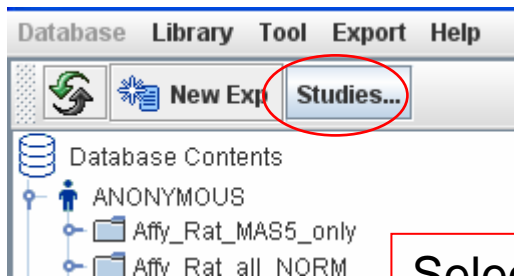


# Tutorial 13: Simple Tox Format



# SimpleTox for Toxicogenomics Study

- Used directly for data uploading for toxicogenomics experiment (non-clinical data and clinical data)  
<http://www.cdisc.org/models/send/v1.4/index.html>
- Rationale behind SimpleTox
  - To capture essential information related to microarray and toxicity study to attain sufficient information for cross-study analysis
  - To mimic the way of biologists managing/organizing data
  - To be compliant with MIAME and SEND
- Format
  - Excel spreadsheet format
  - Contains required and optional fields
  - Customization: Users be able to add new fields
  - Searchable



Click “Studies...” button to bring out the window below.

Select one study, the experiment that references the selected Study will be shown below

Search data by study and individual

STUDY_NAME	STUDY_ID	SUBJVAR	Allowed...	Class	ClassCode	Compound	Laboratory N...	Organ	Route	Sex	Species	Strain	Study Title	Study Type	Tissue
Hamner Mice Lung tumor F	311	Animal_ID	View Only	Non-lungtumor	LT   NLT	1,5-Naphthalene	Hamner	Lung	Diet   Gavag	F	Mouse	B6C3F1	Hamner Mice	Repeat Dose	Lung
Simple ToxFormat Demo	317	Animal_ID	View Only	Liver Toxicity	LT	Cd	Cedars_Sinai	Cell Culture	M	Rat	Fischer 3	Simple ToxFo	single Dose		

Exps ( 1 ) Hybs ( 59 )

Experiments Referencing Selected Studies Above

EXPID *	EXPTITLE *	EXPDATE	ARRAYPLATFORM	EXPTYPE	KEYWORD	DESCRIPTION	OWNERID	EXPERIMENTER	INSTITUTE	DIVISION	COMMENTS	PHENOTYPE
1270	Simple_ToxFormat_						ANONYMO					

Select the study named “Simple\_ToxFormat”, then click “View Observation”.

Highlight the exp and click “Select Exp Dataset” button will select all the data (or just raw/normalized data) in the data panel for data analysis purpose (see the screen shot in next slide)

The screenshot shows a software interface with a 'Studies' window. At the top, there is a 'View Observations' button and a 'Search Studies' section with a search box and checkboxes for 'case sensitive' and 'search individual observations'. Below this is a table of studies:

	STUDY_NAME	STUDY_ID	SUBJVAR	Allowed Access	Class	ClassCode	
26	Hamner Mice Lung tumor F	311	Animal_ID	View & Modify	Non-lungtumorigen   lung tumorigen	LT   NLT	1,5-N
27	Simple ToxFormat Demo	317	Animal_ID	View Only	Liver Toxicity	LT	Cd

Below the studies table, there are tabs for 'Exps ( 1 )' and 'Hybs ( 59 )'. Under the 'Exps ( 1 )' tab, there is a section titled 'Experiments Referencing Selected Studies Above'. This section contains a 'Select Exp Datasets' button (circled in red) and a dropdown menu for 'of type' (also circled in red) with options 'any', 'raw', and 'normalized'. Below this is a table of experiments:

	EXPID *	EXPTITLE *	ARRAYPLATFORM	EXPTYPE	KEYWORD	DESCRIPTION	OWNERID	EXPERIMENTER	INSTITU
1	1270	Simple_ToFormat_get					ANONYMO		

You can select the study named “Simple\_ToFormat”, then click “View Observation” to view the detail of the observation including sample info and toxicological info. See the observation viewer in slide 6.

# Data analysis

- View data set(s) as wide spreadsheet - datasets side by side
- Export
- Convert affy cel files to probe sets
- Mixed scatterplot
- Virtual array images for data
- Actual array images for data <<Dev. Only>>
- Rank intensity plots for data
- Bar Chart
- Create gene list by data filtering...
- Analysis**
- Quality Control
- Normalize...
- Duplicate data sets
- Copy data sets for pasting elsewhere
- Studies
- Tree options...

