Using Cvt2Mae to Convert a Separate GIPO and Scanalyze Array Data for MAExplorer

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

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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, or simply Location 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.

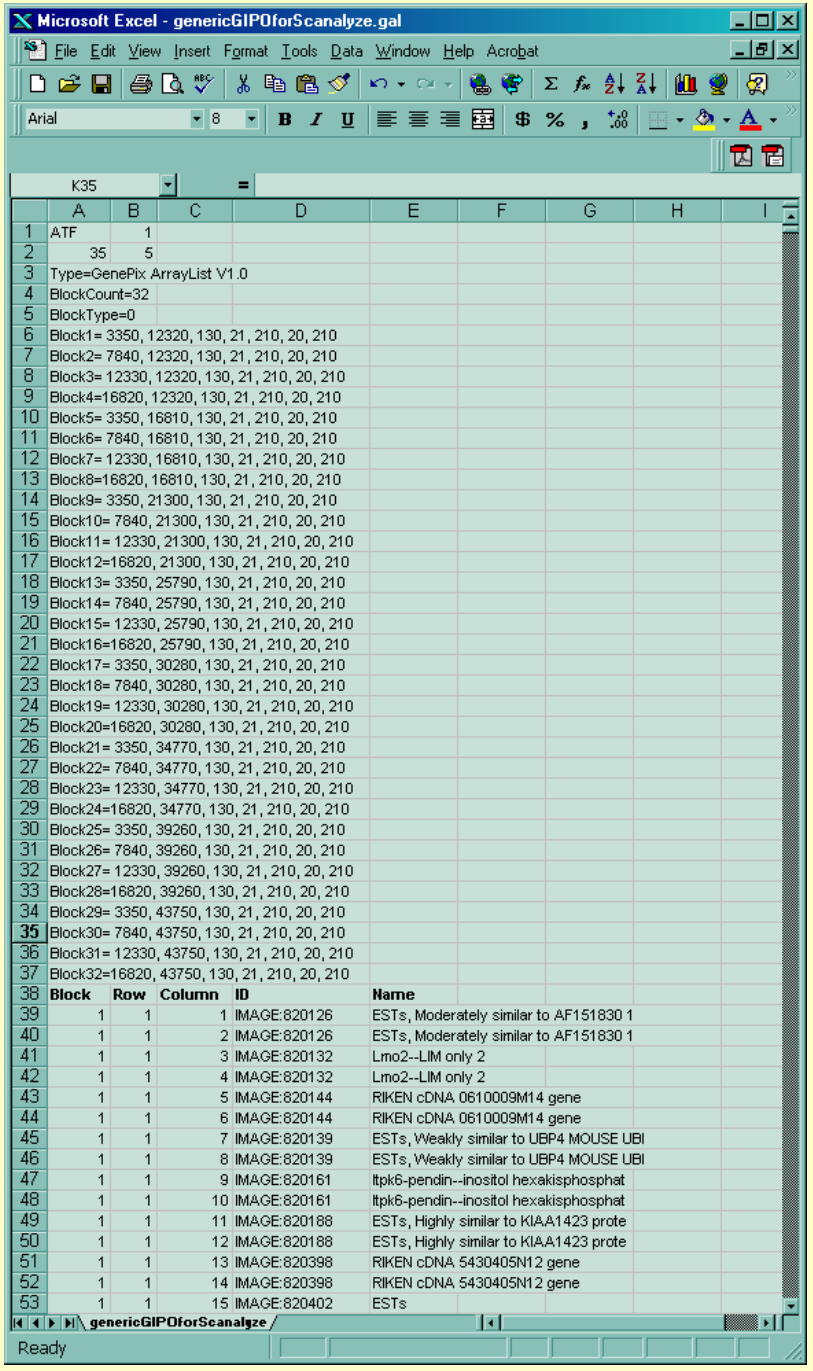
S.1.4 MAExplorer Spot Quantification Files

- 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 GIPO Data



Microsoft Excel - genericGIPOforScanalyze.gal

File Edit View Insert Format Tools Data Window Help Acrobat

Arial 8

K35 =

	A	B	C	D	E	F	G	H	I
1	ATF	1							
2	35	5							
3	Type=GenePix ArrayList V1.0								
4	BlockCount=32								
5	BlockType=0								
6	Block1= 3350, 12320, 130, 21, 210, 20, 210								
7	Block2= 7840, 12320, 130, 21, 210, 20, 210								
8	Block3= 12330, 12320, 130, 21, 210, 20, 210								
9	Block4=16820, 12320, 130, 21, 210, 20, 210								
10	Block5= 3350, 16810, 130, 21, 210, 20, 210								
11	Block6= 7840, 16810, 130, 21, 210, 20, 210								
12	Block7= 12330, 16810, 130, 21, 210, 20, 210								
13	Block8=16820, 16810, 130, 21, 210, 20, 210								
14	Block9= 3350, 21300, 130, 21, 210, 20, 210								
15	Block10= 7840, 21300, 130, 21, 210, 20, 210								
16	Block11= 12330, 21300, 130, 21, 210, 20, 210								
17	Block12=16820, 21300, 130, 21, 210, 20, 210								
18	Block13= 3350, 25790, 130, 21, 210, 20, 210								
19	Block14= 7840, 25790, 130, 21, 210, 20, 210								
20	Block15= 12330, 25790, 130, 21, 210, 20, 210								
21	Block16=16820, 25790, 130, 21, 210, 20, 210								
22	Block17= 3350, 30280, 130, 21, 210, 20, 210								
23	Block18= 7840, 30280, 130, 21, 210, 20, 210								
24	Block19= 12330, 30280, 130, 21, 210, 20, 210								
25	Block20=16820, 30280, 130, 21, 210, 20, 210								
26	Block21= 3350, 34770, 130, 21, 210, 20, 210								
27	Block22= 7840, 34770, 130, 21, 210, 20, 210								
28	Block23= 12330, 34770, 130, 21, 210, 20, 210								
29	Block24=16820, 34770, 130, 21, 210, 20, 210								
30	Block25= 3350, 39260, 130, 21, 210, 20, 210								
31	Block26= 7840, 39260, 130, 21, 210, 20, 210								
32	Block27= 12330, 39260, 130, 21, 210, 20, 210								
33	Block28=16820, 39260, 130, 21, 210, 20, 210								
34	Block29= 3350, 43750, 130, 21, 210, 20, 210								
35	Block30= 7840, 43750, 130, 21, 210, 20, 210								
36	Block31= 12330, 43750, 130, 21, 210, 20, 210								
37	Block32=16820, 43750, 130, 21, 210, 20, 210								
38	**Block**	**Row**	**Column**	**ID**	**Name**				
39	1	1	1	IMAGE:820126	ESTs, Moderately similar to AF151830 1				
40	1	1	2	IMAGE:820126	ESTs, Moderately similar to AF151830 1				
41	1	1	3	IMAGE:820132	Lmo2--LIM only 2				
42	1	1	4	IMAGE:820132	Lmo2--LIM only 2				
43	1	1	5	IMAGE:820144	RIKEN cDNA 0610009M14 gene				
44	1	1	6	IMAGE:820144	RIKEN cDNA 0610009M14 gene				
45	1	1	7	IMAGE:820139	ESTs, Weakly similar to UBP4 MOUSE UBI				
46	1	1	8	IMAGE:820139	ESTs, Weakly similar to UBP4 MOUSE UBI				
47	1	1	9	IMAGE:820161	Itpk6-pendin--inositol hexakisphosphat				
48	1	1	10	IMAGE:820161	Itpk6-pendin--inositol hexakisphosphat				
49	1	1	11	IMAGE:820188	ESTs, Highly similar to KIAA1423 prote				
50	1	1	12	IMAGE:820188	ESTs, Highly similar to KIAA1423 prote				
51	1	1	13	IMAGE:820398	RIKEN cDNA 5430405N12 gene				
52	1	1	14	IMAGE:820398	RIKEN cDNA 5430405N12 gene				
53	1	1	15	IMAGE:820402	ESTs				

genericGIPOforScanalyze

Ready

S.3.1 Example of tab-delimited Scanalyze Data

Microsoft Excel - genericData1.DAT

File Edit View Insert Format Tools Data Window Help Acrobat

W2 =

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T
1	HEADER	SPOT	GRID	TOP	LEFT	BOT	RIGHT	ROW	COL	CH1I	CH1B	CH1AB	CH2I	CH2B	CH2AB	SPIX	BGPIX	EDGE	RAT2	MRAT
2	REMARK	SOFTWARE	ScanAlyze																	
3	REMARK	SOFTVERS	2.44																	
4	REMARK	CH1 IMAGE	4_Cy3m																	
5	REMARK	CH2 IMAGE	4_Cy5m																	
6	REMARK	GRID FILE	C:generic.SAG																	
7	REMARK	DATE	10/1/2002																	
8	REMARK	TIME	11:45:03																	
9	SPOT	1	1	90	116	103	129	1	1	2690	2196	3150	2122	806	1706	137	1392	0	2.664	1.819
10	SPOT	2	1	90	137	103	150	1	2	2763	2174	3051	995	670	1598	137	1302	0	0.552	0.555
11	SPOT	3	1	90	158	103	171	1	3	6861	2162	2957	1454	548	1480	137	1302	0	0.193	0.266
12	SPOT	4	1	90	179	103	192	1	4	8181	2046	2843	1221	512	1461	137	1302	0	0.116	0.288
13	SPOT	5	1	90	200	103	213	1	5	3139	1912	2772	1060	446	1346	137	1302	0	0.5	0.58
14	SPOT	6	1	90	221	103	234	1	6	3105	1864	2685	1185	406	1259	137	1302	0	0.628	0.474
15	SPOT	7	1	90	242	103	255	1	7	2286	2032	2966	1273	380	1253	137	1302	0	3.516	0.827
16	SPOT	8	1	90	263	103	276	1	8	3374	2234	3197	1165	392	1234	137	1302	0	0.678	0.62

genericData1

Ready

Microsoft Excel - genericData1.DAT

File Edit View Insert Format Tools Data Window Help Acrobat

AJ16 =

	U	V	W	X	Y	Z	AA	AB	AC	AD	AE	AF	AG	AH
1	REGR	CORR	LFRAT	CH1GTB1	CH2GTB1	CH1GTB2	CH2GTB2	CH1EDGEA	CH2EDGEA	FLAG	CH1KSD	CH1KSP	CH2KSD	CH2KSP
2														
3														
4														
5														
6														
7														
8														
9	0.021	0.0227	0.1211	0.438	0.4818	0.2774	0.4161	0.3673	0.4854	0	0.1081	1.01E-01	0.2106	2.42E-05
10	0.031	0.0447	0.0589	0.4672	0.3796	0.3212	0.3504	0.3587	0.4844	0	0.05403	8.53E-01	0.2482	3.26E-07
11	0.022	0.0471	0.029	0.781	0.5036	0.6423	0.4234	0.3311	0.51	0	0.3562	2.10E-14	0.2351	1.62E-06
12	-0.044	-0.101	18.64	0.854	0.4526	0.7591	0.4088	0.3139	0.5587	0	0.4484	1.39E-22	0.2808	4.07E-09
13	-0.007	-0.008	50.75	0.5474	0.4453	0.4672	0.3796	0.329	0.5362	0	0.1123	8.15E-02	0.3135	2.96E-11
14	-0.021	-0.032	25.62	0.562	0.4818	0.4453	0.4234	0.3673	0.5413	0	0.1034	1.33E-01	0.2351	1.62E-06
15	-0.005	-0.007	132.2	0.3796	0.4526	0.2701	0.4161	0.3813	0.5888	0	0.1274	3.27E-02	0.2874	1.59E-09
16	0.032	0.053	0.0511	0.562	0.5182	0.4526	0.4672	0.3439	0.5401	0	0.1013	1.48E-01	0.2678	2.51E-08

genericData1

Ready

I. Procedure: Convert Data for Array Layouts

1. Select the Chip Set array layout (**Scanalyze**) if in list,
   otherwise pick <User-defined>)

2. Select separate GIPO file if needed using the "Browse GIPO file" .

2.1 Repeatedly 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"

I. Procedure: continued...

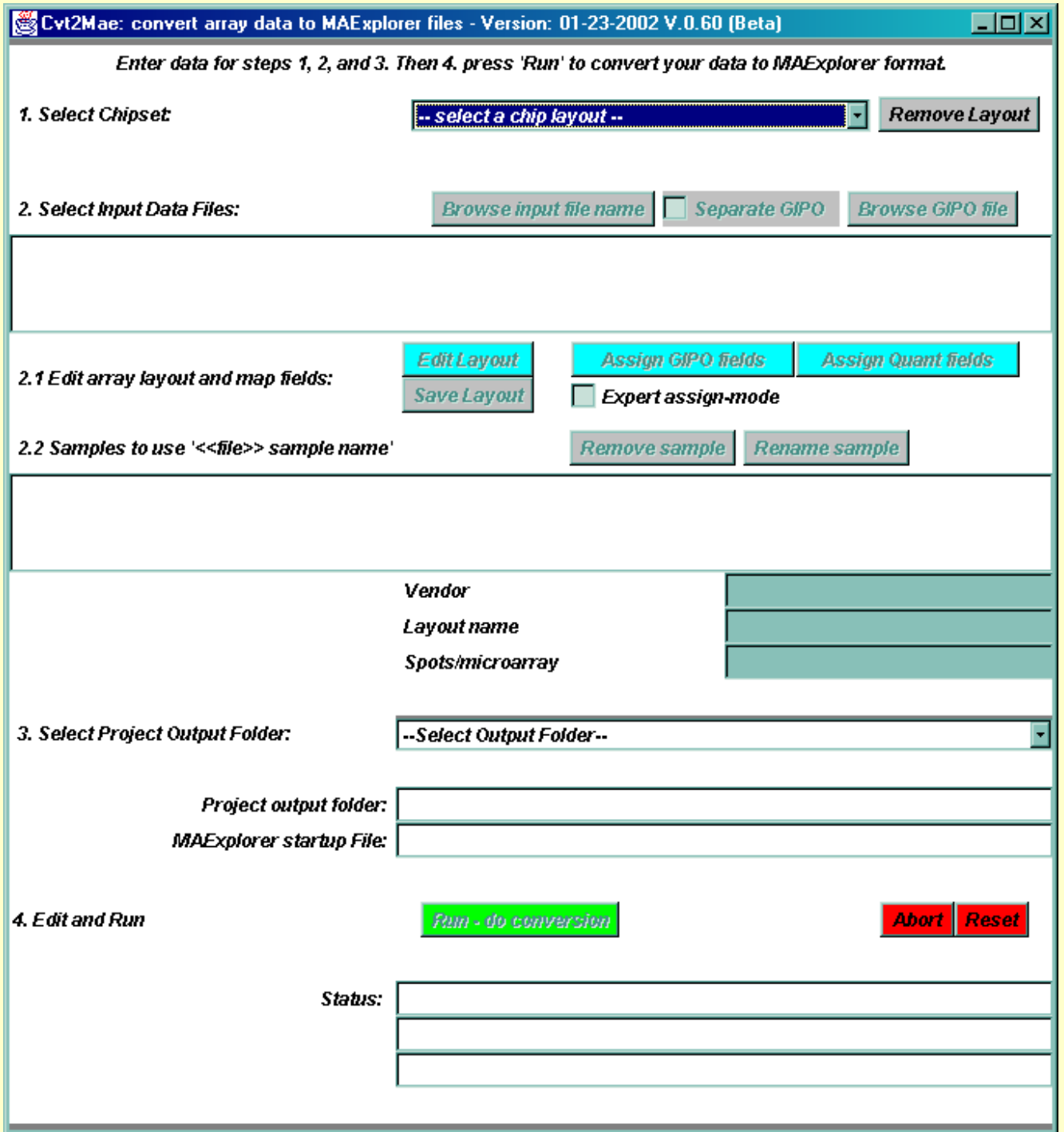
4. Select the project output directory (i.e., folder) to save generated files

