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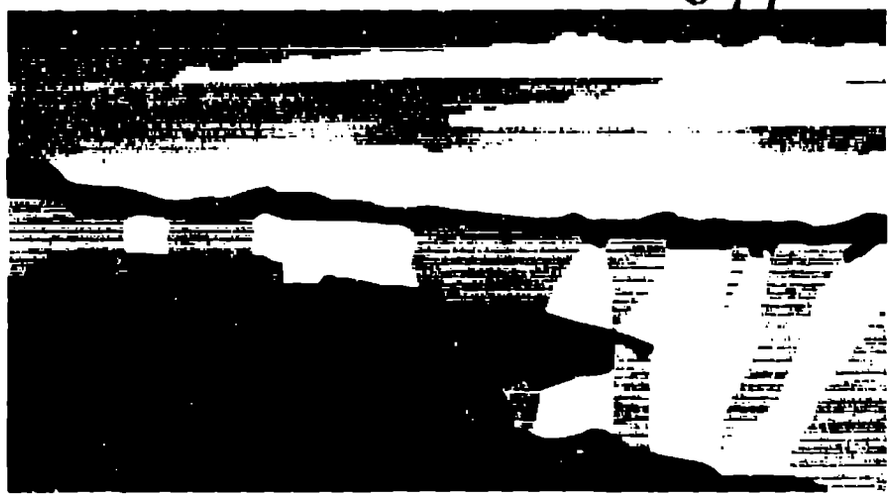

Los Alamos
NATIONAL LABORATORY

WIDER AVAILABILITY OF PARMILA AND RECENT IMPROVEMENTS TO PARMILA [a]

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ABSTRACT

PARMILA (Phase And Radial Motion in Ion Linear Accelerators) is a drift-tube linac (DTL) ion-beam dynamics code. Over its long life, many versions have developed. The Los Alamos Accelerator Code Group distributes a version, for which a manual[1] is available. Unless otherwise specified, all mentions of PARMILA in this document refer to that LAACG-distributed version. Until recently, this documented and distributed version functioned only under CTSS. Users who wished to run on a different operating system needed to convert the code themselves. PARMILA now operates under UNICOS, a much more widely available CRAY operating system, and under VAX/VMS. This paper describes some new features of the code, and gives directions for obtaining the manual and the UNICOS and VMS versions of the code.

INTRODUCTION

Reference 1, the PARMILA manual, describes the major features of PARMILA as it is distributed by the LAACG. Unless otherwise specified, all mentions of PARMILA in this document refer to the LAACG-distributed version. This paper emphasizes features that have been added since the first version of that report was published in 1990, and those that are not well documented. The 1992 revision to the manual was minor. The new features include the ability to scale data from SUPERFISH, availability of a second linac generation subroutine, two new output files giving emittances and power requirements, and the ability to handle comments in the input file.

We also describe a post-processor for PARMILA, named NBEAM6.

[a]Work supported by U S Department of Energy, Office of Energy Research: Office of High Energy and Nuclear Physics, Office of Basic Energy Sciences, Office of Fusion Energy, Office of Superconducting Super Collider, and Scientific Computing Staff.

SCALED SFDATA INFORMATION

A table of information generated by running the cavity code SUPERFISH[2,3] provides the basis for generating a linac. PARMILA now has the ability to scale information in an SFDATA table based on SUPERFISH analysis of cells having one resonate frequency to a different design frequency[4]. In order to utilize this feature, the user must specify the reference frequency for which the SUPERFISH runs were done, FREQREF. The fifth data element after the LINAC label is set equal to the value of FREQREF, in megahertz. Then PARMILA multiplies each shunt impedance, Z, in the SFDATA table by the square root of the ratio of the design frequency to the reference frequency. (The design frequency is the third data element following the LINAC label, as described in the manual.) If no value for FREQREF is given, PARMILA assumes it to be equal to the design frequency. This scaling is done in the main program, and is independent of the linac generation routine selected for use (see next section).

CHOICE OF ROUTINE TO GENERATE LINAC

PARMILA now contains two routines that the user can select to generate the linac. The two routines have somewhat different capabilities, and even for the same input data, they generate slightly different linacs. The new routine, which is named GENLAT1 in PARMILA, is similar to the linac-generating routine used in the AT-1 PC version of PARMILA. It is the routine that is called by default when all the cells for which SFDATA information is provided are symmetric.

The old routine, GENLIN2, can deal with asymmetric cells, and is called automatically if any asymmetric cells are represented in the SFDATA input. If the SFDATA is for a symmetric cell, entry number 8 equals zero ,and entries 9 and 10 are ignored but must be present for spacing. For an asymmetric cell, entry number 8 is nonzero, and it, along with entries 9 and 10, gives the characteristics of the second half of the cell. See reference 1 for details. GENLIN2 also generates a file of power requirements, described below.

In order to use GENLIN2 when all cells are actually symmetric, an artificial value for SFDATA entry 8 is used. Set entry number 8 in the SFDATA information for at least one cell equal to 9000.0. PARMILA will reset it to zero but will set a flag to cause GENLIN2 to be called.

The new routine, GENLAT1, allows an automatic ramp of phase, either with or without ramping E0[5] . To ramp phase only, set vv(30) [6] following a TANK label to 1, and vv(5) following the TANK label to less than 0.1e10. To ramp both phase and E0, set vv(5) equal to 1.0e10 and VV(30) to 1. For ramp of E0 only, see the manual. (The E0 only ramp capabilities are similar in GENLAT1 and GENLIN2.) A 10-cm delay in the phase ramp is programmed into GENLAT1. It can be changed by changing the numeric value in one "if" statement that checks

[6] vv(n) is the nth data element following its associated label

"(gnlen .le. 10.00)" and recompiling. Similarly, the phase limit can be changed by changing the value assigned to SPMINV in the routine and recompiling. This assignment occurs immediately after the comment "generate linac".

NEW OUTPUT FILES

Two additional output files not documented in the manual are now available. The file EMITT contains 100%, 90%, and rms emittances, as well as α and β in the x-xprime, y-yprime and phase-energy phase space planes at each cell, and the number of particles that have not been lost to that point. The file is written by subroutine EMIT.

POWFILE contains the power requirement in megawatts for each cell and the cumulative power requirement to that cell in the tank. It is written by subroutine GENLIN2.

COMMENTS

Data on a line that starts with a COMMENT label will now be ignored. This permits comments to be included in input files.

POST-PROCESSOR

A post-processor named NBEAM6 has been locally available for use with the version of PARMILA but has not been documented. It is now also available for use with UNICOS. It provides graphical and tabular descriptions of a beam from PARMILA, taking the beam particle coordinates from a file named by the user. Histogram plots of the beam particle distributions in x, xprime, y, yprime, phase, and energy are available, either with or without Gaussian curves fitted to the distributions. Figure 1 shows an example histogram plot with fitted Gaussian.

Scatter plots in each of the phase-space planes are available. An example is given in figure 2. Tabular descriptions of either a set of nine percentages of the beam (a "full range analysis") or of a single percentage of the beam specified by the user are presented in the output file named FORT.4. The values of the step, mean, standard deviation, and third moment associated with the fitted Gaussian curves are given in a file named OUTPUT. The program makes use of the proprietary graphics software, DISSPLA.

Use of the program is interactive, and the user is prompted for input. An example interactive session follows.

