Package 'RJafroc'

August 14, 2015

Type Package

Title Analysis of Data Acquired Using the Receiver Operating Characteristic Paradigm and Its Extensions

Version 0.1.1

Date 2015-08-14

Maintainer Xuetong Zhai <xuetong.zhai@gmail.com>

Depends tools, xlsx, ggplot2, stringr, utils, stats, shiny

Suggests knitr

VignetteBuilder knitr

Description A common task in medical imaging is assessing whether a new imaging system or device is an improvement over an existing one. Observer performance methodology, such as receiver operating characteristic analysis, is widely used for this purpose. Receiver operating characteristic studies are often required for regulatory approval of new devices. The purpose of this work is to software for the analysis of data acquired using the receiver operating characteristic paradigm and its location specific extensions. It is an enhanced implementation of existing Windows software (http://www.devchakraborty.com). In this paradigm the radiologist rates each image for confidence in presence of disease. The images are typically split equally between actually non-diseased and diseased. A common figure of merit is the area under the receiver operating characteristic curve, which has the physical interpretation as the probability that a diseased image is rated higher than a non-diseased one. In receiver operating characteristic studies a number of radiologists (readers) rate images in two or more treatments, and the object of the analysis is to determine the significance of the inter-treatment difference between reader-averaged figures of merit. In the free-response paradigm the reader marks the locations of suspicious regions and rates each region for confidence in presence of disease, and credit for detection is only given if a true lesion is correctly localized. In the region of interest paradigm each image is divided into a number of regions and the reader rates each region. Each paradigm requires definition of a valid figure of merit that rewards correct decisions and penalizes incorrect ones and specialized significance testing procedures are applied. The package reads data in all currently used data formats including Excel. Significance testing uses two models in widespread use, a jackknife pseudo-value based model and an analysis of variance model with correlated errors. Included are tools for (1) calculating a variety of free-response figures of merit; (2) sample size estimation for planning a future study based on pilot data; (3) viewing empirical operating characteristics in receiver operating characteristic and free-response paradigms; (4) producing format-

ted report files; and (5) saving a data file in appropriate format for analysis with alternate software. In addition to open-source access to the functions, the package includes a graphical interface for users already familiar with the Windows software, who simply wish to run the program.

License GPL-3

LazyData true

URL http://www.devchakraborty.com

NeedsCompilation no

Author Xuetong Zhai [aut, cre],
Dev Chakraborty [aut, ths]

Repository CRAN

Date/Publication 2015-08-14 20:13:33

R topics documented:

`RJafroc-package` *JAFROC analysis for MRMC data*

Description

Software for the analysis of data acquired in observer performance studies conducted using ROC, FROC or ROI multiple reader multiple case (MRMC) data collection paradigms. It is an R implementation of current JAFROC analysis (http://www.devchakraborty.com) with enhancements including allowing choice between DBM or OR significance testing methods, with Hillis improvements, and choices of several figures of merit, plotting empirical operating characteristics, sample size estimation tools and generating formatted outputs.

Details

Package:	RJafroc
Type:	Package
Version:	1.0
Date:	2015-04-09
License:	GPL-3
URL:	http://www.devchakraborty.com

Abbreviations and definitions

- treatment/modality: used interchangeably, for example, CT images vs. MRI images of the same patients
- reader/observer: used interchangeably, also radiologist
- image/case: used interchangeably; a case can consist of several images of the same patient in the same modality
- MRMC: multiple reader multiple case (each reader interprets each case in each modality, i.e. fully crossed study design)
- DBM: Dorfman-Berbaum-Metz (a significance testing method for detecting a treatment effect in MRMC studies)
- DBMH: Hillis modification of DBM
- OR: Obuchowski-Rockette (a significance testing method for detecting a treatment effect in MRMC studies)
- ORH: Hillis modification of OR
- ROC: receiver operating characteristic (a data collection paradigm where each image yields a single rating)
- mark: the location of a suspected diseased region
- rating: the level of confidence that the image or the location is diseased, higher numbers indicate increasing confidence in presence of disease
- FROC: free-response ROC (a data collection paradigm where each image yields a random number, 0, 1, 2,..., of mark-rating pairs)
- AFROC: alternative FROC
- JAFROC: jackknife AFROC: an integrated software suite for analyzing observer performance data
- ROI: region-of-interest (each case is divided into a fixed number of region and the reader rates each region)
- FOM: figure of merit or quantitative measure of performance
- FP: false positive
- TP: true positive
- FPF: number of FPs divided by number of non-diseased cases

