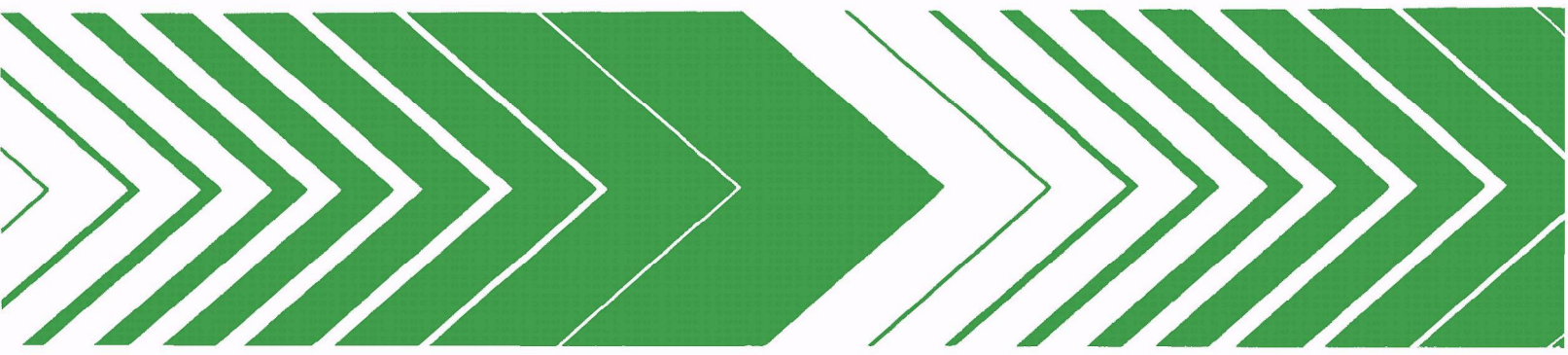


Research and Development



Computer Program for Reducing Mass Spectra Data from GC/MS Systems



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COMPUTER PROGRAM FOR REDUCING MASS SPECTRAL DATA
FROM GC/MS SYSTEMS

by

David Rosenthal
Research Triangle Institute
Post Office Box 12194
Research Triangle Park, North Carolina 27709

Contract No. 68-02-2745

Project Officer

Kenneth Krost
Atmospheric Chemistry and Physics Division
Environmental Sciences Research Laboratory
Research Triangle Park, North Carolina 27711

ENVIRONMENTAL SCIENCES RESEARCH LABORATORY
OFFICE OF RESEARCH AND DEVELOPMENT
U.S. ENVIRONMENTAL PROTECTION AGENCY
RESEARCH TRIANGLE PARK, NORTH CAROLINA 27711

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ABSTRACT

Existing computer programs for deconvoluting mass spectrometry data derived from gas chromatography/mass spectrometry/computer systems were evaluated, and the most efficient method was introduced unto an EPA UNIVAC computer. The program chosen was that reported by Rindfleisch and his co-workers at Stanford University. The accompanying program listing is included. The Rindfleisch program was tested with both standard runs and environmental samples. Sample components were successfully identified by an independent computer search program with an accuracy approaching 80%.

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ABBREVIATIONS

GC/MS	-	Gas Chromatography/Mass Spectrometry
TIC	-	Total Ion Current
A/D	-	Analog to Digital
MS	-	Mass Spectrometry
TUCC	-	Triangle University Computation Center
GC	-	Gas Chromatograph(y)
R	-	Correlation Coefficient
H	-	Hit
M	-	Miss
I/O	-	Input/Output

SECTION 1

INTRODUCTION

Gas Chromatography/Mass Spectrometry (GC/MS) is an analytical method which has the potential capability of allowing the total automated identification of a complex mixture of pollutants. Implementation of such a technique depends on the availability of two types of new technology. The first, the automatic acquisition and storage of fast scan low resolution mass spectrometry data, has been available for some time. The first GC/MS system involving the continuous recording of mass spectral data from a mass spectrometer operating in cyclic mode was first reported by Hites and Biemann in 1968.¹ At the present time these systems are commercially produced by many manufacturers.

The availability of computer programs for the analysis of this kind of data is at present still very limited. Although software development in this field constitutes a very active research area (roughly 100 papers are published yearly), very few integrated systems have yet been developed which are generally useful. This is in part due to the large variety of computer types, each with its own individual characteristics, but more importantly due to a general unavailability of broad based algorithms with an effective philosophy of approach. As a result, the vast majority of mass spectral runs are still being analyzed by hand.

The problem of the development of a generalized system for data analysis has two aspects. The first is how to separate mathematically the raw mixed spectra into well resolved components. The second is to assign a chemical structure to each resolved spectrum. Several approaches have been tried concerning the second problem, and one based on the pioneering work of Grotch² had been successfully implemented and realized in the form of a library search program now resident at the RTI Mass Spectrometry Facility prior to this project. The early results of this search program however, had not been totally satisfactory, usually for the reason that the input spectra were not

sufficiently "clear", to allow unique identification. This problem was in large part alleviated by combining the search algorithm with an appropriate cleanup procedure. The implementation of each of these two stages and their effective combination turned out to enhance the capabilities of the entire system.

After a prototype system was developed which was shown to be effective, the CLEANUP programs which were developed were adapted to the EPA environment. Since manipulation of large data bases are much more easily accomplished in a large computer, it was felt that this process was best carried out by adapting data acquired using EPA's INCOS data system and processing them on a large computer. This approach had the dual advantage of making the programming effort much simpler, since core size limitations did complicate the programming, and in addition the processing could be accomplished independently, thus freeing the INCOS system to do other work. Again, the fact that programs were written in standard FORTRAN facilitated their transfer to the EPA UNIVAC computer.

Completion of the project by delivery of the program and its documentation to the contracting agency, is effected with this report and the accompanying listings (Appendix 1).

SECTION 2

CONCLUSIONS AND RECOMMENDATIONS

The work accomplished under this contract can be divided into four parts: (I) a literature search to determine the most effective algorithm for deconvolution of mass spectra; (II) implementing that algorithm on an existing computer and performing detailed tests of its efficiency, both from a chemical and machine standpoint; (III) making the program operational on the EPA UNIVAC computer installation using for input a tape created using the INCOS data acquisition system; (IV) making the necessary documentation and source code (Appendix 1) available to the contacting agency.

Three techniques were considered in Phase I: background subtraction, mass max analysis, and peak profile analysis. The peak profile analysis proposed in a recent article by Rindfleisch (Appendix 2) was ultimately chosen because of its demonstrated effectiveness in existing systems (the CLEANUP program) and because it incorporated the notions of background subtraction and mass max analysis as a starting point.

Once the Rindfleisch algorithm was chosen, the task of implementing that algorithm on the TUCC 370 was undertaken. First, a detailed study of the published algorithm was made in order to gain a better understanding of what was involved and to determine if improvements were necessary. Next, a copy of the Rindfleisch program modified to run on an IBM 370 was obtained through the cooperation of a group of chemists at the NASA Ames Air Force Base. This copy was then modified to run in a batch environment at TUCC and was subjected to extensive testing, both from a machine and chemical standpoint. This included running the program under the WATFIV compiler to insure program accuracy and machine independence, followed by testing with data acquired by a VARIAN CH-7

mass spectrometer. The test data consisted of three brominated standards, followed by fifteen runs involving a wide variety of environmental samples. The RTI library search program was used throughout to evaluate the output from CLEANUP. The laboratory standards were all correctly identified and correct identifications, approaching 80% were obtained on some environmental samples. In addition, some of the CLEANUP input parameters were studied in order to determine optimum settings.

Phase III, making CLEANUP operational in the EPA environment, consisted of three parts: obtaining a successful run of INCOS test data supplied by EPA on the TUCC 370, obtaining a successful run on the same data using a version of CLEANUP adapted to run on the EPA UNIVAC computer, and finally verifying that the output tape was compatible with the contracting agency's INCOS data acquisition software and yielded plausible output spectra.

This report, together with the accompanying listings and the installing of CLEANUP on the UNIVAC comprise the completion of Phase IV of this project.

It is now necessary to carry out a thorough testing of the programs to determine what conditions and sets of parameters must be used to obtain optimal results. The principles used in developing the software are sound, however, the programs need to be tuned to fit the acquisition conditions. Some attention should be given to control studies using known mixtures, because these give the best opportunity for evaluation of the system. A statistical evaluation of the results, especially when compared with other methods, would be very profitable.

SECTION 3

LITERATURE SEARCH OF EXISTING DECONVOLUTION METHODS

Phase I of this contract consisted of a literature search to consider available alternatives for the treatment of mass spectral mixtures, and thus arrive at a best method for deconvolution. Three general avenues of attack were examined: background subtraction, mass max, and peak profile analysis.

BACKGROUND SUBTRACTION

The technique of background subtraction is basically as follows. In its simplest form, a spectrum from either an unknown GC run or some blank run is chosen as a "background" spectrum. This spectrum is then subtracted from the unknowns within the run, and the resulting difference spectra are used for mass spectral identification.

In a slightly more refined version of the technique, the background spectrum is determined manually by visual inspection of a raw total ion current (TIC) plot, and in some instances several background spectra are chosen for use in different ranges of the chromatogram.

The difficulties associated with this approach are fairly obvious. Background spectra are not constant, either qualitatively or quantitatively. Thus, what constitutes the background in one section of the run may be very different from that in another. Additionally, background peaks arising from contaminants such as column bleed change in intensity especially during temperature programmed runs.

Thus the question of how the background subtraction is to be carried out is very difficult to answer. Even the mechanics of the subtraction can be done in a number of ways. Several unsophisticated schemes exist in which the background spectra are subtracted, peak for peak, from the raw digitized unknown. Invariably, some spectra are undercorrected, while in others, real data is eliminated from the output, making identification very difficult,

either by hand or by machine. Human interpreters often prefer to look at raw data over background subtracted, since they can learn to ignore certain peaks without the removal of key unknown peaks by a clumsy program.

More sophisticated approaches have been tried wherein only a fraction of the background spectrum is subtracted. The problem of course, is to determine the proper size of the fraction.

All in all the background subtraction approach was eliminated since it is not sufficiently flexible, can give erroneous results, and lacks a way in which a consistent algorithm can be proposed for automatic processing.

MASS MAX ANALYSIS

A second and more sophisticated approach to mass spectral deconvolution has been taken by Biemann and co-workers.³ This approach makes use of the principle that when a compound elutes from a GC column and is analyzed by continuous scan MS, the ions of each component show maximum intensity at some mean elution time.

The algorithm chosen, then, searches through each single ion trace for points of maximum intensity. The deconvoluted spectra are then defined as that collection of ions which have shown an intensity maximum within a given time window.

This approach was designed to allow the separation of mixtures of unknowns which are not sufficiently resolved to show individual TIC peaks, but which can be distinguished by the presence of single ion maxima which are not influenced by other ions not present in that particular unknown.

This idea is sound, and in fact, constitutes the first part of the Rindfleisch⁴ procedure, described below. The procedure is very rapid and has actually been incorporated into other commercially available deconvolution software systems.

The program is deficient because it does not take into account a number of facts.

1. If a given ion shows a maximum at one point, it does not by any means guarantee that this ion will not be present in the other component.

2. If, as often occurs, an ion is present in both components in approximately equal amounts, the observed maximum may occur between the maxima of either component and be missed entirely by the system.
3. The technique does not take into account contributions from background noise or column bleed, and treats each ion in an all or nothing manner, and therefore cannot get a proper estimate of the intensity of peaks which derive from more than one source.

The method seems to have some merit for the purpose of identifying the presence of unresolved multiplets. However, it cannot accurately predict the actual spectra, and because of the deficiencies mentioned in the previous paragraphs, sometimes fails entirely, showing specious peaks, or missing multiplets.

PEAK PROFILE ANALYSES

The algorithm for the CLEANUP program herein described was originally due to Rindfleisch and co-workers at Stanford.⁴ Their program was part of an integrated GC/MS data reduction system which ran on a PDP-11/20. Following is a detailed description of the elements and mode of operation of this program. This information was gathered from the published work on the subject as supplemented by our copy of the listings and other documentation.

Raw spectra output from GC/MS systems differ from the library spectra of pure components for at least three definable reasons. CLEANUP attempts to correct mathematically these spectra in three distinct ways, corresponding to these known error sources. These are 1) Background noise and column bleed, 2) Signal saturation, 3) overlapping peaks. We will call the three portions of the program dealing with these problems Tasks 1, 2, and 3.

Errors arise for the following reasons. Superimposed on the eluant spectrum there will always be a certain constant level of background noise, and in addition other extraneous signals which normally rise slowly with increasing column temperature due to the elution of some of the liquid phase of the column. Task 1 is concerned with the distinction between the origin of these kinds of signals. Task 2 tries to reconstruct the actual intensity level of peaks which are so strong that they have exceeded the range of the A/D convertor. This is the problem of peak saturation. Task 3 is the reconstruction of peak intensities of two or more compounds which elute so closely to one another that their

mass spectral peaks are intermixed. The guiding principle which allows the CLEANUP program to function is that it uses information both in advance and after a particular scan to distinguish between real peak unknown information and extraneous data. Such issues as column bleed detection, doublet resolution, background detection, etc. are defined in the context of a region of scans rather than a single scan. The CLEANUP program makes use of fourteen MS scans in core at any one time (Figure 1). For tasks 1 and 2, only the seven innermost scans are used. For some details (e.g., background estimation), all 14 scans are needed. For multiplet resolution, all 14 scans are used. The processing proceeds from the beginning of the run to the end in a single pass always using 14 spectra. The spectrum window in core is progressively updated by the addition of one spectrum from one end and the dropping of one spectrum from the other.

The CLEANUP algorithm can be divided into stages from a programming point of view. The first stage is the examination of the spectral window and determine whether or not an eluant is present at all. When a peak, or group of peaks is detected, then tasks 1, 2, and 3 can be undertaken to improve the quality of the raw data. The detection process is accomplished as follows: The program looks at a window seven scans wide as the input spectra move through the fourteen spectrum window in core. For each of the 411 masses in the seven scan window (each scan covers masses 40 to 450 the program does a primitive check to see if the window contains a simple maximum (Figure 2). As maxima are detected, histogram of the frequency of "singlet" maxima is created. Data are ignored if there are any "lumps" (indicating a doublet) or if peak saturation is observed anywhere in the window (Figure 3). In addition to the histogram of the number of occurrences of maxima (Figure 4), a record of a slightly modified total ion current is kept (Figure 5), i.e., once a singlet maximum is detected, a rudimentary approximation to column bleed and background is subtracted (corresponding to the lowest value in the 14 a.m.u. window), the ion current at the maximum is estimated via interpolation, and the resulting ion current is added into a peak amplitude record. When an appropriate number of scans have passed through the window (the statistics are updated continuously) a decision is made on the basis of the number of maxima observed and the total amplitude of those maxima whether an eluant is present. It should be mentioned here that at this

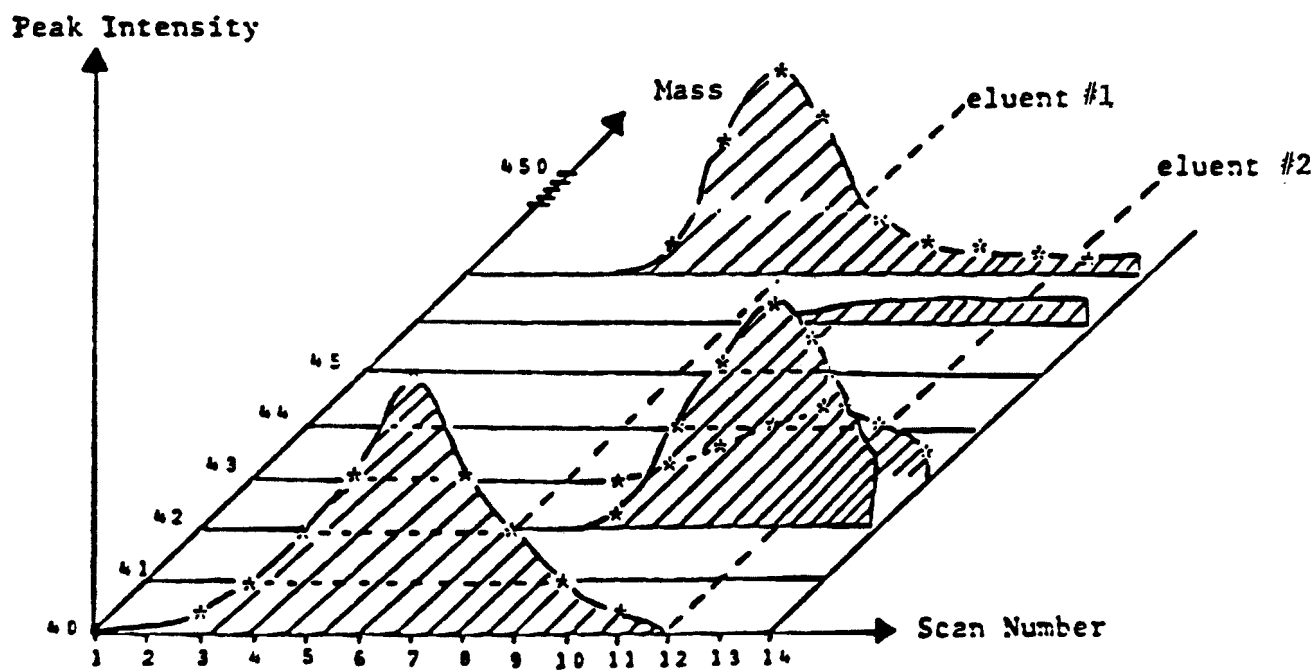


Figure 1. Schematic representation of 14 scan window for Masses 40-450 in core - a typical case.

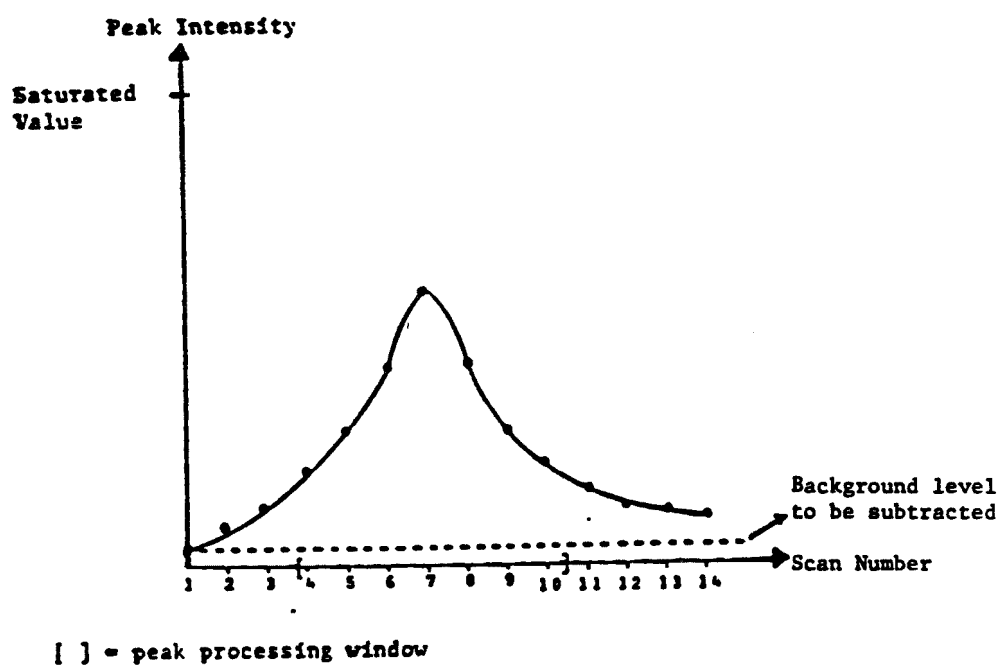


Figure 2. A typical singlet peak model for a given mass.

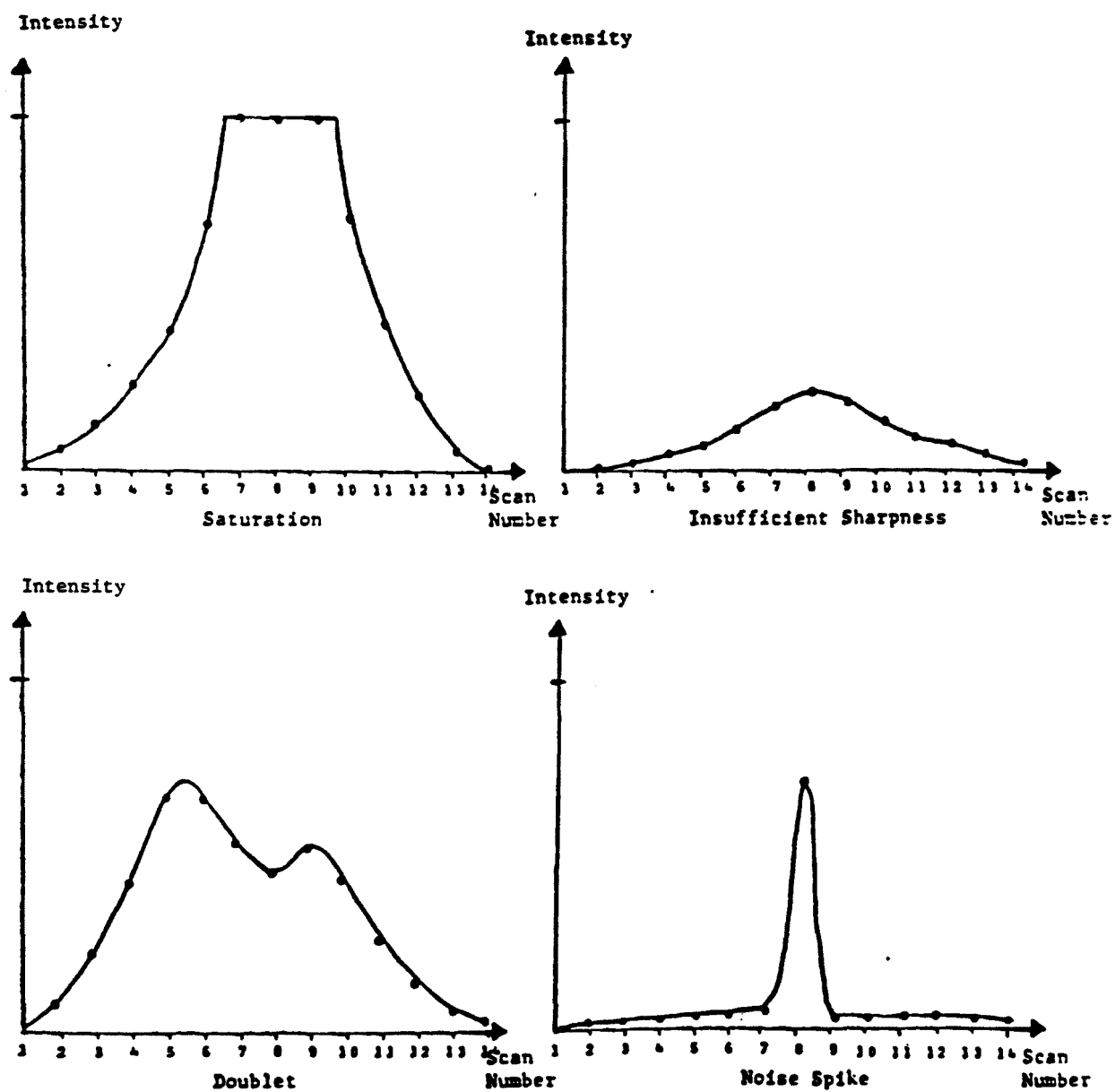


Figure 3. Various types of situations which do not qualify in histogram calculation.

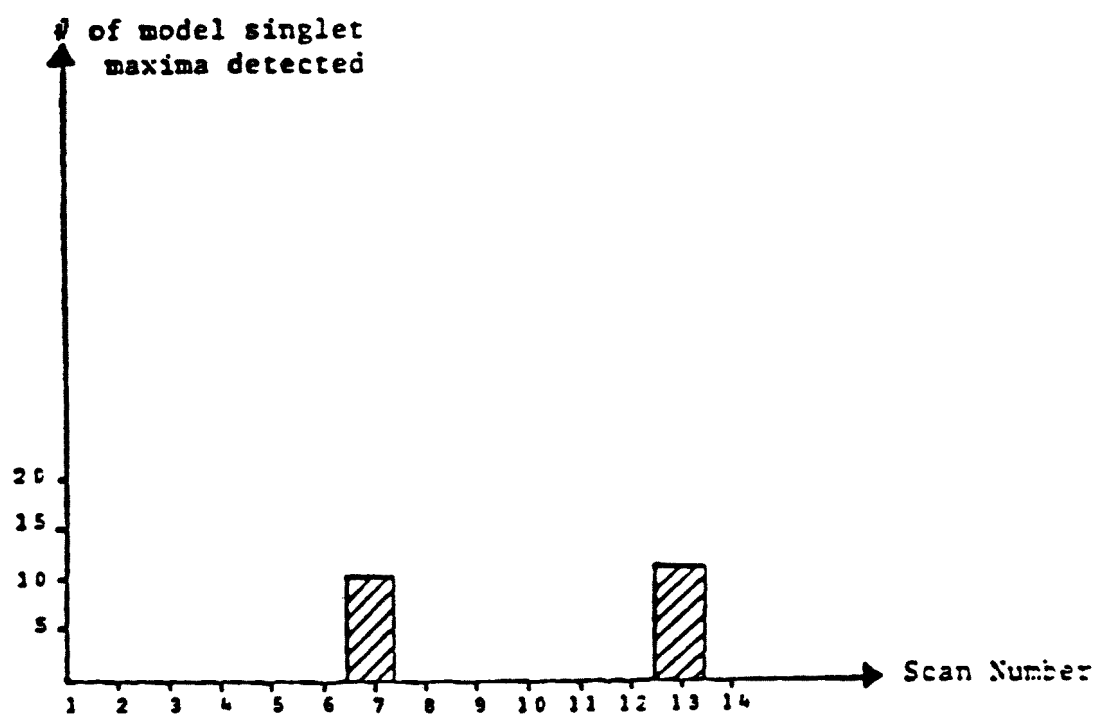


Figure 4. Peak detection histograms for sample processing window of Figure 1.

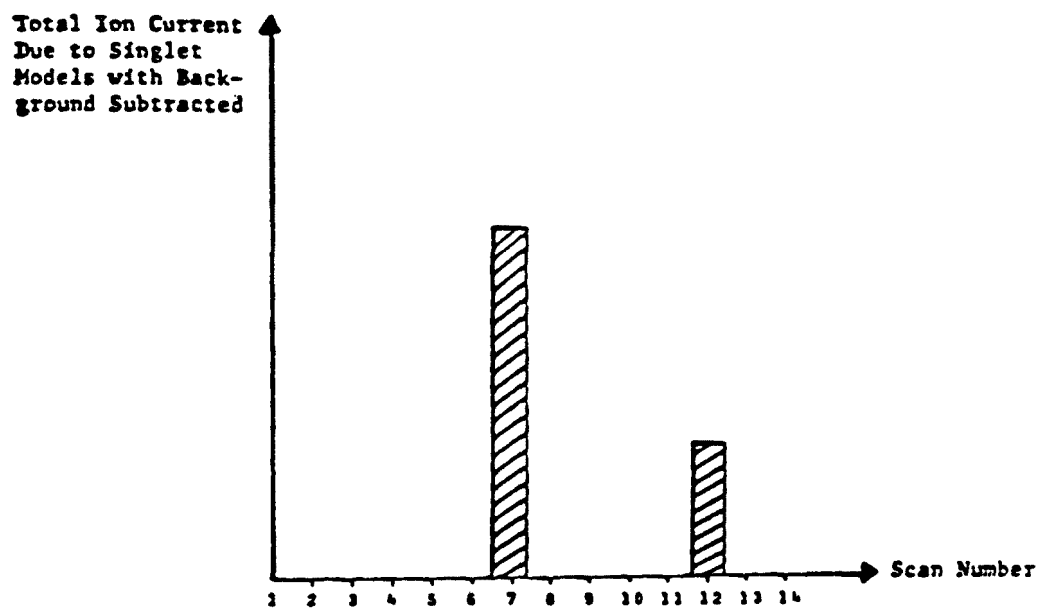


Figure 5. Statistics of TIC vs. scan number.

point in the program the "sharpness" of each candidate peak is computed. This number is a numerical approximation of the theoretical expression

$$\int \left| \frac{dy}{y} \right|$$

which is a measure of the relative steepness of each individual peak. It is to be noted that this number is independent of the height of the peak. There is a provision in the CLEANUP program for the rejection of peaks not meeting a minimum sharpness threshold (Figure 3). Noise spikes are eliminated by the property of the steepness function which favors wider peaks over very narrow ones.

Once the presence of a peak is detected, the CLEANUP program begins its real work, namely, the deconvolution of the peak mixtures and the accounting for bleed, noise, etc. The CLEANUP program assumes linear superposition of ion currents due to different causes, i.e., at any given point in time the total ion current can be represented as a simple sum of a background, column bleed, and whatever eluants are present. For the case of a singlet, the total ion current for a given mass $Y(t)$ may be represented as a sum of three functions

$$Y(t) = P(t) + dt + c,$$

when the term dt represents the contribution to column bleed, c represents the contribution due to background noise, and $P(t)$ is the peak contribution due to the signal. The problem lies in making an initial choice for the function $P(t)$. The method used by CLEANUP is to examine the mass in the window with the sharpest non-saturated singlet maximum. This mass was stored by the previous phase of the program. The column bleed and background are then subtracted out (see Figure 6). Once the functional form of the model peak for a given mass is known, the contribution to the ion current due to the eluant compound at other masses can be computed via a least squares process, i.e., for any given mass

$$Y(t) \sim pP(t) + dt + c$$

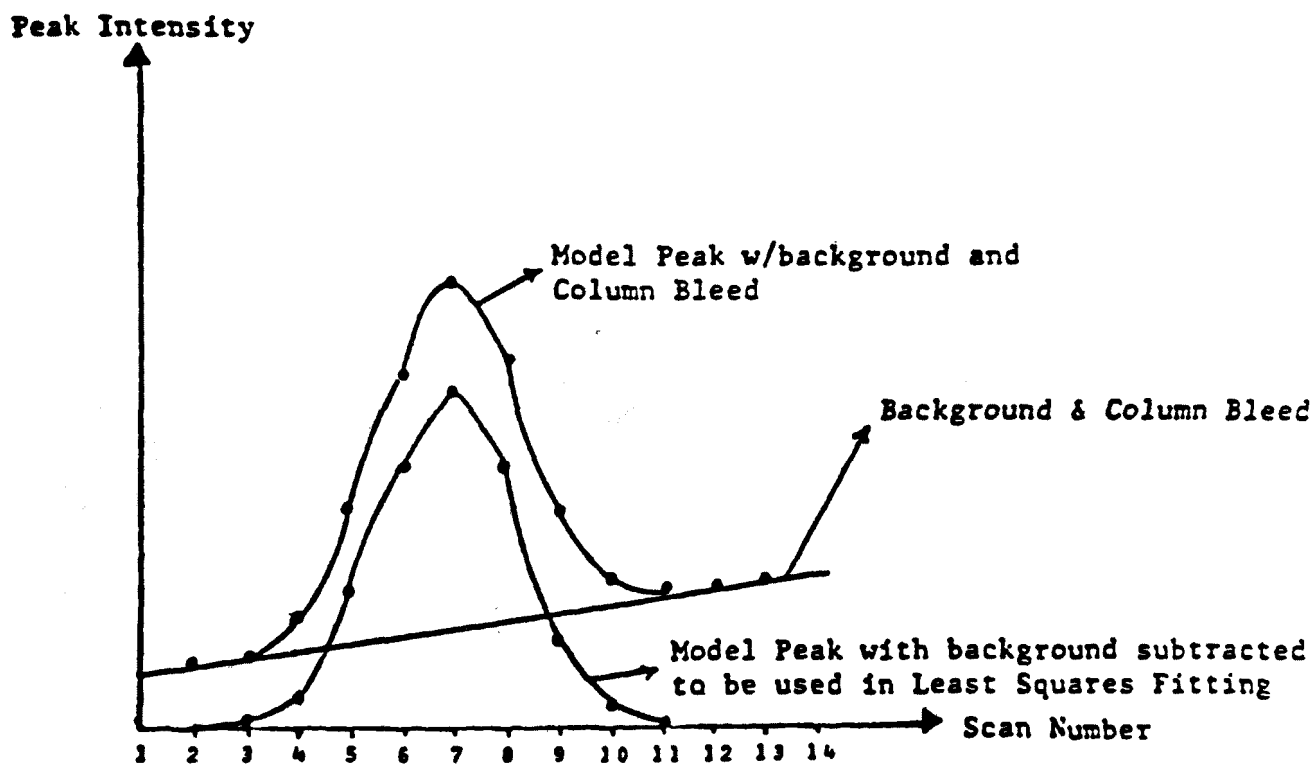


Figure 6. Example of background subtraction for model peak.

Here $Y(t)$ is the total signal for that mass, which is made up of a contribution of the signal, column bleed, and background. The aim is to minimize

$$D = [Y(t_i) - pP(t_i) - dt_i - c]^2$$

in the interval covered by the peak, subject to the conditions

$$\frac{\delta D}{\delta p} = 0; \quad \frac{\delta D}{\delta d} = 0; \quad \frac{\delta D}{\delta c} = 0$$

This is done by a standard method.⁵ It is important to realize that p , d and c are being varied in order to find the best possible match of three functions of fixed form (the model function P , a line through the origin, and a constant) to the given Function Y . The idea is that for a given eluant, all peaks will have the same functional form $P(t)$ and that peaks of different masses corresponding to that eluant differ only in relative amplitude - something which is taken account for in the factor p in $pP(t)$. Once the model function $P(t)$ is determined for a mass that is relatively free of background noise, neighboring eluents, column bleed, etc., a meaningful interpolation can be made for those masses which are contaminated with noise and bleed, or which are saturated. In the case of saturated peaks, a routine is used which interpolates an approximation of the functional form of $P(t)$ to obtain correct signal contributions for saturated points based on the non-saturated points on the fringe of each peak.

For doublet resolution, the model peak for the neighboring spectrum is added to the approximating function. $Y(t)$ is then approximately by

$$Y(t) \approx pP(t) + rR(t) + dt + c$$

where $R(t)$ is the model function for the second peak and r is its corresponding parameter. The idea is graphically illustrated for several cases in Figure 7.

A diagram of the detailed subroutines of the CLEANUP program, along with a short description of these function is shown in Chart 1 and Table 1.

SCOPE AND LIMITATIONS

Some comments regarding the scope and limitations of the CLEANUP program are in order.

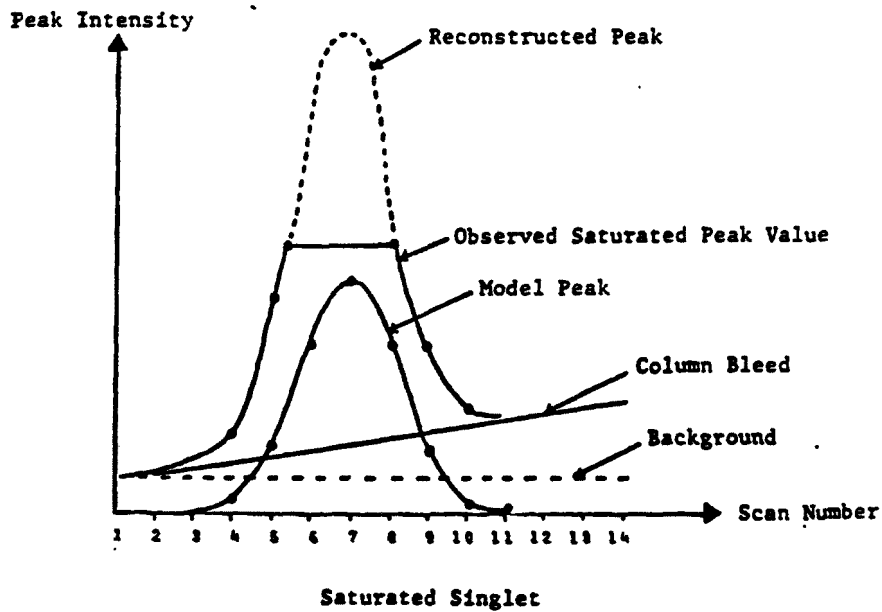
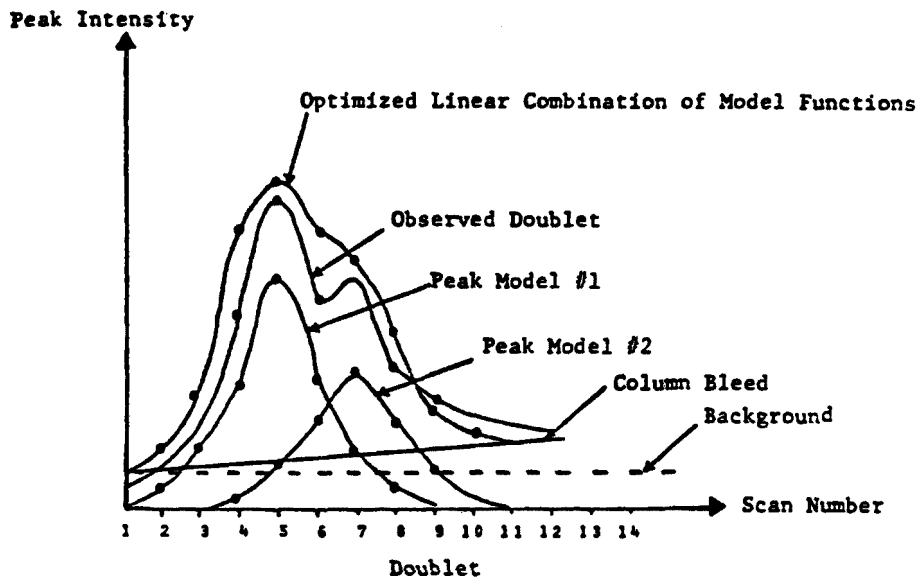


Figure 7. Peak model resolutions: two possible situations.

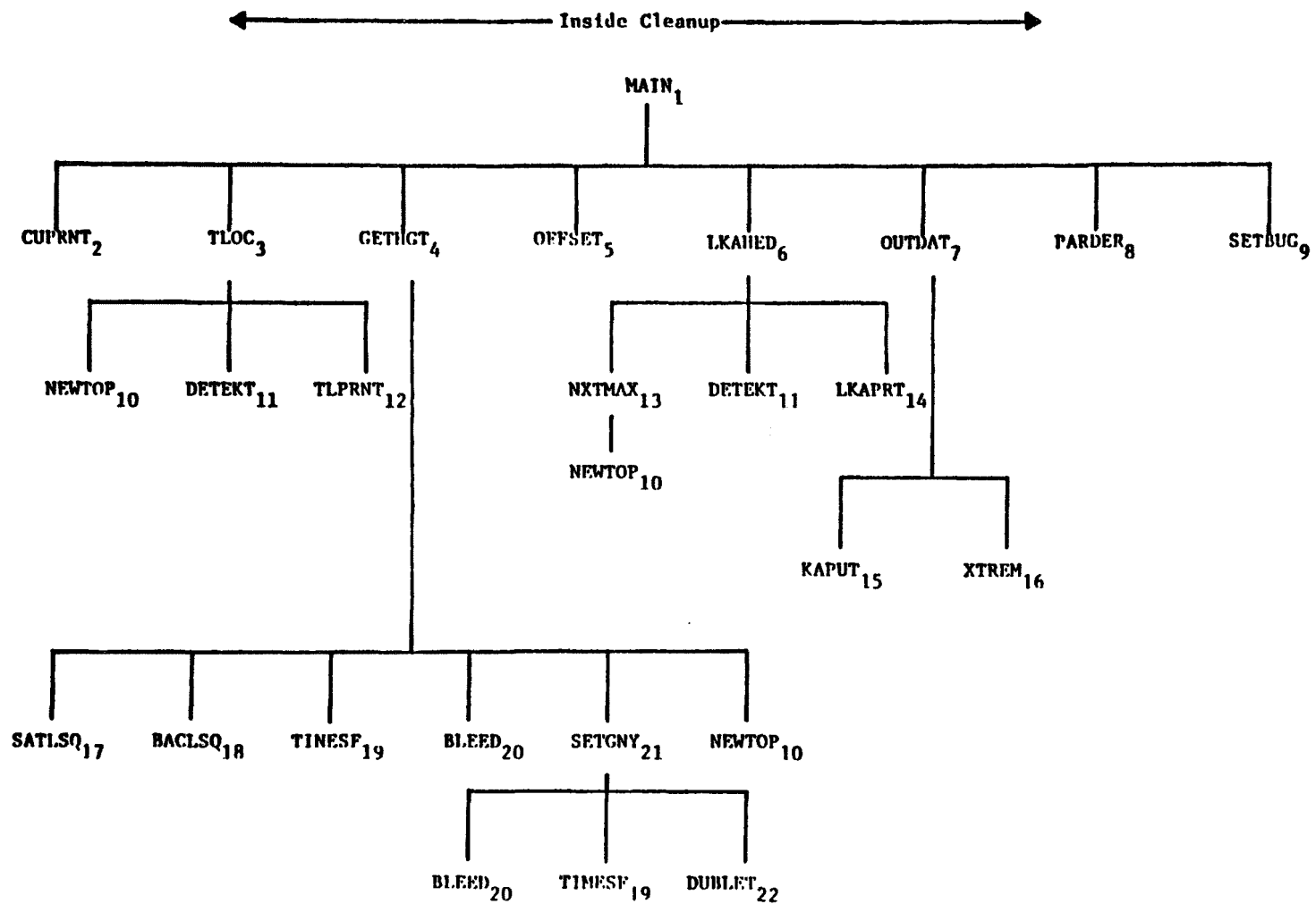


Chart 1. Summary of calling structure and subroutine function.

TABLE 1. SUBROUTINES OF CLEANUP BY FUNCTION

-
1. MAIN
is the root segment which calls all other routines.
 2. CUPRNT
prints some debugging messages for MAIN.
 3. TLOC
builds histograms for eluant detection, and selects the model peak for each compound. A model peak is the singlet which is sharpest, and its mass fragmentogram is 9 spectra wide. It is important to note that histograms contain "singlet" information, and we use this information to detect eluants.
 4. GETHGT
is called after a spectrum has been detected, and is the executive for building the cleaned up spectrum from the raw data.
 5. OFFSET
is called only in the event that an overlapping situation arises, and aligns the model peaks with respect to their modes in arrays GMN and HNU in anticipation of processing a doublet.
 6. LKAHED
is called only if an eluant is detected. It looks ahead to see if another is present in the 14 spectrum window, and if so assigns the model peak and sets the flag OVLAP.
 7. OUTDAT
prints report information for the run and writes the clean up spectra to disk.
 8. PARDIR
is the operator communication subroutine. It sets some parameters which can be entered either from cards or from a terminal.
 9. SETBUG
does some initialization of output buffers, and reads in the first 13 spectra.
 10. NEWTOP
finds the actual mode and the displacement of this mode from the assumed mode as well as computing the integral $|dy|/y$ (rate) from a singlet peak profile.

(continued)

TABLE 1 (continued)

11. DETEKT
examines histograms to determine if an eluant is present.
The major criterion for an eluant to be detected is that its histogrammed total ion current be greater than MINTIC.
12. TLPRNT
prints some debugging messages for TLOC.
13. NXTMAX
builds histograms in the look ahead mode. Due to core limitations, it can only look ahead 3 spectra, and in the extreme case, i.e., the 3rd spectrum ahead is determined to be an eluant, the determination is done with less information than its predecessors. If 16 spectra are in core, NXTMAX can easily be set up to use exactly the same criteria as TLOC in building histograms. Some heuristics have been put in TLOC and DETEKT to take care of the minimal cases. This minimal situation occurs when a very weak eluant is found ahead, and then passed up when it becomes a primary candidate.
14. LKAPRT
prints some debugging message for LKAHED.
15. KAPUT
outputs to the line printer a short summary of the results of the programs processing.
16. XTREM
determines the minimum value and its subscript given an integer array and its length.
17. SATLSQ
processes saturated peaks, and tries to compute actual peak heights by taking the ratios of nonsaturated amplitudes in the saturated peak profile with their corresponding amplitudes in the model peak.
18. BACLSQ
does a least squares fit using the peak profile of a singlet, and a model peak to determine the singlets contribution to a detected spectrum.
19. TIMESF
uses a parabolic interpolation to place a peak profile on the same time co-ordinate as the model peak for a detected elutant.
20. BLEED
fits a line to a peak profile and uses goodness of fit, and average value of Y, where $Y=mx+b$, to see if the profile is column bleed.

(continued)

TABLE 1 (continued)

21. SETGHY

is called only in the event of a doublet situation, and decides whether or not a given peak profile will be passed through the doublet resolver.

22. DUBLET

is the doublet resolver, and does the least square fit of two model peaks, and a doublet peak profile and puts the second peak contribution in a different array.

The construction of model peaks for an eluant depends on at least one mass in the processing window having a well defined, well resolved singlet. This requirement will not be satisfied if two eluants are within roughly one scan time of each other, or if there is an unsaturated peak for use as a model, i.e. in extremely bad run conditions.

Also the CLEANUP procedure breaks down in the case of interacting elutents because the ion currents are not longer a simple sum. This is an inherent limitation of the linear reconstruction model.

Finally, the program currently lacks the capability of providing the user with a visual TIC plot. This is essential in order to allow the user to analyze the final results.

SECTION 4

IMPLEMENTATION AND TESTING OF CLEANUP

Phase II of the contract consisted of implementing a version of the Rindfleisch program on the TUCC 370 and testing its performance. This involved obtaining an existing copy of CLEANUP and modifying it to run at TUCC, developing support software to facilitate the analysis of CLEANUP output, and extensive testing of CLEANUP on a variety of environmental samples.

INITIAL PROGRAM MANIPULATION

The first step in implementation of the CLEANUP program was to obtain a listing and initial documentation from the author. This was achieved with relatively little difficulty. Dr. Rindfleisch and his colleagues were very generous in providing us with full listings and some documentation of their program. Since these programs were designed to run on a PDP-11 computer, they were written in a combination of PDP-11 assembler language and a PDP-11 version of Fortran, which would have made their translation into standard Fortran a very difficult task. We were informed by the Stanford group, however, that another group of chemists at the NASA Ames Air Force Base had been working on a Fortran implementation of the Rindfleisch program and we were referred to that group.

The Ames scientists were cooperative in forwarding their versions of the Rindfleisch programs to us, however it was immediately clear when we received tapes from them that there were large discrepancies between their programs and a working system. There were numerous errors in the program, indicating that they had not been fully tested.

After some additional conversations with the Ames group, an improved version of their Rindfleisch program was sent to us which we began to use. The new program had been changed, and some of the errors, detected previously had been corrected. This new program was then reorganized to make it operational in the TUCC environment. The mode of inserting variable data and

options into the program was completely altered. The original programs were designed to operate interactively from a terminal, and the variables for each run were introduced in a conversational mode. If the results are not satisfactory, then the parameters are changed and the program re-run, etc. This process is continued until the operator is satisfied with the results, or feels that no further improvements can be made. Since in our environment programs must be run in a batch process, it was necessary to proceed somewhat differently. A set of trial parameters were obtained from the program authors, which were entered into the RTI program from cards. The effect of the program parameters on the output is discussed in 3.4.

The main body of the program was debugged by the use of the WATFIV compiler. This compiler is useful, not only because of its very well documented error messages, but because the compiler, by its nature, cannot operate using special system subroutines. This means that the entire program, if run under WATFIV, is insured to be compatible with other computers running with standard Fortran packages. By this procedure, the entire program was debugged and freed from a number of errors, particularly those relating to the initialization of variables prior to their use, which in our experience, has proven very difficult to trace down at later stages of program development.

SUPPORT SOFTWARE FOR CLEANUP

After the program ran freely, it was necessary to test it on some typical environmental data. In order to do this, GC/MS data which previously had been generated from environmental samples in the RTI laboratory were adapted to the CLEANUP program. This required the writing of several sets of programs: one translated raw mass spectral data into the input format required by CLEANUP; a second translated the output data from CLEANUP into a format required by the search program; a third set generated plot output from CLEANUP on an in-house VERSATEC plotter. A more detailed description of this software follows.

RTI Search System Interfacing

These programs accepted mass spectral data, which had been acquired on a Varian CH-7 mass spectrometer, and automatically selected spectra for introduction into a library search program. Selection of specific spectra was carried

out by the analysis of the total ion current (TIC) profile of the GC run. In the case of spectra acquired using the Varian system, the TIC profile was very easy to analyze numerically, because the data system was designed to acquire TIC information simultaneously with MS information throughout the course of the run. By means of a multiplexer, the data system acquired ca. 100 TIC points, which were received from an ion current electrode placed at the exit of the source of the spectrometer, during each MS scan. These TIC points were recorded on the output tape in a Varian coded format and it was possible to regenerate this TIC information in both numeric and graphic form from the original tape.

Whereas most other GC/MS computer systems generate TIC data by the summation of ion intensities for each mass spectrum run (software TIC), the hardware TIC data is much richer in detail since it produces ca. 100 points per GC scan rather than one in the software method. This advantage is particularly important when data are being scanned relatively slowly as compared with the TIC peak width. The TIC trace generated from the data encoded on the tape was very useful to evaluate the CLEANUP program, since CLEANUP does not produce any visual record of the GC run, but simply selects specific peaks for subsequent evaluation, in our case by means of library search. We compared the selection of spectra made by analysis of the hardware TIC trace with those spectra chosen by CLEANUP. This approach was extremely useful in the evaluation of the CLEANUP program. Figure 8 shows a schematic diagram of the RTI data processing system.

Splicing the CLEANUP program into the RTI data processing system consisted of two parts: formatting the data generated by the MS-7 GC/MS system so that it could be read as input by CLEANUP (Chart 2) and formatting the output generated by CLEANUP so that it could be used as input to the RTI library search program (Chart 3).

As these programs were being written, a tape was prepared of a standard GC/MS run on the RTI MS-7 GC/MS system and was hand carried to TUCC. After a few trials, we were successful in creating CLEANUP-compatible input data, getting CLEANUP to run to completion on that data, and finally obtaining a successful run on that data with the RTI search program.

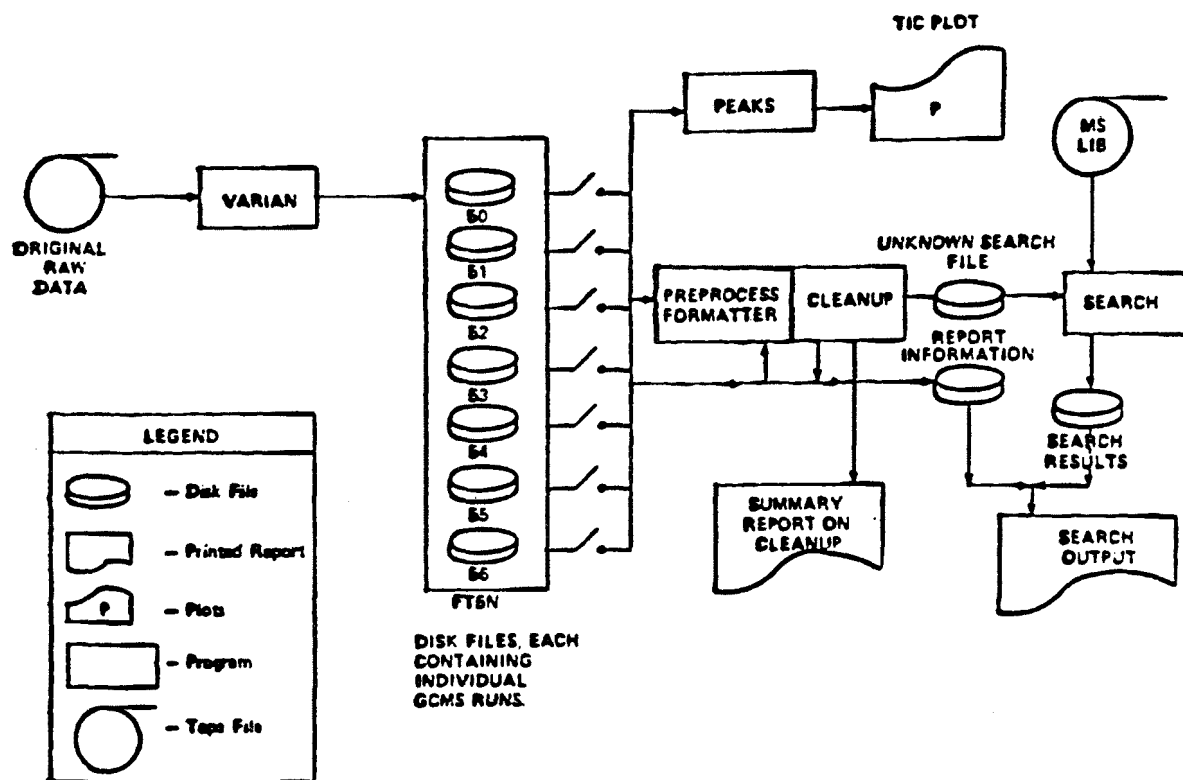


Figure 8. Overall schematic of computer assisted qualitative analysis of GC/MS data.

Files Generated

Varian data tape containing
raw output from GC/MS

Intermediate step, output
file from VARIAN

Output file of VARTRN in
CLEANUP compatible input
format

Output file of CLEANUP
containing resolved spectra

Chart 4:
Display of input and output
spectra on VERSATEC plotter

Programs Involved

Translates raw Varian data to
Fortran compatible format

VARTRN is an intermediate program
which transforms the output of
VARTRN into CLEANUP compatible
input

CLEANUP is the main processing
program which:
(1) Eliminates column bleed
and background
(2) Reconstructs saturated peaks
(3) Resolves mixed doublets

Chart 3:
Examination of results when
fed into RTI Search System

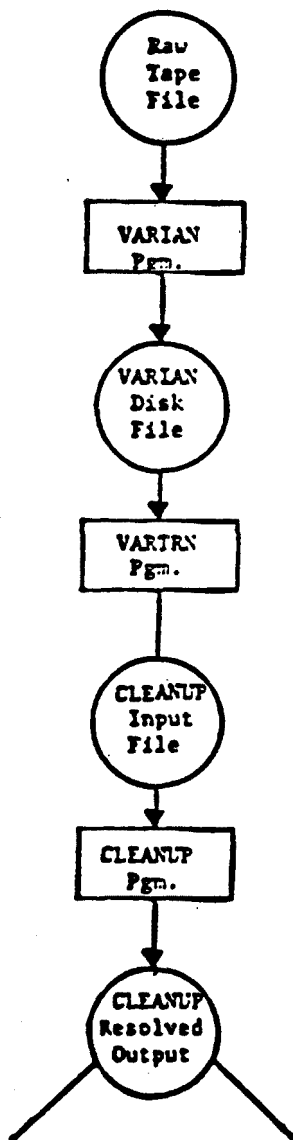
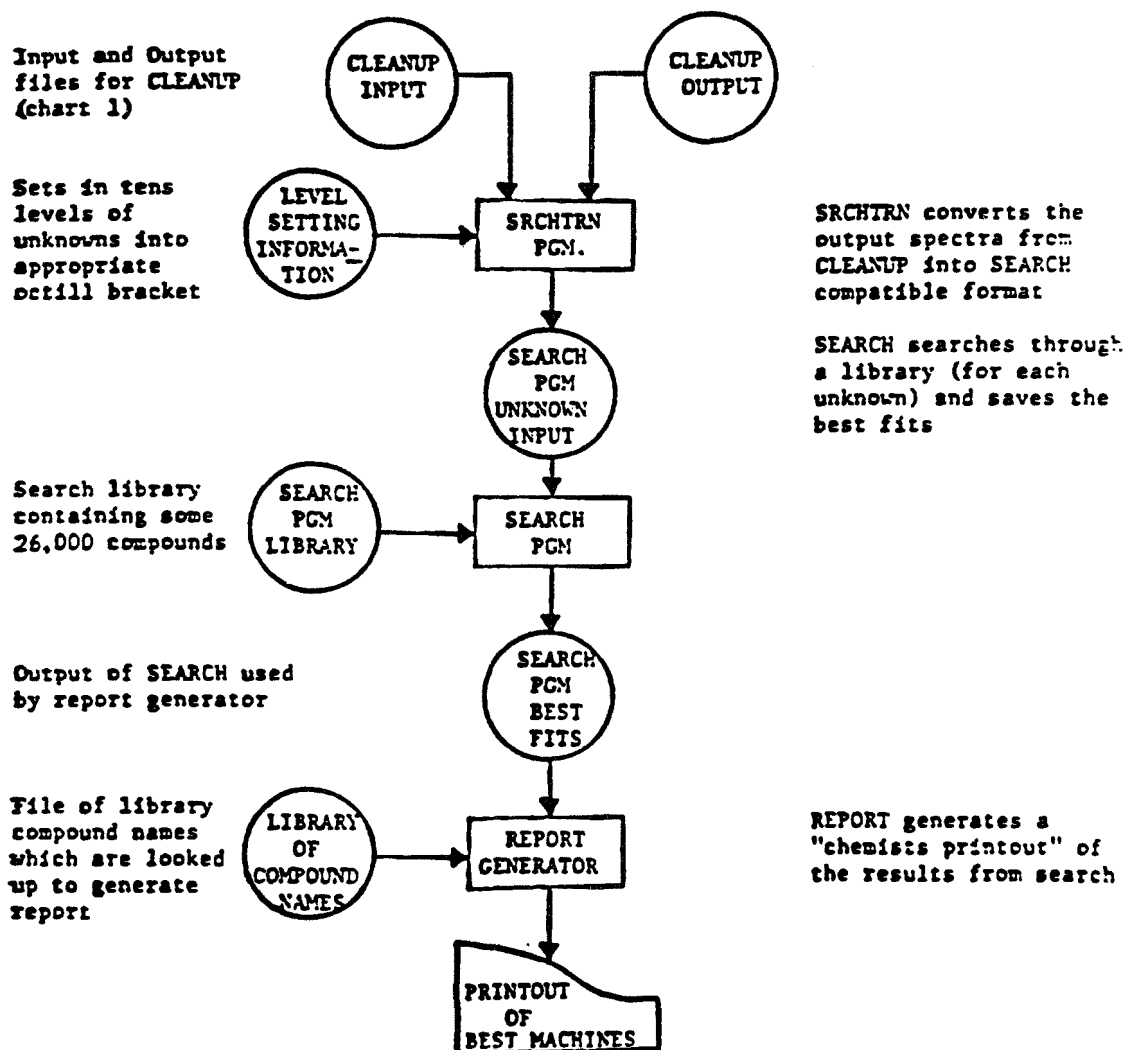


Chart 2. Steps involved in processing of CLEANUP test data (1).
Preparation for and interface to CLEANUP program.



