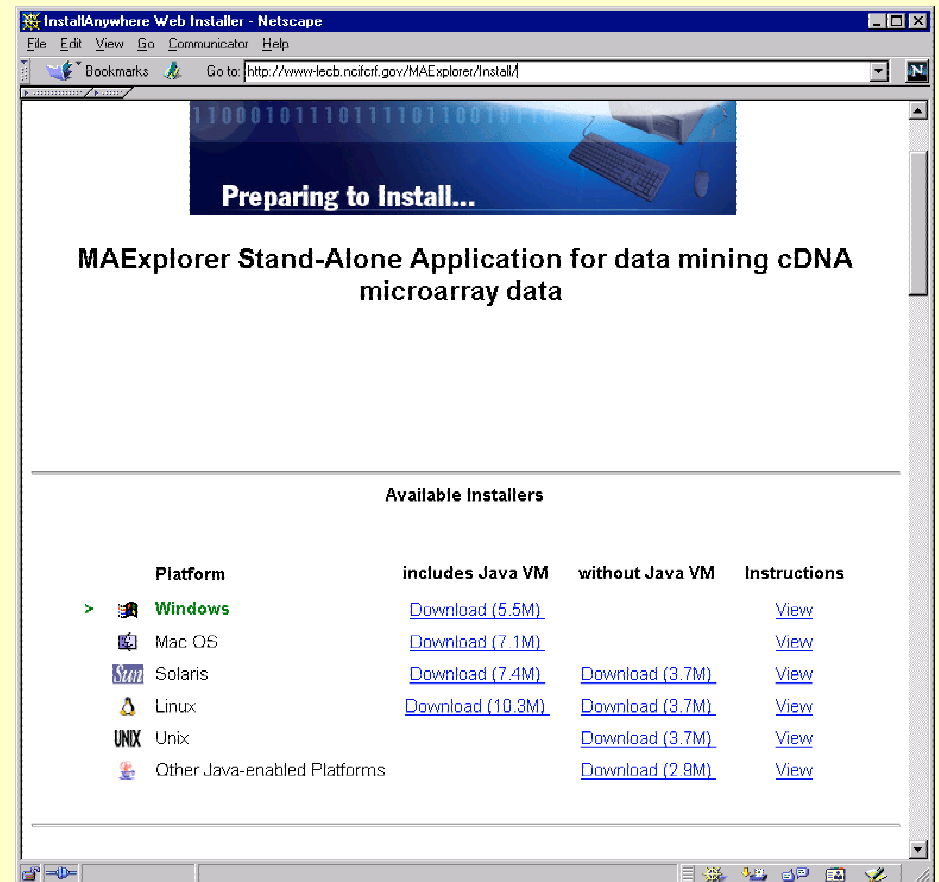


III. Installing MicroArray Explorer on Your Computer



Outline

1. MAExplorer home page
2. Download installer to your computer
3. Run the installer
4. Test it on MGAP sample database

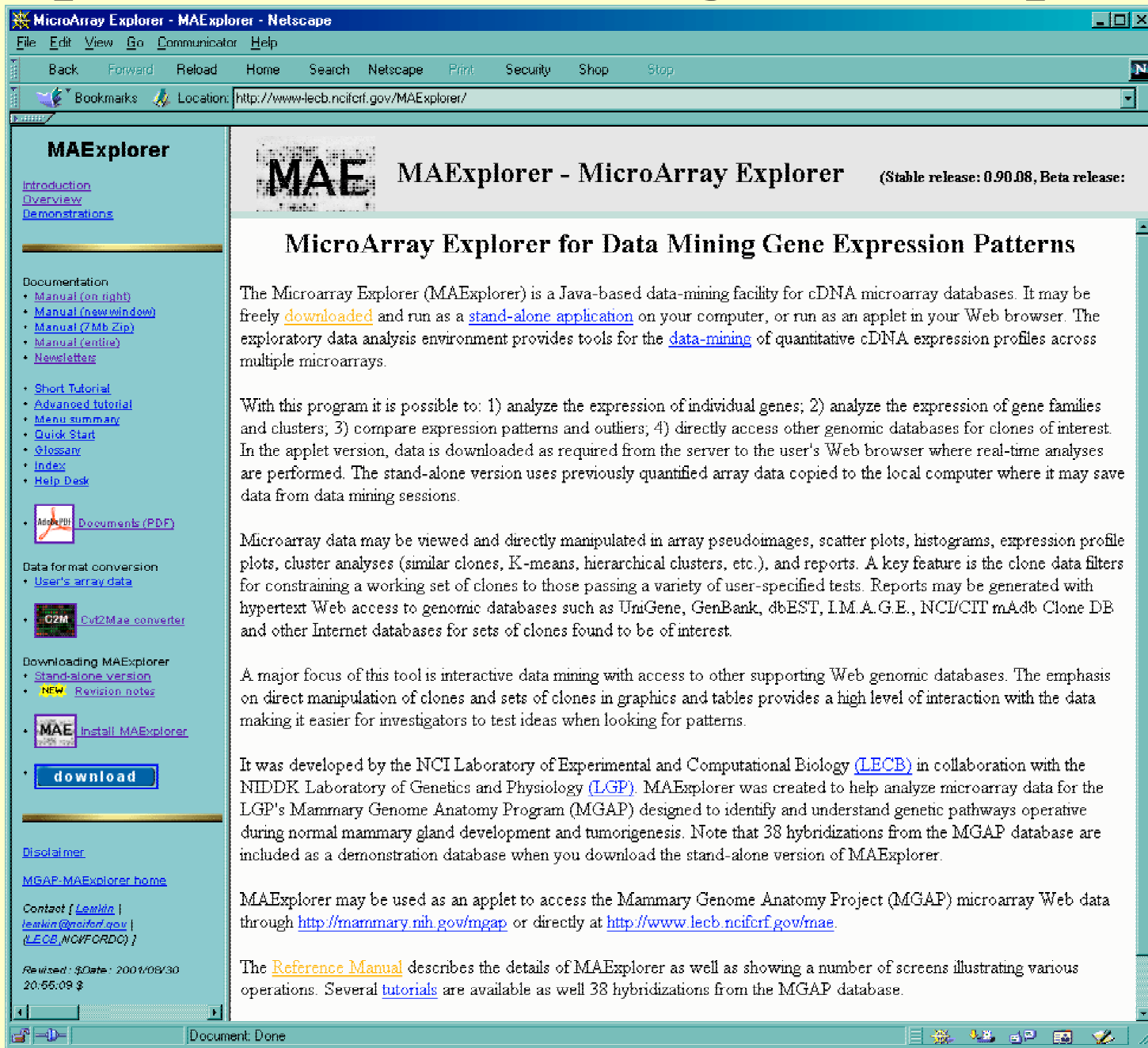


III. Procedure to Download & Install MAExplorer

- 1. Go to **<http://www.lecb.ncifcrf.gov/MAExplorer>** with your Web browser.
- 2. Select **Download** to start the install process. It uses the InstallAnywhere™ program. You have a choice of:
 - 3.1 Allow InstallAnywhere™ to select and run the installer requesting where you want to install it (eg. in Windows this would be C:\Program Files\MAExplorer),
 - 3.2 Or, you may download the installer file **installMae** and run it yourself.
 - a) Find your computer **Platform** in the list. Click on the corresponding **Download** word and save the installer on your computer.
 - b) Go to **View** for your platform in the same download Web page to see how to finish the installation for your particular platform.
 - c) Now run the **installMae** on your computer to install MAExplorer where you want.
- 4. You are ready to use MAExplorer. In Windows Start menu, click on MAExplorer. After it starts, select “Open file DB” in the File | Database menu, and select a one of the demo startup files.

III.1 MAExplorer Home Page - Press “download”

<http://www.lecb.ncifcrf.gov/MAExplorer>



The screenshot shows a Netscape browser window titled "MicroArray Explorer - MAExplorer - Netscape". The address bar displays "http://www.lecb.ncifcrf.gov/MAExplorer/". The page content is organized into a left sidebar and a main content area.

MAExplorer

[Introduction](#)
