives exactly the same final results (F-statistic, ddf and p-value) as "1T-RRRC" but the intermediate quantities are meaningless.

Value

If method = "1T-RRRC" the return value is a list with the following elements:

fomCAD   The observed FOM for CAD.

fomRAD   The observed FOM array for the readers.

avgRadFom   The average FOM of the readers.

avgDiffFom   The mean of the difference FOM, RAD - CAD.

ciAvgDiffFom   The 95-percent CI of the average difference, RAD - CAD.

varR   The variance of the radiologists.

varError   The variance of the error term in the single-treatment multiple-reader OR model.

cov2   The covariance of the error term.

tstat   The observed value of the t-statistic; it's square is equivalent to an F-statistic.

df	The degrees of freedom of the t-statistic.
pval	The p-value for rejecting the NH.
Plots	If argument plots = TRUE, a **ggplot** object containing empirical operating characteristics corresponding to specified FOM. For example, if FOM = "Wilcoxon" an ROC plot object is produced where reader 1 is CAD. If an LROC FOM is selected, an LROC plot is displayed.

If method = "2T-RRRC" the return value is a list with the following elements:

fomCAD	The observed FOM for CAD.
fomRAD	The observed FOM array for the readers.
avgRadFom	The average FOM of the readers.
avgDiffFom	The mean of the difference FOM, RAD - CAD.
ciDiffFom	A data frame containing the statistics associated with the average difference, RAD - CAD.
ciAvgRdrEachTrt	
	A data frame containing the statistics associated with the average FOM in each "treatment".
varR	The variance of the pure reader term in the OR model.
varTR	The variance of the treatment-reader term error term in the OR model.
cov1	The covariance1 of the error term - same reader, different treatments.
cov2	The covariance2 of the error term - different readers, same treatment.
cov3	The covariance3 of the error term - different readers, different treatments.
varError	The variance of the pure error term in the OR model.
FStat	The observed value of the F-statistic.
ndf	The numerator degrees of freedom of the F-statistic.
ddf	The denominator degrees of freedom of the F-statistic.
pval	The p-value for rejecting the NH.
Plots	see above.

References

Hillis SL (2007) A comparison of denominator degrees of freedom methods for multiple observer ROC studies, Statistics in Medicine. 26:596-619.

Chakraborty DP (2017) *Observer Performance Methods for Diagnostic Imaging - Foundations, Modeling, and Applications with R-Based Examples*, CRC Press, Boca Raton, FL. https://www.crcpress.com/Observer-Performance-Methods-for-Diagnostic-Imaging-Foundations-Modeling/Chakraborty/p/book/9781482214840

Hupse R, Samulski M, Lobbes M, et al (2013) Standalone computer-aided detection compared to radiologists performance for the detection of mammographic masses, Eur Radiol. 23(1):93-100.

Kooi T, Gubern-Merida A, et al. (2016) A comparison between a deep convolutional neural network and radiologists for classifying regions of interest in mammography. Paper presented at: International Workshop on Digital Mammography, Malmo, Sweden.

Examples

```
ret1M <- StSignificanceTestingCadVsRadiologists (dataset09,
FOM = "Wilcoxon", method = "1T-RRRC")

## Not run:
## takes longer than 5 sec on OSX
retLroc1M <- StSignificanceTestingCadVsRadiologists (datasetCadLroc,
FOM = "PCL", method = "1T-RRRC", FPFValue = 0.05)

retLroc2M <- StSignificanceTestingCadVsRadiologists (datasetCadLroc,
FOM = "PCL", method = "2T-RRRC", FPFValue = 0.05)

## test with fewer readers
dataset09a <- DfExtractDataset(dataset09, rdrs = seq(1:7))
ret1M7 <- StSignificanceTestingCadVsRadiologists (dataset09a,
FOM = "Wilcoxon", method = "1T-RRRC")

datasetCadLroc7 <- DfExtractDataset(datasetCadLroc, rdrs = seq(1:7))
ret1MLroc7 <- StSignificanceTestingCadVsRadiologists (datasetCadLroc7,
FOM = "PCL", method = "1T-RRRC", FPFValue = 0.05)

ret2MLroc7 <- StSignificanceTestingCadVsRadiologists (datasetCadLroc7,
FOM = "PCL", method = "2T-RRRC", FPFValue = 0.05)

## End(Not run)
```

