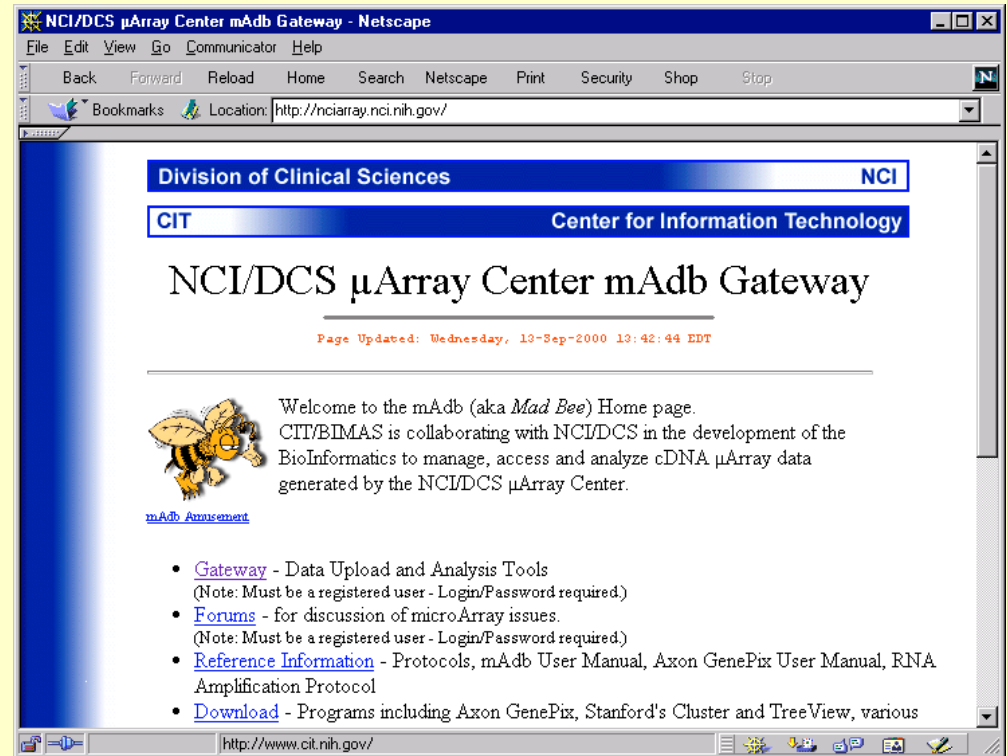



IV. Using NCI/CIT mAdb data with MicroArray Explorer



Outline

1. Log into mAdb
2. Select your data
3. Download it as a Zip file to your computer
4. Unpack the Zip file
5. Click on the  Start.mae

IV. Procedure to Use MAExplorer on mAdb Data

- 1. Install MAExplorer if not already installed (see MAExplorer installation Procedure).
- 2. Go to <http://nciarray.nci.nih.gov/> with your Web browser
- 3. Go to "**Gateway**"
- 4. Go to "**Tools**"
- 5. Select the set of projects to be exported from the scrollable list.
- 6. Select "**BETA formatted array data retrieval tool**".
- 7. Select "**LECB/NCI MAExplorer**" for the "Retrieval format".
- 8. **Submit**. This will eventually replace the Web page with a new page containing a numbered (number related to date and time of day) file ending in **.zip**. The file will be purged after a while, so it should not be treated as a permanent link.
- 9. Click on the **.zip** file to download and save it locally to your disk.
- 10. Unpack the **.zip** file to a new directory, for example "*myData*"
- 11. On Windows systems, double click on Start.mae in the *myData\MAE* directory. This will start up MAExplorer.

MAExplorer is Compatible with mAdb Data

mAdb Downloads - Netscape

File Edit View Go Communicator Help






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NCI/DCS μ Array Center mAdb Downloads

