RJafroc Documentation

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Contents

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 desribing 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

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

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

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

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

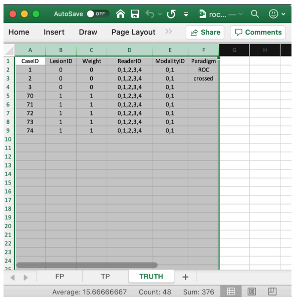
- *Toy files* are artificial small datasets intended to illustrate essential features of the data format.

- 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`).



CaseID	LesionID	Weight	ReaderID	ModalityID	Paradigm
1	0	0	0,1,2,3,4	0,1	ROC
2	0	0	0,1,2,3,4	0,1	crossed
3	0	0	0,1,2,3,4	0,1	
70	1	1	0,1,2,3,4	0,1	
71	1	1	0,1,2,3,4	0,1	
72	1	1	0,1,2,3,4	0,1	
73	1	1	0,1,2,3,4	0,1	
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 ...
```

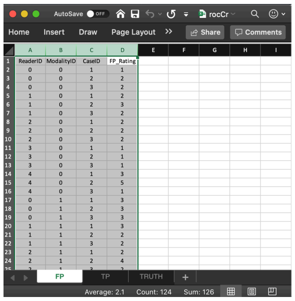
- In the above code chunk flag `newExcelFileFormat` is set to `TRUE` as otherwise columns D - F in the `Truth` worksheet are ignored and the dataset is assumed to be crossed, with `dataType` automatically determined from the contents of the FP and TP worksheets.
- Flag `newExcelFileFormat = FALSE` is 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$NL member, with dimension [2, 5, 8, 1], contains the ratings of normal cases. The extra values in the third dimension, filled with NAs, are needed for compatibility with FROC datasets, as unlike ROC, false positives are possible on diseased cases.
- The x$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.



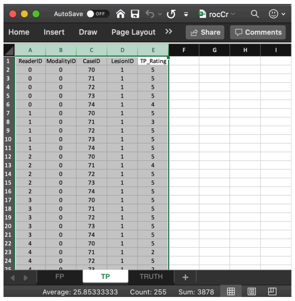
ReaderID	ModalityID	CaseID	FP_Rating
0	0	1	1
0	0	2	2
0	0	3	2
1	0	1	2
1	0	2	3
1	0	3	2
2	0	1	2
2	0	2	2
2	0	3	2
3	0	1	1
3	0	2	1
3	0	3	1
4	0	1	3
4	0	2	5
4	0	3	1
0	1	1	3
0	1	2	3
0	1	3	3
1	1	1	3
1	1	2	2
1	1	3	2
2	1	1	2
2	1	2	4

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.



	A	B	C	D	E
1	ReaderID	ModalityID	CaseID	LesionID	TP_Rating
2	0	0	70	1	5
3	0	0	71	1	5
4	0	0	72	1	5
5	0	0	73	1	5
6	0	0	74	1	4
7	1	0	70	1	5
8	1	0	71	1	3
9	1	0	72	1	5
10	1	0	73	1	5
11	1	0	74	1	5
12	2	0	70	1	5
13	2	0	71	1	4
14	2	0	72	1	5
15	2	0	73	1	5
16	2	0	74	1	5
17	3	0	70	1	5
18	3	0	71	1	5
19	3	0	72	1	5
20	3	0	73	1	5
21	3	0	74	1	5
22	4	0	70	1	5
23	4	0	71	1	2
24	4	0	72	1	5
25	4	0	73	1	2

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$NL` is an array with `dim = c(2,5,8,1)`.
  - The first dimension (2) comes from the number of modalities.
  - The second dimension (5) comes from the number of readers.
  - The third dimension (8) comes from the **total** number of cases.
  - The fourth dimension is alway 1 for an ROC dataset.
- The value of `x$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$LL` is an array with `dim = c(2,5,5,1)`.
  - The first dimension (2) comes from the number of modalities.
  - The second dimension (5) comes from the number of readers.
  - The third dimension (5) comes from the number of diseased cases.
  - The fourth dimension is alway 1 for an ROC dataset.
- The value of `x$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

FROC data format

3.1 Purpose

- Explain the data format of the input Excel file for FROC datasets.
- Explain the format of the FROC dataset.
- Explain the lesion distribution array returned by `UtilLesionDistr()`.
- Explain the lesion weights array returned by `UtilLesionWeightsDistr()`.
- Details on the FROC paradigm are in my book.

3.2 Introduction

- See my book Chakraborty (2017) for full details.
- In the Free-response Receiver Operating Characteristic (FROC) paradigm (Chakraborty, 1989) the observer searches each case for signs of **localized disease** and marks and rates localized regions that are sufficiently suspicious for disease presence.
- FROC data consists of **mark-rating pairs**, where each mark is a localized-region that was considered sufficiently suspicious for presence of a localized lesion and the rating is the corresponding confidence level.
- By adopting a proximity criterion, each mark is classified by the investigator as a lesion localization (`LL`) - if it is close to a real lesion - or a non-lesion localization (`NL`) otherwise.
- The observer assigns a rating to each region. The rating, as in the ROC paradigm, 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 a lesion at the indicated region.

3.3 The Excel data format

The Excel file has three worsheets. These are named `Truth`, `NL` or `FP` and `LL` or `TP`.

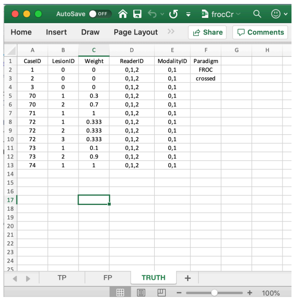
3.4 The `Truth` worksheet

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

- Since a diseased case may have more than one lesion, the first five columns contain **at least** 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, 1, 2, etc., with each 0 representing a non-diseased case, 1 representing the *first* lesion on a diseased case, 2 representing the second lesion on a diseased case, if present, and so on.
- The non-diseased cases are labeled `1`, `2` and `3`, while the diseased cases are labeled `70`, `71`, `72`, `73` and `74`.
- There are 3 non-diseased cases in the dataset (the number of 0's in the `LesionID` column).
- There are 5 diseased cases in the dataset (the number of 1's in the `LesionID` column of the `Truth` worksheet).
- There are 3 readers in the dataset (each cell in the `ReaderID` column contains `0, 1, 2`).
- There are 2 modalities in the dataset (each cell in the `ModalityID` column contains `0, 1`).
- `Weight`: floating point; 0, for each non-diseased case, or values for each diseased case that add up to unity.

- Diseased case `70` has two lesions, with `LesionID`s 1 and 2, and weights 0.3 and 0.7. Diseased case `71` has one lesion, with `LesionID` = 1, and `Weight` = 1. Diseased case `72` has three lesions, with `LesionID`s 1, 2 and 3 and weights 1/3 each. Diseased case `73` has two lesions, with `LesionID`s 1, and 2 and weights 0.1 and 0.9. Diseased case `74` has one lesion, with `LesionID` = 1 and `Weight` = 1.
- `ReaderID`: a comma-separated listing of readers, each represented by a unique **integer**, that have interpreted the case. In the example shown below each cell has the value `0, 1, 2`. **Each cell has to be text formatted. Otherwise Excel will not accept it.**
- `ModalityID`: a comma-separated listing of modalities (or treatments), each represented by a unique **integer**, that apply to each case. In the example each cell has the value `0, 1`. **Each cell has to be text formatted.**

- Paradigm: In the example shown below, the contents are FROC and crossed. It informs the software that this is an FROC dataset and the design is “crossed”, as in **Vignette #1**.



	A	B	C	D	E	F	G	H
1	CaseID	LesionID	Weight	ReaderID	ModalityID	Paradigm		
2	1	0	0	0,1,2	0,1	FROC		
3	2	0	0	0,1,2	0,1	crossed		
4	3	0	0	0,1,2	0,1			
5	70	1	0.3	0,1,2	0,1			
6	70	2	0.7	0,1,2	0,1			
7	71	1	1	0,1,2	0,1			
8	72	1	0.333	0,1,2	0,1			
9	72	2	0.333	0,1,2	0,1			
10	72	3	0.333	0,1,2	0,1			
11	73	1	0.1	0,1,2	0,1			
12	73	2	0.9	0,1,2	0,1			
13	74	1	1	0,1,2	0,1			

Figure 3.1: Truth worksheet for file inst/extdata/toyFiles/FROC/frocCr.xlsx

3.5 The structure of an FROC dataset

The example shown above corresponds to Excel file `inst/extdata/toyFiles/FROC/frocCr.xlsx` in the project directory.

```
frocCr <- system.file("extdata", "toyFiles/FROC/frocCr.xlsx",
                        package = "RJafroc", mustWork = TRUE)
x <- DfReadDataFile(frocCr, newExcelFileFormat = TRUE)
str(x)
#> List of 12
#>  $ NL           : num [1:2, 1:3, 1:8, 1:2] 1.02 2.89 2.21 3.01 2.14 ...
#>  $ LL           : num [1:2, 1:3, 1:5, 1:3] 5.28 5.2 5.14 4.77 4.66 4.87 3.01 3.27 3.31 3.19 ..
#>  $ lesionVector : int [1:5] 2 1 3 2 1
#>  $ lesionID     : num [1:5, 1:3] 1 1 1 1 1 ...
#>  $ lesionWeight : num [1:5, 1:3] 0.3 1 0.333 0.1 1 ...
#>  $ dataType     : chr "FROC"
#>  $ modalityID   : Named chr [1:2] "0" "1"
#>   ..- attr(*, "names")= chr [1:2] "0" "1"
#>  $ readerID     : Named chr [1:3] "0" "1" "2"
#>   ..- attr(*, "names")= chr [1:3] "0" "1" "2"
#>  $ design       : chr "CROSSED"
#>  $ normalCases  : int [1:3] 1 2 3
#>  $ abnormalCases: int [1:5] 70 71 72 73 74
#>  $ truthTableStr: num [1:2, 1:3, 1:8, 1:4] 1 1 1 1 1 1 1 1 1 1 ...
```

- This follows the general description in **Vignette #1**. The differences are described below.

- The `x$dataType` member indicates that this is an `FROC` dataset.
- The `x$lesionVector` member is a vector whose contents reflect the number of lesions in each diseased case, i.e., 2, 1, 3, 2, 1 in the current example.
- The `x$lesionID` member indicates the labeling of the lesions in each diseased case.

```
x$lesionID
#>      [,1] [,2] [,3]
#> [1,]    1    2 -Inf
#> [2,]    1 -Inf -Inf
#> [3,]    1    2    3
#> [4,]    1    2 -Inf
#> [5,]    1 -Inf -Inf
```

- This shows that the lesions on the first diseased case are labeled 1 and 2. The `-Inf` is a filler used to denote a missing value. The second diseased case has one lesion labeled 1. The third diseased case has three lesions labeled 1, 2 and 3, etc.
- The `lesionWeight` member is the clinical importance of each lesion. Lacking specific clinical reasons, the lesions should be equally weighted; this is *not* true for this toy dataset.

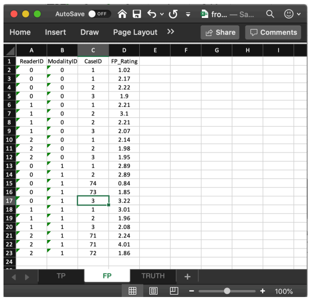
```
x$lesionWeight
#>           [,1]      [,2]      [,3]
#> [1,] 0.3000000 0.7000000      -Inf
#> [2,] 1.0000000      -Inf      -Inf
#> [3,] 0.3333333 0.3333333 0.3333333
#> [4,] 0.1000000 0.9000000      -Inf
#> [5,] 1.0000000      -Inf      -Inf
```

- The first diseased case has two lesions, the first has weight 0.3 and the second has weight 0.7. The second diseased case has one lesion with weight 1.The third diseased case has three equally weighted lesions, each with weight 1/3. Etc.

3.6 The false positive (FP) ratings

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

- It consists of 4 columns, of equal length. **The common length is unpredictable.** It could be zero if the dataset has no NL marks (a distinct possibility if the lesions are very easy to find and the modality and/or observer has high performance). All one knows is that the common length is an integer greater than or equal to zero.



	A	B	C	D
1	ReaderID	ModalityID	CaseID	FP_Rating
2	0	0	1	1.02
3	0	0	1	2.17
4	0	0	2	2.22
5	0	0	3	1.9
6	1	0	1	2.21
7	1	0	2	3.1
8	1	0	2	2.21
9	1	0	3	2.07
10	2	0	1	2.14
11	2	0	2	1.98
12	2	0	3	1.95
13	0	1	1	2.89
14	0	1	2	2.89
15	0	1	74	0.84
16	0	1	73	1.85
17	0	1	3	3.22
18	1	1	1	3.01
19	1	1	2	1.96
20	1	1	3	2.08
21	2	1	71	2.24
22	2	1	71	4.01
23	2	1	72	1.86
24				

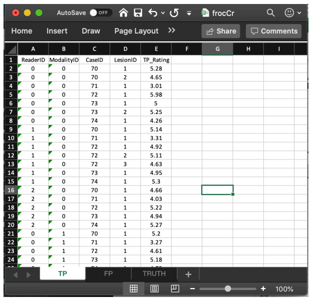
Figure 3.2: Fig. 2: FP/NL worksheet for file inst/extdata/toyFiles/FROC/frocCr.xlsx

- In the example dataset, the common length is 22.
- `ReaderID`: the reader labels: these must be `0`, `1`, or `2`, as declared in the `Truth` worksheet.
- `ModalityID`: the modality labels: must be `0` or `1`, as declared in the `Truth` worksheet.
- `CaseID`: the labels of cases with `NL` marks. In the FROC paradigm, `NL` events can occur on non-diseased **and** diseased cases.
- `FP_Rating`: the floating point ratings of `NL` marks. Each row of this worksheet yields a rating corresponding to the values of `ReaderID`, `ModalityID` and `CaseID` for that row.
- For `ModalityID` 0, `ReaderID` 0 and `CaseID` 1 (the first non-diseased case declared in the `Truth` worksheet), there is a single `NL` mark that was rated 1.02, corresponding to row 2 of the `FP` worksheet.
- Diseased cases with `NL` marks are also declared in the `FP` worksheet. Some examples are seen at rows 15, 16 and 21-23 of the `FP` worksheet.
- Rows 21 and 22 show that `caseID` = 71 got two `NL` marks, rated 2.24, 4.01.
- That this is the *only* case with two marks determines the length of the fourth dimension of the `x$NL` list member, 2 in the current example. Absent this case, the length would have been one.
- In general, the case with the most `NL` marks determines the length of the fourth dimension of the `x$NL` list member.
- The reader should convince oneself that the ratings in `x$NL` reflect the contents of the `FP` worksheet.

3.7 The true positive (TP) ratings

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

- This worksheet can only have diseased cases. The presence of a non-



	A	B	C	D	E
1	ReaderID	ModalityID	CaseID	LesionID	TP_Rating
2	0	0	70	1	5.28
3	0	0	70	2	4.65
4	0	0	71	1	3.01
5	0	0	72	1	5.98
6	0	0	73	1	5
7	0	0	73	2	5.25
8	0	0	74	1	4.26
9	1	0	70	1	5.14
10	1	0	71	1	3.31
11	1	0	72	1	4.92
12	1	0	72	2	5.11
13	1	0	72	3	4.63
14	1	0	73	1	4.95
15	1	0	74	1	5.3
16	2	0	70	1	4.66
17	2	0	71	1	4.03
18	2	0	72	1	5.22
19	2	0	73	1	4.94
20	2	0	74	1	5.27
21	0	1	70	1	5.2
22	0	1	71	1	3.27
23	0	1	72	1	4.61
24	0	1	73	1	5.18

Figure 3.3: Fig. 3: TP/LL worksheet for file inst/extdata/toyFiles/FROC/frocCr.xlsx

diseased case in this worksheet will generate an error.

- The common vertical length, 31 in this example, is a-priori unpredictable. Given the structure of the `Truth` worsheet for this dataset, the maximum length would be 9 times 2 times 3, assuming every lesion is marked for each modality, reader and diseased case. The 9 comes from the total number of non-zero entries in the `LesionID` column of the `Truth` worksheet.
- The fact that the length is smaller than the maximum length means that there are combinations of modality, reader and diseased cases on which some lesions were not marked.
- As an example, the first lesion in `CaseID` equal to `70` was marked (and rated 5.28) in `ModalityID 0` and `ReaderID 0`.
- The length of the fourth dimension of the `x$LL` list member, 3 in the present example, is determined by the diseased case with the most lesions in the `Truth` worksheet.
- The reader should convince oneself that the ratings in `x$LL` reflect the contents of the `TP` worksheet.

3.8 On the distribution of numbers of lesions in abnormal cases

- Consider a much larger dataset, `dataset11`, with structure as shown below:

```
x <- dataset11
str(x)
#> List of 12
#>  $ NL            : num [1:4, 1:5, 1:158, 1:4] -Inf -Inf -Inf -Inf -Inf ...
#>  $ LL            : num [1:4, 1:5, 1:115, 1:20] -Inf -Inf -Inf -Inf -Inf ...
#>  $ lesionVector  : int [1:115] 6 4 7 1 3 3 3 8 11 2 ...
#>  $ lesionID      : num [1:115, 1:20] 1 1 1 1 1 1 1 1 1 1 ...
#>  $ lesionWeight : num [1:115, 1:20] 0.167 0.25 0.143 1 0.333 ...
#>  $ dataType     : chr "FROC"
#>  $ modalityID   : Named chr [1:4] "1" "2" "3" "4"
#>   ..- attr(*, "names")= chr [1:4] "1" "2" "3" "4"
#>  $ readerID     : Named chr [1:5] "1" "2" "3" "4" ...
#>   ..- attr(*, "names")= chr [1:5] "1" "2" "3" "4" ...
#>  $ design       : chr "CROSSED"
#>  $ normalCases  : int [1:43] 6 9 14 27 62 66 70 71 83 91 ...
#>  $ abnormalCases: int [1:115] 1 2 3 5 7 8 10 11 13 17 ...
#>  $ truthTableStr: num [1:4, 1:5, 1:158, 1:21] 1 1 1 1 1 1 1 1 1 1 ...
```

- Focus for now in the 115 abnormal cases.
- The numbers of lesions in these cases is contained in `x$lesionVector`.

```
x$lesionVector
#>   [1]  6  4  7  1  3  3  3  8 11  2  4  6  2 16  5  2  8  3  4  7 11  1  4  3  4
#>  [26]  4  7  3  2  5  2  2  7  6  6  4 10 20 12  6  4  7 12  5  1  1  5  1  2  8
#>  [51]  3  1  2  2  3  2  8 16 10  1  2  2  6  3  2  2  4  6 10 11  1  2  6  2  4
#>  [76]  5  2  9  6  6  8  3  8  7  1  1  6  3  2  1  9  8  8  2  2 12  1  1  1  1
#> [101]  1  3  1  2  2  1  1  1  1  3  1  1  1  2  1
```

- For example, the first abnormal case contains 6 lesions, the second contains 4 lesions, the third contains 7 lesions, etc. and the last abnormal case contains 1 lesion.
- To get an idea of the distribution of the numbers of lesions per abnormal cases, one could interrogate this vector as shown below using the `which()` function:

```
for (el in 1:max(x$lesionVector)) cat(
  "abnormal cases with", el, "lesions = ",
  length(which(x$lesionVector == el)), "\n")
#> abnormal cases with 1 lesions =  25
#> abnormal cases with 2 lesions =  23
#> abnormal cases with 3 lesions =  13
#> abnormal cases with 4 lesions =  10
#> abnormal cases with 5 lesions =  5
#> abnormal cases with 6 lesions =  11
#> abnormal cases with 7 lesions =  6
#> abnormal cases with 8 lesions =  8
#> abnormal cases with 9 lesions =  2
#> abnormal cases with 10 lesions =  3
#> abnormal cases with 11 lesions =  3
#> abnormal cases with 12 lesions =  3
#> abnormal cases with 13 lesions =  0
#> abnormal cases with 14 lesions =  0
#> abnormal cases with 15 lesions =  0
#> abnormal cases with 16 lesions =  2
#> abnormal cases with 17 lesions =  0
#> abnormal cases with 18 lesions =  0
#> abnormal cases with 19 lesions =  0
#> abnormal cases with 20 lesions =  1
```

- This tells us that 25 cases contain 1 lesion
- Likewise, 23 cases contain 2 lesions
- Etc.

3.8.1 Definition of `lesDistr` array

- Let us ask what is the fraction of (abnormal) cases with 1 lesion, 2 lesions etc.

```
for (el in 1:max(x$lesionVector)) cat("fraction of abnormal cases with", el, "lesions =
                                              length(which(x$lesionVector == el))/leng
#> fraction of abnormal cases with 1 lesions =  0.2173913
#> fraction of abnormal cases with 2 lesions =  0.2
#> fraction of abnormal cases with 3 lesions =  0.1130435
#> fraction of abnormal cases with 4 lesions =  0.08695652
#> fraction of abnormal cases with 5 lesions =  0.04347826
#> fraction of abnormal cases with 6 lesions =  0.09565217
#> fraction of abnormal cases with 7 lesions =  0.05217391
#> fraction of abnormal cases with 8 lesions =  0.06956522
#> fraction of abnormal cases with 9 lesions =  0.0173913
#> fraction of abnormal cases with 10 lesions =  0.02608696
#> fraction of abnormal cases with 11 lesions =  0.02608696
#> fraction of abnormal cases with 12 lesions =  0.02608696
#> fraction of abnormal cases with 13 lesions =  0
#> fraction of abnormal cases with 14 lesions =  0
#> fraction of abnormal cases with 15 lesions =  0
#> fraction of abnormal cases with 16 lesions =  0.0173913
#> fraction of abnormal cases with 17 lesions =  0
#> fraction of abnormal cases with 18 lesions =  0
#> fraction of abnormal cases with 19 lesions =  0
#> fraction of abnormal cases with 20 lesions =  0.008695652
```

- This tells us that fraction 0.217 of (abnormal) cases contain 1 lesion
- And fraction 0.2 of (abnormal) cases contain 2 lesions
- Etc.

- This information is contained the the `lesDistr` array
- It is coded in the `Utility` function `UtilLesionDistr()`

```
lesDistr <- UtilLesionDistr(x)
lesDistr
#>       [,1]        [,2]
#>  [1,]    1 0.217391304
#>  [2,]    2 0.200000000
#>  [3,]    3 0.113043478
#>  [4,]    4 0.086956522
#>  [5,]    5 0.043478261
#>  [6,]    6 0.095652174
#>  [7,]    7 0.052173913
#>  [8,]    8 0.069565217
#>  [9,]    9 0.017391304
#> [10,]   10 0.026086957
#> [11,]   11 0.026086957
#> [12,]   12 0.026086957
#> [13,]   16 0.017391304
#> [14,]   20 0.008695652
```

- The `UtilLesionDistr()` function returns an array with two columns and number of rows equal to the number of distinct values of lesions per case.
- The first column contains the number of distinct values of lesions per case, 14 in the current example.
- The second column contains the fraction of diseased cases with the number of lesions indicated in the first column.
- The second column must sum to unity

```
sum(UtilLesionDistr(x)[,2])
#> [1] 1
```

- The lesion distribution array will come in handy when it comes to predicting the operating characteristics from using the Radiological Search Model (RSM), as detailed in Chapter 17 of my book.

3.9 Definition of `lesWghtDistr` array

- This is returned by `UtilLesionWeightsDistr()`.
- This contains the same number of rows as `lesDistr`.
- The number of columns is one plus the number of rows as `lesDistr`.
- The first column contains the number of distinct values of lesions per case, 14 in the current example.

- The second column contains the weights of cases with number of lesions per case corresponding to row 1.
- The third column contains the weights of cases with number of lesions per case corresponding to row 2.
- Etc.
- Missing values are filled with `-Inf`.

