

Manual for the Noise Model and Event Ratio programs

A. Download Python program

Python is an *interpreted, interactive, object-oriented* programming language. It is often compared to Tcl, Perl, Scheme or Java. The Python implementation is portable: it runs on many brands of UNIX, on Windows, OS/2, Mac, Amiga, and many other platforms. The Python implementation is copyrighted but freely usable and distributable, even for commercial use. (<http://www.python.org/>)

For windows machines:

1) Download and install Python from this link

<http://downloads.activestate.com/ActivePython/windows/2.3/ActivePython-2.3.4-233-win32-ix86.msi>

2) Download and install the “numarray” extension for python version 1.1

<http://prdownloads.sourceforge.net/numpy/numarray-1.1.win32-py2.3.exe?download>

3) Download and install the graphical user interface extension wxPython2.5-win32-ansi-2.5.3.1-py23.exe

<http://prdownloads.sourceforge.net/wxpython/wxPython2.5-win32-ansi-2.5.3.1-py23.exe>

For Macs and Linux machine, download **Python 2.3.4** from

<http://www.python.org/download/>, and the corresponding numarray and graphical interface extension.

B. Download the Noise model and Event Ration program

Download the Aris.zip file from <http://www.cag.icph.org/bioinformatics.html>. Unzip the file and place the content (model.py, aris.py and main.py) in a folder in the python program location (i.e.: C:\Python23\Aris)

C. Run the noise model

To run the noise model double click on model.py

The following window will appear (figure 1) as well as an MS-Dos prompt. Closing one or the other will terminate the program.

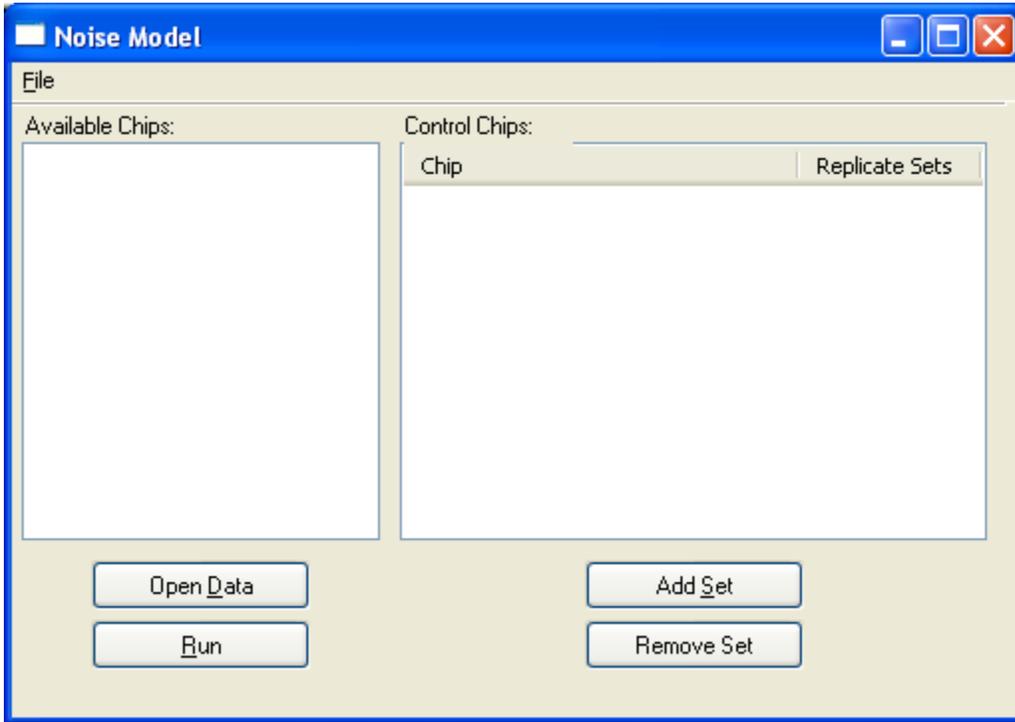


Figure 1

The data to be loaded must be in **one text** file and contain the following information in columns separated by tabs (Figure2):

probedata name_Chip1 name_Chip1_call name_Chip2 name_Chip2_call.....

