RJafroc documentation

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Contents

Chapter 1

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 2

Introduction

- This is the book desribing the **RJafroc** packages.
- 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

Chapter 3

ROC data format

3.1 Introduction

- In the receiver operating characteristic (**ROC**) paradigm (Metz, 1978) the observer's task is to **rate** (i.e., assign an ordered label representing the degree of suspicion) each case for confidence in presence of disease. The rating is frequently called a *confidence level*.
- 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 case [1].
- For human observer studies a 6-point rating scale is recommended, collected via two questions (Chakraborty, 2017):
  - Is the case diseased?
    - Binary response: *Yes* or *No*.
  - What is your confidence in the preceding decisions?
    - Three level response: *Low*, *Medium* or *High*.
- With algorithmic readers, e.g., computer aided detection algorithms a floating point rating, if possible, should be retained.
- In the most common study design, termed multiple-reader multiple-case (**MRMC**), the rating collection procedure is repeated for all cases, treatments and readers.

[1] The directionaliy of the rating is not a limitation. If lower values correspond to increased confidence level, it is only necessary to transform the observed rating by subtracting it from a constant value. The constant value can be chosen arbitrarily, typically as the maximum of all observed ratings, thereby ensuring that the transformed value is always non-negative.

3.2 An actual MRMC ROC dataset

An actual MRMC ROC dataset (Van Dyke et al., 1993) is included as `dataset02`. It has the following structure:

```
str(dataset02)
#> List of 8
#>  $ 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 ...
#>  $ lesionNum   : 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" ...
```

3.2.1 Overview of the data structure

- The `dataset` structure is a `list` variable with 8 members [2].
    - Ratings of non-diseased cases are stored in the `NL` list member.
    - Ratings of diseased cases are stored in the `LL` list member.
    - The `lesionNum` list member is an array of length 45, filled with ones. It lists the number of lesions per case, which for ROC data, is always unity. The length of this array equals the number of diseased cases `K2`, see below.
    - The `lesionID` list member is a `[45 x 1]` array, also filled with ones. [3]
    - The `LesionWeight` list member is also a `[45 x 1]` array filled with ones.
    - The `dataType` list member equals the string `"ROC"`, identifying it as an ROC dataset.
    - The `modalityID` list member is a string array identifying the names of the treatments (see below).
    - The `readerID` list member is a string array, identifying the names of the readers (see below).

3.2.2 Details of the `modalityID` and `readerID` list members

- The names of the treatments are in the `modalityID` list member:

[2] This is true for ROC, FROC and ROI datasets. LROC datasets have 9 `list` members.
[3] The second "unnecessary" dimension is necessary for compatibility with FROC datasets.

```
attributes(dataset02$modalityID)
#> $names
#> [1] "0" "1"
```

For example, the name of the first treatment is `"0"`. The names can be longer strings, but use of very long string names may mess up the output formats of the analysis report. As per the **KISS** principle [4], keep the names short.

- The names of the readers are in the `readerID` array:

```
attributes(dataset02$readerID)
#> $names
#> [1] "0" "1" "2" "3" "4"
```

For example, the name of the second reader is `"1"`. A similar caveat regarding long reader names applies.

3.2.3 Details of the `NL` and `LL` list members

- For either `NL` or `LL` list members, the fourth dimension has unit length. This dimension, which is strictly speaking unnecessary for ROC data, is retained for ease of generalizability to the FROC and ROC paradigms, where more than one rating per case is possible.
- `dataset02` is a 2-treatment 5-reader dataset (the lengths of the first and second dimensions, respectively, of the `NL` and `LL` list members).

3.2.3.1 Numbers of non-diseased and diseased cases

```
K <- length(dataset02$NL[1,1,,1])
K2 <- length(dataset02$LL[1,1,,1])
K1 <- K - K2
```

- `K1` is the number of non-diseased cases, while `K2` is the number of diseased cases.
- The third dimension of the `NL` array is the total number of **all** cases, i.e., `K` = 114, and the third dimension of the `LL` array, i.e., `K2` = 45, is the total number of diseased cases.
- Subtracting the number of diseased cases from the number of all cases yields the number of non-diseased cases.
- Therefore, in this dataset, there are **45** diseased cases and **69** non-diseased cases.

[4] For those not familiar, KISS stands for Keep It Simple, Stupid.

3.2.3.2 Why dimension the NL array for the total number of cases?

- Again, this is for ease of generalizability to the FROC and ROI paradigms.