5. Press “Run” to convert the data

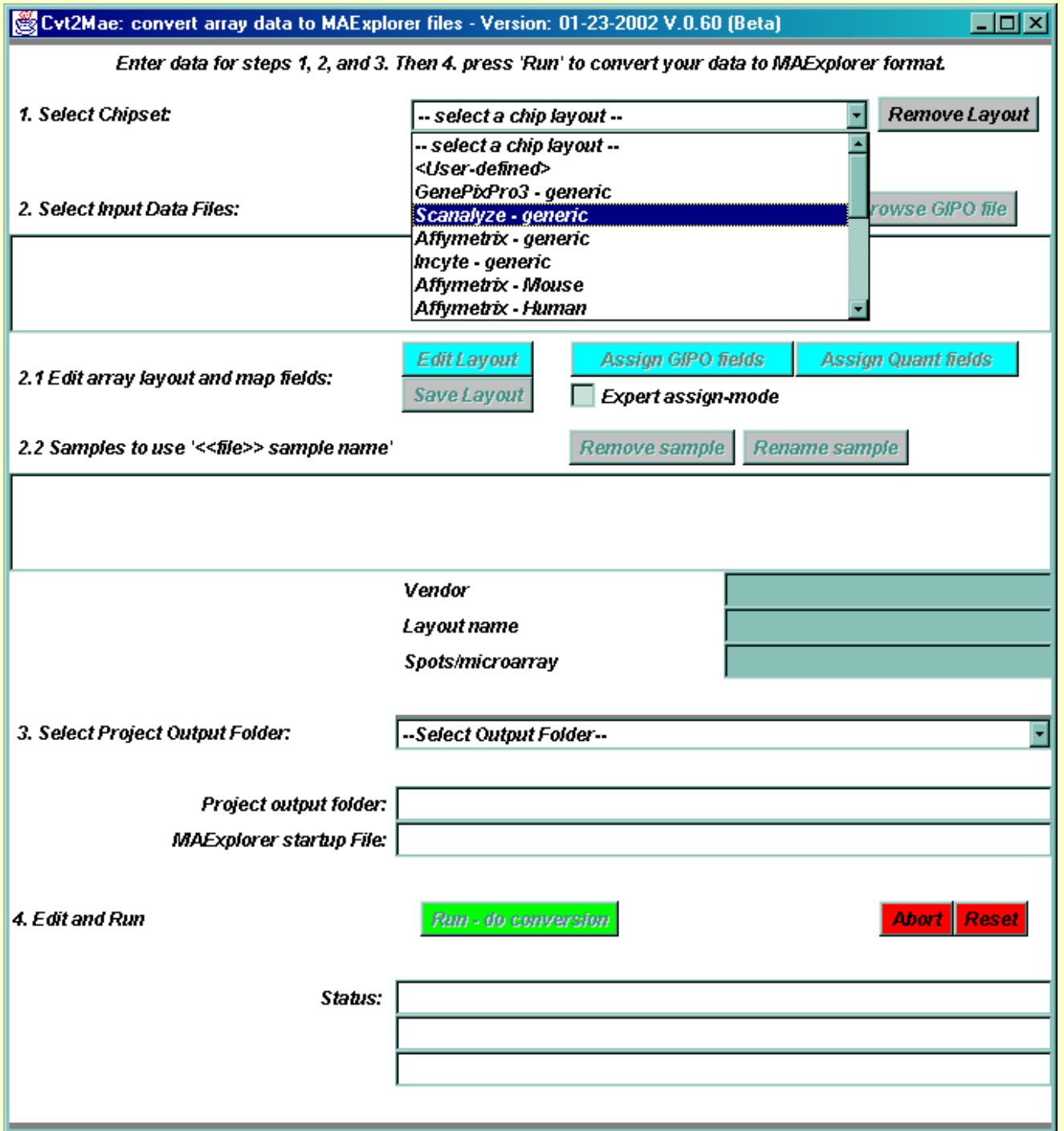
6. Press “Done” when it is finished.

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

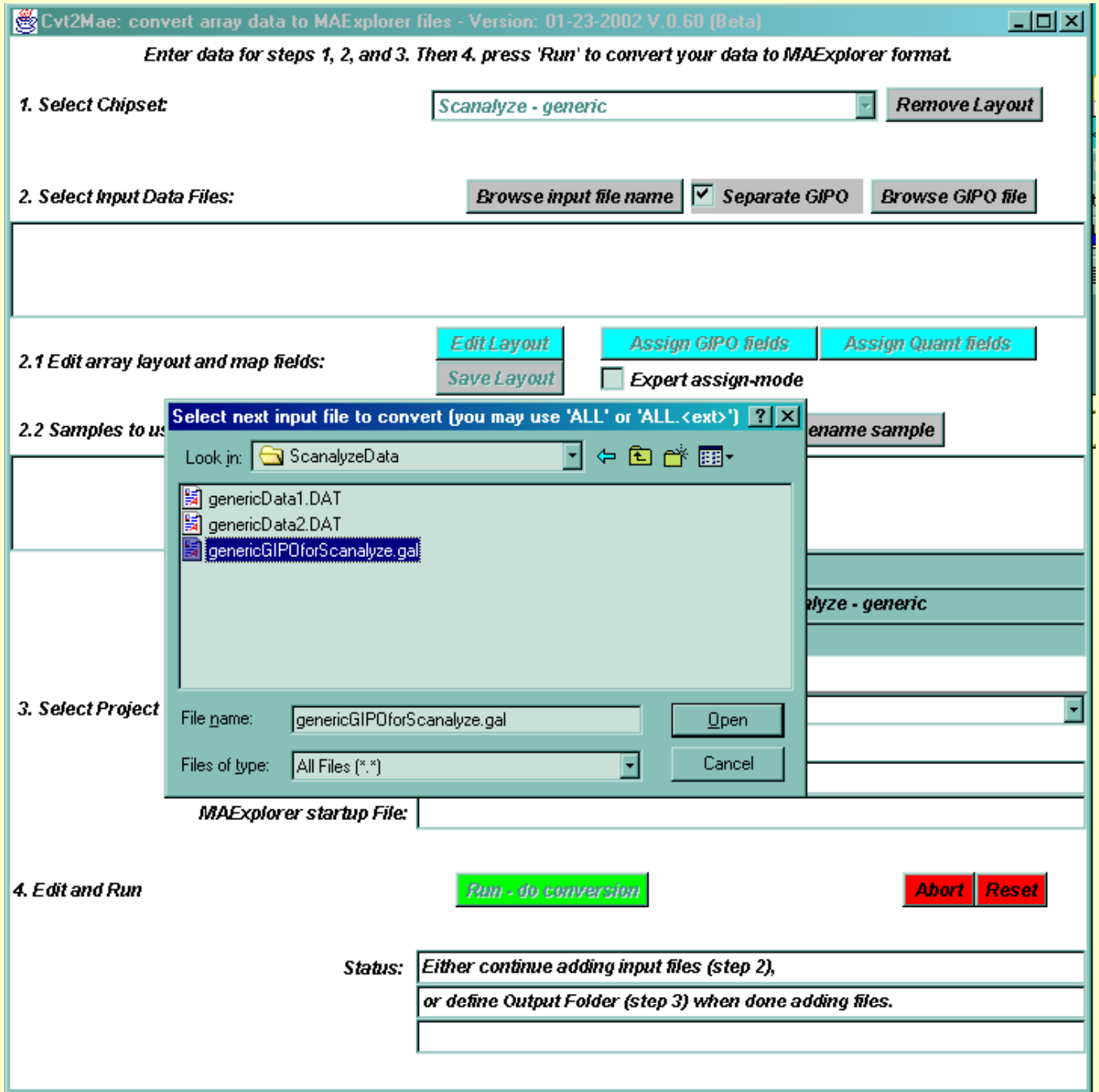
1. Initial State of Cvt2Mae Program



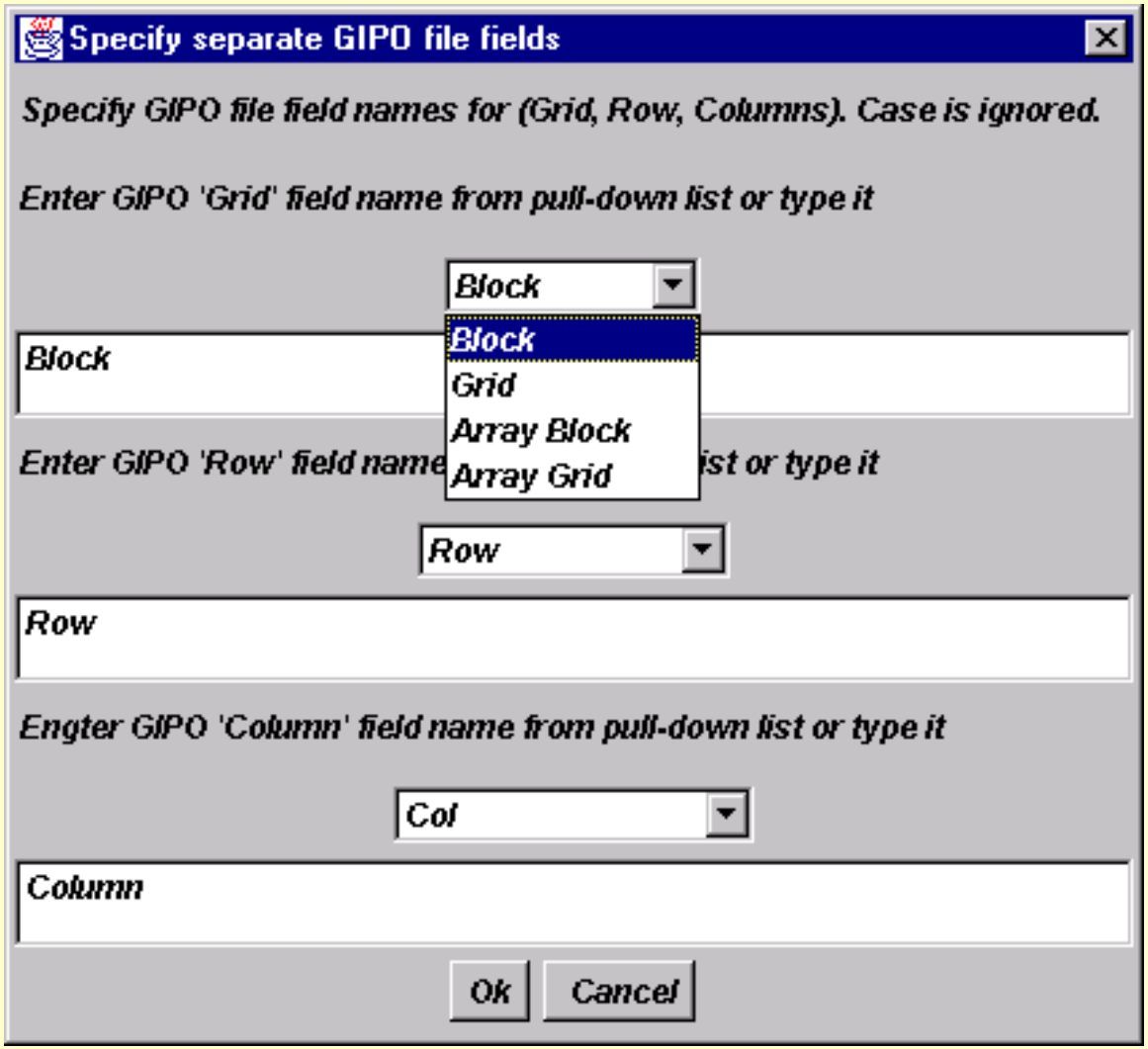
2. Selecting Scanalyze Chipset Array-Layout



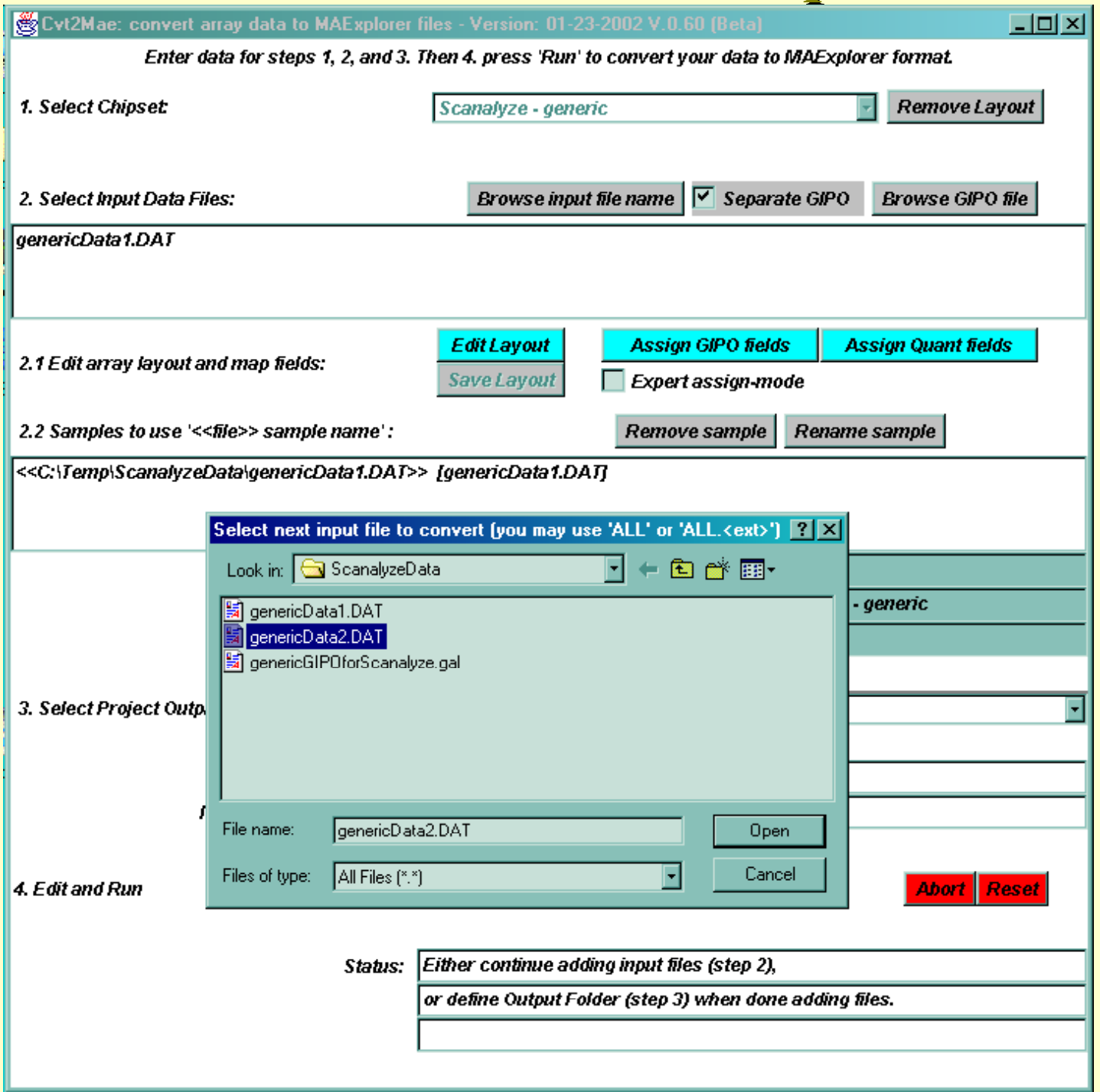
3.1 Select GIPO Input File with "Browse GIPO file"



