

# RJafroc Documentation

Dev P. Chakraborty, PhD

2020-03-17



# Contents

<b>Preface</b>	<b>5</b>
<b>1 Introduction</b>	<b>7</b>
1.1 References . . . . .	7
<b>2 ROC DATA FORMAT</b>	<b>9</b>
2.1 Introduction . . . . .	9
2.2 Note to existing users . . . . .	10
2.3 The Excel data format . . . . .	10
2.4 Illustrative toy file . . . . .	10
2.5 The <b>Truth</b> worksheet . . . . .	10
2.6 The structure of an ROC dataset . . . . .	12
2.7 The false positive (FP) ratings . . . . .	13
2.8 The true positive (TP) ratings . . . . .	14
2.9 Correspondence between NL member of dataset and the FP work- sheet . . . . .	15
2.10 Correspondence between LL member of dataset and the TP work- sheet . . . . .	15
2.11 Correspondence using the <b>which</b> function . . . . .	15
2.12 References . . . . .	16
<b>3 Proper ROCs</b>	<b>17</b>
3.1 Helper functions . . . . .	17
3.2 Definitions of PROPROC parameters in terms of binormal model parameters . . . . .	17

3.3	Main code and output . . . . .	17
3.4	Discussion . . . . .	20
<b>4</b>	<b>Metz Eqn36 numerical check</b>	<b>23</b>
4.1	Helper functions . . . . .	23
4.2	Main code and output . . . . .	23
4.3	Discussion . . . . .	24
<b>5</b>	<b>CBM Plots</b>	<b>25</b>
5.1	Helper functions . . . . .	25
5.2	Main code and output . . . . .	25
5.3	Comments . . . . .	28
5.4	pdf plots . . . . .	28
5.5	Comments . . . . .	30
5.6	likelihood ratio plots . . . . .	30
5.7	Comments . . . . .	33
<b>6</b>	<b>ROI paradigm data</b>	<b>35</b>
6.1	Introduction; this vignette is under construction! . . . . .	35
6.2	An example ROI dataset . . . . .	36
6.3	The ROI Excel data file . . . . .	37
6.4	Next, TBA . . . . .	39
6.5	References . . . . .	39
<b>7</b>	<b>Analyzing data acquired according to the ROI paradigm</b>	<b>41</b>
7.1	Introduction; this vignette is under construction! . . . . .	41
7.2	Note to self (10/29/19) !!!DPC!!! . . . . .	41
7.3	Introduction . . . . .	41
7.4	The ROI figure of merit . . . . .	42
7.5	Calculation of the ROI figure of merit. . . . .	42
7.6	Significance testing . . . . .	43
7.7	Summary . . . . .	47
7.8	References . . . . .	47

# Preface

- This book, an extended documentation of the **RJafroc** package, is undergoing extensive edits.
- It should not be used by the casual user until I give the go ahead.
- It bypasses the file size limits of **CRAN**, currently 5 MB, which severely limits the extent of the documentation that can be included with the CRAN version of the package.
- I welcome corrections and comments by the not-so-casual-user.
- Please use the GitHub website to raise issues and comments:
  - <https://github.com/dpc10ster/RJafrocBook>



# Chapter 1

## Introduction

- This is the book describing the **RJafroc** package.
- The name of the book is RJafrocBook
- Modality and treatment are used interchangeably.
- Reader is a generic radiologist, or a computer aided detection algorithm, or any algorithmic “reader”
- TBA

### 1.1 References





## Chapter 2

# ROC DATA FORMAT

$$\theta = \frac{1}{N_L N_N} \sum_k \sum_{k'} \sum_{r=1}^{n_k^L} \sum_{r'=1}^{n_{k'}^N} \psi(X_{kr}, Y_{k'r'})$$

$$\frac{d}{dx} \left( \int_a^x f(u) du \right) = f(x)$$

$$\theta = \frac{1}{N_L N_N}$$

### 2.1 Introduction

- The purpose of this vignette is to explain the data format of the input Excel file and to introduce the capabilities of the function `DfReadDataFile()`. Background on observer performance methods are in my book (Chakraborty, 2017).
- I will start with Receiver Operating Characteristic (ROC) data (Metz, 1978), as this is by far the simplest paradigm.
- In the ROC paradigm the observer assigns a rating to each image. A rating is an ordered numeric label, and, in our convention, higher values represent greater certainty or **confidence level** for presence of disease. With human observers, a 5 (or 6) point rating scale is typically used, with 1 representing highest confidence for *absence* of disease and 5 (or 6) representing highest confidence for *presence* of disease. Intermediate values represent intermediate confidence levels for presence or absence of disease.
- Note that location information associated with the disease, if applicable, is not collected.

- There is no restriction to 5 or 6 ratings. With algorithmic observers, e.g., computer aided detection (CAD) algorithms, the rating could be a floating point number and have infinite precision. All that is required is that higher values correspond to greater confidence in presence of disease.

## 2.2 Note to existing users

- The Excel file format has recently undergone changes resulting in 4 extra `list` members in the final created `dataset` object (i.e., 12 members instead of 8).
- Code should run on the old format Excel files as the 4 extra list members are simply ignored.
- Reasons for the change will become clearer in these vignettes
- Basically they are needed for generalization to other data collection paradigms instead of crossed, for example to the split-plot data acquisition paradigm, and for better data entry error control.

## 2.3 The Excel data format

- The Excel file has three worksheets.
- These are named
  - `Truth`,
  - `NL` (or `FP`),
  - `LL` (or `TP`).

## 2.4 Illustrative toy file

- *Toy files* are artificial small datasets intended to illustrate essential features of the data format.
- The examples shown in this vignette corresponds to Excel file `inst/extdata/toyFiles/ROC/rocCr.xlsx` in the project directory.
- To view these files one needs to `clone` the source files from [GitHub](#).

## 2.5 The Truth worksheet

- The `Truth` worksheet contains 6 columns: `CaseID`, `LesionID`, `Weight`, `ReaderID`, `ModalityID` and `Paradigm`.

- For ROC data the first five columns contain as many rows as there are cases (images) in the dataset.
- **CaseID**: unique integers, one per case, representing the cases in the dataset.
- **LesionID**: integers 0 or 1, with each 0 representing a non-diseased case and each 1 representing a diseased case.
- In the current toy dataset, the non-diseased cases are labeled 1, 2 and 3, while the diseased cases are labeled 70, 71, 72, 73 and 74. The values do not have to be consecutive integers; they need not be ordered; the only requirement is that they be **unique**.
- **Weight**: Not used for ROC data, a floating point value, typically filled in with 0 or 1.
- **ReaderID**: a **comma-separated** listing of reader labels, each represented by a **unique string**, that have interpreted the case. In the example shown below each cell has the value 0, 1, 2, 3, 4 meaning that each of the readers, represented by the strings "0", "1", "2", "3" and "4", have interpreted all cases (hence the "crossed" design). **With reader names that could be confused with integers, each cell in this column has to be text formatted as otherwise Excel will not accept it.** [Try entering 0, 1, 2, 3, 4 in a numeric formatted Excel cell.]
- The reader names could just as well have been Rdr0, Rdr1, Rdr2, Rdr3, Rdr4. The only requirement is that they be unique strings.
- Look in in the `inst/extdata/toyFiles/ROC` directory for files `rocCrStrRdrsTrts.xlsx` and `rocCrStrRdrsNonUnique.xlsx` for examples of data files using longer strings for readers. The second file generates an error because the reader names are not unique.
- **ModalityID**: a comma-separated listing of modalities (one or more modalities), each represented by a **unique string**, that are applied to each case. In the example each cell has the value "0", "1". **With treatment names that could be confused with integers, each cell has to be text formatted as otherwise Excel will not accept it.**
- The treatment names could just as well have been Trt0, Trt1. Again, the only requirement is that they be unique strings.
- **Paradigm**: this column contains two cells, **ROC** and **crossed**. It informs the software that this is an ROC dataset, and the design is crossed, meaning each reader has interpreted each case in each modality (in statistical terminology: modality and reader factors are "crossed").
- There are 5 diseased cases in the dataset (the number of 1's in the **LesionID** column of the **Truth** worksheet).
- There are 3 non-diseased cases in the dataset (the number of 0's in the **LesionID** column).
- There are 5 readers in the dataset (each cell in the **ReaderID** column contains the string 0, 1, 2, 3, 4).
- There are 2 modalities in the dataset (each cell in the **ModalityID** column contains the string 0, 1).

	A	B	C	D	E	F
	CaseID	LesionID	Weight	ReaderID	ModalityID	Paradigm
1	1	0	0	0,1,2,3,4	0,1	ROC
2	2	0	0	0,1,2,3,4	0,1	crossed
3	3	0	0	0,1,2,3,4	0,1	
4	70	1	1	0,1,2,3,4	0,1	
5	71	1	1	0,1,2,3,4	0,1	
6	72	1	1	0,1,2,3,4	0,1	
7	73	1	1	0,1,2,3,4	0,1	
8	74	1	1	0,1,2,3,4	0,1	

Figure 2.1: Truth worksheet for file rocCr.xlsx

## 2.6 The structure of an ROC dataset

In the following code chunk the first statement retrieves the name of the data file, located in a hidden directory that one need not be concerned with. The second statement reads the file using the function `DfReadDataFile()` and saves it to object `x`. The third statement shows the structure of the dataset object `x`.

```
rocCr <- system.file("extdata", "toyFiles/ROC/rocCr.xlsx",
                     package = "RJaFroc", mustWork = TRUE)
x <- DfReadDataFile(rocCr, newExcelFileFormat = TRUE)
str(x)
#> List of 12
#> $ NL          : num [1:2, 1:5, 1:8, 1] 1 3 2 3 2 2 1 2 3 2 ...
#> $ LL          : num [1:2, 1:5, 1:5, 1] 5 5 5 5 5 5 5 5 5 5 ...
#> $ lesionVector : int [1:5] 1 1 1 1 1
#> $ lesionID     : num [1:5, 1] 1 1 1 1 1
#> $ lesionWeight : num [1:5, 1] 1 1 1 1 1
#> $ dataType     : chr "ROC"
#> $ modalityID   : Named chr [1:2] "0" "1"
#> ..- attr(*, "names")= chr [1:2] "0" "1"
#> $ readerID     : Named chr [1:5] "0" "1" "2" "3" ...
#> ..- attr(*, "names")= chr [1:5] "0" "1" "2" "3" ...
#> $ design       : chr "CROSSED"
#> $ normalCases  : int [1:3] 1 2 3
#> $ abnormalCases: int [1:5] 70 71 72 73 74
#> $ truthTableStr: num [1:2, 1:5, 1:8, 1:2] 1 1 1 1 1 1 1 1 1 1 ...
```

- In the above code chunk flag `newExcelFileFormat` is set to `TRUE` as otherwise columns D - F in the Truth worksheet are ignored and the dataset is assumed to be crossed, with `dataType` automatically determined from the contents of the FP and TP worksheets.
- Flag `newExcelFileFormat = FALSE` is for compatibility with older

JAFROC format Excel files, which did not have these columns in the Truth worksheet. Its usage is deprecated.