3.2.3.3 Ratings on a non-diseased case

- For ROC data a non-diseased case can have only one, and exactly one, `NL` rating.
- For treatment 1, reader 1 and case 1 (the first non-diseased case), the NL rating is `"1"`:

```
dataset02$NL[1,1,1,1]
#> [1] 1
mean(dataset02$NL[,,1:K1,1])
#> [1] 1.784058
```

- This study utilized a 5-point rating scale, 1 thru 5, so non-diseased cases are expected to have low ratings; in this case the lowest rating was observed.
- The mean rating over all non-diseased cases, treatments and readers, is 1.784058.

3.2.3.4 Ratings on a diseased case

- For ROC data a diseased case can have only one, and exactly one, `LL` rating.
- For treatment 1, reader 1, case 1 (the first diseased case) the LL rating is:

```
dataset02$LL[1,1,1,1]
#> [1] 5
mean(dataset02$LL)
#> [1] 4.297778
```

- As noted previously, this study utilized a 5-point rating scale, 1 thru 5, so diseased cases are expected to have high ratings; in this case the highest rating was observed.
- The mean rating over all diseased cases, treatments and readers, is 4.2977778.

3.3 The ROC Excel data file

- An Excel file in JAFROC format containing ROC data corresponding to `dataset02` is included with the **RJafroc** package. The first command (below) finds the location of the file and the second command reads it and saves it to a dataset object `ds`.

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

- `DfReadDataFile` is short for *Data File Function to Read a Data File*.
- All data file related functions start with `Df`, and a similar organization applies to other functions. This makes it easier, in my opinion, to find a function in the `R` help system.
- To see the online help files, use the following command:

```
help("RJafroc-package")
```

- Click the `"Show in new window"` button to see it full screen.
- This bit of experiential advice applies, of course, to all help files.

3.3.1 The ROC Excel file organization

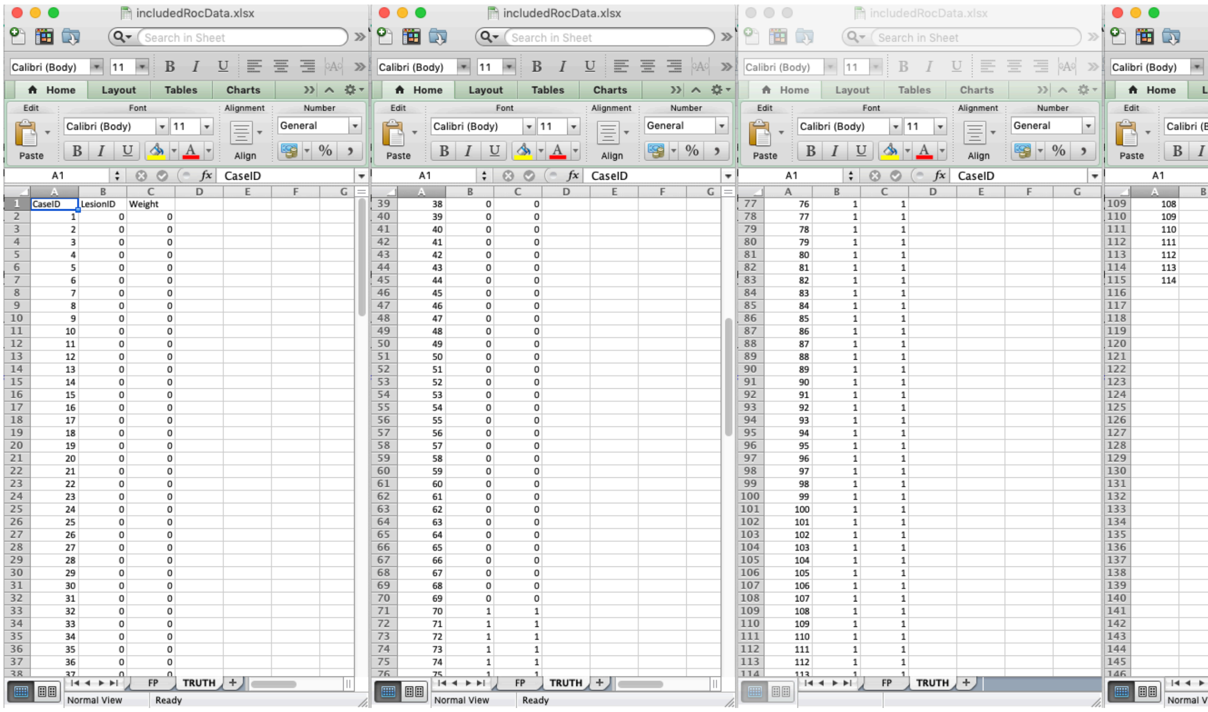
- It contains three worksheets, `Truth`, `TP` and `FP`.
- The `Truth` worksheet defines the ground-truth of each case. It indicates which cases are diseased and which are non-diseased.
- The `FP` worksheet lists the ratings of non-diseased cases.
- The `TP` worksheet lists the ratings of diseased cases [5].

