Package 'RJafroc'

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Type Package

Title Modeling, Analysis, Validation and Visualization of Observer Performance Studies in Diagnostic Radiology

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Maintainer Dev Chakraborty <dpc10ster@gmail.com>

Depends xlsx

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

LinkingTo Rcpp

Suggests knitr

VignetteBuilder knitr

Description Tools for quantitative assessment of medical imaging systems, radiologists or computer aided ('CAD') algorithms. Implements methods described in a book: 'Chakraborty' 'DP' (2017), ``Observer Performance Methods for Diagnostic Imaging - Foundations, Modeling, and Applications with R-Based Examples", Taylor-Francis <https://www.crcpress.com/9781482214840>. Data collection paradigms include receiver operating characteristic ('ROC') and its location specific extensions, primarily free-response 'ROC' ('FROC'). 'ROC' data consists of a single rating per image, where the rating is the perceived confidence level the image is 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 true lesion. The software supersedes the current Windows version of 'JAFROC' software <http://www.devchakraborty.com>. 'RJafroc' is derived from it being an enhanced R version of original Windows 'JAFROC'. Implemented are a number of figures of merit quantifying performance, functions for visualizing operating characteristics; three ROC ratings data curve-fitting algorithms: the 'binormal' model ('BM'), the contaminated binormal model ('CBM') and the radiological search model ('RSM'). Unlike the 'BM', the 'CBM' and the 'RSM' predict proper ROC curves that do not cross the chance diagonal or display inappropriate hooks near the upper right corner of the plots. 'RSM' fitting additionally yields measures of search and lesion-classification performances, in addition to the usual case-classification performance measured by the area under the 'ROC' curve. Search performance is the ability to find lesions while avoiding finding non-lesions. Lesion-classification performance is the ability to discriminate between found lesions and non-lesions. For fully crossed study designs, termed multiple-reader multiple-case, significance testing of reader-averaged figure-of-merit differences between modalities is implemented via both 'Dorfman', 'Berbaum' and 'Metz' ('DBM') and the 'Obuchowski' and 'Rock-

ette' ('OR') methods. Single treatment analysis allows comparison of performance of a group of radiologists to a specified value, or comparison of 'CAD' performance to a group of radiologists interpreting the same cases. Sample size estimation tools are provided for 'ROC' and 'FROC' studies that allow estimation of relevant variances from a pilot study to predict required numbers of readers and cases in a pivotal study. 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 package is used extensively in the online appendices of the cited book. Directions for accessing the online material are available by following the software tab of <http://www.devchakraborty.com>.

License GPL-3

LazyData true

URL http://www.devchakraborty.com

RoxygenNote 6.0.1

Author Xuetong Zhai [cre, aut],
Dev Chakraborty [aut],
Lucy D'Agostino McGowan [ctb]

R topics documented:

`RJafroc-package` *Modeling, Analysis, Validation and Visualization of Observer Performance Studies in Diagnostic Radiology*

Description

Software for assessing medical imaging systems, radiologists or computer aided detection (CAD) algorithms. Models of observer performance include the binormal model, the contaminated binormal model (CBM) and the radiological search model (RSM). The software and its 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**. The observer performance data collection paradigms include 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. The rating is the perceived confidence level that the image is 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 true lesion. LROC data consists of a rating and a forced localization of the most suspicious region on every image. *In this software higher ratings always represent greater confidence in presence of disease.* The software supersedes the Windows version of **JAFROC** software V4.2.1, `http://www.devchakraborty.com`. **This package is incompatible with `RJafroc` version 0.1.1**. In addition to improvements and new functions, existing functions have been renamed for better

organization. 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*. The software implements a number of figures of merit (FOMs) for quantifying performance, functions for visualizing empirical operating characteristics: e.g., ROC, FROC, alternative FROC (AFROC) and weighted AFROC (wAFROC). Three ROC ratings data curve-fitting algorithms are implemented: the Binormal Model (BM), the Contaminated Binormal Model (CBM) and the Radiological Search Model (RSM). Unlike the BM, the CBM and the RSM predict "proper" ROC curves that do not cross the chance diagonal or display inappropriate "hooks" near the upper right corner of the plots. RSM fitting additionally yields measures of search and lesion-classification performances in addition to the usual case-classification accuracy measured by the area under the ROC curve. 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, termed multiple-reader multiple-case (MRMC), significance testing of reader-averaged FOM differences between modalities is implemented via both Dorfman-Berbaum-Metz and the Obuchowski-Rockette methods. 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. A 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. The package is used extensively in online appendices of the referenced book.

Details

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Abbreviations and definitions

- a: The separation or "a" parameter of the conventional 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 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 modality
- iMRMC: A text file format used for ROC data by FDA/CDRH researchers
- individual dataset: A single modality 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: total number of readers, indexed by j
- JAFROC file format: A .xlsx file format, applicable to ROCX, FROC and LROC paradigms
- JAFROC FOM: trapezoidal area under AFROC curve; this term is obsolete; 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
- JAFROC1 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 modality, 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 paramter
- 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 threhold 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-ζ1: 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
- Signficance testing: determining the p-value of a statistical test
- SP: specificity, same as $1 - FPF$
- Threshold: Reporting criteria: if confidence exceeds a threhold 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 images (MRI)
- 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**
- wJAFROC FOM: weighted trapezoidal area under AFROC curve: this term is obsolete; use wAFROC-AUC instead;**this is the recommended FOM**
- wJAFROC1 FOM: weighted trapezoidal area under AFROC1 curve: only use if there are zero non-diseased cases is always number of treatments minus one

Dataset

Dataset, an object, can be created by the user or read from an external text of Excel file. The dataset is a list generally containing 8 elements (9 elements for crossed-modality or LROC datasets): **Note:** `-Inf` **is used to indicate the ratings of unmarked lesions and/or to indicate unavailable 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: **the word "dataset" used 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 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]`.
- `lesionNum`: 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 string variable: `"ROC"`, `"ROI"` or `"FROC"`.
- `modalityID`: a string vector of length I, which labels the modalities in the dataset.
- `readerID`: a string 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`.

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 `-Inf`s.
- `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.
- `lesionNum`: 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 string 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.
- lesionNum: same as general case.
- lesionID: same as general case.
- lesionWeight: same as general case.
- dataType: a string 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 string field uniquely labeling the readers (radiologists).
     - 'ModalityID', a string 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.
- 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.
- 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.

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.
- 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.