- The dataset object `x` is a `list` variable with 12 members.
- The `x$NL` member, with dimension `[2, 5, 8, 1]`, contains the ratings of normal cases. The extra values in the third dimension, filled with `NA`s, are needed for compatibility with FROC datasets, as unlike ROC, false positives are possible on diseased cases.
- The `x$LL`, with dimension `[2, 5, 5, 1]`, contains the ratings of abnormal cases.
- The `x$lesionVector` member is a vector with 5 ones representing the 5 diseased cases in the dataset.
- The `x$lesionID` member is an array with 5 ones.
- The `x$lesionWeight` member is an array with 5 ones.
- The `lesionVector`, `lesionID` and `lesionWeight` members are not used for ROC datasets. They are there for compatibility with FROC datasets.
- The `dataType` member indicates that this is an ROC dataset.
- The `x$modalityID` member is a vector with two elements "0" and "1", naming the two modalities.
- The `x$readerID` member is a vector with five elements "0", "1", "2", "3" and "4", naming the five readers.
- The `x$design` member is `CROSSED`; specifies the dataset design, which is "CROSSED".
- The `x$normalCases` member lists the integer names of the normal cases, 1, 2, 3.
- The `x$abnormalCases` member lists the integer names of the abnormal cases, 70, 71, 72, 73, 74.
- The `x$truthTableStr` member quantifies the structure of the dataset, as explained in **Chapter 00 Vignette #3-#5**.

## 2.7 The false positive (FP) ratings

These are found in the FP or NL worksheet, see below.

ReaderID	ModalityID	CaseID	FP Rating
0	0	1	1
0	0	2	2
0	0	3	2
0	1	1	2
0	1	2	3
0	1	3	2
0	2	0	2
0	2	1	2
0	2	2	2
0	2	3	2
0	2	4	1
0	3	0	2
0	3	1	1
0	3	2	1
0	3	3	1
0	3	4	5
0	4	0	3
0	4	1	3
0	4	2	3
0	4	3	3
0	4	4	3
0	4	5	2
0	4	6	2
0	4	7	2
0	4	8	4

Figure 2.2: FP worksheet for file rocCr.xlsx

- It consists of 4 columns, each of length 30 (= # of modalities times number of readers times number of non-diseased cases).
- **ReaderID**: the reader labels: 0, 1, 2, 3 and 4. Each reader label occurs 6 times (= # of modalities times number of non-diseased cases).
- **ModalityID**: the modality or treatment labels: 0 and 1. Each label occurs 15 times (= # of readers times number of non-diseased cases).
- **CaseID**: the case labels for non-diseased cases: 1, 2 and 3. Each label occurs 10 times (= # of modalities times # of readers).
- The label of a diseased case cannot occur in the FP worksheet. If it does the software generates an error.
- **FP\_Rating**: the floating point ratings of non-diseased cases. Each row of this worksheet contains a rating corresponding to the values of **ReaderID**, **ModalityID** and **CaseID** for that row.

## 2.8 The true positive (TP) ratings

These are found in the TP or LL worksheet, see below.

ReaderID	ModalityID	CaseID	LesionID	TP_Rating
0	0	70	1	5
0	0	71	1	5
0	0	72	1	5
0	0	73	1	5
0	0	74	1	4
1	0	70	1	5
1	0	71	1	5
1	0	72	1	5
1	0	73	1	5
1	0	74	1	5
2	0	70	1	5
2	0	71	1	5
2	0	72	1	5
2	0	73	1	5
2	0	74	1	5
3	0	70	1	5
3	0	71	1	5
3	0	72	1	5
3	0	73	1	5
3	0	74	1	5
4	0	70	1	5
4	0	71	1	2
4	0	72	1	5
4	0	73	1	5
4	0	74	1	5
0	1	1	1	5
0	1	2	1	5
0	1	3	1	5
0	1	1	1	5
0	1	2	1	5
0	1	3	1	5
1	1	1	1	5
1	1	2	1	5
1	1	3	1	5
1	1	1	1	5
1	1	2	1	5
1	1	3	1	5
2	1	1	1	5
2	1	2	1	5
2	1	3	1	5
2	1	1	1	5
2	1	2	1	5
2	1	3	1	5
3	1	1	1	5
3	1	2	1	5
3	1	3	1	5
3	1	1	1	5
3	1	2	1	5
3	1	3	1	5
4	1	1	1	5
4	1	2	1	5
4	1	3	1	5
4	1	1	1	5
4	1	2	1	5
4	1	3	1	5

Figure 2.3: TP worksheet for file rocCr.xlsx

- It consists of 5 columns, each of length 50 (= # of modalities times number of readers times number of diseased cases).
- **ReaderID**: the reader labels: 0, 1, 2, 3 and 4. Each reader label occurs 10 times (= # of modalities times number of diseased cases).
- **ModalityID**: the modality or treatment labels: 0 and 1. Each label occurs 25 times (= # of readers times number of diseased cases).
- **LesionID**: For an ROC dataset this column contains fifty 1's (each diseased case has one lesion).
- **CaseID**: the case labels for non-diseased cases: 70, 71, 72, 73 and 74. Each label occurs 10 times (= # of modalities times # of readers). The label of a non-diseased case cannot occur in the TP worksheet.
- **TP\_Rating**: the floating point ratings of diseased cases. Each row of this worksheet contains a rating corresponding to the values of **ReaderID**, **ModalityID**, **LesionID** and **CaseID** for that row.

## 2.9 Correspondence between NL member of dataset and the FP worksheet

- The list member `x$NL` is an array with `dim = c(2,5,8,1)`.
  - The first dimension (2) comes from the number of modalities.
  - The second dimension (5) comes from the number of readers.
  - The third dimension (8) comes from the **total** number of cases.
  - The fourth dimension is always 1 for an ROC dataset.
- The value of `x$NL[1,5,2,1]`, i.e., 5, corresponds to row 15 of the FP table, i.e., to `ModalityID = 0`, `ReaderID = 4` and `CaseID = 2`.
- The value of `x$NL[2,3,2,1]`, i.e., 4, corresponds to row 24 of the FP table, i.e., to `ModalityID 1`, `ReaderID 2` and `CaseID 2`.
- All values for case index  $> 3$  are `-Inf`. For example the value of `x$NL[2,3,4,1]` is `-Inf`. This is because there are only 3 non-diseased cases. The extra length is needed for compatibility with FROC datasets.

## 2.10 Correspondence between LL member of dataset and the TP worksheet

- The list member `x$LL` is an array with `dim = c(2,5,5,1)`.
  - The first dimension (2) comes from the number of modalities.
  - The second dimension (5) comes from the number of readers.
  - The third dimension (5) comes from the number of diseased cases.
  - The fourth dimension is always 1 for an ROC dataset.
- The value of `x$LL[1,1,5,1]`, i.e., 4, corresponds to row 6 of the TP table, i.e., to `ModalityID = 0`, `ReaderID = 0` and `CaseID = 74`.
- The value of `x$LL[1,2,2,1]`, i.e., 3, corresponds to row 8 of the TP table, i.e., to `ModalityID = 0`, `ReaderID = 1` and `CaseID = 71`.
- There are no `-Inf` values in `x$LL`: `any(x$LL == -Inf) = FALSE`.

## 2.11 Correspondence using the which function

- Converting from **names** to **subscripts** (indicating position in an array) can be confusing.
- The following example uses the `which` function to help out.
- The first line says that the `abnormalCase` named 70 corresponds to subscript 1 in the LL array case dimension.
- The second line prints the NL rating for `modalityID = 0`, `readerID = 1` and `normalCases = 1`.

- The third line prints the LL rating for `modalityID = 0`, `readerID = 1` and `abnormalCases = 70`.
- The last line shows what happens if one enters an invalid value for name; the result is a `numeric(0)`.
- Note that in each of these examples, the last dimension is 1 because we are dealing with an ROC dataset.
- The reader is encouraged to examine the correspondence between the NL and LL ratings and the Excel file using this method.

```
which(x$abnormalCases == 70)
#> [1] 1
x$NL[which(x$modalityID == "0"),which(x$readerID == "1"),which(x$normalCases == 1),1]
#> [1] 2
x$LL[which(x$modalityID == "0"),which(x$readerID == "1"),which(x$abnormalCases == 70),1]
#> [1] 5
x$LL[which(x$modalityID == "a"),which(x$readerID == "1"),which(x$abnormalCases == 70),1]
#> numeric(0)
```

