

# Using Cvt2Mae to Convert Incyte 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 “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
- $^{33}\text{P}$  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 Incyte Data

Microsoft Excel - genericIncyte1.cgi.xls

File Edit View Insert Format Tools Data Window Help Acrobat

Arial 8 B I U

H1 =

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1	Experiment Results Generated by GEMTools 2.4													
2	Client:	Genome_Systems												
3	Export Date:	1-Jun-00												
4														
5	GEM:	0225AXSK	BalanceC	Min S/B: 2.5	Min Area: 40%									
6														
7	<b>GEMID</b>	<b>Location</b>	<b>DiffExpr</b>	<b>BalancedDiffExpr</b>	<b>P1Signal</b>	<b>P1S/B</b>	<b>P1Area%</b>	<b>P2BalancedSignal</b>	<b>P2Signal</b>	<b>P2S/B</b>	<b>P2Area%</b>	<b>Probe1</b>	<b>P1Description</b>	<b>Probe2</b>
8	#													
9	0225AXSK	5083	81.5	76.4	4888	47.6	93	64	60	1.5	93	12316130	r41.rc	123T6134
10	0225AXSK	10183	70.7	66.1	6148	42.8	74	93	87	1.5	74	12316130	r41.rc	123T6134
11	0225AXSK	2533	68.7	64.2	3914	42.2	65	61	57	1.7	65	12316130	r41.rc	123T6134
12	0225AXSK	7633	64.9	60.9	3959	34.8	65	65	61	1.5	65	12316130	r41.rc	123T6134

genericIncyte1.cgi/

Ready

# S.3.1 Example of tab-delimited Incyte Data

Microsoft Excel - genericIncyte1.cgi.xls

File Edit View Insert Format Tools Data Window Help Acrobat

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

H1 =

	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA
1													
2													
3													
4													
5													
6													
7	<b>P2Description</b>	<b>GeneID</b>	<b>PlateRow</b>	<b>PlateCol</b>	<b>PlateID</b>	<b>GeneName</b>	<b>CloneID</b>	<b>CloneSource</b>	<b>AccessionNum</b>	<b>Locus</b>	<b>IncyteCloneID</b>	<b>PCRStatus</b>	<b>GeneReferenceID</b>
8													
9	r42.rc	-40175	E		2	2149980 Control: YCFR 27	YC 27.2000.X	Controls					NA
10	r42.rc	-40182	F		2	2149980 Control: YCFR 27	YC 27.2000.Y	Controls					NA
11	r42.rc	-40174	E		1	2149980 Control: YCFR 27	YC 27.2000.W	Controls					NA
12	r42.rc	-40181	F		1	2149980 Control: YCFR 27	YC 27.2000.Z	Controls					NA

genericIncyte1.cgi /

Ready

## S.3.2 Example of tab-delimited Incyte Data

Microsoft Excel - genericIncyte1.cgi.xls

File Edit View Insert Format Tools Data Window Help Acrobat

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

H1 =

	AA	AB	AC	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN
1														
2														
3														
4														
5														
6														
7	<b>GeneReferenceID</b>	<b>GeneNotes</b>	<b>GenBankId</b>	<b>ClonId</b>	<b>Vector</b>									
8														
9	NA	NA	NA											
10	NA	NA	NA											
11	NA	NA	NA											
12	NA	NA	NA											

genericIncyte1.cgi /

Ready

# I. Procedure: Convert Data for Array Layouts

1. Select the Chip Set array layout (**Incyte - 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 Incyte Chipset Array-Layout

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: -- select a chip layout -- Remove Layout

2. Select Input Data Files: Browse GPO file

- Affymetrix - Mouse
- Affymetrix - Human
- Affymetrix - Mouse, use Genomic Descriptions
- Affymetrix - Human, use Genomic Descriptions
- Incyte - Mouse**
- Incyte - Human
- GenePixPro3 - Human
- GenePixPro3 - Mouse

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	2703

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

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':

3. Select Project Output Folder:  
Project output folder  
MAExplorer startup File

4. Edit and Run

Status: *Either continue adding input files (step 2),  
or define Output Folder (step 3) when done adding files.*