[Overview](#)
[Demonstrations](#)

Documentation

- [Manual \(on right\)](#)
- [Manual \(new window\)](#)
- [Manual \(7 Mb Zip\)](#)
- [Manual \(entire\)](#)
- [Newsletter](#)

• [Short Tutorial](#)

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Data format conversion

- [User's array data](#)

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Downloading MAExplorer

- [Stand-alone version](#)
- **NEW** [Revision notes](#)

•  [Install MAExplorer](#)

download

[Disclaimer](#)

[MGAP-MAExplorer home](#)

Contact ([Leatkin](#) | leatkin@ncifcrf.gov | LECB@NCIFCRFDC)

Revised: \$Date: 2001/08/30 20:55:09 \$

MAExplorer - MicroArray Explorer (Stable release: 0.90.08, Beta release:)

MicroArray Explorer for Data Mining Gene Expression Patterns

The Microarray Explorer (MAExplorer) is a Java-based data-mining facility for cDNA microarray databases. It may be freely [downloaded](#) and run as a [stand-alone application](#) on your computer, or run as an applet in your Web browser. The exploratory data analysis environment provides tools for the [data-mining](#) of quantitative cDNA expression profiles across multiple microarrays.

With this program it is possible to: 1) analyze the expression of individual genes; 2) analyze the expression of gene families and clusters; 3) compare expression patterns and outliers; 4) directly access other genomic databases for clones of interest. In the applet version, data is downloaded as required from the server to the user's Web browser where real-time analyses are performed. The stand-alone version uses previously quantified array data copied to the local computer where it may save data from data mining sessions.