```
lesWghtDistr <- UtilLesionWeightsDistr(x)
cat("dim(lesDistr) =", dim(lesDistr),"\n")
#> dim(lesDistr) = 14 2
cat("dim(lesWghtDistr) =", dim(lesWghtDistr),"\n")
#> dim(lesWghtDistr) = 14 21
cat("lesWghtDistr = \n\n")
#> lesWghtDistr =
lesWghtDistr
#>       [,1]       [,2]       [,3]       [,4]       [,5]       [,6]       [,7]
#>  [1,]    1 1.00000000       -Inf       -Inf       -Inf       -Inf       -Inf
#>  [2,]    2 0.50000000 0.50000000       -Inf       -Inf       -Inf       -Inf
#>  [3,]    3 0.33333333 0.33333333 0.33333333       -Inf       -Inf       -Inf
#>  [4,]    4 0.25000000 0.25000000 0.25000000 0.25000000       -Inf       -Inf
#>  [5,]    5 0.20000000 0.20000000 0.20000000 0.20000000 0.20000000       -Inf
#>  [6,]    6 0.16666667 0.16666667 0.16666667 0.16666667 0.16666667 0.16666667
#>  [7,]    7 0.14285714 0.14285714 0.14285714 0.14285714 0.14285714 0.14285714
#>  [8,]    8 0.12500000 0.12500000 0.12500000 0.12500000 0.12500000 0.12500000
#>  [9,]    9 0.11111111 0.11111111 0.11111111 0.11111111 0.11111111 0.11111111
#> [10,]   10 0.10000000 0.10000000 0.10000000 0.10000000 0.10000000 0.10000000
#> [11,]   11 0.09090909 0.09090909 0.09090909 0.09090909 0.09090909 0.09090909
#> [12,]   12 0.08333333 0.08333333 0.08333333 0.08333333 0.08333333 0.08333333
#> [13,]   16 0.06250000 0.06250000 0.06250000 0.06250000 0.06250000 0.06250000
#> [14,]   20 0.05000000 0.05000000 0.05000000 0.05000000 0.05000000 0.05000000
#>             [,8]       [,9]      [,10]      [,11]      [,12]      [,13]  [,14]
#>  [1,]       -Inf       -Inf       -Inf       -Inf       -Inf       -Inf   -Inf
#>  [2,]       -Inf       -Inf       -Inf       -Inf       -Inf       -Inf   -Inf
#>  [3,]       -Inf       -Inf       -Inf       -Inf       -Inf       -Inf   -Inf
#>  [4,]       -Inf       -Inf       -Inf       -Inf       -Inf       -Inf   -Inf
#>  [5,]       -Inf       -Inf       -Inf       -Inf       -Inf       -Inf   -Inf
#>  [6,]       -Inf       -Inf       -Inf       -Inf       -Inf       -Inf   -Inf
#>  [7,] 0.14285714       -Inf       -Inf       -Inf       -Inf       -Inf   -Inf
#>  [8,] 0.12500000 0.12500000       -Inf       -Inf       -Inf       -Inf   -Inf
#>  [9,] 0.11111111 0.11111111 0.11111111       -Inf       -Inf       -Inf   -Inf
#> [10,] 0.10000000 0.10000000 0.10000000 0.10000000       -Inf       -Inf   -Inf
#> [11,] 0.09090909 0.09090909 0.09090909 0.09090909 0.09090909       -Inf   -Inf
#> [12,] 0.08333333 0.08333333 0.08333333 0.08333333 0.08333333 0.08333333   -Inf
#> [13,] 0.06250000 0.06250000 0.06250000 0.06250000 0.06250000 0.06250000 0.0625
#> [14,] 0.05000000 0.05000000 0.05000000 0.05000000 0.05000000 0.05000000 0.0500
#>        [,15]  [,16]  [,17] [,18] [,19] [,20] [,21]
#>  [1,]   -Inf   -Inf   -Inf  -Inf  -Inf  -Inf  -Inf
#>  [2,]   -Inf   -Inf   -Inf  -Inf  -Inf  -Inf  -Inf
#>  [3,]   -Inf   -Inf   -Inf  -Inf  -Inf  -Inf  -Inf
#>  [4,]   -Inf   -Inf   -Inf  -Inf  -Inf  -Inf  -Inf
#>  [5,]   -Inf   -Inf   -Inf  -Inf  -Inf  -Inf  -Inf
#>  [6,]   -Inf   -Inf   -Inf  -Inf  -Inf  -Inf  -Inf
#>  [7,]   -Inf   -Inf   -Inf  -Inf  -Inf  -Inf  -Inf
#>  [8,]   -Inf   -Inf   -Inf  -Inf  -Inf  -Inf  -Inf
#>  [9,]   -Inf   -Inf   -Inf  -Inf  -Inf  -Inf  -Inf
#> [10,]   -Inf   -Inf   -Inf  -Inf  -Inf  -Inf  -Inf
#> [11,]   -Inf   -Inf   -Inf  -Inf  -Inf  -Inf  -Inf
#> [12,]   -Inf   -Inf   -Inf  -Inf  -Inf  -Inf  -Inf
#> [13,] 0.0625 0.0625 0.0625  -Inf  -Inf  -Inf  -Inf
#> [14,] 0.0500 0.0500 0.0500  0.05  0.05  0.05  0.05
```

- Row 3 corresponds to 3 lesions per case and the weights are 1/3, 1/3 and 1/3.
- Row 13 corresponds to 16 lesions per case and the weights are 0.06250000, 0.06250000, …, repeated 13 times.
- Note that the number of rows is less than the maximum number of lesions per case (20).
- This is because some configurations of lesions per case (e.g., cases with 13 lesions per case) do not occur in this dataset.

3.10 Summary

- The FROC dataset has far less regularity in structure as compared to an ROC dataset.
- The length of the first dimension of either `x$NL` or `x$LL` list members is the total number of modalities, 2 in the current example.
- The length of the second dimension of either `x$NL` or `x$LL` list members is the total number of readers, 3 in the current example.
- The length of the third dimension of `x$NL` is the total number of cases, 8 in the current example. The first three positions account for `NL` marks on non-diseased cases and the remaining 5 positions account for `NL` marks on diseased cases.
- The length of the third dimension of `x$LL` is the total number of diseased cases, 5 in the current example.
- The length of the fourth dimension of `x$NL` is determined by the case (diseased or non-diseased) with the most `NL` marks, 2 in the current example.
- The length of the fourth dimension of `x$LL` is determined by the diseased case with the most lesions, 3 in the current example.

3.11 References

Chapter 4

ROC split plot data format

4.1 Introduction

- The purpose of this vignette is to explain the data format of the input Excel file for an ROC *split-plot* dataset.
- In a split-plot dataset each reader interprets a *different* sub-set of cases in all modalities, i.e., the cases interpreted by different readers have no overlap.
- Each sub-set of cases can have different numbers of non-diseased and diseased cases.
- The example below assumes the same numbers of non-diseased and diseased cases.
- The data format has been extended to `NewFormat` to allow such datasets.

4.2 The Excel data format

As before,the Excel file has three worsheets named `Truth`, `NL` or `FP` and `LL` or `TP`. The Excel file corresponding to the example that follows is `inst/extdata/toyFiles/ROC/rocSp.xlsx`.

4.3 The `Truth` worksheet

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

- The first five columns contain as many rows as there are cases in the dataset.

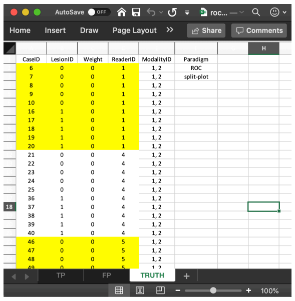
- `CaseID`: unique **integers**, one per case, representing the cases in the dataset.
- `LesionID`: integers 0, representing non-diseased cases and 1 representing the diseased cases.
- The `ReaderID` column is a listing of readers each represented by a **unique string**. Note that, unlike the crossed design, the `ReaderID` column has *single values*. **Each cell has to be text formatted.**
- The non-diseased cases interpreted by reader with `ReaderID` value `1` are labeled `6`, `7`, `8`, `9` and `10`, each with `LesionID` value `0`.
- The diseased cases interpreted by this reader are labeled `16`, `17`, `18`, `19` and `20`, each with `LesionID` value `1`.

- The second reader, with `ReaderID` value `4`, interprets five non-diseased cases labeled `21`, `22`, `23`, `24` and `25`, each with `LesionID` value `0`, and five diseased cases labeled `36`, `37`, `38`, `39` and `40`, each with `LesionID` value `1`.

- The third reader, with ReaderID value `5`, interprets five non-diseased cases labeled `46`, `47`, `48`, `49` and `50`, each with `LesionID` value `0` and five diseased cases labeled `51`, `52`, `53`, `54` and `55`, each with `LesionID` value `1`.

- `Weight`: floating point value 0 - this is not used for ROC data.

- `ModalityID`: a comma-separated listing of modalities, each represented by a **unique string**. In the example shown below each cell has the value `1, 2`. **Each cell has to be text formatted.**
- `Paradigm`: In the example shown in this vignette, the contents are `ROC` and `split-plot`.



CaseID	LesionID	Weight	ReaderID	ModalityID	Paradigm
6	0	0	1	1, 2	ROC
7	0	0	1	1, 2	split-plot
8	0	0	1	1, 2	
9	0	0	1	1, 2	
10	0	0	1	1, 2	
16	1	0	1	1, 2	
17	1	0	1	1, 2	
18	1	0	1	1, 2	
19	1	0	1	1, 2	
20	1	0	1	1, 2	
21	0	0	4	1, 2	
22	0	0	4	1, 2	
23	0	0	4	1, 2	
24	0	0	4	1, 2	
25	0	0	4	1, 2	
36	1	0	4	1, 2	
37	1	0	4	1, 2	
38	1	0	4	1, 2	
39	1	0	4	1, 2	
40	1	0	4	1, 2	
46	0	0	5	1, 2	
47	0	0	5	1, 2	
48	0	0	5	1, 2	
49	0	0	5	1, 2	

Figure 4.1: Fig. 1: Truth worksheet for file inst/extdata/toyFiles/ROC/rocSp.xlsx

4.4 The structure of the ROC split plot dataset

- The example shown in Fig. 1 corresponds to Excel file `inst/extdata/toyFiles/ROC/rocSp.xlsx` in the project directory.

```
rocSp <- system.file("extdata", "toyFiles/ROC/rocSp.xlsx",
                        package = "RJafroc", mustWork = TRUE)
x <- DfReadDataFile(rocSp, newExcelFileFormat = TRUE)
str(x)
#> List of 12
#>  $ NL           : num [1:2, 1:3, 1:30, 1] 1 1 -Inf -Inf -Inf ...
#>  $ LL           : num [1:2, 1:3, 1:15, 1] 5 2.3 -Inf -Inf -Inf ...
#>  $ lesionVector : int [1:15] 1 1 1 1 1 1 1 1 1 1 ...
#>  $ lesionID     : num [1:15, 1] 1 1 1 1 1 1 1 1 1 1 ...
#>  $ lesionWeight : num [1:15, 1] 1 1 1 1 1 1 1 1 1 1 ...
#>  $ dataType     : chr "ROC"
#>  $ modalityID   : Named chr [1:2] "1" "2"
#>   ..- attr(*, "names")= chr [1:2] "1" "2"
#>  $ readerID     : Named chr [1:3] "1" "4" "5"
#>   ..- attr(*, "names")= chr [1:3] "1" "4" "5"
#>  $ design       : chr "SPLIT-PLOT"
#>  $ normalCases  : int [1:15] 6 7 8 9 10 21 22 23 24 25 ...
#>  $ abnormalCases: int [1:15] 16 17 18 19 20 36 37 38 39 40 ...
#>  $ truthTableStr: num [1:2, 1:3, 1:30, 1:2] 1 1 NA NA NA NA 1 1 NA NA ...
```

- `DfReadDataFile()` flag `newExcelFileFormat` **must** be set to `TRUE` for split plot data.
- The dataset object `x` is a `list` variable with 12 members.
- There are 15 diseased cases in the dataset (the number of 1's in the `LesionID` column of the `Truth` worksheet) and 15 non-diseased cases (the number of 0's in the `LesionID` column).
- `x$NL`, with dimension [2, 3, 30, 1], contains the ratings of normal cases. The extra values in the third dimension, filled with `NA`s, are needed for compatibility with FROC datasets.
- `x$LL`, with dimension [2, 3, 15, 1], contains the ratings of abnormal cases.
- The `x$lesionVector` member is a vector with 15 ones representing the 15 diseased cases in the dataset.
- The `x$lesionID` member is an array with 15 ones (this member is needed for compatibility with FROC datasets).
- The `x$lesionWeight` member is an array with 15 ones (this member is needed for compatibility with FROC datasets).
- The `dataType` member is ROC which specifies the data collection method ("ROC", "FROC", "LROC" or "ROI").
- The `x$modalityID` member is a vector with two elements `"1"` and `"2"`, naming the two modalities.

- The `x$readerID` member is a vector with three elements `"1"`, `"4"` and `"5"`, naming the three modalities.
- The `x$design` member is SPLIT-PLOT; specifies the dataset design, which can be either "CROSSED" or "SPLIT-PLOT".
- The `x$normalCases` member lists the names of the normal cases, 6, 7, 8, 9, 10, 21, 22, 23, 24, 25, 46, 47, 48, 49, 50.
- The `x$abnormalCases` member lists the names of the abnormal cases, 16, 17, 18, 19, 20, 36, 37, 38, 39, 40, 51, 52, 53, 54, 55.
- The `x$truthTableStr` member quantifies the structure of the dataset, as explained next. **It is used in the `DfReadDataFile()` function to check for data entry errors.**

4.5 The `truthTableStr` member

- This is a `2 x 3 x 30 x 2` array, i.e., I x J x K x (maximum number of lesions per case plus 1). The `plus 1` is needed to accommodate normal cases with `lesionID` = 0. [Zero is not a valid array subscript in `R`.]
- Each entry in this array is either `1`, meaning the corresponding interpretation exists, or `NA`, meaning the corresponding interpretation does not exist.
- For example, `x$truthTableStr[1,1,1,1]` is 1. This means that an interpretation exists for the first treatment (`modalityID` = 1), first reader (`readerID` = 1) and first (normal) case (`caseID` = 6 and `lesionID` = 0). This example corresponds to row 2 in the `TRUTH` worksheet.
- The following shows that the first reader interprets the first five normal cases in both modalities.

```
x$truthTableStr[,1,1:15,1]
#>      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12] [,13] [,14]
#> [1,]    1    1    1    1    1   NA   NA   NA   NA    NA    NA    NA    NA    NA
#> [2,]    1    1    1    1    1   NA   NA   NA   NA    NA    NA    NA    NA    NA
#>      [,15]
#> [1,]    NA
#> [2,]    NA
```

- In the following all elements are `NA` because normal cases correspond to lesionID = 1.

```
x$truthTableStr[,1,1:15,2]
#>      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12] [,13] [,14]
#> [1,]   NA   NA   NA   NA   NA   NA   NA   NA   NA    NA    NA    NA    NA    NA
#> [2,]   NA   NA   NA   NA   NA   NA   NA   NA   NA    NA    NA    NA    NA    NA
#>      [,15]
#> [1,]    NA
#> [2,]    NA
```

- The following shows that the second reader interprets the next group of five normal cases, indexed 6 through 10, in both modalities.

```
x$truthTableStr[,2,1:15,1]
#>      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12] [,13] [,14]
#> [1,]   NA   NA   NA   NA   NA    1    1    1    1     1    NA    NA    NA    NA
#> [2,]   NA   NA   NA   NA   NA    1    1    1    1     1    NA    NA    NA    NA
#>      [,15]
#> [1,]    NA
#> [2,]    NA
```

- The following shows that the third reader interprets the next group of five normal cases, indexed 11 through 15, in both modalities.

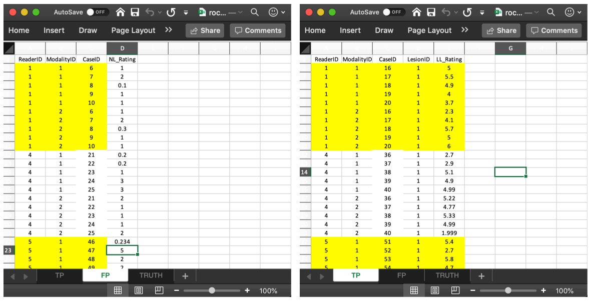
```
x$truthTableStr[,3,1:15,1]
#>      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12] [,13] [,14]
#> [1,]   NA   NA   NA   NA   NA   NA   NA   NA   NA    NA     1     1     1     1
#> [2,]   NA   NA   NA   NA   NA   NA   NA   NA   NA    NA     1     1     1     1
#>      [,15]
#> [1,]     1
#> [2,]     1
```

- The following shows that the first reader interprets the first group of five abnormal cases, indexed 16 through 20, in both modalities.

```
x$truthTableStr[,1,16:30,2]
#>      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12] [,13] [,14]
#> [1,]    1    1    1    1    1   NA   NA   NA   NA    NA    NA    NA    NA    NA
#> [2,]    1    1    1    1    1   NA   NA   NA   NA    NA    NA    NA    NA    NA
#>      [,15]
#> [1,]    NA
#> [2,]    NA
```

- In the following all elements are `NA` because abnormal cases correspond to `lesionID` = 2.

```
x$truthTableStr[,1,16:30,1]
#>      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12] [,13] [,14]
#> [1,]   NA   NA   NA   NA   NA   NA   NA   NA   NA    NA    NA    NA    NA    NA
#> [2,]   NA   NA   NA   NA   NA   NA   NA   NA   NA    NA    NA    NA    NA    NA
#>       [,15]
#> [1,]     NA
#> [2,]     NA
```



ReaderID	ModalityID	CaseID	NL_Rating
1	1	6	1
1	1	7	2
1	1	8	0.1
1	1	9	1
1	1	10	1
1	2	6	1
1	2	7	2
1	2	8	0.3
1	2	9	1
1	2	10	1
4	1	21	0.2
4	1	22	0.2
4	1	23	1
4	1	24	3
4	1	25	3
4	2	21	2
4	2	22	1
4	2	23	1
4	2	24	1
4	2	25	2
5	1	46	0.234
5	1	47	5
5	1	48	2
5	1	49	2

ReaderID	ModalityID	CaseID	LesionID	LL_Rating
1	1	16	1	5
1	1	17	1	5.5
1	1	18	1	4.9
1	1	19	1	4
1	1	20	1	3.7
1	2	16	1	2.3
1	2	17	1	4.1
1	2	18	1	5.7
1	2	19	1	5
1	2	20	1	6
4	1	36	1	2.7
4	1	37	1	2.9
4	1	38	1	5.1
4	1	39	1	4.9
4	1	40	1	4.99
4	2	36	1	5.22
4	2	37	1	4.77
4	2	38	1	5.33
4	2	39	1	4.99
4	2	40	1	1.999
5	1	51	1	5.4
5	1	52	1	2.7
5	1	53	1	5.8
5	1	54	1	4.7

Figure 4.2: Fig. 2 FP/TP worksheets; LEFT=FP, (b) RIGHT=TP

4.6 The false positive (FP) ratings

- These are found in the FP or NL worksheet, see Fig. 2, left panel.
- This worksheet has the ratings of non-diseased cases.
- The common vertical length is 30 in this example (2 modalities times 3 readers times 5 non-diseased cases per reader).
- ReaderID: the reader labels: these must be from 1, 4 or 5, as declared in the Truth worksheet.
- ModalityID: the modality labels: 1 or 2, as declared in the Truth worksheet.
- CaseID: the labels of non-diseased cases. Each CaseID - ReaderID combination must be consistent with that declared in the Truth worsheet.

- NL_Rating: the floating point ratings of non-diseased cases. Each row of this worksheet yields a rating corresponding to the values of ReaderID, ModalityID and CaseID for that row.

```
x$NL[,1,1:15,1]
#>      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12] [,13] [,14]
#> [1,]    1    2  0.1    1    1 -Inf -Inf -Inf -Inf  -Inf  -Inf  -Inf  -Inf  -Inf
#> [2,]    1    2  0.3    1    1 -Inf -Inf -Inf -Inf  -Inf  -Inf  -Inf  -Inf  -Inf
#>      [,15]
#> [1,]  -Inf
#> [2,]  -Inf
x$NL[,2,1:15,1]
```

```
#>      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12] [,13] [,14]
#> [1,] -Inf -Inf -Inf -Inf -Inf  0.2  0.2    1    3     3  -Inf  -Inf  -Inf  -Inf
#> [2,] -Inf -Inf -Inf -Inf -Inf  2.0  1.0    1    1     2  -Inf  -Inf  -Inf  -Inf
#>      [,15]
#> [1,]  -Inf
#> [2,]  -Inf
x$NL[,3,1:15,1]
#>      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12] [,13] [,14]
#> [1,] -Inf -Inf -Inf -Inf -Inf -Inf -Inf -Inf -Inf  -Inf 0.234     5     2     2
#> [2,] -Inf -Inf -Inf -Inf -Inf -Inf -Inf -Inf -Inf  -Inf 3.000     2     2     2
#>      [,15]
#> [1,]  2.00
#> [2,]  0.33
```

- The first line of the above code shows the ratings, in both modalities, of the first five non-diseased cases with `CaseIDs` `6,7,8,9,10` (indexed 1, 2, 3, 4, 5 and appearing in the first five columns) interpreted by the first reader (`ReaderID` 1).
- The second line shows the ratings, in both modalities, of the next five non-diseased cases with `CaseIDs` `21,22,23,24,25` (indexed 6, 7, 8, 9, 10and appearing in the next five columns) interpreted by the second reader (`ReaderID` 4).
- The third line shows the ratings, in both modalities, of the final five non-diseased cases with `CaseIDs` `46,47,48,49,50` (indexed 11, 12, 13, 14, 15and appearing in the final five columns) interpreted by the third reader (`ReaderID` 5).
- Values such as `x$NL[,,16:30,1]`, which are there for compatibility with FROC data, are all filled with `-Inf`.

4.7 The true positive (TP) ratings

- These are found in the `TP` or `LL` worksheet, see Fig. 2, right panel.
- This worksheet has the ratings of diseased cases.
- The common vertical length is 30 in this example (2 modalities times 3 readers times 5 diseased cases per reader).
- `ReaderID`: the reader labels: these must be from `1`, `4` or `5`, as declared in the `Truth` worksheet.
- `ModalityID`: the modality labels: `1` or `2`, as declared in the `Truth` worksheet.
- `CaseID`: the labels of diseased cases. Each `CaseID` - `ReaderID` combination must be consistent with that declared in the `Truth` worsheet.

- `LL_Rating`: the floating point ratings of diseased cases. Each row of this worksheet yields a rating corresponding to the values of `ReaderID`, `ModalityID` and `CaseID` for that row.

