

# JAFROC 4.0 User Manual

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Windows XP and Windows 7 compatible software to perform JAFROC analysis.

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## Features

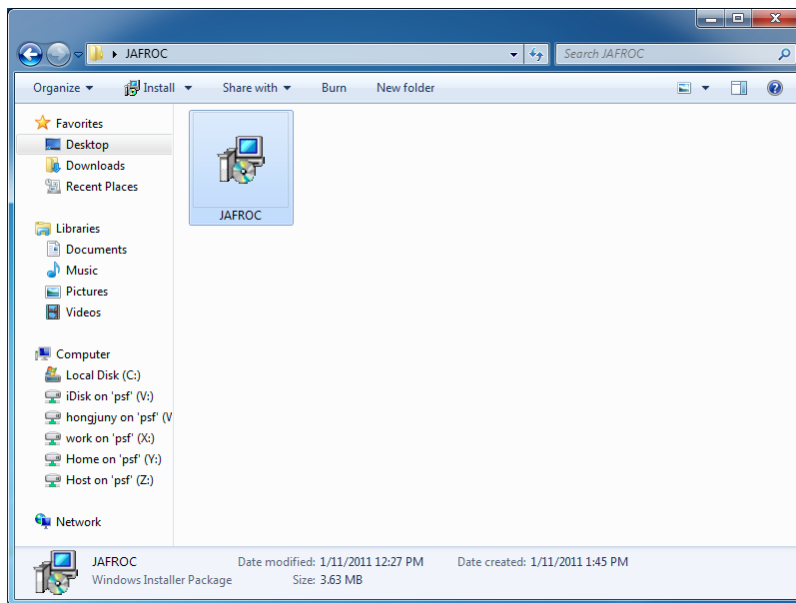
JAFROC analysis is described in Ref. (1). Basic ROC references are (2-4).

1. Standalone windows compatible software (XP, Vista, 7).
2. Convenient FROC raw data plotting: this is a quick way to check the quality of the FROC data and train readers in optimal usage of the rating scale (5).
3. Integrated plotting routine – uses maximum likelihood method to fit the search model (6, 7) to ROC, FROC and AFROC data.
4. Integrated sample size analysis using an adaptation of the Hillis-Berbaum method (8).
5. Ability to perform user-defined FROC analysis by accessing the built in DLLs (e.g., jackknifing, figure of merit and ANOVA). See JAFROC Development Kit Guide.doc.

## Installing the software

Install “Microsoft Visual C++ 2010 Redistributable Package (x86)” before installing JAFROC software. It is available at <http://www.microsoft.com/downloads/en/details.aspx?familyid=A7B7A05E-6DE6-4D3A-A423-37BF0912DB84&displaylang=en>. Search for “Microsoft Visual C++ 2010 Redistributable Package (x86)” on Google to get to this site.

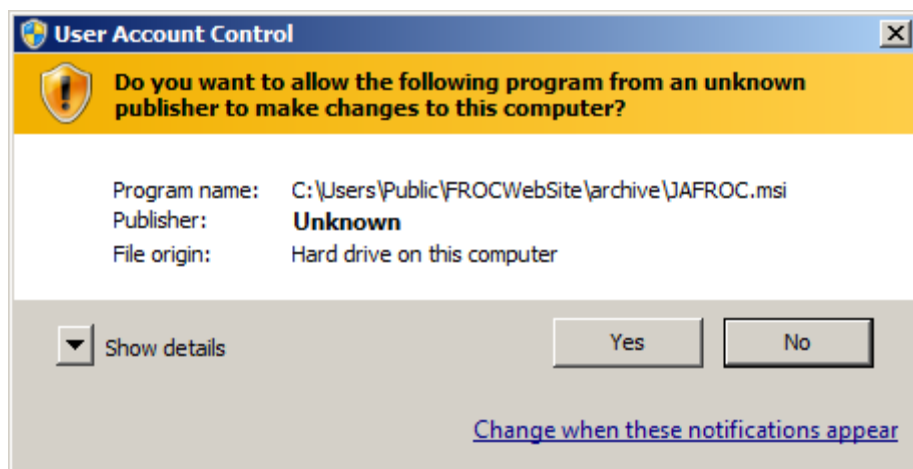
Double-click JAFROC.MSI file.



Installation creates a “JAFROC” folder in the “Program Files” folder and “JAFROC Data” folder in “Documents” folder and copies a sample JAFROC data file "DataFile.xls" and “plot\_template.xls” file to this folder. Click on "Next"

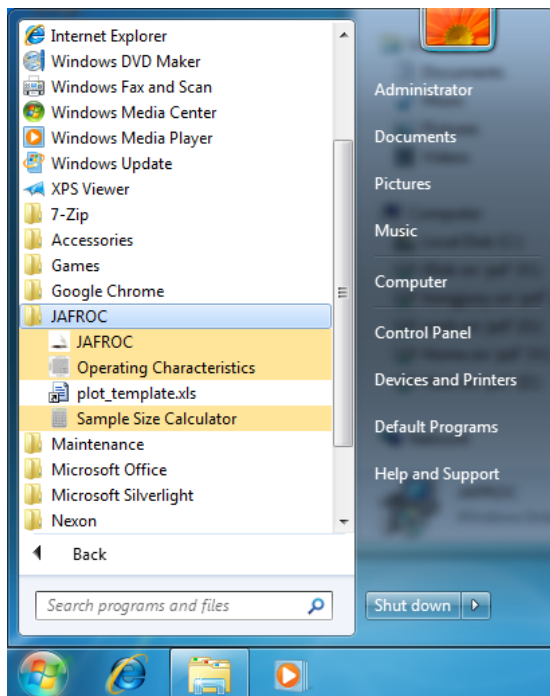


If running under Windows 7 the following screen may appear:



Click on "Yes".