STUDY_NAME	STUDY_ID	SUBJVAR	Allowed Access
Lung tumor	311	Animal_ID	View & Modify
Format Demo	317	Animal_ID	View Only

Selected Studies Above

of type raw

- T-Test/ANOVA
- SAM-Test
- R-Interface
- Correlation Matrix
- Correlate Study Data vs. Gene Expression Data
- T-Test with custom data options

Select Dataset Group Assignments for T-Test / ANOVA / Pairwise Tests

### Assign Data Sets Into Groups

View Obs

Hybridization	SampleName	Subject	BioRepl	TechRepl	Compound	Control	TreatmentGroup	Dose
2	D2_T24_B_a 42	D2_T24_B	D2_T24_B_B	a	Cd	N		2
2	D2_T24_B_b 43	D2_T24_B	D2_T24_B_B	b	Cd	N		2
2	D2_T24_C_a 44	D2_T24_C	D2_T24_C_C	a	Cd	N		2
2	D2_T24_C_b 45	D2_T24_C	D2_T24_C_C	b	Cd	N		2
2	D2_T24_D_a 46	D2_T24_D	D2_T24_D_D	a	Cd	N		2
2	D2_T24_D_b 47	D2_T24_D	D2_T24_D_D	b	Cd	N		2
1	D2_T3_B_a 48	D2_T3_B	D2_T3_B_B	a	Cd	N		2
1	D2_T3_B_b 49	D2_T3_B	D2_T3_B_B	b	Cd	N		2
1	D2_T3_C_a 50	D2_T3_C	D2_T3_C_C	a	Cd	N		2
1	D2_T3_C_b 51	D2_T3_C	D2_T3_C_C	b	Cd	N		2

2 groups, sizes = [4, 6]

T-Test fold changes are computed as  $grp\ 1/grp\ 2$ , so "up" regulation will mean  $grp\ 1 > grp\ 2$  in any further analysis.

Next >

Group data according to sample info and toxicological info.

Obs Viewer

File Observations Related-Obs Analysis

Search  case sensitive

Domain: **inst - NCTR Simple Tox Data**

Filter->	Compound	Compound Class	Is Control Y/N	Treatment	Unit for Dose	Species	Strain
1		Liver Toxicity	Y	C	0	ug/Kg	Rat
2		Liver Toxicity	Y	C	0	ug/Kg	Rat
3	Cd	Liver Toxicity	N		2	ug/Kg	Rat
4		Liver Toxicity	Y	C	0	ug/Kg	Rat
5	Cd	Liver Toxicity	N		2	ug/Kg	Rat
6		Liver Toxicity	Y	C	0	ug/Kg	Rat
7		Liver Toxicity	Y	C	0	ug/Kg	Rat
8		Liver Toxicity	Y	C	0	ug/Kg	Rat
9	Cd	Liver Toxicity	N		2	ug/Kg	Rat
10	Cd	Liver Toxicity	N		2	ug/Kg	Rat
11	Cd	Liver Toxicity	N		2	ug/Kg	Rat
12	Cd	Liver Toxicity	N		2	ug/Kg	Rat
13	Cd	Liver Toxicity	N		2	ug/Kg	Rat
14	Cd	Liver Toxicity	N		2	ug/Kg	Rat
15	Cd	Liver Toxicity	N		2	ug/Kg	Rat
16	Cd	Liver Toxicity	N		2	ug/Kg	Rat
17	Cd	Liver Toxicity	N		2	ug/Kg	Rat
18		Liver Toxicity	Y	C	0	ug/Kg	Rat
19	Cd	Liver Toxicity	N		2	ug/Kg	Rat

Switch to study summary domain

Obs Viewer

File Observations Related-Obs Analysis

Search  case sensitive

Domain: **SS - Study Summary**

Filter->	Parameter Short Name	Parameter Name	Parameter Value
1	Study Title	Study Title	Simple ToxFormat Demo
2	Laboratory Name	Laboratory Name	Cedars_Sinai Medical Center
3	Study Type	Study Type	single Dose
4	Species	Species	Rat
5	Sex	Sex	M
6	Strain	Strain	Fischer 344
7	Class	Class	Liver Toxicity
8	Route	Route	Cell Culture
9	Compound	Compound	Cd
10	ClassCode	ClassCode	LT