Microarray data may be viewed and directly manipulated in array pseudomages, scatter plots, histograms, expression profile plots, cluster analyses (similar clones, K-means, hierarchical clusters, etc.), and reports. A key feature is the clone data filters for constraining a working set of clones to those passing a variety of user-specified tests. Reports may be generated with hypertext Web access to genomic databases such as UniGene, GenBank, dbEST, I.M.A.G.E., NCI/CIT mAdb Clone DB and other Internet databases for sets of clones found to be of interest.

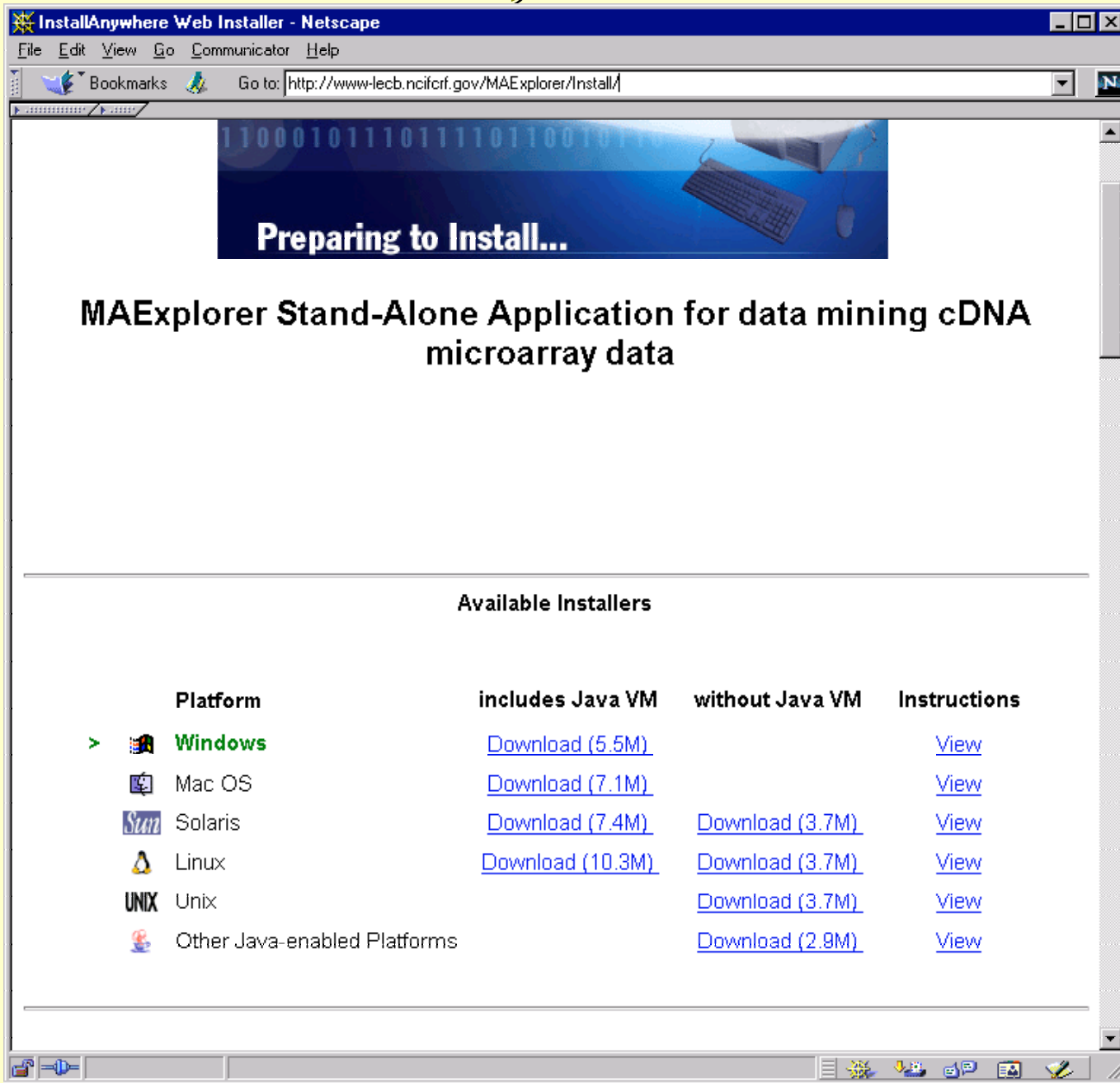
A major focus of this tool is interactive data mining with access to other supporting Web genomic databases. The emphasis on direct manipulation of clones and sets of clones in graphics and tables provides a high level of interaction with the data making it easier for investigators to test ideas when looking for patterns.

It was developed by the NCI Laboratory of Experimental and Computational Biology ([LECB](#)) in collaboration with the NIDDK Laboratory of Genetics and Physiology ([LGP](#)). MAExplorer was created to help analyze microarray data for the LGP's Mammary Genome Anatomy Program (MGAP) designed to identify and understand genetic pathways operative during normal mammary gland development and tumorigenesis. Note that 38 hybridizations from the MGAP database are included as a demonstration database when you download the stand-alone version of MAExplorer.