3.3.1.1 The Truth worksheet organization

- The `CaseID` column lists the numeric labels identifying each case. Again, string names are possible, but keep them short.
- A `1` in the `LesionID` column denotes a diseased case.
- A `0` in the `LesionID` column denotes a non-diseased case.
- The `Weight` column is irrelevant for ROC data [6].
- The contents of the `Truth` worksheet corresponding to `dataset02` are displayed next:

[5] OK, I am being inconsistent. I am using `NL`, `LL` for the ratings and `FP`, `TPj` for the worksheets. The worksheet format will accept `NL` and `LL` instead of `FP` and `TP`. However, for ease of generalization to the FROC pardigm it is necessary to use `NL` and `LL` for the list members of the dataset object.

[6] It is only needed for FROC data.

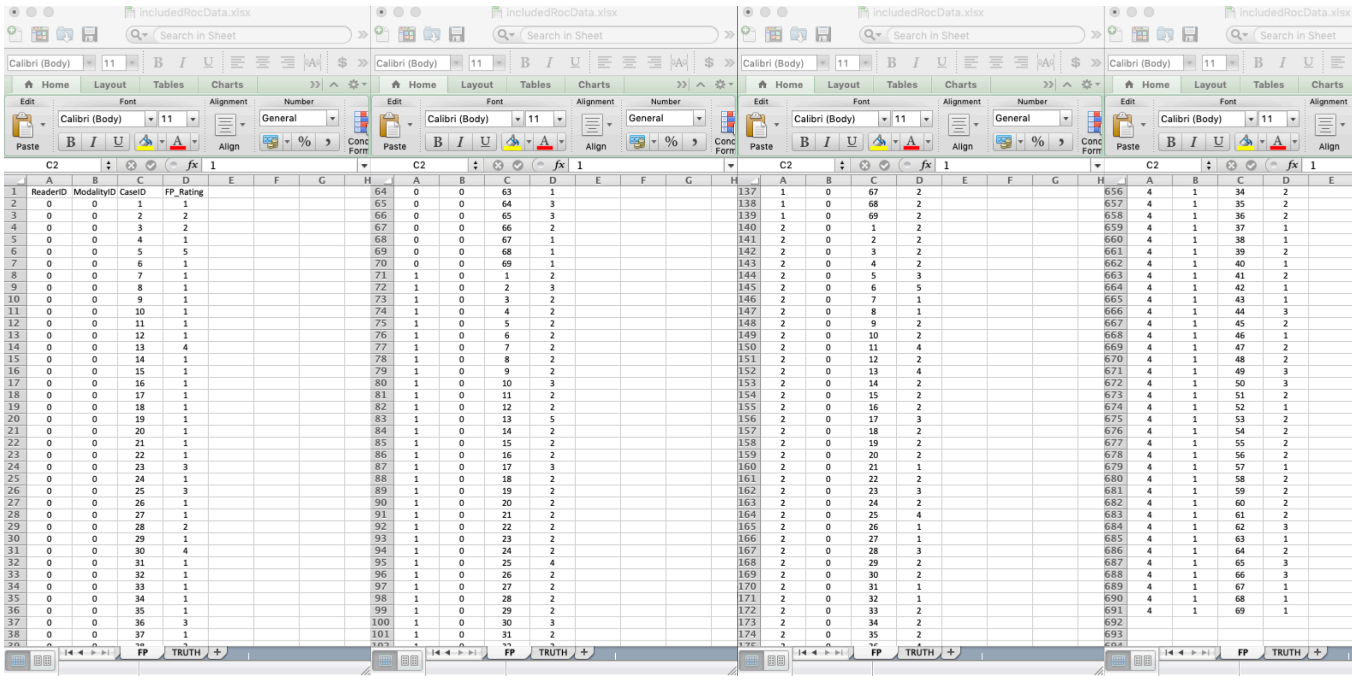


- There are 69 non-diseased cases (labeled 1-69) under column `CaseID`.
- There are 45 diseased cases (labeled 70-114) under column `CaseID`.

- The `LesionID` field for each non-diseased case (e.g., `CaseID` = 1) is zero. A zero in this field defines a non-diseased case.
- The `LesionID` field for each diseased case (e.g., `CaseID` = 70) is unity. A unit value in this field defines a diseased case.
- The `Weights` field is irrelevant for ROC datasets. For convenience it is filled with zeroes.

