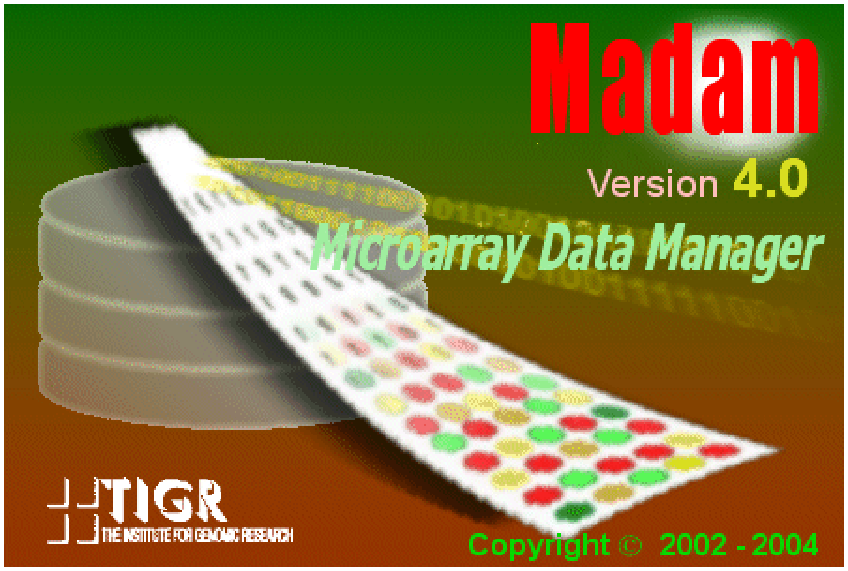
MADAM

Microarray Data Manager

(Version 4.0)



January, 2004

Microarray Software Group

The Institute for Genomic Research

Table of Contents

Table of Contents

Madam (Microarray Data Manager, version 4.0) is a suite of tools used to upload, download, and display a plethora of microarray data to and from a database management system (MySql). Working as an interface for the MySql, Madam allows scientists and researchers to manage their microarray data efficiently to meet the requirement of experiment annotation and data mining.

The database working as a repository was designed and guided by MIAME. This version of MADAM allows users to export the data in MAGE-ML format if the data are uploaded into the database.

If you have any questions about this software and need technical support, please contact madam@tigr.org for the help. We appreciate your comments.

Platform / System Requirements

Java Runtime Environment (JRE) 1.3 or later
Java Virtual Machine 1.3 or later
Platform: Windows/95/98/2000/XP/NT
Hard disk: more then 2 GB.

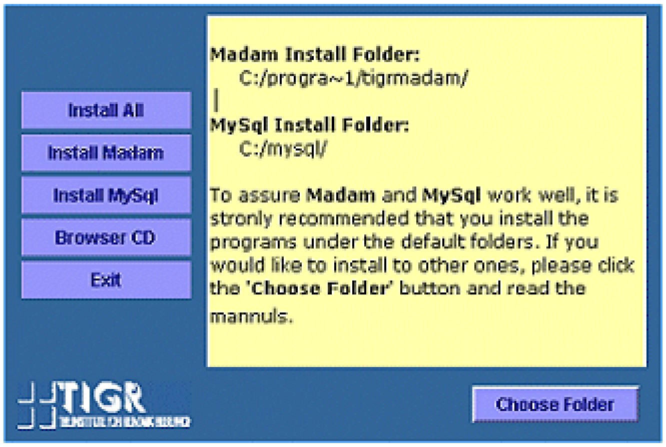
1. Installation

Notice: You must have administrative privilege for your system to install Madam.

Because MySql, a product of open source project for Database Management System (DBMS), is used as a back end for data storage, it must be installed and configured on your system before you operate the Madam. The configuration involves creating databases, setting up user privileges, and making communication protocol with Madam. This is a complicate task. However, we have developed an installer to complete the task smoothly for you.

The installation is straightforward and involves three major steps: installing Madam, installing MySql, and tuning up the Madam and MySql. What you need to do is to run the setup.bat file in the **application** folder. The entire process of installation may take 20 minutes, depending on the CPU speed of your system. Following steps will guide you to install the software.

(1) Run 'setup.bat' to have an Installer Window.



Madam Install Folder:
C:/progra~1/tigrmadam/

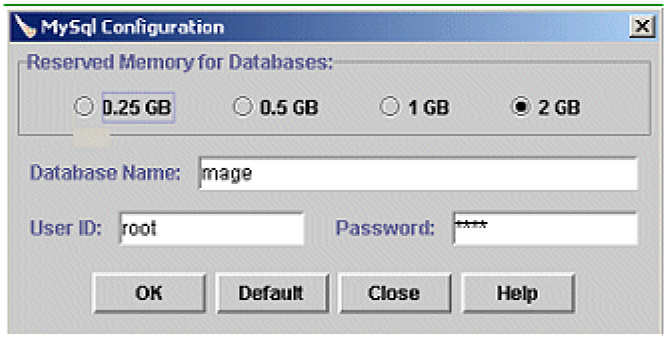
MySql Install Folder:
C:/mysql/

To assure **Madam** and **MySql** work well, it is stronly recommended that you install the programs under the default folders. If you would like to install to other ones, please click the **'Choose Folder'** button and read the mannuls.

(2) Click **Install All** button to install both Madam and MySql. If you have MySql previously installed on your system, you need to remove it before the installation. You can install either of the programs by clicking 'Install Madam' or 'Install MySql' respectively.

(3) Follow the instructions of the installers to complete the installation of both programs. It is strongly recommended to install the programs at the default directories (c:\program files\tigrmadam\ for Madam, and c:\mysql for MySql). If you really want to install the programs at other directories, you must click the 'Choose Folder" button and provide the locations for installations. Please note that you MUST set the same locations when you have install windows again for installing Madam and MySql respectively.

(4) After installations of Madam and MySql, you will have a configuration window. Set the memory size for MySql to store data. We recommend setting more than 1 GB.



Reserved Memory for Databases:

○ 0.25 GB ○ 0.5 GB ○ 1 GB ● 2 GB

Database Name: mage

User ID: root Password: ****

(5) The default database name is 'mage'; and use-id and password are 'root'. You can change them to yours (You can add more databases with Madam Administrator or Preference … in the program). Then, click 'OK' button.
(6) It will take a couple of minutes to create databases and insert data to a testing database (test_mage). The process of inserting data could be very slow at some point, so that the installer seems to be frozen. If the timer is counting, you should wait for a while. Please be patient.
(7) Click **Exit** to close the Installer Window. Now, it is ready to use Madam.

2. Uninstallation

To uninstall Madam, from **'Start --> Programs --> TigrMadam'**, click **'Uninstall Tigr Madam'**. To uninstall MySql, open **'Control Panel'** from **'Start --> Setting'**; click **'Add/Remove Programs'** and select 'MySql'. If you cannot remove the entire programs, you might need to manually delete the mysql and tigrmadam folders under c:\ and c:\program files\ respectively (or at your selected locations).

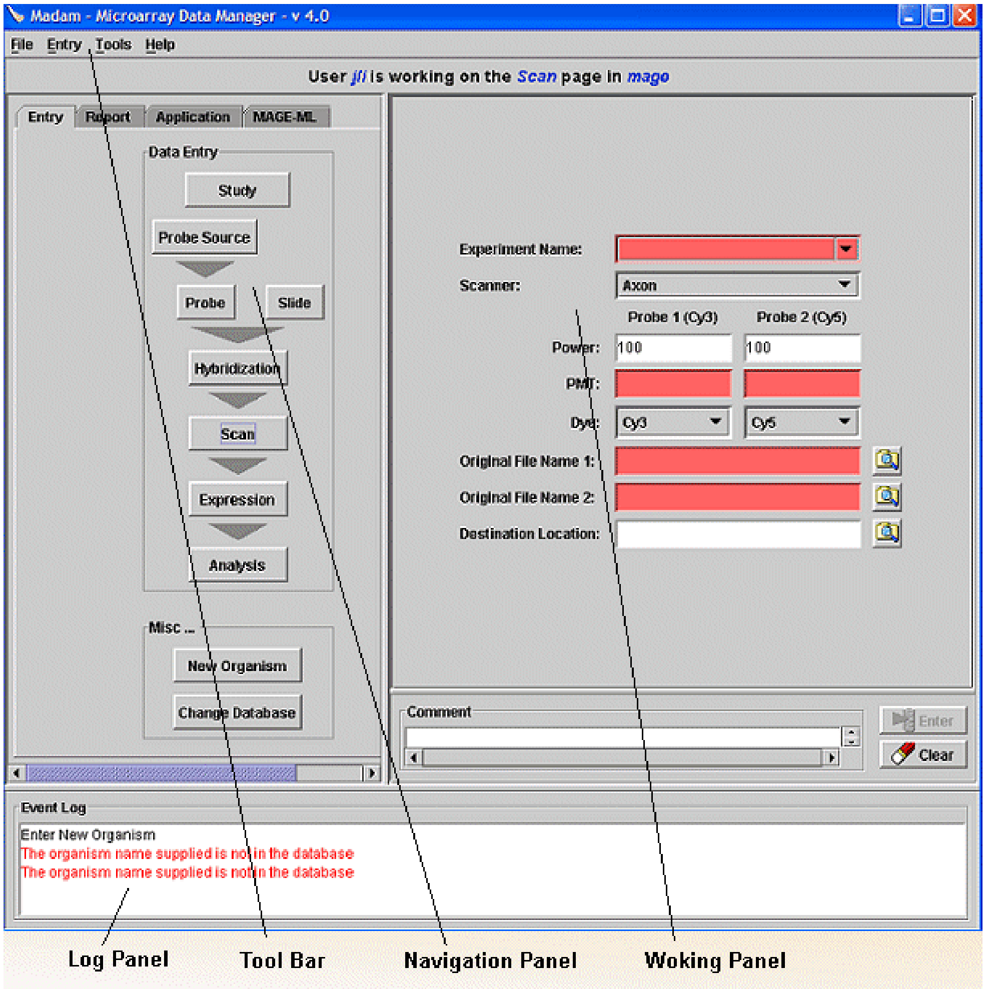
1. Start the application

From **'Start --> Programs --> TigrMadam'**, click Madam. Alternatively, you can run the madam.bat under "..\tigrmadam\" folder to start the program.