```
x$LL[,1,1:15,1]
#>      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12] [,13] [,14]
#> [1,]  5.0  5.5  4.9    4  3.7 -Inf -Inf -Inf -Inf  -Inf  -Inf  -Inf  -Inf  -Inf
#> [2,]  2.3  4.1  5.7    5  6.0 -Inf -Inf -Inf -Inf  -Inf  -Inf  -Inf  -Inf  -Inf
#>      [,15]
#> [1,]  -Inf
#> [2,]  -Inf
x$LL[,2,1:15,1]
#>      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12] [,13] [,14]
#> [1,] -Inf -Inf -Inf -Inf -Inf 2.70 2.90 5.10 4.90 4.990  -Inf  -Inf  -Inf  -Inf
#> [2,] -Inf -Inf -Inf -Inf -Inf 5.22 4.77 5.33 4.99 1.999  -Inf  -Inf  -Inf  -Inf
#>      [,15]
#> [1,]  -Inf
#> [2,]  -Inf
x$LL[,3,1:15,1]
#>      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12] [,13] [,14]
#> [1,] -Inf -Inf -Inf -Inf -Inf -Inf -Inf -Inf -Inf  -Inf   5.4   2.7   5.8   4.7
#> [2,] -Inf -Inf -Inf -Inf -Inf -Inf -Inf -Inf -Inf  -Inf   5.4   2.7   5.8   4.7
#>      [,15]
#> [1,]     5
#> [2,]     5
```

- The first line of code shows the ratings, in both modalities, of the first five diseased cases with `CaseIDs` `16,17,18,19,20` (indexed 1, 2, 3, 4, 5and appearing in the first five columns) interpreted by the first reader (`ReaderID` 1).
- The second line shows the ratings, in both modalities, of the next five diseased cases with `CaseIDs` `36,37,38,39,40` (indexed 6, 7, 8, 9, 10and appearing in the next five columns) interpreted by the second reader (`ReaderID` 4).
- The third line shows the ratings, in both modalities, of the final five non-diseased cases with `CaseIDs` `51,52,53,54,55` (indexed 11, 12, 13, 14, 15and appearing in the final five columns) interpreted by the third reader (`ReaderID` 5).

4.8 Summary

- The FROC dataset has far less regularity in structure as compared to an ROC dataset.

- The length of the first dimension of either `x$NL` or `x$LL` list members is the total number of modalities, 2 in the current example.
- The length of the second dimension of either `x$NL` or `x$LL` list members is the total number of readers, 3 in the current example.
- The length of the third dimension of `x$NL` is the total number of cases, 8 in the current example. The first three positions account for `NL` marks on non-diseased cases and the remaining 5 positions account for `NL` marks on diseased cases.
- The length of the third dimension of `x$LL` is the total number of diseased cases, 5 in the current example.
- The length of the fourth dimension of `x$NL` is determined by the case (diseased or non-diseased) with the most `NL` marks, 2 in the current example.
- The length of the fourth dimension of `x$LL` is determined by the diseased case with the most lesions, 3 in the current example.

4.9 References

Chapter 5

FROC ROC DATA FORMAT SPLIT PLOT

5.1 Introduction

- The purpose of this vignette is to explain the data format of the input Excel file for an FROC *split-plot* dataset.
- In a split-plot dataset each reader interprets a sub-set of cases in all modalities.
- The cases interpreted by different readers have no overlap.
- It is assumed, for now, that each sub-set of cases has the same numbers of non-diseased and diseased cases.

5.2 The Excel data format

The Excel file has three worsheets named `Truth`, `NL` or `FP` and `LL` or `TP`.

5.3 The `Truth` worksheet

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

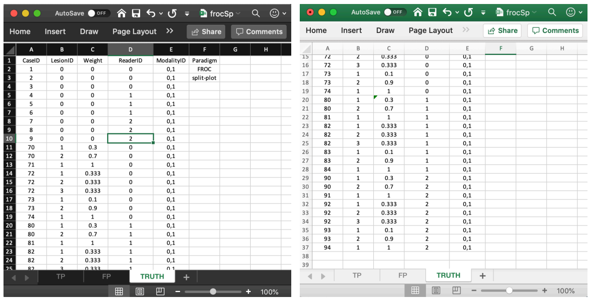
- The first five columns contain as many rows as there are non-diseased cases (9) plus total number of lesions (27) in the dataset (each row with a non-zero `LesionID` corresponds to a lesion).

- `CaseID`: unique **integers**, one per case, representing the cases in the dataset.
- `LesionID`: integers 0, 1, 2, etc., with each 0 representing a non-diseased case, 1 representing the *first* lesion on a diseased case, 2 representing the second lesion on a diseased case, if present, and so on.
- The three non-diseased cases interpreted by reader with `ReaderID` value `0` are labeled `1`, `2`, `3`, while the diseased cases interpreted by this reader are labeled `70`, `71`, `72`, `73` and `74`, with `LesionID` values ranging from 1 to 3.

- The second reader, with `ReaderID` value `1`, interprets three non-diseased cases labeled `4`, `5` and `6`, each with `LesionID` value `0`, and five diseased cases labeled `80`, `81`, `82`, `83` and `84`, with `LesionID` values ranging from 1 to 3.

- The third reader, with `ReaderID` value `2`, interprets three non-diseased cases labeled `7`, `8` and `9`, each with `LesionID` value `0` and five diseased cases labeled `90`, `91`, `92`, `93` and `94`, with `LesionID` values ranging from 1 to 3.

- `Weight`: floating point value adding upto unity for diseased cases as required for FROC data.
- `ModalityID`: a comma-separated listing of modalities, each represented by a unique **integer**. In the example shown below each cell has the value `0, 1`. **Each cell has to be text formatted.**
- `Paradigm`: In the example shown below, the contents are `FROC` and `split-plot`.



	A	B	C	D	E	F	G	H
1	CaseID	LesionID	Weight	ReaderID	ModalityID	Paradigm		
2	1	0	0	0	0,1	FROC		
3	2	0	0	0	0,1	split-plot		
4	3	0	0	0	0,1			
5	4	0	0	1	0,1			
6	5	0	0	1	0,1			
7	6	0	0	1	0,1			
8	7	0	0	2	0,1			
9	8	0	0	2	0,1			
10	9	0	0	2	0,1			
11	70	1	0.3	0	0,1			
12	70	2	0.7	0	0,1			
13	71	1	1	0	0,1			
14	72	1	0.333	0	0,1			
15	72	2	0.333	0	0,1			
16	72	3	0.333	0	0,1			
17	73	1	0.1	0	0,1			
18	73	2	0.9	0	0,1			
19	74	1	1	0	0,1			
20	80	1	0.3	1	0,1			
21	80	2	0.7	1	0,1			
22	81	1	1	1	0,1			
23	82	1	0.333	1	0,1			
24	82	2	0.333	1	0,1			
25	82	3	0.333	1	0,1			
26	83	1	0.1	1	0,1			
27	83	2	0.9	1	0,1			
28	84	1	1	1	0,1			
29	90	1	0.3	2	0,1			
30	90	2	0.7	2	0,1			
31	91	1	1	2	0,1			
32	92	1	0.333	2	0,1			
33	92	2	0.333	2	0,1			
34	92	3	0.333	2	0,1			
35	93	1	0.1	2	0,1			
36	93	2	0.9	2	0,1			
37	94	1	1	2	0,1			
38								
39								

Figure 5.1: Two views of Truth worksheet for file frocSp.xlsx

5.4 The structure of the FROC split plot dataset

The example shown in Fig. 1 corresponds to Excel file `inst/extdata/toyFiles/FROC/frocSp.xlsx` in the project directory.

```
frocSp <- system.file("extdata", "toyFiles/FROC/frocSp.xlsx",
                        package = "RJafroc", mustWork = TRUE)
x <- DfReadDataFile(frocSp, newExcelFileFormat = TRUE)
str(x)
#> List of 12
#>  $ NL           : num [1:2, 1:3, 1:24, 1:3] 1.02 2.89 -Inf -Inf -Inf ...
#>  $ LL           : num [1:2, 1:3, 1:15, 1:3] 5.28 5.2 -Inf -Inf -Inf ...
#>  $ lesionVector : int [1:15] 2 1 3 2 1 2 1 3 2 1 ...
#>  $ lesionID     : num [1:15, 1:3] 1 1 1 1 1 1 1 1 1 1 ...
#>  $ lesionWeight : num [1:15, 1:3] 0.3 1 0.333 0.1 1 ...
#>  $ dataType     : chr "FROC"
#>  $ modalityID   : Named chr [1:2] "0" "1"
#>   ..- attr(*, "names")= chr [1:2] "0" "1"
#>  $ readerID     : Named chr [1:3] "0" "1" "2"
#>   ..- attr(*, "names")= chr [1:3] "0" "1" "2"
#>  $ design       : chr "SPLIT-PLOT"
#>  $ normalCases  : int [1:9] 1 2 3 4 5 6 7 8 9
#>  $ abnormalCases: int [1:15] 70 71 72 73 74 80 81 82 83 84 ...
#>  $ truthTableStr: num [1:2, 1:3, 1:24, 1:4] 1 1 NA NA NA NA 1 1 NA NA ...
```

- Flag `newExcelFileFormat` **must** be set to `TRUE` for split plot data.
- The dataset object `x` is a `list` variable with 12 members.
- Note that the `dataType` member is FROC and the `design` member is SPLIT-PLOT.
- There are 15 diseased cases in the dataset (the number of 1's in the `LesionID` column of the `Truth` worksheet) and 9 non-diseased cases (the number of 0's in the `LesionID` column).
- The `x$lesionVector` member is a vector with 15 ones representing the 15 diseased cases in the dataset.
- The `x$lesionID` member is a 15 x 3 array labeling the lesions in the dataset.
- The `x$lesionWeight` member is a 15 x 3 array.

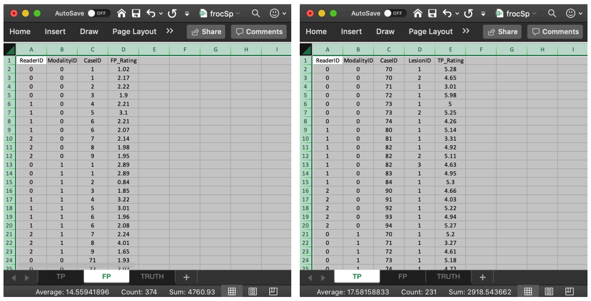
```
x$lesionVector
#>  [1] 2 1 3 2 1 2 1 3 2 1 2 1 3 2 1
x$lesionID
#>       [,1] [,2] [,3]
#>  [1,]    1    2 -Inf
#>  [2,]    1 -Inf -Inf
#>  [3,]    1    2    3
#>  [4,]    1    2 -Inf
#>  [5,]    1 -Inf -Inf
#>  [6,]    1    2 -Inf
#>  [7,]    1 -Inf -Inf
#>  [8,]    1    2    3
#>  [9,]    1    2 -Inf
#> [10,]    1 -Inf -Inf
#> [11,]    1    2 -Inf
#> [12,]    1 -Inf -Inf
#> [13,]    1    2    3
#> [14,]    1    2 -Inf
#> [15,]    1 -Inf -Inf
x$lesionWeight
#>            [,1]      [,2]      [,3]
#>  [1,] 0.3000000 0.7000000      -Inf
#>  [2,] 1.0000000      -Inf      -Inf
#>  [3,] 0.3333333 0.3333333 0.3333333
#>  [4,] 0.1000000 0.9000000      -Inf
#>  [5,] 1.0000000      -Inf      -Inf
#>  [6,] 0.3000000 0.7000000      -Inf
#>  [7,] 1.0000000      -Inf      -Inf
#>  [8,] 0.3333333 0.3333333 0.3333333
#>  [9,] 0.1000000 0.9000000      -Inf
#> [10,] 1.0000000      -Inf      -Inf
#> [11,] 0.3000000 0.7000000      -Inf
#> [12,] 1.0000000      -Inf      -Inf
#> [13,] 0.3333333 0.3333333 0.3333333
#> [14,] 0.1000000 0.9000000      -Inf
#> [15,] 1.0000000      -Inf      -Inf
```

- The `x$truthTableStr` member is a `2 x 3 x 24 x 4` array, i.e., I x J x K x (maximum number of lesions per case plus 1). The `plus 1` is needed to accommodate normal cases with `lesionID` = 0.
- Each entry in this array is either `1`, meaning the corresponding interpretation exists, or `NA`, meaning the corresponding interpretation does not exist.
- For example, `x$truthTableStr[1,1,1,1]` is 1. This means that an interpretation exists for the first treatment (`modalityID` = 0), first reader (`readerID` = 0) and first (normal) case `caseID` = 1 and `lesionID` = 0. This example corresponds to row 2 in the `TRUTH` worksheet.
- `x$truthTableStr[1,1,4,1]` is NA, which means an interpretation does not exist for the first treatment, first reader and fourth (normal) case.
- However, `x$truthTableStr[1,2,4,1]` is 1, which means an interpretation does exist for the first treatment, second reader and fourth (normal) case. This example corresponds to row 5 in the `TRUTH` worksheet.

- Likewise, `x$truthTableStr[1,1,10,3]` is 1, which means an interpretation does exist for the first treatment, first reader, tenth (abnormal) case and `lesionID` = 2. This example corresponds to row 12 in the `TRUTH` worksheet.
- As an aside, in the FROC paradigm an interpretation need not yield a mark-rating pair. An interpretation means the reader was "exposed to" and had the opportunity to mark the corresponding treatment-reader-case-lesion combination.
- The reader should confirm that the contents of `x$truthTableStr` summarizes the structure of the data in the `TRUTH` worksheet.

5.5 The false positive (FP) ratings

These are found in the `FP` or `NL` worksheet, see Fig. 2.



	ReaderID	ModalityID	CaseID	FP_Rating
1	ReaderID	ModalityID	CaseID	FP_Rating
2	0	0	1	1.02
3	0	0	1	2.17
4	0	0	2	2.22
5	0	0	3	1.9
6	1	0	4	2.21
7	1	0	5	3.1
8	1	0	6	2.21
9	1	0	6	2.07
10	2	0	7	2.14
11	2	0	8	1.98
12	2	0	9	1.95
13	0	1	1	2.89
14	0	1	1	2.89
15	0	1	2	0.84
16	0	1	3	1.85
17	1	1	4	3.22
18	1	1	5	3.01
19	1	1	6	1.96
20	1	1	6	2.08
21	2	1	7	2.24
22	2	1	8	4.01
23	2	1	9	1.65
24	0	0	71	1.93
25	0	0	72	2.07

Average: 14.55941896 Count: 374 Sum: 4760.93

	ReaderID	ModalityID	CaseID	LesionID	TP_Rating
1	ReaderID	ModalityID	CaseID	LesionID	TP_Rating
2	0	0	70	1	5.28
3	0	0	70	2	4.65
4	0	0	71	1	3.01
5	0	0	72	1	5.98
6	0	0	73	1	5
7	0	0	73	2	5.25
8	0	0	74	1	4.26
9	1	0	80	1	5.14
10	1	0	81	1	3.31
11	1	0	82	1	4.92
12	1	0	82	2	5.11
13	1	0	82	3	4.63
14	1	0	83	1	4.95
15	1	0	84	1	5.3
16	2	0	90	1	4.66
17	2	0	91	1	4.03
18	2	0	92	1	5.22
19	2	0	93	1	4.94
20	2	0	94	1	5.27
21	0	1	70	1	5.2
22	0	1	71	1	3.27
23	0	1	72	1	4.61
24	0	1	73	1	5.18
25	0	1	74	1	4.72

Average: 17.58158833 Count: 231 Sum: 2918.543662

Figure 5.2: NL/FP worksheet, left, and LL/TP worksheet, right, for file frocSp.xlsx

- This worksheet has the ratings of non-diseased cases.
- The common vertical length is 30 in this example (2 modalities times 3 readers times 5 non-diseased cases per reader).
- `ReaderID`: the reader labels: these must be from `0`, `1` or `2`, as declared in the `Truth` worksheet.
- `ModalityID`: the modality labels: `0` or `1`, as declared in the `Truth` worksheet.
- `CaseID`: the labels of non-diseased cases. Each `CaseID`, `ModalityID`, `ReaderID` combination must be consistent with that declared in the `Truth` worsheet.

- `FP_Rating`: the floating point ratings of non-diseased cases. Each row of this worksheet yields a rating corresponding to the values of `ReaderID`, `ModalityID` and `CaseID` for that row. Each `CaseID`, `ModalityID`, `ReaderID` combination must be consistent with that declared in the `Truth` worsheet.

```
x$NL[,1,1:9,1]
#>      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9]
#> [1,] 1.02 2.22 1.90 -Inf -Inf -Inf -Inf -Inf -Inf
#> [2,] 2.89 0.84 1.85 -Inf -Inf -Inf -Inf -Inf -Inf
x$NL[,2,1:9,1]
#>      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9]
#> [1,] -Inf -Inf -Inf 2.21 3.10 2.21 -Inf -Inf -Inf
#> [2,] -Inf -Inf -Inf 3.22 3.01 1.96 -Inf -Inf -Inf
x$NL[,3,1:9,1]
#>      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9]
#> [1,] -Inf -Inf -Inf -Inf -Inf -Inf 2.14 1.98 1.95
#> [2,] -Inf -Inf -Inf -Inf -Inf -Inf 2.24 4.01 1.65
```

- The first line of the above code shows the ratings, in both modalities, of the first three non-diseased cases with `CaseIDs` `1,3,3` (indexed 1, 2, 3 and appearing in the first three columns) interpreted by the first reader (`ReaderID` `0`).
- The second line shows the ratings, in both modalities, of the next three non-diseased cases with `CaseIDs` `4,5,6` (indexed 4, 5, 6and appearing in the next three columns) interpreted by the second reader (`ReaderID` `1`).
- The third line shows the ratings, in both modalities, of the final three non-diseased cases with `CaseIDs` `7,8,9` (indexed 7, 8, 9and appearing in the final three columns) interpreted by the third reader (`ReaderID` `2`).
- Values such as `x$NL[,,16:30,1]`, which are there for compatibility with FROC data, are all filled with `-Inf`.

5.6 The true positive (TP) ratings

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

- This worksheet has the ratings of diseased cases.
- The common vertical length is 30 in this example (2 modalities times 3 readers times 5 diseased cases per reader).
- `ReaderID`: the reader labels: these must be from `0`, `1` or `2`, as declared in the `Truth` worksheet.
- `ModalityID`: the modality labels: `0` or `1`, as declared in the `Truth` worksheet.
- `CaseID`: the labels of diseased cases. Each `CaseID`, `ModalityID`, `ReaderID` combination must be consistent with that declared in the `Truth` worsheet.

- `TP_Rating`: the floating point ratings of diseased cases. Each row of this worksheet yields a rating corresponding to the values of `ReaderID`, `ModalityID` and `CaseID` for that row. Each `CaseID`, `ModalityID`, `ReaderID` combination must be consistent with that declared in the `Truth` worsheet.

```
x$LL[,1,1:15,1]
#>      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12] [,13] [,14]
#> [1,] 5.28 3.01 5.98 5.00 4.26 -Inf -Inf -Inf -Inf  -Inf  -Inf  -Inf  -Inf  -Inf
#> [2,] 5.20 3.27 4.61 5.18 4.72 -Inf -Inf -Inf -Inf  -Inf  -Inf  -Inf  -Inf  -Inf
#>      [,15]
#> [1,]  -Inf
#> [2,]  -Inf
x$LL[,2,1:15,1]
#>      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12] [,13] [,14]
#> [1,] -Inf -Inf -Inf -Inf -Inf 5.14 3.31 4.92 4.95  5.30  -Inf  -Inf  -Inf  -Inf
#> [2,] -Inf -Inf -Inf -Inf -Inf 4.77 3.19 5.20 5.39  5.01  -Inf  -Inf  -Inf  -Inf
#>      [,15]
#> [1,]  -Inf
#> [2,]  -Inf
x$LL[,3,1:15,1]
#>      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12] [,13] [,14]
#> [1,] -Inf -Inf -Inf -Inf -Inf -Inf -Inf -Inf -Inf  -Inf  4.66  4.03  5.22  4.94
#> [2,] -Inf -Inf -Inf -Inf -Inf -Inf -Inf -Inf -Inf  -Inf  4.87  1.94  -Inf  -Inf
#>      [,15]
#> [1,]  5.27
#> [2,]  4.78
```

- The first line of code shows the ratings, in both modalities, of the first five diseased cases with `CaseIDs` `70,71,72,73,74` (indexed 1, 2, 3, 4, 5 and appearing in the first five columns) interpreted by the first reader (`ReaderID` `0`).
- The second line shows the ratings, in both modalities, of the next five diseased cases with `CaseIDs` `80,81,82,83,84` (indexed 6, 7, 8, 9, 10 and appearing in the next five columns) interpreted by the second reader (`ReaderID` `1`).
- The third line shows the ratings, in both modalities, of the final five non-diseased cases with `CaseIDs` `90,91,92,93,94` (indexed 11, 12, 13, 14, 15 and appearing in the final five columns) interpreted by the third reader (`ReaderID` `2`).

5.7 Summary

- TBA

5.8 References

Chapter 6

QUICK START DBM1

6.1 Introduction

- This vignette is intended for those seeking a quick transition from Windows **JAFROC** to `RJafroc`.
- Described first is the structure of an `RJafroc` dataset followed by how to read a *JAFROC* format Excel file to create an `RJafroc` dataset.

6.2 An ROC dataset

Dataset `dataset03` corresponding to the Franken ROC data (Franken et al., 1992) is predefined. The following code shows the structure of this dataset.

```
str(dataset03)
#> List of 12
#>  $ NL           : num [1:2, 1:4, 1:100, 1] 3 3 4 3 3 3 4 1 1 3 ...
#>  $ LL           : num [1:2, 1:4, 1:67, 1] 5 5 4 4 5 4 4 5 2 2 ...
#>  $ lesionVector : num [1:67] 1 1 1 1 1 1 1 1 1 1 ...
#>  $ lesionID     : num [1:67, 1] 1 1 1 1 1 1 1 1 1 1 ...
#>  $ lesionWeight : num [1:67, 1] 1 1 1 1 1 1 1 1 1 1 ...
#>  $ dataType     : chr "ROC"
#>  $ modalityID   : Named chr [1:2] "TREAT1" "TREAT2"
#>   ..- attr(*, "names")= chr [1:2] "TREAT1" "TREAT2"
#>  $ readerID     : Named chr [1:4] "READER_1" "READER_2" "READER_3" "READER_4"
#>   ..- attr(*, "names")= chr [1:4] "READER_1" "READER_2" "READER_3" "READER_4"
#>  $ design       : chr "CROSSED"
#>  $ normalCases  : int [1:33] 1 2 3 4 5 6 7 8 9 10 ...
#>  $ abnormalCases: int [1:67] 34 35 36 37 38 39 40 41 42 43 ...
#>  $ truthTableStr: num [1:2, 1:4, 1:100, 1:2] 1 1 1 1 1 1 1 1 1 1 ...
```

- It is a list with 8 members. The false positive ratings are contained in `{NL}`, an array with dimensions `[1:2,1:4,1:100,1]`. The first index corresponds to treatments, and since the dataset has 2 treatments, the corresponding dimension is 2. The second index corresponds to readers, and since the dataset has 4 readers, the corresponding dimension is 4. The third index corresponds to the total number of cases. Since the dataset has 100 cases, the corresponding dimension is 100. But, as you can see from the code below, the entries in this array for cases 34 through 100 are `-Inf`: i.e., `all(dataset03$NL[1,1,34:100,1] == -Inf)` = TRUE.
- This is because in the ROC paradigm false positive are not possible on diseased cases. So the actual FP ratings are contained in the first 33 elements of the array. How did I know that there are 33 non-diseased cases? This can be understood in several ways.
- `LL` is an array with dimensions `[1:2,1:4,1:67,1]`. This implies 67 diseased cases, and by subtraction from 100, there must be 33 non-diseased cases.
- The list member `lesionVector` is a vector with length 67, implying 33 non-diseased cases.
- The list members `lesionID` and `lesionWeight` are arrays with dimensions `[1:67,1]` containing ones. Again, these imply 67 diseased cases.
- The fields `lesionVector`, `lesionID` and `lesionWeight`, while not needed for ROC data, are needed for the FROC paradigm.

The `dataType` list member is the character string `"ROC"`, characterizing the ROC dataset.

```
dataset03$dataType
#> [1] "ROC"
```

The `modalityID` list member is a character string with two entries, `"TREAT1"` and `"TREAT2"`, corresponding to the two modalities.

```
dataset03$modalityID
#>   TREAT1   TREAT2
#> "TREAT1" "TREAT2"
```

The `readerID` list member is a character string with four entries, `"READER_1"`, `"READER_2"`, `"READER_3"` and `"READER_4"` corresponding to the four readers.