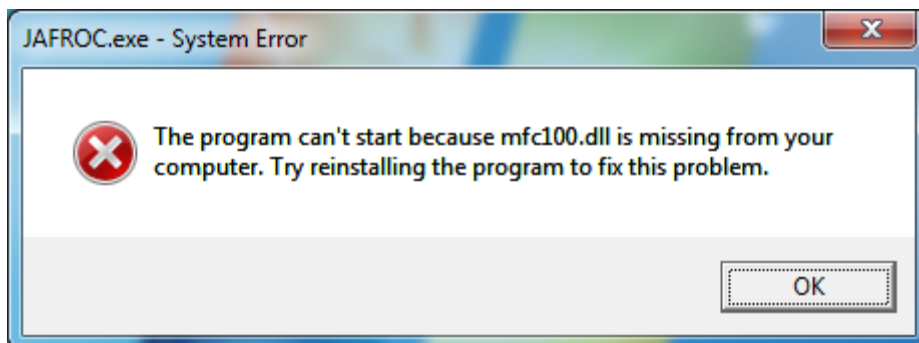
After installation, click on [Start] menu and check that the JAFROC folder was created with four icons in.



If you get the error message shown below when you start JAFROC software, try installing “Microsoft Visual C++ 2010 Redistributable Package (x86)” available at

<http://www.microsoft.com/downloads/en/details.aspx?familyid=A7B7A05E-6DE6-4D3A-A423-37BF0912DB84&displaylang=en>

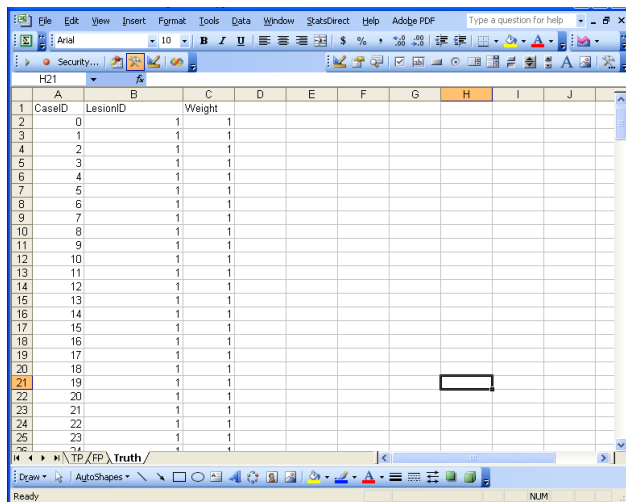
and restart JAFROC.



## 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 for creating FROC and AFROC plots. Note: text input format is no longer supported.

## Truth worksheet



	A	B	C	D	E	F	G	H	I	J
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							

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	<p>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.</p> <p>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).</p> <p>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.</p>



## 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						

Label	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.

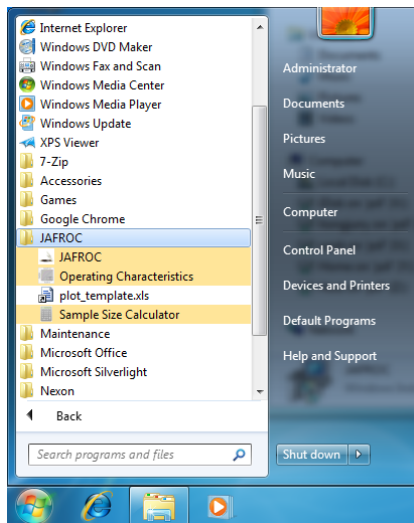
## FP (non-lesion localization) Worksheet

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
4	1	111	4

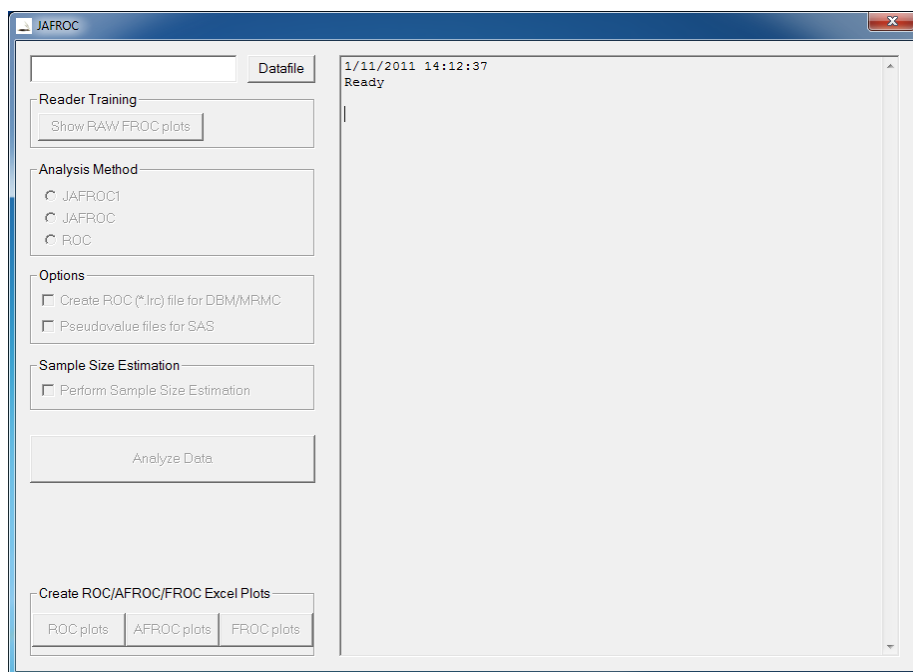
Label	Meaning
ReaderID	As in Table 2
ModalityID	As in Table 2
CaseID	As in Table 1, but on this sheet the cases must be grouped: if two or more false positives occur for the same reader, modality and case then they should appear consecutively and not be separated by data for other cases.
FP_Rating	This <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