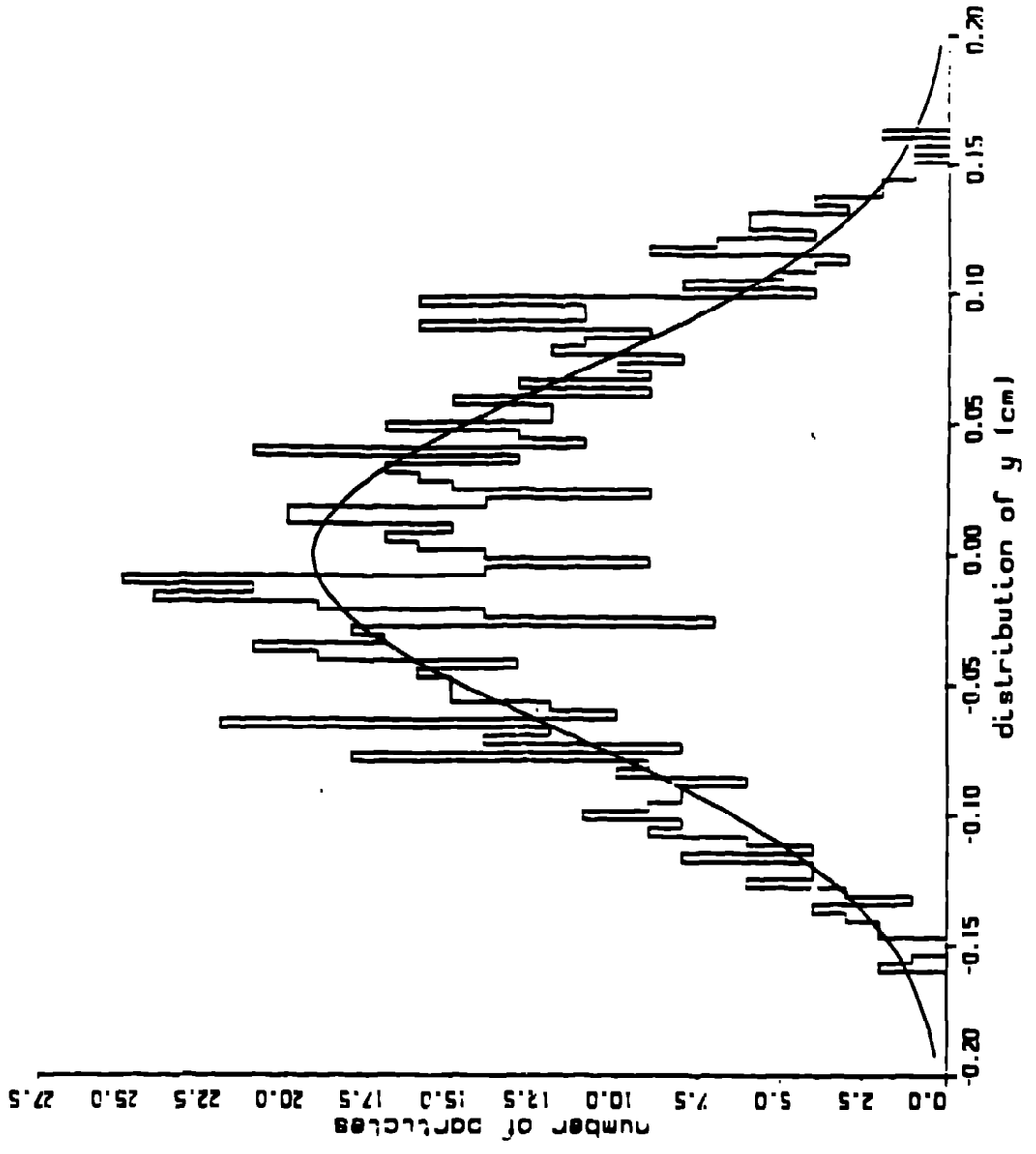


Fig. 1. Histogram plot of particle distribution in y, with fitted Gaussian.

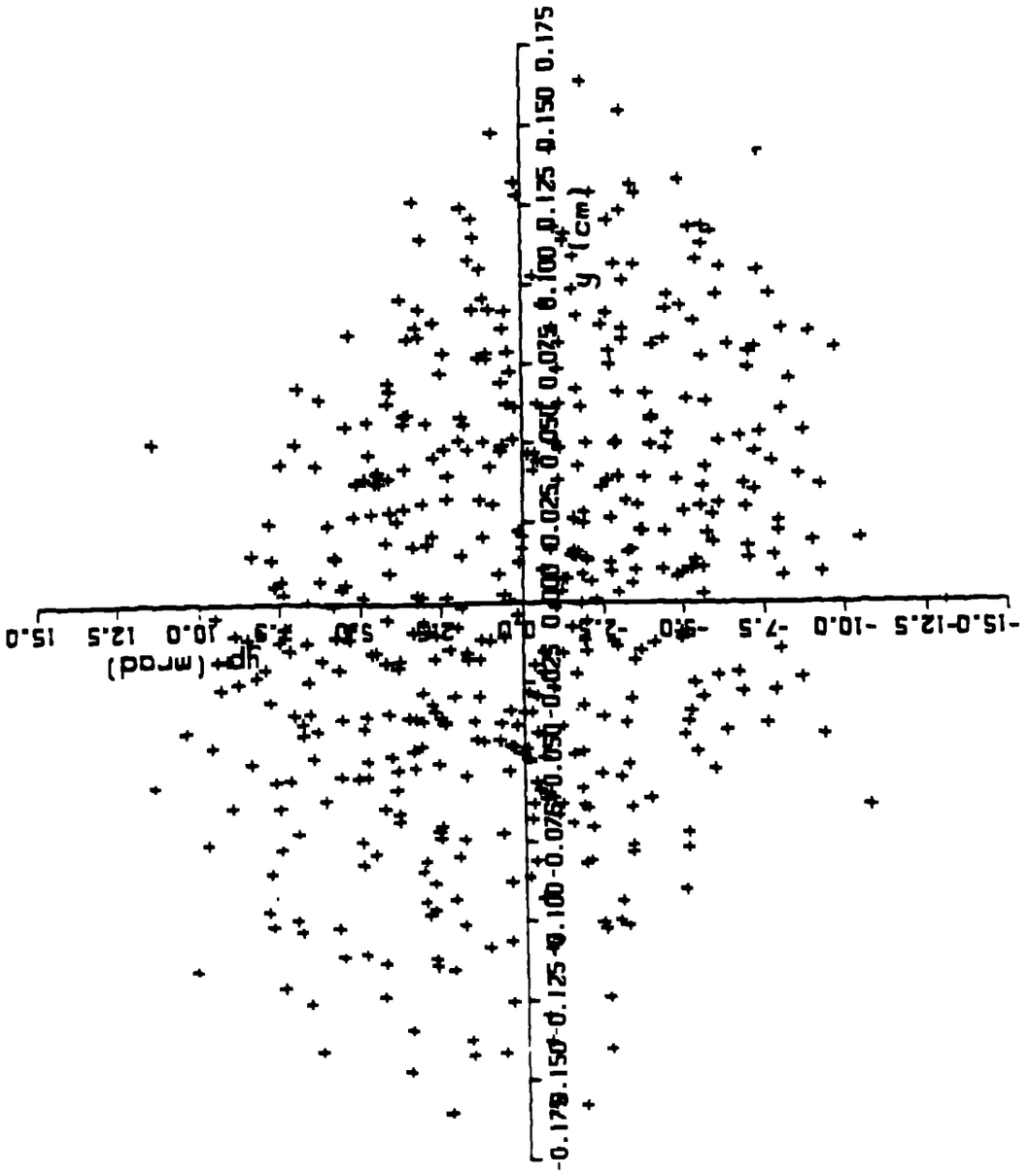


Fig. 2. Phase-space distribution in y vs. y-prime.

```
 give coordinate input file name.
tape25
 what is dimension of cord on input file?
6
 give first four letters of type of particle.
try <prot>,<deut>,or <hmin> or <stop> to exit code.
hmin
want to use synch energy-synch phase <y> <cr>?
if <cr>, will use wbar-pbar calculated in this code.
y

 read from tape5      synch energy       5.0504 mev
                      synch phase       -0.6981 radians

do you want a full range analysis? <y> or <cr>
y

parmila short input file

 do you want plot output ? <y> or <cr>
y

do you want histograms plotted? <y> or <cr>
y
 do you want plots of fitted gaussian distribution? <y> or <cr>
y
to change distribution limits enter any or all xl,xpl,yl,ypl,phimin,phimax,
wlow,whigh,npar. namelist format. namelist name=limits
 $limits$
 do you want sample emittance plots? <y> or <cr>)
y
to change plot limits enter any or all xmx,xpmx,ymx,ypmx,wmx,pmx
use namelist format. namelist name is maxs
 $maxs$
 plot    done.  pages =   11.  words =    10517
 graphics cl = u
 END OF DISSPLA 11.0 9003, DRIVERS 9003 -- 20519 VECTORS IN 10
 PLOTS.
 RUN ON 1/12/93 USING SERIAL NUMBER 2545 AT LOS ALAMOS NATIONAL
 LABORATORY
 PROPRIETARY SOFTWARE PRODUCT OF COMPUTER ASSOCIATES, INC.
 9763 VIRTUAL STORAGE REFERENCES; 7 READS; 0 WRITES.
```

