

Using Cvt2Mae to Convert Affymetrix Array Data for MAExplorer

<http://www.lecb.ncifcrf.gov/Cvt2Mae>

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Cvt2Mae version 0.60

Accessing Arrays with MAExplorer

- MAExplorer works with any arrays using the schema (see Appendix C of MAExplorer Reference Manual for details)
- All data files are tab-delimited text files
- Databases could be constructed with tools like Excel for editing user data into the schema format
- The Cvt2Mae array data converter “Wizard” tool converts non-standard <User-defined> academic or commercial data to MAExplorer format
- **Affymetrix**, Incyte, GenePix, Scanalyze, and other array data formats may be converted using predefined “Array Layouts”

S.1 MAExplorer Data Schema

- MAExplorer works with any array data using our data schema
- The schema is described in detail in MAExplorer Reference Manual Appendix C.
- Data Schema: tab-delimited experiment data files:
 1. GIPO (Gene In Plate Order or “array print” file)
 2. List of hybridized samples in database
 3. Configuration data describing the array and conventions
 4. Separate spot quantification data files
- The Cvt2Mae “wizard” tool converts user array data to this schema

S.1.1 MAExplorer GIPO or Print File

- GIPO file maps a spot on the array to a particular gene
- Contains:
 1. location or grid-geometry
 2. one or more genomic identifiers (e.g., Clone ID, GenBank ID, LocusID, etc.)
 3. gene description as Gene Name (or other description)
 4. Optional: global spot quality (QualCheck)
 5. optional: plate coordinates for clones

S.1.2 MAExplorer Samples Database File

- List of hybridized samples file SamplesDB.txt file contains:
 1. full sample description
 2. base file name of quantification file (without .quant file extension)
 3. optional sample ID number
 4. other data you wish to carry with the samples (used in array reports)

S.1.3 MAExplorer Configuration Database File

- Configuration data file MaeConfig.txt describes particular type of array and hybridization labeling you are using. This includes:
 - grid-geometry - # of replicate fields, grids, rows/grid, columns/grid
 - spot hybridization labeling - intensity or ratio data, dye names
 - various presentation options - use pseudo-array or actual (x,y) coordinates, etc.

S.1.4 MAExplorer Spot Quantification Files

- Separate spot quantification data files (with .quant file extension) are used for each hybridized sample
- ^{33}P or biotin labeled samples are specified as one hybridization intensity information per file
- Fluorescent Cy3/Cy5-dye labeled samples are specified as two channels of hybridization intensity information per file
- Intensity background data is optional
- Spot quality (QualCheck) data is optional
- Grid-coordinates are specified the same as for GIPO file

S.2 Assumptions About User Data - Array Layout

- User data is tab-delimited ASCII text files (could generate with Excel)
- If the array geometry (#fields, grids, rows/grid, columns/grid) is known, that geometry may be used in MAExplorer
- Otherwise, a pseudo-array geometry is generated for visual use in MAExplorer from the total # of spots in the user data
- An Array Layout describes the user data. It may be edited and saved for subsequent use in converting other array data files of the same type
- The <User-defined> array layout gives users complete flexibility in describing the array

S.3 Example of tab-delimited Affymetrix Data

Microsoft Excel - generic-U937-Affymetrx.txt.xls

File Edit View Insert Format Tools Data Window Help Acrobat

Arial 8 B I U \$ % , +.0 +.00

A2 =

	A	B	C	D	E	F	G	H	I	J	K	L	M
1	Expression Analysis: Pivot Tab												
2													
3		Sample-1A-1-U95A		Sample-1B-1-U95A		Sample-1B-1-1A		Sample-2A-1-U95A		Sample-2B-1-U95A		Sample-2A-1-1A	
4	probe set	Avg Diff	Abs Call	Avg Diff	Abs Call	Diff Call	Fold Change	Avg Diff	Abs Call	Avg Diff	Abs Call	Diff Call	Fold Change
5	100_g_at	204.1	P	160	A	NC	-1.3	233.8	P	141.7	P	NC	1.1
6	1000_at	157.2	P	207.2	P	NC	1.3	159.4	P	101.2	P	NC	-1.8
7	1001_at	33.7	A	-5.7	A	NC	-1.3	47.3	A	11.4	A	NC	1.2
8	1002_f_at	8.9	A	34.9	A	NC	1.3	9.2	A	14.8	A	NC	1
9	1003_s_at	-22.8	A	-2.1	A	NC	-1.4	35.2	A	14.5	A	NC	-1.4