Sample size Functions

- SsFROCPowerGivenJK: Calculate statistical power given numbers of readers J and cases K from a pilot FROC dataset.
- 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

- ExampleCompare3ProperRocFits: 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.
- UtilLesionDistribution: Calculates the lesion distribution matrix.
- UtilLesionWeights: 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.

Author(s)

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

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

Zhai X, Chakraborty DP. A bivariate contaminated binormal model for robust fitting of proper ROC curves to a pair of correlated, possibly degenerate, ROC datasets. Medical Physics. 2017. doi: 10.1002/mp.12263:2207–2222.

Hillis SL, Chakraborty DP, Orton CG. ROC or FROC? It depends on the research question. Medical Physics. 2017.

Chakraborty DP, Nishikawa RM, Orton CG. Due to potential concerns of bias and conflicts of interest, regulatory bodies should not do evaluation methodology research related to their regulatory missions. Medical Physics. 2017.

Dobbins III JT, McAdams HP, Sabol JM, Chakraborty DP, 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.

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

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.

Chakraborty DP, Zhai X. On the meaning of the weighted alternative free-response operating characteristic figure of merit. Medical physics. 2016;43(5):2548-2557.

Chakraborty DP, Observer Performance Methods for Diagnostic Imaging - Foundations, Modeling, and Applications with R-Based Examples. Taylor-Francis LLC; 2017

`dataset01` *dataset01*

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 modalities ("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 modality 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
- `lesionNum` 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 importances) of lesions
- `dataType` "FROC", the data type
- `modalityID` [1:2] "BT" "DM", modality 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` *dataset02*

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 modalities ("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 grenerates one rating per case. Often referred to in the ROC literature as the Van Dyke dataset, which, along the the Franken dataset, has been widely used to illustrate advances in ROC methodology. The example below displays the ROC plot for the first modality 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
- `lesionNum` 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 importances) of lesions, all set to 1
- `dataType` "ROC", the data type
- `modalityID` [1:2] "0" "1", modality 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)$Plot
```

dataset03 *dataset03*

Description

This is referred to in the book as the "FR" dataset. It consists of 100 cases, 69 of which are diseased, interpreted in two modalities, "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
- `lesionNum` 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 importances) of lesions, all set to 1
- `dataType` "ROC", the data type
- `modalityID` [1:2] "0" "1", modality labels
- `readerID` [1:4] "0" "1" "2" ..., 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)$Plot
```

dataset04 *dataset04*

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 modalities (basically different image processing algorithms), by four radiologists using the FROC paradigm. 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
- `lesionNum` 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 importances) of lesions, all set to 1
- `dataType` "FROC", the data type
- `modalityID` [1:5] "1" "2" ... modality 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 *dataset05*

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 modalities ("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
- `lesionNum` 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 importances) of lesions, all set to 1
- `dataType` "FROC", the data type
- `modalityID` [1:2] "1" "2", modality 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-modality JAFROC observer study. Medical Physics. 2016;43(3):1265-1274.

Examples

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

dataset06 *dataset06*

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 modalities ("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
- `lesionNum` 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 importances) of lesions, all set to 1
- `dataType` "FROC", the data type
- `modalityID` [1:2] "1" "2", modality 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 *dataset07*

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 modalities (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
- lesionNum 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 importances) of lesions, all set to 1
- dataType "FROC", the data type
- modalityID [1:5] "1" "2", ..., modality 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 *dataset08*

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 modalities (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
- lesionNum 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 importances) of lesions, all set to 1
- dataType "ROC", the data type
- modalityID [1:5] "0" "1", modality 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)$Plot
```

---

dataset09 *dataset09*

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-modality** 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
- lesionNum 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 importances) of lesions, all set to 1
- dataType "ROC", the data type
- modalityID [1] "1" modality 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)$Plot
```

---

dataset10 *dataset10*

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 modalities. "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
- lesionNum 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 importances) of lesions, all set to 1
- dataType "ROC", the data type
- modalityID [1:3] "1" "2" "3", modality 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)$Plot
```

`dataset11` *dataset11*

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 modalities 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
- `lesionNum` 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 importances) of lesions, all set to 1
- `dataType` "FROC", the data type
- `modalityID` [1:4] "1" "2" ..., modality 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` *dataset12*

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
- `lesionNum` 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 importances) of lesions, all set to 1
- `dataType` "ROC", the data type
- `modalityID` [1:2] "0" "1", modality 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 *dataset13*

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 modalities.

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
- `lesionNum` 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 importances) of lesions, all set to 1
- `dataType` "FROC", the data type
- `modalityID` [1:4] "1" "2" ..., modality 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 *dataset14*

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 modalities "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 num 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
- lesionNum 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 importances) of lesions, all set to 1
- dataType "ROC", the data type
- modalityID [1:2] "1" "2", modality 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)
```

---

datasetCadLroc *datasetCadLroc*

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, LLC1, representing true positives where the lesions were correctly localized, and LLI1, 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
- lesionNum 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 importances) of lesions, all set to 1
- dataType "LROC", the data type
- modalityID [1:2] "0" "1", modality 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)
```

---

datasetCrossedModality

datasetCrossedModality

Description

This is a crossed modality dataset, see book Section 18.5. There are two modality factors. The first modality factor modalityID1 can be "F" or "I", which represent two CT reconstruction algorithms. The second modality 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
- lesionNum 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 importances) of lesions, all set to 1
- dataType "FROC", the data type
- modalityID1 [1:2] "F" "I", modality labels
- modalityID2 [1:4] "20" "40" "60" "80", modality 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-modality JAFROC observer study. Medical Physics. 43(3):1265-1274.

Examples

```
str(datasetCrossedModality)
```

---

datasetDegenerate *datasetDegenerate*

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
- lesionNum 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 importances) of lesions, all set to 1
- dataType "ROC", the data type
- modalityID "1", modality label
- readerID "1", reader label

Examples

```
str(datasetDegenerate)
```

`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. `lesionNum` **must** be specified if an FROC dataset is to be returned. 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 `lesionNum`. 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 absence of lesionNum;  # 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,
lesionNum = Lk2)
NL <- drop(frocDataRaw$NL)
LL <- drop(frocDataRaw$LL)
dataset <- Df2RJafrocDataset(NL, LL, lesionNum = Lk2)
## note presence of lesionNum, signalling an FROC dataset

## Simulated FROC dataset, convert to dataset object, and 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, lesionNum = 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, lesionNum = 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:
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)$Plot
y <- PlotEmpiricalOperatingCharacteristics(datasetB)$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)
print(xx$Points)

## End(Not run)
```

