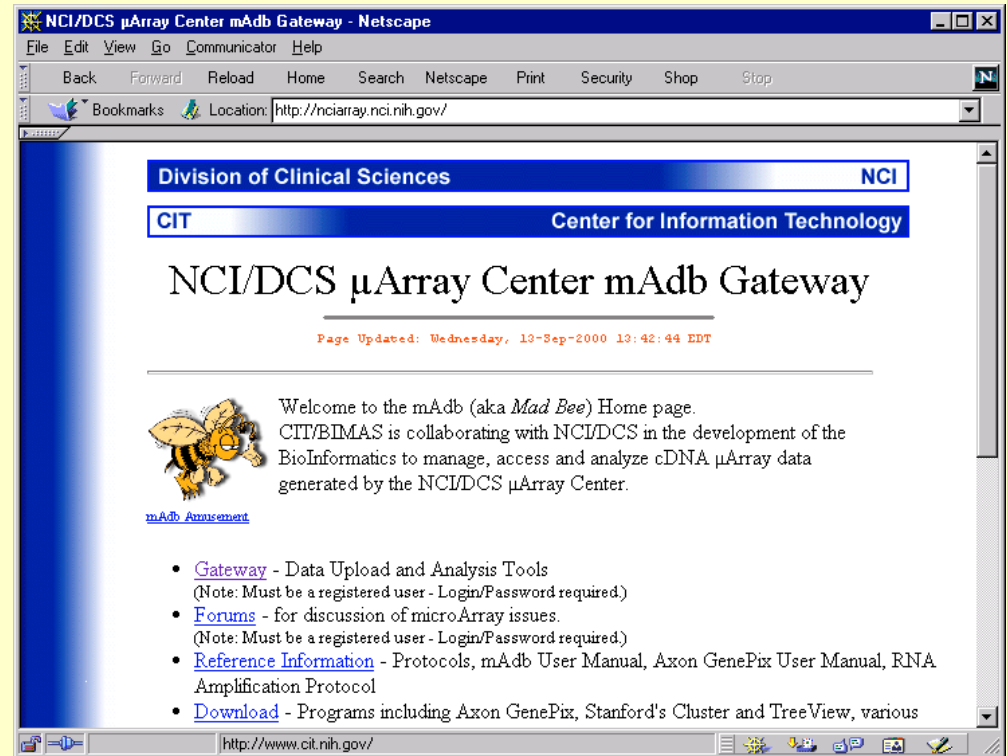# IV. Using NCI/CIT mAdb data with MicroArray Explorer

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 MAE Start.mae

IV. <u>Procedure</u> 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 **"Tool**s"
- 5. Select the set of projects to be exported from the scrollable list.
- 6. Select **"BETA formated 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