- TPF: number of TPs divided by number of diseased cases
- SP: specificity, same as $1 - FPF$
- SE: sensitivity, same as TPF
- ROC operating characteristic: plot of TPF (ordinate) vs. FPF
- AUC: trapezoidal area under the ROC curve as estimated by the Wilcoxon statistic
- 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)
- LL: lesion localization, of which TP is a special case, i.e., a mark that correctly locates an existing localized lesion
- LLF: number of LLs divided by the total number of lesions
- NLF: number of NLs divided by the total number of cases
- FROC curve: plot of LLF (ordinate) vs. NLF
- AFROC curve: plot of LLF (ordinate) vs. FPF, where FPF is inferred using highest rating of NL marks on non-diseased cases only
- AFROC1 curve: plot of LLF (ordinate) vs. $FPF1$, where $FPF1$ is inferred using highest rating of NL marks on all cases
- JAFROC FOM: trapezoidal area under AFROC curve
- JAFROC1 FOM: trapezoidal area under AFROC1 curve
- alpha/α: The significance level of the test of the null hypothesis of no treatment effect
- p-value: the probability, under the null hypothesis, that the observed treatment effects, or larger, could occur by chance
- NH: The null hypothesis that all treatments effects are zero; rejected if the p-value is smaller than α
- RRRC: Analysis that treats both readers and cases as random factors
- RRFC: Analysis that treats readers as random and cases as fixed factors
- FRRC: Analysis that treats readers as fixed and cases as random factors
- ddf: Denominator degrees of freedom of appropriate F-test, the numerator df (ndf) is always number of treatments minus one
- CI: The $1 - \alpha$ confidence interval for the stated statistic
- I: total number of modalities, indexed by i; I must be at least 2 to perform null hypothesis testing
- J: total number of readers, indexed by j
- K1: total number of non-diseased cases, indexed by $k1$
- K2: total number of diseased cases, indexed by $k2$
- K: total number of cases, $K = K1 + K2$, indexed by k
- maxNL: maximum number of NL marks per case in dataset
- maxLL: maximum number of lesions per case in dataset

Dataset

Dataset, an R object, can be created by the user or read from an external data file. **Note**: **the word "dataset" used in this package always represents an R object with following structure**.

Data structure: The dataset is an R list containing 9 elements: **Note**: `-Inf` is assigned to any missing/unavailabe element, e.g., an unmarked true lesion.

- `NL`: a floating-point array with a dimension of `c(I, J, K, maxNL)` that contains the ratings of NL marks for specified modality, reader and case. For ROC datasets FP ratings are assigned to `NL` with `maxNL = 1`, i.e., the last index is set to 1.
- `LL`: a floating-point array with a dimension of `c(I, J, K2, maxLL)`that contains the ratings of all LL marks for specified modality, reader and case. For ROC datasets TP ratings are assigned to `LL` with `maxLL = 1`.
- `lesionNum`: a integer vector with a length of `K2`, whose elements indicate the number of lesions in each diseased case.
- `lesionID`: a integer array with a dimnsion of `c(K2, maxLL)`. **Note** that ratings of lesions in `LL` must appear in the same sequence as `lesionID` for that case. For example, if the `lesionID` field for the first diseased case is `c(4, 2, 3, 1)`, i.e., there are 4 lesion on this case labeled 4, 2, 3 and 1, the ratings in `LL` for this case must appear in the same sequence, with the first rating corresponding to the lesion labeled 4, the second corresponding to the lesion labeled 2, etc.
- `lesionWeight`: a floating point array with a dimension of `c(K2, maxLL)`, representing the relative importance of detecting each lesion. For each case, the weights must sum to unity. If zero is assigned to all elements of this array, then the software assigns equal weighting, e.g., `c(0.5, 0.5)` to an image with two lesions.
- `maxNL`: the maximum number of `NL` marks per case over the entire dataset.
- `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 contains the ID of each reader. **Note** that the order of elements in `modalityID` and `readerID` must match that in `NL` and `LL`. For example, `NL[1, 2, , ]` indicates the ratings of the reader with the second ID in `readerID` using the modality with the first ID in `modalityID`.

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 ReadDataFile.

- **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 lesion localization worksheet and (3) the '`FP`' or non-lesion localization 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 format is described in the iMRMC website, currently https://code.google.com/p/imrmc/.

Functions

- DBMHAnalysis: Performs Dorfman-Berbaum-Metz analysis with Hillis improvements for the specified dataset.
- EmpiricalOpCharac: Plot empirical curves for specified modalities and readers in the dataset.
- FigureOfMerit: Calculate the figure of merit for each reader using each modality.
- FROC2HrROC: Convert an FROC dataset to a highest rating inferred ROC dataset.
- ORHAnalysis: Performs Obuchowski-Rockette analysis with Hillis improvements for the specified dataset.
- OutputReport: Save the results of the analysis to a text file.
- PowerGivenJK: Calculate the statistical power with the given number of readers, number of cases and DBM or OR variances components.
- PowerTable: Calculate required sample size for the specified dataset with given significance level, effect size and desired power.
- ReadDataFile: Read the dataset that will be analysis from data file.
- SampleSizeGivenJ: Calculate required number of cases with the given number of readers and DBM variances components.
- SaveDataFile: Save data file in specified format.

Author(s)

Xuetong Zhai, Dev Chakraborty

Maintainer: Xuetong Zhai <xuetong.zhai@gmail.com>

References

Basics of ROC

Metz, C. E. (1978). Basic principles of ROC analysis. In Seminars in nuclear medicine (Vol. 8, pp. 283–298). Elsevier.

Metz, C. E. (1986). ROC Methodology in Radiologic Imaging. Investigative Radiology, 21(9), 720.

Metz, C. E. (1989). Some practical issues of experimental design and data analysis in radiological ROC studies. Investigative Radiology, 24(3), 234.

Metz, C. E. (2008). ROC analysis in medical imaging: a tutorial review of the literature. Radiological Physics and Technology, 1(1), 2–12.

Wagner, R. F., Beiden, S. V, Campbell, G., Metz, C. E., & Sacks, W. M. (2002). Assessment of medical imaging and computer-assist systems: lessons from recent experience. Academic Radiology, 9(11), 1264–77.