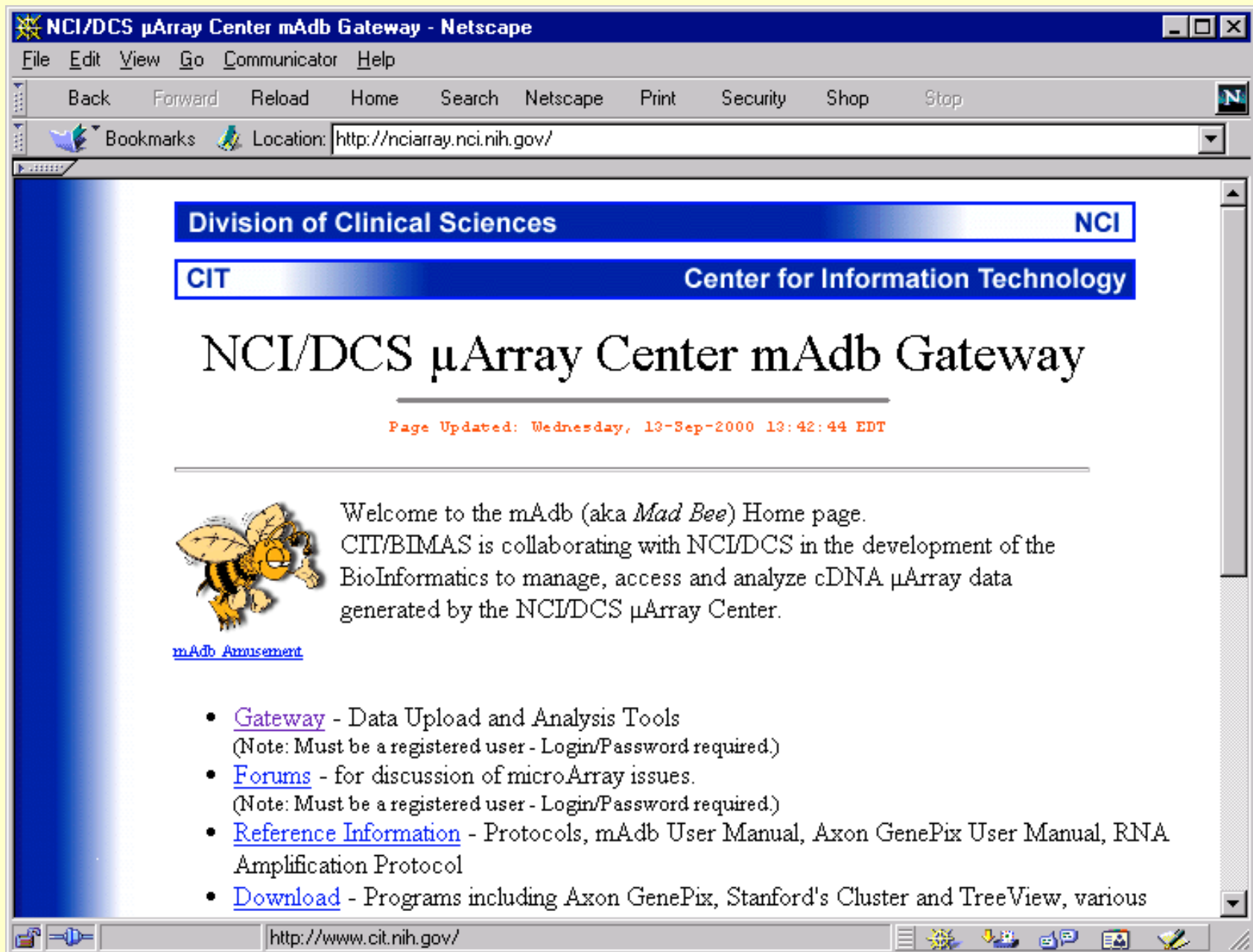
Page Updated: Thursday, 24-May-2001 14:01:17 EDT

		Program	Description	Author	Version	Updated	Download	Manual
<p>Axon Inc. Software</p> <p>This is commercial, licensed software and the GenePix application requires a "dongle" attached to the parallel port to run. The manual is accessible to all.</p> <p>Axon's Web Site</p>		GenePix Pro 3	Fully integrated acquisition and analysis software for the GenePix 4000A. Download to a folder of your choice and then run to extract the installation files. Then run the extracted file setup.exe and follow installation instructions		3.0.6.66 History	(Posted here 05/24/2001)	Download	GenePix3.0 Manual Axon Scanner Manual (PDFs)
<p>Stanford Genome Analysis Group Software</p> <p>It is available free of charge to academic and non-profit institutions.</p> <p>Stanford Download Site</p>		ScanAlyze	Image Analysis (extracts data from fluorescence images of arrays)	Michael Eisen	2.44	11/15/99	Download	Manual (PDF)
		Cluster	Perform Hierarchical Clustering, Self-organizing Maps, k-Means Clustering, and More	Michael Eisen	2.11.01	7/10/2000 (Posted here 10/26/2000)	Download	Manual (PDF)
		TreeView	Graphical Viewing and Browsing of Cluster Results	Michael Eisen	1.45	9/28/99	Download	
<p>MAExplorer</p> <p>Developed by and Available from LECB/FCRF/NCI.</p> <p>MAExplorer Web Site</p>		MAExplorer	A Java data mining application for gene expression data using a variety of statistical, clustering, direct-manipulation graphical, spreadsheet and Web access methods.	Peter Lemkin	Revision History	Current version	Link to Download	Manual (Online) Use with mAdb data (PDF)