## 2.12 References



## Chapter 3

# Proper ROCs

### 3.1 Helper functions

### 3.2 Definitions of PROPROC parameters in terms of binormal model parameters

$$c = \frac{b-1}{b+1}$$
$$d_a = \frac{\sqrt{2}a}{\sqrt{1+b^2}}$$

### 3.3 Main code and output

```
c1Arr <- c(-0.1322804, 0.2225588); daArr <- c(1.197239, 1.740157)
myLabel <- c("A", "B", "C", "D")
myLabelIndx <- 1
for (i in 1:2)
{
  c1 <- c1Arr[i]
  da <- daArr[i]
  ret <- Transform2ab(da, c1)
  a <- ret$a; b <- ret$b
  if (i == 1) z <- seq(-3, 0, by = 0.01) # may need to adjust limits to view detail of slope plot
  if (i == 2) z <- seq(-3, 5, by = 0.01) # may need to adjust limits to view detail of slope plot
```

```

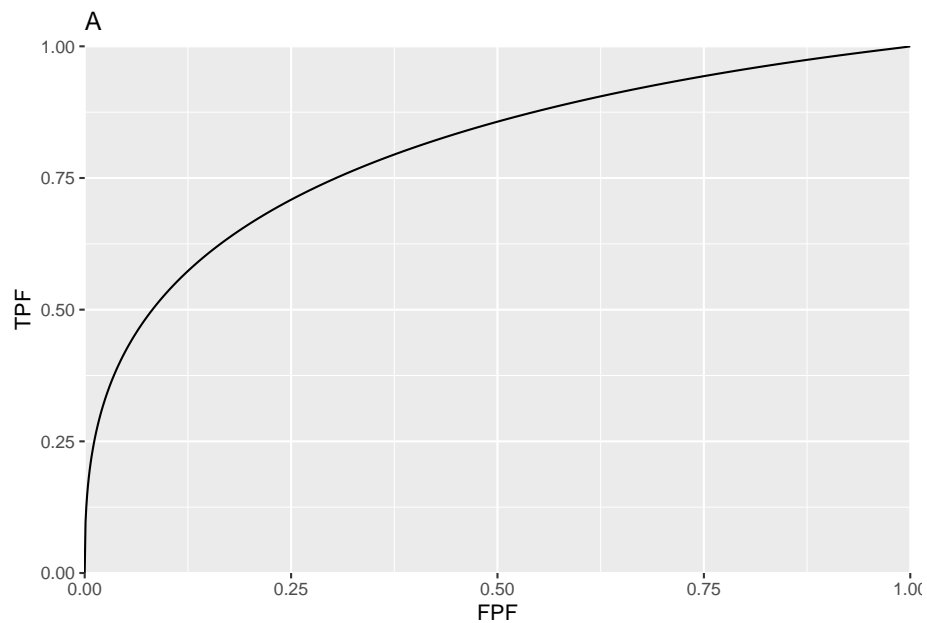
FPF <- seq(0.0, 1, 0.001)
TPF <- rocY(FPF, a, b)

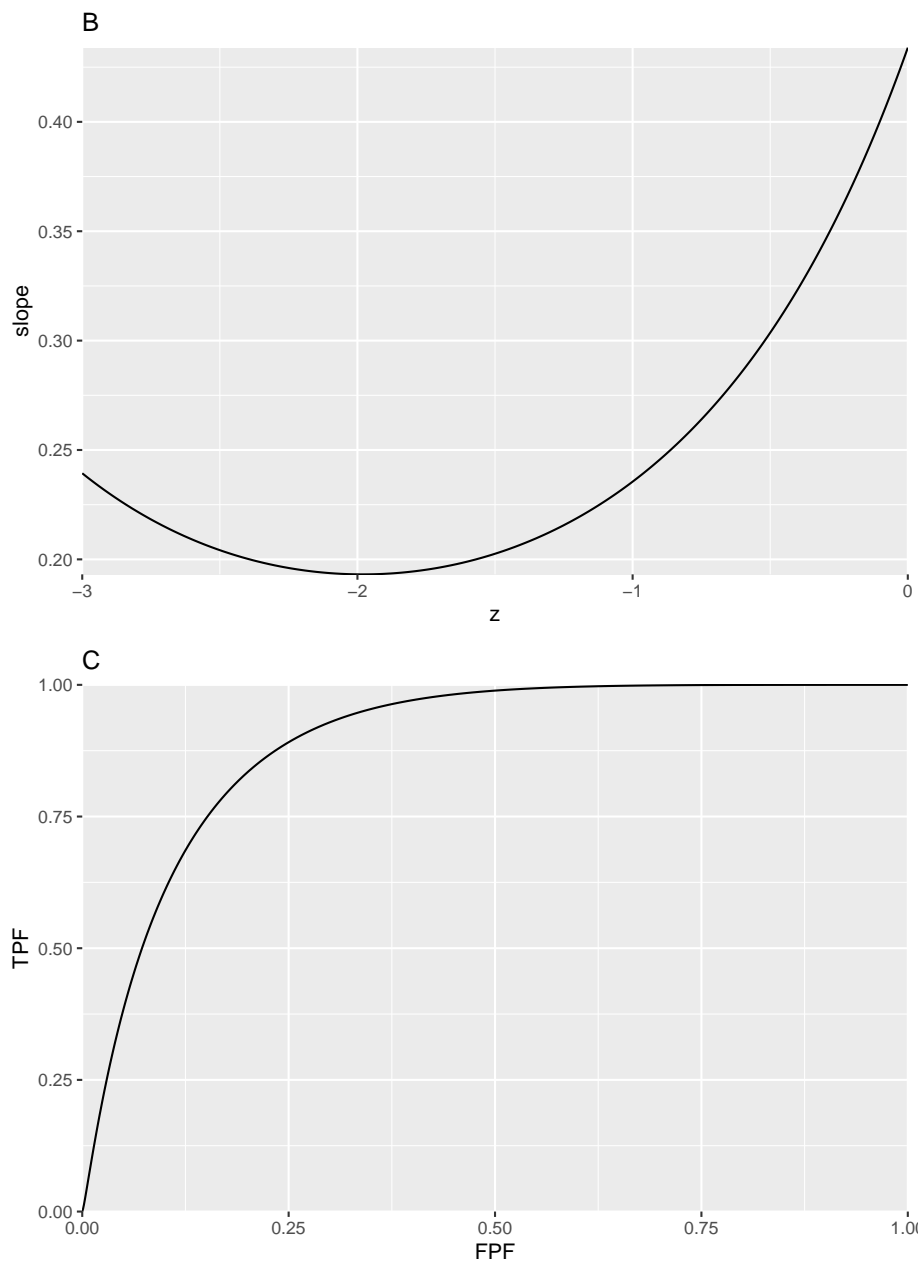
rocPlot <- data.frame(FPF = FPF, TPF = TPF)
plotRoc <- ggplot(rocPlot, aes(x = FPF, y = TPF)) +
  geom_line() +
  scale_x_continuous(expand = c(0, 0)) +
  scale_y_continuous(expand = c(0, 0)) +
  ggtitle(myLabel[myLabelIndx]); myLabelIndx <- myLabelIndx + 1

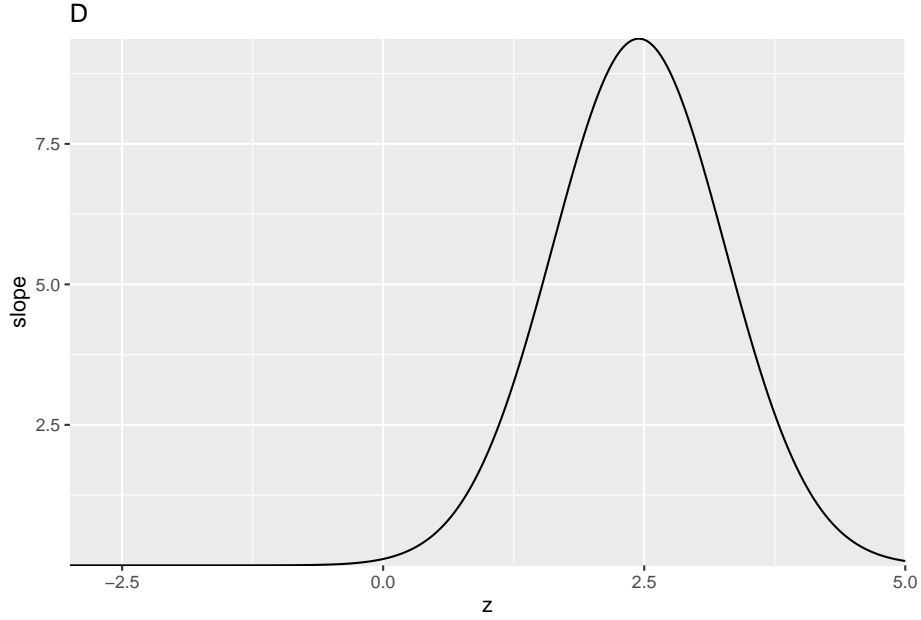
slope <- -b*dnorm(a-b*z)/dnorm(-z) # same as likelihood ratio

slopePlot <- data.frame(z = z, slope = slope)
p <- ggplot(slopePlot, aes(x = z, y = slope)) +
  geom_line() +
  scale_x_continuous(expand = c(0, 0)) +
  scale_y_continuous(expand = c(0, 0)) +
  ggtitle(myLabel[myLabelIndx]); myLabelIndx <- myLabelIndx + 1
print(plotRoc); print(p)
}

```







### 3.4 Discussion

Plot A is for  $c1 = -0.1322804$ ,  $da = 1.197239$  while plot C is for  $c1 = 0.2225588$ ,  $da = 1.740157$ . Plots B and D are the corresponding slope plots as functions of the binormal model  $z$ -sample. In plot A, the slope is infinite near the origin and the curve approaches the upper-right corner with finite slope. The situation is reversed in plot C where the slope is finite near the origin and the curve approaches the upper-right corner with zero slope.

These two readers are from a clinical dataset, `dataset01`. Highest rating inferred ROC data from original FROC data, were analyzed by PROPROC and the resulting parameter values are coded here. They were chosen as they demonstrate key differences in the shapes of proper ROC plots. Plot A corresponds to a negative value of  $c1$ , which implies  $b < 1$ . The slope of the proper ROC is infinite near the origin and approaches a positive constant near the upper right corner of the ROC. Plot C is for a positive value of  $c1$ , i.e., for  $b > 1$ . Now the slope of the proper ROC is finite near the origin and approaches zero near the upper right corner.

Considering plot D, as one “cuts” the slope axis horizontally with a sliding threshold, starting with very high values and moving downwards, the slope of the ROC curve starts at the origin with a large but finite value. This corresponds to the peak in plot D. Above the peak, there are no solutions for  $z$ . The slope decreases monotonically to zero, corresponding to the flattening out of the slope

at zero for  $z \sim -2$ .

The two values of  $z$  corresponding to each cut implies, of course, that the binormal model based proper algorithm has to do a lot of bookkeeping, since each horizontal cut splits the decision axis into 3 regions. One can think of shrinking each of plots B & D horizontally to zero width, and all that remains is the slope axis with a thick vertical line superimposed on it, corresponding to the horizontally collapsed curves. In plot B the vertical line extends from positive infinity down to about 0.1, and represents the range of decision variable samples encountered by the observer on the likelihood ratio scale. In plot D the vertical line extends from a finite value ( $\sim 9.4$ ) to zero. For the stated binormal model parameters values outside of these ranges are not possible.



