# Table of Contents

1 Introduction ................................................................................. 1-1  
   1.1 Overview .............................................................................. 1-1  
   1.2 Copyright ............................................................................. 1-1  

2 Installation ................................................................................... 2-1  
   2.1 Overview .............................................................................. 2-1  

3 The Main Window ......................................................................... 3-1  
   3.1 Overview .............................................................................. 3-1  
   3.2 The Menu Bar ........................................................................ 3-2  
   3.3 Accessing the Main Window .................................................. 3-2  

4 Add New Experiments ................................................................. 4-1  
   4.1 Overview .............................................................................. 4-1  
      4.1.1 The Add New Experiments Window ............................... 4-1  
   4.2 Select an Array Database ..................................................... 4-2  
   4.3 File Options .......................................................................... 4-2  
   4.4 Add Files .............................................................................. 4-3  
      4.4.1 Add New Experiments .................................................... 4-3  
      4.4.2 Add SVM Files .............................................................. 4-3  
   4.5 Add Experiments to Database .............................................. 4-3  

5 Customize a File for Clustering ................................................... 5-1  
   5.1 Overview .............................................................................. 5-1  
      5.1.1 The Customize a File for Clustering Window .................. 5-1  
   5.2 Select an Array Database ..................................................... 5-2  
   5.3 Experiments to be Added to Cluster File .............................. 5-2  
   5.4 Add the Gene’s/ORF’s to Cluster File ................................... 5-2  
   5.5 Generate the Cluster File ..................................................... 5-2  

6 Customize a File for SVM .......................................................... 6-1  
   6.1 Overview .............................................................................. 6-1  

6.1.1 The Customize a File for SVM Window .............................. 6-1
6.2 Select an Array Database .............................................. 6-2
6.3 Experiments to be Added to SVM Files ............................. 6-2
6.4 Add Gene’s/ORF’s to the Positive Set ............................... 6-2
6.5 Selecting Output File Options ........................................ 6-2
   6.5.1 Class File Options .............................................. 6-2
   6.5.2 Test Output Options ............................................ 6-4
6.6 Generate SVM Files .................................................... 6-4

7 Quick View ........................................................................ 7-1

7.1 Overview ........................................................................ 7-1
   7.1.1 The Quick View Window .......................................... 7-1
7.2 Select an Array Database .............................................. 7-2
7.3 Select a Custom File .................................................... 7-2
7.4 Adding Experiments to be Viewed ................................. 7-2
7.5 Quick View Options ..................................................... 7-2
   7.5.1 Quick View Options Window ................................... 7-3
      7.5.1.1 Colour of Missing Values .................................. 7-3
      7.5.1.2 Colour of Zero Values ...................................... 7-3
      7.5.1.3 Start Colouring .............................................. 7-4
      7.5.1.4 Report Options ............................................. 7-4
7.6 Quick View .................................................................... 7-5
7.7 The Quick View Output ................................................ 7-5
   7.7.1 The Quick View Option Toolbar ................................. 7-5
      7.7.1.1 The AFM 3.0 Toolbar Option ............................... 7-5
      7.7.1.2 The Zoom In Toolbar Option ............................... 7-5
      7.7.1.3 The Zoom Out Toolbar Option ............................. 7-6
      7.7.1.4 The Filter Toolbar Option ................................. 7-6
         7.7.1.4.1 The Filter Window ...................................... 7-6
         7.7.1.4.2 The Similarities Filter ................................ 7-7
         7.7.1.4.3 The Differences Filter ................................. 7-8
      7.7.1.5 The Colour Option Toolbar Option ....................... 7-9
      7.7.1.6 The SGD Toolbar Option .................................. 7-9