StSignificanceTestingCrossedModalities
                    Perform significance testing using crossed treatments analysis

Description

Performs ORH analysis for specified crossed treatments dataset averaged over specified treatment
factor

Usage

```
StSignificanceTestingCrossedModalities(
  crossedData,
  avgIndx,
  FOM = "wAFROC",
  alpha = 0.05,
  option = "ALL"
)
```

Arguments

`crossedData`	The crossed treatments dataset
`avgIndx`	The index of the treatment to be averaged over
`FOM`	See StSignificanceTesting
`alpha`	See StSignificanceTesting
`option`	See StSignificanceTesting

Value

The return list contains the same items with StSignificanceTesting.

Examples

```
## read the raw data file in extdata directory
crossedFileName <- system.file("extdata", "CrossedModalitiesData.xlsx",
package = "RJafroc", mustWork = TRUE)
crossedData <- DfReadCrossedModalities(crossedFileName)
retCrossed1 <- StSignificanceTestingCrossedModalities(crossedData, 1)

## read the built in dataset
retCrossed2 <- StSignificanceTestingCrossedModalities(datasetCrossedModality, 1)
```

StSignificanceTestingSingleFixedFactor

Perform significance testing for single fixed factor analysis

---

Description

Significance testing for datasets with a single reader in multiple (at least two) treatments, or a single treatment with multiple (at least two) readers, where reader or treatment, respectively, is regarded as a fixed factor and a common case-set, regarded as random, is assumed.

Usage

```
StSignificanceTestingSingleFixedFactor(
  dataset,
  FOM,
  FPFValue = 0.2,
  alpha = 0.05
)
```

Arguments

dataset	A single-treatment or single-reader dataset.
FOM	The figure of merit, see [UtilFigureOfMerit]().
FPFValue	Only needed for LROC data **and** FOM = "PCL" or "ALROC"; where to evaluate a partial curve based figure of merit. The default is 0.2.
alpha	The significance level (alpha, default 0.05) of the test of the null hypothesis that FOMs of all levels of the fixed factor are identical.

Details

This function performs implements Hillis et al. 2005, Eqn. 23. Following an overall F-test, reader-pairings are compared using paired t-tests. **In order for a specific pairing to be declared significant, the F-test must also be significant.**

Value

The return value is a list containing:

f	The observed F-statistic for testing the null hypothesis of no treatment effect.
ddf	The denominator degrees of freedom of the F statistic. The numerator degrees of freedom is always the number of levels of the fixed factor minus one.
pValue	The p-value for rejecting the NH.
fomStats	Statistics for FOM for each level of the fixed factor.
diffFomStats	Statistics for FOM-differences for all distinct pairings of the levels of the fixed factor

References

Hillis SL, Obuchowski NA, Schartz KM, Berbaum KS (2005) A comparison of the Dorfman-Berbaum-Metz and Obuchowski-Rockette methods for receiver operating characteristic (ROC) data, Statistics in Medicine, 24(10), 1579-607.

Hillis SL (2007) A comparison of denominator degrees of freedom methods for multiple observer ROC studies, Statistics in Medicine. 26:596-619.

Hillis SL (2014) A marginal mean ANOVA approach for analyzing multireader multicase radiological imaging data, Statistics in medicine 33, 330-360.

Examples

```
## Create a single treatment ROC dataset with one treatment and four readers
singleFactorData <- DfExtractDataset(dataset02, 1, 1:4)

## Performs single treatment fixed reader analysis
StSignificanceTestingSingleFixedFactor(singleFactorData, FOM = "Wilcoxon")
```

StSingleTreatmentRandomReader

Significance testing for single random factor

Description

Significance testing for datasets with multiple readers in a single treatment, compare average FOM to specified NH value.

