

Using Cvt2Mae to Convert GenePix 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 Orders or “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 (with .quant file extension) files 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 GenePix Data

Microsoft Excel - genericGenePix-Cy3Cy5-DataFile1.txt.xls

File Edit View Insert Format Tools Data Window Help Acrobat

Arial 8 B I U

P1 =

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P
1	ATF	1														
2	27	43														
3	Type=GenePix Results 1.4															
4	DateTime=2001/06/01 13:30:07															
5	Settings=C:\Axon\GenePixPro3\XXXX.gps															
6	GalFile=C:\Documents and Settings\Desktop\XXXX\XXXX.gal															
7	Scanner=GenePix 4000A [47890]															
8	Comment=															
9	PixelSize=10															
10	ImageName=635 nm□532 nm															
11	FileName=C:\Documents and Settings\XXXX\Desktop\XXXX\Sample1.tif□C:\Documents and Settings\Desktop\XXXX\Sample1.tif															
12	PMTVolts=630□710															
13	ScanPower=100□100															
14	FocusPosition=0															
15	NormalizationFactor:RatioOfMedians=0.498487															
16	NormalizationFactor:RatioOfMeans=0.484085															
17	NormalizationFactor:MedianOfRatios=0.494956															
18	NormalizationFactor:MeanOfRatios=0.494158															
19	NormalizationFactor:RegressionRatio=0.453322															
20	JpegImage=C:\Documents and Settings\Desktop\XXXX\Sample1.tif															
21	RatioFormulation=W1/W2 (635 nm/532 nm)															
22	Barcode=															
23	ImageOrigin=0, 17400															
24	JpegOrigin=890, 18360															
25	Creator=GenePix Pro 3.0.6.66															
26	Temperature=37.53															
27	LaserPower=1.28□1.03															
28	LaserOnTime=71108□71129															
29	Supplier=															
30	Block	Column	Row	Name	ID	X	Y	Dia.	F635 Median	F635 Mean	F635 SD	B635 Median	B635 Mean	B635 SD	% > B635+1SD	% > B635+2SD
31	1	1	1	ltgb7--adhesio	IMAGE:604856	2050	18570	170	310	325	105	299	302	59	22	10
32	1	2	1	Gjb1--adhesio	IMAGE:442991	2350	18570	170	293	331	129	294	299	61	25	16
33	1	3	1	adhesion inte	IMAGE:522319	2650	18570	170	334	364	124	302	306	58	38	23
34	1	4	1	adhesion throi	IMAGE:533853	2950	18570	170	312	381	220	302	305	60	28	20
35	1	5	1	adhesion inte	IMAGE:538626	3260	18580	120	2571	2370	761	307	311	62	100	100

genericGenePix-Cy3Cy5-DataFile1 /

Ready

S.3.1 Example of tab-delimited GenePix Data

Microsoft Excel - genericGenePix-Cy3Cy5-DataFile1.txt.xls

File Edit View Insert Format Tools Data Window Help Acrobat

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

P1 =

	Q	R	S	T	U	V	W	X	Y	Z	AA	AB
30	F635 % Sat.	F532 Median	F532 Mean	F532 SD	B532 Median	B532 Mean	B532 SD	% > B532+1SD	% > B532+2SD	F532 % Sat.	Ratio of Medians	Ratio of Means
31	0	578	591	106	599	600	71	16	6	0	-0.524	-3.25
32	0	563	577	124	581	583	72	18	11	0	0.056	-9.25
33	0	574	588	109	592	592	72	19	7	0	-1.778	-15.5
34	0	586	606	149	587	589	73	26	13	0	-10	4.158
35	0	1609	1584	398	586	588	71	98	98	0	2.213	2.067

genericGenePix-Cy3Cy5-DataFile1/

Ready

Microsoft Excel - genericGenePix-Cy3Cy5-DataFile1.txt.xls

File Edit View Insert Format Tools Data Window Help Acrobat

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

P1 =

	AC	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	
30	Median of Ratios	Mean of Ratios	Ratios SD	Rgn Ratio	Rgn R²	F Pixels	B Pixels	Sum of Medians	Sum of Means	Log Ratio	F635 Median	F532 Median	F635
31	0.675	0.732	3.705	0.665	0.047	208	1548	-10	18 Error		11	-21	
32	0.749	0.838	3.934	0.86	0.057	208	1492	-19	33	-4.17	-1	-18	
33	1.05	1.069	4.695	1.087	0.023	208	1534	14	58 Error		32	-18	
34	1.094	0.914	3.898	1.788	0.148	208	1563	9	98 Error		10	-1	
35	1.962	2.067	1.865	2.221	0.773	120	820	3287	3061	1.146	2264	1023	

genericGenePix-Cy3Cy5-DataFile1/

Ready

I. Procedure: Convert Data for Array Layouts

1. Select the Chip Set array layout (**GenePixPro3 - generic**) if in list, otherwise pick <User-defined>)
2. Select 1 or more input files using the “Browse filename” .
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':