CONCLUSIONS

The manual, the UNICOS version of PARMILA, or the VAX/VMS version can be obtained by sending a request to The Los Alamos Accelerator Code Group by one of the means given below.

Mail request to:

Los Alamos Accelerator Code Group (LAACG)
Mail Stop H825
Los Alamos National Laboratory
Los Alamos, New Mexico 87545
USA

Phone:

(505) 667-9131

E-Mail:

laacg@lanl.gov

Please include the following information with your request: code and/or documentation requested, your name, organization, address, phone number, fax number, and E-mail address, and the computer and operating system on which you intend to use the program.

The LAACG is restricted in its dealings with persons from countries on the U.S. Department of Energy's sensitive countries list. The code group can send such persons documentation, but they must request software from the Energy Science and Technology Software Center (ESTSC). For those who must request software from the ESTSC, the center can be reached as follows:

Phone: (615) 576-2606
Fax: (615) 576-2865
Mail: Energy Science and Technology Software Center
P.O. Box 1020
Oak Ridge, TN 37831
USA

The Los Alamos Accelerator Code Group is able to send the manual to requestors in sensitive countries.

References

[1] G. Boicourt and J. Merson, "PARMILA Users and Reference Manual," Los Alamos National Laboratory report LA-UR-90-127 (January 10, 1990, revised September 25, 1992)

[2] M.T. Menzel and H.K. Stokes,"User's Guide for the POISSON/SUPERFISH Group of Codes," Los Alamos National Laboratory report LA-UR-87-115 (January 1987)

[3] Los Alamos Accelerator Code Group,"POISSON/SUPERFISH Reference Manual," Los Alamos National Laboratory report LA-UR-87-126 (January 1987)

[4] Thomas P. Wangler, private communication, October 1991

[5] George H. Neuschaefer, private communication, December 21, 1992

Fig 1

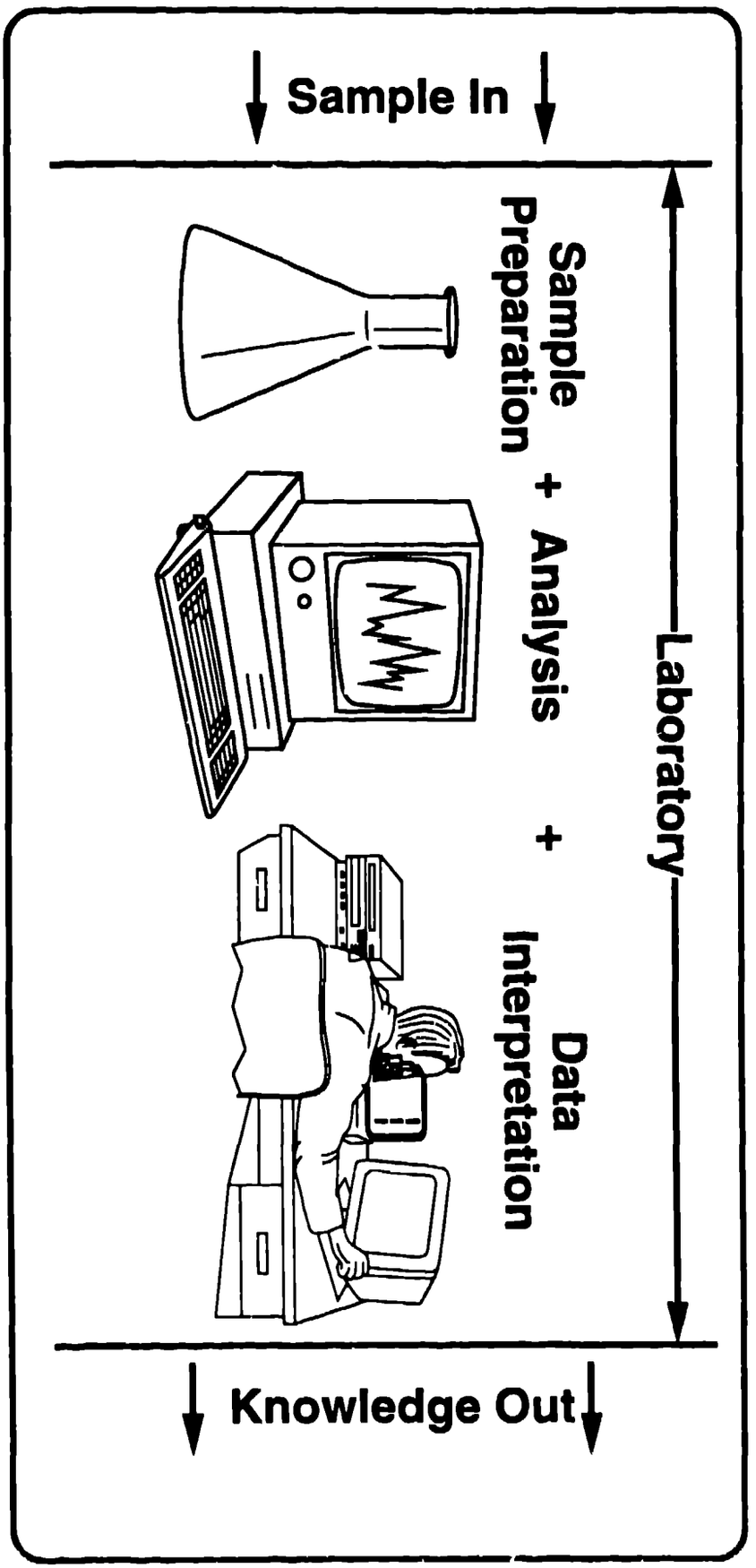

Sample In
Sample Preparation + Analysis + Data Interpretation
Laboratory
Knowledge Out