Wagner, R. F., Metz, C. E., & Campbell, G. (2007). Assessment of medical imaging systems and computer aids: a tutorial review. Academic Radiology, 14(6), 723–48.

DBM/OR methods and extensions

DORFMAN, D. D., BERBAUM, K. S., & Metz, C. E. (1992). Receiver operating characteristic rating analysis: generalization to the population of readers and patients with the jackknife method. Investigative Radiology, 27(9), 723.

Obuchowski, N. A., & Rockette, H. E. (1994). HYPOTHESIS TESTING OF DIAGNOSTIC ACCURACY FOR MULTIPLE READERS AND MULTIPLE TESTS: AN ANOVA APPROACH WITH DEPENDENT OBSERVATIONS. Communications in Statistics-Simulation and Computation, 24(2), 285–308.

Hillis, S. L., Berbaum, K. S., & Metz, C. E. (2008). Recent developments in the Dorfman-Berbaum-Metz procedure for multireader ROC study analysis. Academic Radiology, 15(5), 647–61.

Hillis, S. L., Obuchowski, N. A., & Berbaum, K. S. (2011). Power Estimation for Multireader ROC Methods: An Updated and Unified Approach. Acad Radiol, 18, 129–142.

Hillis, S. L. S. L. (2007). A comparison of denominator degrees of freedom methods for multiple observer ROC analysis. Statistics in Medicine, 26(3), 596–619.

FROC paradigm

Chakraborty, D. P., & Berbaum, K. S. (2004). Observer studies involving detection and localization: modeling, analysis, and validation. Medical Physics, 31(8), 1–18.

Chakraborty, D. P. (2006). A search model and figure of merit for observer data acquired according to the free-response paradigm. Physics in Medicine and Biology, 51(14), 3449–62.

Chakraborty, D. P. (2006). ROC curves predicted by a model of visual search. Physics in Medicine and Biology, 51(14), 3463–82.

Chakraborty, D. P. (2011). New Developments in Observer Performance Methodology in Medical Imaging. Seminars in Nuclear Medicine, 41(6), 401–418.

Chakraborty, D. P. (2013). A Brief History of Free-Response Receiver Operating Characteristic Paradigm Data Analysis. Academic Radiology, 20(7), 915–919.

Chakraborty, D. P., & Yoon, H.-J. (2008). Operating characteristics predicted by models for diagnostic tasks involving lesion localization. Medical Physics, 35(2), 435.

ROI paradigm

Obuchowski, N. A., Lieber, M. L., & Powell, K. A. (2000). Data analysis for detection and localization of multiple abnormalities with application to mammography. Academic Radiology, 7(7), 553–4; discussion 554–6.

`DBMHAnalysis` *DBM analysis with Hillis improvements*

Description

Performs Dorfman-Berbaum-Metz significance testing, with Hillis improvements, for the specified dataset.

Usage

```
DBMHAnalysis(dataset, fom = "wJAFROC", alpha = 0.05, option = "ALL")
```

Arguments

dataset	The dataset to be analyzed, see RJafroc-package.
fom	The figure of merit to be used in the analysis, default is "wJAFROC", see FigureOfMerit.
alpha	The significance level of the test of the null hypothesis that all treatment effects are zero (default alpha is 0.05).
option	The analysis option: it can be "RRRC", "FRRC", "RRFC" or "ALL" (the default), corresponding random readers and random cases, fixed readers and random cases and random readers and fixed cases, respectively; this option indicates which factors are treated as random and/or fixed factors in the analysis.

Value

The return value is a list with following elements:

fomArray	The figure of merit array of each reader and modality.
anovaY	The ANOVA table of the pseudovalues.
anovaYi	The ANOVA table of the pseudovalues for each modality.
varComp	The DBM variance components estimates.
fRRRC	The F statistic for testing the null hypothesis, for the RRRC condition.
ddfRRRC	The denominator degrees of freedom of the F statistic, for the RRRC condition.
pRRRC	The p-value of the significance test of the NH for the RRRC condition.
ciDiffTrtRRRC	The confidence intervals and related tests for the FOM differences between pairs of modalities, for the RRRC condition.
ciAvgRdrEachTrtRRRC	The confidence intervals and related tests for rdr. avg. FOM in each modality, for the RRRC condition.
fFRRC	The F statistic for testing the null hypothesis, for the FRRC condition.
ddfFRRC	The denominator degrees of freedom of the FRRC F statistic.
pFRRC	The p-value of the significance test of the NH, for the FRRC condition.
ciDiffTrtFRRC	The confidence intervals and related tests for the FOM differences between pairs of modalities, for the FRRC condition.
ciAvgRdrEachTrtFRRC	The confidence intervals and related tests for rdr. avg. FOM in each modality, for the FRRC condition.
ssAnovaEachRdr	The sum of squares table of the ANOVA of the pseudovalues for each reader (based on the data only for the specified reader).
msAnovaEachRdr	The mean squares table of the ANOVA of the pseudovalues for each reader (based on the data only for the specified reader).
ciDiffTrtEachRdr	The confidence intervals and related tests of the FOM differences between pairs of modalities for each reader.
fRRFC	The F statistic for testing the null hypothesis, for the RRFC condition.

ddfRRFC	The denominator degrees of freedom of the F statistic, for the RRFC condition.
pRRFC	The p-value of the significance test of the NH, for the RRFC condition.
ciDiffTrtRRFC	The confidence intervals and related tests for the FOM differences between pairs of modalities, for the RRFC condition.
ciAvgRdrEachTrtRRFC	The confidence intervals and related tests for rdr. avg. FOM in each modality, for the RRFC condition.