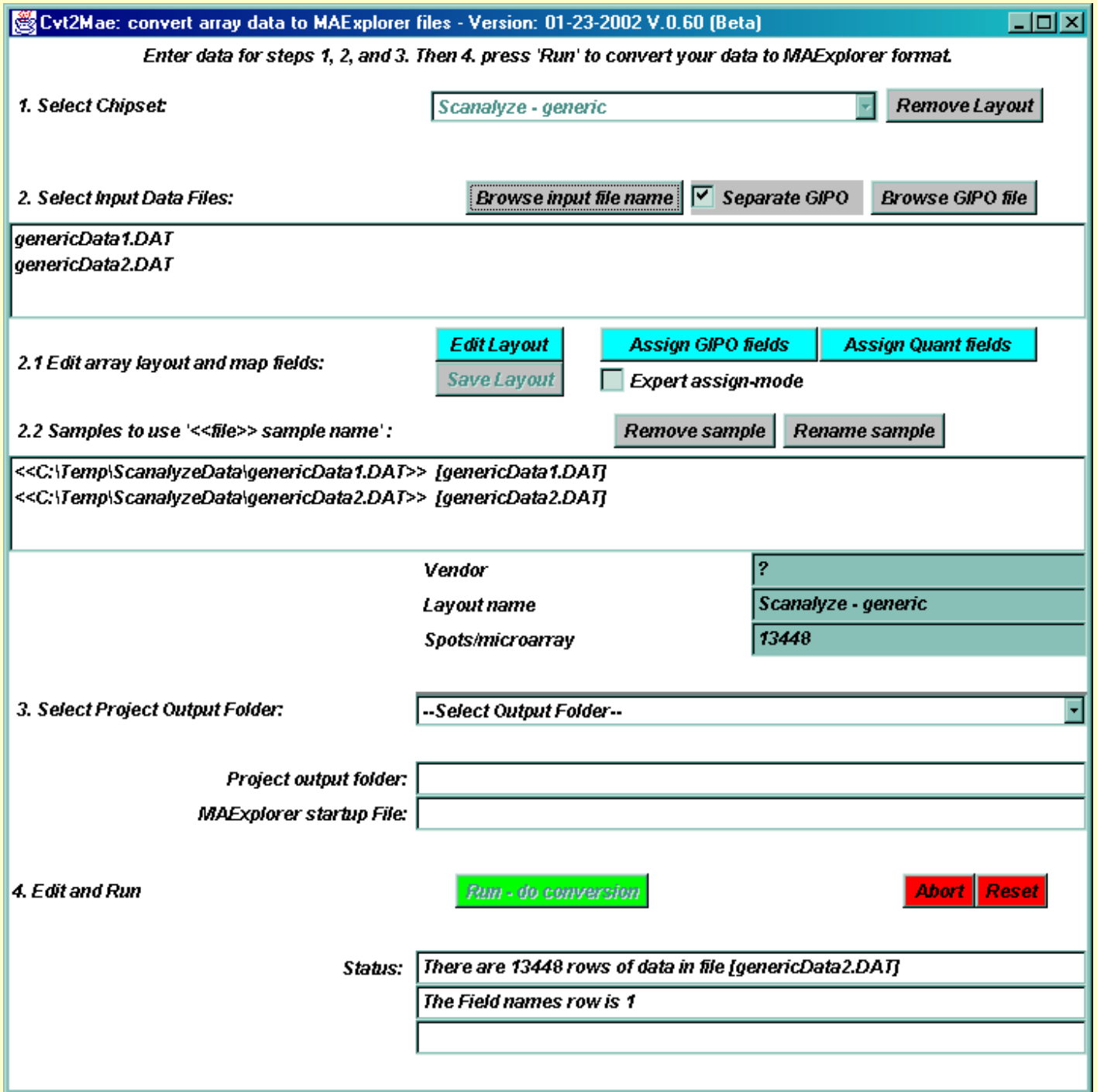
3.2 Specify GIPO Field Names for Grid, Row & Column



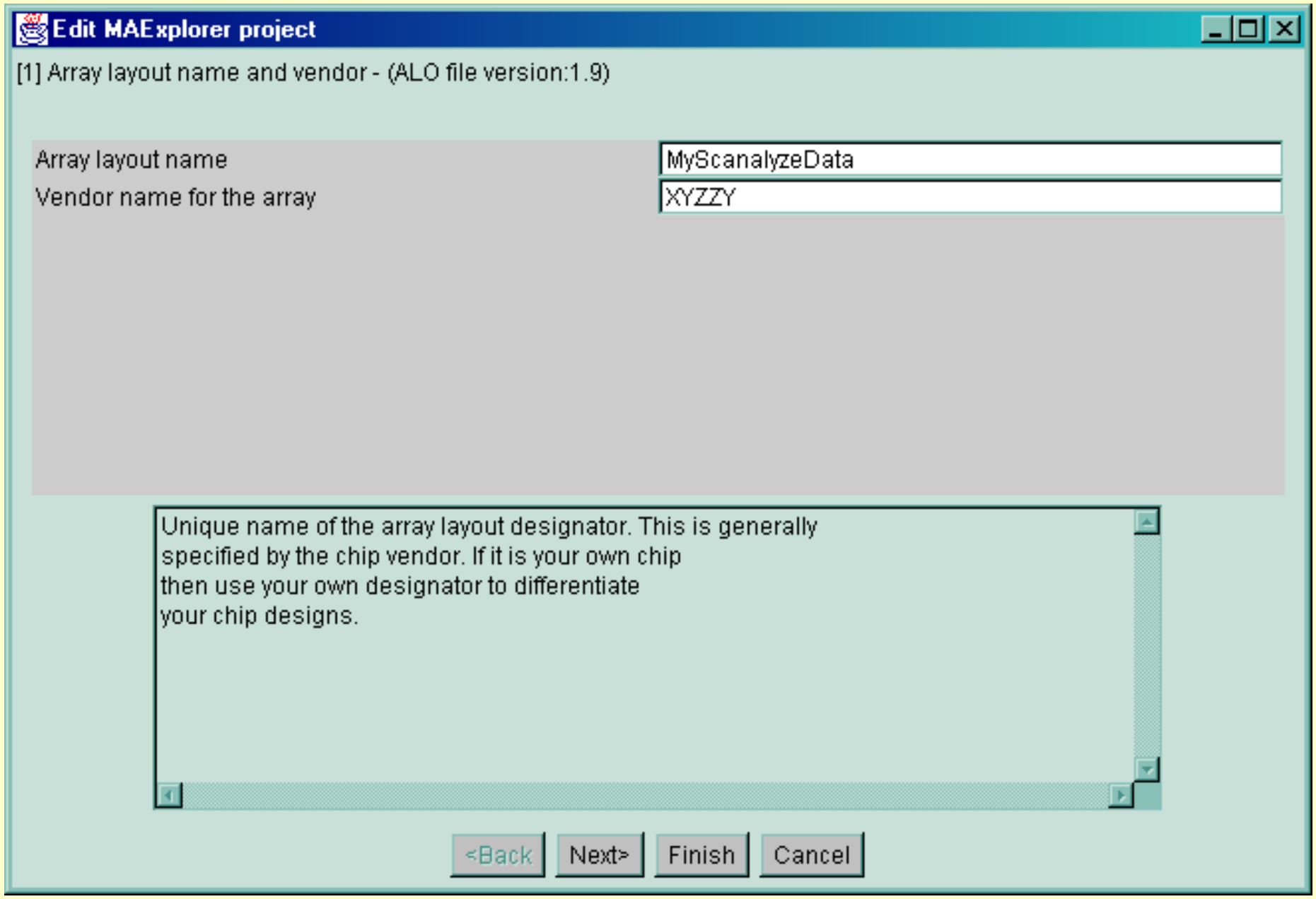
3.3 Select Files with “Browse input file” Name



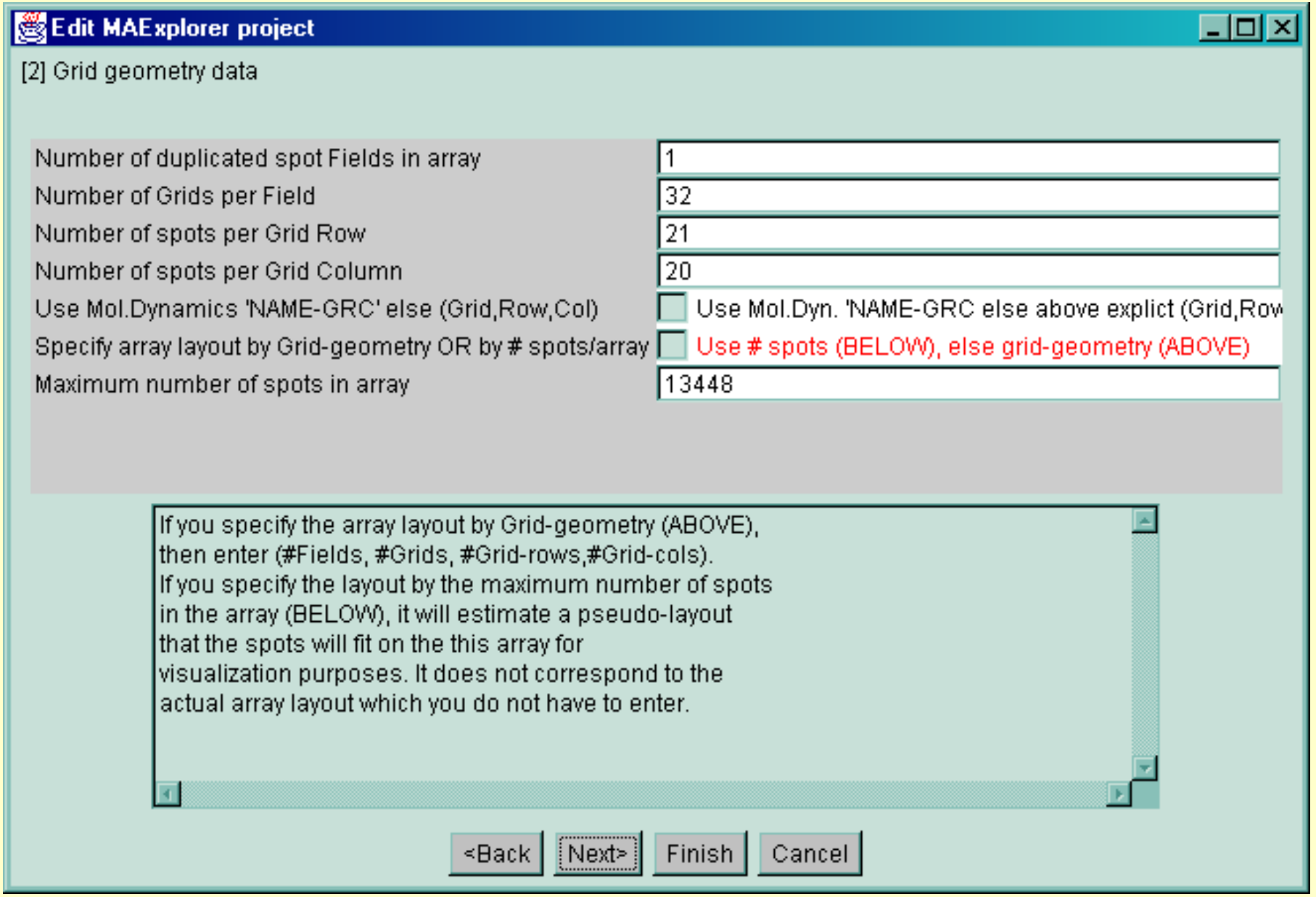
4. Continue Adding Input Files If Needed



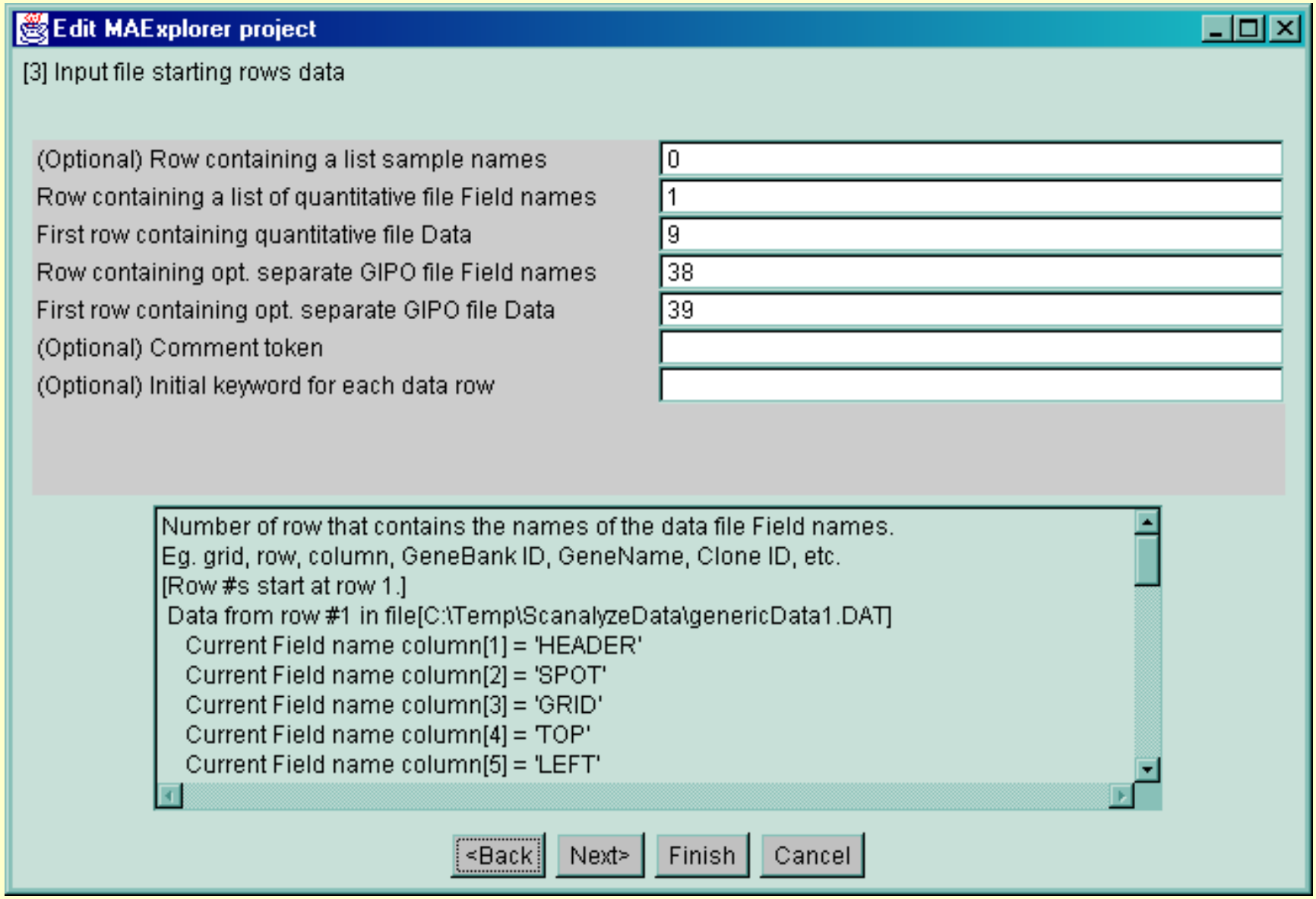
5.1 Edit Layout 'Wizard' Values for This Array