Usage

```
StSingleTreatmentRandomReader(
  dataset,
  fomNh,
  FOM,
  FPFValue = 0.2,
  alpha = 0.05
)
```

Arguments

dataset	A single-treatment multipe-reader dataset.
fomNh	The comparison value that the reader average FOM is compared to.
FOM	The figure of merit, see UtilFigureOfMerit.
FPFValue	Only needed for LROC data **and** FOM = "PCL" or "ALROC"; where to evaluate a partial curve based figure of merit. The default is 0.2.
alpha	The significance level (alpha, default 0.05) of the test of the null hypothesis that the reader averaged FOMs and the specified NH value fomNh are identical.

Details

This function performs implements Hillis et al. 2005, Eqn. 23.

Value

The return value is a list containing:

- fom Observed reader FOMs.
- avgFom Average reader FOM.
- CIAvgFom Confidence interval of the reader averaged FOM.
- vaR Reader variance term of the Obuchowski-Rockette model.
- cov2 cov2 of the Obuchowski-Rockette model.
- var Error term of the Obuchowski-Rockette model.
- Tstat The observed value of the t-statistic.
- df The degrees of freedom associated with the t-statistic.
- pValue The p-value for rejecting the NH.

References

Hillis SL, Obuchowski NA, Schartz KM, Berbaum KS (2005) A comparison of the Dorfman-Berbaum-Metz and Obuchowski-Rockette methods for receiver operating characteristic (ROC) data, Statistics in Medicine, 24(10), 1579-607.

Hillis SL (2007) A comparison of denominator degrees of freedom methods for multiple observer ROC studies, Statistics in Medicine. 26:596-619.

Hillis SL (2014) A marginal mean ANOVA approach for analyzing multireader multicase radiological imaging data, Statistics in medicine 33, 330-360.

Examples

```
## Create a single treatment ROC dataset with four readers
singleFactorData <- DfExtractDataset(dataset02, trts = 1, rdrs = seq(1,4))

## Perform single-treatment random-reader analysis
StSingleTreatmentRandomReader(singleFactorData, fomNh = 0.8, FOM = "Wilcoxon")
```

UtilAucBinormal   *Binormal model AUC function*

Description

Returns the Binormal model ROC-AUC corresponding to specified parameters. See also `UtilAucsRSM`, `UtilAucPROPROC` and `UtilAucCBM`

Usage

```
UtilAucBinormal(a, b)
```

Arguments

a	The a parameter of the binormal model (separation of non-diseased and diseased pdfs)
b	The b parameter of the binormal model (std. dev. of non-diseased diseased pdf; diseased pdf has unit std. dev)

Value

Binormal model-predicted ROC-AUC

References

Dorfman DD, Alf E (1969) Maximum-Likelihood Estimation of Parameters of Signal-Detection Theory and Determination of Confidence Intervals - Rating-Method Data, Journal of Mathematical Psychology. 6:487-496.

Examples

```
a <- 2;b <- 0.7
UtilAucBinormal(a,b)
```

UtilAucCBM   *CBM AUC function*

Description

Returns the CBM ROC-AUC See also `UtilAucsRSM`, `UtilAucPROPROC` and `UtilAucBinormal`

Usage

```
UtilAucCBM(mu, alpha)
```

Arguments

mu	The `mu` parameter of CBM (separation of non-diseased and diseased pdfs)
alpha	The `alpha` parameter of CBM, i.e., the fraction of diseased cases on which the disease is visible

Value

CBM-predicted ROC-AUC for the specified parameters

References

Dorfman DD, Berbaum KS (2000) A contaminated binormal model for ROC data: Part II. A formal model, Acad Radiol 7:6 427–437.

Examples

```
mu <- 2;alpha <- 0.8
UtilAucCBM(mu,alpha)
```

UtilAucPROPROC *PROPROC AUC function*

Description

Returns the PROPROC ROC-AUC corresponding to specified parameters. See also `UtilAucsRSM`, `UtilAucBinormal` and `UtilAucCBM`

Usage

```
UtilAucPROPROC(c1, da)
```

Arguments

c1   The c-parameter of the PROPROC model, since **c is a reserved function in R**.

da   The da-parameter of the PROPROC model.