"Chemists Printout" of best choices for unknowns

Chart 3. Steps involved in processing of CLEANUP test data (2). Preparation for and interface to search program.

Plot Out for CLEANUP

At this stage it was necessary to carry out a critical evaluation of the results to determine the efficacy of the CLEANUP algorithm. Although the CLEANUP program executed successfully, preliminary examination of the printed data for a few isolated cases indicated that the initial parameters chosen were not ideal, and that although the program seemed to recognize the presence of individual components in the GC run, the output spectra were not yet suitable for characterization of the unknown GC component. In order to proceed in an orderly manner, then, it was felt that a method for displaying the results of CLEANUP needed to be developed. Software to generate plots from MS data have been available for some time, however, these programs generate output intended for the university operated CALCOMP plotters which were entirely too slow to generate the hundreds of plots needed in the course of this investigation. An alternative approach of writing software to generate plots on an in-house VERSATEC electrostatic plotter (several orders of magnitude faster than the CALCOMP incremental plotters) was adopted. The process consisted of two steps. First a program at TUCC read the CLEANUP output spectra as input and generated picture records which were then written to tape. The tape was then hand carried to the RTI laboratory and read by a PDP-12 program which generated the actual plots. This method proved very economical, since plots were generated at low costs (50¢ per picture) and high speeds (ca. 20/30 sec/plot). In this fashion it was possible to generate up to 100 plots in an hour, a task which would have tied up the TUCC network CALCOMP plotters for several days. The entire scheme for generating plots together with already existing software is shown in Chart 4 with sample output in Figures 9-11.

TEST RUNS WITH CLEANUP

Brominated Standards

A preliminary evaluation of the CLEANUP program using two GC/MS runs was made. The first was a relatively simple mixture of a series of

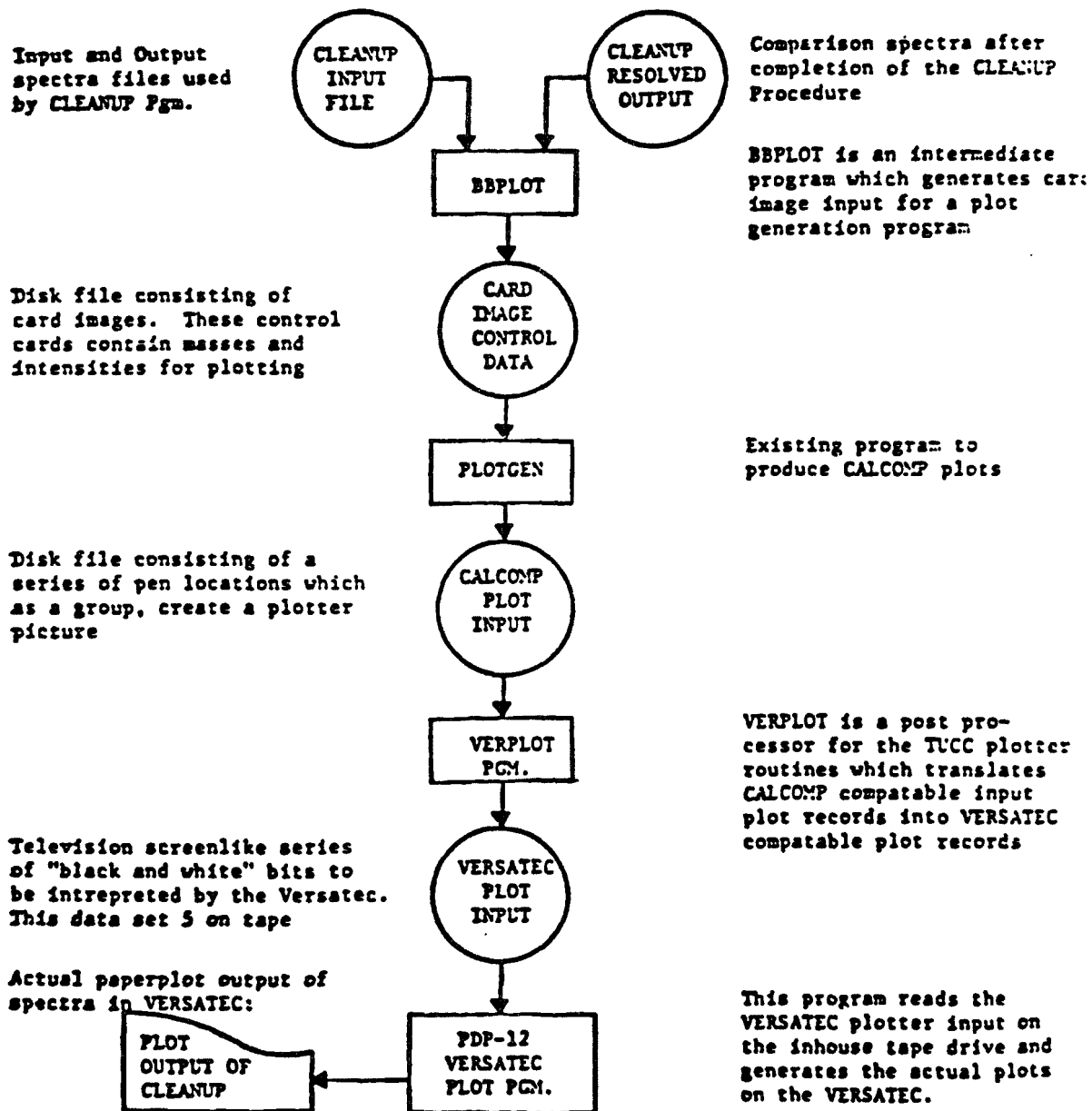


Chart 4. Steps involved in processing of CLEANUP test data (3).
Generation of Versatec MS plots from CLEANUP files.

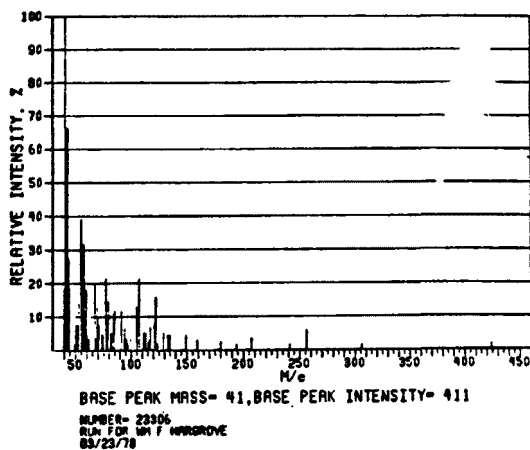
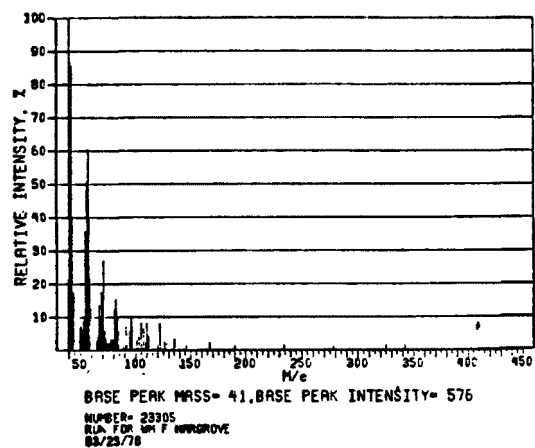
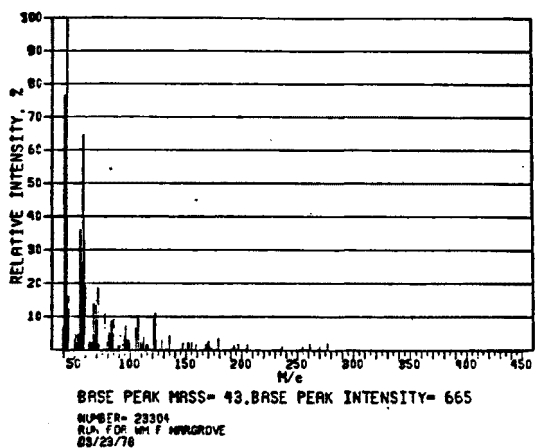
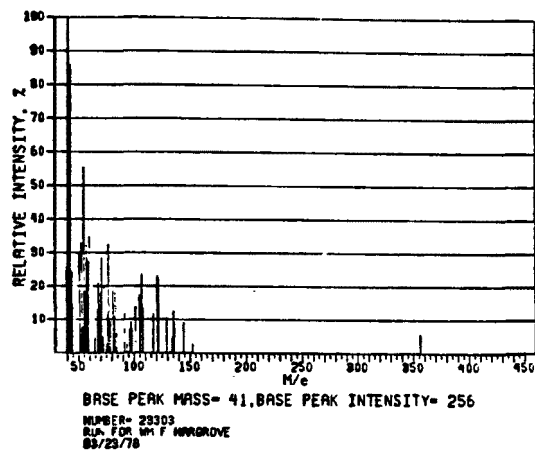
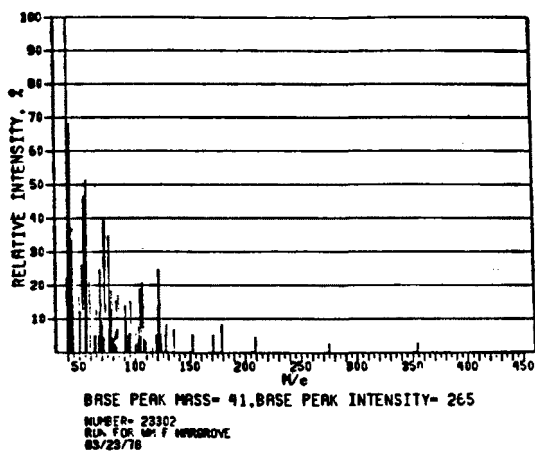


Figure 9. Five "raw" spectra used as input to CLEANUP.

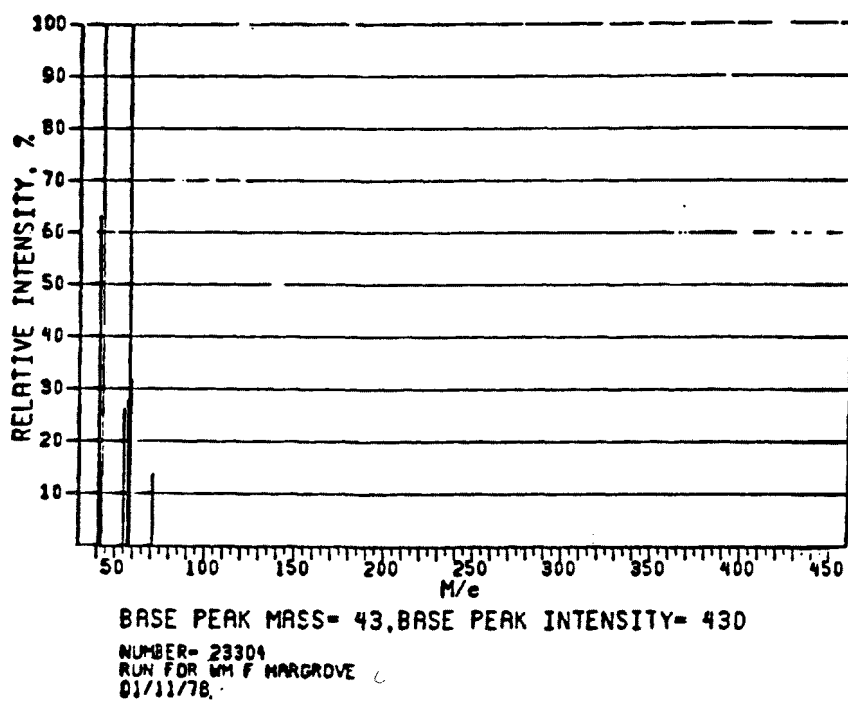


Figure 10. Resultant "cleaned-up" spectrum from Figure 9.

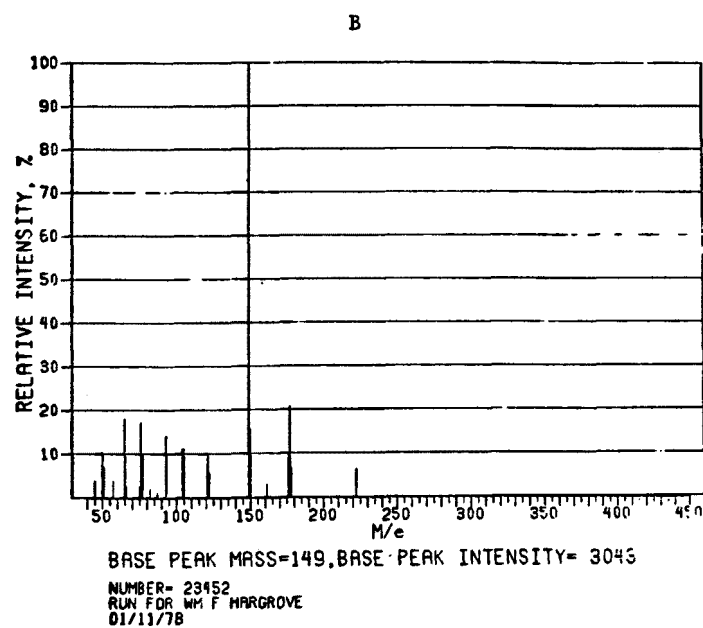
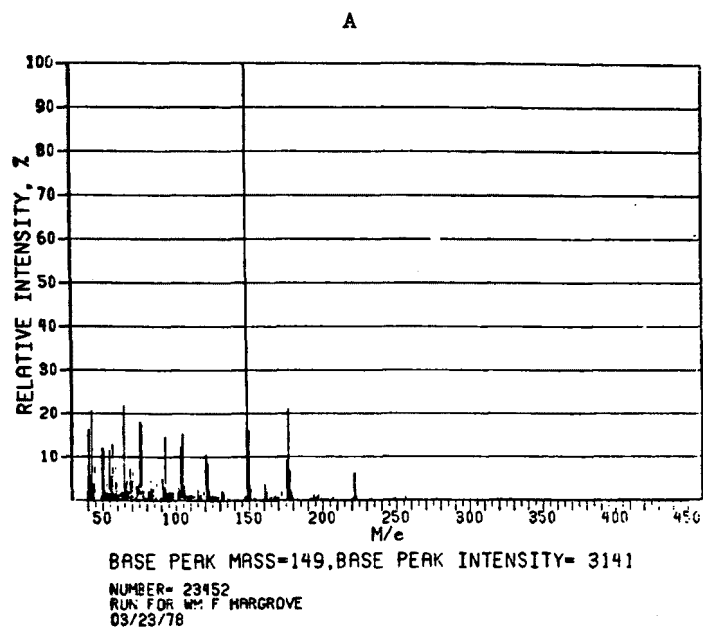


Figure 11. Precleanup - A, postcleanup - B.

brominated standard compounds. This series was chosen to serve as a control. The compounds in the run were known, and they were reasonably easy to identify.

In the case of the brominated standards, the CLEANUP procedure worked essentially perfectly. In the first section of the GC run the spectra were relatively free of background noise and the output spectra from the CLEANUP program resembled the original spectra very closely. This fact is not trivial in that it shows the CLEANUP procedure is essentially benign for the case of uncomplicated spectral data. Thus, if the original data are good, then the CLEANUP step does not alter them or degrade them in any way. This is a necessary condition of performance for a good CLEANUP program.

In the latter portions of the run, increasing amounts of background noise from column bleed became evident. In the case of weak spectra near the end of the run, the CLEANUP procedure became indispensable for the identification of several components. As it turned out, in addition to the brominated standards which were specifically put into the mixture, several additional components, many of them not containing bromine, were found. For example, spectrum number 23469 in the run had been seen many times previously during manual identification and never been identified. With the help of CLEANUP and SEARCH it was possible to identify this component as an alkylated phenol. The TIC trace of the run is given in Figure 12.

The results from the CLEANUP program are shown graphically in Figures 9 through 11. Figure 9 shows five successive spectra (the computer actually uses 7) from which a cleaned up spectrum is derived (Figure 10). Another pair of pre and postCLEANUP spectra are shown in Figure 11. A summary of the run is shown in Table 2.

Coal Run

The second GC/MS data set which was examined consisted of a low boiling fraction from a coal gasification process. With this data the situation was virtually the opposite from the previous case, i.e.,

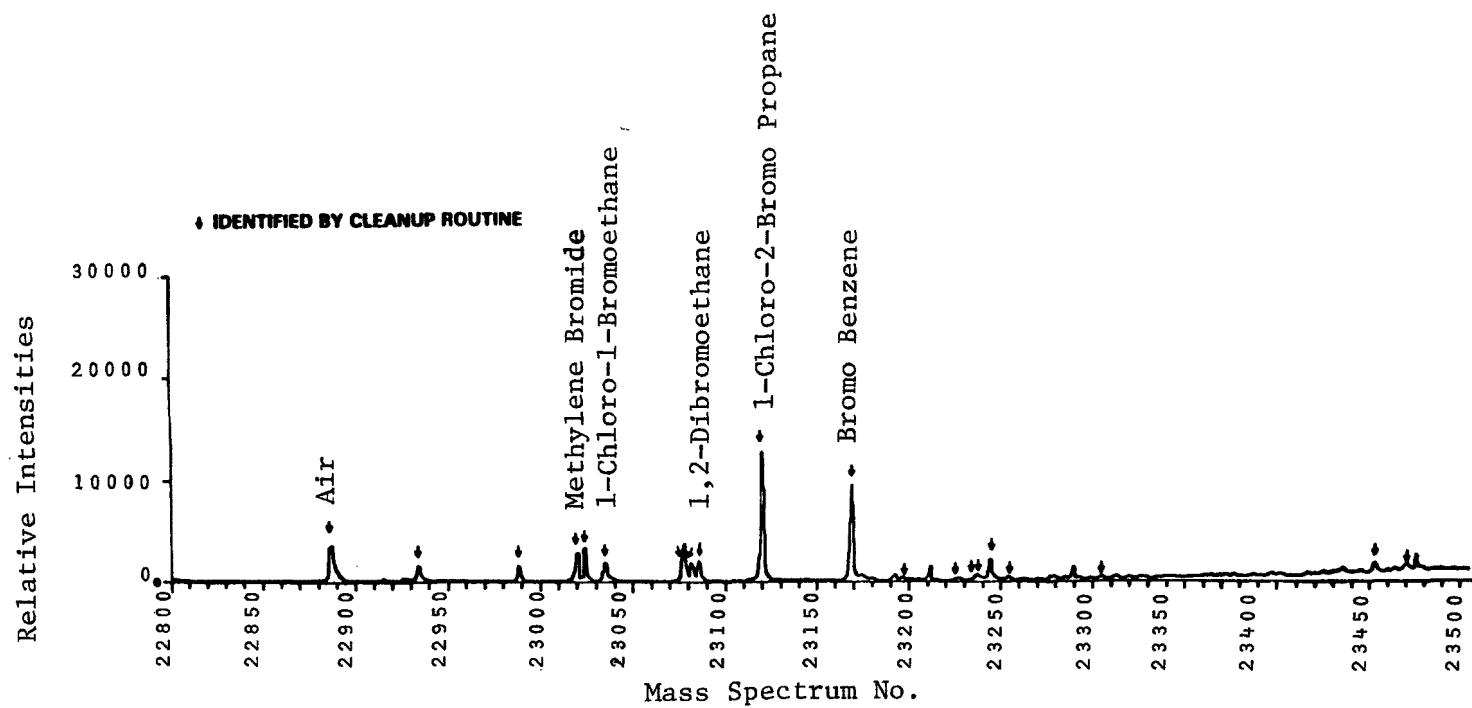


Figure 12. TIC plot of brominated standards.

Table 2. RESULTS OF COMPARISON OF CLEANUP WITH BROMINATED STANDARDS
SEARCHED FOR 26,209 STANDARDS

Compound	<u>Precleanup</u>		TIC Max.	<u>Postcleanup</u>		Elution Time
	Rank ^b	R		Rank	R	
1. methylene chloride ^a	1	.31	752	1	.67	15.63
2. 1,2-dichloroethane ^a	1	.33	672	1	.54	21.93
3. methylene bromide	1	.36	720	1	.49	25.55
4. bromodichloromethane	1	.37	688	1	.43	26.00
5. 1-chloro-2-bromoethane	1	.30	704	1	.43	27.30
6. <u>n</u> -butyl bromide	>5	<.19	512	2	.33	32.43
7. ethylene bromide	3	.17	800	1	.31	33.25
8. chlorobromopropane ^a	1	.28	1392	1	.37	37.22
9. bromobenzene	>5	<.18	1088	2	.27	42.93
10. dimethylphenol ^a	1	.31	320	1	.45	46.20
11. <u>n</u> -butane ^a	>5	<.19	304	1	.53	49.35
12. acetophenone ^a	>5	<.22	320	1	.39	51.10
13. toluene ^a	>5	<.21	304	1	.60	52.97
14. diethyl phthalate ^a	1	.33	478	1	.52	76.07
15. octyl phenol ^a	>5	<.15	432	1	.52	78.05

^a Compound was not knowingly part of standard mixture.

^b The ordinal number of the similarity of the library component to the unknown. The program normally prints out the 5 best fits.

this sample consisted of a deliberately chosen, highly complex mixture, which would test the system to its limit to determine the most that could be expected from this program.

In this GC/MS data set, the chromatography conditions and the relatively slow sampling rate assured that the majority of MS scans would consist of mixtures, contain also background noise, column bleed, and other components in the system. Although the specific components in the mixture were not known, the nature of the sample gave strong clues as to what kinds of compounds were to be expected. A TIC plot of this run is shown in Figure 13.

Not surprisingly then, when raw coal run MS data were introduced into the MS search routines, the output was nearly totally useless, since the correlation coefficients were almost uniformly low and those compounds which were chosen as the closest fitting were obviously completely erroneous. We believe that we understand why this occurred. When samples are highly impure, numerous additional small peaks, particularly in the high molecular weight regions usually appear. The search system normally has no way of distinguishing these weak noise peaks from similar weak peaks which may be present in high molecular weight components. As a result, these peaks are picked up as possible molecular ions for high molecular weight components, and the results are entirely erroneous.

After the CLEANUP program had been applied to this set of data, the results, although far from perfect, improved noticeably. A sample of the search program output is shown in Table 3. Most of the high molecular weight noise was removed by CLEANUP, resulting in the identified compounds being of a much more "reasonable" nature. In addition, the search program's correlation coefficients rose dramatically, and indeed, most of the identified components seemed to be reasonable, based on the known origin of the sample. Thus hydrocarbons, low molecular weight phenols, and specific compounds containing heteroatoms such as thiophene and carbon disulfide were identified correctly by the search system with good correlation coefficients. We feel that this represents a remarkable achievement for such a difficult mixture. Figures 14 and 15 show a

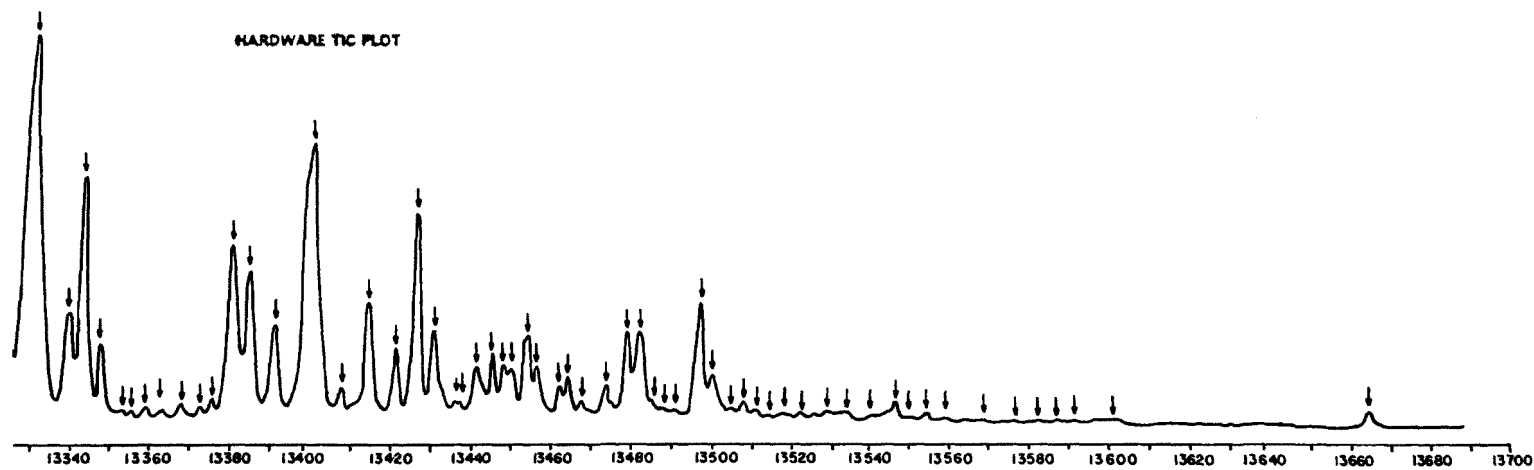
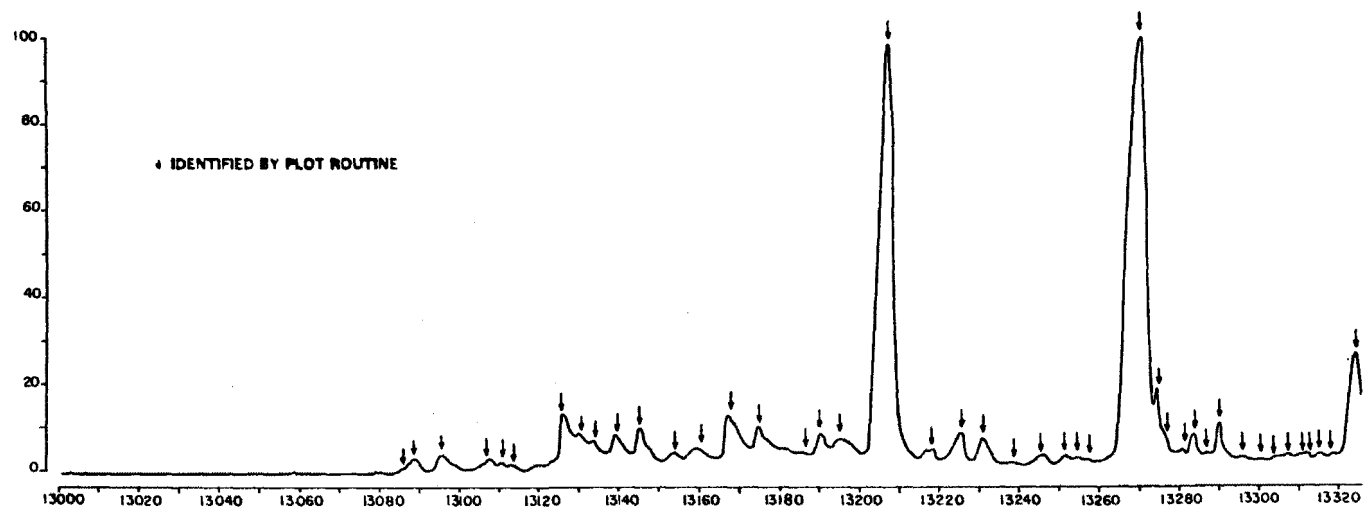


Figure 13. Hardware TIC plot of GC/MS analysis of organics from coal pyrolysis.

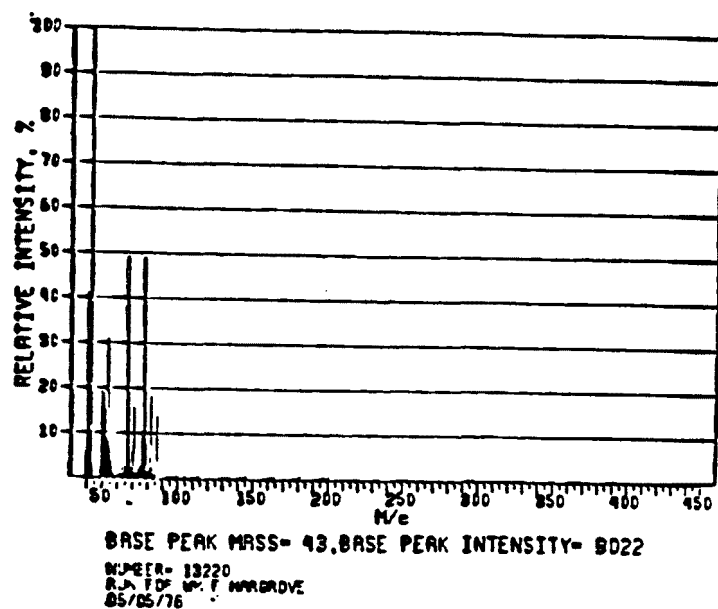


Figure 14. Typical precleanup of mass spectrum.

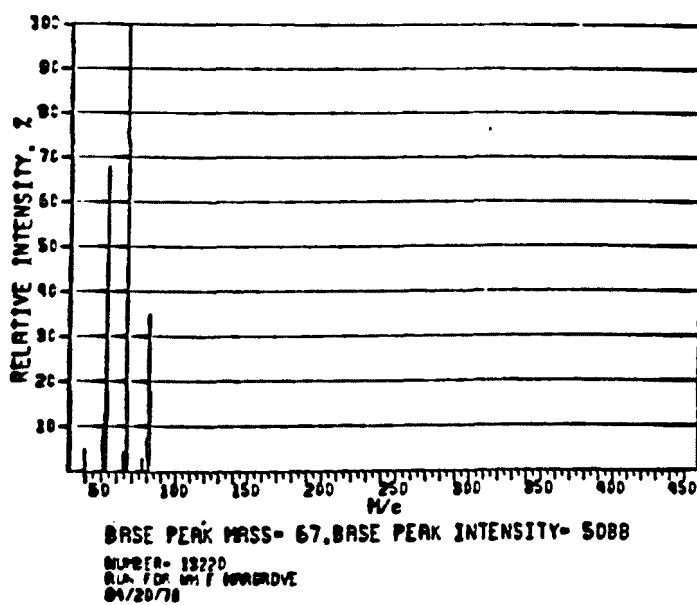


Figure 15. Same spectrum after CLEANUP.

TABLE 3. TYPICAL PRINTOUT FOR IDENTIFICATION OF COAL COMPONENTS
(AFTER CLEANUP)

SPEC # 4211 ELUTION TIME= 24.62 MIN ELUTION TEMP= 0 TIC MAX= 928									
ID#	R	MWT	FORMULA	NAME					
1.	622 0.47	88 C	4 H 8 O 2	ETHYL ACETATE					
2.	2234 0.38	118 C	6 H 14 O 2	1-ISOPROPOXY-2-PROPANOL					
3.	2210 0.37	118 C	5 H 10 O 3	2-METHOXYETHYL ACETATE					
4.	649 0.34	88 C	5 H 12 O 1	ETHYL ISOPROPYL ETHER					
5.	615 0.33	88 C	4 H 8 O 2	BUTANOIC ACID (BUTYRIC ACID)					
SPEC # 4221 ELUTION TIME= 25.78 MIN ELUTION TEMP= 0 TIC MAX= 848									
ID#	R	MWT	FORMULA	NAME					
1.	14543 0.59	236 C	7 F 8	TRIFLUOROMETHYL-PENTAFLUOROBENZENE					
2.	9749 0.35	186 C	6 F 6	HEXAFLUOROBENZENE					
3.	14540 0.35	236 C	6 F 7 P 1	PENTAFLUOROPHENYLDIFLUOROPHOSPHINE					
4.	14395 0.17	234 C	6 Cl 1 F 5 S 1	PENTAFLUOROBENZENE SULPHENYL CHLORIDE					
5.	13839 0.17	227 C	9 H 13 N 3 O 4	2-DEOXYCYTIDINE					
SPEC # 4224 ELUTION TIME= 26.13 MIN ELUTION TEMP= 0 TIC MAX= 1568									
ID#	R	MWT	FORMULA	NAME					
1.	471 0.50	84 C	6 H 12	1-HEXENE					
2.	477 0.46	84 C	6 H 12	2-METHYL-1-PENTENE					
3.	475 0.46	84 C	6 H 12	METHYLCYCLOPENTANE					
4.	462 0.44	84 C	6 H 12	CIS-2-HEXENE					
5.	483 0.44	84 C	6 H 12	TRANS-2-HEXENE					
SPEC # 4241 ELUTION TIME= 28.12 MIN ELUTION TEMP= 0 TIC MAX= 1696									
ID#	R	MWT	FORMULA	NAME					
1.	354 0.69	78 C	6 H 6	2,4-HEXADIENE					
2.	353 0.68	78 C	6 H 6	1,5-HEXADIENE					
3.	352 0.68	78 C	6 H 6	1,5-HEXADIENE-3-YNE (DIVINYL ACETYLENE)					
4.	351 0.68	78 C	6 H 6	BUTADIENYL ACETYLENE					
5.	350 0.51	78 C	6 H 6	BENZENE					
SPEC # 4247 ELUTION TIME= 28.82 MIN ELUTION TEMP= 0 TIC MAX= 960									
ID#	R	MWT	FORMULA	NAME					
1.	471 0.54	84 C	6 H 12	1-HEXENE					
2.	470 0.50	84 C	6 H 12	HEXENE-2					
3.	445 0.48	84 C	5 H 8 O 1	CYCLOPENTANONE					
4.	453 0.48	84 C	5 H 8 O 1	2-METHYLCYCLOBUTANONE					
5.	1235 0.46	102 C	6 H 14 O 1	1-HEXANOL					
SPEC # 4256 ELUTION TIME= 29.87 MIN ELUTION TEMP= 0 TIC MAX= 1136									
ID#	R	MWT	FORMULA	NAME					
1.	136 0.81	64 O	2 S 1	SULFUR DIOXIDE					
2.	358 0.29	80 C	1 H 4 O 2 S 1	METHANESULFINIC ACID					
3.	2175 0.29	118 Cl	2 O 1 S 1	THIONYL CHLORIDE					
4.	6579 0.24	159 C	2 F 3 N 1 O 2 S 1	TRIFLUOROMETHANESULFINIC ACID ISOCYANATE					
5.	11530 0.23	203 H	1 N 3 O 4 S 3	2H-1,3,5,2,4,6-TRITHIATRIAZIN-1,1,3,3-TETROXIDE					

typical "before" and "after" pair of spectra from the coal run. Table 4 shows a comparison of a small selection of the data before and after CLEANUP. Complete accuracy is not claimed for this run, but CLEANUP improves the hit rate from nearly zero to an estimated 50%.

Several defects in the system emerged from this series of experiments. The most obvious defect involves situations in which strong peaks emerge from the column at sufficient amplitude to saturate the data acquisition system for a number of ions in several mass spectra. The most obvious case of this involves the component benzene (Figure 13, spectrum number ca. 13207), which eluted from the column as a very broad band extending for about 9 spectra (at 6 sec/scan this corresponds to a 54 second peak). This component showed saturated peak intensities for five major ions at m/z 50, 51, 52, 77, and 78. As a result of this situation, the ^{13}C isotope at m/e 79 was computed to have a relative intensity of 50%. As a result, the search program subsequently misidentified the major peaks in the spectrum and the search for benzene failed. This problem was compounded because, in addition, the large amount of benzene present caused other components, mainly from the "stationary" phase in the column to coelute, giving rise to a series of small peaks at high masses which the CLEANUP program dutifully processed and included in the unknown spectrum.

The problem of saturated peaks in spectrum identification is a serious one. Notwithstanding the fact that it is obviously wrong to try to identify components from a GC run when the amounts injected saturate the data acquisition system, these components are so strong and obvious that most investigators would be highly dissatisfied if simple compounds such as benzene were misidentified by a computer software system. There are several ways to remedy this situation. Currently, compounds with saturated peaks are labelled on the output printout (Figure 16) and thus warn the investigator of a potential problem. Also, a possible remedy for future development would be to raise cutoff limits on peak intensities when saturation was encountered so as to exclude weak peaks which otherwise would be accepted for searching.

Table 3. COMPARISON OF SELECTED SPECTRA FROM COAL GASIFICATION SAMPLE
SEARCHED BEFORE AND AFTER CLEANUP

Before CLEANUP			After CLEANUP		
MWT	NAME	R	R	NAME	MWT
Spectrum #13209					
Elution Time = 24.38					
TIC Max. 8081					
218	(AK-33)Methylcyclopentadienyl Manganese Tricarbonyl	0.19	0.21	Ethyl 2-Keto-2-Penylethandate	178
200	Alpha-(Bromoethyl)Benzyl Alcohol	0.16	0.20	Ethyl 2-Hydroxy-2-Phenylethandate	180
160	P-Phenylene Diisocyanate	0.15	0.20	P-Phenylene Diisocyanate	160
133	2-Methylphenyl Azide (D-Tolyl Azide)	0.15	0.20	Alpha-(Bromomethyl)Benzyl Alcohol	200
Spectrum #13219					
Elution Time = 25.55					
TIC Max. 654					
198	7-Methyltridecane	0.15	0.43	2-pentanone	86
142	2,6-Dimethyl-3-Heptanone	0.14	0.42	Tri-Methylacetamide	101
121	3-Acetylpyridine	0.13	0.42	2-methyl-Pentanal	100
178	Ethyl 2-Keto-2-Phenylethandate	0.13	0.38	N-Butanal-D-Methyloxime	101
Spectrum #13227					
Elution Time = 26.48					
TIC Max. 984					
130	Trichloroethylene	0.22	0.38	Trichloroethylene	130
132	1,1,1-Trifluoro-3-Chloropropane	0.16	0.23	1,1,1-Trifluoro-3-Chloropropane	132
146	N-Carbamoyl-2-Imino-1,3-Oxathiolane	0.15	0.22	1,2-Dichloro-1,2-Difluoroethylene	132
132	2-Thiadatane	0.15	0.22	1,1-Dichlorodifluoroethylene	132
Spectrum #13233					
Elution Time = 27.18					
TIC Max. 862					
202	1,4-Dibutoxybutane	0.16	0.56	N-Heptane	100
132	1,3-Dimethoxy-2,2-Dimethylpropane	0.15	0.47	3-Methylhexane	100
162	1-(2-Butoxyethoxy)Ethanol	0.14	0.44	2,3-Dimethylpentane	100
158	2,2-Dimethyl-5-Methylene-3,7-Dioxa-Octane	0.14	0.42	2-Methyl-3-Pentanone	100
Spectrum #13248					
Elution Time = 28.93					
TIC Max. 559					
98	Methylcyclohexane	0.28	0.75	Methylcyclohexane	98
98	Cycloheptane	0.24	0.74	Cycloheptane	98
112	1-Methyl-1-Ethylcyclopentane	0.22	0.60	Cyclohexanone	98
98	Cyclohexanone	0.22	0.58	2-Methylcyclopentandne	98
Spectrum #13254					
Elution Time = 29.63					
TIC Max. 514					
146	2-Thianonane	0.21	0.40	2,2-Dimethylcyclobutanone	98
146	1-Octanethiol	0.19	0.37	2-Cyclohexene-1-ol	98
188	1-Undecanethiol	0.17	0.37	Cycloheptane	98
132	1-Heptanethiol (N-Heptyl) Mercaptan	0.16	0.36	3-Cyclohexenol	98

CLEAN UP OF RAW DATA FILE CLEANUP TEST #1 ON 10/28/78						
SLOT	SPEC.#	RETENTION	TICRAT	MAX. AMP	DOUBLET?	SAY. PEAKS
1	7110	16352.	99	32699.	NC	1
2	7130	1714.	47	747.	NC	0
3	7143	19136.	99	61726.	YES	1
4	7144	16010.	33	7089.	NC	0
5	7153	1090.	13	456.	NC	0
6	7155	15939.	90	585.	NC	0
7	7159	2706.	44	684.	NC	0
8	7165	7353.	37	767.	NC	0
9	7175	23997.	99	10775.	YES	0
10	7177	6379.	37	2954.	YES	0
11	7178	3256.	25	1906.	NC	0
12	7182	18789.	99	9435.	NC	0
13	7197	13812.	85	4184.	YES	0
14	7189	118588.	92	28657.	NC	0
15	7191	34309.	75	13336.	NC	0
16	7202	6717.	43	1687.	NC	0
17	7204	23102.	99	9807.	NC	0
18	7209	8299.	87	2605.	NC	0
19	7216	12211.	18	6535.	YES	0
20	7217	57833.	93	27078.	NC	0
21	7221	12304.	42	4179.	YES	0
22	7225	35864.	99	13092.	NC	0
23	7230	32738.	76	8797.	YES	0
24	7236	8971.	31	2252.	NC	0
25	7238	18402.	88	3776.	NC	0
26	7244	55210.	99	25520.	NC	0
27	7259	26381.	71	7812.	NC	0
28	7265	7530.	50	1209.	NC	0
29	7292	137667.	99	32699.	NC	3
30	7299	37614.	47	9796.	YES	0
31	7292	11621.	16	4320.	YES	0
32	7293	14134.	23	3074.	NC	0
33	7295	7720.	17	2132.	NC	0
34	7299	7522.	8	1151.	YES	0
35	7302	3439.	3	1280.	YES	0
36	7304	45877.	42	70393.	YES	1
37	7308	110416.	99	32699.	NC	4
38	7315	1760.	6	1171.	NC	0
39	7322	9331.	37	3156.	YES	0
40	7325	111516.	90	37699.	NC	1
41	7336	51139.	99	32695.	NC	1
42	7341	144658.	70	32699.	NC	1
43	7346	32112.	39	16745.	NC	0
44	7351	38519.	46	13943.	YES	0
45	7355	70510.	99	32699.	YES	3
46	7356	5220.	7	1280.	YES	0
47	7358	3937.	7	2368.	YES	0
48	7362	34024.	99	32699.	YES	2
49	7365	2319.	5	744.	NC	0
50	7369	3231.	9	1244.	NC	0
51	7373	8612.	21	3104.	NC	0
52	7392	8114.	14	2778.	YES	0
53	7393	40291.	63	6558.	NC	0
54	7394	27476.	32	5946.	YES	0
55	7385	30808.	25	2245.	NC	0
56	7390	177912.	55	32699.	YES	2
57	7392	194676.	78	20230.	NC	3
58	7399	73934.	30	16678.	YES	0
59	7403	34758.	26	7014.	YES	0
60	7404	5880.	4	1480.	YES	0
61	7408	6438.	5	2012.	YES	0
62	7409	4782.	4	1985.	YES	0
63	7411	9557.	7	4904.	YES	0
64	7413	9112.	9	2847.	YES	0
65	7417	44985.	34	16888.	YES	0
66	7421	288286.	97	32759.	NC	2
67	7431	161146.	53	32699.	NC	1
68	7433	122713.	99	32699.	YES	1
69	7437	67547.	38	15925.	YES	0

Figure 16. Chemist's printout from CLEANUP.

70	7439	27009.	14	5233.	NC	0
71	7445	48464.	43	15673.	YES	0
72	7447	14978.	11	4088.	YES	0
73	7448	32380.	28	7289.	NC	0
74	7453	12165.	10	1736.	NC	0
75	7458	5804.	5	1529.	YES	0
76	7459	15665.	15	3084.	YES	0
77	7463	20917.	22	6761.	NC	0
78	7468	80867.	99	32699.	YES	2
79	7469	3856.	3	1986.	YES	0
80	7471	5719.	6	1777.	YES	0
81	7472	21524.	28	3765.	NC	0
82	7478	259586.	74	32699.	NC	7
83	7482	22038.	21	3463.	YES	0
84	7483	7770.	8	1012.	YES	0
85	7484	4966.	6	713.	YES	0
86	7486	5304.	4	1393.	YES	0
87	7439	124812.	67	18205.	NC	3
88	7490	101103.	54	29322.	NC	0
89	7497	19823.	22	2731.	YES	0
90	7498	18524.	12	2777.	NC	0
91	7504	13503.	6	1424.	YES	0
92	7505	81709.	39	14400.	NC	0
93	7511	307985.	97	32699.	NC	2
94	7513	33757.	17	7284.	NC	0
95	7516	2664.	3	514.	NC	0
96	7520	48239.	42	9673.	NC	0
97	7524	65144.	57	9421.	YES	0
98	7528	18459.	27	4667.	NC	0
99	7532	4643.	7	946.	NC	0
100	7544	5306.	9	1000.	NC	0
101	7544	17751.	29	2080.	NC	0
102	7546	14371.	25	3540.	NC	0
103	7552	26178.	48	5355.	NC	0
104	7556	94184.	53	20048.	YES	0
105	7557	100720.	99	22306.	NC	0
106	7559	2218.	3	540.	NC	0
107	7562	79264.	88	15105.	NC	0
108	7564	13380.	23	3684.	NC	0
109	7569	57043.	79	13283.	YES	0
110	7571	20409.	31	4879.	YES	0
111	7573	29182.	42	6078.	YES	0
112	7577	10942.	17	3371.	NC	0
113	7588	27725.	40	6134.	YES	0
114	7590	38307.	56	9176.	NC	0
115	7596	97445.	93	22153.	NC	0
116	7602	3966.	6	1505.	NC	0
117	7606	2180.	3	1642.	NC	0
118	7615	6393.	10	1785.	NC	0
119	7619	3496.	5	1390.	YES	0
120	7623	16928.	24	2310.	NC	0
121	7629	3851.	6	771.	YES	0
122	7630	6274.	10	700.	YES	0
123	7634	74127.	56	16870.	NC	0
124	7637	3056.	4	772.	YES	0
125	7639	4655.	7	1607.	NC	0
126	7648	3291.	6	880.	NC	0
127	7659	4311.	5	1597.	YES	0
128	7670	21496.	34	8647.	NC	0
129	7672	38809.	99	32699.	NC	2
130	7674	40036.	48	15488.	YES	0
131	7675	1338.	2	1022.	NC	0
132	7698	19246.	34	6173.	NC	0
133	7703	3835.	8	1041.	NC	0
134	7705	1325.	3	615.	NC	0
135	7710	1563.	3	1278.	NC	0
136	7717	36074.	44	8902.	NC	0
137	7723	29546.	53	7979.	NC	0
138	7775	10576.	26	1758.	NC	0

Figure 16, Continued.

Analysis of Environmental Samples

As a further test of the proper operation of the CLEANUP program, a series of runs were processed at RTI using data which had been previously analyzed by hand. Seven runs were processed which represented a selection of different types of samples which possessed a variety of functional group types. These runs are briefly described in Table 5. Of all of the runs for which data were available, one represented a very complex mixture containing a wide variety of components and was chosen for extended study. The sample was that derived from ambient air in a basement of a residence which had been built over an industrial chemical dump and which had been perfused with a large variety of organic components. The air sample when analyzed by GC/MS, showed the presence of in excess of 100 components. A total ion current plot of this run is shown in Figure 17. The sample was first processed by the CLEANUP program using the best available values for the input parameters, and the results compared with the manual identification. The results of this comparison are shown in Table 6.

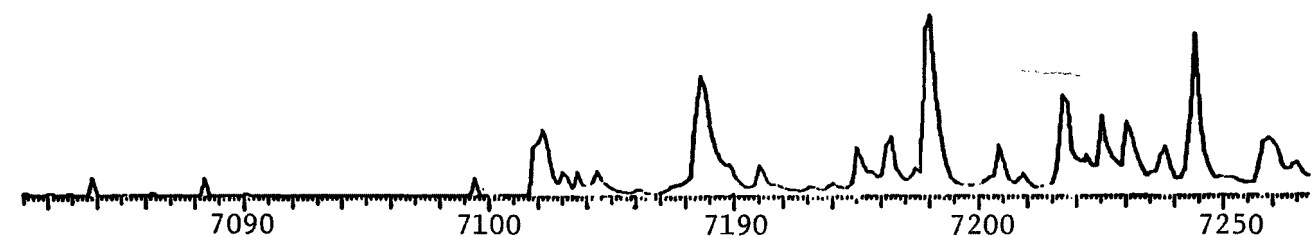
Notwithstanding a small number of errors, it is obvious that the CLEANUP program is operating very successfully, and is capable of extracting correct spectra from mixtures and identifying them even in very difficult and complex mixtures. The table shows a number of interesting results. It should be noted that in the majority of cases, the manual identification and the computer results were the same. When this is combined with a high correlation coefficient ($R > 0.6$), then the identification can be said to be correct and confirmed. In such cases the table entry is marked with an H (hit).

In some cases the computer results identified a component which is known to have a spectrum very similar to the manually identified compound. The correct identity often can be deduced by inspection, e.g. toluene might be identified as a methyl hexatriyne, or vinylidene chloride confused with dichloroethylene. This category comprises mainly isomers or homologues. These cases were also marked with an H. When the computer printed the manually identified compound as a 2nd to 5th choice, this number was also included in the table under the column heading, "Found".

TABLE 5. DESCRIPTION OF TYPES OF SAMPLES INVESTIGATED TO TEST OUT CLEANUP

All samples were run by desorption from TENAX GC cartridges.

Type of Sample	Contents
1. UNC smog chamber	esters nitrates dioxanes nitriles aldehydes hydrocarbons low m.w. alkyl aromatics ketones
2. Oil shale volatiles	nitriles alcohols sulfur compounds ketones pyridines pyrazoles quinolines hydrocarbons aromatics
3. Volatiles from in situ coal gasification (tar fraction)	alkanes alkyl aromatics very few hetero atom containing compounds
4. Volatiles from in situ coal gasification (water fraction)	alkanes sulfur compounds pyridines oxygenated hydrocarbons
5. Organics from air in basements	alkanes aromatics chlorines, bromine and fluorine containing compounds
6. Organics in air in the vicinity of a Du Pont plant	halogenated hydrocarbons aldehydes ketones phenols nitro aromatics
7. Organics near a pesticide plant	halogenated hydrocarbons sulfur compounds oxygenated hydrocarbons (aldehydes, ketones, phenols, esters)



300-7849 LM 1510/CAB383N/FNYNFKA/T1/27FEB70/105MSF30 STEP SPECN. 1 INT. 1000

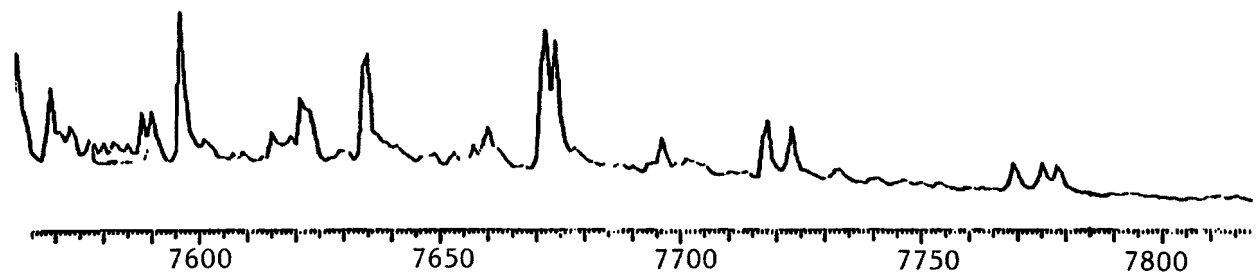
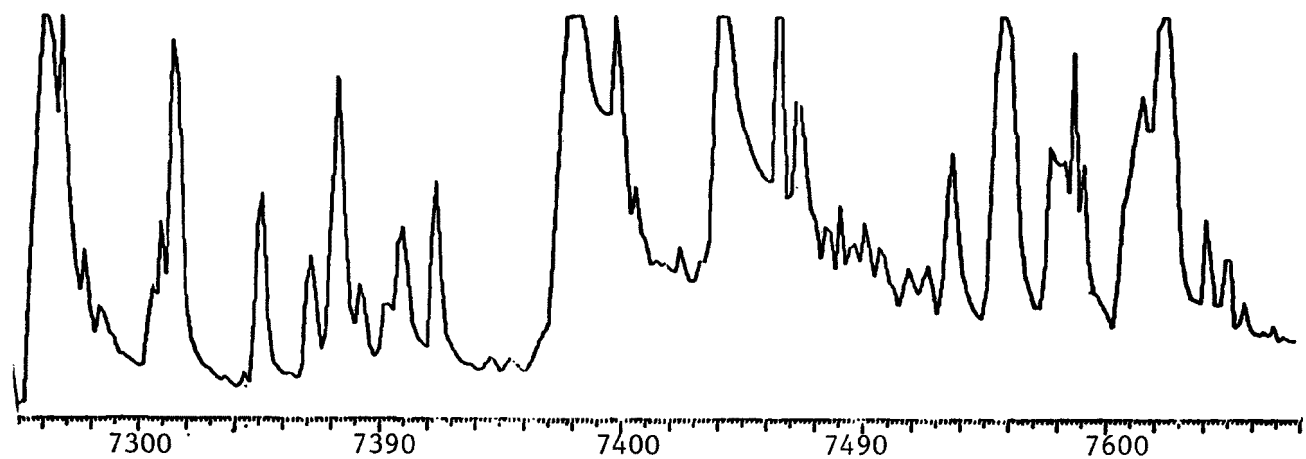


Figure 17. Total ion current plot from test run.