You will be asked to provide your user-id and password you set during the installation. Having provided the correct user-id and password, Madam will start MySql and be ready to use.

2. Interface

The interface of Madam could be categorized into four parts, as indicated in the picture 2.1. The Tool Bar shows the database and page you are working on. Also the tool bar allows you to terminate the Madam or use other tools, such as **Query Window**, **PCR Score**, and others. On the left side of the page is a **Navigation Panel** that allows you to open pages in the **Working Panel** to process different jobs. The Working Panel on the right shows you the pages corresponding to the buttons on the Navigation Panel. The **Log Panel** is at the bottom that keeps a log of the operations performed and an Event Log window informs you about the events.



Madam - Microarray Data Manager - v 4.0

User *jli* is working on the *Scan* page in *mago*

Scanner: Axon

Power: 100 100

Dye: Cy3 Cy5

Enter New Organism
The organism name supplied is not in the database
The organism name supplied is not in the database

Figure 2.1: The Interface of Madam

2.1 Tool Bar

The **Tool Bar** contains four menus: **File**, **Entry**, **Tools**, and **Help** (see Figure 2.2). Clicking **QUIT** from the file menu terminates Madam. The **Entry** menu functions as the buttons in the **Entry** tab (see picture 2.1 above) and presents corresponding pages for data entry. The **Tools** menu allows you to open **Query Window (**a friendly tool used to query the Database), **PCR Score**, **Miner**, **Express Converter**, and **Experiment Designer**. By clicking **Help** menu, you can get more information about how to use the program.

Figure 2.2: The tool bar

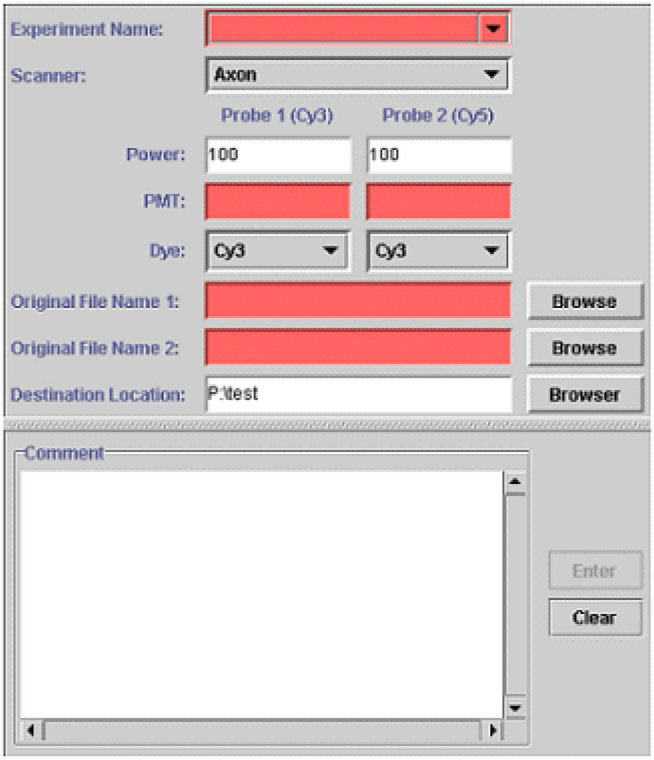
2.2 Navigation Panel

The **Navigation Panel** provides you with four tabs, **Entry**, **Report**, **Application**, and **MAGE-ML** (Figure 2.3), for job selections. **Entry** tab shows a set of buttons to trigger different pages for data entry. The buttons represent the data flow in the microarray research and you must follow the flow to enter data. **Report** tab presents a list of selections for Study, Experiment, Slide, Slide Type, and Probe. With the list, you can have a report about the selected items. MAGE-ML tab allows you to export the data in MAGE-ML format. **Application** tab brings about buttons through which you can launch a program for data management.

Figure 2.3: Navigation panel

2.3 Working Panel

The **Working Panel** shows you different pages based on the buttons you clicked in the **Navigation Panel** (Figure 2.4). All the pages have a Comment area and two buttons: **Enter** and **Clear**. You can write some comments for the pages you are working on. When all the entry fields have qualified data, the **Enter** button will be activated. Clicking **Clear** button will erase what you have typed in that entry.



Experiment Name:
Scanner: Axon

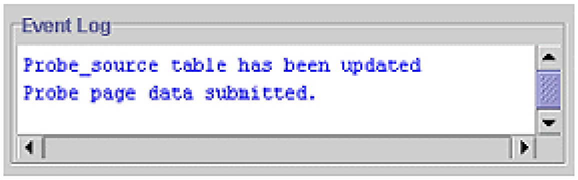
	Probe 1 (Cy3)	Probe 2 (Cy5)
Power:	100	100
PMT:		
Dye:	Cy3	Cy3

Original File Name 1:
Original File Name 2:
Destination Location: P:\test
Comment

Figure 2.4: Working panel showing entries of San.

2.4 Log Panel

The **Log Panel** contains an Event Log window that shows you messages about your operations (Figure 2.5). The messages are printed in three colors. Blue indicates that your job has been successfully completed; red indicates errors; and black suggests a general message.



```
Probe_source table has been updated
Probe page data submitted.
```

Figure 2.5: Log panel showing process messages.

2.5 Data Validation

Madam has a data auto-validation function for data entry. In the course of your data entry, once the field becomes red, it indicates that some errors had occurred. You can move the mouse over the color to see what the error is. If the red color is gone, it suggests that your entry was valid. Only when all entry fields have white colors, is the **Enter** button activated. Figure 2.6 shows the data in the field Sample Name is "required".

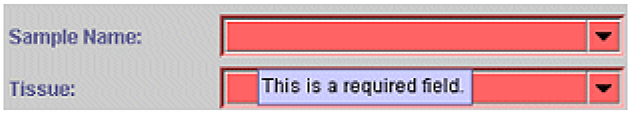


Figure 2.6: Red background suggests the errors.

2.6 Smart List

Madam is equipped with a feature called **Smart List** that allows you to search data quickly. If you click the arrow at the right of an entry field, a list of valid data will be shown. You can focus or shorten the list by typing the beginning of your entry. The top of the figure 2.7 shows a list of data for Sample Name and the bottom represents that when "Om" is typed, the list shows only data starting with "Om".

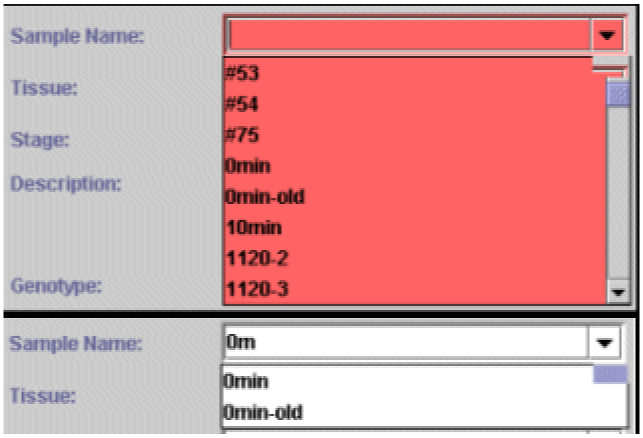


Figure 2.7: The entry can shorten the list.

2.7 Informative Label

Informative Label is a tool to keep track of where the data are saved in the databases. If you move your mouse over a label of an entry field for 1-2 seconds, a small box will show you the table name and field name. For example, figure 2.8 shows you that the Project Name in Slide Page will go to slide_name in the table Slide.

