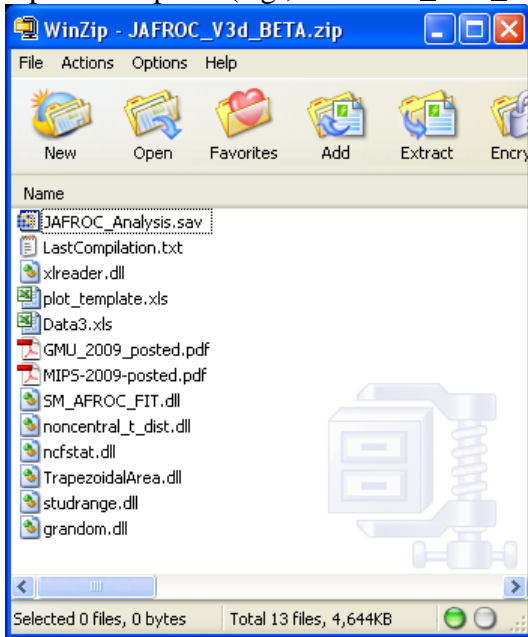


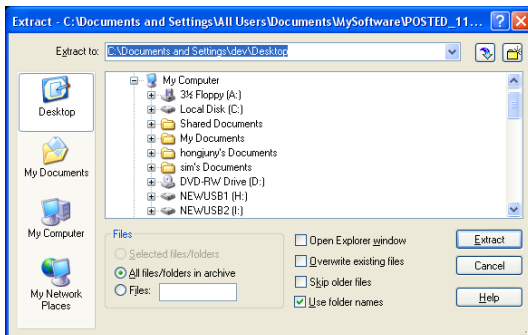
# Installing the software

The IDL Virtual Machine (IDL VM) is available at <http://www.itvis.com/idlvm> .  
Download and install the latest version of IDL VM.

Open the zip file (e.g., JAFROC\_V3d\_BETA.zip).

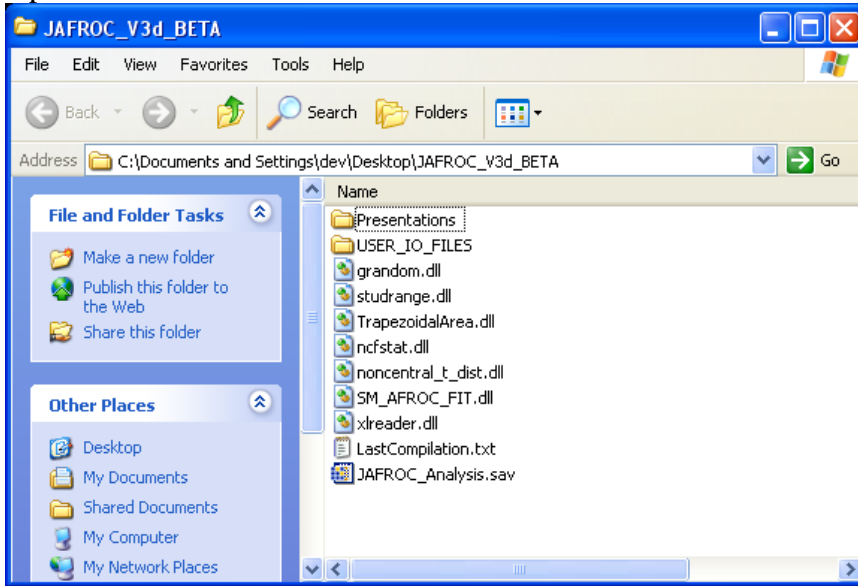


Click on "Extract" and make sure the selected options are as shown below.



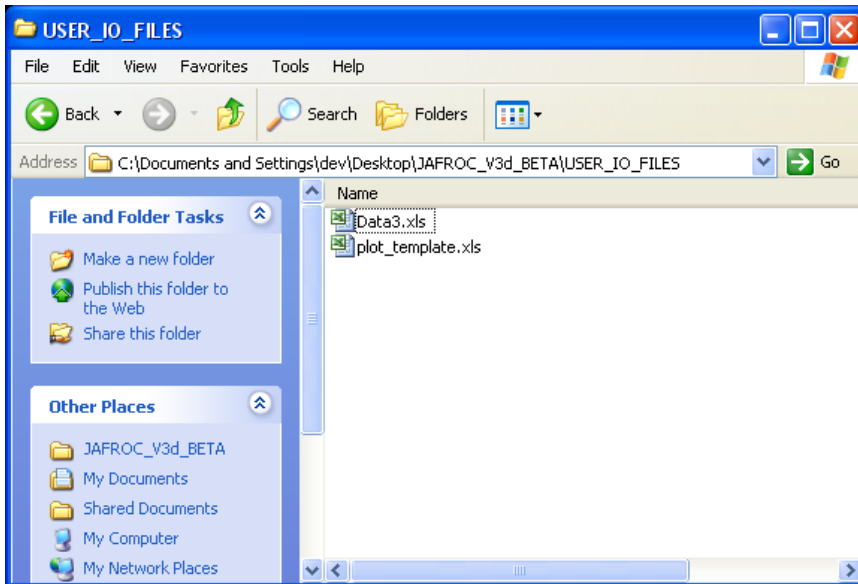
Again click on "Extract". A folder "JAFROC\_V3d\_BETA" will be created in the same directory containing the original zip file. You will see the zip file still open. Close it (click on the cross mark).