generic-U937-Affymetrx.txt /

Ready

Microsoft Excel - generic-U937-Affymetrx.txt.xls

File Edit View Insert Format Tools Data Window Help Acrobat

Arial 8 B I U \$ % , +.0 +.00

A2 =

	N	O	P	Q	R	S	T	U	V	W	X	Y	Z
1													
2													
3	Sample-2A-1-1B		Sample-2B-1-1A		Sample-2B-1-1B		Sample-2B-1-12A						
4	Diff Call	Fold Chang	Diff Call	Fold Chang	Diff Call	Fold Change	Diff Call	Fold Change	Probe Set	Identifier	Description		
5	NC	1.5	NC	-1.4	NC	-1.1	NC	-1.6	100_g_at	Y08200	Y08200 =HSRABGTRA Hor		
6	NC	-2.3	NC	-1.6	NC	-2	NC	1.1	1000_at	X60188	X60188 =mRNA /DEFINIO		
7	NC	1.5	NC	-1.1	NC	1.3	NC	-1.2	1001_at	X60957	X60957 =cds /DEFINITION=		
8	NC	-1.3	NC	1.1	NC	-1.3	NC	1.1	1002_f_at	X65962	X65962 =cds /DEFINITION=		
9	NC	1.5	MD	-1.5	NC	1.2	NC	-1.3	1003_s_at	X68149	X68149 =cds /DEFINITION=		

generic-U937-Affymetrx.txt /

Ready

I. Procedure: Convert Data for Array Layouts

1. Select the Chip Set array layout (**Affymetrix - generic**) if in list, otherwise pick <User-defined>)
2. Select 1 or more input files using the “Browse input files” .
3. You may edit or change various array layout parameters at this time
 - 3.1 you may edit the array layout with “Edit Layout”
 - 3.2 you may “Assign GIPO fields” in user data file
 - 3.3 you may “Assign Quantification fields” in user data file
 - 3.4 if you changed any array layout parameters, you may save it with “Save Layout”
4. Select the project output directory (i.e., folder) to save generated files

I. Procedure: continued...

5. Press “Run” to convert the data
6. Press “Done” when it is finished.
7. Go to the project directory and then to the MAE sub-directory, click on the Start.mae file to start MAExplorer on the new data

1. Initial State of Cvt2Mae Program

Cvt2Mae: convert array data to MAExplorer files - Version: 01-23-2002 V.0.60 (Beta)

Enter data for steps 1, 2, and 3. Then 4. press 'Run' to convert your data to MAExplorer format.

1. Select Chipset:

2. Select Input Data Files:

2.1 Edit array layout and map fields:

2.2 Samples to use '<<file>> sample name':

3. Select Project Output Folder:

Vendor

Layout name

Spots/microarray

Project output folder:

MAExplorer startup File:

4. Edit and Run

Status:

2. Selecting Affymetrix Chipset Array-Layout

Cvt2Mae: convert array data to MAExplorer files - Version: 01-23-2002 V.0.60 (Beta)

Enter data for steps 1, 2, and 3. Then 4. press 'Run' to convert your data to MAExplorer format.

1. Select Chipset: -- select a chip layout --

2. Select Input Data Files: -- select a chip layout --
<User-defined>
GenePixPro3 - generic
Scanalyze - generic
Affymetrix - generic
Incyte - generic
Affymetrix - Mouse
Affymetrix - Human

2.1 Edit array layout and map fields:
 Expert assign-mode

2.2 Samples to use '<<file>> sample name':

3. Select Project Output Folder: --Select Output Folder--

Project output folder:
MAExplorer startup File:

4. Edit and Run

Status:

3. Select Files with “Browse input file” Name

Cvt2Mae: convert array data to MAExplorer files - Version: 01-23-2002 V.0.60 (Beta)

Enter data for steps 1, 2, and 3. Then 4. press 'Run' to convert your data to MAExplorer format.