## Chapter 4

# Metz Eqn36 numerical check

### 4.1 Helper functions

### 4.2 Main code and output

```
npts <- 10000
for (i in 1:2) {
  for (j in 1:5) {
    C <- c1[i,j]
    da <- d_a1[i,j]
    ret <- GetLimits(da,C)
    LL <- ret$LL;UL <- ret$UL
    vc <- seq (LL, UL, length.out = npts)
    TPF <- TruePositiveFraction (vc, da, C)
    FPF <- FalsePositiveFraction (vc, da, C)
    FPF <- rev(FPF);TPF <- rev(TPF)
    df2 <- data.frame(FPF = FPF, TPF = TPF)
    # do integral numerically
    numAuc <- trapz(FPF, TPF)
    # Implement Eqn. 36 from Metz-Pan paper
    rho <- -(1-C^2)/(1+C^2);sigma <- rbind(c(1, rho), c(rho, 1))
    lower <- rep(-Inf,2);upper <- c(-da/sqrt(2),0)
    aucProproc <- pnorm(da/sqrt(2)) + 2 * pmvnorm(lower, upper, sigma = sigma)
    aucProproc <- as.numeric(aucProproc)
    cat("i = ", i,"j = ", j,"C = ", C, ", da = ", da, "aucProproc =", aucProproc, "Norm. Diff. = "
```

```

    }
  }
#> i = 1 j = 1 C = -0.1322804 , da = 1.197239 aucProproc = 0.8014164 Norm. Diff. =
#> i = 1 j = 2 C = -0.08696513 , da = 1.771176 aucProproc = 0.8947898 Norm. Diff. =
#> i = 1 j = 3 C = -0.1444419 , da = 1.481935 aucProproc = 0.8526605 Norm. Diff. =
#> i = 1 j = 4 C = 0.08046016 , da = 1.513757 aucProproc = 0.8577776 Norm. Diff. =
#> i = 1 j = 5 C = 0.2225588 , da = 1.740157 aucProproc = 0.8909392 Norm. Diff. =
#> i = 2 j = 1 C = -0.08174248 , da = 0.6281251 aucProproc = 0.6716574 Norm. Diff. =
#> i = 2 j = 2 C = 0.04976448 , da = 0.9738786 aucProproc = 0.7544739 Norm. Diff. =
#> i = 2 j = 3 C = -0.1326126 , da = 1.155871 aucProproc = 0.7931787 Norm. Diff. =
#> i = 2 j = 4 C = 0.1182226 , da = 1.620176 aucProproc = 0.8740274 Norm. Diff. =
#> i = 2 j = 5 C = 0.0781033 , da = 0.8928816 aucProproc = 0.7360989 Norm. Diff. =

```

### 4.3 Discussion

Note the close correspondence between the formula, Eqn. 36 in the Metz-Pan paper and the numerical estimate. As a historical note, Eqn. 31 and Eqn. 36 (they differ only in parameterizations) in the referenced publication are provided without proof – it was probably obvious to Prof Metz or he wanted to leave it to us “mere mortals” to figure it out, as a final parting gesture of his legacy. The author once put a significant effort into proving it and even had a bright graduate student from the biostatistics department work on it to no avail. The author has observed that these equations always yield very close to the numerical estimates, to within numerical precisions, so the theorem is correct empirically, but he has been unable to prove it analytically. It is left as an exercise for a gifted reader to prove/disprove these equations.



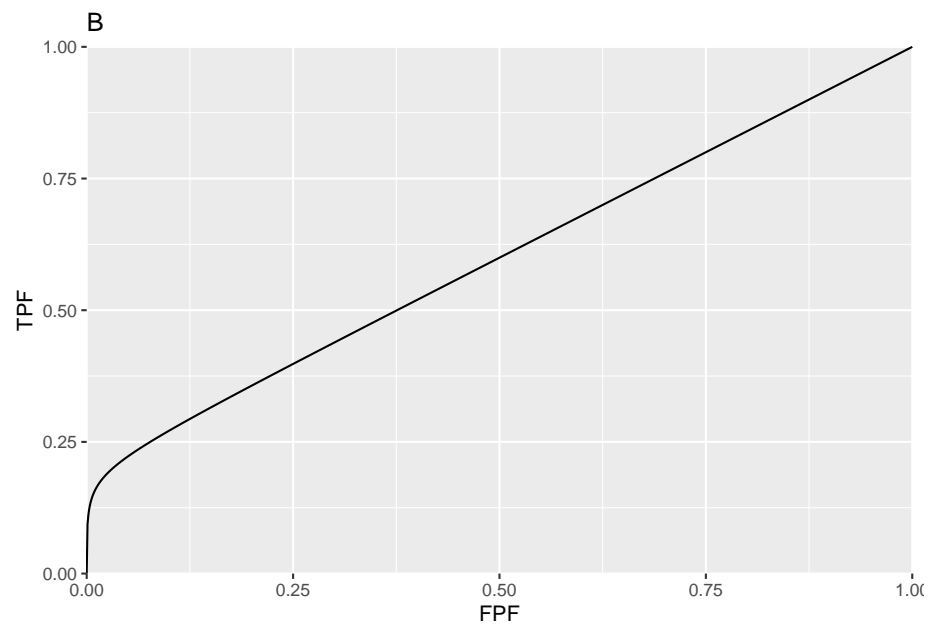
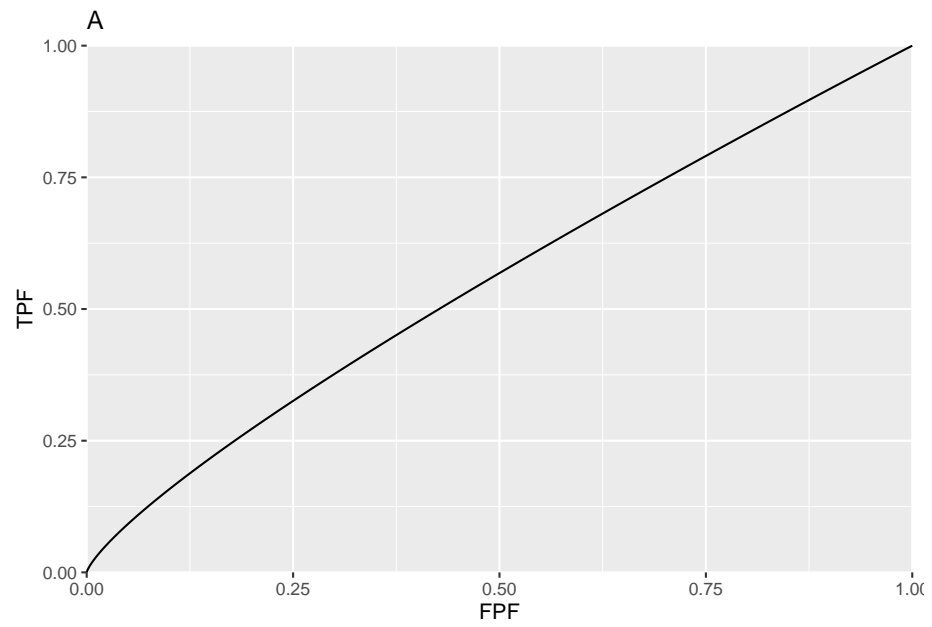
## Chapter 5

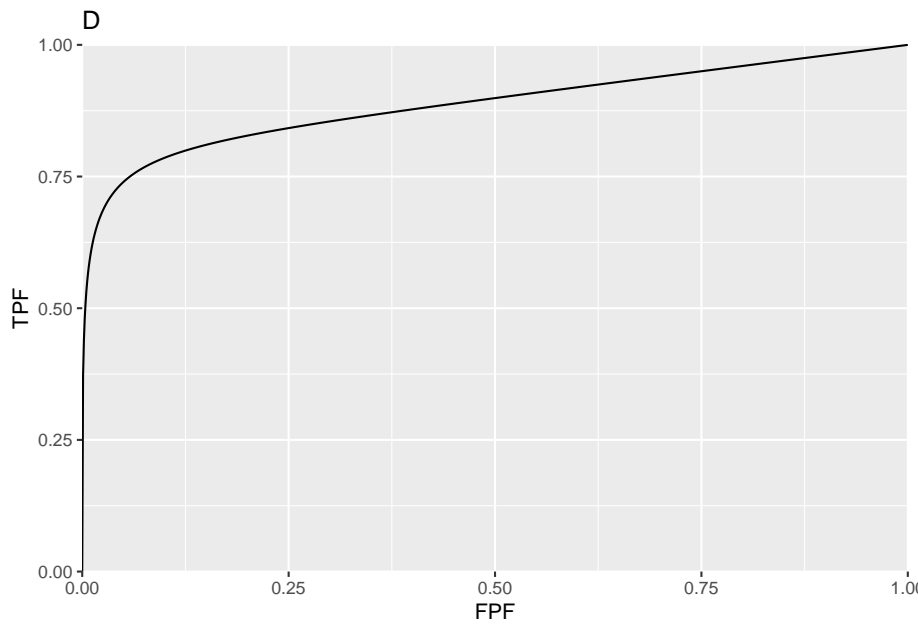
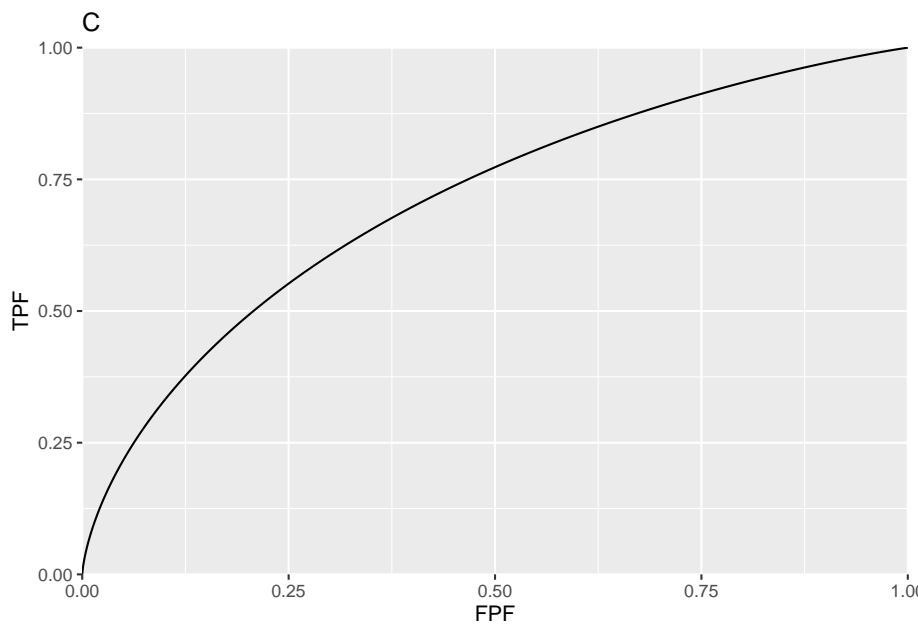
# CBM Plots