Obs Viewer

File Observations Related-Obs Analysis

Column Naming  Variable Labels

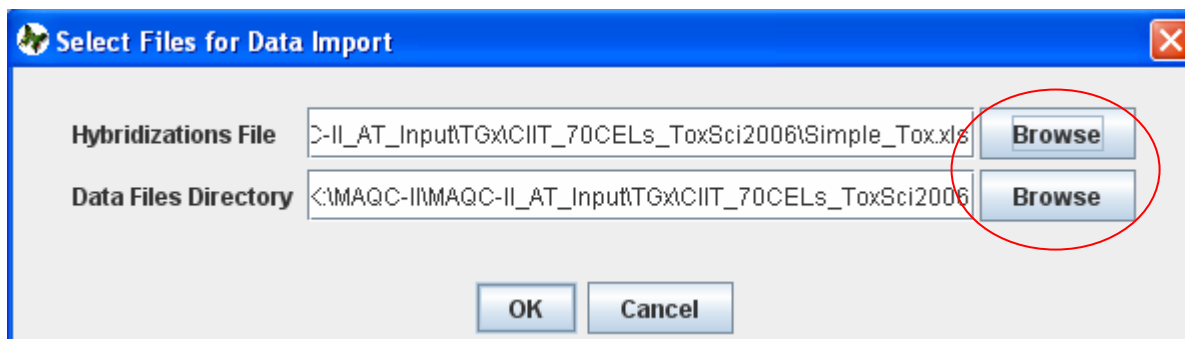
Refresh Active Variables and Domains From Database  Official Variable Names (Short Names)

User can also change the display of column naming

# Batch Import – Simple Tox Format



Right-click the experiment, choose “Batch Import Data – Simple Tox Format”

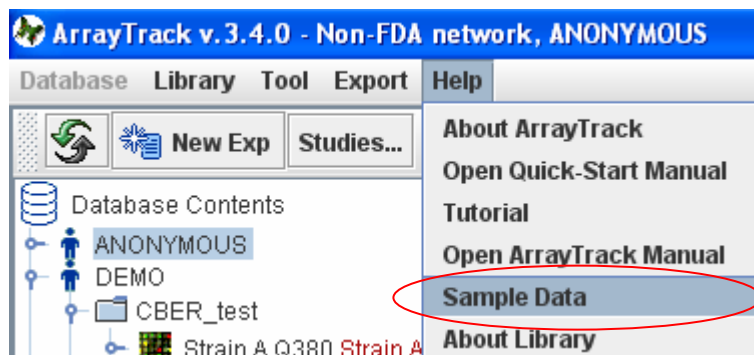


Click Browse button to locate the hybridization file and data files directory. The next slide shows an example of hybridization table file.

# Batch Import – Simple Tox Format

This is an example of hybridization table file (which can be downloaded from ArrayTrack help pull-down menu.). User can use this as a template to make his own hybridization file. Just make sure that your column titles are exactly same as this template. You are allowed to add new columns, however formatted columns Designed for toxicogenomics study will benefit for future across study analysis.