`DfExtractDataset` *Extract a subset of modalities 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
`trts`	A vector contains the indices of the modalities to be extracted. **If this parameter is not supplied, all modalities 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 modalities and readers that were extracted from the original dataset

Examples

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

## Extract the data of the first and third reader in all modality from the include 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
- `lesionNum` 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)
```

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 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
- lesionNum 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

Examples

```
rocDataSet <- DfFroc2Roc(dataset05)
p <- PlotEmpiricalOperatingCharacteristics(rocDataSet, trts = 1, rdrs = 1)
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, lesionNum = 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
```

`DfLroc2Roc` *Convert an LROC dataset to a ROC dataset*

Description

Converts an LROC dataset to a ROC dataset

Usage

```
DfLroc2Roc (dataset)
```

Arguments

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

Details

The conversion is effected by taking the maximum rating on each diseased case, which could be a TPCl or a TPIl, whichever has the higher rating.

Value

An ROC dataset

Examples

```
dataset <- DfReadLrocDataFile()
str(dataset)
rocDataSet <- DfLroc2Roc(dataset)
str(rocDataSet)
```

DfReadCrossedModalities

Read a crossed-modality data file

Description

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

Usage

```
DfReadCrossedModalities (fileName, renumber = 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 modality factor.
renumber	If TRUE, consecutive integers (starting from 1) will be used as the modality and reader IDs. Otherwise, modality 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 modality factors. A sample crossed modality file "includedCrossedModalities-Data.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 modality factor, NL and LL are each five dimensional arrays. There are also two modality 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-modality 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

```
## Not run:
crossedFileName <- system.file("extdata",
   "includedCrossedModalitiesData.xlsx", package = "RJafroc", mustWork = TRUE)
crossedData <- DfReadCrossedModalities(crossedFileName)
str(crossedData)

## End(Not run)
```

DfReadDataFile *Read a data file*

Description

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

Usage

```
DfReadDataFile(fileName, format = "JAFROC",
   delimiter = ",", renumber = 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/.
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.

renumber A logical varible: if TRUE, consecutive integers (starting from 1) will be used as the modality and reader IDs. Otherwise, modality 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", "includedRocData.xlsx",
package = "RJafroc", mustWork = TRUE)
RocDataXlsx <- DfReadDataFile(fileName)

## Not run:
fileName <- system.file("extdata", "includedRocData.csv",
package = "RJafroc", mustWork = TRUE)
RocDataCsv<- DfReadDataFile(fileName, format = "MRMC")

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

fileName <- system.file("extdata", "includedFrocData.xlsx",
package = "RJafroc", mustWork = TRUE)
FrocDataXlsx <- DfReadDataFile(fileName, renumber = TRUE)


## End(Not run)
```

DfReadLrocDataFile *Read a LROC data file*

Description

Read the Hupse-Karssemeijer LROC data file, a study comparing standlalone 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) 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 modality 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
- `lesionNum` 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], modality 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 decription 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")
```

ExampleCompare3ProperRocFits *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

```
ExampleCompare3ProperRocFits(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

allResults is a list-array with length equal to (endIndx - startIndx + 1), where each element of the list-array consists of 10 elements, see above. For example, allResults[[1]] corresponds to the dataset corresponding to startIndx. allResults[[2]] corresponds to the dataset corresponding to startIndx+1, etc. A specific member, e.g., allResults[[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 modalities
- 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. The corresponding returned objects contain all relevant parameters. Chapter 18 of the author's book has further details. If saveProprocLrcFile is TRUE, the .lrc files will be written to the File-Panes directory, **overwriting** any existing files with the same names.

Notes on updating the results ## First run PROPROC on all datasets ## 1. ret14 <- ExampleCompare3ProperRocFits(saveProprocLrcFile = TRUE) ## this generates 14 .lrc files in rjafroc ## 2. Move these files to VmWareShared folder ## 3. Start VmWare and Windows 8 ## 4. Start OR DBM MRMC, select .lrc file, set PROPROC AUC and run all ## 5. Repeat for each datset ## 6. Move 2 files (ending with .lroc and proproc area pooled.csv) from ## VmWareShared to rjafroc/inst/MRMCRuns to appropriate subdirectories. ## 7. Remove spaces in names of all "proproc area pooled.csv" files ## 8. ret14 <- ExampleCompare3ProperRocFits(reAnalyze = TRUE) ## this generates new results files in rjafroc/inst/ANALYZED/RSM6

Value

The returned value `allResults` is a `list` containing all results from the three parameteric model fits. 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

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

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

Examples

```
## Not run:
ExampleCompare3ProperRocFits(1,1)$allResults

## End(Not run)
```

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

Description

Fit the binormal model-predicted ROC curve for an individual 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 included degenerate ROC data
```

```
## Not run:
retFit <- FitBinormalRoc(datasetDegenerate);print(retFit$fittedPlot)

## End(Not run)
```

`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 modality 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 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

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

```
## 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 <- FitCbmRoc(dataset);print(retFit$fittedPlot)

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

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

Description

Fit an RSM-predicted ROC curve to a binned dataset

Usage

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

Arguments

dataset	The **binned** dataset containing the data
lesDistr	The lesion distribution matrix
trt	The desired treatment, default is 1
rdr	The desired reader, default is 1

Details

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. MLE ROC algorithms require binned datasets. Use DfBinDataset to perform the binning prior to calling this function. 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 <- UtilLesionDistribution(dataset02)
retFit <- FitRsmRoc(dataset02, lesDistr)
print(retFit$fittedPlot)

## Test with included degenerate ROC data
lesDistr <- UtilLesionDistribution(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))
dataset <- Df2RJafrocDataset(fp, tp)
lesDistr <- UtilLesionDistribution(dataset)
retFit <- FitRsmRoc(dataset, 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))
dataset <- Df2RJafrocDataset(fp, tp)
lesDistr <- UtilLesionDistribution(dataset)
retFit <- FitRsmRoc(dataset, 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
dataset <- Df2RJafrocDataset(fp, tp)
lesDistr <- UtilLesionDistribution(dataset)
retFit <- FitRsmRoc(dataset, lesDistr);print(retFit$fittedPlot)
```

`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 for specified dataset, treatment and reader*

Description

Plot emprirical operating characteristics (operating points connected by straight lines) for specified treatments and readers, or if desired, plots only (no operating points) averaged over specified treatments and / or readers

Usage