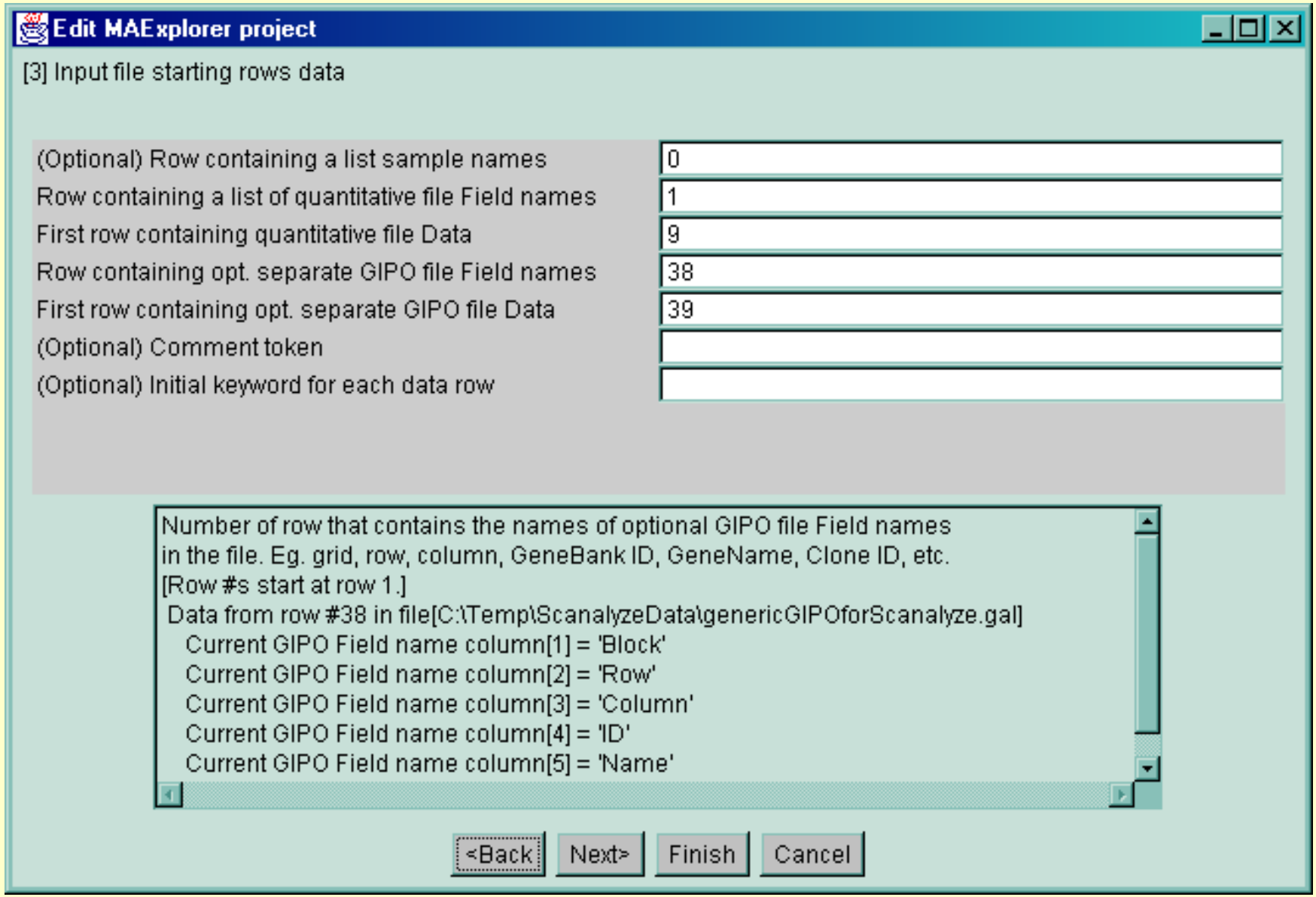
5.2 Edit Layout 'Wizard' - Grid Geometry. Enter (Grid, Rows/Grid, Columns/Grid) Values



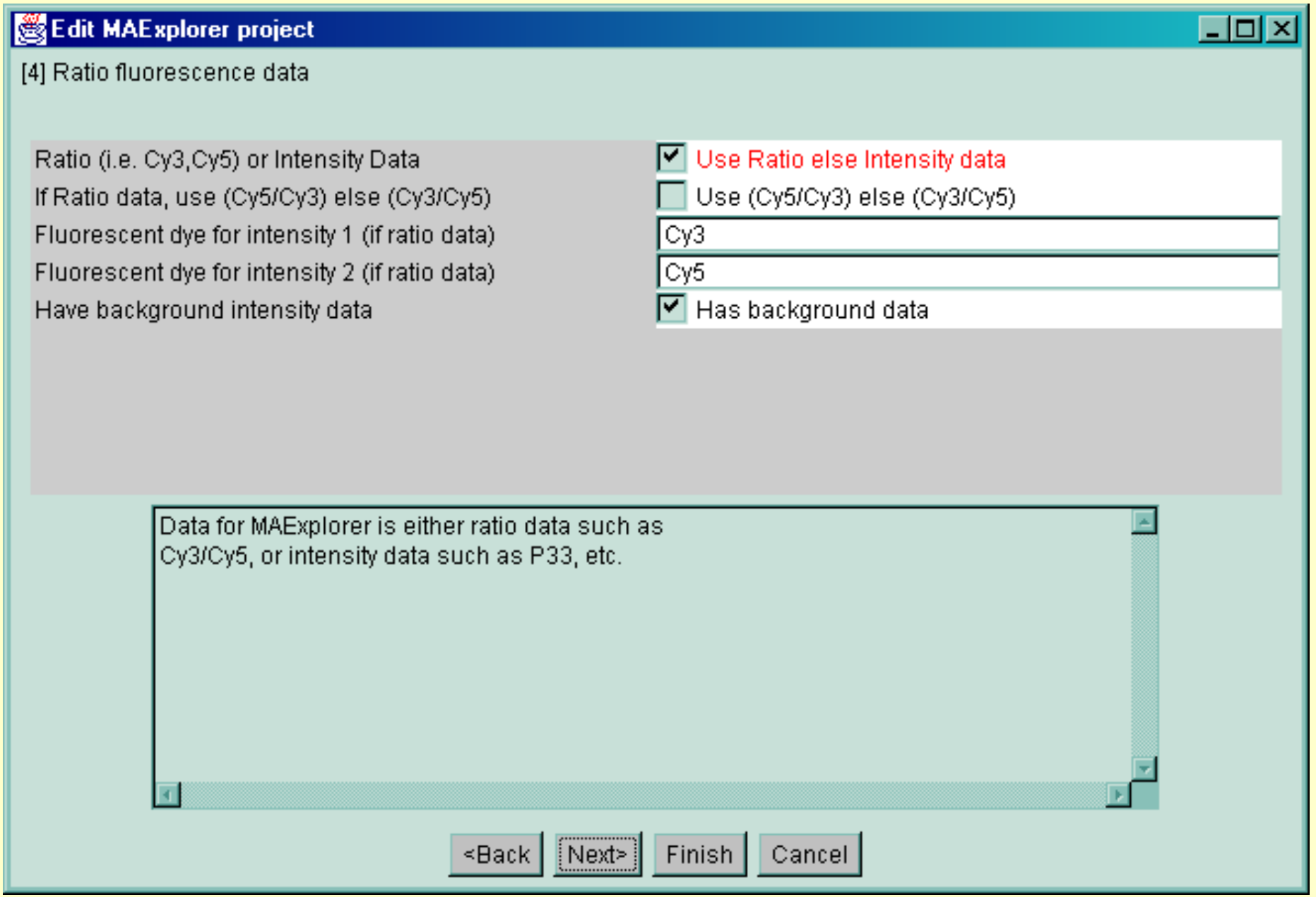
5.3 Edit Layout 'Wizard' Input Data File Row Values. Verify Row Where Field Names Defined



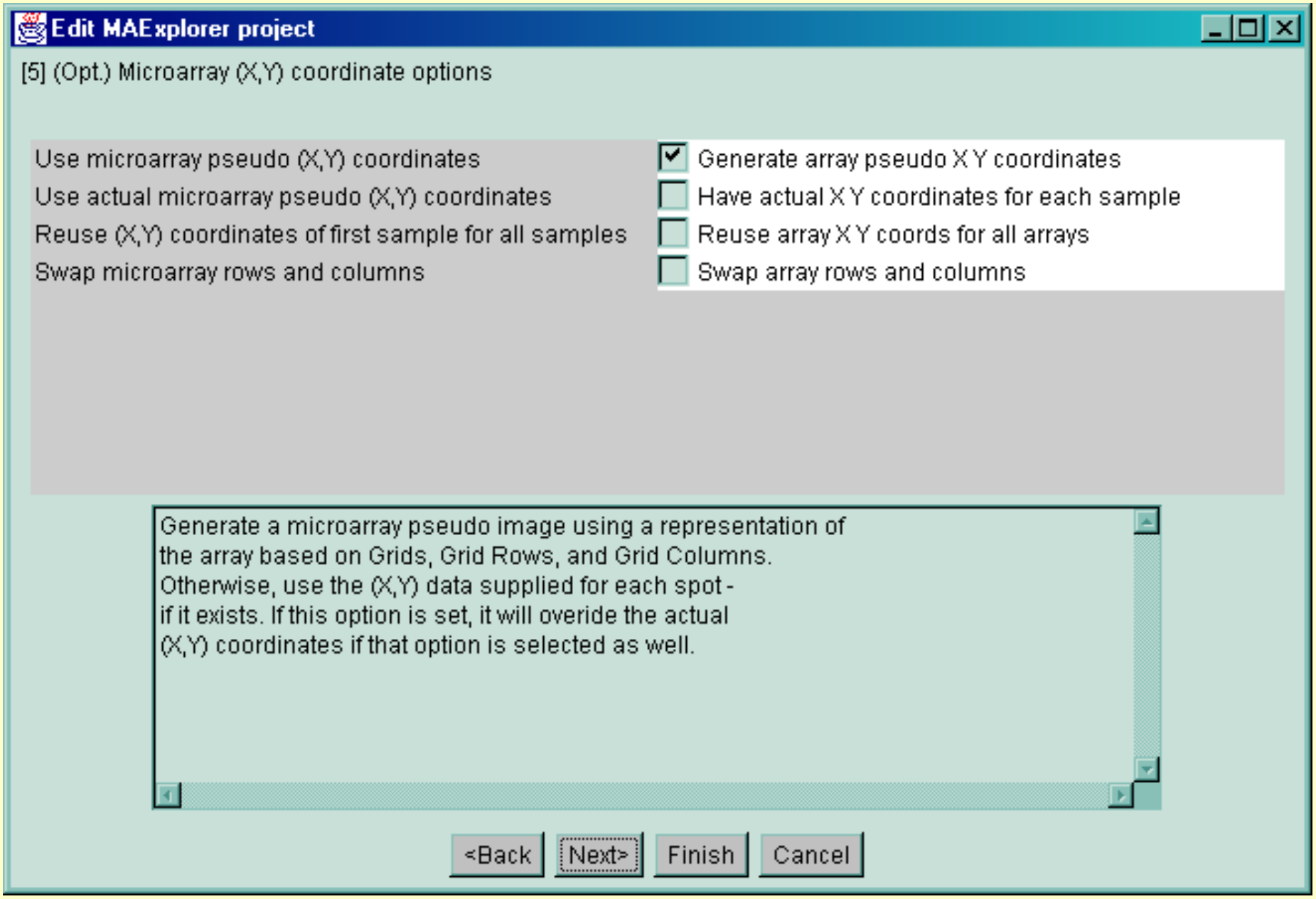
5.3.1 Edit Layout 'Wizard' Input GIPO File Row Values. Verify Row Where Field Names Defined