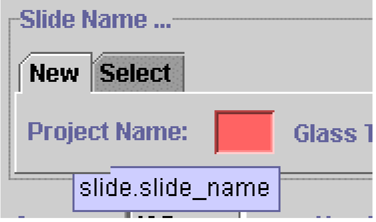
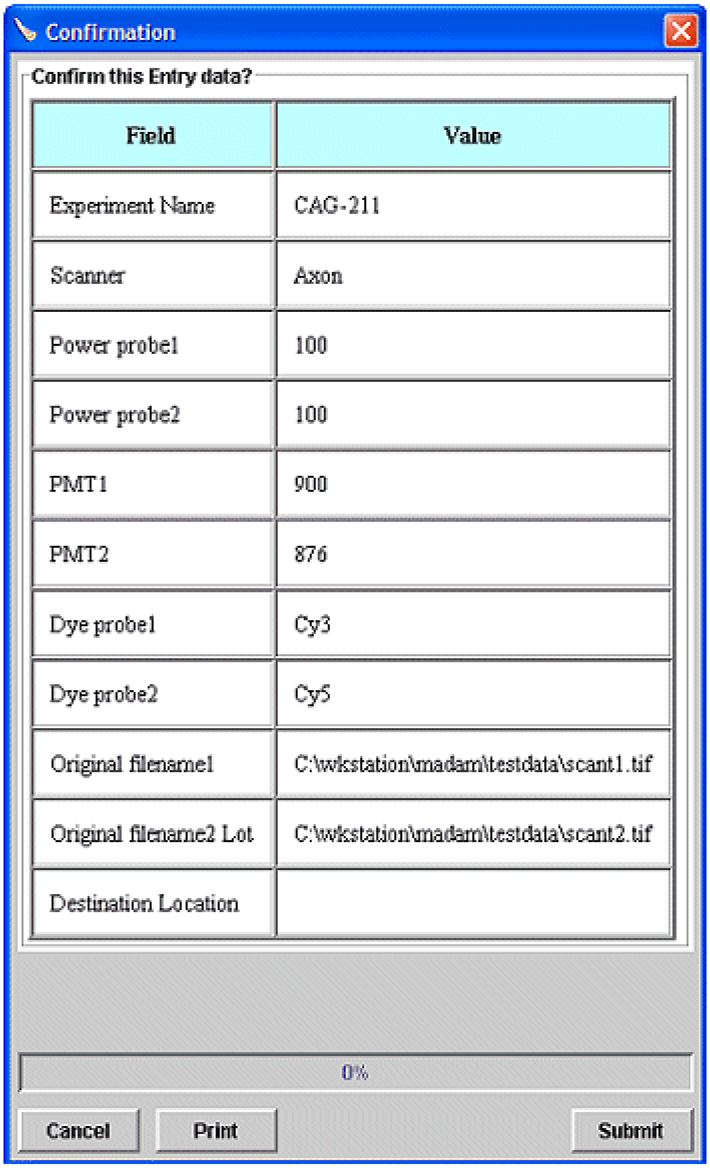


Figure 2.8: The label can show where data are inserted.

2.8 Confirmation Window

The **Confirmation Window** or **Confirmation Page** allows you to check your data entry before you submit to the database. Other than a table that contains the entry, there are a progress bar and three buttons (see Figure 2.9). If you find a mistake, you can close the window by click the **Cancel** button. Clicking the **Submit** button will start the process of updating the database. The progress bar shows you the percentage of the process that is done. You can print the data entry by clicking the **Print** button as you print a report (see section 4.7, Print a Report You Are Viewing).



Confirm this Entry data?

Field	Value
Experiment Name	CAG-211
Scanner	Axon
Power probe1	100
Power probe2	100
PMT1	900
PMT2	876
Dye probe1	Cy3
Dye probe2	Cy5
Original filename1	C:\wkstation\madam\testdata\scant1.tif
Original filename2 Lot	C:\wkstation\madam\testdata\scant2.tif
Destination Location	

Figure 2.9: Confirmation Window shows what will be inserted.

3. Data Entry

Madam is an interface for data entry. There are 8 pages for Study, Probe Source, Probe, Slide, Hybridization, Scan, Expression, and Analysis respectively. You can switch among them by clicking buttons in the Navigation Panel. The buttons are arranged in sequential order, so you should enter data in that order. In other words, only after you enter probe and slide information, can you enter hybridization data. Entering data is straightforward, just following the instructions in each page. If you create a **new** database, the correct procedure for uploading data is:]

(1) Enter an organism using **New Organism Window**.
(2) Enter an organism using **New Organism Window.**
(3) Upload your plate and PCR information with **PCR Score.**
(4) Insert study information with **study** page.
(5) Insert probe source data with **Probe Source** page.
(6) Use other pages ...

3.1 Entering Study Information

Study page collects sgeneral information about a research project. A study can have a set of experiments (hybridizations).

(1) Fill in New Study Name, Investigator, and Study Variables by typing or selecting from the list.
(2) Enter Factor and Values. You can leave the Values and Unit blank, but you must enter the Factor. Once the Factor is entered, the red square at the right up corner will change to gray, suggesting that you have entered qualified data.
(3) You can leave other entries blank.
(4) Type your comment in the Comment field if you want. Right-clicking mouse will allow you to zoom in the Comment to have a large writing place.
(5) If **Enter** button is activated, click it to open **Confirmation Page**; otherwise, correct mistake to activate **Enter** button.
(6) Check if all entered data are correct. If they are, click **Submit** button on the **Confirmation Page**.

3.2 Entering Probe Source Information

(1) Fill in Sample Name, Tissue, Organism, and Provider fields by typing or selecting from the list.
(2) You can leave other entries blank.
(3) Select Source Nucleic Acid and Isolation Date.
(4) Type your comment in the **Comment** field if you want.
(5) If **Enter** button is activated, click it to open **Confirmation Page**; otherwise, correct mistake to activate **Enter** button.
(6) Check if all entered data are correct. If they are, click **Submit** button on the **Confirmation Page**.

3.3 Entering Probe Data

Note: You must complete Probe Source entry before processing following steps.

(1) Fill in Probe Name, Sample Name, and Protocol Name by typing or selecting from the list.
(2) You can leave other entries blank.
(3) Select Dye Label and Nucleic Acid Produced, and Primer Type.
(4) Type your comment in the **Comment** field if you want.
(5) If **Enter** button is activated, click it to open **Confirmation Page**; otherwise, correct mistake to activate **Enter** button.
(6) Check if all the entered data are correct. If they are, click **Submit** button on the Confirmation Page.

3.4 Entering Slide Data

The slide data involves slide name and slide type that describes how an array is designed. This makes the entering slide data a relatively complicated and resulted in three methods.

3.4.1 Naming New Slide and Slide Type

Note: To create a new slide type, you must uploaded plate information with PCR Score. Also, you might need to complete Probe Source and Probe entries before processing following steps.

(1) Click **New** tab under Slide Name.
(2) Enter three letters as Project Name.
(3) Select Glass Type and Number of Slide.
(4) Fill in Surface Type, Surface Name**,** Attachment Method**,** and Protocol Name fields by type or selection from the list.
(5) Click **New** tab under Slide Type.
(6) Select a machine from Arrayer.
(7) Fill in Type Name.
(8) Select Number of Cols, Number of Rows, Columns of Pens, and Columns of Pens for array printing configuration if you select Generic for the Arrayer. Also select Pattern and Repeats on ... for Rows and Columns. It is recommended to select the same number for Number of Spots and Pattern.
(9) Set Plate Order ... by using either Direct Set (see Creating Plate Order by Direct Setting) or Allies Set (see Create Plate Order by Alias Setting). The plate order is the sequence of plates that are used to print a slide, consisting of a set of numbers, which represent the ids of plates and are created by Madam.
(10) If **Enter** button is activated, click it to open **Confirmation Page**; otherwise, correct mistake to activate **Enter** button.
(11) Check if all the entered data are correct. If they are, click **Submit** button on the **Confirmation Page**.

3.4.1.1 Create Plate Order with Direct Setting

Plate order is the consequence of plates that provide the samples for printing spots on a slide. To set the order, you should have plate numbers (e.g. plate id) stored in the database with PCR Score.

(1) Click **Direct Set** tab under Plate Order.
(2) Set Start number by clicking the arrow or direct type the number.
(3) Use the same way to set End number.
(4) Click **Set** button and the plate order will show in the field. You can edit the order by typing. Click **Reset** to erase plate order if you need to re-set.

3.4.1.2 Create Plate Order with Alias Setting

(1) Click **Alias Set** tab under Plate Order ...
(2) Enter a few of starting letters for alias name to Alias field, and hit **Return** key. A list of alias name starting with what you typed will show under All Alias. If you type nothing, all aliases in the database will show.
(3) Select those aliases you need to get their Plate Number. You can do multiple selections by holding **Ctrl** key during your selecting.
(4) Move the selected alias name to Selected Alias by clicking the Right Arrow or double-clicking your selections.
(5) Click **Set** button and the plate order will show in the field. You can edit the order by typing. Click **Reset** to erase plate order if you need to re-set.

3.4.2 Naming New Slide with Existing Slide Type

(1) Click **New** tab under Slide Name.
(2) Enter three letters as Project Name.
(3) Select Glass Type and Number of Slide
(4) Fill in Surface Type, Surface Name**,** Attachment Method**,** and Protocol Name fields by type or selection from the list.
(5) Click **Select** tab under Slide Type (**Select** is default when you select **New** for Slide Name).
(6) Select a Slide Type from the list.
(7) If **Enter** button is activated, click it to open **Confirmation Page**; otherwise, correct mistake to activate **Enter** button.
(8) Check if all the entered data are correct. If they are, click **Submit** button on the **Confirmation Page**.

3.4.3 Numbering Slides with Existing Name

(1) Click **Select** tab under Slide Name.
(2) Select a slide name from the list (Note: Madam will give your slide a new name based on your selection, but not use what you select as the name).
(3) Select a number from Number of Slide.
(4) If **Enter** button is activated, click it to open **Confirmation Page**; otherwise, correct mistake to activate **Enter** button.
(5) Check if all the entered data are correct. If they are, click **Submit** button on the **Confirmation Page**.