	A	B	C	D	E	F	G	H	I	J	K
1	probedata	L1	L1_call	L1R	L1R_call	L2	L2_call	L2R	L2R_call	L3	L3_call
2	AFFX-MurL2_at	6.9	P	5.9	P	5.5	P	6.9	P	2.4	P
3	AFFX-MurL10_at	5.7	P	5	P	5.3	P	1.3	P	1.9	P
4	AFFX-MurL4_at	1.7	P	3.8	P	1.5	P	0.1	P	3.4	P
5	AFFX-MurFAS_at	7.5	P	5.8	P	3.3	P	1.3	P	13.4	P
6	AFFX-BioB-5_at	2.8	P	7.9	P	5.4	P	1.7	P	2.2	P
7	AFFX-BioB-M_at	1.9	P	2.7	P	2.6	P	1.3	P	0.9	P
8	AFFX-BioB-3_at	0.8	P	1.5	P	1	P	0.8	P	1.8	P
9	AFFX-BioC-5_at	2.3	P	5.3	P	21.3	P	4.8	P	4.5	P
10	AFFX-BioC-3_at	1.4	P	2.7	P	1.9	P	1.3	P	0.8	P
11	AFFX-BioDn-5_at	0.4	P	1	P	0.9	P	0.4	P	0.7	P
12	AFFX-BioDn-3_at	18.1	P	103.8	P	101.7	P	10.9	P	34.7	P
13	AFFX-CreX-5_at	0.2	P	0.3	P	0.4	P	0.4	P	0.3	P
14	AFFX-CreX-3_at	1.4	P	20.8	P	2.6	P	6.3	P	1.8	P

Figure 2

You can obtain such a file from the pivot table of the Affymetrix MAS5 Software or create one in excel saving it as a tab delimited text file (.txt).

Load the data using Open Data button

Load the replicate sets by holding down the control key (click on each member of the replicate set) and then click on Add Set (Figure 3).

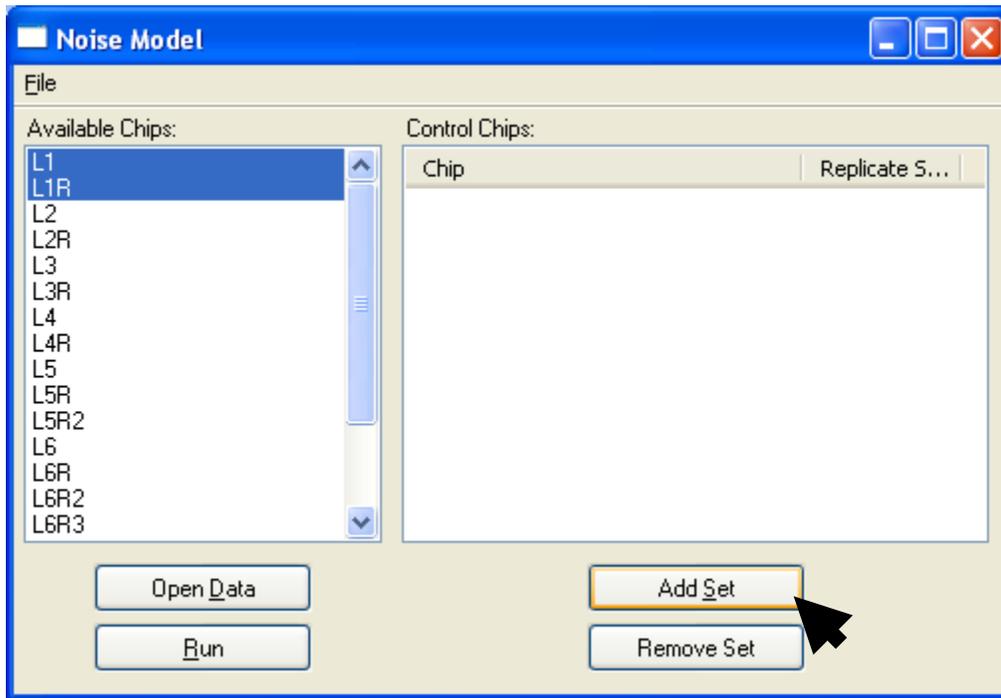


Figure 3

Repeat the operation for each set of replicate. You have the ability to load duplicates, triplicates...of the same samples. A replicate set number is assigned to each members of the set (Figure 4).