Vendor:

Layout name:

Spots/microarray:

3. Select Project Output Folder:

Project output folder:

MAExplorer startup File:

4. Edit and Run

Status:

2. Selecting GenePix 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: GenePixPro3 - Human Remove Layout

2. Select Input Data Files: Affymetrix - Human Affymetrix - Mouse, use Genomic Descriptions Affymetrix - Human, use Genomic Descriptions Incyte - Mouse Incyte - Human GenePixPro3 - Human GenePixPro3 - Mouse GenePixPro3 Browse GPO file

2.1 Edit array layout and map fields: Edit Layout Assign GPO fields Assign Quant fields Save Layout Expert assign-mode

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

Vendor	Axon
Layout name	GenePixPro3 - Human
Spots/microarray	0

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

Project output folder:

MAExplorer startup File:

4. Edit and Run Run - do conversion Abort Reset

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: Separate GIPO

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

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:

- Cache
- Config
- MAE
- Quant
- Report
- State
- genericArrayVision.txt
- genericGenePix-Cy3Cy5-DataFile1.txt
- genericGenePix-Cy3Cy5-DataFile2.txt
- genericGenePix-Cy3Cy5-DataFile3.txt
- genericIncyte1.cgi
- genericIncyte2.cgi

File name:

Files of type:

4. Continue Adding Input Files If Needed

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

genericGenePix-Cy3Cy5-DataFile1.txt
genericGenePix-Cy3Cy5-DataFile2.txt
genericGenePix-Cy3Cy5-DataFile3.txt

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

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

<<C:\Temp\junk\genericGenePix-Cy3Cy5-DataFile1.txt>> [*genericGenePix-Cy3Cy5-DataFile1.txt*]
<<C:\Temp\junk\genericGenePix-Cy3Cy5-DataFile2.txt>> [*genericGenePix-Cy3Cy5-DataFile2.txt*]
<<C:\Temp\junk\genericGenePix-Cy3Cy5-DataFile3.txt>> [*genericGenePix-Cy3Cy5-DataFile3.txt*]

Vendor	<input type="text" value="Axon"/>
Layout name	<input type="text" value="GenePixPro3 - Human"/>
Spots/microarray	<input type="text" value="2703"/>

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: GenePixPro3

Vendor name for the array: Axon

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. Enter (Grid, Rows/Grid, Columns/Grid) Values

Edit MAExplorer project

[2] Grid geometry data

Number of duplicated spot Fields in array	1
Number of Grids per Field	16
Number of spots per Grid Row	13
Number of spots per Grid Column	13
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 type="checkbox"/> Use # spots (BELOW), else grid-geometry (ABOVE)
Maximum number of spots in array	2703

Number of Grids per Field. A grid contains Grid Rows X Grid Columns of spots.

<Back Next> Finish Cancel

5.3 Edit Layout 'Wizard' Input File Row Values. Verify Row Where Field Names Are Defined

MAEdit MAExplorer project

[3] Input file starting rows data

(Optional) Row containing a list sample names	0
Row containing a list of quantitative file Field names	30
First row containing quantitative file Data	31
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 #30 in file[C:\Temp\junk\genericGenePix-Cy3Cy5-DataFile1.txt]
Current Field name column[1] = 'Block'
Current Field name column[2] = 'Column'
Current Field name column[3] = 'Row'
Current Field name column[4] = 'Name'

<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

If Ratio data, 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

Use Ratio else Intensity data

Use (Cy5/Cy3) else (Cy3/Cy5)

Cy3

Cy5

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

Edit MAExplorer project

[5] (Opt.) Microarray (X,Y) coordinate options

<input type="checkbox"/> Use microarray pseudo (X,Y) coordinates	<input checked="" type="checkbox"/> Generate array pseudo X Y coordinates
<input type="checkbox"/> Use actual microarray pseudo (X,Y) coordinates	<input checked="" type="checkbox"/> Have actual X Y coordinates for each sample
<input type="checkbox"/> Reuse (X,Y) coordinates of first sample for all samples	<input type="checkbox"/> Reuse array X Y coords for all arrays
<input type="checkbox"/> Swap microarray rows and columns	<input type="checkbox"/> 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 checked="" type="checkbox"/> User data file has Clone ID data
Has GenBank data	<input 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 I.M.A.G.E 'Clone ID' data.

<Back **Next>** Finish Cancel

5.7 Edit Layout 'Wizard' Gene Names Description

Edit MAExplorer 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 checked="" 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 'Quant' QualCheck data. This data is on a per-spot basis for each array hybridization. The code (see MAExplorer Reference Manual Appendix C Table C.4.2) may be used to flag bad spots or missing spot data.