TABLE 6. COMPARISON OF MANUAL VS. COMPUTER IDENTIFICATION OF GC-MS RUN

Run #: 1510-CAB-3B3W-FNYNFKB

SP #	Retention Time	Compound Identification	R	Hit or Miss	Found	Manual Identification
7110	12.72	Dimethylamine	.84	M	5	Carbon dioxide
7130	15.05	Vinyl fluoride	.63	H		C ₃ H ₈ O?
7143	16.57	Acetone	.89	H		Acetone
7144	16.68	Fluorotrichloromethane	.85	H		--
84 7153	17.73	Vinylidene chloride	.78	H		Dichloroethylene
7155	17.97	Dichloromethane	.96	H		Dichloromethane
7159	18.43	Freon 113	.54	H		--
7165	19.13	Acetic acid	.71	M		C ₄ H ₈ O?
7175	20.30	2-Methylpentane	.80	H		2-Methylpentane
7177	20.55	1,2-Dimethylpropyl acetate	.55	M		C ₅ H ₁₀
7178	20.65	<u>n</u> -Butanal	.75	H		Butanal
7182	21.12	2,2-Dimethylbutane	.69	H		3-methylpentane
7187	21.70	Hexafluorobenzene	.78	H		Hexafluorobenzene
7189	21.93	<u>n</u> -Hexane	.82	H		<u>n</u> -Hexane
7191	22.17	Chloroform	.63	H		Chloroform
7202	23.45	Perfluorotoluene	.71	H		Perfluorotoluene
7204	23.68	Methylcyclopentane	.77	H		Methylcyclopentane
7209	24.27	1,1,1-Trichloroethane	.68	H		1,1,1-Trichloroethane
7216	25.08	Isopropyl acetate	.76	H		Isopropyl acetate

(continued)

TABLE 6 (continued)

SP #	Retention Time	Compound Identification	R	Hit or Miss	Found	Manual Identification
7218	25.20	Benzene	.90	H		Benzene
7220	25.67	Acetic acid	.67	H		Acetic acid
7225	26.13	2-Methylhexane	.78	H		2-Methylhexane
7230	26.72	3-Methylhexane	.89	H		3-Methylhexane
7235	27.42	Dimethylcyclopentane	.82	H		C ₉ H ₁₄
7238	27.65	Trichloroethylene	.75	H		Trichloroethylene
7244	28.35	<u>n</u> -Heptane	.97	H		<u>n</u> -Heptane
7259	30.10	Methyl isobutyl ketone	.54	H		4-Methyl-2-pentanone
64 7265	30.80	<u>n</u> -Heptyl formate	.76	?		C ₈ H ₁₈
7281	32.78	1,5-Heptadien-3-yne	.60	H	5	Toluene
7289	33.60	3-methylheptane	.91	H		C ₈ H ₁₈
7292	33.95	Hexanal	.61	H		C ₆ H ₁₂ O?
7293	34.07	1,3-Dimethylcyclohexane	.62	H		C ₈ H ₁₆
7295	34.30	Ethyl <u>n</u> -butanoate	.52	H		--
7300	34.77	4-Methyltriazole	.46	?		C ₈ H ₁₆
7303	35.12	<u>n</u> -Butyl acetate	.42	H		<u>n</u> -Butyl acetate
7305	35.35	3,4-Epoxy-2-hexanone	.52	M		<u>n</u> -Octane
7309	35.82	Tetrachloroethylene	.58	H		Tetrachloroethylene
7315	36.63	Hexamethylenecyclohexasiloxane	.57	?		--
7322	37.45	2,6-Dimethylheptane	.78	H		C ₉ H ₂₀
7325	37.80	Chlorobenzene	.80	H		Chlorobenzene

(continued)

TABLE 6 (continued)

SP #	Retention Time	Compound Identification	R	Hit or Miss		Manual Identification
				Found		
7336	39.08	1,3-Dimethylbenzene	.83	H		Ethylbenzene
7342	39.67	N-Methyl-n-pentylhydrazine	.74	M	3	Xylene isomer
7346	40.25	3-Methyloctane	.81	H		C ₉ H ₂₀
7351	40.83	Benzocyclobutane	.75	H	3	Styrene
7355	41.30	p-Xylene	.77	H	3	o-Xylene
7356	41.42	1,3-Dimethylcyclopentane	.40	?		--
7358	41.65	1-Methyl-4-ethylcyclohexane	.43	H		C ₉ H ₁₈
50 7361	42.16	n-Nonane	.69	H		n-Nonane
7365	42.47	Diethyl methylvinylsilane	.51	?		--
7369	42.93	1-Methylethylcyclohexane	.75	H		C ₉ H ₁₈
7373	43.40	Isopropylbenzene	.56	H		Isopropylbenzene
7381	44.45	Cyclohexyl acrylate	.63	?		C ₃ -Alkylcyclohexane
7383	44.57	3-Methylnonane	.52	H		C ₁₀ H ₂₂
7384	44.68	Di(2-ethylhexyl) ether	.56	H		--
7385	44.80	2-Methyl-5-ethyl heptane	.28	H		C ₁₀ H ₂₂
7390	43.38	Benzyl chloride	.58	H	2	Chlorotoluene
7392	45.62	4-Azido-3-nitrotoluene	.37	M		--
7399	46.43	Isopropylbenzene	.38	H		C ₃ -Alkylbenzene
7403	46.90	3-Methylnonane	.77	H		C ₁₀ H ₂₂
7404	47.02	3-Phenyl-3-methylazetidine	.66	?		--
7408	47.48	p-Menthan-9-ol	.45	H	2	C ₁₀ H ₂₀

(continued)

TABLE 6 (continued)

SP #	Retention Time	Compound Identification	R	Hit or Miss	Found	Manual Identification
7409	47.60	β -Thujene	.41	H		C ₁₀ H ₂₀
7412	47.83	Valeric acid	.66	H	3	Heptanoic acid?
7413	48.07	4- <u>n</u> -Propyl-3-heptene	.42	M		C ₃ -Alkylbenzene
7417	48.53	Octamethylcyclooctasiloxane	.52	?		--
7420	49.00	o-Chlorobenzoyl chloride	.43	H	2	Dichlorobenzene isomer
7431	50.17	1,3-Dichlorobenzene	.53	?		C ₄ -Alkylbenzene
7433	50.40	Cuminic aldehyde	.48	?		C ₃ -Alkylbenzene
7438	50.87	1- <u>p</u> -Menthadiene	.76	H		C ₁₁ + C ₁₀ isomer
7439	51.10	Isobutylcyclohexane	.51	M		Bromotoluene isomer
7444	51.80	<u>p</u> -Methylacetophenone	.68	H	4	C ₄ -Alkylbenzene
7447	52.03	4-Ethylheptane	.53	H	2	C ₁₁ H ₂₄ Isomer
7448	52.15	O-Decyl-hydroxylamine	.50	?		C ₁₁ H ₂₄ Isomer
7453	52.73	Bicyclo(4.4.0)decane	.42	?		C ₁₁ H ₂₄
7458	53.32	3,5-dimethylmethyl benzoate	.33	M		C ₄ -Alkylbenzene
7459	53.43	Ar, α -dimethylstyrene	.50	H		--
7463	53.90	Linalol	.39	?		C ₁₁ H ₂₂
7468	54.48	<u>n</u> -Undecane	.87	H		<u>n</u> -Undecane
7469	54.60	<u>t</u> -Butylbenzene	.28	?		--
7471	54.83	Methyl benzoylacetylene	.36	M		Tetrachlorobenzene
7472	54.95	o, α -Dichlorotoluene	.38	H		Trichlorotoluene
7478	55.65	2,6-Dichlorotoluene	.70	H		Dichlorotoluene

(continued)

TABLE 6 (continued)

SP #	Retention Time	Compound Identification	R	Hit or Miss	Found	Manual Identification
7482	56.12	α -Neoisomenthol	.21	M		Pentachlorobutadiene
7484	56.23	Bicyclo(3.3.1)nonane-2-ol	.28	M		Trichlorobenzene
7485	56.35	Methyldichlorocyclopentadiene	.25	M	2	Trichlorobenzene
7486	56.58	3,4-Dimethylstyrene	.45	?		C ₅ -Alkylbenzene
7488	56.82	α -Pinene oxide	.77	H		C ₄ H ₁₆ O
7490	57.05	2,6-Dichlorotoluene	.85	H		Dichlorotoluene
7497	57.87	N-Acetyl-phenylalanine	.21	M		--
7498	57.98	2-Methylnonane	.43	H		--
52 7504	58.68	1,2,4-Trichlorobenzene	.43	H		Trichlorobenzene
7506	58.80	1,2,4-trichlorobenzene	.48	H		Trichlorobenzene
7511	59.50	Quinoline butiodide	.43	M	3	Naphthalene
7513	59.73	<u>n</u> -Dodecane	.65	?		Methyl salicylate
7515	60.08	Verbenone	.33	?		C ₁₂ H ₂₆
7520	60.55	1,3,5-Trichlorobenzene	.72	H		Trichlorobenzene
7525	61.02	Hexachlorobutadiene	.69	H		Hexachlorobutadiene
7528	61.48	Carvone	.74	H		?
7532	61.95	Pentobarbital-TMS ether	.20	M		Unsat. hydrocarbon
7534	62.18	Cyclohexylmethanol	.31	M		C ₁₃ H ₂₆
7544	63.35	α ,2,4-trichlorotoluene	.37	H		Trichlorotoluene
7546	63.58	2-Methyl-5-ethylheptane	.64	?		C ₁₄ H ₂₈

(continued)

TABLE 6 (continued)

SP #	Retention Time	Compound Identification	R	Hit or Miss	Found	Manual Identification
7552	64.28	Bornyl formate	.59	H		C ₁₀ H ₁₆ (?)
7556	64.75	<u>n</u> -Tridecane	.67	H		<u>n</u> -Tridecane
7558	64.87	α ,3,4-Trichlorotoluene	.67	H		Trichlorotoluene
7559	65.10	Haloperidol	.28	M		Methylnaphthalene
7561	65.45	α ,3,4-Trichlorotoluene	.25	H		Trichlorotoluene
7564	65.68	1-Methylnaphthalene	.61	H		α -Methylnaphthalene
7568	66.27	Chlorophenyldibenzoazepine	.32	M		C ₁₄ H ₃₀ ?
7571	66.50	1,2,3,4-Tetrachlorobenzene	.68	H		Tetrachlorobenzene
53 7573	66.73	α ,2,4-Trichlorotoluene	.63	H		Trichlorotoluene
7577	67.20	2,5-Dimethylundecane	.48	H		C ₁₃ H ₂₆ isomer
7588	68.48	Acenaphthene	.50	H	2	Biphenyl
7590	68.72	1,2,3,4-Tetrachlorobenzene	.68	H		Tetrachlorobenzene
7596	69.42	<u>n</u> -Tetradecane	.79	H		<u>n</u> -Tetradecane
7602	70.12	2,6-Dimethylnaphthalene	.47	H		C ₂ -Alkyl naphthalene
7607	70.58	2-Amino-4-hydroxupteridine	.40	M		C ₂ -alkyl naphthalene
7615	71.63	α -murolene	.24	M		Alkylbenzene?
7619	72.10	1-Cyclohexyloctane	.39	H	2	C ₁₆ H ₃₂
7623	72.57	2,6-Di-t-butyl-1,4-benzoquinone	.61	H		C ₆ H ₂₄ O?
7624	73.27	7-Acetoxy-p-menth-1-en-3-one	.31	?		--
7630	73.38	2,6-Dichlorobenzal chloride	.32	H	2	Tetrachlorotoluene
7634	73.85	<u>n</u> -Pentadecane	.82	H		<u>n</u> -Pentadecane
7637	74.20	Methyl laurate	.38	?		C ₁₅ H ₃₀

(continued)

TABLE 6 (continued)

SP #	Retention Time	Compound Identification	R	Hit or Miss	Found	Manual Identification
7639	74.43	Trihydroxy benzoic acid, TMS	.19	M		C ₃ -Alkyl naphthalene
7649	75.60	Pentachlorobenzene	.38	?		C ₅ -Alkyl benzene
7659	76.77	Dicyclohexyl ether	.30	?		--
7660	76.88	Diethyl phthalate	.68	H		Diethyl phthalate
7672	78.28	Neopentylphosphonyldichloride	.41	M		Trimethylpentadiol diacetate
7674	78.52	<u>n</u> -Hexadecane	.58	H		<u>n</u> -Hexadecane
7675	78.63	2-Phenyldecane	.39	H		Sat. hydrocarbon
7696	81.08	Pristane	.66	H		C ₁₈ H ₃₈
7703	81.90	Dimethylbenzylisobutyl ether	.23	M		C ₁₆ H ₃₂
7705	82.13	Methylfuranyl THP-ether	.29	M		--
7710	82.72	Trimethylamine	.65	M		--
7718	83.53	<u>n</u> -Tetradecane	.77	H	3	<u>n</u> -Heptadecane
7723	84.23	Pristane	.82	H		C ₁₉ H ₄₀
7775	90.30	Myristic acid	.48	H		?

An interesting situation occurred in a few cases in which manual identification was not possible or uncertain. In those cases the manual identification column contains a question mark. If in addition the R factor from the computer is sufficiently high, it is reasonable to assume that the computer identification is correct and the manual identification is incorrect. This is particularly true with closely spaced doublets where frequently it is nearly impossible to separate components manually. In these cases, the computer identification is more certain than the human one. When this occurred, a question mark or even an H was entered in the hit column. Components missed in the manual interpretation were marked with a dash in the appropriate column.

In a small number of cases, computer identification is undoubtedly wrong. This is usually accompanied by low R factors ($R < 0.3$). Also when peaks are weak or small components of multiplets, it is difficult to identify them by computer. Such cases are marked with an M in the hit column ("Miss").

Comparison of figures clearly shows that the CLEANUP program materially simplifies the spectra prior to their submission to the search program. The data here presented show that by combining CLEANUP with an efficient search procedure, results can be obtained which are comparable with human interpretation. In summary, of 138 components, definite hits were obtained on 90 components, clear misses occurred in 26 cases, with 22 cases unclear. Removing the questionable category, the system recorded 78% hits and 22% misses; a rather remarkable performance for this very complex and convoluted mixture.

CLEANUP CONTROL PARAMETERS

The conclusion of Phase II consisted of variation of the CLEANUP control parameters in order to determine their effect on the output spectra and to arrive at an optimum setting for each. The fifth of the eight runs described above was chosen as a test case. Most of the parameters represent threshold settings concerned with eluant detection: peak sharpness requirements, total ion current threshold, closest expected distance between neighboring eluants, the percent of each peak attributable to background, etc. Two parameters are simply switches controlling optional diagnostic messages useful for program debugging.

An attempt was made to determine optimal parameter settings by varying parameters in a regular manner and analyzing the results using the SPSS statistical package. This approach was not fruitful since there was no obvious demarcation between what constitutes peak peaks and noise peaks, and so the statistics did not show a clear preference for one setting of the parameters, but only a continuum of change. Trial and error variation of the parameters, though less sophisticated, proved more effective. The general procedure was to vary each parameter in both directions about the value suggested by the program authors in the original CLEANUP documentation. A summary of conclusions and recommended values is shown in Table 7. The two things which most aided determining the effects of parameter variation were the "chemist's summary printout" of CLEANUP (Figure 17) and the output of the RTI search program (Table 4). It is to be emphasized that these values represent optimum settings for a VARIAN CH-7. Our suggested values for the INCOS test data are shown in Figure 27.

The chemist's printout is a summary list of components found by CLEANUP, along with information regarding the presence of doublets and saturated peaks. By comparing the change of the number of eluants indicated in the chemist's printout together with the most likely candidates for those eluants found by the RTI search program, it was possible to determine when erroneous peaks were beginning to be picked up by CLEANUP.

Following is a technical review of the analysis of parameters, primarily of interest to programming specialists.

The first two variables control the print options of the CLEANUP program and do not affect any internal calculations. Either variables can be set to 0 (do not print) or 1 (print). The first option (IPFLAG) determines whether or not the chemist's printout is to be printed. The listing of all eluants found by CLEANUP takes relatively little space, and has proved helpful in almost all test runs. We feel that the chemist's printout should always be requested. The second option (IDEBUG) determines whether or not intermediate calculations and decisions inside CLEANUP are to be printed. Information printed includes histogram

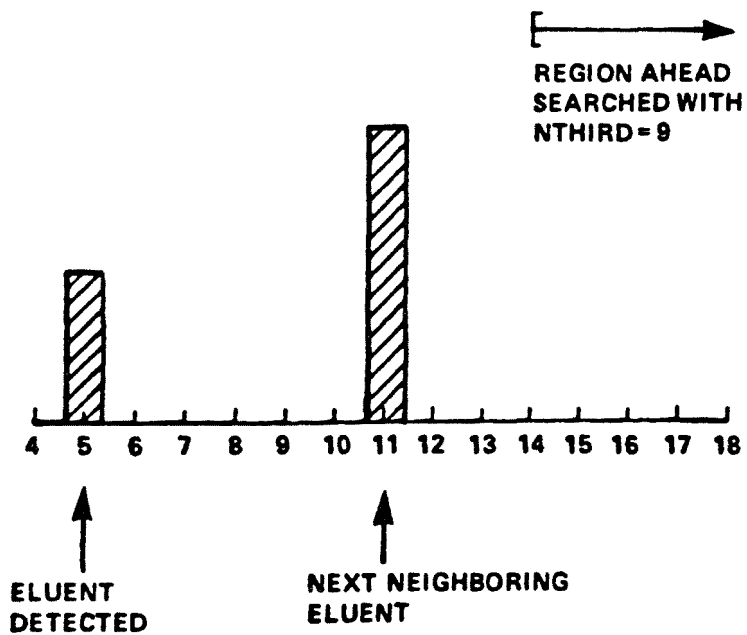
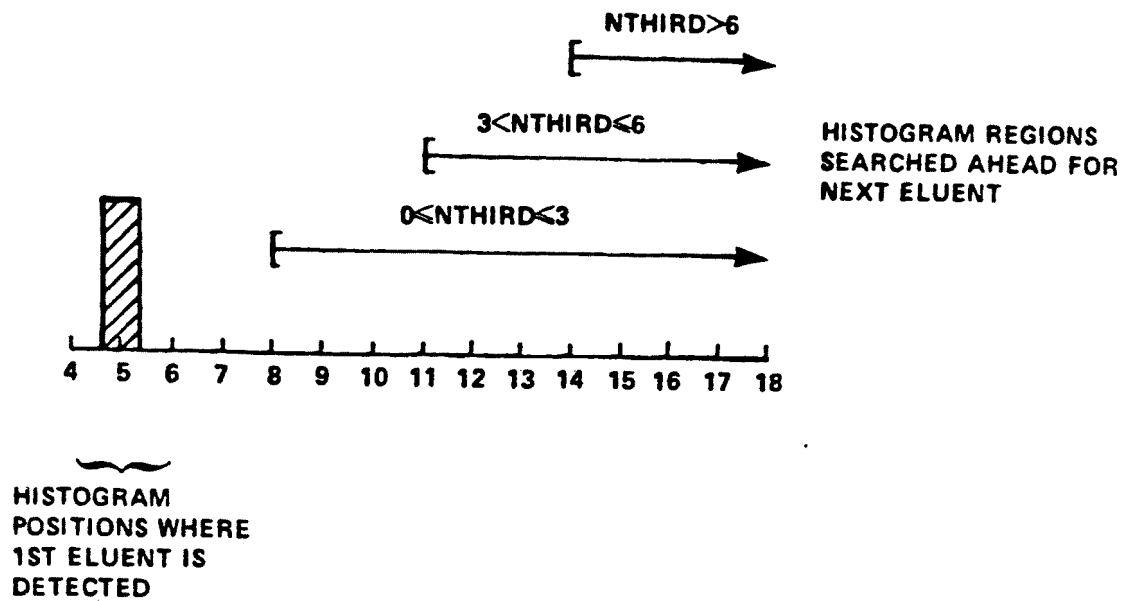
TABLE 7. CLEANUP INPUT PARAMETER SUMMARY

Name	Function	Possible values	Suggested values
IPFLAG	Determine whether or not to generate chemist's printout	1 = Generate printout 0 = Suppress printout	1 = Chemist's printout is helpful in all cases
IDBUG	Determine whether or not to generate debugging output	1 = Generate printout 0 = Suppress printout	0 = Printout necessary only when looking for errors
NTHIRDS	Set minimum # of scans for expected doublets	3,6,9 in units of 1/3 scan	3 = Expected distance as short possible
ITOM	Set neighborhood in histogram window for eluent detection	1,2 units of 1/3 scans	2 = Widest setting
MINNY	Set minimum histogram ion current for 1 to 4 peak eluents	Any integer greater than or equal to 0	1000 currently used, setting greater than 0 recommended
MINTIC	Set minimum histogram ion current for eluents with more than 5 peaks	Any integer greater than or equal to 0	1000 currently used and recommended, critical that setting greater than zero is used
RATM	Minimum rate for eluent detection	Any real number greater than 0.0	0.0 = No minimum cutoff for peak rates appears necessary at this time
RATMOX	Eliminate column bleed from detected eluents by linear error ratio test	0.0 to 1.0	= .1, current value is .0756. It is critical that this parameter not be 0.0
ILEFT	Set number of scans required for increasing ion current prior to prospective model peak mode	1,2	2 = As wide a neighborhood about the mode as possible is recommended to ensure model accuracy
IRIGHT	Set number of scans required for decreasing ion current after prospective model mode	1,2,3	3 = Same as above
SATVAL	Tells CLEANUP instrument saturation value	All integers	= 200 below instrument saturation value (see text)

printouts, complete peak models, and decisions made as to whether the peak encountered was dismissed as noise, qualified as a singlet eluant, or whether the doublet resolver was invoked. With an average of 1 page of printout per eluant detected, the full printout for some test runs has frequently exceeded 200 pages. Although this information proved very helpful in finding some bugs in CLEANUP, we feel that unless there is a specific need, this diagnostic output should be suppressed.

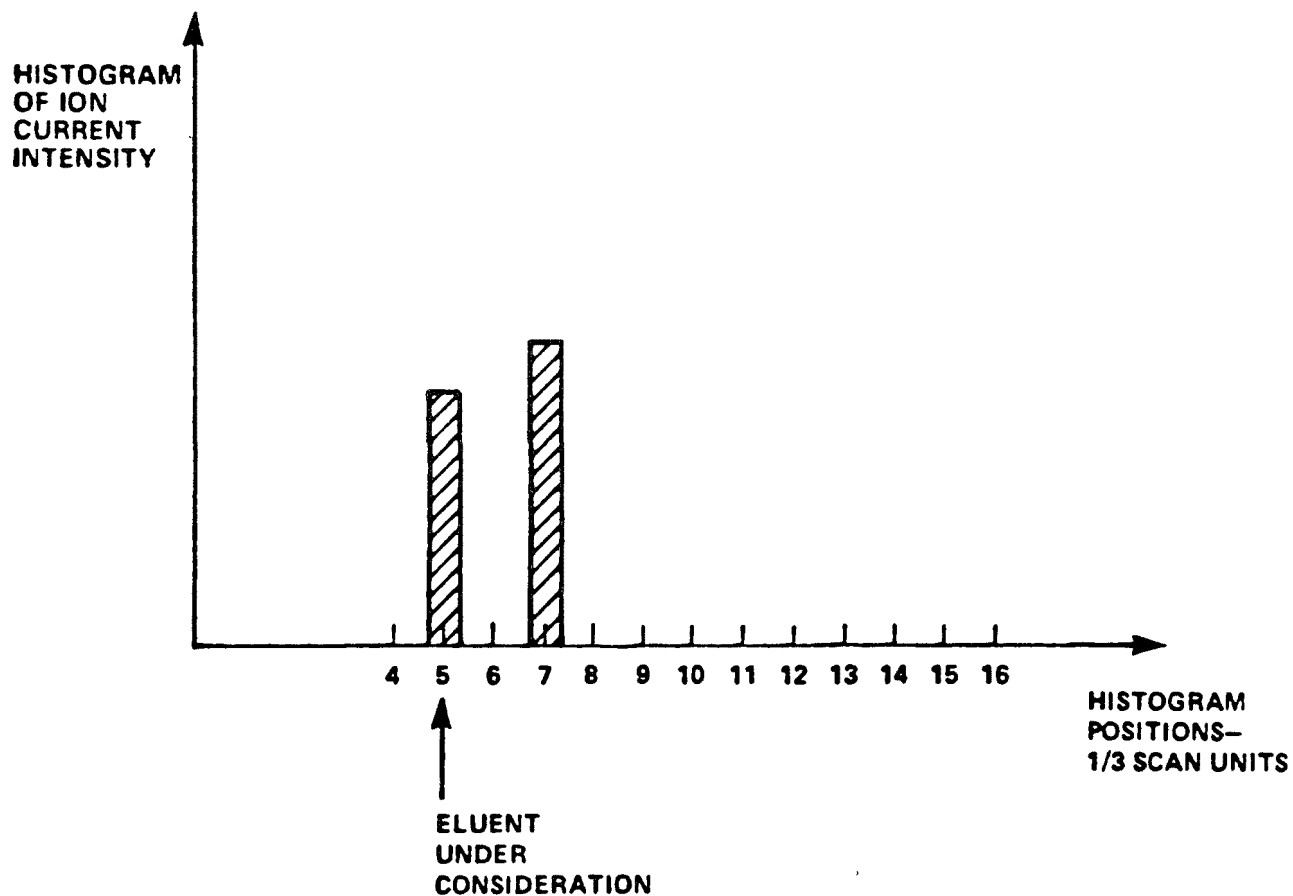
The first of the parameters affecting output spectra (NTHIRD) determines the closest distance which CLEANUP expects between neighboring eluants. Once the CLEANUP program detects an eluant from histograms of the ion current, it looks ahead in the histogram to determine if another eluant is in the vicinity just ahead. Although the variable NTHIRD is given in units of thirds of scans, only three values make a difference in terms of CLEANUP internal calculations. A value for NTHIRD of 3 means that neighboring eluants are expected no closer than 1 scan away, 6 means no closer than 2 scans, and 9 means that neighboring eluants are expected no closer than 3 scans from each other. The function of NTHIRD is shown graphically in Figure 18. From a theoretical point of view, there is no reason why this parameter should not be set to 3, setting the CLEANUP program to look for doublets within the finest possible grid. The danger of using a coarser setting is that some close pairs of eluants could be interpreted by the CLEANUP program as singlets, resulting in incorrect peak model choices and the deletion of unknowns. Our experience with varying this parameter over the test run however, showed only a mild dependence of results on the expected minimum distance, with the number of eluants decreasing by only 5% from the finest to the coarsest possible setting.

The detection window size (ITOM), has two possible values; 1 and 2, corresponding to the number of histogram positions which must be less than the central maximum in order for an eluant to qualify for detection. This is shown graphically in Figure 19. Currently, the most stringent setting is being used, requiring that histograms of ion currents for 2 members on either side of the central position be lower than the central value in order for an eluant to be detected. Statistics on this



Example of Eluent Missed Due to Incorrect Setting of $NTHIRD$ Parameter

Figure 18. Graphic representation of possible settings of $NTHIRD$.



The ion at position 5 would be rejected with ITOM = 2 because of the neighboring eluent at position 7, whereas with ITOM = 1, it would be accepted.

Figure 19. Function of ITOM histogram window setting.

parameter were obtained, but in view of the fact that the CLEANUP algorithm does not try to resolve doublets closer than 1 scan apart and breaks down entirely for a distance of 1/3 scan, it was decided to keep ITOM at its most rigorous value, 2.

The input parameters MINNY and MINTIC are minimum TIC histogram intensity thresholds for eluant detection. It is important to note that these ion currents are tested after background noise is subtracted. There are two threshold settings, one for spectra containing very few ions, (e.g. coronene), and one for spectra containing 5 or more ions. In addition, the reconstructed spectrum is required to have a total ion current equal or greater than MINTIC otherwise it is not written to the output file or noted in the chemist's printout. TIC threshold requirement was tested first by setting both parameters to 0, effectively eliminating the TIC minimum cutoff. The result of this test was to more than double the number of eluants detected by CLEANUP. Many of these eluants when processed by the RTI search program were found to have less than 5 compounds in the entire library which passed its two out of six strongest peaks presearch test, indicating that the peaks consisted mainly of noise. It is thus concluded that some TIC requirement is necessary. We now believe that the value of 1000, presently used, is too high. The optimum setting of this threshold must be determined individually for every data system.

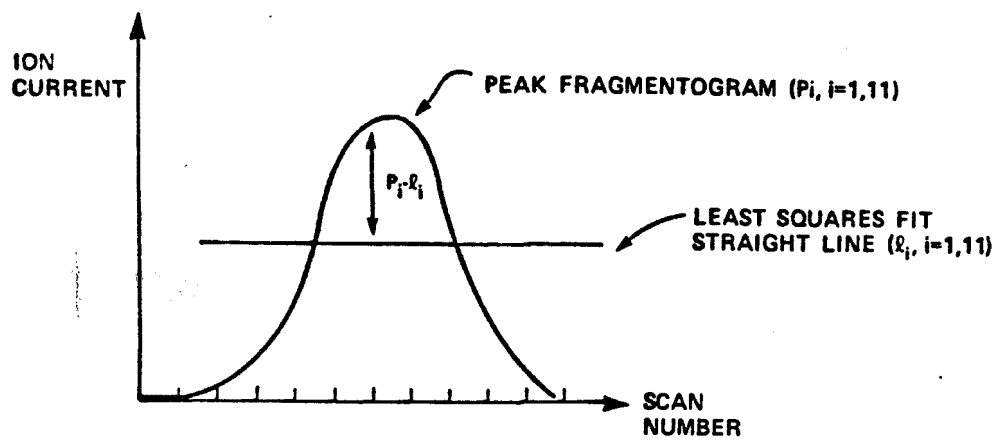
The parameter (RATM) sets a minimum sharpness on each model peak before it can qualify as an eluant. The suggested value is 0, meaning that no eluents are rejected, sharpness being positive definite. This parameter was left at 0 for two reasons. First, there was no evidence of spurious eluants being introduced due to insufficient sharpness, and second, the distribution of sharpness values for the test run gave no clues as to a best setting.

The function of the linear error ratio (RATMXX) is to remove those single ion traces (fragmentograms) which contain column bleed. In order to do this, a least squares fit to a straight line is calculated for an 11 scan window (5 scans on each side scan under consideration) and then

the ratio of the root mean square deviation of the peak shape about the line to the average value of the line is calculated (Figure 20). As indicated, peak shapes which are "too flat" can be eliminated by the error ratio criterion. Another useful property of the error ratio is that small peaks against very limited background noise will still be considered as eluants (b), whereas the same small ripple against a strong background would be dismissed as noise (c). We have varied the minimum error ratio requirement and we have demonstrated that the correct assignment of this variable is critical. The minimum error ratio requirement was reduced from the suggested .0756 to .002. Under these conditions CLEANUP found the same number of peaks as it had with the higher value found (the error ratio test is applied after an eluant has been detected in order to determine if reconstruction is worthwhile), but the CPU time required by the search program doubled and recognition performance markedly deteriorated. Extraneous peaks were admitted by CLEANUP, causing a large fraction of the unknowns to pass the presearch cycle of SEARCH and also causing misidentification in the search program due to the presence of those peaks.

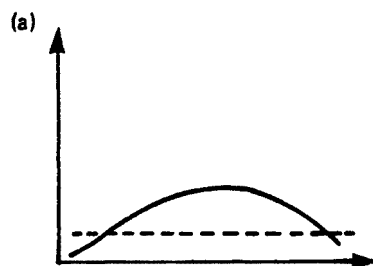
The parameter ILEFT sets the number of scans which must show an increasing ion current prior to the mode in order for an ion fragmentogram to be considered as a model peak. Correspondingly, IRIGHT sets the number of scans required to show a decreasing ion current after the mode for model consideration. We feel that ILEFT and IRIGHT should be left at their maximum permissible values, 2 scans prior to and 3 scans after the mode. The CLEANUP algorithm achieves maximum efficiency when a typical singlet peak is 5 to 10 scans wide. If the scan rate is correctly "tuned" the most stringent setting for ILEFT and IRIGHT ensures that well-behaved individual ion traces are used as model peaks.

The parameter SATVAL defines the saturation value used by the program in order to determine when peaks are saturated and need to be reconstructed via a ratio approach. Although this number would be expected to be the theoretical maximum for the A/D convertor used in the data acquisition system, we have found it necessary to set SATVAL to a value slightly below the theoretical maximum. Thus, for the VARIAN

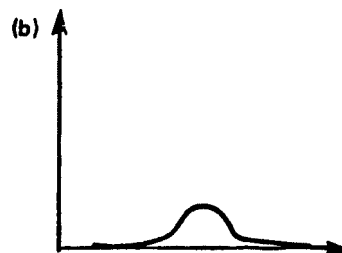


$$\text{ERROR RATIO} = \frac{\sqrt{\sum_{i=1}^{i=11} (P_i - l_i)^2}}{\sum_{i=1}^{i=11} l_i}$$

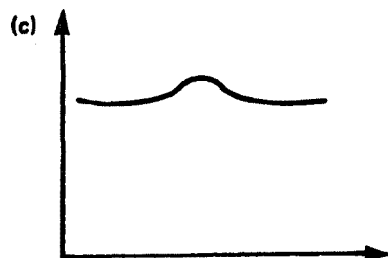
EXAMPLES:



Peak thrown out because error ratio is too low



Small, relatively sharp peak admitted because of small denominator in error ratio

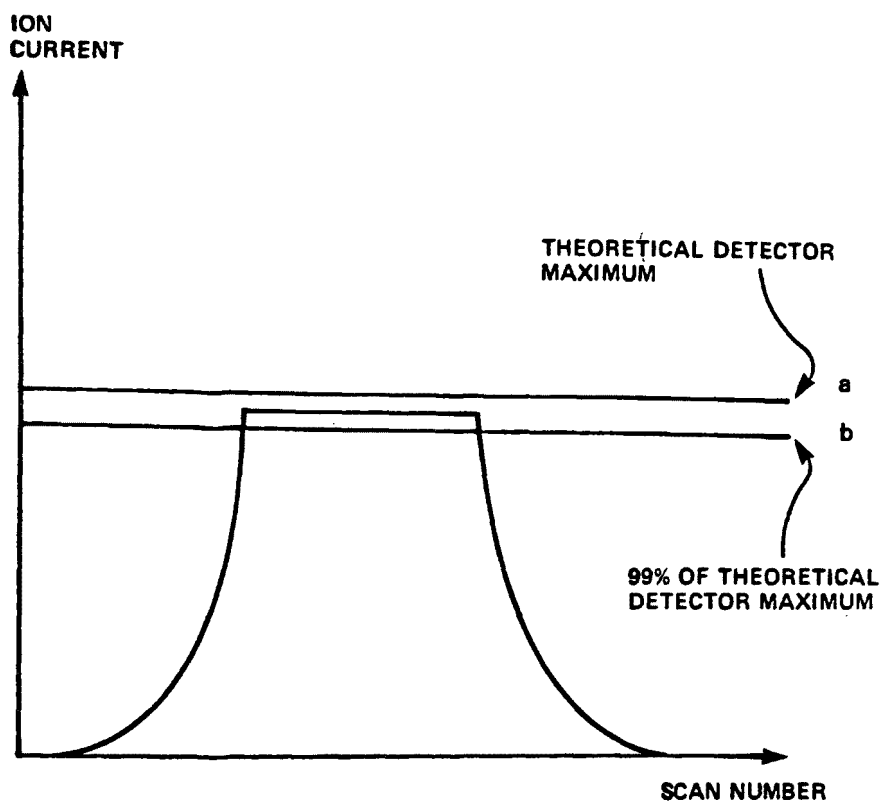


Same small peak here is thrown out as noise because of large denominator in linear error ratio

Figure 20. Effects of linear error ratio.

system, the maximum A/D output is 32,767 ($2^{15}-1$), we currently have SATVAL set to 32,000. For unknown reasons, A/D convertors often register values less than their maximum for known, saturated peaks. In such cases, saturated peaks can inadvertently be eliminated entirely as background noise (Figure 21).

Again, the values for the parameters shown in Table 7 are satisfactory for VARIAN CH-7 data. It must be realized however, that these values are instrument and data dependent, and optimum values for any particular data system must be determined empirically by adjustment of parameters, which will require some experience gained only with time.



With SATVAL setting at value (a), the saturated peak is constructed by CLEANUP to be entirely background noise, but with a slightly reduced setting (b) for SATVAL, the peak is recognized as saturated and handled by the correct routines.

Figure 21. Effect of SATVAL on CLEANUP.

SECTION 5

IMPLEMENTATION OF THE CLEANUP PROGRAM ON THE UNIVAC COMPUTER

Phase III of this contract consisted of making the CLEANUP program developed at RTI operational on the UNIVAC computer located at EPA. This work was carried out simultaneously with some improvements being made in the organization of the data formats in CLEANUP.

Because RTI's and EPA's environment for using the CLEANUP program are similar, it was decided to use the same CLEANUP source version for each. The general plan was to change the READ and WRITE statements inside CLEANUP to subroutine calls and then write a set of I/O subroutines for EPA and later a set of I/O routines for RTI's system.

There were two advantages to this approach. First, the CLEANUP program would require substantially less modification. In addition, if any bugs were to occur in CLEANUP in the future, it would be possible to investigate the problem by carrying out a debugging run at TUCC. This would verify whether the bug was a system oriented problem or an algorithm deficiency inside CLEANUP proper. If the problem was indeed a bug in CLEANUP, it could be corrected at TUCC. Systems problems at the UNIVAC would be corrected there. Modules required for these programs are shown on Figure 22. The code to be delivered to EPA consists of sections 1, 2 and 3. A short description of each of these modules follows.

Some minor modifications to the original CLEANUP program besides changing READ and WRITE statements were made. The most important of these was to expand the CLEANUP program so that it could process multiple runs on the same tape data set. To include this facility, the routines PARDIR (reading in the CLEANUP input parameters) and SETRUG (initializing the 14 spectra window with the first 13 spectra) had to be repositioned and rewritten.

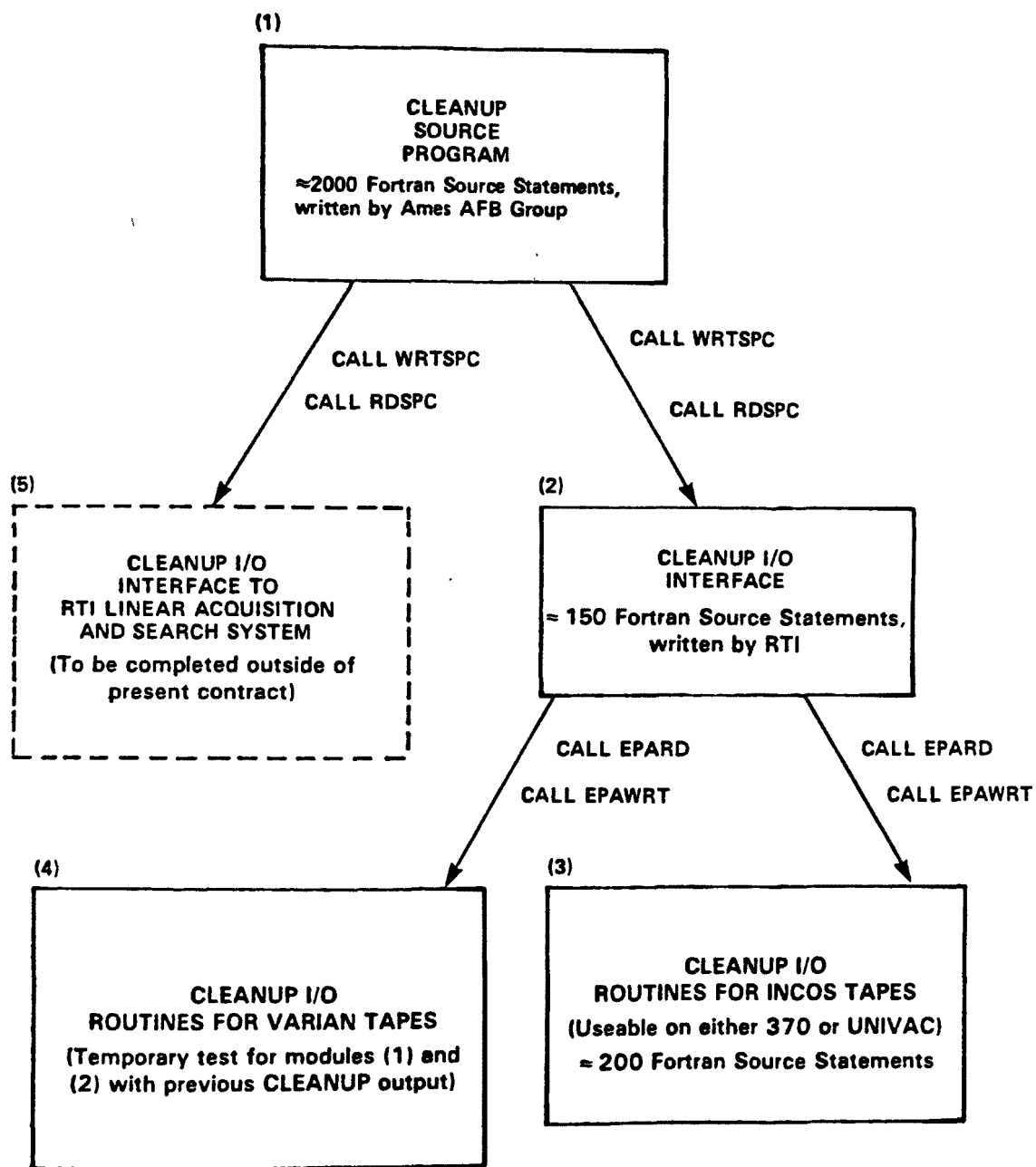


Figure 22. Modules required for transfer of CLEANUP program to UNIVAC.

Rather than have CLEANUP call the I/O routines directly, it was decided to create an intermediate step consisting of an I/O interface called by CLEANUP which would in turn call the I/O routines. This was necessary because the only data used by CLEANUP for internal calculations are individual ion intensities while the INCOS tape data contained much additional identification information. Although not used by CLEANUP, these items were carried along to be able to write output spectra in the same format as on the original input tape. The interface served the dual function of keeping track of data not used directly inside CLEANUP and of making the I/O routines more versatile for use with other tasks.

The modification of the CLEANUP program involved roughly 500 statements: 100 statements for the rewritten routines inside CLEANUP, 200 statements for the I/O interface, and 200 statements for the I/O routines. To assure accuracy and quality control, several cross checks were made.

In order to insure the correctness of the modified CLEANUP source (1) and the I/O interface (2) a temporary set of I/O routines for reading the VARIAN CH 7 data (4) were written. These routines purposefully had exactly the same calling arguments as the INCOS tape I/O routines (3). These routines were written in standard FORTRAN and involved little more than READ and WRITE statements. It was then possible to test CLEANUP and the I/O interface on one of the eight trial runs. The prototype run was much more difficult to achieve than anticipated, mainly due to communication problems between the main CLEANUP source module and the I/O interface. However, because everything was in strict FORTRAN it was possible to use the WATFIV interpreter to find the majority of the CLEANUP bugs. The WATFIV interpreter again proved itself invaluable, not only in solving otherwise very subtle problems but also by insuring machine independence of the code. Thus, output of the CLEANUP source with the new I/O interface was verified against earlier output from the version of the CLEANUP program which was "spliced" into the RTI system.

It remained to test out the I/O routines (3) on an INCOS tape data set. After we were convinced that the I/O routines were operating properly, a program was written to generate a TIC plot of the first INCOS test run with the aid of the UNC plotter facility and the TUCC plotter routines. A reproduction of this plot is shown in Figure 23. This plot confirms that the data were correctly read and interpreted by the program.

Initially, running CLEANUP with INCOS test data on the TUCC IBM/370 detected only 8 eluants in the entire run. Closer examination of the data revealed that the average peak width for the INCOS runs extended over some 25 scans. Since the CLEANUP program derives its model singlets from a 7 scan window, not enough peak profile was available to obtain a good model shape (Figure 24). The simplest solution to this problem was to incorporate another parameter into the CLEANUP program which would average over a specified number of input spectra before any internal calculations were made. Once this modification was incorporated into CLEANUP, the same run was processed again, averaging over three spectra at a time. The results were much improved, showing a total of 72 eluants detected in the run (Figure 25).

After verification that the scan numbers of detected eluants agreed with the TIC plot (Figure 23) and checking the masses and intensities of detected eluants on the output tape against CLEANUP diagnostic printout, the task of duplicating this run with the same input tape on the UNIVAC computer was undertaken. A card copy of the CLEANUP source code was generated on the TUCC 370 and transported to the EPA UNIVAC when the source was recompiled and cross checking of its output. The chemist's printout of the test run on the UNIVAC is shown in Figure 26. The small discrepancies between this printout and the chemist's printout generated at TUCC are of a round-off type arising from hardware differences (i.e. word length, floating point arithmetic) between the two machines. These differences are too small to affect the performance of CLEANUP.

A second problem of greater concern occurred when trying to process multiple runs on a single tape with the EPA UNIVAC. Problems were encountered either when attempting to write a file mark at the end of

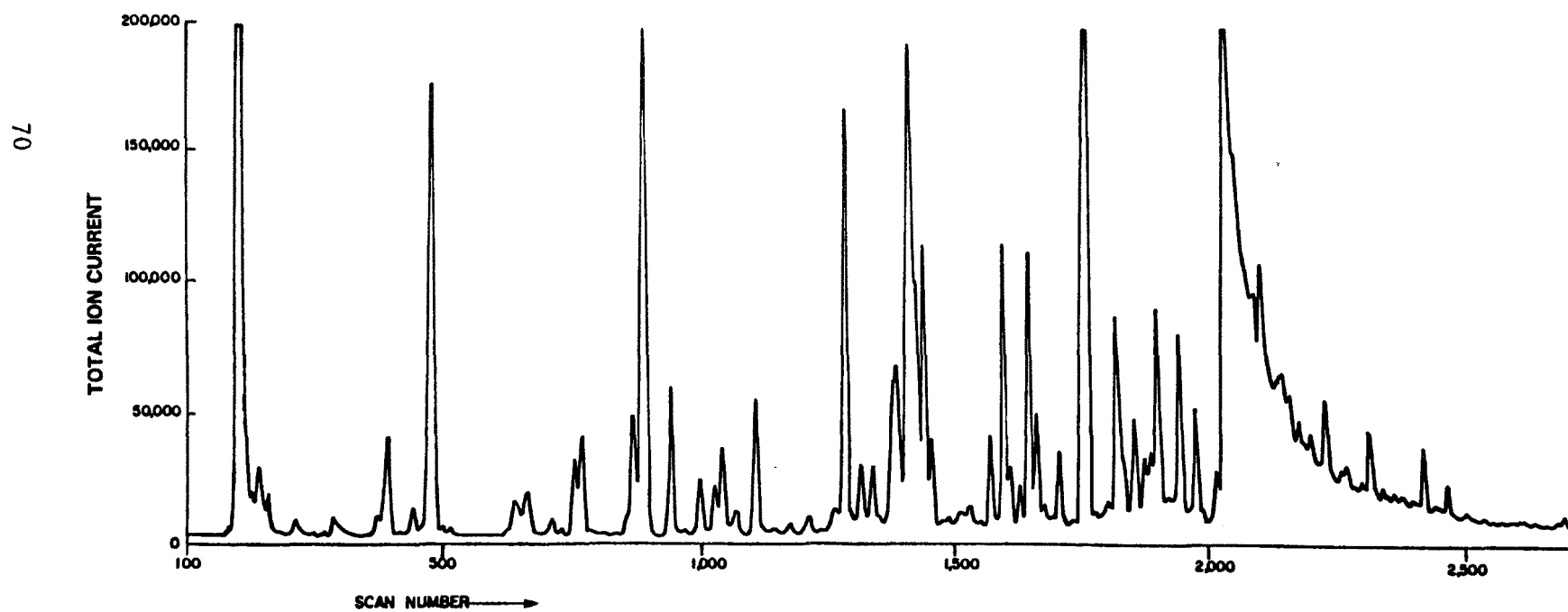
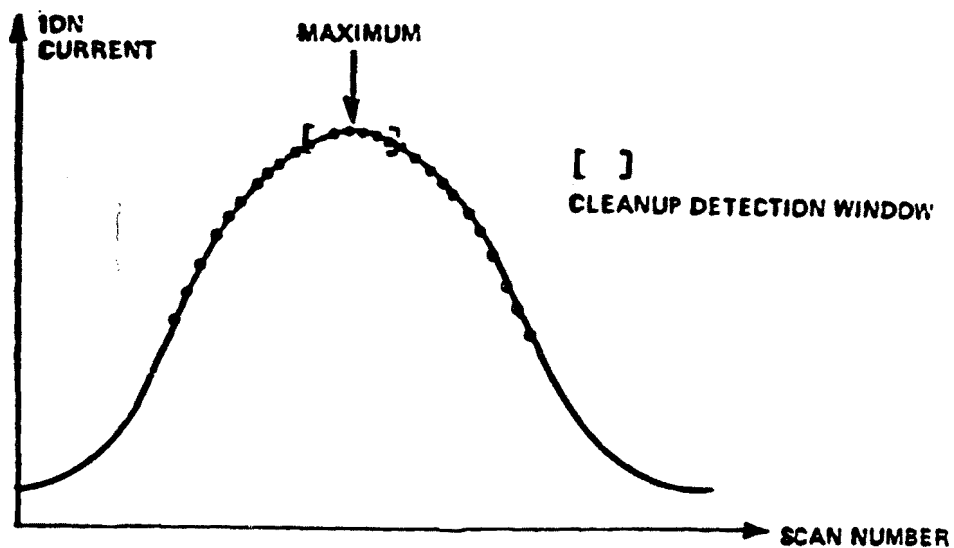
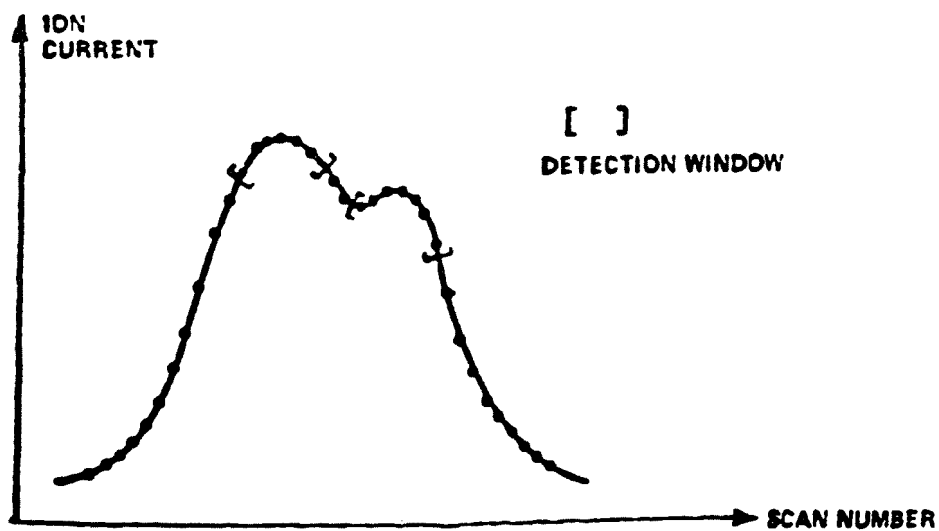


Figure 23. Raw TIC of INCOS test data.



VALID PEAK DISCARDED DUE TO FAILURE OF LINEAR ERROR RATIO TEST



DOUBLET INCORRECTLY INTERPRETED AS TWO SINGLETs

Figure 24. Possible consequences of scan rate too rapid for CLEANUP.

SLUT	SPEC.#	TUTION	TICRAI	MAX. AMP	DOUBLET?	SAT. PEAKS
1	85	1936.	31	1775.	NO	0
2	97	166999.	57	104876.	NO	0
3	130	2347.	13	1197.	YES	0
4	142	14250.	47	4738.	NO	0
5	145	14453.	51	8170.	NO	0
6	169	2224.	33	1366.	NO	0
7	217	4049.	54	2213.	NO	0
8	442	5897.	44	2573.	NO	0
9	475	147816.	92	53347.	NO	0
10	499	1770.	25	857.	NO	0
11	658	13973.	72	5954.	NO	0
12	709	6051.	65	1896.	NO	0
13	856	5265.	45	1925.	YES	0
14	866	41455.	99	9156.	NO	0
15	886	166097.	91	41310.	NO	0
16	904	1142.	23	561.	NO	0
17	940	47802.	98	19716.	NO	0
18	967	1046.	18	359.	NO	0
19	1066	4617.	37	1066.	NO	0
20	1108	44296.	99	13477.	NO	0
21	1150	1070.	18	400.	NO	0
22	1216	4953.	51	1057.	NO	0
23	1265	87303.	59	24632.	YES	0
24	1288	69335.	55	24065.	NO	0
25	1321	18167.	69	5751.	NO	0
26	1381	7455.	12	4126.	YES	0
27	1384	35357.	59	10480.	NO	0
28	1387	3959.	6	2111.	NO	0
29	1390	32665.	50	15483.	NO	0
30	1417	116639.	73	32767.	YES	0
31	1420	16945.	13	8773.	YES	0
32	1429	61522.	67	12418.	NO	0
33	1435	5456.	13	2191.	NO	0
34	1444	74565.	73	18173.	NO	0
35	1513	3418.	26	950.	YES	0
36	1522	2746.	24	520.	YES	0
37	1534	4649.	33	2156.	NO	0
38	1576	29853.	97	12032.	NO	0
39	1600	60520.	61	18903.	NO	0
40	1636	11792.	64	4708.	NO	0
41	1648	1246.	1	677.	NO	0
42	1651	77545.	84	16005.	NO	0
43	1666	19490.	45	11114.	NO	0
44	1681	2603.	18	663.	NO	0
45	1711	24234.	72	7455.	NO	0
46	1759	440631.	90	68273.	NO	0
47	1822	69229.	98	21607.	YES	0
48	1831	14281.	44	2935.	NO	0
49	1837	7724.	29	4362.	NO	0
50	1876	1203.	3	491.	YES	0
51	1897	4384.	6	1063.	YES	0
52	1903	60098.	93	8852.	NO	0
53	1906	10533.	27	3897.	NO	0
54	1939	4987.	11	909.	YES	0
55	1945	56164.	88	15042.	NO	0
56	1978	36425.	95	9039.	NO	0
57	2020	11452.	49	3519.	YES	0
58	2029	227926.	81	32760.	NO	0
59	2050	3858.	2	1514.	NO	0
60	2104	31191.	31	7311.	NO	0

Figure 25. Chemist's printout of EPA test run generated at TUCC.

SLOT	SPEC.#	TOTION	TICRAT	MAX. AMP	DOUBLET?	SAT. PEAKS
1	85	1938.	31	1775.	NO	0
2	97	167000.	57	104876.	NO	0
3	130	2347.	13	1197.	YES	0
4	142	14250.	47	4738.	NO	0
5	145	14453.	51	8170.	NO	0
6	169	2224.	33	1366.	NO	0
7	217	4049.	54	2213.	NO	0
8	442	5897.	44	2573.	NO	0
9	475	147816.	92	53347.	NO	0
10	499	1770.	25	857.	NO	0
11	658	13973.	72	5954.	NO	0
12	709	6052.	65	1898.	NO	0
13	856	5285.	45	1925.	YES	0
14	868	41455.	99	9156.	NO	0
15	886	166097.	91	41310.	NO	0
16	904	1143.	23	562.	NO	0
17	940	47802.	98	19716.	NO	0
18	967	1046.	18	359.	NO	0
19	1066	4617.	37	1068.	NO	0
20	1108	44296.	99	13477.	NO	0
21	1150	1070.	18	400.	NO	0
22	1216	4953.	51	1057.	NO	0
23	1285	87303.	59	24832.	YES	0
24	1288	69335.	55	24065.	NO	0
25	1321	18167.	69	5751.	NO	0
26	1381	7455.	12	4126.	YES	0
27	1384	35358.	59	10481.	NO	0
28	1387	3959.	6	2111.	NO	0
29	1390	32685.	50	15483.	NO	0
30	1417	116839.	73	32767.	YES	0
31	1420	16945.	13	8773.	YES	0
32	1429	61523.	67	12418.	NO	0
33	1435	5456.	13	2191.	NO	0
34	1444	74385.	73	18173.	NO	0
35	1513	3418.	28	950.	YES	0
36	1522	2746.	24	520.	YES	0
37	1534	4649.	33	2156.	NO	0
38	1576	29853.	97	12032.	NO	0
39	1600	60520.	61	18903.	NO	0
40	1636	11792.	64	4708.	NO	0
41	1648	1246.	1.	677.	NO	0
42	1651	77546.	84	16003.	NO	0
43	1666	19490.	45	11114.	NO	0
44	1681	2603.	18	663.	NO	0
45	1711	24234.	72	7455.	NO	0
46	1759	440632.	90	68274.	NO	0
47	1822	69229.	98	21607.	YES	0
48	1831	14281.	44	2935.	NO	0
49	1837	7724.	29	4362.	NO	0
50	1876	1203.	3	491.	YES	0
51	1897	4384.	6	1083.	YES	0
52	1903	60098.	93	8852.	NO	0
53	1906	10533.	27	3897.	NO	0
54	1939	4987.	11	909.	YES	0
55	1945	56184.	88	15042.	NO	0
56	1978	36425.	95	9039.	NO	0
57	2020	11452.	49	3519.	YES	0
58	2029	227926.	81	32760.	NO	0
59	2050	3858.	2	1514.	NO	0
60	2104	31191.	31	7311.	NO	0
61	2134	2738.	4	1084.	YES	0
62	2140	1990.	3	850.	NO	0
63	2179	8014.	19	3174.	NO	0
64	2200	2661.	6	607.	NO	0
65	2227	14861.	27	3754.	NO	0
66	2266	5288.	17	2042.	NO	0
67	2314	18434.	43	5317.	NO	0
68	2341	2516.	12	643.	NO	0
69	2422	21199.	84	10656.	NO	0
70	2455	1045.	7	657.	NO	0
71	2467	10041.	43	2636.	NO	0
72	2698	3222.	29	835.	NO	0

Figure 26. Chemist's printout of EPA test run.

the output cleaned up spectra tape or when attempting to locate the beginning of a subsequent run on the input test tape. Because it was possible to detect file marks separating the three runs on the EPA test tape at TUCC with no difficulty, it was concluded that the problem lay with the UNIVAC. Notwithstanding that the systems staff for the EPA UNIVAC have been alerted to these difficulties, we recommend that for the present CLEANUP runs on the UNIVAC be limited to one input and output file per tape.