Value

PROPROC model-predicted ROC-AUC for the specified parameters

References

Metz CE, Pan X (1999) Proper Binormal ROC Curves: Theory and Maximum-Likelihood Estimation, J Math Psychol 43(1):1-33.

Examples

```
c1 <- .2;da <- 1.5
UtilAucPROPROC(c1,da)
```

UtilAucsRSM *RSM ROC/AFROC AUC calculator*

Description

Returns the ROC and AFROC AUCs corresponding to specified RSM parameters. See also `UtilAucPROPROC`, `UtilAucBinormal` and `UtilAucCBM`

Usage

```
UtilAucsRSM(mu, lambdaP, nuP, lesDistr)
```

Arguments

mu	The mean(s) of the Gaussian distribution(s) for the ratings of latent LLs (continuous ratings of lesions that are found by the search mechanism)
lambdaP	The Poisson distribution parameter(s), which describes the random number of latent NLs (suspicious regions that do not correspond to actual lesions) per case; these are the *physical* parameters.
nuP	The *physical* nuP parameters, each of which is the success probability of the binomial distribution(s) describing the random number of latent LLs (suspicious regions that correspond to actual lesions) per diseased case.
lesDistr	See PlotRsmOperatingCharacteristics.

Details

The RSM parameters (mu, lambdaP and nuP) can be vectors, provided they are of the same length; the first parameter of each array is used, followed by the second, etc; a common lesion distribution is assumed.

Value

A list containing the ROC and AFROC AUCs corresponding to the specified parameters

References

Chakraborty DP (2017) *Observer Performance Methods for Diagnostic Imaging - Foundations, Modeling, and Applications with R-Based Examples*, CRC Press, Boca Raton, FL. https://www.crcpress.com/Observer-Performance-Methods-for-Diagnostic-Imaging-Foundations-Modeling/Chakraborty/p/book/9781482214840

Chakraborty DP (2006) A search model and figure of merit for observer data acquired according to the free-response paradigm, Phys Med Biol 51, 3449-3462.

Chakraborty DP (2006) ROC Curves predicted by a model of visual search, Phys Med Biol 51, 3463–3482.

Examples

```
mu <- 1;lambdaP <- 1;nuP <- 1
lesDistr <- rbind(c(1, 0.9), c(2, 0.1))
## i.e., 90% of dis. cases have one lesion, and 10% have two lesions
UtilAucsRSM(mu, lambdaP, nuP, lesDistr)$aucROC
UtilAucsRSM(mu, lambdaP, nuP, lesDistr)$aucAFROC


mu <- c(1,2);lambdaP <- c(1,0.5);nuP <- c(1, 0.8)
lesDistr <- rbind(c(1, 0.9), c(2, 0.1))
## i.e., 90% of dis. cases have one lesion, and 10% have two lesions
UtilAucsRSM(mu, lambdaP, nuP, lesDistr)$aucROC
UtilAucsRSM(mu, lambdaP, nuP, lesDistr)$aucAFROC
```

UtilFigureOfMerit   *Calculate empirical figures of merit (FOMs) for specified dataset*

Description

Calculate the specified empirical figure of merit for each treatment-reader combination in the ROC, FROC, ROI or LROC dataset

Usage

```
UtilFigureOfMerit(dataset, FOM = "wAFROC", FPFValue = 0.2)
```

Arguments

dataset	The dataset to be analyzed, `RJafroc-package`
FOM	The figure of merit; the default is `"wAFROC"`
FPFValue	Only needed for `LROC` data **and** FOM = "PCL" or "ALROC"; where to evaluate a partial curve based figure of merit. The default is 0.2.

Details

The allowed FOMs depend on the `dataType` field of the `dataset` object.

For a `dataType = "ROC"` dataset **only** `FOM = "Wilcoxon"` **is allowed**.