3.5 Entering Hybridization Data

Note: You must complete Probe Source, Probe, and Slide entries before entering hybridization information.

(1) Fill in Study Name and Slide Name fields by typing or selecting from the list.
(2) Fill in New Experiment Name field with whatever you want to name. If you leave it blank, the slide name you selected will be used as the name.
(3) Fill in Probe fields for Probe1 and Probe2. You can filter the probe names by selecting My Probes or All Probes.
(4) Indicate which probe works as reference by clicking Reference under the probe name.
(5) If there are experiment factors associated with probe, click the Expt. Factor button under the probe name and select them.
(6) Fill in Protocol Name**,** Protocol**,** Block Agent**,** Wash Method**,** Instrument**,** Volume**,** Time, and Temperature fields.
(7) Select or un-select Biological Replicates, PolyA, Low Complexity, and Unspecific Binding.
(8) Type your comment in the Comment field if you want.
(9) If **Enter** button is activated, click it to open **Confirmation Page**; otherwise, correct mistake to activate **Enter** button.
(10) Check if all entered data are correct. If they are, click **Submit** button on the **Confirmation Page**.

3.6 Entering Scan Data

Note: You must complete Probe Source, Probe, Slide, and Hybridization entries before entering scan information.

(1) Fill in Experiment Name field by typing or selecting from the list.
(2) Select a scanner from Scanner list. If there is no scanner for your selection, you can add a scanner from Preference Window.
(3) Fill in Power and PMT fields for **Probe 1** and **Probe 2**.
(4) Select Dye.
(5) Fill in Original File Name 1**,** Original File Name 2, and Destination Location fields by typing the path and name directly or clicking the **Browse** button.
(6) Type your comment in the Comment field if you want.
(7) If **Enter** button is activated, click it to open **Confirmation Page**; otherwise, correct mistake to activate **Enter** button.
(8) Check if all entered data are correct. If they are, click **Submit** button on the **Confirmation Page**.

3.7 Entering Expression Data

Note: You must complete Probe Source, Probe, Slide, Hybridization, and Scan entries before entering expression information.

(1) Fill in Experiment Name field by typing or selecting from the list.
(2) Select Reference Data Column. 7 and 8 refer the intensity columns in the TIGR-TAV/MEV files.
(3) Fill in TAV/MEV File Name filed by typing the path and name directly or clicking the **Browse** button.
(4) Type your comment in the Comment field if you want.

(5) If **Enter** button is activated, click it to open **Confirmation Page**; otherwise, correct mistake to activate **Enter** button.
(6) Check if all entered data are correct. If they are, click **Submit** button on the **Confirmation Page**.

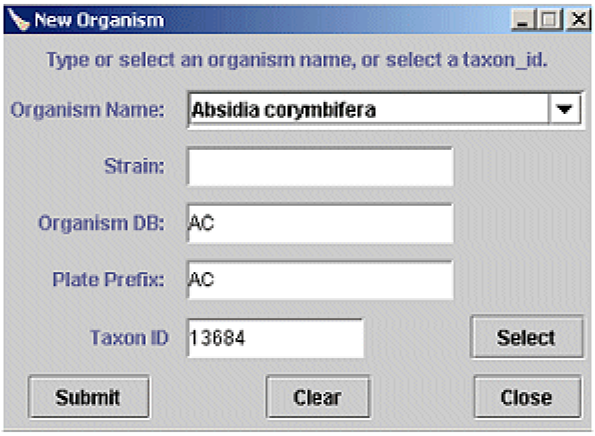
3.8 Entering Analysis Data

Note: You must complete Probe Source, Probe, Slide, Hybridization, Scan, and Expression entries before entering analysis information.

(1) Fill in Experiment Name**,** File Name 1**,** Normalization 1**,** File Name 2, and Normalization 2 fields by typing or selecting from the list.
(2) You can leave Program Name filed blank.
(3) Type your comment in the Comment field if you want.
(4) If **Enter** button is activated, click it to open **Confirmation Page**; otherwise, correct mistake to activate **Enter** button.
(5) Check if all entered data are correct. If they are, click **Submit** button on the **Confirmation Page**.

3.9 Entering New Organism Data

When you click **New Organism** button in the Navigation Panel, a small window, New Organism window, will be presented (see Figure 3.1). This window allows you to search or submit an organism from or to database.



Type or select an organism name, or select a taxon_id.

Organism Name: Absidia corymbifera
Strain:
Organism DB: AC
Plate Prefix: AC
Taxon ID 13684

Figure 3.1: New organism window.

3.9.1 Searching an Organism From Database

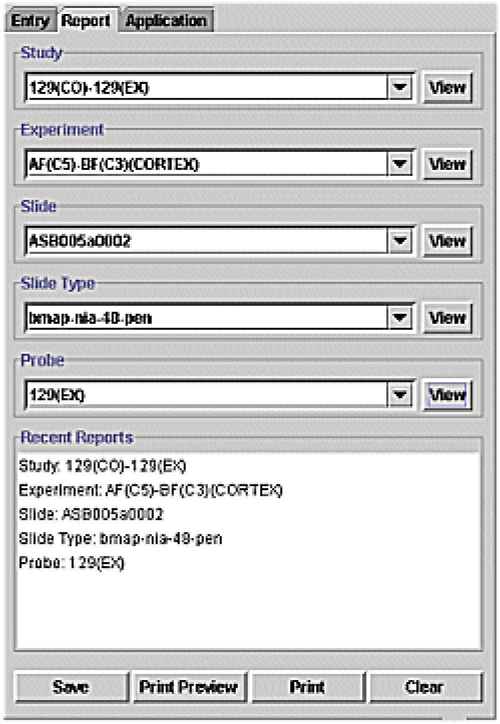
Select an organism from the Organism Name list. You can find a name quickly by typing the starting letters and hit the **Return** key. When you select an organism, the Organism DB, Plate Prefix, and Taxon ID fields will be filled with related information. If you want to erase what you have typed, click **Clear** button.

3.9.2 Submitting an Organism to Database

(1) Fill in Organism Name field by typing or selecting the list. You can find a name quickly by typing the starting letters and hit the **Return** key. If you know the taxon id, you can fill in the Taxon ID filed and click **Select** button. Then, the organism will show in the Organism Name field.
(2) Click **Submit** button.

4. Data Report (Query)

Madam is also an interface for data retrieval. You can view Study, Experiment, Slide, Slide Type, and Probe data by clicking the **View** buttons at the Report tab in the Navigation Panel (see Figure 4.1). Once you click the button, the reports will be presented on the Working Panel. The history of your viewing will show in a list under Recent Reports. You can view any history report by clicking it. You can save or print the reports (see 4.6 and 4.7).



Study: 129(CO)-129(EX)
Experiment: AF(C5)-BF(C3)(CORTEX)
Slide: ASB005a0002
Slide Type: bmap-nia-40-pen
Probe: 129(EX)

Recent Reports
Study: 129(CO)-129(EX)
Experiment: AF(C5)-BF(C3)(CORTEX)
Slide: ASB005a0002
Slide Type: bmap-nia-48-pen
Probe: 129(EX)

Figure 4.1: The report panel

4.1 Viewing Study Report

(1) Click Report tab in the Navigation Panel.
(2) Fill in Study field by typing or selecting from the list.
(3) Click the **View** button. If there are data for the *Study* you entered or selected, the report will show in the Working Panel.

4.2 Viewing Experiment Report

(1) Click Report tab in the Navigation Panel.
(2) Fill in Experiment field by typing or selecting from the list.
(3) Click the **View** button. If there are data for the *Experiment* you entered or selected, the report will show in the Working Panel.

4.3 Viewing Slide Report

(1) Click Report tab in the Navigation Panel.
(2) Fill in Slide field by typing or selecting from the list.
(3) Click the **View** button. If there is already data for the Slide you had entered or selected, the report will be displayed in the Working Panel.

4.4 Viewing Slide Type Report

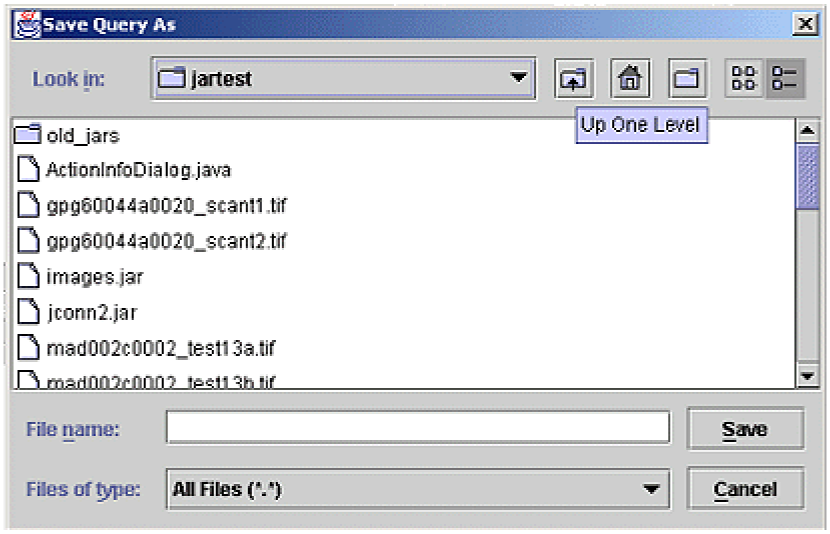
(1) Click Report tab in the Navigation Panel.
(2) Fill in Slide Type field by typing or selecting it from the list.
(3) Click the **View** button. If there is already data for the Slide Type you had entered or selected, the report will be displayed in the Working Panel.

