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USER'S MANUAL FOR ANALYST,

A COMPUTER PROGRAM FOR CONTROL OF AN ISOMASS 54E THERMAL-IONIZATION, SINGLE-COLLECTOR MASS-SPECTROMETER

by

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USER'S MANUAL FOR ANALYST, A COMPUTER PROGRAM FOR CONTROL OF AN ISOMASS 54E THERMAL-IONIZATION, SINGLE-COLLECTOR MASS-SPECTROMETER

INTRODUCTION

ANALYST is a computer program for controlling an Isomass 54E mass-spectrometer, written in Hewlett-Packard BASIC 2.1 for an HP-9836 computer. A second-generation program evolved from the HP-9835/9845 programs DBAT1B and DBAT2B (Ludwig, 1982), ANALYST is intended to be extremely easy and straightforward to use, both for manual and fully-automatic running, and yet permit the flexibility and range of operations that are required for use in a research mode by experienced operators. Though similar in many of its functions to these earlier programs, ANALYST was designed after two years of observing the day-to-day interaction of users with DBAT1B and DBAT2B, and was designed in part to rectify some of the difficulties in operator interaction in these programs. Another goal, of course, was to exploit the inherent advantages of the much-greater speed and memory of the HP-9836 computer compared to the HP-9835/9845 used for DBAT1B and DBAT2B. The general characteristics of the program are summarized below.

Characteristics of ANALYST

1) most functions of ANALYST can be used with virtually no reference to this documentation - even for inexperienced users;

2) real-time graphics are provided for functions of the mass-spectrometer wherever possible and appropriate;

3) the operator is always able to interrupt an operation and rapidly return to a "home base" without unforeseen or negative consequences;

4) simple functions are accessed via clearly-defined menus and single keystrokes of the labeled computer softkeys;

5) all continuous functions of the mass-spectrometer (such as filament-currents, focus-settings...) are controllable from the computer using the computer KNOB;

6) once the samples are loaded, the source-can pumped down, and all appropriate switches turned on, all further operator interaction with the mass-spectrometer takes place through the computer;

7) nonreversible operations, such as rotating the barrel to a new sample or turning filament-currents off, require confirmation by the operator;

8) operator-requested operations that affect the physical state of the mass-spectrometer are reflected by real-time feedback, in the form of either alphanumeric data, graphics, or both;

9) isotope-ratio data-taking is available in two modes: fully-automatic, where no further operator attention is required once the automatic-running parameters have been defined; and "manual" (really semi-automatic), where the operator is responsible for taking up the filament-currents (through the computer), focusing the ion-optics (through the computer), and deciding when the data-taking operation is to begin;

10) even in the manual mode, most mass-spectrometer operations are available either semi-automatically or under complete operator control. Such operations include ion-optics focussing, optimization of barrel-position, filament-current control, and magnet-scanning;

11) for semi-automatic or automatic operations where there are several parameters that the operator needs to define, such as magnet-scanning, filament-current take-up, or data-taking, the program requests input of these parameters in a highly flexible and convenient "form-entry" mode. This "form-entry" mode is essentially self-explanatory, appears with useful default values wherever possible, permits simple and rapid correction of errors, and protects against both logical and typographical errors;

12) for complex "forms", such as for the definition of the fully-automatic running parameters, "HELP" screens are available to explain the computer's requests to the inexperienced user;

13) definition of the parameters necessary for a full-automatic run is extremely rapid and simple. The time necessary to define a new automatic run ranges from only a few seconds to a minute or so;

14) the operator can intervene at will during a full-automatic run, request various mass-spectrometer operations, and then return to full-automatic running via a simple and smooth process;

15) full-automatic runs are extensively protected against unpredictable running-conditions and hardware malfunctions;

16) the data-taking algorithm chooses optimum parameters for critical parameters such as integration and delay times, location of background positions, and the order of peak-switching;

17) the data-taking algorithm is unusually time-efficient, without sacrificing accuracy.

How Should You Use This Guide?

For your first session with **ANALYST**, start with the **TUTORIAL - MANUAL RUNNING** section. This will give you some familiarity with the way you will interact with **ANALYST** and get you to the stage of actually running samples in a fairly short time.

When you're comfortable with doing manual runs and are ready to experiment with fully-automatic runs, use the **TUTORIAL - AUTOMATIC RUNNING** section. You might then try fully-automatic runs of whatever samples you had been experimenting with in the manual-running mode.

To access some of the less-frequently used functions of **ANALYST**, to deal with nonroutine situations, or just to understand more about the capabilities and logic of **ANALYST**, you will eventually want to consult the **REFERENCE GUIDE**. The **REFERENCE GUIDE** is less-coherently arranged than the Tutorials, but is better-suited to finding out how to access specific functions of **ANALYST** (or to find out if a function is available at all). The **REFERENCE GUIDE** also contains instructions on how to load **ANALYST** from scratch and what to do after changing the samples in the barrel.

If you really want to dig into the nuts and bolts of the program, the program list is available as a separate report (Ludwig, 1985). If you want to do this, I suggest that you have the program loaded into the computer so that you can find the subprograms that you're interested in (since there are about 100 of them, they can be hard to find from the list alone).

Hardware Required

The particular mass-spectrometer for which **ANALYST** was written is a Micromass Isomass 54E, built in 1979. This instrument is equipped with a single Faraday-cup collector using a 10^{11}-ohm resistor, a Daly detector, a 16-bit GPIO interface, and a 16-sample barrel. The computer for which **ANALYST** was written is a Hewlett-Packard HP-9836 running under the **HP EXTENDED BASIC 2.1** language, including the Hewlett-Packard Advanced Programming and Graphics Extensions binary programs, and at least 1 megabyte of total RAM. An HP-9816 computer with similar language and RAM and the equivalent to the HP-9836 keyboard (keyboard option 805; ASCII Extended Keyboard Character Set) should also be compatible with the program.

TUTORIAL - MANUAL RUNNING

This section is intended to be used while you are sitting down at the computer and actually running a trial sample. To start, you'll have to have a sample in the barrel that you can play with, and have the mass-spectrometer pumped down, all switches turned to their proper settings (see the **Reference Manual**), a good vacuum, and the beam-valve open. Check with an experienced operator to make sure that this is the case. Ask this person to also make sure that **ANALYST** is currently in the Beam-Monitor Condition.

How to Use the HP-9836 Computer

If you've worked with the HP-9836 computer before, you can skip this section. Otherwise, read on.

Compared to other computers that you may have used before, the HP-9836 has some unique features (or peculiarities if you prefer) that you'll have to get used to, so I'll try and briefly go through the more important ones.

The Softkeys

The keys numbered **k0** through **k9** at the top left of the keyboard are called the **softkeys**. The functions of the softkeys are defined by the computer program, and will change depending on what part of the program you're in. When the softkeys are active (that is, when they can actually do something when you press one), the program will indicate their function by labels in the ten white boxes at the bottom of the CRT. These labels "map" to the softkeys, so that the label in the upper-left box indicates the function of the upper-left softkey (k0), the label in the lower-right box indicates the function of the lower-right softkey (k9), and so on. In many cases, **ANALYST** will also list the functions of the softkeys in more detail above the softkey labels. Whenever you press a softkey that has a softkey-label, **ANALYST** will usually immediately start to perform the function indicated by the softkey label (though some functions require operator confirmation).

The KNOB

At the upper-left of the keyboard is a circular device called the **KNOB**. The KNOB is used by **ANALYST** to let you perform continuous functions, such as changing the filament current manually or changing the focus potentials manually. So its function depends again on what part of the program you're in (in most cases, it won't do anything at all). Whenever the KNOB is active, though, there will be a message somewhere on the CRT telling you what it will do.

Changing or Dumping the ALPHA and GRAPHICS Screens

The HP-9836 can use the CRT to display alphanumeric information, graphics information, or both at the same time. Sometimes, you might want to unclutter the CRT display by clearing either the alpha or graphics part of the display, or you might want to redisplay a graphics screen that isn't present at the moment, but you suspect hasn't been overwritten yet. To do this, just use the **ALPHA** and/or **GRAPHICS** keys to the upper-left of the keyboard. To invoke the graphics screen when only the alpha screen is displayed, press the **GRAPHICS** key once (both alpha and graphics present at once) or twice (graphics screen only). To have the alpha screen reappear, just press the **ALPHA** key once (again, to get alpha plus graphics) or twice (to get alpha only).

If you want to "dump" the graphics display to the printer (assuming that the printer is one that can accept a graphics-dump, such as the HP-2225 [ThinkJet] printer), just press SHIFT-GRAPHICS (labeled in blue as DUMP GRAHICS). To dump just the alpha display, press SHIFT-ALPHA (DUMP ALPHA in blue). These dumps take about 30 seconds with the ThinkJet printer.

Entering Responses to Queries

To answer one of ANALYST's queries, type in your response and press the ENTER key. Don't use the EXECUTE key - the computer will respond with an error-message. Also, don't use the CONTINUE key unless you want to accept the default response (indicated in the query itself).

Editing Your Responses

To correct mistakes in your responses to ANALYST's queries, there are several keys just for editing your input. To move the cursor to where you want to change part of your response, use the left- and right-arrow keys at the top center of the keyboard. To delete a character or insert a character at the cursor position, use the DEL CHR or INS CHR keys, also at the top-center of the keyboard. To erase your input and start over again, use the CLR LN key towards the top right of the keyboard. Press the EXECUTE key to enter your edited response.

Recovering from I/O Errors

If you forgot to turn the printer on, or if one of the critical switches on the panel of the mass spectrometer was not turned on, the computer will become hung up waiting for a response from that device. If this happens, just correct the problem (for example, turn the printer on), press the CLR I/O key (in the upper-right area of the keyboard), then the CONTINUE key, and you'll be back in business.

The HP-9836 Floppy-Disk Drives

The HP-9836 has two floppy-disk drives, located between the keyboard and the CRT. These drives must always contain a DATA disk in the left-hand drive and a SYSTEM disk in the right-hand drive. When ANALYST is accessing one of these disks, the yellow light by that disk drive will be on, and ANALYST won't respond to any commands. DON'T ever open the door of the floppy-disk drives while the yellow light is on!.

Starting to Use ANALYST

First, press the "?" key (you don't have to press the shift key at the same time if you don't want to) on the computer to make sure that the full menu and status information is displayed on the CRT (the CRT is the computer's TV-monitor). This state of the program is called the **Beam-Monitor Condition.** You can tell when the program is in this state because the letters bmc appear in the lower-right corner of the screen. When you're at the Beam-Monitor Condition (bmc for short), ANALYST is waiting for a command from you, while at the same time monitoring the intensity of the ion-beam arriving at the collector. The bmc is a "home-base" of the program that ANALYST returns to after completing any operation or function that you request, and from which you can command any operation or function of the computer or mass-spectrometer. So it's important that you recognize when you're at the bmc.

Now look at the lowest line of the CRT that isn't highlighted. This line should look something like this,

206 Pb PEAK 6722 CF=1.234 SF=0.000 2642 mV CUP bmc

with the number before "mV" changing 5 times per second.

The leftmost number ("206" above) indicates the mass-number (strictly speaking, mass/charge ratio) of the nuclide arriving at the collector, and the next letters to the right ("Pb" above) indicate the expected dominant element or molecule for that nuclide. The next word ("PEAK" above) indicates whether you are on the peak-top (PEAK), about halfway down or up the side of the peak (-SIDE or +SIDE), or 1/2 mass above or below the peak-top (ABOVE or BELOW).

"CF=1.234 SF=0.000" in the above example indicates how much current, in amperes, is going through the center (CF) and side (SF) filaments, if any, of the sample. The next number ("2642 mV") indicates the intensity of the beam, in millivolts, arriving at the collector. Because the resistor of the amplifier is assumed to be a 10^{11}-ohm resistor, you can convert the "mV" value to amperes by multiplying by 10^{-14}. When the Daly-detector is in use, this relationship is still valid; in other words, a given beam should appear to have the same intensity to ANALYST regardless of the detector (except for small differences due to errors in the gain-setting of the Daly detector). The next word (CUP in the above example) indicates which collector is in use (CUP or DALY).

One Way of Changing Filament Currents

The next line or two above the bmc line should be,

USE KNOB with CTRL key to change Center-Filament Current
" " CTRL-SHIFT keys to change Side-Filament Currents

These lines (the second line appears only if you're running a triple-filament) tell you one of the ways of changing the filament currents of your sample: to turn up the center-filament current, for example, hold down the CTRL key while at the same time rotating the KNOB (the round knob at the upper-left of the computer keyboard) clockwise. To turn up the side-filament current, do the same but also hold down the SHIFT key at the same time (note that the message about changing the side-filament current will only appear if the sample currently being run is a triple-filament assembly). Try taking up the center-filament current to, say, 1 ampere or so at this point. Notice that the bmc-line display changes its value for the center-filament current as you rotate the knob. **IMPORTANT: This method of turning up the filament-currents works only from the bmc. If you don't see the bmc letters at the lower-right of the CRT, this method of changing the filament currents won't work!**

Other Ways of Changing Filament Currents

You can change the filament currents from the bmc in several other ways as well. The up-arrow and down-arrow keys (at the center-top of the keyboard) will raise or lower the center-filament current of the sample by 0.01 amperes for each keystroke, and change the side-filament currents in a similar way if the SHIFT key is held down at the same time.