Fig 2

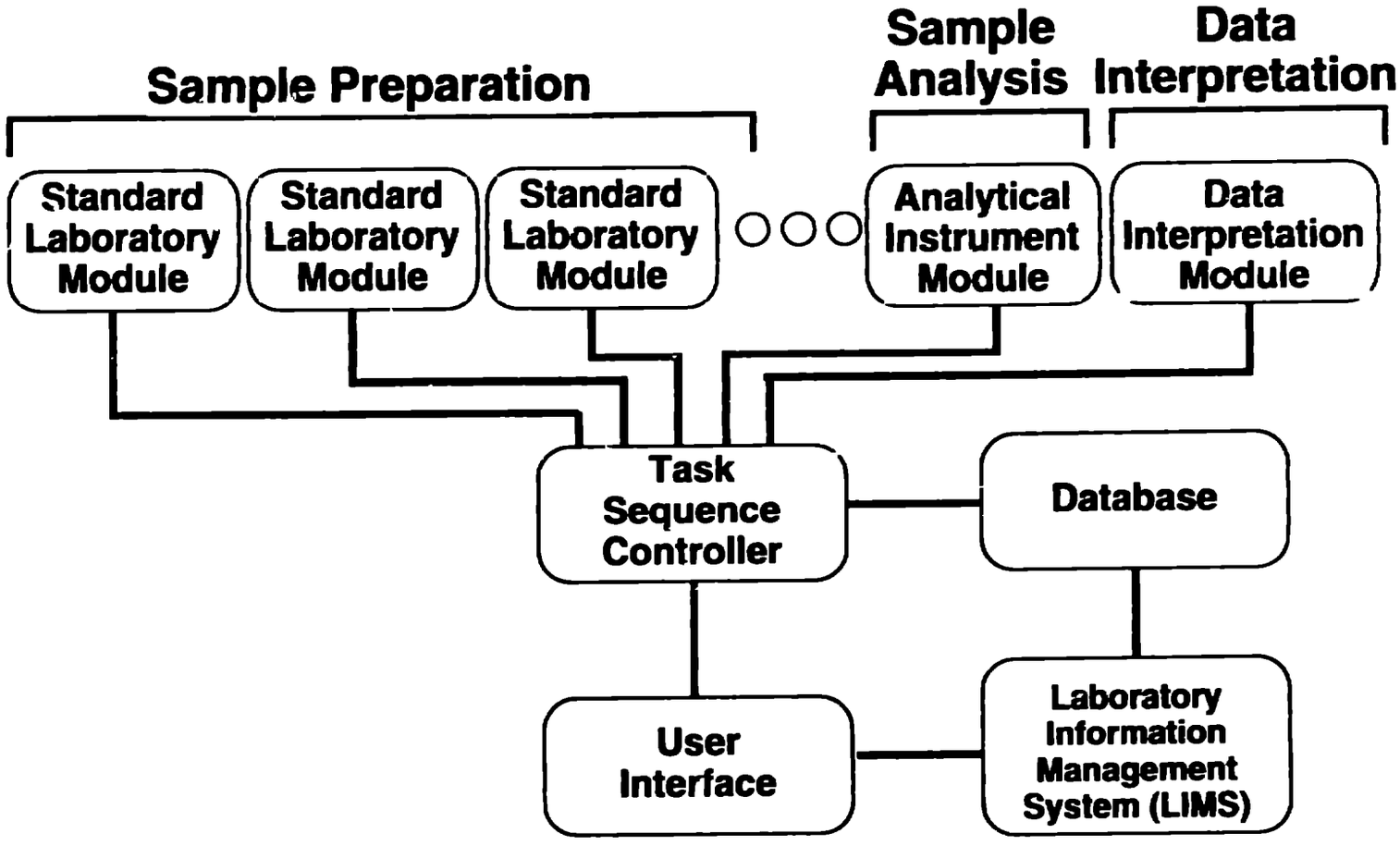

Sample Preparation
Sample Analysis
Data Interpretation
Standard Laboratory Module
Standard Laboratory Module
Standard Laboratory Module
Analytical Instrument Module
Data Interpretation Module
Task Sequence Controller
Database
User Interface
Laboratory Information Management System (LIMS)