1. Select Chipset:

2. Select Input Data Files:

2.1 Edit array layout and map fields:

2.2 Samples to use '<<file>> sample name':

3. Select Project Output Folder:

4. Edit and Run

Status:

Select next input file to convert (you may use 'ALL' or 'ALL.<ext>') ? X

Look in:

- genericArrayVision.txt
- genericGenePix-Cy3Cy5-DataFile1.txt
- genericGenePix-Cy3Cy5-DataFile2.txt
- genericGenePix-Cy3Cy5-DataFile3.txt
- genericIncyte1.cgi
- genericIncyte2.cgi
- genericIncyte3.cgi
- generic-U937-Affymetrix.txt

File name:

Files of type:

4. Input File(s) Analyzed for Multiple Samples

Cvt2Mae: convert array data to MAExplorer files - Version: 01-23-2002 V.0.60 (Beta)

Enter data for steps 1, 2, and 3. Then 4, press 'Run' to convert your data to MAExplorer format.

1. Select Chipset:

2. Select Input Data Files: Separate GIPO

2.1 Edit array layout and map fields:
 Expert assign-mode

2.2 Samples to use '<<file>> sample name':

<<C:\Temp\GenericData\generic-U937-Affymetrix.txt>> [Sample-1A-1-U95A]
<<C:\Temp\GenericData\generic-U937-Affymetrix.txt>> [Sample-1B-1-U95A]
<<C:\Temp\GenericData\generic-U937-Affymetrix.txt>> [Sample-2A-1-U95A]
<<C:\Temp\GenericData\generic-U937-Affymetrix.txt>> [Sample-2B-1-U95A]

Vendor	Affymetrix
Layout name	Affymetrix - generic
Spots/microarray	12630

3. Select Project Output Folder:

Project output folder:

MAExplorer startup File:

4. Edit and Run

Status:

5.1 Edit Layout 'Wizard' Values for This Array

Edit MAExplorer project

[1] Array layout name and vendor - (ALO file version:1.7)

Array layout name: Affymetrix - Human

Vendor name for the array: Affymetrix

Name of the array layout designator. This is generally specified by the chip vendor. If it is your own chip then use your own designator to differentiate your chip designs.

<Back Next> Finish Cancel

5.2 Edit Layout 'Wizard' Grid Geometry Values

MAE Explorer Edit MAE explorer project

[2] Grid geometry data

Number of duplicated spot Fields in array	1
Number of Grids per Field	11
Number of spots per Grid Row	29
Number of spots per Grid Column	40
Use Mol.Dynamics 'NAME-GRC' else (Grid,Row,Col)	<input type="checkbox"/> Use Mol.Dyn. 'NAME-GRC' else above explicit (Grid,Row
Specify array layout by Grid-geometry OR by # spots/array	<input checked="" type="checkbox"/> Use # spots (BELOW), else grid-geometry (ABOVE)
Maximum number of spots in array	12630

If you specify the array layout by Grid-geometry (ABOVE), then enter (#Fields, #Grids, #Grid-rows,#Grid-cols).
If you specify the layout by the maximum number of spots in the array (BELOW), it will estimate a pseudo-layout that the spots will fit on the this array for visualization purposes. It does not correspond to the actual array layout which you do not have to enter.

<Back Next> Finish Cancel

5.3 Edit Layout 'Wizard' Input File Row Values. Verify Rows for Sample & Field Names Defined

Edit MAExplorer project

[3] Input file starting rows data

(Optional) Row containing a list sample names	3
Row containing a list of quantitative file Field names	4
First row containing quantitative file Data	5
Row containing opt. separate GIPO file Field names	0
First row containing opt. separate GIPO file Data	0
(Optional) Comment token	
(Optional) Initial keyword for each data row	

Number of row that contains the names of the data file Field names.
Eg. grid, row, column, GeneBank ID, GeneName, Clone ID, etc.
[Row #s start at row 1.]
Data from row #4 in file[C:\Temp\GenericData\generic-U937-Affymetrx.txt]
Current Field name column[1] = 'probe set'
Current Field name column[2] = 'Avg Diff'
Current Field name column[3] = 'Abs Call'
Current Field name column[4] = 'Avg Diff'

<Back Next> Finish Cancel

5.4 Edit Layout 'Wizard' Ratio or Intensity Values

Edit MAExplorer project

[4] Ratio fluorescence data

Ratio (i.e. Cy3,Cy5) or Intensity Data Use Ratio else Intensity data

If Ratio data, use (Cy5/Cy3) else (Cy3/Cy5) Use (Cy5/Cy3) else (Cy3/Cy5)

Fluorescent dye for intensity 1 (if ratio data)

Fluorescent dye for intensity 2 (if ratio data)

Have background intensity data Has background data

Data for MAExplorer is either ratio data such as Cy3/Cy5, or intensity data such as P33, etc.