8 Chromosome Counter ....................................................... 8-1

8.1 Overview ........................................................................ 8-1
   8.1.1 The Chromosome Counter Window ............................ 8-1
8.2 Selecting your Database .............................................. 8-2
8.3 Saving the Output File ................................................ 8-2
8.4 Chromosome Counter Options ...................................... 8-2
   8.4.1 By Mean ............................................................. 8-2
<table>
<thead>
<tr>
<th>Section</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>8.4.1 By Median</td>
<td>8-2</td>
</tr>
<tr>
<td>8.5 Adding the Experiments</td>
<td>8-2</td>
</tr>
<tr>
<td>8.6 Start Counting</td>
<td>8-2</td>
</tr>
<tr>
<td><strong>Appendix A File Formats</strong></td>
<td>A-1</td>
</tr>
<tr>
<td>A.1 Overview</td>
<td>A-1</td>
</tr>
<tr>
<td>A.2 Array Database Format</td>
<td>A-1</td>
</tr>
<tr>
<td>A.2.1 Overview</td>
<td>A-1</td>
</tr>
<tr>
<td>A.2.2 Database Settings</td>
<td>A-2</td>
</tr>
<tr>
<td>A.3 Ready for Database Format</td>
<td>A-2</td>
</tr>
<tr>
<td>A.4 Custom File Format</td>
<td>A-3</td>
</tr>
<tr>
<td>A.5 Generate Venn Diagram Option</td>
<td>A-4</td>
</tr>
<tr>
<td></td>
<td>A-5</td>
</tr>
</tbody>
</table>
1 Introduction

1.1 Overview

The Array File Maker 4.0 (AFM 4.0) application is designed to help organize and interpret the massive amounts of data produced from microarray experiments. The AFM program allows the user to quickly add his/her experiments into an excel spreadsheet for further manipulation and investigation. The user can then take this Array Database and quickly generate the input files necessary for the two popular freewares available for clustering array experiments:

a.) Michael Eisen’s cluster program
b.) William Noble Grundy’s svm v1.0 program

The AFM program, Quick View option, can transform the database into a wash of colour, where the intensity of colour signifies the extent of gene induction. Once you have the coloured database, AFM can generate Venn diagrams that show the similarities and differences of gene’s in your experiments.

1.2 Copyright

Copyright Notice

Copyright ©2001 Mount Sinai Hospital, Toronto, Canada. All Rights Reserved.

Disclaimer

All downloads and use of the Array File Maker 4.0 is subject to the following terms:

Permission is hereby granted to use, copy, modify, and distribute this software, its source code, and its documentation for educational, research, and not-for-profit purposes, without fee and without a signed licensing agreement, provided that the above copyright notice, this paragraph and the following paragraphs appear in all copies, modifications, and distributions, and related documentation. The right to use, copy, modify, and distribute this software, its source code and its documentation by companies or other for profit organizations or in conjunction with for profit activities, are not granted except by prior arrangement and written consent of the copyright holder. Contact Terry Donaghue, The Office of Technology Transfer, Mount Sinai Hospital at donaghue@mshri.on.ca, for commercial licensing opportunities.

IN NO EVENT SHALL MOUNT SINAI HOSPITAL BE LIABLE TO ANY PARTY FOR DIRECT, INDIRECT, SPECIAL, INCIDENTAL, OR CONSEQUENTIAL
DAMAGES, INCLUDING LOST PROFITS, ARISING OUT OF THE USE OF THIS SOFTWARE AND ITS DOCUMENTATION, EVEN IF MOUNT SINAI HOSPITAL HAS BEEN ADVISED OF THE POSSIBILITY OF SUCH DAMAGE.

MOUNT SINAI HOSPITAL SPECIFICALLY DISCLAIMS ANY IMPLIED WARRANTIES OF MERCHANTABILITY AND FITNESS FOR A PARTICULAR PURPOSE. THE SOFTWARE AND ACCOMPANYING DOCUMENTATION, IF ANY, PROVIDED HEREUNDER IS PROVIDED "AS IS". MOUNT SINAI HOSPITAL HAS NO OBLIGATION TO PROVIDE MAINTENANCE, SUPPORT, UPDATES, ENHANCEMENTS, OR MODIFICATIONS.

Published research assisted by this software should cite:

2 Installation and Setting up Your Database

2.1 Overview

AFM 4.0 is indifferent to the number of spots on the array and to the organism represented by the array.