Fig 3

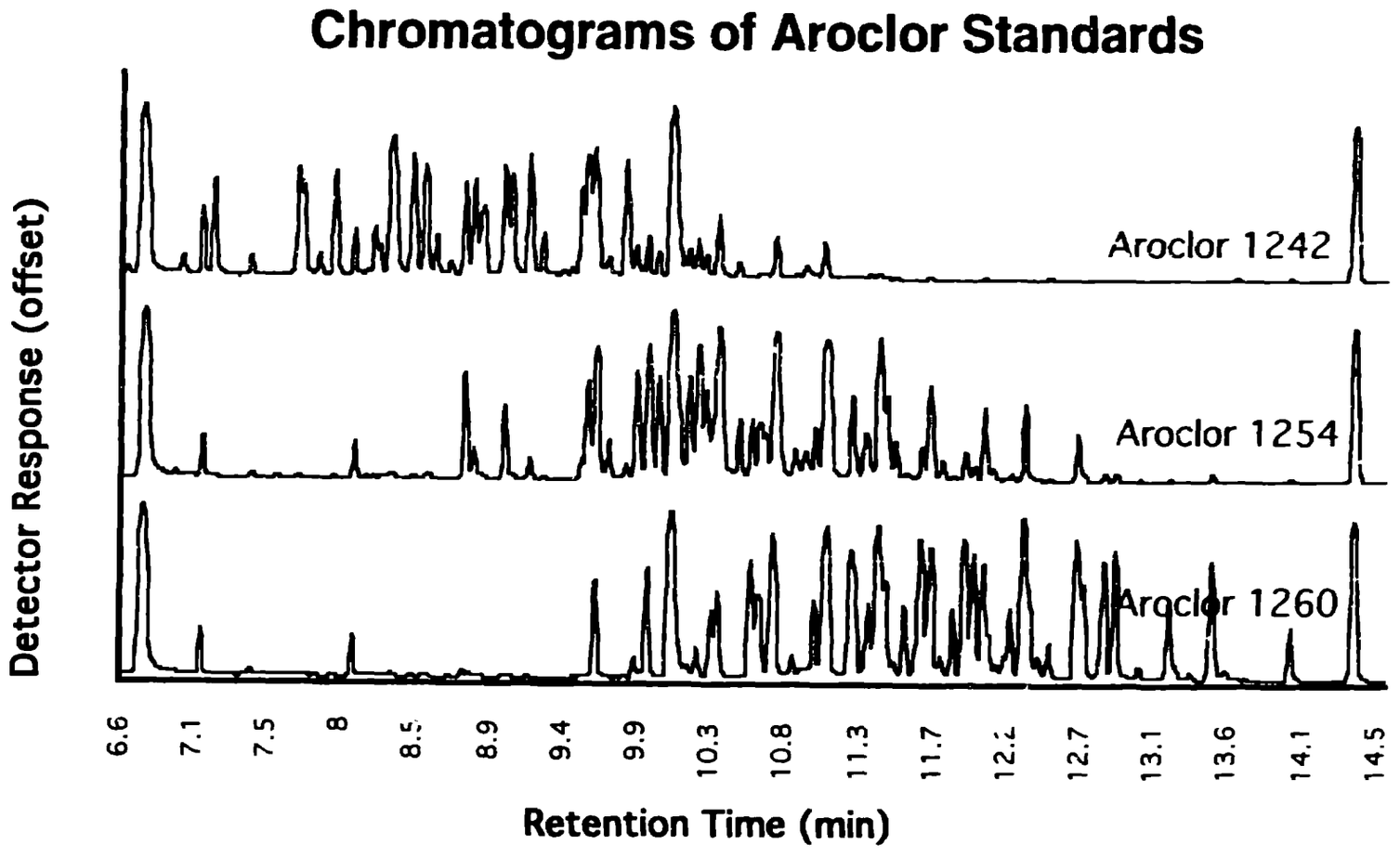
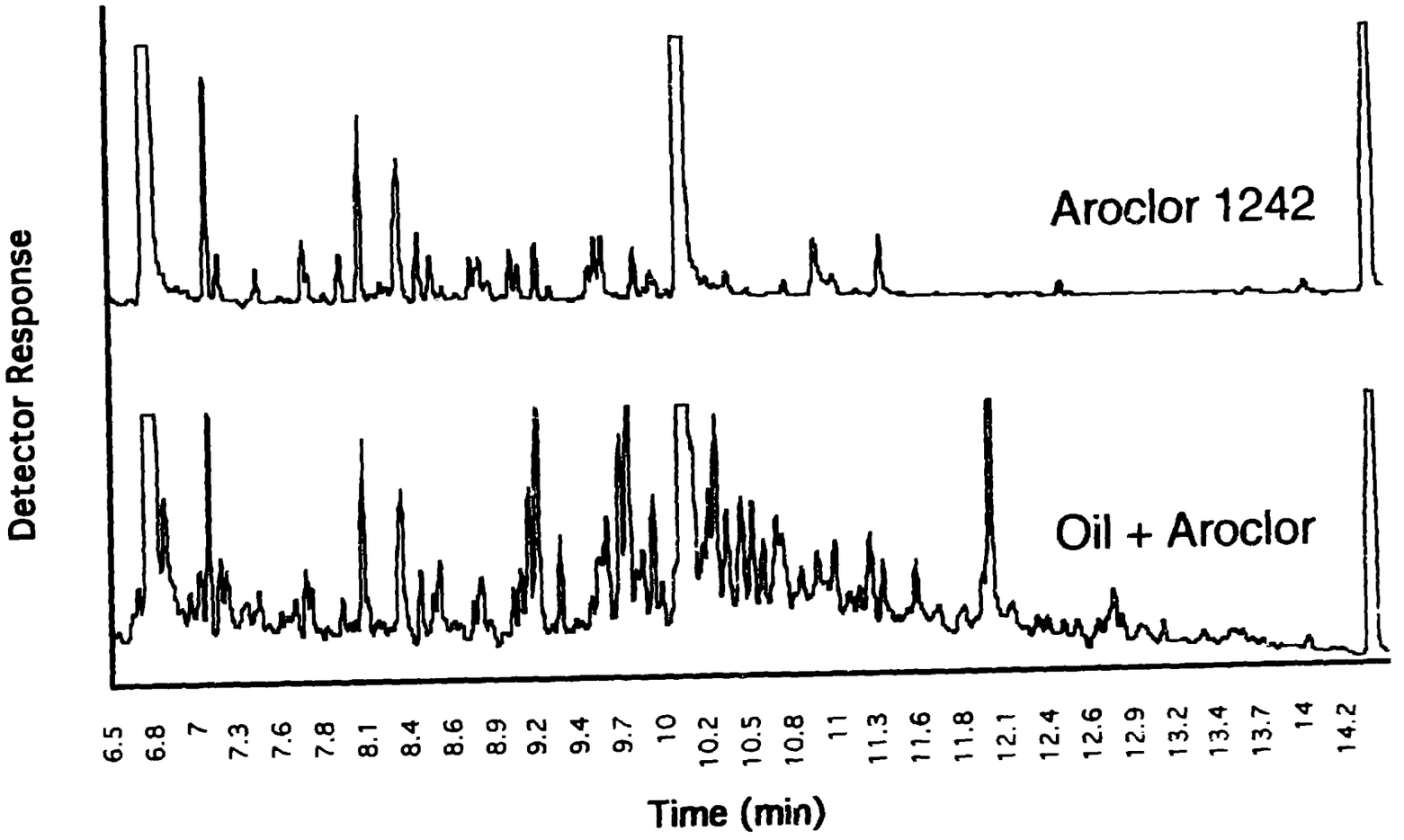
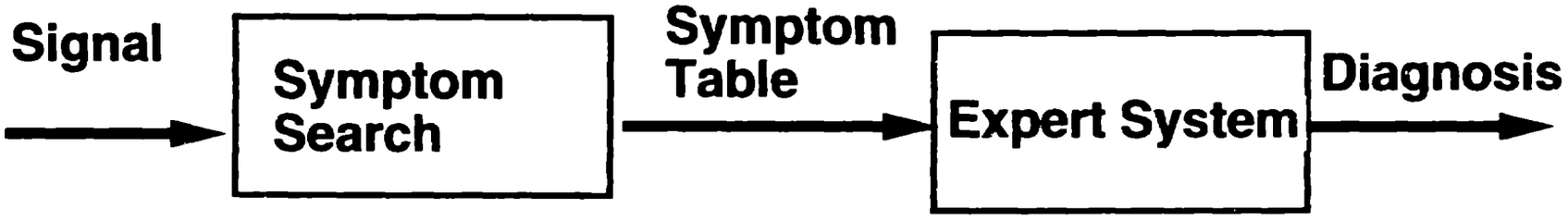
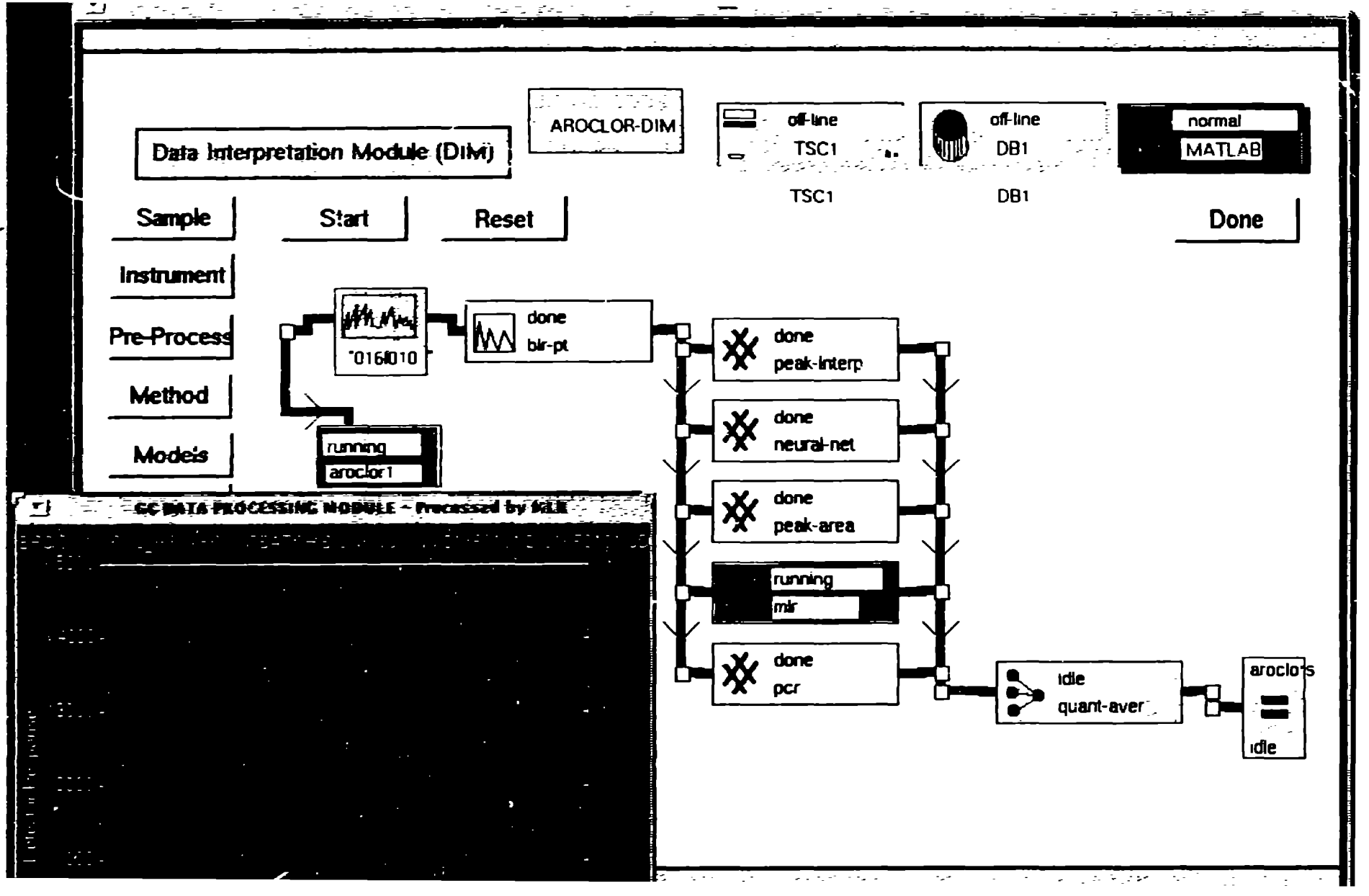
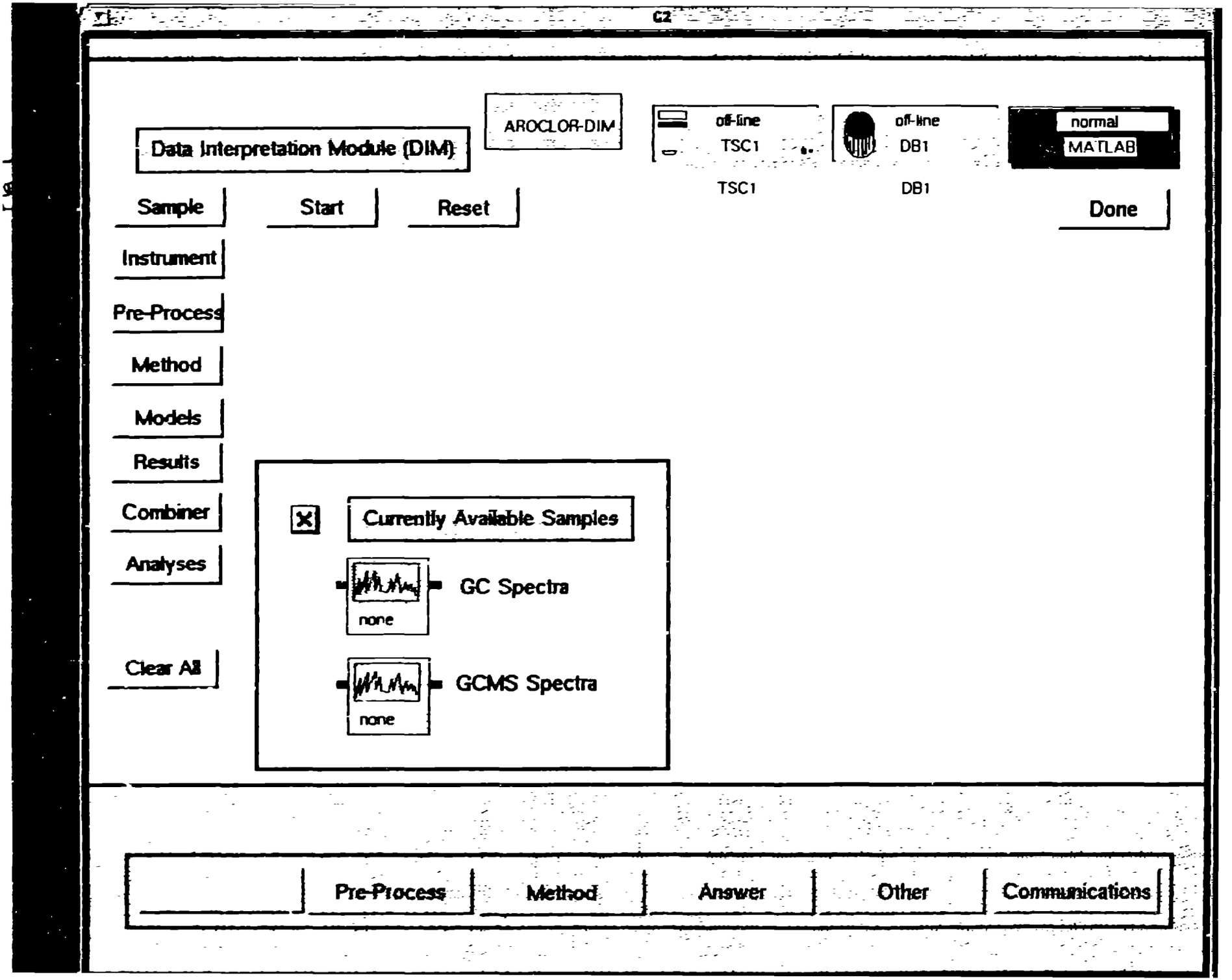

