

RJafroc Documentation

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2020-03-17

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Preface

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

Chapter 1

Introduction

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

1.1 References

Chapter 2

ROC DATA FORMAT

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

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

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

2.1 Introduction

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

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

2.2 Note to existing users

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

2.3 The Excel data format

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

2.4 Illustrative toy file

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

2.5 The Truth worksheet

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

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

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

Figure 2.1: Truth worksheet for file rocCr.xlsx

2.6 The structure of an ROC dataset

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

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

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

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

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

2.7 The false positive (FP) ratings

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

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

Figure 2.2: FP worksheet for file rocCr.xlsx

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

2.8 The true positive (TP) ratings

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

| | ReaderID | ModalityID | CaseID | LesionID | TP_Rating |
|----|----------|------------|--------|----------|-----------|
| 1 | 0 | 0 | 70 | 1 | 5 |
| 2 | 0 | 0 | 71 | 1 | 5 |
| 3 | 0 | 0 | 72 | 1 | 5 |
| 4 | 0 | 0 | 73 | 1 | 5 |
| 5 | 0 | 0 | 74 | 1 | 4 |
| 6 | 1 | 0 | 70 | 1 | 5 |
| 7 | 1 | 0 | 71 | 1 | 5 |
| 8 | 1 | 0 | 72 | 1 | 5 |
| 9 | 1 | 0 | 73 | 1 | 5 |
| 10 | 1 | 0 | 74 | 1 | 5 |
| 11 | 2 | 0 | 70 | 1 | 5 |
| 12 | 2 | 0 | 71 | 1 | 5 |
| 13 | 2 | 0 | 72 | 1 | 5 |
| 14 | 2 | 0 | 73 | 1 | 5 |
| 15 | 2 | 0 | 74 | 1 | 5 |
| 16 | 3 | 0 | 70 | 1 | 5 |
| 17 | 3 | 0 | 71 | 1 | 5 |
| 18 | 3 | 0 | 72 | 1 | 5 |
| 19 | 3 | 0 | 73 | 1 | 5 |
| 20 | 3 | 0 | 74 | 1 | 5 |
| 21 | 4 | 0 | 70 | 1 | 5 |
| 22 | 4 | 0 | 71 | 1 | 5 |
| 23 | 4 | 0 | 72 | 1 | 5 |
| 24 | 4 | 0 | 73 | 1 | 5 |
| 25 | 4 | 0 | 74 | 1 | 5 |
| 26 | 0 | 1 | 1 | 1 | 5 |
| 27 | 0 | 1 | 2 | 1 | 5 |
| 28 | 0 | 1 | 3 | 1 | 5 |
| 29 | 0 | 1 | 4 | 1 | 5 |
| 30 | 0 | 1 | 5 | 1 | 5 |
| 31 | 1 | 1 | 1 | 1 | 5 |
| 32 | 1 | 1 | 2 | 1 | 5 |
| 33 | 1 | 1 | 3 | 1 | 5 |
| 34 | 1 | 1 | 4 | 1 | 5 |
| 35 | 1 | 1 | 5 | 1 | 5 |
| 36 | 2 | 1 | 1 | 1 | 5 |
| 37 | 2 | 1 | 2 | 1 | 5 |
| 38 | 2 | 1 | 3 | 1 | 5 |
| 39 | 2 | 1 | 4 | 1 | 5 |
| 40 | 2 | 1 | 5 | 1 | 5 |
| 41 | 3 | 1 | 1 | 1 | 5 |
| 42 | 3 | 1 | 2 | 1 | 5 |
| 43 | 3 | 1 | 3 | 1 | 5 |
| 44 | 3 | 1 | 4 | 1 | 5 |
| 45 | 3 | 1 | 5 | 1 | 5 |
| 46 | 4 | 1 | 1 | 1 | 5 |
| 47 | 4 | 1 | 2 | 1 | 5 |
| 48 | 4 | 1 | 3 | 1 | 5 |
| 49 | 4 | 1 | 4 | 1 | 5 |
| 50 | 4 | 1 | 5 | 1 | 5 |

Figure 2.3: TP worksheet for file rocCr.xlsx

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

2.9 Correspondence between NL member of dataset and the FP worksheet

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

2.10 Correspondence between LL member of dataset and the TP worksheet

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

2.11 Correspondence using the which function

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

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

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

2.12 References

Chapter 3

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 worksheets. 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 **LesionIDs** 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 **LesionIDs** 1, 2 and 3 and weights 1/3 each. Diseased case 73 has two lesions, with **LesionIDs** 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 |
|----|--------|----------|--------|----------|------------|----------|---|---|
| | CaseID | LesionID | Weight | ReaderID | ModalityID | Paradigm | | |
| 1 | 1 | 0 | 0 | 0.12 | 0.1 | FROC | | |
| 2 | 2 | 0 | 0 | 0.12 | 0.1 | crossed | | |
| 3 | 3 | 0 | 0 | 0.12 | 0.1 | | | |
| 4 | 3 | 0 | 0 | 0.12 | 0.1 | | | |
| 5 | 70 | 1 | 0.3 | 0.12 | 0.1 | | | |
| 6 | 70 | 2 | 0.7 | 0.12 | 0.1 | | | |
| 7 | 71 | 1 | 1 | 0.12 | 0.1 | | | |
| 8 | 72 | 1 | 0.333 | 0.12 | 0.1 | | | |
| 9 | 72 | 2 | 0.333 | 0.12 | 0.1 | | | |
| 10 | 72 | 3 | 0.333 | 0.12 | 0.1 | | | |
| 11 | 73 | 1 | 0.3 | 0.12 | 0.1 | | | |
| 12 | 73 | 2 | 0.3 | 0.12 | 0.1 | | | |
| 13 | 73 | 2 | 0.3 | 0.12 | 0.1 | | | |
| 14 | 74 | 1 | 1 | 0.12 | 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.

| ReaderID | ModalityID | CaseID | FP_Rating |
|----------|------------|--------|-----------|
| 0 | 0 | 1 | 1.02 |
| 0 | 0 | 1 | 2.17 |
| 0 | 0 | 2 | 2.22 |
| 0 | 0 | 3 | 1.9 |
| 1 | 0 | 1 | 2.23 |
| 1 | 0 | 2 | 3.1 |
| 1 | 0 | 2 | 2.23 |
| 1 | 0 | 3 | 2.07 |
| 2 | 0 | 1 | 2.14 |
| 2 | 0 | 2 | 1.86 |
| 2 | 0 | 3 | 1.95 |
| 0 | 1 | 1 | 2.89 |
| 0 | 1 | 2 | 2.89 |
| 0 | 1 | 74 | 0.84 |
| 0 | 1 | 72 | 1.85 |
| 0 | 1 | 5 | 3.22 |
| 1 | 1 | 1 | 3.01 |
| 1 | 1 | 2 | 1.96 |
| 1 | 1 | 3 | 2.08 |
| 2 | 1 | 71 | 2.24 |
| 2 | 1 | 71 | 4.01 |
| 2 | 1 | 72 | 1.86 |

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-

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** worksheet 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 ...
```

3.8. ON THE DISTRIBUTION OF NUMBERS OF LESIONS IN ABNORMAL CASES²⁷

```
#> $ 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))/length(x$lesionVector), "\n")
#> 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 worksheets 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 | ROC |
| 8 | 0 | 0 | 1 | 1,2 | ROC |
| 9 | 0 | 0 | 1 | 1,2 | ROC |
| 10 | 0 | 0 | 1 | 1,2 | ROC |
| 16 | 1 | 0 | 1 | 1,2 | split-plot |
| 17 | 1 | 0 | 1 | 1,2 | split-plot |
| 18 | 1 | 0 | 1 | 1,2 | split-plot |
| 19 | 1 | 0 | 1 | 1,2 | split-plot |
| 20 | 1 | 0 | 1 | 1,2 | split-plot |
| 21 | 0 | 0 | 4 | 1,2 | ROC |
| 22 | 0 | 0 | 4 | 1,2 | ROC |
| 23 | 0 | 0 | 4 | 1,2 | ROC |
| 24 | 0 | 0 | 4 | 1,2 | ROC |
| 25 | 0 | 0 | 4 | 1,2 | ROC |
| 36 | 1 | 0 | 4 | 1,2 | split-plot |
| 37 | 1 | 0 | 4 | 1,2 | split-plot |
| 38 | 1 | 0 | 4 | 1,2 | split-plot |
| 39 | 1 | 0 | 4 | 1,2 | split-plot |
| 40 | 1 | 0 | 4 | 1,2 | split-plot |
| 46 | 0 | 0 | 5 | 1,2 | ROC |
| 47 | 0 | 0 | 5 | 1,2 | ROC |
| 48 | 0 | 0 | 5 | 1,2 | ROC |
| 49 | 0 | 0 | 5 | 1,2 | ROC |
| 50 | 0 | 0 | 5 | 1,2 | ROC |
| 51 | 1 | 0 | 5 | 1,2 | split-plot |
| 52 | 1 | 0 | 5 | 1,2 | split-plot |
| 53 | 1 | 0 | 5 | 1,2 | split-plot |
| 54 | 1 | 0 | 5 | 1,2 | split-plot |
| 55 | 1 | 0 | 5 | 1,2 | split-plot |

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

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 1 ...
#> $ lesionID     : num [1:15, 1] 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 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.

- #### 4.5 The truthTableStr member

- ```
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
```

- [illegible]

```
#> [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
#> [,15]
#> [1,] NA
#> [2,] NA
```

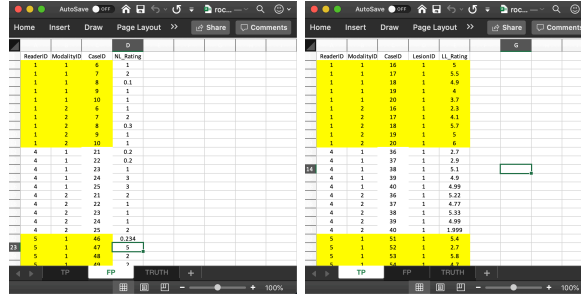


Figure 4.2: Fig. 2 FP/TP worksheets; LEFT=FP, (b) RIGHT=TP

## 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** worksheet.
- **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 -Inf 0.234 5 2 2
#> [2,] -Inf -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, 10 and 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, 15 and 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** worksheet.

- **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, 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 diseased cases with **CaseIDs** 36,37,38,39,40 (indexed 6, 7, 8, 9, 10 and 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, 15 and 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  $\mathbf{x}_{NL}$  or  $\mathbf{x}_{LL}$  list members is the total number of modalities, 2 in the current example.
- The length of the second dimension of either  $\mathbf{x}_{NL}$  or  $\mathbf{x}_{LL}$  list members is the total number of readers, 3 in the current example.
- The length of the third dimension of  $\mathbf{x}_{NL}$  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  $\mathbf{x}_{LL}$  is the total number of diseased cases, 5 in the current example.
- The length of the fourth dimension of  $\mathbf{x}_{NL}$  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  $\mathbf{x}_{LL}$  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 worksheets 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.

| CaseID | LesionID | Weight | ReaderID | ModalityID | Paradigm   | Truth | TP | FP |
|--------|----------|--------|----------|------------|------------|-------|----|----|
| 1      | 0        | 0      | 0        | 0, 1       | FROC       | 0     |    |    |
| 2      | 0        | 0      | 0        | 0, 1       | split plot | 0     |    |    |
| 3      | 0        | 0      | 0        | 0, 1       |            | 0     |    |    |
| 4      | 0        | 0      | 1        | 0, 1       |            | 0     |    |    |
| 5      | 0        | 0      | 1        | 0, 1       |            | 0     |    |    |
| 6      | 0        | 0      | 1        | 0, 1       |            | 0     |    |    |
| 7      | 0        | 0      | 2        | 0, 1       |            | 0     |    |    |
| 8      | 0        | 0      | 2        | 0, 1       |            | 0     |    |    |
| 9      | 0        | 0      | 2        | 0, 1       |            | 0     |    |    |
| 10     | 1        | 0.1    | 0        | 0, 1       |            | 1     |    |    |
| 11     | 1        | 0.2    | 0        | 0, 1       |            | 1     |    |    |
| 12     | 1        | 0.3    | 0        | 0, 1       |            | 1     |    |    |
| 13     | 1        | 0.4    | 0        | 0, 1       |            | 1     |    |    |
| 14     | 1        | 0.5    | 0        | 0, 1       |            | 1     |    |    |
| 15     | 1        | 0.6    | 0        | 0, 1       |            | 1     |    |    |
| 16     | 1        | 0.7    | 0        | 0, 1       |            | 1     |    |    |
| 17     | 1        | 0.8    | 0        | 0, 1       |            | 1     |    |    |
| 18     | 1        | 0.9    | 0        | 0, 1       |            | 1     |    |    |
| 19     | 1        | 1.0    | 0        | 0, 1       |            | 1     |    |    |
| 20     | 1        | 0.1    | 1        | 0, 1       |            | 1     |    |    |
| 21     | 1        | 0.2    | 1        | 0, 1       |            | 1     |    |    |
| 22     | 1        | 0.3    | 1        | 0, 1       |            | 1     |    |    |
| 23     | 1        | 0.4    | 1        | 0, 1       |            | 1     |    |    |
| 24     | 1        | 0.5    | 1        | 0, 1       |            | 1     |    |    |
| 25     | 1        | 0.6    | 1        | 0, 1       |            | 1     |    |    |
| 26     | 1        | 0.7    | 1        | 0, 1       |            | 1     |    |    |
| 27     | 1        | 0.8    | 1        | 0, 1       |            | 1     |    |    |
| 28     | 1        | 0.9    | 1        | 0, 1       |            | 1     |    |    |
| 29     | 1        | 1.0    | 1        | 0, 1       |            | 1     |    |    |
| 30     | 1        | 0.1    | 2        | 0, 1       |            | 1     |    |    |
| 31     | 1        | 0.2    | 2        | 0, 1       |            | 1     |    |    |
| 32     | 1        | 0.3    | 2        | 0, 1       |            | 1     |    |    |
| 33     | 1        | 0.4    | 2        | 0, 1       |            | 1     |    |    |
| 34     | 1        | 0.5    | 2        | 0, 1       |            | 1     |    |    |
| 35     | 1        | 0.6    | 2        | 0, 1       |            | 1     |    |    |
| 36     | 1        | 0.7    | 2        | 0, 1       |            | 1     |    |    |
| 37     | 1        | 0.8    | 2        | 0, 1       |            | 1     |    |    |
| 38     | 1        | 0.9    | 2        | 0, 1       |            | 1     |    |    |
| 39     | 1        | 1.0    | 2        | 0, 1       |            | 1     |    |    |

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.