Document: Done

IV.1 NCI/CIT mAdb Web Server Home Page

<http://nciarray.nci.nih.gov/>



The screenshot shows a Netscape browser window titled "NCI/DCS μ Array Center mAdb Gateway - Netscape". The address bar shows the URL "http://nciarray.nci.nih.gov/". The page content includes a blue header with "Division of Clinical Sciences" and "NCI", and "CIT" and "Center for Information Technology". The main heading is "NCI/DCS μ Array Center mAdb Gateway". Below this, a red text line indicates the page was updated on Wednesday, 13-Sep-2000 at 13:42:44 EDT. A cartoon bee logo is positioned to the left of the welcome text. The text reads: "Welcome to the mAdb (aka *Mad Bee*) Home page. CIT/BIMAS is collaborating with NCI/DCS in the development of the BioInformatics to manage, access and analyze cDNA μ Array data generated by the NCI/DCS μ Array Center." Below this is a link for "mAdb Amusement". A bulleted list of links is provided: "Gateway" (Data Upload and Analysis Tools, login required), "Forums" (discussion of microArray issues, login required), "Reference Information" (Protocols, mAdb User Manual, Axon GenePix User Manual, RNA Amplification Protocol), and "Download" (Programs including Axon GenePix, Stanford's Cluster and TreeView, various).

NCI/DCS μ Array Center mAdb Gateway - Netscape

File Edit View Go Communicator Help

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Bookmarks Location: <http://nciarray.nci.nih.gov/>

Division of Clinical Sciences NCI

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NCI/DCS μ Array Center mAdb Gateway

Page Updated: Wednesday, 13-Sep-2000 13:42:44 EDT



Welcome to the mAdb (aka *Mad Bee*) Home page.
CIT/BIMAS is collaborating with NCI/DCS in the development of the BioInformatics to manage, access and analyze cDNA μ Array data generated by the NCI/DCS μ Array Center.

[mAdb Amusement](#)

- [Gateway](#) - Data Upload and Analysis Tools
(Note: Must be a registered user - Login/Password required.)
- [Forums](#) - for discussion of microArray issues.
(Note: Must be a registered user - Login/Password required.)
- [Reference Information](#) - Protocols, mAdb User Manual, Axon GenePix User Manual, RNA Amplification Protocol
- [Download](#) - Programs including Axon GenePix, Stanford's Cluster and TreeView, various

<http://www.cit.nih.gov/>

IV.2 Press “Gateway” & Log on to mAdb Server

NCI/DCS μArray Center mAdb Gateway - Netscape

File Edit View Go Communicator Help

Back Forward Reload Home Search Netscape Print Security Shop Stop


Bookmarks Location: <http://nciarray.nci.nih.gov/>

Division of Clinical Sciences NCI

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NCI/DCS μArray Gateway

Welcome to the NCI/DCS μArray Gateway. This site provides a central location for the development of the μArray data.

 mAdb Amusement

[Gateway](#) - Data Upload and Analysis Tools
(Note: Must be a registered user - Login/Password required.)

[Forums](#) - for discussion of microArray issues.
(Note: Must be a registered user - Login/Password required.)

[Reference Information](#) - Protocols, mAdb User Manual, Axon GenePix User Manual, RNA Amplification Protocol

[Download](#) - Programs including Axon GenePix, Stanford's Cluster and TreeView, various

Connect: Please enter password for host...