If you don't like the inconvenience of holding down the CONTROL key while raising the filament currents with the KNOB, press SHIFT-k9 while in the bmc. ANALYST will then allow you to use the softkeys to choose which filament is controlled by the KNOB, while at the same time displaying the beam size in real time. This is the only way to control the preheat filament-currents using the KNOB, incidentally.

Finally, you can use a semi-automatic mode of changing the filament currents by pressing k4 during the bmc. This method is explained in detail in a later section.

What Sample Am I Running?

In the lower-middle of the CRT, you'll see something like this:

Barrel# 9, Run# 4 PCG-1047 Feldspar

The Barrel# is the location of the current sample in the sample-barrel (the circular carrier for the loaded filament-assemblies in the source-can), and corresponds to the numbers stamped on the barrel- from 1 to 16. The Run# is what you'll use to retrieve data for this sample from the disks; otherwise (except for full-automatic running), don't worry about it. "PCG-1047 Feldspar" is an example of a sample name. If there isn't any sample name on the CRT, that means that it hasn't been defined yet.

Now look at the rest of the CRT (above the softkey labels). The upper part should be,

USE THESE SHIFTED SOFTKEYS (k0-k9) TO OBTAIN OTHER FUNCTIONS FOR:

k0 ----- MAGNET
k1 ----- ION OPTICS
k2 ----- BARREL
k3 ----- COLLECTORS
k4 ----- ISOTOPE-RATIO DATA
k5 ----- SPIKES
k6 ----- MASS-SPEC STATUS (pressure,HV,time,contacts..)
k7 ----- AUTOMATIC-RUNNING VARIABLES
k8 ----- STARTING AUTOMATIC RUNNING
k9 ----- CHANGING ANY FILAMENT-CURRENT USING KNOB

Pressing a shifted softkey from the bmc generally gives you access to a variety of other functions. The type of functions that you can access with a given shifted softkey are indicated in the menu above. I'll discuss some of them in this tutorial and others in the Reference Guide.

Functions of Other Keys

And finally, look at the sheet of paper taped to the right of the CRT (figure 5). This sheet indicates what some of the more-important non-softkey keys will do during the bmc. Let's try one of the most useful of these. First (you should still be in the bmc), while looking at the bmc line, press the + key. The value of the isotope should increase by one or more, and the fine-magnet setting should also change. You can go back to the isotope that you started from by pressing the - key. So the + and - keys cause the magnet to immediately jump up or down to the next-defined isotope for whatever element (Pb, Sr, Nd, etcetera) that you're using.

The parentheses keys and the left- and right-arrow keys are used to step off either to the next half-mass higher or next half-mass lower, or to the above or below half-peak positions, respectively. These keys are useful for looking at zeroes or for checking if the peak is adequately centered. To return to the peak-top after pressing one of these keys, press either the ^ key or the space-bar.

To turn a filament **off** immediately (as opposed to slowly turning the current down to zero), hold down the **CONTROL** key, then press the **1**, **2**, **3**, or **4** key twice within a half-second. This will turn off the center or side filament in the **running** position (**1** or **2**), or the center or side filament in the **preheat** position (**3** or **4**).

Recovering From Mistaken Commands

It's easy, of course, to hit the wrong key by mistake and invoke a function that you really didn't want. How to "back up" or "escape" from such a situation depends on just what the situation is, but is never difficult. There several possible "escape" routes:

1) For commands that invoke one of **ANALYST's FORM**s (discussed in a later section), softkey **k9** is always defined as an **ESCAPE** or **RETURN TO BMC** key.

2) For commands that invoke a function needing only a single response (such as the "Which Element?" response to a change-elements command), you can escape by either a response of zero or by pressing the **CONTINUE** key. The CRT will tell you which to do.

3) If the operation that you want to escape from is in progress (such as focussing the beam), the **k9** key again is almost always defined as an **ESCAPE** key.

4) If none of the above apply, or in some apparent run-emergencies, you can always press the **PAUSE** key to immediately stop the program, then press the **RUN** key to restart **ANALYST** at its "waiting for commands" state - the **bmc**.

5) If nothing else works, pressing the **RESET** key (**SHIFT-PAUSE**) will stop the program. This is a drastic measure, however, and contains a small risk of bombing the program. So **RESET** is a last resort.

Getting a Beam

To go any further, you'll need to get an ion-beam from your sample. First, using the + or - keys, jump to the most-abundant isotope that you expect is present in your sample. Then, holding down the **CTRL** key, turn the knob until you get a beam (look at the part of the **bmc** line that tells you the intensity of the ion beam as you turn the filament-current up). When you have a 20-30 millivolt beam, stop turning up the filament-current and press the **k0** softkey (the one labelled **CENTER PEAK**). This function adjusts the magnet so that the peak is precisely centered at the collector. Now, press the **k1** softkey (the one labeled **FOCUS BEAM**). This function adjusts the potentials on each of the source assembly plates (the ion-optics) to maximize the size of the beam arriving at the collector. Several iterations of adjustment are usually required for the first focus of a beam, taking 1 or 2 minutes. The graphics accompanying the focus procedure shows you the result of each focus operation for each "plate".

When the beam is focused (the CRT will give you a message saying so, and the computer will make an affirmative-sounding chirp), press the **k2** softkey (the one labelled **CENTER BARREL**). This function rotates the barrel slightly to obtain maximum beam-intensity. The accompanying graphics will show you how sensitive the beamsize is to the barrel position.

You now have a centered, focused ion-beam. If you expect more intensity than you have at this point, just increase the filament-current until you have a reasonable beam-size. (Note: you can duplicate the beam-tuneup that you've just done with just one command, if you like, by pressing **CTRL** * during the **bmc**. **ANALYST** will then center, focus, optimize the barrel, and refocus the beam without additional commands.)

Real-Time Ion-Beam Graphics

To have ANALYST simulate a stripchart recorder (figure 1) for the ion-beam as you take up the filament-current, press the BEAM CHART key (k3) during the bmc. The CRT display will immediately change to show the softkey definitions below.

KEY#	FUNCTION
0	START LINEAR GRAPHICS BEAM-MONITOR
1	START LOGARITHMIC GRAPHICS BEAM-MONITOR
2	DOUBLE X-AXIS TIME-PERIOD (now 8 mins)
3	DOUBLE Y-AXIS HT (now 1.5X initial beam)
4	ENABLE AUTO PRTR-DUMP OF GRAPHICS BEAM-MONITOR
7	HALVE X-AXIS TIME-PERIOD (now 8 mins)
8	HALVE Y-AXIS HT (now 1.5X initial beam)
9	RETURN TO BMC

Using these softkey-commands, you can expand or contract the horizontal and vertical scales of the beam-chart, request that each full chart be automatically dumped to the printer when the chart is full, and request that the chart have either a linear or logarithmic scale. For example, the softkey-menu above indicates that the X-axis of the beam-chart can record up to 8 minutes of running time, after which the chart may be dumped to the printer, and will be restarted. If you press k2, the explanation for k2 will change to indicate that the maximum X-axis time is now 16 minutes. You can cut the X-axis time in half, or double/halve the Y-axis height (that is, the maximum beamsize in millivolts that will be contained in the chart) in a similar way.

For now, change the X-axis time period to 4 minutes using the k7 and/or k2 softkeys, then change the Y-axis height to 1.5 times the existing beam using the k3 and/or k8 keys. Now start the chart with the START LINEAR GRAPHICS BEAM-MONITOR key (k0). When the chart has been drawn, try switching isotopes with the + and - keys, noticing how the trace of the beam changes on the CRT beam-chart. Now try turning up the center-filament current (using the KNOB while holding down the CTRL key), and see if the beamsize changes the way you expect on the CRT beam-chart. Note that as long as you have the beam chart on the CRT, ANALYST can't display the barrel-number, sample-name, or run-number, nor the definitions of the shifted-softkeys. If you want these to reappear (at the expense of the beam-chart), just press the ? key (or the / key) during the bmc.

Of course, if you increase the beam-size so that it disappears off the top of the beam-chart, you won't get much information from it. There are three ways of getting around this. First, during the bmc, just press the **BEAM CHART** key (**k3**), then the **k0** key (defined as **START LIN-GBM** as soon as **k3** was pressed). Because you had previously defined the Y-axis height as 1.5 times the entering beam, the new beam-chart will be drawn with about 30% "headroom" over the beamsize. Second, you could change the Y-axis height to greater than 1.5 times the entering beam (using the **DOUBLE Y-AXIS** softkey after calling up the **BEAM CHART** screen) to, say, 3 times the entering beam. This would give you substantially more "headroom" for a growing beam. Third, you could press the **START LOG-GBM** key (**k1**) after calling up the **BEAM CHART** screen. Because the beam-chart is then drawn with a logarithmic Y-axis, the beam can grow several orders of magnitude and still be contained in the beam chart.

Switching Collectors - Faraday Cup and Daly Detector

The Daly detector permits a large amplification of the ion-beam with almost no amplification of signal noise, as well as almost completely eliminating background noise. The limitations of the device are that:

1) the intensity of the ion-beam arriving at the Daly must be no more than about 50 millivolts to avoid damage,

2) the gain of the Daly varies slightly with the mass of the arriving nuclide, resulting in a near-linear mass-discrimination of about 0.2% per mass-unit,

3) there seems to be a significant nonlinearity in the response of the Daly as a function of the intensity of the arriving ion-beam.

The latter two points are discussed further in a later section, but for now just regard the Daly as a device which greatly increases the signal-to-noise ratio of an ion-beam.

To toggle between from the Faraday Cup and the Daly detector, press softkey **k5** while in the bmc. If you're switching to the Daly and the nuclide presently arriving at the collector wasn't previously "cleared" at the present filament-current for use with the Daly, **ANALYST** will quickly look in the immediate region of the peak to make sure that the beam is not too intense before switching the Daly on. If you have the CRT stripchart in operation, you'll probably notice a slight apparent change in the beamsize and a marked reduction

in the beam noise. If the beamsize discrepancy between the Faraday Cup and Daly detector is significant (more than 10 or 20 percent), you might want to recalibrate the Daly gain by obtaining a 5 to 40 mV beam and then requesting a calibration of the Daly gain (see the Reference Guide for instructions).

Reaction of the BMC to Large Beams

ANALYST will not "tolerate" an ion beam that is too intense for the collector in use. The maximum acceptable beam for the Faraday cup is 10 volts (100 picoamperes), and the maximum acceptable beam for the Daly detector is 50 millivolts (0.5 picoamperes). If, while in the bmc, a beam of more than 10 volts arrives at the Faraday cup, ANALYST will immediately switch to the next-higher or next-lower isotope. If the next isotope also has too intense a beam, another jump yet will be made, until a beam of less than 10 volts is obtained. If such a large beam is obtained while **not** in the bmc (for example, while focussing), ANALYST will turn down the sample-filament current in 3% increments until an acceptable beam is obtained.

If the Daly detector is in use when an unacceptably intense beam ()50 millivolts) is obtained, ANALYST will immediately switch to the Faraday cup. Should this occur, there will be a 5 or 6 second delay before the beam will be detected at the Faraday cup.

Using ANALYST's FORM Screens

There are some operations that just can't be initiated with just a keystroke-command or two: several items of information might be required for the particular task. For such operations, ANALYST will present you with a "FORM" to fill out, correct any errors on, and then submit. If you've filled out the "FORM" without any errors or misunderstanding, ANALYST will proceed with the requested task as described in the "FORM". Though this may sound like a very formal and somewhat tedious way of communicating what you want, in practice the actual procedure is nothing of the kind.

As an example, try one of the several ways of changing filament-current. Press the FIL. CURRS key (k4) during the bmc. A short "FORM" will appear on the CRT that looks something like this:

PARAMETER	RESPONSE
FILAMENT-NUMBER (1=center-sample, 2=side-sample, 3=center-preheat, 4=side-preheat)	1
NEW CURRENT (amperes) ---------- (present CF current is 2.052 amps)	??
RATE (milliamps/second)	10

Use ARROWS, (CTRL)CONTINUE, or KNOB to move cursor to different parameters

ENTER new value (press EXECUTE when all parameters defined, k9 to escape)

Notice that one of the values on the right (probably the NEW CURRENT value) is shown highlighted and with a dashed line pointing to it. This is the value that the FORM is requesting you to type in. You can move the "parameter cursor" to any parameter you want by rotating the KNOB, by pressing the up-arrow or down-arrow keys, or by pressing the CONTINUE key (next parameter down) or CTRL-CONTINUE keys (next parameter up). Try some of these keys now.