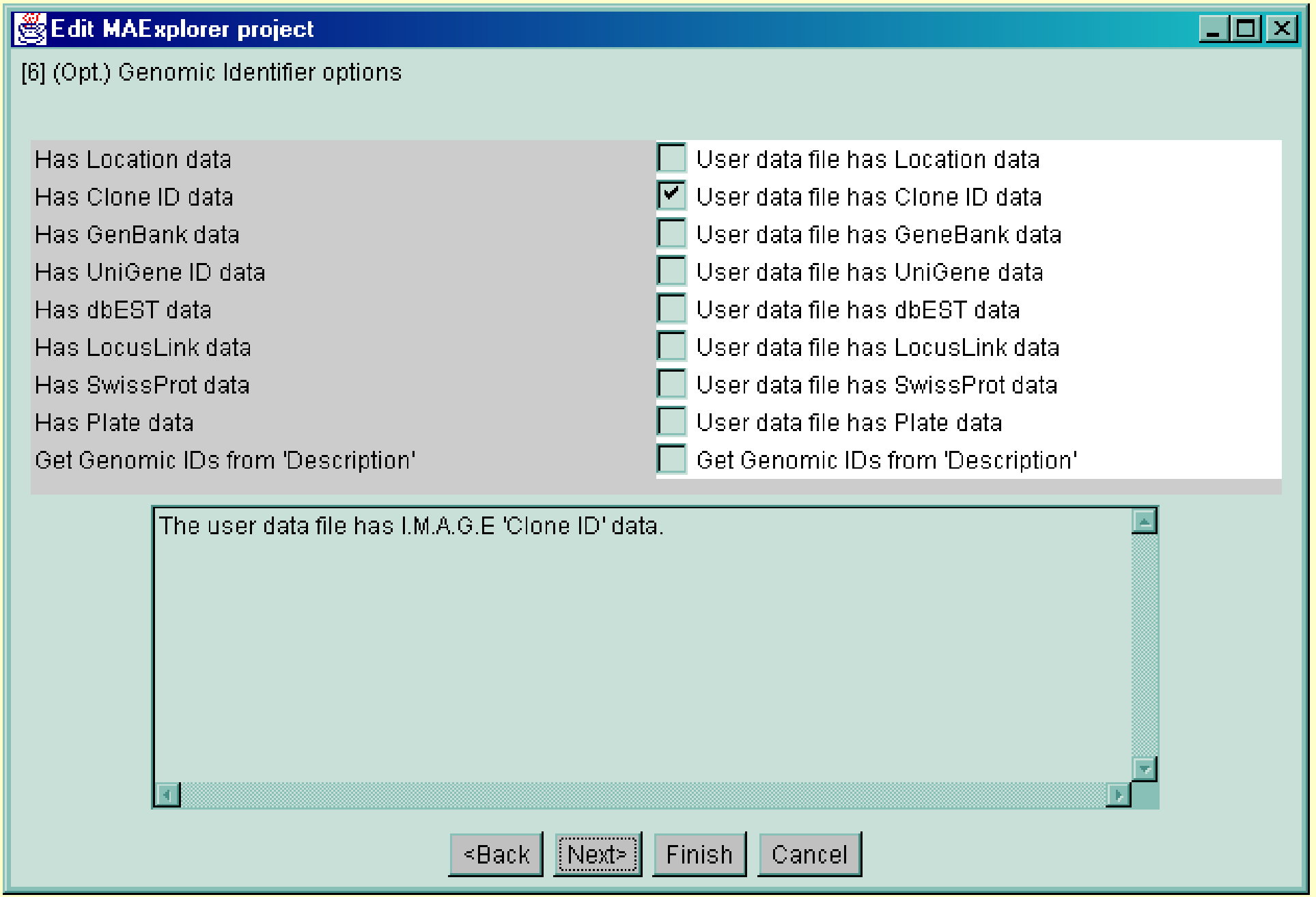
5.4 Edit Layout 'Wizard' Ratio or Intensity Values



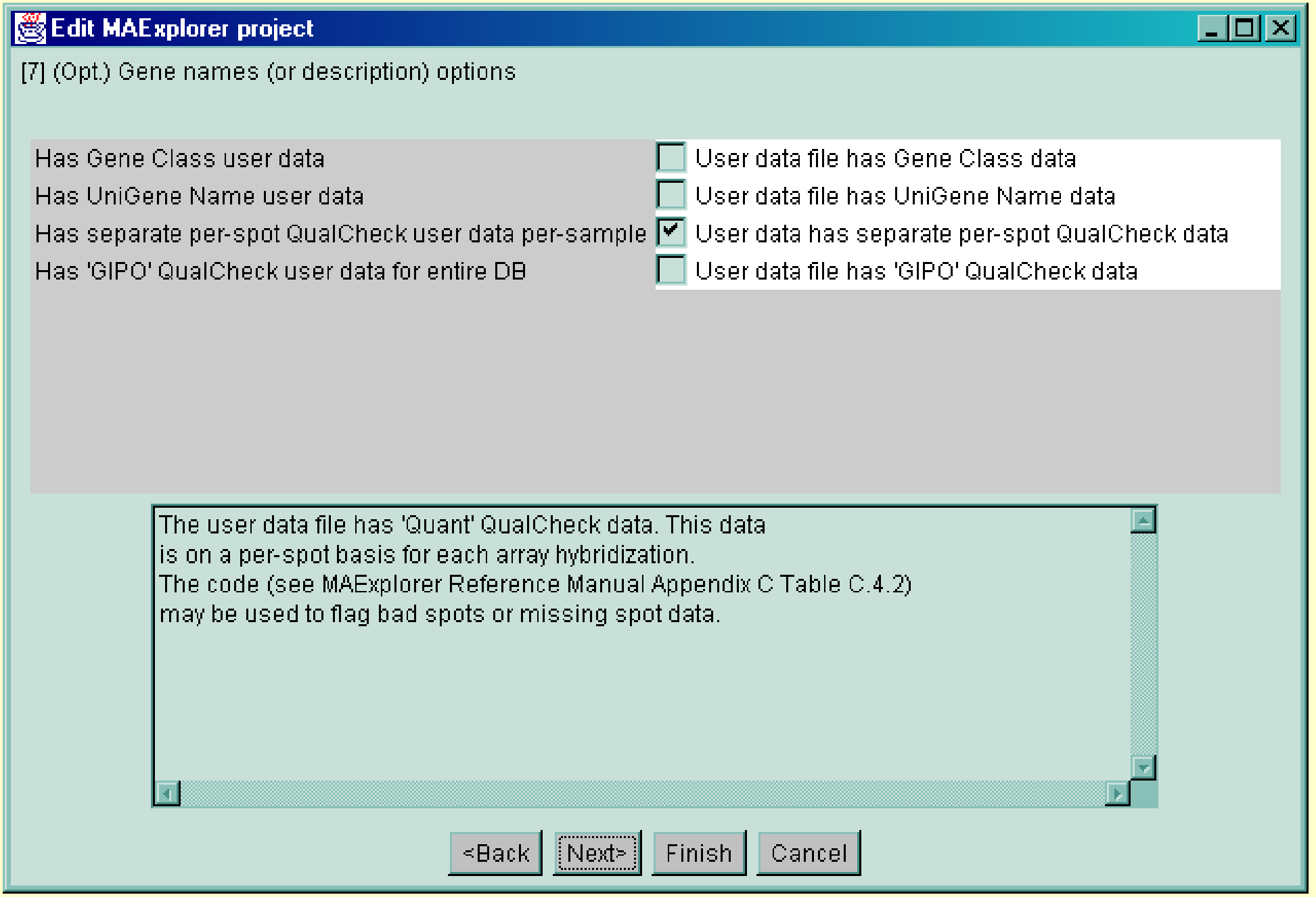
5.5 Edit Layout 'Wizard' optional (X,Y) Coordinate Values



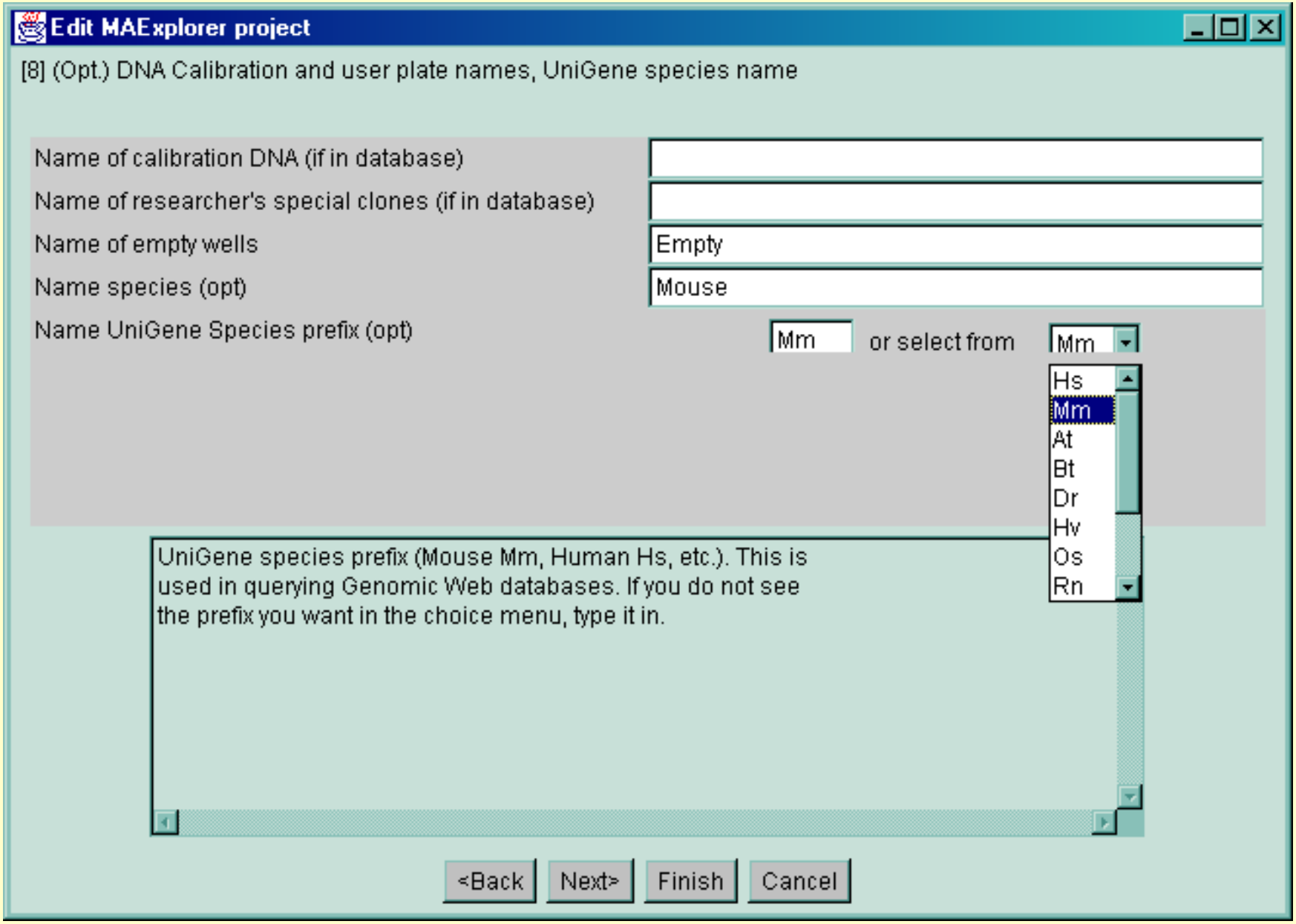
5.6 Edit Layout ‘Wizard’ Genomic ID Values



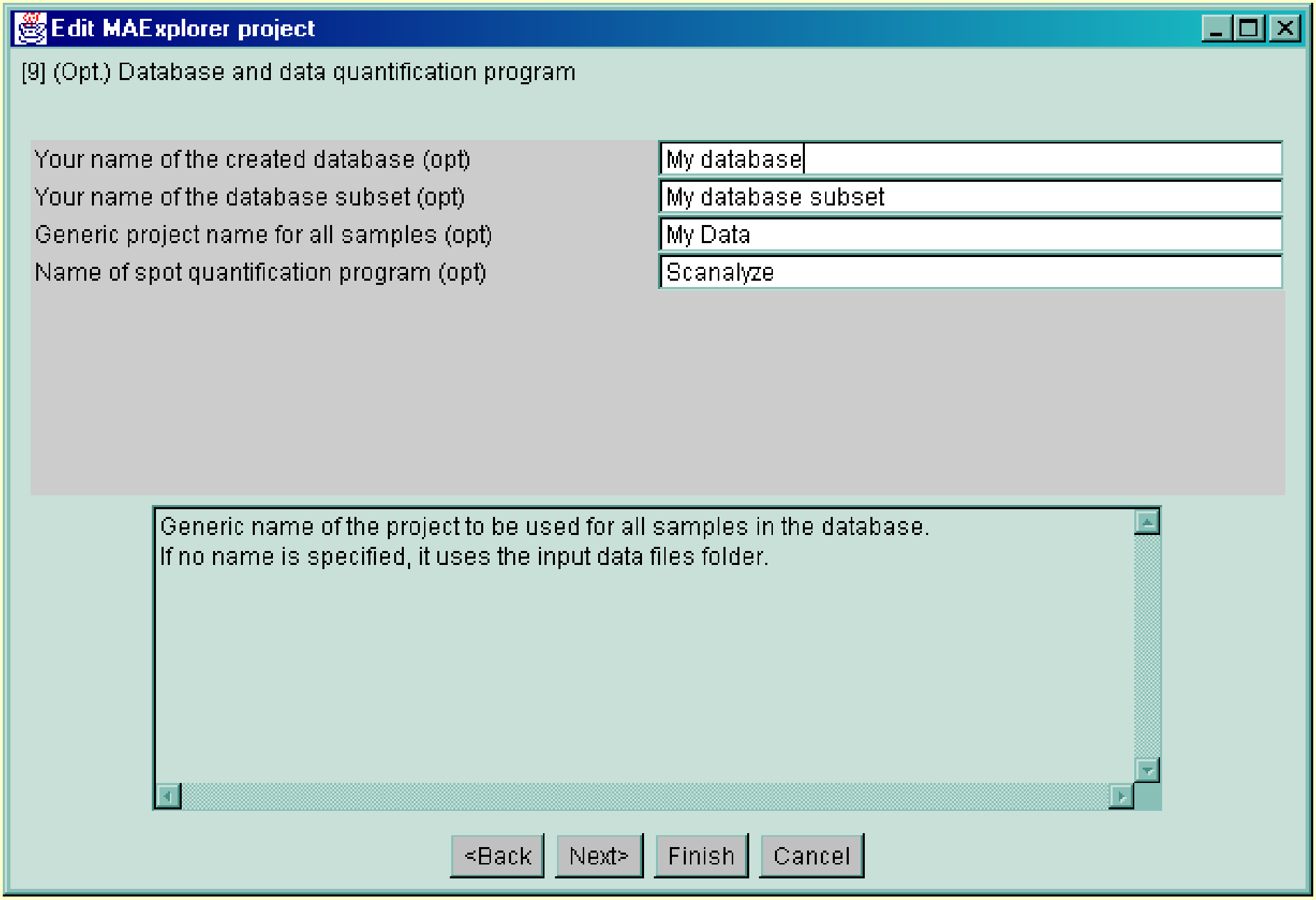
5.7 Edit Layout ‘Wizard’ Gene Names Description