Examples

```
retDbmRoc  <- DBMHAnalysis(rocData, fom = "Wilcoxon")

## Not run:
retDbmwJAFROC  <- DBMHAnalysis(frocData) # default is weighted JAFROC

retDbmHrAuc  <- DBMHAnalysis(frocData, fom = "HrAuc")
print(retDbmHrAuc)

retDbmSongA1  <- DBMHAnalysis(frocData, fom = "SongA1")
print(retDbmSongA1)

retDbmSongA2  <- DBMHAnalysis(frocData, fom = "SongA2")
print(retDbmSongA2)

retDbmwJafroc1  <- DBMHAnalysis(frocData, fom = "wJAFROC1")
print(retDbmwJafroc1)

retDbmJafroc1  <- DBMHAnalysis(frocData, fom = "JAFROC1")
print(retDbmJafroc1)

retDbmJAFROC  <- DBMHAnalysis(frocData, fom = "JAFROC")
print(retDbmJAFROC)

retDbmROI  <- DBMHAnalysis(roiData, fom = "ROI")
print(retDbmROI)

## End(Not run)
```

EmpiricalOpCharac *Plot empirical operating characteristic*

Description

Plot empririca operating characteristics (operating points connected by straight lines) for specified trts and rdrs in the dataset.

Usage

```
EmpiricalOpCharac(dataset, trts, rdrs, lgdPos, opChType = "ROC")
```

Arguments

dataset	Dataset to be used for plotting.
trts	List or vector: indices of modalities to be plotted. See "Details".
rdrs	List or vector. indices of readers to be plotted. See "Details".
lgdPos	The positioning of the legend: "right"(the default), "left", "top" or "bottom".
opChType	Type of operating characteristic to be plotted. Available choices are "ROC"(the default), "AFROC" and "FROC".

Details

Note that trts and rdrs are the vectors or list 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**.

If both of trts and rdrs are vectors, all possible combinations will be plotted.

If both of trts and rdrs are lists, they must have same length. Only the combination of modality and reader at same position will be plotted. If some elements of the lists are vectors, the averaged operating characteristic over them will be plotted. See "Examples".

Value

A **ggplot2** object of the plotted operating characteristics and a data frame containing the points of the operating characteristics are returned. Following are the returned objects of "ROC" operating characteristics.

ROCPlot	**ggplot2** object: Use print function to display the saved object.
ROCPoints	Data frame with four columns: abscissa, ordinate, class (coding modality and reader) and type, which can be "individual" or "averaged".

Examples

```
plotM <- c(1:2)
plotR <- c(1:3)
EmpiricalOpCharac(dataset = rocData, trts = plotM, rdrs = plotR,
                  lgdPos = "bottom", opChType = "ROC")
## Above is the example of plotting individual ROC operating characteristics of modalities
## 1 and 2 and readers 1 to 3. Six operating characteristics will be plotted, which are
## operating characteristics of reader 1 modality 1, reader 1 modality 2, reader 2 modality
## 1, reader 2 modality 2, reader 3 modality 1 and reader 3 modality 2.

plotM <- list(1, 2, c(1:2))
plotR <- list(2, c(2:3), c(1:3))
EmpiricalOpCharac(dataset = rocData, trts = plotM, rdrs = plotR,
                  lgdPos = "bottom", opChType = "ROC")
EmpiricalOpCharac(dataset = frocData, trts = plotM, rdrs = plotR,
                  lgdPos = "bottom", opChType = "AFROC")
EmpiricalOpCharac(dataset = frocData, trts = plotM, rdrs = plotR,
                  lgdPos = "bottom", opChType = "FROC")
## Above is the example of plotting three ROC, AFROC and FROC operating characteristics.
## They are the individual operating characteristic of modality 1 reader 2, the
```

```
## averaged operating characteristic of modality 2 and reader 2 and 3 and the averaged
## operating characteristic of modality 1 and 2 and reader 1 to 3.
```

`FigureOfMerit` *Calculate figure of merit*

Description

Caclulate the figure of merit (an objective measure of observer performance) for each treatment-reader combination.

Usage

```
FigureOfMerit(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 "Details".

Details

Allowed figures of merit are: (1) `"Wilcoxon"` for ROC data; (2) `"JAFROC1"`, `"JAFROC"`, `"wJAFROC1"`, `"wJAFROC"` (the default), `"HrAuc"`, `"SongA1"`, `"SongA2"`**, `"HrSe"`, `"HrSp"`, `"MaxLLF"`, `"MaxNLF"`, `"MaxNLFAllCases"`, `"ExpTrnsfmSp"`, for free-response data and (3) `"ROI"` for ROI data. The JAFROC FOMs are described in the paper by Chakraborty and Berbaum. The Song FOMs are described in the paper by Song et al. The `"MaxLLF"`, `"MaxNLF"` and `"MaxNLFAllCases"` FOMs correspond to ordinate, abscissa and abscissa, respectively, of the highest point on the FROC operating characteristic obtained by counting all the LL marks on diseased, all NL marks on non-diseased cases, and all NL marks on all cases, respectively). The `"ExpTrnsfmSp"` FOM is described in the paper by Popescu. The `"ROI"` FOM is described in the paper by Obuchowski et al.

** **The Song A2 figure of merit is computationally very intensive.**

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, D. P., & Berbaum, K. S. (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, L. M. (2011). Nonparametric signal detectability evaluation using an exponential transformation of the FROC curve. Medical Physics, 38(10), 5690.

Obuchowski, N. A., Lieber, M. L., & Powell, K. A. (2000). Data Analysis for Detection and Localization of Multiple Abnormalities with Application to Mammography. Academic Radiology, 553-554.

Examples