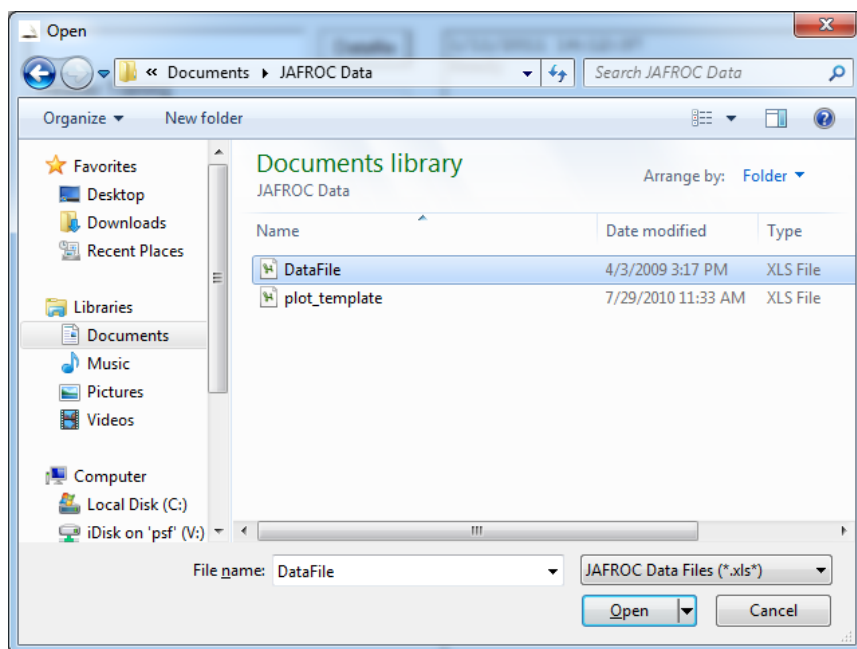
Click [Start] menu and select JAFROC icon.



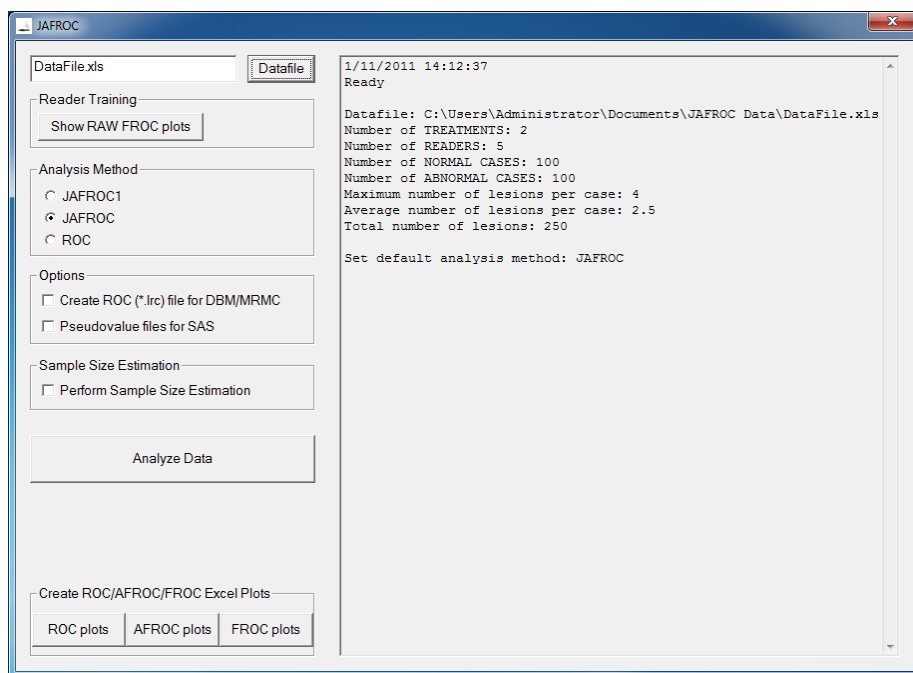
The following screen will show. Click on the “Datafile” button located at top-left.

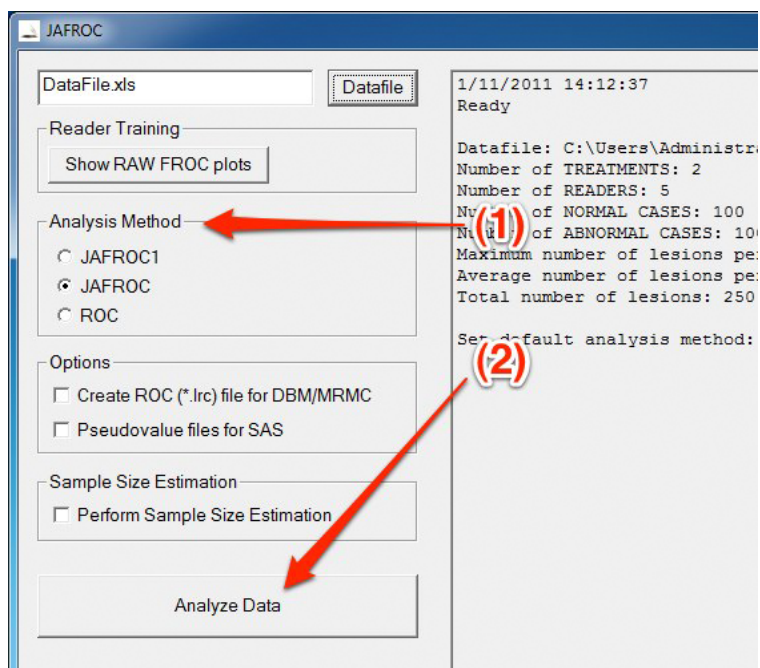


Locate your data file in “Documents\JAFROC Data” folder. Select your data file and double click or click “Open”.



If there are errors (e.g., the selected file is not a valid input file, or the data is inconsistent) the program will display appropriate error messages on the console. Other wise the screen will show the following.