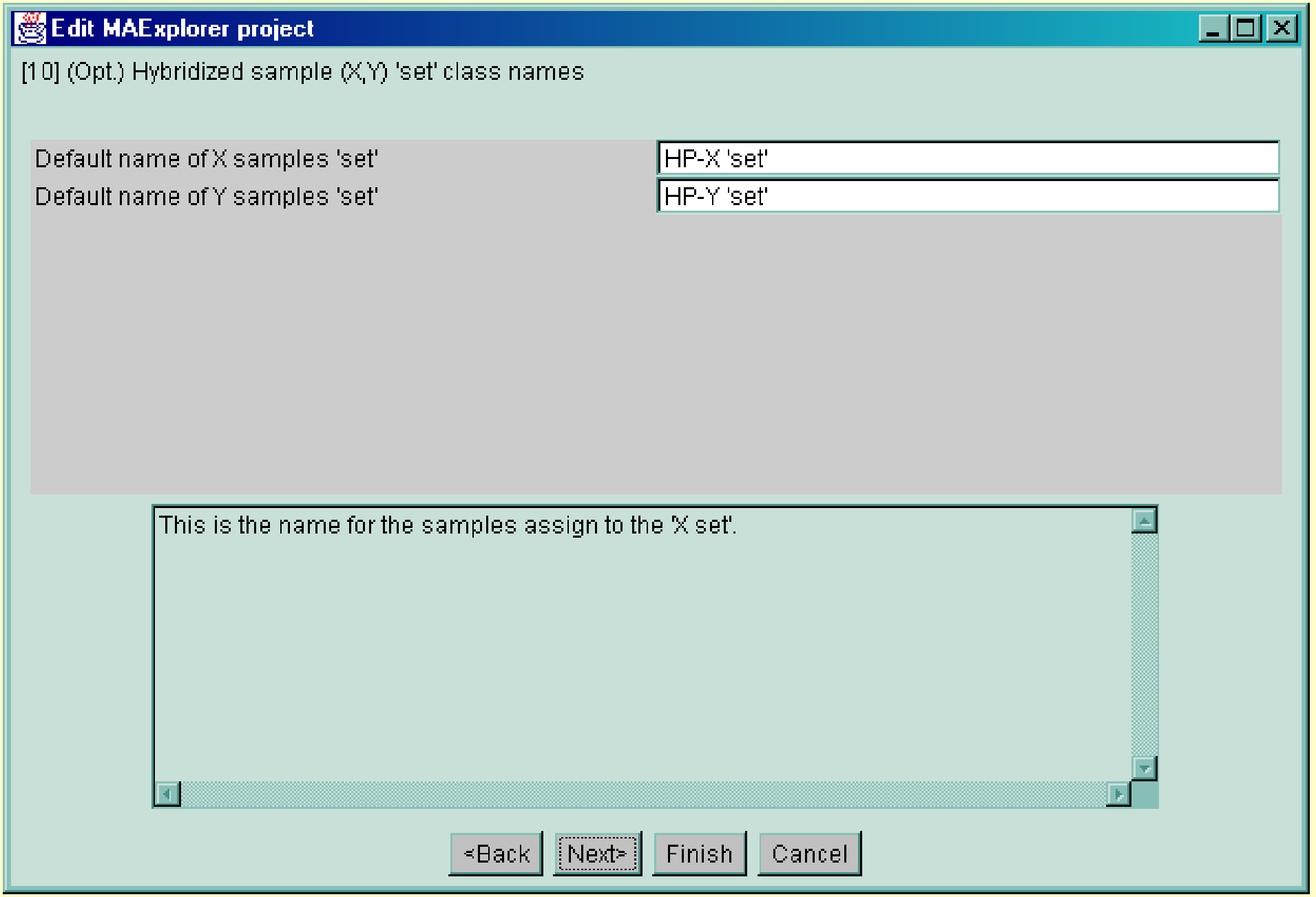
5.8 Edit Layout 'Wizard' Calibration Values. Define UniGene Species prefix



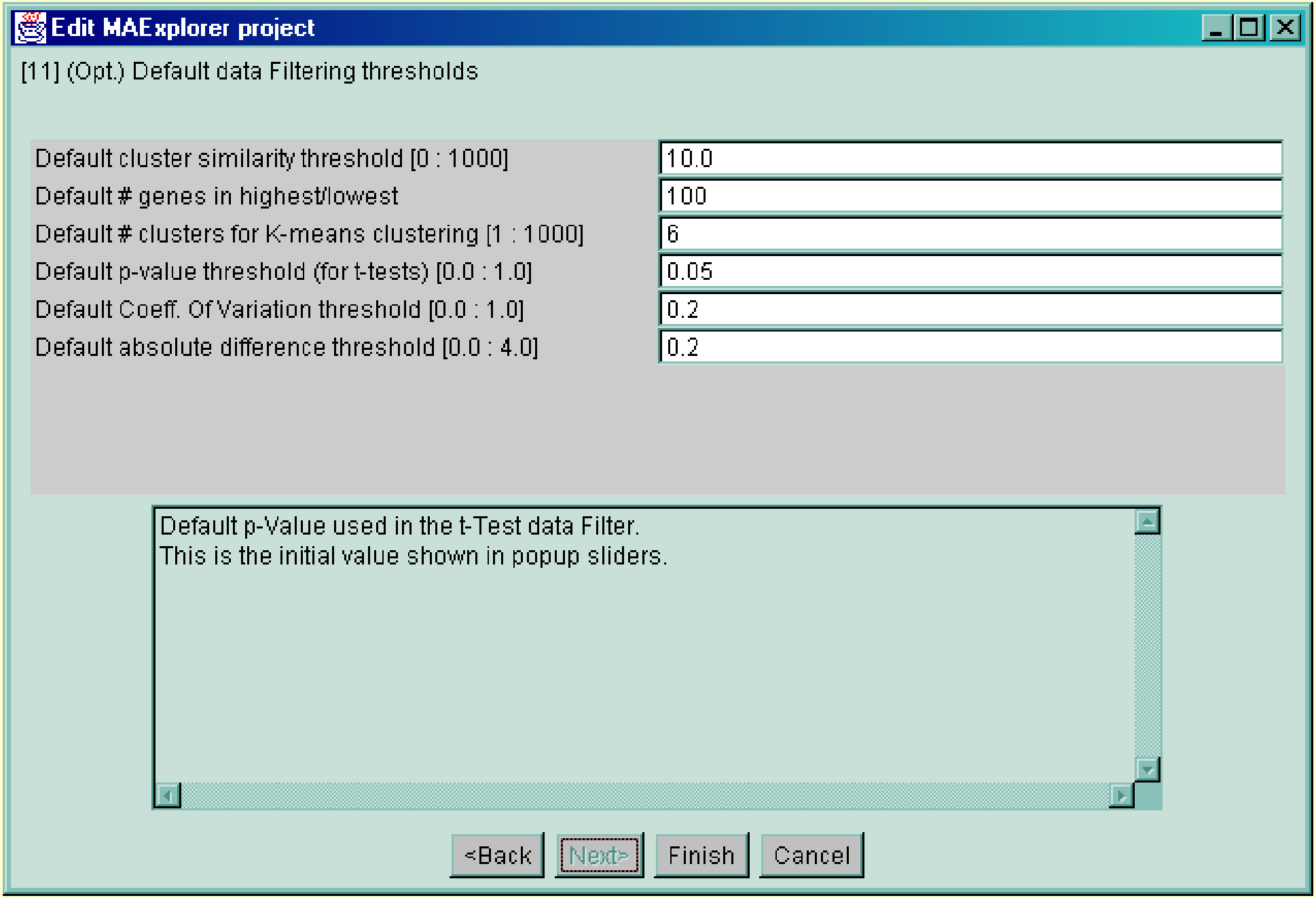
5.9 Edit Layout 'Wizard' Database Name Values. Define Optional Names for Database



5.10 Edit Layout ‘Wizard’ HP-X,-Y Class Names



5.11 Edit Layout 'Wizard' Default Thresholds

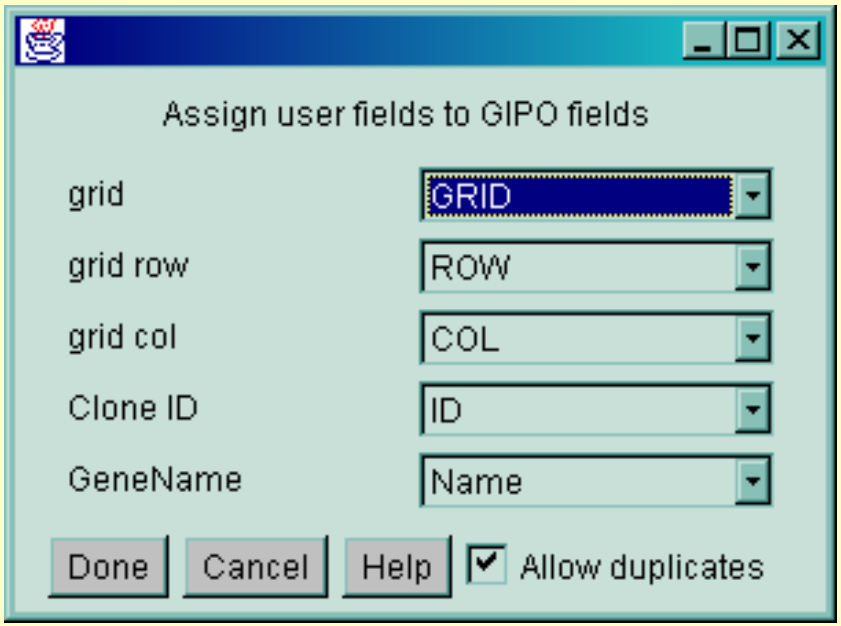


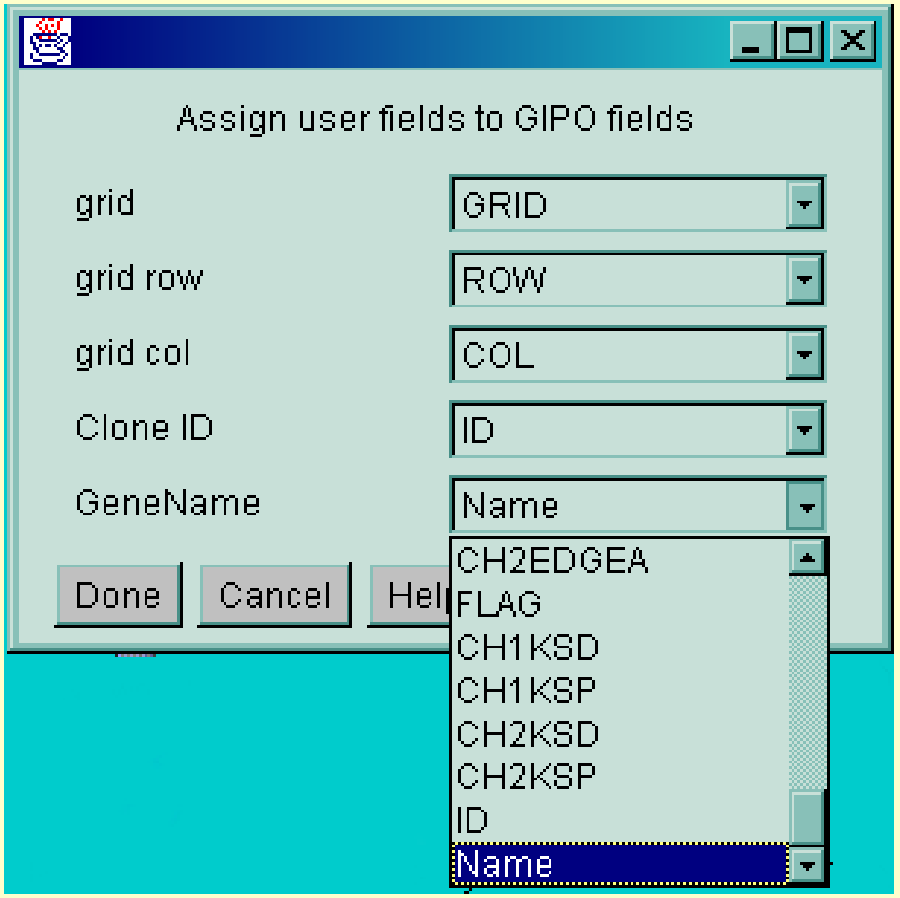
6. Other Options - Assigning User Data Fields to MAExplorer Fields

- 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.

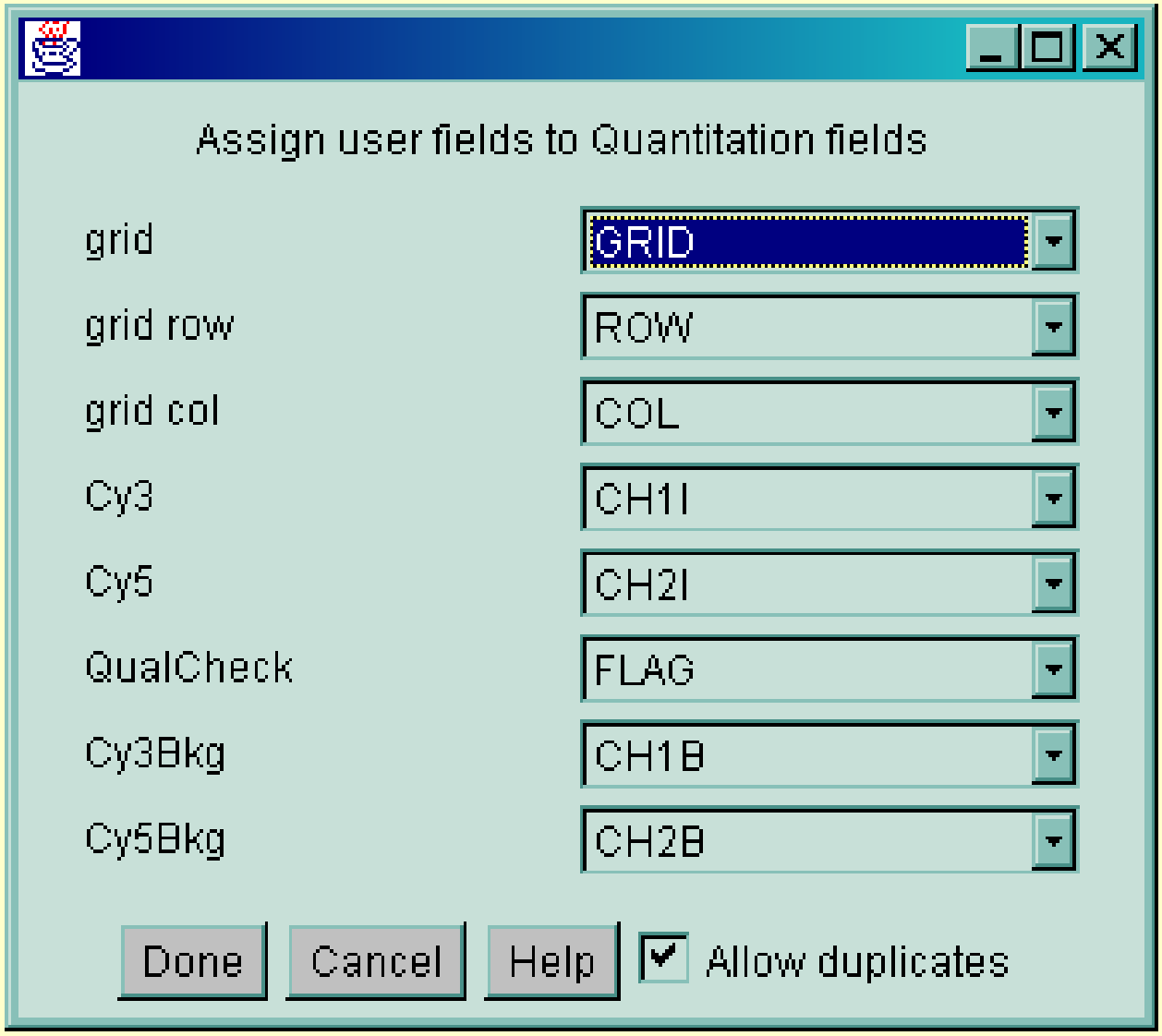
- Quant data - assigns names of quantified data in the user file to MAExplorer data (e.g. Cy3 intensity to RawIntensity1, Cy5 to RawIntensity2, etc).