```
dataset03$readerID
#>   READER_1   READER_2   READER_3   READER_4 
#> "READER_1" "READER_2" "READER_3" "READER_4"
```

Here are the actual ratings for cases 1:34.

```
dataset03$NL[1,1,1:33,1]
#>  [1] 3 1 2 2 2 2 2 4 1 1 4 2 1 2 4 2 1 2 1 2 4 2 3 2 2 2 4 3 2 2 2 5 3
```

- This says that for treatment 1 and reader 1, (non-diseased) case 1 was rated 3, case 2 was rated 1, cases 3-7 were rated 2, case 8 was rated 4, etc.
- As another example, for treatment 2 and reader 3, the FP ratings are:

```
dataset03$NL[2,3,1:33,1]
#>  [1] 3 1 2 2 2 2 4 4 2 3 2 2 1 3 2 4 2 3 2 2 2 2 2 4 2 2 1 2 2 2 2 4 2
```

6.3 Creating a dataset from a JAFROC format file

There is a file `RocData.xlsx` that is part of the package installation. Since it is a system file one must get its name as follows.

```
fileName <- "RocData.xlsx"
sysFileName <- system.file(paste0("extdata/",fileName), package = "RJafroc", mustWork = TRUE)
```

Next, one uses `DfReadDataFile()` as follows, assuming it is a JAFROC format file.

```
ds <- DfReadDataFile(sysFileName, newExcelFileFormat = FALSE)
str(ds)
#> List of 12
#>  $ NL           : num [1:2, 1:5, 1:114, 1] 1 3 2 3 2 2 1 2 3 2 ...
#>  $ LL           : num [1:2, 1:5, 1:45, 1] 5 5 5 5 5 5 5 5 5 5 ...
#>  $ lesionVector : int [1:45] 1 1 1 1 1 1 1 1 1 1 ...
#>  $ lesionID     : num [1:45, 1] 1 1 1 1 1 1 1 1 1 1 ...
#>  $ lesionWeight : num [1:45, 1] 1 1 1 1 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 [1:69] 1 2 3 4 5 6 7 8 9 10 ...
#>  $ abnormalCases: int [1:45] 70 71 72 73 74 75 76 77 78 79 ...
#>  $ truthTableStr: num [1:2, 1:5, 1:114, 1:2] 1 1 1 1 1 1 1 1 1 1 ...
```

Analysis is illustrated for `dataset03`, but one could have used the newly created dataset `ds`.

6.4 Analyzing the ROC dataset

This illustrates the `StSignificanceTesting()` function. The significance testing method is specified as `"DBMH"` and the figure of merit `FOM` is specified as "Wilcoxon".

```
ret <- StSignificanceTesting(dataset03, FOM = "Wilcoxon", method = "DBMH")
print(ret)
#> $fomArray
#>           RdrREADER_1 RdrREADER_2 RdrREADER_3 RdrREADER_4
#> TrtTREAT1   0.8534600   0.8649932   0.8573044   0.8152420
#> TrtTREAT2   0.8496156   0.8435097   0.8401176   0.8143374
#>
#> $anovaY
#>       Source          SS  DF          MS
#> 1      Row1_T  0.02356541   1 0.023565410
#> 2      Row2_R  0.20521800   3 0.068406000
#> 3      Row3_C 52.52839868  99 0.530589886
#> 4     Row4_TR  0.01506079   3 0.005020264
#> 5     Row5_TC  6.41004881  99 0.064747968
#> 6     Row6_RC 39.24295381 297 0.132131158
#> 7    Row7_TRC 22.66007764 297 0.076296558
#> 8 Row8_Total 121.08532315 799          NA
#>
#> $anovaYi
#>   Source  DF  TrtTREAT1  TrtTREAT2
#> 1       R   3 0.04926635 0.02415991
#> 2       C  99 0.29396753 0.30137032
#> 3      RC 297 0.10504787 0.10337984
#>
#> $varComp
#>           varR       varC         varTR        varTC     varRC     varErr
#> 1 3.775568e-05 0.05125091 -0.0007127629 -0.002887147 0.0279173 0.07629656
#>
```

```
#> $FTestStatsRRRC
#>      fRRRC ndfRRRC ddfRRRC     pRRRC
#> 1 4.694058       1       3 0.1188379
#> 
#> $ciDiffTrtRRRC
#>               TrtDiff   Estimate      StdErr DF        t     PrGTt      CILower
#> 1 TrtTREAT1-TrtTREAT2 0.01085482 0.005010122  3 2.166577 0.1188379 -0.005089627
#>      CIUpper
#> 1 0.02679926
#> 
#> $ciAvgRdrEachTrtRRRC
#>   Treatment      Area     StdErr        DF   CILower   CIUpper
#> 1 TrtTREAT1 0.8477499 0.02440215  70.12179 0.7990828 0.8964170
#> 2 TrtTREAT2 0.8368951 0.02356642 253.64403 0.7904843 0.8833058
#> 
#> $FTestStatsFRRC
#>      fFRRC ndfFRRC ddfFRRC    pFRRC
#> 1 0.363956       1      99 0.547697
#> 
#> $ciDiffTrtFRRC
#>             Treatment   Estimate     StdErr DF         t    PrGTt     CILower
#> 1 TrtTREAT1-TrtTREAT2 0.01085482 0.01799277 99 0.6032876 0.547697 -0.02484675
#>      CIUpper
#> 1 0.04655638
#> 
#> $ciAvgRdrEachTrtFRRC
#>   Treatment      Area     StdErr DF   CILower   CIUpper
#> 1 TrtTREAT1 0.8477499 0.02710939 99 0.7939590 0.9015408
#> 2 TrtTREAT2 0.8368951 0.02744860 99 0.7824311 0.8913591
#> 
#> $msAnovaEachRdrFRRC
#>   Source DF  RdrREADER_1 RdrREADER_2 RdrREADER_3  RdrREADER_4
#> 1      T  1 0.0007389761  0.02307702  0.01476929 4.091217e-05
#> 2      C 99 0.2038747746  0.22344191  0.21424677 2.854199e-01
#> 3     TC 99 0.0915587344  0.08027926  0.06122898 6.057067e-02
#> 
#> $ciDiffTrtEachRdrFRRC
#>        Reader           Treatment     Estimate     StdErr DF          t
#> 1 RdrREADER_1 TrtTREAT1-TrtTREAT2 0.0038444143 0.04279223 99 0.08983908
#> 2 RdrREADER_2 TrtTREAT1-TrtTREAT2 0.0214834916 0.04006975 99 0.53615233
#> 3 RdrREADER_3 TrtTREAT1-TrtTREAT2 0.0171867933 0.03499399 99 0.49113552
#> 4 RdrREADER_4 TrtTREAT1-TrtTREAT2 0.0009045681 0.03480536 99 0.02598933
#>       PrGTt     CILower    CIUpper
#> 1 0.9285966 -0.08106465 0.08875348
#> 2 0.5930559 -0.05802359 0.10099057
#> 3 0.6244176 -0.05224888 0.08662247
#> 4 0.9793182 -0.06815683 0.06996596
#> 
#> $FTestStatsRRFC
#>      fRRFC ndfRRFC ddfRRFC     pRRFC
#> 1 4.694058       1       3 0.1188379
#> 
#> $ciDiffTrtRRFC
#>               Treatment   Estimate      StdErr DF        t     PrGTt      CILower
#> 1 TrtTREAT1-TrtTREAT2 0.01085482 0.005010122  3 2.166577 0.1188379 -0.005089627
#>      CIUpper
#> 1 0.02679926
#> 
#> $ciAvgRdrEachTrtRRFC
#>   Treatment      Area     StdErr DF   CILower   CIUpper
#> 1 TrtTREAT1 0.8477499 0.01109801  3 0.8124311 0.8830687
#> 2 TrtTREAT2 0.8368951 0.00777173  3 0.8121620 0.8616282
```

6.5 Explanation of the output

The function returns a long unwieldy list. Let us consider them one by one. The function `UtilOutputReport()`, which can generate an Excel file report, making it much easier to visualize the results, is described in another vignette.

6.5.1 FOMs

- `fomArray` contains the `[1:2,1:4]` FOM values.

```
ret$fomArray
#>           RdrREADER_1 RdrREADER_2 RdrREADER_3 RdrREADER_4
#> TrtTREAT1   0.8534600   0.8649932   0.8573044   0.8152420
#> TrtTREAT2   0.8496156   0.8435097   0.8401176   0.8143374
```

This shows the 2 x 4 array of FOM values.

6.5.2 Pseudovalue ANOVA table

- `anovaY`, where the Y denotes that these are pseudovalue based, is the ANOVA table.

```
ret$anovaY
#>       Source          SS  DF          MS
#> 1     Row1_T   0.02356541   1 0.023565410
#> 2     Row2_R   0.20521800   3 0.068406000
#> 3     Row3_C  52.52839868  99 0.530589886
#> 4    Row4_TR   0.01506079   3 0.005020264
#> 5    Row5_TC   6.41004881  99 0.064747968
#> 6    Row6_RC  39.24295381 297 0.132131158
#> 7   Row7_TRC  22.66007764 297 0.076296558
#> 8 Row8_Total 121.08532315 799          NA
```

6.5.3 Pseudovalue ANOVA table, each treatment

- `anovaYi` is the ANOVA table for individual treatments.

```
ret$anovaYi
#>   Source  DF  TrtTREAT1  TrtTREAT2
#> 1      R   3 0.04926635 0.02415991
#> 2      C  99 0.29396753 0.30137032
#> 3     RC 297 0.10504787 0.10337984
```

The `0` and `1` headers come from the treatment names.

6.5.4 Pseudovalue Variance Components

- `varComp` is the variance components (needed for sample size estimation).

```
ret$varComp
#>             varR       varC          varTR         varTC      varRC     varErr
#> 1 3.775568e-05 0.05125091 -0.0007127629 -0.002887147 0.0279173 0.07629656
```

6.5.5 Random-reader random-case (RRRC) analysis

- `ret$FTestStatsRRRC$fRRRC` is the F-statistic for testing the NH that the treatments have identical FOMs. RRRC means random-reader random-case generalization.

```
ret$FTestStatsRRRC$fRRRC
#> [1] 4.694058
```

6.5.5.1 F-statistic and p-value for RRRC analysis

- `ret$FTestStatsRRRC$ddfRRRC` is the denominator degrees of freedom of the F-statistic.

```
ret$FTestStatsRRRC$ddfRRRC
#> [1] 3
```

- `ret$FTestStatsRRRC$pRRRC` is the p-value of the test.

```
ret$FTestStatsRRRC$pRRRC
#> [1] 0.1188379
```

6.5.5.2 Confidence Intervals for RRRC analysis

- `ciDiffTrtRRRC` is the 95% confidence interval of reader-averaged differences between treatments.

```
ret$ciDiffTrtRRRC
#>               TrtDiff   Estimate      StdErr DF        t     PrGTt      CILower
#> 1 TrtTREAT1-TrtTREAT2 0.01085482 0.005010122  3 2.166577 0.1188379 -0.005089627
#>      CIUpper
#> 1 0.02679926
```

- `ciAvgRdrEachTrtRRRC` is the 95% confidence interval of reader-averaged FOMs for each treatments.

```
ret$ciAvgRdrEachTrtRRRC
#>   Treatment      Area     StdErr        DF   CILower   CIUpper
#> 1 TrtTREAT1 0.8477499 0.02440215  70.12179 0.7990828 0.8964170
#> 2 TrtTREAT2 0.8368951 0.02356642 253.64403 0.7904843 0.8833058
```

6.5.6 Fixed-reader random-case (FRRC) analysis

6.5.6.1 F-statistic and p-value for FRRC analysis

- `ret$FTestStatsFRRC$fFRRC` is the F-statistic for fixed-reader random-case analysis.

```
ret$FTestStatsFRRC$fFRRC
#> [1] 0.363956
```

- `ret$FTestStatsFRRC$ndfFRRC` is the numerator degrees of freedom of the F-statistic, always one less than the number of treatments.

```
ret$FTestStatsFRRC$ndfFRRC
#> [1] 1
```

- `ret$FTestStatsFRRC$ddfFRRC` is the denominator degreesof freedom of the F-statistic, for fixed-reader random-case analysis.

```
ret$FTestStatsFRRC$ddfFRRC
#> [1] 99
```

- `ret$FTestStatsFRRC$pFRRC` is the p-value for fixed-reader random-case analysis.

```
ret$FTestStatsFRRC$pFRRC
#> [1] 0.547697
```

6.5.6.2 Confidence Intervals for FRRC analysis

- `ciDiffTrtFRRC` is the 95% CI of reader-average differences between treatments for fixed-reader random-case analysis

```
ret$ciDiffTrtFRRC
#>             Treatment   Estimate     StdErr DF         t    PrGTt     CILower
#> 1 TrtTREAT1-TrtTREAT2 0.01085482 0.01799277 99 0.6032876 0.547697 -0.02484675
#>      CIUpper
#> 1 0.04655638
```

- `ret$ciAvgRdrEachTrtFRRC` is the 95% CI of reader-average FOMs of each treatment for fixed-reader random-case analysis

```
ret$ciAvgRdrEachTrtFRRC
#>   Treatment      Area     StdErr DF   CILower   CIUpper
#> 1 TrtTREAT1 0.8477499 0.02710939 99 0.7939590 0.9015408
#> 2 TrtTREAT2 0.8368951 0.02744860 99 0.7824311 0.8913591
```

6.5.6.3 ANOVA for FRRC analysis

- `ret$msAnovaEachRdrFRRC` is the mean-squares ANOVA for each reader

```
ret$msAnovaEachRdrFRRC
#>   Source DF  RdrREADER_1 RdrREADER_2 RdrREADER_3  RdrREADER_4
#> 1      T  1 0.0007389761  0.02307702  0.01476929 4.091217e-05
#> 2      C 99 0.2038747746  0.22344191  0.21424677 2.854199e-01
#> 3     TC 99 0.0915587344  0.08027926  0.06122898 6.057067e-02
```

6.5.6.4 Confidence Intervals for FRRC analysis

- `ciDiffTrtFRRC` is the CI for reader-averaged treatment differences, for fixed-reader random-case analysis

```
ret$ciDiffTrtFRRC
#>            Treatment   Estimate     StdErr DF         t    PrGTt     CILower
#> 1 TrtTREAT1-TrtTREAT2 0.01085482 0.01799277 99 0.6032876 0.547697 -0.02484675
#>      CIUpper
#> 1 0.04655638
```

6.5.7 Random-reader fixed-case (RRFC) analysis

6.5.7.1 F-statistic and p-value for RRFC analysis

- `ret$FTestStatsRRFC$fRRFC` is the F-statistic for for random-reader fixed-case analysis

```
ret$FTestStatsRRFC$fRRFC
#> [1] 4.694058
```

- `ret$FTestStatsRRFC$ddfRRFC` is the ddf for for random-reader fixed-case analysis

```
ret$FTestStatsRRFC$ddfRRFC
#> [1] 3
```

- `ret$FTestStatsRRFC$pRRFC` is the p-value for for random-reader fixed-case analysis

```
ret$FTestStatsRRFC$pRRFC
#> [1] 0.1188379
```

6.5.7.2 Confidence Intervals for RRFC analysis

- `ciDiffTrtRRFC` is the CI for reader-averaged inter-treatment FOM differences for random-reader fixed-case analysis

```
ret$ciDiffTrtRRFC
#>              Treatment   Estimate      StdErr DF        t     PrGTt      CILower
#> 1 TrtTREAT1-TrtTREAT2 0.01085482 0.005010122  3 2.166577 0.1188379 -0.005089627
#>      CIUpper
#> 1 0.02679926
```

- `ciAvgRdrEachTrtRRFC` is the CI for treatment FOMs for each reader for random-reader fixed-case analysis

```
ret$ciAvgRdrEachTrtRRFC
#>   Treatment      Area     StdErr DF   CILower   CIUpper
#> 1 TrtTREAT1 0.8477499 0.01109801  3 0.8124311 0.8830687
#> 2 TrtTREAT2 0.8368951 0.00777173  3 0.8121620 0.8616282
```

6.6 ORH significance testing

Simply change `method = "DBMH"` to `method = "ORH"`.

```
ret <- StSignificanceTesting(dataset03, FOM = "Wilcoxon", method = "ORH")
str(ret)
#> List of 14
#>  $ fomArray            : num [1:2, 1:4] 0.853 0.85 0.865 0.844 0.857 ...
#>   ..- attr(*, "dimnames")=List of 2
#>   .. ..$ : chr [1:2] "TrtTREAT1" "TrtTREAT2"
#>   .. ..$ : chr [1:4] "RdrREADER_1" "RdrREADER_2" "RdrREADER_3" "RdrREADER_4"
#>  $ meanSquares         :'data.frame':    1 obs. of  3 variables:
#>   ..$ msT : num 0.000236
#>   ..$ msR : num 0.000684
#>   ..$ msTR: num 5.02e-05
#>  $ varComp             :'data.frame':    1 obs. of  6 variables:
#>   ..$ varR : num 2.33e-05
#>   ..$ varTR: num -0.000684
#>   ..$ cov1 : num 0.000792
#>   ..$ cov2 : num 0.000484
#>   ..$ cov3 : num 0.000513
#>   ..$ var  : num 0.00153
#>  $ FTestStatsRRRC      :'data.frame':    1 obs. of  4 variables:
#>   ..$ fRRRC  : num 4.69
#>   ..$ ndfRRRC: num 1
#>   ..$ ddfRRRC: num 3
#>   ..$ pRRRC  : num 0.119
#>  $ ciDiffTrtRRRC       :'data.frame':    1 obs. of  8 variables:
#>   ..$ Treatment: chr "TrtTREAT1-TrtTREAT2"
#>   ..$ Estimate : num 0.0109
#>   ..$ StdErr   : num 0.00501
#>   ..$ DF       : num 3
#>   ..$ t        : num 2.17
#>   ..$ PrGTt    : num 0.119
#>   ..$ CILower  : num -0.00509
#>   ..$ CIUpper  : num 0.0268
#>  $ ciAvgRdrEachTrtRRRC :'data.frame':    2 obs. of  6 variables:
#>   ..$ Treatment: Factor w/ 2 levels "TrtTREAT1","TrtTREAT2": 1 2
#>   ..$ Area     : num [1:2] 0.848 0.837
#>   ..$ StdErr   : num [1:2] 0.0244 0.0236
#>   ..$ DF       : num [1:2] 70.1 253.6
#>   ..$ CILower  : num [1:2] 0.799 0.79
#>   ..$ CIUpper  : num [1:2] 0.896 0.883
#>  $ FTestStatsFRRC      :'data.frame':    1 obs. of  4 variables:
#>   ..$ fFRRC  : num 0.364
#>   ..$ ndfFRRC: num 1
#>   ..$ ddfFRRC: num Inf
#>   ..$ pFRRC  : num 0.546
#>  $ ciDiffTrtFRRC       :'data.frame':    1 obs. of  8 variables:
#>   ..$ Treatment: chr "TrtTREAT1-TrtTREAT2"
#>   ..$ Estimate : num 0.0109
#>   ..$ StdErr   : num 0.018
#>   ..$ DF       : num Inf
#>   ..$ t        : num 0.603
#>   ..$ PrGTt    : num 0.546
#>   ..$ CILower  : num -0.0244
#>   ..$ CIUpper  : num 0.0461
#>  $ ciAvgRdrEachTrtFRRC :'data.frame':    2 obs. of  6 variables:
#>   ..$ Treatment: Factor w/ 2 levels "TrtTREAT1","TrtTREAT2": 1 2
#>   ..$ Area     : num [1:2] 0.848 0.837
#>   ..$ StdErr   : num [1:2] 0.0271 0.0274
#>   ..$ DF       : num [1:2] Inf Inf
#>   ..$ CILower  : num [1:2] 0.795 0.783
#>   ..$ CIUpper  : num [1:2] 0.901 0.891
#>  $ ciDiffTrtEachRdrFRRC:'data.frame':    4 obs. of  9 variables:
#>   ..$ Reader   : Factor w/ 4 levels "RdrREADER_1",..: 1 2 3 4
#>   ..$ Treatment: Factor w/ 1 level "TrtTREAT1-TrtTREAT2": 1 1 1 1
#>   ..$ Estimate : num [1:4] 0.003844 0.021483 0.017187 0.000905
#>   ..$ StdErr   : num [1:4] 0.0428 0.0401 0.035 0.0348
#>   ..$ DF       : num [1:4] Inf Inf Inf Inf
#>   ..$ t        : num [1:4] 0.0898 0.5362 0.4911 0.026
#>   ..$ PrGTt    : num [1:4] 0.928 0.592 0.623 0.979
#>   ..$ CILower  : num [1:4] -0.08 -0.0571 -0.0514 -0.0673
#>   ..$ CIUpper  : num [1:4] 0.0877 0.1 0.0858 0.0691
#>  $ varCovEachRdr      :'data.frame':    4 obs. of  3 variables:
#>   ..$ Reader: Factor w/ 4 levels "RdrREADER_1",..: 1 2 3 4
#>   ..$ Var   : num [1:4] 0.00148 0.00152 0.00138 0.00173
#>   ..$ Cov1  : num [1:4] 0.000562 0.000716 0.000765 0.001124
#>  $ FTestStatsRRFC     :'data.frame':    1 obs. of  4 variables:
#>   ..$ fRRFC  : num 4.69
#>   ..$ ndfRRFC: num 1
#>   ..$ ddfRRFC: num 3
#>   ..$ pRRFC  : num 0.119
#>  $ ciDiffTrtRRFC      :'data.frame':    1 obs. of  8 variables:
#>   ..$ Treatment: chr "TrtTREAT1-TrtTREAT2"
#>   ..$ Estimate : num 0.0109
#>   ..$ StdErr   : num 0.00501
#>   ..$ DF       : num 3
#>   ..$ t        : num 2.17
#>   ..$ PrGTt    : num 0.119
#>   ..$ CILower  : num -0.00509
#>   ..$ CIUpper  : num 0.0268
#>  $ ciAvgRdrEachTrtRRFC :'data.frame':    2 obs. of  6 variables:
#>   ..$ Treatment: Factor w/ 2 levels "TrtTREAT1","TrtTREAT2": 1 2
#>   ..$ Area     : num [1:2] 0.848 0.837
#>   ..$ StdErr   : num [1:2] 0.0111 0.00777
#>   ..$ DF       : num [1:2] 3 3
#>   ..$ CILower  : num [1:2] 0.812 0.812
#>   ..$ CIUpper  : num [1:2] 0.883 0.862
```

6.7 References

Chapter 7

QUICK START DBM2

7.1 Introduction

This vignette illustrates significance testing using the DBMH method. But, instead of the unwieldy output in *QuickStartDBMH.html*, it generates an Excel output file containing the following worksheets:

- `Summary`
- `FOMs`
- `RRRC`
- `FRRC`
- `RRFC`
- `ANOVA`

7.2 Generating the Excel output file

This illustrates the `UtilOutputReport()` function. The significance testing `method` is “DBMH”, the default, and the figure of merit `FOM` is “Wilcoxon”. Note `ReportFileExt` = “xlsx”‘ telling the function to create an Excel output file. The Excel output is created in a temporary file.

```
ret <- UtilOutputReport(dataset03, FOM = "Wilcoxon", overWrite = TRUE, ReportFileExt = "xlsx")
#>
#> Output file name is:      /var/folders/d1/mx6dcbzx3v39r260458z2b200000gn/T//RtmpugyZds/RJafro
```

7.3 ORH significance testing

Simply change `method = "DBMH"` (the default) to `method = "ORH"`.