Chromatograms of Aroclor Standards
Detector Response (offset)
Aroclor 1242
Aroclor 1254
Aroclor 1260
6.6
7.1
7.5
8
8.5
8.9
9.4
9.9
10.3
10.8
11.3
11.7
12.2
12.7
13.1
13.6
14.1
14.5
Retention Time (min)

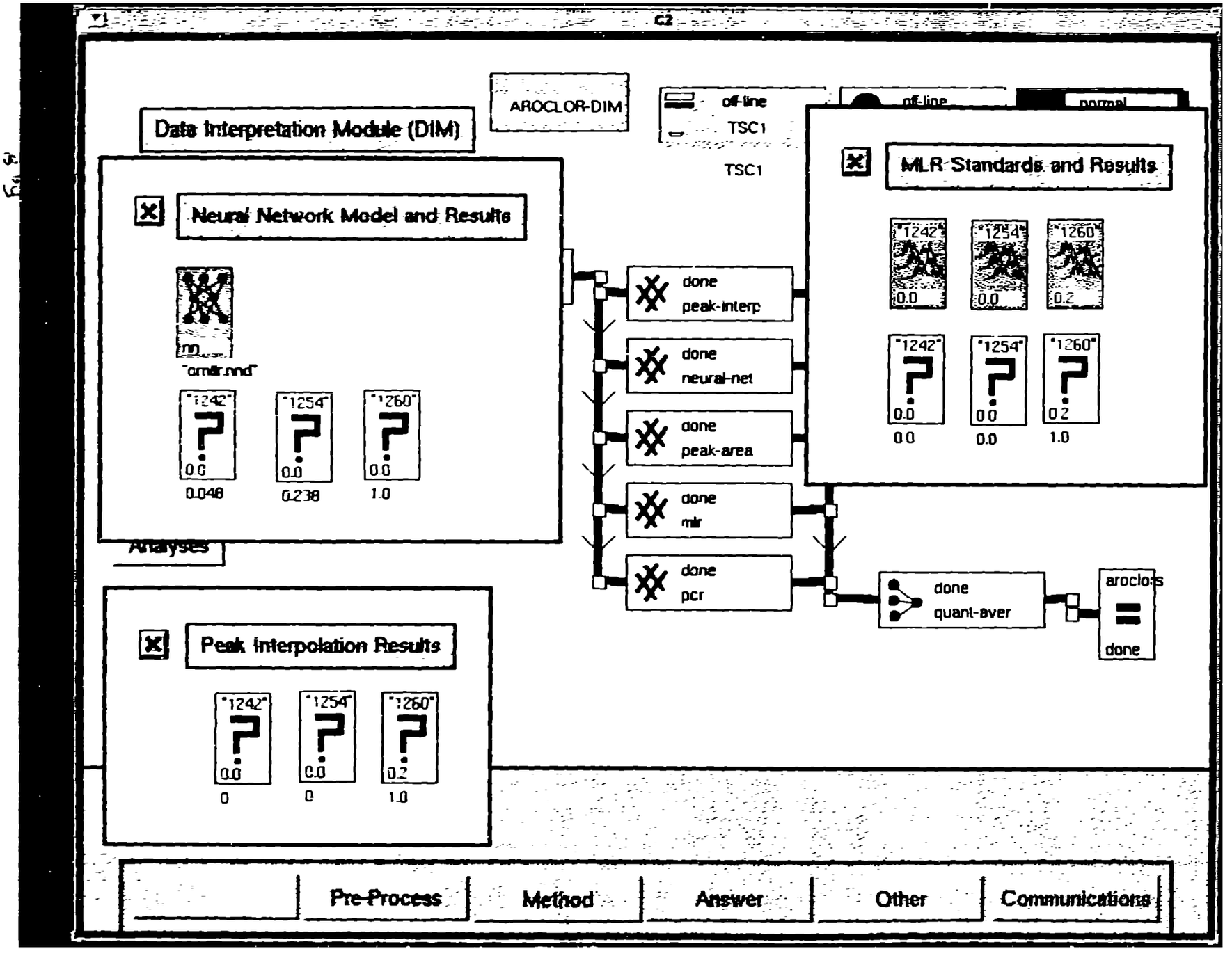
Fig 4


Aroclor 1242
Oil + Aroclor
Detector Response
6.5
6.8
7
7.3
7.6
7.8
8.1
8.4
8.6
8.9
9.2
9.4
9.7
10
10.2
10.5
10.8
11
11.3
11.6
11.8
12.1
12.4
12.6
12.9
13.2
13.4
13.7
14
14.2
Time (min)