4.5 Viewing Probe Report

(1) Click Report tab in the Navigation Panel.
(2) Fill in Probe field by typing or selecting from the list.
(3) Click the **View** button. If there is already data for the Probe you had entered or selected, the report will be displayed in the Working Panel.

4.6 Saving the Report You Are Viewing

(1) Click **Save** button to open a file choose window (see Figure 4.2).
(2) Set the file location (directory) by selecting from Look in and the folder in the window.
(3) Fill in the File name field.
(4) Click the **Save** button. The file will be saved as a HTML file so that you can open it with a web browser.



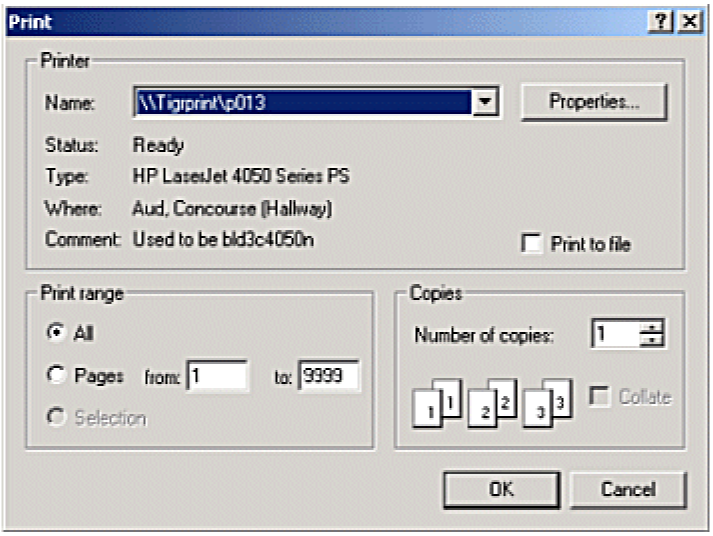
Look in: jartest
Files of type: All Files (*.*)

Figure 4.2: The file chooser window allows you to save a file.

4.7 Printing the Report You Are Viewing

(1) Click **Print** button to open a **Print** window (see Figure 4.3).

(2) Select a printer from the Name in the Printer group.
(3) Click the **OK** button. If you are not sure what you will print out, click **Print Preview** button to view the pages. You can click the **Print** button on the Report Preview window to print the report.



Printer
Name: \\Tigprint\p013
Status: Ready
Type: HP LaserJet 4050 Series PS
Where: Aud, Concourse (Hallway)
Comment: Used to be bld3c4050n
☐ Print to file

Print range
● All
○ Pages from: 1 to: 9999
○ Selection

Copies
Number of copies: 1
☐ Collate

Figure 4.3: Printer chooser window.

4.8 Preview the Report to Be Printed

(1) Click **Print Preview** button to open a **Report Preview** window (see Figure 4.4) and what you will print out is showed in the window.
(2) Click **Next** button to view the next page and click the **Previous** button to view the last page
(3) Click the **Print** button to print out the report.

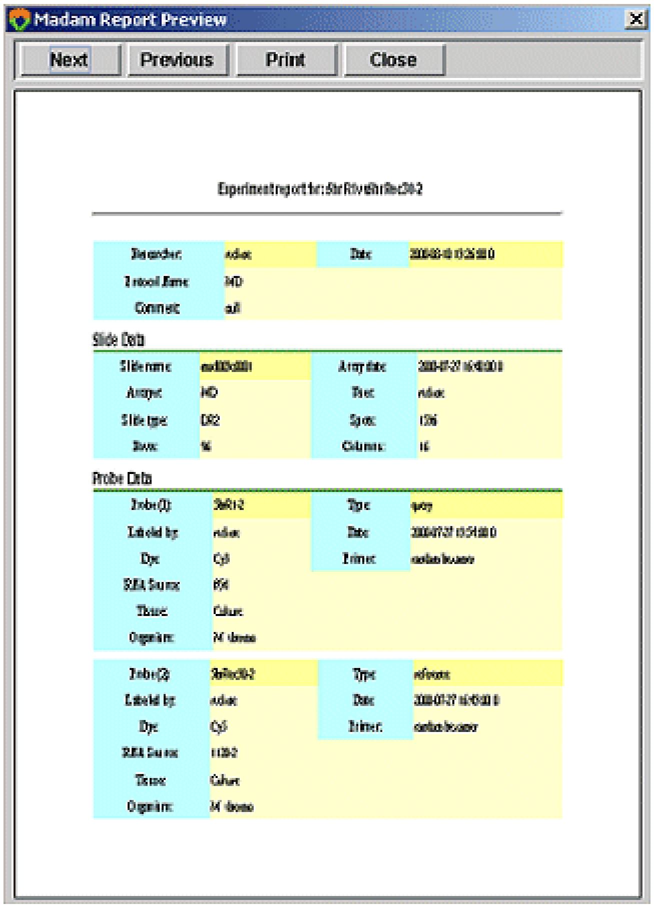


Figure 4.4: Preview window.

5. Applications

Other than the interface for data management, **Madam** allows you to run many useful applications such as Experiment Designer, PCR Score, Miner, Query Window, and Express Converter by clicking the **Experiment Designer**, **PCR Score**, **Miner**, **Query Window**, and **Express Converter** buttons (see Figure 5.1). Also, you can launch them from the **Tools** menu.

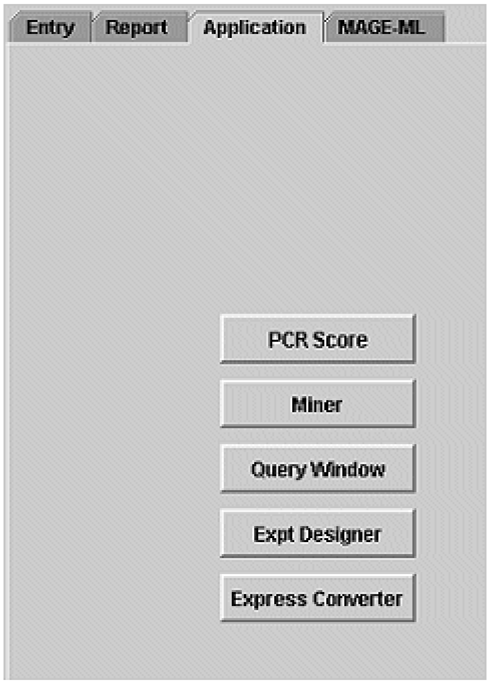


Figure 5.1: Navigation panel.

5.1 Running Experiment Designer

Experiment Designer is a tool that can facilitate your experiment design. Using it, you can easily to draw a design graph and save the design as a file.

(1) Click Application tab in the Navigation Panel; or click **Tools** at the tool bar.
(2) Click **Expt Designer** button to launch the program. You can get detailed information by clicking the Help button in the program.

5.2 Running PCR Score

(1) Click Application tab in the Navigation Panel; or click **Tools** at the tool bar.
(2) Click **PCR Score** button to run the program. You can have more information from PCR Score Manual.

5.3 Running Miner

Miner is a tool that allows you to retrieve the data from database for an experiment and save the data as a TIGR mev or tav file, so that the data can be analyzed with MIDAS and MEV. Clicking the Miner button in the Application tab in the Navigation Panel or selecting Miner under Tools menu at the tool bar will present an interface (see Figure 5.2) in the Working Panel. Process following steps:

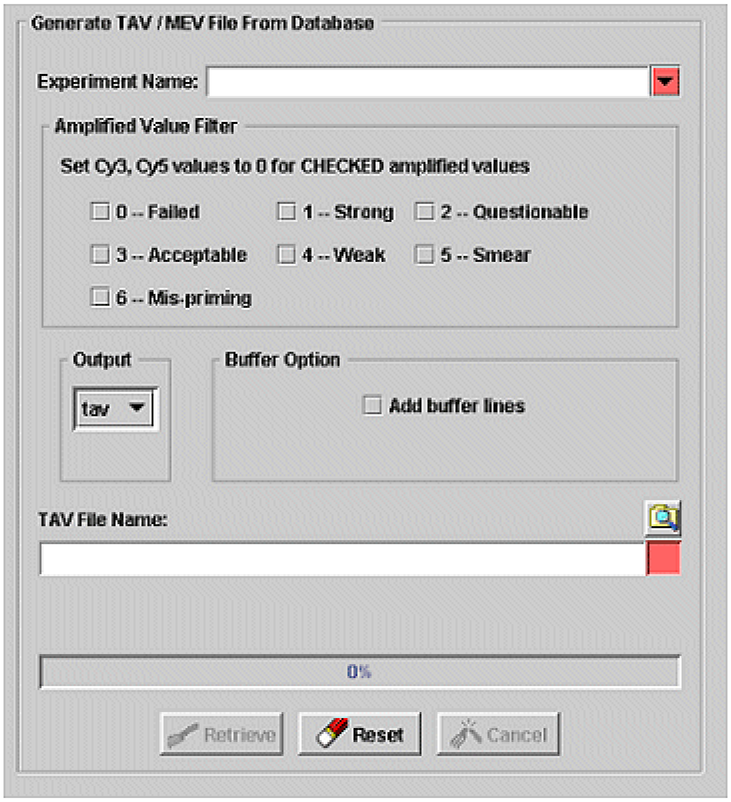


Figure 5.2: Miner interface.