```
FigureOfMerit(dataset = rocData, fom = "Wilcoxon")

FigureOfMerit(dataset = frocData)
```

`FROC2HrROC` *Convert FROC dataset*

Description

Convert an FROC dataset to a highest rating inferred ROC dataset

Usage

```
FROC2HrROC(dataset)
```

Arguments

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

Value

An ROC dataset, where each case is represented by the highest rating of the case in FROC dataset.

Examples

```
FROC2HrROC(dataset = frocData)
```

`frocData` *An example FROC dataset provided by Dr. Federica Zanca.*

Description

In this example dataset there are 100 non-diseased and 100 lesion containing mammography images. The maximum number of lesions per diseased case is 3. Four radiologists intepreted all images using five image processing algorithms (modalities). They marked and rated suspicious regions on an integer 1 - 5 scale, where larger ratings represented greater confidence in presence of disease. Only modalities 4 and 5 have been retained in this dataset. The *.xlsx file can be downloaded from http://www.devchakraborty.com/FrocData/frocData.xlsx. The dataset file can then be read into a dataset object using ReadDataFile function.

Usage

```
frocData
```

Format

A dataset object consisting of a list containing 8 elements, see RJafroc-package.

Source

Zanca, F., Chakraborty, D. P., Van Ongeval, C., Jacobs, J., Claus, F., Marchal, G., & Bosmans, H. (2008). An improved method for simulating microcalcifications in digital mammograms. Medical Physics, 35(9), 4012-8.

ORHAnalysis *Obuchowski-Rockette analysis with Hillis improvements*

Description

Performs Obuchowski-Rockette analysis with Hillis improvements for the specified dataset.

Usage

```
ORHAnalysis(dataset, fom = "wJAFROC", alpha = 0.05,
  covEstMethod = "Jackknife", nBoots = 200, option = "ALL")
```

Arguments

dataset	See DBMHAnalysis.
fom	See DBMHAnalysis.
alpha	See DBMHAnalysis.
covEstMethod	The method used to estimate the covariance matrix; can be "Jackknife", "Bootstrap" or "DeLong", the last assumes the Wilcoxon FOM is chosen, otherwise an error will result.
nBoots	The number of bootstraps (default is 200), used only if the "Bootstrap" method is used to estimate the covariance matrix.
option	See DBMHAnalysis.

Value

The return value is a list with following elements:

fomArray	Figures of merit array. See the return of FigureOfMerit.
msT	Mean square of the figure of merit corresponding to the the treatment effect.
msTR	Mean square of the figure of merit corresponding to the the treatment-reader effect.

varComp	Obuchowski-Rockette variance component and covariance estimates.
fRRRC	See DBMHAnalysis.
ddfRRRC	See DBMHAnalysis.
pRRRC	See DBMHAnalysis.
ciDiffTrtRRRC	See DBMHAnalysis.
ciAvgRdrEachTrtRRRC	See DBMHAnalysis.
fFRRC	See DBMHAnalysis.
ddfFRRC	See DBMHAnalysis.
pFRRC	See DBMHAnalysis.
ciDiffTrtFRRC	See DBMHAnalysis.
ciAvgRdrEachTrtFRRC	See DBMHAnalysis.
ciDiffTrtEachRdr	See DBMHAnalysis.
varCovEachRdr	Obuchowski-Rockette Variance and Cov1 estimates for each reader.
fRRFC	See DBMHAnalysis.
ddfRRFC	See DBMHAnalysis.
pRRFC	See DBMHAnalysis.
ciDiffTrtRRFC	See DBMHAnalysis.
ciAvgRdrEachTrtRRFC	See DBMHAnalysis.

Examples

```
retOR <- ORHAnalysis(rocData, fom = "Wilcoxon")
print(retOR)
```

`OutputReport` *Generate a formatted report of the analysis*

Description

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

Usage

```
OutputReport(fileName, format = "JAFROC", delimiter = ",", dataset,
  dataDscrpt = deparse(substitute(dataset)), reportFile, method = "DBMH",
  fom = "wJAFROC", alpha = 0.05, covEstMethod = "Jackknife",
  nBoots = 200, showWarnings = TRUE)
```

Arguments

fileName	A string variable containing the name of the data file to be analyzed, see ReadDataFile and "Details".
format	The format of the data specified in fileName: see ReadDataFile and "Details".
delimiter	See ReadDataFile.
dataset	The dataset object to be analyzed, see RJafroc-package and "Details".
dataDscrpt	Only needed if a dataset object is specified. It is a string descriptor of the dataset object, the default is the variable name of dataset, see "Details".
reportFile	The file name of the output report file. If this parameter is missing, the function will use fileName or dataDscrpt followed by the underscore separated concatenation of method and fom as the output report file.
method	The analysis method: "ORH" or "DBMH".
fom	See DBMHAnalysis.
alpha	See DBMHAnalysis.
covEstMethod	See ORHAnalysis.
nBoots	See ORHAnalysis.
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 dataDscrpt must be specified. If both are specified, the data file fileName is analyzed and the dataset object dataset is ignored.

Value

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

Examples