To enter a value into the FORM, just type in the appropriate value (or words). Your response will appear in the appropriate space in the FORM as you type it in. To correct mistakes, use the right/left arrows (to move the character-cursor), the DEL CHR key (to delete a character), the INSERT CHR key (to insert a character), or the CLR LINE key (to erase all characters and start your response for this parameter over). When you've typed in your response and edited it, press the ENTER key to enter your reponse into the FORM. If you haven't made any errors, ANALYST will beep, and the cursor will move on to the next parameter.

But if you made an error of the type that ANALYST can recognize (for example, entering letters instead of numbers where a numeric value was requested, or entering an unreasonable value, such as a request for more than 7 amperes filament-current), an error-sound will occur, and a brief message indicating the problem will appear towards the bottom of the CRT for a few seconds. In this case, just enter the requested value again (correctly).

Notice that when the FORM appears on the CRT that some of the parameters already have reasonable-looking responses filled in, but others have a double question-mark as a response. The double question-mark indicates a parameter that must be filled in. For the other parameters, however, ANALYST will have chosen a default response. For many FORMs, the default responses will simply be whatever you entered the last time you submitted this FORM, so that you may have to type in only one response (or none at all) even for a fairly lengthy FORM.

For several of the FORM screens, you can get more detailed explanations of just what the parameters are and how to fill in the FORM by pressing CTRL-H. The CRT will then clear and give you some "help" for whatever parameter the cursor was on when you pressed CTRL-H. You can tell if help-screens are available for a FORM by looking at the next-to-bottom line of the CRT for the phrase "CTRL-H(elp) for help".

After you submit the FORM (by pressing the EXECUTE key), ANALYST may check your values once more; this time for the internal consistency of the values. For example, in the MAGNET-SCAN FORM, if you request a scan from a lower isotope of 209 to an upper isotope of 203, ANALYST will indicate an error and ask you to enter these values again.

Notice that if you type a response into the FORM and then move the parameter cursor without pressing the ENTER key, your response will be ignored. Also note that if you type in a response and then press the EXECUTE key, this is equivalent to pressing the ENTER key followed directly by the EXECUTE key (saves you a whole keystroke!).

If you called up a FORM by mistake, or changed your mind halfway through filling out one, just press the ESCAPE softkey (k9) to return to whatever state ANALYST was in when you called the form up.

As long as you have the semi-automatic filament-current FORM on the CRT, let's go through its use. The topmost parameter of the FORM indicates the filament for the current change. As the FORM indicates, a value of 1 is for the center filament of the sample in running position, 2 is for the side filaments of sample in running position, 3 is for the center filament of the sample in the preheat position (the sample whose barrel-number is 1 greater than the sample currently in running position), and 4 is for the side filaments of the sample in the preheat position. Be careful that you don't accidentally enter the wrong filament!

The NEW CURRENT is just the current that you want the filament taken to, in amperes. You can go up or down.

The RATE refers to how rapidly you want the NEW CURRENT to be attained. For example, if you choose a RATE of 10, the filament-current will be changed at a nominal rate of 10 milliamperes per second. So to go from 1 to 2 amperes would take roughly (2-1)*1000/10/60 = 1.7 minutes. No matter how fast you choose to take the filament-current up, though (unless the NO PRESS. CHECK key is pressed - see below), ANALYST will check the source-pressure every .4 amperes, and if the pressure is too high (more than about 10^{-6}), will wait until the pressure goes down before increasing the filament-current again.

Complete the FORM and submit it to ANALYST by pressing the EXECUTE key. The CRT will then display the changing filament-current in real time, and also offer you (via the softkeys) a few options as the filament-current is changed. For example, one the the softkeys is labeled DOUBLE RATE, and another HALVE RATE. If you press one of these softkeys while the filament-current is being changed, the RATE will immediately be doubled or halved, and the display line of the CRT will indicate the change. Using these keys, you can override whatever rate you indicated in the FORM you just completed.

Also, one of the softkeys will be labeled as \NO PRESS.-CHECKS. If you press that softkey, then ANALYST will not check the source-pressure every 0.4 amperes during a filament-current take-up. Because checking the source-pressure takes several seconds, you may find this option convenient if you know that the filament will not outgas severely as its current is increased.

Scanning the Magnet

To scan the magnet with real-time beam-versus-magnet graphics, press the softkey labeled MAGNET SCAN (k6) during the bmc. One of ANALYST's forms will appear on the CRT, looking something like this:

PARAMETER	RESPONSE
Start scan at isotope -------	203.5
End scan at isotope	209.5
Max. beam on graph (mV)	1200
Scan-speed (a.m.u./second)	.2
Linear or Log scan (Lin/Log)	LIN
Coarse-Magnet Range	8

Use ARROWS,(CTRL)CONTINUE,or KNOB to move cursor,CTRL-H for help

ENTER new value (press EXECUTE when all parameters defined,
k9 to escape)

In this example, the scan would start at mass 203.5 and scan up-mass to mass 209.5 at a rate of about 0.2 mass-units per second. Useful values for the scan-speed are typically between .05 (slow scan) to 1 (very fast scan). You can speed up or slow down the scan as it is being performed, though, so don't worry about the exact value. Examples of magnet-scan graphics are shown in figures 2 and 3.

The Max. beam on graph is the Y-axis height for the CRT graphics. Generally, you'll want a value of 10% - 30% greater than the size of the largest peak to be encountered in the scan. You can choose to have the CRT graphics with either a linear or logarithmic scale. The latter is very useful if the scan will encounter peaks of extremely different sizes. You must enter the word LIN for a linear scan (default) or LOG for a logarithmic scan.

The scan will start with whatever collector was in use when the Magnet-Scan FORM was invoked, so if you want the scan to be done with the Daly detector, make sure that the collector in use is the Daly. You may need to jump to another isotope in order to turn the Daly on. If a peak of more than 50 mV is encountered during the scan, ANALYST will just revert to the Faraday Cup and then finish the scan.

The **Coarse-Magnet Range** refers to which of the 10 coarse ranges the magnet is set to, with the default coarse range being the one appropriate to the current **ELEMENT**. For example, if the current **ELEMENT** were Pb, and you wanted to see if any potassium peaks were present, you would have to change the **Coarse-Magnet Range** to some lower value (or temporarily change the **ELEMENT** to potassium). As soon as you submit the **MAGNET SCAN FORM** with some other coarse-range value, the **FORM** will reappear and ask you to define the starting and ending magnet values instead of the starting and ending isotopes. These magnet values may be between 0 and 9999.

Changing Elements

An **ELEMENT** is a set of data that tells **ANALYST** what element you're running, what nuclides can be present, what nuclide to use as the reference-isotope for isotope ratios, what isobaric interferences to expect and how to monitor and correct for them, and whether or not it is possible to normalize for mass-fractionation using some specific isotope ratio. The most common **ELEMENT**s, such as Pb, U, Sr, Nd, and miscellaneous rare earths, have probably already been defined using conventional constants for isobaric interferences and fractionation-normalization. When you get more familiar with **ANALYST**, you can easily define a new **ELEMENT** of your own, or perhaps define another version of some existing **ELEMENT** (for example, if you wanted to normalize your Nd runs to the 148/144 ratio instead of 146/144).

For example, try changing from the **ELEMENT** that you're now using to another one - say Nd. Press the **CHANGE ELEMENTS** softkey (**k7**) during the **bmc**. The CRT will then show you a list of **ELEMENT**s that have been defined (and stored on the **DATA** disk). Choose the **Nd ELEMENT**.

ANALYST will retrieve the information for running Neodymium from the DATA disk, and display the information in the format below:

```
Ba-134  Ba-135  Ba-136  Ba-137 Ba-138 La-139  Ce-140  Pr-141
Nd(Ce)-142 Nd-143 Nd(Sm)-144 Nd-145 Nd-146 Sm-147 Nd(Sm)-148
Sm-149 Nd(Sm)-150 Eu-151 Sm-152 Eu-153 Sm-154 Gd-155  Gd/Dy-
156 Gd-157

COARSE-MAGNET RANGE:  7

 134  135  136  137  138  139  140  141  142  143  144  145
 749  989  1227 1465 1702 1937 2172 2406 2639 2871 3102 3332

 146  147  148  149  150  151  152  153  154  155  156  157
 3561 3789 4017 4243 4469 4693 4917 5140 5361 5582 5802 6021

  ELEMENT:  Nd       REF. PEAK: 144       DEFINED FOR HV=7800

  NORMALIZING RATIO:  144/146=1.385233

    MONITOR ISOT.     INTERFERING ISOT.          RATIO
        147                 144              144/147=.2097
        147                 148              148/147=.7478
        147                 150              150/147=.4957
        140                 142              142/140=.1251
```

The first several lines of the display show which nuclides have been defined for this ELEMENT. This is followed by the default magnet-settings for each nuclide. Though you can scan over any mass-position from any ELEMENT, you can only peak-jump to and take isotope-ratio data for those nuclides which have been defined for the ELEMENT currently in use. If none of the existing ELEMENTs include the isotopes you want (or if none of them does the fractionation or isobaric-interference corrections the way you like), you'll have to define a new ELEMENT. This procedure is described in the Reference Guide.

The name of the ELEMENT (Nd in the example above) is important if you will be using it for fully-automatic running; otherwise, it just indicates its main use (in this case, taking data for neodymium isotopes). The REF. PEAK isotope is important: this is the isotope to which all others will be ratioed to during automatic-run data-taking. In other words, if the reference isotope is 144, the data will be calculated either as i/144 or 144/i, where i is some other isotope. Ratios that don't contain 144 will not be calculated directly. Whether 144 appears in the numerator or the denominator depends on what the person who defined the ELEMENT selected - either is permissible.

The accelerating voltage (HV) that the mass spectrometer must be set to for the magnet-settings of the isotopes to be valid is indicated by the "DEFINED FOR HV=7800" line. If the HV differs by more than 3 volts from this value, ANALYST will continue to query the HV until either this condition is met, or you escape by pressing the ESCAPE softkey (k9). Note that the HV that ANALYST looks at is the digital value received by the computer when it queries the mass spectrometer, and not the setting on the dial of the instrument panel. To find out what the current HV setting is, press SHIFT-k6 during the bmc (to get the STATUS menu), then k2 (or you can use the shortcut method of just pressing CTRL-V during the bmc).

The NORMALIZING RATIO ("146/144=1.385233" in the example) is the isotope ratio that will be used to normalize for mass-dependent fractionation. If such a ratio exists, then all blocks of data for this ELEMENT must contain this ratio.

The next lines indicate what isobaric interferences may be present and how to correct for them. In the example above, ANALYST will know that there may be interferences at masses 144, 148, 150, and 142, and that they may be corrected by monitoring masses 147, 147, 147, and 140, respectively, and subtracting the interferences using the assumed ratios of 144/147=.2097, 148/147=.7478, 150/147=.4957, and 142/140=.1251, respectively. In other words, the latter ratios pertain to the ratios of naturally occurring Sm, Sm, Sm, and Ce, respectively.

If you've ever run one of the more-common commercially available software packages for an automated mass-spectrometer, you may recall that in these programs the information in ANALYST's ELEMENT data-files tend to be bundled together with the information on how to do a fully-automatic run. ANALYST doesn't do this because ELEMENTs need to be defined only rarely, and having to do so each time an automatic run is modified is somewhat of a nuisance. Also, of course, the existence of independent ELEMENT files permits the operator to run in the manual (actually semi-automatic) mode with a minimum of query/response interactions with the computer.

Looking at the Rhenium Beam

You can always switch the magnet to the ^{187}Re peak regardless of the ELEMENT you're using, just by pressing CTRL - during the bmc. The first time you do this for a particular run, you should then center the peak using the k0 softkey. To switch back to whatever peak you were on when you pressed CTRL - , press CTRL + during the bmc. A rhenium beam should be present whenever the a center rhenium filament is hotter than 1800^{o}-1850^{o}.

Changing Samples

To change samples (that is, to rotate another filament-assembly into the running position), press the NEW SAMPLE key (k8) during the bmc. ANALYST will then ask you

ENTER THE BARREL# OF THE NEW SAMPLE, NUMBER OF FILAMENTS FOR THIS SAMPLE?