Open the ""JAFROC\_V3d\_BETA" folder.



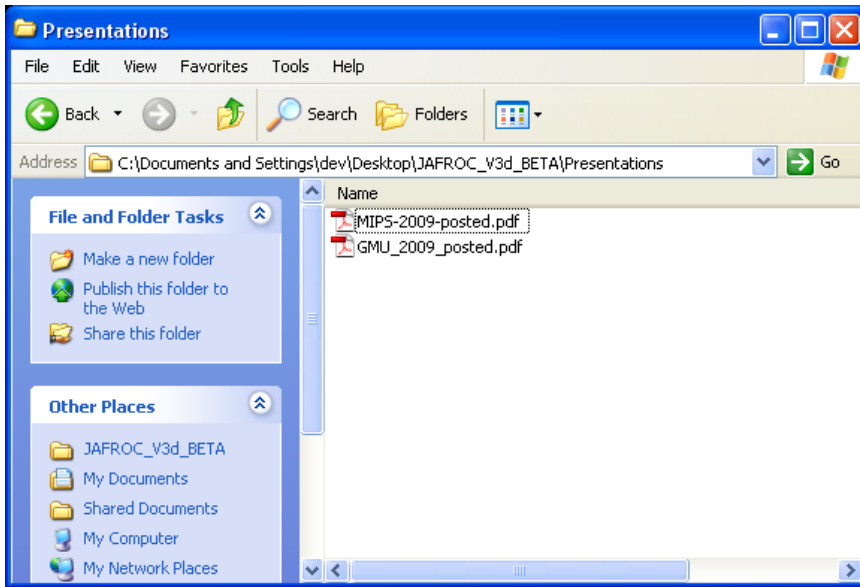
The "JAFROC\_Analysis.sav" file runs under the IDL Virtual machine and is effectively an exe file for the Virtual machine "operating system". If the extension ".sav" is reserved by some other program (SAS or SPSS) you need to disable that hold on this extension.

Click on the folder "USER\_IO\_FILES".



"Data3.xls" is a sample data file and ""plot\_template.xls" is an Excel macro file to allow you to plot FROC and AFROC curves. It is most convenient to put your data file in this folder, as this is where the program looks first.

Move up one directory and click on the "Presentations" directory. These contain some recent talks that illustrate basic ROC/FROC methodology and the sample size estimation routine which is built into JAFROC V3.



You have completed the installation.

# Data format

For an intuitive understanding of the format see the sample input file "Data3.xls" included in the zip file. The file plot\_template.xls is not an input file. It is intended to create FROC and AFROC plots. [Note: text input format is no longer supported.]

## Truth worksheet

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

Label	Meaning
CaseID	This <b>integer</b> field identifies the case (or patient or image). Cases must be <b>uniquely</b> labeled with integers; the integers do not have to be sequentially numbered.
LesionID	This <b>integer</b> field tells the program how many lesions are in a particular image and uniquely identifies them. If this number is zero the case is considered to be normal. If a case has multiple lesions then these must be uniquely identified with integers (they do not need to be sequential). For weighted analysis the lesion IDs in the Truth and TP worksheets must refer to the same lesions. For un-weighted analysis matching is not necessary. E.g., 11, 2, 31 and 4 for an abnormal case with 4-lesions; 1 and 2 for an abnormal case with 2-lesions; 0 for a normal case.
Weight	This <b>positive floating-point</b> value is the weight corresponding to the lesion ID. For each abnormal case there must be as many weights as there are lesions. e.g., 0.1, 0.2, 0.3, and 0.4 for a 4-lesion case; 0.5 and 0.5 for a 2-lesion case (equally weighted). Note that the sum of weights for a case must be 1.0 (to within 1%). For a normal case the weight field must be zero.