For a `dataType = "FROC"` dataset the following FOMs are allowed:

- FOM = "AFROC1"
- FOM = "AFROC"
- FOM = "wAFROC1"
- FOM = "wAFROC" (the default)
- FOM = "HrAuc"
- FOM = "SongA1"
- FOM = "SongA2"
- FOM = "HrSe"
- FOM = "HrSp"
- FOM = "MaxLLF"
- FOM = "MaxNLF"
- FOM = "MaxNLFAllCases"
- FOM = "ExpTrnsfmSp"

"MaxLLF", "MaxNLF" and "MaxNLFAllCases" correspond to ordinate, and abscissa, respectively, of the highest point on the FROC operating characteristic obtained by counting all the marks. The "ExpTrnsfmSp" FOM is described in the paper by Popescu. Given the large number of FOMs possible with FROC data, it is appropriate to make a recommendation: **it is recommended that one use the wAFROC FOM.**

For a dataType = "ROI" **dataset only** FOM = "ROI" **is allowed**.

For a dataType = "LROC" dataset the following FOMs are allowed:

- FOM = "Wilcoxon" for ROC data inferred from LROC data
- FOM = "PCL" the probability of correct localization at specified FPFValue
- FOM = "ALROC" the area under the LROC from zero to specified FPFValue

FPFValue The FPF at which to evaluate PCL or ALROC; the default is 0.2; only needed for LROC data.

Value

An c(I,J) array, where the row names are modalityID's of the treatments and column names are the readerID's of the readers.

References

Chakraborty DP (2017) *Observer Performance Methods for Diagnostic Imaging - Foundations, Modeling, and Applications with R-Based Examples*, CRC Press, Boca Raton, FL. https://www.crcpress.com/Observer-Performance-Methods-for-Diagnostic-Imaging-Foundations-Modeling/Chakraborty/p/book/9781482214840

Chakraborty DP, Berbaum KS (2004) Observer studies involving detection and localization: modeling, analysis, and validation, Medical Physics, 31(8), 1–18.

Song T, Bandos AI, Rockette HE, Gur D (2008) On comparing methods for discriminating between actually negative and actually positive subjects with FROC type data, Medical Physics 35 1547–1558.

Popescu LM (2011) Nonparametric signal detectability evaluation using an exponential transformation of the FROC curve, Medical Physics, 38(10), 5690.

Obuchowski NA, Lieber ML, Powell KA (2000) Data Analysis for Detection and Localization of Multiple Abnormalities with Application to Mammography, Acad Radiol, 7:7 553–554.

Swensson RG (1996) Unified measurement of observer performance in detecting and localizing target objects on images, Med Phys 23:10, 1709–1725.

Examples

```
UtilFigureOfMerit(dataset02, FOM = "Wilcoxon") # ROC data
UtilFigureOfMerit(DfFroc2Roc(dataset01), FOM = "Wilcoxon") # FROC dataset, converted to ROC
UtilFigureOfMerit(dataset01) # FROC dataset, default wAFROC FOM
UtilFigureOfMerit(datasetCadLroc, FOM = "Wilcoxon") #LROC data
UtilFigureOfMerit(datasetCadLroc, FOM = "PCL") #LROC data
UtilFigureOfMerit(datasetCadLroc, FOM = "ALROC") #LROC data
UtilFigureOfMerit(datasetROI, FOM = "ROI") #ROI data
## Not run:  # these are meant to illustrate conditions which will throw an error
```

```
UtilFigureOfMerit(dataset02, FOM = "wAFROC") #error
UtilFigureOfMerit(dataset01, FOM = "Wilcoxon") #error

## End(Not run)
```

UtilIntrinsic2PhysicalRSM

Convert from intrinsic to physical RSM parameters

Description

Convert **intrinsic** RSM parameters $lambda$ and nu correspond to the **physical** RSM parameters $lambda'$ and nu'. The physical parameters are more meaningful but they depend on mu. The intrinsic parameters are independent of mu. See book for details.

Usage

```
UtilIntrinsic2PhysicalRSM(mu, lambda, nu)
```

Arguments

mu	The mean of the Gaussian distribution for the ratings of latent LLs, i.e. continuous ratings of lesions that were found by the search mechanism ~ N(μ,1). The corresponding distribution for the ratings of latent NLs is N(0,1).
lambda	The Poisson *intrinsic* parameter, related to λ', the latter is the mean of the Poisson distribution of numbers of latent NLs (suspicious regions that do not correspond to actual lesions) per case.
nu	The *intrinsic* ν parameter; the corresponding *physical* parameter is the success probability of the binomial distribution of random numbers of latent LLs (suspicious regions that correspond to actual lesions) per diseased case, i.e., the chance that a lesion is "found".