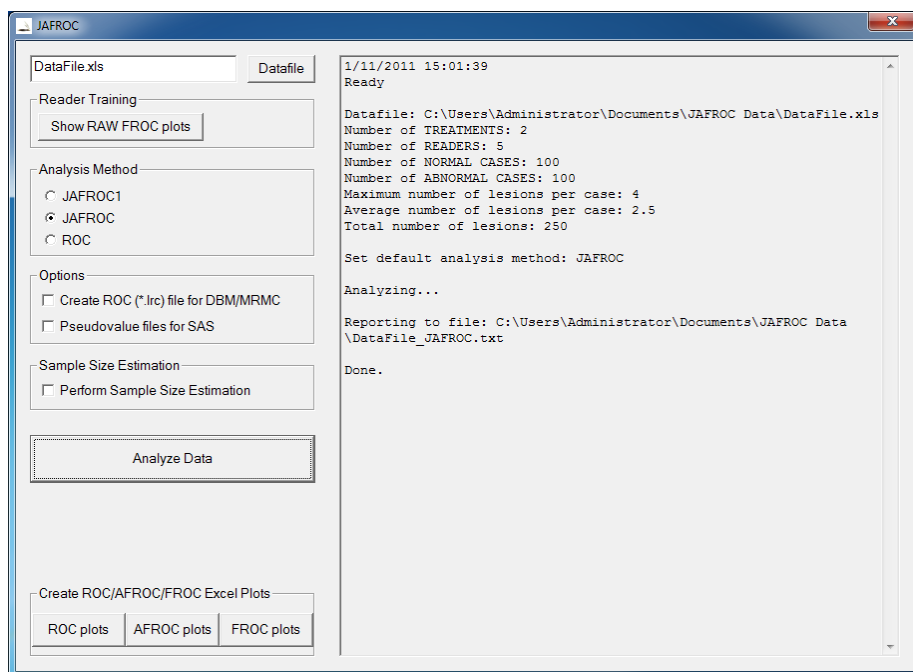




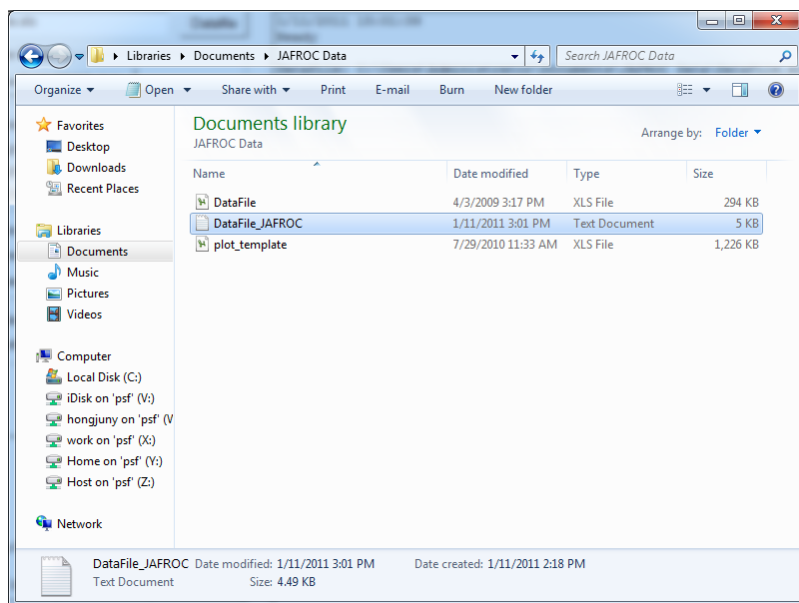
(1) First, select the analysis option. The simplest way is to keep the defaults.

(2) Then click on "Analyze Data" button.

Upon successful completion the following will show



Open the JAFROC Data folder.



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

## Output file for the sample data set

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=====

JAFROC Version 4.0

Last Compilation Date

JAFROC\_CORE.DLL : Jan 10 2011 12:34:00

JAFROC.EXE : Jan 11 2011 12:27:18

=====

This run date: 1/11/2011 15:01:46

Input Data Filename : DataFile.xls

Output Data Filename : DataFile\_JAFROC.txt

Analysis method: : JAFROC FOM DBM-MRMC SIGNIFICANCE TESTING

Number of Readers : 5

Number of Treatments : 2



Number of Normal Cases : 100  
 Number of Abnormal Cases : 100  
 fraction normal cases : 0.500  
 min LESIONS\_PER\_IMAGE : 1  
 max LESIONS\_PER\_IMAGE : 4  
 mean LESIONS\_PER\_IMAGE : 2.5  
 Total LESIONS : 250  
 Inc. Loc. Frac. : 0.031

=====

For TRT = 1	, and RDR = 1	, max FPF = 0.990.
For TRT = 1	, and RDR = 2	, max FPF = 0.990.
For TRT = 1	, and RDR = 3	, max FPF = 1.000.
For TRT = 1	, and RDR = 4	, max FPF = 0.990.
For TRT = 1	, and RDR = 5	, max FPF = 0.990.
For TRT = 2	, and RDR = 1	, max FPF = 1.000.
For TRT = 2	, and RDR = 2	, max FPF = 1.000.
For TRT = 2	, and RDR = 3	, max FPF = 1.000.
For TRT = 2	, and RDR = 4	, max FPF = 1.000.
For TRT = 2	, and RDR = 5	, max FPF = 1.000.