## TP (lesion localization) Worksheet

	A	B	C	D	E	F	G	H	I	J	K
1	ReaderID	ModalityID	CaseID	LesionID	TP_Rating						
2	1	1	0	1	4						
3	1	1	1	1	5						
4	1	1	2	1	5						
5	1	1	4	1	5						
6	1	1	5	1	5						
7	1	1	6	1	2						
8	1	1	7	1	3						
9	1	1	8	1	3						
10	1	1	9	1	5						
11	1	1	10	1	5						
12	1	1	15	1	4						
13	1	1	16	1	4						
14	1	1	17	1	4						
15	1	1	18	1	5						
16	1	1	19	1	4						
17	1	1	20	1	4						
18	1	1	21	1	5						
19	1	1	22	1	5						
20	1	1	23	1	4						
21	1	1	24	1	5						
22	1	1	25	1	4						
23	1	1	26	1	5						
24	1	1	27	1	5						
25	1	1	28	1	3						
26	1	1	29	1	5						

Entry	Meaning
ReaderID	This <b>integer</b> field identifies the readers. The entries must be unique integers, e.g., 1 or 2 or 3 for 3 readers.
ModalityID	This <b>integer</b> field identifies the modalities, e.g., 1 or 2 for 2 modalities.
CaseID	As in Table 1
LesionID	As in Table 1
TP_Rating	This <b>positive integer / floating-point</b> value is the rating assigned to a particular TP mark. <b>Higher numbers represent greater confidence</b> that the location is actually a lesion. For images with multiple lesions the ratings must correspond to the LesionIDs in the truth table unless the lesions are equally weighted. Otherwise the rating associated with a particular lesion will not match its weight.

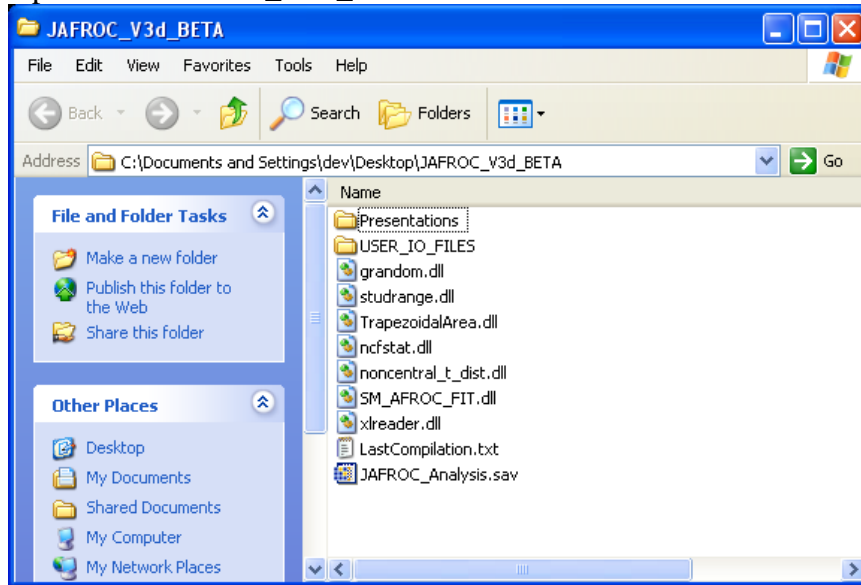
## FP (non-lesion localization) Worksheet

ReaderID	ModalityID	CaseID	FP_Rating
1	1	1	2
1	1	2	1
1	1	2	2
1	1	13	2
1	1	14	2
1	1	23	1
1	1	37	2
1	1	38	3
1	1	44	4
1	1	46	3
1	1	47	2
1	1	52	3
1	1	54	1
1	1	54	1
1	1	62	3
1	1	72	1
1	1	77	2
1	1	91	3
1	1	95	2
1	1	95	2
1	1	103	3
1	1	105	3
1	1	107	4
1	1	109	2
1	1	111	4

Entry	Meaning
ReaderID	As in Table 2.
ModalityID	As in Table 2.
CaseID	As in Table 1.
FP_Rating	This <b>positive integer / floating-point</b> value is the rating assigned to a particular FP mark. Multiple false positive are indicated on multiple lines.