**AFM 4.0 works strictly with log base 2 values.** Expression ratios are easier to work with when in log form and log base 2 is an intuitive and standard format. AFM 4.0 only works on a database with a defined format, see Appendix A.2 for details, which requires that the user first set up a database template. Proceed to the Excel sheet labeled “Database Settings” (click the button on the bottom left hand side of the Excel sheet). There are six settings that need to be defined, see Appendix A.2.2 for details.
3 The Main Window

3.1 Overview

The Main window of the AFM 4.0 application program (Figure 3-1) is used to access one of the following five options currently available:

a.) Add New Experiments (presented in chapter 4)
b.) Customize a File for Clustering (presented in chapter 5)
c.) Customize a File for SVM (presented in chapter 6)
d.) Quick View (presented in chapter 7)
e.) Chromosome Counter (presented in chapter 8)

Figure 3-1: The Main Window
3.2 The Menu Bar

Accessing the various options available in AFM is the role of the menu bar, which is located across the top of the main window (Figure 3-2). Note: The darker Grey shading indicates which option is currently active.

![Figure 3-2: The Menu Bar](image)

3.3 Accessing the Main Window

You can access the main window (figure 3-1) in two different ways:

a.) The easiest way, and the one we recommend is to go to the “AFM 4.0” sheet (Figure 3-3) in the workbook that contains the application. From here you can access the Main Window by clicking on the RUN button. This sheet also contains the copyright (chapter 2.2).

![Figure 3-3: The AFM 4.0 Sheet](image)
b.) Load the workbook that contains the application and go to the Tools menu (Figure 3-4). Select the run Macros… options (or press Alt + F8). This will bring up the window shown in figure 3-5, select the macro named “ArrayFileMaker” and click on the Run button.

Figure 3-4: Excel Tools Menu

Figure 3-5: Run Macro Menu
4 Add New Experiments to the Array Database

4.1 Overview

The Add New Experiments to the Array Database option allows the user to quickly add experiments and SVM output files into the Array Database in four easy steps as indicated by the red boxes.

4.1.1 The Add New Experiments Window

The Add New Experiments Window (Figure 4-1)

![Add New Experiments Window](image)

Figure 4-1: The Add New Experiments Window
4.2 Select an Array Database

The role of Select an Array Database step (step 1 of 4) is to select the database in which you want to add the new experiments to. This can be accomplished by simply clicking on the “Browse” button and selecting the database you want.

**NOTE:** It is very important that the database that you select is in compliance with your database settings, see Appendix A section A.2.2 for more information on database settings.

4.3 Files Option

The role of the Files Option (Figure 4-2) step (step 2 of 4) is to tell the AFM program the type of files you are adding to the Array Database. There are two options available:

a.) Add New Experiments

This option is used to add files that are in the *ready for database format* (see Appendix A section A.3 for more details).

b.) Add SVM files

This option will be implemented in future versions of AFM to add the output files produced from running the svm 1.0 program to your database.

Figure 4-2: File Options
4.4 Add Files

4.4.1 Add New Experiments

The role of the Add New Experiments step (step 3 of 4) is to browse the computers file structure and add the files that contain the new experiments which have to be in the correct format (see Appendix A section A.3 for details) to your database.

4.4.2 Add SVM Files

The role of the Add SVM Files step (step 3 of 4) is to add the output file produced from the SVM program.

4.5 Add Experiments to Database

The role of the Add Experiments to Database step (step 4 of 4) is to add the experiments from the files provided to the database.
5 Customize a File for Clustering

5.1 Overview

The role of the Customize a File for Clustering option is to allow the user to generate the input files that can be used in Michael Eisen’s cluster program in four easy steps as indicated by the red boxes in figure 5-1. For more information on the cluster program please visit http://rana.stanford.edu/software/.

5.1.1 The Customize a File for Clustering Window

The Customize a File for Clustering Window (Figure 5-1)

![Figure 5-1: Customize a File for Clustering Window](image-url)
5.2 Select an Array Database

The role of Select an Array Database step (step 1 of 4) is to select the database that contains the experiments that you want to cluster. This can be accomplished by simply clicking on the “Browse” button and selecting the database you want.