```
PlotEmpiricalOperatingCharacteristics(dataset, trts = 1,
   rdrs = 1, opChType = "ROC")
```

Arguments

`dataset`	Dataset to be used for plotting
`trts`	List or vector: **integer** indices of modalities to be plotted
`rdrs`	List or vector: **integer** indices of readers to be plotted
`opChType`	Type of operating characteristic to be plotted: `"ROC"`(the default), `"FROC"`, `"AFROC"`, `"wAFROC"`, `"AFROC1"`, or `"wAFROC1"`

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 shows the string IDs.

If both of `trts` and `rdrs` are vectors, all combinations of treatments 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 treatments and / or readers lists are vectors, the average operating characteristic over the implied treatments and / or readers are plotted. See Example 2.

Value

A **ggplot2** object containing the operating characteristic plot(s) and a data frame containing the points defining the operating characteristics are returned. For example, the returned objects for `"ROC"` operating characteristics are as follows:

`Plot`	**ggplot2** object. For continous 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"` or `"average"`; `"individual"` refers to a one modality and one reader.

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))
print(ret$Plot)

## Example 2
## Empirical ROC, FROC, AFROC and wAFROC plots. Each plot consists of
## three parts (see Example 3 for correspondences between indices and string identifiers
## for modalities and readers):
## (1) plot for the 1st modality (string ID "1") and the 2nd reader (string ID "3")
## (2) plot for the 2nd modality (string ID "2") AVERAGED over the 2nd and 3rd readers
##     (string IDs "3" and "4"), and
## (3) plot 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")

plotT <- list(1, 2, c(1:2))
plotR <- list(2, c(2:3), c(1:3))
ret <- PlotEmpiricalOperatingCharacteristics(dataset = dataset04, trts = plotT, rdrs = plotR)
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 -Inf -Inf -Inf ...
## $ LL          : num [1:5, 1:4, 1:100, 1:3] 5 4 4 3 5 5 4 2 4 5 ...
## $ lesionNum   : 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,
   lesionWeights, type = "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 upto 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 upto 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.
`lesionWeights`	Array, [1:maxLL,1:maxLL]. The weights (or clinical importances) of the lesions. The 1st row contains the weight of the lesion on cases with one lesion only, necessarily 1; 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`. 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. This parameter is not to be confused with the lesionWeights field in an FROC dataset with enumerates the weights of lesions on individual cases.
`type`	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 6 elements containing six **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 arugment is missing, the default value of one lesion per diseased case applies.

In lesionWeights, 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 (eg., 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 `lesionWeights` matrix will be `[1:3,1:3]`, where each row will sum to one (excluding negative infinites).

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:
lesionWeights <- rbind(c(1.0, -Inf, -Inf, -Inf),
                       c(0.4,  0.6, -Inf, -Inf),
                       c(0.2,  0.3,  0.5, -Inf),
                       c(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, lesionWeights = lesionWeights,
   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.
```

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

Description

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

Usage

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

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 modalities
J	The number of readers
K1	The number of non-diseased cases
K2	The number of diseased cases
lesionNum	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;lesionNum <- 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, lesionNum = lesionNum )

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

SimulateRocDataset *Simulates an individual binormal model ROC dataset*

Description

Simulates a binormal model ROC dataset for a single modality 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)
```

SsFROCPowerGivenJK *Statistical power in ROC and FROC paradigms from an ROC/FROC/LROC NH binned dataset*

Description

Compares statistical power using ROC and FROC paradigms, over a range of ROC effect sizes, from variability information obtained from a null hypothesis **binned** dataset, which can be in ROC/FROC/LROC paradigms, for J readers and K cases in the pivotal study.

Usage

```
SsFROCPowerGivenJK(dataset, trts, rdrs, effectSizeROC, J, K)
```

Arguments

dataset	The pilot dataset to be analyzed, see RJafroc-package, for variability information. The dataType can be "ROC", "FROC", or "LROC".
trts	The indices of the modalities in the pilot dataset that will be regarded as representive of null hypothesis modalities. Two or more modalities, specified by indices, e.g., c(1,2,3).
rdrs	The indices of the readers in the pilot dataset that will be regarded as representative of the NH readers; this can be used for example to exclude an atypical reader.
effectSizeROC	Array, the range of expected ROC effect sizes to scan; see book Chapter 11 for guidelines, e.g., seq(0.01, 0.09, 0.005).
J	The number of readers in the pivotal study.
K	The number of cases in the pivotal study.

Value

The returned list contains following items.

powerROC	Array, length(effectSizeROC), the statistical power using ROC methodology.
powerwAFROC	Array, length(effectSizeROC), the statistical power using wAFROC methodology.

potential project for summer student

Note

The pilot dataset must have at least 2 modalities; this is a temporary limitation to be removed in a future update

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

```
## Not run:
SsFROCPowerGivenJK(dataset04, trts = c(1,2), rdrs = c(1,2,3,4),
   effectSizeROC = seq(0.01, 0.09, 0.005), J = 5, K = 200)

##SsFROCPowerGivenJK(datasetCadLroc, trts = 1, rdrs = seq(2,9),
##    effectSizeROC = seq(0.01, 0.09, 0.005), J = 5, K = 200)


## End(Not run)
```

`SsPowerGivenJK` *Statistical power for specified numbers of readers and cases in an ROC study*

Description

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

Usage

```
SsPowerGivenJK(J, K, effectSize, method, option = "ALL", alpha = 0.05, ...)
```

Arguments

`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 calculation, the sign is unimportant, see Ch 11 in book for guidance.
`method`	"DBMH" or "ORH"
`option`	"RRRC", "FRRC", "RRFC" or "ALL"; the default is "ALL"
`alpha`	The significance level, default is 0.05.
`...`	Other necessary parameters, OR or DBM variance components, see details

Details

Regarding other parameters (...) needed are **either** the set of of DBM variance components, i.e, (`varYTR`, `varYTC`, and `varYEps`), **or** the set of OR covariance matrix elements, the treatment-reader variance and number of cases in pilot study i.e, (`cov1`, `cov2`, `cov3`, `varEps`, `varTR` and `KStar`).

If both of are given, DBM variance components are used and the OR values are ignored.

Either numeric values, for example, of `varYTR`, `varYTC`, `varYEps` can be supplied, **provided they are in that order**, or the function call must explicitly state, for example, `cov1 = value1`, `cov2 = value2`, `cov3 = value3`, `varTR = value4`, `varEps = value5`, `KStar = value6`, i.e., in any order.

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