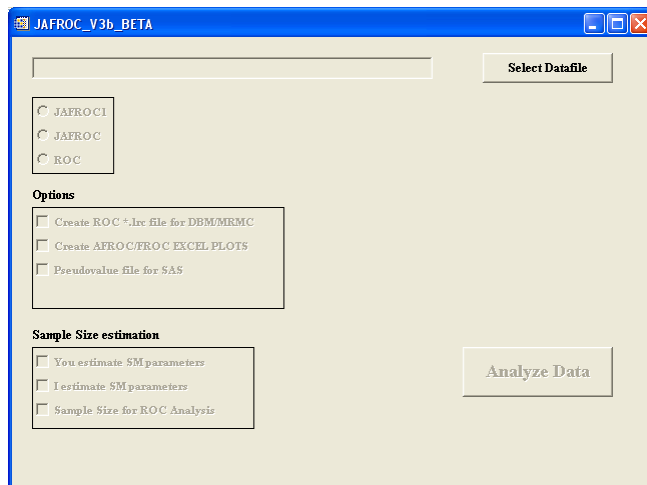
# Running the software

Open the "JAFROC\_V3d\_BETA" folder.

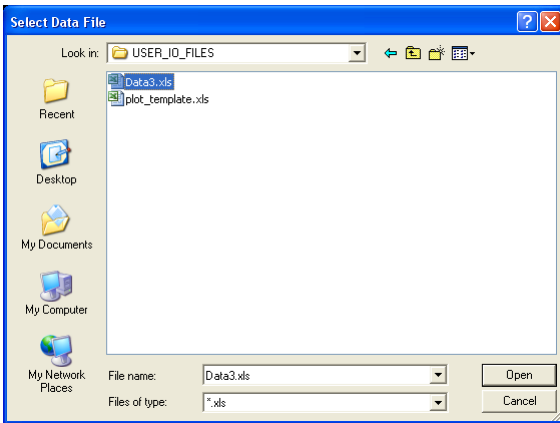


The "JAFROC\_Analysis.sav" file runs under the IDL Virtual machine and is effectively an exe file for the Virtual machine "operating system". If the extension ".sav" is reserved by some other program (SAS or SPSS) you need to disable that hold on this extension.

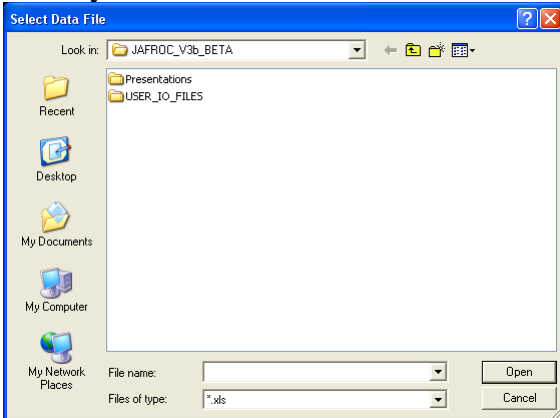
The following screen will show.



There is only one active button "Select Datafile". Upon clicking it you will see

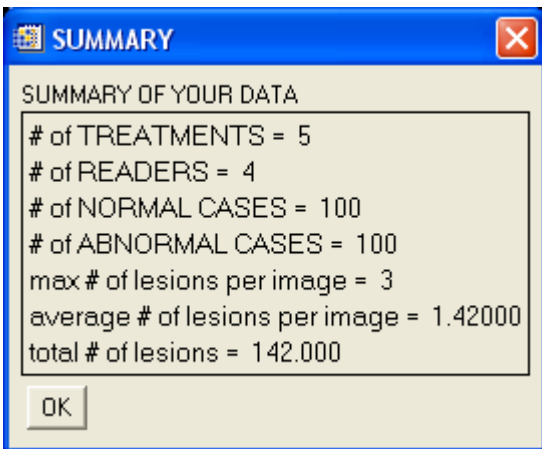


Select your data file and double click or "Open".