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
1	Array_ID	SubjectID	Institution	StudyTitle	StudyType	CompoundClass	ClassReference	Compound	CAS	Control	Treatmen	Dose	DoseUnit	HybName	SampleName
2	792	1-22	Hamner	Hamner Mice Lu	Repeat Dose			Corn Oil		Y	C	0	mg/kg	RT_0_13_22	RT_0_13_22_Lung_CornOil
3	793	1-24	Hamner	Hamner Mice Lu	Repeat Dose			Corn Oil		Y	C	0	mg/kg	RT_0_13_24	RT_0_13_24_Lung_CornOil
4	794	1-25	Hamner	Hamner Mice Lu	Repeat Dose			Corn Oil		Y	C	0	mg/kg	RT_0_13_25	RT_0_13_25_Lung_CornOil
5	795	1-27	Hamner	Hamner Mice Lu	Repeat Dose			Rodent Chow		Y	C	0	ppm	RT_0_13_27	RT_0_13_27_Lung_RodentCho
6	796	1-28	Hamner	Hamner Mice Lu	Repeat Dose			Rodent Chow		Y	C	0	ppm	RT_0_13_28	RT_0_13_28_Lung_RodentCho
7	797	1-29	Hamner	Hamner Mice Lu	Repeat Dose			Rodent Chow		Y	C	0	ppm	RT_0_13_29	RT_0_13_29_Lung_RodentCho
8	798	1-12	Hamner	Hamner Mice Lu	Repeat Dose	Non-lungtumorigen	NTP_No168	N-(1-naphthyl)et	1465-25-4	N	NLT	2000	ppm	RT_2000_13	RT_2000_13_12_Lung_ethylen
9	799	1-14	Hamner	Hamner Mice Lu	Repeat Dose	Non-lungtumorigen	NTP_No168	N-(1-naphthyl)et	1465-25-4	N	NLT	2000	ppm	RT_2000_13	RT_2000_13_14_Lung_ethylen
10	800	1-15	Hamner	Hamner Mice Lu	Repeat Dose	Non-lungtumorigen	NTP_No168	N-(1-naphthyl)et	1465-25-4	N	NLT	2000	ppm	RT_2000_13	RT_2000_13_15_Lung_ethylen
11	801	1-2	Hamner	Hamner Mice Lu	Repeat Dose	lung tumorigen	NTP_No143	1,5-Naphthalene	2243-62-1	N	LT	2000	ppm	RT_2000_13	RT_2000_13_2_Lung_Naphthal



The next slide shows a table that explains the meaning of the column heads. The order for each column doesn't matter.

