EPA/600/R-94/033
March 1994

GeneTox Manager System (GENETOX)

PROGRAMMER'S GUIDE VAX Component

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Prepared Under
Contract # 68-W0-0043
Delivery Order # 507

June 1993
Version 2.0

Printed on Recycled Paper

PREFACE

This programmer's guide is the reference manual explaining how the EPA GeneTox Manager System operates on the VAX. It is intended for use by anyone who has to perform program maintenance of the application.

GeneTox Manager is a data capture, data management, and statistical analysis program used for microbial mutagenicity data. Its main purpose is to provide a homogeneous environment for the collection, organization, and analysis of data generated in the laboratory while also supporting a quality assurance program. The complete system consists of both a personal computer (PC) system and a microcomputer (VAX) system although the PC system can be used as a stand-alone system. The system controls the data collection and management through a user-friendly menu driven system that requests specific information and provides uniform methods for data and information entry. GeneTox Manager is capable of performing specialized statistical analysis of the data and creating tabular and graphical summaries. The PC system is designed to function with the VAX FOCUS databases so that the VAX can be used for long-term storage, archiving of files, and the analysis of large groups of data.

Acknowledgements

We would like to acknowledge those individuals who used prototype versions of this software and gave us useful, productive comments. Without their suggestions, this product could have not been done. In this regard, we give our thanks to Sarah Warren, Erica Perry, Virginia Houk, and Maria Taylor.

We also want to thank those who gave us permission to use the statistical analysis programs that they developed. These include Dr. L. Berstein, Dr. D. Krewski, and Mr. A. Stead. If you use information from these statistical programs, we hope that you will give proper acknowledgement to the authors of the statistical manuscripts.

We also want to thank Mr. Ken Laws for providing administrative support that made this project possible, and Drs. Lawrence W. Reiter and Michael D. Waters for creating the scientific support that made our endeavors a joy. Thanks are also extended to Mr. Ken Mullins and Dr. David Svendsgaard for review of this document.

Notice

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CHAPTER 1

INTRODUCTION

The GeneTox Manager System is an U.S. EPA system for the collection, organization, retrieval, and analysis of microbial mutagenicity data. Although the system was designed primarily for the *Salmonella typhimurium* plate incorporation assay, it will accept data and information for any mutagenicity assay where similar information is obtained.

Microbial assays, especially *Salmonella* bioassays, are the most common type of mutation tests. These tests determine whether or not a substance interacts with the DNA of the organism in such a way as to create permanent, heritable changes within the DNA. These tests are important because they can be used to screen for both mutagens and genotoxic carcinogens. The *Salmonella* assay has been reported to have been used by over 2000 laboratories. In comparison to other genotoxicity assays, these microbial assays are relatively rapid and inexpensive. These tests, therefore, generate very large databases.

In order to collect, manage, and analyze microbial mutagenicity data in an orderly and rapid manner, the U.S. EPA (through the services of Computer Sciences Corporation) developed the GeneTox Manager system. Using this system, investigators can use a PC to collect information and data, to provide short-term storage of the information, and to provide selected types of statistical analysis. The complete GeneTox Manager system also includes a VAX FOCUS system that can be used for the archiving of databases and for the analysis of large groupings of data. The total system is designed to achieve compatibility between the PC and VAX system environments. The GeneTox Manager system is designed to be user friendly through the use of a structured menu system, screen entry helps, and other help screens. Reports are both tabular and graphical in nature, and they can be seen on the computer screen, sent to a printer, or written to a PC file.

It is the hope of EPA that GeneTox Manager will not only be of benefit to the Agency but will also be of constructive use to others outside of the EPA.

CHAPTER 2

ORGANIZATION OF GENETOX MANAGER ON THE VAX

The VAX component of the GeneTox Manager System is implemented on the VAX Cluster of EPA's National Computer Center (NCC). The specific VAX machine on which GeneTox Manager is installed is VAXTM1.