3.3.1.2 The FP/NL worksheet organization

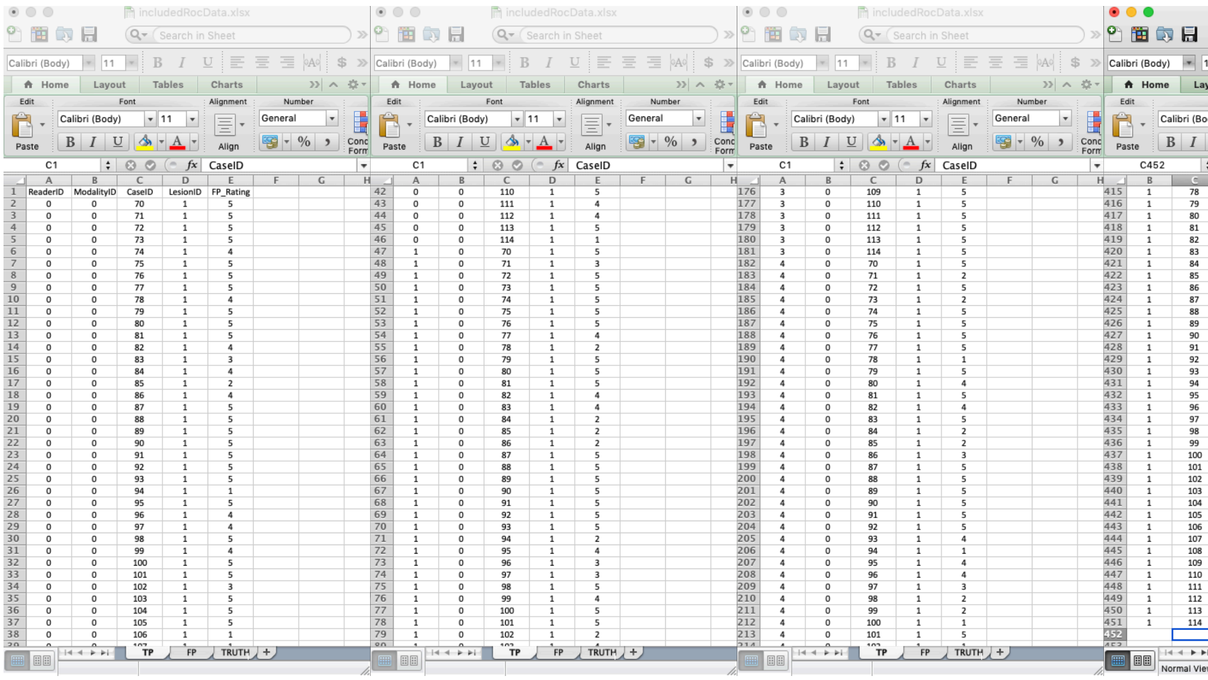
The following screen-shots show different parts of the `FP` worsheet for `dataset02`.



- The `FP` (or `NL`) worksheet lists the ratings of non-diseased cases.
- The **ModalityID** values range from `0` to `1`, corresponding to two treatments.
- The **ReaderID** values range from `0` to `4`, corresponding to five readers.
- The **CaseID** values range from `1` to `69`, corresponding to non-diseased cases **only**.
- For each reader and treatment, each non-diseased case gets one rating; therefore the length of the column labeled **FP-Rating** is **69 x 2 x 5 = 690**.
- The FP ratings tend to be low, there are a lot of ones, fewer twos, even fewer threes, and an ocassional four and a five rating may be found.

3.3.1.3 The TP/LL worksheet organization

The following screen-shots show different parts of the `FP` worsheet for `dataset02`.



* The TP (or LL) worksheet lists the ratings of diseased cases. * The **ModalityID** values range from 0 to 1, corresponding to two treatments. * The **ReaderID** values range from 0 to 4, corresponding to five readers. * The **CaseID** values range from 70 to 114, corresponding to diseased cases **only**. * For each reader and treatment, each non-diseased case gets one rating; therefore the length of the column labeled **FP-Rating** is **45 x 2 x 5 = 450**. * The TP ratings tend to be high, there are a lot of fives, fewer fours, even fewer threes, and an ocassional two and a one rating may be found.

3.4 Summary

- Since each case gets one rating, the ROC data structure is relatively easy to visualize. All of the information in the three Excel worksheets can be summarize by a two-row five column table (with 10 values), with one row listing the number of non-diseased cases rated 1, the number rated two, etc., upto the number rated five, and a corresponding row for diseased cases. These 10 values contain all of the information contained in the Excel file.