Remove unwanted sets or chips by selecting the chips to be removed and clicking on Remove Set

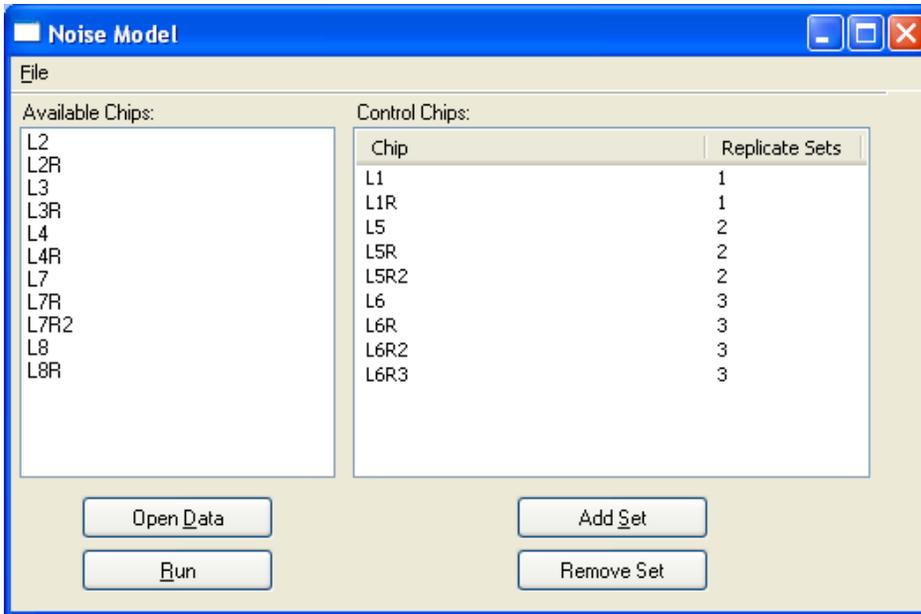


Figure 4

To run the model, click Run, you will be prompted for a file name to save the model parameters in.

This file can be opened using a text editor and contains 3 values:

0.000 the regression slope of the 80% percentile and the intercept

Computation is almost immediate depending on the computer speed and the results are saved immediately in the file specified, without any prompt.

The program can now be closed and you can proceed to the next step for computing the Event ratios.

D. Calculation the Event Ratios

To run the Event Ratio program double click on main.py

A window will appear (Figure 5) as well as an MS-Dos prompt. Closing one or the other will terminate the program.

Load the model you created above with the load model button.

Load the data as **one text** file containing the following information in columns separated by tabs (Figure 6):

probedata name_Chip1 name_Chip1_call name_Chip2 name_Chip2_call.....

You can obtain such a file from the pivot table of the Affymetrix MAS5 Software or create one in excel saving it as a tab delimited text file (.txt).