(1) Select an experiment name from the Experiment Name list.
(2) If you want to filter those spots with some degree of PCR qualities, check them under Amplified Value Filter. The intensities of those spots will be set to zero. Please refer to **PCR Score** manual for detailed information about the scores.
(3) Checking the Add buffer box will keep the empty spots on the array in the mev/tav file.
(4) Select the Output for the file type.
(5) Provide a file name in the TAV File Name field. You can click Browser button to find where you want to save on your system.
(6) Click Retrieve button to start.
(7) Clicking **Reset** button can erase what you have set.
(8) You can stop the retrieving at any time by clicking the **Cancel** button.

5.4 Running Query Window

The **Query Window** provides you a tool to query databases with SQL programming. As the following pictures (Figure 5.3) shows, the window consists of a Query and Results areas, plus several buttons. With the window, you can manipulate the data in database by SQL programming or SQL files. Also, you can save your SQL programs and the query results.

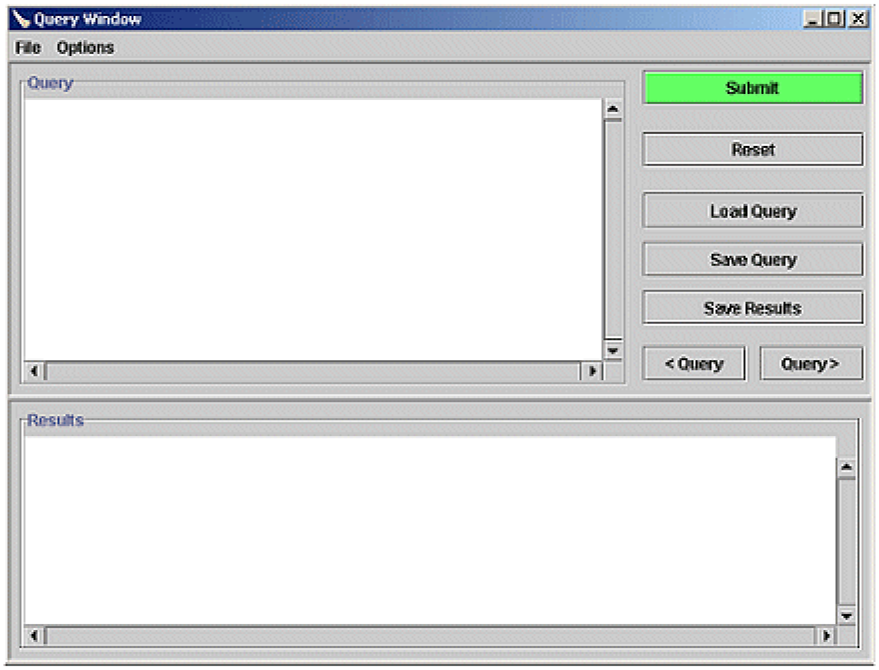


Figure 5.3: Query window.

5.4.1 Query Data by SQL Programming

(1) Type SQL codes in the Query filed (you can enter multiple lines by typing the **Return** key).
(2) Click **Submit** button; if no error occurs, the query results will show in the Results field.
(3) Clicking **Reset** button can erase the Query filed;

You can use the previous SQL codes by keeping clicking the **"‹Query";** or **"Query›"** buttons. Also, you can save your SQL codes and the query results as a file.

5.4.2 Query Data by SQL File

If you have saved your SQL codes as a file, you can query a database by following the steps.

(1) Click the **Load Query** button to open a File Choose Windows.
(2) Fill in the File Name by typing the path and name of the file or selecting from the Look in list and the window.
(3) Click the **Open** button and the SQL codes will show in the Query filed.
(4) Click **Submit** button and query results will be presented the Results field.

5.4.3 Saving SQL Codes as a File

(1) Click the **Save Query** button to open a File Choose Window.
(2) Fill in the File Name by typing the path and name of the file or selecting from the Look in list and the window;.
(3) Click the **Save** button.

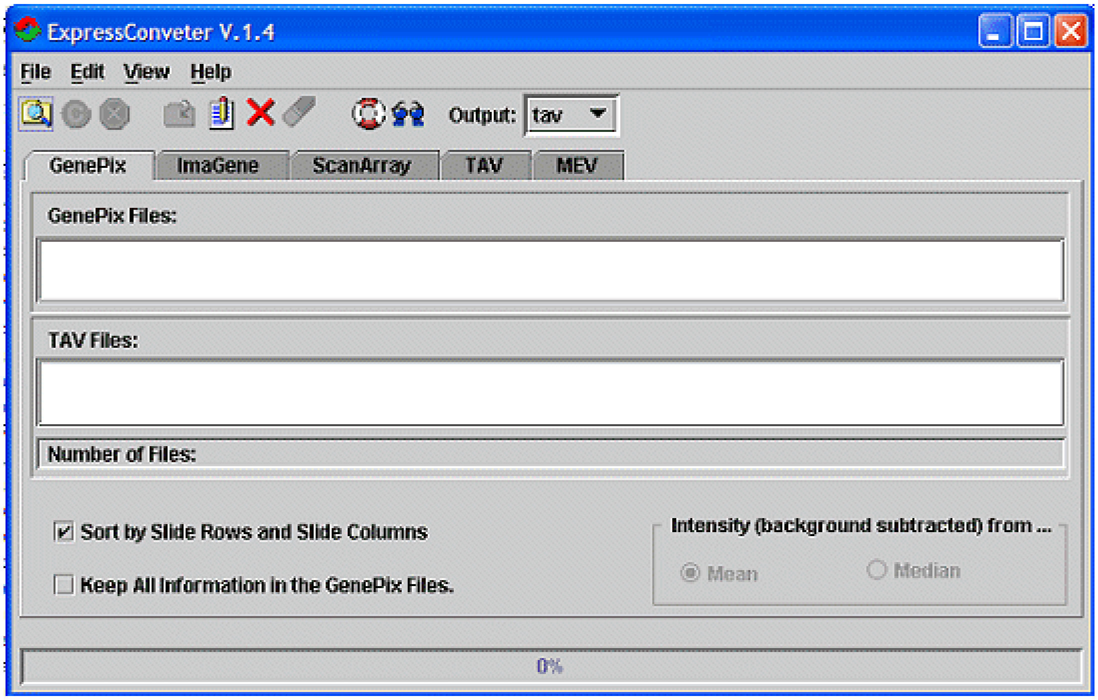
5.4.4 Saving SQL Results as a File

(1) Click the **Save Results** button to open a File Choose Window.
(2) Fill in the File Name by typing the path and name of the file or selecting from the Look in list and the window.
(3) Click the **Save** button.

5.5 Running ExpressConverter

ExpressConverter is a file format conversion tool that can change a variety of microarray data files to TIGR Mev/Tav files; as a result the data files are accessible by TIGR MIDAS and MEV. At time being, the ExpressConverter can take GenePix, ImaGene, and ScanArray files as inputs.

(1) Click Application tab in the Navigation Panel; or click **Tools** at the tool bar.
(2) Click **Express Converter** button to launch the program. For detail information, please read the help manual by clicking the **Help** button in the ExpressConverter tool bars.



Output: tav

☑ Sort by Slide Rows and Slide Columns

☐ Keep All Information in the GenePix Files.