<Back Next> Finish Cancel

5.8 Edit Layout 'Wizard' Calibration Values. Define UniGene Species prefix

The screenshot shows a software window titled "Edit MAExplorer project" with a subtitle "[8] (Opt.) DNA Calibration and user plate names, UniGene species name". The window contains several input fields and a dropdown menu. The fields are: "Name of calibration DNA (if in database)", "Name of researcher's special clones (if in database)", "Name of empty wells" (containing "Empty"), and "Name species (opt)" (containing "Mouse"). Below these is a section for "Name UniGene Species prefix (opt)" with a text box containing "Mm" and a dropdown menu labeled "or select from" with "Mm" selected. The dropdown menu lists "Hs", "Mm", "At", "Bt", "Dr", "Hv", "Os", and "Rn". A text box at the bottom provides instructions: "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." At the bottom of the window are four buttons: "<Back", "Next>", "Finish", and "Cancel".

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
Empty

Name species (opt)
Mouse

Name UniGene Species prefix (opt) Mm or select from Mm

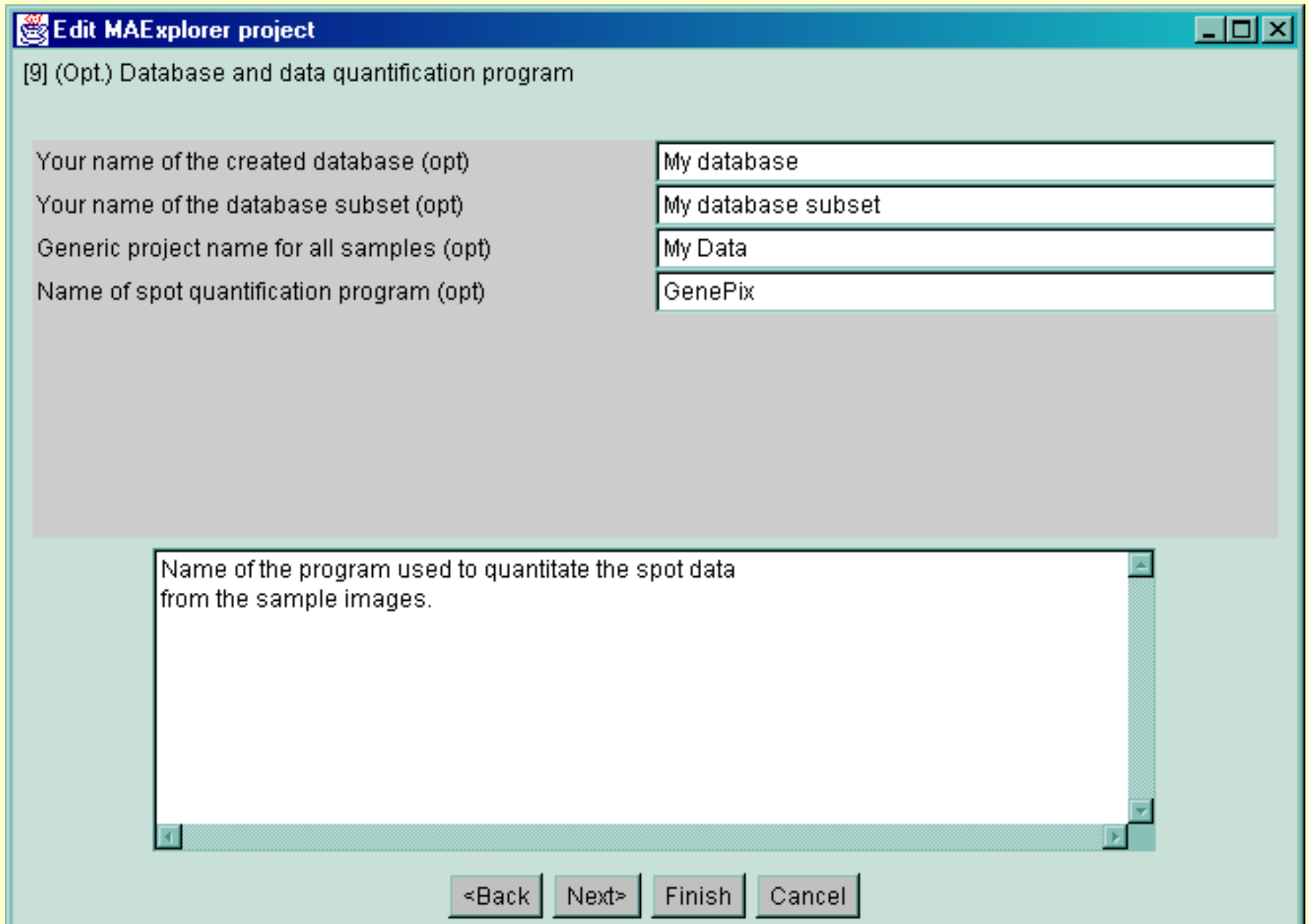
- Hs
- Mm**
- At
- Bt
- Dr
- Hv
- Os
- Rn

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.