6.1 “Assign user fields to GIPO fields”

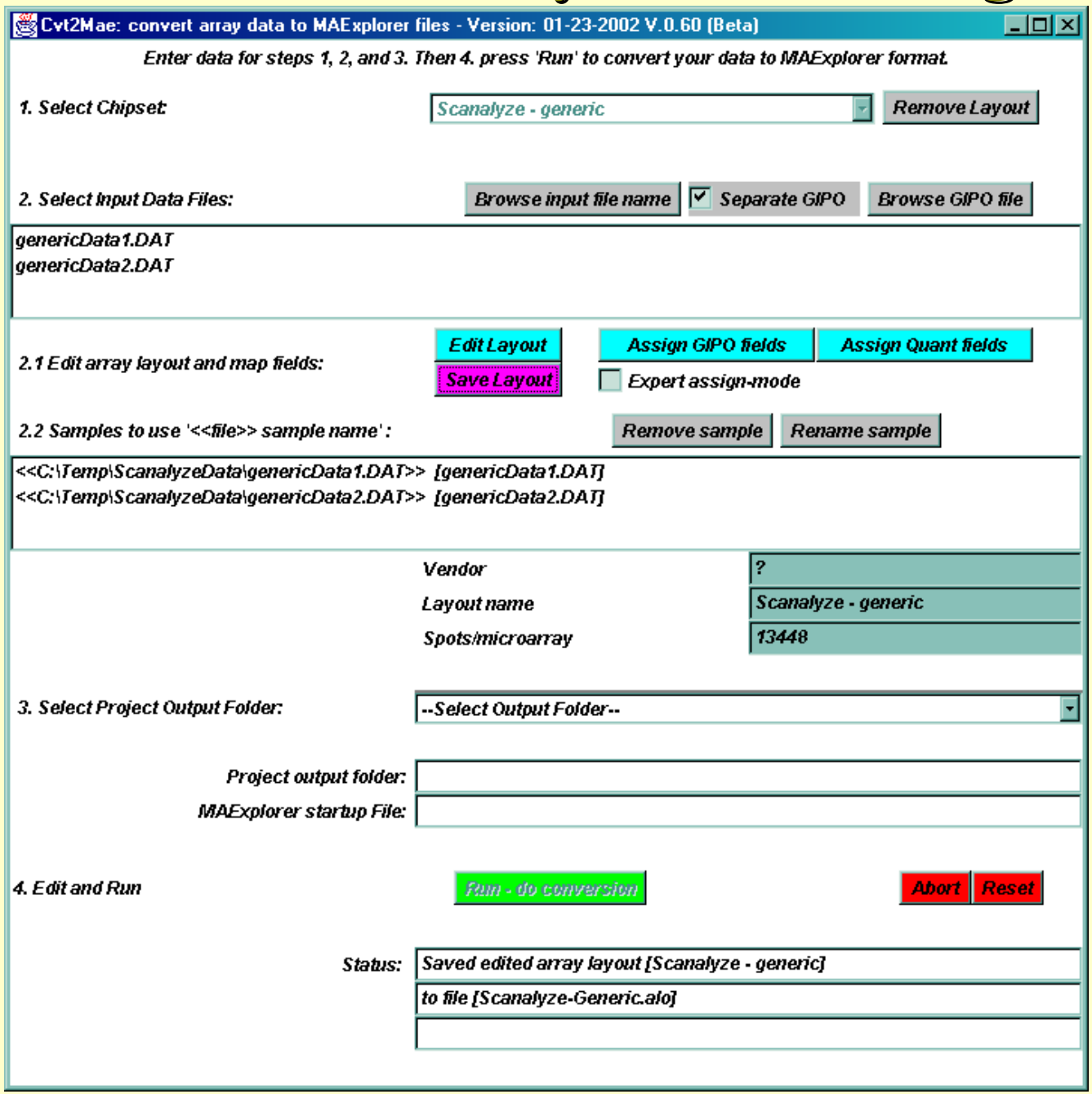




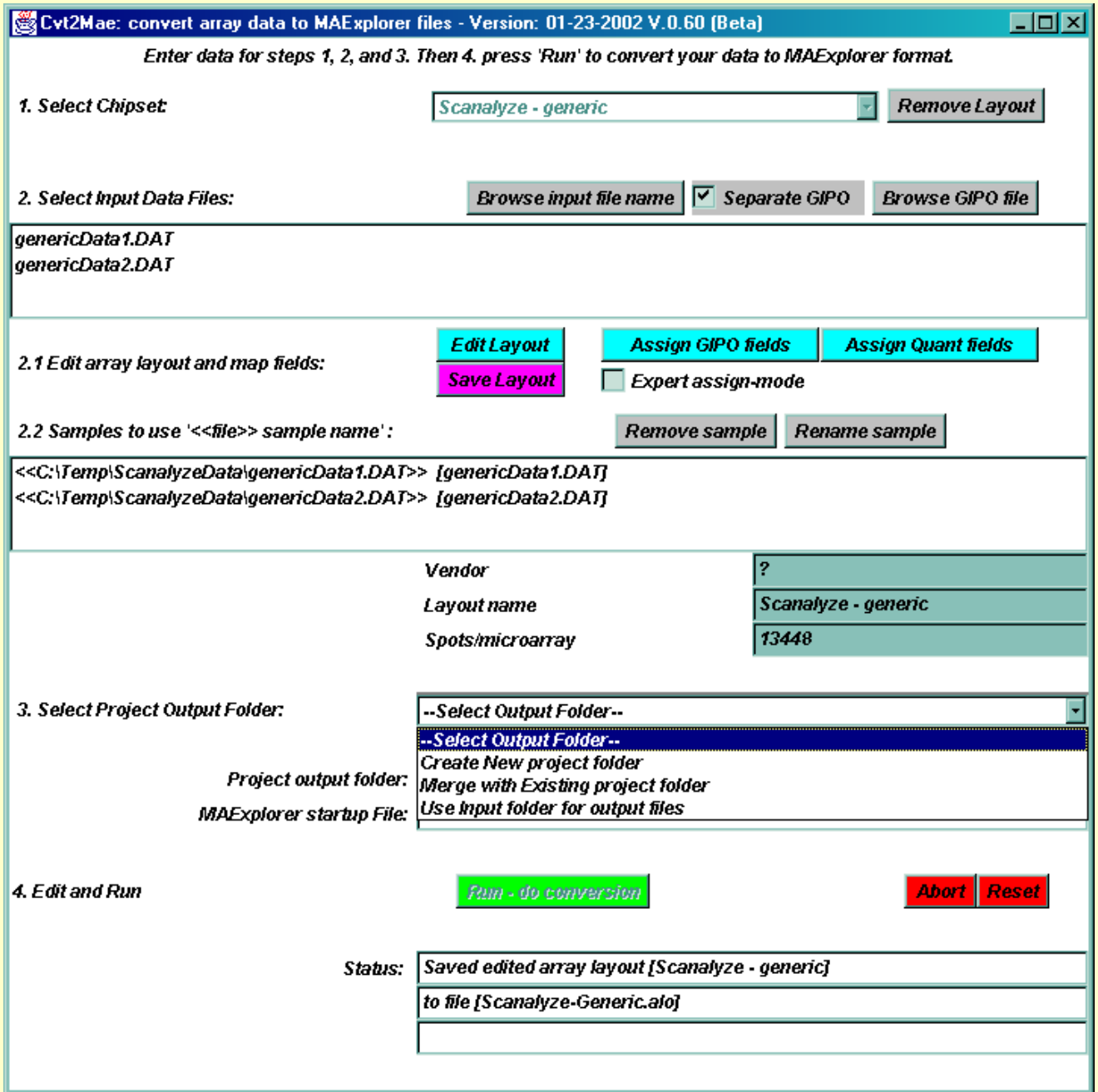
6.2 “Assign user fields to Quant fields”



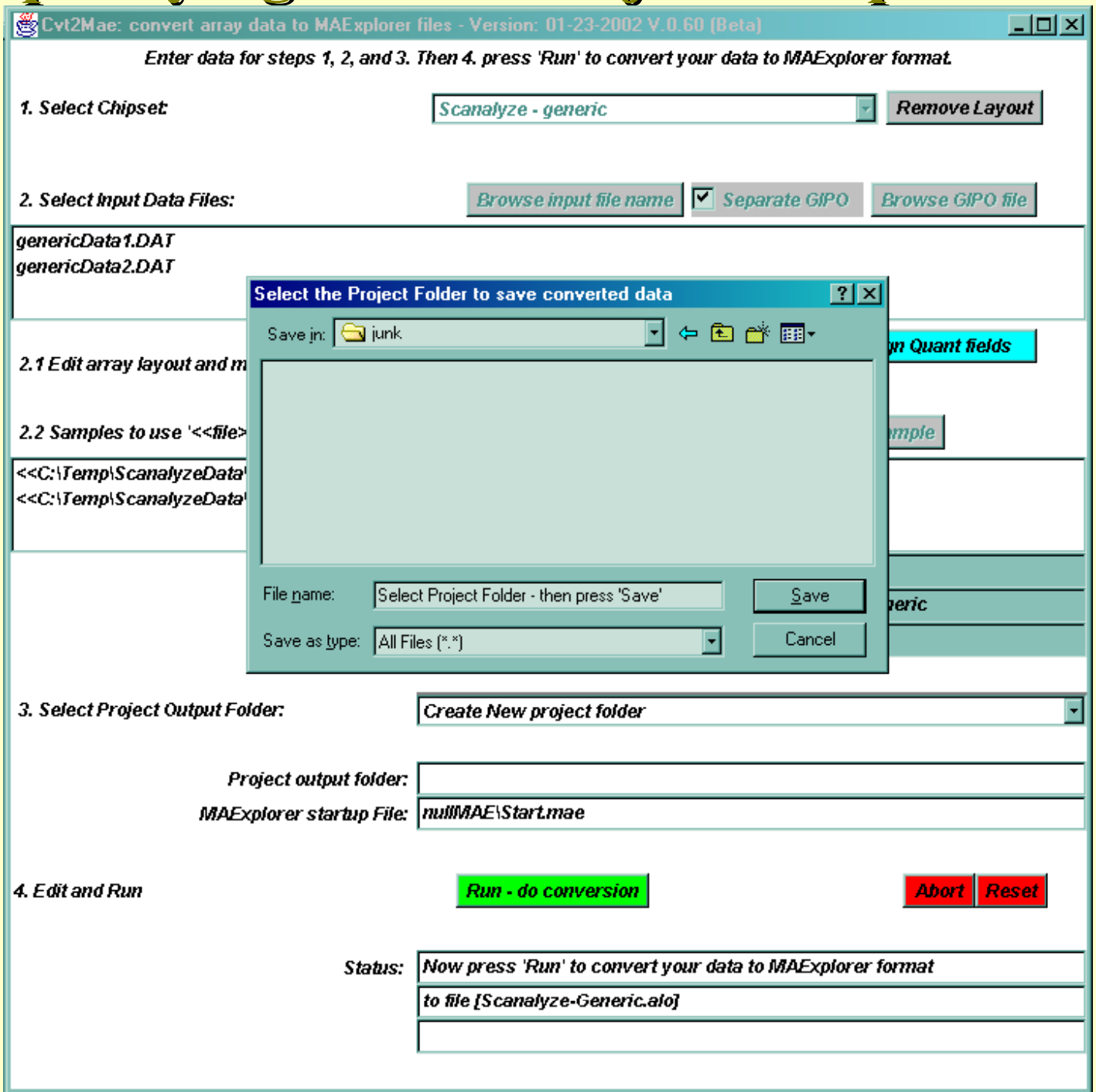
7. Optional "Save Layout" to Array Layout Database After Edit Layout and Assign fields



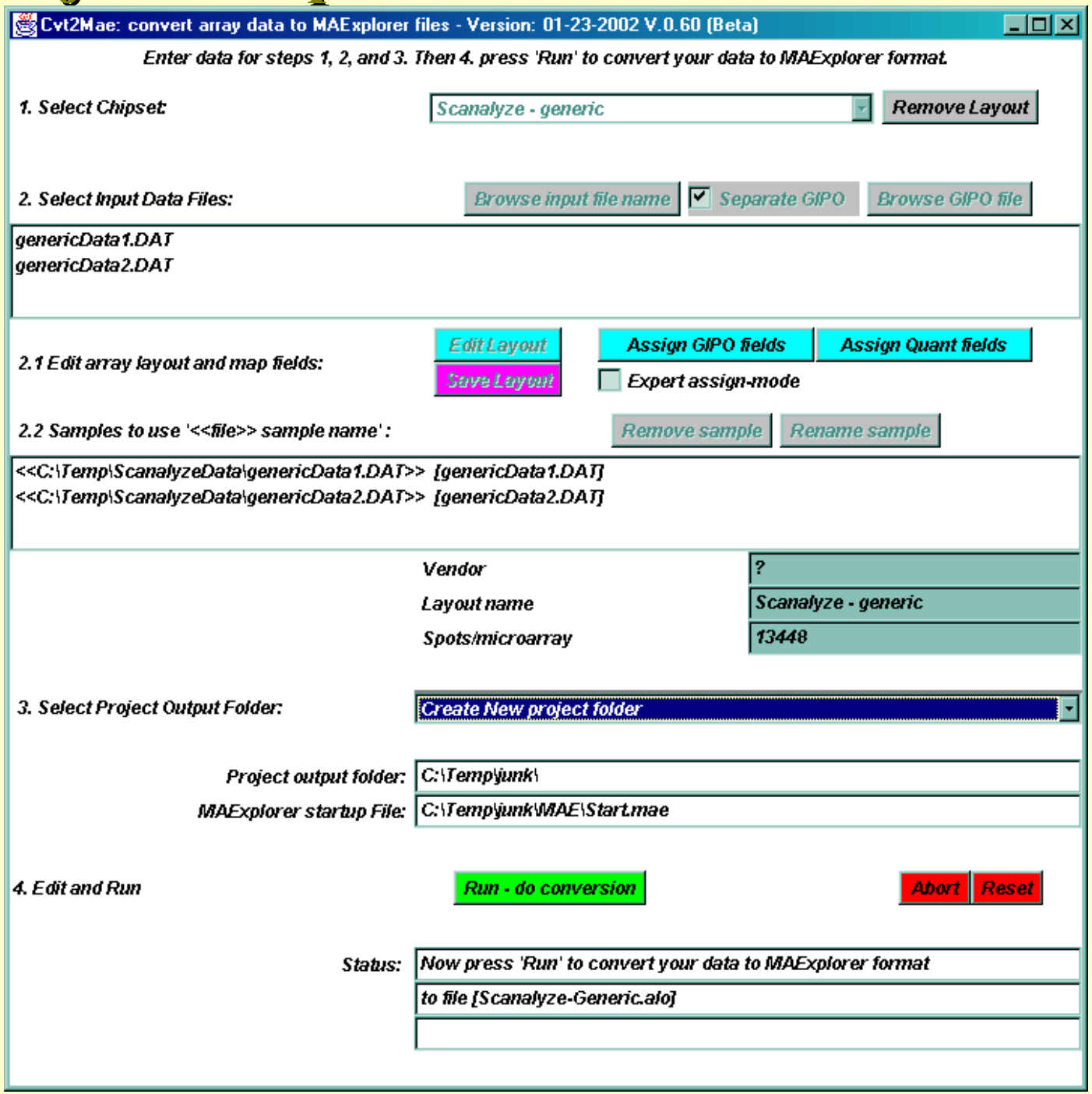
8. Specifying “Create new project folder” Option Where Generated Database Will Be Saved