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

Look in:

- junk
- genericArrayVision.txt
- genericGenePix-Cy3Cy5-DataFile1.txt
- genericGenePix-Cy3Cy5-DataFile2.txt
- genericGenePix-Cy3Cy5-DataF
- genericIncyte1.cgi
- genericIncyte2.cgi
- genericIncyte3.cgi
- generic-scanalyze.dat
- generic-scanalyze-separateGIPO.gal
- 7-Affymetrx.txt

Type: Text Document  
Size: 576 KB

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

*genericlncyte1.cgi*  
*genericlncyte2.cgi*  
*genericlncyte3.cgi*

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

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

<<C:\Temp\GenericData\genericlncyte1.cgi>> [genericlncyte1.cgi]  
<<C:\Temp\GenericData\genericlncyte2.cgi>> [genericlncyte2.cgi]  
<<C:\Temp\GenericData\genericlncyte3.cgi>> [genericlncyte3.cgi]

Vendor	Axon
Layout name	GenePixPro3 - Human
Spots/microarray	7244

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)

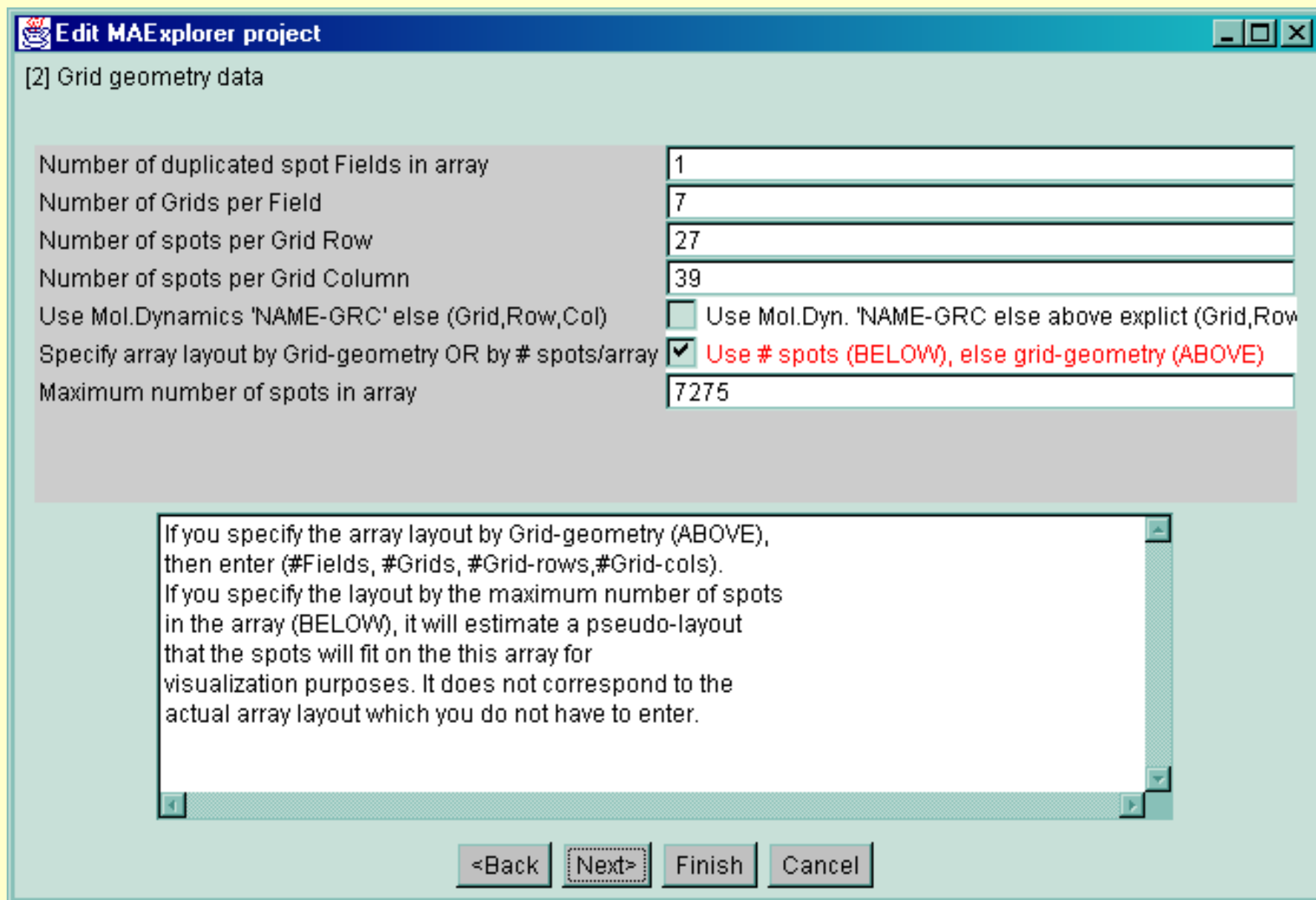
Array layout name: Incyte - Mouse

Vendor name for the array: Incyte

Name of the chip vendor. If your are specifying a <User-defined> chip, then you can use whatever you wish - eg. your organization.

<Back Next> Finish Cancel

## 5.2 Edit Layout 'Wizard' - Grid Geometry. Enter (Grid, Rows/Grid, Columns/Grid) Values



The screenshot shows a dialog box titled "Edit MAExplorer project" with a sub-header "[2] Grid geometry data". It contains several input fields