Chapter 4

FROC data format

4.1 Introduction

- In the free-response ROC (**FROC**) paradigm (Bunch et al., 1978) the observer's task is to indicate (i.e., **mark** the location of) and **rate** (i.e., assign an ordered label - or confidence level - representing the degree of suspicion) regions in the image that are perceived as suspicious for presence of disease. Accordingly, FROC data consists of **mark-rating pairs**, where each mark indicates a region [1] that was considered suspicious for presence of a localized lesion and the rating is the corresponding confidence level. The number of mark-rating pairs on any particular case is a-priori unpredictable. It is a non-negative random integer (i.e., 0, 1, 2, ...) that depends on the case, the reader and the modality. The relatively unstructured nature of FROC data makes FROC paradigm data more difficult to analyze than ROC paradigm data [2].

- 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 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 [3].

[1] In order to avoid confusion with the ROI-paradigm, I do not like to use the term ROI to describe the marks made by the observer.

[2] Recall that the ROC paradigm always yields a single rating per case.

[3] The directionaliy of the rating is not a limitation. If lower values correspond to increased confidence level, it is only necessary to transform the observed rating by subtracting it from a constant value. The constant value can be chosen arbitrarily, typically as the maximum of all observed ratings, thereby ensuring that the transformed value is always non-negative.

- Region-level-normal ratings are stored in the `NL` field and region-level-abnormal ratings are stored in the `LL` field.

4.2 An actual FROC dataset

An actual FROC dataset (Zanca et al., 2009) is included as `dataset04`, which has the following `dataset` structure:

```
str(dataset04)
#> List of 8
#>  $ NL          : num [1:5, 1:4, 1:200, 1:7] -Inf -Inf 1 -Inf -Inf ...
#>  $ LL          : num [1:5, 1:4, 1:100, 1:3] 4 5 4 5 4 3 5 4 4 3 ...
#>  $ lesionNum   : int [1:100] 1 1 1 1 1 1 1 1 1 1 ...
#>  $ lesionID    : num [1:100, 1:3] 1 1 1 1 1 1 1 1 1 1 ...
#>  $ lesionWeight: num [1:100, 1:3] 1 1 1 1 1 1 1 1 1 1 ...
#>  $ dataType    : chr "FROC"
#>  $ modalityID  : Named chr [1:5] "1" "2" "3" "4" ...
#>   ..- attr(*, "names")= chr [1:5] "1" "2" "3" "4" ...
#>  $ readerID    : Named chr [1:4] "1" "3" "4" "5"
#>   ..- attr(*, "names")= chr [1:4] "1" "3" "4" "5"
```

Examination of the output reveals that:

- The `dataset` structure is a list with 8 members.
- This is a 5-treatment 4-reader dataset (the lengths of the first and second dimensions, respectively, of the `NL` and `LL` arrays). The names of the treatments are in the `modalityID` array:

```
attributes(dataset04$modalityID)
#> $names
#> [1] "1" "2" "3" "4" "5"
```

For example, the name of the second treatment is `"2"`.

- The names of the readers are in the `readerID` array:

```
attributes(dataset04$readerID)
#> $names
#> [1] "1" "3" "4" "5"
```

For example, the name of the second reader is `"3"`. Apparently reader `"2"` “dropped out” of the study.

4.2.1 Numbers of non-diseased and diseased cases

```
length(dataset04$NL[1,1,,1])
#> [1] 200
length(dataset04$LL[1,1,,1])
#> [1] 100
```

- The third dimension of the `NL` array is the total number of **all** cases, i.e., 200, and the third dimension of the `LL` array, i.e., 100, is the total number of diseased cases.
- Subtracting the number of diseased cases from the number of all cases yields the number of non-diseased cases.
- Therefore, in this dataset, there are 100 diseased cases and 100 non-diseased cases.

4.2.2 Why dimension the `NL` array for the total number of cases?

- Because, in addition to `LLs`, `NLs` are possible on diseased cases.
- Only `LLs` are possible on diseased cases.
- Only `NLs` are possible on non-diseased cases.
- The missing values are filled in with `-Inf`.

4.2.3 Ratings on a non-diseased case

- For treatment 1, reader 1 and case 1 (the first non-diseased case), the NL ratings are:

```
dataset04$NL[1,1,1,]
#> [1] -Inf -Inf -Inf -Inf -Inf -Inf -Inf
```

4.2.4 The meaning of a negative infinity rating

- Obviously, a real rating cannot be negative infinity [4]. This value is reserved for **missing ratings**, and more generally, **missing marks** [5]. For

[4] If an observer is so highly confident in the *absence* of a localized lesion, he will simply *not mark* the location in question; if he did, then, logically, he should mark *all* areas in the image that are definitely not lesions; in the FROC paradigm only regions with a reasonable degree of suspicion are marked. The radiologist only wishes to draw attention to regions that are reasonably suspicious; the definition of "reasonable" is determined by clinical considerations.