The figure shows two side-by-side Excel spreadsheets. The left spreadsheet is titled 'NL/FP' and the right is titled 'LL/TP'. Both spreadsheets have a similar structure with columns for ReaderID, ModalityID, CaseID, and a rating column (FP\_Rating or TP\_Rating). The data is organized into 30 rows, with the first 10 rows having a rating of 0 and the next 20 rows having a rating of 1. The spreadsheets are displayed in a window titled 'frocSp'.

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** worksheet.
- **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** worksheet.

```

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, 6 and 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, 9 and 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** worksheet.
- **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 worksheet.

```
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 -Inf 5.14 3.31 4.92 4.95 5.30 -Inf -Inf -Inf -Inf
#> [2,] -Inf -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 -Inf 4.66 4.03 5.22 4.94
#> [2,] -Inf -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 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 degrees of 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//RtmpkqP1cY/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//RtmpkqP
```

## 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  $\Delta$  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.

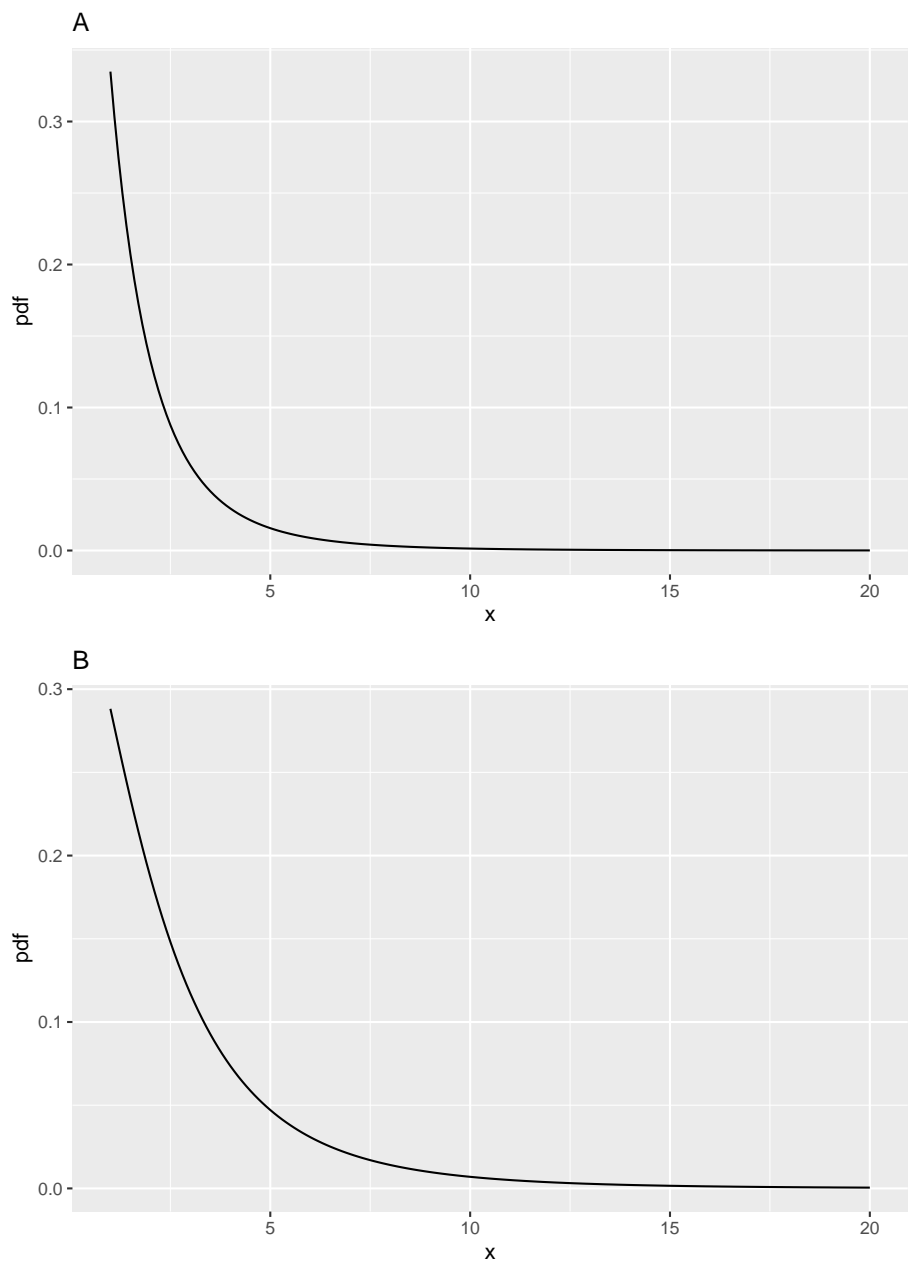
- `fCrit` is the critical value of the F distribution, i.e., that value such that fraction  $\alpha$  of the area is to the right of the critical value, i.e., `fCrit` is identical to:

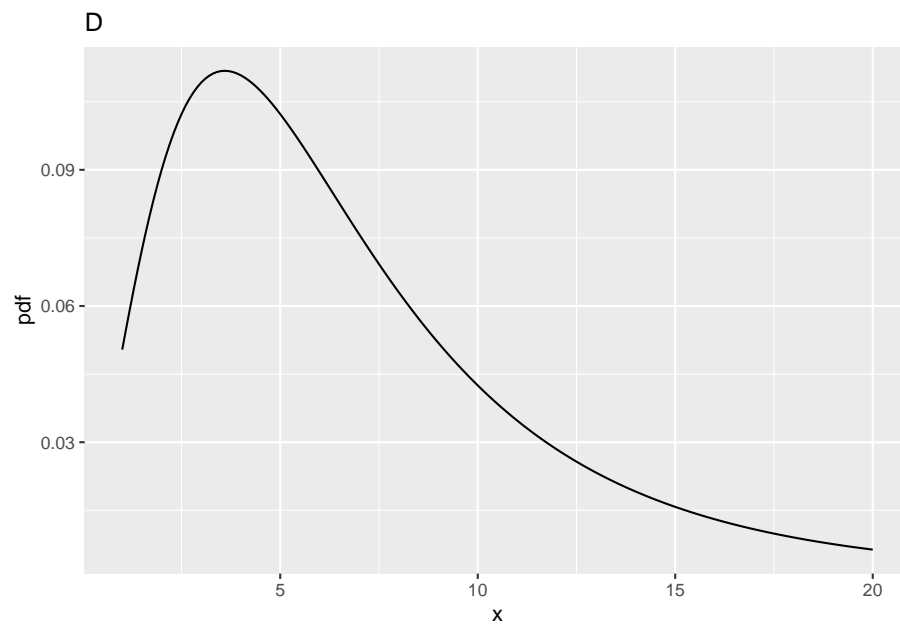
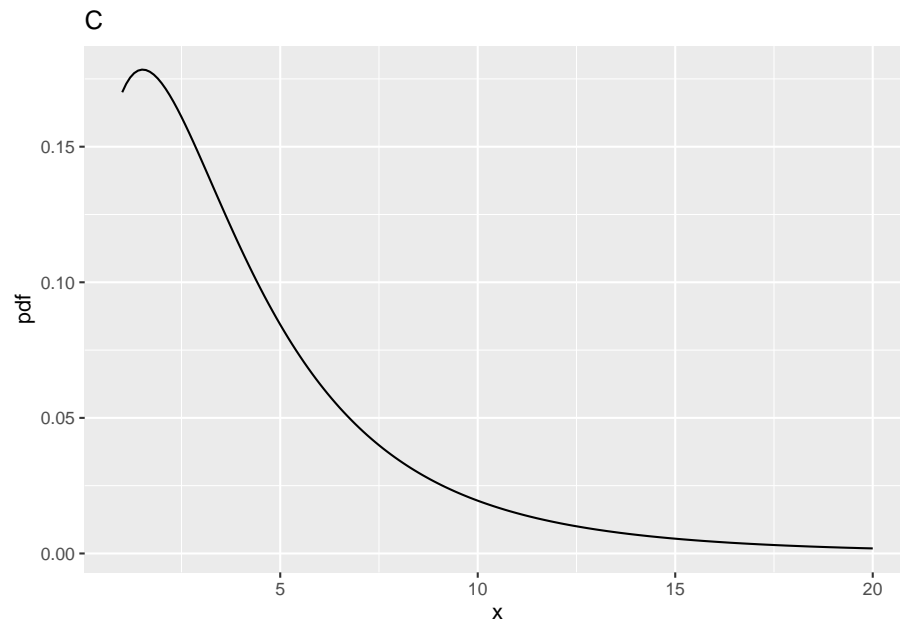
$$F_{1-\alpha, ndf, ddf}$$