SECTION 6

USER DESCRIPTION OF PROGRAM OPERATION

The final phase of implementing CLEANUP in the EPA environment consisted of testing the output tape written by the UNIVAC on the contracting agency's INCOS acquisition system. Although numerous problems were encountered, they were all of a systems oriented nature (incorrect tape density, incomplete format information, etc.) which commonly occur with machine transfer. No internal algorithm changes to the CLEANUP program were necessary in order to successfully read the test tape and obtain plausible output spectra with the INCOS software.

A user oriented description for running CLEANUP on the UNIVAC follows. To execute CLEANUP at the UNIVAC, it is necessary to deliver two tapes (one containing the INCOS raw input spectra and one for the output spectra) along with a card deck containing program control information (Figure 27). Cards 1 through 5 and 19 through 25 comprise the Executive Control Language necessary for the UNIVAC system to recognize and run the CLEANUP program. Of these, it is necessary to change the underlined portions of cards 19 and 20 with each run because they specify the tape serial numbers for CLEANUP to use. Cards 21 and 22 specify the positions of the data sets on the input and output tapes - in this example the input is read from the second file of tape B003KK and the output is written to the third file of tape B334KK. Cards 21 and 22 should be omitted if only one run is present on the input tape, and the cleaned up run is to be written on the beginning of the output tape. Card 1 - the "run" card contains the job name (CLNP) and the maximum time estimate in minutes (5). Although none of the present tests exceeded three minutes, it is conceivable that an increase of the time requirement could become necessary in the future.

@RUN 26CLNP/45/2,64026SA010/KJK,5A010,5	1
@PASSWD KJK	2
@ASG,A A.	3
@ASG,T 4. . CONTAINS THE CONTROL CARD DATA	4
@DATA,I 4. . THE ACTUAL CONTROL CARD DATA FOLLOWS	5
1 CLEANUP PRINT FLAG (IN 11)	6
0 DEBUG PRINT SWITCH IN 11 (0=NO,1=YES)	7
3 NUMBER OF INPUT SPECTRA TO AVERAGE (IN 12)	8
6 MINIMUM THIRDS BETWEEN ELUANTS (IN 11)	9
2 DETECTION WINDOW (IN 14)	10
1000 MINIMUM FOR LESS THAN 5 PEAKS (IN 16)	11
1000 MINIMUM FOR MORE THAN 4 PEAKS (IN 16)	12
.0000 MINIMUM QUALIFYING RATE (IN F8.4)	13
.0350 ERROR RATIO (IN F8.4)	14
2 POINTS TO LEFT OF MODE (IN 13)	15
3 POINTS TO RIGHT OF MODE (IN 13)	16
130000 SATURATION VALUE (IN F6.0)	17
@END	18
@ASG,TJH 7.,16D/////0,B003KK . INPUT TAPE	19
@ASG,TJH/W 9.,16D/////0,B334KK . OUTPUT TAPE	20
@MOVE 7.,1 .SKIP 1 FILE ON INPUT TAPE-USE 2ND FILE	21*
@MOVE 9.,2 .SKIP 2 FILES ON OUTPUT TAPE-USE 3RD FILE	22*
@XOT,F A.CLEANUP	23
@MARK 9. . PUT A 'SAFETY' END OF FILE ON OUTPUT TAPE	24
@FIN: . END OF RUN	25

*omit until multiple run processing is implemented.

Figure 27. Example of CLEANUP control cards for EPA UNIVAC.

Cards 6 through 17 comprise the control cards used by the CLEANUP program. It is important to note that the variables shown here have been optimized with respect to the EPA test data taken on the INCOS system and hence differ from those in Table 7 which were optimized with respect to the VARIAN CH-7 at RTI. The most important difference is the additional control card (card 8) which instructs CLEANUP to average over 3 spectra. Also the instrument saturation value was changed to 130,000 (card 17), the minimum thirds between ellutants was increased from 3 to 6 (card 9), and the error ratio requirement was reduced from .0756 to .035 (card 14). The changes in minimum thirds and error ratio were made in order to accommodate the wider peak width and smoother data generated on the INCOS system.

SECTION 7

DELIVERY TO EPA

Accompanying this report are listings of the CLEANUP program which currently is being run on the UNIVAC, completing Phase IV of the contract. A backup tape of the same programs will be kept by RTI as well as the version of CLEANUP at TUCC which runs on INCOS tapes.

It still will be necessary for the contracting agency to carry out a series of test runs in order to determine the best operating parameters for CLEANUP. The system will respond differently to data derived from different mass spectrometers, as well as data run under differing GC conditions.

The program affords considerable flexibility in operation by the suitable adjustment of variable input parameters. These will still need to be exercised until optimum operational conditions are determined.

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4. "Extraction of Mass Spectra Free of Background and Neighboring Component Contributions from Gas Chromatography/Mass Spectrometry Data," R. G. Dromey, M. J. Stefik, T. C. Rindfleisch, and A. M. Duffield, *Anal. Chem.*, 48, 1368 (1976).
5. Stephen M. Pizer, "Numerical Computing and Analysis," Science Research Associates, Inc., Chicago, 1975, p. 358ff.

APPENDIX A
CLEANUP SOURCE LISTING

```

C      SUBROUTINE EPARD
C
C      THIS ENTRY POINT READS ONE SCAN'S WORTH OF DATA PER CALL AND RETURNS
C      IT TO THE CALLING ROUTINE IN COMMON BLOCKS IHDR AND INDATA.
C
C      COMMON /HDR1/ NAME,HDRFLG,DATE,RUNHR,RUNMIN
C      COMMON /HDR2/ SAMPID,INAM
C      COMMON /HDR3/ RUNCON,SECSCN
C      COMMON /HDR4/ BUF4,LOPMAS,HIPMAS
C      COMMON /IHDR/ JNAM,ISCN,IDBUF,IDHR,IDMIN,IRTMIN,IRTSEC,INMBAS,
C      * IRBAS,IRTIC
C      COMMON /INDATA/ INBUF,INSEQ,NIN
C      COMMON /QHDR/ ONAM,OSCN,ODBUF,ODHR,ODMIN,ORTMIN,ORTSEC,ONMBAS,
C      * ORBAS,ORTIC
C      COMMON /OTDATA/ OTBUFF,OTSEQ,NOUT
C      COMMON /FLAGS/ EOF
C      COMMON /UNITS/ IRDR,IPTR1,IPTR2,IPTR3,IIN,IOUT
C      COMMON /IOBUF/ ITBUF1,CNTIN,CNTOUT,IOERR,ITBUF2
C      INTEGER*4 NAME(3),HDRFLG,DATE(2),RUNHR,RUNMIN,SAMPID(16),INAM(2),
C      * RUNCON(16),BUF4(11),LOPMAS,HIPMAS,JNAM(3),ONAM(3),ISCN,OSCN,
C      * IDBUF(2),ODBUF(2),IDHR,ODHR,IDMIN,ODMIN,IRTMIN,ORTMIN,IRTSEC,
C      * ORTSEC,INMBAS,ONMBAS,EOF
C      * INSEQ,OTSEQ,NIN,NOUT,INBUF(411),OTBUFF(411)
C      INTEGER*4 RCDLEN/80/,CNTIN,CNTOUT,ITBUF1(20),IBLANK/4H /,
C      * INSPC(26),IDD(11),OTSPC(26),SCNEND/0/,ITBUF2(20)
C      INTEGER*4 OTSPCX(3,26),OTSEQX,OTSEQY
C      REAL*4 SECSCN,ORBAS,IRBAS,IRTIC,ORTIC
C
C      SET SCAN FLAG, COUNTER.
C
C      SCNEND=0
C      NIN=0
C
C      CLEAR TRANSFER ARRAY IN 'INDATA' BLOCK.
C
C      DO 5 I=1,411
C      5 INBUF(I)=0
C
C      CALL BLKRD TO BRING A LOGICAL RECORD INTO THE BUFFER.
C
C      CALL BLKRD
C      IF (IOERR.LT.0) GO TO 1000
C
C      DECODE A LOGICAL RECORD (ASSUMED TO BE A SCAN HEADER).
C
C      DECODE(RCDLEN,5000,ITBUF1) JNAM,IDD(1),ISCN,IDD(2),IDBUF,IDHR,
C      * IDD(3),IDMIN,IDD(4),IDD(5),IRTMIN,IDD(6),
C      * IRTSEC,IDD(7),IDD(8),INMBAS,IDD(9),IRBAS,IDD(10),IDD(11),IRTIC
C      5000 FORMAT(3A4,A1,15,A2,2A4,13,A1,12,A4,A1,13,A1,12,A4,A2,14,A1,F9.0,
C      * A4,A1,F10.0)
C
C      STOP IF NEW HEADER FOR RUN IS ENCOUNTERED. (ISCN=0)
C
C      IF (ISCN.EQ.0) GO TO 110
C
C      HANDLE SPECTRUM RECORD(S). AT LEAST ONE IS ASSUMED TO BE PRESENT.

```

C		00036310
C	CHECK BUFFER VIA POINTERS TO DETERMINE AMOUNT OF REMAINING DATA.	00036320
C	RETURN HERE IF MORE THAN ONE SCAN RECORD.	00036330
C		00036340
C	45 CALL BLKRD	00036350
C	IF (IOERR.LT.0) GO TO 2000	00036360
C		00036370
C	DECODE A SPECTRUM RECORD.	00036380
C		00036390
C	80 CONTINUE	00036400
C		00036430
C	DECODE(RCDLEN,5005,ITBUF1) INSPC,INSEQ	00036450
C		00036460
C	5005 FORMAT(2613,12)	00036470
C		00036480
C	STORE THIS RECORD'S DATA IN INBUF USING SPECTRUM MASS AS INDEX OF IN	00036490
C		00036510
C	DO 86 I=1,25,2	00036520
C	J=I+1	00036530
C	L=INSPC(I)	00036540
C	IF (L.NE.0) GO TO 83	00036550
C	SCNEND=1	00036560
C	GO TO 86	00036570
C	83 L=L-39	00036580
C	IF (L.LT.1.OR.L.GT.411) GO TO 86	00036590
C	INBUF(L)=INSPC(J)	00036600
C	NIN=NIN+1	00036610
C	86 CONTINUE	00036620
C		00036630
C	CHECK WHETHER END-OF-SCAN ENCOUNTERED (MASS VALUE = 0).	00036640
C		00036650
C	IF (SCNEND.EQ.0) GO TO 45	00036660
C		00036670
C	RETURN WHEN SCAN ENDS (SCNEND = 1).	00036680
C		00036690
C	SCNEND=SCNEND+1	00036700
C	RETURN	00036710
C		00036720
C	ENTRY POINT FOR WRITING OUTPUT TAPE FOR INCOS USE.	00036730
C		00036740
C	ENTRY EPAURT	00036750
C		00036760
C	WRITE SCAN HEADER TO TEMPORARY BUFFER FROM COMMON BLOCK OHDR.	00036770
C		00036780
C		00036850
C	ENCODE(RCDLEN,5000,ITBUF2) ONAM,IDD(1),OSCN,IDD(2),ODBUF,ODHR,	00036190
C	* IDD(3),ODMIN,IDD(4),IDD(5),ORTMIN,IDD(6),	00036200
C	* ORTSEC,IDD(7),IDD(8),ONMBAS,IDD(9),ORBAS,IDD(10),IDD(11),ORTIC	00036880
C		00036890
C	MOVE ENCODED HEADER RECORD TO OUTPUT BUFFER. WRITE A FULL BUFFER AS	00036900
C	REQUIRED VIA NTRAN (CALLED FROM SUBROUTINE BLKWRT).	00036910
C		00036920
C	CALL BLKWRT	00036930
C		00036940
C	STORE ODBUFF (PROCESSED OUTPUT SCAN) IN OTJPC AS MANY TIMES AS	00036950

C	WHEN OTSPC IS FULL. IT IS ENCODED INTO ITBUF2.	00036970
C	J=-1	00036980
	OTSEQ=1	00036990
	DO 87 I=1,26	00037000
	OTSPC(I)=0	
	DO 87 M=1,3	
	87 OTSPCX(M,I)=0	
	DO 100 I=1,411	
C		00037010
C	LOOP ENDING AT 100 USES J & L AS INDICES TO OTSPC;	00037020
C		00037030
C	DATA IN OTSPC ARE:	00037040
C	MASS (I+39, WHERE 'I' IS THE INDEX OF OTBUFF);	00037050
C	AND INTENSITY, THE CONTENTS OF OTBUFF(I).	00037060
C		00037070
C	MASS IS STORED IN OTSPC(J) AND INTENSITY IS STORED IN OTBUFF(L),	00037080
C	WHERE L = J + 1.	00037090
C		00037100
	IF (OTBUFF(I).LE.0) GO TO 100	00037110
	J=J+2	00037120
	L=J+1	00037130
	OTSPC(J)=I+39	00037140
	OTSPC(L)=OTBUFF(I)	00037150
	IF (J.LT.25) GO TO 100	00037160
C		00037170
C	ENCODE SCAN DATA FROM OTSPC TO ITBUF2.	00037180
C		00037190
C		00037200
	DO 88 M=1,26	00037250
	I1=OTSPC(M)	
	I2=I1/100	
	I3=I1/10-I2*10	
	I4=I1-I3*10-I2*100	
	OTSPCX(1,M)=I2	
	OTSPCX(2,M)=I3	
	88 OTSPCX(3,M)=I4	
	OTSEQX=OTSEQ/10	
	OTSEQY=OTSEQ-OTSEQX*10	
	ENCODE(RCDLEN,5040,ITBUF2) OTSPCX,OTSEQX,OTSEQY	
	5040 FORMAT(80I1)	
C		00037270
C	TRANSFER CARD IMAGE IN ITBUF2 TO OUTPUT BUFFER IN SUBROUTINE BLKWRT.	00037280
C		00037290
C	CALL BLKWRT	00037300
C		00037310
C	CLEAR OTSPC AND INCREMENT OTSEQ.	00037320
C		00037330
	DO 90 K=1,26	00037340
	OTSPC(K)=0	00037350
	DO 90 M=1,3	00037360
	90 OTSPCX(M,K)=0	
	OTSEQ=OTSEQ+1	
	J=-1	
	100 CONTINUE	00037370
C		00037380
		00037390
C	SOME DATA REMAINS IN OTSPC (EVEN IF IT IS END-OF-SCAN ZEROS):	00037400
		00037410

C	WRITE IT OUT.	00037420
C		00037490
	DO 103 M=1.26	
	11=OTSPC(M)	
	12=11/100	
	13=11/10-12*10	
	14=11-13*10-12*100	
	OTSPCX(1,M)=12	
	OTSPCX(2,M)=13	
	OTSPCX(3,M)=14	
103	CONTINUE	
	OTSEQX=OTSEQ/10	
	OTSEQY=OTSEQ-OTSEQX*10	
	ENCODE(RCDLEN,5040,ITBUF2) OTSPCX,OTSEQX,OTSEQY	
C		00037510
C	TRANSFER SCAN RECORD FROM ITBUF2 TO OUTPUT BUFFER.	00037520
C		00037530
	CALL BLKWRT	00037540
	RETURN	00037550
	ENTRY EPAHDR	00037560
C		00037570
C	ENTRY POINT TO READ FILE HEADER RECORDS (4) AND TRANSFER TO OUTPUT	00037580
C	BUFFER.	00037590
C		00037600
C	HERE WE CHECK FOR A PREVIOUS EOF...	00037610
	IF (EOF.EQ.0) GO TO 105	00037620
	EOF=1	00037630
	RETURN	00037640
105	CONTINUE	00037650
	CALL BLKRD	00037660
	IF (IOERR.LT.0) GO TO 2000	00037670
110	CONTINUE	
C		00037740
	DECODE(RCDLEN,5010,ITBUF1) NAME,HDRFLG,DATE,RUNHR,RUNMIN	00037750
5010	FORMAT(3A4,1X,15,2X,2A4,13,1X,12,46X)	
C		00037760
	DO 120 I=1,20	00037770
120	ITBUF2(I)=ITBUF1(I)	00037780
	CALL BLKWRT	00037790
	CALL BLKRD	00037800
	IF (IOERR.LT.0) GO TO 2000	00037810
C		00037880
	DECODE(RCDLEN,5015,ITBUF1) SAMPID,INAM	00037890
5015	FORMAT(16A4,10X,A4,A2)	
C		00037900
	DO 130 I=1,20	00037910
130	ITBUF2(I)=ITBUF1(I)	00037920
	CALL BLKWRT	00037930
	CALL BLKRD	00037940
	IF (IOERR.LT.0) GO TO 2000	00037950
C		00038020
	DECODE(RCDLEN,5020,ITBUF1) RUNCON,SECSCN	00038030
5020	FORMAT(16A4,10X,F6,2)	
C		00038040
	DO 140 I=1,20	00038050
140	ITBUF2(I)=ITBUF1(I)	00038060
	CALL BLKWRT	00038070
	CALL BLKRD	00038080

C	IF (IOERR.LT.0) GO TO 1000	00038090
	DECODE(RCDLEN,5025,ITBUF1) BUF4.LOPMAS,HIPMAS	00038160
5025	FORMAT(6X,2A4,6X,2A4,6X,2A4,6X,5A4,5X,13,1X,13)	00038170
C	DO 150 I=1,20	00038180
150	ITBUF2(I)=ITBUF1(I)	00038190
	CALL BLKWRT	00038200
	RETURN	00038210
C	END-OF-FILE PROCESSING (IOERR < 0).	00038220
C	1000 IF (IOERR.NE.-2) GO TO 2000	00038230
	EOF=1	00038240
	CALL BLKWRT	00038250
	CALL NTRAN\$(IOUT,9,22)	00038260
	WRITE(IPTR1,5030) CNTIN,CNTOUT,EOF	00038270
5030	FORMAT(' AT EOF CNTIN =',16,' CNTOUT =',16,' EOF = ',110)	00038280
	RETURN	00038290
C	ERROR PROCESSING.	00038300
C	IOERR<-2	00038310
C	2000 EOF=-IOERR	00038320
	CALL BLKWRT	00038330
	CALL NTRAN\$(IOUT,9,22)	00038340
	WRITE(IPTR1,5035) CNTIN, CNTOUT, EOF	00038350
5035	FORMAT(' AT ERROR CNTIN =',16,' CNTOUT =',16,' EOF = ',110)	00038360
	RETURN	00038370
	END	
	SUBROUTINE BLKRD	
C	THIS SUBROUTINE TRANSFERS INPUT DATA FROM THE INCOS TAPE OF 128-WORD	00038430
C	(512-CHARACTER) BLOCKS INTO A 20-WORD (80-CHARACTER) BUFFER.	00038440
C	WHEN THE NTRAN BUFFER NO LONGER CONTAINS ENOUGH DATA FOR ONE LOGICAL	00038450
C	RECORD (<20 WORDS), THE TAIL OF THE BUFFER IS WRAPPED AROUND TO THE	00038460
C	BEGINNING OF THE BUFFER AND A NEW BLOCK READ INTO THE END OF THE	00038470
C	BUFFER VIA A CALL TO NTRAN\$.	00038480
C	COMMON /UNITS/ IRDR,IPTR1,IPTR2,IPRT3,IIN,IOUT	00038490
	COMMON /IDBUF/ ITBUF1,CNTIN,CNTOUT,IOERR,ITBUF2	00038500
	INTEGER*4 ITBUF1(20), CNTIN,CNTOUT,IOERR,ITBUF2(20)	00038510
	INTEGER*4 IISTRT/1/, BLKLEN/128/,RCDLEN/20/,IIEND/0/.	00038520
	* IBUF(148)	00038530
C	CHECK STARTING POSITION IN BUFFER. IF IISTRT > (IIEND-RCDLEN+1)	00038540
C	READ A NEW BLOCK.	00038550
C	IF (IISTRT.LE.(IIEND-RCDLEN+1)) GO TO 40	00038560
C	IF (IISTRT.EQ.(IIEND+1)) GO TO 20	00038570
C	IF BUFFER HAS INSUFFICIENT DATA TO READ, MOVE RECORD TO BEGINNING OF	00038580
C	BUFFER AND STRING A NEW INPUT BLOCK BEHIND IT.	00038590
C	J=0	00038600
	DO 10 I=IISTRT,IIEND	00038610
	J=J+1	00038620

10	IBUF(J)=IBUF(I)	00038700
	IISTRT=J+1	00038710
	GO TO 30	00038720
20	IISTRT=1	00038730
C		00038740
C	CALL BLOCK READ SUBROUTINE (SIMULATED FOR IBM 370 TESTING).	00038750
C		00038760
30	CALL NTRAN\$(IIN,3,BLKLEN,IBUF(IISTRT),IOERR,22)	00038770
	CNTIN=IISTRT+1	00038780
C		00038790
C	UPDATE BUFFER LENGTH TO REFLECT NEWLY READ DATA.	00038800
C		00038810
	IIEND=IISTRT+BLKLEN-1	00038820
	IISTRT=1	00038830
C		
C	PROCESS NEXT LOGICAL RECORD.	
C		
40	J=0	00038840
	IEND=IISTRT+19	00038850
	DO 50 I=IISTRT,IEND	00038860
	J=J+1	00038870
	ITBUF1(J)=IBUF(I)	00038880
50	CONTINUE	00038890
C	CALL TRACE(IISTRT)	00038900
	IISTRT=IEND+1	00038910
	RETURN	00038920
	END	00038930
	SUBROUTINE BLKWRT	00038940
C		00038950
C	THIS SUBROUTINE FILLS A 512-CHARACTER (128-WORD) OUTPUT BUFFER	00038960
C	WITH 80-CHARACTER RECORDS. WRAPAROUND IS USED TO MAKE THE BUFFER	00038970
C	COMPLETELY FULL AS REQUIRED BY INCOS. THE BLOCKS, WHEN FULL, ARE	00038980
C	ACTUALLY WRITTEN ON TAPE BY SUBROUTINE NTRAN\$.	00038990
C		00039000
	COMMON /UNITS/ IRDR,IPTR1,IPTR2,IPRT3,IIN,IOUT	00039010
	COMMON /FLAGS/EOF	00039020
	COMMON /IOBUF/ ITBUF1,CNTIN,CNTOUT,IOERR,ITBUF2	00039030
	INTEGER*4 ITBUF1(20), CNTIN,CNTOUT,IOERR,ITBUF2(20)	00039040
	INTEGER*4 IBUF(20), OBUF(148)/148*4H /,BLKLEN/128/,	00039050
	* RCDLEN/80/,IOSTRT/1/,IBLANK/4H /,IOEND/20/	00039060
	EQUIVALENCE (IBUF(1),ITBUF2(1))	00039070
C		00039080
C	CHECK TO SEE WHETHER BUFFER IS ALREADY FULL TO 512 CHARACTERS.	00039090
C		00039100
C	ALSO, PUT OUT THE LAST BLOCK(S) (THERE MAY BE TWO REQUIRED) AT END-	00039110
C	OF-FILE OR ERROR IN READING OR WRITING.	00039120
	IF (IOSTRT.GT.128.OR.EOF.NE.0) GO TO 30	00039140
C		00039150
C	STORE FILLED TRANSFER BUFFER INTO OUTPUT BUFFER OBUF.	00039160
C		00039170
10	IOEND=IOSTRT+19	00039180
	J=0	00039190
	DO 20 I=IOSTRT,IOEND	00039210
	J=J+1	00039220
20	OBUF(I)=IBUF(J)	00039230
	IOSTRT=IOEND+1	00039240
	RETURN	00039250
C		00039260

C	UPON ENTERING AND FINDING A FULL BUFFER, WRITE IT TO TAPE.	00039270
C	30 CALL NTRANS(IOUT,1,BLKLEN,OBUF(1),IDERR,22)	00039280
	31 CNTOUT=IOUT+1	00039290
C	ADJUST CONTENTS OF OBUF SO THAT IT CONTAINS THE UNWRITTEN PORTION OF	00039300
C	A 80-CHARACTER RECORD. FILL THE REST OF OBUF WITH BLANKS.	00039310
C	32 IOSTRT=1	00039320
	33 IF (IEND.LE.128) GO TO 50	00039330
	34 J=0	00039340
	DO 40 I=129,IEND	00039350
	J=J+1	00039360
	40 OBUF(J)=OBUF(I)	00039370
	IOSTRT=J+1	00039380
	IEND=J	00039390
		00039400
	STORE BLANKS IN REMAINDER OF OBUF.	00039410
		00039420
	50 DO 60 I=IOSTRT,148	00039430
	60 OBUF(I)=IBLANK	00039440
		00039450
	GET THE LAST BIT OF DATA ONTO TAPE IF EOF OR ERROR.	00039460
	IF (IEND.LT.IOSTRT.AND.EOF.GT.0) GO TO 30	00039470
	IF (EOF.EQ.0) GO TO 10	00039480
	OTHERWISE, FINISHED.	00039510
		00039520
	RETURN	00039530
	END	00039540
	BLOCK DATA	00039550
	COMMON /FLAGS/ EOF	00039560
	INTEGER*4 EOF/0/	00039570
	COMMON /IOBUF/ ITBUF1,CNTIN,CNTOUT,IDERR,ITBUF2	00039770
	INTEGER*4 ITBUF1(20),CNTIN,CNTOUT,IDERR,ITBUF2(20)	00039780
	DATA CNTIN/0/,CNTOUT/0/,ITBUF1/20*4H /,IDERR/0/,	00039790
	ITBUF2/20*4H /	00039800
	END	00039810
C	THIS SUBROUTINE WAS CALLED ONLY FROM CUEXEC SO	00039820
C	CUEXEC WAS ELIMINATED AND ITS STATEMENTS WERE	00000010
C	INSERTED IN GCMSOL WHICH WAS IN TURN MADE THE MAIN PGM.	00000020
C	WM.F. HARGROVE 9/30/77	00000030
C..	SUBROUTINE GCMSOL(CLNFLG)	00000040
	INTEGER CLNFLG	00000050
C	THIS COMPUTER PROGRAM WAS DEVELOPED WITH THE FUNDING SUPPORT	00000060
C	FROM THE NATIONAL INSTITUTES OF HEALTH (GRANTS RR-612 AND	00000070
C	GM-20832) AND THE NATIONAL AERONAUTICS AND SPACE ADMINISTRATION	00000080
C	(GRANT NGR-05-020-632).	00000090
	INTEGER MASBUF(6),VALBUF(6),AJACEN,AHEAD,ISO(1000)	00000100
	INTEGER NAME,RDATE,BITMAP,GCTIME,LIBMAP,INTEG.LOMASS,MAD,ADS	00000110
	INTEGER HIMASS,POINTS,TAPCNT,MAXSP,LSTCNT,DEVICE,SPCNO	00000120
	INTEGER LSTMIN,SPEC,IND,IR,BK,NM,NTM,PNAME(32)	00000130
	INTEGER HIST(10),UNIT,NNAME(18),IRNO	00000140
	INTEGER NUSPEC,NMASS,OVLAP,EXPNAM,SRLB(5),SECOND	00000150
	INTEGER ODUBLT,QSATS,NLINE,RAWBUF,FSTPGE,FSTREC	00000160
	INTEGER SATLST,SATINX,PASS1,ITOM,EOF	00000170
	INTEGER GPEAK,SPARE1,SPARE2,SPARE3,SPARE4,SPARE7	00000180
		00000190

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INTEGER*4 TIMREM,TIMCNT                                00000200
REAL      SPARE5,SPARE6                                00000210
REAL      ISVP8,ISVP9                                  00000220
REAL      QNORM                                         00000230
REAL*8    C4,C1,C2,SGX,SHX                             00000240
DIMENSION G(9),H(11),GNU(18),HNU(18)                 00000250
COMMON    PKHIST(20),NPHIST(20)                        00000260
COMMON    Y15,Y14,Y13,Y12,Y11,Y0,Y1,Y2,Y3,Y4,Y5      00000270
COMMON    GM4,GM3,GM2,GM1,G0,GP1,GP2,GP3,GP4         00000280
COMMON    SG,SG2,SIG,S1,S12,AN,AA,BB,CC,DD           00000290
COMMON    NAME(32),RDATE(5),BITMAP(64),GCTIME        00000300
COMMON    LIBMAP(17),INTEG,LOMASS,HIMASS,POINTS,TAPCNT 00000310
COMMON    MAXSP,LSTCNT,DEVICE(5),SPCNO               00000320
COMMON    SPEC(14,411),IND(3,411),NUSPEC(411),NMASS  00000330
COMMON    RMAX(3),IR(3),BK(3),NM(3),NTM(3),GPEAK(3,11) 00000340
COMMON    SPARE1,SPARE2,SPARE3,SPARE4,SPARE5,SPARE6,SPARE7 00000350
COMMON    RATMIN,RATEMX,SIGY0,SIGNXT,SIGLST          00000360
COMMON    ISVN8,ISVN9,ISVP8,ISVP9,SIGMA7,SATVAL,SATMAX 00000370
COMMON    MODE1,MODE2,NLWCUT,NUPCUT,SATPKS(25),NSAT,EXPNAM(5) 00000380
COMMON    /CSATLS/SATLST(25),SATINX                 00000390
COMMON    /CAHEA/AHEAD(5)                            00000400
COMMON    /PRNTFG/IPFLAG                             00000410
COMMON    /MODES/ SGMODE(3),SHMODE(3),GMODE,HMODE    00000420
COMMON    /MASSES/ ISGMAS(3),ISHMAS(3),IGMASS,IHMASS 00000430
COMMON    /ERRORS/RMASS,ERRMAX,NERR,SIGERR,SECOND(411) 00000440
COMMON    /IFF/IFLAG(3)                              00000450
COMMON    /AJACNT/AJACEN(2)                          00000460
COMMON    /BACKER/SUMG,SUMG2                         00000470
COMMON    /DUBBER/C4,C1,C2,SGX,SHX                  00000480
COMMON    /PARAMS/MINTIC,MINNY,NTHIRD,RATM          00000490
COMMON    /HIND/IH1,IH2,MSINGS(2,50),MINX,LINGS(50),LINX 00000500
COMMON    /DUBFLG/IDUB                               00000510
COMMON    /CRATMX/RATMX                               00000520
COMMON    /LFTRIT/ILEFT,IRIGHT                     00000530
COMMON    /DUBBUG/IDEBUG                            00000540
COMMON    /MONITOR/MONSPC,MONMAS                    00000550
COMMON    /SLOTNO/NSLOT                             00000560
COMMON    /CHEMPO/QDUBLT,QNORM,QSATS,NLINE          00000570
COMMON    /CFSTPG/FSTPGE                             00000580
COMMON    /CRAWBU/RAWBUF(411)                       00000590
COMMON    /LSD/PASS1                                 00000600
COMMON    /CFSTRE/FSTREC                             00000610
COMMON    /TOMS/ITOM                                  00000620
COMMON    /IMAD/MAD                                   00000630
COMMON    /IADS/ADS                                   00000640
COMMON    /NA/PNAME                                   00000650
COMMON    /UNITS/ IRDR,IPTR1,IPTR2,IPTR3,IIN,IOUT   00000660
C      IH1,IH2,IFLAG1,IFLAG2 USED IN TLOC AND ITS BRANCHES. 00000670
C HERE CLEANUP HAS BEEN GIVEN THE CAPABILITY OF MULTIPLE RUN 00000680
C PROCESSING - AND THE I/O UNIT NUMBERS HAVE BEEN PUT IN A 00000690
C COMMON BLOCK NAMED /UNITS/                          00000700
C                                                         00000710
C                                                         00000720
C                                                         00000730
C                                                         00000740
C                                                         00000750
C                                                         00000760
C                                                         00000770

                                WM F HARGROVE
                                11/29/78

IRDR=4
IPTR1=6
IPTR2=6
IPTR3=6
IIN=7

```

IOUT=9	00000780
IRNO=0	00000790
CALL CUPRNT(3,NPHIST,MASEUF,PKHIST,AVE,	00000800
1ERRMAX,ERR2,MODE1,MODE1,MODE2)	00000810
C GET CONTROL PARAMETERS - PARDIR HAS BEEN REWRITTEN AS OF	00000820
C 12/12/78 WFH - RTI	00000830
CALL PARDIR	00000840
C OPEN PRIMARY INPUT AND OUTPUT FILES	00000850
CALL OPNFIL	00000860
C START OF RUN PROCESSING LOOP	00000870
35 IRNO=IRNO+1	00000880
EOF=0	00000890
MU=0	00000900
IH1 = 1	00000910
IH2 = 2	00000920
IFLAG(1) = 0	00000930
IFLAG(2) = 0	00000940
TAPCNT = 0	00000950
AJACEN(2) = 0	00000960
C THIS MOD INSERTED TO HELP WITH UNINITIALIZED G ARRAY	00000970
C DOWN INSIDE SATLSQ.	00000980
C RTI WFH 11/21/78	00000990
DO 17 I=1.9	00001000
17 G(I)=0.0	00001010
DO 10 I = 1.5	00001020
10 AHEAD(I) = 0	00001030
C THIS MOD INSERTED TO INITIALIZE THE ARRAY GPEAK	00001040
C INSERTED 11/14/78 - AT RTI BY WFH	00001050
DO 11 I=1.3	00001060
DO 11 J=1.11	00001070
11 GPEAK(I,J)=0	00001080
C THIS MOD TO INITIALIZE ARRAY MSINGS...	00001090
C INSERTED 4/12/78 - AT RTI BY WFH	00001100
DO 13 I=1.2	00001110
DO 13 J=1.50	00001120
13 MSINGS(I,J)=0	00001130
C THIS MOD ALSO TO INITIALIZE AN ARRAY LINGS...	00001140
C INSERTED 4/13/78 - AT RTI BY WFH	00001150
DO 14 I=1.50	00001160
14 LINGS(I)=0	00001170
C THESE MODS ARE ALSO TO INITIALIZE ISVN8, ISVN9, ISVP8, ISVP9...	00001180
C INSERTED 4/14/78 - AT RTI BY WFH	00001190
ISVP8=0.0	00001200
ISVP9=0.0	00001210
ISVN8=0	00001220
ISVN9=0	00001230
C YET ANOTHER MOD TO INITIALIZE THE HISTOGRAMS - NPHIST,PKHIST	00001240
C INSERTED 4/14/78 - AT RTI BY WFH	00001250
DO 15 I=1.20	00001260
PKHIST(I)=0.0	00001270
15 NPHIST(I)=0	00001280
C STILL ANOTHER MOD TO INITIALIZE THINGS FOR TLOC - SPARE3 TO SPARE7	00001290
C INSERTED 4/17/78 BY WFH AT RTI	00001300
SPARE3=0	00001310
SPARE4=0	00001320
SPARE5=0.0	00001330
SPARE6=0.0	00001340
C ONCE AGAIN AN UNINITIALIZED VARIABLE - THIS TIME IN LKAHD	00001350
	00001360
	00001370

```

C MOD INSERTED 4/20/78 AT RTI BY WFH
OVLAP=0
DO 12 I = 1,25
12 SATLST(I) = 0
SATINX = 1
C THIS MOD INSERTED TO INITIALIZE ISGMAS FOR A
C MOD DOWN INSIDE TLOC TO PREVENT LOOKING FOR
C ELUTANTS WHICH HAVE NO SUITABLE MODEL....
C RTI - BY WFH 5/24/78
DO 16 I=1,3
ISHMAS(I)=1
16 ISGMAS(I)=1
C NSLOT,NLINE USED IN KAPUT VIA OUTDAT.
NSLOT = 0
NLINE = 0
FSTPGE = 1
FSTREC = 1
C ANOTHER RANDOM VOID .. EH .. HUI NENG ...
NMASS=411
LSTCNT=0
C HERE THE CALL TO PARDIR HAS BEEN SHIFTED TO THE TOP
C AND CALLING ARGUMENTS TO SETBUG HAVE BEEN MODIFIED
C WM F HARGROVE
C 11/29/78
C CALL PARDIR(CLNFLG,UNIT,NNAME)
C CALL SETBUG(NNAME,EOF)
C IF(EOF.NE.0)GO TO 30
C LOOP CONTROL MODIFIED SO PROGRAM WILL TERMINATE INSIDE MAIN
C CSECT - WFH RTI 9/31/78
C MAXSP=MAXSP-10
NS=13
40 NS=NS+1
C THE UPDATING OF SPCNO IS NOW DONE INSIDE TLOC
C WHERE THE SPECTRUM RECORDS ARE INPUT...
C THIS WAS DONE SO THAT SPCNO COULD KEEP UP WITH
C GAPS IN THE SCAN NUMBERS...
C WFH - RTI 6/15/78
C SPCNO=SPCNO+1
C ALSO AN EOF FLAG WAS ADDED TO ENSURE TERMINATION INSIDE THE
C MAIN ROUTINE....
C WFH - RTI 9/31/78
C CALL TLOC(NS,M1,M2,M3,IFOUND,EOF)
C IF(EOF.EQ.1)GO TO 30
C IFOUND = 0 IF NO SPECTRUM DETECTED.
C IF(IFOUND.EQ.0) GO TO 40
MU=MU+1
C IF(MU.LE.1000)GO TO 23
C CALL CUPRNT(4,NPHIST,MASBUF,PKHIST,AVE,ERRMAX,
1ERR2,SPCNO,MODE2,MODE2)
C WRITE(IPTR2,24) SPCNO
C 24 FORMAT(' ','*** CLEANUP TERMINATING DUE TO TABLE OVERFLOW ***',
C 1/,1X,'LAST SPECTRUM NO. IS ',15)
C STOP 12
23 ISQ(MU)=SPCNO
20 CALL LKAHED(NS,M2,M3,OVLAP,G,H)
C OVLAP = 1 IF ELUTANT DETECTED AHEAD.
C IF(OVLAP.EQ.0) GO TO 25
CALL OFFSET(G,H,GNU,HNU,MODE1,MODE2)

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C	HOPEFULLY THE LAST FIX TO CUPRNT IN ORDER TO MAKE	00001950
C	WATFIV HAPPY... THE ONLY ARGUMENTS USED IN THIS CALL ARE	00001960
C	MODE1 AND MODE2	00001970
C	WFH,RTI 4/26/78	00001980
	CALL CUPRNT(1,NPHIST,MASBUF,PKHIST,AVE,ERRMAX,	00001990
	IERR2,MODE1,MODE2,MODE2)	00002000
C	ABOVE PRINTS MODE1 AND MODE2	00002010
25	CONTINUE	00002020
	ISKP=0	00002030
	PASS1 = 0	00002040
	NDIS=1	00002050
C	THIS PASS FOR MASSES DETECTED TO LEFT OF DETECTED SPECTRUM	00002060
C	AND NOT RESOLVED	00002070
C	IT SHOULD BE NOTED THAT THE DOUBLET RESOLVER IS ONLY RUN ON	00002080
C	PASS 2.	00002090
C	CALL GETHGT(NS-2,M1,ISKP,OVLAP,NDIS,G,H,GNU,HNU)	00002100
C	THIS PASS FOR MASSES DETECTED AT THE SPECTRUM	00002110
C	---	00002120
	NDIS=2	00002130
	CALL GETHGT(NS-1,M2,ISKP,OVLAP,NDIS,G,H,GNU,HNU)	00002140
	ISKP=1	00002150
	NDIS=3	00002160
C	THIS PASS FOR MASSES DETECTED TO THE RIGHT OF THE SPECTRUM	00002170
C	CALL GETHGT(NS,M3,ISKP,OVLAP,NDIS,G,H,GNU,HNU)	00002180
C	PRINT LEAST SQUARE ERROR STUFF IF DOUBLET FOUND	00002190
	IF(OVLAP.EQ. 0) GO TO 550	00002200
	IF (IDEBUG.EQ. 0) GO TO 550	00002210
	AVE = SIGERR/NERR	00002220
	ERRMAX = ERRMAX/NERR	00002230
	IMASS = RMASS	00002240
C	HOPEFULLY THE LAST FIX TO CUPRNT IN ORDER TO MAKE	00002250
C	WATFIV HAPPY... THE ONLY ARGUMENTS USED IN THIS CALL ARE	00002260
C	AVE AND ERRMAX	00002270
C	WFH,RTI 4/26/78	00002280
	CALL CUPRNT(2,NPHIST,MASBUF,PKHIST,AVE,ERRMAX,ERR2,	00002290
	1MODE1,MODE2,MODE2)	00002300
C	* * *	00002310
C	WRITE OUT 0*(IHSPEC) STUFF	00002320
	CALL CUPRNT(5,NPHIST,MASBUF,PKHIST,AVE,ERRMAX,	00002330
	IERR2,SPCNO,MODE2,MODE2)	00002340
C	WRITE(IPTR2,900)	00002350
C	WRITE(IPTR2,910)	00002360
	ICOUNT = 0	00002370
	DO 600 I = 1,6	00002380
	MASBUF(I) = 0	00002390
600	VALBUF(I) = 0	00002400
	DO 650 I = 1,411	00002410
	IMASS = I + 39 - MAD	00002420
	IF(SECOND(I).EQ. 32767) GO TO 650	00002430
	ICOUNT = ICOUNT + 1	00002440
	IF (ICOUNT.LT. 7) GO TO 620	00002450
C	WRITE(IPTR2,920) (MASBUF(J),VALBUF(J), J = 1,6)	00002460
	CALL CUPRNT(6,MASBUF,VALBUF,PKHIST,AVE,ERRMAX,ERR2,	00002470
	1SPCNO,MODE2,MODE2)	00002480
	ICOUNT = 1	00002490
	DO 610 J = 1,6	00002500
	MASBUF(J) = 0	00002510
610	VALBUF(J) = 0	00002520

620	MASBUF(ICOUNT) = IMASS	00002530
	VALBUF(ICOUNT) = SECOND(I)	00002540
650	CONTINUE	00002550
	IF (MASBUF(I) .EQ. 0) GO TO 550	00002560
C	WRITE(IPTR2,920) (MASBUF(J),VALBUF(J),J=1,6)	00002570
	CALL CUPRINT(6,MASBUF,VALBUF,PKHIST,AVE,ERRMAX,ERR2,	00002580
	ISPCNO,MODE2,MODE2)	00002590
C	THE ABOVE EMPTIES THE BUFFER.	00002600
550	CALL OUTDAT(SRLIB,NNAME)	00002610
	GO TO 40	
C	THIS MOD INSERTED IN CONJUNCTION WITH THE EOF FLAG ADDITION TO	00002630
C	TLOC	00002640
	WFH - RTI 9/31/78	00002650
C	THE END OF THE CLEANUP MAIN CSECT HAS BEEN MODIFIED	00002660
C	TO HANDLE MULTIPLE RUN PROCESSING.	00002670
	WM F HARGROVE	00002680
	11/29/78	00002690
C	END OF SPECTRUM RUN	00002700
30	CONTINUE	00002710
	CALL CLSRUN(ISQ,MU)	00002740
	GO TO 35	00002750
C	END OF FILE AND TERMINATION OF CLEANUP PROGRAM	00002760
50	CALL CUPRINT(8,NNAME,VAIBUF,PKHIST,AVE,ERRMAX,	00002770
	ZERR2,TIMCNT,MODE2,MODE2)	00002780
	CALL CLSFIL	00002790
	STOP	00002800
	END	00002810
	SUBROUTINE BACLSQ(PKHGT)	00002820
C		00002830
C	THIS COMPUTER PROGRAM WAS DEVELOPED WITH THE FUNDING SUPPORT	00002840
C	FROM THE NATIONAL INSTITUTES OF HEALTH (GRANTS RR-612 AND	00002850
C	GM-20832) AND THE NATIONAL AERONAUTICS AND SPACE ADMINISTRATION	00002860
C	(GRANT NGR-05-020-632).	00002870
C		00002880
C	*** THIS ROUTINE USES A MODEL PEAK AND CURRENT PEAK	00002890
C	*** AND DOES A LEAST SQUARES TO COMPUTE THE	00002900
C	*** BACKGROUND AT PEAK CENTRE (ASSUMES LINEAR BACKGROUND).	00002910
C		00002920
	INTEGER PKHGT,PASS1	00002930
	COMMON PKHIST(20),NPHIST(20)	00002940
	COMMON YMS,Y(9),YP5	00002950
	COMMON G(9)	00002960
	COMMON /LSQ/PASS1	00002970
	COMMON /BACKER/SG,SG2	00002980
	REAL P,C	00002990
C		00003000
C	*** SOLUTION OF THREE LINEAR EQUATIONS.	00003010
C		00003020
C		00003030
C		00003040
C	P * SG**2 + C = SGY	00003050
C		00003060
C	P * SG + C = SY	00003070
C		00003080
C		00003090
C	WHICH RESULT FROM THE LEAST SQUARE FITTING OF THE	00003100
C	ERROR TERMS.	00003110
		00003120

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C          E(I) = P * G(I) + C - Y(I)      .  I = 1.9      00003130
C          WE SOLVE FOR P AND SET PEAKHGT = P * GTOP.      00003140
C          WHERE GTOP IS THE INTERPOLATED VALUE AT THE SPECTRUMS HISTOGRAM POSITION. 00003150
C          00003160
C          00003170
C          00003180
C          IF( PASS1 .EQ. 1 ) GO TO 10      00003190
C          PASS1 = 1      00003200
C          SG = 0      00003210
C          SG2 = 0      00003220
C          DO 5 I = 1.9      00003230
C          SG = SG + G(I)/9      00003240
5          SG2 = SG2 + G(I) * G(I)/9      00003250
10         CONTINUE      00003260
C          SY = 0      00003270
C          SYG = 0      00003280
C          DO 20 I = 1.9      00003290
C          SY = SY + Y(I)/9      00003300
20         SYG = SYG + Y(I) * G(I)/9      00003310
C          P = ( SYG - SY * SG ) / ( SG2 - SG * SG )      00003320
C          PKHGT = P * G(5)      00003330
C          C = SY - P * SG      00003340
C          RETURN      00003350
C          END      00003360
C          SUBROUTINE BLEED(Y,RATIO)      00003370
C          LEAST SQUARE FITS A LINE TO DATA TO DETERMINE ITS LINEARITY.      00003380
C          REAL AVY,AXY,AXX,X,B,M,RATIO      00003390
C          INTEGER N,I      00003400
C          REAL Y(7),ERROR,FIT(7)      00003410
C          AVY = 0      00003420
C          AXY = 0      00003430
C          AXX = 0      00003440
C          DO 200 I = 1.7      00003450
C          X = I - 4      00003460
C          AVY = AVY + Y(I)      00003470
C          AXY = AXY + X * Y(I)      00003480
200         AXX = AXX + X*X      00003490
C          AVY = AVY/7      00003500
C          AXY = AXY/7      00003510
C          AXX = AXX/7      00003520
C          AXY = AXY/7      00003530
C          B = AVY      00003540
C          M = AXY/AXX      00003550
C          Y = M * X + B      00003560
C          00003570
C          00003580
C          00003590
C          THE ERROR RATIO CALCULATION HAS BEEN MODIFIED SUBSTANTIALLY      00003600
C          BECAUSE IT WAS FOUND TO BE HAYWIRE IN THE PREVIOUS VERSION.      00003610
C          THE MOD IS A JOINT EFFORT OF DR/SHAH/PC/WFH      00003620
C          ENTERED BY WFH-RTI 9/31/78      00003630
C          00003640
C          00003650
C          IF(AVY.EQ.0)GO TO 400      00003660
C          RMS=0.0      00003670
C          DO 300 I=1.7      00003680
C          FIT(I)=M*(I-4)+B      00003690
C          ERROR=FIT(I)-Y(I)      00003700
300         RMS=RMS+ERROR*ERROR      00003700
C          RMS=SQRT(RMS)/7.0      00003700
C          RATIO=RMS/AVY      00003700

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RETURN	00003710
C	00003720
400 RATIO=0.0	00003730
RETURN	00003740
END	00003750
C THIS SUBROUTINE DOES ALL PRINTING	00003760
C FOR CLEANUP. PLEASE USE IT TO ADD NEW PRINTING	00003770
C IN ANY SUBROUTINE.	00003780
C	00003790
C THE CALL STATEMENT ALLOWS FOR PASSING OF ARRAYS	00003800
C REALS AND INTEGERS.	00003810
C	00003820
C	00003830
C THIS COMPUTER PROGRAM WAS DEVELOPED WITH THE FUNDING SUPPORT	00003840
C FROM THE NATIONAL INSTITUTES OF HEALTH (GRANTS RR-612 AND	00003850
C GM-20832) AND THE NATIONAL AERONAUTICS AND SPACE ADMINISTRATION	00003860
C (GRANT NGR-05-020-632).	00003870
C	00003880
SUBROUTINE CUPRNT(N,IAR,IAR2,AR,R1,R2,R3,I1,I2,I3)	00003890
INTEGER N,I1,I2,I3,IONE,NINE	00003900
REAL R1,R2,R3	00003910
C THE DIMENSIONS OF IAR AND AR HAVE BEEN CHANGED TO SUIT WATFIV	00003920
C THEY WERE AT 9....MUCH OF THIS CODE SEEMS NONSENSE...	00003930
C WFM RTI 26/4/78	00003940
C	00003950
DIMENSION IAR(1),AR(1),IAR2(1)	00003960
COMMON /DUBBUG/IFLAG	00003970
COMMON /UNITS/ IRDR,IPTR1,IPTR2,IPTR3,IIN,IOUT	00003980
DATA IONE,NINE/1.9/	00003990
C	00004000
IFLAG IS RESET IF NO PRINTING IS TO BE DONE/	00004010
C	00004020
IF (IFLAG.EQ.0) RETURN	00004030
GO TO (10,140,150,160,170,180,200,210),N	00004040
C	00004050
THE ABOVE IS A CASE STATEMENT FOR EXECUTING PRINT	00004060
C OPTIONS.C	00004070
C	00004080
GCMSOL PRINTING OF MODE1,MODE2	00004090
10 IF(IFLAG.EQ.0)RETURN	00004100
WRITE(IPTR2,510) I1,I2	00004110
RETURN	00004120
C	00004130
140 IF(IFLAG.EQ.0)RETURN	00004140
WRITE(IPTR2,1400) R1,R2	00004150
RETURN	00004160
FORMAT STATEMENTS FOLLOW.	00004170
C	00004180
510 FORMAT(/IX,' HISTOGRAM LOCATIONS OF THE TWO SPECTRA ARE:/'	00004190
-BX,'G-POSITION = ',I2,2X,'H-POSITION = ',I4)	00004200
1400 FORMAT(/' LEAST SQUARES ERROR STUFF FOR DOUBLET:/'	00004210
-' AVE. ERR. AVE RMS ERR'	00004220
-',,IX,E15.8,4X,E15.8,/'	00004230
C THESE PRINT STATEMENTS HAVE BEEN ADDED AS PART OF THE	00004240
C GENERAL REVAMPING OF CUPRNT.... WFM RTI 9/31/78	00004250
C	00004260
150 WRITE(IPTR2,101)	00004270
101 FORMAT(' ','START OF CONVERTED MASS SPEC CLEANUP PROGRAM')	00004280
RETURN	

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C 160 WRITE(IPTR2,24) I1 00004290
24 FORMAT('-', '*** CLEANUP TERMINATING DUE TO TABLE OVERFLOW ***', 00004300
1/, I1, 'LAST SPECTRUM NO. IS ', I5) 00004310
RETURN 00004320
C 00004330
170 IF(IFLAG.EQ.0)RETURN 00004340
WRITE(IPTR2,900) 00004350
900 FORMAT('/', 20X, 'COMPUTED H(MODE) * Q', /) 00004360
WRITE(IPTR2,910) 00004370
910 FORMAT(' MASS VALUE MASS VALUE MASS VALUE MASS VALUE MASS VAL 00004380
*UE MASS VALUE' /) 00004390
RETURN 00004400
C 00004410
C 00004420
180 IF(IFLAG.EQ.0)RETURN 00004430
WRITE(IPTR2,920) (IAR(I), IAR2(I), I=1,6) 00004440
920 FORMAT(6(3X, I3, 1X, I5)) 00004450
RETURN 00004460
C 00004470
CUPRNT STATEMENTS 7 AND 8 HAVE BEEN MODIFIED TO 00004480
FIT IN WITH THE SCHEME OF MULTIPLE RUN PROCESSING. 00004490
WM F HARGROVE 00004500
11/29/78 RTI 00004510
C 200 WRITE(IPTR2,11) I2, (IAR(I), I=1,18) 00004520
11 FORMAT(1X, 'END OF PROCESSING FOR RUN ', I2, 00004530
2' RUN TITLE: ', I8A4) 00004550
RETURN 00004560
C 00004570
210 WRITE(IPTR2,102) 00004580
102 FORMAT('-', '***END OF CLEANUP PROCESSING***') 00004590
RETURN 00004600
END 00004610
SUBROUTINE DETEKT (PKHIST,NPHIST,DTFLAG,NLWCUT,NUPCUT 00004620
& ,NL,NU,IDX,IDXU,INDX) 00004630
C 00004640
C THIS COMPUTER PROGRAM WAS DEVELOPED WITH THE FUNDING SUPPORT 00004650
FROM THE NATIONAL INSTITUTES OF HEALTH (GRANTS RR-612 AND 00004660
GM-20832) AND THE NATIONAL AERONAUTICS AND SPACE ADMINISTRATION 00004670
(GRANT NGR-05-020-632). 00004680
C 00004690
C INTEGER PLIMIT,DTFLAG,CPLMIT,SVFLAG,CASE1 00004700
REAL MX,MX2,INTSUM 00004710
DIMENSION PKHIST(20),NPHIST(20) 00004720
COMMON /PARAMS/MINTIC,MINNY,NTHIRD,RATM 00004730
C MINNY IS USED FOR FEWER THAN 5 PEAKS 00004740
C REQUIRE TOTAL ION CURRENT FOR DETECTED SPECTRUM TO BE MINTIC 00004750
C IN AND AROUND THE MAX IF 5 PEAKS LOCALLY. 00004760
COMMON /TOMS/ITOM 00004770
COMMON /CAHEA/AHEAD(5) 00004780
C INTEGER AHEAD,ITOM 00004790
C ***** 00004800
C WE SCAN THE HISTOGRAMIC WINDOW +NL,NU@ FOR A MAXIMUM 00004810
DTFLAG=0 00004820
INDX=NL 00004830
NUM=NPHIST(NL) 00004840
MX=PKHIST(NL) 00004850
C THE HISTOGRAMIC WINDOW +IDX,IDXU@ IS WHERE A MAXIMUM 00004860
C WILL OCCUR IF A SPECTRUM IS ELUTING. 00004870