Details

RSM is the Radiological Search Model described in the book. A latent mark becomes an actual mark if the corresponding rating exceeds the lowest reporting threshold $\zeta 1$. See also UtilPhysical2IntrinsicRSM.

Value

A list containing λ' and ν'

References

Chakraborty DP (2006) A search model and figure of merit for observer data acquired according to the free-response paradigm, Phys Med Biol 51, 3449–3462.

Chakraborty DP (2006) ROC Curves predicted by a model of visual search, Phys Med Biol 51, 3463–3482.

Chakraborty DP (2017) *Observer Performance Methods for Diagnostic Imaging - Foundations, Modeling, and Applications with R-Based Examples*, CRC Press, Boca Raton, FL. https://www.crcpress.com/Observer-Performance-Methods-for-Diagnostic-Imaging-Foundations-Modeling/Chakraborty/p/book/9781482214840

Examples

```
mu <- 2;lambda <- 20;nu <- 1.1512925
lambdaP <- UtilIntrinsic2PhysicalRSM(mu, lambda, nu)$lambdaP
nuP <- UtilIntrinsic2PhysicalRSM(mu, lambda, nu)$nuP
## note that the physical values are only constrained to be positive, but the physical variable nuP
## must obey 0 <= nuP <= 1
```

UtilLesionDistr   *Lesion distribution matrix*

Description

The lesion distribution matrix for a dataset.

Usage

```
UtilLesionDistr(dataset)
```

Arguments

dataset   The dataset

Details

lesDistr The lesion distribution matrix, an [1:nRow,2] array, where nRow is the number of **unique** values of lesions per case in the dataset. The first column contains the number of lesions. The second column contains the fraction of diseased cases with the number of lesions indicated in the first column. See PlotRsmOperatingCharacteristics for a function that depends on lesDistr. See Chapter00Vignette2 for more details.

Value

The lesion distribution matrix

Examples

```
UtilLesionDistr (dataset01) # FROC data
UtilLesionDistr (dataset02) # ROC data
UtilLesionDistr (datasetCadLroc) # LROC data
```

```
UtilLesionWeightsDistr
```
Lesion weights distribution

Description

The lesion weights distribution, assuming equal weights. Needed to plot empirical curves for FROC data (ROC, wAFROC).

Usage

```
UtilLesionWeightsDistr(dataset)
```

Arguments

dataset   The supplied dataset.

Value

lesWghtDistr The lesion weights distribution, an [1:nRow,1:(maxLL+1)] array, where nRow is the number of lesions per case in the dataset and maxLL is the maximum number of lesions per case in the dataset. The first column contains the number of lesions per case, while the remaining columns contain the weights (equal weighting assumed). Missing values are filled with -Inf. This parameter is not to be confused with the lesionWeight list member in an FROC dataset, which enumerates the weights of lesions on **individual** cases. See PlotRsmOperatingCharacteristics for a function that depends on lesWghtDistr.See Chapter00Vignette2 for fuller explanation.

Examples

```
UtilLesionWeightsDistr (dataset11) # FROC data
UtilLesionWeightsDistr (dataset02) # ROC data
UtilLesionWeightsDistr (datasetCadLroc) # LROC data
```

UtilMeanSquares   *Calculate mean squares*

Description

Calculates the mean squares used in the DBMH and ORH methods

Usage

```
UtilMeanSquares(dataset, FOM = "Wilcoxon", FPFValue = 0.2, method = "DBMH")
```

Arguments

dataset   The dataset to be analyzed, see `RJafroc-package`.

FOM   The figure of merit to be used in the calculation. The default is `"FOM_wAFROC"`.
                 See `UtilFigureOfMerit`.