2.1 GeneTox Manager Logicals and Symbols

In order to access GeneTox, there are two items related to the user's VAX ID that must be completed. The first of these is the allocation of an appropriate GeneTox Access Control List (ACL) entry for the user's ID. See the GeneTox Application Manager for issuance of a GeneTox ACL for your VAX ID.

The second item is the definition of VAX 'Symbols' and 'Logicals' on the user's ID that are specific to GeneTox. (An understanding of 'Symbols' and 'Logicals' is not required, but the user may reference VAX documentation for further information on these constructs if desired.) Upon logon to the VAX, the system will check a file called LOGIN.COM in the user's root directory for initialization of the user environment. The following two commands must be added to the user's LOGIN.COM file (or a .COM file called by LOGIN.COM) in order to initialize the GeneTox environment for the user.

(1) The following command invokes a .COM file that will establish required GeneTox logicals:

```
@$2$DUA90:[INVITRO]GTMSET
```

(2) The following command establishes a symbol for invocation of GeneTox:

```
GENETOX :== "@GTM$SYS:GENETOX"
```

To define a printer to accept GeneTox output, include the following command as well:

DEFINE GTMSYSPRINTER ppppppp

where:
ppppppp is the name of a printer defined on the VAX network

2.2 Invoking the GeneTox Application

2.2.1 End User Access

After logging on to the VAX computer, enter "GeneTox" at the DCL prompt ($) to start the application. (Moving into a separate subdirectory (SET DEFAULT) before initiating this application will isolate print listings and various work files that the application will produce from outputs from other programs or tasks.)

$ GeneTox<RET>

The GeneTox Main Menu is then displayed on the screen. The main menu presents a list of options and corresponding functions; a function is selected by entering the appropriate letter at the command prompt.