<Back Next> Finish Cancel

5.5 Edit Layout 'Wizard' optional (X,Y) Coordinate Values

The image shows a software dialog box titled "Edit MAExplorer project". The main heading is "[5] (Opt.) Microarray (X,Y) coordinate options". There are four radio button options on the left and four checkbox options on the right. A text box at the bottom provides a detailed explanation of the "Generate array pseudo X Y coordinates" option. At the bottom of the dialog are four buttons: "<Back", "Next>", "Finish", and "Cancel".

Use microarray pseudo (X,Y) coordinates Generate array pseudo X Y coordinates

Use actual microarray pseudo (X,Y) coordinates Have actual X Y coordinates for each sample

Reuse (X,Y) coordinates of first sample for all samples Reuse array X Y coords for all arrays

Swap microarray rows and columns Swap array rows and columns

Generate a microarray pseudo image using a representation of the array based on Grids, Grid Rows, and Grid Columns. Otherwise, use the (X,Y) data supplied for each spot - if it exists. If this option is set, it will override the actual (X,Y) coordinates if that option is selected as well.

<Back Next> Finish Cancel

5.6 Edit Layout 'Wizard' Genomic ID Values

Edit MAExplorer project


[6] (Opt.) Genomic Identifier options

Has Location data	<input type="checkbox"/>	User data file has Location data
Has Clone ID data	<input type="checkbox"/>	User data file has Clone ID data
Has GenBank data	<input checked="" type="checkbox"/>	User data file has GeneBank data
Has UniGene ID data	<input type="checkbox"/>	User data file has UniGene data
Has dbEST data	<input type="checkbox"/>	User data file has dbEST data
Has LocusLink data	<input type="checkbox"/>	User data file has LocusLink data
Has SwissProt data	<input type="checkbox"/>	User data file has SwissProt data
Has Plate data	<input type="checkbox"/>	User data file has Plate data
Get Genomic IDs from 'Description'	<input type="checkbox"/>	Get Genomic IDs from 'Description'

The user data file has 'GenBank' identifier data.
See <http://ncbi.nlm.nih.gov/> for more information.

<Back Next> Finish Cancel

5.7 Edit Layout 'Wizard' Gene Names Description

 Edit MA Explorer project

[7] (Opt.) Gene names (or description) options

Has Gene Class user data	<input type="checkbox"/>	User data file has Gene Class data
Has UniGene Name user data	<input type="checkbox"/>	User data file has UniGene Name data
Has separate per-spot QualCheck user data per-sample	<input type="checkbox"/>	User data has separate per-spot QualCheck data
Has 'GIPO' QualCheck user data for entire DB	<input type="checkbox"/>	User data file has 'GIPO' QualCheck data

The user data file has UniGene Name data. This could be used if the default 'GeneName' description is not available.

<Back Next> Finish Cancel

5.8 Edit Layout 'Wizard' Calibration Values

Edit MAExplorer project

[8] (Opt.) DNA Calibration and user plate names, UniGene species name

Name of calibration DNA (if in database)

Name of researcher's special clones (if in database)

Name of empty wells

Name species (opt)

Name UniGene Species prefix (opt) or select from

- Hs
- Mm**
- At
- Bt
- Dr
- Hv
- Os
- Rn

UniGene species prefix (Mouse Mm, Human Hs, etc.). This is used in querying Genomic Web databases. If you do not see the prefix you want in the choice menu, type it in.

<Back Next> Finish Cancel

5.9 Edit Layout 'Wizard' Database Name Values

Edit MAExplorer project

[9] (Opt.) Database and data quantification program

Your name of the created database (opt)	My project description
Your name of the database subset (opt)	My sub project description
Generic project name for all samples (opt)	My Data
Name of spot quantification program (opt)	Affymetrix

Generic name of the project to be used for all samples in the database.
If no name is specified, it uses the input data files folder.

<Back Next> Finish Cancel

5.10 Edit Layout 'Wizard' HP-X,-Y Class Names

Edit MAExplorer project

[10] (Opt.) Hybridized sample (X,Y) 'set' class names

Default name of X samples 'set' HP-X 'set'

Default name of Y samples 'set' HP-Y 'set'

This is the name for the samples assign to the 'X set'.