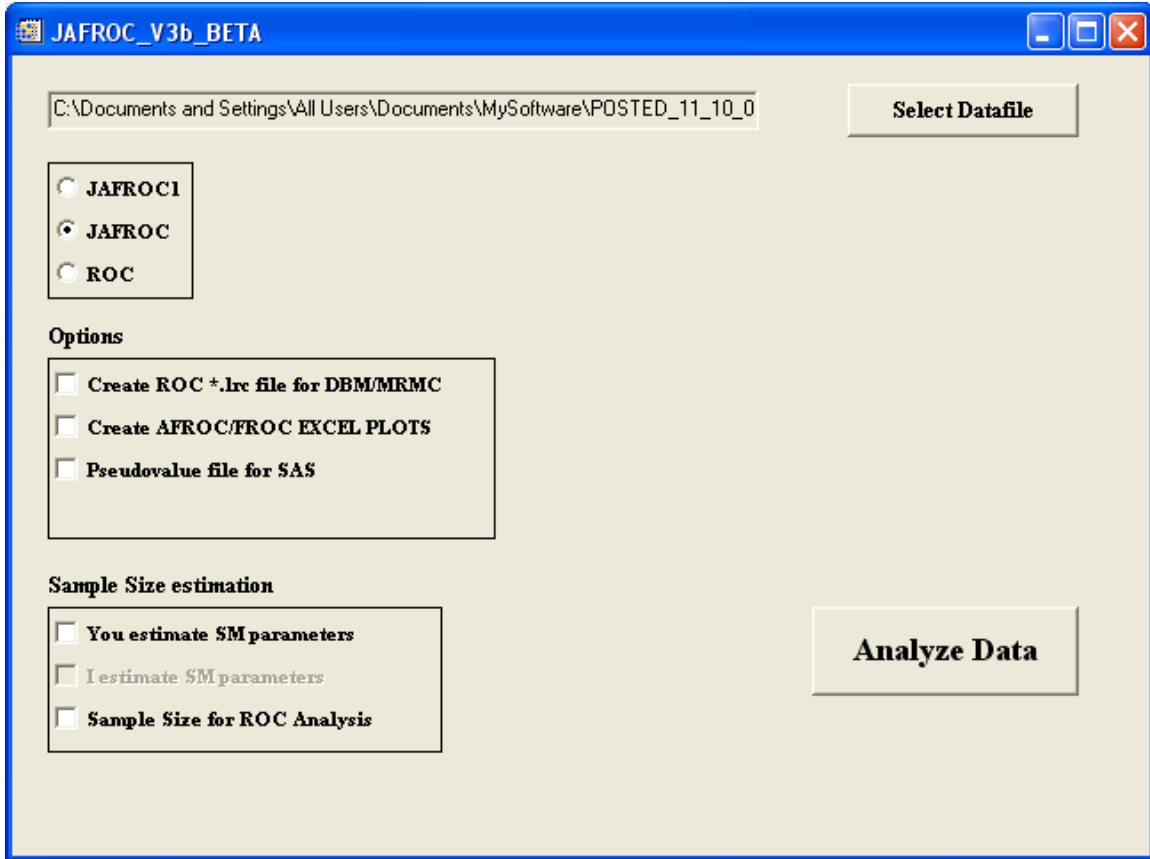


If there are errors (e.g., the selected file is not a valid input file, or the data is inconsistent) the program will exit with appropriate error messages.

Other wise the following screen will show.