```

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

```





|   | 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  $\alpha$ . 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  $F \geq fCrit$ . 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.

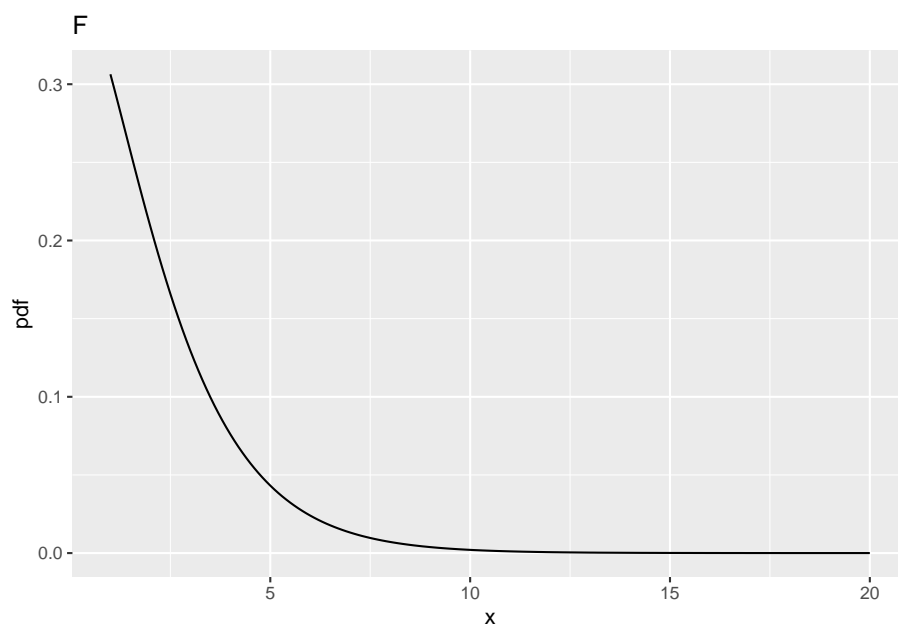
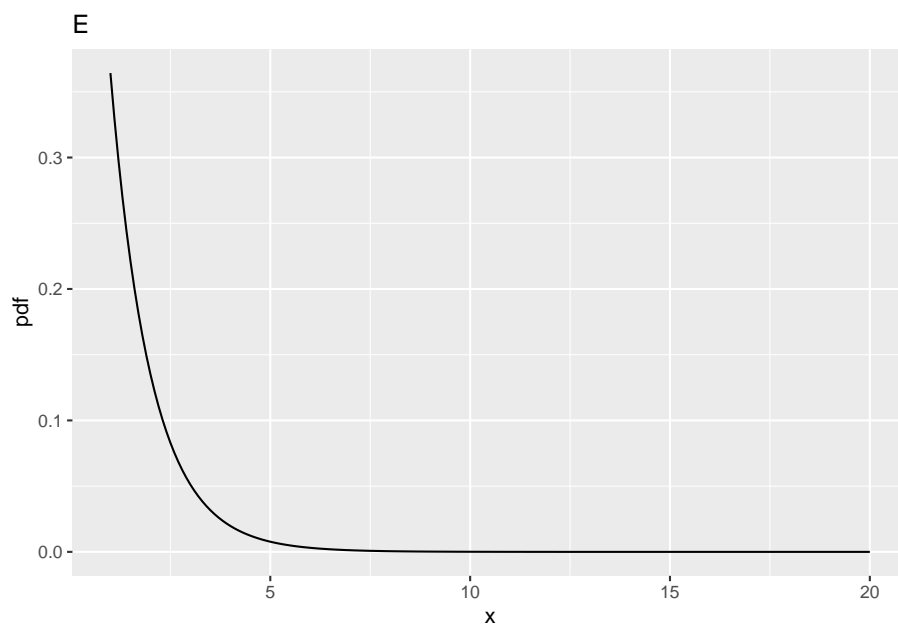
### 8.3.4 Fig. D

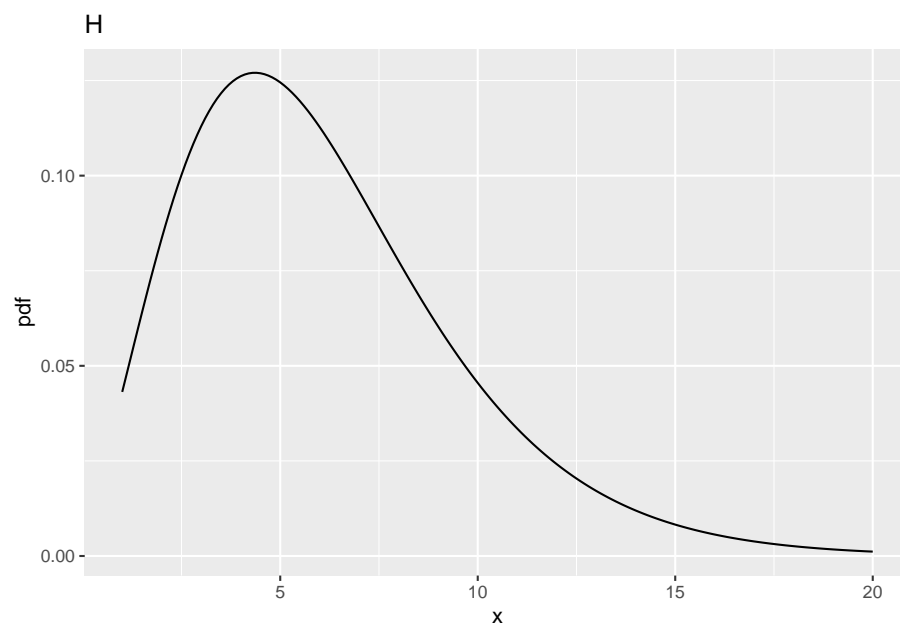
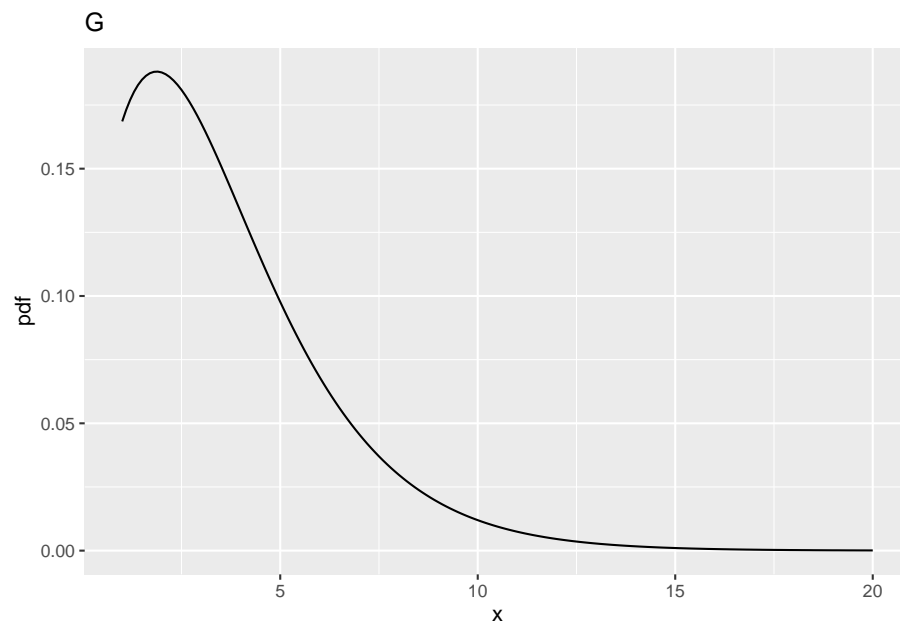
- This corresponds to `ncp = 10`, `ndf = 2` and `ddf = 10`.
- Now `prob > fCrit` is 0.6769776.
- Power has increased compared to Fig. C.
- The effect of the shift is most obvious in Fig. C and Fig. D.
- Considering a vertical line at `x = 4.102821`, fraction 0.6769776 of the probability distribution 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  $ddf = 100$** 



|   | 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.

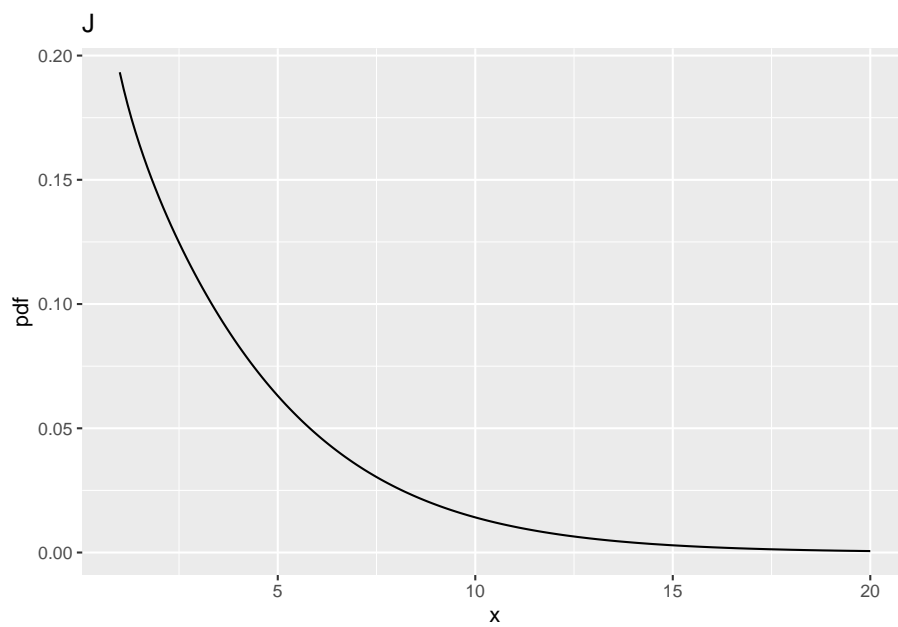
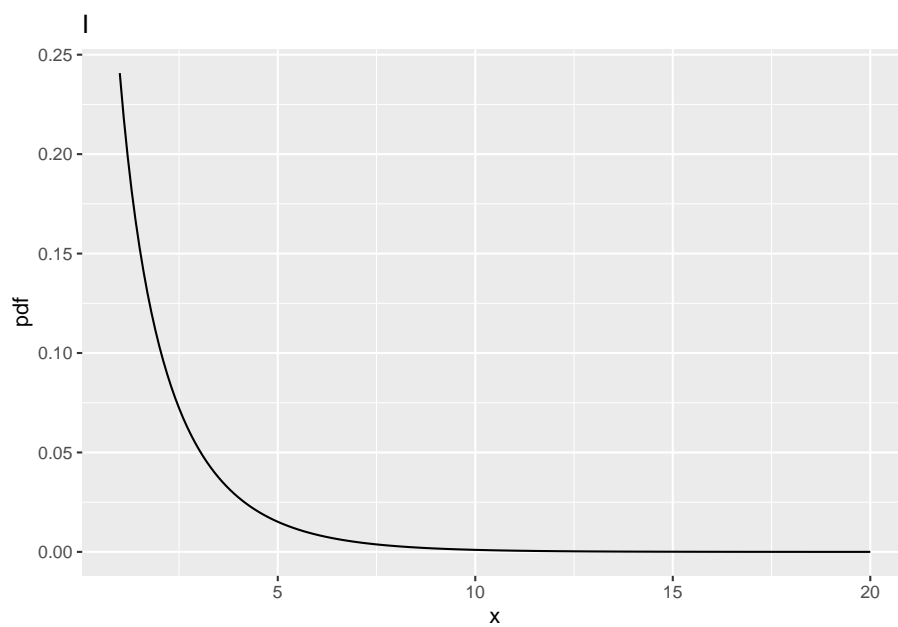
### 8.5.3 Fig. G

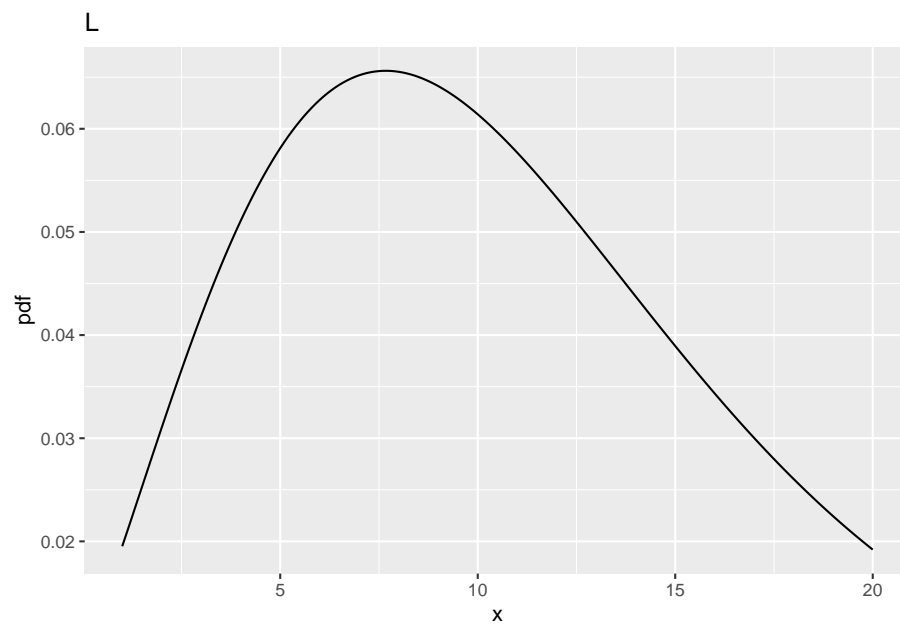
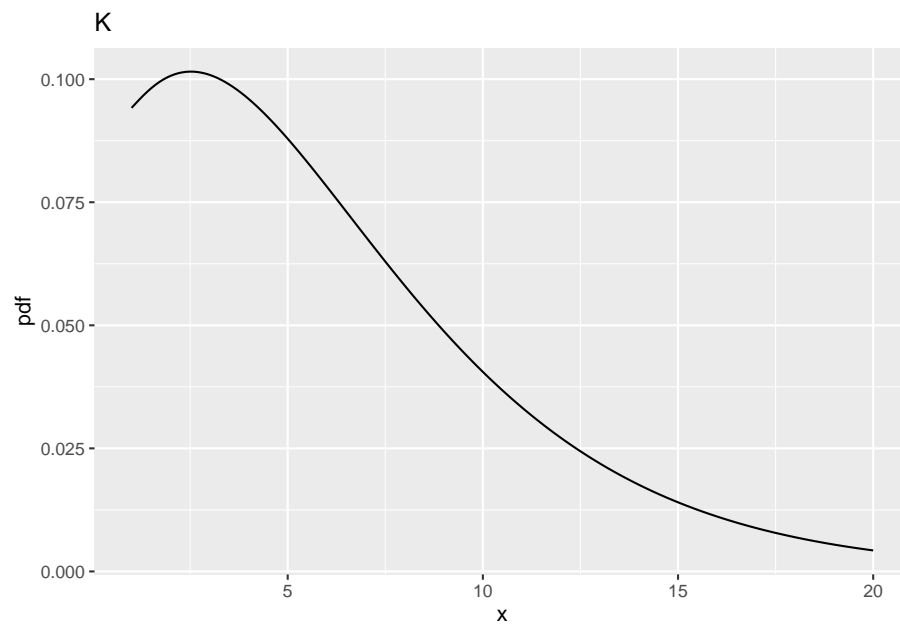
- This corresponds to **ncp** = 5, **ndf** = 2 and **ddf** = 100.
- The probability of exceeding the critical value is **prob** > **fCrit\_2\_100** = 0.4910802.
- This is greater than the previous value, i.e., 0.3876841 for **ddf** = 10.

### 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  $ndf = 1$ ,  $ddf = 100$** 



|   | 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$varComp$varEps
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:

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

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, by 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:

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

```
#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, by design, this is close to 80%.

## 9.3 Summary

For 10 readers, the numbers of cases needed for 80% power is largest (163) for RRRRC, 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  $\alpha$  is 0.05 and default power ( $1-\beta$ ) 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 (FRRRC) **option** = "FRRRC" 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.

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

The returned value is a list containing the expected power `power`, the non-centrality 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.

```
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"

```
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.

```
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

```

#### 10.4. ILLUSTRATION OF `SSSAMPLESIZEKGIVENJ()` USING `METHOD = "DBMH"`<sup>91</sup>

```
#> 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 = "RRRC")
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 = "RRRC", desiredPower = 0.9)
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 = "RF
```

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 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

# Choosing a realistic effect size

### 12.1 Introduction

- The value of the true FOM difference between the treatments, i.e., the true effect-size (ES) is, of course, unknown. If it were known, there would be no need to conduct an ROC study. One would simply adopt the treatment with the higher FOM. Sample-size estimation involves making an educated guess regarding the ES, called the *anticipated* ES, and denoted by  $\mathbf{d}$ . To quote (ICRU, 2008): “any calculation of power amounts to specification of the anticipated effect-size”. Increasing the anticipated ES will increase statistical power but may represent an unrealistic expectation of the true difference between the treatments, in the sense that it overestimates the ability of technology to achieve this much improvement. An unduly small might be clinically insignificant, besides requiring a very large sample-size to achieve sufficient power.
- There is a key difference between *statistical* significance and *clinical* significance. An effect-size in AUC units could be so small, e.g., 0.001, as to be clinically insignificant, but by employing a sufficiently large sample size one could design a study to detect this small and clinically meaningless difference with high probability, i.e., high statistical power.
- What determines clinical significance? A small effect-size, e.g., 0.01 AUC units, could be clinically significant if it applies to a large population, where the small benefit in detection rate is amplified by the number of patients benefiting from the new treatment. In contrast, for an “orphan” disease, i.e., one with very low prevalence, an effect-size of 0.05 might not

be enough to justify the additional cost of the new treatment. The improvement might have to be 0.1 before it is worth it for a new treatment to be brought to market. One hates to monetize life and death issues, but there is no getting away from it, as cost/benefit issues determine clinical significance. The arbiters of clinical significance are engineers, imaging scientists, clinicians, epidemiologists, insurance companies and those who set government health care policies. The engineers and imaging scientists determine whether the effect-size the clinicians would like is feasible from technical and scientific viewpoints. The clinician determines, based on incidence of disease and other considerations, e.g., altruistic, malpractice, cost of the new device and insurance reimbursement, what effect-size is justifiable. Cohen has suggested that  $d$  values of 0.2, 0.5, and 0.8 be considered small, medium, and large, respectively, but he has also argued against their indiscriminate usage. However, after a study is completed, clinicians often find that an effect-size that biostatisticians label as small may, in certain circumstances, be clinically significant and an effect-size that they label as large may in other circumstances be clinically insignificant. Clearly, this is a complex issue. Some suggestions on choosing a clinically significant effect size are made in **Chapter 11**.