and a checkbox. The fields are: "Number of duplicated spot Fields in array" (value: 1), "Number of Grids per Field" (value: 7), "Number of spots per Grid Row" (value: 27), "Number of spots per Grid Column" (value: 39), "Use Mol.Dyn. 'NAME-GRC' else (Grid,Row,Col)" (checkbox: unchecked), "Specify array layout by Grid-geometry OR by # spots/array" (checkbox: checked, with red text "Use # spots (BELOW), else grid-geometry (ABOVE)"), and "Maximum number of spots in array" (value: 7275). Below the fields is a text box with instructions: "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." At the bottom are buttons for "<Back", "Next>", "Finish", and "Cancel".

Number of duplicated spot Fields in array	1
Number of Grids per Field	7
Number of spots per Grid Row	27
Number of spots per Grid Column	39
Use Mol.Dyn. 'NAME-GRC' else (Grid,Row,Col)	<input type="checkbox"/> Use Mol.Dyn. 'NAME-GRC' else above explicit (Grid,Row,Col)
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	7275

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 Row Where Field Names Are Defined

Configuration Option	Value
(Optional) Row containing a list sample names	0
Row containing a list of quantitative file Field names	7
First row containing quantitative file Data	0
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	GEMID

If a line starts with this token (eg. #), the line will be skipped.  
Leave it blank, if there are no comment lines.