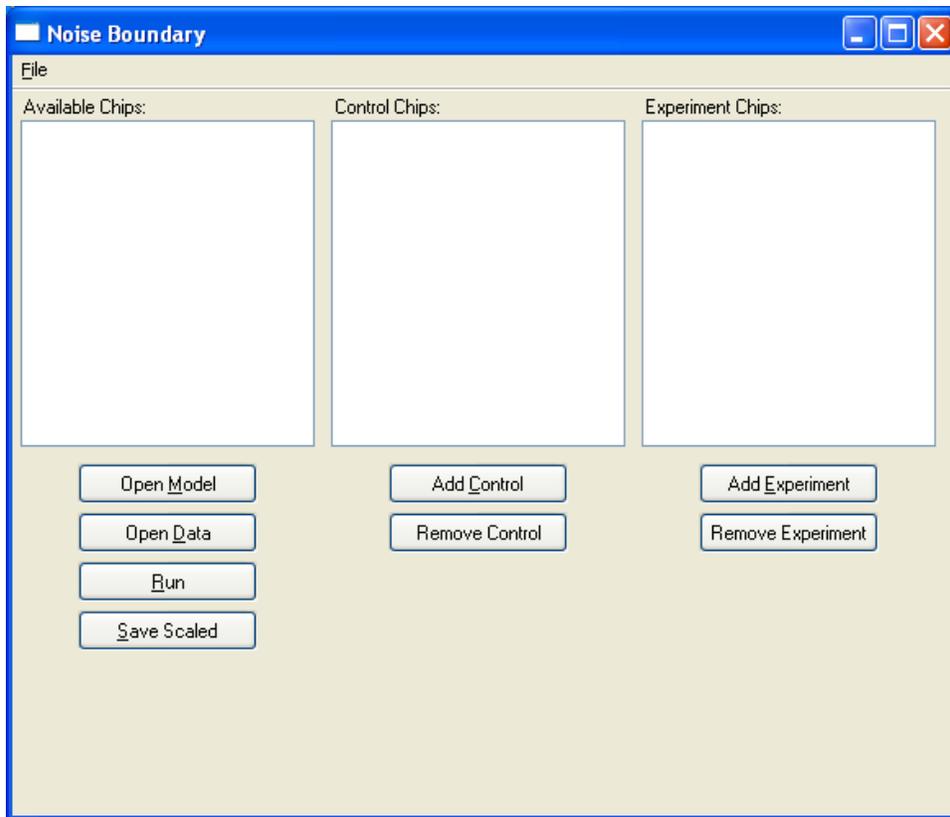


Figure 5

Microsoft Excel - data2.txt

File Edit View Insert Format Tools Data Window Help

A1 = probedata

	A	B	C	D	E	F	G
1	probedata	Normal 1	Normal 1 call	Normal 2	Normal 2 call	Normal 3	Normal 3 call
2	AFFX-MurlL2_at	6.9	P	5.5	P	2.4	P
3	AFFX-MurlL10_at	5.7	P	5.3	P	1.9	P
4	AFFX-MurlL4_at	1.7	P	1.5	P	3.4	P
5	AFFX-MurFAS_at	7.5	P	3.3	P	13.4	P
6	AFFX-BioB-5_at	2.8	P	5.4	P	2.2	P
7	AFFX-BioB-M_at	1.9	P	2.6	P	0.9	P
8	AFFX-BioB-3_at	0.8	P	1	P	1.8	P
9	AFFX-BioC-5_at	2.3	P	21.3	P	4.5	P
10	AFFX-BioC-3_at	1.4	P	1.9	P	0.8	P
11	AFFX-BioDn-5_at	0.4	P	0.9	P	0.7	P
12	AFFX-BioDn-3_at	18.1	P	101.7	P	34.7	P
13	AFFX-CreX-5_at	0.2	P	0.4	P	0.3	P
14	AFFX-CreX-3_at	1.4	P	2.6	P	1.8	P
15	AFFX-BioB-5_st	6.6	P	24.8	P	6.7	P

Figure 6

The name of the chips will appear in the left panel (figure 7).
Select the chips to be placed in the control group by selecting them holding down the Ctrl or Shift key, and then click Add Control.
Those chips named will be moved to the Control Chips panel (figure 8).
Then selects the chips to be added to the Experiment group and add them to the Experiment Chips panel by clicking Add Experiment. The Remove Control and Experiment buttons remove selected chips from the experiment of control panel.