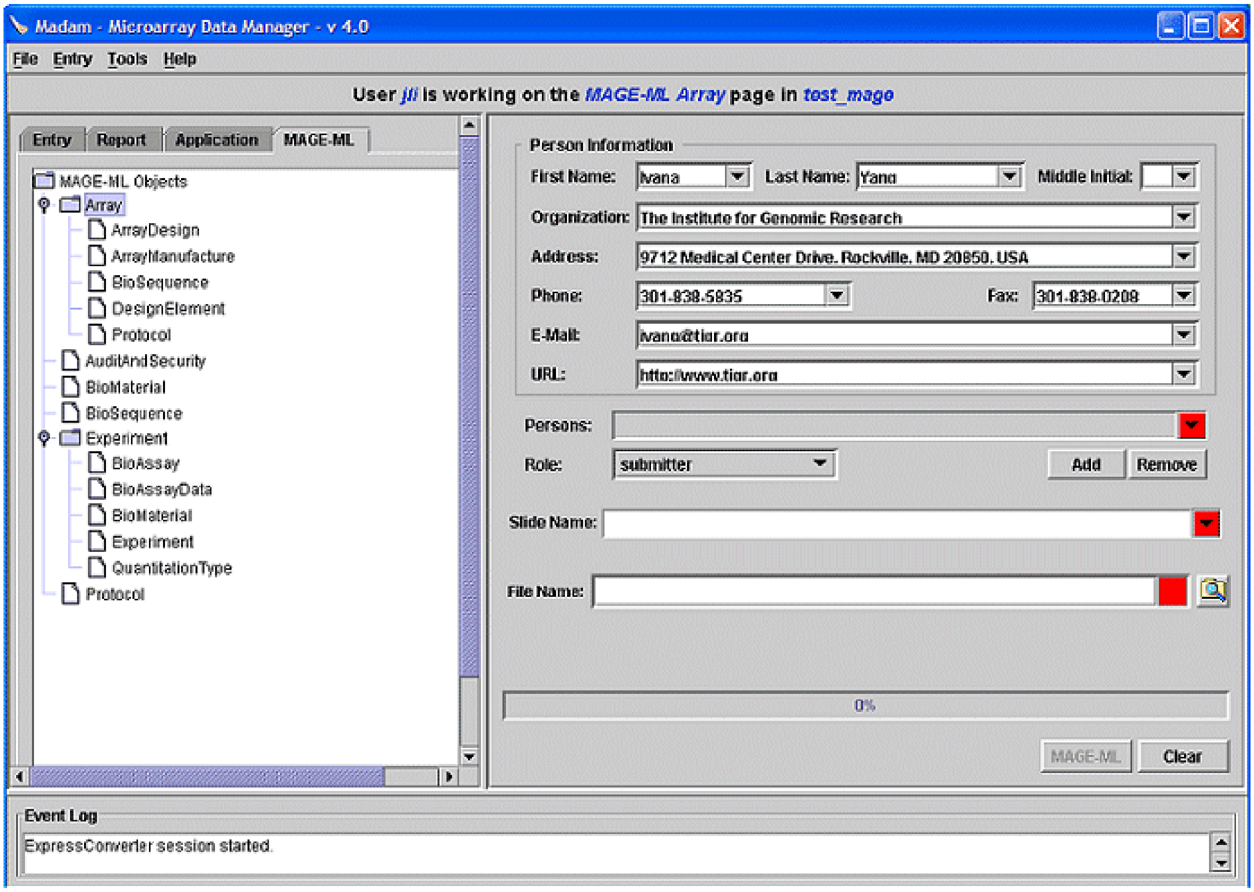
Intensity (background subtracted) from ...

● Mean ○ Median

Figure 5.4: ExpressConverter interface.

6. MAGE-ML Writing

After you upload your microarray data into the database, you can export them in MAGE-ML format so that the data could be exchangeable among your colleagues or submitted to public database such as ArrayExpress. Clicking the MAGE-ML tab in the Navigation Panel will show a MAGE-ML tree; when a branch or a node of the tree, representing a MAGE-ML object, is clicked, an interface that is suitable to the object will be presented in the Work Panel showed in picture 6.1.



User *jli* is working on the *MAGE-ML Array* page in *test_mage*

First Name: Ivana
Last Name: Yang
Middle Initial:
Organization: The Institute for Genomic Research
Address: 9712 Medical Center Drive. Rockville. MD 20850. USA
Phone: 301-838-5835
Fax: 301-838-0208
E-Mail: ivana@tigr.org
URL: http://www.tigr.org
Role: submitter

ExpressConverter session started.

Figure 6.1: The interface for writing MAGE-Ml files

You can select one or multiple objects under the same branch to export MAGE-ML files. As soon as all the required fields contain qualified entries, the MAGE-ML button will be activated. Clicking it will start the writing.

6.1 Write Array Out

The **Array** branch deals with the information about how arrays are created and deviated, and grouped. You can write all nodes (objects) at the same time by clicking the Array or any of the objects separately by clicking it (i.e. ArrayDesign, ArrayManufacture, and so on). The general steps are;

(1) Select the MAGE-ML object by clicking it. You can select multiple objects by holding the [Ctr] key while selecting.
(2) In the Work Panel, add person names to the Persons list and indicate who will be the submitter, researcher, supervisor, or curator. You can select the person by choosing the First Name, Last Name, Organization or others in the Person Information area, then select a Role for the person, and click the Add button. If you make a mistake for the setting, you can click Remove to drop the person from the list.
(3) Select a slide name from the Slide Name list.
(4) Provide a file name and path in the File Name field. You can click 🔍 icon to find the path on your system.
(5) Click MAGE-ML button to start writing.

6.2 Write AuditAndSecurity Out

The **AuditAndSecurity** is used for tracking of changes and information on user permissions to view the data and annotation. It is written out with every object in the tree.

(1) Select the AuditAndSecurity in the **MAGE-ML** pane.
(2) In the Work Panel, add person names to the Persons list and indicate who will be the submitter, researcher, supervisor, or curator. You can select the person by choosing the First Name, Last Name, Organization or others in the Person Information area, then select a Role for the person, and click the Add button. If you make a mistake for the setting, you can click Remove to drop the person from the list.
(3) The AuditAndSecurity should be associated with one of the MAGE-ML objects: Study Name, Experiment Name, or Slide Name. Select one of them by clicking the radio button before them.
(4) Select appropriate name from the list you have selected in above step.
(5) Provide a file name and path in the File Name field. You can click 🔍 icon to find the path on your system.
(6) Click MAGE-ML button to start writing.

6.3 Write BioMaterial Out

The **BioMaterial** describes how a BioSource is treated for making an array and hybridization.

(1) Select the BioMaterial in the **MAGE-ML** pane.
(2) In the Work Panel, add person names to the Persons list and indicate who will be the submitter, researcher, supervisor, or curator. You can select the person by choosing the First Name, Last Name, Organization or others in the Person Information area, then select a Role for the person, and click the Add button. If you make a mistake for the setting, you can click Remove to drop the person from the list. s
(3) Select a probe from the Probe Name from the list.
(4) Provide a file name and path in the File Name field. You can click 🔍 icon to find the path on your system.
(5) Click MAGE-ML button to start writing.

6.4 Write BioSequence Out

The **BioSequence** describes a known gene or sequence in the BioMaterial.

(1) Select the BioSequence in the **MAGE-ML** pane.
(2) In the Work Panel, add person names to the Persons list and indicate who will be the submitter, researcher, supervisor, or curator. You can select the person by choosing the First Name, Last Name, Organization or others in the Person Information area, then select a Role for the person, and click the Add button. If you make a mistake for the setting, you can click Remove to drop the person from the list. Select a slide name from the Slide Name list.
(3) Provide a file name and path in the File Name field. You can click 🔍 icon to find the path on your system.
(4) Click MAGE-ML button to start writing.

6.5 Write Experiment Out

The **Experiment** represents the container for a hierarchical grouping of BioAssays. It can have the end results of Clustering Analysis specified and, through the ExperimentDesign, a description and annotation of the overall design of the experiment and what it was to show. You can write all nodes (objects) at the same time by clicking the Experiment or any of the objects separately by clicking it (i.e. BioAssay, BioAssayData, and so on). The general steps are;

(1) Select the MAGE-ML object by clicking it. You can select multiple objects by holding the [Ctr] key while selecting.
(2) In the Work Panel, add person names to the Persons list and indicate who will be the submitter, researcher, supervisor, or curator. You can select the person by choosing the First Name, Last Name, Organization or others in the Person Information area, then select a Role for the person, and click the Add button. If you make a mistake for the setting, you can click Remove to drop the person from the list.
(3) If you want to write out all experiments (hybridizations) at the same time, click Study tab and select a study name from the drop-down list.
(4) If you want to write some experiments of a study, click the Experiment tab, select a study name, and press **RETURN** key. The all experiments of the study will show on the left list. Select those you want and click the arrow button to move them to the right list. Double-clicking the selected experiments will move them between the left and right lists. You can save the selected experiment into a file by clicking Save button; and later you can load the file by clicking Import button.
(5) Select the Internal or External for your BioAssayData (expressions) output type. The internal suggests that the data are embraced into the MAGE-ML file; and external means the data are saved as other files that can be referenced by the MAGE-ML file.
(6) Provide a file name and path in the File Name field. You can click 🔍 icon to find the path on your system.
(7) Click MAGE-ML button to start writing.

6.6 Write Protocol Out

The **Protocol** describes a generic laboratory procedure or analysis algorithm.

(1) Select the Protocol in the **MAGE-ML** pane.
(2) In the Work Panel, add person names to the Persons list and indicate who will be the submitter, researcher, supervisor, or curator. You can select the person by choosing the First Name, Last Name, Organization or others in the Person Information area, then select a Role for the person, and click the Add button. If you make a mistake for the setting, you can click Remove to drop the person from the list.
(3) Select a protocol name from the Protocol Name list.
(4) Provide a file name and path in the File Name field. You can click 🔍 icon to find the path on your system.
(5) Click MAGE-ML button to start writing.s

7. Configuration

Madam can be customized to meet your requirements by **Administrator** or **Preference Window**. For example, you can create a new database, change name of a scanner, add researcher or organization information for writing MAGE-ML, and even alter JDBC settings for other DBMS (i.e. Sybase/Oracle).

To launch the Administrator, click Start --> All Programs --> TigrMadam --> Administrator. If have your current Madam updated, you need to go to "*..\TigrMadam*" folder to execute *MadamAdministratorW.exe* file by double-clicking it.