```
## deliberately overriding the default for showWarnings, so as to not confuse
## timing tests run by CRAN; you should not need to do this
OutputReport(dataset = rocData, method = "DBMH", fom = "Wilcoxon",
             dataDscrpt = "MyROCData", showWarnings = FALSE)

## Not run:
## Generate a analysis report for a data file.
fileName <- system.file("tests", "rocData.xlsx", package = "RJafroc")
OutputReport(fileName = fileName, method = "DBMH", fom = "Wilcoxon",
             showWarnings = FALSE)

## Output report for an existing dataset
OutputReport(dataset = rocData, method = "DBMH", fom = "Wilcoxon",
```

```
            reportFile = "MyROCDataAnalysis.txt", showWarnings = FALSE)
OutputReport(dataset = rocData, method = "ORH", fom = "Wilcoxon", showWarnings = FALSE)
OutputReport(dataset = frocData, method = "DBMH", fom = "Wilcoxon") # ERROR!
OutputReport(dataset = frocData, method = "ORH") # default fom is wJAFROC
OutputReport(dataset = frocData, method = "DBMH", fom = "HrAuc")
OutputReport(dataset = roiData, method = "ORH", fom = "ROI")
## End(Not run)
```

PowerGivenJK *Calculate statistical power given numbers of readers J and cases K for ROC studies*

Description

Calculate the statistical power with the given number of readers, number of cases and DBM or OR variances components.

Usage

```
PowerGivenJK(J, K, varYTR, varYTC, varYEps, cov1, cov2, cov3, varEps, msTR,
  KStar, alpha = 0.05, effectSize = 0.05, randomOption = "ALL")
```

Arguments

J	The number of readers to be used in the calculation.
K	The number of cases to be used in the calculation.
varYTR	The DBM variance component of treatment(modality)-by-reader interaction term.
varYTC	The DBM variance component of treatment(modality)-by-case interaction term.
varYEps	The variance component of DBM error term.
cov1	The OR covariances of the figure of merit estimates of same reader and different modalities.
cov2	The OR covariances of the figure of merit estimates of same reader and different modalities.
cov3	The OR covariances of the figure of merit estimates of same reader and different modalities.
varEps	The variance component of OR error term.
msTR	Treatment(modality)-by-reader mean square of the figure of merit.
KStar	See SampleSizeGivenJ.
alpha	The significantce level.
effectSize	The effect size to be used in the calculation.
randomOption	The random option. It can be "ALL", "READERS" or "CASES", which indicate predictions for (1) random readers and random cases, (2) random readers only and (3) random cases only.

Details

To calculate the statistical power, either the group of DBM variance components (varYTR, varYTC, and varYEps) or OR variance components (cov1, cov2, cov3, varEps, msTR and KStar) should be specified. If both of them are given, DBM variance components are used and OR variance components are ignored.

Value

The statistical power with given components and condition.

References

Hillis, S. L., Obuchowski, N. A., & Berbaum, K. S. (2011). Power Estimation for Multireader ROC Methods: An Updated and Unified Approach. Acad Radiol, 18, 129-142.

Hillis, S. L., Obuchowski, N. a, Schartz, K. M., & Berbaum, K. S. (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 with DBM variance componements.
retDbm <- DBMHAnalysis(data = rocData, fom = "Wilcoxon")
effectSize <- retDbm$ciDiffTrtRRRC$Estimate
varCompDBM <- retDbm$varComp
varYTR <- varCompDBM$varComp[3]
varYTC <- varCompDBM$varComp[4]
varYEps <- varCompDBM$varComp[6]
PowerGivenJK(J = 6, K = 251, varYTR = varYTR, varYTC = varYTC,
             varYEps = varYEps, effectSize = effectSize)

## Following is an example of sample size calculation with OR variance componements.
retOR <- ORHAnalysis(data = rocData, fom = "Wilcoxon", covEstMethod = "Jackknife")
effectSize <- retDbm$ciDiffTrtRRRC$Estimate
varCompOR <- retOR$varComp
cov1 <- varCompOR$varCov[3]
cov2 <- varCompOR$varCov[4]
cov3 <- varCompOR$varCov[5]
varEps <- varCompOR$varCov[6]
KStar <- length(rocData$NL[1,1,,1])
msTR <- retOR$msTR
PowerGivenJK(J = 6, K = 251, cov1 = cov1, cov2 = cov2, cov3 = cov3,
             varEps = varEps, msTR = msTR, KStar = KStar, effectSize = effectSize)
```

PowerTable — *Calculate power table, different combinations, of J and K for desired power for ROC studies.*

Description

Calculate required sample size for the specified dataset with given significance level, effect size and desired power

Usage

```
PowerTable(dataset, alpha = 0.05, effectSize = 0.05, desiredPower = 0.8,
  randomOption = "ALL")
```

Arguments

dataset	The dataset to be analyzed, see RJafroc-package.
alpha	The significantce level.
effectSize	The effect size to be used in the calculation.
desiredPower	The desired statistical power.
randomOption	The random option. It can be "ALL", "READERS" or "CASES", which indicate predictions for (1) random readers and random cases, (2) random readers only and (3) random cases only.