=====

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

FOMs for TREATMENTS (columns) and READERS (rows)

1	2
---	---

	-----	-----
1	0.6654	0.6486
2	0.6867	0.6963
3	0.7447	0.7067
4	0.7118	0.7602
5	0.6416	0.7416

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

F-statistic and p-value

Significance level of test (alpha) = 0.05

F-statistic : 0.382

p-value : 5.469E-001

DF (Num,Den) : ( 1, 1.370E+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	0.6901, ( 0.6286, 0.7515 )
2	0.7107, ( 0.6506, 0.7708 )

INTER-TREATMENT differences and 95% confidence intervals:

FOM(1) - FOM(2) = -0.0206, (-0.0923, 0.0511 )

Variance components needed for sample-size estimation:

var\_tr : 1.2143E-003  
var\_tc : 5.1149E-002  
var\_trc : 5.7859E-002

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

F-statistic and p-value

Significance level of test (alpha) = 0.05

F-statistic : 0.677

p-value : 4.116E-001

DF (Num,Den) : ( 1, 1.990E+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 0.6901, ( 0.6390, 0.7411 )  
2 0.7107, ( 0.6649, 0.7565 )

INTER-TREATMENT differences and 95% confidence intervals:

FOM(1) - FOM(2) = -0.0206, (-0.0700, 0.0288 )

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

F-statistic and p-value

Significance level of test (alpha) = 0.05

F-statistic : 0.706

p-value : 4.480E-001

DF (Num,Den) : ( 1, 4.000E+000 )

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 0.6901, ( 0.6403, 0.7398 )

2 0.7107, ( 0.6570, 0.7644 )

INTER-TREATMENT differences and 95% confidence intervals:

FOM(1) - FOM(2) = -0.0206, (-0.0887, 0.0475 )

=====

## Interpretation of the output file

Inc. Loc. Frac. : 0.031

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\_MPMC software.

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

F-statistic and p-value

Significance level of test (alpha) = 0.05

F-statistic : 0.382

p-value : 5.469E-001

DF (Num,Den) : ( 1, 1.370E+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 0.6901, ( 0.6286, 0.7515)

2 0.7107, ( 0.6506, 0.7708)

Lists the reader-averaged figures of merit for the 2 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) = -0.0206, (-0.0923, 0.0511 )

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 (more than one pair). 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:

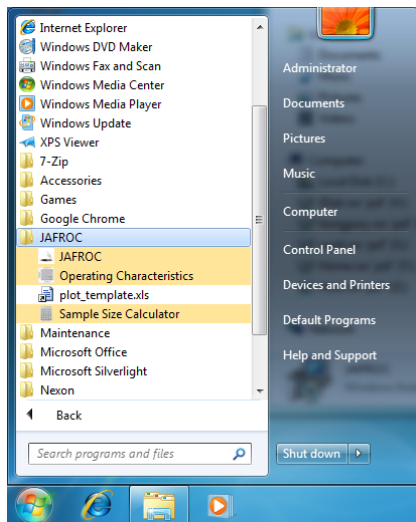
var\_tr : 1.2143E-003

var\_tc : 5.1149E-002

var\_trc : 5.7859E-002

## ROC sample size calculator

[This could be used for sample size estimation for JAFROC but you don't know the JAFROC effect size corresponding to a given ROC effect size, so it is best to use the built in capability in JAFROC described after this section.] This is an implementation of the Hillis Berbaum method (8). Click [Start] menu and select the "Sample Size Calculator" icon.



The following screen will show. Enter the three variance components, set the appropriate parameters, and press [Recalculate].

A screenshot of the 'Sample Size Calculator' dialog box. The dialog box has a title bar with the text 'Sample Size Calculator'. Inside the dialog box, there are several sections. The first section is 'Generalization To:' with three radio buttons: 'Random ALL' (selected), 'Random CASES', and 'Random READERS'. The second section is 'Needed Input:' with four input fields: 'Number of Readers:' (5), 'Effect Size:' (0.114222), 'VAR\_TR:' (0.00121427), and 'VAR\_TC:' (0.0511491). The 'VAR\_TR:' and 'VAR\_TC:' fields are highlighted with a red rectangle, and a red arrow points to the 'VAR\_TC:' field. Below these fields are two more input fields: 'VAR\_TRC:' (0.0578592) and 'Desired Power (1-beta):' (0.8). The third section is 'Alpha:' (0.05). The fourth section is 'Prediction:' with an input field 'Number of Cases:' (126). At the bottom of the dialog box, there are two buttons: 'Recalculate' and 'Close'.

## JAFROC sample size calculator

If you had selected "Perform Sample Size Estimation" in the main screen, repeated below, the program will walk you through one more step. You will not have to re-enter the variance components manually.

The screenshot displays the JAFROC sample size calculator interface. On the left, there are three main sections: 'JAFROC' (selected with a radio button), 'ROC' (unselected), and 'Options' (containing two unchecked checkboxes: 'Create ROC (.lrc) file for DBM/MRMC' and 'Pseudovalue files for SAS'). Below these is the 'Sample Size Estimation' section, which contains a checked checkbox for 'Perform Sample Size Estimation'. A red arrow points to the word 'Checked' in red text above this checkbox. At the bottom of the left panel is an 'Analyze Data' button. The right panel displays the following text: 'Total number of lesions: 250', 'Set default analysis method: JAFROC', and 'Select Sample Size Estimation.'

Upon the "Sample Size Estimation" screen, you will enter appropriate parameters as for your request, then click on "Recalculate" button. Required number of cases per number of readers will be shown. Press "OK" to report the result.



**Sample Size Estimation**

ROC Effect Size  
0.05

Modality  
☒ 1  
☒ 2

Alpha  
0.05

Desired Power (1-beta)  
0.8

Recalculate

NH ROC FOM: 0.777212  
AH ROC FOM: 0.827212  
ROC Effect Size: 0.0500001

NH JAFROC FOM: 0.545253  
AH JAFROC FOM: 0.659475  
JAFROC Effect Size: 0.114222

Alpha: 0.05  
Desired power: 0.8

Prediction  
Random All

# Readers: 4	# Cases: 188
# Readers: 5	# Cases: 126
# Readers: 6	# Cases: 105
# Readers: 7	# Cases: 97
# Readers: 8	# Cases: 88
# Readers: 9	# Cases: 86
# Readers: 10	# Cases: 82
# Readers: 11	# Cases: 80
# Readers: 12	# Cases: 79
# Readers: 13	# Cases: 78
# Readers: 14~15	# Cases: 74
# Readers: 16~20	# Cases: 72
# Readers: 21~23	# Cases: 71

OK - Send the result to report

Cancel - Do not report

The rest of the output is for random cases and random readers analyses, as per the DBM-MRMC documentation (9).