<Back Next> Finish Cancel

5.11 Edit Layout 'Wizard' Default Thresholds

Edit MAExplorer project

[11] (Opt.) Default data Filtering thresholds

Default cluster similarity threshold [0 : 1000]	10.0
Default # genes in highest/lowest	100
Default # clusters for K-means clustering [1 : 1000]	6
Default p-value threshold (for t-tests) [0.0 : 1.0]	0.05
Default Coeff. Of Variation threshold [0.0 : 1.0]	0.2
Default absolute difference threshold [0.0 : 4.0]	0.2

Default p-Value used in the t-Test data Filter.
This is the initial value shown in popup sliders.

<Back Next> Finish Cancel

6. Other Options - Assigning User Data Fields to MAExplorer Fields

- GIPO (Gene In Plate Order or “array print” table) - assigns genes to positions on the array as well as GeneBank ID, Clone ID, LocusID (if available), Gene Name, etc.
- Quant data - assigns names of quantified data in the user file to MAExplorer data (e.g. Cy3 intensity to RawIntensity1, Cy5 to RawIntensity2, etc).

6.1 “Assign user fields to GIPO fields”

Assign user fields to GIPO fields

Location: probe set

Identifier: <not used>

GeneName: Description

Done Cancel Help Allow Duplicate

Assign user fields to GIPO fields

Location: probe set

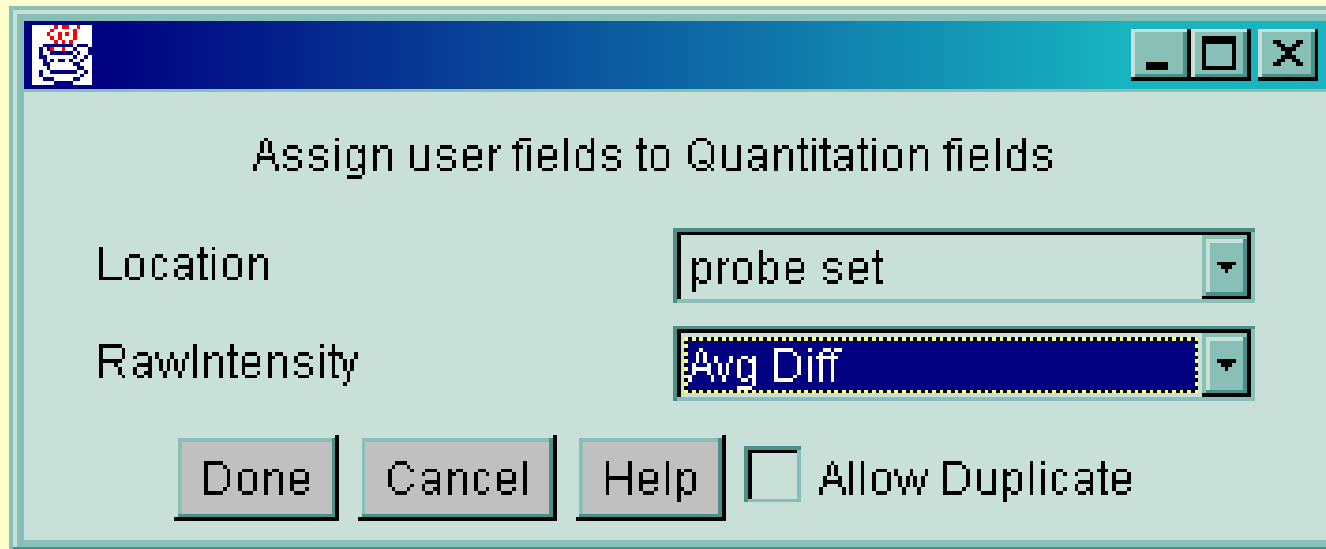
Identifier: <not used>

GeneName: Identifier

Done Cancel Help

- Diff Call
- Fold Change
- Diff Call
- Fold Change
- Probe Set
- Identifier
- Description

6.2 “Assign user fields to GIPO fields”



7. Optional “Save Layout” to Array Layout Database After Edit Layout and Assign fields

Cvt2Mae: convert array data to MAExplorer files - Version: 01-23-2002 V.0.60 (Beta)

Enter data for steps 1, 2, and 3. Then 4. press 'Run' to convert your data to MAExplorer format.