<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

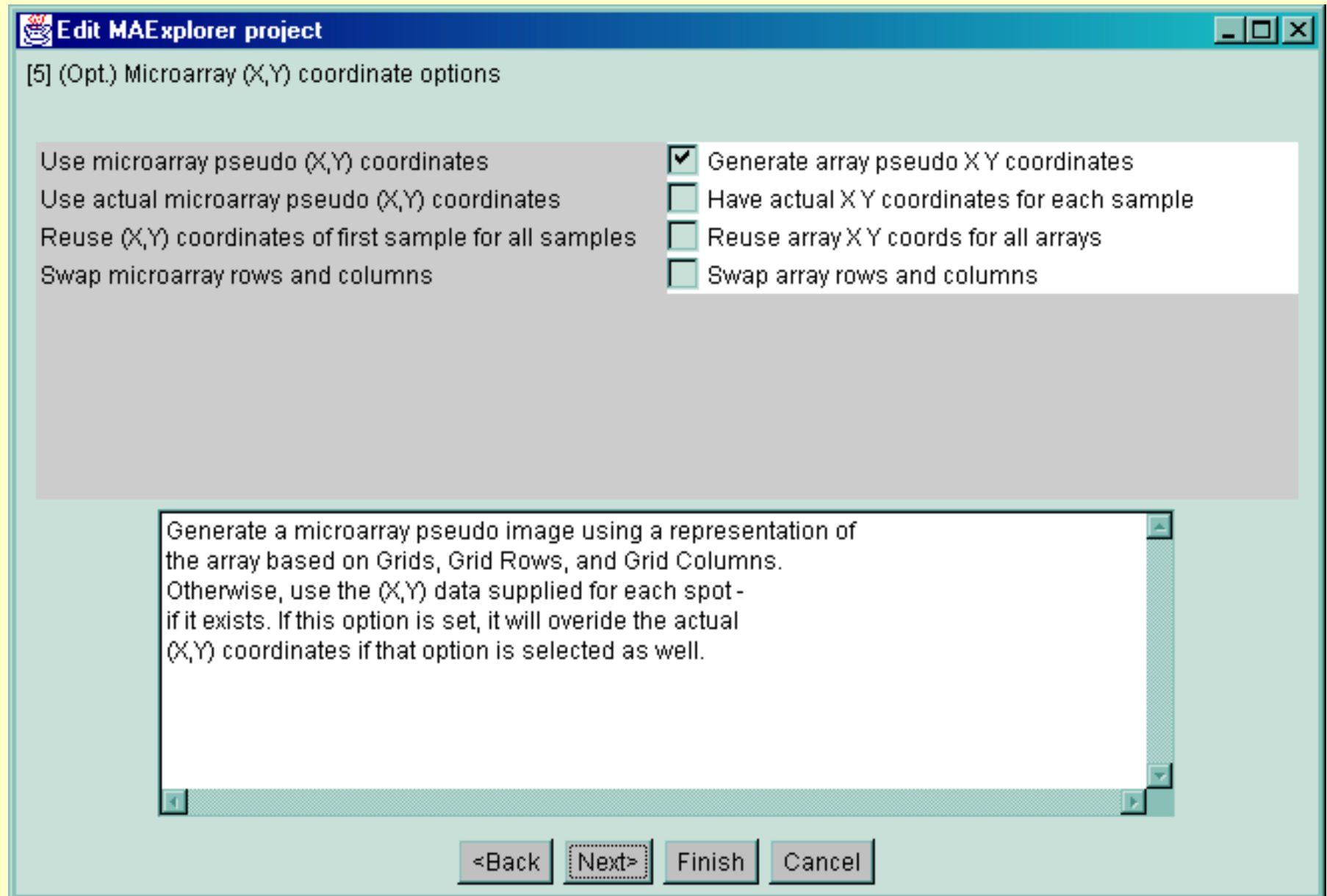
Use Ratio else Intensity data  
 Use (Cy5/Cy3) else (Cy3/Cy5)

Cy3  
Cy5

Has background data

<Back Next> Finish Cancel

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



# 5.6 Edit Layout 'Wizard' Genomic ID Values

The screenshot shows a Windows-style dialog box titled "Edit MAExplorer project". The main content area is titled "[6] (Opt.) Genomic Identifier options". It contains two columns of options, each with a checkbox. The first column lists data sources, and the second column lists whether the user data file has that data. Below the options is a text box with the message "The user data file has I.M.A.G.E 'Clone ID' data." At the bottom are four buttons: "<Back", "Next>", "Finish", and "Cancel".

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

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 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. Define UniGene Species prefix

**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.

## Define Optional Names for Database

Edit MAExplorer project

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

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)	GemTool

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

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

Location	Location
Clone ID	CloneID
GenBankAcc	AccessionNum
GenBankAcc3'	<not used>
GenBankAcc5'	<not used>
Plate	PlateID
Plate row	PlateRow
Plate col	PlateCol
GeneName	GeneName