NOTE: It is very important that the database that you select is in compliance with your database settings, see Appendix A section A.2.2 for more information on database settings.

5.3 Experiments to be Added to the Cluster File

The role of the Experiments to be Added to the Cluster File step (step 2 of 4) is to select the experiments from the experiments available list and add them to the Experiments to be Added to Cluster File list. You need to first highlight the experiments and then click on the “ADD” button to add the highlighted experiments.

5.4 Add the Gene’s/ORF’s to the Cluster File

The role of the Add the Gene’s/ORF’s to the Cluster File step (step 3 of 4) is to Select the genes/ORF’s that you would like to include in your input file. This can be done a few ways:

a.) Typing your genes/ORF’s in and pressing the enter key or pressing the Find Button.

b.) Pressing the Open File for Cutting and Pasting button to open a file that contains the genes/ORF’s (can be more than one) you are interested in. Then you can simply cut and paste them into the text box and hit enter or press the “Find” button.

c.) Highlighting the ORF’s from the list box and pressing the add ORF’s button.

d.) Pressing the Add all ORF’s button will add all the available genes/ORF’s in your database to the input file.

5.5 Generate the Cluster File

The role of the Generate the Cluster File step (step 4 of 4) is to generate the input file for Michael Eisen’s cluster program.
6 Customize a file for SVM

6.1 Overview

The role of the Customize a File for SVM Window (Figure 6-1) is to allow the user to generate the input files that can be used in William Noble Grundy’s svm v1.0 program in six easy steps as indicated by the red boxes in Figure 6-1. For more information on SVM visit http://www.cs.columbia.edu/~bgrundy/svm/doc/svm.html.

6.1.1 The Customize a file for SVM Window

The Customize a File for SVM Window (Figure 6-1)
6.2 Select an Array Database

The role of Select an Array Database step (step 1 of 5) is to select the database that contains the experiments that you want to include in your SVM input files. This can be accomplished by simply clicking on the “Browse” button and selecting the database you want.

**NOTE:** It is very important that the database that you select is in compliance with your database settings, see Appendix A section A.2.2 for more information on database settings.

6.3 Experiments to be Added to SVM Files

The role of the Experiments to be Added to SVM Files step (step 2 of 6) is to select from your database the experiments you want to include in your SVM input files. This can be accomplished by simple highlighting the experiments you are interested in and clicking on the “ADD” button.

6.4 Add Gene’s/ORF’s to the Positive Set

The role of the Add Gene’s/ORF’s to the Positive Set step (step 3 of 6) is to select the specific Gene’s/ORF’s that belong to the Positive Set.

6.5 Selecting Output File Options

The role of the Selecting Output File Options step (step 4 of 6) is to let the AFM program know how you want the Class File and Test File to be generated.

6.5.1 Class File Options

After you have selected the ORF’s that belong to your positive set you have a choice on how you choose your ORF’s that make up the negative set. As you can see from figure 6-1 you have two different options:

a.) You can randomly generate the negative set by selecting the random options and supply the AFM program with a number greater than one and less than the total number of negative ORF’s available.

b.) You can add your own ORF’s to the negative set by choosing the Add your Own ORFs to the Negative Set option. Once you select this option the
Customize a File for SVM window (Figure 6-1) will be transformed into Figure 6-2 to give you the ability to *Add your Own ORF’s to the Negative Set* step (step 5 of 6).

**NOTE:** You do not need to do this step if you have chosen to randomly generate the negative set. If you need to make any changes to the positive set you will be prompted with the message shown in figure 6-3, and will need to reenter your positive set ORF’s.

![Figure 6-2: Customize a File for SVM with Add to negative set Window](image)

![Figure 6-3: Message Box](image)
6.5.2 Test Output File Options

The role of the Test Output File Options is to let the AFM program know whether or not you want to include all the training ORFs in your test file or exclude them based on which option you choose.