[5] Since there is a one-to-one correspondence between marks and ratings.

example, since all values in the above code chunk are negative infinities, this means this treatment-reader-case combination did not yield any mark-rating pairs. This possibility, alluded to above, is only possible with FROC data. All other paradigms (ROC, LROC and ROI) yield at least one rating per case.
- The length of the fourth dimension of the `NL` array is determined by that treatment-reader-case combination yielding the maximum number of `NLs`. Consider the following chunk:

```
for (i in 1:5)
  for (j in 1:4)
    for (k in 1:200)
      if (all(dataset04$NL[i,j,k,] != -Inf))
        cat(i, j, k, all(dataset04$NL[i,j,k,] != -Inf),"\n")
#> 5 4 192 TRUE
```

- This shows that the fourth dimension of the `NL` array has to be of length 7 because *one, and only reader*, specifically reader "4", made 7 `NL` marks on a diseased case in treatment "5"!

4.2.5 Ratings on a non-diseased case

Unlike non-diseased cases, diseased cases can have both `NL` and `LL` ratings.

- For treatment 1, reader 1, case 51 (the 1st diseased case) the NL ratings are:

```
dataset04$NL[1,1,51,]
#> [1] -Inf -Inf -Inf -Inf -Inf -Inf -Inf
dataset04$lesionNum[1]
#> [1] 1
dataset04$LL[1,1,1,]
#> [1]    4 -Inf -Inf
mean(is.finite(dataset04$LL))
#> [1] 0.3043333
```

. There are only two finite values because this case has two ROI-level-abnormal regions, and 2 plus 2 makes for the assumed 4-regions per case. The corresponding `$lesionNum` field is 1.

```
mean(is.finite(dataset04$NL[,,1:50,]))
#> [1] 0.05942857
dataset04$NL[1,1,51,]
```

```
#> [1] -Inf -Inf -Inf -Inf -Inf -Inf -Inf
dataset04$lesionNum[1]
#> [1] 1
dataset04$LL[1,1,1,]
#> [1]    4 -Inf -Inf
mean(is.finite(dataset04$LL))
#> [1] 0.3043333
```

```
mean(is.finite(dataset04$NL[,,1:50,]))
#> [1] 0.05942857
dataset04$NL[1,1,51,]
#> [1] -Inf -Inf -Inf -Inf -Inf -Inf -Inf
dataset04$lesionNum[1]
#> [1] 1
dataset04$LL[1,1,1,]
#> [1]    4 -Inf -Inf
mean(is.finite(dataset04$LL))
#> [1] 0.3043333
```

- The ratings of the 2 ROI-level-abnormal ROIs on this case are 4. The mean rating over all ROI-level-abnormal ROIs is 3.6785323.

```
mean(is.finite(dataset04$NL[,,1:50,]))
#> [1] 0.05942857
dataset04$NL[1,1,51,]
#> [1] -Inf -Inf -Inf -Inf -Inf -Inf -Inf
dataset04$lesionNum[1]
#> [1] 1
dataset04$LL[1,1,1,]
#> [1]    4 -Inf -Inf
mean(is.finite(dataset04$LL))
#> [1] 0.3043333
```