Done Cancel Help  Allow Duplicate

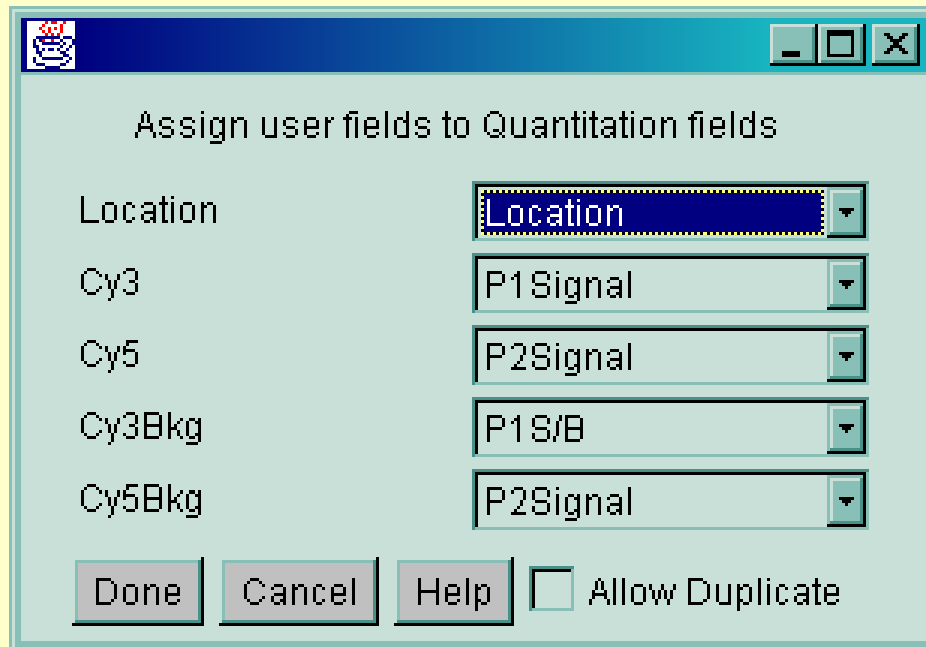
Assign user fields to GIPO fields

Location	Location
Clone ID	CloneID
GenBankAcc	AccessionNum
GenBankAcc3'	<not used>
GenBankAcc5'	<not used>
Plate	<not used>
Plate row	<not used>
Plate col	PlateID
GeneName	Probe2

Done Cancel Help

- Probe2
- P2Description
- GeneID
- PlateRow
- PlateCol
- PlateID
- GeneName
- CloneID

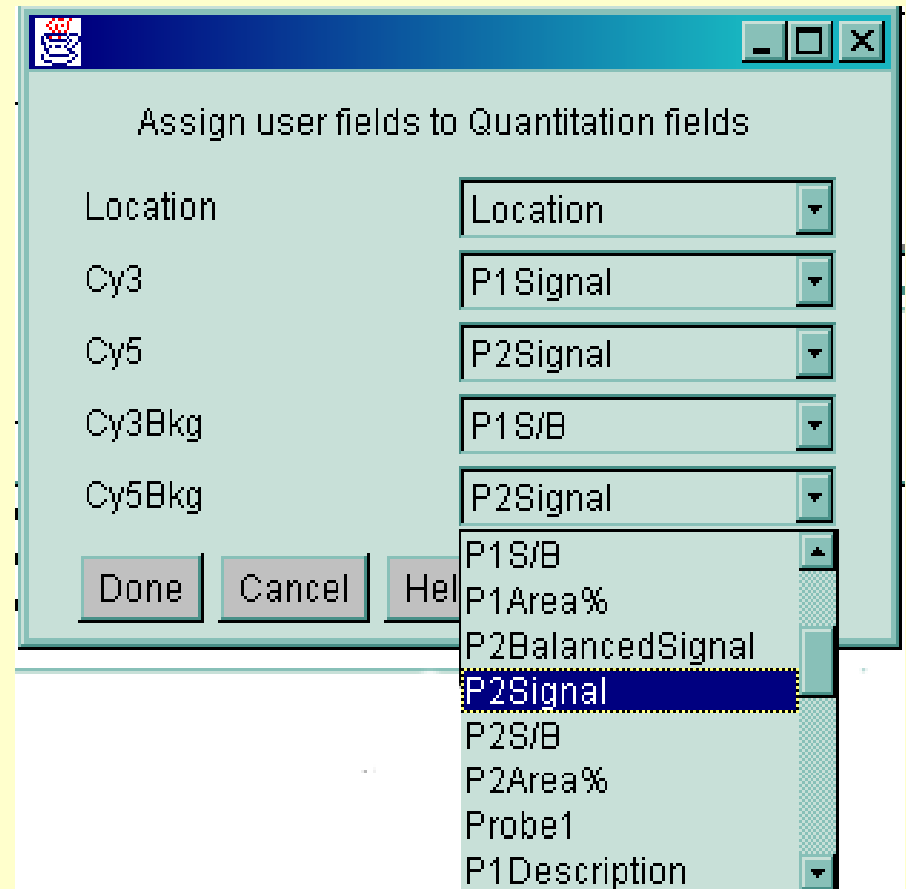
## 6.2 “Assign user fields to GIPO fields”