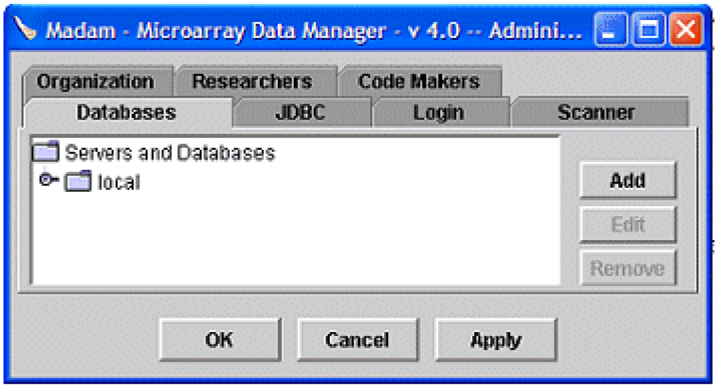


Figure 7.1: Configuration window.

7.1 Create New Databases

Note: Creation of databases is functional only on MySql DBMS installed on your local machine.

You can create a new database that has the identical schema as ***test_mage*** by using Madam Administrator or Preference Window. To open the Preference Window, click Preference ... under the File menu.

(1) Open Preference Window or launch Madam Administrator.
(2) Click Database tab.
(3) Click local node or any database name.
(4) Click Add button to open an input dialog.
(5) Type a database name and click OK button to close the dialog; the new database will show under local node.
(6) Click the OK button to close the Preference Window (You can click Apply button in the **Administrator** without closing the window). At the same time, a process dialog will show up. When the dialog close, the database is created.

7.2 Delete Databases

Note: You can only delete the name of database in the list without affecting the database. To remove the database, you must use MySql commands.

(1) Open Preference Window or Madam Administrator.
(2) Click Databases tab.
(3) Select a database name you want to delete.
(4) Click Remove button.
(5) Click the OK button to close the Preference Window (You can click Apply button in the **Administrator** without closing the window).

7.3 Change Database Name

Note: You can only change the name of database in the list to match the name on DBMS. To make really change, you have to use MySql commands.

(1) Open Preference Window or Madam Administrator.
(2) Select a database name you want to change.
(3) Click Edit button to open an input dialog.
(4) Type new database name and click OK button to close the dialog; the new database name will show under local node.
(5) Click the OK button to close the Preference Window (You can click Apply button in the **Administrator** without closing the window).

7.4 Modify JDBC Settings

If your databases are set on other DBMS (i.e. Sybase/Oracle), you can change the JDBC parameters to make Madam accessible to the DBMS.

(1) Open Preference Window or Madam Administrator.
(2) Click JDBC tab.
(3) Select a DBMS name from the Database Management System list. When selected, the corresponding JDBC Driver will show.
(4) Click the OK button to close the Preference Window (You can click Apply button in the **Administrator** without closing the window).

If there is no suitable DBMS name, click the Add button to open a **New JDBC Window** to add. You can get more information by clicking the Help button in the New JDBC Window.

If the DBMS name or JDBC Driver string is not correct, click the Edit button to open a **New JDBC Window** to change. You can get more information by clicking the Help button in the New JDBC Window.

Clicking Remove button will delete the selected DBMS and JDBC driver from the list.

7.5 Change Scanner Names

When entering data with Scan page, you need to select a scanner. If there is no your scanner, you can change the name of (or add) a scanner.

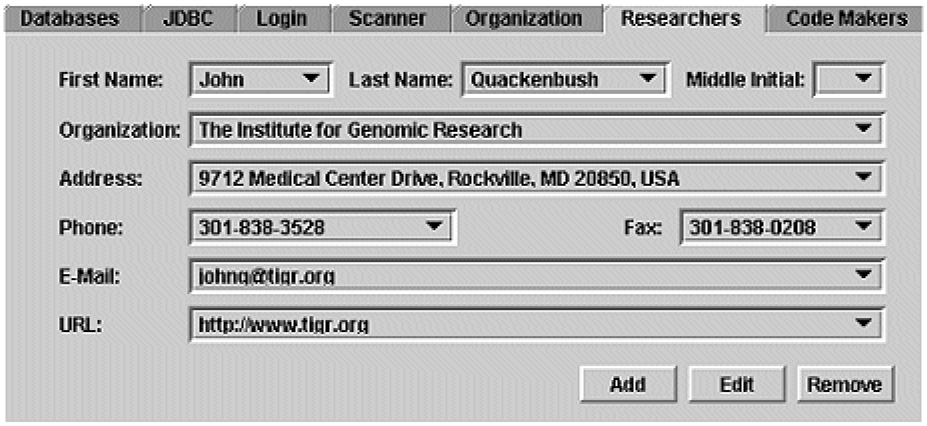
(1) Open Preference Window or Madam Administrator.
(2) Click Scanner tab.

(3) Click Edit button to open an input dialog. If you want to add a scanner, click Add button.
(4) Type new scanner name and click OK button to close the dialog; the new scanner name will show in the Scanner list.
(5) Click the OK button to close the Preference Window (You can click Apply button in the **Administrator** without closing the window).

7.6 Manage Person Information

Person information required to export MAGE-ML refers to the names and contact information of researchers and code makers. You can set them with **Administrator** or **Preference Window**. Both have the same interface as following (Figure 7.2).

It is straightforward to see that the Add, Edit, and Remove buttons allow you to add, change, and delete the person information from the lists.



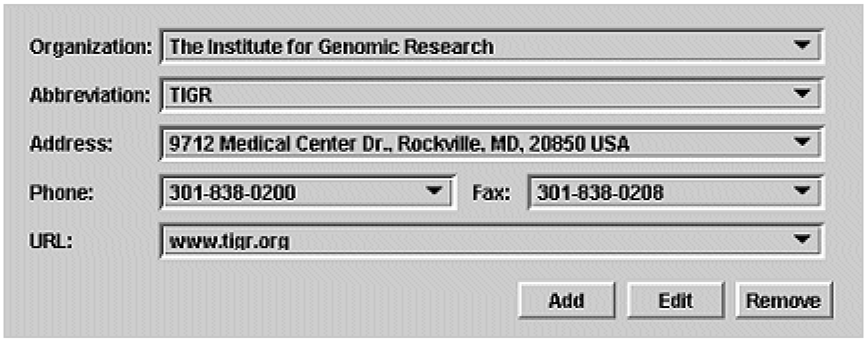
First Name: John
Last Name: Quackenbush
Middle Initial:
Organization: The Institute for Genomic Research
Address: 9712 Medical Center Drive, Rockville, MD 20850, USA
Phone: 301-838-3528
Fax: 301-838-0208
E-Mail: johnq@tigr.org
URL: http://www.tigr.org

Figure 7.2: Person information window.

7.7 Manage Organization Information

The information about your organization is required to export MAGE-ML files, especially its URL on internet. You can set the Organization with **Administrator** or **Preference Window**. Both have the same interface as following (Picture 7.3)

As managing person information, the tree buttons, (Add, Edit, and Remove), allow you to add, change, and delete the organization information from the lists.


Organization: The Institute for Genomic Research

Abbreviation: TIGR

Address: 9712 Medical Center Dr., Rockville, MD, 20850 USA

Phone: 301-838-0200

Fax: 301-838-0208

URL: www.tigr.org

Figure 7.3: Organization window

7.8 Set User-Id and Passwords

If you have difficulty to login the databases, it might need to set user-id and password again.

(1) Run Madam Administrator.
(2) Click Login tab.
(3) Fill in the User ID and Password fields.
(4) Click the OK button to close the Administrator (You can click Apply button in the **Administrator** without closing the window).

8. Troubleshooting

8.1 *I cannot start Madam Installer.*

ERROR: When I double-click the 'setup.bat' from the CD, a black window opened and closed.

ANSWER: You need to install Java Running Environment (JRE) on your system. Open the folder 'jvsuport' and double click 'jre-1_3_1_02-win.exe'. Follow the instructions to install the JRE.

8.2 *I cannot change the reserved memory for MySql DBMS.*

ERROR: I removed MySql with 'Add/Remove Program' from 'control panel'. When I reinstalled MySql and wanted to change the reserved memory, I failed to do that.

ANSWER: You might need to manually delete 'mysql' folder and its content before you re-install the MySql. If you cannot delete the 'mysql' folder, it might result from the running of Mysql. Refer to the next question to stop MySql.

8.3 *I cannot re-install MySql*

ERROR: I failed to install TIGR Madam and MySql at a time. When I re-install the programs, I always get failed.

ANSWER: The MySql might be running and keep you from starting it again. You need to shutdown or kill MySql by following steps:

(1) Open 'Window Task Manager' by right clicking the window menu bar and select 'Task Manager'. You can open it by pressing 'Ctrl', 'Alt', and 'Delete' keys simultaneously, and click 'Task Manager' button (for Window2000).
(2) Click 'Processes' tab and select 'mysql-max.exe' under the 'image name'.
(3) Right click mouse button and select 'End Process'.
(4) Click 'OK' button to kill MySql (It will take about 10 seconds to completely stop MySql).

8.4 *I cannot login the database*

ERROR: When I run Madam and tried to login a database, I got 'Unable to connect to server' error message.

ANSWER: There could be two causes:

Did you type right user-id and password?
(Please note, user-id and password are case sensitive).

Do you have the database in MySql?

Following steps help you to check the database.

(1) Leave the error message showing. This will allow MySql to keep running.
(2) Open a DOS window and change the directory to 'c:\mysql\bin' by typing 'cd mysql\bin'.
(3) Type 'mysql' and hit 'Return'.
(4) Type 'show databases;'

If the database you want to login is not in the list, you need to add the database to MySql.