## Options

Analysis Method

☐ JAFROC1

☒ JAFROC (1)

☐ ROC

Option

☐ Create ROC (\*.lrc) file for DBM/MRMC (2)

☐ Pseudo-value files for SAS

Sample Size Estimation

☐ Perform Sample Size Estimation

Analyze Data

(1) Convert FROC data into ROC and save it to the file compatible to DBM-MRMC software (\*.lrc).

(2) Save pseudo-values to a file in plain text format, consists of four columns of numbers. For each row, there are Reader Index, Treatment Index, Case Index, and the corresponding pseudo-value.

## Plots

Press “Show RAW FROC plots” button in the Reader Training section.

JAFROC

DataFile.xls Datafile 1/11/20 Ready

Reader Training

Show RAW FROC plots

Analysis Method

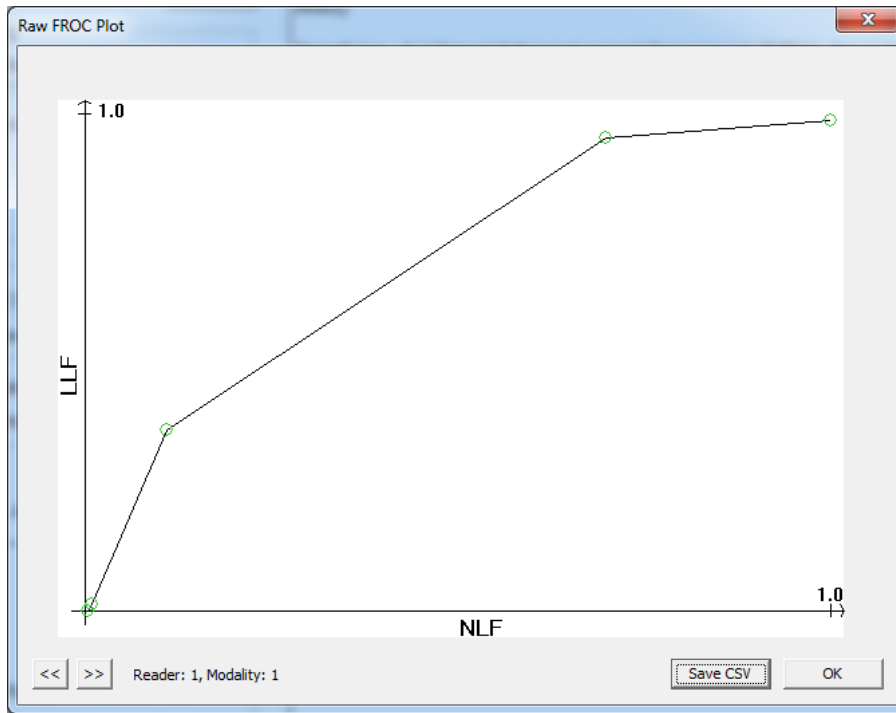
☐ JAFROC1

☒ JAFROC

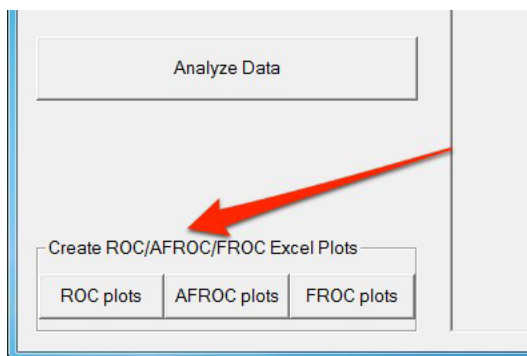
☐ ROC

Datafile Number Number Number Number Maximum Average Total n Set def

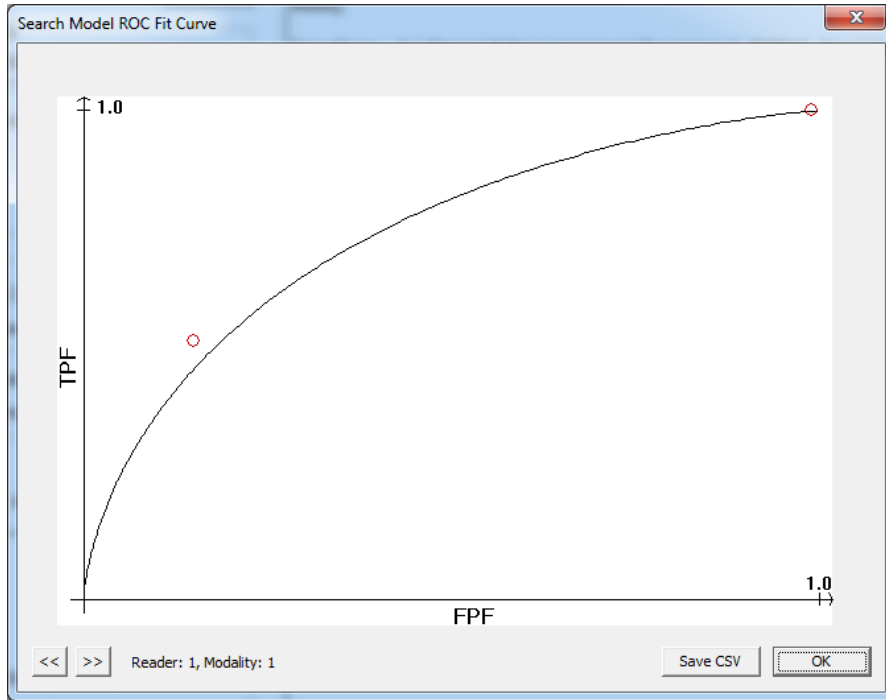
Shown is the raw FROC plot for each reader and modality. Press << and >> button to browse other reader and modality. Or, you can save the raw plot as CSV file.