Assign user fields to Quantitation fields

Location	Location
Cy3	P1Signal
Cy5	P2Signal
Cy3Bkg	P1S/B
Cy5Bkg	P2Signal

Done Cancel Help  Allow Duplicate



Assign user fields to Quantitation fields

Location	Location
Cy3	P1Signal
Cy5	P2Signal
Cy3Bkg	P1S/B
Cy5Bkg	P2Signal

Done Cancel Help

- P1S/B
- P1Area%
- P2BalancedSignal
- P2Signal**
- P2S/B
- P2Area%
- Probe1
- P1Description

# 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

*genericncyte1.cgi*  
*genericncyte2.cgi*  
*genericncyte3.cgi*

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

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

<<C:\Temp\GenericData\genericncyte1.cgi>> [genericncyte1.cgi]  
<<C:\Temp\GenericData\genericncyte2.cgi>> [genericncyte2.cgi]  
<<C:\Temp\GenericData\genericncyte3.cgi>> [genericncyte3.cgi]

Vendor	Axon
Layout name	GenePixPro3 - Human
Spots/microarray	7371

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

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

genericIncyte1.cgi  
genericIncyte2.cgi  
genericIncyte3.cgi

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

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

<<C:\Temp\GenericData\genericIncyte1.cgi>> [genericIncyte1.cgi]  
<<C:\Temp\GenericData\genericIncyte2.cgi>> [genericIncyte2.cgi]  
<<C:\Temp\GenericData\genericIncyte3.cgi>> [genericIncyte3.cgi]

Vendor	Axon
Layout name	GenePixPro3 - Human
Spots/microarray	7371

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”

**Lvt2Mae: 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:**

*genericncyte1.cgi*  
*genericncyte2.cgi*  
*genericncyte3.cgi*

**2.1 Edit array layout and map fields:**

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

<<C:\Temp\GenericData\genericncyte1.cgi>>  
<<C:\Temp\GenericData\genericncyte2.cgi>>  
<<C:\Temp\GenericData\genericncyte3.cgi>>

**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

*genericlncyte1.cgi*  
*genericlncyte2.cgi*  
*genericlncyte3.cgi*

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

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

<<C:\Temp\GenericData\genericlncyte1.cgi>> [genericlncyte1.cgi]  
<<C:\Temp\GenericData\genericlncyte2.cgi>> [genericlncyte2.cgi]  
<<C:\Temp\GenericData\genericlncyte3.cgi>> [genericlncyte3.cgi]

Vendor	Axon
Layout name	GenePbxPro3 - Human
Spots/microarray	7371

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

genericIncyte1.cgi  
genericIncyte2.cgi  
genericIncyte3.cgi

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

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

<<C:\Temp\GenericData\genericIncyte1.cgi>> [genericIncyte1.cgi]  
<<C:\Temp\GenericData\genericIncyte2.cgi>> [genericIncyte2.cgi]  
<<C:\Temp\GenericData\genericIncyte3.cgi>> [genericIncyte3.cgi]

Vendor	Axon
Layout name	GenePixPro3 - Human
Spots/microarray	7371

3. Select Project Output Folder:

Project output folder: C:\Temp\junk\  
MAExplorer startup File: C:\Temp\junk\MAE\Start.mae