```
ret <- UtilOutputReport(dataset03, FOM = "Wilcoxon", method = "ORH", overWrite = TRUE,
#>
#> Output file name is:      /var/folders/d1/mx6dcbzx3v39r260458z2b200000gn/T//Rtmpugy
```

Chapter 8

BACKGROUND ON THE F-DISTRIBUTION

8.1 Introduction

Since it plays an important role in sample size estimation, it is helpful to examine the behavior of the F-distribution. In the following `ndf` = numerator degrees of freedom, `ddf` = denominator degrees of freedom and `ncp` = non-centrality parameter (i.e., the Δ appearing in Eqn. (11.6) of (Chakraborty, 2017)).

The use of three `R` functions is demonstrated.

- `qf(p,ndf,ddf)` is the *quantile* function of the F-distribution for specified values of `p`, `ndf` and `ddf`, i.e., the value `x` such that fraction `p` of the area under the F-distribution lies to the right of `x`. Since `ncp` is not included as a parameter, the default value, i.e., zero, is used. This is called the *central* F-distribution.

- `df(x,ndf,ddf,ncp)` is the probability density function (*pdf*) of the F-distribution, as a function of `x`, for specified values of `ndf`, `ddf` and `ncp`.

- `pf(x,ndf,ddf,ncp)` is the probability (or cumulative) distribution function of the F-distribution for specified values of `ndf`, `ddf` and `ncp`.

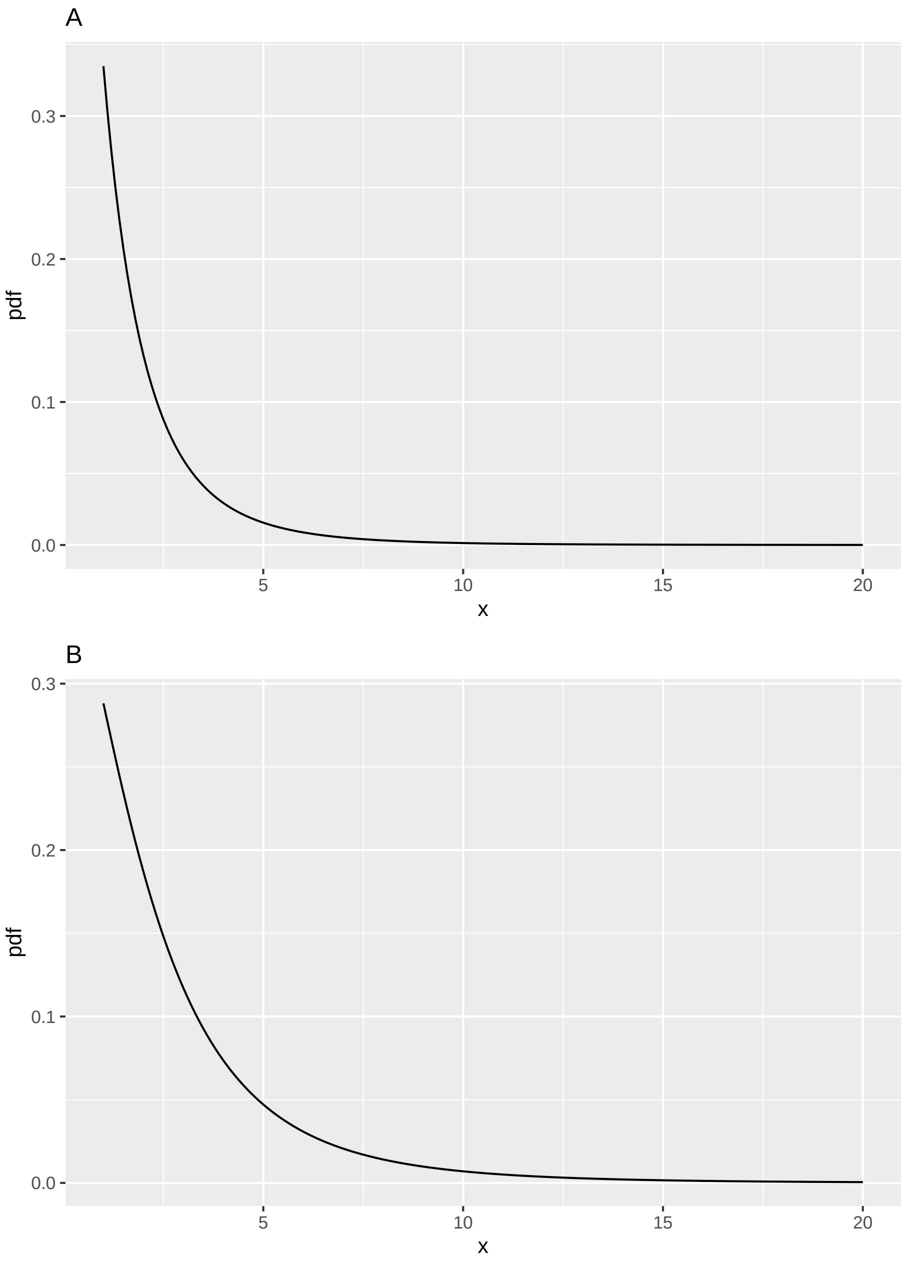
8.2 Effect of `ncp` for `ndf` = 2 and `ddf` = 10

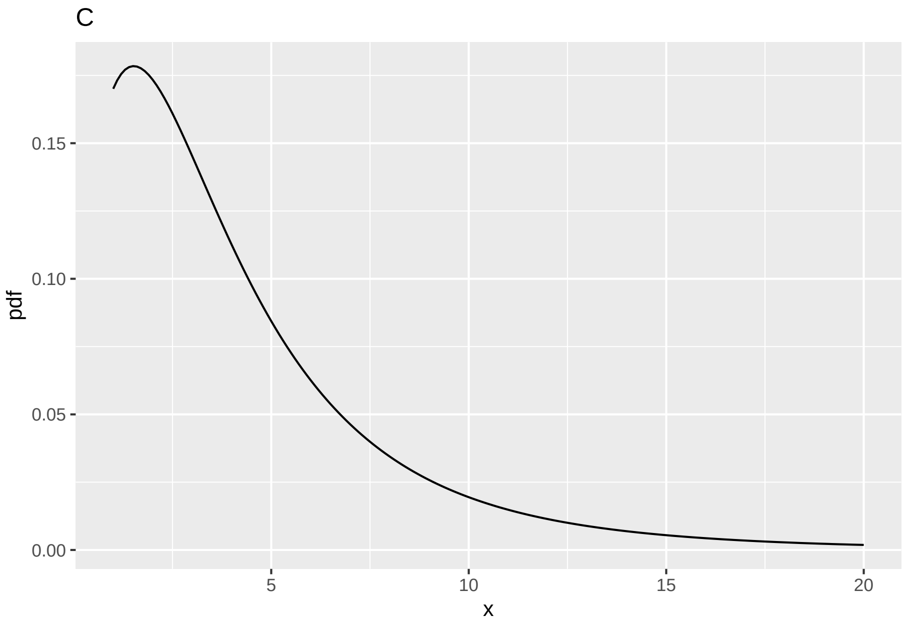
- Four values of `ncp` are considered (0, 2, 5, 10) for `ddf` = 10.

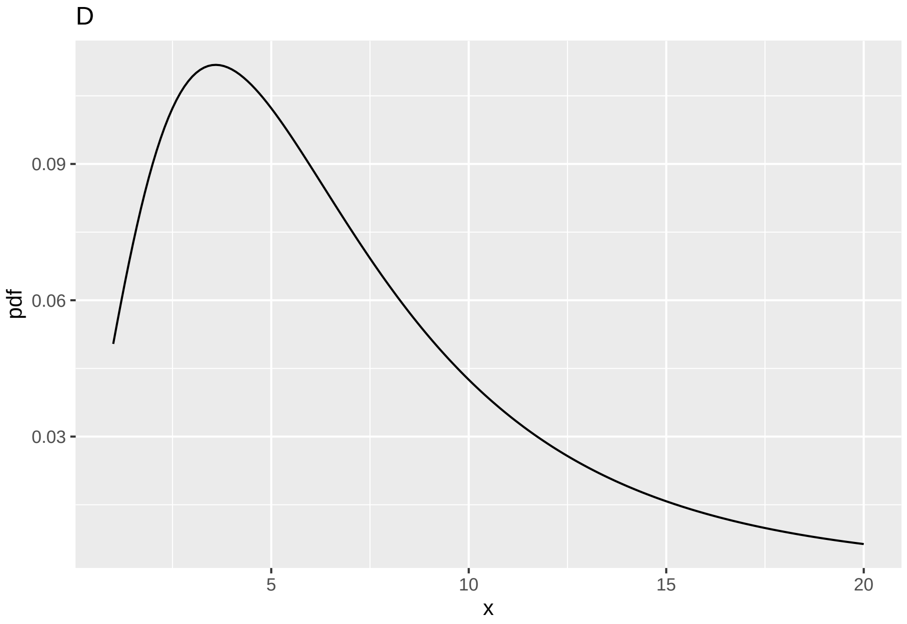
- fCrit is the critical value of the F distribution, i.e., that value such that fraction α of the area is to the right of the critical value, i.e., fCrit is identical to:

$$F_{1-\alpha,ndf,ddf}$$

```
ndf <- 2;ddf <- 10;ncp <- c(0,2,5,10)
alpha <- 0.05
fCrit <- qf(1-alpha, ndf,ddf)
x <- seq(1, 20, 0.1)
myLabel <- c("A", "B", "C", "D")
myLabelIndx <- 1
pFgtFCrit <- NULL
for (i in 1:length(ncp))
{
  y <- df(x,ndf,ddf,ncp=ncp[i])
  pFgtFCrit <- c(pFgtFCrit, 1-pf(fCrit, ndf, ddf, ncp = ncp[i]))
}
for (i in 1:length(ncp))
{
  y <- df(x,ndf,ddf,ncp=ncp[i])
  curveData <- data.frame(x = x, pdf = y)
  curvePlot <- ggplot(data = curveData, mapping = aes(x = x, y = pdf)) +
    geom_line() +
    ggtitle(myLabel[myLabelIndx]);myLabelIndx <- myLabelIndx + 1
  print(curvePlot)
}
fCrit_2_10 <- fCrit # convention fCrit_ndf_ddf
```


A
pdf
0.3
0.2
0.1
0.0
5
10
15
20
x
B
pdf
0.3
0.2
0.1
0.0
5
10
15
20
x





	ndf	ddf	fCrit	ncp	pFgtFCrit
A	2	10	4.102821	0	0.0500000
B	2	10	4.102821	2	0.1775840
C	2	10	4.102821	5	0.3876841
D	2	10	4.102821	10	0.6769776

8.3 Comments

8.3.1 Fig. A

- This corresponds to `ncp = 0`, i.e., the *central* F-distribution.
- The integral under this distribution is unity (this is also true for all plots in this vignette).
- The critical value, `fCrit` in the above code block, is the value of `x` such that the probability of exceeding `x` is α. The corresponding parameter `alpha` is defined above as 0.05.
- In the current example `fCrit` = 4.102821. Notice the use of the quantile function `qf()` to determine this value, and the default value of `ncp`, namely zero, is used; specifically, one does not pass a 4th argument to `qf()`.
- **The decision rule for rejecting the NH uses the NH distribution of the F-statistic**, i.e., reject the NH if F >= `fCrit`. As expected, `prob > fCrit` = 0.05 because this is how `fCrit` was defined.

8.3.2 Fig. B

- This corresponds to `ncp = 2`, `ndf` = 2 and `ddf` = 10.
- The distribution is slightly shifted to the right as compared to Fig. A, thereby making it more likely that the observed value of the F-statistic will exceed the critical value determined for the NH distribution.
- In fact, `prob > fCrit` = 0.177584, i.e., the *statistical power* (compare this to Fig. A where `prob > fCrit` was 0.05).

8.3.3 Fig. C

- This corresponds to `ncp = 5`, `ndf` = 2 and `ddf` = 10.
- Now `prob > fCrit` = 0.3876841.
- Power has increased compared to Fig. B.

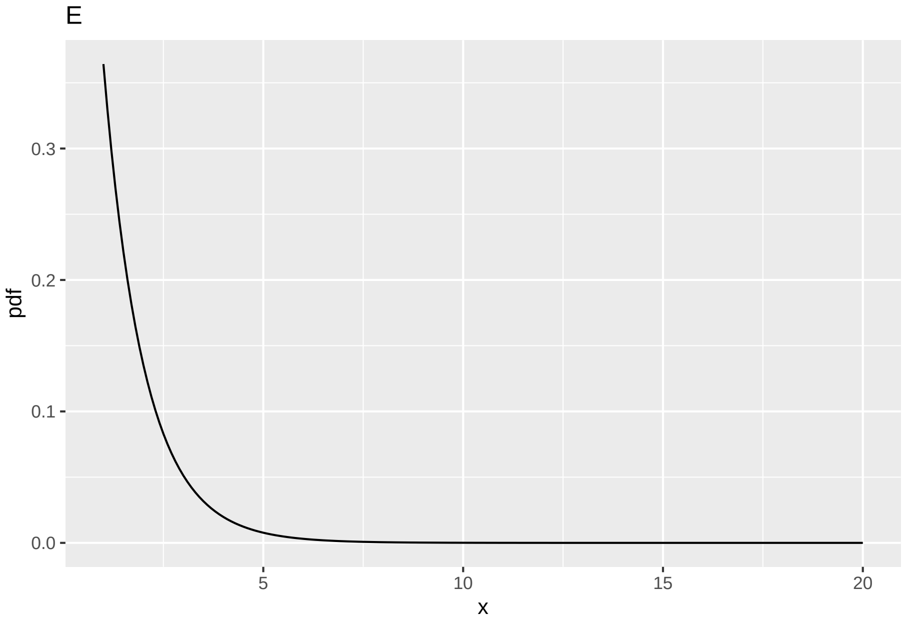
8.3.4 Fig. D

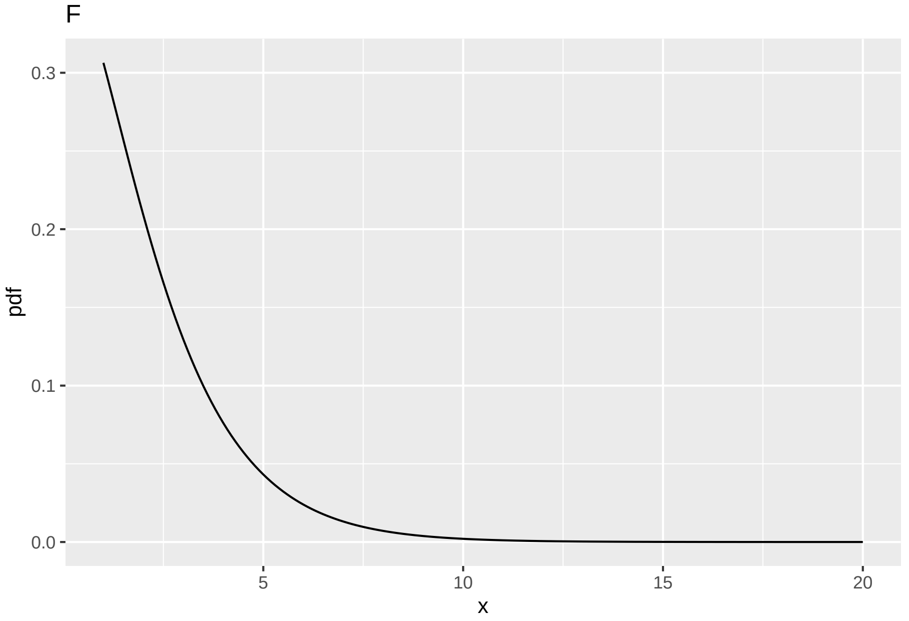
- This corresponds to `ncp = 10`, `ndf` = 2 and `ddf` = 10.
- Now `prob > fCrit` is 0.6769776.
- Power has increased compared to Fig. C.
- The effect of the shift is most obvious in Fig. C and Fig. D.
- Considering a vertical line at `x` = 4.102821, fraction 0.6769776 of the probability distribution in Fig. D lies to the right of this line
- Therefore the NH is likely to be rejected with probability 0.6769776.

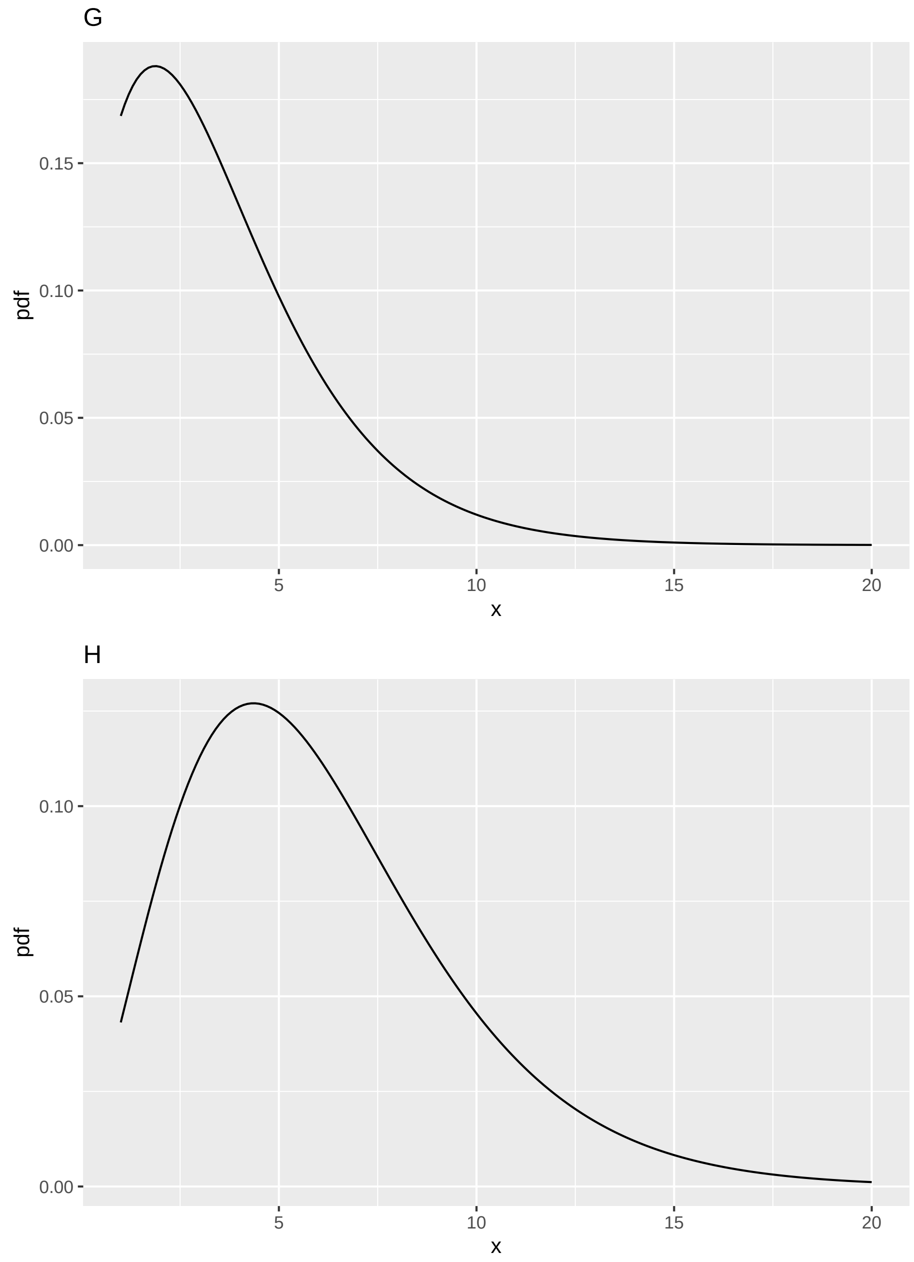
8.3.5 Summary

The larger that non-centrality parameter, the greater the shift to the right of the F-distribution, and the greater the statistical power.

8.4 Effect of `ncp` for `ndf` = 2 and `ddf` = 100






G
pdf
0.15
0.10
0.05
0.00
5
10
15
20
x
H
pdf
0.10
0.05
0.00
5
10
15
20
x

	ndf	ddf	fCrit	ncp	pFgtFCrit
A	2	10	4.102821	0	0.0500000
B	2	10	4.102821	2	0.1775840
C	2	10	4.102821	5	0.3876841
D	2	10	4.102821	10	0.6769776
E	2	100	3.087296	0	0.0500000
F	2	100	3.087296	2	0.2199264
G	2	100	3.087296	5	0.4910802
H	2	100	3.087296	10	0.8029764

8.5 Comments

- All comparisons in this sections are at the same values of `ncp` defined above.
- And between `ddf` = 100 and `ddf` = 10.

8.5.1 Fig. E

- This corresponds to `ncp` = 0, `ndf` = 2 and `ddf` = 100.
- The critical value is `fCrit_2_100` = 3.0872959. Notice the decrease compared to the previous value for `ncp` = 0, i.e., 4.102821, for `ddf` = 10.
- One expects that increasing `ddf` will make it more likely that the NH will be rejected, and this is confirmed below.
- All else equal, statistical power increases with increasing `ddf`.

8.5.2 Fig. F

- This corresponds to `ncp` = 2, `ndf` = 2 and `ddf` = 100.
- The probability of exceeding the critical value is `prob > fCrit_2_100` = 0.2199264, greater than the previous value, i.e., 0.177584 for `ddf` = 10.

8.5.3 Fig. G

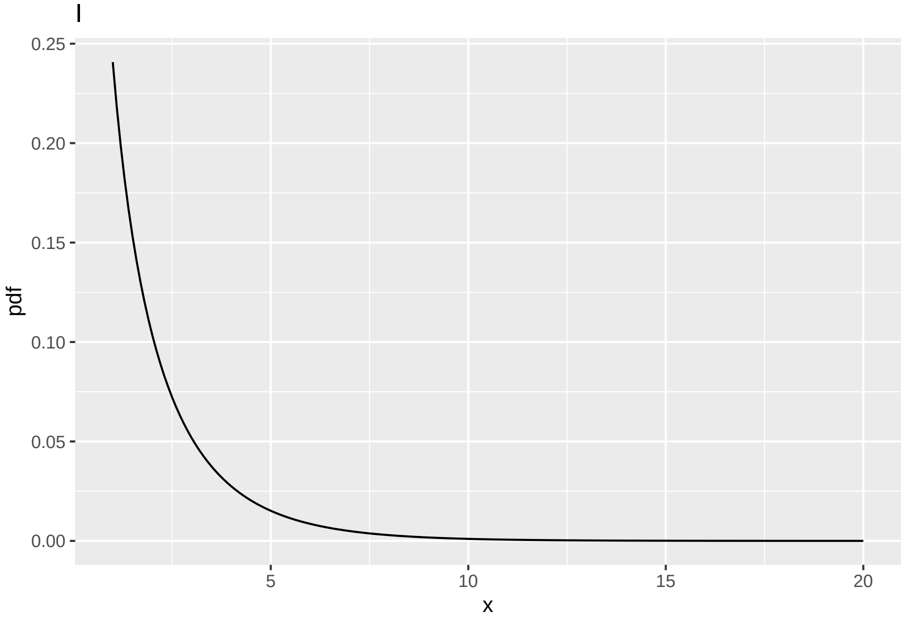
- This corresponds to `ncp = 5`, `ndf` = 2 and `ddf` = 100.
- The probability of exceeding the critical value is `prob > fCrit_2_100` = 0.4910802.
- This is greater than the previous value, i.e., 0.3876841 for `ddf` = 10.

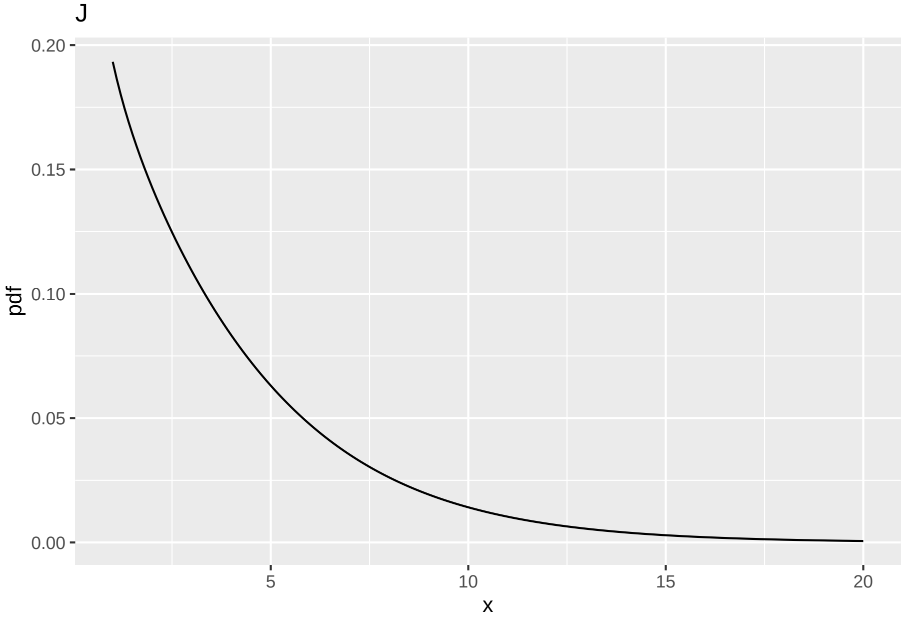
8.5.4 Fig. H

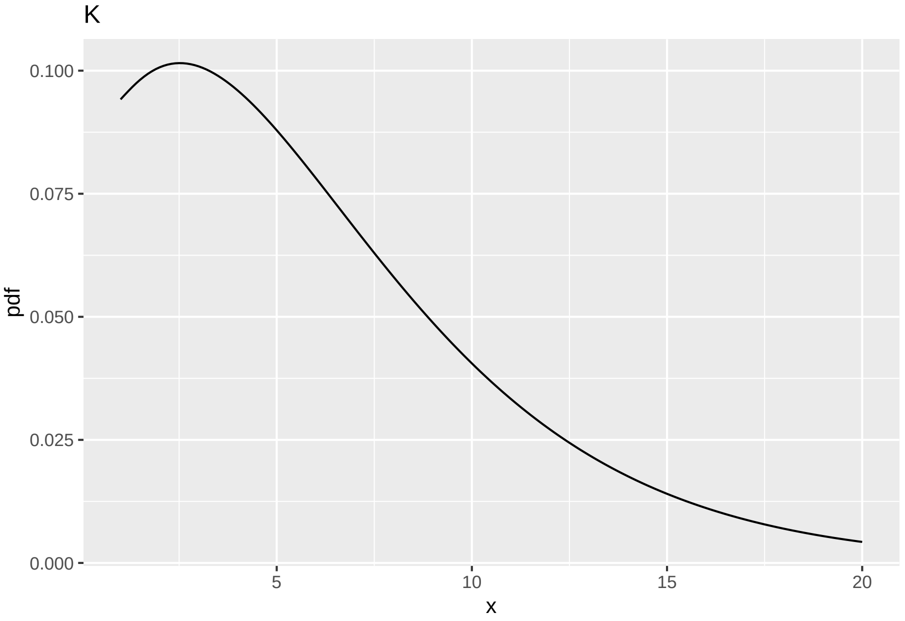
- This corresponds to `ncp = 10`, `ndf` = 2 and `ddf` = 100.

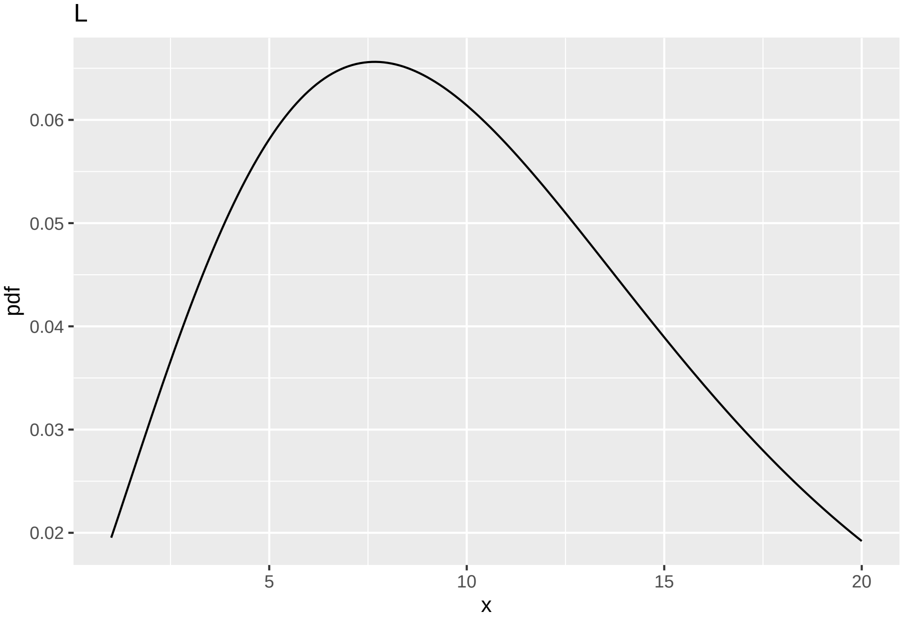
- The probability of exceeding the critical value is `prob > fCrit_2_100` is 0.8029764.
- This is greater than the previous value, i.e., 0.6769776 for `ddf` $= 10$.

8.6 Effect of `ncp` for `ndf` = 1, `ddf` = 100






K
0.100
0.075
0.050
0.025
0.000
pdf
5
10
15
20
x


L
0.06
0.05
0.04
0.03
0.02
pdf
5
10
15
20
x

	ndf	ddf	fCrit	ncp	pFgtFCrit
A	2	10	4.102821	0	0.0500000
B	2	10	4.102821	2	0.1775840
C	2	10	4.102821	5	0.3876841
D	2	10	4.102821	10	0.6769776
E	2	100	3.087296	0	0.0500000
F	2	100	3.087296	2	0.2199264
G	2	100	3.087296	5	0.4910802
H	2	100	3.087296	10	0.8029764
I	1	100	3.936143	0	0.0500000
J	1	100	3.936143	2	0.2883607
K	1	100	3.936143	5	0.6004962
L	1	100	3.936143	10	0.8793619

8.7 Comments

- All comparisons in this sections are at the same values of `ncp` defined above and at `ddf` = 100.
- And between `ndf` = 1 and `ndf` = 2.

8.7.1 Fig. I

- This corresponds to `ncp` = 0, `ndf` = 1 and `ddf` = 100.
- The critical value is `fCrit_1_100` = 3.936143.
- Notice the increase in the critical value as compared to the corresponding value for `ndf = 2`, i.e., 3.0872959.
- One might expect power to decrease, **but see below**.

8.7.2 Fig. J

- This corresponds to `ncp` = 2, `ndf` = 1 and `ddf` = 100.
- Now `prob > fCrit_1_100` = 0.2883607, larger than the previous value 0.2199264.
- The power has actually increased.

8.7.3 Fig. K

- This corresponds to `ncp` = 5, `ndf` = 1 and `ddf` = 100‘’,
- Now `prob > fCrit_1_100` = 0.6004962, larger than the previous value 0.4910802.
- Again, the power has actually increased.

8.7.4 Fig. L

- This corresponds to `ncp` = 10, `ndf` = 1 and `ddf` = 100
- Now `prob > fCrit_1_100` is 0.8793619, larger than the previous value 0.8029764.
- The power has actually increased.

8.8 Summary

- Power increases with increasing `ddf` and `ncp`.
- The effect of increasing `ncp` is quite dramatic. This is because power depends on the square of `ncp`.
- Decreasing `ndf` also **increases** power. At first glance this may seem counterintuitive, as `fCrit` has gone up, but is explained by the differing shapes of the two distributions: the pdf is broader for `ndf` = 1 as compared to `ndf` = 2 (compare Fig. L to H).

8.9 References

Chapter 9

ROC-DBMH sample size from first principles

9.1 Introduction

The starting point is a **pilot** study. The variability in this dataset (specifically the variance components, subsequently converted to mean squares), obtained by running the significance testing function `StSignificanceTesting()`, is used to extrapolate to the necessary numbers of readers and cases, in the **pivotal** study, to achieve the desired power. In this example, the observed effect size in the pilot study is used as the anticipated effect size for the pivotal study – this is generally not a good idea as discussed in **Chapter 11** under "Cautionary notes". Shown below, and the reader should confirm, is a first principles implementation of the relevant formulae in **Chapter 11**.

9.2 Sample size estimation using the DBMH method

The Van Dyke dataset in file `VanDyke.lrc`, in `"MRMC"` format, is regarded as a pilot study. The command `rocData <- DfReadDataFile(fileName, format = "MRMC")` reads the data and saves it to a `dataset` object `rocData`. For more on data formats click here. The next line uses the function `StSignificanceTesting()` to apply `method = "DBMH"` analysis, the default, using the `FOM = "Wilcoxon"` figure of merit. The next line extracts the variance components `varYTR`, `varYTC` and `varYEps` (the Y's denote pseudovalue based values). The next line extracts the effect size.