6.6 Generate SVM Files

The role of the Generate SVM Files step (step 6 of 6) is to generate the three input files (Class File, Train File, and Test File) that are necessary for the SVM program.
7 Quick View

7.1 Overview

Quick View allows the user to transform the contents of the cells from numbers to colours, where the intensity of the colour signifies the extent of gene induction.

7.1.1 The Quick View Window

The Quick View Window (Figure 7-1)

![Quick View Window](image)

Figure 7-1: The Quick View Window
7.2 Select an Array Database

The role of Select an Array Database step (step 1 of 4) is to select the database that contains the experiments that you want to view in colour. This can be accomplished by simply clicking on the “Browse” button and selecting the database you want.

NOTE: It is very important that the database that you select is in compliance with your database settings, see Appendix A section A.2.2 for more information on database settings.

7.3 Select a Custom File

The role of Select a Custom File step (step 1 of 4) is to select the file that contains the experiments that you want to view. This can be accomplished by simply clicking on the “Browse” button and selecting the custom file you want.

NOTE: It is very important that the custom file that you select is in the correct format, see Appendix A section A.4 for more information on custom file format.

7.4 Add Experiments to be Viewed

The role of the Add Experiments to be Viewed step (step 2 of 4) is to add the experiments from the experiments available in the array database list to the Experiments to be Viewed list by simple clicking on the “ADD” button.

7.5 Quick View Options

The role of the Quick View Options step (step 3 of 4) is to set the various options available for colouring the cells. You can also set the options for generating a report that is explained in section 7.5.1.4.
7.5.1 Quick View Options Window

The Quick View Options Window (Figure 7-2)

![Quick View Options Window](image)

Figure 7-2: The Quick View Options Window

7.5.1.1 Colour of Missing Values

There are four colours that you can choose from to colour the blank cells.

7.5.1.2 Colour of Zero Values

There are four colours that you can choose from to colour the cells that contain a value of zero.
7.5.1.3 Start Colouring

The role of the Start Colouring options is to set the fold value at which to start colouring the cells.

7.5.1.4 Report Options

The role of the Report Options, if selected, is to generate a report found on the “Report” sheet (Figure 7-3) in the workbook that contains the application. The report will tell you four things:

a.) How many gene’s/ORF’s that are repressed by the value inputted.
b.) How many gene’s/ORF’s that are induced by the value inputted.
c.) How many gene’s/ORF’s there were total for a given experiment
d.) How many gene’s/ORF’s there are available in your database

![Figure 7-3: The Report Sheet](image-url)
7.6 Quick View

The role of the Quick View step (step 4 of 4) is to initiate the colouring of the cells and generation of the report.

7.7 The Quick View Output

Once Quick View has finished colouring all the cells you will be taken to the Quick View Sheet so that you can view the output produced by Quick View.

7.7.1 The Quick View Options Toolbar

The role of the Quick View Options Toolbar (Figure 7-4) is to help manipulate the data. The toolbar is loaded automatically with the workbook that contains the AFM program, and should appear with the other toolbars.

![Figure 7-4: The Quick View Options Toolbar](image)

7.7.1.1 The AFM 4.0 Toolbar Option

The role of the AFM 4.0 Toolbar Option is to gain access to the main window of the AFM program (see chapter 3).

7.7.1.2 The Zoom In Toolbar Option

The role of the Zoom In Toolbar Option (Figure 7-5) is to zoom in on both the rows and columns of the coloured cells.

![Figure 7-5: The Zoom in Toolbar Option](image)
7.7.1.3 **The Zoom Out Toolbar Option**

The role of the Zoom out Toolbar Option (Figure 7-6) is to Zoom out on both the rows and columns of the coloured cells.

![Figure 7-6: The Zoom out Toolbar Options](image)

7.7.1.4 **The Filter Toolbar Option**

The role of the Filter Toolbar Option is to show the Filter Window shown in figure 7-7.