### 5.1 Helper functions

### 5.2 Main code and output

```
#> Fig. A : mu = 1 , alpha = 0.2  
#> Fig. B : mu = 3 , alpha = 0.2  
#> Fig. C : mu = 1 , alpha = 0.8  
#> Fig. D : mu = 3 , alpha = 0.8
```



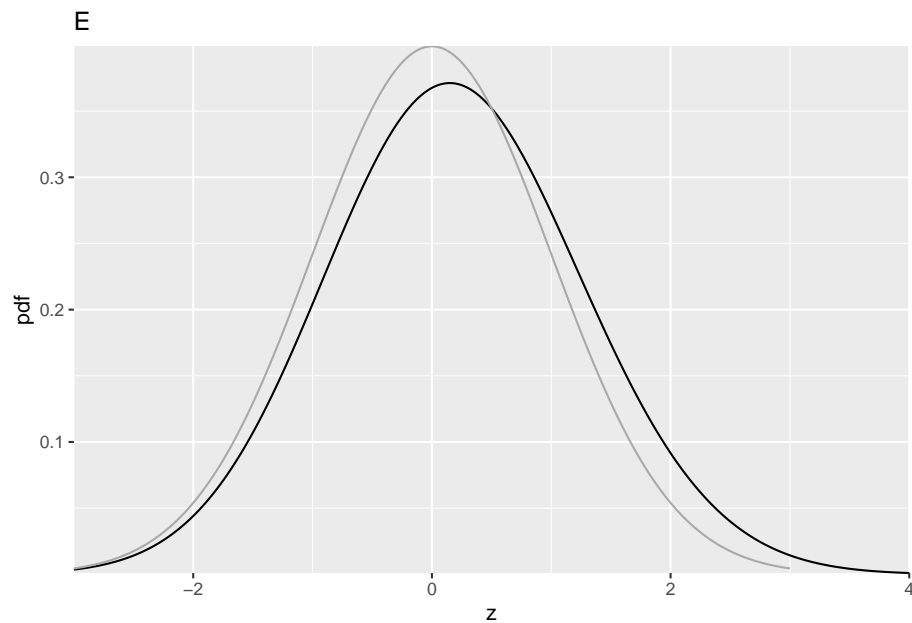


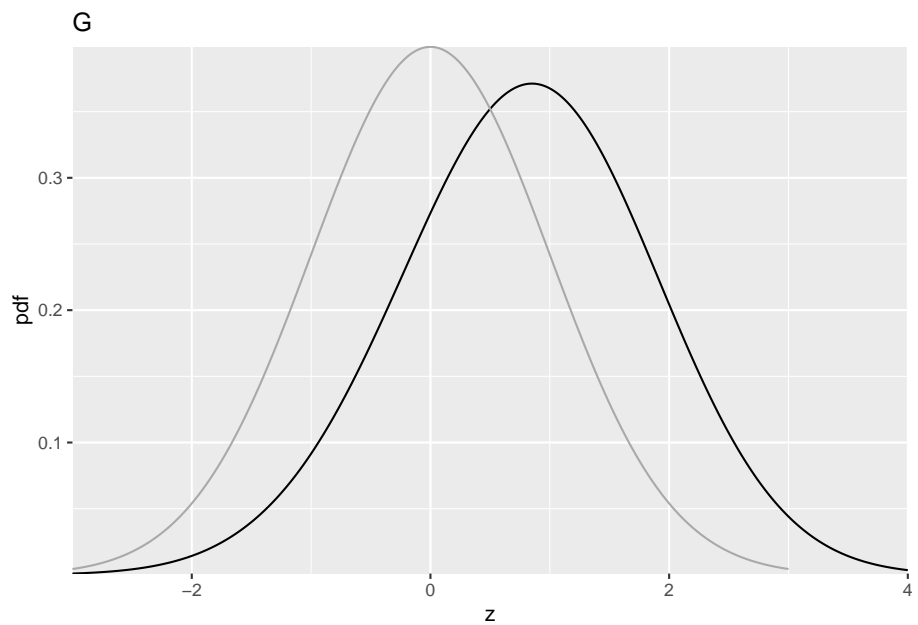
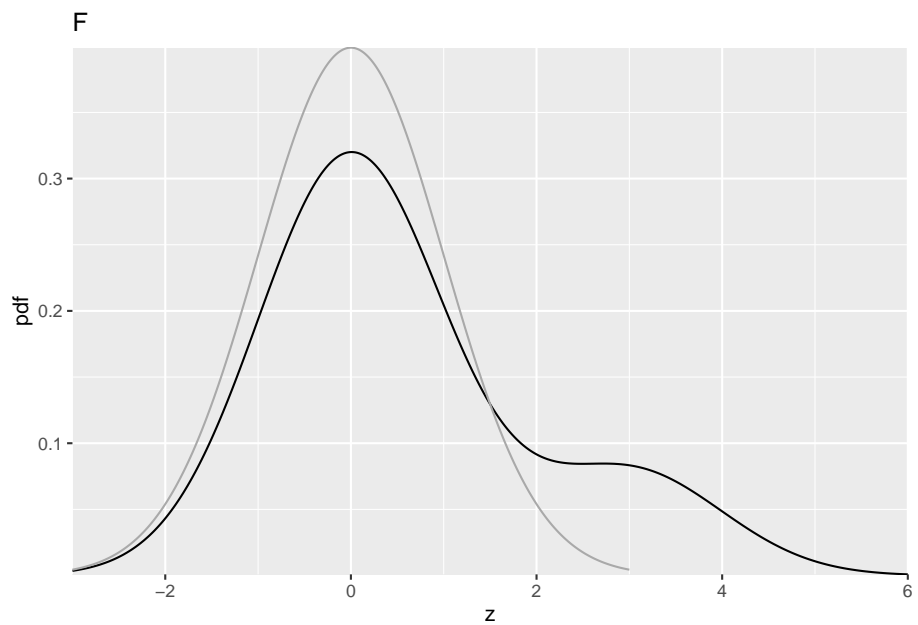
### 5.3 Comments

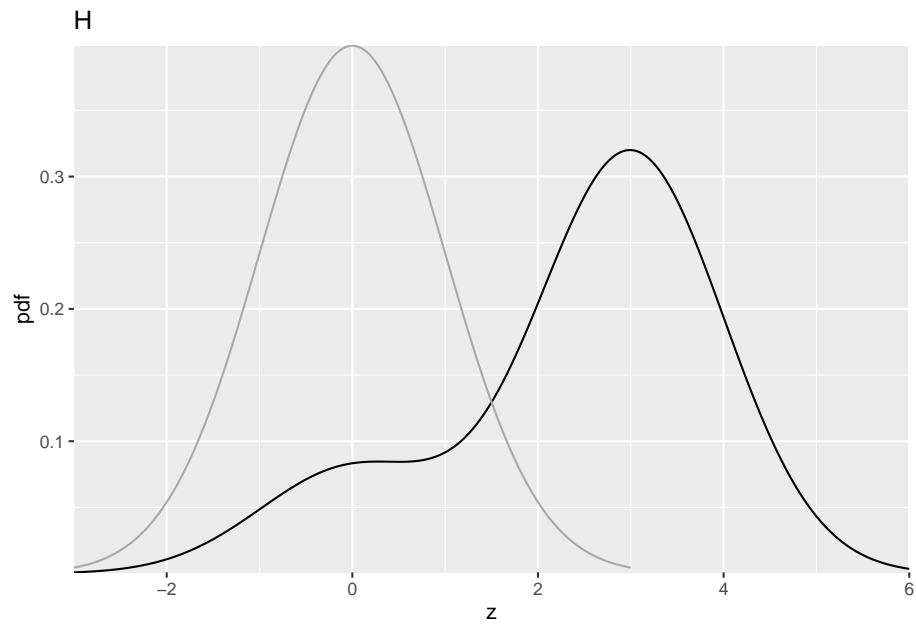
Plots A - D show ROC curves predicted by the CBM model; the corresponding values of the  $\mu$  and  $\alpha$  parameters are indicated above the plots. For small  $\mu$  and/or  $\alpha$  the curve approaches the chance diagonal, consistent with the notion that if the lesion is not visible, performance can be no better than chance level.