```
alpha <- 0.05
rocData <- dataset02 ##"VanDyke.lrc"
#fileName <- dataset03 ## "Franken1.lrc"
retDbm <- StSignificanceTesting(dataset = rocData, FOM = "Wilcoxon", method = "DBMH")
varYTR <- retDbm$varComp$varTR;varYTC <- retDbm$varComp$varTC;varYEps <- retDbm$varCom
effectSize <- retDbm$ciDiffTrtRRRC$Estimate
```

The *observed* effect size is `effectSize` = -0.0438003, which, in this example, is used as the *anticipated* effect size, generally not a good idea. **See Chapter 11 for nuances regarding the choice of this all important value.** The following code snippet reveals the names and array indexing of the pseudovalue variance components.

```
retDbm$varComp
#>          varR       varC        varTR     varTC      varRC    varErr
#> 1 0.001534999 0.02724923 0.0002004025 0.0119753 0.01226473 0.0399716
```

For example, the treatment-reader pseudovalue variance component is the third element of `retDbm$varComp`.

9.2.1 Random reader random case (RRRC)

This illustrates random reader random case sample size estimation. Assumed are 10 readers and 163 cases in the pivotal study. The non-centrality parameter is defined by:

$$\Delta = \frac{JK\sigma_{Y;\tau}^2}{\left(\sigma_{Y;\varepsilon}^2 + \sigma_{Y;\tau RC}^2\right) + K\sigma_{Y;\tau R}^2 + J\max\left(\sigma_{Y;\tau C}^2, 0\right)}$$

The sampling distribution of the F-statistic under the AH is:

$$F_{AH|R} \equiv \frac{MST}{MSTC} \sim F_{I-1,(I-1)(K-1),\Delta}$$

Also, $\sigma_{Y;\tau}^2 = d^2/2$, where `d` is the observed effect size, i.e., `effectSize`. The formulae for calculating the mean-squares are in (Hillis and Berbaum, 2004), implemented in `UtilMeanSquares()`.

```
#RRRC
J <- 10;K <- 163
ncp <- (0.5*J*K*(effectSize)^2)/(K*varYTR+max(J*varYTC,0)+varYEps)
MS <- UtilMeanSquares(rocData, FOM = "Wilcoxon", method = "DBMH")
ddf <- (MS$msTR+max(MS$msTC-MS$msTRC,0))^2/(MS$msTR^2)*(J-1)
```

```
FCrit <- qf(1 - alpha, 1, ddf)
Power1 <- 1-pf(FCrit, 1, ddf, ncp = ncp)
```

The next line calculates the non centrality parameter, `ncp` = 8.1269825. Note that `effectSize` enters as the **square**. The `UtilMeanSquares()` function returns the mean-squares as a `list` (ignore the last two rows of output for now).

```
str(MS)
#> List of 9
#>  $ msT        : num 0.547
#>  $ msR        : num 0.437
#>  $ msC        : num 0.397
#>  $ msTR       : num 0.0628
#>  $ msTC       : num 0.0521
#>  $ msRC       : num 0.0645
#>  $ msTRC      : num 0.04
#>  $ msCSingleT: num [1:2] 0.336 0.16
#>  $ msCSingleR: num [1:5] 0.1222 0.2127 0.1365 0.0173 0.1661
```

The next line calculates `ddf` = 12.822129. The remaining lines calculate the critical value of the F-distribution, `FCrit` = 4.680382 and statistical power = 0.7494133, which by design is close to 80%, i.e., the numbers of readers and cases were chosen to achieve this value.

9.2.2 Fixed reader random case (FRRC)

This code illustrates fixed reader random case sample size estimation. Assumed are 10 readers and 133 cases in the pivotal study. The formulae are:

$$\Delta = \frac{JK\sigma_{Y;\tau}^2}{\sigma_{Y;\varepsilon}^2 + \sigma_{Y;\tau RC}^2 + J\sigma_{Y;\tau C}^2}$$

The sampling distribution of the F-statistic under the AH is:

$$F_{AH|R} \equiv \frac{MST}{MSTC} \sim F_{I-1,(I-1)(K-1),\Delta}$$

```
#FRRC
ncp <- (0.5*J*K*(effectSize)^2)/(max(J*varYTC,0)+varYEps)
ddf <- (K-1)
FCrit <- qf(1 - alpha, 1, ddf)
Power2 <- 1-pf(FCrit, 1, ddf, ncp = ncp)
```

This time non centrality parameter, `ncp` = 7.9873835, `ddf` = 132, `FCrit` = 3.912875 and statistical power = 0.8011167. Again, be design, this is close to 80%. Note that when readers are regarded as a fixed effect, fewer cases are needed to achieve the desired power. Freezing out a source of variability results in a more stable measurement and hence fewer cases are needed to achieve the desired power.

9.2.3 Random reader fixed case (RRFC)

This code illustrates random reader random case sample size estimation. Assumed are 10 readers and 53 cases in the pivotal study. The formulae are:

$$\Delta = \frac{JK\sigma_{Y;\tau}^2}{\sigma_{Y;\varepsilon}^2 + \sigma_{Y;\tau RC}^2 + K\sigma_{Y;\tau R}^2}$$

The sampling distribution of the F-statistic under the AH is:

$$F_{AH|C} \equiv \frac{MST}{MSTR} \sim F_{I-1,(I-1)(J-1),\Delta}$$

```r
#RRFC
ncp <- (0.5*J*K*(effectSize)^2)/(K*varYTR+varYEps)
ddf <- (J-1)
FCrit <- qf(1 - alpha, 1, ddf)
Power3 <- 1-pf(FCrit, 1, ddf, ncp = ncp)
```

This time non centrality parameter, `ncp` = 10.0487164, `ddf` = 9, `FCrit` = 5.117355 and statistical power = 0.8049666. Again, be design, this is close to 80%.

9.3 Summary

For 10 readers, the numbers of cases needed for 80% power is largest (163) for RRRC, intermediate (133) for FRRC and least for RRFC (53). For all three analyses, the expectation of 80% power is met.

9.4 References

Chapter 10

ROC-DBMH sample size using RJafroc

10.1 Introduction

This illustrates the `RJafroc` implementation of sample-size estimation. Default α is 0.05 and default power (1-β) is 0.8. Three functions are provided. Each of these functions can be used with `method "DBMH"` (illustrated here, the default) or `method = "ORH"` (next vignette). Illustrated below, for the most part, is the random-reader random-case (RRRC) option, i.e., `option = "RRRC"`. The last two examples illustrate fixed-reader random-case (FRRC) `option = "FRRC"` and random-reader fixed-case (RRFC) `option = "RRFC"` options.

- `SsPowerGivenJK()` Statistical power for specified numbers of readers and cases in an ROC study.
- `SsPowerTable()` Generate a power table, i.e., combinations of numbers of readers and cases yielding the desired power.
- `SsSampleSizeKGivenJ` Number of cases, for specified number of readers, to achieve desired power.

10.2 Illustration of `SsPowerGivenJK()` using `method = "DBMH"`

The selected dataset corresponds to the Van Dyke data.

```r
power <- SsPowerGivenJK(dataset02, FOM = "Wilcoxon", J = 6, K = 112, option = "RRRC")
```

The returned value is a list containing the expected power `power`, the noncentrality parameter `ncp`, the denominator degrees of freedom `ddf` and the F-statistic `f`. The numerator degrees of freedom `ndf` is always `I - 1`, i.e., unity for this dataset.

```r
str(power)
#> 'data.frame':    1 obs. of  4 variables:
#>  $ powerRRRC: num 0.556
#>  $ ncpRRRC  : num 4.8
#>  $ ddfHRRRC : num 23.1
#>  $ fRRRC    : num 4.28
```

Expected power is 0.5555789.

10.3 Illustration of `SsPowerTable()` using `method = "DBMH"`

```r
powTab <- SsPowerTable(dataset02, FOM = "Wilcoxon", method = "DBMH", option = "RRRC")
```

Now show the power table `powTab`. Note that the last column is always close to 0.8, the desired power. The 2nd and 3rd columns show the number of readers and number of cases to achieve the desired power.

```r
powTab
#>    numReaders numCases power
#> 1           3    >2000  <NA>
#> 2           3    >2000  <NA>
#> 3           4     1089   0.8
#> 4           4     1089   0.8
#> 5           5      344 0.801
#> 6           5      344 0.801
#> 7           6      251 0.801
#> 8           6      251 0.801
#> 9           7      211 0.801
#> 10          7      211 0.801
#> 11          8      188 0.801
#> 12          8      188 0.801
#> 13          9      173 0.801
#> 14          9      173 0.801
#> 15          10      163 0.802
#> 16          10      163 0.802
#> 17          11      155 0.801
#> 18          11      155 0.801
#> 19          12      149 0.802
#> 20          12      149 0.802
#> 21          13      144 0.801
#> 22          13      144 0.801
#> 23          14      140 0.802
#> 24          14      140 0.802
#> 25          15      137 0.802
#> 26          15      137 0.802
#> 27          16      134 0.802
#> 28          16      134 0.802
#> 29          17      131 0.801
#> 30          17      131 0.801
#> 31          18      129 0.801
#> 32          18      129 0.801
#> 33          19      127 0.801
#> 34          19      127 0.801
#> 35          20      126 0.802
#> 36          20      126 0.802
#> 37          21      124 0.801
#> 38          21      124 0.801
#> 39          22      123 0.802
#> 40          22      123 0.802
#> 41          23      122 0.802
#> 42          23      122 0.802
#> 43          24      121 0.803
#> 44          24      121 0.803
#> 45          25      120 0.802
#> 46          25      120 0.802
#> 47          26      119 0.802
#> 48          26      119 0.802
#> 49          27      118 0.802
#> 50          27      118 0.802
#> 51          28      117 0.801
#> 52          28      117 0.801
#> 53          29      117 0.803
#> 54          29      117 0.803
#> 55          30      116 0.802
#> 56          30      116 0.802
#> 57          31      115 0.801
#> 58          31      115 0.801
#> 59          32      115 0.803
#> 60          32       115 0.803
#> 61          33       114 0.801
#> 62          33       114 0.801
#> 63          34       114 0.803
#> 64          34       114 0.803
#> 65          35       113 0.801
#> 66          35       113 0.801
#> 67          36       113 0.802
#> 68          36       113 0.802
#> 69          37       112   0.8
#> 70          37       112   0.8
#> 71          38       112 0.802
#> 72          38       112 0.802
#> 73          39       112 0.803
#> 74          39       112 0.803
#> 75          40       111 0.801
#> 76          40       111 0.801
#> 77          41       111 0.802
#> 78          41       111 0.802
#> 79          42       111 0.803
#> 80          42       111 0.803
#> 81          43       110 0.801
#> 82          43       110 0.801
#> 83          44       110 0.802
#> 84          44       110 0.802
#> 85          45       110 0.802
#> 86          45       110 0.802
#> 87          46       110 0.803
#> 88          46       110 0.803
#> 89          47       109 0.801
#> 90          47       109 0.801
#> 91          48       109 0.802
#> 92          48       109 0.802
#> 93          49       109 0.802
#> 94          49       109 0.802
#> 95          50       109 0.803
#> 96          50       109 0.803
#> 97          51       108   0.8
#> 98          51       108   0.8
#> 99          52       108 0.801
#> 100         52       108 0.801
#> 101         53       108 0.802
#> 102         53       108 0.802
#> 103         54       108 0.802
#> 104         54       108 0.802
#> 105         55      108 0.803
#> 106         55      108 0.803
#> 107         56      107   0.8
#> 108         56      107   0.8
#> 109         57      107 0.801
#> 110         57      107 0.801
#> 111         58      107 0.801
#> 112         58      107 0.801
#> 113         59      107 0.802
#> 114         59      107 0.802
#> 115         60      107 0.802
#> 116         60      107 0.802
#> 117         61      107 0.803
#> 118         61      107 0.803
#> 119         62      107 0.803
#> 120         62      107 0.803
#> 121         63      106   0.8
#> 122         63      106   0.8
#> 123         64      106 0.801
#> 124         64      106 0.801
#> 125         65      106 0.801
#> 126         65      106 0.801
#> 127         66      106 0.802
#> 128         66      106 0.802
#> 129         67      106 0.802
#> 130         67      106 0.802
#> 131         68      106 0.802
#> 132         68      106 0.802
#> 133         69      106 0.803
#> 134         69      106 0.803
#> 135         70      106 0.803
#> 136         70      106 0.803
#> 137         71      106 0.804
#> 138         71      106 0.804
#> 139         72      105   0.8
#> 140         72      105   0.8
#> 141         73      105 0.801
#> 142         73      105 0.801
#> 143         74      105 0.801
#> 144         74      105 0.801
#> 145         75      105 0.801
#> 146         75      105 0.801
#> 147         76      105 0.802
#> 148         76      105 0.802
#> 149         77      105 0.802
#> 150         77       105 0.802
#> 151         78       105 0.802
#> 152         78       105 0.802
#> 153         79       105 0.803
#> 154         79       105 0.803
#> 155         80       105 0.803
#> 156         80       105 0.803
#> 157         81       105 0.803
#> 158         81       105 0.803
#> 159         82       105 0.803
#> 160         82       105 0.803
#> 161         83       104   0.8
#> 162         83       104   0.8
#> 163         84       104   0.8
#> 164         84       104   0.8
#> 165         85       104 0.801
#> 166         85       104 0.801
#> 167         86       104 0.801
#> 168         86       104 0.801
#> 169         87       104 0.801
#> 170         87       104 0.801
#> 171         88       104 0.801
#> 172         88       104 0.801
#> 173         89       104 0.802
#> 174         89       104 0.802
#> 175         90       104 0.802
#> 176         90       104 0.802
#> 177         91       104 0.802
#> 178         91       104 0.802
#> 179         92       104 0.802
#> 180         92       104 0.802
#> 181         93       104 0.802
#> 182         93       104 0.802
#> 183         94       104 0.803
#> 184         94       104 0.803
#> 185         95       104 0.803
#> 186         95       104 0.803
#> 187         96       104 0.803
#> 188         96       104 0.803
#> 189         97       104 0.803
#> 190         97       104 0.803
#> 191         98       104 0.804
#> 192         98       104 0.804
#> 193         99       104 0.804
#> 194         99       104 0.804
#> 195         100       103    0.8
#> 196         100       103    0.8
```

10.4 Illustration of SsSampleSizeKGivenJ() using method = "DBMH"

This function illustrates how the number of cases for 10 readers, used in Vignette 2, were chosen. In all but one example the default value of the `desiredPower` argument is used, namely 0.8 (if the argument is absent, its default value is used).

10.4.1 RRRC

```
ncases <- SsSampleSizeKGivenJ(dataset02, FOM = "Wilcoxon", J = 10, method = "DBMH", option = "RRR
str(ncases)
#> 'data.frame':    1 obs. of  2 variables:
#>  $ KRRRC    : num 163
#>  $ powerRRRC: num 0.802
```

`ncases` is a list containing the number of cases 163 and expected power 0.8015625. Compare the number of cases to the RRRC value used in vignette 2.

10.4.1.1 Non default value of `desiredPower`

This is illustrated below for 90% desired power.