(press CONTINUE to escape)

Enter the barrel# (the position in the barrel as indicated by the stamped number on the barrel itelf) of the sample that you want, then a number indicating whether the sample is a single (1) or triple (3) filament assembly, in the format

12,1

ANALYST will then reset the barrel (rotate it to its reset position, just past barrel# 1), rotate to the approximate position of the sample that you requested, and find the valid contact-interval of barrel rotation. When the sample-change operation is done, the CRT will display the barrel-positions (in arbitrary barrel-units, which give about 187 barrel units between adjacent samples), where filament-contact was just made and just lost (for a counter-clockwise rotation), and the width, in barrel-units, of valid contact. This valid-contact width should be at least 15-20 units (and usually 30-35 units); if less, a warning message will appear on the CRT to indicate that you have potential contact problems. If nothing seems to happen for a long time after your sample-change request, you might check to see that the barrel-motor switch is really in the ON position (down). If ANALYST indicates that no filament contacts were found for the sample, check that the filament-control knobs are really in the ON position and that they were turned all the way to the RESET position.

Then, if no collector-zeroes have been taken in the last hour, ANALYST will measure the collector zeroes (and, no oftener than 4 times a day, the collector noise). Finally, just before returning you to the bmc, ANALYST will retrieve the standard focus-settings from the SYSTEM disk and use these as the default focus-settings.

Taking Isotope-Ratio Data Manually

Once you have a beam large enough for data-taking, you can ask ANALYST to take either as little or as much data as you want, without worrying about drifting off peak-tops, changing focus-positions, a dying beam, or out-of-control beam-growth. Though this mode of data-taking will be referred to as "manual", it is really a type of automatic mode that lacks only the capability for obtaining the proper beam-size to start with, and for changing samples and continuing with more runs. Nonetheless, only a few keystrokes and a few seconds are necessary to describe and initiate "manual" data-taking.

The Manual Data-Taking FORM:

To initiate manual data-taking, press the TAKE DATA key (k9) during the bmc. If the ELEMENT that you're using is one that will be normalized for mass-dependent fractionation using an internal isotope ratio, such as Sr or Nd, the first FORM to appear will look like this:

PARAMETER	RESPONSE
Sample Name ----------	??
Spike Number (0 if an unspiked run)	0
Normalize data to ratios of first block (Y/N)?	NO

The **Sample Name** is just the name that will be assigned to this run of this sample. It can be up to 50 characters long, so you can be fairly descriptive.

The **Spike Number** tells ANALYST if this sample has been spiked, and if so, with which spike. Spiked runs will be discussed in a later section, but for now just be aware that you can store the isotope ratios of a spike for a fractionation-normalizable element on the DATA disk. Then, ANALYST can calculate both the relative concentrations of the spike and sample isotopes, as well as the spike and fractionation-corrected radiogenic-isotope ratio for each block as it is completed. If you've forgotten which spike you used, enter a question-mark in response to the **Spike Number**, and ANALYST will display the spikes that are defined on the DATA disk.

The Normalize Ratios to First Block query asks whether, instead of using the usual value of the normalizing ratio for fractionation-normalization, you'd rather use the appropriate normalizing ratio of the first block. For example, suppose that you want to determine the isotope ratios for a Nd-150 spike, and your usual normalizing ratio for Nd runs is 146/144 =.7219. The spike, however, might have a 144/146=3.425, in which case using .7219 would give very strange results. But if you choose to normalize the ratios for all of the blocks of this run to whatever 146/144 ratio you get for the first block, the normalized ratios will be reasonable-looking (though not accurate), and you'll be able to combine the data for several blocks to do weighted averages on all of the ratios. You can then correct these final, averaged ratios for whatever fractionation you estimate was present in the first block's data.

The next FORM (or the first one, if the ELEMENT doesn't have a ratio for fractionation-normalization, such as Pb, U, Rb ...), will look something like this:

PARAMETER	RESPONSE
Sample Name ----------	??
Isotopes (Reference-Isotope First)	238,235
Number of Sets in a Block	15
Number of Blocks	1
Beam Window (most-intense peak):	
Minimum Beam (volts)	0
Maximum Beam (volts)	10
Maximum Filament-Current (amps)	6
Maximum Beam-Growth (%/minute)	100
Final Filament-Currents (amps) (sa-Cen,sa-Si,preh-Cen,preh-Si)	2.234,0,0,0
Daly Status (0,1,2) (0: Disabled 1: OK for data 2: Beam-tuneup only)	1
Dump Graphics Each Block? (Y/N)	N

Use ARROWS,(CTRL)CONTINUE,or KNOB to move cursor,CTRL-H for help

ENTER new value (press EXECUTE when all parameters defined, k9 to escape)

Notice that at most, only one of the queries (the sample name) must be answered, and that if the ELEMENT is fractionation-normalizable or if the sample names for the whole barrel were already entered by whomever installed the barrel earlier, even that query already has a response. So when this FORM appears for the first time, it's already almost competely filled out with default responses. As a general rule, if you're not sure of a response to this FORM, accept the default responses - they'll give you a simple but adequate mode of data-taking. But to really take advantage of the manual mode of ANALYST, you'll want to know how to customize your data-taking for your particular samples.

The Isotopes Query (for an ELEMENT without Internally-Normalized Fractionation):

This query and its reponse will differ depending on whether or not there is an internal ratio used for fractionation-normalization, such as for Sr, Nd, Sm.... For ELEMENTs with no such correction possible (Pb, U, Rb...), the query will appear as in the example above. Your response must include a list of the isotopes that you want isotope-ratio data for, **with the reference isotope first in the list.** For example, if you wanted 206/208 and 206/207 ratios, your response would be,

206,207,208

or

206,208,207

Note that for data-taking of ELEMENTs without fractionation-normalization, you can choose any isotope defined in the ELEMENT as the reference isotope.

Don't include isotopes whose only purpose is to monitor for isobaric interferences, such as Rb-85 for Sr runs, Sm-147 for Nd runs, or Tl-203 for 205-spiked Pb runs. These isotopes will automatically be monitored by ANALYST if one or more of the isotopes that are being interfered with were included in the **Isotopes** list.

The Isotopes query (for an ELEMENT with Internally-Normalized Fractionation):

For an element such as Sr, where the $^{86}Sr/^{88}Sr$ ratio is used to normalize the other ratios for mass-dependent fractionation, the Isotopes query will look like this:

Isotopes (must include 86 and 88)?

In other words, no matter what other isotopes you wish to include, you must include the two isotopes (86 and 88) that will be used to correct for mass-depended fracionation. If the run is for a fractionation-normalizable ELEMENT and you told ANALYST that it was spiked with one of the spikes defined on the DATA disk, the query will insist on one more isotope, for example

Isotopes (must include 86, 88, and 84)?

The Number of Sets in a Block and Number of Blocks Queries:

A Set is defined as one complete sequence of peak-top jumps during data-taking. For example, if data were being taken for isotopes 206, 207, and 208, a Set would include the peak-jumping sequence of 208, 206, 207 (the exact order depends on the relative intensities of the peaks). A Block of data consists of backgrounds, isobaric-interference monitoring (if required), the specified number of sets of peak-top jumps, backgrounds and interference-monitoring again, and caclulation of the corrected isotope-ratio data. Typical Blocks usually include from 10 to 25 Sets. The more the number of Sets, the longer it will take to do a Block and the more precise the data in the Block. On the other hand, focusing and peak-centering (with the exception of a block of Pb 204, 206, 207, and 208) is done only at the beginning of each Block, so you should usually restrict the Block length to take no more than about 15 minutes. The number of Blocks can range from 1 to more than 100.

If this is your first experience with ANALYST, you can skip the remaining parameters in the manual data-taking FORM for now, since their default values are adequate for simple runs. Otherwise, or if you're just curious, please read on.

The Beam Window Queries:

After each block, ANALYST checks to see if the intensity of the Most-Intense Peak (MIP for short) lies within the Minimum Beam and Maximum Beam values (in millivolts). If the MIP doesn't lie within these limits, ANALYST will raise or lower the sample-filament currents (center filament if a single-filament assembly, side-filaments if a triple) until the MIP does lie within the specified window. Note that the default values of 0 to 10 volts are equivalent to specifying no control on the beam-intensity.

The Maximum Filament-Current value puts a limit on how high the sample-filament current can be raised to satisfy the Minimum Beam requirement. For example, if the MIP fell below the Minimum Beam and the Maximum Filament-Current were 2.8 amps, ANALYST would not take the filament-current past 2.8 amps even though the Minimum Beam limit were not met.

The Growth Limit Query:

The Growth Limit value restricts how fast ANALYST will allow the ion-beam to grow during a block. After each block, ANALYST checks to see whether the growth-rate of the beam (printed out in the block-results printout) is less than the specified Growth Limit. If not, ANALYST will lower the sample-filament current by 2.3 percent.

The default Growth Limit of 100%/minute in effect places no limit on the allowed rate of beam-growth. This is appropriate for samples whose ion beam will respond quickly to a change in filament current, such as Pb or U. For samples such as Sr, Th, or Nd, however, rapid growth (greater than about 2% - 3% per minute) generally indicates that the run will soon "die" by decaying rapidly and irreversibly in the near future. But for most runs, if the sample-filament current is reduced within a few minutes of the onset of rapid growth, this early run-death can be avoided. So for runs of this type, try restricting the growth-rate to 2% - 3% per minute.

The Final Filament-Currents (amps) Query:

After completion of the blocks specified in the Number of Blocks query, ANALYST will turn the filaments down (or up) to the values specified in the Final Filament-Currents query. The response to this query is in the form of 4 values, separated by commas, such as

2.2,1.8,3.5,1.2

The order of the values corresponds to the filaments that they affect, so that

Value 1 = Center Filament, Sample Position

Value 2 = Side Filament, Sample Position

Value 3 = Center Filament, Preheat Position

Value 4 = Side Filament, Preheat Position

The default values are the filament-currents that were in effect when the Manual Data FORM was invoked. So if the default values are used, ANALYST won't change any of the filament-currents after the end of last block.

The Daly Status (0,1,2) Query:

This query specifies under what conditions the Daly detector can be used. A value of zero indicates that the Daly is malfunctioning or absent, and should not be used under any circumstances. **DON'T USE ZERO UNLESS THE DALY IS ACTUALLY NOT WORKING.** A value of 2 indicates that the Daly can be used for tuning up the beam if necessary (that is, for small beams), but not for data-taking under any circumstances. A value of 1 indicates that the Daly can be used for beam tuneup of small beams, and will be used for taking data if the beam-sizes for all of the data-taking isotopes are less than 35 millivolts.

The advantage of the Daly detector is that the background noise is reduced to almost nothing and the peak-top noise reduced to mainly that from ion-counting statistics, so that the internal precision of a block of data can be drastically improved compared to Faraday Cup data under the same conditions. The disadvantage is that the Daly detector introduces both a pseudolinear, mass-dependent bias (about 0.2% per mass-unit) and a nonlinearity (the gain for smaller peaks is less than the gain for larger peaks). If you're doing only concentration work, these biases are not usually intolerable, and generally no greater than about 1 percent. If you wish to do work at level of accuracy of 01.% - 0.2%, you should either calibrate the Daly for nonlinearity, or check the consistency of the Daly data with Faraday Cup data on the same isotopes to estimate the bias in specific ratios for the particular run. Using this technique, Pb isotope ratios can be easily obtained with accuracies of better than 0.2 percent.

If you wish to take ratios using the Daly detector with accuracies of better than .05%, you will have to very carefully calibrate the gain of the Daly as a function of beam-size. This is possible but not generally done.

The Dump Graphics Each Block (Y/N) Query:

If you answer Y(es) to this query,. ANALYST will dump the peak-jumping graphics for each block to the printer after each block. This may effectively substitute for a real strip-chart recorder, though the resolution of the CRT screen won't show the noise of a beam that is only slightly unstable. The printer that is hooked up to the computer, of course, must be the type that can accept a graphics dump, such as the HP-2225 (ThinkJet) printer.

Incidentally, you may have noticed that the manual data-taking FORM has its own HELP screens, as indicated by the "CTRL-H for help" phrase at the bottom of the form. So you can get most of the above information about this FORM by just pressing CONTROL-H when the parameter-cursor is at the parameter of interest.

The Data-Taking Procedure

The data-taking procedure begins as soon as you submit the manual data-taking FORM to ANALYST (by pressing the EXECUTE key). First, ANALYST checks to see if the ion-optics have been focused for this sample. If you've forgotten to do so, ANALYST will focus the beam at this point. Then, ANALYST will center all of the peaks requested for data-taking, and do a quick step-scan over each isotope. From this quick-scan, ANALYST will know the approximate intensities and ratios of each peak, and from this information select

1) the order of peak-switching during data-taking (from most-intense peak to least-intense peak),

2) The delay times before integration for each peak (the greater the ratio of the previous peak to the present peak, the larger the delay time),

3) The integration times for each peak (the smaller the peak, the larger the integration time),

4) The amount of time spent on backgrounds, and

5) The mass positions where the backgrounds are taken.