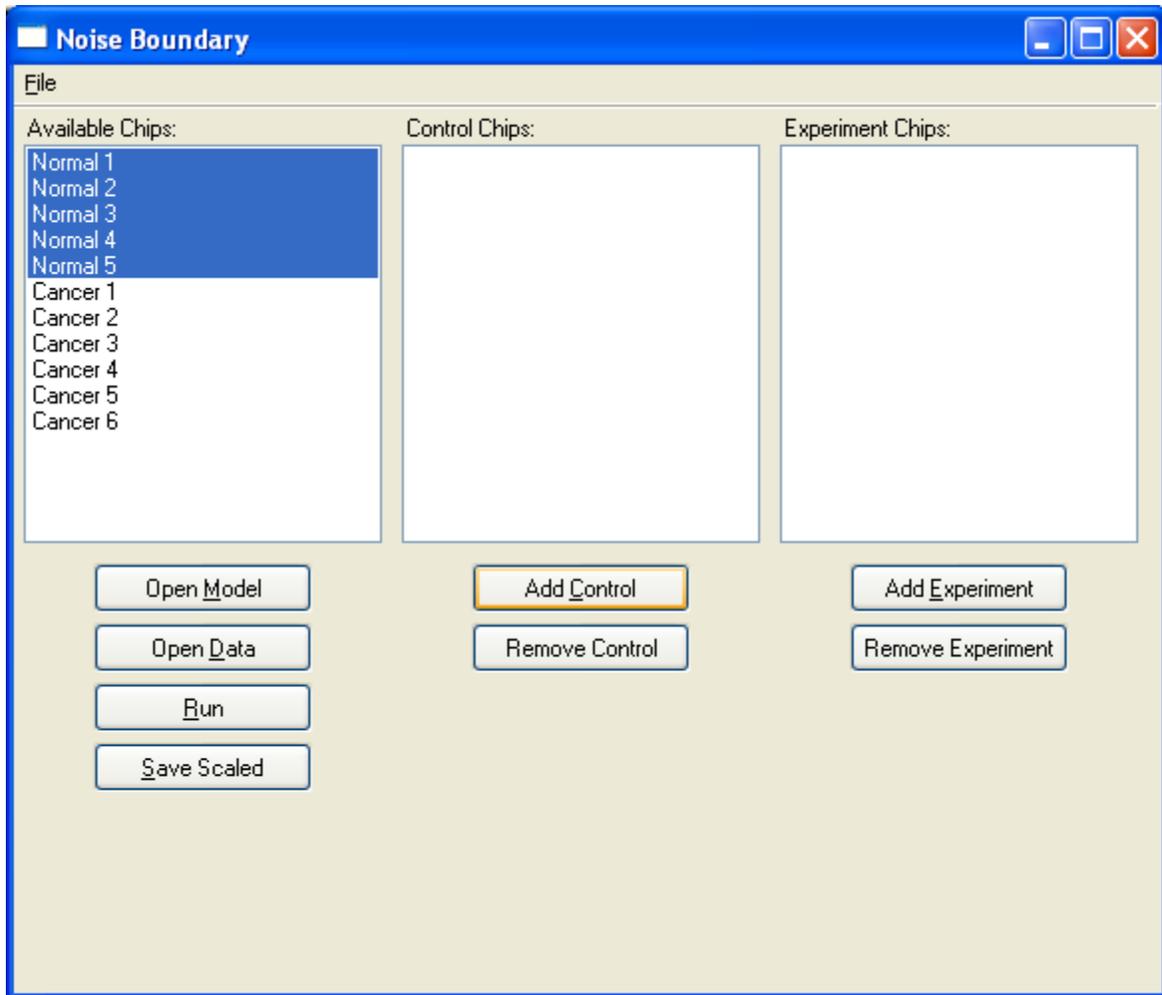


Figure 7

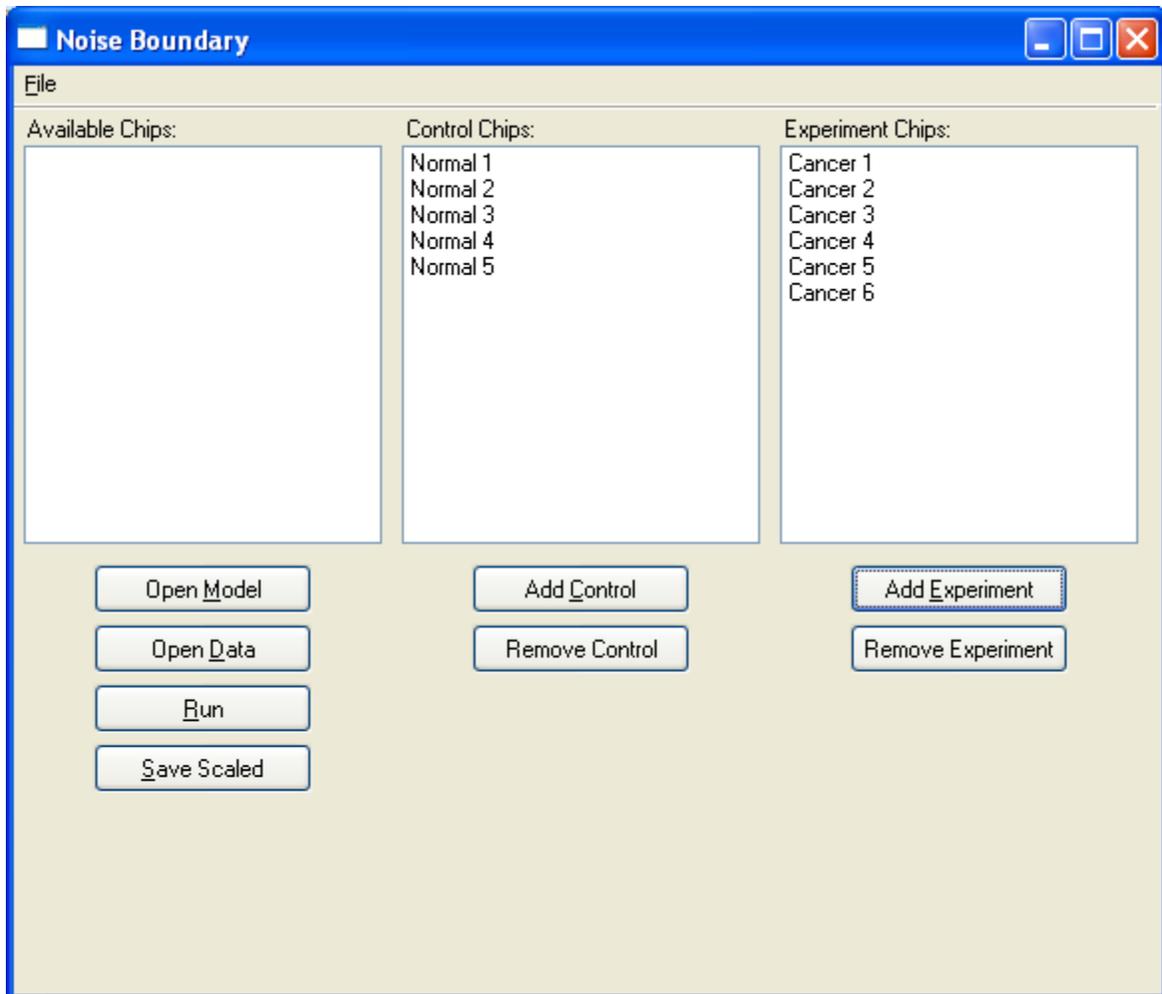


Figure 8

To compute the Event Ratios, click the Run button.
 The result file is a tab delimited text file that can be opened by Excel.

The following is a description of the columns contents:

probe_set: Probe set name

FC: Fold Change

Pos. Er Score: #positive change/# comparisons

Neg. Er Score: #negative change/# comparisons

Tendency: max(#pos,#neg) ie.: Overall direction: up regulated (+), down regulated (-) or no change(0)

ER Score: max(#pos,#neg) /# comparisons

T Score Prob: Standard T-test p-value for the comparison of the 2 groups

NNB Pos. Er Score: #positive change/# comparisons without the noise model

NNB Neg. Er Score: #negative change/# comparisons without the noise model

NNB Tendency: max(#pos,#neg) ie.: Overall direction: up regulated (+), down regulated (-) or no change(0) without the noise model

NNB ER Score: max(#pos,#neg) /# comparisons without the noise model

Control Mean: Average of the intensity values in the control group

Control SD: Standard deviation of the intensity values in the control group

Experiment Mean: Average of the intensity values in the experiment group

Experiment SD: Standard deviation of the intensity values in the experiment group

To save the data scaled to a trimmed mean of 300, as per the MAS 5 program (2% of the top and bottom intensities were removed from the mean computation) click the Save Scaled button