IV.3 Select: a) Projects, b) “Formatted Array Data Retrieval Tool”, c) then press “Continue”

mArray Tools - Netscape

File Edit View Go Communicator Help

Back Forward Reload Home Search Netscape Print Security Shop Stop

Bookmarks Location: <http://nciarrray.nci.nih.gov/cgi-bin/restricted/beta/cgi-bin/MAAccessTools.pl>

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Top Level Analysis Selection

Choose one or more Projects, Analysis Tool and then Continue

Note: Tools marked with "*" only support selection of one project

Projects:

- quest - Time Course Demo Set #1
- quest - Repeats and Reciprocal Retests Demo Set #3

Tool: BETA Formatted Array Data Retrieval Tool

Continue

Document: Done

IV.4 Set a) Format Option to “MAExplorer”, b) Select Arrays to be Analyzed, c) Press “Submit”

Division of Clinical Sciences **NCI**

CIT **Center for Information Technology**

mAdb: Data Retrieval Form

Format Options

Dataset Formatted for NCI/LECB's MAExplorer

Array Selection

--	A	<input type="button" value="Submit"/>
	A	Array Name & Description
<input type="radio"/>	<input checked="" type="radio"/>	MmOC8p6-46 4 Hrs A
<input type="radio"/>	<input checked="" type="radio"/>	MmOC8p6-47 4 Hrs B
<input type="radio"/>	<input checked="" type="radio"/>	MmOC8p6-48 8 Hrs A
<input type="radio"/>	<input checked="" type="radio"/>	MmOC8p6-49 8 Hrs B

IV.5 Click on Resulting Zip File (e.g. 319-103653.zip) to Download Data to Your Computer

Division of Clinical Sciences **NCI**

CIT **Center for Information Technology**

mAdb WAIT Data Retrieval Tool 1.00

The Data Retrieval process is running. This page monitors the progress and allows you to continue when the results are available.

Please wait for completion.

Working

Done! To retrieve the dataset Link as ..." or Save

[319_103653.zip](#)

To unpack the dataset, you will need an uncompress utility which can handle ZIP compressed files. One such utility is WINZIP available on the mAdb [Program Downloads](#) page.

Viewing Location

Location: http://nciarray...n/319_103653.zip
Viewer: "C:\Program File...t.exe" /download
Status: 72K of 637K (at 2.1K/sec)
Time Left: 00:04:24