File Edit View Go Communicator Help

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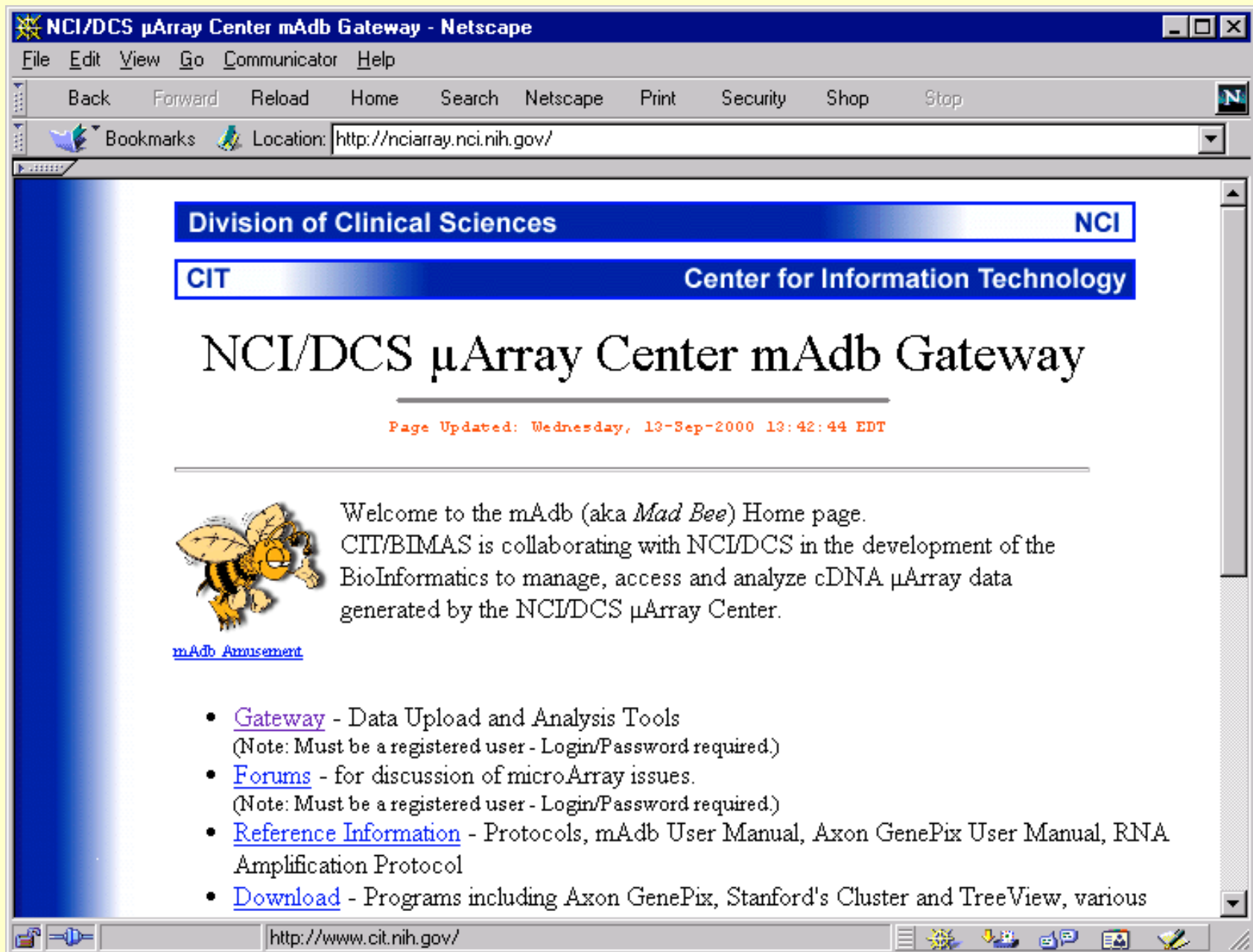**CIT**   **Center for Information Technology**

NCI/DCS μArray Center mAdb Downloads

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

		Program	Description	Author	Version	Updated	Download	Manual
Axon Inc. Software 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. **Axon's** Web Site		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)
Stanford Genome Analysis Group Software It is available free of charge to academic and non-profit institutions. **Stanford** Download Site		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	
MAExplorer Developed by and Available from LECB/FCRF/NCI. **MAExplorer** Web Site		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/

NCI/DCS µArray Center mAdb Gateway - Netscape

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

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NCI/DCS µArray 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 µArray data
generated by the NCI/DCS µArray 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

IV.3 Select: a) Projects, b) "Formated Array Data Retrieval Tool", c) then press "Continue"