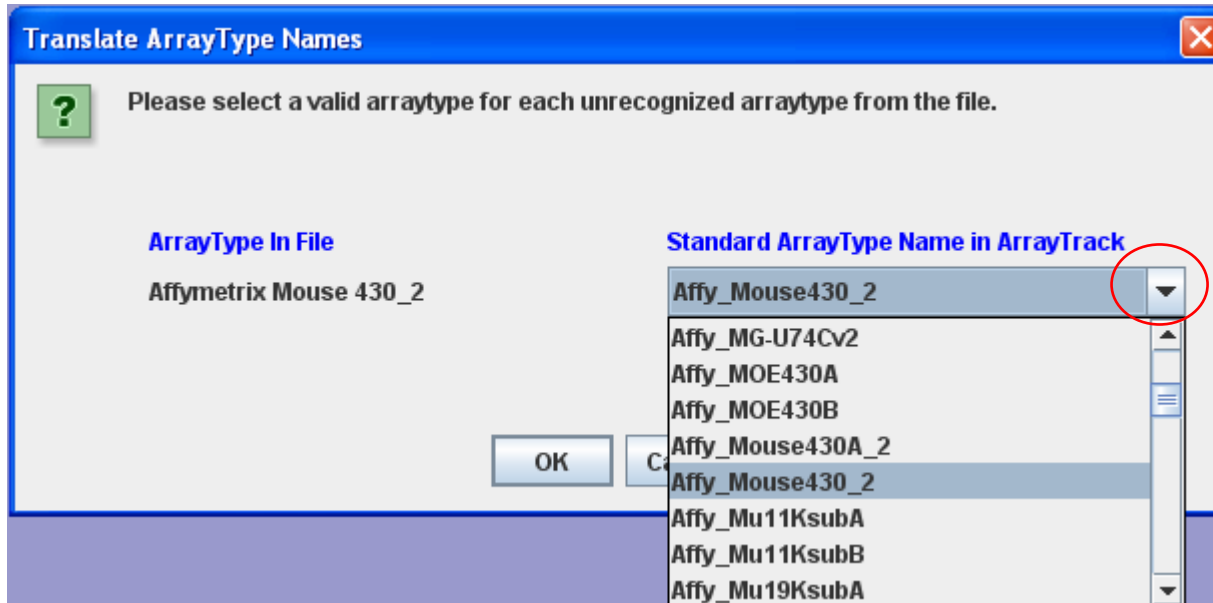


# SimpleTox

SimpleTox Column Head	Description	Example
<b>Institution</b>	Laboratory or institution name	NCTR/FDA, EPA
<b>DataFile</b>	Microarray data file	GSM142129.CEL
<b>HybName</b>	User specified identifier for a hybridization name	APAP_D100_T6_Jun04; APAP_D0_T6_Jun04
<b>SampleName</b>	Sample name	APAP_Dose100_Time6; APAP_Dose0_Time6
<b>Array_ID</b>	User-specified identifier for a hybridization	1,2,3 ... or p1002356
<b>Label</b>	RNA label reagent	Biotin; Cy3
<b>ArrayType</b>	Array type	Affymetrix Mouse 430_2
<b>Subject_ID</b>	Subject identifier	
<b>StudyTitle</b>	Study title	6 days repeating toxicity study
<b>Tech_Rep</b>	Technical replicates; microarray specific	A, B or C; 1,2, or 3
<b>Bio_Rep</b>	Biological replicates	A, B or C; 1,2, or 3
<b>HybDate</b>	Hybridization date	2/25/2007
<b>StudyType</b>	Study type	Single Dose Toxicity or Repeat Dose Toxicity
<b>Compound</b>	Compound name	Carbon Tetrachloride; Acetaminophen
.....	.....	.....

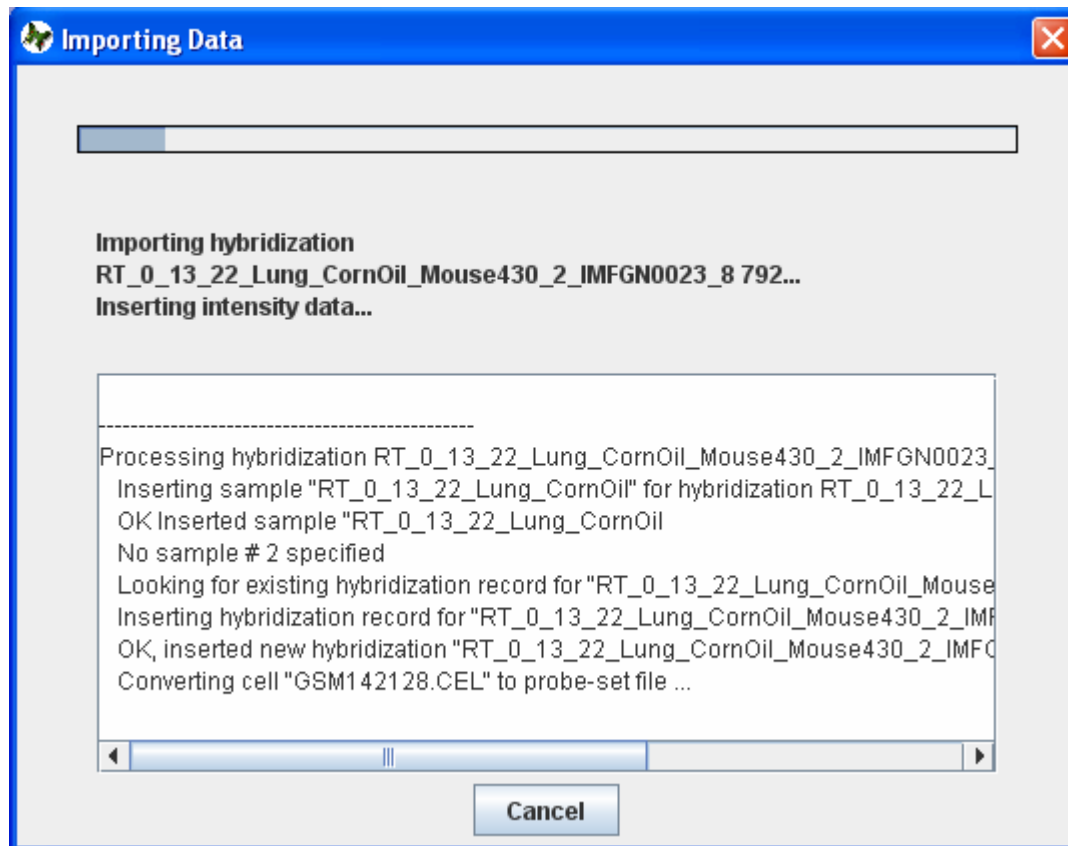
The red-colored part are required fields, while black-colored are optional fields. If you don't have Array\_ID, you can use subject\_ID as Array\_ID.