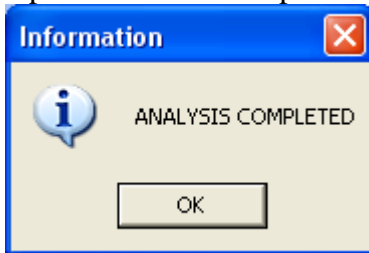


Clicking on "OK" will show the following screen

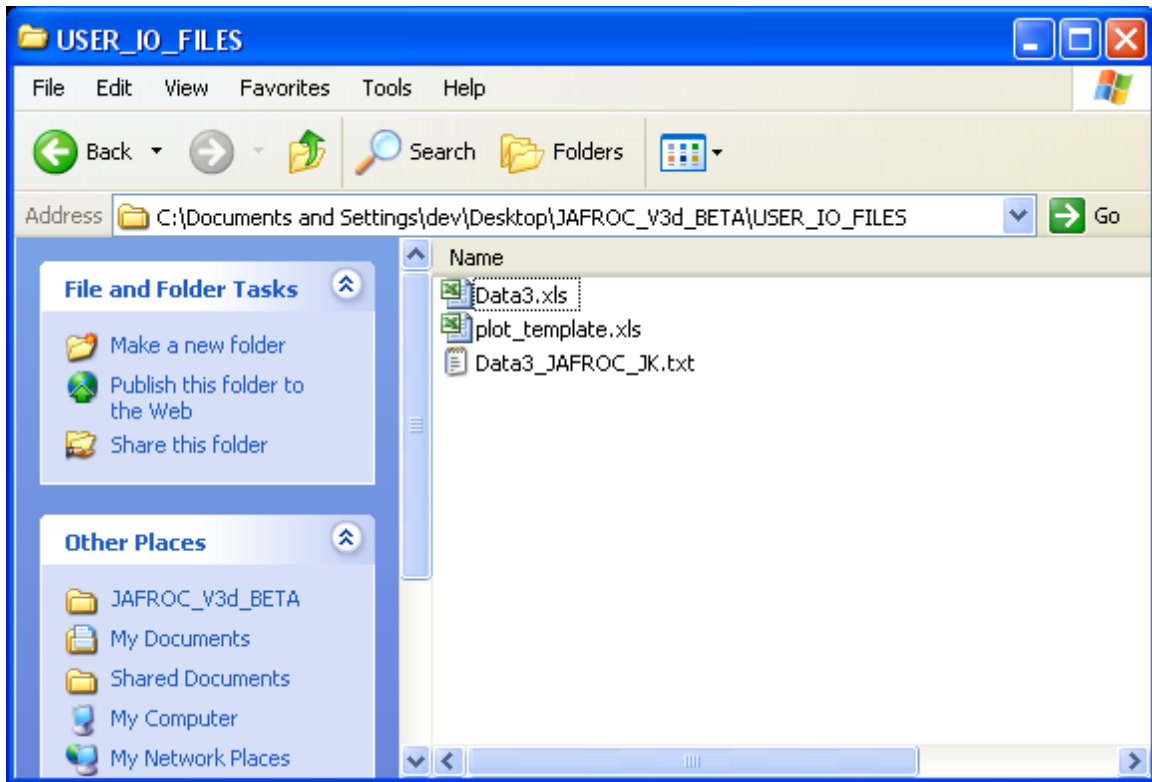


Here is where you select the analysis option. The simplest way is to keep the defaults. Click on "Analyze Data" button.

Upon successful completion the following will show



Click OK. Open the USER\_IO\_FILES folder.



The output file is Data3\_JAFROC\_JK.txt. It will contain the following (for the sample data set):

# Output file (for the sample data set)

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=====

JAFROC\_V3d\_BETA  
Last Compilation Date: Fri Nov 20 17:24:44 2009

=====

This run date : Tue Dec 08 15:38:45 2009

Input Data Filename : Data3.xls  
Output Data Filename : Data3\_JAFROC\_JK.txt

Analysis method: : JAFROC2  
Number of Readers : 4  
Number of Treatments : 5  
Number of Normal Cases : 100  
Number of Abnormal Cases : 100  
fraction normal cases : 0.500  
min LESIONS\_PER\_IMAGE : 1  
max LESIONS\_PER\_IMAGE : 3  
mean LESIONS\_PER\_IMAGE : 1.420  
Total LESIONS : 142  
Inc. Loc. Frac. : 0.132

=====

For TRT = 1 and RDR = 1 , max FPF = 0.480.  
For TRT = 1 and RDR = 3 , max FPF = 0.190.  
For TRT = 1 and RDR = 4 , max FPF = 0.410.  
For TRT = 1 and RDR = 5 , max FPF = 0.160.  
For TRT = 2 and RDR = 1 , max FPF = 0.360.  
For TRT = 2 and RDR = 3 , max FPF = 0.380.  
For TRT = 2 and RDR = 4 , max FPF = 0.580.  
For TRT = 2 and RDR = 5 , max FPF = 0.220.

For TRT = 3 and RDR = 1 , max FPF = 0.480.  
 For TRT = 3 and RDR = 3 , max FPF = 0.160.  
 For TRT = 3 and RDR = 4 , max FPF = 0.390.  
 For TRT = 3 and RDR = 5 , max FPF = 0.280.  
 For TRT = 4 and RDR = 1 , max FPF = 0.400.  
 For TRT = 4 and RDR = 3 , max FPF = 0.250.  
 For TRT = 4 and RDR = 4 , max FPF = 0.500.  
 For TRT = 4 and RDR = 5 , max FPF = 0.220.  
 For TRT = 5 and RDR = 1 , max FPF = 0.420.  
 For TRT = 5 and RDR = 3 , max FPF = 0.240.  
 For TRT = 5 and RDR = 4 , max FPF = 0.480.  
 For TRT = 5 and RDR = 5 , max FPF = 0.250.

=====

FOM = Trapezoidal area under AFROC curve, ignoring NLS on abnormal cases

FOMs for TREATMENTS (columns) and READERS (rows)

	1	2	3	4
1	0.7427	0.7587	0.6983	0.7818
3	0.7105	0.7162	0.6955	0.7235
4	0.7003	0.7225	0.6778	0.7133
5	0.7910	0.7927	0.7548	0.8136

	1
1	0.7170
3	0.6691
4	0.6587
5	0.7682

===== Results: RANDOM\_ALL =====

F-statistic and p-value

Significance level of test (alpha) = 0.05

F-statistic : 8.508

p-value : 1.544E-005

DF (Num,Den) : ( 4, 6.195E+001)

N.B. If the p-value is less than 0.05 there is a significant difference between at least one pair of TREATMENTS

READER-averaged FOMs for TREATMENTS and 95% confidence intervals:

1 0.7361, ( 0.6750, 0.7973)  
2 0.7475, ( 0.6929, 0.8021)  
3 0.7066, ( 0.6541, 0.7591)  
4 0.7580, ( 0.6883, 0.8278)  
5 0.7032, ( 0.6300, 0.7765)

INTER-TREATMENT differences and 95% confidence intervals:

FOM(1)-FOM(2) = -0.0114, (-0.0351, 0.0123)  
FOM(1)-FOM(3) = 0.0295, ( 0.0058, 0.0532)  
FOM(1)-FOM(4) = -0.0219, (-0.0456, 0.0018)  
FOM(1)-FOM(5) = 0.0329, ( 0.0092, 0.0566)  
FOM(2)-FOM(3) = 0.0409, ( 0.0172, 0.0646)  
FOM(2)-FOM(4) = -0.0105, (-0.0342, 0.0132)  
FOM(2)-FOM(5) = 0.0443, ( 0.0206, 0.0680)  
FOM(3)-FOM(4) = -0.0514, (-0.0751,-0.0277)  
FOM(3)-FOM(5) = 0.0034, (-0.0204, 0.0271)  
FOM(4)-FOM(5) = 0.0548, ( 0.0311, 0.0785)

Variance components needed for sample-size estimation:

var\_tr : -3.3255E-004  
var\_tc : 7.8742E-003  
var\_trc : 9.1269E-002

===== Results: RANDOM\_CASES =====

F-statistic and p-value

Significance level of test (alpha) = 0.05  
F-statistic : 3.899  
p-value : 3.830E-003  
DF (Num,Den) : ( 4, 7.960E+002)

N.B. If the p-value is less than 0.05 there is a significant difference  
between at least one pair of TREATMENTS

READER-averaged FOMs for TREATMENTS and 95% confidence intervals:

1 0.7361, ( 0.6943, 0.7779)  
2 0.7475, ( 0.7062, 0.7889)

3 0.7066, ( 0.6638, 0.7494)  
 4 0.7580, ( 0.7190, 0.7970)  
 5 0.7032, ( 0.6613, 0.7452)

INTER-TREATMENT differences and 95% confidence intervals:

FOM(1)-FOM(2) = -0.0114, (-0.0458, 0.0230)  
 FOM(1)-FOM(3) = 0.0295, (-0.0049, 0.0639)  
 FOM(1)-FOM(4) = -0.0219, (-0.0563, 0.0125)  
 FOM(1)-FOM(5) = 0.0329, (-0.0015, 0.0673)  
 FOM(2)-FOM(3) = 0.0409, ( 0.0065, 0.0753)  
 FOM(2)-FOM(4) = -0.0105, (-0.0449, 0.0239)  
 FOM(2)-FOM(5) = 0.0443, ( 0.0099, 0.0787)  
 FOM(3)-FOM(4) = -0.0514, (-0.0858,-0.0170)  
 FOM(3)-FOM(5) = 0.0034, (-0.0310, 0.0377)  
 FOM(4)-FOM(5) = 0.0548, ( 0.0204, 0.0892)

===== Results: RANDOM\_RDRS =====

F-statistic and p-value

Significance level of test (alpha) = 0.05

F-statistic : 19.332

p-value : 3.641E-005

DF (Num,Den) : ( 4, 1.200E+001)

N.B. If the p-value is less than 0.05 there is a significant difference  
 between at least one pair of TREATMENTS

READER-averaged FOMs for TREATMENTS and 95% confidence intervals:

1 0.7361, ( 0.6712, 0.8010)  
 2 0.7475, ( 0.6911, 0.8040)  
 3 0.7066, ( 0.6535, 0.7597)  
 4 0.7580, ( 0.6820, 0.8341)  
 5 0.7032, ( 0.6234, 0.7831)

INTER-TREATMENT differences and 95% confidence intervals:

FOM(1)-FOM(2) = -0.0114, (-0.0286, 0.0057)  
 FOM(1)-FOM(3) = 0.0295, ( 0.0124, 0.0467)  
 FOM(1)-FOM(4) = -0.0219, (-0.0390,-0.0048)  
 FOM(1)-FOM(5) = 0.0329, ( 0.0157, 0.0500)

FOM(2)-FOM(3) = 0.0409, ( 0.0238, 0.0581)  
FOM(2)-FOM(4) = -0.0105, (-0.0276, 0.0066)  
FOM(2)-FOM(5) = 0.0443, ( 0.0271, 0.0614)  
FOM(3)-FOM(4) = -0.0514, (-0.0686,-0.0343)  
FOM(3)-FOM(5) = 0.0034, (-0.0138, 0.0205)  
FOM(4)-FOM(5) = 0.0548, ( 0.0376, 0.0719)

=====

Total number of warnings = 0

===== DONE =====

# Interpretation of the output file

Inc. Loc. Frac. : 0.132

This is the incorrect localization fraction (ILF): the fraction of abnormal images on which the highest rated location was a false positive (and not a lesion). See my 2004 Med Phys paper. If ILF is large then one expects a large power advantage of JAFROC over ROC analysis. If it is zero, one does not expect a power advantage and you might as well analyze your data with DBM\_MRMC software.