```
## An example of sample size calculation with DBM variance componements
retDbm <- StSignificanceTesting(data = dataset02,
FOM = "Wilcoxon", method = "DBMH")
effectSize <- retDbm$ciDiffTrtRRRC$Estimate
varCompDBM <- retDbm$varComp
varYTR <- varCompDBM$varComp[3]
varYTC <- varCompDBM$varComp[4]
varYEps <- varCompDBM$varComp[6]
## should give close to 80% power for RRRC
SsPowerGivenJK(6, 251, effectSize, "DBMH", varYTR = varYTR, varYTC = varYTC,
            varYEps = varYEps)

## An example of sample size calculation with OR variance componements.
retOR <- StSignificanceTesting(data = dataset02,
FOM = "Wilcoxon", covEstMethod = "Jackknife", method = "ORH")
effectSize <- retOR$ciDiffTrtRRRC$Estimate
varCompOR <- retOR$varComp
varTR <- varCompOR$varCov[2]
cov1 <- varCompOR$varCov[3]
cov2 <- varCompOR$varCov[4]
cov3 <- varCompOR$varCov[5]
varEps <- varCompOR$varCov[6]
KStar <- length(dataset02$NL[1,1,,1])
## same sample size as above, different method, should again give close to 80% power for RRRC
SsPowerGivenJK(6, 251, effectSize, "ORH", cov1 = cov1, cov2 = cov2, cov3 = cov3,
            varEps = varEps, varTR = varTR, KStar = KStar)
```

`SsPowerTable` *Generate a power table*

Description

Generate combinations of numbers of readers J and numbers of cases K for desired power and specified generalizations (i.e., RRRC or FRRC or RRFC)

Usage

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

Arguments

effectSize	The postulated effect size
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; the default is "RRRC", for random-reader random-cases
...	Other necessary parameters, OR or DBM variance components, see details

Details

Regarding other parameters (...), see details in SsPowerGivenJK

Value

A data frame containing following three columns.

numReaders	The number of readers in the pivotal study.
numCases	The number of cases in the pivotal study.
power	The calculated statistical power corresponding to the indicated numbers of readers and cases.

Note

The procedure is valid for ROC studies only; for FROC studies see SsFROCPowerGivenJK.

Examples

```
## Example of sample size calculation with DBM method
retDbm <- StSignificanceTesting (dataset02, FOM = "Wilcoxon", method = "DBMH")
effectSize <- retDbm$ciDiffTrtRRRC$Estimate
varYTR <- retDbm$varComp$varComp[3]
varYTC <- retDbm$varComp$varComp[4]
varYEps <- retDbm$varComp$varComp[6]
powTab <- SsPowerTable(
effectSize = effectSize,
method = "DBMH",
varYTR = varYTR,
varYTC = varYTC,
varYEps = varYEps)
print(powTab)

## Example of sample size calculation with OR method
retOR <- StSignificanceTesting (dataset02, FOM = "Wilcoxon", method = "ORH")
effectSize <- retOR$ciDiffTrtRRRC$Estimate
varCompOR <- retOR$varComp
varTR <- varCompOR$varCov[2]
cov1 <- varCompOR$varCov[3]
cov2 <- varCompOR$varCov[4]
cov3 <- varCompOR$varCov[5]
varEps <- varCompOR$varCov[6]
KStar <- length(dataset02$NL[1,1,,1])
powTab <- SsPowerTable(
effectSize = effectSize,
```

```
method = "ORH",
KStar = KStar,
varTR = varTR,
cov1 = cov1,
cov2 = cov2,
cov3 = cov3,
varEps = varEps)
print(powTab)
```

`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 DBM or OR variance components.

Usage

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

Arguments

`J`	The number of readers in the pivotal study
`alpha`	The significance level of the study, default value is 0.05.
`effectSize`	The effect size to be used in the study, default value is 0.05.
`desiredPower`	The desired statistical power, default value is 0.8.
`option`	Desired generalization, "RRRC", "FRRC", "RRFC" or "ALL" (the default).
`method`	"DBMH" (default) or "ORH".
`...`	Other necessary parameters, OR or DBM variance components, see details

Details

Regarding other parameters (...), see details in SsPowerGivenJK. An additional parameter `KStar`, the number of cases in the pilot study, **is required when using OR variability parameters**.

Value

A list of two elements:

`K`	The minimum number of cases K in the pivotal study to just achieve the desired statistical power.
`power`	The predicted statistical power.

Note

The procedure is valid for ROC studies only; for FROC studies see SsFROCPowerGivenJK.

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

```
## Following is an example of sample size calculation using the DBM variance
## components and jackknifing (the default) to
## estimate the variance components
retDbm <- StSignificanceTesting(data = dataset02,
FOM = "Wilcoxon", method = "DBMH")
effectSize <- retDbm$ciDiffTrtRRRC$Estimate
varCompDBM <- retDbm$varComp
varYTR <- varCompDBM$varComp[3]
varYTC <- varCompDBM$varComp[4]
varYEps <- varCompDBM$varComp[6]
SsSampleSizeKGivenJ(J = 6, varYTR = varYTR, varYTC = varYTC, varYEps = varYEps,
                 effectSize =effectSize)

## Following is an example of sample size calculation using the OR variance components
retOR <- StSignificanceTesting(data = dataset02, FOM = "Wilcoxon",
covEstMethod = "Jackknife", method = "ORH")
effectSize <- retOR$ciDiffTrtRRRC$Estimate
varCompOR <- retOR$varComp
varTR <- varCompOR$varCov[2]
cov1 <- varCompOR$varCov[3]
cov2 <- varCompOR$varCov[4]
cov3 <- varCompOR$varCov[5]
varEps <- varCompOR$varCov[6]
KStar <- 114
SsSampleSizeKGivenJ(J = 6, cov1 = cov1, cov2 = cov2, cov3 = cov3, varTR = varTR, varEps= varEps,
                KStar = KStar, effectSize =effectSize, method = "ORH")