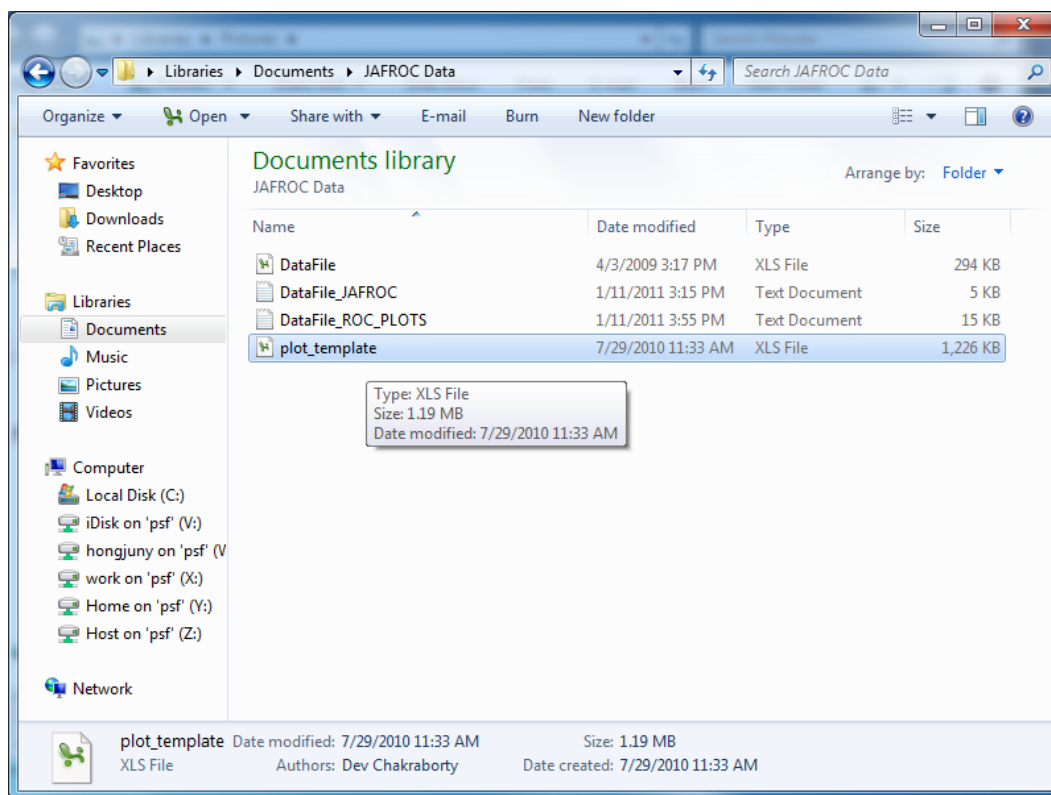
Press "ROC plots", "AFROC plots", and/or "FROC plots" button in the "Create ROC/AFROC/FROC Excel Plots" section.



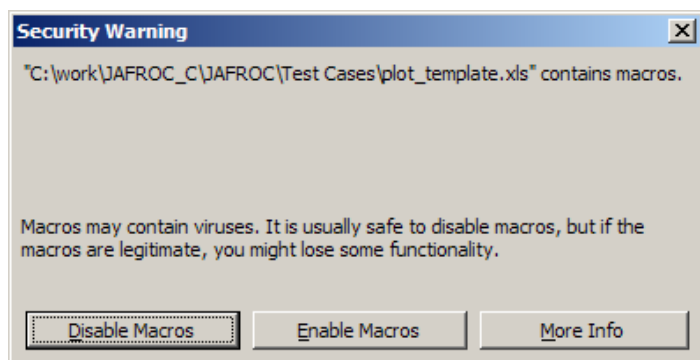
Shown is the Search Model fitted curve for each reader and modality. Press << and >> button to browse other reader and modality. Or, you can save the raw plot as CSV file.



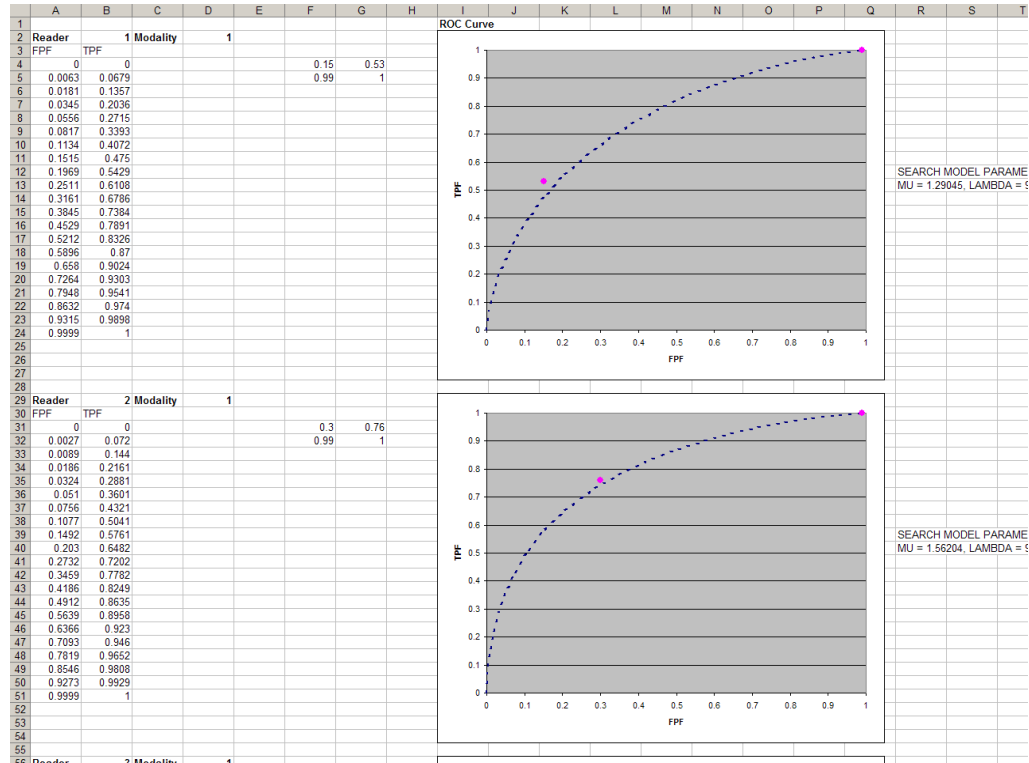
Also, the search model fitted curves for every reader and modality pairs can be shown in Excel worksheet. Open the JAFROC Data folder.