### 5.4 pdf plots

```
#> Fig. E : mu = 1 , alpha = 0.2  
#> Fig. F : mu = 3 , alpha = 0.2  
#> Fig. G : mu = 1 , alpha = 0.8  
#> Fig. H : mu = 3 , alpha = 0.8
```





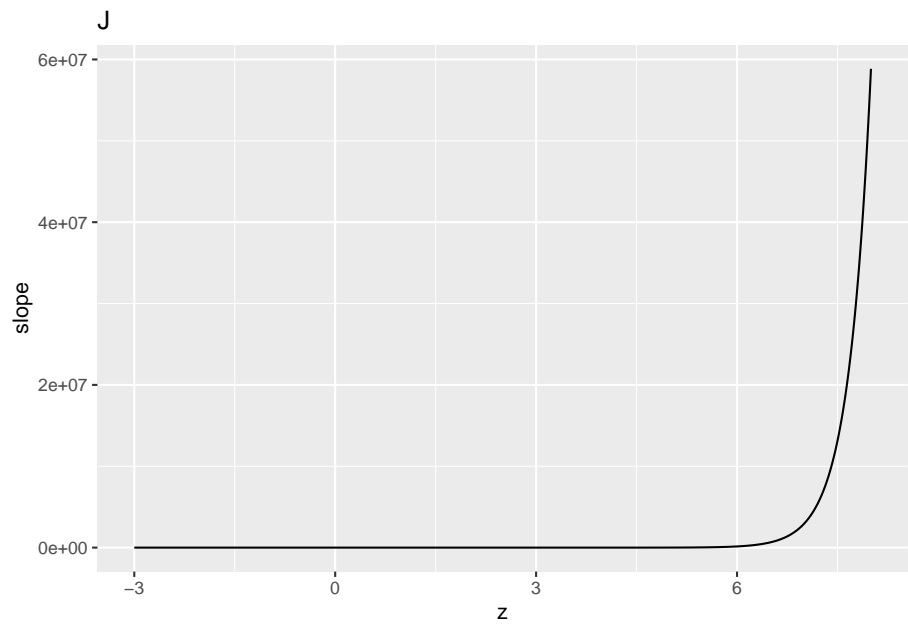
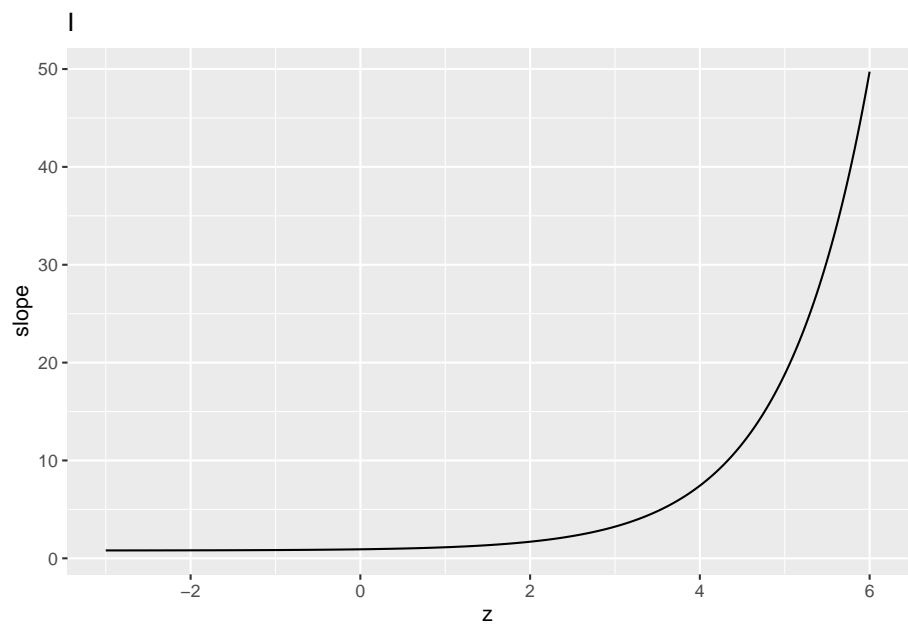


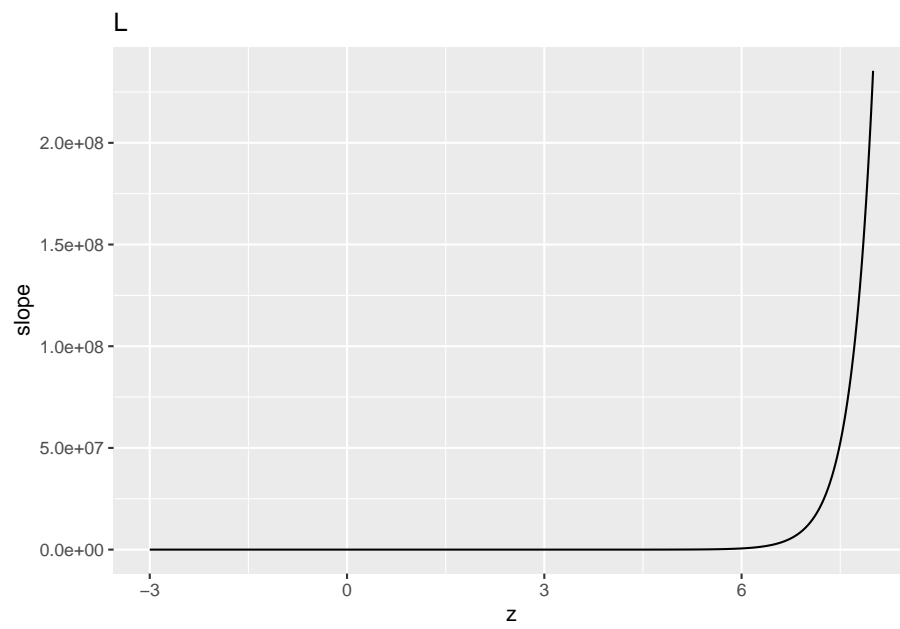
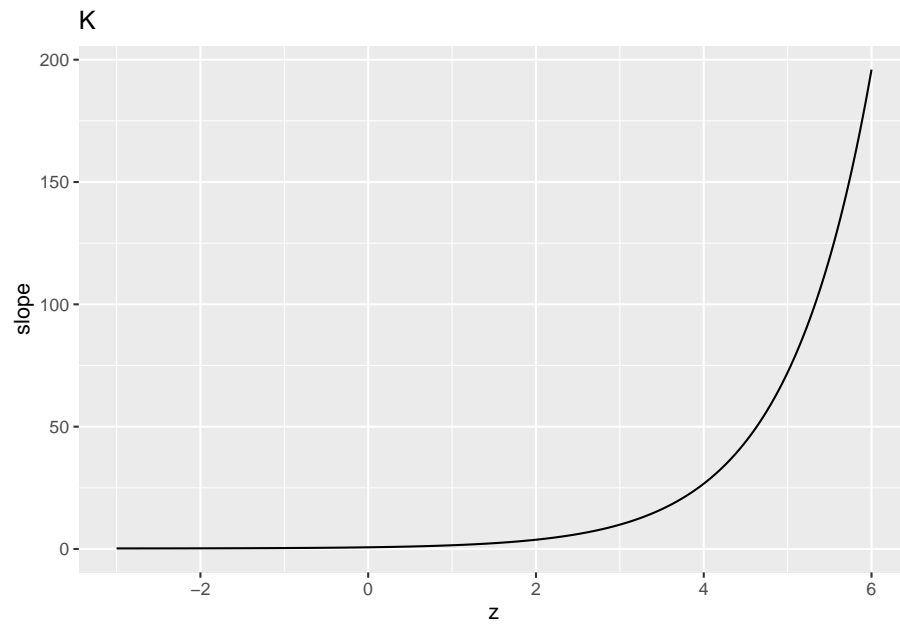
## 5.5 Comments

The dark line is the diseased distribution. The grey line is the non-diseased distribution. The bimodal diseased distribution is clearly evident in plots F and H.

## 5.6 likelihood ratio plots

```
#> Fig. I : mu = 1 , alpha = 0.2  
#> Fig. J : mu = 3 , alpha = 0.2  
#> Fig. K : mu = 1 , alpha = 0.8  
#> Fig. L : mu = 3 , alpha = 0.8
```







## 5.7 Comments

Close examination of the region near the flat part shows it does not plateau at zero; rather the minimum is at  $1 - \alpha$ , explaining the non-zero limiting slope of the predicted curve near  $(1, 1)$ .



## Chapter 6

# ROI paradigm data

### 6.1 Introduction; this vignette is under construction!

- In the region-of-interest (ROI) paradigm (Obuchowski, 1997, Obuchowski et al. (2000)) each case is regarded as consisting of  $Q_k$  ( $Q_k \geq 1$ ) “quadrants” or “regions-of-interest” or ROIs, where  $k$  is the case index ( $k = 1, 2, \dots, K$ ) and  $K$  is the total number of cases (i.e., case-level non-diseased plus case-level diseased cases). Each ROI needs to be classified, by the investigator, as either ROI-level-non-diseased (i.e., it has no lesions) or ROI-level-diseased (i.e., it has at least one lesion). **Note the distinction between case-level and ROI-level truth states.** One can have ROI-level non-diseased regions in a case-level diseased case. A case-level diseased case must contain at least one ROI-level diseased region and a case-level non-diseased case cannot have any ROI-level diseased regions.
- The observer gives a single rating (in fact an ordered label) to each ROI, denoted  $R_{kr}$  ( $r = 1, 2, \dots, Q_k$ ). Here  $r$  is the ROI index and  $k$  is the case index. The rating can be an integer or quasi-continuous (e.g., 0 – 100), or a floating point value, as long as higher numbers represent greater confidence in presence of one or more lesions in the ROI.
- The ROI paradigm is not restricted to 4 or even a constant number of ROIs per case. That is the reason for the  $k$  subscript in  $Q_k$ .
- The ROI data structure is a special case of the FROC data structure, the essential difference being that the number of ratings per case is an a-priori known value, equal to  $Q_k$ .
- ROI-level non-diseased region ratings are stored in the NL field and ROI-level diseased region ratings are stored in the LL field.
- One can think of the ROI paradigm as similar to the FROC paradigm, but

with localization accuracy restricted to belonging to a region (one cannot distinguish multiple lesions within a region). Unlike the FROC paradigm, a rating *is required* for every ROI.

## 6.2 An example ROI dataset

An example simulated ROI dataset is included as `datasetROI`.

```
str(datasetROI)
#> List of 8
#> $ NL          : num [1:2, 1:5, 1:90, 1:4] 0.95 0.927 0.556 0.805 1.421 ...
#> $ LL          : num [1:2, 1:5, 1:40, 1:4] 1.57 2.31 2.3 2.34 2.34 ...
#> $ lesionVector: int [1:40] 2 3 2 2 3 3 1 2 3 3 ...
#> $ lesionID    : num [1:40, 1:4] 2 1 1 1 1 2 4 1 1 1 ...
#> $ lesionWeight: num [1:40, 1:4] 0.5 0.333 0.5 0.5 0.333 ...
#> $ dataType    : chr "ROI"
#> $ modalityID  : Named chr [1:2] "1" "2"
#> ..- attr(*, "names")= chr [1:2] "1" "2"
#> $ readerID    : Named chr [1:5] "1" "2" "3" "4" ...
#> ..- attr(*, "names")= chr [1:5] "1" "2" "3" "4" ...
datasetROI$NL[1,1,1,]
#> [1] 0.9498680 -0.0582497 -0.7763780 0.0120730
mean(datasetROI$NL[,1:50,])
#> [1] 0.1014348
datasetROI$NL[1,1,51,]
#> [1] 1.01867 0.34710 -Inf -Inf
datasetROI$lesionVector[1]
#> [1] 2
datasetROI$LL[1,1,1,]
#> [1] 1.56928 2.05945 -Inf -Inf
x <- datasetROI$LL;mean(x[is.finite(x)])
#> [1] 1.815513
```

Examination of the output reveals that:

- This is a 2-treatment 5-reader dataset, with 50 non-diseased cases and 40 diseased cases, and  $Q_k = 4$  for all  $k$ .
- For treatment 1, reader 1, case 1 (the 1st non-diseased case) the 4 ratings are 0.949868, -0.0582497, -0.776378, 0.012073. The mean of all ratings on non-diseased cases is 0.1014348.
- For treatment 1, reader 1, case 51 (the 1st diseased case) the NL ratings are 1.01867, 0.3471. There are only two finite values because this case

has two ROI-level-diseased regions, and 2 plus 2 makes for the assumed 4-regions per case. The corresponding `$lesionVector` field is 2.