# Batch Import – Simple Tox Format

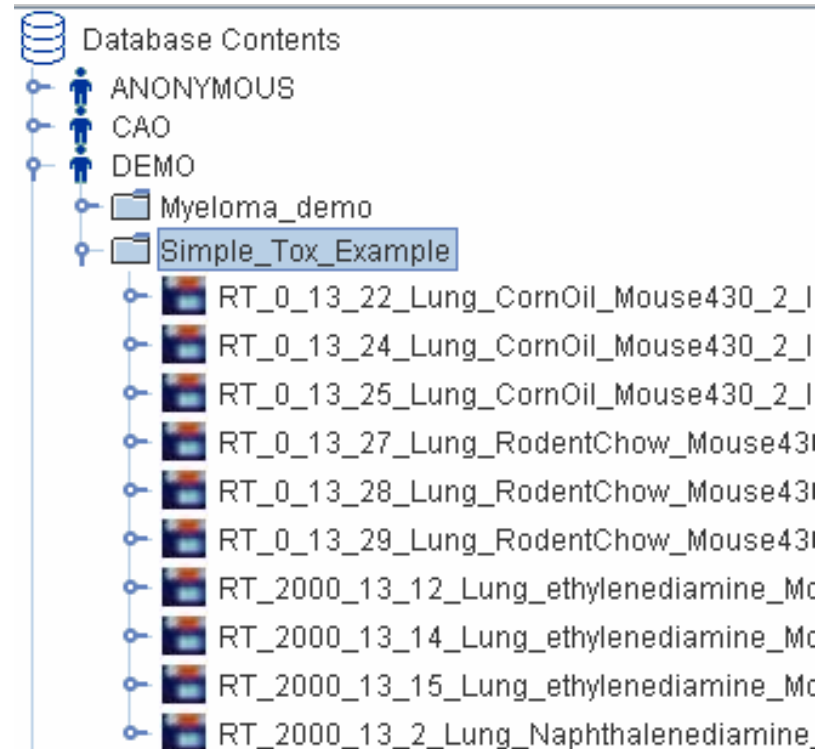
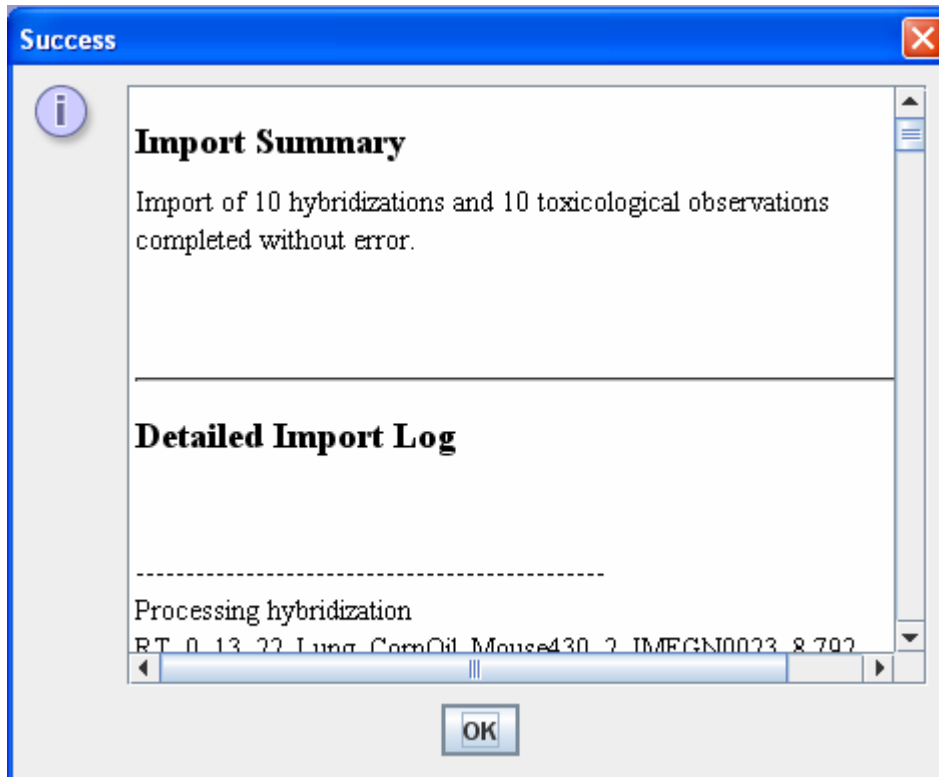


Select the right array type.