Define Optional Names for Database



The screenshot shows a Windows-style dialog box titled "Edit MAExplorer project". The main content area is labeled "[9] (Opt.) Database and data quantification program". It contains four input fields with the following labels and values:

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

Below these fields is a large text area with the label "Name of the program used to quantitate the spot data from the sample images." and a scroll bar on the right. At the bottom of the dialog are four buttons: "<Back", "Next>", "Finish", and "Cancel".

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

Edit MAExplorer project

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

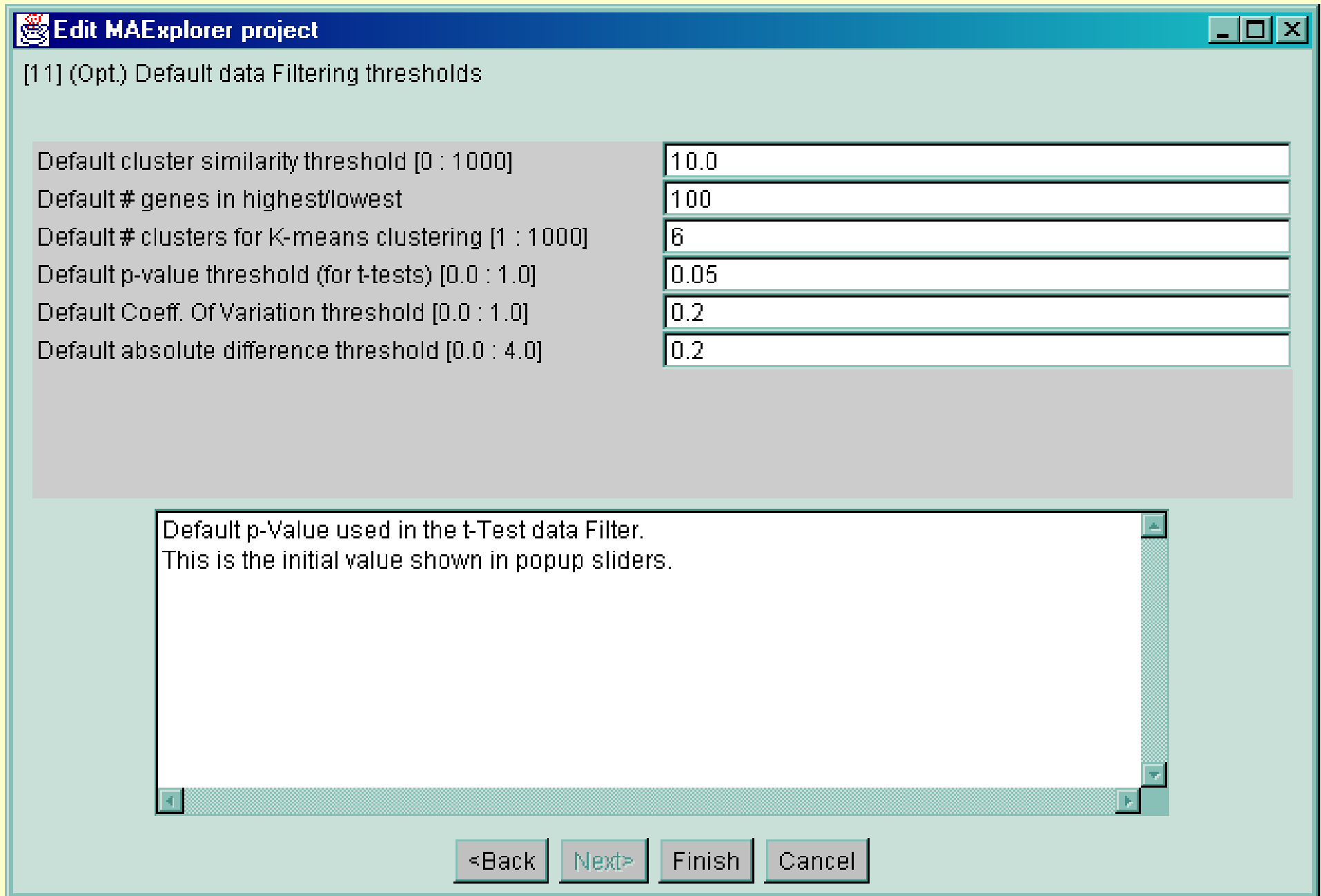
Default name of X samples 'set' HP-X 'set'

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



The screenshot shows a dialog box titled "Edit MAExplorer project" with a standard Windows window title bar. The main content area is titled "[11] (Opt.) Default data Filtering thresholds". It contains a list of six parameters, each with a text input field to its right. The parameters and their values are:

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

Below this list is a scrollable text box containing the following text:

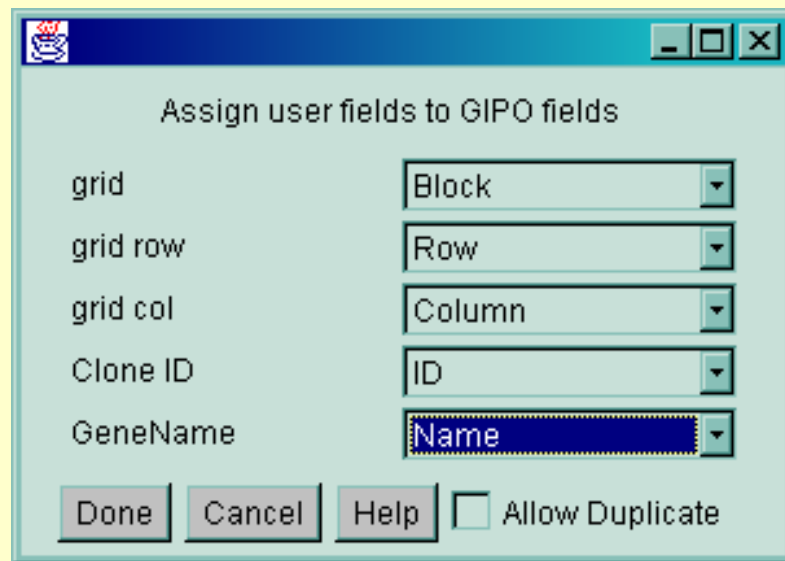
Default p-Value used in the t-Test data Filter.
This is the initial value shown in popup sliders.

At the bottom of the dialog are four buttons: "<Back", "Next>", "Finish", and "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).

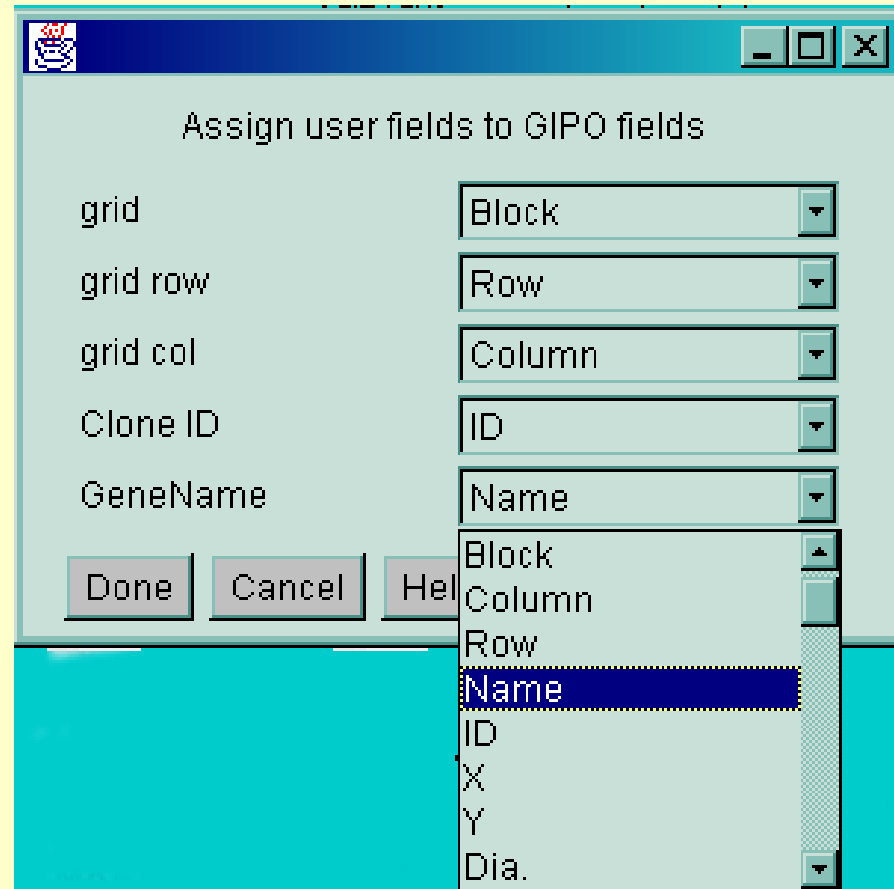
6.1 “Assign user fields to GIPO fields”



Assign user fields to GIPO fields

grid	Block
grid row	Row
grid col	Column
Clone ID	ID
GeneName	Name

Done Cancel Help Allow Duplicate



Assign user fields to GIPO fields

grid	Block
grid row	Row
grid col	Column
Clone ID	ID
GeneName	Name

Done Cancel Help

- Block
- Column
- Row
- Name
- ID
- X
- Y
- Dia.