FPFValue   Only needed for `LROC` data **and** FOM = "PCL" or "ALROC"; where to evaluate
                 a partial curve based figure of merit. The default is 0.2.

method   The method, in which the mean squares are calculated. The two valid options
                 are `"DBMH"` (default) and `"ORH"`.

Details

For `DBMH` method, `msT,msTR,msTC,msTRC` will not be available if the dataset contains only one
treatment. Similarly, `msR,msTR,msRC,msTRC` will not be returned for single reader dataset. For `ORH`
method, `msT,msR,msTR` will be returned for multiple reader multiple treatment dataset. `msT` is not
available for single treatment dataset, and `msR` is not available for single reader dataset.

Value

A list containing all possible mean squares

Examples

```
UtilMeanSquares(dataset02, FOM = "Wilcoxon")
UtilMeanSquares(dataset05, FOM = "wAFROC", method = "ORH")
```

UtilOutputReport *Generate a text formatted report file or an Excel file*

Description

Generates a formatted report of the analysis and saves it to a text or an Excel file

Usage

```
UtilOutputReport(
  dataset,
  dataDescription = "MyDataDescription: ",
  ReportFileBaseName = NULL,
  ReportFileExt = "txt",
  method = "DBMH",
  FOM,
  alpha = 0.05,
  covEstMethod = "Jackknife",
  nBoots = 200,
  sequentialNames = FALSE,
  overWrite = FALSE
)
```

Arguments

dataset
: The dataset object to be analyzed (*not the file name*), see Dataset in RJafroc-package.

dataDescription
: A short string describing the dataset, the default is "MyDataDescription: "; it is inserted, for reference, in the output file.

ReportFileBaseName
: The file base name (sans the extension) for the desired report; the default is NULL, in which case the system generates a temporary text file, whose name is displayed.

ReportFileExt
: The report file extension determines the type of output. txt, the default, for a text file, xlsx for an Excel file.

method
: The significance testing method, "ORH" or (the default) "DBMH".

FOM
: The figure of merit; see StSignificanceTesting.

alpha
: See StSignificanceTesting; the default is 0.05.

covEstMethod
: See StSignificanceTesting; only needed for method = "ORH"; the default is "Jackknife".

nBoots
: See StSignificanceTesting; only needed for "ORH" analysis; the default is 200.

sequentialNames

> A logical variable: if TRUE, consecutive integers (staring from 1) will be used as the treatment and reader IDs in the output report. Otherwise, treatment and reader IDs in the original data file will be used. This option may be needed for aesthetics. The default is FALSE.

overWrite

> A `logical` variable: if FALSE, a warning will be issued if the report file already exists and the program will wait until the user inputs "y" or "n" to determine whether to overwrite the existing file. If TRUE, the existing file will be silently overwritten. The default is FALSE.

Details

A formatted report of the data analysis is written to the output file in either text or Excel format.

Value

sigTestResult The object returned by StSignificanceTesting.

Examples

```
 # text output is created in a temporary file
UtilOutputReport(dataset03, FOM = "Wilcoxon")
# Excel output is created in a temporary file
UtilOutputReport(dataset03, FOM = "Wilcoxon", ReportFileExt = "xlsx")
```

UtilPhysical2IntrinsicRSM

Convert from physical to intrinsic RSM parameters

Description

Convert **physical** RSM parameters λ' and ν' to the **intrinsic** RSM parameters λ and ν. The physical parameters are more meaningful but they depend on μ. The intrinsic parameters are independent of μ. See book for details.

Usage

```
UtilPhysical2IntrinsicRSM(mu, lambdaP, nuP)
```

Arguments

mu	The mean of the Gaussian distribution for the ratings of latent LLs, i.e. continuous ratings of lesions that were found by the search mechanism ~ $N(\mu,1)$. The corresponding distribution for the ratings of latent NLs is $N(0,1)$
lambdaP	The Poisson *physical* parameter, which describes the distribution of random numbers of latent NLs (suspicious regions that do not correspond to actual lesions) per case; the mean of these random numbers asymptotically approaches lambdaP
nuP	The *physical* ν parameter; it is the success probability of the binomial distribution describing the random number of latent LLs (suspicious regions that correspond to actual lesions) per diseased case

Details

RSM is the Radiological Search Model described in the book. A latent mark becomes an actual mark if the corresponding rating exceeds the lowest reporting threshold zeta1. See also UtilIntrinsic2PhysicalRSM.