```
ncases <- SsSampleSizeKGivenJ(dataset02, FOM = "Wilcoxon", J = 10, method = "DBMH", option = "RRR
str(ncases)
#> 'data.frame':    1 obs. of  2 variables:
#>  $ KRRRC    : num 236
#>  $ powerRRRC: num 0.9
```

The required number of cases is 236 and expected power is 0.9003501.

10.4.2 FRRC

```
ncases <- SsSampleSizeKGivenJ(dataset02, FOM = "Wilcoxon", J = 10, method = "DBMH", op
str(ncases)
#> 'data.frame':    1 obs. of  2 variables:
#>  $ KFRRC    : num 133
#>  $ powerFRRC: num 0.801
```

The required number of cases is 133 and expected power is 0.8011167. Compare the number of cases to the FRRC value used in vignette 2.

10.4.3 RRFC

```
ncases <- SsSampleSizeKGivenJ(dataset02, FOM = "Wilcoxon", J = 10, method = "DBMH", op
str(ncases)
#> 'data.frame':    1 obs. of  2 variables:
#>  $ KRRFC    : num 53
#>  $ powerRRFC: num 0.805
```

The required number of cases is 53 and expected power is 0.8049666. Compare the number of cases to the RRFC value used in vignette 2.

Chapter 11

ROC-ORH sample size using RJafroc

11.1 Introduction

The use of the functions introduced in vignette 3, but this time using the ORH method to estimate the variance components, is illustrated here. The reader should confirm that these give the same results as the corresponding ones obtained using the DBMH method. When the figure of merit is the empirical AUC, the two methods can be shown to be identical.

11.2 Illustration of SsPowerGivenJK() using method = "ORH"

```
power <- SsPowerGivenJK(dataset02, FOM = "Wilcoxon", J = 6, K = 251, method = "ORH", option = "RR
```

The returned value is a `list` containing the expected power, the non-centrality parameter, the denominator degrees of freedom and the F-statistic (the numerator degrees of freedom is always one less than the number of treatments, i.e., unity in this example).

```
str(power)
#> 'data.frame':    1 obs. of  4 variables:
#>  $ powerRRRC: num 0.801
#>  $ ncpRRRC  : num 8.91
#>  $ ddfHRRRC : num 16.1
#>  $ fRRRC    : num 4.49
```

Expected power is 0.8005403.

11.3 Illustration of `SsPowerTable()` using `method = "ORH"`

```
powTab <- SsPowerTable(dataset02, FOM = "Wilcoxon", method = "ORH", option = "RRRC")
```

Now show the power table `powTab`.

```
powTab
#>    numReaders numCases power
#> 1           3    >2000  <NA>
#> 2           3    >2000  <NA>
#> 3           4     1089   0.8
#> 4           4     1089   0.8
#> 5           5      344 0.801
#> 6           5      344 0.801
#> 7           6      251 0.801
#> 8           6      251 0.801
#> 9           7      211 0.801
#> 10          7      211 0.801
#> 11          8      188 0.801
#> 12          8      188 0.801
#> 13          9      173 0.801
#> 14          9      173 0.801
#> 15         10      163 0.802
#> 16         10      163 0.802
#> 17         11      155 0.801
#> 18         11      155 0.801
#> 19         12      149 0.802
#> 20         12      149 0.802
#> 21         13      144 0.801
#> 22         13      144 0.801
#> 23         14      140 0.802
#> 24         14      140 0.802
#> 25         15      137 0.802
#> 26         15      137 0.802
#> 27         16      134 0.802
#> 28          16      134 0.802
#> 29          17      131 0.801
#> 30          17      131 0.801
#> 31          18      129 0.801
#> 32          18      129 0.801
#> 33          19      127 0.801
#> 34          19      127 0.801
#> 35          20      126 0.802
#> 36          20      126 0.802
#> 37          21      124 0.801
#> 38          21      124 0.801
#> 39          22      123 0.802
#> 40          22      123 0.802
#> 41          23      122 0.802
#> 42          23      122 0.802
#> 43          24      121 0.803
#> 44          24      121 0.803
#> 45          25      120 0.802
#> 46          25      120 0.802
#> 47          26      119 0.802
#> 48          26      119 0.802
#> 49          27      118 0.802
#> 50          27      118 0.802
#> 51          28      117 0.801
#> 52          28      117 0.801
#> 53          29      117 0.803
#> 54          29      117 0.803
#> 55          30      116 0.802
#> 56          30      116 0.802
#> 57          31      115 0.801
#> 58          31      115 0.801
#> 59          32      115 0.803
#> 60          32      115 0.803
#> 61          33      114 0.801
#> 62          33      114 0.801
#> 63          34      114 0.803
#> 64          34      114 0.803
#> 65          35      113 0.801
#> 66          35      113 0.801
#> 67          36      113 0.802
#> 68          36      113 0.802
#> 69          37      112   0.8
#> 70          37      112   0.8
#> 71          38      112 0.802
#> 72          38      112 0.802
#> 73          39      112 0.803
#> 74          39      112 0.803
#> 75          40      111 0.801
#> 76          40      111 0.801
#> 77          41      111 0.802
#> 78          41      111 0.802
#> 79          42      111 0.803
#> 80          42      111 0.803
#> 81          43      110 0.801
#> 82          43      110 0.801
#> 83          44      110 0.802
#> 84          44      110 0.802
#> 85          45      110 0.802
#> 86          45      110 0.802
#> 87          46      110 0.803
#> 88          46      110 0.803
#> 89          47      109 0.801
#> 90          47      109 0.801
#> 91          48      109 0.802
#> 92          48      109 0.802
#> 93          49      109 0.802
#> 94          49      109 0.802
#> 95          50      109 0.803
#> 96          50      109 0.803
#> 97          51      108   0.8
#> 98          51      108   0.8
#> 99          52      108 0.801
#> 100         52      108 0.801
#> 101         53      108 0.802
#> 102         53      108 0.802
#> 103         54      108 0.802
#> 104         54      108 0.802
#> 105         55      108 0.803
#> 106         55      108 0.803
#> 107         56      107   0.8
#> 108         56      107   0.8
#> 109         57      107 0.801
#> 110         57      107 0.801
#> 111         58      107 0.801
#> 112         58      107 0.801
#> 113         59      107 0.802
#> 114         59      107 0.802
#> 115         60      107 0.802
#> 116         60      107 0.802
#> 117         61      107 0.803
#> 118         61       107 0.803
#> 119         62       107 0.803
#> 120         62       107 0.803
#> 121         63       106   0.8
#> 122         63       106   0.8
#> 123         64       106 0.801
#> 124         64       106 0.801
#> 125         65       106 0.801
#> 126         65       106 0.801
#> 127         66       106 0.802
#> 128         66       106 0.802
#> 129         67       106 0.802
#> 130         67       106 0.802
#> 131         68       106 0.802
#> 132         68       106 0.802
#> 133         69       106 0.803
#> 134         69       106 0.803
#> 135         70       106 0.803
#> 136         70       106 0.803
#> 137         71       106 0.804
#> 138         71       106 0.804
#> 139         72       105   0.8
#> 140         72       105   0.8
#> 141         73       105 0.801
#> 142         73       105 0.801
#> 143         74       105 0.801
#> 144         74       105 0.801
#> 145         75       105 0.801
#> 146         75       105 0.801
#> 147         76       105 0.802
#> 148         76       105 0.802
#> 149         77       105 0.802
#> 150         77       105 0.802
#> 151         78       105 0.802
#> 152         78       105 0.802
#> 153         79       105 0.803
#> 154         79       105 0.803
#> 155         80       105 0.803
#> 156         80       105 0.803
#> 157         81       105 0.803
#> 158         81       105 0.803
#> 159         82       105 0.803
#> 160         82       105 0.803
#> 161         83       104   0.8
#> 162         83       104   0.8
#> 163         84      104   0.8
#> 164         84      104   0.8
#> 165         85      104 0.801
#> 166         85      104 0.801
#> 167         86      104 0.801
#> 168         86      104 0.801
#> 169         87      104 0.801
#> 170         87      104 0.801
#> 171         88      104 0.801
#> 172         88      104 0.801
#> 173         89      104 0.802
#> 174         89      104 0.802
#> 175         90      104 0.802
#> 176         90      104 0.802
#> 177         91      104 0.802
#> 178         91      104 0.802
#> 179         92      104 0.802
#> 180         92      104 0.802
#> 181         93      104 0.802
#> 182         93      104 0.802
#> 183         94      104 0.803
#> 184         94      104 0.803
#> 185         95      104 0.803
#> 186         95      104 0.803
#> 187         96      104 0.803
#> 188         96      104 0.803
#> 189         97      104 0.803
#> 190         97      104 0.803
#> 191         98      104 0.804
#> 192         98      104 0.804
#> 193         99      104 0.804
#> 194         99      104 0.804
#> 195        100      103   0.8
#> 196        100      103   0.8
```

Since the default `FOM = "Wilcoxon"`, the table is identical to that generated in vignette 3, which used `method = "DBMH"`.

11.4 Illustrations of SsSampleSizeKGivenJ() using method = "ORH"

11.4.1 For RRRC generalization

```
ncases <- SsSampleSizeKGivenJ(dataset02, FOM = "Wilcoxon", J = 10, method = "ORH", option = "RRRC
```

`ncases` is a list containing the number of cases `ncases$KRRRC` and expected power `ncases$powerRRRC`.

```
str(ncases)
#> 'data.frame':    1 obs. of  2 variables:
#>  $ KRRRC    : num 163
#>  $ powerRRRC: num 0.802
```

The required number of cases is 163 and expected power is 0.8015625.

11.4.2 For FRRC generalization

```
ncases <- SsSampleSizeKGivenJ(dataset02, FOM = "Wilcoxon", J = 10, method = "ORH", option = "FRRC
```

The required number of cases is 133 and expected power is 0.8011167.

11.4.3 For RRFC generalization

```
ncases <- SsSampleSizeKGivenJ(dataset02, FOM = "Wilcoxon", J = 10, method = "ORH", option = "RRFC
```

The required number of cases is 53 and expected power is 0.8049666.

Chapter 12

Proper ROCs

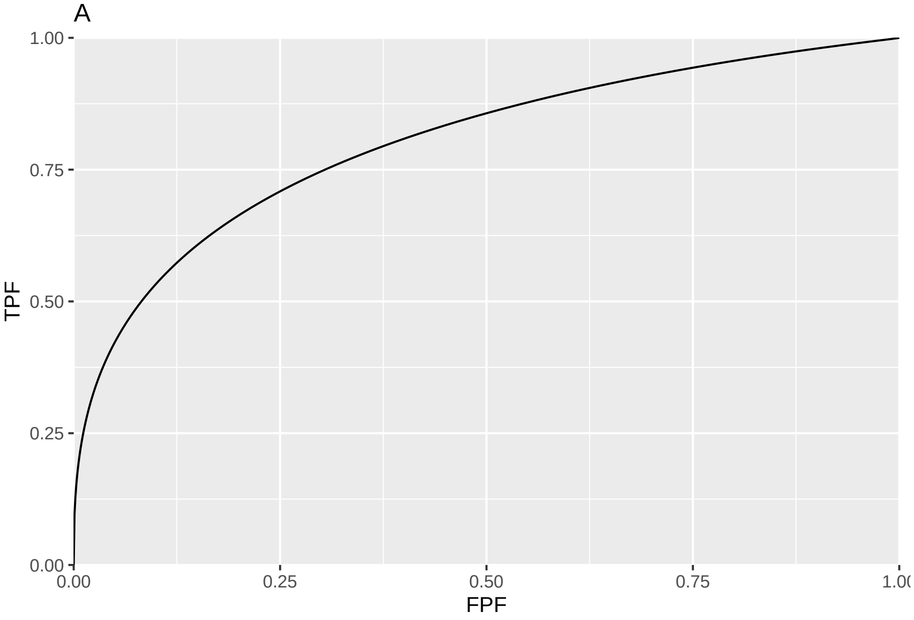
12.1 Helper functions

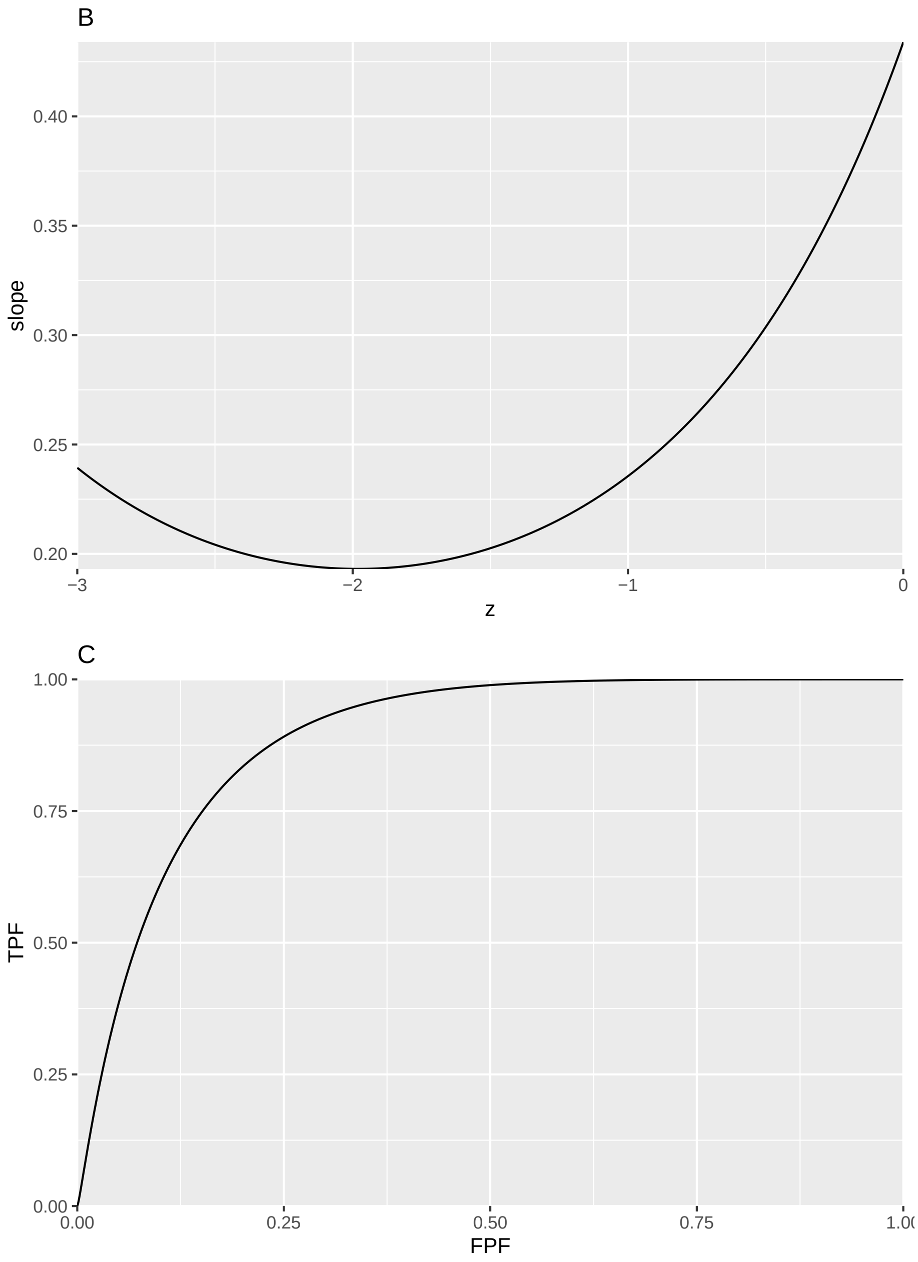
12.2 Definitions of PROPROC parameters in terms of binormal model parameters

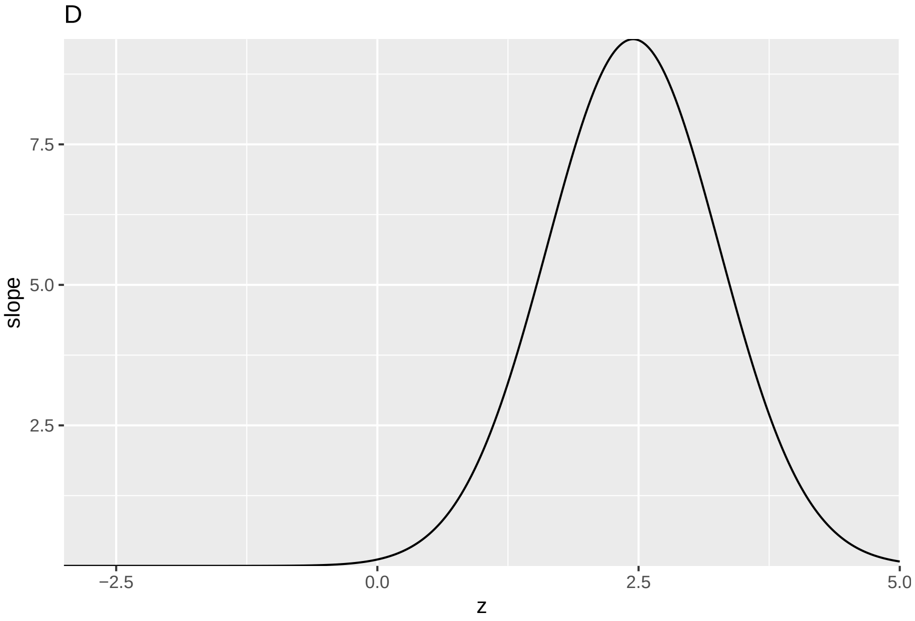
$$
\begin{aligned}
c &= \frac{b-1}{b+1} \\
d_a &= \frac{\sqrt{2}a}{\sqrt{1+b^2}}
\end{aligned}
$$

12.3 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 plo
  if (i == 2) z <- seq(-3, 5, by = 0.01) # may need to adjust limits to view detail of slope plo
  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)
}
```




B
slope
0.40
0.35
0.30
0.25
0.20
−3
−2
−1
0
z
C
TPF
1.00
0.75
0.50
0.25
0.00
0.00
0.25
0.50
0.75
1.0
FPF



12.4 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 ~   -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 (~9.4) to zero. For the stated binormal model parameters values outside of these ranges are not possible.

Chapter 13

Metz Eqn36 numerical check

13.1 Helper functions

13.2 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. =
```

13.3 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.

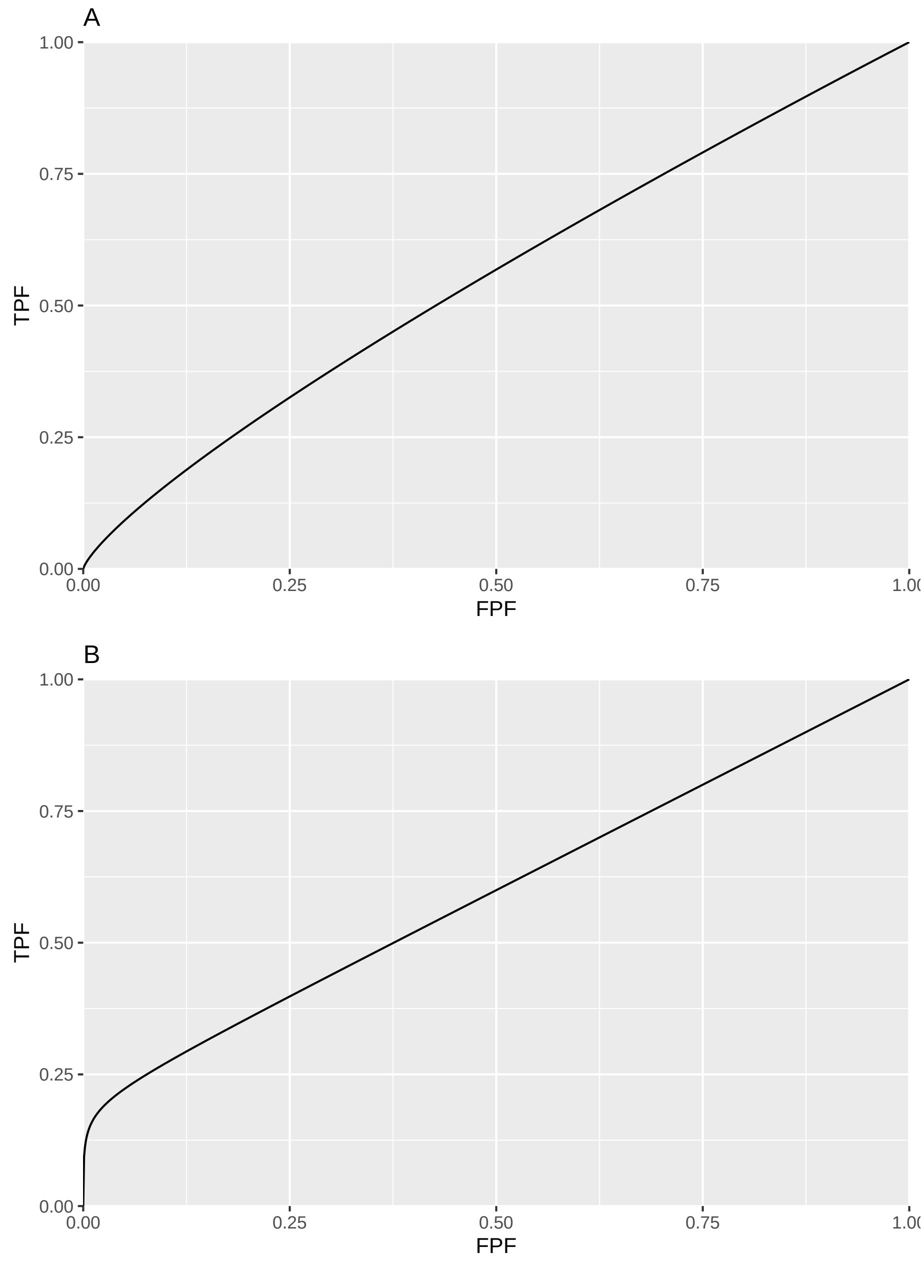
Chapter 14

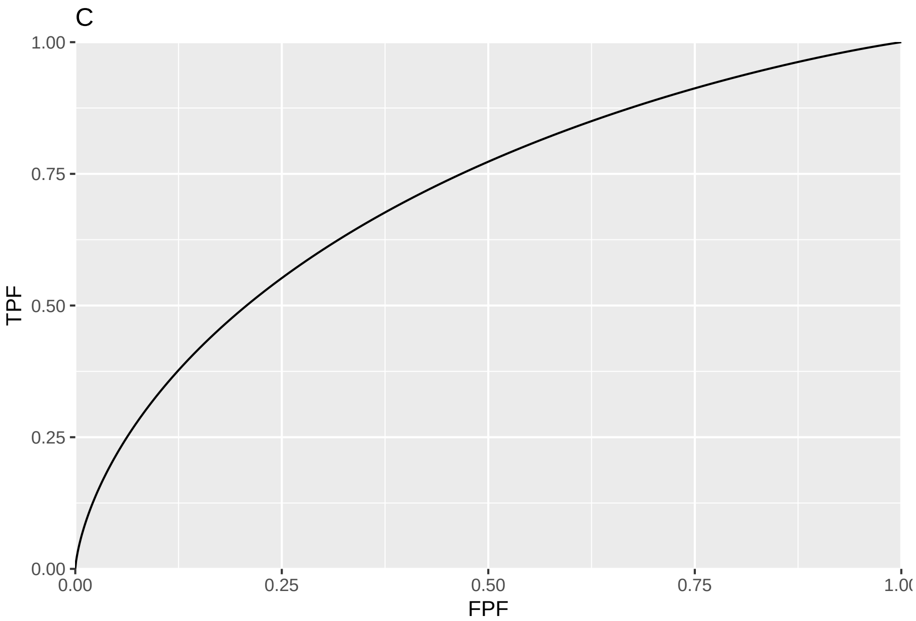
CBM Plots

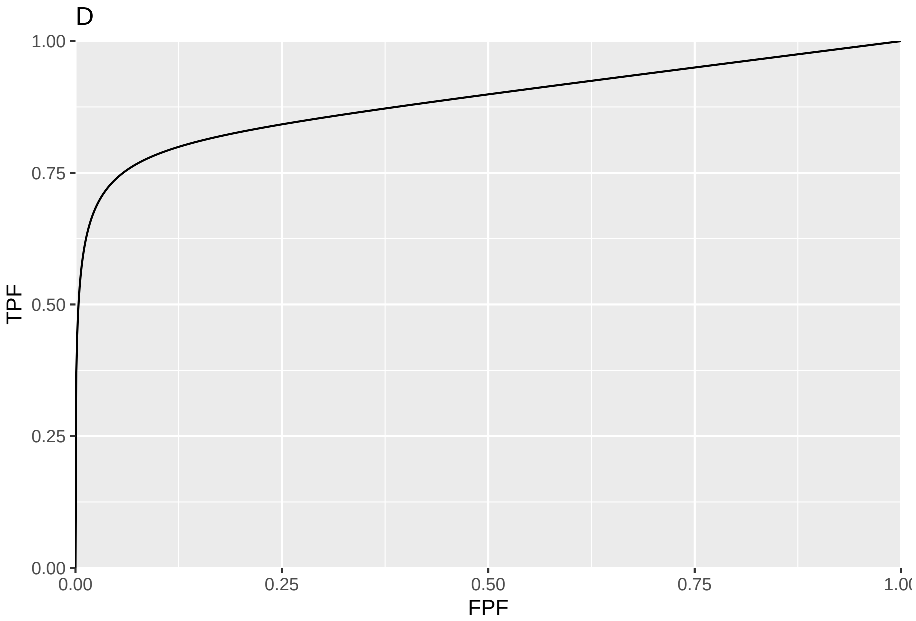
14.1 Helper functions

14.2 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
```