4. Edit and Run

Status: **Generating sorted 'Location' IDs with 'INFILL' spots.**  
For sample #1 [genericIncyte1.cgi]

# 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

*genericIncyte1.cgi*  
*genericIncyte2.cgi*  
*genericIncyte3.cgi*

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

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

<<C:\Temp\GenericData\genericIncyte1.cgi>> [*genericIncyte1.cgi*]  
<<C:\Temp\GenericData\genericIncyte2.cgi>> [*genericIncyte2.cgi*]  
<<C:\Temp\GenericData\genericIncyte3.cgi>> [*genericIncyte3.cgi*]

Vendor	<input type="text" value="Axon"/>
Layout name	<input type="text" value="GenePixPro3 - Human"/>
Spots/microarray	<input type="text" value="7371"/>

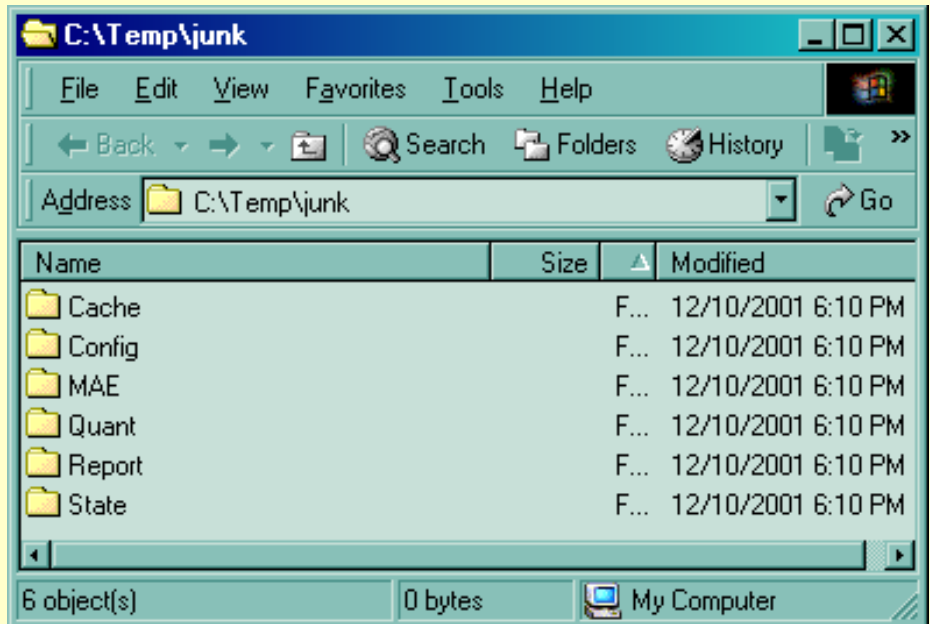
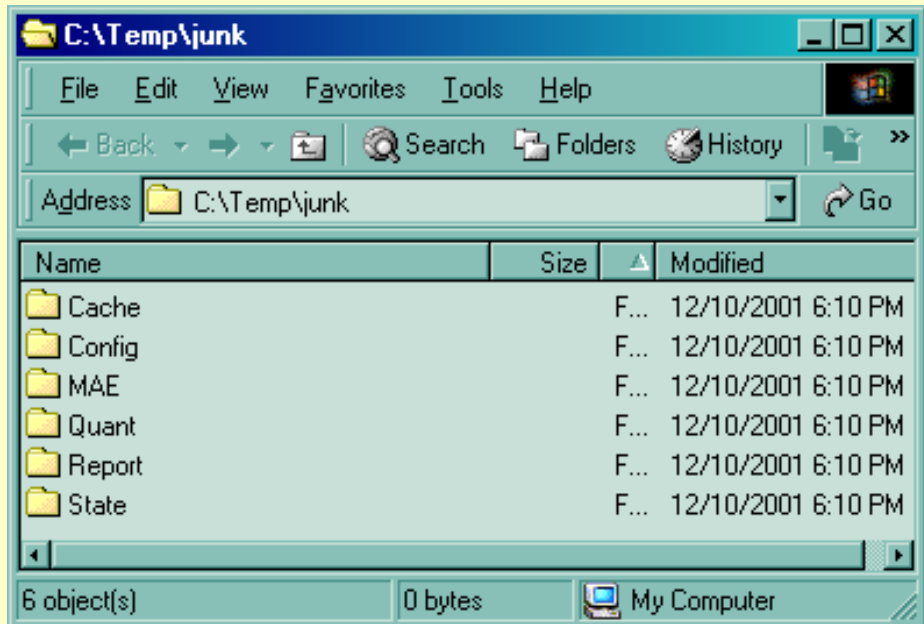
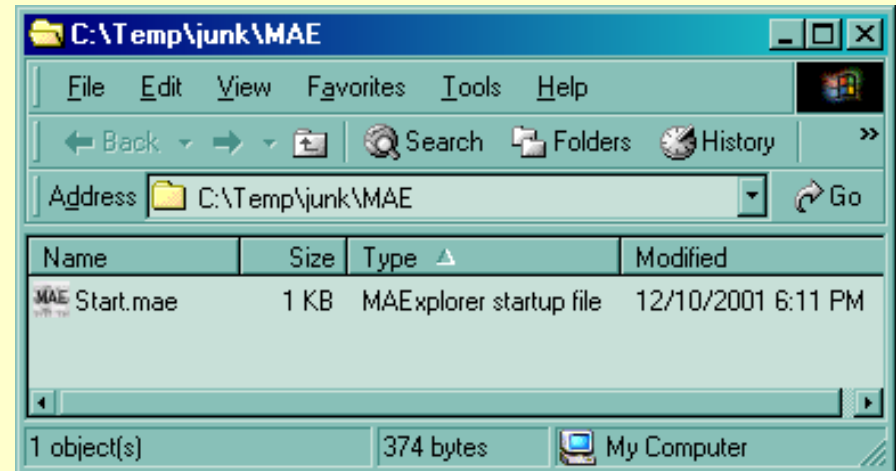
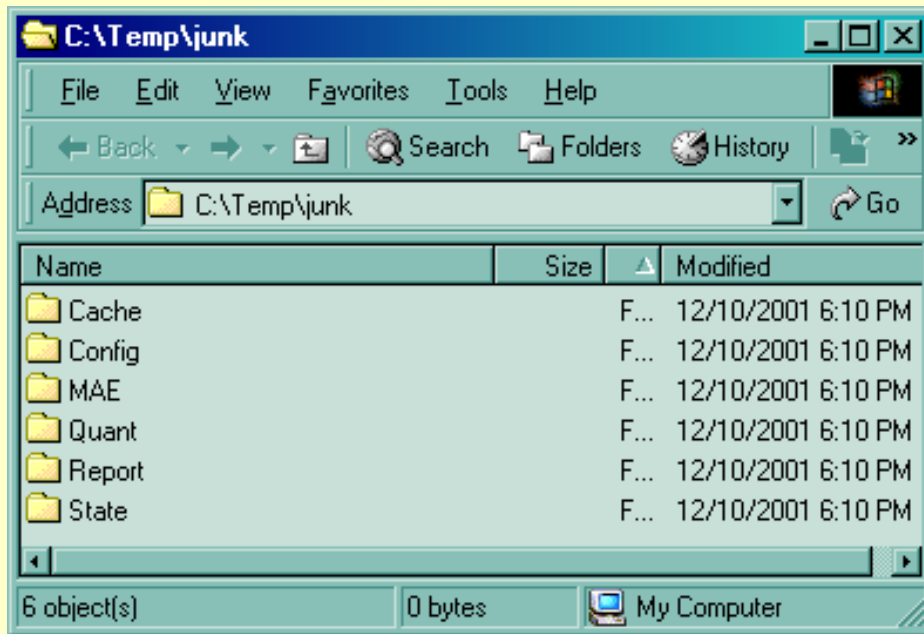
3. Select Project Output Folder:

Project output folder:   
MAExplorer startup File:

4. Edit and Run

Status:

# 11. MAExplorer Data Created By Cvt2Mae



# 12. Running MAExplorer on the Converted Data