- Does one even need to perform a pivotal study? If the pilot study returns a significant difference, one has rejected the  $H_0$  and that is all there is to it. There is no need to perform the pivotal study, unless one “tweaks” the new treatment and/or casts a wider sampling net to make a stronger argument, perhaps to the FDA, that the treatments are indeed generalizable, and that the difference is in the right direction (new treatment FOM > conventional treatment FOM). If a significant difference is observed in the opposite direction (e.g., new treatment FOM < conventional treatment FOM) one cannot justify a pivotal study with an expected effect-size in the “other or favored” direction; see example below. Since the Van Dyke pilot study came close to rejecting the  $H_0$  and the observed effect size, see below, is not too small, a pivotal study is justified.
- This vignette discusses choosing a realistic effect size based on the pilot study. Illustrated first is using Van Dyke dataset, regarded as the pilot study.

## 12.2 Illustration of `SsPowerGivenJK()` using `method = "ORH"`

```
rocData <- dataset02 ##"VanDyke.lrc"
#fileName <- dataset03 ## "Franken1.lrc"
retDbm <- StSignificanceTesting(dataset = rocData, FOM = "Wilcoxon", method = "DBMH")
```

```
str(retDbm$ciDiffTrtRRRC)
#> 'data.frame': 1 obs. of 8 variables:
#> $ TrtDiff : chr "Trt0-Trt1"
#> $ Estimate: num -0.0438
#> $ StdErr : num 0.0207
#> $ DF : num 15.3
#> $ t : num -2.11
#> $ PrGtT : num 0.0517
#> $ CILower : num -0.088
#> $ CIUpper : num 0.000359
```

- Lacking any other information, the observed effect-size is the best estimate of the effect-size to be anticipated. The output shows that the FOM difference, for treatment 0 minus treatment 1, is -0.0438003. In the actual study treatment 1 is the new modality which hopes to improve upon 0, the conventional modality. Since the sign is negative, the difference is going the right way and is justified in moving forward with planning a pivotal study. [If the difference went the other way, there is little justification for a pivotal study].
- The standard error of the difference is 0.0207486.
- An optimistic (but not unduly so) effect size is given by:

```
effectSizeOpt <- abs(retDbm$ciDiffTrtRRRC$Estimate) + 2*retDbm$ciDiffTrtRRRC$StdErr
```

- The observed effect-size is a realization of a random variable. The lower limit of the 95% confidence interval is given by -0.0879595 and the upper limit by  $3.5885444 \times 10^{-4}$ . CI's generated like this, with independent sets of data, are expected to encompass the true value with 95% probability. The lower end (greatest magnitude of the difference) of the confidence interval is -0.0852976, and this is the optimistic estimate. Since the sign is immaterial, one uses as the optimistic estimate the value 0.0852976.
- While the sign is immaterial for sample size estimates, the decision to conduct the pivotal most certainly is material. If the sign went the other way, with the new modality lower than the conventional modality, one would be unjustified in conducting a pivotal study.

## 12.3 References





## Chapter 13

# FROC sample size estimation and comparison to ROC

### 13.1 Introduction

- FROC sample size estimation is not fundamentally different from the previously outlined procedure (see vignettes corresponding to Chapter 11) for the ROC paradigm. To recapitulate, based on analysis of a pilot ROC dataset and using a specified FOM, e.g., `FOM = Wilcoxon`, and either `method = "DBMH"` or `method = "ORH"` for significance testing, one estimates the intrinsic variability of the data expressed in terms of variance components or the covariance matrix. The second step is to postulate a clinically realistic effect-size, e.g., the anticipated AUC difference between the two treatments. Given these values, the sample size functions implemented in `RJaFroc` (beginning with `Ss`) allow one to estimate the number of readers and cases necessary to detect (i.e., reject the null hypothesis) the specified effect size at specified Type II error rate, typically chosen to be 20% (corresponding to 80% statistical power) and specified Type I error rate, typically chosen to be 5%.
- In FROC analysis the only difference, **indeed the critical difference**, is the choice of FOM; e.g., `FOM = "wAFROC"` instead of the inferred ROC-AUC, `FOM = "HrAuc"`. The FROC dataset is analyzed using either the DBMH or the ORH method. This yields the necessary variance components or the covariance matrix corresponding to the wAFROC-AUC. The next step is to specify the effect-size **in wAFROC-AUC units**, and therein lies the rub. What value does one use? The ROC-AUC has a his-

torically well-known interpretation: the classification ability at separating diseased patients from non-diseased patients, while the wAFROC-AUC does not. Needed is a way of relating the effect-size in ROC-AUC units to one in wAFROC-AUC units: as should be obvious this requires a physical model, e.g., the RSM, that predicts both ROC and wAFROC curves and the respective AUCs.

1. One chooses an ROC-AUC effect-size that is realistic, one that clinicians understand and can therefore participate in, in the effect-size postulation process.
  2. One converts the ROC effect-size to a wAFROC-AUC effect-size. The method for this is described in the next section.
  3. One uses the sample size tools in `RJafroc` to determine sample size or power.
- **It is important to recognize is that all quantities have to be in the same units.** When performing ROC analysis, everything (variance components and effect-size) has to be in units of the selected FOM, e.g., `FOM = "Wilcoxon"` which is identical to the empirical ROC-AUC. When doing wAFROC analysis, everything has to be in units of the wAFROC-AUC. The variance components and effect-size in wAFROC-AUC units will be different from their corresponding ROC counterparts. In particular, as shown next, an ROC-AUC effect-size of 0.05 generally corresponds to a larger effect-size in wAFROC-AUC units. The reason for this is that the range over which wAFROC-AUC can vary, namely 0 to 1, is twice the corresponding ROC-AUC range.
  - The next section explains the steps used to implement step #2 above.

## 13.2 Relating an ROC effect-size to a wAFROC effect-size

- If the original data is FROC, one needs to first convert it to ROC, using `DfFroc2Roc()`: **the RSM fits ROC data.**
- For each treatment and reader the inferred ROC data is fitted by `FitRsmRoc()`, yielding estimates of the RSM *physical* (or primed) parameters (not the *intrinsic* values).
- The following example uses the *first two* treatments of the “FED” dataset, `dataset04`, which is a 5 treatment 4 radiologist FROC dataset acquired by Dr. Federica Zanca et. al. (Zanca et al., 2009). The dataset has 5 treatments and 4 readers and 200 cases and was acquired on a 5-point integer scale, i.e., it is already binned. If not one needs to bin the dataset

using `DfBinDataset()`. I need to emphasize this point: **if the dataset represents continuous ratings, as with a CAD algorithm, one must bin the dataset to (ideally) about 5 bins**. The number of parameters that must be estimated increases with the number of bins (for each bin one needs to estimate a cutoff parameter).

- The reason for using RSM parameter values only for the first two treatments is that these were found (Zanca et al., 2009) to be almost equivalent (more precisely, the NH could not be rejected for the first two treatments, so it makes sense to regard them as “almost” NH treatments.
- The following code block defines the pilot FROC data `frocData` (corresponding to `dataset04`, which is the “FED” dataset, but with only treatments 1 and 2 extracted, using `DfExtractDataset()`) and `rocData`, i.e., the highest-rating ROC dataset inferred from the FROC dataset using `DfFroc2Roc()`.

```
frocData <- DfExtractDataset(dataset04, trts = c(1,2))
rocData <- DfFroc2Roc(frocData)
```

The next code block determines `lesDistr`, the lesion distribution array, which has `Lmax` (maximum number of lesions per diseased case over the dataset) rows and two columns. The first column contains the integers 1, 2, ..., `Lmax` and the second column contains the fraction of diseased cases with the number of lesions per case specified in the first column. The second column will sum to unity. The RSM fitting algorithm needs to know how lesion-rich the dataset is, as the RSM predicted ROC-AUC depends on the lesion-richness of the dataset. For reasons that will become clear below, one also needs `lesWghts`, the distribution of the lesion weights.

```
lesDistr <- UtilLesionDistr(frocData)
lesWghts <- UtilLesionWeightsDistr(frocData) # this is needed later
```

The meanings of `lesDistr` and `lesWghts` is clear from examining their values:

```
print(lesDistr)
#> [,1] [,2]
#> [1,] 1 0.69
#> [2,] 2 0.20
#> [3,] 3 0.11
print(lesWghts)
#> [,1] [,2] [,3] [,4]
#> [1,] 1 1.0000000 -Inf -Inf
#> [2,] 2 0.5000000 0.5000000 -Inf
#> [3,] 3 0.3333333 0.3333333 0.3333333
```

For this dataset `Lmax` is 3, and 69 percent of the diseased cases have one lesion, 20 percent have two lesions and 11 percent have three lesions. Since the lesions are equally weighted, on cases with one lesion the weight of the lesion is unity, on cases with two lesions the weights of each lesion is 0.5 and on cases with three lesions the weight of each lesion is 1/3.

The next code block determines the number of treatments and readers (`I` and `J`) from the dimensions of the `frocData$NL` array. It creates an array `RsmParms` to hold the RSM fitted parameter values. For each treatment and reader it applies the fitting algorithm `FitRsmRoc()`. The first three returned values are `mu`, `lambdaP` and `nuP`, corresponding to RSM parameters  $\mu$ ,  $\lambda'$  and  $\nu'$ .

```
I <- dim(frocData$NL)[1]
J <- dim(frocData$NL)[2]
RsmParms <- array(dim = c(I,J,3))
for (i in 1:I) {
 for (j in 1:J) {
 x1 <- FitRsmRoc(rocData, trt = i, rdr = j, lesDistr)
 RsmParms[i,j,1] <- x1[[1]] # mu
 RsmParms[i,j,2] <- x1[[2]] # lambdaP
 RsmParms[i,j,3] <- x1[[3]] # nuP
 }
}
```

I recommend taking the median of each of the parameters, over all treatment-reader indices, as representing the average NH dataset. The median is less sensitive to outliers than the mean.

```
muMed <- median(RsmParms[, ,1])
lambdaPMed <- median(RsmParms[, ,2])
nuPMed <- median(RsmParms[, ,3])
```

The defining values of the fitting model are `muMed` = 3.3105557, `lambdaPMed` = 1.714368 and `nuPMed` = 0.7036567. Note that these obey the constraints `lambdaPMed` > 0 and `0` < `nuP` < 1. One then converts the physical parameters to the intrinsic values:

```
temp <- UtilPhysical2IntrinsicRSM(muMed, lambdaPMed, nuPMed)
lambdaMed <- temp$lambda
nuMed <- temp$nu
```

In terms of intrinsic parameters, the defining values of the fitting model are `muMed` = 3.3105557, `lambdaMed` = 5.6755108 and `nuMed` = 0.3673814. We are now ready to calculate the expected NH FOMs using the ROC -AUC and the wAFROC FOM.

```

aucRocNH <- PlotRsmOperatingCharacteristics(muMed, lambdaMed, nuMed,
 lesDistr = lesDistr,
 lesWghtDistr = lesWghts, OpChType = "ROC")$aucROC
aucwAfrocNH <- PlotRsmOperatingCharacteristics(muMed, lambdaMed, nuMed,
 lesDistr = lesDistr,
 lesWghtDistr = lesWghts, OpChType = "wAFROC")$aucwAfrocNH