Value

The return is a data frame containing following three columns.

numReaders	The number of readers.
numCases	The number of cases.
power	The statistical power for the number of readers and cases combination.

Examples

```
retDbm <- DBMHAnalysis(data = rocData, fom = "Wilcoxon")
effectSize <- retDbm$ciDiffTrtRRRC$Estimate
PowerTable(dataset = rocData, effectSize = effectSize)
```

ReadDataFile *Reads the data file and creates a dataset object*

Description

Reads the dataset file to be analyzed and creates a dataset object for subsequent analysis.

Usage

```
ReadDataFile(fileName, format = "JAFROC", delimiter = ",")
```

Arguments

fileName	A string specifying the name of the file that contains the dataset. The extension of the file must match the corresponding format specified below.
format	A string specifying the format of the data file. It can be "JAFROC" (the default), "MRMC" or "iMRMC". For "MRMC" the format is determined by the extension of the data file as specified in http://perception.radiology.uiowa.edu/: the file extension can be .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.

Value

A dataset with the specified structure, see RJafroc-package.

Examples

```
fileName <- system.file("tests", "rocData.xlsx", package = "RJafroc")
RocDataXlsx<- ReadDataFile(fileName)

## Not run:
fileName <- system.file("tests", "rocData.csv", package = "RJafroc")
RocDataCsv<- ReadDataFile(fileName, format = "MRMC")

fileName <- system.file("tests", "rocData.imrmc", package = "RJafroc")
RocDataImrmc<- ReadDataFile(fileName, format = "iMRMC")

fileName <- system.file("tests", "frocData.xlsx", package = "RJafroc")
FrocDataXlsx <- ReadDataFile(fileName)

fileName <- system.file("tests", "roiData.xlsx", package = "RJafroc")
RoiDataXlsx <- ReadDataFile(fileName)

## End(Not run)
```

RJafrocGui *Graphical user interface to* **RJafroc** *functions*

Description

Start a graphical user interface which is functionally similar to Windows JAFROC software (Version 4.2.1)

Usage

```
RJafrocGui(useBrowser = FALSE)
```

Arguments

useBrowser	a logical variable, if TRUE the default internet browser is used, otherwise RStudio's internal browser is used. Default is FALSE. See "Details".

Details

For Windows users, we suggest setting useBrowser to TRUE due to a bug in RStudio's (Version 0.99.467) internal broswer which prevents saving plots.

Examples

```
## Not run:
## For Windows users:
RJafrocGui(useBrowser = TRUE)

## For other users:
RJafrocGui()

## End(Not run)
```

---

rocData *An ROC dataset originally provided by Dr. Kevin Berbaum, U of Iowa, ca. 2002.*

Description

This ROC dataset was collected by Carolyn Van Dyke, MD, in an ROC study that compared the performance of two modalities (Spin Echo MRI and cine MRI). There are 69 non-diseased and 45 diseased cases. Five radiologists interpreted all images in both modalities using an integer 1 - 5 ratings scale, where larger ratings represented stronger confidence for presence of disease. The *.xlsx file can be downloaded from http://www.devchakraborty.com/RocData/rocData.xlsx. The dataset file can then be read into a dataset object using ReadDataFile function. The *.csv and *.lrc files can be downloaded from OR-DBM MRMC website, currently http://perception.radiology.uiowa.edu/. Alternatively they can be downloaded from http://www.devchakraborty.com/RocData/rocData.csv or http://www.devchakraborty.com/RocData/rocData.lrc. The iMRMC file can be downloaded from http://www.devchakraborty.com/RocData/rocData.imrmc.

Usage

```
rocData
```

Format

A dataset object consisting of a list containing 8 elements, see RJafroc-package.

Source

Van Dyke, C. W., et al. "Cine MRI in the diagnosis of thoracic aortic dissection." 79th Annual Meeting of the Radiological Society of North America, Radiological Society of North America, Chicago, Illinois. 1993.

`roiData` *An ROI dataset produced by a data simulator*

Description

This ROI dataset represents a simulation study in which two modalities are compared. There are 50 non-diseased and 40 diseased cases and each case is divided into 4 ROIs. Five simulated readers rated each ROI in both modalities using a floating point scale, where larger ratings represented stronger confidence for presence of disease. The NL array contains the ratings of all non-diseased ROIs while the LL array contains the ratings of all diseased ROIs. The *.xlsx file can be downloaded from `http://www.devchakraborty.com/RoiData/roiData.xlsx`. The dataset file can then be read into a dataset object using ReadDataFile function.

Usage

```
roiData
```

Format

A dataset object consisting of a list containing 8 elements, see RJafroc-package.

Source

The simulator used to generate the values is availabe from Dr. Chakraborty's website `http://www.devchakraborty.com/RoiData/RoiSimulator.zip`.

`SampleSizeGivenJ` *Calculate number of cases for specified number of readers J to achieve the desired power for ROC studies.*

Description

Calculate required number of cases to achieve the desired power for specified number of readers J and DBM or OR variability parameters.