Signal
Symptom Search
Symptom Table
Expert System
Diagnosis


Data Interpretation Module (DIM)
AROCLOR-DIM
off-line
TSC1
TSC1
off-line
DB1
DB1
normal
MATLAB
Sample
Start
Reset
Done
Instrument
Pre-Process
Method
Models
done
blr-pt
done
peak-interp
done
neural-net
done
peak-area
running
mlr
done
pcr
idle
quant-aver
idle
running
aroclor1


Data Interpretation Module (DIM)
AROCLOR-DIM
off-line
TSC1
TSC1
off-line
DB1
DB1
normal
MATLAB
Sample
Start
Reset
Done
Instrument
Pre-Process
Method
Models
Results
Combiner
Analyses
Clear All
Currently Available Samples
GC Spectra
none
GCMS Spectra
none
Pre-Process
Method
Answer
Other
Communications


C2
AROCLOR-DIM
off-line
TSC1
TSC1
off-line
normal
Data Interpretation Module (DIM)
Neural Network Model and Results
"1242"
0.0
0.048
"1254"
0.0
0.238
"1260"
0.0
1.0
Analyses
done
peak-interp
done
neural-net
done
peak-area
done
mlr
done
pcr
MLR Standards and Results
"1242"
0.0
"1254"
0.0
"1260"
0.2
"1242"
0.0
0.0
"1254"
0.0
0.0
"1260"
0.2
1.0
done
quant-aver
aroclors
done
Peak Interpolation Results
"1242"
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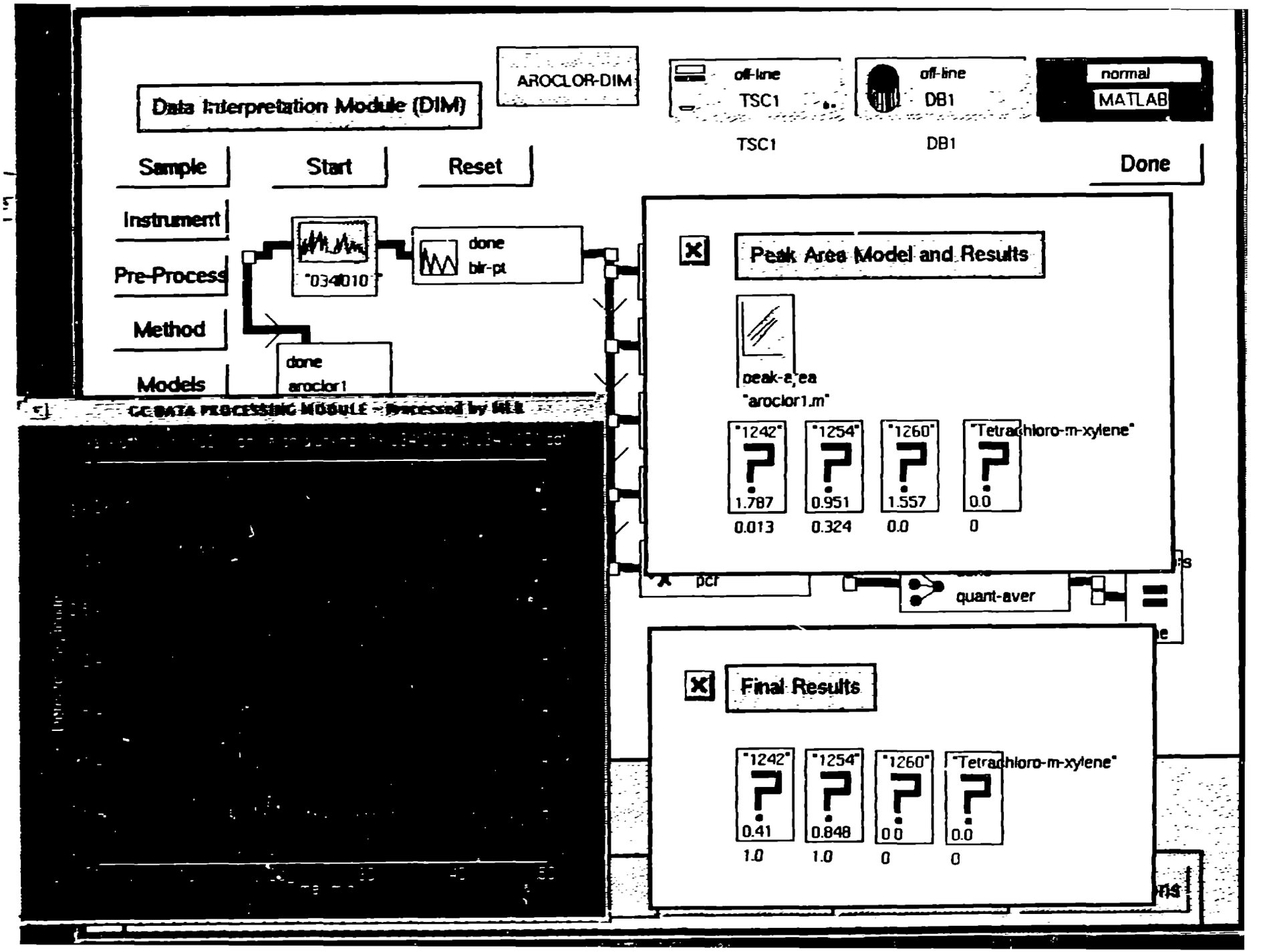
0
"1254"
0.0
0
"1260"
0.2
1.0
Pre-Process
Method
Answer
Other
Communications


Data Interpretation Module (DIM)
AROCLOR-DIM
off-line
TSC1
off-line
DB1
normal
MATLAB
TSC1
DB1
Sample
Start
Reset
Done
Instrument
Pre-Process
Method
Models
done
blr-pt
done
aroclor1
Peak Area Model and Results
peak-area
"aroclor1.m"
"1242"
"1254"
"1260"
"Tetrachloro-m-xylene"
1.787
0.951
1.557
0.0
0.013
0.324
0.0
0
pcr
quant-aver
Final Results
"1242"
"1254"
"1260"
"Tetrachloro-m-xylene"
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0.848
0.0
0.0
1.0
1.0
0
0