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NUM2=NPHIST(IDXL)
MX2=PKHIST(IDXL)
INDX2=IDXL
C      MX.NUM = MAX *NL.NU0 & MX2.NUM2 = MAX *IDXL.IDXU0
DO 10 I=NL.NU
  IF ( MX.GE. PKHIST(I) ) GO TO 9
  MX=PKHIST(I)
  NUM=NPHIST(I)
  INDX=I
9    CONTINUE
C      NOTE: *IDXL.IDXU0 IS WINDOW FOR DETECTING ELUTANT NOW
  IF ( 1.LE. IDXL .OR. 1.GT. IDXU ) GO TO 10
  IF ( MX2.GE. PKHIST(I) ) GO TO 10
C      GET MAXIMUM IN WINDOW * IDXL,IDXU 0
  MX2=PKHIST(I)
  NUM2=NPHIST(I)
  INDX2=I
10   CONTINUE
C      SEE IF IN RIGHT HISTOGRAM WINDOW, *IDXL.IDXU0
  IF ( INDX.GE. IDXL .AND. INDX.LE. IDXU ) GO TO 15
C      IF WE GET HERE THE ABSOLUTE MAXIMUM WAS NOT IN *IDXL.IDXU0
  AND IDXL.LE. INDX2.LE. IDXU
C      REQUIRE: 1. THAT TIC (INDX2) BE LARGER THAN ITS IMMEDIATE
C      NEIGHBORS.
C      2. THAT PKHIST(IDXU) + PKHIST(IDXU+1)
C      + PKHIST(IDXL) .GE. MINTIC.
  IF ( MX2.LT. PKHIST(INDX2-1) ) RETURN
  IF ( MX2.LT. PKHIST(INDX2+1) ) RETURN
C      CHECK ON HOW CLOSE WE WILL ALLOW HISTOGRAM BUMPS.
C      DEFAULTS TO 2 SLOTS APART. SPECIAL FLAG ITOM IS
C      USED FOR FRAGMENTOGRAPHY RUNS TO TRY TO SEPARATE
C      DEUTERATED PEAKS FROM NON-DEUTERATED PEAKS.
C      THIS IS A TEMPORARY MOD IN ORDER TO GATHER STATISTICS ON
C      THE INPUT PARAMETER ITOM - CODE 6
C      WFH RTI 9/31/78
C      ISPC=0
C      ITYP=6
C      WRITE(20,6251) ITYP,ISPC
C6251 FORMAT(A4,A4)
C      IF ( ITOM.EQ. 1 ) GO TO 79
C      IF ( MX2.LT. PKHIST(INDX2-2) ) RETURN
C      IF ( MX2.LT. PKHIST(INDX2+2) ) RETURN
C      TEMPORARY MOD IN ORDER TO GATHER STATISTICS ON
C      THE INPUT PARAMETER ITOM - CODE 7
C      WFH RTI 9/31/78
C      ISPC=0
C      ITYP=7
C      WRITE(20,6254) ITYP,ISPC
C6254 FORMAT(A4,A4)
79   CONTINUE
  PKSUM = PKHIST(IDXL) + PKHIST(IDXL+1) + PKHIST(IDXU)
  IF ( IDXL.NE. 4 ) GO TO 12
  IF ( AHEAD(1).EQ. 1 ) PKSUM = MINTIC
C      THE ABOVE GUARANTEES DETECTION IF SPECTRUM WAS DETECTED

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C	AHEAD.	00005460
12	CONTINUE	00005470
C		00005480
C	THIS IS A TEMPORARY MOD IN ORDER TO GATHER STATISTICS ON	00005490
C	THE INPUT PARAMETER ITOM - CODE 5	00005500
C		00005510
C	ISPC=0	00005520
C	ITYP=5	00005530
C	WRITE(20,6252) ITYP,ISPC,PKSUM	00005540
C6252	FORMAT(A4,A4,36X,A4)	00005550
C	IF (PKSUM .LT. MINTIC) RETURN	00005560
C	NLWCUT=INDX2-2	00005570
C	NUPCUT=INDX2+2	00005580
C	INDX=INDX2	00005590
C	DTFLAG = 1 SAYS WE'VE FOUND ONE	00005600
C	DTFLAG=1	00005610
C	RETURN	00005620
15	CONTINUE	00005630
C	WE NOW SUM NUMBER OF PEAKS AND TIC.	00005640
C	IF (IDXL .LT. 7) GO TO 16	00005650
C	MAKE SURE WE HAVE A HISTOGRAMIC BUBBLE	00005660
C	IF LOOKING AHEAD.	00005670
C	BUBBLE = PKHIST(INDX)	00005680
C	IF (BUBBLE .LT. PKHIST(INDX-1)) RETURN	00005690
C	IF (BUBBLE .LT. PKHIST(INDX-2)) RETURN	00005700
16	CONTINUE	00005710
C	PKSUM = NPHIST(IDXL)	00005720
C	INTSUM = PKHIST(IDXL)	00005730
C	IF IDXL = 9 THEN WE ARE LOOKING AHEAD. AND AN EARLIER	00005740
C	ELUTANT WAS DETECTED AT 6. WE ONLY SCANNED +9.100.	00005750
C	IF (IDXL .EQ. 9) GO TO 150	00005760
C	PKSUM = PKSUM + NPHIST(IDXL + 1)	00005770
C	INTSUM = INTSUM + PKHIST(IDXL + 1)	00005780
C	IF (IDXL .EQ. 8) GO TO 100	00005790
C	HERE WE ONLY SCANNED +8.100	00005800
C	PKSUM = PKSUM + NPHIST(IDXU)	00005810
C	INTSUM = INTSUM + PKHIST(IDXU)	00005820
C	IF (IDXL .EQ. 7) GO TO 100	00005830
C	HERE WE SCANNED +7.100. IN ALL SPECIAL CASES A ELUTANT WAS	00005840
C	DETECTED IN +4.5.60 SO WE DO NO LEFT BOUNDARY CHECKING.	00005850
C	SEE IF MAXIMUM OCCURRED ON LEFT BOUNDARY	00005860
C	IF (INDX .NE. IDXL) GO TO 100	00005870
C	PKSUM = PKSUM + NPHIST(IDXL-1)	00005880
C	INTSUM = INTSUM + PKHIST(IDXL-1)	00005890
C	GO TO 150	00005900
C	SEE IF MAXIMUM OCCURRED ON RIGHT BOUNDARY	00005910
100	CONTINUE	00005920
C	IF (INDX .NE. IDXU) GO TO 150	00005930
C	PKSUM = PKSUM + NPHIST(IDXU+1)	00005940
C	INTSUM = INTSUM + PKHIST(IDXU+1)	00005950
150	CONTINUE	00005960
C	GUARANTEE SPECTRUM DETECTION IF DETECTED AHEAD.	00005970
C	IF (IDXL .NE. 4) GO TO 155	00005980
C	IF (AHEAD(1) .EQ. 0) GO TO 155	00005990
C	PKSUM = MINTIC	00006000
C	IF (PKSUM .LT. MINNY) PKSUM = MINNY	00006010
155	CONTINUE	00006020
C	CHECK FOR FEWER THAN 5 PEAKS.	00006030

C		00006040
C	THIS IS A TEMPORARY MOD IN ORDER TO GATHER STATISTICS ON	00006050
C	THE INPUT PARAMETER ITOM - CODE 4	00006060
C		00006070
C	ISPC=0	00006080
C	ITYP=4	00006090
C	WRITE(20,6257) ITYP,ISPC,PKSUM,INTSUM	00006100
C6257	FORMAT(A4,A4,28X,A4,A4)	00006110
	IF (PKSUM .GE. 5) GO TO 200	00006120
	IF(INTSUM .GE. MINNY) GO TO 18	00006130
	RETURN	00006140
200	CONTINUE	00006150
C	IF AT LEAST 5 PEAKS. THEN REQUIRE INTSUM > MINTIC.	00006160
	IF(INTSUM .LT. MINTIC) RETURN	00006170
18	CONTINUE	00006180
	DTFLAG=1	00006190
	IF (NL .NE. 1) RETURN	00006200
C	NL = 1 --> WE ARE NOT LOOKING AHEAD, AND NEED HISTOGRAMIC	00006210
C	BOUNDS, NLWCUT AND NUPCUT.	00006220
	SLEFT=0.0	00006230
	SRIGHT=0.0	00006240
	NUM1=INDX+1	00006250
	NUM3=INDX+3	00006260
C	GET HISTOGRAMIC "WEIGHTS" TO THE LEFT AND RIGHT OF THE	00006270
C	MAXIMUM AT PKHIST(INDX).	00006280
	J = 0	00006290
	DO 20 I=NUM1,NUM3	00006300
	J = J + 1	00006310
	JJ = INDX - J	00006320
	SLEFT = SLEFT + PKHIST(JJ)	00006330
	SRIGHT = SRIGHT + PKHIST(I)	00006340
20	CONTINUE	00006350
	NLWCUT = INDX - 2	00006360
	NUPCUT = INDX + 2	00006370
	IF (SLEFT - SRIGHT) 30,40,50	00006380
C	MORE "WEIGHT" TO RIGHT IF WE GET HERE	00006390
30	NUPCUT = NUPCUT + 1	00006400
	GO TO 40	00006410
C	MORE "WEIGHT" TO LEFT IF WE GET HERE	00006420
50	NLWCUT = NLWCUT - 1	00006430
40	RETURN	00006440
	END	00006450
	SUBROUTINE DUBLET (G,H,Y,STORE,M,IHSPEC,GHGT,ISWD,NS)	00006460
	REAL GHGT	00006470
	INTEGER STORE,M,IHSPEC,ISWD,SECOND,NS,MAD	00006480
	REAL KK,LL,MM,NN	00006490
	COMMON /DUBBER/C4,C1,C2,SG,SH	00006500
	COMMON /MONITOR/MONSPC,MONMAS	00006510
	COMMON /ERRORS/RMASS,ERRMAX,NERR,SIGERR,SECOND(411)	00006520
	COMMON /IMAD/MAD	00006530
	COMMON /UNITS/ IRDR,IPTR1,IPTR2,IPTR3,IIN,IOUT	00006540
	INTEGER I32766	00006550
	REAL*8 C4,C1,C2,SG,SH	00006560
	REAL*8 SY,SGY,SHY,SG2,SH2,SGH	00006570
	REAL ERR,ERRM	00006580
C	*** ROUTINE TO RESOLVE A DUBLET USING TWO MODEL	00006590
C	*** PEAKS BY A LEAST SQUARES METHOD. THE MODEL	00006600
C	*** INCLUDES A LINEAR BACKGROUND.	00006610

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C      THE LEAST SQUARE NORMAL EQUATIONS ARE DERIVED FROM
C      THE FOLLOWING EQUATION FOR ERROR MINIMAZATION:
C       $E(I) = P * G(I) + Q * H(I) + C - Y(I)$  , I = 1,14
C      <X> = AVERAGE VALUE OF X
C      THIS LEADS TO THE FOLLOWING SYSTEM OF EQUATIONS :
C       $P * \langle SG^{**2} \rangle + Q * \langle SGH \rangle + C * \langle SG \rangle = \langle SGY \rangle$ 
C       $P * \langle SGH \rangle + Q * \langle SH^{**2} \rangle + C * \langle SH \rangle = \langle SHY \rangle$ 
C       $P * \langle SG \rangle + Q * \langle SH \rangle + C = \langle SY \rangle$ 
C      REAL G(18),H(18),Y(18)
C      REAL ERRT1(14),FIT(14)
C      REAL P,Q,C,ZERO,HMD(14),GMD(14)
C      INTEGER ILOW,IUP
C      DATA ZERO/0.0/
C      DATA 132766/32768/
C      *****HI THERE*****
C      INITIALIZE SOME VARIABLES
C      ILOW = 3
C      IUP = 11
C      WE TRUNCATE THE SECOND MODEL AT THE 11TH POSITION SO AS
C      ONLY TO USE POINT WHERE REAL DATA WAS SUPPLIED.
C      AN = IUP - ILOW + 1
C      TEST TO SEE IF WE'VE ALREADY BEEN BY FOR THIS SPECTRUM
C      IF( ISWD .EQ. 0) GO TO 20
C      ISWD = 0
C      SG2 = 0
C      SGH = 0
C      SG = 0
C      SH2 = 0
C      SH = 0
C      DO SOME SUMS.
C      DO 10 I = ILOW,IUP
C      SG = SG + G(I)
C      SG2 = SG2 + G(I) * G(I)
C      SH = SH + H(I)
C      SH2 = SH2 + H(I) * H(I)
C      SGH = SGH + G(I) * H(I)
10  CONTINUE
C      MAKE ALL AVERAGE VALUES
C      SG = SG/AN
C      SG2 = SG2/AN
C      SH = SH/AN
C      SH2 = SH2/AN
C      SGH = SGH/AN
C      NOW DO WHAT COMPUTING WE CAN FOR MODEL STUFF
C      C4 = SG2 - SG * SG
C      C1 = SGH - SG * SH
C      C2 = SH2 - SH * SH
20  CONTINUE
C      SY=0
C      SGY=0
C      SHY=0
C      DO 30 I = ILOW,IUP
C      SY=SY + Y(I)
C      SGY=SGY + G(I) * Y(I)
C      SHY=SHY + H(I) * Y(I)
30  CONTINUE
C      SY = SY/AN
C      SGY = SGY/AN

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C      SHY = SHY/AN
      NOW SOLVE FOR P,Q,C
      C5 = SGY - SY * SG
      C3 = SHY - SY * SH
      P = ( C5 * C2 - C3 * C1 ) / ( C4 * C2 - C1 * C1 )
      Q = ( C3 - P * C1 ) / C2
      C = SY - P * SG - Q * SH
      GHGT = P * G(7)
      HHGT = Q * H(IHSPEC)
      IF( GHGT .LT. ZERO ) GHGT = ZERO
      IF( HHGT .LT. ZERO ) HHGT = ZERO
C      DO MEAN SQUARE ERROR CALCULATION
      ERR = 0
      ERRM = 0
      DO 40 I = ILOW,IUP
      GMD(I) = P * G(I)
      HMD(I) = Q * H(I)
      FIT(I) = GMD(I) + HMD(I) + C
      ERRT1(I) = Y(I) - FIT(I)
      ERRM = ERRM + ERRT1(I)
40     ERR = ERR + ERRT1(I) * ERRT1(I)
      ERRM = ERRM/AN
      RMS = ERR/AN - ERRM * ERRM
      IF( RMS .LT. 0 ) RMS = 0
      ERR = SQRT(RMS)
      SIGERR = SIGERR + ERRM
      ERRMAX = ERRMAX + ERR
      NERR = NERR + 1
      STORE = 1
C      FLAG FOR SETGHY TO SIGNAL STORING OF NEW VALUE IN NUSPEC(M)
      IF(HHGT .GT. I32766) HHGT = I32766
200    SECOND(M) = HHGT
      CONTINUE
      RETURN
C THIS SECTION OF DOUBLET DEALS WITH PRINTING
C OUT OF MONITORED SPECTRA AND MONITORED MASSES
C IT WAS COMMENTED OUT BECAUSE NO EASY WAY OF
C INCORPORATING THIS DIAGNOSTIC INTO THE
C MULTIPLE RUN PROCESSING SCHEME COULD
C BE THOUGHT OF. IT MAY BE REINSTITUTED IN THE
C EVENT OF SUBTLE DOUBLET RESOLUTION PROBLEMS.
C                                     WM F HARGROVE
C                                     12/7/78 - RTI
C      IF ( MONMAS .EQ. 0 ) RETURN
C      IM = M + 39-MAD
C      IS = NS - 6
C      IF ( MONMAS .NE. IM .OR. MONSPC .NE. IS ) RETURN
C      WRITE(IPTR2,2500) ERR,ERRM
C      WRITE(IPTR2,2000) IM,P,Q,C
C      WRITE(IPTR2,2100) (Y(I),I = 3 , 11)
C      WRITE(IPTR2,2200) (G(I),I = 3 , 11)
C      WRITE(IPTR2,2300) (H(I),I = 3 , 11)
C      BAK = C
C      SQHT = GHGT + Q * H(7) + BAK
C      WRITE(IPTR2,2400) GHGT,BAK,SQHT
C999  RETURN
C2000 FORMAT(//,' DOUBLET STUFF FOR MASS = ',I3,'//',
C      -,' P Q C

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C      -.3(2X,F10.3))
C2100 FORMAT(///.Y-VALUES'.,.5(2X,F7.0),.4(2X,F7.0))
C2200 FORMAT(///.G-VALUES'.,.5(2X,F7.4),.4(2X,F7.4))
C2300 FORMAT(///.H-VALUES'.,.5(2X,F7.4),.4(2X,F7.4))
C2400 FORMAT(///.P * G(7) BACK GROUND P*G + Q*H + C '.
C      -.3(4X,F8.0)/)
C2500 FORMAT(///.RMS ERROR = '.E14.8.' MEAN ERROR = '.E20.8)
END
SUBROUTINE GETHGT(NS,MN,ISKP,OVLAP,NDIS,G,H,GNU,HNU)
INTEGER PKHGT,MNB,MI,MN,ISKP,JMPK,NUHGT
DIMENSION G(9),H(11),GNU(18),HNU(18)
C      *** THIS ROUTINE IS THE MAIN PROCESSING ROUTINE. IT
C      *** PICKS UP THE MASS INDICES THAT HAVE BEEN FLAGGED
C      *** IN THE DETECTION PHASE AND PROCEEDS TO HANDLE
C      *** BACKGROUND REMOVAL AND DOUBLET RESOLUTION AND
C      *** THE PROCESSING OF SATURATED PEAKS. IT IS CALLED
C      *** THREE TIMES IN PROCESSING ANY ONE COMPONENT DUE TO
C      *** THE SPREAD THAT CAN EXIST IN PEAK MODES FOR ANY
C      *** COMPONENT (PARTICULARLY THE LOW INTENSITY ONES).
INTEGER NAME,RDATE,BITMAP,GCTIME,LIBMAP,INTEG,LOMASS
INTEGER HIMASS,POINTS,TAPCNT,MAXSP,LSTCNT,DEVICE,SPCNO
INTEGER SPEC,IND,IR,BK,NM,NTM
INTEGER GPEAK,SPARE1,SPARE2,SPARE3,SPARE4,SPARE7
INTEGER ISWD,MAD
INTEGER NUSPEC,NMASS,OVLAP
INTEGER SECOND
INTEGER PASS1
INTEGER QDUBLT,OSATS,NLINE,BEDROK,AJACEN,SATLST,SATINX
REAL ISVP8,ISVP9
REAL HIST(10),YVAL
REAL SPARE5,SPARE6
REAL QNORM,RATIO
REAL PERCNT
REAL*8 GTHT
COMMON PKHIST(20),NPHIST(20)
COMMON YVAL(11)
COMMON GM4,GM3,GM2,GM1,G0,GP1,GP2,GP3,GP4
COMMON SG,SG2,SG,SI,S12,AN,AA,BB,CC,DD
COMMON NAME(32),RDATE(5),BITMAP(64),GCTIME
COMMON LIBMAP(17),INTEG,LOMASS,HIMASS,POINTS,TAPCNT
COMMON MAXSP,LSTCNT,DEVICE(5),SPCNO
COMMON SPEC(14,411),IND(3,411),NUSPEC(411),NMASS
COMMON RMAX(3),IR(3),BK(3),NM(3),NTM(3),GPEAK(3,11)
COMMON SPARE1,SPARE2,SPARE3,SPARE4,SPARE5,SPARE6,SPARE7
COMMON RATMIN,RATEMX,SIGY0,SIGNXT,SIGLST
COMMON ISVN8,ISVN9,ISVP8,ISVP9,SIGMA7,SATVAL,SATMAX
COMMON MODE1,MODE2,NLWCUT,NUPCUT,SATPKS(25),NSAT,EXPNAM(5)
COMMON /CSATLS/SATLST(25),SATINX
COMMON /MODES/SGMODE(3),SHMODE(3),GMODE,HMODE
COMMON /ERRORS/RMASS,ERRMAX,NERR,SIGERR,SECOND(411)
COMMON /DUBFLG/IDUB
COMMON /AJACNT/AJACEN(2)
COMMON /DUBBUG/IDEBUG
COMMON /CHEMPO/QDUBLT,QNORM,OSATS,NLINE
COMMON /QUIXOT/IQUIT
COMMON /LSO/PASS1
COMMON /CRATM/RATMDX
COMMON /IMAD/MAD

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COMMON /UNITS/ IRDR,IPTR1,IPTR2,IPTR3,IIN,IOUT          00008360
EQUIVALENCE (YVAL(1),YM5),(YVAL(2),YM4),(YVAL(3),YM3)    00008370
EQUIVALENCE (YVAL(4),YM2),(YVAL(5),YM1),(YVAL(6),Y0)    00008380
EQUIVALENCE (YVAL(7),YP1),(YVAL(8),YP2),(YVAL(9),YP3)    00008390
EQUIVALENCE (YVAL(10),YP4),(YVAL(11),YP5)                00008400
DATA HIST/-1.0,-.6667,-.3333,0...3333,.6667,1.,1.3333,1.6667,2./ 00008410
DATA PERCENT/.0125/                                       00008420
DATA GTHT/'GETHGT'/                                       00008430
DATA BEDROK/40/                                           00008440
I1=NS-13-14*((NS-14)/14)                                  00008450
I2=NS-12-14*((NS-13)/14)                                  00008460
I3=NS-11-14*((NS-12)/14)                                  00008470
I4=NS-10-14*((NS-11)/14)                                  00008480
I5=NS-9-14*((NS-10)/14)                                    00008490
I6=NS-8-14*((NS-9)/14)                                    00008500
I7=NS-7-14*((NS-8)/14)                                    00008510
I8=NS-6-14*((NS-7)/14)                                    00008520
I9=NS-5-14*((NS-6)/14)                                    00008530
I10=NS-4-14*((NS-5)/14)                                   00008540
I11=NS-3-14*((NS-4)/14)                                   00008550
I12=NS-2-14*((NS-3)/14)                                   00008560
I13=NS-1-14*((NS-2)/14)                                   00008570
I14=NS-14*((NS-1)/14)                                     00008580
C *** ONLY GO HERE ON FIRST PASS TO COLLECT ANY PEAKS    00008590
C *** THAT MIGHT HAVE BEEN INVOLVED IN A DOUBLET WITH    00008600
C *** THE LAST COMPONENT THAT WAS PROCESSED ALSO         00008610
C *** ZERO OUT SATURATION PARAMETERS.                    00008620
C STATEMENT BELOW HAS BEEN COMMENTED OUT BECAUSE OF CALL TO 00008630
C FUNCTION SUBROUTINE SCAN.....RTI - WFH 11/20/78         00008640
C DIVIS = HIMASS - LOMASS                                  00008650
C IF ( NDIS .EQ. 2 .AND. AJACEN(1) .EQ. 1 ) PASS1 = 0     00008660
C MAKE SURE WE SET UP RIGHT IN BACKSLQ IF WE DON'T SCAN FOR M10 00008680
C IF ( NDIS .NE. 1 ) GO TO 6                               00008690
C NDIS = 1 ON FIRST PASS                                   00008700
C NSAT=0                                                    00008710
C SATMAX=0                                                  00008720
C RMASS = 32000                                             00008730
C ERRMAX = 0                                                00008740
C NERR = 0                                                  00008750
C SIGERR = 0                                                00008760
C QHDEM = 1.0                                              00008770
C QDUBLT = 0                                                00008780
C QSATS = 0                                                 00008790
C HELLO JOEF DROMEY.....WHERE EVER YOU ARE...TAO        00008800
C DO 1 I = 1,411                                           00008810
C SECOND(I) = 32767                                        00008820
C IF(QVLAP.EQ.0) GO TO 6                                   00008830
C HERE IF OVERLAPPING ELUTANT AHEAD.                      00008840
C GMX=0.0                                                  00008850
C HMX=0.0                                                  00008860
C QDUBLT = 1                                               00008870
C IDUB IS FLAG FOR SETGHY                                  00008880
C IDUB = 1                                                 00008890
C DO 5 J=1,14                                              00008900
C IF(GMX.LT.GNU(J)) GMX=GNU(J)                            00008910
C IF(HMX.LT.HNU(J)) HMX=HNU(J)                            00008920
C CONTINUE                                                 00008930

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C      NORMALIZE MODELS TO 1.0
      GMX=1.0/GMX
      HMX=1.0/HMX
      DO 7 J=1,14
      GNU(J)=GNU(J)*GMX
      HNU(J)=HNU(J)*HMX
7      CONTINUE
6      CONTINUE
C      *** NOW START LOOPING THROUGH ALL THE SAVED MASSES
      NMS=NM(MN)
      DO 500 MD=1,411
      IF ( NUSPEC(MD) .NE. -1 ) GO TO 500
C      NUSPEC(M) NE -1 IF INTENSITIES FROM EARLIER ELUTANT HAVE
C      BEEN ALREADY COMPUTED.
      M=IND(MN,MD)
      IMASS = M
C      M < 0 MEANS MASS ALREADY CONSIDERED AS A COMPONENT OF PREVIOUS
C      SPECTRUM.
      IF (M .LT. 0) GO TO 500
C      IF M = 0 THEN MASS WAS NOT DETECTED AS PEAKING IN TLOC, SO TRY
C      FOR POSSIBLE DOUBLET.
      IF(M.EQ.0) M = MD
      MI=M+39
      Y0=SPEC(18,M)
C THIS MOD MADE AT RT1 BECAUSE NO POSSIBLE REASON WAS SEEN
C FOR HAVING AN EQ INSTEAD OF A GE IN
C THIS SITUATION.
C      WFH - RT1 6/14/78
      IF(Y0.GE.SATVAL) GO TO 120
C      IF A DOUBLET IS DETECTED RUN ALL MASSES THROUGH DOUBLET RESOLVER
      IF(OVLAP.EQ.1) GO TO 130
C      IF IMASS IS ZERO ,THEN
C      NO SINGLET CONTRIBUTION DETECTED IN TLOC.
      IF(IMASS .EQ. 0) GO TO 500
      IF ( NDIS .EQ. 1 .AND. AJACEN(1) .EQ. 1 ) GO TO 500
C      DON'T PROCESS ANY PASS ONE SINGLET(MN=M1) IF A SPECTRUM
C      IMMEDIATELY PRECEDING THE CURRENTLY DETECTED SPECTRUM
C      WAS DETECTED.SINCE THIS SPECTRUM IS FOR MN=M2,
C      AND WE DON'T WANT TO INCLUDE SINGLET FROM PREVIOUS SPECTRUM
C      IN IT'S IMMEDIATE SUCCESSOR.
C      BUT, WE MUST PROCESS SATURATED PEAKS IN ALL CASES.
      YM1=SPEC(17,M)
      YP1=SPEC(19,M)
      YM5=SPEC(13,M)
      YP5=SPEC(113,M)
      YM4 = SPEC(14,M)
      YP4=SPEC(112,M)
      YM2=SPEC(16,M)
      YP2=SPEC(110,M)
      YM3=SPEC(15,M)
      YP3=SPEC(111,M)
C      PUT MASSES ON MODE OF PEAK USING CUBIC INTERPOLATION
      CALL NEWTOP(YVAL,RATEST,XTOP,YTOP,4)
C      MAKE SURE PEAKS ARE RISING FASTER THAN BACKGROUND.
C      THIS IS A VERY MINIMAL APPROXIMATIO OF BACKGROUND.
      IF( (YTOP-YM5) .LT. 90 .AND. (YTOP-YP5) .LT. 90 ) GOTO 500
C      *** APPLY MINIMUM RATE CRITERION FOR HIGH MASS
C      *** PEAKS THAT CAN'T BE ISOTOPE PEAKS. TH'S ELIMINATES

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C      *** BACKGROUND PEAKS AT THE LEADING EDGE OF COMPONENTS      00009520
C      *** NOTE THE COMPUTED RATES FOR BACKGROUND PEAKS ARE      00009530
C      *** ARE ALWAYS LOW BECAUSE THEIR INTENSITY VARIATION      00009540
C      *** IS CAUSED BY A DIFFERENT PROCESS TO NORMAL MASS      00009550
C      *** CHROMATOGRAM PROFILES FOR REAL COMPONENTS.      00009560
C      IF(RATEST.LT..095) GO TO 500      00009570
C      IF(M.LT. 140) GO TO 25      00009580
C      IF(RATEST.LT. RATMIN) GO TO 500      00009590
C      *** CORRECT FOR FINITE SWEEP OFFSET      00009600
C      *** REJECT ODDBALL PEAK-MODES      00009610
C      CONTINUE      00009620
C      CONTINUE      00009630
C      *** HERE FOR EXCLUSION TEST ON PEAK TOP RELATIVE TO      00009640
C      *** HISTOGRAM MODE - IF "IH" IS OUTSIDE LIMITS THEN      00009650
C      *** PEAK IS REJECTED.      00009660
C      IF(XTOP.LE. -1.5 .OR. XTOP.GE. 1.5) GO TO 500      00009670
C      THE ABOVE REJECTS ANY PEAKS WITH FUNNY SHAPES, OR MODES NOT      00009680
C      IN HISTOGRAMMIC WINDOW.      00009690
C      MI=M+39      00009700
C      MI=M+39      00009700
C      FUNCTION SUBROUTINE CALL HAS BEEN SUBSTITUTED FOR ARITHMETIC      00009710
C      IN ORDER TO ACCOMODATE MAGNETIC INSTRUMENTS...      00009720
C      RTI - WFM 11/20/78      00009730
C      TSHIFT = (MI - LDMASS)/DIVIS      00009740
C      TSHIFT = SCAN(MI)      00009750
C      XTOP = XTOP + TSHIFT      00009760
C      DO 600 IJ = 1,10      00009770
C      IF(XTOP.LT. HIST(IJ)) GO TO 700      00009780
C      CONTINUE      00009790
600      IH = IJ + (NDIS-1) * 3 - 4      00009800
700      IH IS IN ONE THE THREE SETS 1-3 TO 60, 10 TO 90, 13 TO 120      00009810
C      AS A FUNTION OF NDIS = 1,2,3      00009820
C      SEE IF HISTOGRAM INDEX IS OUT OF RANGE OF DETECTED SPECTRUM      00009830
C      ***** BELOW USED TO SAY IH.GE.NLWCUT*****12/19 CHANGED      00009840
C      IF(IH.LT.NLWCUT.OR.IH.GT.NUPCUT) GO TO 500      00009850
C      WE NOW SEE IF THE DATA WILL PASS OVER A FLOOR      00009860
C      BELOW YTOP.      00009870
C      FLUSH = PERCNT * YTOP      00009880
C      BUBBLE = PERCNT * G(5)      00009890
C      GET MAX+ FLUSH,BUBBLE 0      00009900
C      IF ( FLUSH.LT. BUBBLE ) FLUSH = BUBBLE      00009910
C      GET MIN+ 70,FLUSH 0      00009920
C      IF ( 70.LT. FLUSH ) FLUSH = 70      00009930
C      GET MAX+ BEDROK,FLUSH 0      00009940
C      IF ( BEDROK.GT. FLUSH ) FLUSH = BEDROK      00009950
C      FLOOR = YTOP - FLUSH      00009960
C      *      00009970
C      *      00009980
C      *      00009990
C      *      00010000
C      *      00010010
C      *      00010020
C      *      00010030
C      *      00010040
C      *      00010050
C      *      00010060
C      *      00010070
C      *      00010080
C      Y13      YTOP      YP3
C      IF THE CURVE STAYS ABOVE THE FLOOR IT GETS FLUSHED ← FLOOR
C      DO 110 II = 3,9
C      IF ( YVAL(II) .LE. FLOOR ) GO TO 111
110      CONTINUE
GO TO 500

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C      .... AND AWAY WE GOOOOOOOOOOOOOOOO ..... BLUB ...
111  CONTINUE
    CALL BLEED(YVAL(3),OITAR)
C
C THIS IS A TEMPORARY MOD IN ORDER TO GATHER STATICS ON
C THE INPUT PARAMETER ERRATIO - CODE 2
C      LFH RTI 9/31/78
C      ISPC=SPCND
C      ITYP=2
C      WRITE(20,6250) ITYP,ISPC,OITAR,OITAR
C6250  FORMAT(A4,A4,16X,A4,4X,A4)
C      IF ( OITAR .LT. RATMAX ) GO TO 500
C      THE ABOVE FITS A LINE TO Y13 THRU YP3, AND
C      RETURNS OITAR = (MEAN SQUARE ERR)/(AVERAGE VALUE Y )
C      *** THROW AWAY MASS INDEX SO THAT IT CAN'T BE INCLUDED
C      *** IN SPECTRUM OF NEXT-DETECTED COMPONENT
C      IND(MN,MD) = -1
C      PUT MASSES ON SAME TIME CO-ORDINATE AS MODEL
C      CALL TIMESF(TSHIFT,YVAL,11,GMODE)
C      *** NOW COMPUTE AND REMOVE LINEAR BACKGROUND BY
C      *** LEAST SQUARES METHOD USING MODEL PEAK - THE
C      *** CORRECTED INTENSITY IS RETURNED AS *PKHGT*
C      CALL BACLSQ(PKHGT)
C      PEAKS OF INTENSITY < 10 ARE CONSIDERED AS ARTIFACTS OF
C      THE SINGLET RESOLVER
C      IF ( PKHGT .LT. 10 ) GO TO 500
C      NUSPEC(M)=PKHGT
C      GO TO 500
C      *** HERE FOR HANDLING SATURATED PEAKS BY RATIO
C      *** APPROACH THAT USES NON - SATURATED VALUES OF PEAK
C      *** TOGETHER WITH THE MODEL PEAK FOR THE COMPONENT TO
C      *** COMPUTE THE AMPLITUDE (LESS BACKGROUND) OF THE
C      *** SATURATED PEAK, JUMP OVER IF SATURATED PEAK HAS BEEN
C      *** PROCESSED IN AN EARLIER PASS BY *GETHGT*
120  CONTINUE
    NUSE = NUSPEC(M)
    IF ( NUSE .LT. 0 .AND. NUSE .NE. -1 ) GO TO 500
C      NUSE < 0 IF THIS PEAK HAS BEEN PROCESSED IN EARLIER PASS
C      NOTE: IF NUSE = -1 IT HASN'T BEEN PROCESSED YET.
    IF (NSAT.GE.25) GO TO 500
    NSS=NS+2-NDIS
    CALL SATLSQ(NSS,M,RPKHGT,G,SPEC,SATVAL,MODE1,OVLAP,MODE2,PKH1ST)
C      *** SAVE COMPUTED HEIGHT FOR LATER SO THAT IT CAN BE
C      *** NORMALIZED TO INTEGER SIZE
    IF ( IQUIT .EQ. 1 ) GO TO 500
C      IQUIT = 1 IF SATURATED VALUES MODE IS NOT "NEAR"
C      SPECTRUM.
C      IQUIT = 2 IF WE WANT TO SKIP PEAK BECAUSE IT DOESN'T
C      BELONG IN THIS SPECTRUM, IT WAS IN OVERLAPPING PREDECESSOR.
    IF ( IQUIT .NE. 2 ) GO TO 125
    NUSPEC(M) = -2
    GO TO 500
125  CONTINUE
    NSAT=NSAT+1
    SATPKS(NSAT)=RPKHGT
C      RPKHGT IS < 0 IF SUPERSATURATION ENCOUNTERED
    NUSPEC(M) = -NSAT - 2
C      SAVE MAXIMUM SATURATED VALUE ENCOUNTERED FOR NORMALIZATION

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	IF(SATMAX.GT.RPKHGT) GO TO 500	00010670
	SATMAX=RPKHGT	00010680
	GO TO 500	00010690
C	*** HERE FOR HANDLING DOUBLETS IN THE SET	00010700
130	CONTINUE	00010710
C	RUN ALL MASSES THROUGH DOUBLET RESOLVER IF OVLAP=1, IE,	00010720
C	DOUBLET SITUATION DETECTED.	00010730
	IGPOS=MODE1	00010740
	IHPOS=MODE2	00010750
C	NSD=NS+3-NDIS	00010760
	IF(NDIS .NE. 2) GO TO 500	00010770
C	ONLY GO THROUGH DOUBLET RESOLVER WHEN WE ARE LOOKING AT	00010780
C	"SPECTRUM 7".	00010790
	CALL SETGHY(NS,M,GNU,HNU,IGPOS,IHPOS,1DUB,GMX)	00010800
C	DO NOT MARK MASS AS ALREADY FOUND "CONTRIBUTION" BY SETTING	00010810
C	IND(MH,MO) = 0.	00010820
C	SINCE THE DOUBLET RESOLVER SAVES THE LARGEST CONTRIBUTION IN	00010830
C	THE ARRAY NUSPEC(M).	00010840
500	CONTINUE	00010850
C	*** HERE ONLY ON THIRD PASS AND ONLY THEN IF ANY	00010860
C	*** SATURATED PEAKS HAVE BEEN FOUND. NEED TO NORMALIZE	00010870
C	*** SO THAT EXTRAPOLATED VALUES CAN BE SAVED AS INTEGERS	00010880
	IF(NSAT .EQ. 0 .OR. NDIS .NE. 3) RETURN	00010890
C	SET LOWER BOUND ON SATINX. THIS ARRAY IS USED IN SATLSQ.	00010900
	J = 26	00010910
	DO 723 1 = 1,25	00010920
	J = J - 1	00010930
	IF (SATLST(J) .NE. 0) GO TO 750	00010940
723	CONTINUE	00010950
750	CONTINUE	00010960
	SATINX = J	00010970
	AMXNU=0.0	00010980
C	GET MAXIMUM VALUE IN SPECTRUM	00010990
	DO 503 J=1,411	00011000
	IF(NUSPEC(J).GT.AMXNU) AMXNU=NUSPEC(J)	00011010
503	CONTINUE	00011020
C	SATMAX WILL BE 0 IF ONLY SUPERSATURATION ENCOUNTERED..	00011030
	IF (SATMAX .EQ. 0) SATMAX = SATVAL	00011040
	IF(AMXNU.GT.SATMAX) SATMAX=AMXNU	00011050
	AMXNU = SATMAX	00011060
C	NORMALIZE TO 32000	00011070
	SATMAX=32000.0/SATMAX	00011080
C	NUSPEC(J) < 0 .IF SATURATED VALUE FOR THAT MASS	00011090
	DO 530 J=1,411	00011100
	IF(NUSPEC(J)) 510,530,520	00011110
C	HERE IF SATURATED VALUE	00011120
510	IF (NUSPEC(J) .EQ. -1) GO TO 530	00011130
	IF (NUSPEC(J) .EQ. -2) GO TO 530	00011140
	NC = -NUSPEC(J) - 2	00011150
C	SATPKS(NC) < 0 IF SUPER SATURATION.	00011160
	IF (SATPKS(NC) .LT. 0) SATPKS(NC) = AMXNU	00011170
	NUSPEC(J)=SATPKS(NC)*SATMAX	00011180
	QSATS = QSATS + 1	00011190
C	*** USE C13 ISOTOPE TO ASSIGN SATURATED PEAK TO THE	00011200
C	*** APPROPRIATE COMPONENT WHEN THERE ARE TWO COMPONENTS	00011210
C	*** CLOSE TOGETHER	00011220
C	OVLAP = 0 MEANS NO ELUTANT DETECTED AHEAD AND CLOSE	00011230
	IF(OVLAP .EQ. 0) GO TO 530	00011240

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C      NUSPEC(J+1) NOT EQUAL ZERO MEAN ISOTOPE PRESENT IN THIS      00011250
C      ELUTANT                                                       00011260
      IF ( NUSPEC(J+1) .EQ. 0 ) GO TO 511                             00011270
      IF ( NUSPEC(J+1) .EQ. -1 ) GO TO 511                             00011280
      GO TO 530                                                         00011290
511    NUSPEC(J) = 0                                                  00011300
      MY = J + 39-MAD                                                 00011310
      QSATS = QSATS - 1                                               00011320
      IF ( IDEBUG .EQ. 0 ) GO TO 530                                   00011330
      WRITE(IPTR2,1000) MY                                           00011340
      GO TO 530                                                         00011350
520    NUSPEC(J)=NUSPEC(J)*SATMAX                                     00011360
530    CONTINUE                                                       00011370
      IF ( QSATS .GE. 1 ) QNORM = SATMAX                              00011380
      RETURN                                                           00011390
C3222  FORMAT(// ' ADJACENT FLAG =',I3//)                             00011400
1000    FORMAT(// ' MASS ',I3,' HAS NO C13 ISOTOPE PEAK ',//)        00011410
      END                                                             00011420
      SUBROUTINE KAPUT( SPECNO,TOTION,TICRAT,ABMAX )                  00011430
      REAL TOTION,ABMAX                                              00011440
      INTEGER SPECNO,TICRAT                                          00011450
      COMMON /SLOTNO/NSLOT                                           00011460
      COMMON /CFSTPG/FSTPGE                                           00011470
      COMMON /CHEMPO/ODUBLT,QNORM,QSATS,NLINE                       00011480
      COMMON /UNITS/ IRDR,IPTR1,IPTR2,IPTR3,IIN,IOUT               00011490
      INTEGER ODUBLT,QSATS,NLINE,ITOTS,NSLOT,FSTPGE                 00011500
      REAL QNORM                                                      00011510
      REAL YES1// 'YES'//YES// 'NO'//                                00011520
      THIS ROUTINE DOES THE CHEMIST'S PRINTOUT                       00011530
      ODUBLT 1 IF THE SPECTRA IS FIRST ELUTANT OF DUBLET.           00011540
      QSATS   NO. OF SATURATED PEAKS IN SPECTRUM.                  00011550
      NLINE   LINE COUNT FOR EACH PAGE.                             00011560
      SPECNO   SPECTRUM NUMBER                                       00011570
      TOTION   TOTAL ION CURRENT OF SPECTRUM.                      00011580
      TICRAT   CLEANUP RATIO(SEE OUTDAT FOR DETAILS).              00011590
      ABMAX    MAXIMUM AMPLITUDE OF SPECTRUM.                      00011600
      NSLOT = NSLOT + 1                                              00011610
      IF(NSLOT.EQ.1)WRITE(IPTR3,1000)                                00011620
      YES1=YES                                                         00011630
      IF ( ODUBLT .EQ. 0 )YES1=YN0Y                                    00011640
      WRITE(IPTR3,2000) NSLOT,SPECNO,TOTION,TICRAT,ABMAX,YES1,QSATS 00011650
      RETURN                                                           00011660
1000    FORMAT(' SLOT SPEC.* TOTION TICRAT MAX. AMP DOUBLET?      00011670
      *SAT. PEAKS '//)                                                00011680
2000    FORMAT(3X,I3,5X,I5,3X,F8.0,3X,I3,4X,F8.0,4X,A4,6X,I3)      00011690
      END                                                             00011700
      SUBROUTINE LKAHED(NS,M2,M3,OVLAP,G,H)                          00011710
      THIS COMPUTER PROGRAM WAS DEVELOPED WITH THE FUNDING SUPPORT 00011720
      FROM THE NATIONAL INSTITUTES OF HEALTH (GRANTS RR-612 AND    00011730
      GM-20832) AND THE NATIONAL AERONAUTICS AND SPACE ADMINISTRATION 00011740
      (GRANT NGR-05-020-632).                                         00011750
      *** THIS ROUTINE USES THE SAME TECHNIQUES AS 'TLOC'          00011760
      *** TO LOOK BEYOND THE PROCESSING WINDOW AND DETECT         00011770
      *** IF THERE ARE ANY NEW COMPONENTS NEARBY. THIS IS         00011780
      *** IMPORTANT FOR COMPENSATING FOR OVERLAP                   00011790
      ***                                                           00011800
      ***                                                           00011810
      ***                                                           00011820

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C      *** INTERACTIONS USING THE DOUBLET RESOLVER. 00011830
C      *** A MODEL PEAK IS SELECTED FOR ANY COMPONENT THAT 00011840
C      *** IS COMING UP DIRECTLY. THE RELATIVE DISTANCE 00011850
C      *** BETWEEN NEIGHBORING COMPONENTS IS ESTABLISHED 00011860
C      *** ACCURATELY FROM THE LOCAL HISTOGRAM PROFILES. 00011870
C 00011880
C      REAL ISVP8,ISVP9 00011890
C      INTEGER NAME,RDATE,BITMAP,GCTIME,LIBMAP,INTEG,LOMASS 00011900
C      INTEGER HIMASS,POINTS,TAPCNT,MAXSP,LSTCNT,DEVICE,SPCNO 00011910
C      INTEGER SPEC,IND,IR,BK,NM,NTM,BUBBLE 00011920
C      INTEGER GPEAK,SPARE1,SPARE2,SPARE3,SPARE4,SPARE7 00011930
C      REAL SPARE5,SPARE6 00011940
C      INTEGER NUSPEC,NMASS,OVLAP 00011950
C      INTEGER NSP2,NSP3,NT2,NT3,SCNDPK,NERR,SECOND 00011960
C      REAL NXTRTE,RASS,ERRMAX,SIGERR 00011970
C 00011980
C      DIMENSION SCNDPK(3,11),NXTRTE(3),H(11),G(9) 00011990
C      COMMON PKHIST(20),NPHIST(20) 00012000
C      COMMON Y15,Y14,Y13,Y12,Y11,Y0,YP1,YP2,YP3,YP4,YP5 00012010
C      COMMON GM4(9) 00012020
C      COMMON SG,SG2,SIG,S1,S12,AN,AA,BB,CC,DD 00012030
C      COMMON NAME(32),RDATE(5),BITMAP(64),GCTIME 00012040
C      COMMON LIBMAP(17),INTEG,LOMASS,HIMASS,POINTS,TAPCNT 00012050
C      COMMON MAXSP,LSTCNT,DEVICE(5),SPCNO 00012060
C      COMMON SPEC(14,411),IND(3,411),NUSPEC(411),NMASS 00012070
C      COMMON RMAX(3),IR(3),BK(3),NM(3),NTM(3),GPEAK(3,11) 00012080
C      COMMON SPARE1,SPARE2,SPARE3,SPARE4,SPARE5,SPARE6,SPARE7 00012090
C      COMMON RATMIN,RATEMX,SIGY0,SIGNXT,SIGLST 00012100
C      COMMON ISVN8,ISVN9,ISVP8,ISVP9,SIGMA7,SATVAL,SATMAX 00012110
C      COMMON MODE1,MODE2,NLWCUT,NUPCUT,SATPKS(25),NSAT,EXPNAM(5) 00012120
C      COMMON /CAHEA/AHEAD(5) 00012130
C      COMMON /ERRORS/RASS,ERRMAX,NERR,SIGERR,SECOND(411) 00012140
C      COMMON /MODES/ SGMODE(3),SHMODE(3),GMODE,HMODE 00012150
C      COMMON /IFF/JFLAG(3) 00012160
C      COMMON /PARAMS/MINTIC,MINNY,NTHIRD,RATM 00012170
C      COMMON /MASSES/ISGMAS(3),ISHMAS(3),IGMASS,IHMASS 00012180
C      COMMON /UNITS/ IRDR,IPTR1,IPTR2,IPTR3,IIN,IOUT 00012190
C      INTEGER ONE,TWO,THREE,FOUR,FIVE,SIX,UNION,AHEAD 00012200
C      DIMENSION IFLAG(3) 00012210
C 00012220
C 00012230
C      REAL*8 ILKA 00012240
C      DATA ONE/ 1/,TWO/2/,THREE/3/,FOUR/4/,FIVE/5/,SIX/6/ 00012250
C      DATA ILKA/'LKAHED'/ 00012260
C      ***** 00012270
C      DO 3 I=12,20 00012280
C      NPHIST(I)=0 00012290
C      PKHIST(I)=0 00012300
C      CONTINUE 00012310
C      DO 4 I=1,25 00012320
C      SATPKS(I)=0.0 00012330
C      NSHIFT=0 00012340
C      NSP2=NS+1 00012350
C      REINITIALIZE ARRAY FOR SAVING SPECTRUM 00012360
C      DO 5 M=1,411 00012370
C      NUSPEC(M)=-1 00012380
C      UNION = 0 00012390
C      IF(OVLAP.EQ.0) GO TO 7 00012400

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C      OVLAP SET MEANS PRECEDING SPECTRUM CONTRIBUTED TO THIS ONE.      00012410
      OVLAP=0      00012420
      UNION = 1      00012430
C      UNION IS SET TO INDICATE WE WILL UNION SPECTRUM N-1'S      00012440
C      CONTRIBUTIONS WITH SPECTRUM N ONLY IF SPECTRUM N      00012450
C      DOESN'T HAVE AN OVERLAPPING ELUTANT.      00012460
7      CONTINUE      00012470
      CALL NXTMAX(SPEC,NSP2,RNS2,YNS2,NT2,SATVAL      00012480
&      ,SCNDPK,NXTRTE,NSHIFT,IFLAG)      00012490
      NSHIFT=1      00012500
      NSP3=NS+2      00012510
      CALL NXTMAX(SPEC,NSP3,RNS3,YNS3,NT3,SATVAL      00012520
&      ,SCNDPK,NXTRTE,NSHIFT,IFLAG)      00012530
      NSHIFT=2      00012540
      NSP4=NS+3      00012550
      CALL NXTMAX(SPEC,NSP4,RNS4,YNS3,NT4,SATVAL      00012560
&      ,SCNDPK,NXTRTE,NSHIFT,IFLAG)      00012570
C      SCAN FROM MODE1 + NTHIRD TO 13, SINCE THE CURRENT SPECTRUM      00012580
C      EFFECTS HIST(2-8) WITH MODE1 VARYING FROM 4 TO 6.      00012590
C      LOOKING FOR SPECTRUM IN +MODE1+NTHIRD,9 @      00012600
      NL=MODE1 + NTHIRD      00012610
C      SEE IF WE HAVE TO SCAN TOO CLOSE ( +7,8,9@)      00012620
      IF ( NL .GE. 10 ) GO TO 10      00012630
C      SO NL .LE. 9      00012640
      IDXL = NL      00012650
      IDXU = 9      00012660
      NU = 10      00012670
      IAHEAD = 2      00012680
      CALL DETEKT(PKHIST,NPHIST,OVLAP,NLWCUT,NUPCUT,NL,NU,IDXL ,IDXU,MODE      00012690
*DE2)      00012700
      IF ( OVLAP .EQ. 1 ) GO TO 26      00012710
C      SCAN +9,13@ FOR ELUTANT IN +10,12@      00012720
      NL = 9      00012730
10      IF ( NL .GE. 13 ) GO TO 20      00012740
      IAHEAD = 3      00012750
      NU=13      00012760
      IDXL=10      00012770
      IDXU=12      00012780
      CALL DETEKT(PKHIST,NPHIST,OVLAP,NLWCUT,NUPCUT,NL,NU,IDXL      00012790
&      ,IDXU,MODE2)      00012800
      IF(OVLAP.EQ.1) GO TO 26      00012810
      SEE IF SPECTRUM AHEAD IN +13,15@      00012820
C      NL = 12      00012830
20      NU = 16      00012840
      IDXL = 13      00012850
      IDXU = 15      00012860
      IAHEAD = 4      00012870
      CALL DETEKT(PKHIST,NPHIST,OVLAP,NLWCUT,NUPCUT,NL,NU,IDXL,IDXU,MODE      00012880
*2)      00012890
      IF ( OVLAP .EQ. 1 ) GO TO 26      00012900
C      SEE IF SPECTRUM AHEAD IN +16,18@      00012910
      NL = 15      00012920
      NU = 19      00012930
      IDXL = 16      00012940
C      IDXL=18      00012950
C      THIS SEEMED AN OBVIOUS TYPO, SO IDXL HAS BEEN CHANGED      00012960
C      TO IDXU AS IN THE STMT BELOW      00012970
C      WFH RTI 9/31/78      00012980

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IDXJ = 18                                00012990
IAHEAD = 5                                00013000
CALL DETEKT(PKHIST,NPHIST,OVLAP,NLWCUT,NUPCUT,NL,NU,IDXJ,MODE00013010
*2)                                       00013020
IF ( OVLAP .EQ. 0 ) GO TO 30             00013030
26 CONTINUE                             00013040
AHEAD(IAHEAD) = 1                       00013050
C SET SPECTRUM AHEAD FLAG               00013060
30 CONTINUE                             00013070
RC0 = .5                                00013080
RATEMX = RMAX(M2)                       00013090
RATHIN = RATEMX * 0.25 * RC0            00013100
GMODE=SGMODE(M2)                        00013110
JFLAG1 = JFLAG(M2)                     00013120
IGMASS = ISGMAS(M2)                    00013130
C STORE MODEL PEAK FOR THIS SPECTRUM    00013140
DO 2000 IJ=1,9                          00013150
2000 GM4(IJ) = GPEAK(M2,IJ+1)           00013160
IF(OVLAP.EQ.0) GO TO 95                 00013170
C HERE FOR OVERLAPPING SPECTRUM DOWN THE PIPE 00013180
MODEH=6+(MODE2-1)/3                    00013190
C MODEH IS RELATIVE SPECTRUM NUMBER OF OVER LAPPER. 00013200
C LABEL 40 HAS BEEN PUT TO BETTER USE.... 00013210
C RTI WFH 11/20/78                     00013220
IF(MODEH-10) 50,60,70                  00013230
50 INDXH=1                              00013240
GO TO 80                                00013250
60 INDXH=2                              00013260
GO TO 80                                00013270
70 INDXH=3                              00013280
80 CONTINUE                             00013290
SH=0.0                                  00013300
C STORE MODEL H                         00013310
C THIS MOD INSERTED TO HELP WITH POOR INITIALIZATION 00013320
C OF H-PEAK PARAMETERS.....           00013330
C RTI WFH 11/20/78                     00013340
IF(ISHMAS(INDXH).NE.-1)GO TO 40        00013350
OVLAP = 0                               00013360
RETURN                                  00013370
40 IF ( MODEH .NE. 8 ) GO TO 89         00013380
C IF SPECTRUM ELUTING AT SLOT 8,GIVE IT DETECTED THERE. 00013390
DO 88 I = 1,11                          00013400
H(I) = GPEAK(M3,I)                      00013410
SH = SH + H(I)                          00013420
88 IHMASS = ISGMAS(M3)                  00013430
HMODE = SGMODE(M3)                     00013440
IFLAG(INDXH) = JFLAG(M3)               00013450
GO TO 91                                00013460
89 CONTINUE                             00013470
HMODE = SHMODE(INDXH)                   00013480
IHMASS = ISHMAS(INDXH)                  00013490
DO 90 I=1,11                            00013500
H(I) = SCNDPK(INDXH,I)                  00013510
SH=SH + H(I)                            00013520
90 CONTINUE                             00013530
91 CONTINUE                             00013540
C SEE IF WEIRD H MODEL PEAK.           00013550
IF ( SH .LE. 0 ) OVLAP = 0             00013560