===== Results: RANDOM\_ALL =====

## F-statistic and p-value

Significance level of test (alpha) = 0.05

F-statistic : 8.508

p-value : 1.544E-005

DF (Num,Den) : ( 4, 6.195E+001)

N.B. If the p-value is less than 0.05 there is a significant difference between at least one pair of TREATMENTS

If  $p < 0.05$  you have a significant difference.

## READER-averaged FOMs for TREATMENTS and 95% confidence intervals:

1	0.7361, ( 0.6943, 0.7779)
2	0.7475, ( 0.7062, 0.7889)
3	0.7066, ( 0.6638, 0.7494)
4	0.7580, ( 0.7190, 0.7970)
5	0.7032, ( 0.6613, 0.7452)

Lists the reader-averaged figures of merit for the 5 treatments (modalities) and 95% confidence intervals. The confidence intervals have not been corrected for multiple comparisons.

## INTER-TREATMENT differences and 95% confidence intervals:

FOM(1)-FOM(2)	= -0.0114, (-0.0458, 0.0230)
FOM(1)-FOM(3)	= 0.0295, (-0.0049, 0.0639)
FOM(1)-FOM(4)	= -0.0219, (-0.0563, 0.0125)
FOM(1)-FOM(5)	= 0.0329, (-0.0015, 0.0673)

FOM(2)-FOM(3)	= 0.0409, ( 0.0065, 0.0753)
FOM(2)-FOM(4)	= -0.0105, (-0.0449, 0.0239)
FOM(2)-FOM(5)	= 0.0443, ( 0.0099, 0.0787)
FOM(3)-FOM(4)	= -0.0514, (-0.0858,-0.0170)
FOM(3)-FOM(5)	= 0.0034, (-0.0310, 0.0377)
FOM(4)-FOM(5)	= 0.0548, ( 0.0204, 0.0892)

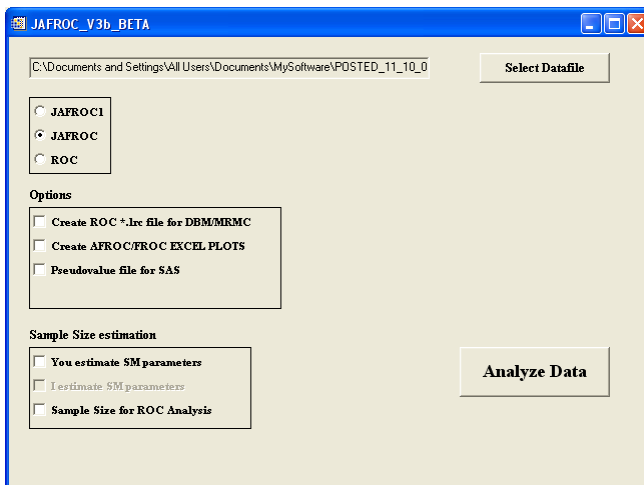
Lists the inter-treatment differences between reader-averaged figures of merit for all pairings of the treatments and 95% confidence intervals for the differences. If the 95% CI does not include 0, then the corresponding modality pairs are significantly different. The confidence intervals have not been corrected for multiple comparisons. If they had been, the corrected CI's would be larger and you would see fewer significant differences. But if  $p < 0.05$  at least one of the differences is significant.

Variance components needed for sample-size estimation:

var\_tr : -3.3255E-004  
var\_tc : 7.8742E-003  
var\_trc : 9.1269E-002

This could be used for sample size estimation but you don't know the JAFROC effect size corresponding to a 5% ROC effect size.

If you had selected the "You estimate SM parameters" in the opening screen, repeated below, the program will walk you through a couple of steps illustrated in the MIPS Power Point presentation. You will not have to re-enter the above values.



The rest of the output is for random cases and random readers analyses, as per the DBM-MRMC documentation.

If warnings or errors are generated a log file is created. If you cannot fix the problem send me the data file.

Please bring errors in the documentation to my attention.

Good luck!

Dev P. Chakraborty

Last revision: 12/8/2009 4:01 PM