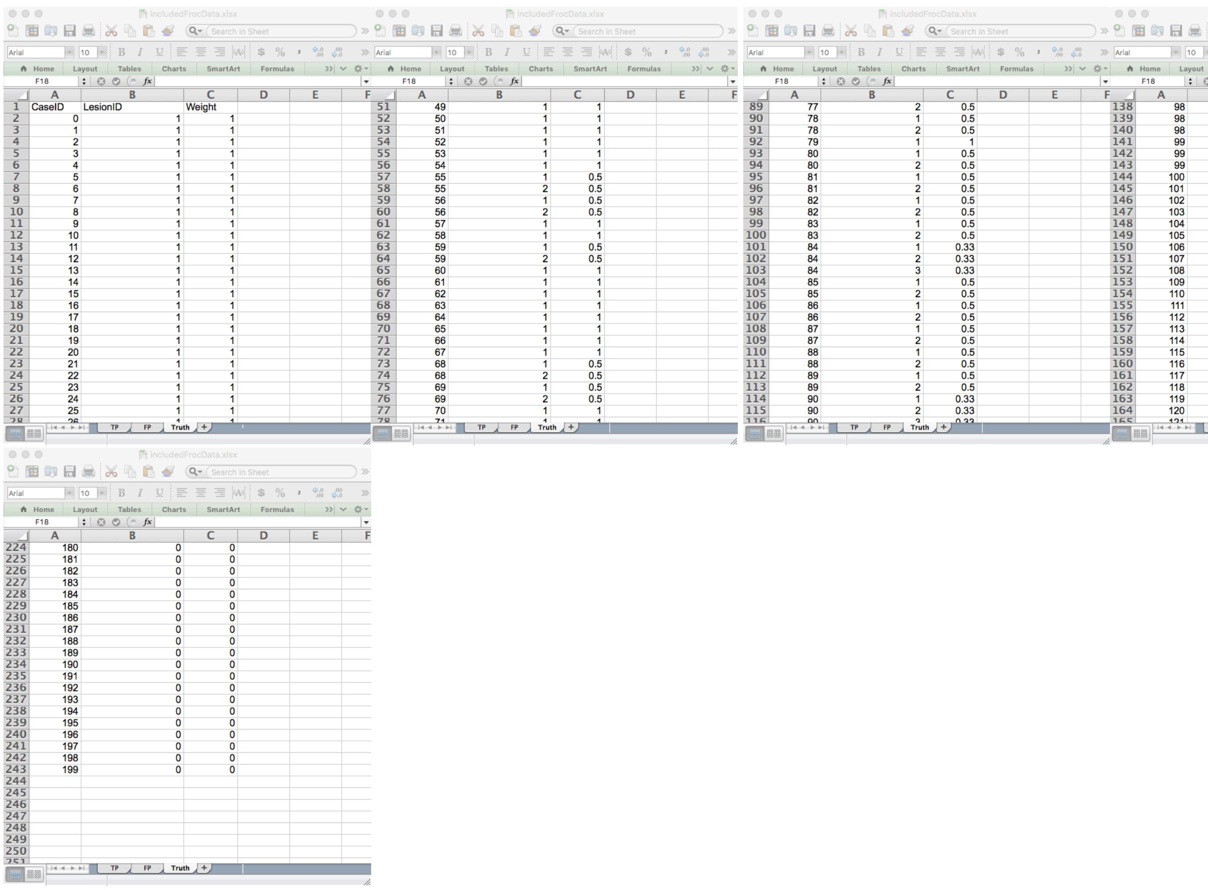
4.3 The FROC Excel data file

An Excel file in JAFROC format containing simulated ROI data corresponding to `dataset04`, 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`.

```
fileName <- system.file(
    "extdata", "includedFrocData.xlsx", package = "RJafroc", mustWork = TRUE)
```

```r
ds <- DfReadDataFile(fileName)
ds$dataType
#> [1] "FROC"
```

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:



	A	B	C
1	CaseID	LesionID	Weight
2	0	1	1
3	1	1	1
4	2	1	1
5	3	1	1
6	4	1	1
7	5	1	1
8	6	1	1
9	7	1	1
10	8	1	1
11	9	1	1
12	10	1	1
13	11	1	1
14	12	1	1
15	13	1	1
16	14	1	1
17	15	1	1
18	16	1	1
19	17	1	1
20	18	1	1
21	19	1	1
22	20	1	1
23	21	1	1
24	22	1	1
25	23	1	1
26	24	1	1
27	25	1	1

	A	B	C
51	49	1	1
52	50	1	1
53	51	1	1
54	52	1	1
55	53	1	1
56	54	1	1
57	55	1	0.5
58	55	2	0.5
59	56	1	0.5
60	56	2	0.5
61	57	1	1
62	58	1	1
63	59	1	0.5
64	59	2	0.5
65	60	1	1
66	61	1	1
67	62	1	1
68	63	1	1
69	64	1	1
70	65	1	1
71	66	1	1
72	67	1	1
73	68	1	0.5
74	68	2	0.5
75	69	1	0.5
76	69	2	0.5
77	70	1	1

	A	B	C
89	77	2	0.5
90	78	1	0.5
91	78	2	0.5
92	79	1	1
93	80	1	0.5
94	80	2	0.5
95	81	1	0.5
96	81	2	0.5
97	82	1	0.5
98	82	2	0.5
99	83	1	0.5
100	83	2	0.5
101	84	1	0.33
102	84	2	0.33
103	84	3	0.33
104	85	1	0.5
105	85	2	0.5
106	86	1	0.5
107	86	2	0.5
108	87	1	0.5
109	87	2	0.5
110	88	1	0.5
111	88	2	0.5
112	89	1	0.5
113	89	2	0.5
114	90	1	0.33
115	90	2	0.33