MAExplorer may be used as an applet to access the Mammary Genome Anatomy Project (MGAP) microarray Web data through <http://mammary.nih.gov/mgap> or directly at <http://www.lecb.ncifcrf.gov/mae>.

The [Reference Manual](#) describes the details of MAExplorer as well as showing a number of screens illustrating various operations. Several [tutorials](#) are available as well 38 hybridizations from the MGAP database.

III.2 Access Stand-Alone Version Web Page - Find Your “Platform”, then Select “Download”



InstallAnywhere Web Installer - Netscape







File Edit View Go Communicator Help

Go to: <http://www-lecb.ncicrf.gov/MAExplorer/Install/>

Preparing to Install...

MAExplorer Stand-Alone Application for data mining cDNA microarray data

Available Installers

	Platform	includes Java VM	without Java VM	Instructions
>	 Windows	Download (5.5M)		View
	 Mac OS	Download (7.1M)		View
	 Solaris	Download (7.4M)	Download (3.7M)	View
	 Linux	Download (10.3M)	Download (3.7M)	View
	 Unix		Download (3.7M)	View
	 Other Java-enabled Platforms		Download (2.8M)	View

III.3 Save the Installer on Your Local Computer

InstallAnywhere Web Installer - Netscape
File Edit View Go Communicator Help

Recommended Installation for Your Platform:
Download Installer for Windows...

Installer created with [InstallAnywhere](#)® by Zero G Software, Inc. Copyright 2000. [www.ZeroG.com](#)

Platform

- > **Windows**
- Mac OS
- Solaris
- Linux
- Other Java-enabled Platforms

Available Installers

Save Downloaded File

Norton AntiVirus has determined that this file is free from viruses.

File Name:

Directories: f:\temp

List Files of Type: All Files (*.*)

Drives: f:

OK Cancel Network...

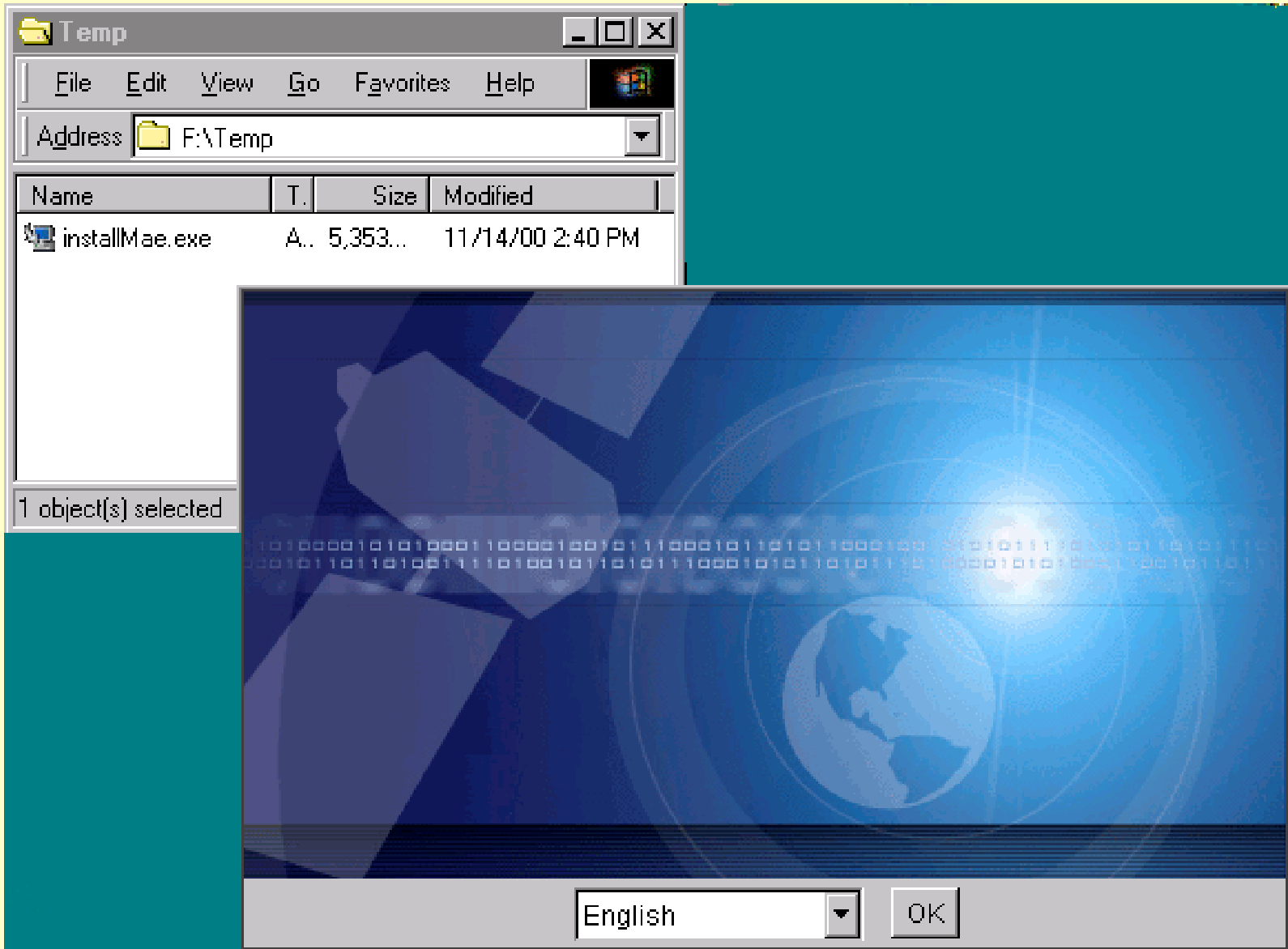
Windows Instructions:

Instructions

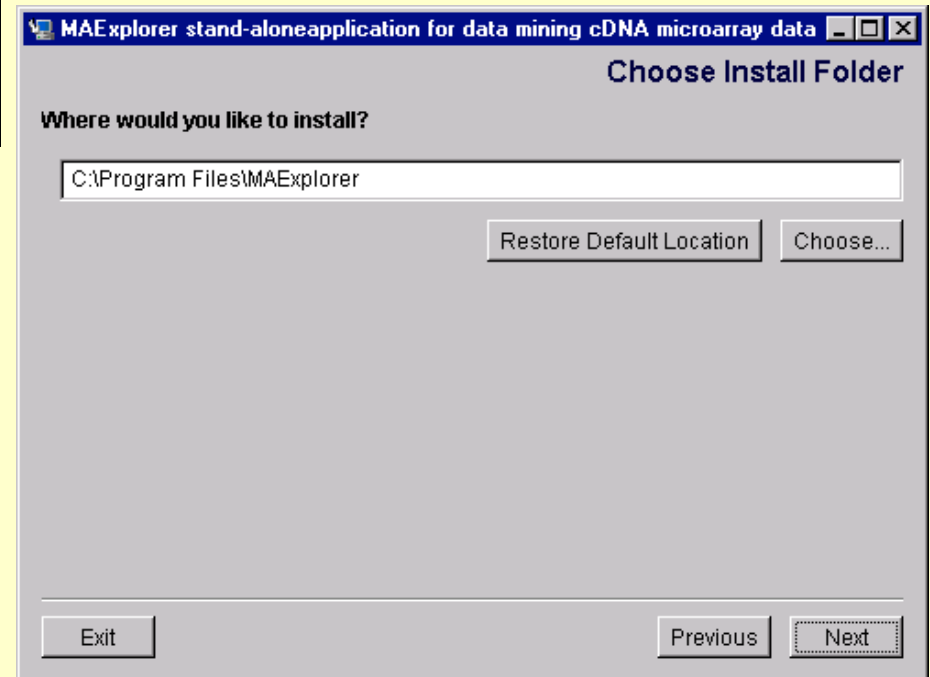
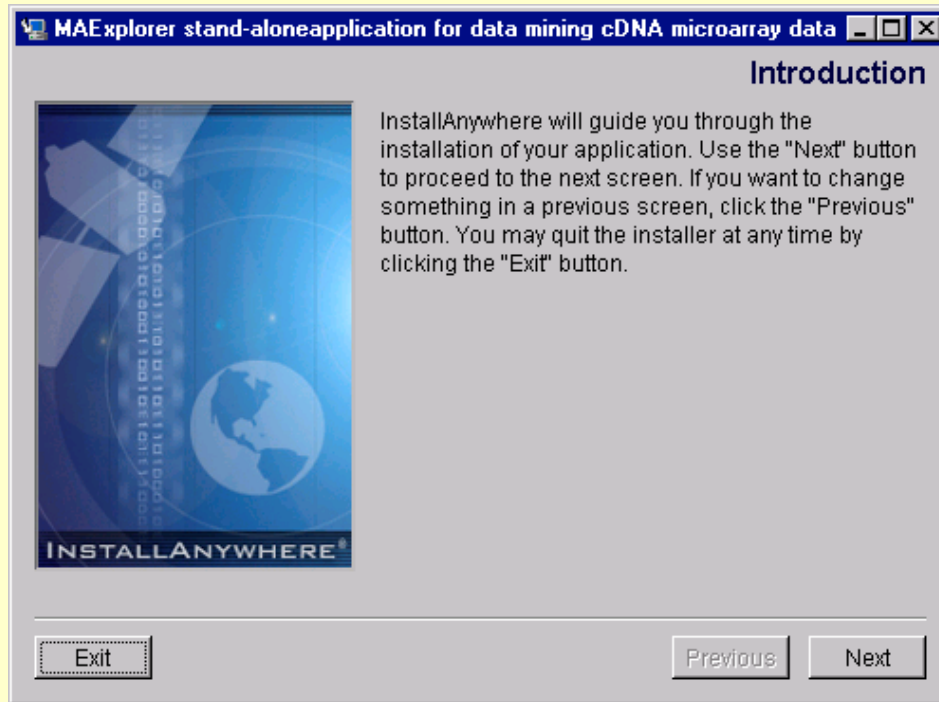
- After downloading, double-click **installMae.exe**

Document: Done

III.4 Start Installer - e.g. in Windows, Click on installMae.exe. Then Answer Questions, “OK” etc.