These parameters are chosen to yield the highest precision in the least amount of time, as well as to minimize the corrections for the resistor time-constants. The actual equations used for this optimization are given in Ludwig (in press).

Basic Data-Taking: No Isobaric Interferences or Fractionation-Correction

In its simplest mode (isotopes without isobaric interferences or internal fractionation-normalization; also, not a Pb 204-206-207-208 block), data-taking proceeds as follows.

1) The pressure for both source-can and flight-tube is checked. If the pressure is $>10^{-6}$ (source) or $>10^{-7}$ (tube), a warning message is printed out. For automatic runs, ANALYST will wait up to an hour for the pressure to improve, then abort the run if satisfactory pressure were not obtained.

2) Backgrounds (zeroes) are taken. If the flight-tube pressure is better than 6×10^{-9}, the greatest ratio of the data-taking isotopes is less than 20, and the Faraday Cup is the collector, backgrounds will be taken 1/2 mass above and below the least-intense peak only. If these conditions are not all met, then backgrounds will be taken 1/2 mass above and below all of the peaks.

3) Peak-top jumping and integration begins. Real-time graphics of the beam (figure 13) appears in the middle of the CRT, and real-time ratios and precisions (1-sigma, in percent) appears below the graphics as the data is accumulated. These data are used only for display purposes, since they are calculated with only the before-peaktop backgrounds, and without isobaric-interference corrections. Outliers are rejected in real time as the data is accumulated.

4) Backgrounds are taken again, in the same manner as the before-peak-top backgrounds.

5) Final isotope ratios are calculated, outliers rejected, and the results printed out.

6) If the auto printer-dump was enabled from the TAKE DATA FORM, the CRT graphics are dumped to the printer.

7) The isotope ratios, precisions, filament-currents, and time since the start of the run are stored on the DATA disk.

8) If the intensity of the most-intense peak fell outside the BEAM WINDOW specified in the TAKE DATA FORM, the sample-filament current will be adjusted until the beam falls within the specified window.

9) If the growth-rate of the beam during the block exceeded the limit specified in the TAKE DATA FORM, the sample-filament current will be reduced by about 2.3 percent.

Data-Taking with Isobaric Interferences

If isobaric interferences are present (remember, they should not have been specified in the TAKE DATA FORM the data-taking procedure is modified as follows:

1) Backgrounds are taken 1/2 mass above and below each monitor isotope (a monitor isotope is an isotope that is used to estimate the intensity of the interfering-isotope peak; for example, 85 for an Rb-85 interference with Sr-87), regardless of the pressure or the ratios of other isotopes.

2) Before starting the peak-top jumping, the monitor isotope(s) are measured for 10-30 seconds.

3) If the degree of interference as calculated from any of the monitor isotopes is greater than 0.1% of the isotope that is interfered with, that monitor isotope is added to the list of isotopes for peaktop-jumping and will appear with them in the peaktop-jump graphics and isotope-ratio results.

4) If the degree of interference calculated from a monitor isotope is less than 0.1%, it will be monitored again only after the peak-jumping sequence.

5) The correction for isobaric interferences is made based on either a linear interpolation of the monitor isotope(s) (case 4, above), or on a least-squares cubic best-fit curve to the monitor isotope(s) (case 3, above).

6) The variance due to the isobaric-interference correction, including an assigned 2% uncertainty in the monitor/interfering isotope ratio, is added to the final uncertainty of the affected ratio.

Data-taking for ^{206}Pb-^{207}Pb-^{208}Pb-^{204}Pb Blocks

Because ^{204}Pb is always a minor isotope for natural Pb, and because its ratio is critical for geochemical studies, blocks of Pb-isotope data with all four natural isotopes are taken in the following sequence:

1) A first series of 206/204 ratios is taken, with the number of sets being about 2/3 the number specified in the TAKE DATA FORM;

2) The ^{206}Pb peak is centered and any magnet-drift corrected for;

3) A block of 206/207/208 ratios is taken with the number of sets specified;

4) The ^{206}Pb peak is again centered to correct for any magnet drift;

5) A second series of 206/204 ratios is taken, again about 2/3 the number specified in the FORM.

6) The statistics for the two 206/204 series are combined to give a single set of statistics for this ratio.

This sequence of peak-switching gives the desired extra time spent on measuring the minor 204 peak, while still retaining short interpolation times for the 206, 207, and 208 peaks

Data-Taking with Fractionation Normalization

If the element is one that has two isotopes whose ratio can be used for normalization of mass-dependent fractionation, such as Sr, Nd, Hf, Sm..., then a linear regression of that isotope ratio during the peak-jumping will be used to estimate the mass fractionation at any time during the data taking. The fractionation law that ANALYST uses is the power law discussed by Russell and others (1978). The uncertainty in the measured normalizing ratio will be included in the calculation of the uncertainty of the radiogenic-isotope ratio.

Data-Taking for Spiked Runs

For runs of a fractionation-normalizable element with an added spike, as indicated in the TAKE DATA FORM, the run will be treated as an unnormalized element until after all the isotope-ratio data has been obtained and printed out. At this point, ANALYST will invoke a subprogram that uses the algorithm of Dodson (1970) to calculate the ratio of the sample reference isotope to the spike's most-abundant isotope (this ratio is called SAM/SPK by ANALYST), and, if a radiogenic isotope is present, the radiogenic-isotope/reference-isotope ratio, corrected for both fractionation and spike isotopes. This latter ratio is indicated with an asterisk (such as 87*86) rather than the usual slash (87/86).

The Block Printout

The printout for each block (figures 6 - 8) is designed to be as compact as possible, yet still contain all the information necessary for an experienced operator to see how good the block's data really is, and whether or not the mass spectrometer seems to be operating properly. If there is no indication of problems after the data has been examined, the block output can be discarded, and either the printout of the Run Summary (figure 9), or the even more-compact weighted averages printout (figure 10), can be used for long-term storage and documentation.

Most of the block printout is self-explanatory, so I'll just go over some of the more important points.

Background values are printed out just under the FOCUS and MAGNET information, and relate to the counts per second (cps) and standard deviation of the cps for each background position. There are 100 cps per millivolt for the Faraday Cup, and about 10,000 cps per millivolt for the Daly detector. So a Faraday Cup background indicated by "503/5" indicates a nominal zero value of 5.03 millivolts with a background noise of .05 millivolts per second. The backgrounds appear under their corresponding isotope in the vertical order of: before peaktop jumping/half-mass below isotope, ditto/half-mass above isotope, after peaktop jumping/half-mass below isotope, ditto/half-mass above isotope. For multiple blocks of the same isotope ratios, though, the after-peaktop backgrounds of block N are used as the before-peaktop backgrounds of block N+1, so only the after-peaktop backgrounds will appear in the block printout for some of the blocks.

If isobaric interferences were monitored for, there will be one or more printed lines under the backgrounds such as:

AVERAGE 85 PEAK=.00736 mV; CORRECTION ON 87=.00561%

This line would indicate that an average of .00736 millivolts of mass 85 was present during the data-taking, so that on the average, .00561% of the observed 87 peak was due to Rb-85 (assuming a natural Rb-87/Rb-85 ratio). So the final 87/86 ratio will be corrected by .00561% for this interference.

If a linear regression of the ratios of each set versus time indicates that there was a real drift in the ratio, this drift will be indicated by a message such as:

RATIO CHANGE DURING BLOCK OF .012% PER MINUTE

The "TIME CONSTANT CORRECTION" in the block printout is the correction applied to the final ratio for the time constants of the 10^{11} ohm resistor. In general, you needn't worry about this correction, since it is usually smaller than the accuracy of the ratio.

If the ratio were corrected for mass-fractionation, the ratio before fractionation-correction (DISCR.-RAW RATIO") is printed out to the right of the Resistor-Decay Correction.

Finally, the information below is printed out:

AVERAGE 87/86 (or other ratio)	---	The final and corrected average value of the ratio
SIGMA% (OBS.)	---	The actual standard deviation of the ratios of the sets, not including rejected ratios, in percent. In parentheses if statistically equivalent to the SIGMA% (THEOR.), below.
SIGMA% (THEOR.)	---	The predicted standard deviation of the sets, in percent, assuming a perfectly stable beam.

SIGMA% (MEAN) --- The standard deviation, in percent, of the mean of the ratio, calculated from the SIGMA% (OBS.), the noise on the backgrounds, the uncertainty introduced by the fractionation correction, and the uncertainty introduced by the isobaric-interference correction. This is a measure of the expected block-to-block precision.

SIGMA MEAN --- Same as SIGMA% MEAN, but in absolute (not percent) units.

DELTA% --- The difference between this block's ratio and the last block's ratio. In parentheses if this difference is not statistically significant.

Using Isotope-Ratio Data Stored on the DATA Disk

After each block, a summary of the isotope-ratio data for that block are stored on the DATA disk. Data for the last 500 blocks are kept stored on this disk, so you should be able to access not only your data for the current run, but data for every run of the last week or two. There are two main ways of using this disk-stored data with ANALYST: obtaining a summary of the data for a run or series of runs, and calculating weighted averages of the data for several blocks in a run. Both these functions are available from the ISOTOPE-RATIO DATA softkey (SHIFT-k4) during the bmc, which will give you the following menu:

KEY# FUNCTION

0 ---- START TAKING ISOTOPE-RATIO DATA
1 ---- ENTER NAMES FOR ALL SAMPLES IN BARREL
2 ---- PRINTOUT SUMMARY OF RUN(S)
3 ---- DISPLAY SUMMARY OF RUN(S)
4 ---- CALCULATE WEIGHTED AVERAGES OF RATIOS FOR A RUN
5 ---- LOCATE RUN DATA ON A DATA DISK
6 ---- SHOW A LIST OF CURRENTLY-DEFINED SAMPLE-NAMES
7 ---- RETURN TO BMC

Run Summaries

A Run Summary (figure 9) is an abbreviated summary of the isotope-ratio data for each block in a run. It includes the average values for the isotope ratios, the observed standard deviation of the ratios within the block, the standard deviation of the means of the ratios, the change in each ratio from the preceeding block, the sample-filament currents, the beam-size of the reference-isotope, and the elapsed time of the block since the start of the run (figure 9).

After pressing k2 or k3 from the ISOTOPE RATIO DATA menu, the CRT will display

STARTING [,ENDING] RUNS FOR PRINTOUT?
(CONTINUE=current run [4], 0=escape)?
(or use negative numbers for file numbers)

If you want the summary for only one run, enter the run-number of that run. If that one run is the current run, though, you can just press CONTINUE. To get summaries of several consecutive runs, enter 2 values; the first and the last run in the sequence (for example, 3,12). The summary will appear on the printer (k2) or the CRT (k3), depending on which softkey you pressed to invoke the above display. To return to the bmc, just enter a value of zero.

Incidentally, if you want just a summary of the current run printed out on the printer, you can do this by just pressing either the RESULT (printer printout) or SHIFT-RESULT (CRT display) keys during the bmc.

Weighted Averages of Isotope Ratios for a Run

To invoke this function, either press k4 from the ISOTOPE-RATIO DATA menu, or just press CTRL-A from the bmc. The CRT will then show

WEIGHTED AVERAGES OF RATIOS:
WHICH RUN#?

Enter 0 to escape, a negative run# (e.g. -9) for CRT-display only,

press CONTINUE for current run (9),

enter 100 to use file numbers rather than Run numbers

If you want to average data for the current run (the one that you're still running or have just finished running), just press **CONTINUE**. To average data for some other run, enter either that run number (for a hard-copy printout) or the negative value of that run number (CRT display only). Don't worry about the last option ("file numbers rather than run numbers") for now.

When you've chosen a run, **ANALYST** will find its data on the **DATA** disk, and ask you to choose one of the ratios (206/204, 206/207, 206/208...) for averaging. If you want the default ratio (shown on the CRT), just press **CONTINUE**. Otherwise, enter the ratio in the exact format requested (numerator isotope-slash-denominator isotope, as shown above). **ANALYST** will then show you a list of all those ratios in the run, and the **SIGMAMEAN%** of those ratios. You can reject any of the ratios from the weighted average calculation by responding to the query

RATIOS TO BE REJECTED? (e.g. 2,5,32) [press CONT for none]?

Enter a list of the sets for any ratios that you don't want to include in the average calculation, separated by commas. **ANALYST** will calculate the weighted averages using an algorithm that

1) first weights the ratios according to the inverse square of their sigma (mean) values,

2) calculates the probability that the actual block-to-block scatter is due to the within-block errors alone,

3) If this probability is low, calculates how much block-to-block variance in excess of the within-block variance must exist, and recalculates the weighted average based on a weighting that combines the within-block and estimated excess block-to-block variance (this approach was developed by Brent Troutman of the U.S. Geological Survey).

4) ratios which are judged by **ANALYST** to be outliers are rejected during the calculation, and are indicated in the weighted-averages graphics by an empty error-box.