- The ratings of the 2 ROI-level-diseased ROIs on this case are 1.56928, 2.05945. The mean rating over all ROI-level-diseased ROIs is 1.8155127.

### 6.3 The ROI Excel data file

- An Excel file in JAFROC format containing simulated ROI data corresponding to `datasetROI`, is included with the distribution. The first command (below) finds the location of the file and the second command reads it and saves it to a dataset object `ds`. !!!DPC!!!
- The `DfReadDataFile` function automatically recognizes that this is an *ROI* dataset. Its structure is similar to the JAFROC format Excel file, with some important differences, noted below. It contains three worksheets:

```
## fileName <- system.file(
##   "extdata", "RoiData.xlsx", package = "RJafroc", mustWork = TRUE)
## ds <- DfReadDataFile(fileName)
## ds$dataType
```

	A	B	C	D	E
1	CaseID	LesionID	Weights		
2	1	0	0		
3	2	0	0		
4	3	0	0		
5	4	0	0		
6	5	0	0		
7	6	0	0		
8	7	0	0		
9	8	0	0		
10	9	0	0		
11	10	0	0		
12	11	0	0		
13	12	0	0		
14	13	0	0		
15	14	0	0		
16	15	0	0		

	A	B	C	D	E
49	48	0	0		
50	49	0	0		
51	50	0	0		
52	51	2	0		
53	51	3	0		
54	52	1	0		
55	52	2	0		
56	52	4	0		
57	53	1	0		
58	53	2	0		
59	54	1	0		
60	54	4	0		
61	55	1	0		
62	55	3	0		
63	55	4	0		
64	56	2	0		

Figure 6.1: Fig. 1 two views of Truth worksheet

- The **Truth** worksheet, Fig. 1, indicates which cases are diseased and which are non-diseased and the number of ROI-level-diseased region on each case.
  - There are 50 non-diseased cases (labeled 1-50) under column **CaseID** and 40 diseased cases (labeled 51-90).
  - The **LesionID** field for each non-diseased case (e.g., **CaseID** = 1) is zero and there is one row per case. For diseased cases, this field has a variable number of entries, ranging from 1 to 4. As an example,

there are two rows for `CaseID = 51` in the Excel file: one with `LesionID = 2` and one with `LesionID = 3`.

- The `Weights` field is always zero (this field is not used in ROI analysis).

	A	B	C	D	E	F
	ReaderID	ModalityID	CaseID	FP_Rating		
1	1	1	1	0.949868		
2	1	1	1	-0.05825		
3	1	1	1	-0.776378		
4	1	1	1	0.012073		
5	1	1	2	-0.641182		
6	1	1	2	-0.140436		
7	1	1	2	-0.669429		
8	1	1	2	-1.15841		
9	1	1	3	0.584815		
10	1	1	3	0.799213		
11	1	1	3	-1.45574		
12	1	1	3	0.53111		
13	1	1	4	0.409021		
14	1	1	4	0.409462		
15	1	1	4	-0.304937		
16	1	1	4	1.04011		
17	1	1	5	0.244483		
18	1	1	5	0.722627		
19	1	1	5	-0.542638		

Figure 6.2: Fig. 2 two views of FP worksheet

- The FP (or NL) worksheet - this lists the ratings of ROI-level-non-diseased regions.
  - For `ReaderID = 1`, `ModalityID = 1` and `CaseID = 1` there are 4 rows, corresponding to the 4 ROI-level-non-diseased regions in this case. The corresponding ratings are 0.949868, -0.0582497, -0.776378, 0.012073. The pattern repeats for other treatments and readers, but the rating are, of course, different.
  - Each `CaseID` is represented in the FP worksheet (a rare exception could occur if a case-level diseased case has 4 diseased regions).

	A	B	C	D	E	F
	ReaderID	ModalityID	CaseID	LesionID	TP_Rating	
1	1	1	51	2	1.56928	
2	1	1	51	3	2.05845	
3	1	1	52	1	3.26529	
4	1	1	52	2	1.98797	
5	1	1	52	4	2.14102	
6	1	1	53	1	1.63172	
7	1	1	53	2	2.45575	
8	1	1	89	2	1.17085	
9	1	1	89	4	1.61856	
10	1	1	90	1	1.64283	
11	1	1	90	2	1.76386	
12	2	1	51	2	2.29811	
13	2	1	51	3	2.09581	
14	2	1	52	1	1.75994	
15	2	1	52	2	2.19357	
16	2	1	52	4	0.472727	
17	2	1	53	1	-0.691873	
18	2	1	53	2	-0.982391	

Figure 6.3: Fig. 2 TP worksheet

- The TP (or LL) worksheet - this lists the ratings of ROI-level-diseased regions.

- Because non-diseased cases generate TPs, one does not find any entry with **CaseID** = 1-50 in the TP worksheet.
- The lowest **CaseID** in the TP worksheet is 51, which corresponds to the first diseased case.
- There are two entries for this case, corresponding to the two ROI-level-diseased regions present in this case. Recall that corresponding to this **CaseID** in the **Truth** worksheet there were two entries with **LesionID** = 2 and 3. These must match the **LesionID**'s listed for this case in the TP worksheet. Complementing these two entries, in the FP worksheet for **CaseID** = 51, there are 2 entries corresponding to the two ROI-level-non-diseased regions in this case.
- One should confirm that for each diseased case the sum of the number of entries in the TP and FP worksheets is always 4.

## 6.4 Next, TBA

The next vignette illustrates significance testing for this paradigm.

## 6.5 References





## Chapter 7

# Analyzing data acquired according to the ROI paradigm

### 7.1 Introduction; this vignette is under construction!

### 7.2 Note to self (10/29/19) !!!DPC!!!

The FOM and DeLong method implementations need checking with a toy dataset.

### 7.3 Introduction

- For an ROI dataset `StSignificanceTesting()` automatically defaults to `method = "ORH"`, `covEstMethod = "DeLong"` and `FOM = "ROI"`.
- The covariance estimation method is based on the original DeLong method (DeLong et al., 1988), which is valid only for the trapezoidal AUC, i.e. ROC data, as extended by (Obuchowski, 1997) to ROI data, see formula below.
- The essential differences from conventional ROC analyses are in the definition of the ROI figure of merit, see below, and the procedure developed by (Obuchowski, 1997) for estimating the covariance matrix. Once the

covariances are known, `method = "ORH"` can be applied to perform significance testing, as described in (Obuchowski and Rockette, 1995) and (Chakraborty, 2017, Chapter 10).

## 7.4 The ROI figure of merit

Let  $X_{kr}$  denote the rating for the  $r^{\text{th}}$  **lesion-containing** ROI in the  $k^{\text{th}}$  case and let  $n_k^L$  be the total number of lesion-containing ROIs in the  $k^{\text{th}}$  case. Similarly, let  $Y_{kr}$  denote the rating for the  $r^{\text{th}}$  **lesion-free** ROI in the  $k^{\text{th}}$  case and  $n_k^N$  denote the total number of lesion-free ROIs in the  $k^{\text{th}}$  case. Let  $N_L$  denote the total number of lesion-containing ROIs in the image set and  $N_N$  denote the total number of lesion-free ROIs. These are given by:

$$N_L = \sum_k n_k^L$$

and

$$N_N = \sum_k n_k^N$$

The ROI figure of merit  $\theta$  is defined by:

$$\theta = \frac{1}{N_L N_N} \sum_k \sum_{k'} \sum_{r=1}^{n_k^L} \sum_{r'=1}^{n_{k'}^N} \psi(X_{kr}, Y_{k'r'})$$

The kernel function  $\Psi(X, Y)$  is defined by:

$$\psi(X, Y) = \begin{cases} 1 & \text{if } X < Y \\ 0.5 & \text{if } X = Y \\ 0 & \text{if } X > Y \end{cases}$$

The ROIs are *effectively regarded as mini-cases* and one calculates the FOM as the Wilcoxon statistic considering the mini-cases as actual cases. The correlations between the ratings of ROIs on the same case are accounted for in the analysis.

## 7.5 Calculation of the ROI figure of merit.

```
UtilFigureOfMerit(datasetROI, FOM = "ROI")
#>           Rdr1           Rdr2           Rdr3           Rdr4           Rdr5
#> Trt1 0.9057239 0.8842834 0.8579279 0.9350207 0.8352103
#> Trt2 0.9297186 0.9546035 0.8937652 0.9531716 0.8770076
fom <- UtilFigureOfMerit(datasetROI, FOM = "ROI")
```

- If the correct FOM is not supplied, it defaults to FOM = ROI.
- This is a 2-treatment 5-reader dataset.
- For treatment 1, reader 1 the figure of merit is 0.9057239.
- For treatment 2, reader 5 the figure of merit is 0.8770076.
- Etc.