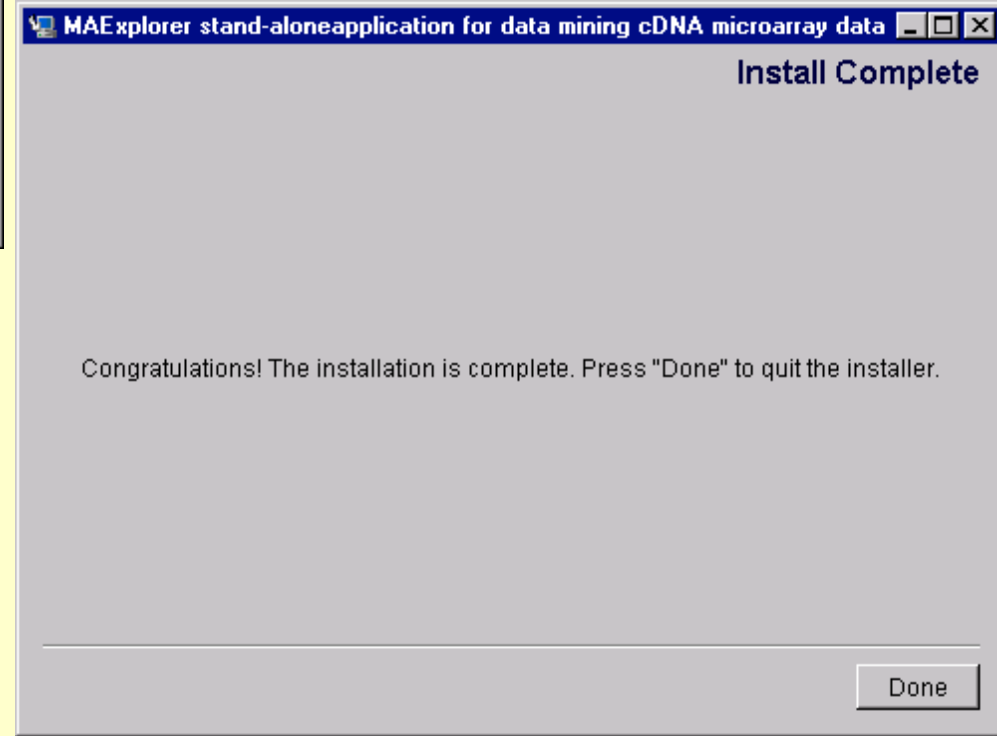
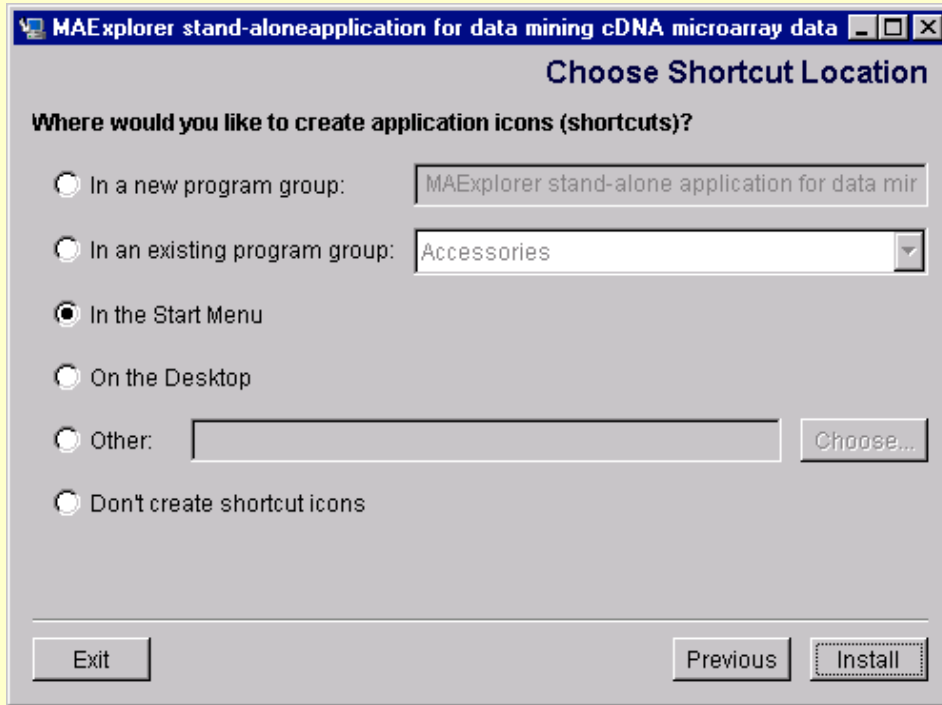