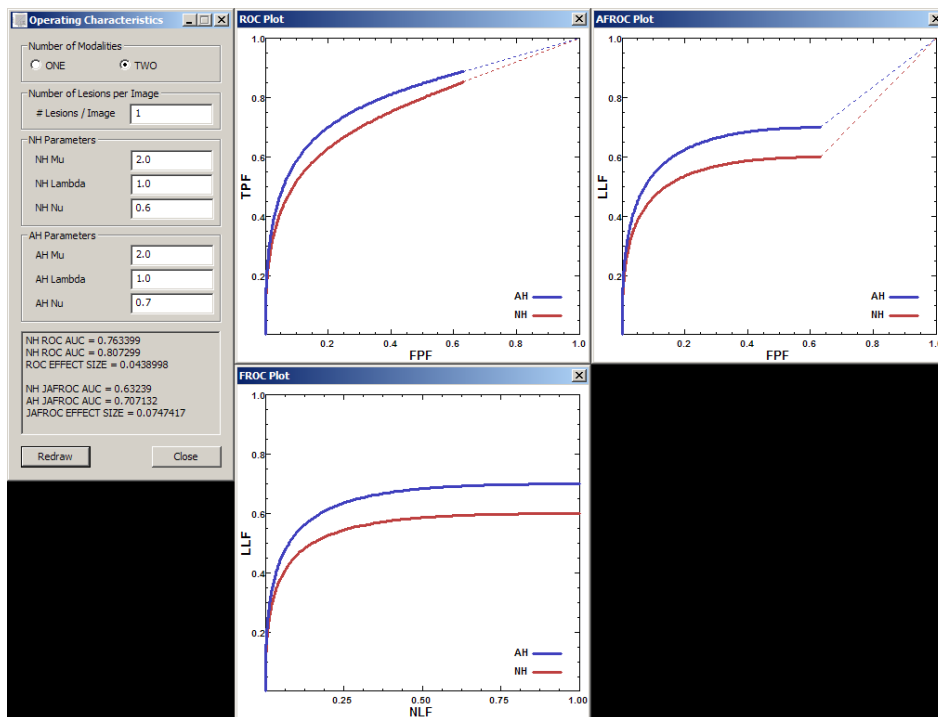
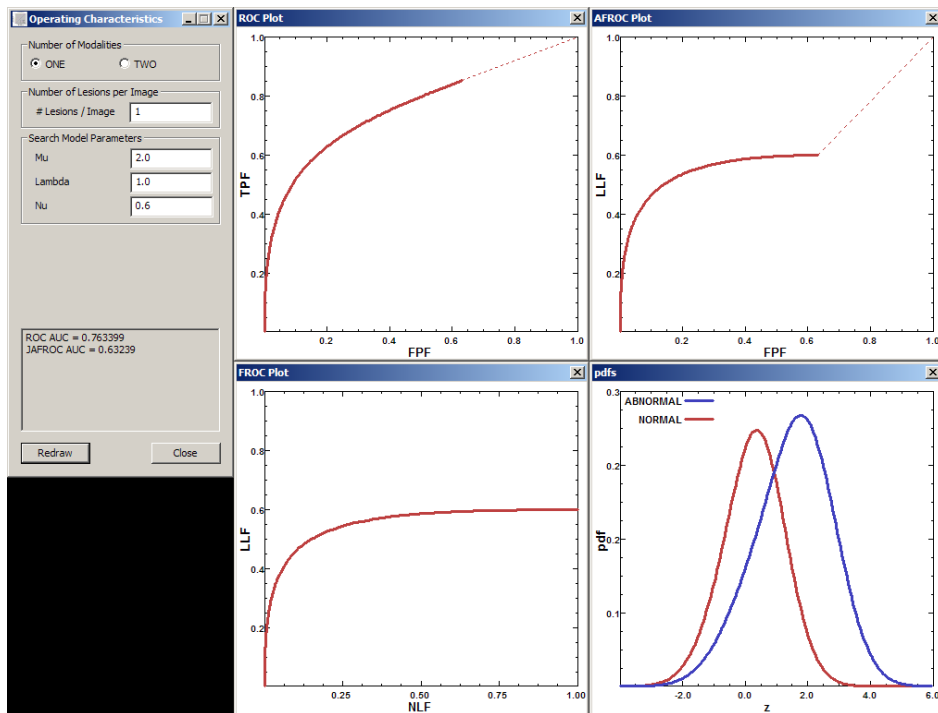
The file “plot\_template.xls” file includes script to read the search model fitted plots data file “DataFile\_ROC\_PLOTS.txt”. Double-click on “plot\_template.xls”, and press “Enable Macros” to allow the script to run reading plots.



Select “DataFile\_ROC\_PLOTS.txt”. Search model fitted ROC curves will be shown on the worksheet, along with the fitted search model parameters.



Reproduce ROC, AFROC, and FROC plots based upon the input search model parameters, observe differences between treatments, and calculate ROC and JAFROC AUC by “Operating Characteristics” software.



If warnings or errors during the analysis, error message is displayed on console window. If you cannot fix the problem send me the data file. Please bring errors on screen to my attention.

Good luck!

Dev P. Chakraborty

Last revision: 2/16/2021



## References

1. Chakraborty DP, Berbaum KS. Observer studies involving detection and localization: Modeling, analysis and validation. *Med Phys*. 2004; 31(8):2313-30.
2. Metz CE. Basic principles of ROC analysis. *Seminars in Nuclear Medicine*. 1978; 8(4):283-98.
3. Metz CE. ROC Methodology in Radiologic Imaging. *Investigative Radiology*. 1986; 21(9):720-33.
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