```

- The plotting function `PlotRsmOperatingCharacteristics()` returns a number of other objects, most importantly the plot, but here we use only the AUC, which is obtained by numerical integration of the predicted operating characteristics. However, it calls for the **intrinsic** RSM parameters, which is why we had to convert the **physical** to the **intrinsic** values.
- One has `aucRocNH = 0.8791301` and `aucwAfrocNH = 0.7198311`. Note that the wAFROC-FOM is smaller than the ROC-FOM as it includes the localization constraint.
- To induce the alternative hypothesis condition, one increments  $\mu_{NH}$  by  $\Delta_\mu$ . The resulting ROC-AUC and wAFROC-AUC are calculated, again by numerical integration of the RSM predicted ROC and wAFROC curves, leading to the corresponding effect-sizes (note that in each equation below one takes the difference between the AH value minus the NH value):
- The next step is to calculate the effect size (new value minus the NH value) using ROC and wAFROC FOMs for a series of specified `deltaMu` values. This generates values that can be used to interpolate a wAFROC effect size for a specified ROC effect size.

```

deltaMu <- seq(0.01, 0.2, 0.01) # values of deltaMu to scan below
esRoc <- array(dim = length(deltaMu)); eswAfroc <- array(dim = length(deltaMu))
for (i in 1:length(deltaMu)) {
 esRoc[i] <- PlotRsmOperatingCharacteristics(
 muMed + deltaMu[i], lambdaMed, nuMed, lesDistr = lesDistr,
 lesWghtDistr = lesWghts, OpChType = "ROC")$aucROC - aucRocNH
 eswAfroc[i] <- PlotRsmOperatingCharacteristics(
 muMed + deltaMu[i], lambdaMed, nuMed, lesDistr = lesDistr,
 lesWghtDistr = lesWghts, OpChType = "wAFROC")$aucwAFROC - aucwAfrocNH
 cat("ES_ROC = ", esRoc[i], ", ES_wAFROC = ", eswAfroc[i], "\n")
}

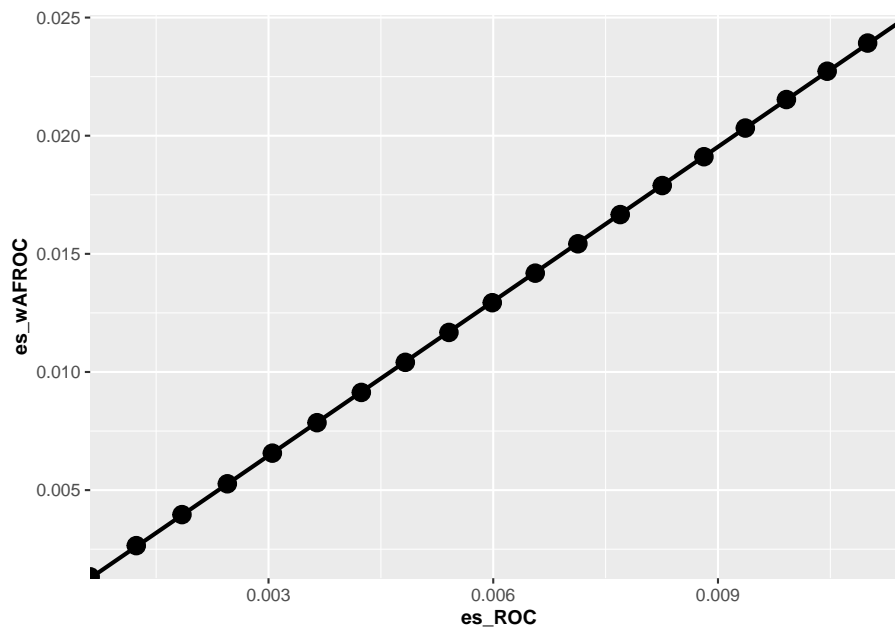
#> ES_ROC = 0.0006197813 , ES_wAFROC = 0.001329066
#> ES_ROC = 0.001234752 , ES_wAFROC = 0.002650005
#> ES_ROC = 0.00184496 , ES_wAFROC = 0.003962878
#> ES_ROC = 0.002450451 , ES_wAFROC = 0.005267748
#> ES_ROC = 0.003051273 , ES_wAFROC = 0.006564677
#> ES_ROC = 0.003647472 , ES_wAFROC = 0.007853725

```

```
#> ES_ROC = 0.004239094 , ES_wAFROC = 0.009134954
#> ES_ROC = 0.004826184 , ES_wAFROC = 0.01040842
#> ES_ROC = 0.005408788 , ES_wAFROC = 0.0116742
#> ES_ROC = 0.00598695 , ES_wAFROC = 0.01293233
#> ES_ROC = 0.006560717 , ES_wAFROC = 0.01418289
#> ES_ROC = 0.007130131 , ES_wAFROC = 0.01542592
#> ES_ROC = 0.007695238 , ES_wAFROC = 0.0166615
#> ES_ROC = 0.00825608 , ES_wAFROC = 0.01788967
#> ES_ROC = 0.008812702 , ES_wAFROC = 0.0191105
#> ES_ROC = 0.009365145 , ES_wAFROC = 0.02032404
#> ES_ROC = 0.009913453 , ES_wAFROC = 0.02153036
#> ES_ROC = 0.01045767 , ES_wAFROC = 0.0227295
#> ES_ROC = 0.01099783 , ES_wAFROC = 0.02392152
#> ES_ROC = 0.01153399 , ES_wAFROC = 0.02510649
```

Here is a plot of wAFROC effect size (y-axis) vs. ROC effect size.

```
df <- data.frame(es_ROC = esRoc, es_wAFROC = eswAfroc)
p <- ggplot(data = df, aes(x = es_ROC, y = es_wAFROC)) +
 geom_smooth(method = "lm", se = FALSE, color = "black", formula = y ~ x) +
 geom_point(size = 4) +
 scale_color_manual(values = "black") +
 theme(axis.title.y = element_text(size = 10, face = "bold"),
 axis.title.x = element_text(size = 10, face = "bold")) +
 scale_x_continuous(expand = c(0, 0)) +
 scale_y_continuous(expand = c(0, 0))
print(p)
```



The plot is very close to linear. This makes it easy to design an interpolation function. In the following code block the first line fits `eswAfroc` vs. `esRoc` using the linear model `lm()` function constrained to pass through the origin (the minus one): `scaleFactor <- lm(eswAfroc ~ -1 + esRoc)`. One expects this constraint since for `deltaMu = 0` the effect size must be zero no matter how it is measured.

```
scaleFactor<-lm(eswAfroc~-1+esRoc) # fit values to straight line thru origin
effectSizeROC <- seq(0.01, 0.1, 0.01)
effectSizewAFROC <- effectSizeROC*scaleFactor$coefficients[1] # r2 = summary(scaleFactor)$r.squa
```

The `scaleFactor` of the straight line fit is `scaleFactor`, where `scaleFactor = 2.1688609` and `R2 = 0.9999904`. Therefore, the conversion from ROC to wAFROC effect size is: `effectSizewAFROC = scaleFactor * effectSizeROC`. The wAFROC effect size is twice the ROC effect size. All that remains is to calculate the variance components using the two FOMs:

### 13.3 Computing the respective variance components

The code block applies `StSignificanceTesting()` to `rocData` and `frocData`, using the appropriate FOM, and extracts the variance components.

```
temp1 <- StSignificanceTesting(rocData, FOM = "Wilcoxon", method = "DBMH", option = "RR")
temp2 <- StSignificanceTesting(frocData, FOM = "wAFROC", method = "DBMH", option = "RR")
varCompROC <- temp1$varComp
varCompwAFROC <- temp2$varComp
```

The observed wAFROC effect-size is -0.0068562. This is a very small effect size; the corresponding ROC effect-size is -0.0051; the sign does not affect the calculations, which is too small to reach 80% power. It is not surprising that the study (Zanca et al., 2009) did not find a significant difference between these two treatments

The respective variance components are:

```
print(varCompROC)
#> varR varC varTR varTC varRC varErr
#> 1 0.000827738 0.03812335 0.0001526507 0.009644327 0.003544196 0.09484637
print(varCompwAFROC)
#> varR varC varTR varTC varRC varErr
#> 1 0.001854229 0.06117805 -0.0004439279 0.01016519 0.01355883 0.0967256
```

Only terms involving treatment are relevant to sample size. The wAFROC `varTC` and `varError` values are slightly larger than the ROC ones - as expected because, again, the range of the wAFROC FOM is twice that of the ROC FOM.

## 13.4 Comparing ROC power to wAFROC power for equivalent effect-sizes

We are now ready to compare ROC and wAFROC powers for equivalent effect sizes. The following example is for 5 readers (JTest) and 100 cases (KTest) in the **pivotal study**.

```
powerROC <- array(dim = length(effectSizeROC)); powerwAFROC <- array(dim = length(effectSizeROC))

JTest <- 5; KTest <- 100
for (i in 1:length(effectSizeROC)) {
 varYTR <- varCompROC$varTR # these are pseudo value based variance components assuming equal effect sizes
 varYTC <- varCompROC$varTC
 varYErr <- varCompROC$varErr
 ret <- SsPowerGivenJKDbmVarComp (J = JTest, K = KTest, effectSize = effectSizeROC[i])
 powerROC[i] <- ret$powerRRRC

 varYTR <- varCompwAFROC$varTR # these are pseudo value based variance components assuming equal effect sizes
 varYTC <- varCompwAFROC$varTC
```



### 13.4. COMPARING ROC POWER TO WAFROC POWER FOR EQUIVALENT EFFECT-SIZES113

```

varYEps <- varCompwAFROC$varErr
ret <- SsPowerGivenJKDbmVarComp (J = JTest, K = KTest, effectSize = effectSizewAFROC[i], varYF
powerwAFROC[i] <- ret$powerRRRC

cat("ROC-ES = ", effectSizeROC[i], ", wAFROC-ES = ", effectSizewAFROC[i],
 ", Power-ROC = ", powerROC[i], ", Power-wAFROC = ", powerwAFROC[i], "\n")
}
#> ROC-ES = 0.01 , wAFROC-ES = 0.02168861 , Power-ROC = 0.06443046 , Power-wAFROC = 0.126631
#> ROC-ES = 0.02 , wAFROC-ES = 0.04337722 , Power-ROC = 0.108789 , Power-wAFROC = 0.3605744
#> ROC-ES = 0.03 , wAFROC-ES = 0.06506583 , Power-ROC = 0.1847115 , Power-wAFROC = 0.6686874
#> ROC-ES = 0.04 , wAFROC-ES = 0.08675444 , Power-ROC = 0.2907927 , Power-wAFROC = 0.8897125
#> ROC-ES = 0.05 , wAFROC-ES = 0.108443 , Power-ROC = 0.4195443 , Power-wAFROC = 0.9777308
#> ROC-ES = 0.06 , wAFROC-ES = 0.1301317 , Power-ROC = 0.5573812 , Power-wAFROC = 0.9973522
#> ROC-ES = 0.07 , wAFROC-ES = 0.1518203 , Power-ROC = 0.6881601 , Power-wAFROC = 0.9998172
#> ROC-ES = 0.08 , wAFROC-ES = 0.1735089 , Power-ROC = 0.7983611 , Power-wAFROC = 0.9999927
#> ROC-ES = 0.09 , wAFROC-ES = 0.1951975 , Power-ROC = 0.8809508 , Power-wAFROC = 0.9999998
#> ROC-ES = 0.1 , wAFROC-ES = 0.2168861 , Power-ROC = 0.936068 , Power-wAFROC = 1

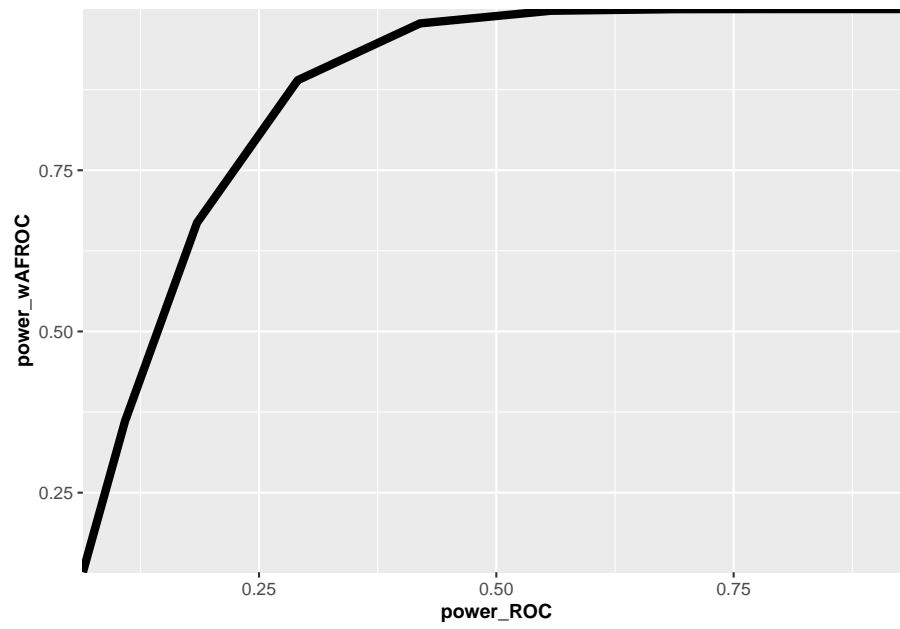
```

Since the wAFROC effect size is about a factor of two larger than the ROC effect size, wAFROC power is larger than that for ROC. The effect is magnified as the effect size enters as the square in the formula for the power (this overwhelms the slight increase in variability of wAFROC-FOM relative to ROC-FOM noted previously). The following is a plot of the respective powers.

```

df <- data.frame(power_ROC = powerROC, power_wAFROC = powerwAFROC)
p <- ggplot(mapping = aes(x = power_ROC, y = power_wAFROC)) +
 geom_line(data = df, size = 2) +
 scale_color_manual(values = "black") +
 theme(axis.title.y = element_text(size = 10, face = "bold"),
 axis.title.x = element_text(size = 10, face = "bold")) +
 scale_x_continuous(expand = c(0, 0)) +
 scale_y_continuous(expand = c(0, 0))
print(p)

```



## 13.5 References

## Chapter 14

# FROC sample size estimation using specified ROC effect

### 14.1 Introduction

This example uses the FED dataset as a pilot FROC study and function `SsFrocNhRsmModel()` to construct the NH model (encapsulating some of the code in the previous vignette).

### 14.2 Constructing the NH model for the dataset

One starts by extracting the first two treatments from `dataset04`, which represent the NH dataset, see previous vignette. Next one constructs the NH model - note that the lesion distribution `lesionPmf` can be specified here independently of that in the pilot dataset. This allows some control over selection of the diseased cases in the pivotal study.

```
frocNhData <- DfExtractDataset(dataset04, trts = c(1,2))
ret <- SsFrocNhRsmModel(frocNhData, lesionPmf = c(0.7, 0.2, 0.1))
muMed <- ret$muMed
lambdaMed <- ret$lambdaMed
nuMed <- ret$nuMed
lesDistr <- ret$lesDistr
lesWghtDistr <- ret$lesWghtDistr
scaleFactor <- ret$scaleFactor
```

The fitting model is defined by `muMed = r muMed`, `lambdaMed = 5.6140942` and `nuMed = 0.3696988` and `lesionPmf`. The effect size scale factor is 2.1542102.

```
aucRocNH <- PlotRsmOperatingCharacteristics(muMed, lambdaMed, nuMed,
 lesDistr = lesDistr,
 lesWghtDistr = lesWghtDistr, OpChType = "R",
aucwAfrocNH <- PlotRsmOperatingCharacteristics(muMed, lambdaMed, nuMed,
 lesDistr = lesDistr,
 lesWghtDistr = lesWghtDistr, OpChType = "R")
```

The null hypothesis ROC AUC is 0.8790725 and the corresponding NH wAFROC AUC is 0.7231709.

