

Description

Package: ÜJAFROC Type: Package

Version: 1.0

Date: 2014-12-09 License: GPL-3

URL: <u>www.devchakraborty.com</u>

Abbreviations

Following abbreviations are used in this package.

- (F)ROC: (free-response) receiver operating characteristic
- · ROI: region-of-interest
- AUC: dæl ^: [ãaælÁarea under the ROC curve
- FOM: figure of merit
- FP: false positive AG LAÜU ÔBÜU OBB accept
- TP: true positive ÁÇI ¦ÁÜU ÔÐÜU ŒÁ æææÐÁ
- NL: non-lesion localization ÁÇI ¦ÁQÜU ÔÁ&æææÐ
- LL: lesion localization ÁÇI ¦ÁØÜUÔÁåæææÐ
- CI: confidence interval
- SE: sensitivityÁÇI ¦ÁÜUÔÐÜUÓÁåæææÐ

ÖÓT PÁMÁ

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Dataset

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Data structure

The structure of the dataset used in analysis functions is an R list containing 9 elements. Following

- are the elements in the list.

 NL: a four dimensions numerical array that contains all non-lesion localization ratings. The dimensions of the array are number of modalities * } umber of readers * number of all cases * { axxã ~ { Ánumber of non-lesion localization marks in a case. Assign -Inf to the ratings of the non-lesion localization that does not exist. Note that this array must have four dimensions. Assign one to the fourth dimension for the condition that the maximum nonlesion localization marks is one. For ROC datasets, false positive ratings are assigned to
 - LL: similar with NL except its dimension only applies to number of abnormal cases and lesion localization. For ROC datasets, true positive ratings are assigned to LL.
 - lesionNum: an integer vector with length of number of abnormal cases indicating the number of lesions in each abnormal cases. Á DEIÁN | \{ \^ \ \& A A \ \ \ A A \ \ A A \ \ A A \ \ A A \ \ A A \
 - lesionID: an integer matrix with dimension of number of abnormal cases by maximum of lesionNum. It gives the ID information of lesions in each abnormal cases. For the cases with lesions less than the maximum lesion number, -Inf are assigned to the unavailable elements. Note that ratings of lesions in LL must appear as the sequence of lesionID for corresponding case. For example, if the **lesionID** for the first abnormal case is c(4, 2, 3, 1), the ratings in **LL** for this case must appear as this sequence.
 - lesionWeight: a numerical matrix with same dimension of lesionID, which is the relative importance of detecting each lesion. The weights must sum to unity for each case. ACE ^æ ^ Á, æ Áq Án} • ˇ ¦ ^ Ánˇ ˇ æ Á, ^ ã ˇ @ēā, ˇ Áā Áq Áæ • ã } Áæ Á ^ ¦ [Á, ^ ã @cÁq Án æ& @Án • ã, } ÉÁ
 - maxNumMarks: the maximum number of non-lesion localization.
 - dataType: the type of the dataset. It { *• of be "ROC", "ROI" or "FROC".
 - modalityID: a vector of strings, which indicates the ID of each modality that is used in the datesetÊA\È ĒÊÃÔO£ÖÄÊATÜQÃÊÁ,¦ÁÀÃÊÁÃFÄÉA\œ&ÉAQ®,Ás Á@;/[]~/Á§,ÁS,c^!;|¦^œā,*Ás@,Á;`q`∽ÁS[;!^&q^È
 - readerID: a vector of strings, which contains the ID of each reader. Note that the order of elements in modalityID and readerID must identical with 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 is able to read JAFROC, OR-DBM MRMC (ROC data only) and iMRMC (ROC data only) data files. They can be imported by using fuctions ReadDataFile.

JAFROC data file format

The JAFROC data file is an Excel file containing three worksheets (*.xls and *.xlsx are supported): (1) Truth (2) 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 normal cases.
- weight, a floating point field, which is the relative importance of detecting each lesion. This field is zero for normal cases and for equally weighted lesions; otherwise the weights must sum to unity for each case. This field is irrelevant unless a weighted figure of merit is selected, see next section.

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 normal 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 lesion-localization mark, with higher numbers represent greater confidence that the location is actually a lesion.

For the stacked input format, the data must be organized in columns following the order:

ReaderID, ModalityID, CaseID, Truth and Rating. The column names can be anything, but they must exist. The columns ReaderID, ModalityID, CaseID and Rating are defined as the same as JAFROC data file format. For the Truth column, use 0 for normal cases and 1 for abnormal. The delimiter in each line must be spaces or commas, but only one delimiter is allowed in a same data file. The data file can be saved as plain text file with *.txt or *.csv extensions.

iMRMC data format

The iMRMC data format contains two parts: the data description and ROC ratings.

- 1. Data description part includes free text information at the top of the file. Following information must be specified in this part as four lines
 - No, number of normal cases.
 - N1, number of abnormal cases.
 - o NR, number of readers.
 - NM, number of modalities.

The symbol and corresponding number are separated by colon (:). For example, 50 normal cases can be indicated by the line N0: 50.

- 2. ROC ratings list starts at the line "BEGIN DATA: ". The list has two parts: truth states and readers' ratings.
 - Truth states has four columns in the following order:
 - -1, lines with -1 in the first column indicate the lines are truth states lines.
 - CaseID, same as JAFROC data format.
 - arbitrary string, can be anything.
 - Truth, same as OR-DBM MRMC format.
 - Readers' ratings list also contains four columns in the following order:
 - ReaderID, same as JAFROC data format. Note that ReaderID can be anything but "-1".
 - CaseID, same as JAFROC data format.
 - ModalityID, same as JAFROC data format.
 - Ratings, same as JAFROC data format.

Columns are separated by commas and the data are saved as plain text file with *.imrmc extension.

Note that JAFROC and OR-DBM MRMC data file have table headers, while the iMRMC data file does not.

Functions

<u>CalculatePower</u>

Calculate the statistical power with the given number of readers,

number of cases and DBMP variances components.

<u>CalculateSampleSize</u> Calcuate required sample size for the specified dataset.

Performs Dorfman-Berbaum-Metz Paja analysis for the specified

dataset.

Visualize the predicted ROC, AFROC, FROC and pdf

OperatingCharacteristics (probability density function) curves for given search model

parameters.

ORAnalysis

Performs Obuchowski-Rockette Paja analysis for the specified

dataset.

<u>OutputReport</u> Output the report of the analysis result.

Plot emprirical curves for specified modalities and readers in the

dataset.

Plot parametric curves for specified modalities and readers in

the dataset.

ReadDataFile Read the dataset that will be analysis from data file

SampleSizeCalculator

Calculate required number of cases with the given number of

readers and DBM variances components.

<u>SaveDataFile</u> Save the dataset into a file as the specified format.

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