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	IF (SH .LE. 0) GO TO 95	00013570
	CALL TIMESF(HMODE,H.11,GMODE)	00013580
C	ALIGN H-MODEL TO G-MODEL'S TIME CO-ORDINATE.	00013590
	.. ANOTHER VOID .. EH DOGEN ..	00013600
95	CONTINUE	00013610
	SEE IF PREVIOUS SPECTRUM OVERLAPPED WITH THIS ONE.	00013620
C	IF (UNION .EQ. 0) GO TO 27	00013630
	BUBBLE = .01 * GM4(5)	00013640
C	UNION = 0 IF PREVIOUS ELUTANT NOT OVERLAPPING WITH THIS ONE.	00013650
C	WE WANT TO MAKE SURE THOSE "SMALL CONTRIBUTIONS"	00013660
C	WHEN CALCULATING THE CURRENT SPECTRUM USING	00013670
C	THE DOUBLET RESOLVER IN CONJUNCTION WITH THE PREVIOUS	00013680
C	OVERLAPPING ELUTANT GET USED IF WE ARE AGAIN IN	00013690
C	AN OVERLAPPING SITUATION.	00013700
	IF (OVLP .EQ. 0) GO TO 29	00013710
C	ONLY DO BELOW IF DOUBLET IS AGAIN A DOUBLET	00013720
	DO 28 M = 1,NMASS	00013730
28	IF (SECOND(M) .LE. BUBBLE) NUSPEC(M) = 0	00013740
	GO TO 27	00013750
C	OVLP = 1. SO AGAIN IN OVERLAPPING SITUATION. DON'T UNION	00013760
C	N-1 WITH N. RATHER, CALCULATE N'S SPECTRUM(EXCEPT FOR	00013770
C	ZERO CONTRIBUTIONS FROM N-1) USING DOUBLET RESOLVER.	00013780
29	CONTINUE	00013790
C	OVERLAP = 0 SO NO DOUBLET SITUATION.THEREFORE UNION.	00013800
C	SINCE UNION = 1 WE'LL UNION SPECTRUM N-1'S CONTRIBUTIONS	00013810
C	WITH OUR CURRENT SPECTRUM. N.	00013820
	DO 6 M = 1,411	00013830
	IF (SECOND(M) .LE. 10) SECOND(M) = 0	00013840
6	IF (SECOND(M) .NE. 32767) NUSPEC(M) = SECOND(M)	00013850
27	CONTINUE	00013860
	DO 2400 IJ=1,9	00013870
2400	G(IJ)=GM4(IJ)	00013880
	CALL LKAPRT(7,NPHIST,PKHIST)	00013890
C	THE ABOVE PRINTS THE SECOND HALF OF THE HISTOGRAMS.	00013900
	IF(JFLAG1 .EQ. 1) CALL LKAPRT(FIVE,I,R)	00013910
C	THIS HAPPENS IF THE MODEL IS FLAGGED AS FUNNY IN TLOC	00013920
	CALL LKAPRT(THREE,IGMASS,G)	00013930
C	PRINT MODELS	00013940
	IF(OVLP .EQ. 0) RETURN	00013950
	CALL LKAPRT(ONE,I,R)	00013960
C	THE ABOVE PRINTS 'OVERLAPPING SPECTRUM FOUND' MSG.	00013970
	IF(MODEH.GE.9.AND.MODEH.LE.11) GOTO 401	00013980
C	THE BELOW WRITES MODEH AS A WARNING THAT THE SECOND	00013990
C	ELUTANT IS VERY CLOSE	00014000
	CALL LKAPRT(TWO,MODEH,H)	00014010
401	CONTINUE	00014020
C	MODEH = 12 ONLY IF NEXT MAX IS IN SLOTS 19,20 OF HISTOS.	00014030
	CALL LKAPRT(FOUR,IMASS,H(2))	00014040
C	SEE IF FLAKEY MODEL WAS USED FOR INTERPOLATION	00014050
	IF(IFLAG(INDXH) .EQ. 1) CALL LKAPRT(SIX,I,H)	00014060
	RETURN	00014070
	END	00014080
C	THE CALL STATEMENT ALLOWS FOR PASSING OF ARRAYS	00014090
C	REALS AND INTEGERS.	00014100
C	THIS COMPUTER PROGRAM WAS DEVELOPED WITH THE FUNDING SUPPORT.	00014110
C	FROM THE NATIONAL INSTITUTES OF HEALTH (GRANTS RR-612 AND	00014120
C	GM-20832) AND THE NATIONAL AERONAUTICS AND SPACE ADMINISTRATION	00014130
C	(GRANT NGR-05-020-632).	00014140

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SUBROUTINE LKAPRT(N,IAR,AR)                                00014150
INTEGER N,IONE,NINE,MAD,IAR(20)                          00014160
INTEGER IAR(1)                                            00014170
REAL AR(1)                                                00014180
COMMON /DUBBUG/IFLAG                                     00014190
COMMON /IMAD/MAD                                          00014200
COMMON /UNITS/ IRDR,IPTR1,IPTR2,IPTR3,IIN,IOUT          00014210
DATA IONE,NINE/1,9/                                       00014220
C   IFLAG IS RESET IF NO PRINTING IS TO BE DONE/         00014230
IF (IFLAG.EQ.0) RETURN                                   00014240
IAR(1)=IAR(1)-MAD                                          00014250
IF(IAR(1).LT.0)IAR(1)=0                                   00014260
GO TO (80,90,100,110,120,130,140),N                     00014270
C   THE ABOVE IS A CASE STATEMENT FOR EXECUTING PRINT    00014280
80  WRITE(IPTR2,580)                                       00014290
RETURN                                                    00014300
C   THE ABOVE WRITE IS CALLED FROM LKAHD(BELOW ALSO)     00014310
90  WRITE(IPTR2,590) IAR(1)                               00014320
RETURN                                                    00014330
100 WRITE(IPTR2,1000) (AR(1), I = IONE,NINE),IAR(1)     00014340
RETURN                                                    00014350
110 WRITE(IPTR2,1100) (AR(1), I = IONE,NINE),IAR(1)     00014360
RETURN                                                    00014370
120 WRITE(IPTR2,1200)                                       00014380
RETURN                                                    00014390
130 WRITE(IPTR2,1300)                                       00014400
RETURN                                                    00014410
140 WRITE(IPTR2,1500)                                       00014420
DO 5 K=2,18                                                00014430
IAR(K)=IAR(K)-MAD                                          00014440
IF(IAR(K).LT.0)IAR(K)=0                                   00014450
5  CONTINUE                                                00014460
WRITE(IPTR2,530) (IAR(1), I = 10,18 )                   00014470
WRITE(IPTR2,535) ( AR(1), I = 10,18 )                   00014480
C   WRITES SECOND HALF OF HISTOGRAMS.                   00014490
RETURN                                                    00014500
580 FORMAT(/,' OVERLAPPING SPECTRUM FOUND')              00014510
590 FORMAT(' OVERLAPPING ELUTANT IS CLOSE. RELATIVE SPEC. =',I4) 00014520
1000 FORMAT(/,' MODEL USED FOR SINGLET RESOLUTION ',/.9F9.0, 00014530
-///,' MASS OF MODEL =',I3)                               00014540
1100 FORMAT(/,' MODEL USED FOR DOUBLET RESOLUTION ',/.9F9.0, 00014550
-///,' MASS OF MODEL =',I3,/,,' NOTE: THIS MODEL HAS BEEN' 00014560
-/,,' INTERPOLATED TO THE MASS OF THE SINGLET MODEL')     00014570
1200 FORMAT(' *** WARNING *** THIS SPECTRUM HAS A SUSPECT G-MODEL ' 00014580
-/,,' PEAK'/,,' POSSIBLE BACKGROUND PEAK USED AS MODEL'/' 00014590
-/,,' EXAMINE MODEL USING LOOK IF YOU ARE WARY'/' )      00014600
1300 FORMAT(' *** WARNING *** THIS SPECTRUM HAS A SUSPECT H-MODEL ' 00014610
-/,,' PEAK'/,,' POSSIBLE BACKGROUND PEAK USED AS MODEL'/' 00014620
-/,,' EXAMINE MODEL USING LOOK IF YOU ARE WARY'/' )      00014630
535  FORMAT(1X,9F9.0)                                     00014640
530  FORMAT(/,' PEAK HIST ',/.8X,9I6/' ION CURRENT HIST ') 00014650
1500 FORMAT(/,' HISTOGRAM POSITIONS 10 - 18 ...'/' )      00014660
END                                                        00014670
SUBROUTINE NEWTOP(Y,RATE,XTOP,YTOP,ISTART)               00014680
REAL RATE,XTOP                                           00014690
DIMENSION Y(11)                                          00014700
INTEGER ISTART                                           00014710
C

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XB = 2 * Y(4) - Y(5) - 2 * Y(6) - Y(7) + 2 * Y(8)
IF (XB .EQ. 0) RETURN
XTOP = .7 * (2 * Y(4) + Y(5) - Y(7) - 2 * Y(8)) / XB
DX = XTOP
K1 = DX - 1
K2 = DX - 2
K3 = DX + 1
C1 = (DX * (K1) * (K2)) / (-6)
C2 = ((K3) * (K1) * (K2)) / 2
C3 = ((K3) * (DX) * (K2)) / (-2)
C4 = ((K3) * (DX) * (K1)) / 6
C
C
C      INTERPOLATE
C
C      YTOP = Y(5) * C1 + Y(6) * C2 + Y(7) * C3 + Y(8) * C4
C      IS = ISTART - 1
C      ... SMOOTH PEAK A LITTLE BEFORE COMPUTING RATE.
C      Z(1) = (Y(1) + 1 * Y(2)) / 1.1
C      DO 275 I = 2, 10
C      Z(I) = (Y(I) + 1 * (Y(I-1) + Y(I+1))) / 1.2
275 CONTINUE
C      Z(11) = (Y(11) + 1 * Y(10)) / 1.1
C SEE MOD NOTE AT BEGINNING WFM RTI 9/31/78
C      DO 250 I = IS, 8
250 IF (Z(I) .EQ. 0) Z(I) = 1
C      CALCULATE RATE TO BE AN APPROXIMATION OF
C
C      INTEGRAL(DY/Y)      ... HIGH RATE FOR SHARP PEAKS.
C      RATE = 0
C SEE MOD NOTE AT BEGINNING WFM RTI 9/31/78
C      DO 300 I = ISTART, 6
300 RATE = RATE + (Z(I) - Z(I-1)) / Z(I-1)
C      DO 400 I = 6, 7
400 RATE = RATE + (Z(I) - Z(I+1)) / Z(I+1)
C      RETURN
C      END
C      SUBROUTINE NXTMAX(SPEC, NS, RATEMX, YMAX, NTMAX, SATVAL
C      , SCNDPK, NXTRTE, NSHIFT, IFLAG)
C
C      THIS COMPUTER PROGRAM WAS DEVELOPED WITH THE FUNDING SUPPORT
C      FROM THE NATIONAL INSTITUTES OF HEALTH (GRANTS RR-612 AND
C      GM-20832) AND THE NATIONAL AERONAUTICS AND SPACE ADMINISTRATION
C      (GRANT NGR-85-828-632). 1, ID2
C
C      INTEGER SPEC, SCNDPK, IFLAG(3)
C      INTEGER RDATE, BITMAP, GCTIME, HIMASS, POINTS, TAPCNT
C      INTEGER NX, NTMAX, IYD, ID1, ID2
C      DIMENSION SPEC(14, 411)
C      DIMENSION SCNDPK(3, 11), NXTRTE(3)
C      COMMON PKHIST(20), NPHIST(20)
C      COMMON YMS(11)
C      COMMON GM4, GM3, GM2, GM1, G0, GP1, GP2, GP3, GP4
C      COMMON SG, SG2, SIG, S1, S12, AN, AA, BB, CC, DD
C      COMMON NAME(32), RDATE(5), BITMAP(64), GCTIME
C      COMMON LIBMAP(17), INTEG, LOMASS, HIMASS, POINTS, TAPCNT
C      COMMON /MODES/SGMODE(3), SHMODE(3), GMODE, HMODE
C      COMMON /LFTRIT/ILEFT, IRIGHT
C      COMMON /MASSES/ISGMAS(3), ISHMAS(3), IGASS, IHMASS

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	EQUIVALENCE (YM4,YM5(2))	00015890
	EQUIVALENCE (YM3,YM5(3)),(YM2,YM5(4)),(YM1,YM5(5))	00015900
	EQUIVALENCE (Y0,YM5(6)),(YP1,YM5(7)),(YP2,YM5(8))	00015910
	EQUIVALENCE (YP3,YM5(9)),(YP4,YM5(10)),(YP5,YM5(11))	00015920
C	INTEGER LOCLBG,ILEFT	00015930
	REAL NXTRTE,SCAN	00015940
	REAL HIST(7),SLOPE,YM5MIN,YP5MIN	00015950
	DATA HIST/-.3333,0.,.3333,.6667,1.0,1.3333,1.6667/	00015960
C	*** ROUTINE TO LOOK AHEAD TO SEE IF THERE ARE ANY OTHER	00015970
C	*** SPECTRA IN THE LOCAL REGION OF CURRENT SPECTRUM	00015980
C		00015990
	I1=NS-13-14*((NS-14)/14)	00016000
	I2=NS-12-14*((NS-13)/14)	00016010
	I3=NS-11-14*((NS-12)/14)	00016020
	I4=NS-10-14*((NS-11)/14)	00016030
	I5=NS-9-14*((NS-10)/14)	00016040
	I6=NS-8-14*((NS-9)/14)	00016050
	I7=NS-7-14*((NS-8)/14)	00016060
	I8=NS-6-14*((NS-7)/14)	00016070
	I9=NS-5-14*((NS-6)/14)	00016080
	I10=NS-4-14*((NS-5)/14)	00016090
	I11=NS-3-14*((NS-4)/14)	00016100
	I12=NS-2-14*((NS-3)/14)	00016110
	I13=NS-1-14*((NS-2)/14)	00016120
	I14=NS-14*((NS-1)/14)	00016130
		00016140
		00016150
C	TAKE OUT - THIS STATEMENT NO LONGER NECESSARY WITH	00016160
C	SCAN SUBROUTINE INSERTED.	00016170
C		00016180
C	DIVISO = HIMASS - LOMASS	00016190
	RATEMX=0.0	00016200
	NTMAX=0	00016210
	NPOS=NSHIFT+1	00016220
C	NOW LOOP THROUGH MASSES	00016230
C		00016240
C	DO 60 M=1,411	00016250
		00016260
C	MI = M + 39	00016270
		00016280
C	MI IS THE ACTUAL MASS NUMBER	00016290
C		00016300
	Y0=SPEC(I8,M)	00016310
C	THIS MOD MADE AT RTI BECAUSE NO POSSIBLE REASON	00016320
C	WAS SEEN FOR HAVING AN ED INSTEAD OF A GE IN	00016330
C	THIS SITUATION.	00016340
		00016350
C	WFM - RTI 6/14/78	00016360
	IF(Y0,GE,SATVAL) GO TO 60	00016370
	YM1=SPEC(I7,M)	00016380
	IF(Y0,LE,YM1) GO TO 60	00016390
C	PEAK TOP A Y0	00016400
	YP1=SPEC(I9,M)	00016410
	IF(YP1,GE,Y0) GO TO 60	00016420
C	WE NOW HAVE Y0 AT TOP OF PEAK	00016430
40	YM2=SPEC(I6,M)	00016440
	YP2=SPEC(I10,M)	00016450
	YP3=SPEC(I11,M)	00016460

	YM3=SPEC(15,M)	00016470
	YM4 = SPEC(14,M)	00016480
	YP4=SPEC(112,M)	00016490
	YM5(1)=SPEC(13,M)	00016500
	YY5 = YM5(1)	00016510
	WE HAVE ONLY 14 SPECTRA IN CORE AT A TIME SO:	00016520
C		00016530
C	NSHIFT SPECTRA AVAILABLE	00016540
C	TO RIGHT OF MODE	00016550
C		00016560
C	0 5	00016570
C	1 4	00016580
C	2 3	00016590
	IF(NSHIFT-1) 41,42,43	00016600
41	YP5=SPEC(113,M)	00016610
	GO TO 44	00016620
42	YP5 = 0.0	00016630
	GO TO 44	00016640
43	YP4 = 0.0	00016650
	YP5 = 0.0	00016660
44	CONTINUE	00016670
C		00016680
C	GET HERE TO QUALIFY AS A SINGLET FOR HISTOGRAMMING	00016690
	IF (YM2 .GE. YM1) GO TO 60	00016700
	IF (YM3 .GE. YM2) GO TO 60	00016710
	IF (ILEFT .EQ. 3) GO TO 100	00016720
	IF (YM4 .GE. YM3) GO TO 60	00016730
100	CONTINUE	00016740
	IF (YP2 .GE. YP1) GO TO 60	00016750
	IF (YP3 .GE. YP2) GO TO 60	00016760
	IF (NSHIFT .EQ. 2) GO TO 200	00016770
	IF (YP4 .GE. YP3) GO TO 60	00016780
200	CONTINUE	00016790
C	PUT Y0 AT TOP OF PEAK	00016800
	CALL NEWTOP(YM5,RATE,XTOP,YTOP,4)	00016810
C	CHECK FOR NARROW RISING PEAK (CHAR. OF BACKGROUND) AND.	00016820
C	CHECK FOR PEAK MODE OUT OF BOUNDS. IF SO THE DATA HAD SOME	00016830
C	INFLECTION POINTS.	00016840
	YYM5=YTOP - YY5	00016850
	IF (NSHIFT .EQ. 0) YXS = YP5	00016860
	IF (NSHIFT .EQ. 1) YXS = YP4	00016870
	IF (NSHIFT .EQ. 2) YXS = YP3	00016880
	YYP5 = YTOP - YXS	00016890
	IF (YYP5 .LT. 30 .AND. YYM5 .LT. 30) GO TO 60	00016900
	IF(XTOP .LE. -1. .OR. XTOP .GE. 1.) GO TO 60	00016910
C	CHECK FOR SATURATION	00016920
	IF (YTOP .GE. SATVAL) GO TO 60	00016930
	IF (YM1 .GE. SATVAL) GO TO 60	00016940
	IF (YM2 .GE. SATVAL) GO TO 60	00016950
	IF (YM3 .GE. SATVAL) GO TO 60	00016960
	IF (YM4 .GE. SATVAL) GO TO 60	00016970
	IF (YP1 .GE. SATVAL) GO TO 60	00016980
	IF (YP2 .GE. SATVAL) GO TO 60	00016990
	IF (YP3 .GE. SATVAL) GO TO 60	00017000
	IF (YP4 .GE. SATVAL) GO TO 60	00017010
C	SEE IF WE HAVE MAXIMUM RATE	00017020
	IF (NSHIFT .GE. 1) GO TO 300	00017030
	SLOPE = (YP5 - YXS)/10.	00017040

300	LOCLBG = YYS + 5 * SLOPE	00017050
	CONTINUE	00017060
C	TSHIFT = (MI - LOMASS)/DIVISO	00017070
C	THIS SECTION CHANGED TO FUNCTION SUBROUTINE TO	00017080
C	GAIN INSTRUMENT COMPATABILITY.	00017090
C	WFH RTI 9/31/78	00017100
	TSHIFT=SCAN(MI)	00017110
	IF(RATE.LT.RATEMX) GO TO 50	00017120
	IF((YTOP - YYS) .GE. 160) GO TO 5000	00017130
C	IFLAG(NPOS) = 1	00017140
	FLAG FUNNY MODEL POSSIBLE	00017150
	GO TO 5500	00017160
5000	IFLAG(NPOS) = 0	00017170
5500	CONTINUE	00017180
C	GET HERE TO QUALIFY AS POSSIBLE MODEL FOR SPECTRUM	00017190
	RATEMX=RATE	00017200
C		00017210
C	USE A LINEAR BACKGROUND FIRST CUT APPROXIMATION.	00017220
C		00017230
	MODBGK = SPEC(I1,M)	00017240
C	PICK MIN + SPEC(IJ,M) : I1 .LE. IJ .LE. I5 0	00017250
	IF (MODBGK .GT. SPEC(I2,M)) MODBGK = SPEC(I2,M)	00017260
	IF (MODBGK .GT. SPEC(I3,M)) MODBGK = SPEC(I3,M)	00017270
	IF (MODBGK .GT. SPEC(I4,M)) MODBGK = SPEC(I4,M)	00017280
	IF (MODBGK .GT. SPEC(I5,M)) MODBGK = SPEC(I5,M)	00017290
	IF (NSHIFT .GE. 1) LOCLBG = MODBGK	00017300
C	USE CONSTANT BACKGROUND IF NO RIGHT END POINT AVAILABLE	00017310
	DO 450 IJ = 1,11	00017320
	SCNDPK(NPOS,IJ) = YMS(IJ) - MODBGK	00017330
450	CONTINUE	00017340
	SHMODE(NPOS) = TSHIFT	00017350
C		00017360
C	SAVE TSHIFT FOR LATER USE	00017370
C		00017380
	ISHMAS(NPOS) = MI	00017390
C	SAVE MASS OF MODEL PEAK	00017400
50	CONTINUE	00017410
	CONTRI = YTOP - LOCLBG	00017420
	IF (CONTRI .LE. 0) GO TO 60	00017430
	TITTY = TSHIFT + XTOP	00017440
	DO 500 I=1,7	00017450
	IF (TITTY .LE. HIST(I)) GO TO 600	00017460
500	CONTINUE	00017470
600	CONTINUE	00017480
	IH = 7 + I + 3*NSHIFT	00017490
C		00017500
C	IH IS IN ONE OF THE THREE SETS +8 TO 140,+11 TO 170 OR	00017510
C	+14 TO 200	00017520
C	AS A FUNCTION OF NSHIFT. NSHIFT = 0, 1 OR 2.	00017530
C		00017540
C	UPDATE HISTOGRAMS	00017550
C		00017560
	PKHIST(IH)=PKHIST(IH)+ CONTRI	00017570
	NPHIST(IH) = NPHIST(IH) + 1	00017580
CJUST A MINOR VOID ..HUI NENG..	00017590
60	CONTINUE	00017600
C		00017610
C		00017620

	NXTRTE(NPOS) = RATEMX	00017630
C	RETURN	00017640
	END	00017650
	SUBROUTINE OFFSET (G,H,GNU,HNU,GPOS,HPOS)	00017660
C		00017670
C	THIS COMPUTER PROGRAM WAS DEVELOPED WITH THE FUNDING SUPPORT	00017680
C	FROM THE NATIONAL INSTITUTES OF HEALTH (GRANTS RR-612 AND	00017690
C	GM-20832) AND THE NATIONAL AERONAUTICS AND SPACE ADMINISTRATION	00017700
C	(GRANT NGR-05-020-632).	00017710
C		00017720
C		00017730
C	*** THIS ROUTINE TAKES THE 'GPOS' AND 'HPOS' INFO	00017740
C	*** WHICH CHARACTERIZES WHERE ON THE SPECTRUM SCALE	00017750
C	*** TWO OVERLAPPING COMPONENTS ARE LOCATED WITH	00017760
C	*** RESPECT TO ONE ANOTHER AND MAKES THE NECESSARY	00017770
C	*** DISPLACEMENTS OF THE TWO MODEL PEAKS (ONE FOR	00017780
C	*** EACH OF THE OVERLAPPING COMPONENTS) WITH	00017790
C	*** RESPECT TO EACH OTHER SO THAT THEY CAN	00017800
C	*** BE USED BY THE DOUBLET RESOLVING ROUTINE	00017810
C	*** IN CONJUNCTION WITH THE RAW DATA FOR	00017820
C	*** THE DOUBLETS THAT HAVE TO BE RESOLVED AND	00017830
C	*** BACKGROUND CORRECTED.	00017840
		00017850
	DIMENSION G(9),H(11),GNU(18),HNU(18)	00017860
	INTEGER GPOS,HPOS,HNU(18),IHSPEC,JLOWER	00017870
	REAL*8 OFST	00017880
	DATA OFST/'OFFSET'/	00017890
C		00017900
C	***STRETCH OUT THE MODEL PEAKS A LITTLE	00017910
C		00017920
	DO 10 I=1,18	00017930
	GNU(I)=0	00017940
	HNU(I)=0	00017950
10	CONTINUE	00017960
C	PUT G AND H INTO LONGER ARRAYS SO THAT THEY CAN BE ALIGNED TO	00017970
C	SPECTRUM HISTOGRAMIC POSITIONS.	00017980
	DO 30 I=1,9	00017990
	GNU(I+2) = G(I)	00018000
30	CONTINUE	00018010
C	DON'T USE H(1), AND H(11).THESE ARE EXTRA FOR INTERPOLATION	00018020
C	IN LKARED.	00018030
	DO 110 I=1,9	00018040
	HNU(I) = H(I+1)	00018050
110	CONTINUE	00018060
C		00018070
C		00018080
C	ALIGN TO SPECTRUM OF H MODEL	00018090
C		00018100
	IHSPEC = 6 + (HPOS - 1)/3	00018110
C		00018120
C	6 .LE. IHSPEC .LE. 11	00018130
C		00018140
	JLOWER = IHSPEC - 4	00018150
	DO 1000 I= 1,9	00018160
	HNU(JLOWER) = HNU(I)	00018170
	JLOWER = JLOWER + 1	00018180
1000	CONTINUE	00018190
		00018200

C	NOU, HNU(IHSPEC) REPRESENTS THE MODE OF THE H-MODEL, AND	00018210
C	GNU(7) IS THE MODE OF THE G-MODEL	00018220
C		00018230
	RETURN	00018240
	END	00018250
	SUBROUTINE OUTDAT(SRLIB,NNAME)	00018260
	INTEGER NNAME(18),MIN,MINI,MAX,MAXI	00018270
	INTEGER MAD	00018280
	INTEGER PDATE(5),PNAME(32),FLAG	00018300
	INTEGER POINTX,TAPCNX,MAXSX	00018310
	INTEGER OUTSLT,MAXAMP,EXPNAM,TICRAT	00018320
	INTEGER NAME,RDATE,BITMAP,GCTIME,LIBMAP,INTEG,LOMASS	00018330
	INTEGER HIMASS,POINTS,TAPCNT,MAXSP,LSTCNT,DEVICE,SPCNO	00018340
	INTEGER SPEC,IND,IR,BK,NM,NTM	00018350
	INTEGER GPEAK,SPARE1,SPARE2,SPARE3,SPARE4,SPARE7	00018360
	INTEGER NUSPEC,NMASS,OVLAP,SRLIB(5)	00018370
	INTEGER JM(411),JSP(411)	00018380
	INTEGER QDUBLT,QSATS,NLINE	00018390
	INTEGER NUZEN,IMDLUT	00018400
	REAL RMT(411),RMSP(411)	00018410
	REAL CLASS(4)/4* ' '//,SUBCL(4)/4* ' '//	00018420
	REAL SPARE5,SPARE6	00018430
	REAL*4 TOTION,SIGMA7	00018440
	REAL ISVP8,ISVP9	00018450
	REAL QNORM,ABMAX	00018460
	REAL SATSUM,FORM(5)	00018470
	REAL*8 OTDT/' OUTDAT '//,SOURCE/' '//	00018480
	DIMENSION G(9),H(9),GNU(18),HNU(18)	00018490
	COMMON PKHIST(20),NPHIST(20)	00018500
	COMMON YM5,YM4,YM3,YM2,YM1,Y0,YP1,YP2,YP3,YP4,YP5	00018510
	COMMON GM4,GM3,GM2,GM1,G0,GP1,GP2,GP3,GP4	00018520
	COMMON SG,SG2,SIG,S1,S12,AN,AB,CC,DD	00018530
	COMMON NAME(32),RDATE(5),BITMAP(64),GCTIME	00018540
	COMMON LIBMAP(17),INTEG,LOMASS,HIMASS,POINTS,TAPCNT	00018550
	COMMON MAXSP,LSTCNT,DEVICE(5),SPCNO	00018560
	COMMON SPEC(14,411),IND(3,411),NUSPEC(411),NMASS	00018570
	COMMON RMAX(3),IR(3),BK(3),NM(3),NTM(3),GPEAK(3,11)	00018580
	COMMON SPARE1,SPARE2,SPARE3,SPARE4,SPARE5,SPARE6,SPARE7	00018590
	COMMON RATMIN,RATEMX,SIGY0,SIGNXT,SIGLST	00018600
	COMMON ISVN8,ISVN9,ISVP8,ISVP9,SIGMA7,SATVAL,SATMAX	00018610
	COMMON MODE1,MODE2,NLWCUT,NUPCUT,SATPKS(25),NSAT,EXPNAM(5)	00018620
	COMMON /PARAMS/INTIC,MINNY,NTHIRD,RATH	00018630
C	COMMON /SCR/ LIBBLK	00018640
	COMMON /ERRORS/ERRMIN,ERRMAX,NERR,SIGERR,IACERR(411)	00018650
	COMMON /PRNTEG/IPFLAG	00018660
	COMMON /MASSES/ISGMAS(3),ISHMAS(3),IGMASS,IHMASS	00018670
	COMMON /DUBBUG/IDEBUG	00018680
	COMMON /CHEMPO/QDUBLT,QNORM,QSATS,NLINE	00018690
	COMMON /IMAD/MAD	00018700
	COMMON /NA/PNAME	00018710
	COMMON /UNITS/ IRDR,IPTR1,IPTR2,IPTR3,IIN,IOUT	00018720
C	THESE EQUIVALENCE STMTS. HAVE BEEN FOUND SUPERFLUOUS IN	00018730
C	THE MULTIPLE RUN PROCESSING STRUCTURE OF CLEANUP	00018740
C	AND HAVE BEEN DELETED. THE VARIABLES INSIDE OUTDAT	00018750
C	WERE MODIFIED IN THE FOLLOWING MANNER:	00018760
C	EXPID,PDATE,AMP,LOMASX,HIMASX,LSTCNX,GCTIMX,	00018770
C	INTEGX - DELETED FROM OUTDAT	00018780
		00018790

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C      SPECNO - INCORPORATED INTO VARIABLE SPCNO          00018800
C      MAXAMP - SHIFTED TO SAVE EXECUTION TIME          00018810
C      TOTION.TICRAT - UNMODIFIED                      00018820
C      WM F HARGROVE                                  00018830
C      12/6/78                                         00018840
C      EQUIVALENCE(EXPID,LIBBLK(84))                   00018850
C      EQUIVALENCE(PDATE,LIBBLK(92))                   00018860
C      EQUIVALENCE(AMP,LIBBLK(257))                    00018870
C      EQUIVALENCE(LOMASX,LIBBLK(75))                  00018880
C      EQUIVALENCE(HIMASX,LIBBLK(74))                  00018890
C      EQUIVALENCE(SPECNO,LIBBLK(78))                  00018900
C      EQUIVALENCE(MAXAMP,LIBBLK(77))                  00018910
C      EQUIVALENCE(TOTION,LIBBLK(1))                   00018920
C      EQUIVALENCE(LSTCNX,LIBBLK(70))                  00018930
C      EQUIVALENCE(GCTIMX,LIBBLK(90))                  00018940
C      EQUIVALENCE(INTEGX,LIBBLK(89))                  00018950
C      EQUIVALENCE(ABMAX,LIBBLK(49))                   00018960
C      EQUIVALENCE(TICRAT,LIBBLK(72))                  00018970
C      DATA HOW/1H /                                  00018980
C      *****HERE WE GO*****                         00018990
C      TAPCNT 1000 IF WE ARE GOING TO WRITE THE BIT MAP 00019000
C      IF ( TAPCNT .EQ. 1000 ) GO TO 12                00019010
C THIS MOD INSERTED TO WEED OUT ELLUTANTS WHICH HAVE NO 00019020
C SUITABLE MODEL.....                                00019030
C      RTI WFH 11/21/78                                00019040
C      IF(IGMASS.GT.0)GO TO 91                          00019050
C      IF(IDEBUG.NE.0)WRITE(IPTR2,3334)                00019060
3334  FORMAT(1X,' SPECTRUM REJECTED FOR LACK OF SUITABLE MODEL') 00019070
C      RETURN                                           00019080
C      91 ISWEAK = IGMAS - 39                          00019090
C      IF ( NUSPEC(ISWEAK) .GT. 0 ) GO TO 93            00019100
C      IF ( IDEBUG .EQ. 0 ) GO TO 92                   00019110
C      INEW=IGMASS-MAD                                00019120
C      CALL TRACE(IGMASS,MAD)                          00019130
C THIS WRITE STMT HAS BEEN MADE CONDITIONAL TO SAVE PAPER 00019140
C      WFH RTI 9/31/78                                00019150
C      IF(IDEBUG.EQ.0)GO TO 92                         00019160
C      WRITE(IPTR2,3333) INEW1                        00019170
92      RETURN                                           00019180
93      CONTINUE                                         00019190
C      CALL ZERO(LIBBLK,1024)                          00019200
C SEE COMMENT AT TOP                                  00019210
C      WFH - RTI 12/6/78                                00019220
C      DO 30 I=1,1024                                  00019230
C30  LIBBLK(I)=0                                         00019240
C      TOTION=0.0                                        00019250
C      CALL TRACE(NMASS)                                00019260
C      DO 4 I = 1,NMASS                                00019270
4      IF ( NUSPEC(I) .LT. 0 ) NUSPEC(I) = 0           00019280
C      SATSUM = 0                                       00019290
C      DO 5 I = 1,NMASS                                00019300
C      NUZEN = NUSPEC(I)                               00019310
C      IF ( NUZEN .GE. SATVAL ) SATSUM = SATSUM + NUZEN 00019320
5      TOTION = TOTION + NUZEN                          00019330
C      REJECT SPECTRUM IF TOTION IS LESS THAN MINIMUM TIC 00019340
C      IF ( TOTION .LT. MINTIC ) RETURN                 00019350
C      TICRAT IS CLEANUP RATIO                         00019360
C      00019370

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C      SIGMA7 = SIGMA7 - QSATS * SATVAL + SATSUM          00019380
C      SINCE COMPUTED SATURATED VALUES MAY CAUSE THE CLEANED UP 00019390
C      TIC TO EXCEED THE RAW, WE SUBSTITUTE CALCULATED VALUES 00019400
C      FOR MAXIMUM VALUES. THIS IS A LIMIT OF OUR 16 BIT INTEGER, 00019410
C      AND 24570 SATURATED DEFAULT VALUE IN OUR GC COLLECTION 00019420
C      PHASE. 00019430
C      IF ( TOTION .GE. SIGMA7 ) TOTION = SIGMA7 - 1 00019440
C      TICRAT=TOTION*100.0/SIGMA7 00019450
C      IF ( IDEBUG .EQ. 0 ) GO TO 6 00019460
C      WRITE(IPTR2,1000) TOTION,SIGMA7,TICRAT,SATSUM 00019470
6      OUTSLT=0 00019480
      LSTCNT=LSTCNT+1 00019490
      CALL MOVE(EXPNAM,EXPID,5) 00019500
C      SEE COMMENT AT TOP 00019510
C      WFH - RTI 12/6/78 00019520
C      DO 39 I=1,5 00019530
C      EXPID(I)=EXPNAM(I) 00019540
C      CALL MOVE(NAME,PNAME,32) 00019550
C      THIS LOOP COMENTED OUT TO SUIT WATFIV AND BECAUSE IT SERVES 00019560
C      NO APPARENT PURPOSE... 00019570
C      WFH AT RTI 4/25/78 00019580
C      DO 32 I=1,32 00019590
C      PNAME(I)=NAME(I) 00019600
C      SEE COMMENT AT TOP 00019610
C      WFH - RTI 12/6/78 00019620
C      INTEG=INTEG 00019630
C      CALL MOVE(RDATE,PDATE,5) 00019640
C      SEE COMMENT AT TOP 00019650
C      WFH - RTI 12/6/78 00019660
C      DO 31 I=1,5 00019670
C      PDATE(I)=RDATE(I) 00019680
C      LOMASX=LOMASS 00019690
C      HIMASX=HIMASS 00019700
C      LSTCNX=LSTCNT 00019710
C      SPECNO=SPCNO 00019720
C      CALL TRACE(NMASS) 00019730
C      MAXAMP DETERMINATION SHIFTED ... 00019740
C      WFH - RTI 12/6/78 00019750
C      IF ( IPFLAG .EQ. 0 ) GO TO 12 00019760
C      MAXAMP=0 00019770
C      DO 10 I=1,NMASS 00019780
C      10 IF(MAXAMP.LT.NUSPEC(I)) MAXAMP=NUSPEC(I) 00019790
C      COMPUTE ABSOLUTE MAXIMUM AMPLITUDE. 00019800
C      ABMAX = MAXAMP/ONORM 00019810
C      CALL KAPUT( SPCNO,TOTION,TICRAT,ABMAX ) 00019820
C      THE ABOVE PRINTS OUT THE "CHEMISTS" MINIMUM STUFF. 00019830
C      11 CONTINUE 00019840
C      CALL SETMAS(LIBMAP,LSTCNT) 00019850
C      CALL PUTFIL(OUTSLT,LIBBLK,LSTCNT) 00019860
C      14... CALL CHKFIL(OUTSLT,FLAG) 00019870
C      IF(FLAG) 13,14,15 00019880
C      15... CONTINUE 00019890
C      15 WRITE(IPTR3,34) (LIBBLK(I),I=1,128) 00019900
C      34 FORMAT(3(/3214)/1314,10A4,9I4/) 00019910
C      12=0 00019920
C      DO 81 I=1,411 00019930
C      IF(NUSPEC(I).LE.0)GO TO 81 00019940
C      12=12+1 00019950

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C      JM(IZ)=1+39-MAD                                00019960
C      MM(IZ)=(1+39-MAD)*10                            00019970
C      RMM(IZ)=1+39-MAD                                00019980
C      JSP(IZ)=NUSPEC(I)                                00019990
C      MSP(IZ)=NUSPEC(I)                                00020000
C      RMSP(IZ)=NUSPEC(I)                              00020010
81     CONTINUE                                         00020020
C THESE WRITE STMTS HAVE BEEN MADE CONDITIONAL FOR CONSISTENCY 00020030
C                                     WFH RTI 9/31/78      00020040
C      IF(IDEBUG.EQ.0)GO TO 85                          00020050
C      WRITE(IPTR2,80)SPCNO,IZ,(NNAME(K),K=1,15)        00020060
80     FORMAT(4X,'SPECTRA = '.15,' NO. OF PEAKS = '.14.2X.15A4,' CLEAN 00020070
C      *D.'/)                                           00020080
C      WRITE(IPTR2,83)(JM(K),JSP(K),K=1,IZ)             00020090
83     FORMAT(46(1016//))                               00020100
85     CALL XTREM(JSP,IZ,MIN,MINI,MAX,MAXI)              00020110
C      BASE=MAX                                         00020120
C      CALL TRACE(IZ)                                   00020130
C      DO 60 I=1,IZ                                     00020140
60     RMSP(I)=(RMSP(I)/BASE)*100.                      00020150
C      RMSP(MAXI)=99.99                                00020160
C      WRITE(8,600)SPCNO,IZ,(NNAME(I),I=1,15),CLASS,SUBCL,HOW,IMOLWT 00020170
C THE FOLLOWING TWO WRITE STATEMENTS WERE CONENCTED OUT BECAUSE 00020180
C THEY SEEM TO YEILD NOTHING INTERESTING AND ALSO BECAUSE NO 00020190
C CARRIAGE CONTROL FOR THE PRINTER HAS BEEN INCLUDED    00020200
C                                     WM.F.HARGROVE - RTI 00020210
C      WRITE(IPTR2,600)SPCNO,IZ,(NNAME(I),I=1,15),CLASS,SUBCL,HOW,IMOLWT 00020220
C600  FORMAT(15,13.15A4,9A1,13)                       00020230
C      HERE IS THE MAIN OUTPUT STATEMENT WRITING THE CLEANUPED 00020240
C      UP SPECTRUM TO A DISK DATASET                    00020250
C THE CHANGE TO A SUBROUTINE CALL HAS BEEN MADE WITH THE 00020260
C ONSET OF MULTIPLE RUN PROCESSING AND A LINEAR SYSTEM. 00020270
C                                     WM F HARGROVE      00020280
C                                     11/29/78            00020290
C      WRITE(9) SPCNO,NUSPEC                            00020300
C      CALL WRTSPC(SPCNO,NUSPEC,QDUBLT,TICRAT,IZ,TOTION) 00020310
C      N=(IZ+7)/8                                        00020320
C      IF=1                                              00020330
C      IT=8                                              00020340
C      DO 62 I=1,N                                       00020350
C THIS MOD INSERTED TO BLOT OUT APPARENTLY USELESS WRITE STMT. 00020360
C                                     WFH - 5/31/78 - RTI 00020370
C      WRITE(8,601)(RMM(K),RMSP(K),K=IF,IT)            00020380
C      ANOTHER WRITE STMT MADE CONDITIONAL FOR CONSISTENCY'S SAKE 00020390
C                                     WFH RTI 9/31/78      00020400
C      IF(IDEBUG.EQ.0)GO TO 63                          00020410
C      WRITE(IPTR2,602)(RMM(K),RMSP(K),K=IF,IT)        00020420
63     CONTINUE                                         00020430
C      IF=IT+1                                           00020440
C      IT=IF+7                                           00020450
62     FORMAT(8(F5.1,F5.2))                             00020460
C601  FORMAT(1X,8(F5.1,F5.2))                          00020470
602  FORMAT(1X,8(F5.1,F5.2))                          00020480
C      DO 61 I=1,411                                    00020490
C      RMM(I)=0.0                                        00020500
61     RMSP(I)=0.0                                       00020510
C      BASM=RMM(MAXI)/10                                00020520
C      BASE=MAX                                          00020530

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C      DO 50 I=1,12
C      HD1=JSP(1)
C      50 MSP(I)=(HD1/BASE)*10000
C      ....
C      ....
C      WRITE(8)MJ,11,12,BASM,NNAME,SOURCE,FORM,(MM(K),MSP(K),K=1,12)
C      12 CONTINUE
C      DON'T WRITE BITMAP UNTIL LAST RECORD.
C      RETURN
C      HERE FOR WRITING BITMAP TO LIST.MAS
C      12 CALL ZERO(LIBBLK,1024)
C      12 DO 33 I=1,1024
C      33 LIBBLK(I)=0
C      OUTSLT = 0
C      LSTCNX=LSTCNT
C      READ(7,20)LIBBLK
C      20 FORMAT(18)
C      CALL GETFIL(OUTSLT,LIBBLK,0)
C      20 CALL CHKFIL(OUTSLT,FLAG)
C      IF(FLAG) 13,20,21
C      21 CONTINUE
C      CALL MOVE(LIBMAP,LIBBLK,17)
C      DO 35 I=1,17
C      35 LIBBLK(I)=LIBMAP(I)
C      WRITE(IPTR3,36)LIBBLK
C      36 FORMAT(18)
C      CALL PUTFIL(OUTSLT,LIBBLK,0)
C      16 CALL CHKFIL(OUTSLT,FLAG)
C      IF(FLAG) 13,16,17
C      13 CALL PUTNUM('FILE ERROR FLAG = ',FLAG)
C      CALL PUTSTR('BOMBED WRITING TO LIST.MAS IN OUTDAT')
C      STOP
C      17 CALL CLSFIL(OUTSLT)
C      RETURN
1000 FORMAT(/,' TOTAL ION CURRENT =',F8.0,/, ' UNC SIG =',E15.8,
-/' TICRAT =',I3,/' SAT PEAK SUM =',F12.0,/)
3333 FORMAT(/,' SPECTRUM REJECTED BECAUSE MASS ',I3,/, 'THE ',
1' MODEL PEAK, HAS 0 CONTRIBUTION ' /)
END
SUBROUTINE PARDIR
C
C      THIS COMPUTER PROGRAM WAS DEVELOPED WITH THE FUNDING SUPPORT
C      FROM THE NATIONAL INSTITUTES OF HEALTH (GRANTS RR-612 AND
C      GM-20832) AND THE NATIONAL AERONAUTICS AND SPACE ADMINISTRATION
C      (GRANT NGR-05-020-632).
C      FURTHER NOTE:
C      THIS VERSION OF PARDIR HAS BEEN COMPLETELY REWRITTEN IN ORDER TO ALLOW
C      FOR PROCESSING OF MULTIPLE RUNS. THIS VERSION OF PARDIR IS ALSO USED
C      IN THE VERSION OF CLEANUP SUPPLIED TO EPA BY RTI. THE FUNCTION OF
C      PARDIR IS TO READ IN CONTROL PARAMETERS FROM A TERMINAL OR
C      CONTROL CARDS THAT ARE CONSTANT ACROSS DIFFERENT RUNS. THE
C      MEANING OF THE VARIABLES READ HEREIN SHOULD BE SELF-DOCUMENTING
C      FROM THE ECHO MESSAGES.
C
C      WM.F.HARGROVE
C      RTI 11/22/78
C
COMMON /UNITS/ IRDR,IPTR1,IPTR2,IPTR3,IIN,IOUT
INTEGER IRDR,IPTR1,IPTR2,IPTR3,IIN,IOUT

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COMMON /TOMS/ITOM	00021120
COMMON /PRNTEG/IPFLAG	00021130
COMMON /LFTRIT/ILEFT,IRIGHT	00021140
COMMON /CRATMX/RATMX	00021150
COMMON /DUBBUG/IDEBUG	00021160
COMMON /PARAMS/MINTIC,MINNY,NTHIRD,RATM	00021170
COMMON /AVG/ NAVG,HAVG	00021180
INTEGER ITOM,IPFLAG,ILEFT,IRIGHT,IDEBUG,NTHIRD	00021190
REAL RATMX,RATM	00021200
INTEGER NAVG,HAVG	00021210
INTEGER MINNY,MINTIC	00021220
C PROMPT AND READ CONTROL PARMS - LIFTED FROM OLD CLEANUP SOURCE	00021230
C AN ADDITIONAL PARAMETER WAS ADDED TO AVERAGE N INPUT	00021240
C SPECTRA IF IT BECAME NECESSARY - AS WITH THE INCOS DATA	00021250
C RTI - WFH 1/14/79	00021260
WRITE(IPTR1,3240)	00021270
3240 FORMAT(1X,'ENTER CLEANUP PRINT FLAG(IN 11):')	00021280
READ(IRDR,3241) IPFLAG	00021290
3241 FORMAT(11)	00021300
WRITE(IPTR1,3242) IPFLAG	00021310
3242 FORMAT(1X,'IPFLAG=',11)	00021320
C	00021330
IPFLAG IS PRINT OPTION FLAG FOR CLEANUP	00021340
C INITIALIZE DEFAULTS FOR VARIOUS PARAMETERS IN COMMON	00021350
WRITE(IPTR1,3100)	00021360
3100 FORMAT(1X,'ENTER DEBUGGING SWITCH IN 11 (0=N,1=Y):')	00021370
READ(IRDR,3101) IDEBUG	00021380
3101 FORMAT(11)	00021390
WRITE(IPTR1,3103) IDEBUG	00021400
3103 FORMAT(1X,'IDEBUG=',11)	00021410
C	00021420
WRITE(IPTR1,123)	00021430
123 FORMAT(1X,'ENTER # OF INPUT SPECTRA TO AVERAGE IN 12:')	00021440
READ(IRDR,121) NAVG	00021450
121 FORMAT(12)	00021460
WRITE(IPTR1,122) NAVG	00021470
122 FORMAT(1X,'NAVG=',12)	00021480
HAVG=NAVG/2+1	00021490
WRITE(IPTR1,3120)	00021500
3120 FORMAT(1X,'MINIMUM THIRDS BETWEEN ELLUANTS IN 11:')	00021510
READ(IRDR,3121) NTHIRD	00021520
3121 FORMAT(11)	00021530
WRITE(IPTR1,3123) NTHIRD	00021540
3123 FORMAT(1X,'THIRDS BETWEEN ELLUANTS=',11)	00021550
C	00021560
WRITE(IPTR1,3130)	00021570
3130 FORMAT(1X,'ENTER DETECTION WINDOW IN 14:')	00021580
READ(IRDR,3131) ITOM	00021590
3131 FORMAT(14)	00021600
WRITE(IPTR1,3132) ITOM	00021610
3132 FORMAT(1X,'DETECTION WINDOW=',14)	00021620
C	00021630
WRITE(IPTR1,3140)	00021640
3140 FORMAT(1X,'ENTER MINIMUM FOR LT 5 PEAKS IN 16:')	00021650
READ(IRDR,3141) MINNY	00021660
3141 FORMAT(16)	00021670
WRITE(IPTR1,3143) MINNY	00021680
3143 FORMAT(1X,'MINNY=',16)	00021690

C	WRITE(IPTR1,3150)	00021700
3150	FORMAT(IX,'ENTER MINIMUM FOR MORE THAN 4 PEAKS IN 16:') READ(IRDR,3151) MINTIC	00021710 00021720
3151	FORMAT(16) WRITE(IPTR1,3152) MINTIC	00021730 00021740
3152	FORMAT(IX,'MINTIC=',16)	00021750 00021760
C	WRITE(IPTR1,3160)	00021770
3160	FORMAT(IX,'ENTER MINIMUM QUALIFYING RATE IN F8.4:') READ(IRDR,3161) RATM	00021780 00021790
3161	FORMAT(F8.4) WRITE(IPTR1,3162) RATM	00021800 00021810
3162	FORMAT(IX,'RATM=',F8.4)	00021820 00021830
C	WRITE(IPTR1,3170)	00021840
3170	FORMAT(IX,'ENTER ERROR RATIO IN F8.4:') READ(IRDR,3171) RATDXX	00021850 00021860
3171	FORMAT(F8.4) WRITE(IPTR1,3172) RATDXX	00021870 00021880
3172	FORMAT(IX,'RATDXX=',F8.4)	00021890 00021900
C	WRITE(IPTR1,3180)	00021910
3180	FORMAT(IX,'ENTER POINTS TO LEFT OF MODE IN I3:') READ(IRDR,3181) ILEFT	00021920 00021930
3181	FORMAT(I3) WRITE(IPTR1,3182) ILEFT	00021940 00021950
3182	FORMAT(IX,'ILEFT=',I3)	00021960 00021970
C	WRITE(IPTR1,3190)	00021980
3190	FORMAT(IX,'ENTER POINTS TO RIGHT OF MODE IN I3:') READ(IRDR,3191) IRIGHT	00021990 00022000
3191	FORMAT(I3) WRITE(IPTR1,3192) IRIGHT	00022010 00022020
3192	FORMAT(IX,'IRIGHT=',I3)	00022030 00022040
	RETURN	00022050
	END	00022060
	SUBROUTINE SATLSQ (NS,M,RPKHGT,G,SPEC,SATVAL,GPOS,OVLAP,HPOS,PKHIS	00022070
	*T)	00022080
C	THIS COMPUTER PROGRAM WAS DEVELOPED WITH THE FUNDING SUPPORT	00022090
C	FROM THE NATIONAL INSTITUTES OF HEALTH (GRANTS RR-612 AND	00022100
C	GM-20832) AND THE NATIONAL AERONAUTICS AND SPACE ADMINISTRATION	00022110
C	(GRANT NGR-05-028-632).	00022120
C		00022130
C		00022140
C	THIS ROUTINE COMPUTES SATURATED VALUES IN THE	00022150
C	FOLLOWING WAY:	00022160
C		00022170
C	1. REMOVE LOCAL BACKGROUND FROM SATURATED PROFILE.	00022180
C		00022190
C	2. COMPUTE THE RATIOS OF PEAK(I)/MODEL(I)	00022200
C	FOR NON-SATURATED POINTS IN THE PEAK.	00022210
C		00022220
C	3. GET THE AVERAGE RATIO, AND MULTIPLY IT TIMES	00022230
C	THE MODEL MODE. THIS IS THE RETURNED SATURATED	00022240
C	VALUE.	00022250
C	REAL LOCLBG,GG,PKHIST(20)	00022260
	INTEGER SPEC(14,411),GPOS,OVLAP,HPOS	00022270


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C      INTEGER MINHGT,SATLST,SATINX
C      INTEGER IJ,IK,IL,LSTOP,RSTART,STOPF,RCOUNT
C      DIMENSION G(9),Y(13),RATIOS(13)
C      COMMON /CSATLS/SATLST(25),SATINX
C      COMMON /MODES/SGMODE(3),SHMODE(3),GMODE,HMODE
C      COMMON /QUIXDT/QUIXDT
C      I2=NS-12-14*((NS-13)/14)
C      I3=NS-11-14*((NS-12)/14)
C      I4=NS-10-14*((NS-11)/14)
C      I5=NS-9-14*((NS-10)/14)
C      I6=NS-8-14*((NS-9)/14)
C      I7=NS-7-14*((NS-8)/14)
C      I8=NS-6-14*((NS-7)/14)
C      I9=NS-5-14*((NS-6)/14)
C      I10=NS-4-14*((NS-5)/14)
C      I11=NS-3-14*((NS-4)/14)
C      I12=NS-2-14*((NS-3)/14)
C      I13=NS-1-14*((NS-2)/14)
C      IK = 13
C      DO 5 I = 1,12
C      IL = IK - 1
C      IJ = NS - IL - 14 * ((NS - IK)/14)
C      Y(I) = SPEC(IJ,M)
C      IK = IK - 1
5      CONTINUE
C      SATVAL WILL BE DEFAULT IN CASE OF SUPER SATURATION
C      RPKHGT = -SATVAL
C      MINHGT = .05 * SATVAL
C      MINHGT IS MINIMUM ACCEPTABLE HEIGHT IN MODEL FOR RATIOING.
C      ILEFT = 0
C      ILEFT = 0
C      IRIGHT = 0
C      NPTS = 12
C      NSATS = 0
C      DO 50 I = 1,NPTS
C      IF (Y(I).GE.SATVAL) GO TO 10
C      IF (ILEFT.EQ.1) GO TO 20
C      COUNT POINTS TO LEFT OF FIRST SATURATED POINT
C      ILEFT = ILEFT + 1
C      GO TO 50
20      CONTINUE
C      COUNT POINTS TO RIGHT OF LAST SATURATED POINT
C      IRIGHT = IRIGHT + 1
C      GO TO 50
C      FOUND FIRST SATURATED POINT
10      ILEFT = 1
C      NSATS = NSATS + 1
C      NSATS COUNTS SATURATED VALUES.
50      CONTINUE
C      ILEFT = NUMBER OF POINTS TO LEFT OF FIRST SATURATED POINT.
C      IRIGHT = NUMBER OF POINTS TO RIGHT OF LAST SATURATED POINT.
C      FIND MIDDLE POINT OF SATURATED VALUES AND MAKE SURE
C      7 IS IN *MID-1,MID+10.NOTE:THE INTERVAL IS CLOSED.
C      IQUIT = 0
C      IFIRST = ILEFT + 1
C      ILAST = ILEFT + NSATS

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00022280
00022290
00022300
00022310
00022320
00022330
00022340
00022350
00022360
00022370
00022380
00022390
00022400
00022410
00022420
00022430
00022440
00022450
00022460
00022470
00022480
00022490
00022500
00022510
00022520
00022530
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00022570
00022580
00022590
00022600
00022610
00022620
00022630
00022640
00022650
00022660
00022670
00022680
00022690
00022700
00022710
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00022750
00022760
00022770
00022780
00022790
00022800
00022810
00022820
00022830
00022840
00022850

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C	LLLLSSSSRRR	00022860
C		00022870
C	IFIRST ILAST	00022880
C		00022890
C	RMID IS MIDDLE POINT OF SATURATED VALUES, AND REAL.	00022900
	RMID = (IFIRST + ILAST)/2.0	00022910
	RWIND = 7.0 - RMID	00022920
C	NOTE: 7 IS INDEX OF CURRENT SPECTRUM.	00022930
C	7 MUST BE WITHIN (RMID-1,RMID+1).	00022940
C		00022950
C		00022960
C	ACTUALLY, RMID MUST BE IN +6.00 FOR SATURATED	00022970
	VALUE TO BE PROCESSED.	00022980
	IF (RWIND .LT. 0) RWIND = -RWIND	00022990
	IF (RWIND .LE. 1.0) GO TO 60	00023000
	IQUIT = 1	00023010
	RETURN	00023020
60	CONTINUE	00023030
C	PRINT SATURATED MASS ENCOUNTERED STUFF	00023040
	MASS = M + 39	00023050
C	SEE IF MASS BELONGS TO PREDESSOR.	00023060
	DO 62 I = 1,SATINX	00023070
	IF (SATLST(I) .NE. MASS) GO TO 62	00023080
	SATLST(I) = 0	00023090
	IQUIT = 2	00023100
	RETURN	00023110
62	CONTINUE	00023120
C	DETERMINE IF THIS MASS BELONGS TO AN AJACENT SPECTRUM	00023130
	IF (OVLAP .EQ. 0) GO TO 70	00023140
	NXTSPC = 6 + (HPOS-1)/3	00023150
C	SEE IF SATVALS OCCUR IN NEXT SPECTRUM CONTINUOUSLY	00023160
	IF (ILAST .LT. NXTSPC) GO TO 70	00023170
	RDIFF = NXTSPC - RMID	00023180
C	SEE IF RMID IS CLOSE TO NEXT SPECTRUM.	00023190
	IF (RDIFF .GT. 1) GO TO 70	00023200
C	GIVE UNDECIDED MASS TO SPECTRUM WITH BIGGEST TIC.	00023210
	IF (PKHIST(GPOS) .GE. PKHIST(HPOS)) GO TO 65	00023220
	IQUIT = 1	00023230
	RETURN	00023240
65	CONTINUE	00023250
C	FLAG FOR NEXT GUY TO AVOID.	00023260
	SATLST(SATINX) = MASS	00023270
	SATINX = SATINX + 1	00023280
	IF (SATINX .EQ. 26) SATINX = 25	00023290
70	CONTINUE	00023300
C	THE LAST THREE ARGUMENTS Y,Y,Y) HAVE BEEN CHANGED TO	00023310
C	SATVAL,SATVAL,SATVAL) TO SUIT WATFIV...THEY HAVE NO	00023320
C	FUNCTION WITHIN SPEPRT.	00023330
C	WFM RTI 4/30/78	00023340
	CALL SPEPRT(1,MASS,Y,SATVAL,SATVAL,SATVAL)	00023350
C	THE LAST TWO ARGUMENTS Y,Y) HAVE ALSO BEEN CHANGED TO SATVAL,SATVAL)	00023360
C	TO SUIT WATFIV... THEY HAVE NO APPARENT FUNCTION INSIDE SPEPRT	00023370
	WFM RTI 4/30/78	00023380
C	PRINT DEFAULT SATURATED VALUE	00023390
	CALL SPEPRT(2,NPTS,Y,SATVAL,SATVAL,SATVAL)	00023400
C	***** NOW BEGIN OUR SATURATION STUFF *****	00023410
	LSTOP = ILEFT	00023420
	RSTART = NPTS - IRIGHT + 1	00023430

	LOCLBG = Y(1)	00023440
C	SUBTRACT LEFT POINT FROM ALL VALUES AS AN APPROXIMATION	00023450
C	OF BACKGROUND. THIS IS TO BE SYMMETRIC WITH MODEL PEAK.	00023460
	STOPF = 0	00023470
	IF (LSTOP .NE. 0) GO TO 90	00023480
	STOPF = 1	00023490
	GO TO 105	00023500
90	CONTINUE	00023510
	DO 100 I = 1, LSTOP	00023520
100	Y(I) = Y(I) - LOCLBG	00023530
105	CONTINUE	00023540
	IF (STOPF .EQ. 1 .AND. RSTART .GT. NPTS) GO TO 900	00023550
C	IF WE GO TO 900 IT MEANS ALL VALUES ARE SATURATED	00023560
	IF (RSTART .GT. NPTS) GO TO 120	00023570
	DO 110 I = RSTART, NPTS	00023580
110	Y(I) = Y(I) - LOCLBG	00023590
120	CONTINUE	00023600
	RATO = 0	00023610
	RCOUNT = 0	00023620
	IF (LSTOP .LT. 3) GO TO 300	00023630
	DO 200 I = 3, LSTOP	00023640
	GG = G(I-2)	00023650
	IF (GG .LT. MINHGT) GO TO 200	00023660
C	NOTE: MINHGT > 0	00023670
	RATIOS(I) = Y(I)/GG	00023680
	RATO = RATO + RATIOS(I)	00023690
	RCOUNT = RCOUNT + 1	00023700
200	CONTINUE	00023710
300	CONTINUE	00023720
	IF (RSTART .GT. 11) GO TO 350	00023730
	DO 325 I = RSTART, 11	00023740
	GG = G(I-2)	00023750
	IF (GG .LT. MINHGT) GO TO 325	00023760
	RATIOS(I) = Y(I)/GG	00023770
	RATO = RATO + RATIOS(I)	00023780
	RCOUNT = RCOUNT + 1	00023790
325	CONTINUE	00023800
350	CONTINUE	00023810
	IF (RCOUNT .LE. 1) GO TO 900	00023820
C	ABOVE TAKES CARE OF SUPER SATURATION	00023830
	RATO = RATO/RCOUNT	00023840
	IF (RATO .LE. 0) GO TO 900	00023850
C	THE ABOVE TAKES CARE OF A VERY FUNNY LOCAL BACKGROUND	00023860
	RPKHGT = RATO * G(5)	00023870
C	THE ABOVE TAKES CARE OF SATURATED PEAKS WITH TOO HIGH	00023880
C	OF BACKGROUND APPROXIMATIONS.	00023890
	CALL SPEPRT(3, 1, RPKHGT, LOCLBG, RATO, G(5))	00023900
	RETURN	00023910
900	CONTINUE	00023920
	CALL SPEPRT(4, 1, RPKHGT, RATO, RATO, RATO)	00023930
	RETURN	00023940
	END	00023950
C		00023960
C	THIS SUBROUTINE WAS INCORPORATED TO ACCOUNT FOR THE POSSIBILITY	00023970
C	OF DIFFERENT SCAN FUNCTIONS ON THE FINNIGAN QUADROPOLE	00023980
C	SPECTROMETER AND TO ALLOW FOR MAGNETIC INSTRUMENTS IN THE FUTURE	00024000
C		00024010
C		00024020

WFH RTI 9/31/78

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      REAL FUNCTION SCAN(MASS)
      INTEGER*4 MASS
      REAL*4 HIMASS/450.,LOMASS/40./
C
      RMASS=MASS
      SCAN=(RMASS-LOMASS)/(HIMASS-LOMASS)
      RETURN
      END
C
      SUBROUTINE SETBUG(NNAME,EOF)
C
      INTEGER CLNFLG
C
      THIS COMPUTER PROGRAM WAS DEVELOPED WITH THE FUNDING SUPPORT
      FROM THE NATIONAL INSTITUTES OF HEALTH (GRANTS RR-612 AND
      GM-20832) AND THE NATIONAL AERONAUTICS AND SPACE ADMINISTRATION
      (GRANT NGR-85-020-632).
C
      C FURTHER NOTE:
      C THIS VERSION OF SUBROUTINE SETBUG HAS REWRITTEN IN ORDER TO PERMIT
      C MULTIPLE RUN PROCESSING AND TO FIT INTO THE CONTEXT OF THE EPA AND
      C RTI ACQUISITION SYSTEMS. ITS FUNCTION IS TO READ AND FILL THE SPECTRUM
      C BUFFER WITH THE FIRST 13 SPECTRA FROM EACH RUN.
      COMMON PKHIST(20),NPHIST(20)
      COMMON YM5,YM4,YM3,YM2,YM1,Y0,YP1,YP2,YP3,YP4,YP5
      COMMON GM4,GM3,GM2,GM1,G0,GP1,GP2,GP3,GP4
      COMMON SG,SG2,SG,S1,S12,AN,AA,BB,CC,DD
      COMMON NAME(32),RDATE(5),BITMAP(64),GCTIME
      COMMON LIBMAP(17),INTEG,LOMASS,HIMASS,POINTS,TAPCNT
      COMMON MAXSP,LSTCNT,DEVICE(5),SPCNO
      COMMON SPEC(14,411),IND(3,411),NUSPEC(411),NMASS
      COMMON RMAX(3),IR(3),BK(3),NM(3),NTM(3),GPEAK(3,11)
      COMMON SPARE1,SPARE2,SPARE3,SPARE4,SPARE5,SPARE6,SPARE7
      COMMON RATMIN,RATEMX,SIGY0,SIGNXT,SIGLST
      COMMON ISVN8,ISVN9,ISVP8,ISVP9,SIGMA7,SATVAL,SATMAX
      COMMON MODE1,MODE2,NLWCUT,NUPCUT,SATPKS(25),NSAT,EXPNAM(5)
      REAL SATVAL
      INTEGER AVGSPC(411),NAVG,HAVG
      INTEGER EOF,LIBBLK,RDATE,LOMASS,HIMASS,ADS,POINTS,
      1SPCNO,SPEC,NNAME(18)
      COMMON /SCR/ LIBBLK(1024)
      COMMON /IADS/ ADS
      COMMON /IMAD/ MAD
      COMMON /AVG/ NAVG,HAVG
C READ IN RUN HEADER AND RETURN IF END OF FILE
      CALL OPNRUN(LIBBLK,EOF)
      IF(EOF.NE.0)RETURN
C HOUSE CLEANING FOR HISTORICAL VARIABLES STILL LEFT IN CLEANUP
      NMASS=411
      DO 10 I=1,2
      10 RDATE(I)=LIBBLK(I+27)
C SETTING OF HIGH MASS, LOMASS AND OF * OF SPECTRA IN RUN
      MAXSP=LIBBLK(38)
      LOMASS=40
      HIMASS=450
      ADS=LIBBLK(36)
      MAD=40-LOMASS
      POINTS=40
C BY SERENDIPIDY NNAME CAN BE MODIFIED TO CONTAIN THE RUN TITLE AND
C EXPNAM TO CONTAIN THE INSTRUMENT TYPE...