1. Select Chipset:

2. Select Input Data Files: Separate GIPO

2.1 Edit array layout and map fields:
 Expert assign-mode

2.2 Samples to use '<<file>> sample name':

<<C:\Temp\GenericData\generic-U937-Affymetrix.txt>> [Sample-1A-1-U95A]
<<C:\Temp\GenericData\generic-U937-Affymetrix.txt>> [Sample-1B-1-U95A]
<<C:\Temp\GenericData\generic-U937-Affymetrix.txt>> [Sample-2A-1-U95A]
<<C:\Temp\GenericData\generic-U937-Affymetrix.txt>> [Sample-2B-1-U95A]

Vendor	Affymetrix
Layout name	Affymetrix - generic
Spots/microarray	12630

3. Select Project Output Folder:

Project output folder:

MAExplorer startup File:

4. Edit and Run

Status: Saved edited array layout [Affymetrix - generic]
to file [Affymetrix-Generic.alo]

8. Specifying “Create new project folder” Option Where Generated Database Will Be Saved

Cvt2Mae: convert array data to MAExplorer files - Version: 01-23-2002 V.0.60 (Beta)

Enter data for steps 1, 2, and 3. Then 4. press 'Run' to convert your data to MAExplorer format.

1. Select Chipset:

2. Select Input Data Files: Separate GIPO

generic-U937-Affymetrix.bt

2.1 Edit array layout and map fields:
 Expert assign-mode

2.2 Samples to use '<<file>> sample name':

<<C:\Temp\GenericData\generic-U937-Affymetrix.bt>> [Sample-1A-1-U95A]
<<C:\Temp\GenericData\generic-U937-Affymetrix.bt>> [Sample-1B-1-U95A]
<<C:\Temp\GenericData\generic-U937-Affymetrix.bt>> [Sample-2A-1-U95A]
<<C:\Temp\GenericData\generic-U937-Affymetrix.bt>> [Sample-2B-1-U95A]

Vendor	Affymetrix
Layout name	Affymetrix - generic
Spots/microarray	12630

3. Select Project Output Folder:

Project output folder:
MAExplorer startup File:

4. Edit and Run

Status: Saved edited array layout [Affymetrix - generic]
to file [Affymetrix-Generic.ato]

8.1 Specifying New “Project Output Folder”

Cvt2Mae: convert array data to MAExplorer files - Version: 01-23-2002 V.0.60 (Beta)

Enter data for steps 1, 2, and 3. Then 4. press 'Run' to convert your data to MAExplorer format.

1. Select Chipset:

2. Select Input Data Files: Separate GIPO

generic-U937-Affymetrix.txt

2.1 Edit array layout and map fields:

2.2 Samples to use '<<file>> sample name':

<<C:\Temp\GenericData\generic-U937-Affym
<<C:\Temp\GenericData\generic-U937-Affym
<<C:\Temp\GenericData\generic-U937-Affym
<<C:\Temp\GenericData\generic-U937-Affym

Select the Project Folder to save converted data

Save in:

File name:

Save as type:

3. Select Project Output Folder:

Project output folder:

MAExplorer startup File:

4. Edit and Run

Status: Saved edited array layout [Affymetrix - generic]
to file [Affymetrix-Generic.ato]

8.2 “Project Output Folder” & MAE startup file

Cvt2Mae: convert array data to MAExplorer files - Version: 01-23-2002 V.0.60 (Beta)

Enter data for steps 1, 2, and 3. Then 4. press 'Run' to convert your data to MAExplorer format.

1. Select Chipset:

2. Select Input Data Files: Separate GIPO

2.1 Edit array layout and map fields:
 Expert assign-mode

2.2 Samples to use '<<file>> sample name':

<<C:\Temp\GenericData\generic-U937-Affymetrix.txt>> [Sample-1A-1-U95A]
<<C:\Temp\GenericData\generic-U937-Affymetrix.txt>> [Sample-1B-1-U95A]
<<C:\Temp\GenericData\generic-U937-Affymetrix.txt>> [Sample-2A-1-U95A]
<<C:\Temp\GenericData\generic-U937-Affymetrix.txt>> [Sample-2B-1-U95A]

Vendor	Affymetrix
Layout name	Affymetrix - generic
Spots/microarray	12630

3. Select Project Output Folder:

Project output folder:
MAExplorer startup File:

4. Edit and Run

Status:

9. Conversion in Process After Pressing “RUN”

Cyt2Mae: convert array data to MAExplorer files - Version: 01-23-2002 V.0.60 (Beta)

Enter data for steps 1, 2, and 3. Then 4. press 'Run' to convert your data to MAExplorer format.