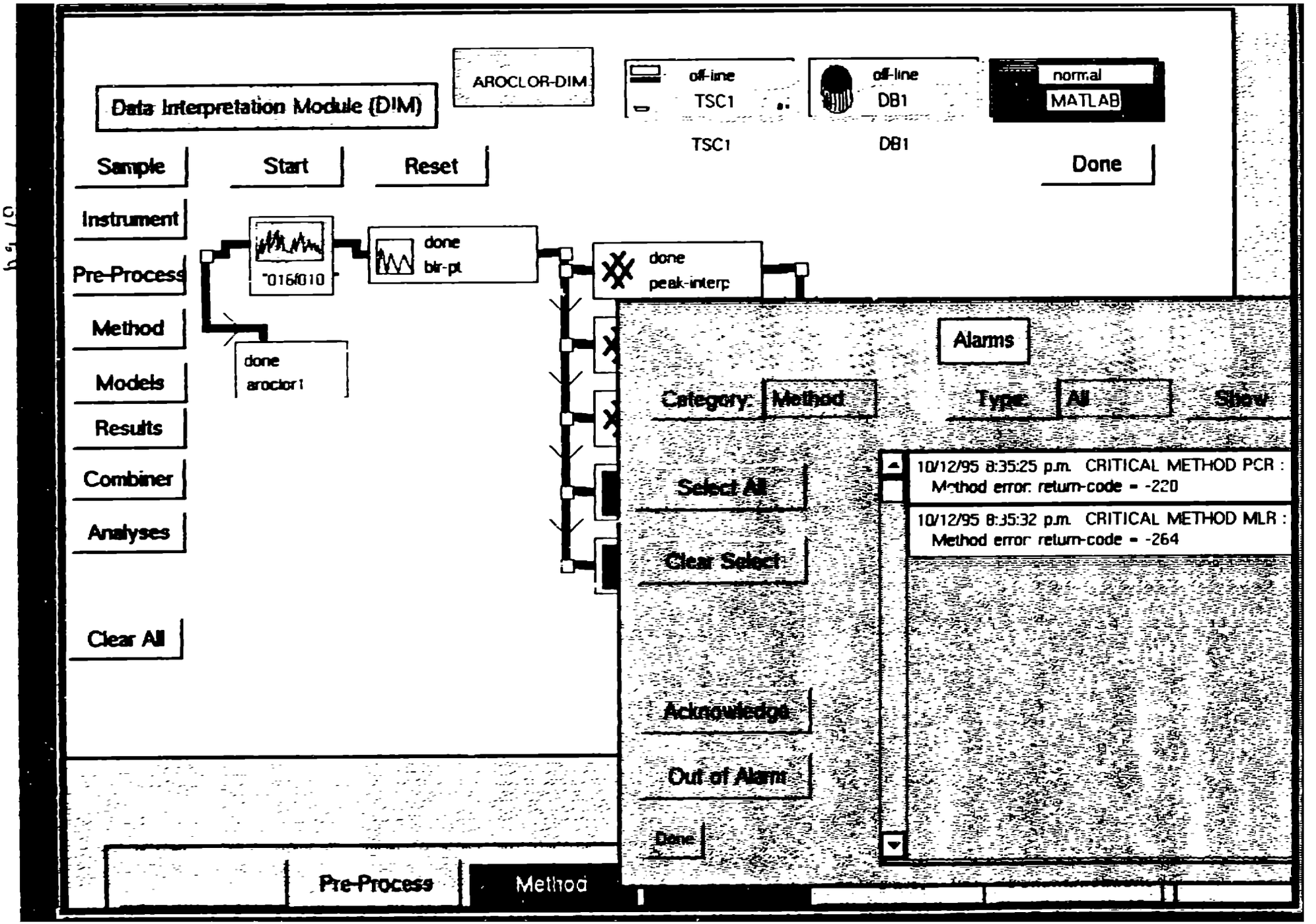
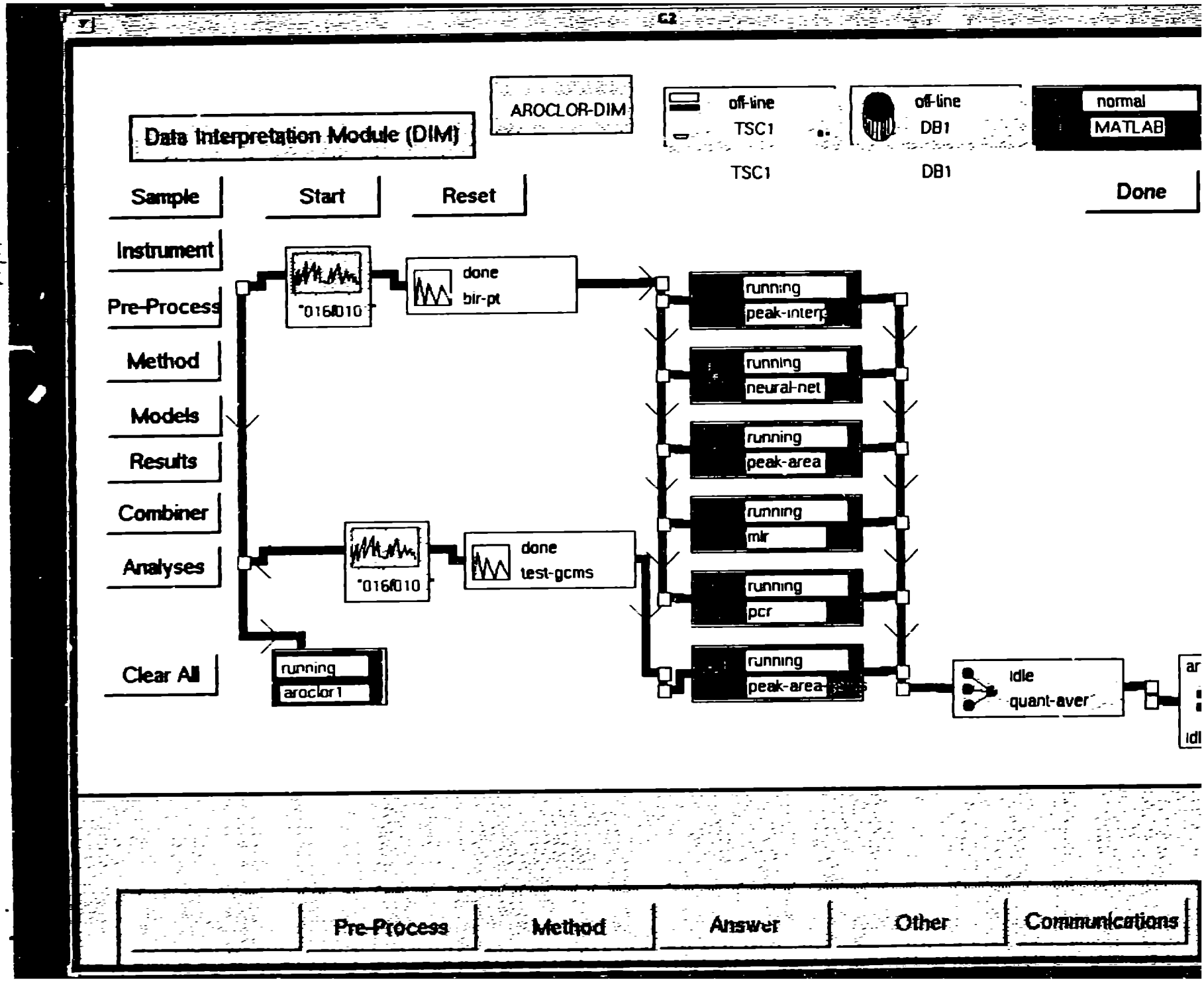

Data Interpretation Module (DIM)
AROCLOR-DIM
off-line
TSC1
TSC1
off-line
DB1
DB1
normal
MATLAB
Done
Sample
Start
Reset
Instrument
Pre-Process
Method
Models
Results
Combiner
Analyses
Clear All
"016f010
done
blr-pt
done
peak-interp
done
aroclor1
Alarms
Category:
Method
Type:
All
Show
Select All
Clear Select
10/12/95 8:35:25 p.m. CRITICAL METHOD PCR :
Method error return-code = -220
10/12/95 8:35:32 p.m. CRITICAL METHOD MLR :
Method error return-code = -264
Acknowledge
Out of Alarm
Done
Pre-Process
Method

Fig 11


Data Interpretation Module (DIM)
AROCLOR-DIM
off-line
TSC1
TSC1
off-line
DB1
DB1
normal
MATLAB
Done
Sample
Start
Reset
Instrument
Pre-Process
Method
Models
Results
Combiner
Analyses
Clear All
"016f010
done
bir-pt
running
peak-interp
running
neural-net
running
peak-area
running
mlr
running
pcr
running
peak-area
"016f010
done
test-gcms
running
aroclor1
idle
quant-aver
Pre-Process
Method
Answer
Other
Communications