## Not run:
## Following is an example of power calculations using the DBM variance components,
## and scanning the number of readers
retDbm <- StSignificanceTesting(data = dataset02,
FOM = "Wilcoxon", method = "DBMH")
effectSize <- retDbm$ciDiffTrtRRRC$Estimate
varYTR <- retDbm$varComp$varComp[3]
varYTC <- retDbm$varComp$varComp[4]
varYEps <- retDbm$varComp$varComp[6]
effectSize <- retDbm$ciDiffTrtRRRC$Estimate
for (J in 6:10) {
 ret <- SsSampleSizeKGivenJ(J = J, varYTR = varYTR, varYTC = varYTC,
 varYEps = varYEps, effectSize =effectSize)
 message("# of readers = ", J, " estimated # of cases = ", ret$K, ", predicted power = ",
    signif(ret$powerRRRC,3), "\n")
}

## Following is an example of power calculations using the ORH variance components,
## using bootstrap to estimate variance components
retOR <- StSignificanceTesting(data = dataset02, FOM = "Wilcoxon",
```

```
covEstMethod = "Bootstrap", method = "ORH")
effectSize <- retOR$ciDiffTrtRRRC$Estimate
varCompOR <- retOR$varComp
varTR <- varCompOR$varCov[2]
cov1 <- varCompOR$varCov[3]
cov2 <- varCompOR$varCov[4]
cov3 <- varCompOR$varCov[5]
varEps <- varCompOR$varCov[6]
KStar <- length(dataset02$NL[1,1,,1])
SsSampleSizeKGivenJ(J = 6, cov1 = cov1, cov2 = cov2, cov3 = cov3,
varTR = varTR, varEps= varEps,
                KStar = KStar, effectSize =effectSize, method = "ORH")

## End(Not run)
```

`StSignificanceTesting` *Perform significance testing, DBMH or ORH*

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 for rejecting a null hypothesis (NH); the most common NH is 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, preferably, Excel-formatted, files produced by UtilOutputReport.

Usage

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

Arguments

`dataset`	The dataset to be analyzed, see RJafroc-package
`FOM`	The figure of merit, default `"wJAFROC"`, see UtilFigureOfMerit
`alpha`	The significance level of the test of the null hypothesis that all treatment effects are zero; the default alpha 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 method used to estimate the covariance matrix in ORH analysis; it can be `"Jackknife"`, `"Bootstrap"` or `"DeLong"`, the last assumes `FOM = "Wilcoxon"`, otherwise an error results. This parameter is not relevant if the analysis method is `"DBMH"`
`nBoots`	The number of bootstraps (default is 200), relevant only if the `"Bootstrap"` method is used to estimate the covariance matrix in the ORH method
`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

VarCompFlag	If TRUE, only the appropriate (DBM or OR) variance components (six in all) are returned, default is FALSE
FPFValue	Only needed for LROC data; where to evaluate a partial curve based figure of merit. The default is 0.2.

Value

For method = "DBMH" the returned value is a list with 22 members:

fomArray	The figure of merit array for each modality-reader combination
anovaY	The ANOVA table of the pseudovalues over all modalities
anovaYi	The ANOVA table of the pseudovalues for each modality
varComp	The variance components of the pseudovalue model underlying the analysis, 6 values, in the following order: c("Var(R)", "Var(C)", "Var(T*R)", "Var(T*C)", "Var(R*C)", "Var(Error)")
fRRRC	For **random-reader random-case** (RRRC) analysis, the F-statistic for rejecting the null hypothesis of no treatment effect
ddfRRRC	For RRRC analysis, the denominator degrees of freedom of the F statistic
pRRRC	For RRRC analysis, the p-value of the significance test of the NH
ciDiffTrtRRRC	For RRRC analysis, the confidence intervals and related test statistics for the FOM differences between pairs of modalities
ciAvgRdrEachTrtRRRC	For RRRC analysis, the confidence intervals and related test statistics for rdr. avg. FOM in each modality
fFRRC	For **fixed-reader random-case** (FRRC) analysis, the F-statistic for rejecting the NH
ddfFRRC	For FRRC analysis, the denominator degrees of freedom of the F-statistic
pFRRC	For FRRC analysis, the p-value of the significance test of the NH
ciDiffTrtFRRC	For FRRC analysis, the confidence intervals and related test statistics for the FOM differences between pairs of modalities
ciAvgRdrEachTrtFRRC	For FRRC analysis, the confidence intervals and related tests for rdr. avg. FOM in each modality
ssAnovaEachRdr	The sum of squares table of the ANOVA of the pseudovalues for each reader (based on data for the specified reader)
msAnovaEachRdr	The mean squares table of the ANOVA of the pseudovalues for each reader (based on data for the specified reader)
ciDiffTrtEachRdr	The confidence intervals and related tests of the FOM differences between pairs of modalities for each reader
fRRFC	For **random-reader fixed-case** (RRFC) analysis, the F statistic
ddfRRFC	For RRFC analysis, the denominator degrees of freedom of the F statistic
pRRFC	For RRFC analysis, the p-value for rejecting the NH
ciDiffTrtRRFC	For RRFC analysis, the confidence intervals and related test statistics for the FOM differences between pairs of modalities

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

For method = "ORH" the return value is a list with with 21 members:

fomArray	Figures of merit array. See the return of UtilFigureOfMerit
msT	Mean square of the figure of merit corresponding to the treatment effect
msTR	Mean square of the figure of merit corresponding to the treatment-reader effect
varComp	The variance components of the pseudovalue model underlying the analysis, 6 values, in the following order: c("Var(R)", "Var(T*R)", "COV1", "COV2", "COV3", "Var(Error)")
fRRRC	Same as DBMH method
ddfRRRC	Same as DBMH method
pRRRC	Same as DBMH method
ciDiffTrtRRRC	Same as DBMH method
ciAvgRdrEachTrtRRRC	Same as DBMH method
fFRRC	Same as DBMH method
ddfFRRC	Same as DBMH method
pFRRC	Same as DBMH method
ciDiffTrtFRRC	Same as DBMH method
ciAvgRdrEachTrtFRRC	Same as DBMH method
ciDiffTrtEachRdr	Same as DBMH method
varCovEachRdr	Obuchowski-Rockette Variance and Cov1 estimates for each reader
fRRFC	Same as DBMH method
ddfRRFC	Same as DBMH method
pRRFC	Same as DBMH method
ciDiffTrtRRFC	Same as DBMH method
ciAvgRdrEachTrtRRFC	Same as 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

```
retDbmRoc  <- StSignificanceTesting(dataset02,
FOM = "Wilcoxon", method = "DBMH")