# Batch Import – Simple Tox Format



# Batch Import – Simple Tox Format

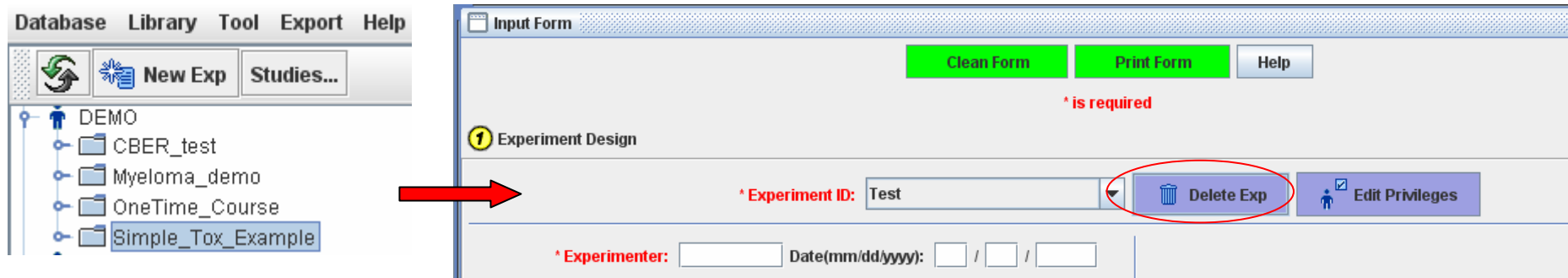


Batch import is successfully finished.

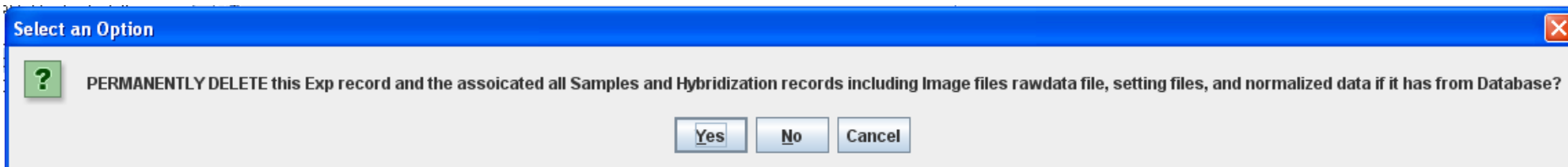
# Delete Data

To delete SimpleTox data you have imported, you need to delete the experiment first and then delete the study.

Double-click the experiment name in the data panel to bring out the Input Form, then click “Delete Exp” button.



You will be asked the following question, click “Yes” button to permanently delete the experiment.



# Delete Data

After deleted experiment, you need to delete the study. Select the study, right-click, Choose “Delete Studies”.

The screenshot shows the ArrayTrack Testing application interface. On the left, a navigation pane shows a tree structure under 'DEMO' with folders like 'CBER\_test', 'Myeloma\_demo', 'OneTime\_Course', and 'Simple\_ToX\_Example'. The 'Studies...' button is circled in red. A red arrow points from this button to the 'Studies' window. The 'Studies' window has a search bar and a table of studies. A context menu is open over the table, with 'Delete Studies' circled in red. Below the table, there are tabs for 'Exps (1)' and 'Hybs (2)', and a section for 'Experiments Referencing Selected Studies Above' with a table of experiments.

	STUDY_NAME	STUDY_ID	SUBJVAR	Allowed Access	
26	Hamner Mice Lung tumor FQIAN - 10/31/07 1:26 PM	311	Animal_ID	View & Modify	Non-lungtumorig
27	Simple ToxFormat Demo	317	Animal_ID	View Only	Liver Toxicity
28	Simple ToxFormat Demo F		ectID	View & Modify	

	EXPID *	EXPTITLE *	EXPDATE	ARRAYPLATFORM	EXPTYPE	KEYWORD	DESCRIPTION	OWNERID	EXPERIMENTER	INS*
1	690	ATvfreshTest						FQIAN	test0	

Click “OK” button.

**Delete Study?**

Delete the selected study and the 10 contained observations?

OK Cancel