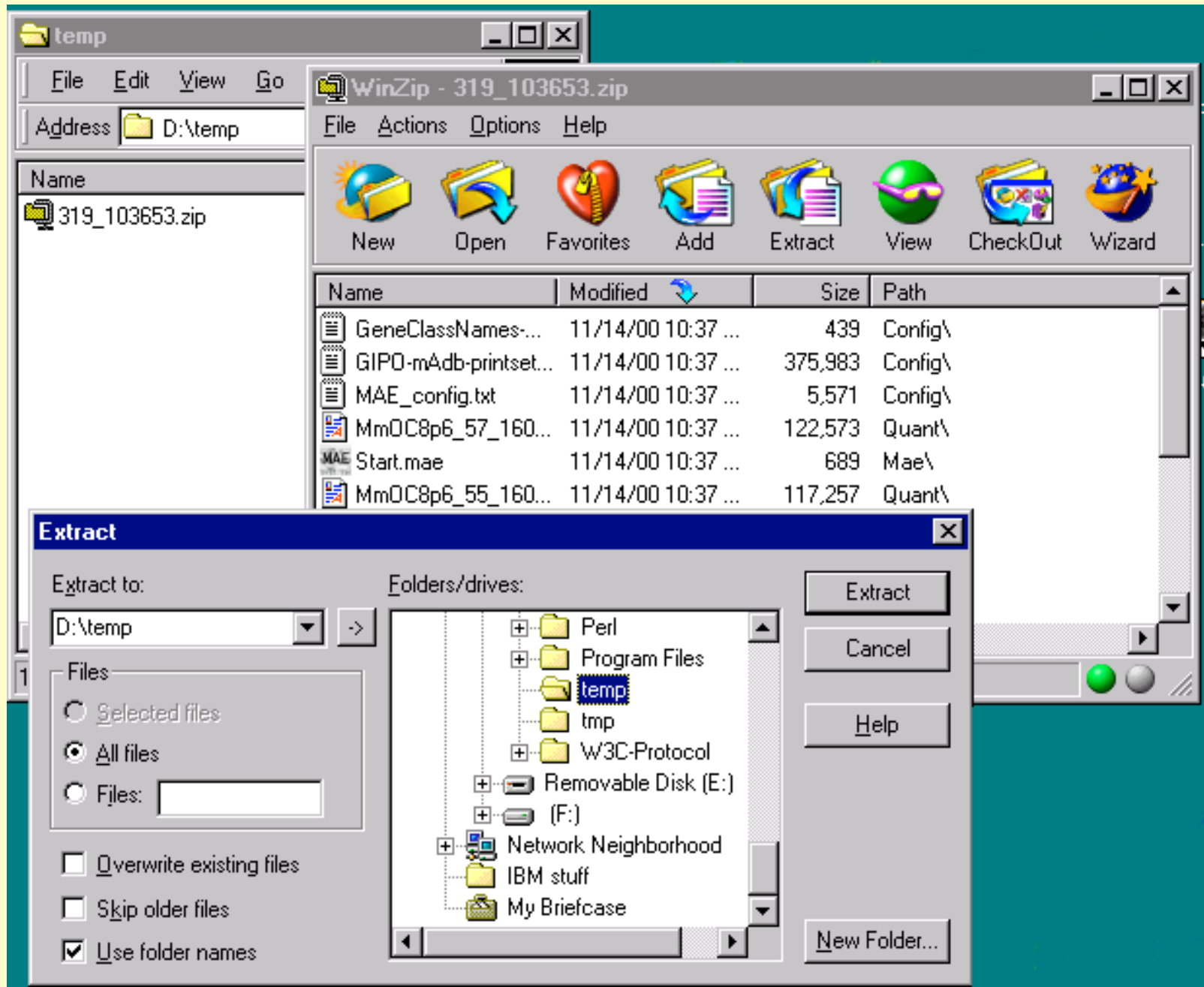
11%

Cancel

Document: Done

IV.6 Save Zip File on your local disk and Unzip it

- (Note: WinZip is available from the mAdb download Web site)



IV.7 Inspecting the Unzipped Data File Folders

The image displays four overlapping Windows Explorer windows showing the directory structure of unzipped data files. The windows are arranged as follows:

- temp** (top-left): Shows the root directory with files and folders: 319_103653.zip, Cache, Config, Mae, and Quant.
- Config** (top-right): Shows the contents of the Config folder: GeneClassNames-mAdb.txt, GIPO-mAdb-printset-10.txt, MAE_config.txt, and Samples-db.txt.
- Quant** (middle-left): Shows the contents of the Quant folder, listing 12 quant files with their names and sizes.
- Mae** (bottom-right): Shows the contents of the Mae folder, containing a single file named Start.mae.

temp

File Edit View Go Favorites Help

Address D:\temp

Name	T.	Modified
319_103653.zip	W.	11/14/00 10:42
Cache	F..	11/14/00 10:36
Config	F..	11/14/00 10:51
Mae	F..	11/14/00 10:51
Quant	F..	11/14/00 10:51

Config

File Edit View Go >>

Address D:\temp\Config

Name	T.
GeneClassNames-mAdb.txt	T.
GIPO-mAdb-printset-10.txt	T.
MAE_config.txt	T.
Samples-db.txt	T.

4 object(s)

Quant

File Edit View Go Favorites >>

Address D:\temp\Quant

Name	T.	Size
MmOC8p6_46_16084.quant	Q..	115KB
MmOC8p6_47_16085.quant	Q..	113KB
MmOC8p6_48_16086.quant	Q..	110KB
MmOC8p6_49_16087.quant	Q..	114KB
MmOC8p6_50_16088.quant	Q..	108KB
MmOC8p6_51_16089.quant	Q..	109KB
MmOC8p6_52_16090.quant	Q..	115KB
MmOC8p6_53_16091.quant	Q..	116KB
MmOC8p6_54_16092.quant	Q..	116KB
MmOC8p6_55_16093.quant	Q..	115KB
MmOC8p6_56_16094.quant	Q..	114KB
MmOC8p6_57_16095.quant	Q..	120KB

12 object(s)

Mae

File Edit View Go Favc >>

Address D:\temp\Mae

MAE

Start.mae

1 object(s)

IV.8 Click MAE "Start.mae" to Start MAExplorer

The screenshot shows the MAExplorer software interface. The title bar reads "mAdb Hs-OC-2-23Cx24R DB - MicroArray Explorer - V0.89.38-Beta - 4Hr vs 7Day A&B replicates". The menu bar includes "File", "HybProbe", "Edit", "Analysis", "View", and "Help". The "Analysis" menu is open, showing options: "GeneClass", "Normalization", "Filter", "Plot", and "Report". The "GeneClass" sub-menu is also open, listing: "All genes", "All named genes", "ESTs similar to genes", "ESTs", "All genes and ESTs", "Good genes", "Replicate genes", "Housekeeping genes", "Set Gene Class subset", and "List current Gene Class".