If the calculated probability is low (less than 10 or 15 percent), there must be some reason besides just the beam noise that is causing the ratios to change from block to block. If the element of the run is one that is not internally corrected for fractionation (such as Pb or Rb), the ratio-change is probably due to changing mass-fractionation.

The **M.S.W.D.** value in the weighted-averages printout refers to the "mean square of weighted deviates", and is essentially the sum of [(the squares of the residuals of the data-points)/(the squares of the assigned sigma-means)] divided by N-1 (N = # of points). The **M.S.W.D.** value should be significantly greater than 1 only if the data scatter more than predicted by their assigned sigma-means.

The **Weighted Averages** graphics (figure 10) displays the averaged data in the form of the ratios (shown as error-boxes) versus the time for each ratio. These graphics can be a very useful aid in the evaluation of the overall quality of a run.

TUTORIAL - AUTOMATIC RUNNING

If you can describe to another person roughly how to run one of your samples, in terms of what beam they might expect at what filament currents or temperatures and how precise you want the data, then you can do the same with ANALYST, and have your routine runs (those without gross unpredictability in running conditions) done with no loss in quality compared to a fully-attended run. This statement is based on extensive personal familiarity with fully-automatic runs on Pb, U, Th, Sr, Rb, Sm, and Nd, and I see no reason for it to be less true for most other elements. In fact, many types of runs actually give better data with full automatic running than manual running, since automatic runs tend to be done more patiently and and in a more repeatable way than manual runs.

What Will You Have to Know to do an Automatic Run?

Not very much. Much of the information is already defined in the ELEMENT data-files, such as the reference-isotope, fractionation-normalization, and isobaric interferences. Besides this, you'll basically need to know,

* at what filament-current to expect at least a small beam,
* how fast you can take the filament(s) up to this current,
* how intense an ion-beam you'd like to have,
* how intense an ion-beam you'll accept if you can't get what you'd really like,
* how much data (blocks, sets) you'll need if the beam is stable,
* how precise you'd like to have the data,
* if a triple-filament run, what criteria to use to determine the current of the center filament: the current only, the rhenium beam, or the beam for the element of interest with no side filament currents.

Defining Run Variables

To tell ANALYST how to do an automatic run, you'll need to define a set of Run Variables for each run. To invoke the Run Variables menu, press SHIFT-k7 during the bmc. Or, press the START AUTOMATIC RUNNING key (SHIFT-k8) and tell ANALYST that your Run Variables are undefined when asked. The Run Variables menu will appear on the CRT, as shown below:

KEY# FUNCTION

0 --- DEFINE A NEW SET OF RUN VARIABLES
1 --- EDIT or VIEW RUN VARIABLES
2 --- ADD TO RUN VARIABLES
3 --- PRINTOUT ALL RUN VARIABLES
4 --- WHAT ARE RUN & STD-RUN VARIABLES ANYWAY?
5 --- HOW TO DEFINE OUTGASSING VARIABLES
6 --- EDIT or VIEW STD-RUN VARIABLES
7 --- ADD TO STD-RUN VARIABLES
8 --- PRINTOUT ALL STD-RUN VARIABLES
9 --- RETURN TO BMC

If you were going to define a set of Run Variables for a newly-loaded barrel, you would start with k0. Try this now. The CRT will then display the Run Variable FORM, as in the example below.

```
RUN# 1                          BARREL# --- ??
ELEMENT ...   ??                ISOTOPES    ??
SAMPLE NAME   ??

SINGLE(1)-TRIPLE(3)   ??        MIN. BEAM (v)          ??
FOCUSING ISOTOPE (CF) ??        MAX. BEAM (v)          10
CENTER-FIL. BEAM (v)  ??        DEFAULT CURR. (amps)   ??
INITIAL CF (amps)     ??        DEFAULT BEAM (v)       ??
DALY ENABLE (0,1,2)   1         FIL. INCR/BLOCK (amps) 0
CURRENT-1 (amps)      ??        MIN# BLOCKS            3
RATE-1 (mA/SEC)       20        MAX# BLOCKS            6
WAIT-1 (min.)         0         MAX SIGMAMEAN(%)       .05
CURRENT-2 (amps)      ??        #SETS/BLOCK            15
RATE-2 (mA/SEC)       2         MAX. GROWTH (%/minute) 100
WAIT-2 (min.)         0         PREHEAT CF (amps)      0
DATA-WAIT (min.)      0         PREHEAT CF (amps)      0
ABORT CURRENT (amps)  ??        NORMSPIKE# (0 if none) 0

(((  for help with a parameter, press CTRL-H(elp) )))

   ENTER value (EXECUTE when done, k9 to escape,
        KNOB, (CTRL)CONTINUE moves cursor)
```

Obviously, with all those double question-marks staring you in the face, there's a lot of information for you to fill in. So how can I say that defining the automatic-run variables could be so easy? Several reasons. First, all these double question-marks will appear only for the first run of the several runs that you'll be defining for this barrel. After you define the first run, the next runs will inherit the values for the previous run as their default values, so if most of your runs in a barrel will be similar to one another, you won't have to enter new values for most of the run-variables. Second, there will usually be **Standard-Run Variables** defined that closely approximate the type of run that you will want to do, and you can insert these **Standard-Run Variables** into the **Run Variable** form with just a couple of keystrokes. Third, though the names for the various run-variables are admittedly pretty cryptic, you can bring up a **HELP** screen to explain any variable by just pressing **CTRL-H** when the cursor is at the confusing variable.

For some examples of typical Run Variables (and an example of the Run-Variable printout), see figure 14. Examples of Standard-Run Variables are given in figure 15.

Overview of an Automatic-Run -- Single-Filament Samples:

Before you proceed further in this explanation of the **Run Variables**, we should briefly go over how the automatic runs will be done by **ANALYST**.

First, of course, the sample at the specified **BARREL#** will be rotated into position. If for some reason valid filament-contacts aren't obtained at this point, **ANALYST** will rotate the sample into position again and re-test the filament contacts before giving up and aborting the sample.

If you specified nonzero values for the **PREHEAT CF** or **PREHEAT SF** variables, the preheat filaments will be taken to these values at a rate that decreases in steps from 30 milliamperes/second to 1 milliampere/second as the target current is approached. The preheat filaments will be held at these currents for two hours or until the run is over, whichever comes first.

Then, the sample filament-current will be raised to **CURRENT-1** amperes at a rate of **RATE-1** milliamperes per second, and left there with no action for **WAIT-1** minutes. After the **WAIT-1** wait, the filament-current will be taken to **CURRENT-2** at a rate of **RATE-2**, and left there with no action for **RATE-2** minutes. So the four variables **CURRENT-1**, **RATE-1**, **WAIT-1**, **CURRENT-2**, **RATE-2**, and **WAIT-2** tell **ANALYST** how you want the sample taken up to running temperature.

ANALYST will then quickly scan over all of the nuclides in the ISOTOPES list of the Run Variables, and select the Most-Intense-Peak (MIP). If a useable (more than a few tenths of a millivolt and reasonably stable) beam is present, ANALYST will center the MIP, focus the ion-optics, and center the barrel. Otherwise, ANALYST will raise the filament-current (beam too small) or wait (unstable beam) until a useable beam is obtained.

By raising or lowering the filament-current, ANALYST will then attempt to adjust the MIP beam until it lies within the window specified by the MAX. BEAM and MIN. BEAM values. If the filament-current exceeds the DEFAULT CURR in this attempt, however, the minimum acceptable MIP beamsize becomes the DEFAULT BEAM value. The DEFAULT CURR/DEFAULT BEAM variables are very useful, so you should understand what their purpose is and how to use them. In essence, these variables are used to permit you to accept an alternate minimum-beamsize if it looks like the beamsize that you'd really rather have will not, in fact, be obtainable.

For example, suppose that you expect at least a 3-volt beam of 206 for your zircon-Pb run. But the zircon turns out to be much younger than you were expecting, or perhaps something was funny about the filament-load, so there is no way that this run could ever give more than, say, an 800 millivolt beam. If data from an 800 millivolt beam would be better than aborting the run and getting no data at all, you should have set the DEFAULT BEAM at 800 millivolts and the DEFAULT CURRENT at some value towards the upper limit for normal Pb runs. This DEFAULT CURRENT value should lie between the ABORT CURRENT and CURRENT-2.

Once ANALYST has obtained an ion-beam that satisfies the above beam-size criteria, it can wait an additional period before taking data; the DATA-WAIT time. This wait can be used to provide an additional and predictable time for un-normalized fractionation to reach a reproducible value. Its advantage over the WAIT-2 wait is that it takes place <u>after</u> any filament-current changes that were required to get the MIP beam to the required size.

Just before starting the first block of data, ANALYST will quickly scan over the isotopes to determine the optimum peak-switching sequence and the integration and delay times for each isotope. The number of sets in the data-blocks are specified by the #SETS/BLOCK variable.

After each block, ANALYST will check the MIP beamsize and the rate of beam growth or decay during the block. The filament-current (center filament if a single-filament sample, side filaments if a triple-filament sample) will be adjusted to keep the MIP within the specified size if necessary. If the rate of beam-growth during the block exceeded the MAX. GROWTH variable and the MIP beam exceeded the MIN. BEAM value, the filament-current will be turned down by about 2.3 percent.

If the filament-current was not changed to control the beamsize or the growth-rate, it will be changed (usually, increased) by the amount specified by the FIL INCR./BLOCK variable. Also, the ion beam will be focused after the first block and then every fourth block.

How many blocks of data are taken depends on the MIN# BLOCKS, MAX# BLOCKS, and MAX. SIGMAMEAN(%) variables. Unless the run is aborted due to insufficient beam or instability, ANALYST will take at least the MIN# BLOCKS, but no more than the MAX# BLOCKS. Once the run has accumulated at least the MIN# BLOCKS, ANALYST checks how many of these blocks meet the criteria imposed by the MAX. SIGMAMEAN(%) variable. The exact conditions that this variable imposes depends on whether it is a positive or negative value. If the MAX. SIGMAMEAN(%) is negative, then to satisfy this variable the mean ratios for all of the isotopes of the block must have a sigma-mean (in percent) that is less than the absolute value. If the MAX. SIGMAMEAN(%) is positive, then mean ratios with a sigma-mean (percent) that is within theoretical limits (and so printed out in parentheses) will also satisfy the criterion. ANALYST will keep on taking data until the number of "good" blocks, as defined by the above criteria, equals the MIN# BLOCKS value or until the MAX# BLOCKS is reached - whichever happens first.

This isn't as complicated as it sounds (well, maybe it is). For example, suppose that the run is for 206/207, 206/208, and 206/204 ratios, and the sigma%/sigmamean% values of these ratios for a given block are .02%/.008%, .01%/.006%, and (.08%)/.03%, respectively. If the MAX. SIGMAMEAN(%) value is .05%, then the block will count as a "good" block since the sigmamean% values for all of the ratios are less than this. If the MAX. SIGMAMEAN(%) value is .025%, the block will still count as a "good" block because the sigma of the 206/204 ratio was within theoretical lmits (and so printed out in parentheses). If the MAX. SIGMAMEAN% value were -.025%, however, the block would not count as a "good" block because the 206/204 precision exceeds this tolerance, regardless of whether the 206/204 precision was within theoretical limits.

The run will end when either the **MIN# BLOCKS** or **MAX# BLOCKS** has been reached, or when the sample-filament current exceeds the **ABORT CURRENT** in the process of trying to obtain the **MIN. BEAM** or **DEFAULT BEAM**. Before going on to the next run, **ANALYST** will print out a run summary for the run (as described in the Manual-Running Tutorial), and calculate the weighted averages for the ratios of all of the blocks.

Overview of an Automatic Run -- Triple-Filament Samples:

For samples loaded on a triple-filament assembly, **ANALYST** will take up the center-filament current before the side filaments. There are three strategies that **ANALYST** can use to control the center-filament current during the run. These strategies depend on the values of the **FOCUSING ISOTOPE**, **CENTER-FIL BEAM**, and **INITIAL CF** run-variables. You may have noticed that these variables disappear from the **Run Variable** FORM if the sample is designated as a single-filament.

The first strategy, and the simplest, occurs when the **FOCUSING ISOTOPE** and **CENTER-FIL BEAM** variables are set to zero. When this is the case, **ANALYST** will take the center filament to the current specified by the **INITIAL CF** variable, and leave it there for the duration of the run. This mode might be appropriate for runs where the center filament isn't rhenium or where the center-filament temperature is too cool to yield a significant rhenium beam. The disadvantage of this mode is that the center-filament temperature at some constant current may vary significantly from run to run due to variations in the filament thickness or outgassing history.