## Not run:
retDbmwJAFROC  <- StSignificanceTesting(dataset05) # default is weighted JAFROC

retDbmHrAuc  <- StSignificanceTesting(dataset05,
FOM = "HrAuc", method = "DBMH")
print(retDbmHrAuc)

retDbmSongA1  <- StSignificanceTesting(dataset05,
FOM = "SongA1", method = "DBMH")
print(retDbmSongA1)

retDbmSongA2  <- StSignificanceTesting(dataset05,
FOM = "SongA2", method = "DBMH")
print(retDbmSongA2)

retDbmwJafroc1  <- StSignificanceTesting(dataset05,
FOM = "wJAFROC1", method = "DBMH")
print(retDbmwJafroc1)

retDbmJafroc1  <- StSignificanceTesting(dataset05,
FOM = "JAFROC1", method = "DBMH")
print(retDbmJafroc1)

retDbmJAFROC  <- StSignificanceTesting(dataset05,
FOM = "JAFROC", method = "DBMH")
print(retDbmJAFROC)


## End(Not run)

retOR <- StSignificanceTesting(dataset02,
FOM = "Wilcoxon", method = "ORH")
print(retOR)
```

`StSignificanceTestingCadVsRadiologists`
Significance testing, CAD vs. radiologists

Description

Significance testing, comparing CAD vs. a group of radiologists interpreting the same cases, an example of single modality analysis

Usage

```
StSignificanceTestingCadVsRadiologists (dataset, FOM = "Wilcoxon",
   option = "RRRC", method = "singleModality", FPFValue = 0.2)
```

Arguments

dataset	**The dataset must be ROC or LROC.**
FOM	The desired FOM, default is "Wilcoxon" for ROC data, or ROC data inferred from LROC data; for LROC data the choices are "PCL" and "ALROC".
option	The desired generalization, the default is "RRRC"; another possibility is "RRFC".
method	"singleModality", the default, or "dualModality", see details.
FPFValue	Only needed for LROC data; where to evaluate a partial curve based figure of merit, see details. The default is 0.2.
	## potential project for summer student

Details

PCL is the probability of a correct localization. The LROC is the plot of PCL (ordinate) vs. FPF. For LROC data "PCL" means interpolated PCL value at specified "FPFValue". "ALROC" is the trapezoidal area under the LROC from FPF = 0 to FPF = FPFValue. If method = "singleModality" the first **reader** is assumed to be CAD. If method = "dualModality" the first **modality** is assumed to be CAD. The NH is that the FOM of CAD equals the average of the readers. The method = "singleModality" analysis uses an adaptation of the single-modality multiple-reader Obuchowski Rockette (OR) model described in a paper by Hillis (2007), section 5.3. The adaptation is characterized by 3 parameters VarR, Var and Cov2, which are returned by the function. The method = "dualModality" analysis replicates CAD data as many times as necessary so as to form one "modality" of an MRMC pairing, the other "modality" being the radiologists. Standard RRRC DBMH/ORH analysis is applied. The method, described in Kooi et al gives exactly the same final results (F-statistic, ddf and p-value) as "singleModality" but the intermediate quantities are questionable. The method is characterized by 6 OR parameters VarR, VarTR, Var, Cov1, Cov2 and Cov3, which are returned by the function.

Value

If method = "singleModality" 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-modality 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	Empirical operating characteristic plots corresponding to specified FOM

If method = "dualModality" 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	Empirical operating characteristic plots corresponding to specified FOM, i.e., if FOM = "Wilcoxon" an ROC plot is produced where reader 1 is CAD. If an LROC FOM is selected, an LROC plot is displayed.

Note

The extension of the code to FROC will be addressed in a future update.

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

```
ret1 <- StSignificanceTestingCadVsRadiologists (dataset09,
FOM = "Wilcoxon", method = "singleModality")
## Not run:
ret2 <- StSignificanceTestingCadVsRadiologists (dataset09,
FOM = "Wilcoxon", method = "dualModality")

ret1 <- StSignificanceTestingCadVsRadiologists (datasetCadLroc,
FOM = "PCL", option = "RRRC", method = "singleModality", FPFValue = 0.05)
```

```
ret2 <- StSignificanceTestingCadVsRadiologists (datasetCadLroc,
FOM = "PCL", option = "RRRC", method = "dualModality", FPFValue = 0.05)

## End(Not run)
```

`StSignificanceTestingCrossedModalities`
Perform significance testing using crossed modalities analysis

---

Description

Performs ORH analysis for specified crossed modalities dataset averaged over specified modality factor

Usage

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

Arguments

`crossedData`	The crossed modalities dataset
`avgIndx`	The index of the modality 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", "includedCrossedModalitiesData.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 single reader in multiple (at least two) modalities, or single modality with multiple (at least two) readers, where reader or modality, respectively, is regarded as a fixed factor and a common case-set, regarded as random, is assumed.

Usage

```
StSignificanceTestingSingleFixedFactor (dataset,
   FOM = "wJAFROC", alpha = 0.05)
```

Arguments

`dataset`	A single-modality or single-reader dataset.
`FOM`	The figure of merit, default `"wJAFROC"`, see UtilFigureOfMerit.
`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 signficant, the F-test must also be significant.**

Value

The return value is a list contaning:

`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 marginalmean ANOVA approach for analyzing multireader multicase radiological imaging data, Statistics in medicine 33, 330-360.

Examples

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

## Performs single modality fixed reader analysis
StSignificanceTestingSingleFixedFactor(singleFactorData, 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 disesed pdfs)
b	The b parameter of the binormal model (std. dev. of non-diseased disesed 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 disesed 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 samne 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 or LROC dataset

Usage

```
UtilFigureOfMerit(dataset, FOM = "wAFROC", 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 `"wJAFROC"`
`FPFValue`	Only needed for LROC data; where to evaluate a partial curve based figure of merit. The default is 0.2.

Details

The allowed FOMs depend on the type of dataset (i.e., `dataType` field of dataset object). For **ROC datasets:** the `"Wilcoxon"` is alllowed. For **FROC datasets:** The following FOMs are allowed: `"AFROC1"`, `"AFROC"`, `"wAFROC1"`, `"wAFROC"` (the default), `"HrAuc"`, `"SongA1"`, `"SongA2"`, `"HrSe"`, `"HrSp"`, `"MaxLLF"`, `"MaxNLF"`, `"MaxNLFAllCases"`, and `"ExpTrnsfmSp"`. The `"MaxLLF"`, `"MaxNLF"` and `"MaxNLFAllCases"` FOMs 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 **LROC datasets:** The following FOMs are allowed:"Wilcoxon" for ROC data inferred from LROC data, which ignores localization information; or "PCL" or "ALROC", in which case one needs to specify an additional argument, FPFValue: the desired FPF at which to evaluate PCL or ALROC; the default is 0.2.