Usage

```
SampleSizeGivenJ(J, varYTR, varYTC, varYEps, cov1, cov2, cov3, varEps, msTR,
  KStar, alpha = 0.05, effectSize = 0.05, desiredPower = 0.8,
  randomOption = "ALL")
```

Arguments

J	The number of readers.
varYTR	The DBM pseudovalue treatment-by-reader variance component.
varYTC	The DBM pseudovalue treatment-by-case variance component.
varYEps	The DBM pseudovalue error variance.
cov1	The covariance of the FOM resampling estimates for same reader and different modalities.
cov2	The covariance of the FOM resampling estimates for different readers and same modalities.
cov3	The covariance of the FOM resampling estimates for different readers and different modalities.
varEps	The variance of the FOM resampling estimates for same reader and same modalities.
msTR	Treatment-by-reader mean square of the FOM.
KStar	The number of cases in the pilot study, only required when using OR variability parameters
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.
randomOption	It can be "ALL", "READERS" or "CASES", which indicate predictions for (1) random readers and random cases, (2) random readers only and (3) random cases only.

Details

To calculate the sample size, either the group of DBM variance components (varYTR, varYTC, and varYEps) or OR covariance matrix elements and mean squares and number of cases in pilot study should be specified. If both of them are given, DBM variance components are used and OR values are ignored. Specifically, either numeric values of varYTR, varYTC, varYEps can be supplied, or the function call must explicitly state cov1 = value1, cov2 = value2, cov3 = value3, varEps = value4, msTR = value5, KStar = value6, as is standard usage in R.

Value

A list of two elements:

K	The minimum number of cases to just achieve the desired statistical power.
power	The predicted statistical power.

References

Hillis, S. L., Obuchowski, N. A., & Berbaum, K. S. (2011). Power Estimation for Multireader ROC Methods: An Updated and Unified Approach. Acad Radiol, 18, 129-142.

Hillis, S. L., Obuchowski, N. A, Schartz, K. M., & Berbaum, K. S. (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 with DBM variance components.
retDbm <- DBMHAnalysis(data = rocData, fom = "Wilcoxon")
effectSize <- retDbm$ciDiffTrtRRRC$Estimate
varCompDBM <- retDbm$varComp
varYTR <- varCompDBM$varComp[3]
varYTC <- varCompDBM$varComp[4]
varYEps <- varCompDBM$varComp[6]
SampleSizeGivenJ(J = 6, varYTR = varYTR, varYTC = varYTC, varYEps = varYEps,
                 effectSize =effectSize)

## Following is an example of sample size calculation with OR variance components.
retOR <- ORHAnalysis(data = rocData, fom = "Wilcoxon", covEstMethod = "Jackknife")
effectSize <- retOR$ciDiffTrtRRRC$Estimate
varCompOR <- retOR$varComp
cov1 <- varCompOR$varCov[3]
cov2 <- varCompOR$varCov[4]
cov3 <- varCompOR$varCov[5]
varEps <- varCompOR$varCov[6]
msTR <- retOR$msTR
KStar <- 114
SampleSizeGivenJ(J = 6, cov1 = cov1, cov2 = cov2, cov3 = cov3, varEps= varEps,
                 msTR = msTR, KStar = KStar, effectSize =effectSize)

## Not run:
## Following is an example of sample size calculation with DBM variance components,
## and scanning the number of readers
retDbm <- DBMHAnalysis(data = rocData, fom = "Wilcoxon")
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 <- SampleSizeGivenJ(J, varYTR, varYTC, varYEps, effectSize =effectSize)
 message("# of readers = ", J, " estimated # of cases = ", ret$K, ", predicted power = ",
    signif(ret$power,3), "\n")
}

## Following is an example of sample size calculation with OR variance components,
## using bootstrap to estimate variance components
retOR <- ORHAnalysis(data = rocData, fom = "Wilcoxon", covEstMethod = "Bootstrap")
effectSize <- retOR$ciDiffTrtRRRC$Estimate
varCompOR <- retOR$varComp
cov1 <- varCompOR$varCov[3]
cov2 <- varCompOR$varCov[4]
cov3 <- varCompOR$varCov[5]
varEps <- varCompOR$varCov[6]
msTR <- retOR$msTR
KStar <- length(rocData$NL[1,1,,1])
SampleSizeGivenJ(J = 6, cov1 = cov1, cov2 = cov2, cov3 = cov3, varEps= varEps,
                 msTR = msTR, KStar = KStar, effectSize =effectSize)
```

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

SaveDataFile *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

```
SaveDataFile(dataset, fileName, format = "JAFROC",
  dataDscrpt = paste0(deparse(substitute(dataset)), " Data File"))
```

Arguments

dataset	The dataset object 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.
dataDscrpt	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

```
SaveDataFile(dataset = rocData, fileName = "rocData2.xlsx", format = "JAFROC")
SaveDataFile(dataset = rocData, fileName = "rocData2.csv", format = "MRMC")
SaveDataFile(dataset = rocData, fileName = "rocData2.lrc", format = "MRMC",
             dataDscrpt = "ExampleROCdata")
SaveDataFile(dataset = rocData, fileName = "rocData2.txt", format = "MRMC",
             dataDscrpt = "ExampleROCdata2")
SaveDataFile(dataset = rocData, fileName = "rocData.imrmc", format = "iMRMC",
             dataDscrpt = "ExampleROCdata3")
```

Index