### 14.3 Extracting the wAFROC variance components

The next code block applies `StSignificanceTesting()` to `frocNhData`, using `FOM = "wAFROC"` and extracts the variance components.

```
varCompwAFROC <- StSignificanceTesting(frocNhData, FOM = "wAFROC", method = "DBMH", opChType = "R")
```

### 14.4 wAFROC power for specified ROC effect size, number of readers J and number of cases K

The following example is for ROC effect size = 0.05, 5 readers (J) and 100 cases (K) in the **pivotal study**.

```
ROC_ES <- 0.05
effectSizewAFROC <- scaleFactor * ROC_ES
J <- 5; K <- 100

varYTR <- varCompwAFROC$varTR
varYTC <- varCompwAFROC$varTC
varYEps <- varCompwAFROC$varErr
ret <- SsPowerGivenJKDbmVarComp (J = J, K = K, effectSize = effectSizewAFROC,
 varYTR, varYTC, varYEps, option = "RRRC")
powerwAFROC <- ret$powerRRRC

cat("ROC-ES = ", ROC_ES, ", wAFROC-ES = ", ROC_ES * scaleFactor, ", Power-wAFROC = ", powerwAFROC, "\n")
#> ROC-ES = 0.05 , wAFROC-ES = 0.1077105 , Power-wAFROC = 0.976293
```

## 14.5 wAFROC number of cases for 80% power for a given number of readers J

```
varYTR <- varCompwAFROC$varTR
varYTC <- varCompwAFROC$varTC
varYEps <- varCompwAFROC$varErr
ret2 <- SsSampleSizeKGivenJ(dataset = NULL, J = 6, effectSize = effectSizewAFROC, method = "DBMH",
 list(varYTR = varYTR, varYTC = varYTC, varYEps = varYEps))

cat("ROC-ES = ", ROC_ES, ", wAFROC-ES = ", ROC_ES * scaleFactor,
 ", K80RRRC = ", ret2$KRRRC, ", Power-wAFROC = ", ret2$powerRRRC, "\n")
#> ROC-ES = 0.05 , wAFROC-ES = 0.1077105 , K80RRRC = 42 , Power-wAFROC = 0.804794
```

## 14.6 wAFROC Power for a given number of readers J and cases K

```
ret3 <- SsPowerGivenJK(dataset = NULL, J = 6, K = ret2$KRRRC, effectSize = effectSizewAFROC, method = "DBMH",
 list(varYTR = varYTR, varYTC = varYTC, varYEps = varYEps))

cat("ROC-ES = ", ROC_ES, ", wAFROC-ES = ", ROC_ES * scaleFactor,
 ", powerRRRC = ", ret3$powerRRRC, "\n")
#> ROC-ES = 0.05 , wAFROC-ES = 0.1077105 , powerRRRC = 0.804794
```

The estimated power is close to 80% as the number of cases (`ret2$KRRRC = 42`) was chosen deliberately from the previous code block.

## 14.7 References



## Chapter 15

# Proper ROCs

### 15.1 Helper functions

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

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

### 15.3 Main code and output

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

```

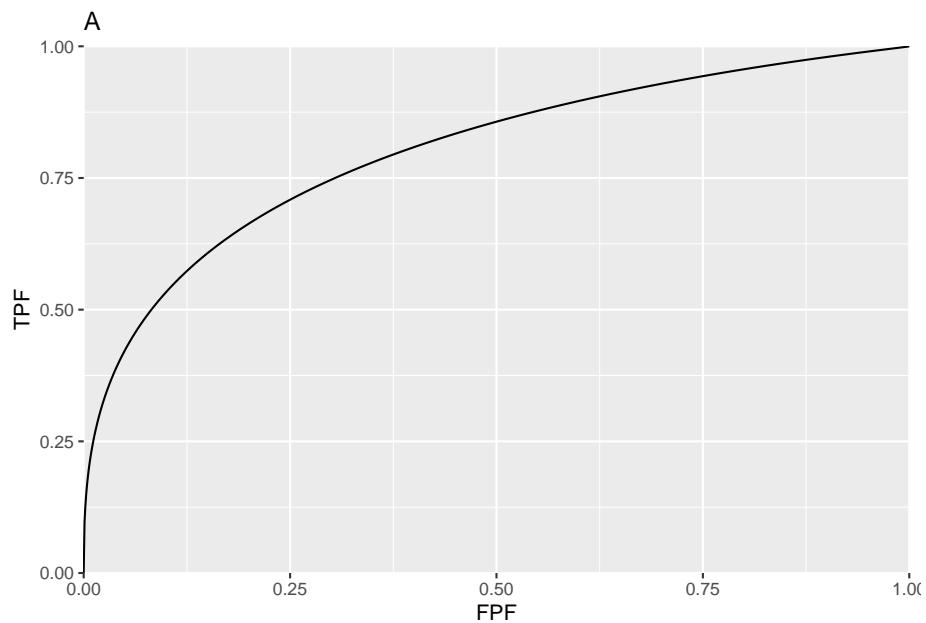
FPF <- seq(0.0, 1, 0.001)
TPF <- rocY(FPF, a, b)

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

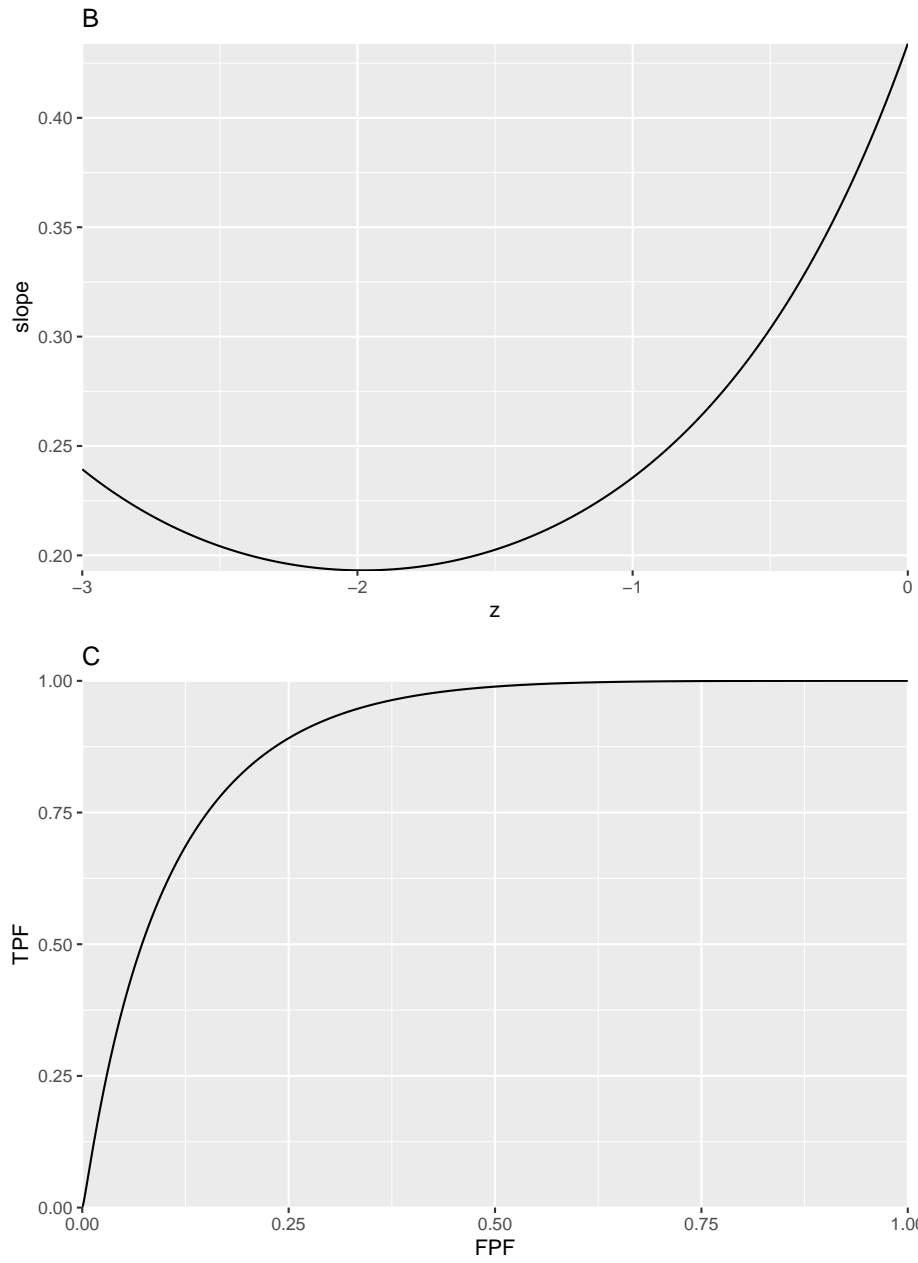
slope <- -b*dnorm(a-b*z)/dnorm(-z) # same as likelihood ratio

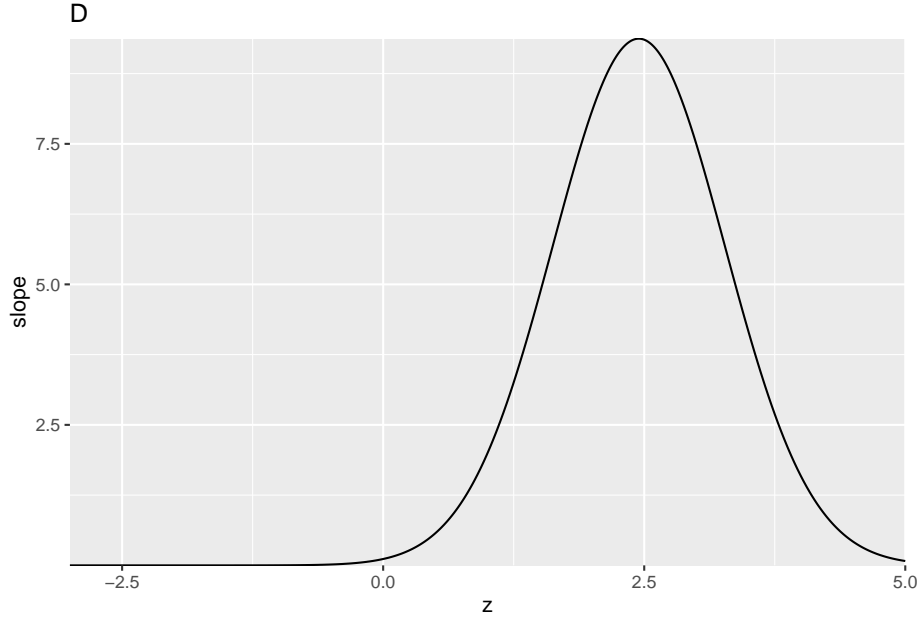
slopePlot <- data.frame(z = z, slope = slope)
p <- ggplot(slopePlot, aes(x = z, y = slope)) +
 geom_line() +
 scale_x_continuous(expand = c(0, 0)) +
 scale_y_continuous(expand = c(0, 0)) +
 ggtitle(myLabel[myLabelIndx]); myLabelIndx <- myLabelIndx + 1
print(plotRoc); print(p)
}

```









## 15.4 Discussion

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

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

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

at zero for  $z \sim -2$ .