The second strategy is to specify the size of the ^{187}Re beam during the run. This is appropriate if the center filament is rhenium, obviously, and if the desired temperature of the filament will be above the threshold for a significant rhenium beam - about 1800°C. To run in this mode, set the **FOCUSING ISOTOPE (CF)** to 187 (defined for all **ELEMENTs**), the **CENTER-FIL BEAM** to whatever rhenium beam corresponds to the center-filament temperature that you want, and the **INITIAL CF** to the approximate current (preferably slightly greater) that will give the desired rhenium beam. **ANALYST** will then start looking for a 187 peak at the **INITIAL CF**, focus on the peak, then raise or lower the center-filament current until the **CENTER-FIL BEAM** is obtained. **ANALYST** will check the size of the 187 peak before each block and adjust the center-filament current to keep the 187 peak within 10% of your specified target. This mode is appropriate for triple-filament runs of U, Th, Nd, Sm, or Hf.

The third strategy is to specify the size of the peak for some non-187 nuclide but still with the side-filaments turned off. For this mode, set the **FOCUSING ISOTOPE (CF)** to the major isotope that will be ionized from the side filaments during the run. After taking the center filament to the **INITIAL CF** current, **ANALYST** will slowly raise or lower the center-filament current until the beam for the **FOCUSING ISOTOPE (CF)** roughly matches the **CENTER-FIL BEAM** value. After this, **ANALYST** will make no further changes in the center-filament current. This mode of triple-filament running is appropriate for runs of Rb, K, and perhaps Sr.

More Information About Specific Run Variables:

The ELEMENT Variable...

This is the **ELEMENT** that will be assigned to the run. The **ELEMENT** must correspond to an **ELEMENT** defined on the **DATA** disk, as discussed in the Manual Running Tutorial. Remember that the **ELEMENT** file contains all the necessary information on the proper accelerating voltage, magnet-settings, reference nuclide, isobaric interferences, and fractionation normalization.

The ISOTOPES Variable...

These are the isotopes or nuclides that you want to take isotope-ratio data on, separated by commas. **Don't** include isotopes that will be used only for correction of isobaric interferences: these are already defined in the **ELEMENT** file. You can enter up to 8 isotopes. If the **ELEMENT** is one with internal fractionation-normalization (such as Sr, Nd...), the isotopes list must contain the **Reference Isotope** as defined in the **ELEMENT** file (such as 86 for Sr), and also include the isotope whose ratio with the reference isotope will be used for the normalization (such as 88 for Sr). And, if the sample was spiked with a spike that is defined on the **DATA** disk (fractionation-normalizable elements only, of course), the **ISOTOPES** list must also include the third nonradiogenic isotope required by the definition of the spike in the **spike** data-file (such as 84 for Sr). If you don't enter the minimum-required isotopes, don't worry. **ANALYST** will make an error-sound, and display a message at the bottom of the CRT explaining the problem before you exit from the **FORM**.

The SAMPLE NAME Variable...

This is just the name (up to 50 characters) that will be assigned to this run. If the names for the samples in each barrel-slot were defined before entering the Run Variable FORM (either after the graphics contact-test or by invoking the DEFINE SAMPLE-NAMES function), the appropriate name should appear automatically as soon as you enter the barrel-number for the run. Of course, you can still change the name at this point.

The DALY ENABLE (0,1,2) Variable...

This variable fulfills the same function as during manual data-dating. A value of 0 indicates that the Daly detector is malfunctioning and must not be used under any circumstances (remember: don't use a value of 0 unless the Daly really isn't working!). A value of 1 indicates that the Daly can be used for beam tuneup and, if all isotopes are less than 35 millivolts, will be used for data-taking also. A value of 2 indicates that the Daly can be used for beam tuneup but not for data-taking.

The PREHEAT CF and PREHEAT SF Variables...

These variables are the currents to which the preheat filament-assembly center (CF) and side (SF) filaments will be taken. If the values are nonzero, this will happen just after the sample filament-assembly is rotated into running position. The preheat filaments will be held at the specified currents for the length of the run or two hours, whichever ends first.

The NORMSPIKE Variable...

If the run were for a fractionation-normalizable element, and the sample were spiked with one of the spikes defined on the DATA disk, this variable indicates the number of this spike (0 indicates an unspiked sample). The data for each block will then be corrected for fractionation and spike isotopes, and the sample/spike ratio calculated. To get a temporary display of the names and isotopes of all of the spikes defined on the DATA disk enter a question-mark for this variable.

Using STANDARD-RUN VARIABLES:

The **Standard-Run Variables** are essentially just a set of **Run Variables** that are typical for several different types of runs and that can be placed in the **Run Variables** FORM with just a few keystrokes. Before I explain in detail how to create and edit the **Standard-Run Variables**, let's just walk through how they're used in practice.

Suppose that you're defining **Run Variables** for a barrel of unspiked and spiked common-Pb samples, and the sample that you want to run first is one of the unspiked samples. Suppose also that someone (perhaps you) has already defined the 7th set of the **Standard-Run Variables** to match the way you want to run your unspiked samples. You would bring up the **Run Variable** FORM as usual, and enter the barrel-number for this sample. Then, instead of entering Pb as the **ELEMENT**, you would enter *7*. A number enclosed in asterisks for the **ELEMENT** in the **Run Variable** FORM is treated as the number of a **Standard-Run Variable**. As soon as you **ENTER** this response, **ANALYST** will access the values for the **Standard-Run Variables** from the **DATA** disk, and insert the values for **Standard-Run** number 7 into the appropriate blanks in the **Run Variables** FORM (with the exceptions, of course, of the **Sample Name** and **Barrel#** responses).

If you wanted to make some changes in the responses at this point, you would do so. Chances are, though, that you would need only one or two such changes, since **Standard-Run** number 7 was already defined to closely match the type of run that you are doing. If you wanted the next run to be for one of the spiked samples and you had previously defined one of the **Standard Runs** to be for a similar type of spiked sample, you would just enter that **Standard Run**-number as the **ELEMENT**, as discussed above.

In other words, the **Standard-Run Variables** are used to define typical ways of running your samples, so that they can be used as the responses to the **Run Variables** FORM without retyping the same (or very similar) responses in each time you change a barrel or a run-type. Up to 32 different **Standard-Run Variables** can be defined on a **DATA** disk. You can find out how the various **Standard-Run Variables** are defined in two ways. To look at **all** of the defined **Standard-Run Variables**, you would press the **PRINT STANDARD-RUN VARIABLES** softkey (k8) during the **RUN VARIABLES** menu. The values for all of the defined **Standard-Run Variables** will then be printed out. To look at just one or two **Standard-Run Variables**, use the **EDIT STANDARD-RUN VARIABLES** key (k6) during the **RUN VARIABLES** menu. A third way of finding out which Standard Run- number to invoke for the Run Variables FORM is to respond to the **ELEMENT** query with *7* . When you enter this response, **ANALYST** will show you the names of all of the defined **Standard-Run**

Variables, then return you to the Run Variables FORM. If these names were descriptive enough, they will probably be enough to let you know which Standard-Run-number to use.

The best way to get a feel for how all this works is to just try invoking a few Standard-Run Variables into a Run Variable FORM as described above.

Defining Standard-Run Variables

Standard-Run Variables are defined in almost exactly the same way as the Run-Variables. Just use the softkeys that refer to the Standard-Run Variables instead of the Run Variables in the RUN VARIABLES menu. The only differences are that the FORM for each Standard-Run will ask for a STD-RUN# instead of a RUN# and a STD RUN NAME instead of a SAMPLE NAME, and that no barrel-number will be required.

Intervening During an Automatic Run

ANALYST is designed to allow you to intervene during an automatic run, perform some series of actions, and then return to the automatic run where you left off. There isn't much limitation on the kinds of actions that you can perform while having temporarily exited from automatic running. For example, you can scan the isotopic spectrum, focus a beam, raise or lower the filament-currents, calculate weighted averages, and even change the Run Variable values (with the exceptions of the Barrel# and Isotopes!) for the run in progress.

To temporarily exit an automatic run once it has started, wait until softkey k0 is labeled BMC. Such a key exists most of the time during an automatic run, so you probably won't have to wait at all. When you press the BMC key, ANALYST will immediately exit to the familiar bmc. You can then invoke any of the functions of ANALYST just as if you were in the Manual-Running mode. To return to the automatic run at about the point where you left it, press the RECALL key during the bmc. That's all there is to it. Keep in mind, though, that if you exit to the bmc in the middle of a block of data, when you re-enter automatic running, ANALYST will start that block over again from the beginning.

If you don't want to just temporarily exit from the automatic run, you have two other options. If you have enough data from the automatic run, or if you decide that the sample just isn't going to give you the quality of data you want, you can command an immediate end to the run by pressing the NEXT RUN softkey (k1), which will exist at the same time as the BMC softkey. If you press the NEXT RUN softkey during the

automatic run, ANALYST will ask you to confirm your request, and if confirmed, end the run in progress and go on to the next automatic run defined in the Run Variables. In effect, you will have just commanded the run to abort.

If you exit to the bmc while ANALYST is in the middle of actually taking data, you will lose the data for any of the sets that had been taken for that block before you intervened. So don't intervene during a data-taking block unless you're willing to lose the existing partial-block data for that block (incidentally, this is also true if you press the ESCAPE key during a block in the manual mode).

If you want to exit automatic running entirely, first exit to the bmc using the BMC softkey as described above. Then press the SHIFT-k8 softkey (REVERT TO MANUAL RUNNING) and choose the MANUAL RUNNING option that follows. You will then have completely exited the automatic-running mode.

Remember to use the BMC key, not the ESCAPE key to temporarily exit from automatic running. If you press the ESCAPE key during automatic running, ANALYST will simply cut short whatever it was doing at the time (such as focussing the beam, taking up a filament-current, or waiting) and go on to its next operation. This may be OK (for example, if focussing were in progress but you were satisfied that the beam were already adequately focussed), but unless you know what you're doing, could bypass an important automatic-running operation.

What Will Cause an Automatic Run to Fail?

It's pretty frustrating to come in in the morning expecting all of your samples to have been run without a hitch, and find out that one or more runs aborted without getting any useable data. Fortunately, this should be an uncommon occurence providing that, 1) the sample would have run satisfactorily under your control in the manual mode, and 2) there were no gross hardware malfunctions during the run. Many of the causes for an early run-abort are preventable, and are listed below.

1) Wrong high-voltage setting for the ELEMENT being run. This will cause an abort without any attempt to run the sample at all. The tolerance is plus or minus 15 volts from the ELEMENT's specified value.

2) Bad filament-contacts. If bad contacts are encountered, ANALYST will try hard to improve the situation, either by slightly wiggling the barrel to rub off any bits of fluff in the contact area, by completely resetting the barrel and refinding the sample, or both. If none of these strategies succeeds in regaining good filament-contact, though, ANALYST will give up and go on to the next run.

3) The Daly Detector was not completely turned on. If your runs assume the presence of an operating Daly detector and you forgot to turn on the FA3 amplifier, the multiplier supply, and the Brandenburg, and pressed the Brandenburg RESET button, the run will abort at an early stage.

4) Unstable beam. If, at the time of the first beam tuneup, the beam persists in being either very noisy or growing/decaying extremely rapidly, the run will abort. Before aborting, though, ANALYST will wait up to 15 minutes for the beam to stabilize. In addition, if the problem is a noisy beam, after this 15-minute wait the filament will be "flashed" to 20% greater filament-current for a few minutes to see if that will decrease the beam-noise.

5) Wrong sample. Obviously, if you mistakenly put in the barrel-number for a uranium sample instead of a lead sample, the run will abort due to insufficient beam.

6) Bad pressure. Bad pressure in the source-can or the flight-tube will cause ANALYST to wait for up to an hour for the pressure to improve, and then abort the run if it didn't. Remember that the liquid N_2 in a full cold trap will last only about 12 hours.

7) Panel switches set to the wrong settings. All panel switches must be set to the heavy black marks, filament-current supplies must have been RESET, beam valve must be open.

Hardware malfunctions, of course, are out of your control. Because of the possibility of a hardware malfunction that could result in the irrevocable loss of every sample in the barrel (such as a malfunction that will cause each filament to be taken up to the ABORT CURRENT in a vain attempt to get a beam), ANALYST will not permit more than two automatic runs in a row to be aborted without ever having a significant beam. If two runs in a row are aborted under such conditions, ANALYST will suspend automatic operation completely.

Automatic Outgassing Runs:

ANALYST recognizes a special kind of outgassing automatic run. An outgassing run is one that is intended only to take the filament(s) up to some target current and wait there in a reproducible way without any intention of taking data. These runs may even be done with the high voltage turned off and the beam-valve closed, to keep any crud that volatilizes from the filament away from the source assembly as much as possible.