Below the menu, there is a text input field with the placeholder "Enter gene name or". To the right, a list of gene identifiers is visible: "6_46_16084] (Cy3/Cy5)" and "6_56_16094] (Cy3/Cy5)".

The main display area shows a heatmap. At the top left of the heatmap, it says "HP-X: [MmOC8p6_46_16084] (Cy3/Cy5)" and "HP-Y: [MmOC8p6_56_16094] (Cy3/Cy5)". Below this, it indicates "Norm.: median intensity" and "HP-XY ratio". A color scale legend on the left ranges from ">4.0" (dark red) to "<0.25" (dark green). The heatmap itself consists of a grid of colored circles representing gene expression levels. Below the heatmap, there are sections for "Active Probe" (listing MmOC8p6_46_160, MmOC8p6_47_160, MmOC8p6_56_160, and MmOC8p6_57_160), "Active Filters" (Gene Class), and "Active GeneClass" (ALL NAMED GENES).

IV.9 Explore Data Using Data Filters, Plots, etc.

mAdb Hs-OC-2-23Cx24R DB - MicroArray Explorer - V0.89.12-Beta - Working title

File HybProbe Edit Analysis View Help

Enter gene name or clone ID Mouse-over info HP-X: [MmOC8p6_46_16084]
HP-Y: [MmOC8p6_52_16090]

[1-B6,28] intensX=21174.64, intensY=48586.707, (X/Y)=0.4358, (Norm.: median intensity)

CloneID: IMAGE:468950, Scatter plot of gene HP-X vs HP-Y (Cy3/Cy5) ratios

GeneName: TF homeo.C

Scatter plot of gene HP-X vs HP-Y (Cy3/Cy5) ratios
[1-B6,28] intensX=1.612, intensY=23.197, (X/Y)=0.0695
CloneID: IMAGE:468950, plate[null,null,null]
GeneName: TF homeo.C8 Mm.4444 Homeo box C6

HP-X: [MmOC8p6_46_16084]
HP-Y: [MmOC8p6_52_16090]

Norm.: median intensity
HP-XY ratio

1-A

- >4.0
- 3.25
- 2.5
- 1.75
- 1.0
- 0.571
- 0.4
- 0.307
- <0.25

[X] Active Probe

- * MmOC8p6_46_16084
- * MmOC8p6_47_16085
- * MmOC8p6_48_16086
- * MmOC8p6_49_16087
- * MmOC8p6_50_16088
- * MmOC8p6_51_16089
- * MmOC8p6_52_16090
- * MmOC8p6_53_16091
- * MmOC8p6_54_16092
- * MmOC8p6_55_16093
- * MmOC8p6_56_16094

HP-Y

HP-X

HP-X: [MmOC8p6_46_16084]
HP-Y: [MmOC8p6_52_16090]
[Norm.: median intensity]
 $rSq=-0.095$, $n=1021$, $X(mn+-sd)=(3.212+-1.552)$, $Y(mn+-sd)=(23.197+-1.552)$

Scatter plot of gene Cy3 vs Cy5 spot intensities for [MmOC8p6_46_16084]
[1-B6,28] intensX=21174.64, intensY=48586.707, (X/Y)=0.4358
CloneID: IMAGE:468950, plate[null,null,null]
GeneName: TF homeo.C8 Mm.4444 Homeo box C6

Cy3

Cy5

Intensity values of Cy3 vs Cy5 for same genes [MmOC8p6_46_16084]

Mouse-over info Filtered genes SaveAs Close

Preference sliders

State scrollers

Spot SI1	<input type="text"/>	7314.066
Spot SI2	<input type="text"/>	241275.69
Ratio R1	<input type="text"/>	0.65
Ratio R2	<input type="text"/>	1.5

IV.10 Summary of Downloading a mAdb Data Set

- This procedure downloads one or more projects into a directory on your local computer.
- At this point, data mining may proceed using MAExplorer independent of the Internet connection to mAdb.
- If you want to add additional hybridized samples, you should download all of the samples again (this will be resolved in the future). Currently, you can't easily merge data from several downloaded data sets.