Value

A list containing λ and ν, the physical parameters

References

Chakraborty DP (2006) A search model and figure of merit for observer data acquired according to the free-response paradigm, Phys Med Biol 51, 3449-3462.

Chakraborty DP (2006) ROC Curves predicted by a model of visual search, Phys Med Biol 51, 3463–3482.

Chakraborty DP (2017) *Observer Performance Methods for Diagnostic Imaging - Foundations, Modeling, and Applications with R-Based Examples*, CRC Press, Boca Raton, FL. https://www.crcpress.com/Observer-Performance-Methods-for-Diagnostic-Imaging-Foundations-Modeling/Chakraborty/p/book/9781482214840

Examples

```
mu <- 2;lambdaP <- 10;nuP <- 0.9
lambda <- UtilPhysical2IntrinsicRSM(mu, lambdaP, nuP)$lambda
nu <- UtilPhysical2IntrinsicRSM(mu, lambdaP, nuP)$nu
## note that the physical values are only constrained to be positive, e.g., nu is not constrained
## to be between 0 and one.
```

UtilPseudoValues   *Calculate pseudovalues*

Description

Calculates **centered** jackknife pseudovalues AND jackknife FOM values

Usage

```
UtilPseudoValues(dataset, FOM, FPFValue = 0.2)
```

Arguments

dataset	The dataset to be analyzed, see `RJafroc-package`.
FOM	The figure of merit to be used in the calculation. The default is `"FOM_wAFROC"`. See `UtilFigureOfMerit`.
FPFValue	Only needed for `LROC` data **and** FOM = "PCL" or "ALROC"; where to evaluate a partial curve based figure of merit. The default is 0.2.

Value

A list containing two `c(I,J,K)` arrays containing the pseudovalues and the jackknife FOM values of the datasets.

Examples

```
UtilPseudoValues(dataset02, FOM = "Wilcoxon")$jkPseudoValues[1,1,1:10]
UtilPseudoValues(dataset02, FOM = "Wilcoxon")$jkFomValues[1,1,1:10]
UtilPseudoValues(dataset05, FOM = "wAFROC")$jkPseudoValues[1,1,1:10]
UtilPseudoValues(dataset05, FOM = "wAFROC")$jkFomValues[1,1,1:10]
```

UtilVarComponentsDBM   *Utility for Dorfman-Berbaum-Metz variance components*

Description

Utility for Dorfman-Berbaum-Metz variance components

Usage

```
UtilVarComponentsDBM(dataset, FOM, FPFValue = 0.2)
```

Arguments

dataset	The dataset object
FOM	The figure of merit
FPFValue	Only needed for LROC data **and** FOM = "PCL" or "ALROC"; where to evaluate a partial curve based figure of merit. The default is 0.2.

Value

A list object containing the variance components.

Examples

```
UtilVarComponentsDBM(dataset02, FOM = "Wilcoxon")
```

UtilVarComponentsOR   *Utility for Obuchowski-Rockette variance components*

Description

Utility for Obuchowski-Rockette variance components

Usage

```
UtilVarComponentsOR(
  dataset,
  FOM,
  FPFValue = 0.2,
  covEstMethod = "Jackknife",
  nBoots = 200
)
```

Arguments

dataset	The dataset object
FOM	The figure of merit
FPFValue	Only needed for LROC data **and** FOM = "PCL" or "ALROC"; where to evaluate a partial curve based figure of merit. The default is 0.2.
covEstMethod	The covariance estimation method, "jackknife" (the default) or "bootstrap".
nBoots	The number of bootstraps, defaults to 200

Details

The variance components are obtained using [StSignificanceTesting](#) with method = "ORH".

Value

A list object containing the variance components.

Examples

```
UtilVarComponentsOR(dataset02, FOM = "Wilcoxon")$varComp
```

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