III.5 Successive Steps During Installation of MAExplorer - Press “Next”

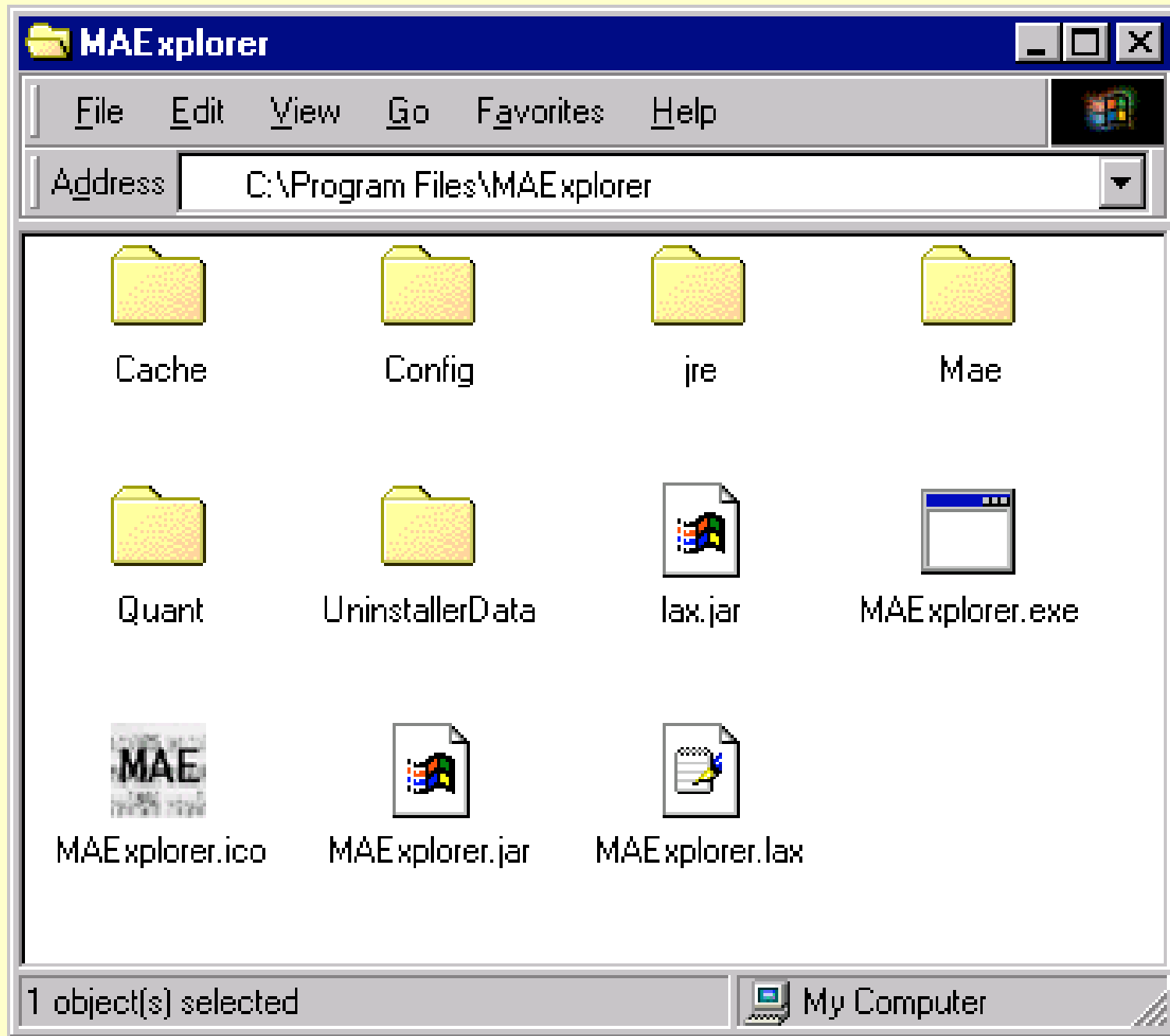


III.6 Finish Installation of MAExplorer:

a) Press “Install”, b) Press “Done”