7.7.1.4.1 **The Filter Window**

The role of the Filter Window (Figure 7-7) is to let the user quickly filter for the ORF’s repressed and induced by the inputted fold value. From this window you can also access the Similarities Filter (see section 7.7.1.4.2) and the Differences Filter (see section 7.7.1.4.3).

![Figure 7-7: The Filter Window](image)
7.7.1.4.2 The Similarities Filter

The role of the Similarities Filter (Figure 7-8) is to show the genes that are induced greater than or repressed less than a user defined fold value. Please see Appendix A.5 for an explanation of the Generate VENN Diagram option. (Note: Can not create Venn diagrams when the number of experiments selected is greater than 4)

![Similarities Filter](image)

Figure 7-8: The Similarities Filter
7.7.1.4.3  The Differences Filter

The role of the Differences Filter (Figure 7-9) is to:

1.) Show the genes that are induced greater than a user defined fold value in experiment list A, and are induced no more than a user defined fold value in Experiment list B.

2.) Show the genes that are repressed less than a user defined fold value in experiment list A, and are induced no less than a user defined fold value in Experiment list B.

\[
( \text{Induced} > X \text{ fold in List A} ) \text{ AND } ( \text{Induced no more than} Y \text{ fold in List B} )
\]

\[
\text{OR} \\
( \text{Repressed} < U \text{ fold in List A} ) \text{ AND } ( \text{Repressed no less than} T \text{ fold in List B} )
\]

Where: X, Y, U, T are user defined fold values

Please see Appendix A.5 for an explanation of the Generate VENN Diagram option. (Note: Can not create Venn diagrams when the number of experiments selected is greater than.

Figure 7-9: The Differences Filter
7.7.1.5 The Colour Options Toolbar Option

The role of the Colour Options (Figure 7-10) is to allow the user to do one of three things: 1) Change the colour of missing values, 2) Change the colour of zero values, and 3) Change the intensity of the coloured cells.

![Colour Options](Image)

Figure 7-10: The Colour Option

7.7.1.6 The SGD Toolbar Option

The role of the SGD Toolbar Option is to provide the user with a hyperlink to Saccharomyces Genome Database (SGD). The user can simply select the gene of interest and then clicking on the SGD Toolbar Option on the toolbar to jump to SGD.
8 Chromosome Counter

8.1 Overview

AFM’s chromosome counter calculates the mean or median expression ratios across each yeast chromosome.

8.1.1 The Chromosome Counter Window

The Chromosome Counter Window (Figure 8-1)

Figure 8-1: Chromosome Counter Window
8.2 Select an Array Database

The role of Select an Array Database step (step 1 of 5) is to select the database that contains the experiments that you want to count the mean/median of the chromosomes. This can be accomplished by simply clicking on the “Browse” button and selecting the Database you want.

**NOTE:** It is very important that the database that you select is in compliance with your database settings, see Appendix A section A.2.2 for more information on database settings.

8.3 Saving the Output File

The role of Saving the Output File step (step 2 of 5) is to let the AFM program know what and where you would like the output file to be saved.

8.4 Chromosome Counter Options

The role of the Chromosome Counter Options step (step 3 of 5) is to let the AFM program know how you would like to count the chromosomes.

8.4.1 By Mean

This option reports the Mean of the chromosome.

8.4.2 By Median

This option reports the Median of the chromosome.

8.5 Adding the Experiments

The role of the Adding the Experiments step (step 4 of 5) is simple to let the AFM program know what experiments you would like counted.

8.6 Start Counting

The role of the Start Counting step (step 5 of 5) is to initiate the counting of the chromosomes.
Appendix A File Formats

A.1 Overview

To avoid problems with using the AFM program it is extremely important that you make sure that all the settings (see section A.2.2) are correct.

A.2 Array Database Format

A.2.1 Overview

The AFM program expects that your database be in a specific format that you determine in your Database Settings (see section A.2.2 for details). Figure A-1 is an example of a typical Array Database. Anything you see in red must be in your database, although the cells can contain any string. There are four major points to each array database:

a.) The Unique ID column must be in the first column and be in ascending alphabetical order.

b.) There can be no blanks in the Unique ID column.

c.) If you do have an EWEIGHT row in your database then you must place it in the second row. Note that after you do a sort on your database you must make sure that if the EWEIGHT row is not placed in the second row you must cut and paste it into the second row manually before running the AFM program.

d.) There can be no blanks across the top row of your database. This is essential to ensure that the AFM program places your experiments in the right location.