6.2 “Assign user fields to GIPO fields”

The image shows a software dialog box with a blue title bar and a light blue background. The title bar contains a small icon on the left and standard window control buttons (minimize, maximize, close) on the right. The main area of the dialog is titled "Assign user fields to Quantitation fields". Below the title, there is a list of user fields on the left and corresponding dropdown menus on the right. The user fields are: grid, grid row, grid col, Cy3, Cy5, X, Y, QualCheck, Cy3Bkg, and Cy5Bkg. The dropdown menus contain the following values: Block, Row, Column, F532 Mean - B532, F635 Mean - B635, X, Y, Flags, B532 Mean, and B635 Mean. At the bottom of the dialog, there are four buttons: "Done", "Cancel", "Help", and "Allow Duplicate". The "Allow Duplicate" button is a checkbox that is currently unchecked.

User Field	Assigned Value
grid	Block
grid row	Row
grid col	Column
Cy3	F532 Mean - B532
Cy5	F635 Mean - B635
X	X
Y	Y
QualCheck	Flags
Cy3Bkg	B532 Mean
Cy5Bkg	B635 Mean

Buttons: Done, Cancel, Help, Allow Duplicate

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

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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

genericGenePix-Cy3Cy5-DataFile1.txt
genericGenePix-Cy3Cy5-DataFile2.txt
genericGenePix-Cy3Cy5-DataFile3.txt

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

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

<<C:\Temp\junk\genericGenePix-Cy3Cy5-DataFile1.txt>> [*genericGenePix-Cy3Cy5-DataFile1.txt*]
<<C:\Temp\junk\genericGenePix-Cy3Cy5-DataFile2.txt>> [*genericGenePix-Cy3Cy5-DataFile2.txt*]
<<C:\Temp\junk\genericGenePix-Cy3Cy5-DataFile3.txt>> [*genericGenePix-Cy3Cy5-DataFile3.txt*]

Vendor	<input type="text" value="Axon"/>
Layout name	<input type="text" value="GenePixPro3 - Human"/>
Spots/microarray	<input type="text" value="2703"/>

3. Select Project Output Folder:

Project output folder:

MAExplorer startup File:

4. Edit and Run

Status:

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

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

genericGenePix-Cy3Cy5-DataFile1.txt
genericGenePix-Cy3Cy5-DataFile2.txt
genericGenePix-Cy3Cy5-DataFile3.txt

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

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

<<C:\Temp\junk\genericGenePix-Cy3Cy5-DataFile1.txt>> [genericGenePix-Cy3Cy5-DataFile1.txt]
<<C:\Temp\junk\genericGenePix-Cy3Cy5-DataFile2.txt>> [genericGenePix-Cy3Cy5-DataFile2.txt]
<<C:\Temp\junk\genericGenePix-Cy3Cy5-DataFile3.txt>> [genericGenePix-Cy3Cy5-DataFile3.txt]

Vendor	Axon
Layout name	GenePixPro3 - Human
Spots/microarray	2703

3. Select Project Output Folder:

Project output folder:
MAExplorer startup File:

4. Edit and Run

Status: Saved edited array layout [GenePixPro3 - Human]
to file [GenePixPro3-Human.alo]

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:

genericGenePix-Cy3Cy5-DataFile1.txt
genericGenePix-Cy3Cy5-DataFile2.txt
genericGenePix-Cy3Cy5-DataFile3.txt

2.1 Edit array layout and map fields:

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

<<C:\Temp\junk\genericGenePix-Cy3Cy5-D
<<C:\Temp\junk\genericGenePix-Cy3Cy5-D
<<C:\Temp\junk\genericGenePix-Cy3Cy5-D

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:

8.2 “Project Output Folder” & MAE startup file

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

genericGenePtx-Cy3Cy5-DataFile1.txt
genericGenePtx-Cy3Cy5-DataFile2.txt
genericGenePtx-Cy3Cy5-DataFile3.txt

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

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

<<C:\Tempjunk\genericGenePtx-Cy3Cy5-DataFile1.txt>> [genericGenePtx-Cy3Cy5-DataFile1.txt]
<<C:\Tempjunk\genericGenePtx-Cy3Cy5-DataFile2.txt>> [genericGenePtx-Cy3Cy5-DataFile2.txt]
<<C:\Tempjunk\genericGenePtx-Cy3Cy5-DataFile3.txt>> [genericGenePtx-Cy3Cy5-DataFile3.txt]

Vendor	Axon
Layout name	GenePtxPro3 - Human
Spots/microarray	2703

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

genericGenePix-Cy3Cy5-DataFile1.txt
genericGenePix-Cy3Cy5-DataFile2.txt
genericGenePix-Cy3Cy5-DataFile3.txt

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

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

<<C:\Temp\junk\genericGenePix-Cy3Cy5-DataFile1.txt>> [*genericGenePix-Cy3Cy5-DataFile1.txt*]
<<C:\Temp\junk\genericGenePix-Cy3Cy5-DataFile2.txt>> [*genericGenePix-Cy3Cy5-DataFile2.txt*]
<<C:\Temp\junk\genericGenePix-Cy3Cy5-DataFile3.txt>> [*genericGenePix-Cy3Cy5-DataFile3.txt*]