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



## Chapter 16

# Metz Eqn36 numerical check

### 16.1 Helper functions

### 16.2 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. =

```

### 16.3 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.

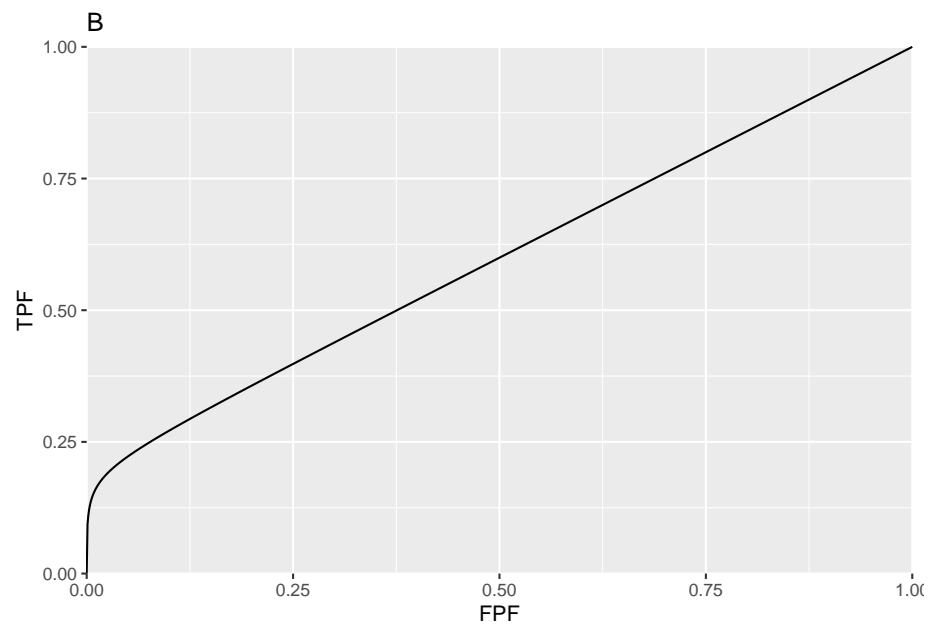
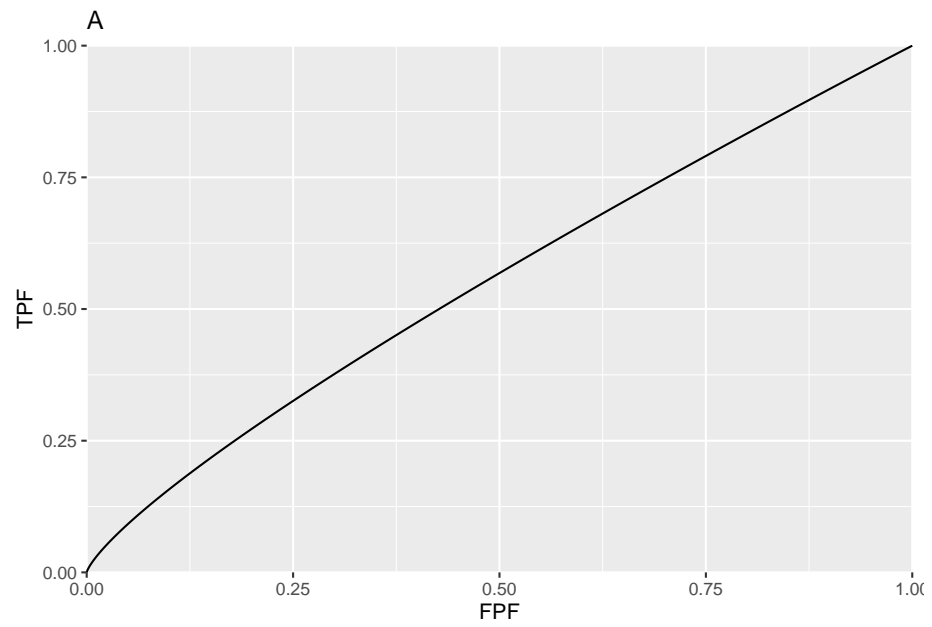
## Chapter 17

# CBM Plots

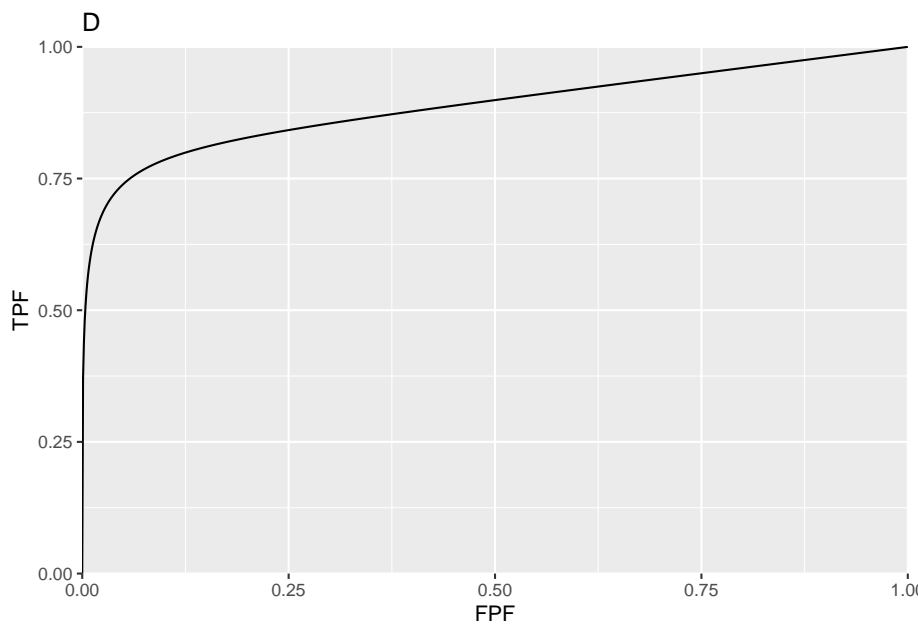
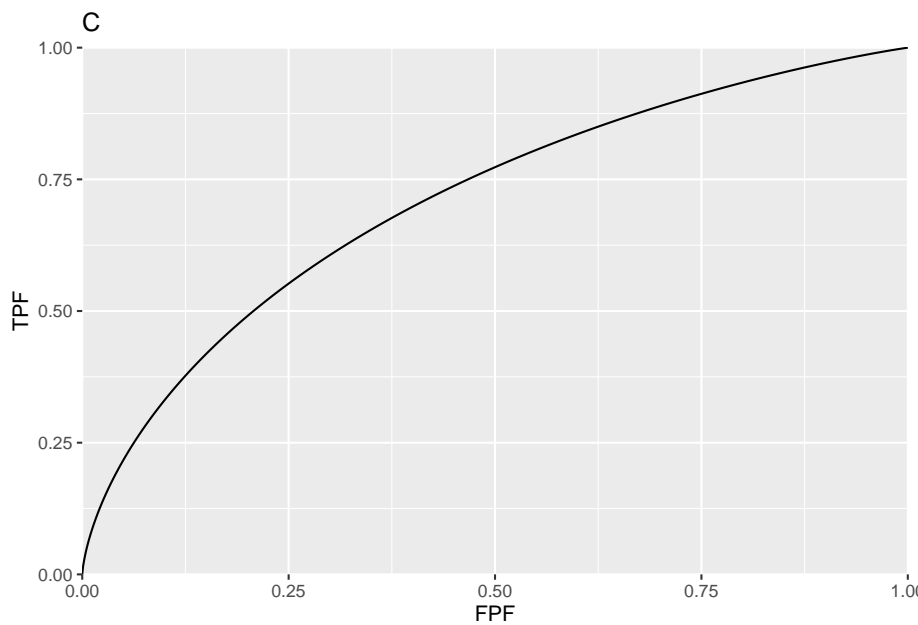
### 17.1 Helper functions

### 17.2 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
```





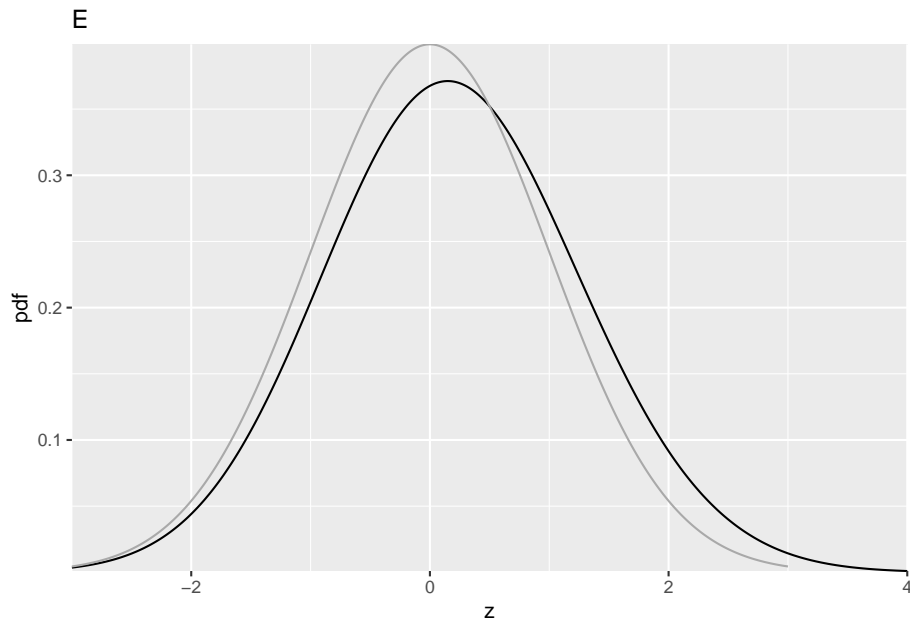


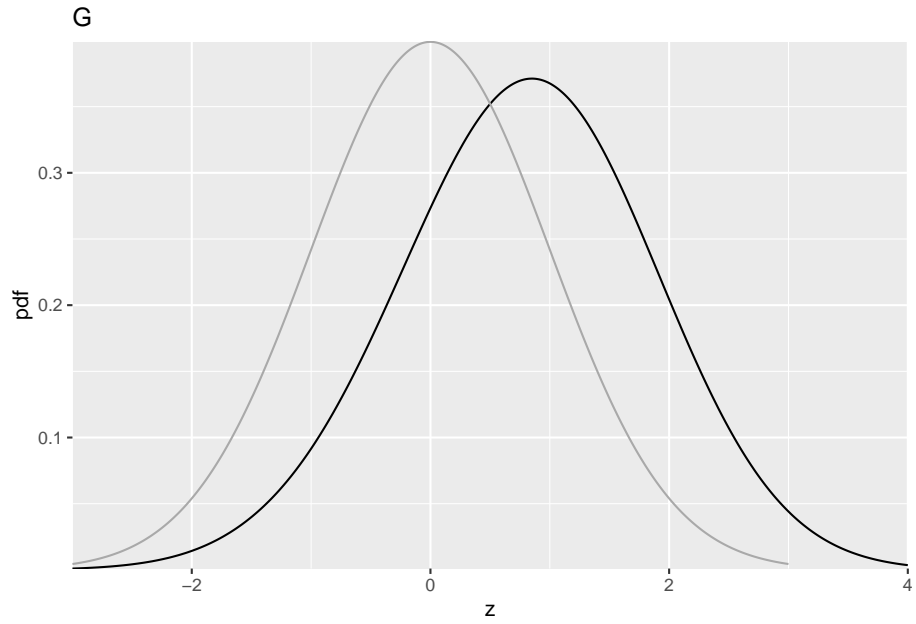
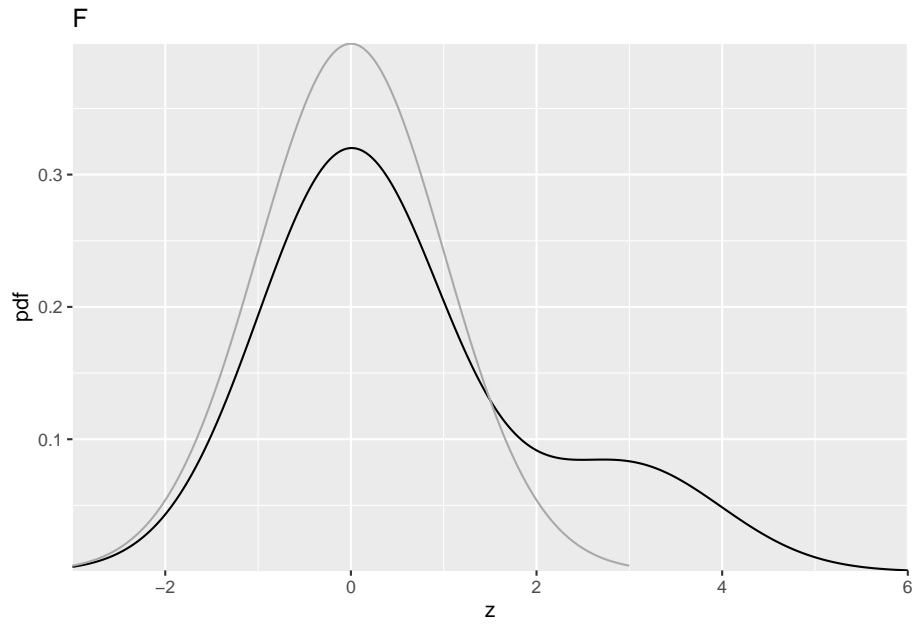
### 17.3 Comments

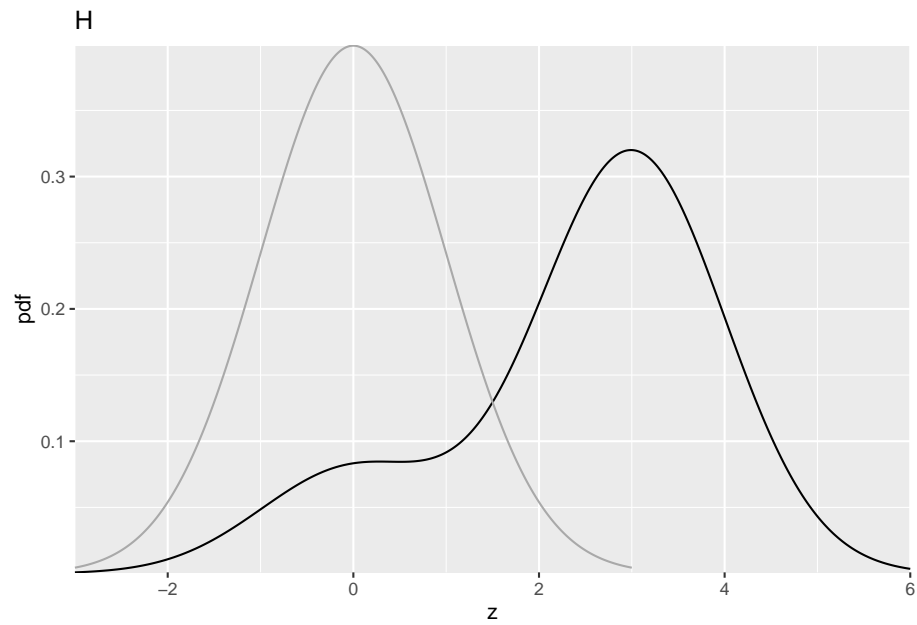
Plots A - D show ROC curves predicted by the CBM model; the corresponding values of the  $\mu$  and  $\alpha$  parameters are indicated above the plots. For small  $\mu$  and/or  $\alpha$  the curve approaches the chance diagonal, consistent with the notion that if the lesion is not visible, performance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