## 7.6 Significance testing

When `dataset$dataType == "ROI"` the FOM defaults to “ROI” (meaning the above formula) and the covariance estimation method defaults to `covEstMethod = "DeLong"`.

```
ret <- StSignificanceTesting(datasetROI, FOM = "Wilcoxon")
#> ROI dataset: forcing method = `ORH`, covEstMethod = `DeLong` and FOM = `ROI`.
str(ret)
#> List of 14
#> $ fomArray          : num [1:2, 1:5] 0.906 0.93 0.884 0.955 0.858 ...
#> ..- attr(*, "dimnames")=List of 2
#> .. ..$ : chr [1:2] "Trt1" "Trt2"
#> .. ..$ : chr [1:5] "Rdr1" "Rdr2" "Rdr3" "Rdr4" ...
#> $ meanSquares       : 'data.frame': 1 obs. of 3 variables:
#> ..$ msT : num 0.00361
#> ..$ msR : num 0.00256
#> ..$ msTR: num 0.000207
#> $ varComp           : 'data.frame': 1 obs. of 6 variables:
#> ..$ varR : num 0.00108
#> ..$ varTR: num 0.000153
#> ..$ cov1 : num 0.000247
#> ..$ cov2 : num 0.000187
#> ..$ cov3 : num 0.000154
#> ..$ var : num 0.000333
#> $ FTestStatsRRRC    : 'data.frame': 1 obs. of 4 variables:
#> ..$ fRRRC : num 9.76
#> ..$ ndfRRRC: num 1
#> ..$ ddfRRRC: num 12.8
#> ..$ pRRRC : num 0.00817
#> $ ciDiffTrtRRRC     : 'data.frame': 1 obs. of 8 variables:
#> ..$ Treatment: chr "Trt1-Trt2"
#> ..$ Estimate : num -0.038
#> ..$ StdErr : num 0.0122
```

```

#> ..$ DF      : num 12.8
#> ..$ t       : num -3.12
#> ..$ PrGTt   : num 0.00817
#> ..$ CILower : num -0.0643
#> ..$ CIUpper : num -0.0117
#> $ ciAugRdrEachTrtRRRC : 'data.frame':  2 obs. of  6 variables:
#> ..$ Treatment: Factor w/ 2 levels "Trt1","Trt2": 1 2
#> ..$ Area      : num [1:2] 0.884 0.922
#> ..$ StdErr    : num [1:2] 0.0232 0.0197
#> ..$ DF        : num [1:2] 12.2 10.1
#> ..$ CILower   : num [1:2] 0.833 0.878
#> ..$ CIUpper   : num [1:2] 0.934 0.966
#> $ FTestStatsFRRC      : 'data.frame':  1 obs. of  4 variables:
#> ..$ fFRRC : num 16.6
#> ..$ ndfFRRC: num 1
#> ..$ ddfFRRC: num Inf
#> ..$ pFRRC : num 4.58e-05
#> $ ciDiffTrtFRRC       : 'data.frame':  1 obs. of  8 variables:
#> ..$ Treatment: chr "Trt1-Trt2"
#> ..$ Estimate : num -0.038
#> ..$ StdErr    : num 0.00933
#> ..$ DF        : num Inf
#> ..$ t         : num -4.08
#> ..$ PrGTt     : num 4.58e-05
#> ..$ CILower   : num -0.0563
#> ..$ CIUpper   : num -0.0197
#> $ ciAugRdrEachTrtFRRC : 'data.frame':  2 obs. of  6 variables:
#> ..$ Treatment: Factor w/ 2 levels "Trt1","Trt2": 1 2
#> ..$ Area      : num [1:2] 0.884 0.922
#> ..$ StdErr    : num [1:2] 0.0163 0.0129
#> ..$ DF        : num [1:2] Inf Inf
#> ..$ CILower   : num [1:2] 0.852 0.896
#> ..$ CIUpper   : num [1:2] 0.916 0.947
#> $ ciDiffTrtEachRdrFRRC: 'data.frame':  5 obs. of  9 variables:
#> ..$ Reader    : Factor w/ 5 levels "Rdr1","Rdr2",...: 1 2 3 4 5
#> ..$ Treatment: Factor w/ 1 level "Trt1-Trt2": 1 1 1 1 1
#> ..$ Estimate : num [1:5] -0.024 -0.0703 -0.0358 -0.0182 -0.0418
#> ..$ StdErr    : num [1:5] 0.01025 0.01448 0.01648 0.00928 0.01398
#> ..$ DF        : num [1:5] Inf Inf Inf Inf Inf
#> ..$ t         : num [1:5] -2.34 -4.86 -2.17 -1.96 -2.99
#> ..$ PrGTt     : num [1:5] 1.93e-02 1.20e-06 2.97e-02 5.05e-02 2.79e-03
#> ..$ CILower   : num [1:5] -0.0441 -0.0987 -0.0681 -0.0363 -0.0692
#> ..$ CIUpper   : num [1:5] -3.90e-03 -4.19e-02 -3.53e-03 3.88e-05 -1.44e-02
#> $ varCovEachRdr      : 'data.frame':  5 obs. of  3 variables:
#> ..$ Reader: Factor w/ 5 levels "Rdr1","Rdr2",...: 1 2 3 4 5

```

```
#> ..$ Var : num [1:5] 0.000269 0.000227 0.000481 0.000168 0.000522
#> ..$ Cov1 : num [1:5] 0.000216 0.000122 0.000345 0.000125 0.000424
#> $ FTestStatsRRFC : 'data.frame': 1 obs. of 4 variables:
#> ..$ fRRFC : num 17.5
#> ..$ ndfRRFC: num 1
#> ..$ ddfRRFC: num 4
#> ..$ pRRFC : num 0.0139
#> $ ciDiffTrtRRFC : 'data.frame': 1 obs. of 8 variables:
#> ..$ Treatment: chr "Trt1-Trt2"
#> ..$ Estimate : num -0.038
#> ..$ StdErr : num 0.00909
#> ..$ DF : num 4
#> ..$ t : num -4.18
#> ..$ PrGtT : num 0.0139
#> ..$ CILower : num -0.0633
#> ..$ CIUpper : num -0.0128
#> $ ciAvgRdrEachTrtRRFC : 'data.frame': 2 obs. of 6 variables:
#> ..$ Treatment: Factor w/ 2 levels "Trt1","Trt2": 1 2
#> ..$ Area : num [1:2] 0.884 0.922
#> ..$ StdErr : num [1:2] 0.0175 0.0157
#> ..$ DF : num [1:2] 4 4
#> ..$ CILower : num [1:2] 0.835 0.878
#> ..$ CIUpper : num [1:2] 0.932 0.965
```

- While `ret` is a list with many (22) members, their meanings should be clear from the notation. As an example:
- The variance components are given by:

```
ret$varComp
#>          varR          varTR          cov1          cov2          cov3          var
#> 1 0.001082359 0.0001526084 0.0002465125 0.0001870571 0.0001543764 0.000333119
```

### 7.6.1 RRRC analysis

```
ret$FTestStatsRRRC$fRRRC
#> [1] 9.763602
ret$FTestStatsRRRC$ndfRRRC
#> [1] 1
ret$FTestStatsRRRC$ddfRRRC
#> [1] 12.82259
ret$FTestStatsRRRC$pRRRC
#> [1] 0.008173042
```

- The F-statistic is , with `ndf` = 1 and `ddf` = , which yields a p-value of .
- The confidence interval for the reader averaged difference between the two treatments is given by:

```
ret$ciDiffTrtRRRC
#>      Treatment      Estimate      StdErr      DF      t      PrGtT      CILower
#> 1 Trt1-Trt2 -0.03802005  0.01216768  12.82259 -3.124676  0.008173042 -0.06434373
#>      CIUpper
#> 1 -0.01169636
```

- The FOM difference (treatment 1 minus 2) is -0.03802, which is significant, p-value = 0.008173, F-statistic = 9.7636016, ddf = 12.8225898. The confidence interval is (-0.0643437, -0.0116964).

### 7.6.2 FRRC analysis

```
ret$FTestStatsFRRC$fFRRC
#> [1] 16.6135
ret$FTestStatsFRRC$ndfFRRC
#> [1] 1
ret$FTestStatsFRRC$ddfFRRC
#> [1] Inf
ret$FTestStatsFRRC$pFRRC
#> [1] 4.582365e-05
```

- The F-statistic is 16.6135014, with `ndf` = 1 and `ddf` = `Inf`, which yields a p-value of  $4.5823651 \times 10^{-5}$ .
- The confidence interval for the reader averaged difference between the two treatments is given by:

```
ret$ciDiffTrtFRRC
#>      Treatment      Estimate      StdErr      DF      t      PrGtT      CILower
#> 1 Trt1-Trt2 -0.03802005  0.009327861  Inf -4.075966  4.582365e-05 -0.05630232
#>      CIUpper
#> 1 -0.01973778
```

### 7.6.3 RRFC analysis

```
ret$FTestStatsRRFC$fRRFC
#> [1] 17.48107
ret$FTestStatsRRFC$ndfRRFC
#> [1] 1
ret$FTestStatsRRFC$ddfRRFC
#> [1] 4
ret$FTestStatsRRFC$pRRFC
#> [1] 0.01390667
```

- The F-statistic is 17.4810666, with `ndf` = 1 and `ddf` = 4, which yields a p-value of 0.0139067.
- The confidence interval for the reader averaged difference between the two treatments is given by:

```
ret$ciDiffTrtRRFC
#>   Treatment   Estimate   StdErr DF      t   PrGtT   CILower
#> 1 Trt1-Trt2 -0.03802005 0.00909345  4 -4.181037 0.01390667 -0.06326751
#>      CIUpper
#> 1 -0.01277258
```

## 7.7 Summary

TBA

## 7.8 References





# Bibliography

- Chakraborty, D. P. (2017). *Observer Performance Methods for Diagnostic Imaging - Foundations, Modeling, and Applications with R-Based Examples*. CRC Press, Boca Raton, FL.
- DeLong, E. R., DeLong, D. M., and Clarke-Pearson, D. L. (1988). Comparing the areas under two or more correlated receiver operating characteristic curves: A nonparametric approach. *Biometrics*, 44:837–845.
- Metz, C. (1978). Basic principles of roc analysis. *Seminars in Nuclear Medicine*, 8(4):283–298.
- Obuchowski, N. A. (1997). Nonparametric analysis of clustered roc curve data. *Biometrics*, 53:567–578.
- Obuchowski, N. A., Lieber, M. L., and Powell, K. A. (2000). Data analysis for detection and localization of multiple abnormalities with application to mammography. *Acad. Radiol.*, 7(7):516–525.
- Obuchowski, N. A. and Rockette, H. (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.