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DO 28 I=1.18	00024610
20 NNAME(I)=LIBBLK(12+I)	00024620
DO 30 I=1.5	00024630
30 EXPNAM(I)=LIBBLK(7+I)	00024640
C THE INTERNALS OF SETBUG HAVE BEEN MODIFIED SO AS TO	00024650
C INCLUDE AN AVERAGING OVER THE INPUT SPECTRA	00024660
C RTI - WFM 1/13/79	00024670
DO 50 I=1.13	00024680
C INITIALIZE MAIN SPECTRUM ARRAY IN CORE FOR ADDITION	00024690
DO 31 IK=1.411	00024700
31 SPEC(I,IK)=0	00024710
C READ IN NAVG SPECTRA FOR THE CURRENT CORE POSITION	00024720
DO 40 IJ=1.NAVG	00024730
IQUPE=0	00024740
C IQUPE ENSURES THAT THE QUE IN THE I/O ROUTINES IS	00024750
C UPDATED ONLY ONCE	00024760
C I14 TELLS WHICH QUEUE LOCATION TO UPDATE	00024770
IF(IJ.EQ.NAVG) IQUPE=1	00024780
CALL RDSPEC(ISCNO,AVGSPC,I,IQUPE,EOF)	00024790
IQUPE=0	00024800
IF(EOF.EQ.0) GO TO 34	00024810
C EOF HAS BEEN ENCOUNTERED BEFORE ALL 13 CORE POSITIONS WERE FILLED	00024820
WRITE(IPTR,60)	00024830
60 FORMAT('---','*** UNABLE TO FILL 13 CORE POSITIONS - EOF ***')	00024840
STOP	00024850
34 CONTINUE	00024860
C NOW INCREMENT MAIN ARRAY IN CORE	00024870
DO 32 IK=1.411	00024880
32 SPEC(I,IK)=SPEC(I,IK)+AVGSPC(IK)	00024890
40 CONTINUE	00024900
C NOW DIVIDE BY NAVG IF NECESSARY	00024910
IF(NAVG.EQ.1) GO TO 47	00024920
DO 46 IK=1.411	00024930
46 SPEC(I,IK)=SPEC(I,IK)/NAVG	00024940
47 CONTINUE	00024950
50 CONTINUE	00024960
C NOW SET INTERNAL SPECTRUM NUMBER	00024970
SPCNO=ISCNO-6*NAVG-NAVG	00024980
RETURN	00024990
END	00025000
SUBROUTINE SETGHY(NS,M,GNU,HNU,GPOS,HPOS,ISW,GMX)	00025010
C	00025020
C *** THIS ROUTINE ACTUALLY DOES THE SETUP AND	00025030
C *** INTERPOLATION PRIOR TO DOUBLET RESOLUTION	00025040
C *** IT CALLS THE DOUBLET RESOLVER.	00025050
C	00025060
INTEGER NAME,RDATE,BITMAP,GCTIME,LIBMAP,INTEG,L0MASS	00025070
INTEGER H1MASS,POINTS,TAPCNT,MAXSP,LSTCNT,DEVICE,SPCNO	00025080
INTEGER SPEC,IND,IR,BK,NM,NTM	00025090
INTEGER GPEAK,SPARE1,SPARE2,SPARE3,SPARE4,SPARE7	00025100
REAL SPARE5,SPARE6	00025110
INTEGER GPOS,HPOS	00025120
INTEGER NUSPEC,NMASS,OVLAP,ISW	00025130
INTEGER STORE	00025140
REAL ISVP8,ISVP9	00025150
REAL DMX	00025160
REAL GMX	00025170
C	00025180

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DIMENSION GNU(18),HNU(18),Y(18)
COMMON PKHIST(20),NPHIST(20)
COMMON Y15,Y14,Y13,Y12,Y11,Y0,YP1,YP2,YP3,YP4,YP5
COMMON GM4,GM3,GM2,GM1,G0,GP1,GP2,GP3,GP4
COMMON SG,SG2,SIG,S1,S12,AN,AA,BB,CC,DD
COMMON NAME(32),RDATE(5),BITMAP(64),GCTIME
COMMON LIBMAP(17),INTEG,LOMASS,HIMASS,POINTS,TAPCNT
COMMON MAXSP,LSTCNT,DEVICE(5),SPCNO
COMMON SPEC(14,411),IND(3,411),NUSPEC(411),NMASS
COMMON RMAX(3),IR(3),BK(3),NM(3),NTM(3),GPEAK(3,11)
COMMON SPARE1,SPARE2,SPARE3,SPARE4,SPARE5,SPARE6,SPARE7
COMMON RATMIN,RATEIX,SIGY0,SIGNXT,SIGLST
COMMON ISVN8,ISVN9,ISVP8,ISVP9,SIGMA7,SATVAL,SATMAX
COMMON MODE1,MODE2,NLWCUT,NUPCUT,SATPKS(25),NSAT,EXPNAM(5)
COMMON /MODES/SGMODE(3),SHMODE(3),GMODE,HMODE
COMMON /CRATMX/RATMX
INTEGER BEDROK
DATA BEDROK/40/

      DO ROTARY BUFFER INDEXING OF SPEC(14,NUMMASSSES)
      J = 13
      DO 1000 I=1,13
      K = J - 1
      IJ = NS - K - 14 * ((NS - J)/14)
      Y(I) = SPEC(IJ,M)
      J = J - 1
1000  CONTINUE
      DO NOT LET ANY PEAKS WITH SATURATED VALUES IN THEIR
      C    PROFILES PASS THROUGH DOUBLET RESOLVER.
      DO 50 I= 1,11
      IF ( Y(I) .GE. SATVAL ) GO TO 5
50    CONTINUE

      WE TRY TO ELIMINATE BACKGROUND PEAKS FROM PASSING THROUGH
      DOUBLET FILTER: SO, LET K1 = .0125 * Y(7), AND K2 = .0125 * G(7).
      THEN: WHERE M = MAX*K1,K20, LET D = MIN*M,700,AND D = MAX*D,300
      (WE USE AN ABSOLUTE MAX OF 70 SO AS NOT TO MISS HIGH MASS
      PEAKS WITH SMALL CONTRIBUTIONS WHEN THE BASE PEAK IS
      LARGE,AND A MIN OF 30 FOR LOW AMPLITUDE DRIBBLE.)

      ----- < Y(7) + E
      . . . * < Y(7) . . . - E
      . . . . . E
      ----- < Y(7) - E

      IF THE FRAGMENTOGRAM STAYS IN THE ABOVE ENVELOPE FROM Y(3) TO
      TO Y(11), THEN WE CONSIDER IT A BACKGROUND PEAK.

      D = .0125
      K1 = D * Y(7)
      WE MUST RECALL THAT G(7) HAS BEEN NORMALIZED IN GETHGT
      K2 = D * GNU(7)/GMX
      DMX = K1
      IF ( DMX .LT. K2 ) DMX = K2
      DMX IS MAX*K1,K20
      IF ( DMX .GT. 70 ) DMX = 70

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00025190
00025200
00025210
00025220
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00025660
00025670
00025680
00025690
00025700
00025710
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00025740
00025750
00025760

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C	DMX = MIN+DMX.700	00025770
	IF(DMX .LT. BEDROK) DMX = BEDROK	00025780
C	DMX = MAX+BEDROK.DMX	00025790
	E1 = Y(7) + DMX	00025800
	E2 = Y(7) - DMX	00025810
	DO 100 I = 3,11	00025820
	IF (Y(I) .GT. E1 .OR. Y(I) .LT. E2) GO TO 200	00025830
100	CONTINUE	00025840
	GHGT = 0	00025850
	RETURN	00025860
200	CONTINUE	00025870
C		00025880
C	WE NOW TRY TO ELIMINATE LOCALLY "NEARLY LINEAR"	00025890
C	CONTRIBUTIONS BY FITTING A LINE TO THE LOCAL FRAGMENTOGRAM	00025900
C	IN A LEAST SQUARES WAY, AND EXAMINING	00025910
C		00025920
C	RATIO = (ROOT MEAN SQUARE ERROR)/(AVERAGE VALUE OF Y(I))	00025930
C		00025940
C		00025950
C	THIS TEST HAS BEEN VERY SUCCESSFUL IN ELIMINATING COLUMN	00025960
C	BLEED.	00025970
C	CALL BLEED(Y(5),RATIO)	00025980
C	THIS MOD INSERTED ON A TEMPORARY BASIS TO GATHER STATISTICS	00025990
C	ON ERROR RATIO - CODE 3	00026000
C		00026010
C	ITYP=3	00026020
C	ISPC=SPCNO	00026030
C	WRITE(20,6250) ITYP,ISPC,RATIO,RATIO	00026040
C6250	FORMAT(2A4,20X,2A4)	00026050
	IF (RATIO .GT. RATIOX) GO TO 290	00026060
	GHGT = 0	00026070
	RETURN	00026080
290	CONTINUE	00026090
C	ALSO, IF Y(I) IS NON INCREASING FOR I=4,9, 1E.Y(I) .GE. Y(I+1),	00026100
C	THEN DON'T CONSIDER, AS IT IS EITHER BACKGROUND	00026110
C	OR TAIL OF PRECEDING PEAK	00026120
	DO 300 I = 4,9	00026130
	IF (Y(I) .LT. Y(I+1)) GO TO 400	00026140
300	CONTINUE	00026150
	GHGT = 0	00026160
	RETURN	00026170
400	CONTINUE	00026180
	MI=M+39	00026190
C	ARITHMETIC BELOW HAS BEEN REPLACED BY FUNCTION SUBROUTINE	00026200
C	IN ORDER TO ACCOMODATE MAGNETIC INSTRUMENTS...	00026210
C		00026220
C	TSHIFT = FLOAT(MI - LOMASS)/(HIMASS - LOMASS)	00026230
C	TSHIFT = SCAN(MI)	00026240
C	INTERPOLATE PEAK PROFILE TO TIME COORDINATE OF MODEL PEAK.G	00026250
	CALL TIMESF(TSHIFT,Y(2),11,GMODE)	00026260
C	CANNOT USE ENDPOINTS AFTER INTERPOLATION	00026270
C		00026280
C		00026290
C	*** NOW USE LEAST SQUARES DOUBLET RESOLVER TO GET	00026300
C	*** THE AMPLITUDE OF THE COMPONENT AT THE DETECTED SPECTRUM.	00026310
C		00026320
C		00026330
C	IHSPEC = 6+(HPOS-1)/3	00026340

C	IHSPEC = 6 - 11	00026350
	STORE = 0	00026360
C	STORE WILL BE SET 1 BY DUBLET IF M QUALIFIES FOR NEW AMPLITUDE.	00026370
	CALL DUBLET(GNU,HNU,Y,STORE,M,IHSPEC,GHGT,ISW,NS)	00026380
C		00026390
C	SAVE THE COMPONENT CONTRIBUTING TO THE DETECTED SPECTRUM.	00026400
C		00026410
C		00026420
C	SAVE CONTRIBUTION WITH MINIMUM ERROR.	00026430
C		00026440
	IF (GHGT .GT. 32767) GHGT = 32767	00026450
C	MADE SURE NO INTEGER OVERFLOW	00026460
	IF (GHGT .LE. 10) GHGT = 0	00026470
C	HEIGHTS LE 10 ARE CONSIDERED ARTIFACTS OF THE DOUBLET RESOLVER	00026480
	IF (STORE .EQ. 1) NUSPEC(M)=GHGT	00026490
C		00026500
S	RETURN	00026510
	END	00026520
C	THIS SUBROUTINE DOES ALL PRINTING	00026530
C	FOR CLEANUP. PLEASE USE IT TO ADD NEW PRINTING	00026540
C	IN ANY SUBROUTINE.	00026550
C	THE CALL STATEMENT ALLOWS FOR PASSING OF ARRAYS	00026560
C	REALS AND INTEGERS.	00026570
C	THIS COMPUTER PROGRAM WAS DEVELOPED WITH THE FUNDING SUPPORT	00026580
C	FROM THE NATIONAL INSTITUTES OF HEALTH (GRANTS RR-612 AND	00026590
C	GM-20832) AND THE NATIONAL AERONAUTICS AND SPACE ADMINISTRATION	00026600
C	(GRANT NGR-05-020-632).	00026610
	SUBROUTINE SPEPRT(N,IAR,AR,R1,R2,R3)	00026620
	INTEGER N,IONE,NINE,MAD	00026630
	REAL R1,R2,R3	00026640
C	THE DIMENSIONS OF AR AND IAR HAVE BEEN SET TO (1),(1) FROM	00026650
C	TO HELP WITH WATFIV....	00026660
	LFH RTI 4/30/78	00026670
C		00026680
	DIMENSION IAR(1),AR(1)	00026690
	COMMON /DUBBUG/IFLAG	00026700
	COMMON /IMAD/MAD	00026710
	COMMON /UNITS/ IRDR,IPTR1,IPTR2,IPTR3,IIN,IOUT	00026720
	DATA IONE,NINE/1,9/	00026730
C	IFLAG IS RESET IF NO PRINTING IS TO BE DONE/	00026740
	IF (IFLAG.EQ.0) RETURN	00026750
	GO TO (40,50,60,70),N	00026760
C	THE ABOVE IS A CASE STATEMENT FOR EXECUTING PRINT	00026770
C	OPTIONS.C	00026780
C	NOW DO STALSO OUTPUT	00026790
40	IAR=IAR(1)-MAD	00026800
	WRITE(IPTR2,600) IAR	00026810
	RETURN	00026820
C	THE ABOVE WRITE IS FOR MASS OF SATURATION	00026830
50	WRITE(IPTR2,550) R1	00026840
	WRITE(IPTR2,610)	00026850
	IUP = IAR(1)	00026860
	WRITE(IPTR2,535) (AR(1),I=IONE,IUP)	00026870
	RETURN	00026880
60	WRITE(IPTR2,800)	00026890
	WRITE(IPTR2,560) AR(1),R1,R2,R3	00026900
	WRITE(IPTR2,900)	00026910
C	WRITES RPKHGT.LOCAL BACKGROUND,RATIO,G(5)	00026920
	RETURN	


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70  WRITE(IPTR2,700)                                00026930
C    THE ABOVE WRITES SATURATED DEFAULT VALUE.      00026940
    RETURN                                           00026950
C    FORMAT STATEMENTS FOLLOW.                       00026960
535  FORMAT(/,8X,7F7.0,/,8X,6F7.0,/)              00026970
550  FORMAT(8X,/, SATURATED VALUE = ',F7.1)        00026980
560  FORMAT(8X,/, PEAK HEIGHT = ',F7.0,/,8X,/, BACK GROUND = ',F7.0,
-/,8X,/, PEAK TO MODEL RATIOS AVERAGE, RATIO = ',E15.8,/,8X,
-/,/, G(5) = ',F7.0,/,/)                          00027000
600  FORMAT(/,/, SATURATION ENCOUNTERED, MASS = ',14,/) 00027010
610  FORMAT(/,/, SATURATED PEAK PROFILE FOLLOWS ',/) 00027020
700  FORMAT(/,/, SUPER SATURATION ENCOUNTERED ',/,8X, 00027030
-PEAK HEIGHT DEFAULTS TO MAXIMUM VALUE ',/)         00027040
800  FORMAT(/,/, SATURATED PEAK ANALYSIS ',/)        00027050
900  FORMAT(/,/, NOTE: PEAK HEIGHT = RATIO X G(5)',/) 00027060
    END                                             00027070
    SUBROUTINE TIMESF(DELTIM,Y,N,GTIME)             00027080
    REAL GTIME                                     00027090
    INTEGER N                                       00027100
    REAL RATE,DELTIM                               00027110
C  Y HAS BEEN REDIMENSIONED DOWN FROM 15 TO 1      00027120
C  TO MAKE THIS THING WATFIV COMPATABLE - WFH RTI 4/25/78 00027130
    DIMENSION Y(1)                                00027140
C  THIS COMPUTER PROGRAM WAS DEVELOPED WITH THE FUNDING SUPPORT 00027150
C  FROM THE NATIONAL INSTITUTES OF HEALTH (GRANTS RR-612 AND 00027160
C  GM-20832) AND THE NATIONAL AERONAUTICS AND SPACE ADMINISTRATION 00027170
C  (GRANT NGR-05-020-632).                          00027180
C  THIS SUBROUTINE TIME ALIGNS A PEAK AT A GIVEN MASS M TO 00027190
C  THE SAME TIME CO-ORDINATE SYSTEM AS THE MODEL'S MASS. 00027200
C  (THE TIME CO-ORDINATE IS GTIME FOR MODEL)          00027210
C  DELTIM=(M-LOMASS)/(HIMASS-LOMASS)                 00027220
C  Y IS THE ABCISSAS OF THE FRAGMENTOGRAM AT MASS M. 00027230
C  THIS ALIGNMENT IS DONE BY A CUBIC FIT USING LAGRANGE'S 00027240
C  METHOD, I.E., GIVEN THE 4 POINTS X0,X1,X2,X3, WE FIND L(X) AS 00027250
C  FOLLOWS:                                           00027260
C  L(X)=+(X-X1)(X-X2)(X-X3)/((X0-X1)(X0-X2)(X0-X3))@Y0 + 00027270
C  +(X-X0)(X-X2)(X-X3)/((X1-X0)(X1-X2)(X1-X3))@Y1 + 00027280
C  +(X-X0)(X-X1)(X-X3)/((X2-X0)(X2-X1)(X2-X3))@Y2 + 00027290
C  +(X-X0)(X-X1)(X-X2)/((X3-X0)(X3-X1)(X3-X2))@Y3 00027300
C  WITH THE X'S INTEGRALLY SPACED.                  00027310
C  IN EACH CASE WE INTERPOLATE FOR A NEW MIDDLE POINT,OR 00027320
C  L(X1+DX), SO, THE ABOVE EQUATION REDUCES TO      00027330
C  L(X1+DX) = C0 * Y0 + C1 * Y1 + C2 * Y2 + C3 * Y3 00027340
C  C0 = DX * (DX-1)(DX-2)/-6                        00027350
C  C1 = (DX+1)(DX-1)(DX-2)/2                        00027360
C  C2 = (DX+1)(DX)(DX-2)/-2                         00027370
C  C3 = (DX+1)(DX)(DX-1)/6                          00027380
C  00027390
C  00027400
C  00027410
C  00027420
C  00027430
C  00027440
C  00027450
C  00027460
C  00027470
C  00027480
C  00027490
C  00027500

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C      WHERE DX = GTIME - DELTIM                                00027510
C      INTEGER I                                                00027520
REAL    C1,C2,C3,DTIME                                         00027530
REAL    Y1,Y11,YMID,K1,K2,K3,K4,DXPOS                         00027540
DIMENSION YOLD(15)                                             00027550
C      DO 50 I=1,N                                              00027560
C      YOLD(I) = Y(I)                                           00027570
C      CONTINUE                                                00027580
C      SAVED OLDIES                                           00027590
C      DX = GTIME - DELTIM                                       00027600
C      DXPOS = DX                                               00027610
C      IF ( DXPOS .LT. 0 ) DXPOS = -DX                          00027620
C      IF ( DXPOS .LT. 0.00001) RETURN                          00027630
C      DON'T INTERPOLATE FOR SMALL VALUES OF DX              00027640
C      K1 = DX - 1                                              00027650
C      K2 = DX - 2                                              00027660
C      K3 = DX + 1                                              00027670
C      K4 = DX + 2                                              00027680
C      C1= (DX * (K1) * (K2))/(-6)                             00027690
C      C2= ((K3) * (K1) * (K2))/2                             00027700
C      C3= ((K3) * (DX) * (K2))/(-2)                          00027710
C      C4= ((K3) * (DX) * (K1))/6                             00027720
C      INTERPOLATE                                             00027730
C      JN = N - 2                                              00027740
C      DO 100 I=2,JN                                           00027750
C      Y(I)=C1*YOLD(I-1) + C2*YOLD(I) + C3*YOLD(I+1) + C4 * YOLD(I+2) 00027760
C      CONTINUE                                                00027770
C      E1= C4                                                  00027780
C      E2= ((K4) * (DX) * (K1))/2                             00027790
C      E3= ((K4) * (K3) * (K1))/(-2)                          00027800
C      E4= ((K4) * (K3) * (DX))/6                             00027810
C      NN = N - 1                                              00027820
C      Y(NN) = Y(N-3) * E1 + Y(N-2) * E2 + Y(NN) * E3 + Y(N) * E4 00027830
C      DO 275 I = 2,NN                                         00027840
C      IF(Y(I) .LT. 0) Y(I) = 0                                00027850
C      CONTINUE                                                00027860
C      RETURN                                                  00027870
C      END                                                    00027880
SUBROUTINE TLOC(NS,M1,M2,M3,IFOUND,EOF)                        00027890
C      THIS COMPUTER PROGRAM WAS DEVELOPED WITH THE FUNDING SUPPORT 00027900
C      FROM THE NATIONAL INSTITUTES OF HEALTH (GRANTS RR-612 AND 00027910
C      GM-20832) AND THE NATIONAL AERONAUTICS AND SPACE ADMINISTRATION 00027920
C      (GRANT NGR-05-020-632).                                00027930
C      *** THE MAIN FUNCTION OF THIS ROUTINE IS TO EXAMINE      00027940
C      *** THE CURRENT DATA IN THE PROCESSING WINDOW          00027950
C      *** AND DETECT WHEN THERE IS A COMPONENT PRESENT IN THE 00027960
C      *** WINDOW. THIS IS DONE BY KEEPING A HISTOGRAM OF      00027970
C      *** HOW MANY PEAK MODES ARE MAXIMIZING WITHIN          00027980
C      *** THE WINDOW. A HISTOGRAM IS ALSO KEPT OF THE        00027990

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C      *** ION CURRENTS ASSOCIATED WITH THE PEAKS THAT ARE      00028090
C      *** ARE MAXIMIZING. THIS LATTER MEASURE IS MORE          00028100
C      *** EFFECTIVE FOR COMPONENT DETECTION. AN INDEX         00028110
C      *** SET IS KEPT OF THOSE MASSES THAT HAVE MAXIMIZED     00028120
C      *** IN THE WINDOW (ARRAY 'IND'). DURING THIS WHOLE      00028130
C      *** PROCESS A MODEL PEAK FOR THE COMPONENT IS ALSO      00028140
C      *** CHOSEN 'GPEAK' USING A SHARPNESS CRITERION.         00028150
C      PARAMETER EOF ADDED - SEE COMMENT NEAR CALL STMT IN MAIN  00028160
C      WFH RTI 9/31/78                                          00028170
C      INTEGER NAME,RDATE,BITMAP,GCTIME,LIBMAP,INTEG,LOMASS     00028180
C      INTEGER HIMASS,POINTS,TAPCNT,MAXSP,LSTCNT,DEVICE,SPCNO   00028190
C      INTEGER SPEC,IND,IR,BK,NM,NTM,RECNO,FLAG,KSTOR(50),MAD,  00028200
C      1KMAD(2,50)                                             00028210
C      INTEGER NUSPEC,NMASS,OVLAP,EOF                           00028220
C      INTEGER MODBK,LOCDBG                                     00028230
C      INTEGER GPEAK,SPARE1,SPARE2,SPARE3,SPARE4,SPARE7        00028240
C      INTEGER FSTREC,AJACEN,AHEAD                             00028250
C      REAL SPARE5,SPARE6                                       00028260
C      THIS HAS BEEN INSERTED FOR THE AVERAGING FACILITY      00028270
C      RTI WFH 1/14/79                                         00028280
C      INTEGER NAVG,HAVG,AVGSPC(411)                            00028290
C      REAL*8 TLC/' TLOCXX '/'                                  00028300
C      REAL ISVP8,ISVP9                                         00028310
C      THE IDENTIFIER DIB HAS BEEN CHANGED TO SCAN TO MAKE    00028320
C      WAY FOR THE NEWLY INCORPORATED FUNCTION SUBROUTINE     00028330
C      WFH RTI 9/31/78                                          00028340
C      REAL F1,F2,F3,YTOP,HIST(7),SLOPE,SCAN                   00028350
C      COMMON PKHIST(20),NPHIST(20)                             00028360
C      COMMON YMS(11)                                           00028370
C      COMMON GM4,GM3,GM2,GM1,G0,GP1,GP2,GP3,GP4              00028380
C      COMMON SG,SG2,SIG,S1,S12,AM,AA,BB,CC,DD                 00028390
C      COMMON NAME(32),RDATE(5),BITMAP(64),GCTIME              00028400
C      COMMON LIBMAP(17),INTEG,LOMASS,HIMASS,POINTS,TAPCNT     00028410
C      COMMON MAXSP,LSTCNT,DEVICE(5),SPCNO                      00028420
C      COMMON SPEC(14,411),IND(3,411),NUSPEC(411),NMASS       00028430
C      COMMON RMAX(3),IR(3),BK(3),NM(3),NTM(3),GPEAK(3,11)    00028440
C      COMMON SPARE1,SPARE2,SPARE3,SPARE4,SPARE5,SPARE6,SPARE7  00028450
C      COMMON RATMIN,RATEMX,SIGY0,SIGNXT,SIGLST                00028460
C      COMMON ISVH8,ISVN9,ISVP8,ISVP9,SIGMA7,SATVAL,SATMAX     00028470
C      COMMON MODE1,MODE2,NLWCUT,NUPCUT,SATPKS(25),NSAT,EXPNAM(5) 00028480
C      COMMON /DUBBUG/IDEBUG                                    00028490
C      COMMON /MODES/SGMODE(3),SHMODE(3),GMODE,HMODE          00028500
C      COMMON /MASSES/ISGMAS(3),ISHMAS(3),IGMASS,IHMASS       00028510
C      COMMON /IFF/IFLAG(3)                                     00028520
C      COMMON /AJACNT/AJACEN(2)                                 00028530
C      COMMON /PARAMS/MINTIC,MINNY,NTHIRD,RATM                 00028540
C      COMMON /LFTRIT/ILEFT,IRIGHT                             00028550
C      COMMON /HIND/IH1,IH2,MSINGS(2,50),MINX,LINGS(50),LINX  00028560
C      COMMON /CRAWBU/RAWBUF(411)                              00028570
C      COMMON /CFSTRE/FSTREC                                    00028580
C      COMMON /AVG/ NAVG,HAVG                                   00028590
C      COMMON /CAHEA/AHEAD(5)                                  00028600
C      COMMON /IMAD/MAD                                         00028610
C      MSINGS SAVES MASSES OF SINGLET IN HISTOGRAMS.          00028620
C      EQUIVALENCE (YM4,YMS(2))                                 00028630
C      EQUIVALENCE (YM3,YMS(3)),(YM2,YMS(4)),(YM1,YMS(5))     00028640
C      EQUIVALENCE (Y0,YMS(6)),(YP1,YMS(7)),(YP2,YMS(8))      00028650
C      EQUIVALENCE (YP3,YMS(9)),(YP4,YMS(10)),(YP5,YMS(11))    00028660

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C	DATA HIST/- .3333,0...3333,.6667,1.0,1.3333,1.6667/	00028670
	*** CIRCULAR QUEUE TO CONTROL CURRENT DATA SET	00028680
	11=NS-13-14*((NS-14)/14)	00028690
	12=NS-12-14*((NS-13)/14)	00028700
	13=NS-11-14*((NS-12)/14)	00028710
	14=NS-10-14*((NS-11)/14)	00028720
	15=NS-9-14*((NS-10)/14)	00028730
	16=NS-8-14*((NS-9)/14)	00028740
	17=NS-7-14*((NS-8)/14)	00028750
	18=NS-6-14*((NS-7)/14)	00028760
	19=NS-5-14*((NS-6)/14)	00028770
	110=NS-4-14*((NS-5)/14)	00028780
	111=NS-3-14*((NS-4)/14)	00028790
	112=NS-2-14*((NS-3)/14)	00028800
	113=NS-1-14*((NS-2)/14)	00028810
	114=NS-14*((NS-1)/14)	00028820
C	*** READ IN NEXT SPECTRUM	00028830
C	NOTE: NS = 14,15,...,MAXSPEC - 10	00028840
C	FIRST RECORD TO BE READ IS NUMBER 13.	00028850
	RECNO = NS	00028860
	INSLT=1	00028870
C		00028880
C	THE PRIMARY INPUT STATEMENT HAS BEEN MODIFIED TO INCLUDE	00028890
C	AN AVERAGING FACILITY OVER NAVG INPUT SPECTRA	00028900
C	RTI - WFH 1/13/79	00028910
C	INITIALIZE CURRENT SPECTRUM IN CORE	00028920
	DO 90 IK=1,411	00028930
	90 SPEC(114,IK)=0	00028940
C	ADD AS MANY INPUT SPECTRA AS NECESSARY TO CORE SPECTRUM	00028950
	DO 92 IJ=1,NAVG	00028960
C	IQUPT ENSURES THAT THE QUEUE DOWN INSIDE THE READ ROUTINES IS	00028970
C	UPDATED ONLY ONCE OVER THE SPREAD OF NAVG INPUT SPECTRA	00028980
	IQUPT=0	00028990
	IF(IJ.EQ.NAVG) IQUPT=1	00029000
C	IQUPT TELLS WHETHER OR NOT TO UPDATE READ ROUTINE QUEUE	00029010
C	I14 TELLS RDSPC QUEUE POSITION	00029020
	CALL RDSPC(ISCNO,AVGSPC,I14,IQUPT,EOF)	00029030
	IQUPT=0	00029040
	IF(EOF.EQ.0) GO TO 4	00029050
	RETURN	00029070
C	READ ONWARD...	00029080
	4 CONTINUE	00029090
	DO 97 IK=1,411	00029100
	97 SPEC(114,IK)=SPEC(114,IK)+AVGSPC(IK)	00029110
	92 CONTINUE	00029120
C	DIVIDE AS NECESSARY	00029130
	IF(NAVG.EQ.1) GO TO 94	00029140
	DO 95 IK=1,411	00029150
	95 SPEC(114,IK)=SPEC(114,IK)/NAVG	00029160
	94 CONTINUE	00029170
C	NOW UPDATE SPECTRUM NUMBER	00029180
	SPCNO=ISCNO-7*NAVG+NAVG-1	00029190
C	THE FOLLOWING TEN STATEMENTS OR SO HAVE BEEN DISCARDED	00029200
C	TO MAKE WAY FOR MULTIPLE RUN PROCESSING AS WELL	00029210
C	AS THE COMMON BLOCK /CRAWBU/ AS NEITHER SERVES ANY	00029220
C	USEFUL PURPOSE.	00029230
C	WFH - RTI	00029240
C	12/6/78	00029250

C	GO TO 620	00029260
C2	WRITE(IPTR2,31)	00029270
C	2 CALL TLPRT(3,NPHIST,PKHIST,XY,XY,XY,1,1,1)	00029280
C	STOP 16	00029290
C	31 FORMAT(' ***FATAL READ ERROR ON MAIN INPUT FILE-IN TLOC***')	00029300
C	RETURN	00029310
C620	DO 10 M=1,NMASS	00029320
C10	SPEC(114,M) = RAWBUF(M)	00029330
C	NOW, WE'RE OFF AND RUNNING WHILE THE DISK IS HUMMING	00029340
	NS3=NS-11	00029350
	M3=NS3-3*((NS3-1)/3)	00029360
	M2=NS3-1-3*((NS3-2)/3)	00029370
	M1=NS3-2-3*((NS3-3)/3)	00029380
	RMAX(M3)=0.0	00029390
	SGMODE(M3)=0	00029400
	BK(M3)=0	00029410
	IR(M3)=0	00029420
	ISGMAS(M3) = -1	00029430
	NMAX=0	00029440
	SIGMA7=0.0	00029450
	IFLAG(M3) = 0	00029460
	NAVE = 0	00029470
C	LINGS IS SET UP IN NXTMAX AND CONTAINS STUFF FROM HIST 10.11	00029480
C	WHICH BECOMES HIST OF 7.8 HERE.	00029490
	DO 12 I = 1,50	00029500
	MSINGS(IH1,I) = MSINGS(IH2,I)	00029510
12	MSINGS(IH2,I) = LINGS(I)	00029520
C	SET MINX FOR STORING IN MSINGS.	00029530
	DO 13 I = 1,49	00029540
	IF (LINGS(I) .EQ. 0) GO TO 14	00029550
13	CONTINUE	00029560
14	MINX = I	00029570
	LINX = I	00029580
	DO 17 J = 1,1	00029590
17	LINGS(J) = 0	00029600
	NINX = I	00029610
	DO 18 I = 1,50	00029620
	IF (MSINGS(IH1,I) .EQ. 0) GO TO 19	00029630
18	CONTINUE	00029640
19	CONTINUE	00029650
	NINX = I	00029660
C	OINX IS USED FOR STORING HISTOGRAMMED MASSES IN H(5-6)	00029670
C	NOW MOVE DETECTION FLAG FOR PREVIOUS SPECTRUM INTO	00029680
C	THE FLAG FOR ITS IMMEDIATE PREDECESSOR. THIS IS USED	00029690
C	IN GETHGT SO SINGLET FROM IMMEDIATE PREDECESSORS	00029700
C	ARE NOT INCLUDED IN THEIR IMMEDIATE SUCCESSORS.	00029710
	AJACEN(1) = AJACEN(2)	00029720
	AJACEN(2) = 0	00029730
C	LOOP THROUGH ALL MASSES AND RESET FOUND INDICES.	00029740
	DO 15 M=1,411	00029750
15	IND(M3,M)=0	00029760
	NPHIST(8) = ISVN8	00029770
	NPHIST(9) = ISVN9	00029780
	PKHIST(8) = ISVP8	00029790
	PKHIST(9) = ISVP9	00029800
	DO 16 J=1,6	00029810
16	PKHIST(J)=PKHIST(J+3)	00029820
	CONTINUE	00029830

C	PKHIST(1)←PKHIST(4),....PSHIST(6)←PKHIST(9)	00029840
	PKHIST(7)= (SPARE5)	00029850
	PKHIST(8)= (SPARE6)	00029860
	PKHIST(9)=0	00029870
	DO 231 J=1.6	00029880
	NPHIST(J)=NPHIST(J+3)	00029890
231	CONTINUE	00029900
C	NPHIST(1)←NPHIST(4),....NPHIST(6)←NPHIST(9)	00029910
	NPHIST(7)= SPARE3	00029920
	NPHIST(8)= SPARE4	00029930
	NPHIST(9)=0	00029940
	NPHIST(10)=0	00029950
	NPHIST(11)=0	00029960
	PKHIST(10)=0	00029970
	PKHIST(11)=0	00029980
	DO 43 I = 2.5	00029990
43	AHEAD(I-1) = AHEAD(I)	00030000
	AHEAD(5) = 0	00030010
C	THE ABOVE IS A BINARY LIST OF SPECTRA DETECTED AHEAD.	00030020
C	WE SHIFT IT LEFT AT EACH NEW SPECTRUM SEARCH.IT IS	00030030
C	USED TO GUARANTEE ANY SPECTRUM DETECTED AHEAD IS ALWAYS	00030040
C	PROCESSED.	00030050
C	STATEMENT REMOVED BECAUSE NO LONGER NEEDED WITH SCAN ROUTINE	00030060
C	WFH RTI 9/31/78	00030070
C	DIB = HIMASS - LOMASS	00030080
	DO 70 M=1.411	00030090
C	RUN THROUGH MASSES	00030100
	Y0=SPEC(18,M)	00030110
C	SAVE FOR CLEAN UP RATIO, TIGRAT	00030120
	SIGMA7 = SIGMA7 + Y0	00030130
	IF(Y0.GE.SATVAL) GO TO 65	00030140
C	*** MARK SATURATED MASSES FOR LATER PROCESSING	00030150
	YM1=SPEC(17,M)	00030160
	YP1=SPEC(19,M)	00030170
C	TEST FOR SINGLET	00030180
C		00030190
C		00030200
C		00030210
C		00030220
C		00030230
C		00030240
	YP4	00030250
	IF(Y0 .LE. YM1) GO TO 70	00030260
	IF(Y0 .LE. YP1) GO TO 70	00030270
	YM2=SPEC(16,M)	00030280
	YP2=SPEC(110,M)	00030290
	YM3=SPEC(15,M)	00030300
	YP3=SPEC(111,M)	00030310
	YM4 =SPEC(14,M)	00030320
	YP4=SPEC(112,M)	00030330
	YM5(1)=SPEC(13,M)	00030340
	YP5=SPEC(113,M)	00030350
	YY5=YM5(1)	00030360
C	TEST LEFT SLOPE OF PEAK	00030370
C	LEFT IS REQUIRED NUMBER OF STRICKLY DECREASING LEFT POINTS	00030380
	IF(YM1 .LE. YM2) GO TO 65	00030390
	IF(ILEFT .EQ. 2) GO TO 44	00030400
	IF(YM2 .LE. YM3) GO TO 65	00030410
	IF(ILEFT .EQ. 3) GO TO 44	