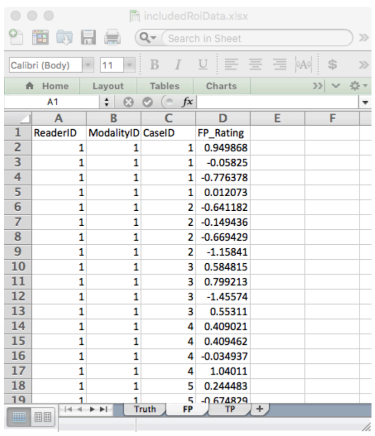
	A
138	98
139	98
140	98
141	99
142	99
143	99
144	100
145	101
146	102
147	103
148	104
149	105
150	106
151	107
152	108
153	109
154	110
155	111
156	112
157	113
158	114
159	115
160	116
161	117
162	118
163	119
164	120

	A	B	C
224	180	0	0
225	181	0	0
226	182	0	0
227	183	0	0
228	184	0	0
229	185	0	0
230	186	0	0
231	187	0	0
232	188	0	0
233	189	0	0
234	190	0	0
235	191	0	0
236	192	0	0
237	193	0	0
238	194	0	0
239	195	0	0
240	196	0	0
241	197	0	0
242	198	0	0
243	199	0	0
244			
245			
246			
247			
248			
249			
250			

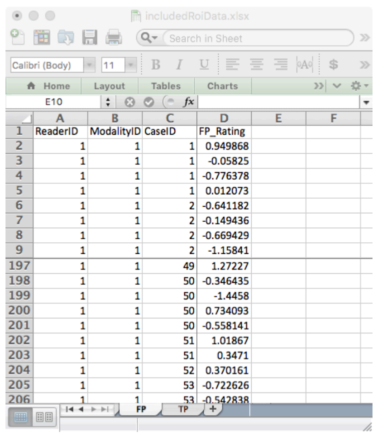
- The `Truth` worksheet - this indicates which cases are diseased and which are non-diseased and the number of ROI-level-abnormal region on each case.
  - There are 50 normal cases (labeled 1-50) under column `CaseID` and 40 abnormal cases (labeled 51-90).
  - The `LesionID` field for each normal case (e.g., `CaseID` = 1) is zero and there is one row per case. For abnormal cases, this field has

a variable number of entries, ranging from 1 to 4. As an example, there are two rows for `CaseID` = 51 in the Excel file: one with `LesionID` = 2 and one with `LesionID` = 3.

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



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

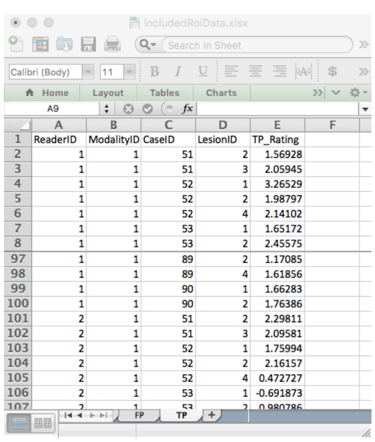


	A	B	C	D	E	F
1	ReaderID	ModalityID	CaseID	FP_Rating		
2	1	1	1	0.949868		
3	1	1	1	-0.05825		
4	1	1	1	-0.776378		
5	1	1	1	0.012073		
6	1	1	2	-0.641182		
7	1	1	2	-0.149436		
8	1	1	2	-0.669429		
9	1	1	2	-1.15841		
197	1	1	49	1.27227		
198	1	1	50	-0.346435		
199	1	1	50	-1.4458		
200	1	1	50	0.734093		
201	1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

- The `FP` (or `NL`) worksheet - this lists the ratings of ROI-level-normal regions.

  - For `ReaderID` = 1, `ModalityID` = 1 and `CaseID` = 1 there are 4 rows, corresponding to the 4 ROI-level-normal regions in this case. The corresponding ratings are . 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 abnormal case has 4 abnormal regions).



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

- The `TP` (or `LL`) worksheet - this lists the ratings of ROI-level-abnormal regions.
  - Because normal 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 abnormal case.
  - There are two entries for this case, corresponding to the two ROI-level-abnormal 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-normal regions in this case.
  - One should be satisfied that for each abnormal case the sum of the number of entries in the `TP` and `FP` worksheets is always 4.

Chapter 5

ROI data format

5.1 ROI paradigm

- 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). The ROIs are defined prior to the study and made known to all observers participating in the study. Unlike the FROC paradigm, a **rating is required for every ROI**.

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