Vendor	Axon
Layout name	GenePixPro3 - Human
Spots/microarray	2703

3. Select Project Output Folder:

Project output folder:
MAExplorer startup File:

4. Edit and Run

Status: ==> re-reading row #2200 [*C:\Temp\junk\genericGenePix-Cy3Cy5-DataFile1.txt*]
For sample #1 [*genericGenePix-Cy3Cy5-DataFile1.txt*]

10. Notification that Conversion is Finished

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

genericGenePix-Cy3Cy5-DataFile1.txt
genericGenePix-Cy3Cy5-DataFile2.txt
genericGenePix-Cy3Cy5-DataFile3.txt

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

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

<<C:\Temp\junk\genericGenePix-Cy3Cy5-DataFile1.txt>> [*genericGenePix-Cy3Cy5-DataFile1.txt*]
<<C:\Temp\junk\genericGenePix-Cy3Cy5-DataFile2.txt>> [*genericGenePix-Cy3Cy5-DataFile2.txt*]
<<C:\Temp\junk\genericGenePix-Cy3Cy5-DataFile3.txt>> [*genericGenePix-Cy3Cy5-DataFile3.txt*]

Vendor	Axon
Layout name	GenePixPro3 - Human
Spots/microarray	2703

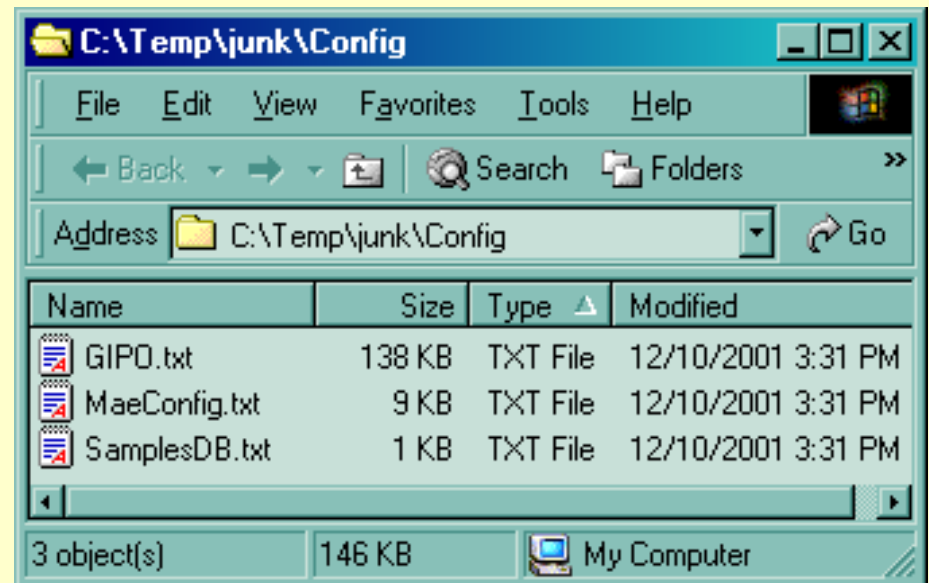
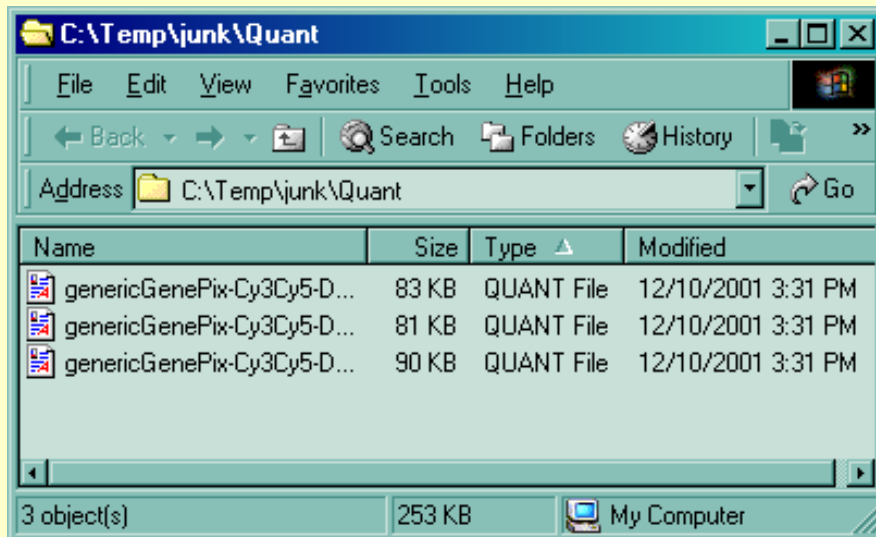
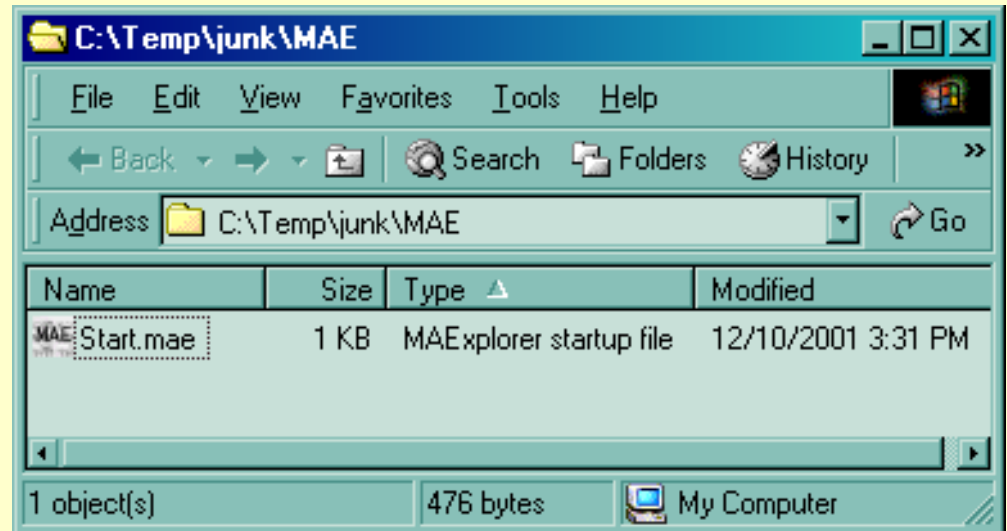
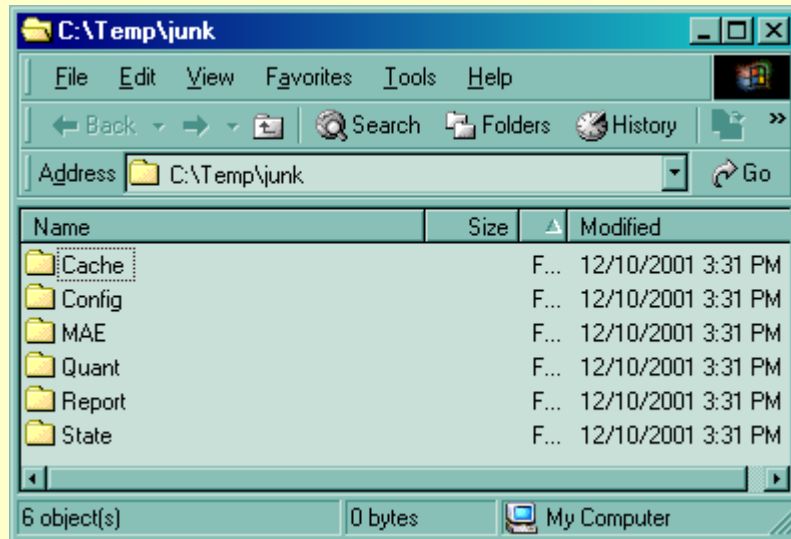
3. Select Project Output Folder:

Project output folder:
MAExplorer startup File:

4. Edit and Run

Status: **===> Finished writing out data files. Press 'Done' to exit**
To start MAExplorer, go to project folder & click on Start.mae.

11. MAExplorer Data Created By Cvt2Mae



12. Running MAExplorer on the Converted Data

MicroArray Explorer - V0.92.19-Beta - My database subset

File HybProbe Edit Analysis View Help

Enter gene name or clone ID Mouse-over info

HP-X: genericGenePix-Cy3Cy5-DataFile1.bt
HP-Y: genericGenePix-Cy3Cy5-DataFile2.bt

[1-A13,3] HP-XY: (X,Y)=(2.405,0.353) XY=6.822, (Norm.: median intensity)

CloneID: IMAGE:457231,
GeneName: M.musculus trop2 gene

HP-X: genericGenePix-Cy3Cy5-DataFile1.txt (Cy3/Cy5)
HP-Y: genericGenePix-Cy3Cy5-DataFile2.txt (Cy3/Cy5)

Norm.: median intensity
HP-XY ratio

>4
3.25
2.5
1.75
1
0.571
0.400
0.308
<0.25

Active Probe
* genericGenePix
* genericGenePix
* genericGenePix

Active Filters
Gene Class
Only quant. data >

Active GeneClass
ALL GENES

Font Family
SansSerif



C:\Temp\junk\MAE

File Edit View Favorites Tools Help

Back Forward Search Folders History

Address C:\Temp\junk\MAE Go

Name	Size	Type	Modified
MAE Start.mae	1 KB	MAExplorer startup file	12/10/2001 3:31 PM

1 object(s) 476 bytes My Computer