1. Select Chipset:

2. Select Input Data Files: Separate GIPO

2.1 Edit array layout and map fields:
 Expert assign-mode

2.2 Samples to use '<<file>> sample name':

<<C:\Temp\GenericData\generic-U937-Affymetrix.txt>> [Sample-1A-1-U95A]
<<C:\Temp\GenericData\generic-U937-Affymetrix.txt>> [Sample-1B-1-U95A]
<<C:\Temp\GenericData\generic-U937-Affymetrix.txt>> [Sample-2A-1-U95A]
<<C:\Temp\GenericData\generic-U937-Affymetrix.txt>> [Sample-2B-1-U95A]

Vendor	Affymetrix
Layout name	Affymetrix - generic
Spots/microarray	12630

3. Select Project Output Folder:

Project output folder:
MAExplorer startup File:

4. Edit and Run

Status: ==> re-reading row #4600 [C:\Temp\GenericData\generic-U937-Affymetrix.txt]
For sample #1 [Sample-1A-1-U95A]

10. Notification that Conversion is Finished

Cvt2Mae: convert array data to MAExplorer files - Version: 01-23-2002 V.0.60 (Beta)

Enter data for steps 1, 2, and 3. Then 4. press 'Run' to convert your data to MAExplorer format.

1. Select Chipset:

2. Select Input Data Files: Separate GIPO

2.1 Edit array layout and map fields:
 Expert assign-mode

2.2 Samples to use '<<file>> sample name':

Vendor	Affymetrix
Layout name	Affymetrix - generic
Spots/microarray	12630

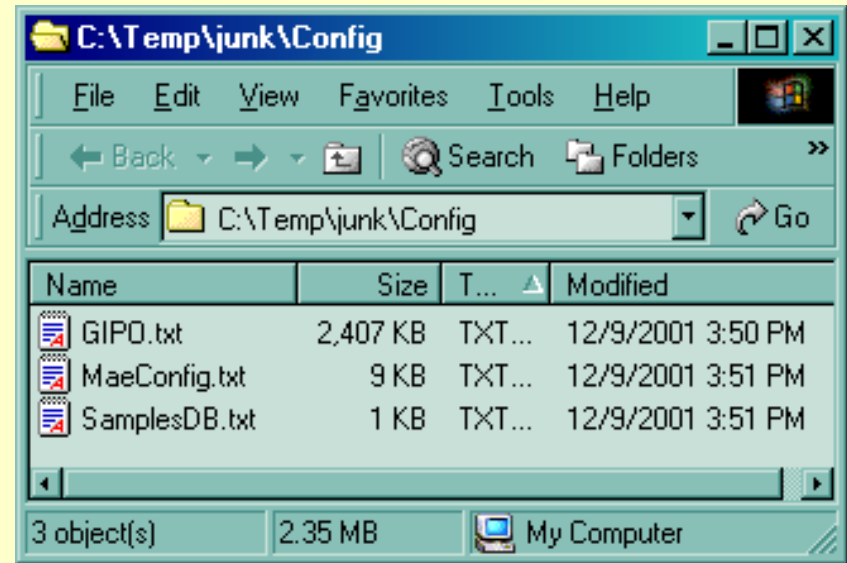
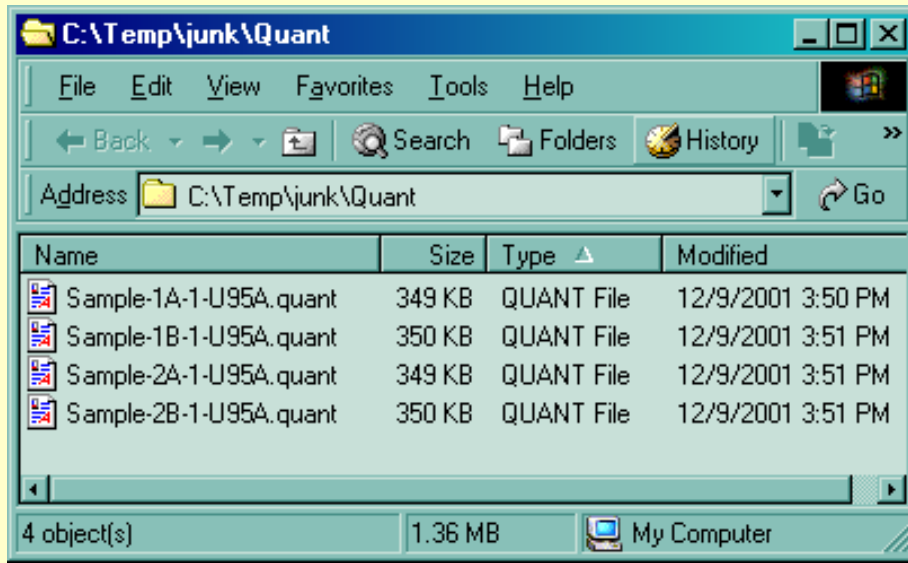
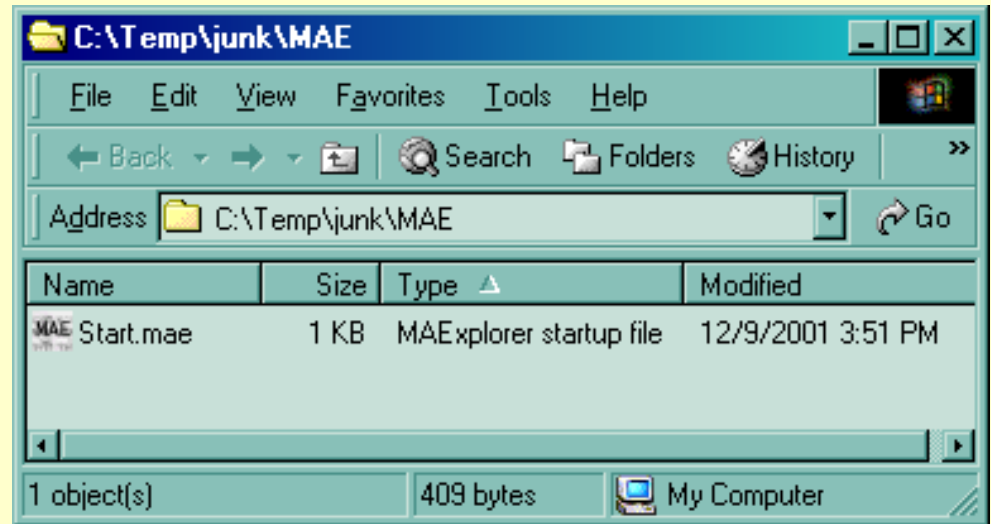
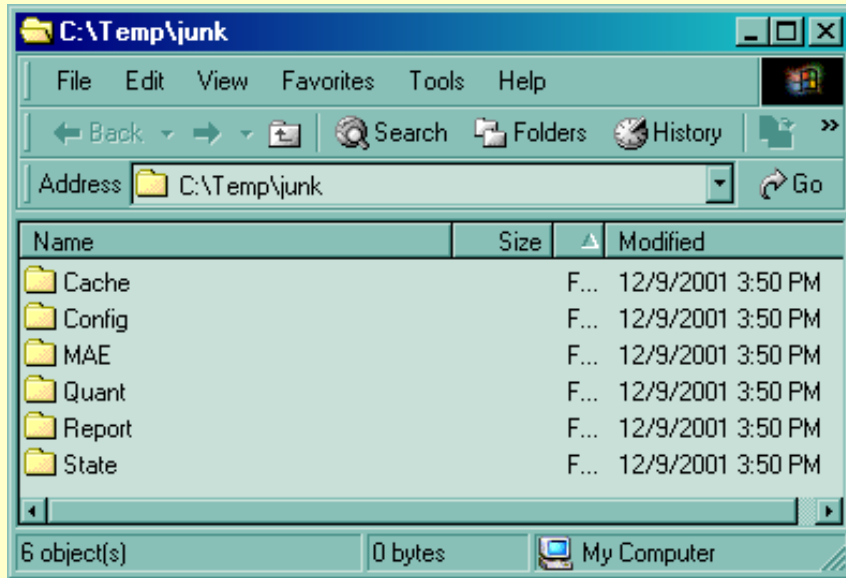
3. Select Project Output Folder:

Project output folder:
MAExplorer startup File:

4. Edit and Run

Status:

11. MAExplorer Data Created By Cvt2Mae



12. Running MAExplorer on the Converted Data