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44      IF(YM3 .LE. YM4) GO TO 65
C      CONTINUE
C      TEST RIGHT SLOPE OF PEAK
C      IRIGHT IS REQUIRED NUMBER OF STRICKLY DECREASING RIGHT POINTS
      IF(YP1 .LE. YP2) GO TO 65
      IF(IRIGHT .EQ. 2) GO TO 45
      IF(YP2 .LE. YP3) GO TO 65
      IF(IRIGHT .EQ. 3) GO TO 45
      IF(YP3 .LE. YP4) GO TO 65
45     CONTINUE
C     CALCULATE VALUE AT MODE OF PEAK, YTOP, AND
C     X DISPLACEMENT, XTOP.
      CALL NEWTOP(YM5,RATE,XTOP,YTOP,4)
C     IF XTOP IS OUT OF RANGE THE PEAK IS NOT ELUTING HERE OR
C     THE DATA HAS TOO MANY INFLECTION POINTS
      IF(XTOP .LE. -1. .OR. XTOP .GE. 1.) GO TO 65
C     MAKE SURE THE PEAK IS INCREASING FASTER THAN BACKGROUND
      IF( (YTOP - YP5).LT.30 .AND. (YTOP - YP5).LT.30 ) GOTO 70
C     SEE IF QUALIFIES FOR MODEL FROM RATE.
      IF(YTOP.GE.SATVAL.OR.YP1.GE.SATVAL.OR.YM1.GE.SATVAL)GO TO 65
      IF(YP2.GE.SATVAL.OR.YP3.GE.SATVAL.OR.YP4.GE.SATVAL) GO TO 65
      IF(YM2.GE.SATVAL.OR.YM3.GE.SATVAL.OR.YM4.GE.SATVAL)GO TO 65
C     PREVENT SUPER SATURATION BY ABOVE
C     SEE IF RATE IS MAXIMUM TO QUALIFY AS MODEL PEAK
      MODEL = 0
      MI = M + 39
      SLOPE = (YP5 - YP5)/10
      LOCLBG = YP5 + SLOPE * 5
C CHANGED TO HAVE FUNCTION SUBROUTINE TO HAVE DIFFERENT INSTRUMENTS
C                                     WFH RTI 9/31/78
      TSHIFT=SCAN(MI)
      TSHIFT = (MI - LOMASS)/DIB
C      IF(RATE.LT.RMAX(M3)) GO TO 50
      MODEL = 1
      IF((YTOP - YP5) .GE. 160) GO TO 2000
      IFLAG(M3) = 1
C      FLAG AS FUNNY MODEL
      GO TO 2500
2000  IFLAG(M3) = 0
2500  CONTINUE
      RMAX(M3)=RATE
      IR(M3)=M
C      USE LINEAR BACKGROUND AS FIRST CUT APPROXIMATION
      MODBGK = SPEC(11,M)
      IF ( MODBGK .GT. SPEC(12,M) ) MODBGK = SPEC(12,M)
      IF ( MODBGK .GT. SPEC(13,M) ) MODBGK = SPEC(13,M)
      IF ( MODBGK .GT. SPEC(14,M) ) MODBGK = SPEC(14,M)
      IF ( MODBGK .GT. SPEC(15,M) ) MODBGK = SPEC(15,M)
      IF ( MODBGK .GT. SPEC(111,M) ) MODBGK = SPEC(111,M)
      IF ( MODBGK .GT. SPEC(112,M) ) MODBGK = SPEC(112,M)
      IF ( MODBGK .GT. SPEC(113,M) ) MODBGK = SPEC(113,M)
      IF ( MODBGK .GT. SPEC(114,M) ) MODBGK = SPEC(114,M)
C      MODBGK = MIN ( SPEC(IJ,M) : 11 .LE. IJ .LE. 1140
      DO 40 IJ = 1,11
      GPEAK(M3,IJ) = YM5(IJ) - MODBGK
40     CONTINUE
      ISGMAS(M3) = MI
      SGMODE(M3)=TSHIFT

```

50	BK(M3) = MODBKG	00031000
	CONTINUE	00031010
	XY=YTOP - (LOCLBG)	00031020
	IF (XY .LE. 0) XY = 1.0	00031030
C	SIGY0 (EXCEPT IN COMMON DECLARATIONS) APPEARS ONLY IN THIS	00031040
C	STATEMENT. HENCE IT HAS BEEN COMMENTED OUT.	00031050
	WFH AT RTI 4/19/78	00031060
C	SIGY0=SIGY0 + XY	00031070
	TITTY = TSHIFT + XTOP	00031080
	DO 800 IJ = 1,7	00031090
	IF (TITTY .LT. HIST(IJ)) GO TO 900	00031100
800	CONTINUE	00031110
900	IH = 4 + IJ	00031120
C	IH = 5 TO 11	00031130
C	HISTOGRAM DATA PKHIST FOR INTENSITY, NPHIST FOR COUNT OF PEAKS	00031140
	PKHIST(IH)=PKHIST(IH) + XY	00031150
	NPHIST(IH)=NPHIST(IH)+1	00031160
C	SAVE MODE OF MODEL PEAK	00031170
C	RESET MODEL FLAG	00031180
	IF (MODEL .EQ. 1) GO TO 925	00031190
C	ALWAYS LOG MASS OF MODEL.	00031200
	NGOGO = IH - 4	00031210
C	NGOGO = 1,2,3,4,5,6,7	00031220
	GO TO (950,950,925,925,925,960,960), NGOGO	00031230
C	SLOT 5 6 7 8 9 10 11	00031240
	HISTOGRAM SLOTS 7,8,9 0	00031250
925	MSINGS(IH2,MINX) = MI	00031260
	MINX = MINX + 1	00031270
	IF(MINX .EQ. 51) MINX = 50	00031280
	IF (MODEL .EQ. 1) GO TO 950	00031290
	GO TO 990	00031300
950	CONTINUE	00031310
C	HISTOGRAM SLOTS 5,6	00031320
	IF (IH .GE. 7) GO TO 960	00031330
	MSINGS(IH1,MINX) = MI	00031340
	MINX = MINX + 1	00031350
	IF(MINX .EQ. 51) MINX = 50	00031360
	IF (MODEL .EQ. 0) GO TO 990	00031370
C	WE HAVE A POSSIBLE MODEL FOR PREVIOUS SPECTRUM SO	00031380
C	IF THE RATE CRITERIA IS SATISFIED, SAVE IT.	00031390
	IF (RATE .LE. RMAX(M2)) GO TO 990	00031400
	ISGMAS(M2) = MI	00031410
	RMAX(M2) = RATE	00031420
	IFLAG(M2) = 0	00031430
	DO 970 IM = 1,11	00031440
970	GPEAK(M2,IM) = GPEAK(M3,IM)	00031450
C	HISTOGRAM SLOTS 10,11	00031460
960	CONTINUE	00031470
	IF (IH .LT. 10) GO TO 990	00031480
	LINGS(LINX) = MI	00031490
	LINX = LINX + 1	00031500
	IF(LINX .EQ. 51) LINX = 50	00031510
990	CONTINUE	00031520
C	SAVE MAXIMUM OF 50 MASSES DUE TO CORE LIMITATIONS	00031530
65	CONTINUE	00031540
	NMAX=NMAX+1	00031550
C	SAVE MASS THAT IS CONSIDERED A CONTRIBUTION	00031560
C	NMAX IS NUMBER OF MASSES MAXIMIZING .	00031570


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70      IND(M3,M) = M                                00031580
        CONTINUE                                    00031590
C      NOW CHECK FOR DETECTED SPECTRUM IN +4.5.60    00031600
        NL=1                                         00031610
        NU=9                                         00031620
        IDXL=4                                       00031630
        IDXU=6                                       00031640
        SPARE3=NPHIST(10)                           00031650
        SPARE4=NPHIST(11)                           00031660
        SPARE5=PKHIST(10)                           00031670
        SPARE6=PKHIST(11)                           00031680
        ISVN8=NPHIST(8)                             00031690
        ISVN9=NPHIST(9)                             00031700
        ISVP8=PKHIST(8)                             00031710
        ISVP9=PKHIST(9)                             00031720
        CALL DETEKT(PKHIST,NPHIST,IFOUND,NLWCUT,NUPCUT 00031730
        & ,NL,NU,IDXL,IDXU,MODE1)                   00031740
C      MODE1 IS THE LOCATION HISTOGRAMMICALY OF THE SPECTRUM, 00031750
C      4.LTE.MODE1.LTE.6                             00031760
C      IFOUND IS 1 IF SPECTRUM DETECTED.             00031770
C      PUT IN HEURISTIC FIX FOR THE CASE WHERE NO SUITABLE 00031780
C      MODEL IS FOUND - INSERTED AT RTI BY WFH - 5/23/78 00031790
C                                                     00031800
        IF (ISGMAS(M3).EQ.-1.AND.ISGMAS(M2).EQ.-1)IFOUND=0 00031810
        IF (IFOUND.NE.1) GO TO 888                   00031820
        AJACEN(2) = 1                                00031830
C      SETS SPECTRUM DETECTED FLAG.                  00031840
C      TEMPORARY MOD HAS BEEN ADDED TO GATHER STATISTICS ON 00031850
C      PEAK RATES- RTI WFH 9/31/78                  00031860
C      IOBS=1                                         00031870
C      WRITE(20,6251) IOBS,SPCNO,RMAX(M3)            00031880
C6251 FORMAT(A4,A4,12X,A4)                          00031890
        IF (RMAX(M3) .GE. RATM) GO TO 889             00031900
        AJACEN(2) = 0                                00031910
        IFOUND = 0                                    00031920
C      CALL PUTNUM('SPEC. REJECTED FOR MIN. RATE. SPEC =',SPCNO) 00031930
C      CALL PUTFLT(' RATE = ',RMAX(M3))              00031940
C      CALL TLPRNT(4,NPHIST,PKHIST,RMAX(M3),XY,XY,SPCNO,1,1) 00031950
C      WRITE(IPTR2,32)SPCNO,RMAX(M3)                 00031960
C32  FORMAT(' SPEC. REJECTED FOR MIN. RATE. SPEC = ',16// RATE = ',F10 00031970
C      *,3//)                                         00031980
        GO TO 888                                     00031990
889  CONTINUE                                         00032000
C      IFOUND = 1 IF SPECTRUM DETECTED.              00032010
        CALL TLPRNT(1,SPEC,SPEC,XY,XY,XY,SPCNO,NLWCUT,NUPCUT) 00032020
        CALL TLPRNT(2,NPHIST,PKHIST,XY,XY,XY,1,1,1) 00032030
        IF ( IDEBUG .EQ. 0 ) GO TO 888              00032040
        CALL TLPRNT(5,NPHIST,PKHIST,XY,XY,XY,1,1,1) 00032050
C      WRITE(IPTR2,5000)                             00032060
        DO 9 KX=1,2                                   00032070
        DO 9 KZ=1,50                                  00032080
        KMAD(KX,KZ)=MSINGS(KX,KZ)-MAD               00032090
        IF (KMAD(KX,KZ) .LE. 0) KMAD(KX,KZ)=0         00032100
9      CONTINUE                                       00032110
        DO 885 I = 1,5                                00032120
        JLOW = (I - 1) * 10 + 1                      00032130
C      JLOW = 1,11,....41                          00032140
        JUP = JLOW + 9                              00032150

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C      JUP = 10.20,....50
C      IF (KMAD(IH1,JLOW) .LE. 0) GO TO 886
C YET ANOTHER MOD TO TLPRT      WFH RT1 10/1/78
C      DO 731 IK=1,50
C      731 KSTOR(IK)=KMAD(IH1,IK)
C      CALL TLPRT(6,KSTOR,PKHIST,XY,XY,XY,JLOW,JUP,1)
C      WRITE(IPTR2,5100) (KMAD(IH1,K), K = JLOW,JUP)
C 885 CONTINUE
C 886 CONTINUE
C 888 CONTINUE
C      NM(M3)=NMAX
C      SAVE NUMBER OF MASSES MAXIMIZING
C      RETURN
C5000 FORMAT(///,' SINGLET MASSES CONTRIBUTING TO DETECTED SPEC. (MAXIMUM
C      * OF 50 PRINTED) '/')
C5100 FORMAT(10(2X,I3))
C      END
C      THIS ROUTINE DOES ALL PRINTING FOR CLEANUP. PLEASE USE IT TO ADD
C      NEW PRINTING IN ANY SUBROUTINE.
C      THE CALL STATEMENT ALLOWS FOR PASSING OF ARRAYS
C      REALS AND INTEGERS.
C      THIS COMPUTER PROGRAM WAS DEVELOPED WITH THE FUNDING SUPPORT
C      FROM THE NATIONAL INSTITUTES OF HEALTH (GRANTS RR-612 AND
C      GM-20832) AND THE NATIONAL AERONAUTICS AND SPACE ADMINISTRATION
C      (GRANT NGR-05-020-632).
C      SUBROUTINE TLPRT(N,IAR,AR,R1,R2,R3,I1,I2,I3)
C      INTEGER N,I1,I2,I3,IONE,NINE,IP/0/
C      REAL R1,R2,R3
C      DIMENSION IAR(1),AR(1)
C      COMMON /DUBBUG/IFLAG
C      COMMON /UNITS/ IRDR,IPTR1,IPTR2,IPTR3,IIN,IOUT
C      DATA IONE,NINE/1,9/
C      IFLAG IS RESET IF NO PRINTING IS TO BE DONE/
C      IF (IFLAG.EQ.0) RETURN
C      GO TO (20,30,40,50,60,70,80),N
C      THE ABOVE IS A CASE STATEMENT FOR EXECUTING PRINT
C20 WRITE(IPTR2,515)
C      20 IF(IFLAG.EQ.0)RETURN
C      WRITE(IPTR2,520) I1,I2,I3
C....WRITE TO TERMINAL
C      IF(IP.EQ.1)RETURN
C      IF(IP.EQ.1)GO TO 21
C THE WRITE TO UNIT 7 STATEMENTS WERE DETERMINED TO BE
C SUPERFLUOUS AND WERE COMMENTED OUT 3/30/78 -
C      WFH
C      WRITE(7,521)
C      IP=1
C 21 WRITE(7,22)I1
C 22 FORMAT(16)
C      THIS DOES TLOC STUFF
C      RETURN
C      30 IF(IFLAG.EQ.0)RETURN
C      WRITE(IPTR2,1400)
C      WRITE(IPTR2,530) (IAR(I),I=IONE,NINE)
C      ABOVE WRITES NPHIST
C      WRITE(IPTR2,535) (AR(I),I=IONE,NINE)
C      ABOVE WRITES PKHIST

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00032160
00032170
00032180
00032190
00032200
00032210
00032220
00032230
00032240
00032250
00032260
00032270
00032280
00032290
00032300
00032310
00032320
00032330
00032340
00032350
00032360
00032370
00032380
00032390
00032400
00032410
00032420
00032430
00032440
00032450
00032460
00032470
00032480
00032490
00032500
00032510
00032520
00032530
00032540
00032550
00032560
00032570
00032580
00032590
00032600
00032610
00032620
00032640
00032650
00032660
00032670
00032680
00032690
00032700
00032710
00032720
00032730
00032740

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RETURN
C515 FORMAT(/,10('-----'))
520 FORMAT(1H1,1X,' ***** SPECTRUM DETECTED *****',/,
-/' SPECTRUM NO. 15 ',15,'. LEFT AND RIGHT HISTOGRAM BOUNDS ',
-' ARE ',15,' AND ',15,'. '/')
530 FORMAT(/,' PEAK HIST ',8X,916,'/' ION CURRENT HIST ')
535 FORMAT(1X,9F9.0)
1400 FORMAT(' HISTOGRAM POSITIONS 1 - 9 ...')
C THESE MODS HAVE BEEN ADDED WITH ADDITIONAL STATEMENTS (WRITE)
C BEING INCORPORATED IN TLOC
C
40 WRITE(IPTR2,31)
31 FORMAT(' ***FATAL READ ERROR ON MAIN INPUT FILE IN TLOC***')
RETURN
50 IF(IFLAG.EQ.0)RETURN
WRITE(IPTR2,32) 11,R1
32 FORMAT(' SPEC. REJECTED FOR MIN. RATE. SPEC = ',16,' RATE = ',F10
*.3/)
RETURN
60 IF(IFLAG.EQ.0)RETURN
WRITE(IPTR2,5000)
5000 FORMAT(/,' SINGLET MASSES CONTRIBUTING TO DETECTED SPEC. (MAXIMUM
* OF 50 PRINTED) '/')
RETURN
C
70 IF(IFLAG.EQ.0)RETURN
WRITE(IPTR2,5100)(IAR(I),I=11,12)
5100 FORMAT(10(2X,13))
RETURN
C
80 WRITE(IPTR2,55)
55 FORMAT(1X,' INCORRECT NUMBER OF RECORDS SPECIFIED - ',
1' EXECUTION NOT AFFECTED')
RETURN
END
SUBROUTINE XTREM(ARRAY,NPTS,XMIN,MININD,XMAX,MAXIND)
INTEGER ARRAY(411),XMIN,MININD,XMAX,MAXIND
XMIN=ARRAY(1)
XMAX=ARRAY(1)
MININD=1
MAXIND=1
IF(NPTS.LE.1)RETURN
DO 2 I=2,NPTS
IF(ARRAY(I).GE.XMIN)GO TO 1
XMIN=ARRAY(I)
MININD=I
GO TO 2
1 IF(ARRAY(I).LE.XMAX)GO TO 2
XMAX=ARRAY(I)
MAXIND=I
2 CONTINUE
RETURN
END
SUBROUTINE OPNFIL
INTEGER CLNFLG
INTEGER MASBUF(6),VALBUF(6),AJACEN,AHEAD,ISQ(1000)
INTEGER NAME,RDATE,BITMAP,GCTIME,L18MAP,INTEG,LOMASS,MAD,ADS
INTEGER HIMASS,POINTS,TAPCNT,MAXSP,LSTCNT,DEVICE,SPCNO

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00032750
00032760
00032770
00032780
00032790
00032800
00032810
00032820
00032830
00032840
00032850
00032860
00032870
00032880
00032890
00032900
00032910
00032920
00032930
00032940
00032950
00032960
00032970
00032980
00032990
00033000
00033010
00033020
00033030
00033040
00033050
00033060
00033070
00033080
00033090
00033100
00033110
00033120
00033130
00033140
00033150
00033160
00033170
00033180
00033190
00033200
00033210
00033220
00033230
00033240
00033250
00033260
00033270
00033280
00033290
00033300
00033310
00033320

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INTEGER LSTMIN, SPEC, IND, IR, BK, NM, NTM, PNAME(32)
INTEGER HIST(10), UNIT, NNAME(18), IRNO
INTEGER NUSPEC, NMASS, OVLAP, EXPNAM, SRLB(5), SECOND
INTEGER QDUBLT, QSATS, NLINE, RAWBUF, FSTPGE, FSTREC
INTEGER SATLST, SATINX, PASS1, ITOM, EOF
INTEGER GPEAK, SPARE1, SPARE2, SPARE3, SPARE4, SPARE7
INTEGER*4 TIMREM, TIMCNT
REAL SPARE5, SPARE6
REAL ISVP8, ISVP9
REAL QNORM
REAL*8 C4, C1, C2, SGX, SHX
DIMENSION G(9), H(11), GNU(18), HNU(18)
COMMON PKHIST(20), NPHIST(20)
COMMON YM5, YM4, YM3, YM2, YM1, Y0, YP1, YP2, YP3, YP4, YP5
COMMON GM4, GM3, GM2, GM1, G0, GP1, GP2, GP3, GP4
COMMON SG, SG2, SIG, S1, S12, AN, AA, BB, CC, DD
COMMON NAME(32), RDATE(5), BITMAP(64), GCTIME
COMMON LIBMAP(17), INTEG, LOMASS, HIMASS, POINTS, TAPCNT
COMMON MAXSP, LSTCNT, DEVICE(5), SPCNO
COMMON SPEC(14, 411), IND(3, 411), NUSPEC(411), NMASS
COMMON RMAX(3), IR(3), BK(3), NM(3), NTM(3), GPEAK(3, 11)
COMMON SPARE1, SPARE2, SPARE3, SPARE4, SPARE5, SPARE6, SPARE7
COMMON RATMIN, RATEMX, SIGY0, SIGNXT, SIGLST
COMMON ISVN8, ISVN9, ISVP8, ISVP9, SIGMA7, SATVAL, SATMAX
COMMON MODE1, MODE2, NLUCUT, NUPCUT, SATPKS(25), NSAT, EXPNAM(5)
COMMON /UNITS/ IRDR, IPTR1, IPTR2, IPTR3, IIN, IOUT
C THIS COMPRISES THE FIRST OF SIX SUBROUTINES FOR THE EPA I/O
C INTERFACE TO THE CLEANUP PROGRAM. IN THE RTI SYSTEM, THE
C PRIMARY INPUT AND OUTPUT FILES WOULD BE OPENED HERE. FOR EPA
C ONLY A DUMMY RETURN IS NECESSARY.
C
C                               WM.F.HARGROVE
C                               RTI 11/25/78
C
EQUIVALENCE (RSEC, ISEC)
C NOW PICK UP SATURATION VALUE FROM TTY...
WRITE(IPTR1, 3110)
3110 FORMAT(IX, 'ENTER SATURATION VALUE IN F6.0:')
READ(IRDR, 3112) SATVAL
3112 FORMAT(F6.0)
WRITE(IPTR1, 3113) SATVAL
3113 FORMAT(IX, 'SATVAL= ', F8.1)
RETURN
END
SUBROUTINE CLSFIL
C THIS COMPRISES THE SECOND OF SIX SUBROUTINES FOR THE EPA I/O
C INTERFACE TO THE CLEANUP PROGRAM. IN THE SYSTEM, THE
C PRIMARY INPUT AND OUTPUT FILES WOULD BE CLOSED HERE. FOR EPA
C ONLY A DUMMY RETURN IS NECESSARY.
C
C                               WM.F.HARGROVE
C                               RTI 11/25/78
C
RETURN
END
SUBROUTINE CLSRUN(ISO, MU)
C THIS COMPRISES THE THIRD OF SIX SUBROUTINES FOR THE EPA I/O
C INTERFACE TO THE CLEANUP PROGRAM. IN THE RTI SYSTEM, THE
C FIRST, LAST, AND NUMBER OF SCANS WOULD BE INSERTED INTO THE HEADER
C RECORD WHICH WOULD THEN BE WRITTEN OUT. FOR EPA ALL THAT IS NEEDED
C IS A RETURN.
INTEGER MU, ISO(1000)

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00033330
00033340
00033350
00033360
00033370
00033380
00033390
00033400
00033410
00033420
00033430
00033440
00033450
00033460
00033470
00033480
00033490
00033500
00033510
00033520
00033530
00033540
00033550
00033560
00033570
00033580
00033590
00033600
00033610
00033620
00033630
00033640
00033650
00033660
00033670
00033680
00033690
00033700
00033710
00033720
00033730
00033740
00033750
00033760
00033770
00033780
00033790
00033800
00033810
00033820
00033830
00033840
00033850
00033860
00033870
00033880
00033890
00033900

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RETURN                                00033910
END                                  00033920
SUBROUTINE OPNRUN(LIBBLK,IEOF)        00033930
C THIS COMPRISES THE FOURTH OF SIX SUBROUTINES FOR THE EPA I/O INTERFACE 00033940
C TO THE CLEANUP PROGRAM. THE HEADER RECORDS ARE READ IN 00033950
C AND WRITTEN OUT AGAIN AND THE CIRCULAR QUEUE FOR KEEPING TRACK OF SCAN 00033960
C TIMES IS INITIALIZED. THE MAIN DIFFERENCE BETWEEN EPA'S OPNRUN AND 00033970
C RTI'S OPNRUN IS THAT HERE FOR EPA SATVAL IS READ IN FROM THE TTY, 00033980
C WHEREAS RTI'S SETUP PICKS IT OFF THE RUN HEADER RECORD. 00033990
C                                     WM.F.HARGROVE 00034000
C                                     RTI 11/25/78 00034010
C
INTEGER LIBBLK(1024),EOF,NS          00034020
INTEGER IRDR,IPTR1,IPTR2,IPTR3,IIN,IOUT,IEOF,ISEC 00034030
REAL SATVAL,SECSCN,RSEC              00034040
INTEGER NAME(3),HDRFLG,DATE(2),RUNHDR,RUNMIN, 00034050
1SAMPID(16),INAM(2),RUNCON(16),BUF4(11),LOPMAS,HIPMAS, 00034060
2RETMIN(14),RETSEC(14),BLANK/' ',INCOS(2)/'INCO','S' '/' 00034070
COMMON /HDR1/ NAME,HDRFLG,DATE,RUNHDR,RUNMIN 00034080
COMMON /HDR2/ SAMPID,INAM 00034090
COMMON /HDR3/ RUNCON,SECSCN 00034100
COMMON /HDR4/ BUF4,LOPMAS,HIPMAS 00034110
COMMON /FLAGS/ EOF 00034120
C
COMMON /UNITS/ IRDR,IPTR1,IPTR2,IPTR3,IIN,IOUT 00034130
COMMON /QUEUE/ RETMIN,RETSEC,NS 00034140
C INITIALIZE CIRCULAR QUEUE FOR SAVING SCAN TIMES 00034150
NS=0 00034160
C HAND CONTROL TO PADDOCK 00034170
CALL EPAHDR 00034180
IEOF=EOF 00034190
IF(IEOF.EQ.1)RETURN 00034200
C NOW PUT THINGS IN THEIR APPROPRIATE PLACES FOR CLEANUP 00034210
IF(HDRFLG.EQ.0)GO TO 10 00034220
WRITE(IPTR1,20) 00034230
20 FORMAT(1X,'*** EXECUTION TERMINATING, INCORRECT FORMAT OF HEADER 00034240
1RECORD DETECTED AT BEGINNING OF FILE IN OPNFI***') 00034250
STOP 00034260
C NOW PICK UP DATE 00034270
10 CONTINUE 00034280
DO 30 I=1,2 00034290
30 LIBBLK(I+30)=DATE(I) 00034300
C SET UP INSTRUMENT NAME 00034310
DO 35 I=10,12 00034320
35 LIBBLK(I)=BLANK 00034330
DO 40 I=1,2 00034340
40 LIBBLK(I+7)=INCOS(I) 00034350
C RUN SAMPLE ID 00034360
LIBBLK(29)=BLANK 00034370
LIBBLK(30)=BLANK 00034380
DO 50 I=1,16 00034390
50 LIBBLK(I+12)=SAMPID(I) 00034400
C REMARKS ON RUN CONDITIONS 00034410
DO 60 I=1,16 00034420
60 LIBBLK(I+137)=RUNCON(I) 00034430
LIBBLK(155)=BLANK 00034440
LIBBLK(154)=BLANK 00034450
C PICK UP SCAN RATE 00034460
RSEC=SECSCN 00034470

```

C	LIBBLK(57)=ISEC	00034490
C	MOVE IN MASS SCAN RANGE	00034500
	LIBBLK(42)=LOPMAS	00034510
	LIBBLK(43)=HIPMAS	00034520
C	SET HDRFLG = FIRST SPECTRUM NUMBER IN RUN	00034530
	LIBBLK(36)=HDRFLG	00034540
C	SET MAXIMUM NUMBER OF SPECTRA IN RUN	00034550
	LIBBLK(38)=100000	00034560
	RETURN	00034570
	END	00034580
	SUBROUTINE RDSPEC(SPCNO,AVGSPC,114,IQUPD,IEOF)	00034590
C	THIS COMPRISES THE FIFTH OF SIX SUBROUTINES FOR EPA I/O	00034600
C	INTERFACE TO THE CLEANUP PROGRAM. HERE IS WHERE CLEANUP	00034610
C	REQUESTS THAT A SCAN RECORD BE READ. ASIDE FROM THE I/O	00034620
C	STATEMENTS, THE LOGIC IS THE SAME AS FOR THE RT1 LINEAR	00034630
C	SYSTEM.	00034640
C		00034650
	WM.F.HARGROVE	00034660
	11/25/78	00034670
	INTEGER AVGSPC(411),SPCNO,114,EOF,IEOF	00034680
	INTEGER INAM(3),ISCN,IDBUF(2),IDHDR,IDMIN,IRTMIN,	00034690
	1IRTSEC,INMBAS,INBUF(411),INSEQ,NIN	00034700
	INTEGER RETMIN(14),RETSEC(14),NS	00034710
	REAL IRBAS,IRTIC,CFACT	00034720
	INTEGER IRDR,IPTR1,IPTR2,IPTR3,IIN,IOUT	00034730
	COMMON /IHDR/ INAM,ISCN,IDBUF,IDHDR,IDMIN,IRTMIN,	00034740
	1IRTSEC,INMBAS,IRBAS,IRTIC	00034750
	COMMON /INDATA/ INBUF,INSEQ,NIN	00034760
	COMMON /FLAGS/ EOF	00034770
	COMMON /UNITS/ IRDR,IPTR1,IPTR2,IPTR3,IIN,IOUT	00034780
	COMMON /QUEUE/ RETMIN,RETSEC,NS	00034790
C	HAND THE BALL TO PADDOCK AND GET A RECORD	00034800
	CALL EPARD	00034810
	IEOF=EOF	00034820
	IF(EOF.LT.2)GO TO 10	00034830
	WRITE(IPTR1,20)	00034840
	20 FORMAT(1X,'***EXECUTION TERMINATING DUE TO IMPROPER EOF CONDITION	00034850
	1DETECTED IN RDSPEC***')	00034860
	STOP	00034870
C	CONTINUE WITH NORMAL PROCESSING	00034880
	10 IF(EOF.EQ.1)RETURN	00034890
C	NORMAL SPECTRUM RETRIEVED - GET SCAN NUMBER	00034900
	SPCNO=ISCN	00034910
C	CALCULATE CORRECTION FACTOR	00034920
	CFACT=IRBAS/999.0	00034930
C	NOW SET UP AND LOOP SPEC ARRAY FROM INBUF	00034940
	DO 60 I=1,411	00034950
	60 AVGSPC(I)=CFACT*INBUF(I)	00034960
C	UPDATE CIRCULAR QUEUE WHEN NECESSARY	00034970
	IF(IQUPD.EQ.0)RETURN	00034980
	NS=NS+1	00034990
	RETMIN(114)=IRTMIN	00035000
	RETSEC(114)=IRTSEC	00035010
C	MISSION ACCOMPLISHED - I HOPE....	00035020
	RETURN	00035030
	END	00035040
	SUBROUTINE WRTSPEC(SPCNO,NUSPEC,DUBLT,RATE,NPK,TICIN)	00035050
C	THIS COMPRISES THE LAST OF SIX SUBROUTINES FOR THE EPA	00035060
C	I/O INTERFACE TO THE CLEANUP PROGRAM. THE CLEANED UP SCAN	

C RECORD IS REFORMATTED AND NECESSARY INFORMATION IS RETRIEVED	00035070
C FROM A CIRCULAR QUEUE. THE LOGIC EXACTLY PARALLELS THAT FOR	00035080
C THE RTI LINEAR ACQUISITION SYSTEM VERSION.	00035090
WM.F.HARGROVE	00035100
RTI 11/26/78	00035110
	00035120
INTEGER SPCNO,NUSPEC(411),DUBLT,NIN,RATE	00035130
REAL TICIN	00035140
INTEGER INAM(3),ISCN,IDBUF(2),IDHDR,IDMIN,IRTMIN,IRTSEC,17,	00035150
1INMBAS,INBUF(411),INSEQ,ONAM(3),OSCN,ODBUFF(2),ODHR,	00035160
2ODMIN,ORTMIN,ORTSEC,ONMBAS,OTBUFF(411),OTSEQ,NOUT,NPK	00035170
REAL IRBAS,IRTIC,ORBAS,ORTIC,CFACT	00035180
INTEGER NS,RETMIN(14),RETSEC(14)	
COMMON /IHDR/ INAM,ISCN,IDBUF,IDHDR,IDMIN,IRTMIN,	00035190
1IRTSEC,INMBAS,IRBAS,IRTIC	00035200
COMMON /INDATA/ INBUF,INSEQ,NIN	00035210
COMMON /CQUEUE/ RETMIN,RETSEC,NS	00035220
COMMON /DHDR/ ONAM,OSCN,ODBUFF,ODHR,ODMIN,ORTMIN,	00035230
2ORTSEC,ONMBAS,ORBAS,ORTIC	00035240
COMMON /OTDATA/ OTBUFF,OTSEQ,NOUT	00035250
COMMON /UNITS/ IRDR,IPTR1,IPTR2,IPTR3,IIN,IOUT	00035260
C NOW START FORMING THE HEADER RECORD	00035270
DO 10 I=1,3	00035280
10 ONAM(I)=INAM(I)	00035290
OSCN=SPCNO	00035300
DO 20 I=1,2	00035310
20 ODBUFF(I)=IDBUF(I)	00035320
ODHR=IDHDR	00035330
ODMIN=IDMIN	00035340
C RETRIEVE SCAN RETENTION TIMES FROM CIRCULAR QUEUE	00035350
I7=NS-7-14*((NS-8)/14)	00035360
ORTMIN=RETMIN(I7)	00035370
ORTSEC=RETSEC(I7)	00035380
C FORM OUTPUT ARRAY AND FIND BASE PEAK MASS AND INTENSITY	00035390
C TRANSFER AND DETERMINE NUMBER OF PEAKS AND BASE PEAK	00035400
ORBAS=0	00035410
ONMBAS=0	00035420
ORTIC=0.0	00035430
NOUT=0	00035440
DO 40 I=1,411	00035450
IF(NUSPEC(I).LE.0)GO TO 30	00035460
ORTIC=ORTIC+NUSPEC(I)	00035470
NOUT=NOUT+1	00035480
30 CONTINUE	00035490
IF(NUSPEC(I).LT.ORBAS)GO TO 40	00035500
ORBAS=NUSPEC(I)	00035510
ONMBAS=1	00035520
40 CONTINUE	00035530
ONMBAS=ONMBAS+39	00035540
C CALCULATE CORRECTION FACTOR	00035550
IF(ORBAS.GT.0)GO TO 50	00035560
WRITE(IPTR2,45) SPCNO	00035570
45 FORMAT('-',/,'*** WARNING - 0 BASE PEAK IN WRTSPC, SCAN #',15,'***')	00035580
RETURN	00035590
C CALCULATE CORRECTION FACTOR	00035600
50 CFACT=999.0/ORBAS	00035610
C NORMALIZE SPECTRUM	00035620
DO 60 I=1,411	00035630

```
      60 OTBUFF(1)=CFAC*#NUSPEC(1)+.05  
C NOW EVERYTHING IS READY FOR PADDOCK'S OUTPUT ROUTINE  
      CALL EPAURT  
      RETURN  
      END
```

```
00035640  
00035650  
00035660  
00035670  
00035680
```


APPENDIX B

"EXTRACTION OF MASS SPECTRA FREE OF BACKGROUND AND NEIGHBORING COMPONENT
CONTRIBUTION FROM GAS CHROMATOGRAPHY MASS SPECTROMETRY DATA"

R. G. DROMEY, M. J. STEFIK, T. C. RINDFLEISCH, AND
A. M. DUFFIELD, ANAL. CHEM., 48, 1368(1976)

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Extraction of Mass Spectra Free of Background and Neighboring Component Contributions from Gas Chromatography/Mass Spectrometry Data

R. G. Dromey,¹ Mark J. Steflk, Thomas C. Rindfleisch,* and Alan M. Duffield²

Departments of Computer Science, Genetics, and Chemistry, Stanford University, Stanford, Calif. 94305

An effective, minicomputer-based method is described for systematically extracting resolved mass spectra of mixture components from GC/MS data. Using tabular peak models derived directly from the raw data, the spectra have column bleed background removed and are corrected for interference from neighboring elutants and peak saturation. Individual components are detected in the data by means of a pair of histograms which statistically characterize the positions of mass fragmentogram peak modes. These data-adaptive cor-

rections avoid costly iterative numerical procedures and allow obtaining representative mass spectra from GC/MS data of complex mixtures on a routine basis. Using this approach, components that elute within less than two spectral scan times of each other can be detected and their mass spectra well resolved.

With the increasing application of gas chromatography/mass spectrometry (GC/MS) systems to mixture component identification in biomedical research (1, 2) and other areas (3), it has become important to be able to systematically isolate and identify minor components in the complex mixtures being analyzed. Because of instrumentation limitations, the mass

¹ Present address, Research School of Chemistry, Australian National University, Canberra, A.C.T., Australia.

² Present address, School of Physiology and Pharmacology, University of New South Wales, 2033, Australia.

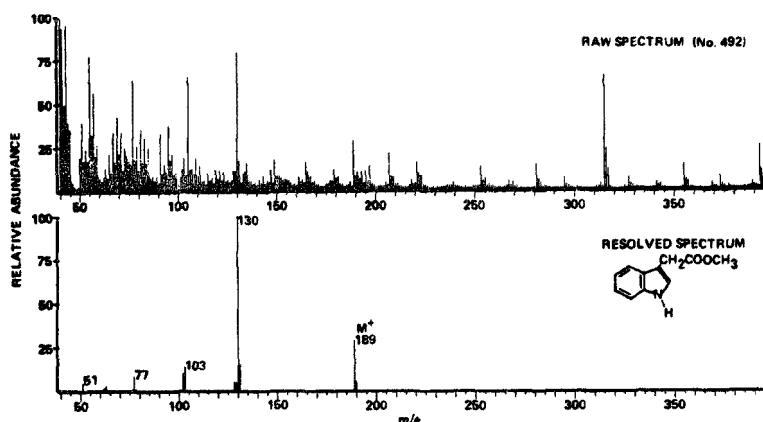


Figure 1. (a) Spectrum of indole acetic acid 3-methyl ester from a GC/MS analysis of human urine before processing. (b) Resolved spectrum of indole acetic acid 3-methyl ester

spectra obtained from a GC/MS analysis of a complex mixture are often markedly different from the spectra of the corresponding pure compounds. Differences may be caused by contributions from unresolved neighboring components during partial separation and also from GC septum and column bleed. These extraneous contributions may severely distort the relative intensities of ions in the mass spectrum of a particular component as well as contribute peaks that are not characteristic of the component being examined. Characterization and removal of these spurious ion contributions is especially important in the analysis of minor constituents where the mass spectra of interest may be substantially masked or distorted.

Our objective has been to implement a solution to these problems which is general and can systematically and reliably resolve GC/MS data with a minimum of human intervention. At the same time we have constrained the design so that the programs can run on a laboratory minicomputer. The first of these objectives has necessitated the use of a relatively complex mathematical treatment of the GC peak profile analyses as compared to that previously reported by Biller and Biemann (4). Both the present approach and that of Ref. 4 are based on analyses of mass fragmentogram profiles (4-6), a method which has been in use in various laboratories including our own, for a number of years. The method described here, however, differs substantially in the extraction of information from the profiles and thereby avoids several serious limitations inherent in the system described previously (4). By using tabular models of the elutant peak shapes together with a polynomial approximation to the GC background, and by deploying the elutant location and multiplicity information gained in analyzing individual fragmentogram profiles to assist in analyzing the others, we can achieve significant advantages in the quality of the reduced data. These include better final GC resolution, the proper assignment of ions to resolved elutant spectra (whether or not they are shared between neighboring components), more accurate spectral amplitudes free from background contributions, and the recovery of usable information from distorted data as in saturated peaks. We feel these improvements are important to a system which can reliably extract component spectra of sufficiently high quality from GC/MS runs to enable more definitive library matching, easier human interpretation of unknowns, and even the addition of extracted spectra to a library as authentic spectra. In our experience, these are essential assets for a GC/MS data system which is to be routinely

applied in medical research and amply justify the complexity of the analysis.

EXPERIMENTAL

The GC/MS computer system used in this investigation consists of a Finnigan 1015 Quadrupole mass spectrometer interfaced to a PDP-11/20 minicomputer system for data acquisition. In one frequent mode of operation a complete mass scan (from mass 40 to 450) is completed each 3.7 s and 600 consecutive mass spectra are collected during a typical GC/MS analysis. Our initial experience of comparing the experimental mass spectra from a complex GC/MS analysis with a library of known mass spectra produced very poor results because of contamination of the experimental data by spectra of column bleed and of neighboring, unresolved components. Tolerable matches were only achieved when a component was present in large quantity in the GC/MS analysis. In order to overcome these problems, we have developed a computer program capable of systematically extracting from the raw GC/MS data, spectra representative of the pure elutant compounds.

The raw mass spectrum (Figure 1a) of indole acetic acid 3-methyl ester obtained from a GC/MS analysis of the acidic fraction (after methylation) of human urine typifies this situation. This component elutes at or near spectrum number 492 in the total ion plot (TIC) shown in Figure 2. Closer examination of Figure 2 shows that this component is submerged both in mass spectral contributions from neighboring components and background from GC column bleed. For comparison, a library spectrum (7) of indole acetic acid 3-methyl ester is shown in Figure 3. Figure 1b shows how, after processing the raw GC/MS data by the method described below, we can retrieve a high quality mass spectrum of indole acetic acid 3-methyl ester free from the environmental perturbations present in Figure 1a.

Thus, in the systematic analysis of GC/MS data the problem is first to detect where in the GC trace each component shows its maximum ion intensity and then to extract from these regions representative spectra for each of the detected components. The extracted mass spectra should be as free as possible from intensity distortions relative to their library counterparts, and from the presence of extraneous ions (e.g., peaks from either neighboring components or gas chromatographic column bleed).

DESCRIPTION OF METHOD

To obtain a reliable solution to these problems, it is necessary to analyze a number of spectra on either side of the ion current maximum for each elutant. A basic assumption of our approach is that the mass spectra of two neighboring unresolved elutants can be distinguished; that is, there exist some masses for which ions occur in the mass spectrum of one component but not in the other and vice versa. A schematic representation for two closely spaced elutants is given in Figure 4. By locating the "resolved" or singlet fragmentogram peaks at such masses (detected on the basis of profile mor-

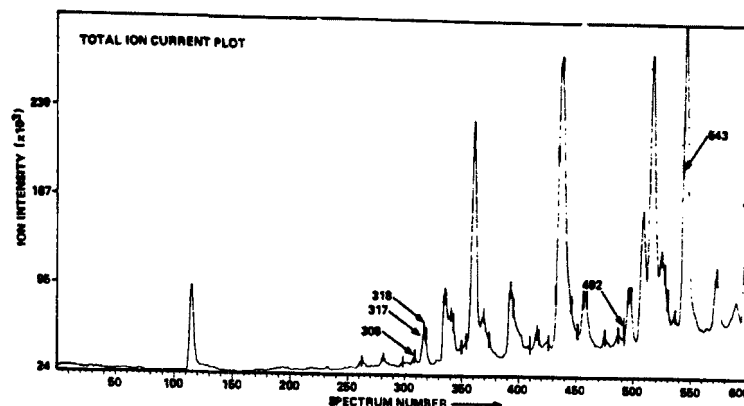


Figure 2. Total ion current plot for a GC/MS analysis of a urine sample. Components were found at vertical bar marks on TIC

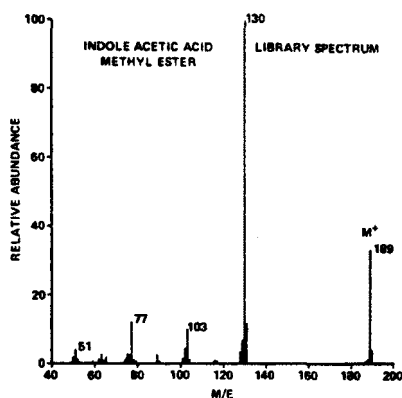


Figure 3. Mass spectrum of indole acetic acid 3-methyl ester taken from a library of biological compounds

phology), one can infer directly the positions of the elutants present and derive tabular models of the individual peak shapes. These models can be used subsequently to separate the unresolved fragmentogram complexes. The use of tabular peak models derived from the data itself accurately accommodates the a priori unknown peak profiles of particular elutants without solving for multiparameter, nonlinear model functions. Since the data are sampled often enough to satisfy the sampling theorem (8), these tabular models contain the necessary information to reconstruct a continuous peak envelope and can therefore be used as if they were continuous analytical models. For the typical peak shapes encountered, the collection of 5-10 mass spectra per singlet elutant peak represents a sampling frequency greater than twice the Fourier bandwidth of the peak. In addition, the mass by mass analysis of the fragmentogram peak complexes facilitates the mass dependent subtraction of background. (The large variation in background levels for different masses is a function of both the type of GC column used and the mixture being analyzed.)

By addressing the problem in this way, we have been able to produce accurate intensity information for the processed mass spectra and simultaneously distinguish with greater confidence which masses contribute to particular elutant spectra. We have been able to distinguish reliably elutants coming off within one and a half to two spectral scan times of each other. The succeeding sections discuss in more detail the

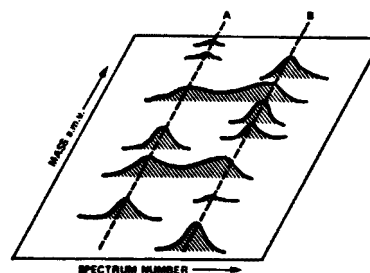


Figure 4. A schematic representation of the set of partial mass fragmentograms for two closely spaced elutants. Components A and B have some masses in common

procedures used to detect and resolve the mass spectra of unique elutants.

Detection of Elutants in GC/MS Data. Elutant detection involves finding the location of each mixture component in the GC/MS data, even if it does not have a corresponding peak maximum in the overall total ion current trace. Ideally for a given elutant, the fragmentograms for all its ion masses will show maxima at the same time and, in practice, this holds for well-resolved materials. However, for partially resolved mixtures, the complicating factors of peak overlap and background contributions can cause fragmentogram maxima for neighboring components to show significant variation in their positions on the time axis. Reliable position information for each elutant is best derived from the fragmentogram profiles containing singlet peaks for that elutant, that is, from fragmentograms at those spectral masses unique to the elutant relative to its neighbors.

The approach used for elutant detection is to compute two histograms of candidate singlet peak positions and to select as elutant locations significant histogram maxima. The first histogram measures the number of singlet mass fragmentogram profiles which reach maxima in each time interval. The second histogram measures the total singlet ion intensity above background at these maxima. These two types of histogram contribute complementary information for judging elutant locations. At a given elution time, the histograms include fragmentogram peak maxima from all masses over seven spectra. The position of each maximum is determined by a parabolic least squares interpolation about the top five points in the sampled peak data. If the intensities of the five points contributing to the maximum are Y_{-2} , Y_{-1} , Y_0 , Y_1 , and Y_2 , then the expression for the time coordinate of the maximum is

$$t = \frac{7(2Y_{-2} + Y_{-1} - Y_1 - 2Y_2)}{10(2Y_{-2} - Y_{-1} - 2Y_0 - Y_1 + 2Y_2)}$$

The time coordinates of maxima are estimated to one third of the time to collect each spectrum in order to separate very close neighbors. Because we measure peak locations to one third of a spectral scan time, appropriate shifts are also included to account for the fact that higher masses are measured later in each spectral scan than lower masses. To build these histograms, the program examines the profiles of each mass fragmentogram in the data. Only peaks with intensities above a prescribed threshold are added into their appropriate time positions in the histograms. Peaks that are obvious multiplets (multiple extrema) are not incorporated into the histograms but are marked for later resolution. After all of the histogram information is collected for a given region, components are defined to be detected at locations where both the intensity and peak count histograms show maxima that are above a threshold. This statistical approach, looking for "clusters" of fragmentogram peaks in the histograms, does not depend upon a correct decision for each peak but rather on a preponderance of good decisions looking over all of the data. It will fail to resolve elutants very close together which do not have enough distinguishing mass spectral components as described above. In general, however, using this approach we are able to detect and resolve spectra reliably that elute with a separation in time as small as one and a half to two spectral scan times. (Two scan times correspond to 25% of a typical GC peak width at the scan rate we use.) Elutants this close often do not show multiple extrema in the fragmentogram profiles of masses common to both spectra and could not be separated properly except for this type of procedure. If two elutants are separated by less than 1.5 scan times, resolution becomes less certain depending on their relative concentrations and mass spectral distinctness.

Estimation of Spectral Intensities and Background for Well Resolved Elutants. Once the locations of elutants in the GC effluent have been determined, we proceed to compute a resolved spectrum for each material. To illustrate the principles involved in spectral amplitude and background estimation, we consider the simple case of an elutant that is well separated in time from its nearest neighbors. This analysis will be extended to the more complicated case of multiplet resolution in a later section. By "well-separated" we imply only that there are no maxima in the elutant detection histograms for three or four spectra on either side of the elutant under consideration. In such a situation, each of the mass fragmentogram profiles in the vicinity of the elutant will consist of a background on which is superimposed a peak with amplitude representative of the elutant spectral component at that mass. The background (contributed by both GC column bleed and possible tailing from nearby, high-concentration elutants) is distinguished from the elutant peak by the fact that it varies much more slowly with time. Reasonable estimates can be made by assuming that, for any particular mass fragmentogram, the background amplitude varies at most linearly with elution time in the vicinity of a given elutant. This approach to background determination, using the actual fragmentogram characteristics around each elutant, automatically tracks changes in the bleed levels observed during a run. It should be noted that our model is a first-order approximation subject to some error. A more accurate approximation would involve representing the background variations over a larger span of spectral scans than we are able to manage with the current program organization and computer memory limitations. We feel that the linear estimate is justified, however, in that it produces results within the error limits from other data uncertainties.

To complete the estimation process, we use a model peak

to determine the contribution of each mass fragmentogram to the elutant spectrum. Much work has been done on the analytic approximation of gas chromatographic peak shapes (9, 10). Our experience has been that relatively simple models do not adequately approximate the range of shapes encountered and more complex models require large amounts of computing to determine model parameters. Noting that a separate model must be developed for each elutant and with a view toward obtaining the peak shape and definition necessary for multiplet resolution within reasonable computing resources, we have approached the problem by using tabular peak models taken from the data itself. Such models, defined at discrete sample points, can be evaluated at any required intermediate point by interpolation (since the sampling theorem is satisfied) and automatically reflect any peak asymmetries which may be present. For a given elutant, the model will be independent of mass, assuming that relative molecular fragmentation probabilities do not change with elutant pressure within the mass spectrometer. A number of criteria should be satisfied by the tabulated model peaks. They should be singlet peaks superimposed on as small a background as possible and they should be relatively intense in order to ensure a good signal-to-noise ratio and good definition of peak skirts.

Candidate singlet peaks may be distinguished from doublet or background peaks by the feature that they are relatively sharp. One way to measure peak "sharpness" is to use a logarithmic rate function defined as follows:

$$\text{rate} = \sum_{i=1}^3 \left[\frac{(Y_{t-1} - Y_t)}{Y_t} + \frac{(Y_{-(t-1)} - Y_{-t})}{Y_{-t}} \right]$$

where the Y_t are evaluated at equal scan widths at each side of the mode of the peak. It can be seen that this rate will be large for peaks which are sharp and smaller for peaks which are broad. The rate as defined is also independent of amplitude for peaks of identical shape. A peak with a computed rate below a threshold appropriate to the experimental conditions is considered to be either an artifact of the gas chromatograph (background peak) or a multiplet and is not included in the detection histograms.

During the process of computing the detection histograms, a list is kept of the unimodal fragmentogram peaks having the highest rate factors in the region under analysis. When a component is detected in a given region, a model peak is then immediately in hand that can be used in the peak height estimation and background removal process. The local minima just on either side of the model peak are used as estimates of the local background (a straight line through the greatest of these minima is removed before the model peak is used for analysis). The selection of the peak with the highest rate factor as our model peak has worked well in producing models which are singlets and suffer least from interference by background and neighboring fragmentogram peaks.

Given the fragmentogram peak model for this case of a well-separated elutant, we can now correct the individual mass fragmentograms for background and estimate true mass spectral intensities for the elutant. For the fragmentograms exhibiting peak maxima "near" the location of this elutant (see below for detailed selection criteria), each peak in the set is quadratically interpolated to align it on a common time origin (this removes the time shift between collection of low and high mass data). This is done by fitting a parabola through successive groups of three points near the peak mode and interpolating to give four equally spaced points about the mode, separated by one spectral scan time. With the peaks in this standard form, they are ready for the least squares analysis below. Assuming a linear background model over the region of 5 to 10 scan intervals under consideration, the local background B_t at time t is approximated by

$$B_t \sim c + dt$$

where c is the background offset and d is its slope. The interpolated elutant peak model is normalized to unit area and has amplitudes P_t at times t . Then for a given mass fragmentogram, the amplitude of the actual fragmentogram profile Y_t at time t can be approximated by

$$Y_t \sim pP_t + (c + dt)$$

where p measures the elutant amplitude above background. Note that this model assumes a superposition principle based on the earlier assumption of constant relative fragmentation probabilities and a linear encoding of ion current information. If ion current data are obtained from nonlinear electronic systems or read from film, the peak model itself would be amplitude dependent and this linear analysis could not be applied until appropriate amplitude linearization corrections were made. From the above model, we can derive a least squares estimate for the elutant amplitude p and the background parameters c and d by minimizing the error function

$$E = \sum (Y_t - pP_t - c - dt)^2$$

according to the conditions

$$\frac{\partial E}{\partial p} = \frac{\partial E}{\partial c} = \frac{\partial E}{\partial d} = 0$$

The summation in the error function is over all available points in the peak profile as well as the neighboring background points within the window of scans contained in the computer's memory. These conditions yield three linear equations in the three parameters which can be solved by standard techniques (11). From the solution of these equations for the value of p , we get the spectral intensity for the mass under consideration. This analysis is applied to all mass fragmentograms with maxima near the elutant location to obtain the complete, intensity-corrected spectrum. It is worth noting that this method, using a tabular model peak derived from the data and elutant locations obtained from the detection histogram analysis, reduces the calculation for each mass spectrum intensity to the solution of a set of linear equations. Specifically, this avoids iterative methods for determining the parameters of a theoretical peak model and for determining elutant time positions.

Fragmentograms are selected for this analysis on the basis of several criteria. Given the nominal elutant position from the detection histogram analysis, a fragmentogram is excluded (mass spectrum assigned zero intensity) if it has no local peak maximum or if its maximum is displaced from the reference elutant position by more than two thirds of a spectral scan time on either side. Each fragmentogram peak meeting this test must also have an acceptably high rate factor, to be included in the analysis. For peaks of masses greater than 200 amu, we require a rate factor greater than 25% of the rate for the model peak. This restriction is useful for eliminating contributions caused by peaking in column bleed components. In carefully examining GC/MS data sets, we can observe that masses characteristic of the spectra of column bleed components show maxima in their mass fragmentograms just prior (one to two spectra) to the elution of an actual component. In essence, the component appears to "push" the bleed out ahead of itself. Because these peaks are formed by a different process than normal elutant mass fragmentogram peaks, they usually have a much broader shape. Consequently their rate factors will be significantly reduced and they can be eliminated by the rate threshold criterion. The combination of the fragmentogram peak location criterion together with the minimum rate criterion effectively discriminates against extra-

neous contributions to the intensity-corrected spectra without removing authentic mass peaks.

Extraction of Poorly Separated Elutant Spectra. Many instances arise in the analysis of GC/MS data where two or more elutants are poorly resolved by the gas chromatograph. The resulting mass spectra in such a region exhibit ion intensity distortions which reflect the interactions (overlap) between adjacent elutants in addition to the ion contributions of background. The extension of the above procedures to the general case is not difficult. Through the histogram detection and model procedures, one can extract normalized peak models P, Q, R, \dots for the various elutants present. Then with the assumption of a linear background, the elutant contributions to each fragmentogram profile Y can be estimated by minimizing the error function

$$E = \sum (Y_t - pP_t - qQ_t - rR_t - \dots - c - dt)^2$$

with respect to the elutant amplitudes p, q, r, \dots , and the background coefficients. Sets of linear equations result for each mass to extract the resolved spectra. In practice, we have not implemented this full procedure beyond the doublet case. Through the following approximations, reasonable results are achievable within available minicomputer resources. Using the histogram method described earlier, neighboring elutants are handled with a "look ahead" procedure. That is, information about an elutant that has just been detected is stored and the detection algorithm is applied to the data in the immediate neighborhood by extending the range over which the detection histograms are calculated. If by including this extended region an additional elutant is detected, we record the position of its mode, select a model peak for this second elutant using the rate criterion, and initiate a doublet resolver algorithm. At present, the extended histograms project four spectral scan widths beyond the position where the first elutant of the multiplet was detected (limited by computer memory). The same criteria are applied as in the singlet case to decide which fragmentogram peaks belong to the pair of detected components. The model used to process the composite fragmentogram peaks (many of which may be singlets belonging to either elutant) assumes that there are two overlapping peaks superimposed on a linear background. The doublet model represents an oversimplification of some situations as, for example, in the case where 3 components elute within a very brief interval. By applying it, however, to successive pairs of elutant peaks (taking first-order account of peak tail contributions from any earlier elutant), it provides acceptable accuracy and peak resolution effectiveness. As indicated above, a fit of the two peak models P and Q with a linear background to the fragmentogram profile Y may be described by the approximation

$$Y_t \sim pP_t + qQ_t + c + dt$$

Minimizing an error function analogous to the earlier singlet case results in 4 linear equations in the peak amplitudes p and q and the background parameters c and d . This set of equations again can be solved by standard methods.

In cases where peaks are actually singlet peaks, the solution should yield zero for the amplitude of the missing component. In practice, for such cases the amplitude of the second component is a very small positive or negative value which is representative of how well the model fits the data. Amplitude results for masses that belong to the second component of the doublet are stored temporarily until this component is moved into the processing window at which time they are incorporated into the analysis of the newly detected component.

Reconstruction of Saturated Peaks in Elutant Spectra. From a practical viewpoint, a fairly common occurrence in

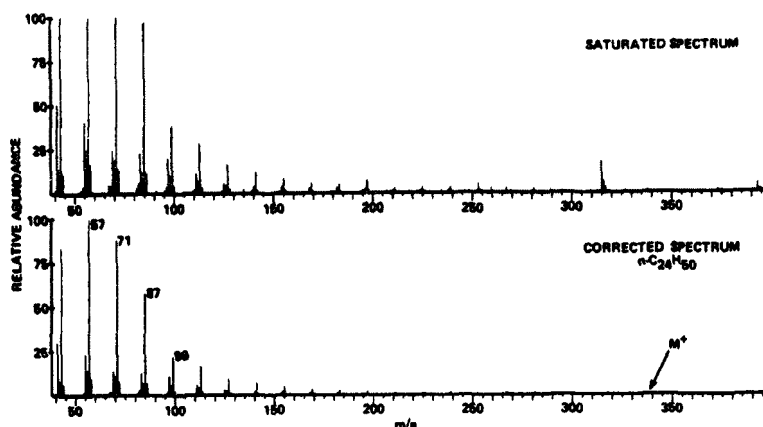


Figure 5. (a) Saturated unprocessed mass spectrum for tetracosane. (b) Spectrum of tetracosane after processing and correction for saturation.

GC/MS data collection systems is the problem of mass peak saturation. Saturated peaks occur when the concentration of a component in the ion source is such that for one or more ion masses the detection system analog-to-digital converter becomes overloaded. Saturated peaks are easily detected because of their characteristic flat tops which have an amplitude determined by the overload limit of the detection system (e.g., the saturation value is 4095 for a twelve-bit analog-to-digital converter).

To obtain accurate amplitudes for component spectra that include saturated mass peaks, we must reconstruct these peaks to estimate their true amplitudes. A convenient way to do this in the singlet case is to use the least squares model that we derived in the preceding sections. To actually apply it for reconstruction of saturated mass fragmentogram peaks, we need to make a small modification to the equations. Instead of summing over all the points in the peak, we sum over only those points that are not saturated in the fragmentogram. As an estimate of the peak mode, we use the mode of the intensity histogram for the component being analyzed. An example of reconstruction of a mass spectrum with saturated ion intensities is given in Figure 5. Figure 5a shows a saturated spectrum of tetracosane (spectrum number 545 in Figure 2) and Figure 5b is the corresponding reconstructed spectrum. It is clear that the reconstructed spectrum will give a far better match with a library spectrum than the saturated spectrum which is badly saturated at masses 43, 57, and 71.

Before leaving the discussion of saturation, we should point out that we have not in practice extended the procedure for saturation correction of singlet peaks to the doublet case as we believe that it would be inadequate for reliable intensity estimates. If too many points are overloaded, there will be insufficient data to accurately estimate the amplitude of each multiplet component. Despite such correction algorithms, there is no substitute for the collection of good quality raw data at the start.

RESULTS AND DISCUSSION

The program based on the algorithm outlined in the preceding sections has been tested on a wide variety of biological samples. It fits comfortably into a DEC PDP 11/45 computer (with 28K words of memory) and takes approximately 8 min to analyze a raw GC/MS data set of 600 mass spectra (scanned from masses 40 to 450). Much of this time is spent in reading the raw data from the disk and other input-output operations. Copies of the program, which is written in FORTRAN, are available from the authors. Currently, this program forms part

of an automated analysis system for the GC/MS analysis of urine and blood samples. The program reduces the raw GC/MS data set of approximately 600 spectra to a set of about 60 resolved elutant spectra which are then matched against a library of mass spectra of biological compounds. This whole process takes about 20 min and produces an analysis of the sample, with known compounds in the mixture identified and the remaining unknown set marked for further study by chemists or other DENDRAL programs (12-14).

In evaluating performance of the program, a major issue is how well it is able to detect elutants in the data. The vertical bars on the TIC (Figure 2) indicate all the places where the program detected and isolated a component from the raw GC/MS data. The program's power of detection is illustrated for example by the elutant detected near spectrum number 492 in the total ion current plot shown in Figure 2. Although there is no evidence of a maximum in the TIC in the region near 492, the program was able to detect and isolate a good quality spectrum of indole acetic acid methyl ester (Figure 1). In the raw data, this spectrum is clearly submerged in background and overlapping contributions. A comparison of the resolved spectrum (Figure 1b) with a library spectrum (Figure 3) shows that the basic spectral intensity profiles are very similar even including the very low intensity ion of mass 89. Some very small ions (of intensity less than 5% relative abundance) are absent from the resolved spectrum because they have been lost in the background noise. It is worth noting that there are no peaks present in the resolved spectrum that are not in the library spectrum, that is, the extraneous mass spectral peaks in the raw data including peaks at masses 105, 253, and 315 are not included in the resolved spectrum. The relative intensities of the mass spectral peaks at masses 51, 62, 65, and 77 have been changed significantly from their levels in the raw data. This illustrates the importance of correcting the intensities for background. The mass spectral peaks at masses 51, 52, 63, 78, and 129 appear to maximize near spectrum 496 in the raw data instead of spectrum 492 because of the overlapping contributions of a poorly resolved elutant. Similar examples of the power of this technique exist in other parts of the GC profile in Figure 2.

The detectability of unresolved elutants is clearly a function of their amplitude relative to neighboring components and background. One way to characterize this is to measure the ratio of the total ion intensity (sum of the mass spectrum amplitudes) in the resolved spectrum compared to that in the unprocessed spectrum including background and overlap effects. The mass spectrum of the processed component at

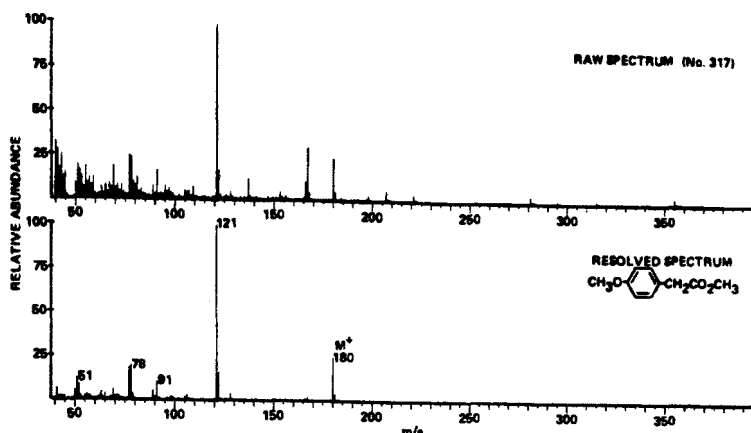


Figure 6. (a) Mass spectrum of 4-methoxyphenylacetic acid methyl ester before processing. (b) Resolved mass spectrum of 4-methoxyphenylacetic acid methyl ester

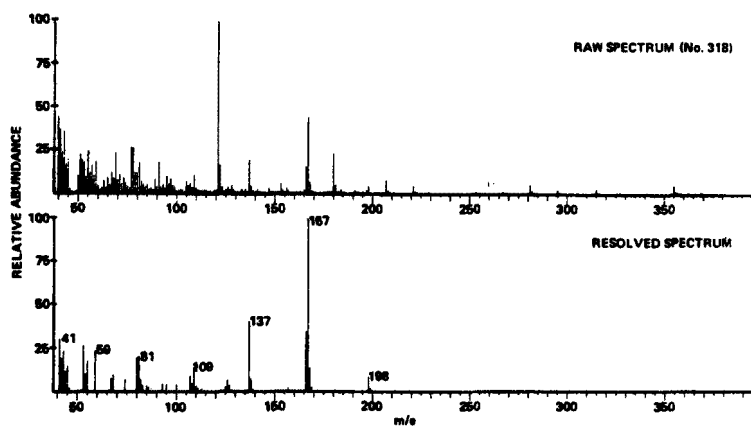


Figure 7. (a) Spectrum of an unknown aromatic ester before processing. (b) Resolved spectrum of unknown ester in Figure 7a

spectrum number 492 comprises only 4% of the total raw ion current. It can be expected that there will be problems detecting components with an ion current ratio that falls much below a level of 4%. Also if two compounds elute within less than 1.5 to 2 spectral scan times of one another, there is an increasing chance that the program will make the wrong decision as to whether there is one or actually two elutants present. Such errors are dependent on the ion current ratio between adjacent elutants, the similarity of their mass spectra, and the stability with which peak positions can be determined.

As an example of doublet resolution, consider the region near spectrum numbers 317 and 318 in Figure 2. The program detects that there are two elutants present and Figures 6 and 7 illustrate the raw and resolved spectra at these locations. The spectrum in Figure 6b is a good representation for 4-methoxyphenylacetic acid methyl ester. The other component is an unknown aromatic ester.

We have evaluated the efficiency of background removal for singlet elutants by examining their mass fragmentograms. After calculating the least squares peak and background levels, we concluded that the computed results are consistent (within 5–10%) with human estimates. They tended to be less accurate for very weak peaks whose shapes were more sensitive to noise distortions.

For the multiplet case, where the peak profiles can be considerably more complex, there is a stronger possibility that

the model will not produce accurate amplitude information. In such cases, as when there are three rather than two elutants present, there is a danger that background contributions will be incorrectly estimated particularly with the limited number of scans that can be held in our minicomputer memory at one time. We feel however that use of a more complex model for triplets is not likely to be able to guarantee much greater precision. A sequential application of the doublet model has produced acceptable results in our experience with the program. Problems most frequently occur when a small amount of an elutant occurs just prior to, or just after, an elutant of high concentration. The intensities of peaks in the small elutant that are common to the large elutant tend to be less accurately calculated than singlet peaks and sometimes may even be discarded as negligible if their intensity relative to the large peak falls much below 10%. This may be especially important for the molecular ions of compounds with the same molecular weight which would be expected to elute near each other.

Comparison with library mass spectra has indicated that correction of intensities for saturated singlet peaks is satisfactory. However, as expected, the accuracy of the calculation decreases as peaks become more heavily saturated. In our case, we are working with model peaks that extend over nine points (i.e., nine scan widths). If more than four of a peak's nine points are saturated, we can expect that its estimated intensity

will have only limited accuracy because there is insufficient information left to accurately characterize its shape.

Conditions arise in the raw GC/MS data for which it is not possible to extract resolved mass spectra unambiguously. One case is when the elutant-to-background ratio falls significantly below 5%. In these cases, the very weak intensity ions, including isotope ions, usually do not appear in the resolved mass spectra. The other difficulties arise when it is not possible to detect the presence of multiple elutants because they occur within less than one mass spectrum scan time of each other. In this case, the processed spectrum represents the mixture of the two elutants.

In general, we have found that the present system works very well and is capable of detecting and isolating high quality representative mass spectra in GC/MS experiments involving complex biological mixtures.

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