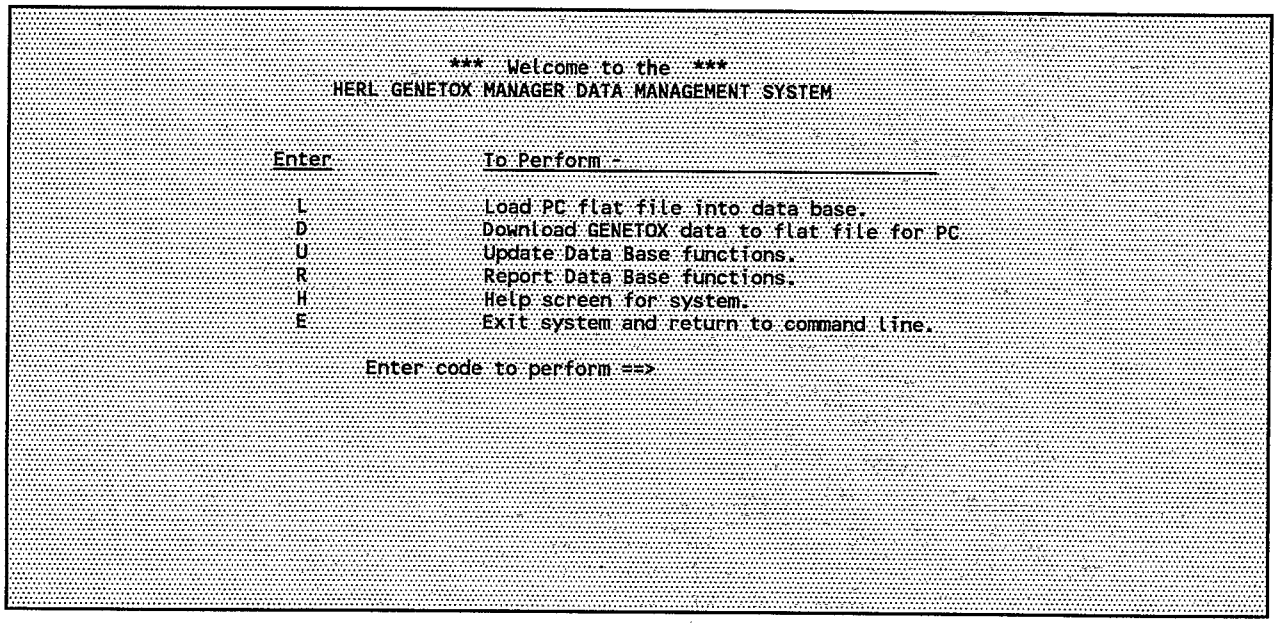

Figure 2-1. Main Menu Screen

2.2.2 Execution Entry Points for Developers

GeneTox Manager actually has four discrete entry points. GENETOX.COM initiates the main menu of the application and is the typical entry point for the end user. However, in support of automatic upload and download to/from the VAX of GeneTox Manager data collected on the PC, there are three additional .COM files that are supported.

PCLOAD.COM is invoked from a SetHost script file on the PC to load new experimental data to the VAX.

PCEDIT.COM is invoked from a SetHost script file on the PC to load 'modified' experimental data to the VAX.

PCDOWN.COM is invoked from a SetHost script file on the PC to download data from the VAX to a PC.

2.3 Developer Access to GeneTox Manager

The GeneTox Manager application is installed on a separate application directory, called INVITRO, on the VAX Cluster machine. Application developers are assigned their own specific, development directory along with their VAX ID. In order to access the code on the INVITRO directory, the developer must be assigned an ACL designation and disk quota for INVITRO. GeneTox ACLs are available as follows:

GENESTAT_CONTROL developer access to modify GeneTox
GENESTAT_USER user access to execute GeneTox

2.4 GeneTox Manager File Organization

The INVITRO directory is divided into a number of sub-directories to store various components of the GeneTox Manager application as follows:

INVITRO root directory stores production data bases
- DEVL development environment for changing application code
- TEST test environment for reviewing application changes
- PROD production location for application code (except statistical models)
- STATS location of statistical models
- DOC location of application documentation
- BAK back-up directory storing previous versions of the application
- SERVER contains pointer information for the FOCUS server for this application

2.5 GeneTox Manager Application Code Notes

GeneTox Manager code on the VAX consists primarily of FOCUS EXEC files (typically known as FEX files). These files are 'fourth generation language' code files which are interpreted at execution time rather than compiled. Most FOCUS code cannot be compiled. All elements of the GeneTox Manager system on the VAX (except for the statistical models) have been developed and are supported by Computer Sciences Corporation. The statistical models, Stead and Bernstein, were developed and are supported by Dr. John Creason, of HERL.

2.6 GeneTox Manager Data Bases

2.6.1 Data Base Definitions

There are currently two data bases on the VAX which serve as a master repository for GeneTox Manager experimental data. The EXPRMNT data base contains all information for an experiment, including sample information related to its analysis under an experiment. The SAMPLES data base contains information specific to a sample independent of an experiment (e.g., sample name). The actual data is stored in Focus data bases with a file extension of .FOC. The master file descriptions which define the fields, data type and relationships for these data bases are in Focus files with a file extension of .MAS. The EXPRMNT and SAMPLES data bases are cross referenced to allow storage and retreival of all GeneTox Manager data by the user.

2.6.2 GeneTox Manager Server to Support Multi-User Access

GeneTox Manager on the VAX supports multi-user access for retrieval of data from the system. It also supports multi-user update of information (as long as two users are not attempting to update the same experiment at the same time - the system will lock out the second user in such a situation). In order to provide multi-user access for GeneTox Manager, a FOCUS server is allocated on the VAX cluster specifically for this application. The server process name is SUSERV_INVITRO, and should be listed as such when it is 'up' by issuing a SHOW SYSTEM command. This server name should also be listed when it is 'up' by issuing a '? SU' command from within interactive Focus.

While an individual developer can disable this server, NCC support personnel are the only staff authorized to re-start the server. Start-up of the INVITRO server is included in VAXTM1 initialization, should the VAX Cluster ever crash or be brought down for maintenance.

2.7 Note on GeneTox Manager Source Code

Because of the rapid changes that occur within computer hardware and software development and because implementation of this portion of the GeneTox Manager System is likely to be very different from location to location, the source code listings have not been included.

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