Value

An c(I, J) array, where the row names are the IDs of the treatments and column names are the IDs 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

```
# ROC data
UtilFigureOfMerit(dataset = dataset02, FOM = "Wilcoxon")
# FROC dataset, converted to ROC, Wilcoxon FOM
UtilFigureOfMerit(DfFroc2Roc(dataset01), FOM = "Wilcoxon")
# FROC dataset, default wAFROC FOM
UtilFigureOfMerit(dataset = dataset01)
#LROC data
UtilFigureOfMerit(dataset = datasetCadLroc, FOM = "ALROC", FPFValue = 0.2)
```

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 paramters 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
```

UtilLesionDistribution *Lesion distribution matrix*

Description

Extracts the lesion distribution matrix for a dataset.

Usage

```
UtilLesionDistribution(dataset)
```

Arguments

dataset	The supplied dataset

Details

The lesion distribution matrix has Lmax rows and two columns. The first column contains the integers 1, 2, ..., Lmax and the second column contains the fraction of diseased cases with the number of lesions per case specified in the first column.

Value

The lesion distribution matrix

Examples

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

UtilLesionWeights *Lesion weights matrix*

Description

Computes the lesion weights matrix, assuming equal weights.

Usage

```
UtilLesionWeights(lesDistr)
```

Arguments

lesDistr	The supplied lesion distribution matrix

Value

The lesion weights matrix, see PlotRsmOperatingCharacteristics

Examples

```
UtilLesionWeights (UtilLesionDistribution(dataset01)) # FROC data
UtilLesionWeights (UtilLesionDistribution(dataset02)) # ROC data
UtilLesionWeights (UtilLesionDistribution(datasetCadLroc)) # LROC data
```

`UtilMeanSquares` *Calculate mean squares*

Description

Calculates the mean squares used in the DBMH and ORH methods

Usage

```
UtilMeanSquares(dataset, FOM = "wJAFROC", 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 `"wJAFROC"`. See UtilFigureOfMerit.
`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 modality. 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 modality dataset. `msT` is not available for sinlge modality dataset, and `msR` is not available for single reader dataset.

Value

A list contating all possible mean squares

Examples

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

UtilMeanSquares(dataset05, method = "ORH")
```

`UtilOutputReport` *Generate a formatted report file*

Description

Generate a formatted report of the analysis and save to a text file

Usage

```
UtilOutputReport (fileName, format = "JAFROC", delimiter = ",", dataset,
  dataDescription = deparse(substitute(dataset)), reportFile, reportFormat = "txt",
   method = "DBMH", FOM = "wJAFROC", alpha = 0.05, covEstMethod = "Jackknife",
   nBoots = 200, renumber = FALSE, showWarnings = TRUE)
```

Arguments

`fileName`	A string variable containing the name of the data file to be analyzed, see DfReadDataFile and "Details".
`format`	The format of the data specified in `fileName`: see DfReadDataFile and "Details".
`delimiter`	See DfReadDataFile.
`dataset`	The dataset to be analyzed, RJafroc-package.
`dataDescription`	Only needed if a dataset is not specified. It is a string descriptor of the dataset; the default is the variable name of `dataset`
`reportFile`	The file name of the output report file. If this parameter is missing, the function will use `fileName` or `dataDescription` followed by the underscore separated concatenation of `method` and `FOM` as the output report file.
`reportFormat`	The format of the output report. The two available formats are "txt" and "xlsx", which correspond to a formatted text file and an Excel file respectively. "txt" is the default.
`method`	The analysis method: `"ORH"` or `"DBMH"`.
`FOM`	See StSignificanceTesting.
`alpha`	See StSignificanceTesting.
`covEstMethod`	See StSignificanceTesting.
`nBoots`	See StSignificanceTesting.
`renumber`	A logical varible: if `TRUE`, consecutive integers (staring from 1) will be used as the modality and reader IDs in the output report. Otherwise, modality and reader IDs in the original data file will be used. This option may be needed for aesthetics.
`showWarnings`	A `logical` variable: if `TRUE`, 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 `FALSE`, the existing file will be silently overwritten.

Details

At least one of the combinations of `fileName` and `format` or `dataset` and `dataDescription` must be specified. If both are specified, the data file `fileName` is analyzed and the dataset `dataset` is ignored.

Value

A formatted report of the data analysis, patterned roughly on that of OR-DBM MRMC V2.5.

Examples

```
## Not run:
UtilOutputReport(dataset = includedRocData, method = "DBMH", FOM = "Wilcoxon",
             dataDescription = "MyROCData", showWarnings = FALSE)

## Generate a analysis report for a data file.
fileName <- system.file("extdata", "includedRocData.xlsx",
package = "RJafroc", mustWork = TRUE)
UtilOutputReport(fileName = fileName, method = "DBMH", FOM = "Wilcoxon",
             showWarnings = FALSE)

## Output report for an existing dataset
UtilOutputReport(dataset = includedRocData, method = "DBMH", FOM = "Wilcoxon",
             reportFile = "MyROCDataAnalysis.txt")
UtilOutputReport(dataset = includedRocData, method = "ORH", FOM = "Wilcoxon", showWarnings = FALSE)
## UtilOutputReport(dataset = dataset05,
## method = "DBMH", FOM = "Wilcoxon") # ERROR!
UtilOutputReport(dataset = dataset05, method = "ORH") # default FOM is wJAFROC
UtilOutputReport(dataset = dataset05, method = "DBMH", FOM = "HrAuc")

## End(Not run)
```

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 paramters 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(μ,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

@usage UtilIntrinsic2PhysicalRSM (mu, lambda, nu)

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 pseudovalues using the jackknife

Usage

```
UtilPseudoValues(dataset, FOM = "wJAFROC")
```

Arguments

dataset	The dataset to be analyzed, see RJafroc-package.
FOM	The figure of merit to be used in the calculation. The default is "wJAFROC". See UtilFigureOfMerit.

Value

An c(I, J, K) array containing the pseudovalues of the datasets.

Examples

```
UtilPseudoValues(dataset02, FOM = "Wilcoxon")[1,1,1:10]

UtilPseudoValues(dataset05)[1,1,1:10] # default FOM is wAFROC for this FROC dataset
```

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