A
1.00
0.75
0.50
0.25
0.00
TPF
0.00
0.25
0.50
0.75
1.00
FPF
B
1.00
0.75
0.50
0.25
0.00
TPF
0.00
0.25
0.50
0.75
1.00
FPF


C
1.00
0.75
0.50
0.25
0.00
TPF
0.00
0.25
0.50
0.75
1.00
FPF

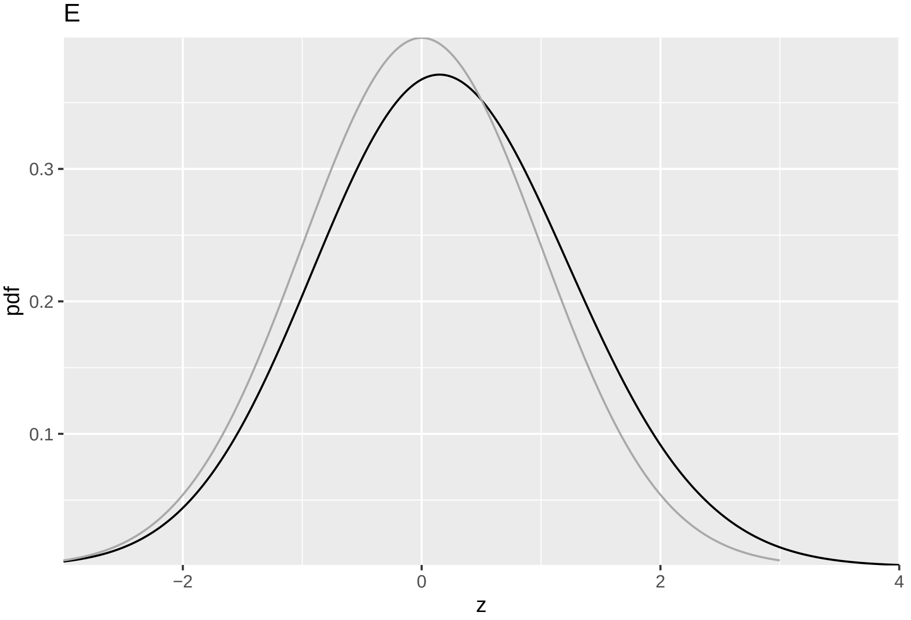

D
1.00
0.75
0.50
0.25
0.00
TPF
0.00
0.25
0.50
0.75
1.00
FPF

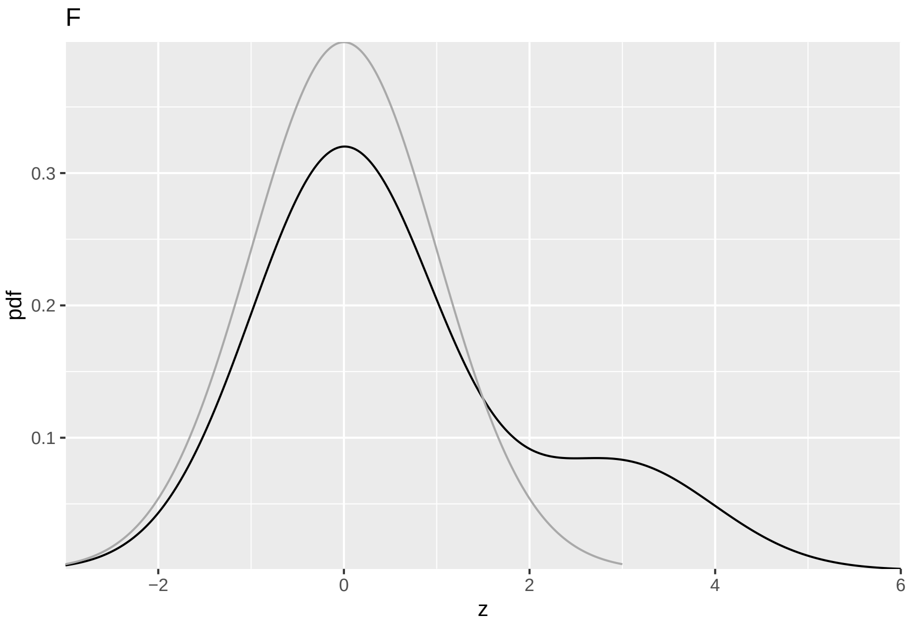
14.3 Comments

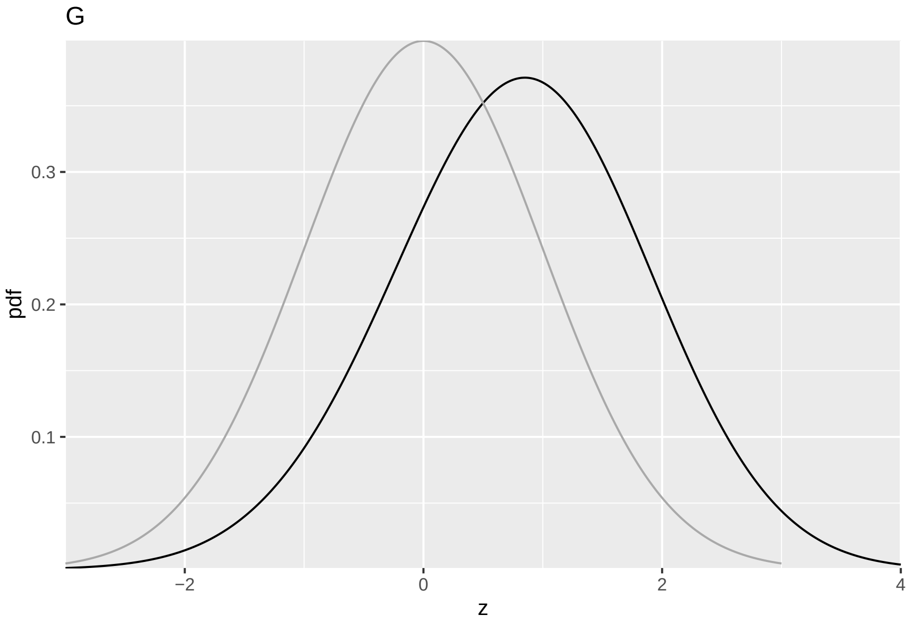
Plots A - D show ROC curves predicted by the CBM model; the corresponding values of the *mu* and *alpha* parameters are indicated above the plots. For small *mu* and/or *alpha* the curve approaches the chance diagonal, consistent with the notion that if the lesion is not visible, performance can be no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

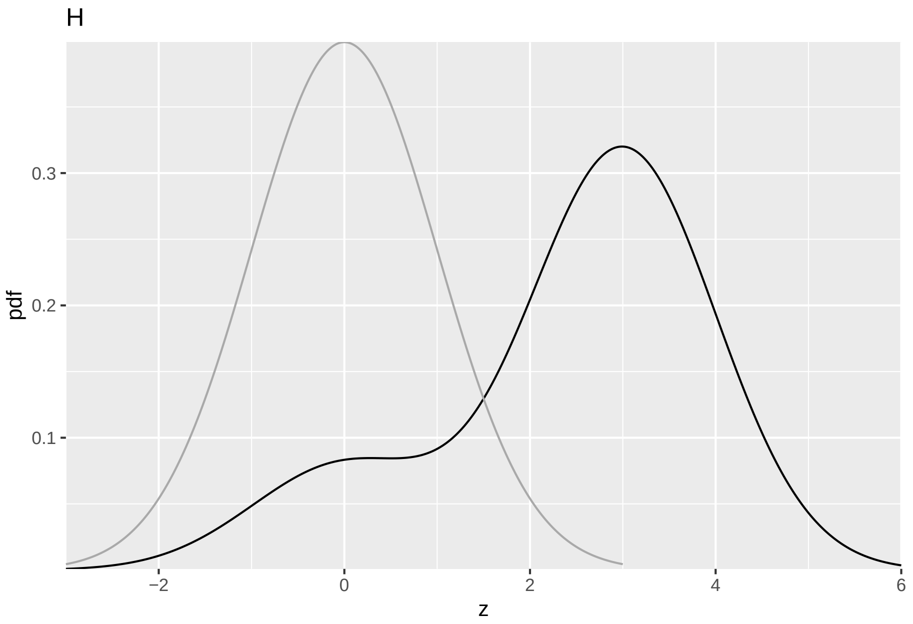
14.4 pdf plots

```
#> 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
```




F
pdf
0.3
0.2
0.1
−2
0
2
4
6
z


G
pdf
0.3
0.2
0.1
−2
0
2
4
z

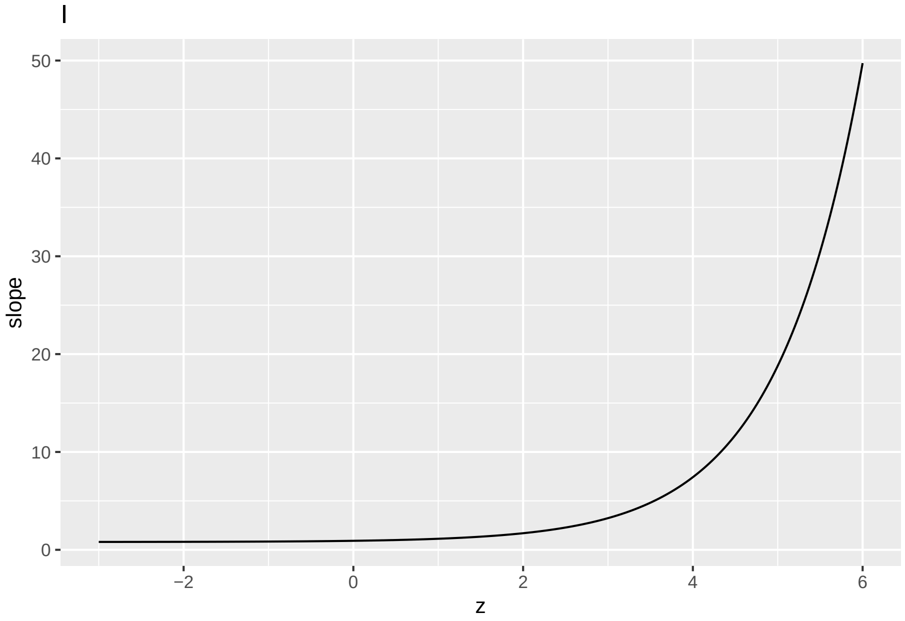


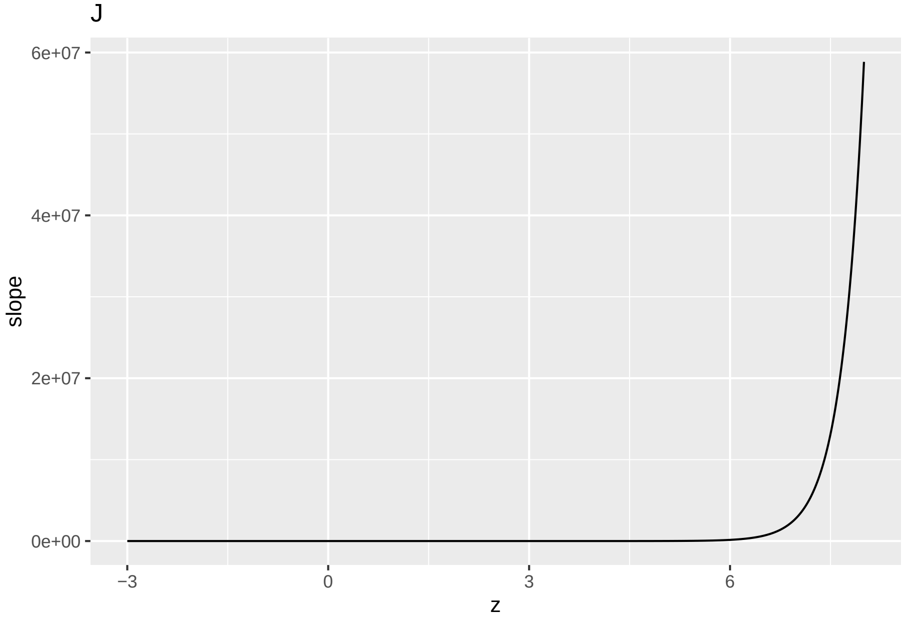
14.5 Comments

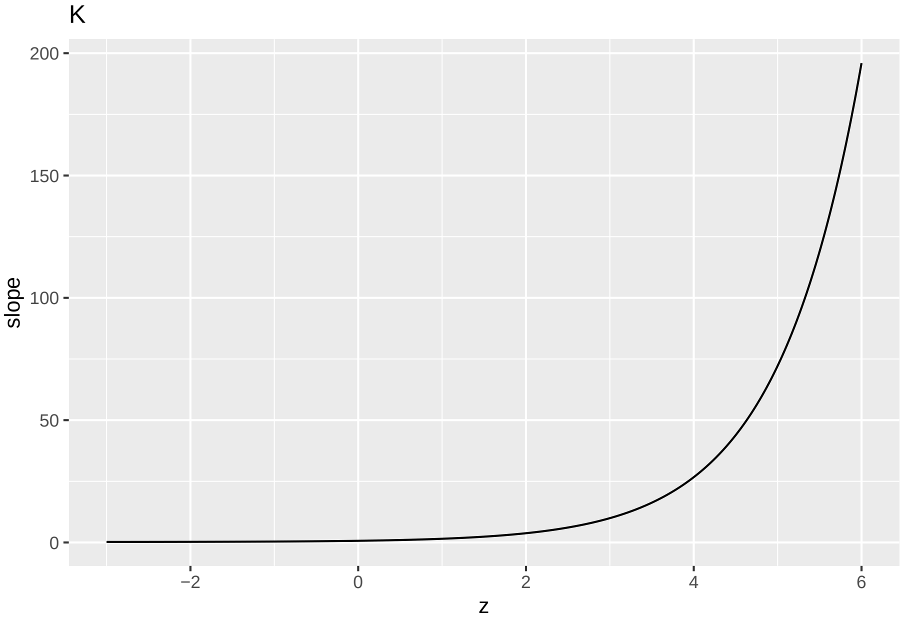
The dark line is the diseased distribution. The grey line is the non-diseased distribution. The bimodal diseased distribution is clearly evident in plots F and H.

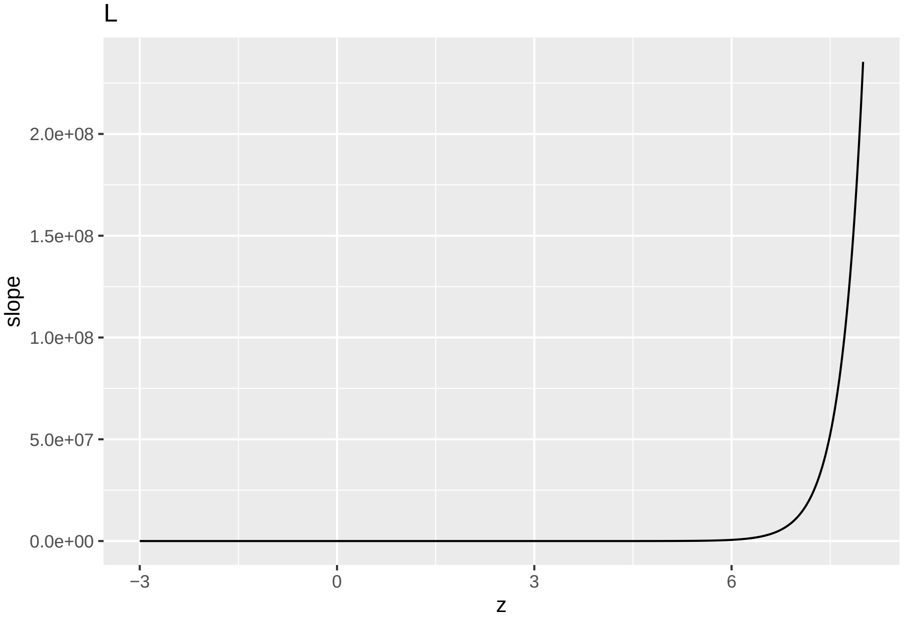
14.6 likelihood ratio plots

```
#> 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
```


I
slope
50
40
30
20
10
0
−2
0
2
4
6
z


J
slope
6e+07
4e+07
2e+07
0e+00
−3
0
3
6
z


K
slope
200
150
100
50
0
−2
0
2
4
6
z


L
slope
2.0e+08
1.5e+08
1.0e+08
5.0e+07
0.0e+00
−3
0
3
6
z

14.7 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 15

ROI paradigm data

15.1 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 ($k = 1, 2, ..., K$) 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, ..., 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.

15.2 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.

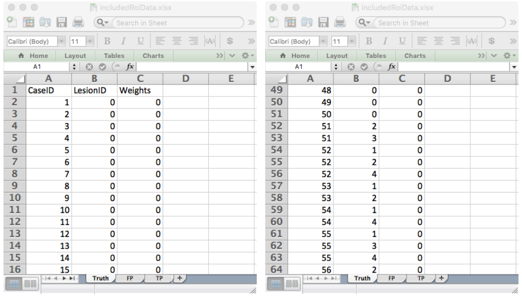
- For treatment 1, reader 1, case 51 (the 1st diseased case) the NL ratings are 1.01867, 0.3471. There are only two finite values because this case has two ROI-level-diseased regions, and 2 plus 2 makes for the assumed 4-regions per case. The corresponding `$lesionVector` field is 2.

- 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.

15.3 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		

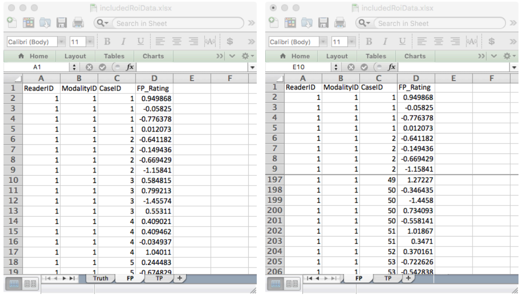
	A	B	C	D	E
49	48	0	0		
50	49	0	0		
51	50	0	0		
52	51	2	0		
53	51	3	0		
54	52	1	0		
55	52	2	0		
56	52	4	0		
57	53	1	0		
58	53	2	0		
59	54	1	0		
60	54	4	0		
61	55	1	0		
62	55	3	0		
63	55	4	0		
64	56	2	0		

Figure 15.1: 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).



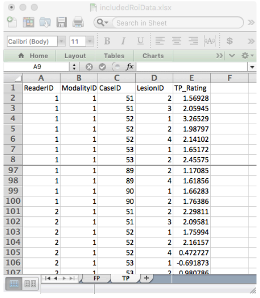
	A	B	C	D	E	F
1	ReaderID	ModalityID	CaseID	FP_Rating		
2	1	1	1	0.949868		
3	1	1	1	-0.05825		
4	1	1	1	-0.776378		
5	1	1	1	0.012073		
6	1	1	2	-0.641182		
7	1	1	2	-0.149436		
8	1	1	2	-0.669429		
9	1	1	2	-1.15841		
10	1	1	3	0.584815		
11	1	1	3	0.799213		
12	1	1	3	-1.45574		
13	1	1	3	0.55311		
14	1	1	4	0.409021		
15	1	1	4	0.409462		
16	1	1	4	-0.034937		
17	1	1	4	1.04011		
18	1	1	5	0.244483		
19	1	1	5	-0.674829		

	A	B	C	D	E	F
1	ReaderID	ModalityID	CaseID	FP_Rating		
2	1	1	1	0.949868		
3	1	1	1	-0.05825		
4	1	1	1	-0.776378		
5	1	1	1	0.012073		
6	1	1	2	-0.641182		
7	1	1	2	-0.149436		
8	1	1	2	-0.669429		
9	1	1	2	-1.15841		
197	1	1	49	1.27227		
198	1	1	50	-0.346435		
199	1	1	50	-1.4458		
200	1	1	50	0.734093		
201	1	1	50	-0.558141		
202	1	1	51	1.01867		
203	1	1	51	0.3471		
204	1	1	52	0.370161		
205	1	1	53	-0.722626		
206	1	1	53	-0.542838		

Figure 15.2: 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
1	ReaderID	ModalityID	CaseID	LesionID	TP_Rating	
2	1	1	51	2	1.56928	
3	1	1	51	3	2.05945	
4	1	1	52	1	3.26529	
5	1	1	52	2	1.98797	
6	1	1	52	4	2.14102	
7	1	1	53	1	1.65172	
8	1	1	53	2	2.45575	
97	1	1	89	2	1.17085	
98	1	1	89	4	1.61856	
99	1	1	90	1	1.66283	
100	1	1	90	2	1.76386	
101	2	1	51	2	2.29811	
102	2	1	51	3	2.09581	
103	2	1	52	1	1.75994	
104	2	1	52	2	2.16157	
105	2	1	52	4	0.472727	
106	2	1	53	1	-0.691873	
107	2	1	53	2	0.980786	

Figure 15.3: 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.

15.4 Next, TBA

The next vignette illustrates significance testing for this paradigm.

15.5 References

Chapter 16

Analyzing data acquired according to the ROI paradigm

16.1 Introduction; this vignette is under construction!

16.2 Note to self (10/29/19) !!!DPC!!!

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

16.3 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).

16.4 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:

$$N_L = \sum\nolimits_k n_k^L$$

and

$$N_N = \sum\nolimits_k n_k^N$$

The ROI figure of merit θ is defined by:

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

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

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

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.

16.5 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.

16.6 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
#>  $ ciAvgRdrEachTrtRRRC :'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
#>  $ ciAvgRdrEachTrtFRRC :'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 0.0003333119
```

16.6.1 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).

16.6.2 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 4.5823651×10^{-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
```

16.6.3 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
```

16.7 Summary

TBA

16.8 References

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