### 17.4 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
```





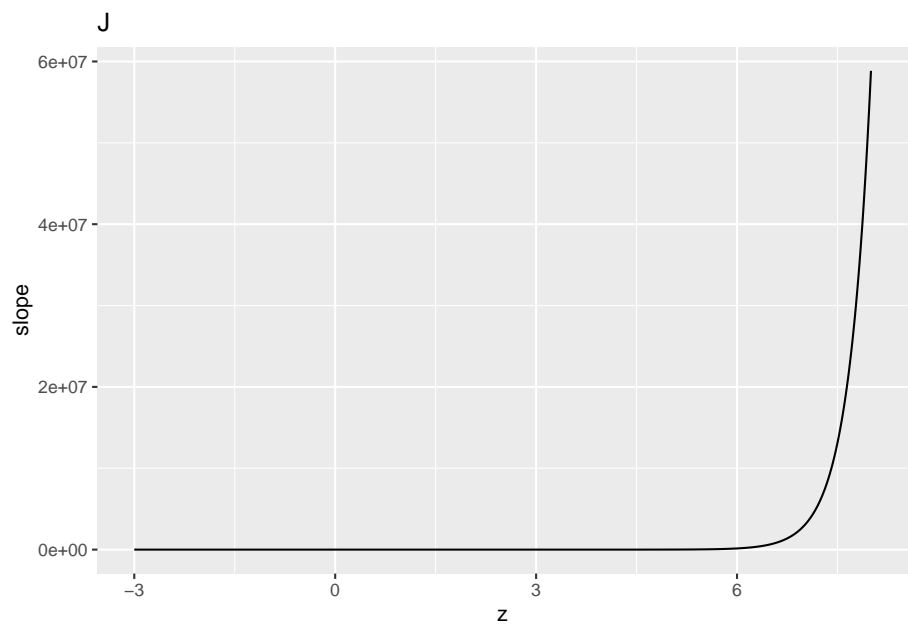
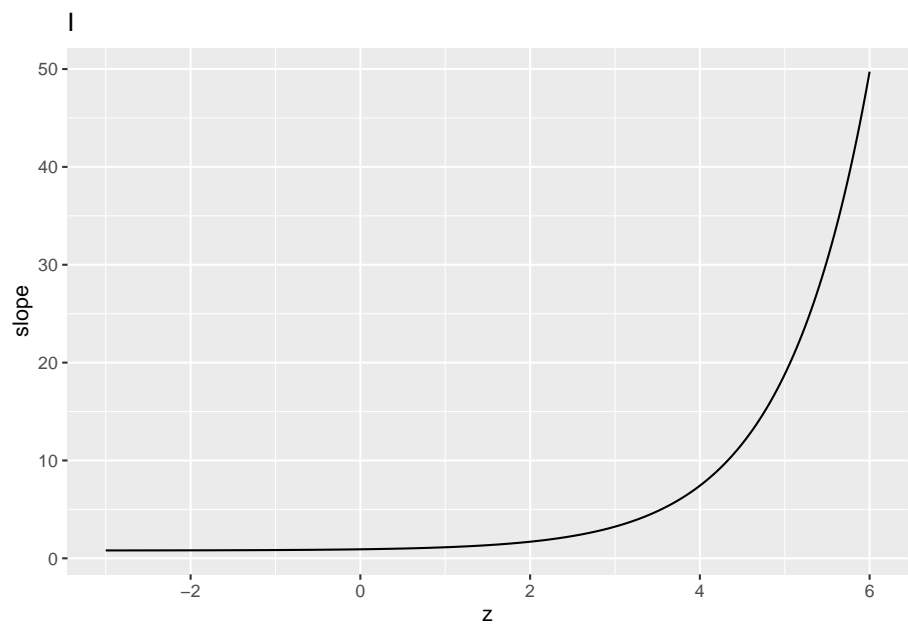


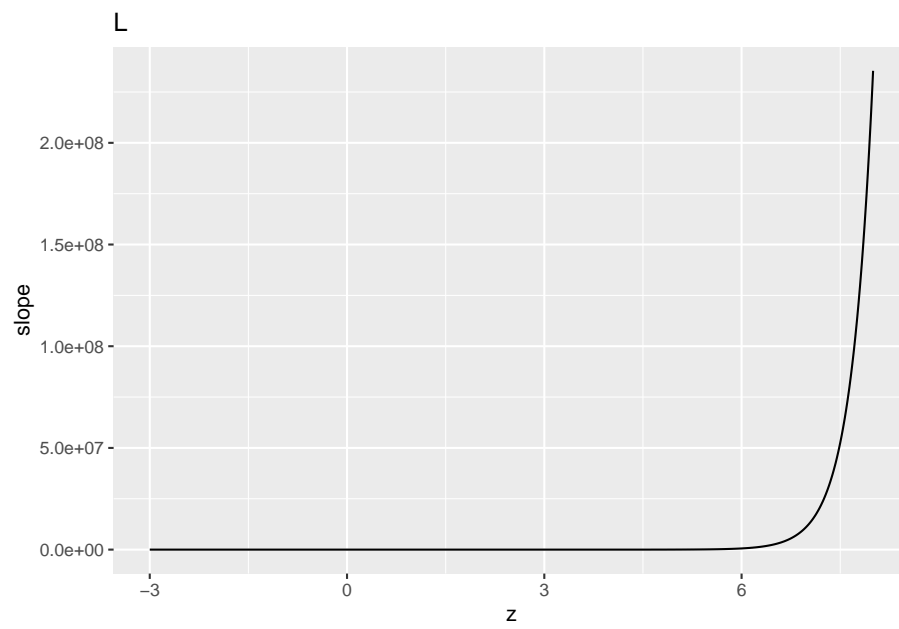
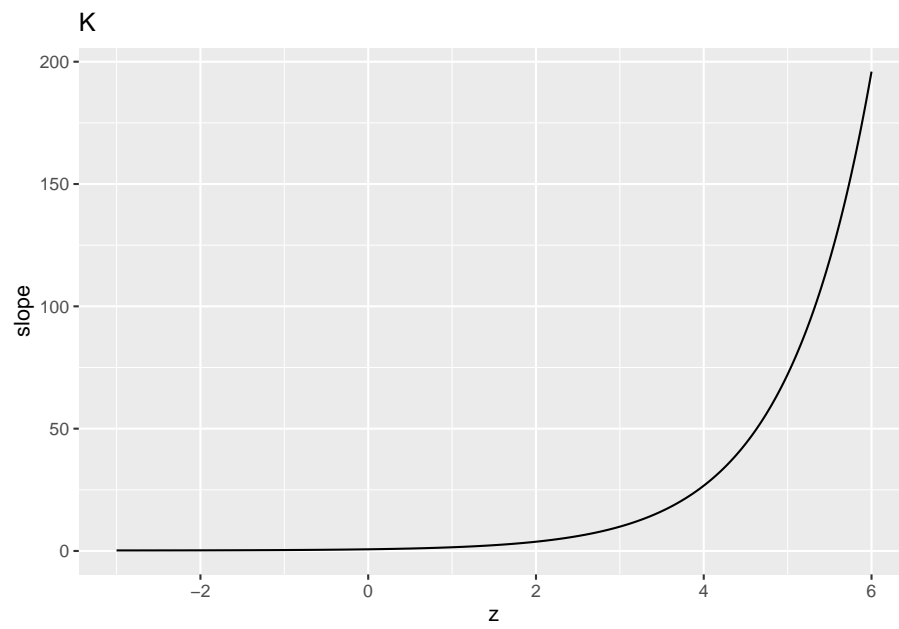
## 17.5 Comments

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.

## 17.6 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
```





## 17.7 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 18

# ROI paradigm data

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

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

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

## 18.2 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.

## 18.3 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
```

| CaseID | LesionID | Weights | D | E |
|--------|----------|---------|---|---|
| 1      | 0        | 0       |   |   |
| 2      | 1        | 0       |   |   |
| 3      | 2        | 0       |   |   |
| 4      | 3        | 0       |   |   |
| 5      | 4        | 0       |   |   |
| 6      | 5        | 0       |   |   |
| 7      | 6        | 0       |   |   |
| 8      | 7        | 0       |   |   |
| 9      | 8        | 0       |   |   |
| 10     | 9        | 0       |   |   |
| 11     | 10       | 0       |   |   |
| 12     | 11       | 0       |   |   |
| 13     | 12       | 0       |   |   |
| 14     | 13       | 0       |   |   |
| 15     | 14       | 0       |   |   |
| 16     | 15       | 0       |   |   |
| 17     | 16       | 0       |   |   |
| 18     | 17       | 0       |   |   |
| 19     | 18       | 0       |   |   |
| 20     | 19       | 0       |   |   |
| 21     | 20       | 0       |   |   |
| 22     | 21       | 0       |   |   |
| 23     | 22       | 0       |   |   |
| 24     | 23       | 0       |   |   |
| 25     | 24       | 0       |   |   |
| 26     | 25       | 0       |   |   |
| 27     | 26       | 0       |   |   |
| 28     | 27       | 0       |   |   |
| 29     | 28       | 0       |   |   |
| 30     | 29       | 0       |   |   |
| 31     | 30       | 0       |   |   |
| 32     | 31       | 0       |   |   |
| 33     | 32       | 0       |   |   |
| 34     | 33       | 0       |   |   |
| 35     | 34       | 0       |   |   |
| 36     | 35       | 0       |   |   |
| 37     | 36       | 0       |   |   |
| 38     | 37       | 0       |   |   |
| 39     | 38       | 0       |   |   |
| 40     | 39       | 0       |   |   |
| 41     | 40       | 0       |   |   |
| 42     | 41       | 0       |   |   |
| 43     | 42       | 0       |   |   |
| 44     | 43       | 0       |   |   |
| 45     | 44       | 0       |   |   |
| 46     | 45       | 0       |   |   |
| 47     | 46       | 0       |   |   |
| 48     | 47       | 0       |   |   |
| 49     | 48       | 0       |   |   |
| 50     | 49       | 0       |   |   |
| 51     | 50       | 0       |   |   |
| 52     | 51       | 2       |   |   |
| 53     | 51       | 3       |   |   |
| 54     | 52       | 1       |   |   |
| 55     | 52       | 2       |   |   |
| 56     | 52       | 4       |   |   |
| 57     | 53       | 1       |   |   |
| 58     | 53       | 2       |   |   |
| 59     | 54       | 1       |   |   |
| 60     | 54       | 4       |   |   |
| 61     | 55       | 1       |   |   |
| 62     | 55       | 3       |   |   |
| 63     | 55       | 4       |   |   |
| 64     | 56       | 2       |   |   |

Figure 18.1: Fig. 1 two views of Truth worksheet

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

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

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

|    | A        | B          | C      | D        | E         | F       |
|----|----------|------------|--------|----------|-----------|---------|
|    | ReaderID | ModalityID | CaseID | LesionID | FP_Rating | Weights |
| 1  | 1        | 1          | 1      | 1        | 0.949868  |         |
| 2  | 1        | 1          | 1      | 2        | -0.05825  |         |
| 3  | 1        | 1          | 1      | 3        | -0.776378 |         |
| 4  | 1        | 1          | 1      | 4        | 0.012073  |         |
| 5  | 1        | 1          | 2      | 1        | -0.641182 |         |
| 6  | 1        | 1          | 2      | 2        | -0.140436 |         |
| 7  | 1        | 1          | 2      | 3        | -0.669429 |         |
| 8  | 1        | 1          | 2      | 4        | -1.15841  |         |
| 9  | 1        | 1          | 3      | 1        | 1.37227   |         |
| 10 | 1        | 1          | 3      | 2        | -0.346435 |         |
| 11 | 1        | 1          | 3      | 3        | -1.45574  |         |
| 12 | 1        | 1          | 3      | 4        | 0.409021  |         |
| 13 | 1        | 1          | 4      | 1        | 0.409462  |         |
| 14 | 1        | 1          | 4      | 2        | -0.304937 |         |
| 15 | 1        | 1          | 4      | 3        | 1.04011   |         |
| 16 | 1        | 1          | 5      | 1        | 0.244483  |         |
| 17 | 1        | 1          | 5      | 2        | 0.702656  |         |
| 18 | 1        | 1          | 5      | 3        | -0.542638 |         |
| 19 | 1        | 1          | 5      | 4        | -0.982391 |         |

Figure 18.2: Fig. 2 two views of FP worksheet

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

|    | A        | B          | C      | D        | E         | F       |
|----|----------|------------|--------|----------|-----------|---------|
|    | ReaderID | ModalityID | CaseID | LesionID | TP_Rating | Weights |
| 1  | 1        | 1          | 51     | 1        | 1.56928   |         |
| 2  | 1        | 1          | 51     | 2        | 2.05845   |         |
| 3  | 1        | 1          | 52     | 1        | 3.26529   |         |
| 4  | 1        | 1          | 52     | 2        | 1.98797   |         |
| 5  | 1        | 1          | 52     | 3        | 2.14102   |         |
| 6  | 1        | 1          | 53     | 1        | 1.63172   |         |
| 7  | 1        | 1          | 53     | 2        | 2.45575   |         |
| 8  | 1        | 1          | 89     | 1        | 1.17085   |         |
| 9  | 1        | 1          | 89     | 2        | 1.61856   |         |
| 10 | 1        | 1          | 90     | 1        | 1.64283   |         |
| 11 | 1        | 1          | 90     | 2        | 1.76386   |         |
| 12 | 2        | 1          | 51     | 1        | 2.29811   |         |
| 13 | 2        | 1          | 51     | 2        | 2.09581   |         |
| 14 | 2        | 1          | 52     | 1        | 1.75994   |         |
| 15 | 2        | 1          | 52     | 2        | 2.16157   |         |
| 16 | 2        | 1          | 52     | 3        | 0.472727  |         |
| 17 | 2        | 1          | 53     | 1        | -0.691873 |         |
| 18 | 2        | 1          | 53     | 2        | -0.982391 |         |

Figure 18.3: 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.

## 18.4 Next, TBA

The next vignette illustrates significance testing for this paradigm.

## 18.5 References



## Chapter 19

# Analyzing data acquired according to the ROI paradigm

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

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

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

### 19.3 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).

## 19.4 The ROI figure of merit

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

$$N_L = \sum_k n_k^L$$

and

$$N_N = \sum_k n_k^N$$

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

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

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

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

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

## 19.5 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.

## 19.6 Significance testing

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

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

```

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

```

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

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

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

### 19.6.1 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).

### 19.6.2 FRRC analysis

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

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

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

### 19.6.3 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
```

## 19.7 Summary

TBA

## 19.8 References



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