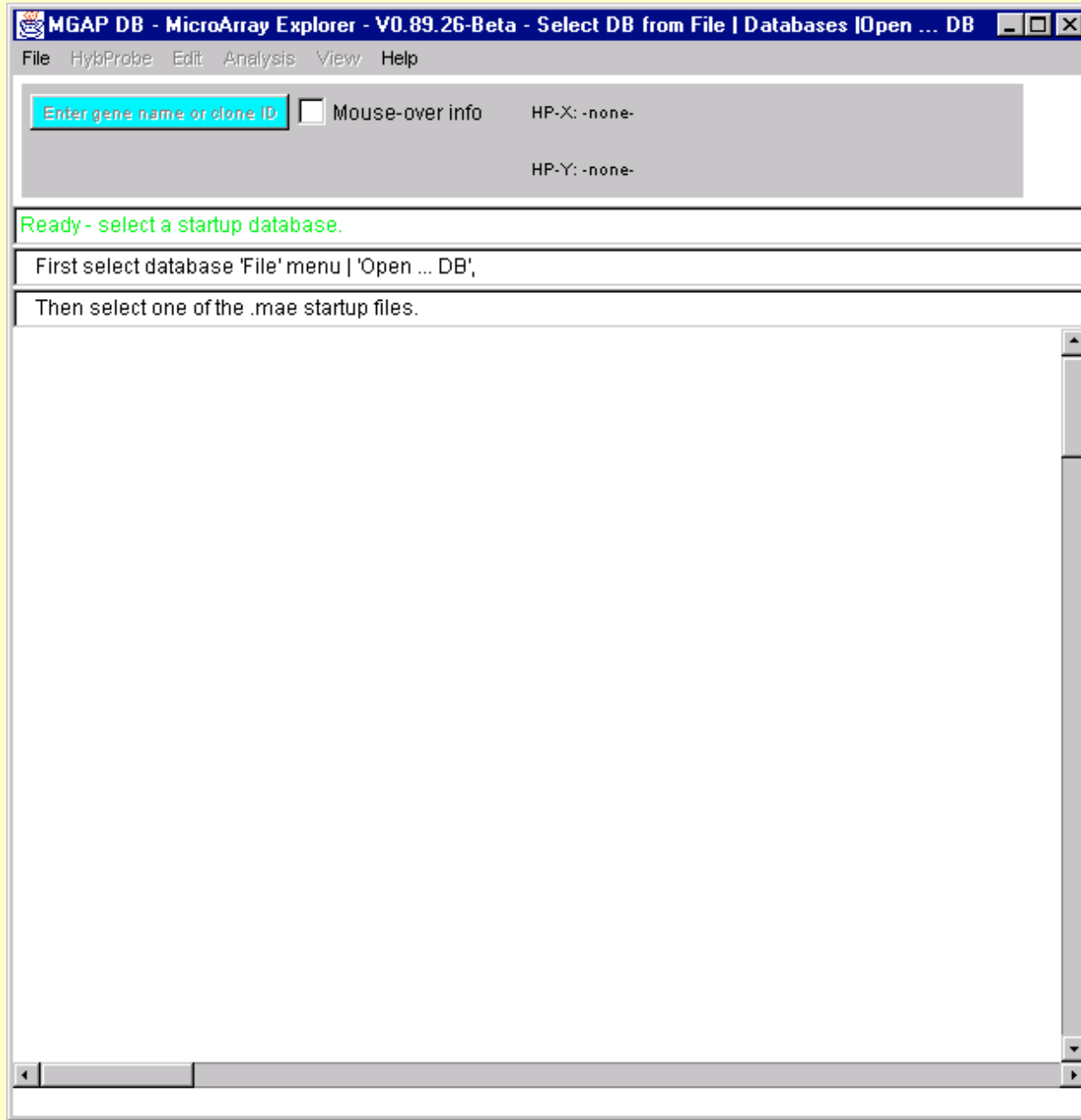


III.7 Folder Structure of Downloaded Files



III.8 Start MAExplorer from Windows PC

“Start” menu. Initially starts with empty database



III.9 Open demo (MGAP) database from local disk

- Browse demo project for startup database. Select File menu, Open file DB, pick startup DB

The screenshot displays the MGAP DB - MicroArray Explorer application window. The title bar reads "MGAP DB - MicroArray Explorer - V0.89.12-Beta - Pregnancy day 13: C57BL/6 vs. stat5a (-,-) ...". The menu bar includes "File", "HybProbe", "Edit", "Analysis", "View", and "Help".

At the top, there is a search bar with the text "Enter gene name or clone ID" and a "Mouse-over info" checkbox. Below this, the current experiment is identified as "HP-X: Pregnancy 13 (1 hr) [C57B6-p13-totalRNA5ug]" and "HP-Y: Pregnancy 13 (15 min) [Stat5a.--.p13-15min]".

The main area is a heatmap with a color scale on the left. The scale ranges from red (>4.0) to green (<0.25). The heatmap is divided into four quadrants labeled 1-A, 1-B, 1-C, and 1-D on the left, and 2-C and 2-D on the right. A legend on the left lists various probes, with "C57 B6-p13-total" highlighted in pink.

An "Open disk DB file" dialog box is open in the foreground, showing the "MAE" directory. The file list includes several .mae files, with "Lact1 vs10-38probes.mae" selected. The "File name" field contains "Lact1 vs10-38probes.mae" and the "Files of type" is set to "All Files (*.*)".