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

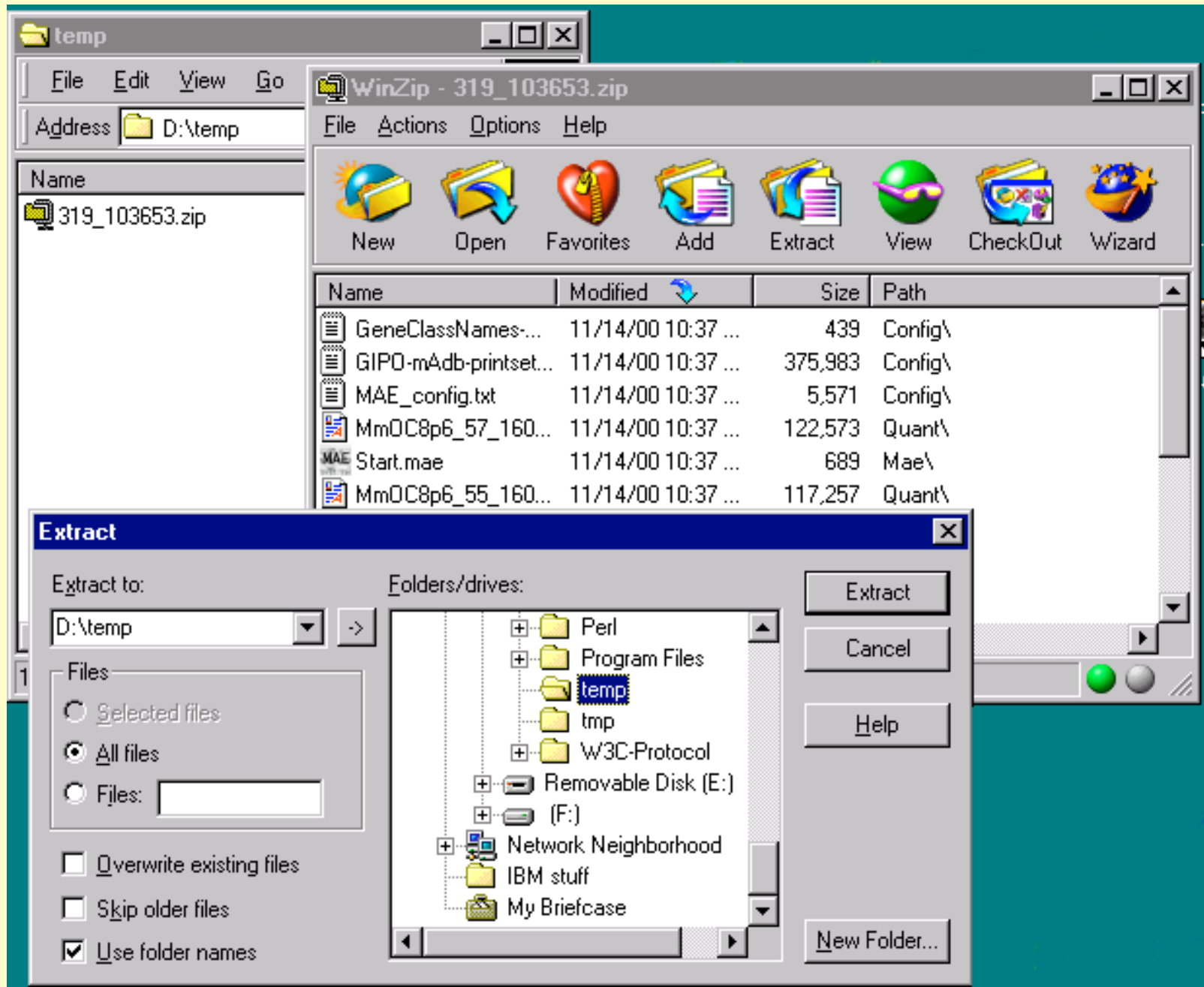# IV.5 Click on Resulting Zip File (e.g. 319-103653.zip) to <u>Download</u> Data to Your Computer

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

- (Note: <u>WinZip</u> is available from the mAdb download Web site)

IV.7 Inspecting the Unzipped Data File Folders

temp — 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 — 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 — 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 — D:\temp\Mae

MAE
Start.mae

1 object(s)

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

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

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.