Figure A-1: Example Array Database
A.2.2 Database Settings

The role of the Database Settings (Figure A-2) is to let the AFM program know how you have set up your database. There are six options that the application can recognize, three of which are essential shown in red in Figure A-2.

a.) The Unique ID Column must be in Column 1 and must be in an ascending alphabetical order, see Figure A-1 for an example.
b.) If you have supplied a Gene Name Column you should insert its column number so the AFM program knows where to look for it.
c.) If you have supplied a Description Column you should insert its column number so the AFM program knows where to look for it.
d.) If you have a EWEIGHT value in your database then you must answer yes to this question, if not then answer no. If you do have an EWEIGHT row in your database it must reside in the second row.
e.) If you have a GWEIGHT value in your database then you should insert its column number so the AFM program knows where to look for it.
f.) You must inform the AFM program about how many columns are in your database template (i.e. The number of columns in your database minus the experiments), so that it knows where the experiments begin.

<table>
<thead>
<tr>
<th>Options</th>
<th>Column Number</th>
</tr>
</thead>
<tbody>
<tr>
<td>Unique ID Column</td>
<td>Must be in Column 1</td>
</tr>
<tr>
<td>Gene Name Column</td>
<td>2</td>
</tr>
<tr>
<td>Description Column</td>
<td>3</td>
</tr>
<tr>
<td>EWEIGHT Included (YES/NO)?</td>
<td>yes</td>
</tr>
<tr>
<td>(If included then must be in the second row of the Unique ID Column)</td>
<td></td>
</tr>
<tr>
<td>GWEIGHT Column</td>
<td>4</td>
</tr>
<tr>
<td>Number of Columns in your database Template</td>
<td>4</td>
</tr>
<tr>
<td>(The number of columns not including the experiments)</td>
<td></td>
</tr>
</tbody>
</table>

Figure A-2: Database Settings
A.3 Ready for Database Format

The *Ready for Database Format* (Figure A-3) is the format the AFM program expects your files to be in if you want to add new experiments (see section 4.4.1) to an Array Database. The Unique ID column has to be the same or a subset of the Unique ID column in your database. It must also be in ascending alphabetical order and cannot contain any blanks. The other columns contain the experiments you would like to add. The top row of each column cannot be blank, but must contain the name of the experiment. The rest of the experiment column must contain numerical values, but blanks are accepted.

![Ready for Database Format Example](image-url)

Figure A-3: Ready for Database Format
A.4 Custom File Format

The Custom File Format (Figure A-4) is the format that is accepted by the custom file option in Quick View (see section 7.3). This format is useful if you want to view pre-clustered files in Quick View. The format expects the first column to be the Unique ID column, which contains no blanks. The next column can be whatever you please, but something has to be put in this column, even if you have to copy and paste your Unique ID column into it. The rest of the columns should contain the log base 2 values with a label for each experiment in the top cell of each column. Note that you do not have to maintain the ascending alphabetical order of the Unique ID column.

Figure A-4: Custom File Format Example
A.5 Generate Venn Diagram Option

If the *Generate Venn Diagram* option is selected, AFM 4.0 will generate a new workbook containing the following:

1.) A Venn diagram (Figure A-5) graphically displaying the results for the experiments the user selected.
2.) Multiple worksheets (Figure A-6) containing the different subsets of the Venn diagram.
3.) Finally, a report (Figure A-7) for each experiment showing the genes that belong exclusively to each set. (NOTE: Each gene name is a hyperlink to SGD)

![Venn Diagram Worksheet](image)

*Figure A-5: Venn Diagram Worksheet*
Figure A-6: Multiple Worksheets containing the Venn Diagram subsets

Figure A-7: Report Worksheet on each Experiment