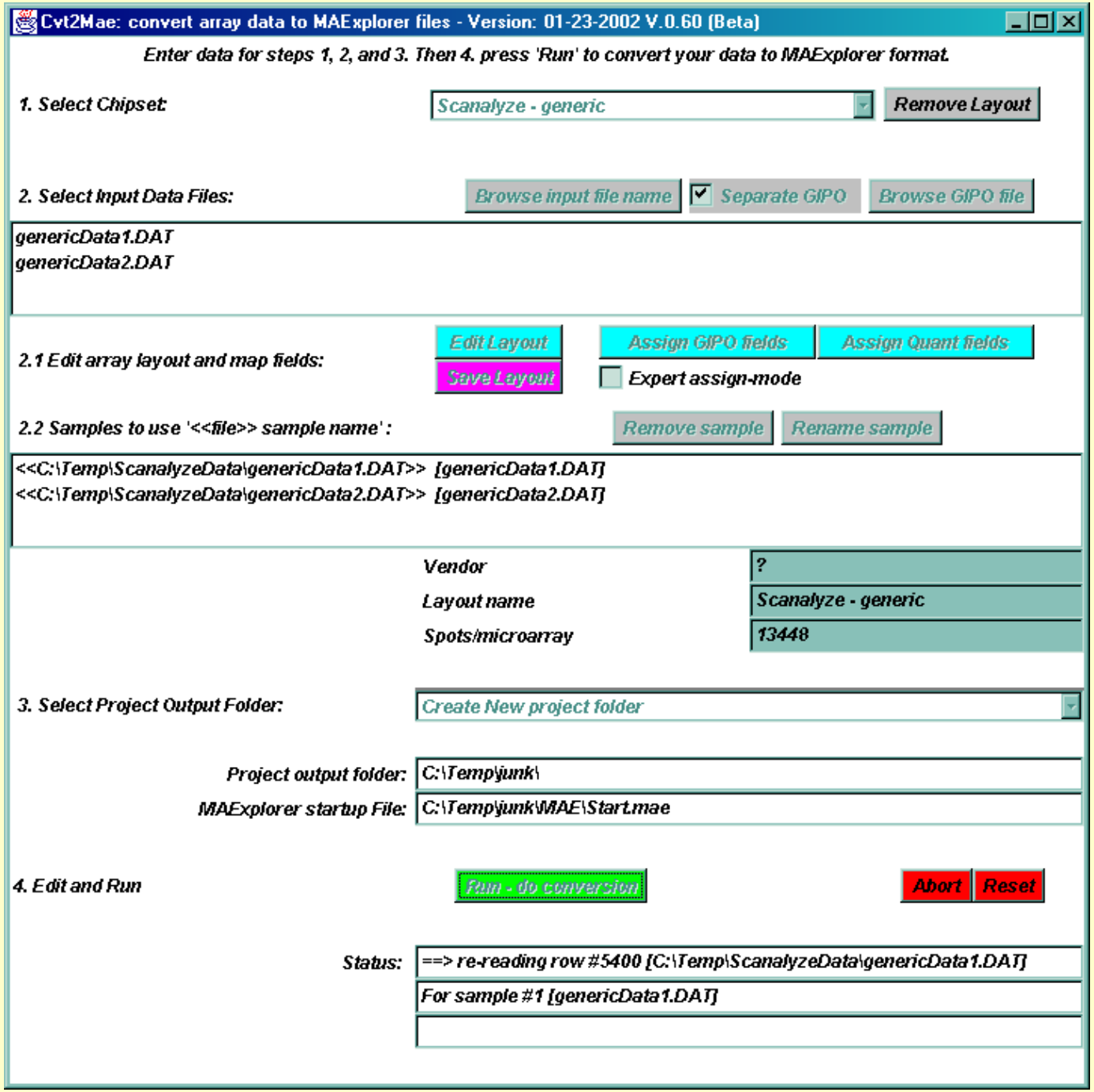
8.1 Specifying New "Project Output Folder"



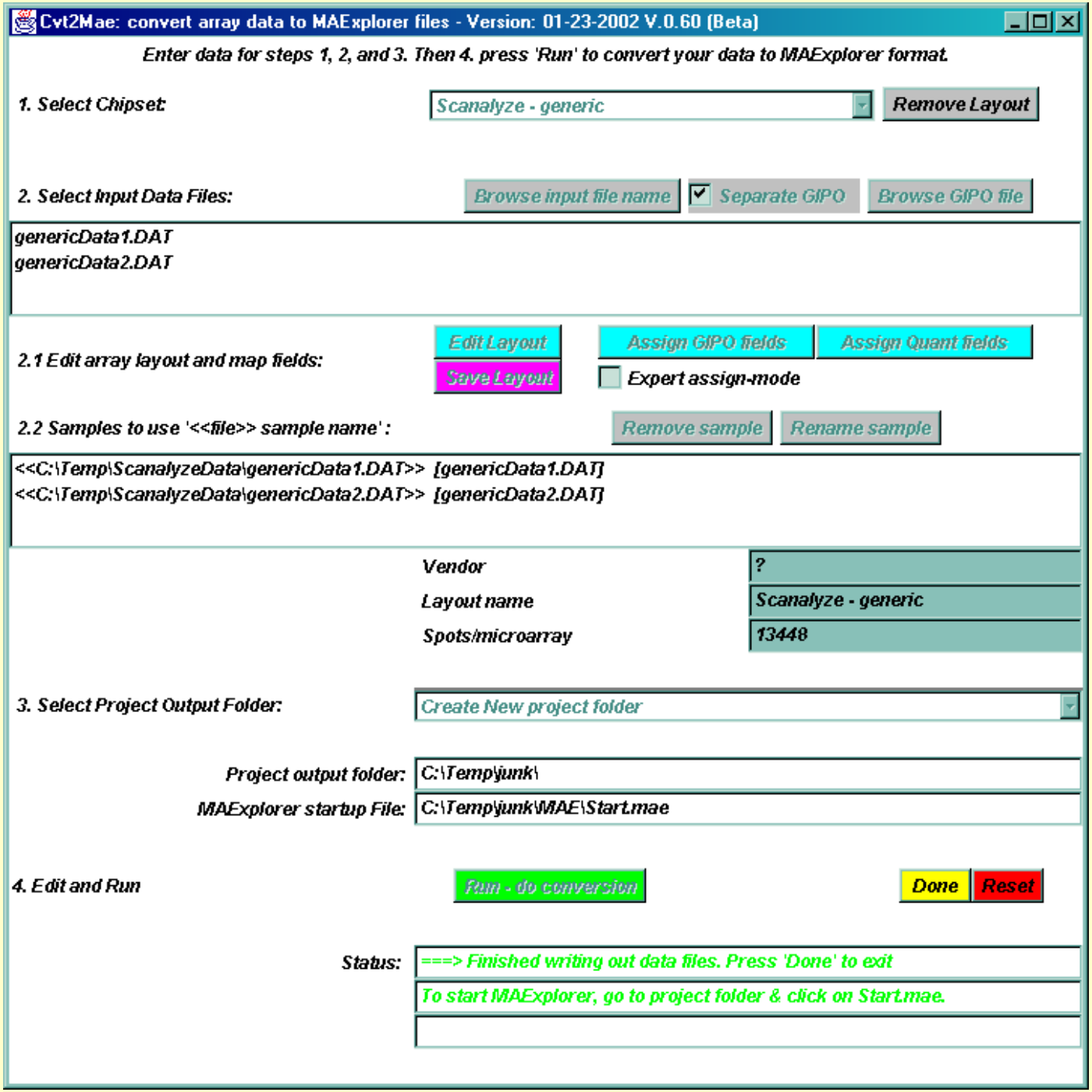
8.2 “Project Output Folder” & MAE startup file



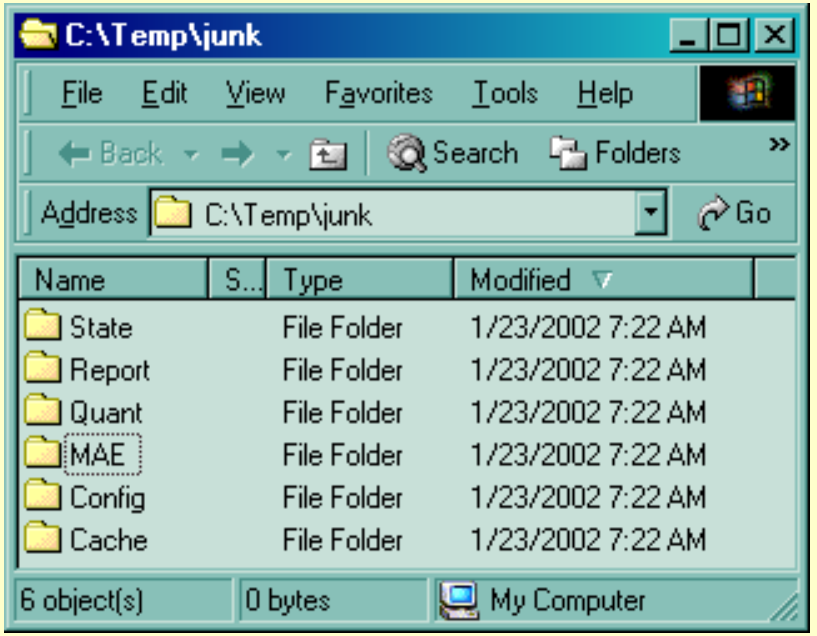
9. Conversion in Process After Pressing "RUN"

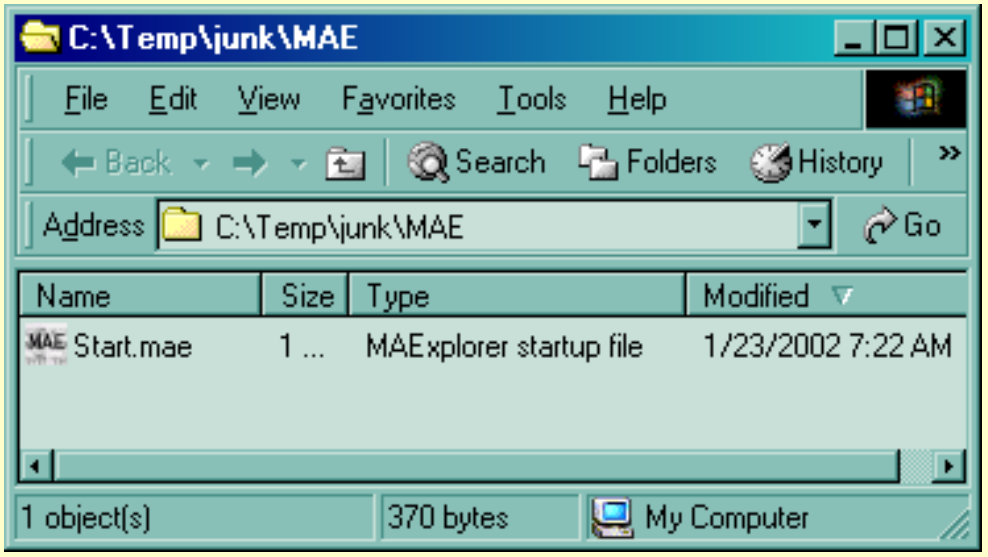


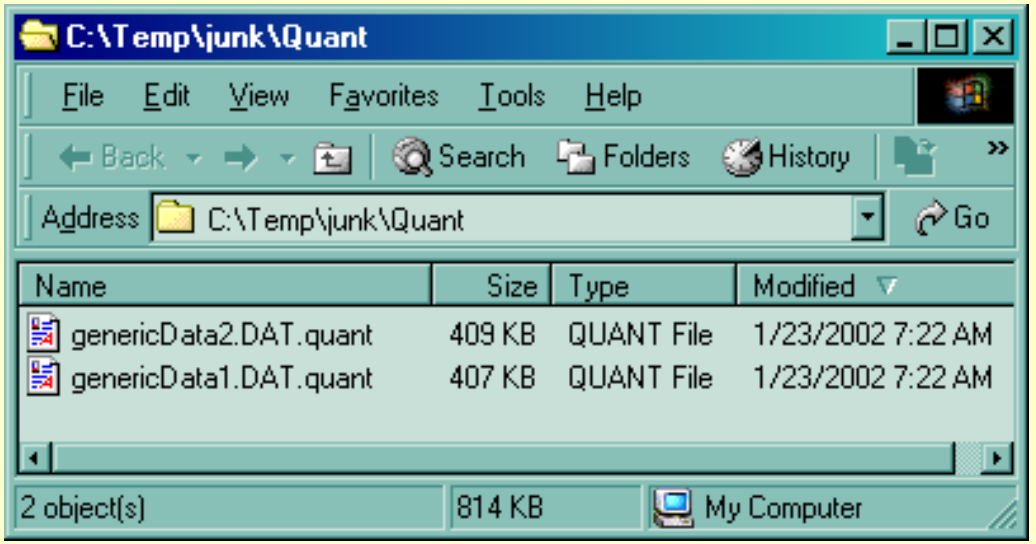
10. Notification that Conversion is Finished

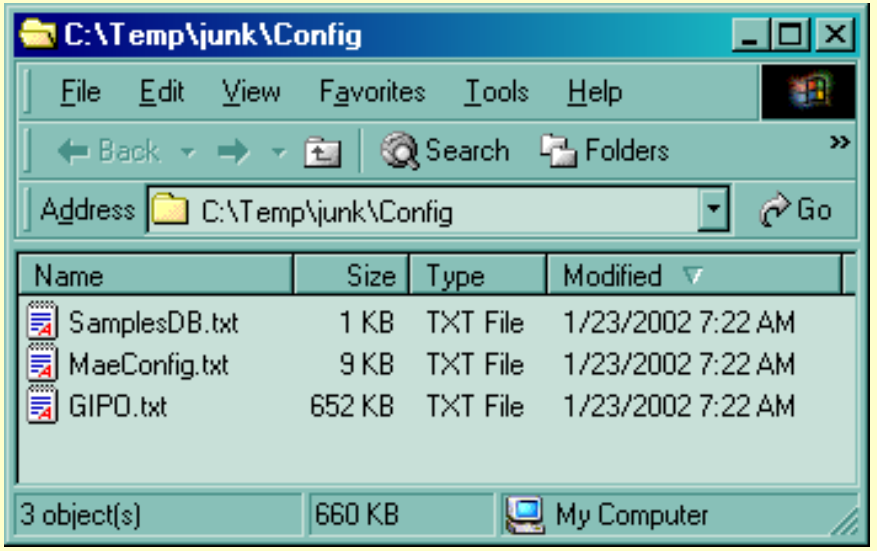


11. MAExplorer Data Created By Cvt2Mae









12. Running MAExplorer on the Converted Data