ANALYST recognizes an outgassing automatic run from the ELEMENT name OUTGAS or P-OUTGAS in the Run Variable FORM. As soon as you enter either of these names as the ELEMENT, all of the parameters in the Run Variable FORM that aren't relevant for just outgassing (such as Isotopes, Sets/Block, Max.# Blocks...) are replaced by asterisks. An ELEMENT name of OUTGAS will result in the specified sample being outgassed in the running position (directly in front of the source assembly), whereas an ELEMENT name of P-OUTGAS will result in automatic outgassing of the specified sample in the preheat position.

An automatic outgassing-run will rotate the sample into position (running position if OUTGAS, preheat position if P-OUTGAS), then take up the sample-filament current according to the RATE-1, CURRENT-1, WAIT-1, RATE-2, CURRENT-2, and WAIT-2 parameters, and then go on to the next run.

Multiple Runs on One Sample:

You can do more than one run on a given filament-assembly without turning off the filaments between runs and completely restarting a new run. For example, suppose that you wanted to take data for uranium, then raise the filament currents enough to grow in a thorium beam, and then take thorium data. All you need do is to define your usual automatic run for uranium, and then define the next run to be a thorium run for the sample at the same barrel-number.

After completing the uranium run (and without turning the filaments down or off), ANALYST will take the sample-filament (center if a single, sides if a triple) directly to the CURRENT-2 target if CURRENT-2 is greater than the sample-filament current at the end of the uranium run. If the sample-filament current at the end of the uranium run were already greater than the new CURRENT-2 value, ANALYST will make no immediate change in the sample-filament current. The CURRENT-1/RATE-1//WAIT-1 variables of the thorium run will be ignored. ANALYST will then adjust the thorium beam-size to the window specified in the Run Variables for that run, and begin taking data.

You can specify as many automatic runs as you like for any given sample. The only restriction is that the total number of automatic runs for a particular suite of unattended runs be no more than 32 - the maximum number of Run Variables that can be defined at any one time.

You can use this multi-run feature in cases where you don't want to really combine runs of different elements on the same sample, but just want to take different isotopes. For example, you might want to specify the first run for a sample as a Pb 206-207-208 run, and the next run on the same sample as a Pb 206-204 run at a higher beamsize and with different requirements on the precision and number of blocks.

REFERENCE GUIDE

Introduction

This part of the guide contains specific information about some of the features of ANALYST that aren't covered in the Tutorial sections. The Reference Guide isn't the easiest way to find out how to use ANALYST -- that's what the tutorial sections are for -- but does contain much of the information you need that doesn't appear in the tutorials.

Nonetheless, you won't find descriptions of all of the features and functions of ANALYST in this section. In fact, you won't find information about some of the features anywhere in this User's Manual at all. There are two reasons for this. The first is, of course, that I just don't have the time to write a really complete manual. That doesn't help you much, but the second reason does: most of the features of ANALYST are more or less self-documenting, and can be both located and used just by intelligently combining the information in the softkey menus, the FORMs, and the HELP screens. I realize that this method of learning is not very convenient if you need to perform some obscure function in a hurry, so I strongly advise you to take some time to sit down with ANALYST and an expendable sample or two, stroll through all of the various menus and functions, and experiment with them.

Loading ANALYST into the Computer from Scratch

If for some reason the computer was turned off or power was lost, you'll have to load ANALYST into the computer using the following procedure:

1) turn the computer off (from the switch below the keyboard, to the right);

2) put the BASIC SYSTEM disk in the right-hand drive, then turn the computer ON. It takes a few minutes to load the BASIC language;

3) When the BASIC language is loaded, put the EXTENDED BASIC 2.1 disk in the right-hand drive, type in LOAD BIN "APZ_1", then press the EXECUTE key;

4) When APZ_1 is loaded, type LOAD BIN "GRAPHZ_1", and press the EXECUTE key again;

5) When GRAPH2_1 is loaded, put in the disk labelled ANALYST - MAIN in the right-hand drive, type CAT, then press EXECUTE. This will give you a catalog on the CRT of the files on the disk. At least one of the files will have a name like MAIN_10_16. This means that this version of the MAIN part of ANALYST was last modified on October 16. Choosing the last-modified version (always towards the front of the disk box), type in GET "MAIN_10_16" if MAIN_10_16 is an ASCII file, or LOAD "MAIN_10_16" if it is a BDAT file. The disk catalog will tell you which type it is. The 10_16 part, of course, is just an example in the above instructions- the file that you load will have its own date-characters. Press the EXECUTE key.

6) When the MAIN part of ANALYST is loaded (takes about a minute for a LOAD operation, or 10-15 minutes for a GET operation), put in the disk labelled ANALYST - SUBS. Get a catalog of the disk as described above, and type in LOADSUB ALL FROM "SUBS_10_16". Again, the 10_16 part is just an example.

7) Put the ANALYST - DATA disk in the left-hand drive and the ANALYST - SYSTEM disk in the right-hand drive. Press the RUN key.

8) After about 30 seconds, ANALYST will begin operation by telling you what settings of the mass-spectrometer switches are required, and ask you to check the beam-valve. When you have acknowledged these requests, ANALYST will ask you to enter the Daly status (disable, enable for beam-tuneup only, or enable for beam-tuneup and data-taking), choose an ELEMENT, and choose a sample in the barrel. When these requests have been answered, ANALYST will perform the appropriate actions and (finally) arrive at the Beam-Monitor Condition (bmc).

Procedures for Starting a New Barrel

When you install a new barrel-load of samples, there are two things that you should do as a routine procedure: perform a contact-test for all of the samples (filament-assemblies) in the barrel, and enter sample-names for all of the samples in the barrel.

The CONTACT TEST procedure:.

The contact-test procedure rotates the barrel past all of the samples, and gives you a graphic display (figure 11) of the contact-width of both the side and center filaments for each sample, both in the running position and the preheat position. You should do this as soon as you are ready to start pumping the source-can down. The procedure is to:

1) install the face plate of the source can and the barrel-motor belt, then start the rough-pump;

2) if you want to use the bypass-plug (which bypasses the high-voltage interlock, so MAKE SURE THAT THE HIGH VOLTAGE IS TURNED OFF), install it now. Otherwise, wait until you have turned on the turbomolecular pump and turned on the high-vacuum gauge for the source;

3) turn all of the filament knobs on the mass-spectrometer to RESET, then ON (both center-filament and side-filaments, both sample and preheats);

4) turn the barrel-motor ON;

5) from the bmc state of ANALYST, invoke the BARREL menu with the SHIFT-k2 softkey, then press the key defined as TEST CONTACTS FOR ALL SAMPLES (k2) (or you could use the short-cut method of pressing CONTROL-B during the bmc);

6) confirm your request when asked.

ANALYST will then reset the barrel, start rotating the barrel slowly so that all of the sixteen possible samples pass through both the sample and preheat filament-contact assemblies, and display graphically the regions where filament-contacts were made for each sample (figure 11). The horizontal line at the zero position of the Y-axis indicates the default barrel-position for each sample. Solid patterns for the boxes to the left of right of the vertical line indicating which sample is being tested indicated that valid contacts were found for both the center filament and the side filaments of that sample. Stippled patterns indicate valid contact for a center filament only, and an empty box indicates valid contacts for the side filaments only.

Boxes to the left of the vertical line indicating the barrel-number indicate contacts in the running position; boxes to the right of the line indicate contacts in the preheat position.

If the region of valid contact is less than about 20 barrel-units, it may be difficult for ANALYST to either "find" the sample or to properly optimize the barrel once a beam is found. If less than 10-12 units of contact exist, you should either vent the source-can and determine the cause of the problem, or accept that you may not be able to get a run from that sample.

When the contact-test is complete, ANALYST will ask you if you want to erase the previously-defined sample-names at this time. Normally, your answer should be YES, since otherwise ANALYST will assign the sample-names for the previous barrel to this barrel's samples.

Entering SAMPLE NAMES for a New Barrel...

If you erased the previously-defined sample names after the completion of the contact test, as recommended above, ANALYST won't suggest default sample-names for manual or automatic running, and won't display the sample names during the bmc. Because not having the sample names displayed (and changed each time a new sample is rotated into running position) increases the risk of the operator trying to run the sample at barrel-number N when actually the sample at barrel-number M is in running position, I strongly recommend that you carefully enter the names for each of the samples as soon as possible after you install a new barrel.

To enter the sample names, invoke the ISOTOPE-RATIO DATA menu by pressing SHIFT-k4 during the bmc, then press then ENTER NAMES FOR ALL SAMPLES key (k1). ANALYST will then ask you to enter the names for the samples at those barrel-numbers which gave valid filament-contacts during the most-recent contact test.

Defining a New ELEMENT

You'll need to define a new ELEMENT for ANALYST if you:

1) start running an element or ionic species that no one else has run before,

2) decide to use a different pair of isotopes for fractionation-normalization or to use a different value for the normalization ratio,

3) decide to use different isotopes to monitor for isobaric interferences or to use different values for the isobaric-interference ratios,

4) decide to use a different reference isotope, or

5) decide to use a different high-voltage setting for your runs.

If you need to define a new ELEMENT for reasons 2, 3, or 4, then you won't need a beam to do so. If you need to define a new ELEMENT for a new element or ionic species, however, you will need a beam unless the isotopes of interest overlap with some previously defined ELEMENT.

The NEW ELEMENT Procedure:

Bring up the MAGNET menu from the bmc by pressing the SHIFT-k0 softkey, then press the key for DEFINE DATA FOR A NEW ELEMENT (k5). The CRT will clear and display:

PRESS k0 TO CHANGE MAGNET-VALUES ONLY,
PRESS k1 TO CHANGE RUNNING-DATA ONLY,
PRESS k2 TO CHANGE BOTH
PRESS k9 TO RETURN TO BMC.

If you press k0, you must have a beam of the nuclides of interest for ANALYST to use for its magnet calibration. The beam must include at least 2 (but try to have 3 or more; the more the better) nuclides present in the magnet-region of interest. If there is already an ELEMENT with nuclides in the same mass-range as the new ELEMENT you're defining), though, just make sure that this was the ELEMENT in use when you called up this NEW ELEMENT function, and choose the CHANGE RUNNING-DATA ONLY option. For example, if you wanted to define an ELEMENT for samarium (mass-numbers 144 to 154) and a neodymium (mass numbers 142 to 150) were already defined, you could just use the CHANGE RUNNING-DATA ONLY option. The CHANGE MAGNET-VALUES ONLY option is also appropriate if you just wanted to update the magnet-calibration for the isotopes of a given ELEMENT (perhaps because of a new high-voltage setting or drift).

You would also use the CHANGE RUNNING-DATA ONLY option if you were just modifying an already-defined ELEMENT to use different values for fractionation-normalization, isobaric interferences, or a different reference-peak.

If you want to define a completely new ELEMENT but no existing ELEMENT has similar nuclides, you'll need to press **k2** (CHANGE BOTH).

Defining new magnet-data...

If you chose either the CHANGE MAGNET-DATA ONLY or CHANGE BOTH option, the CRT will clear and display,

> ENTER THE MAGNET COARSE-RANGE (0-10) AND THE
> MAGNET INTERVAL (300-9700) IN WHICH YOU EXPECT
> TO FIND PEAKS.

You may need to do this part by trial and error, so don't worry if you aren't sure of the values that ANALYST is requesting. The lower the coarse-range, the lighter the isotopes that can be included in the magnet interval. For example, Pb (masses 204 to 208) occurs at a coarse range of 8 for a high voltage of 7800, Nd (masses 142 to 150) at a coarse range of 7, and Sr (masses 84 to 88) at a coarse range of 5. Also, in any coarse range, there are roughly 200 magnet units separating each mass-unit for a high voltage of about 7800.

To get an idea of what ballpark figures to enter for the two values requested, it might be useful to bring up several different ELEMENTs with the CHANGE ELEMENT key from the **bmc** and look at the coarse and fine magnet values that are displayed with them. Of course, you'll need to do this before you request the NEW ELEMENT procedure.

After you enter the coarse-magnet range and the magnet interval for the peak scan, ANALYST will ask you to choose whether the scan is to be done with the Faraday cup or the Daly detector as the collector. Choose the Faraday cup unless all of the peaks that will be encountered in the scan will be less than 50 millivolts.

ANALYST will then do a graphics magnet-scan over the interval that you requested, with a logarithmic Y-axis (beam-size). As soon as the scan is finished, ANALYST will indicate the first peak encountered with a large arrow on the graphics, and query,

> ENTER THE MASS & NUCLIDE OF THIS PEAK
> (e.g. "88,Sr", "160,NdO", "87,Sr(Rb)"

Enter the mass-number of the peak, comma, nuclide or ionic species of the peak. Don't enter the precise atomic weight of the peak - for example, enter **206** rather than **205.973**. Note that the "NUCLIDE" can indicate any information you want, so long as you use no more than 6 characters.

The large arrow will then move and point to the next peak encountered in the scan, and ask the above question again until you have entered the mass and nuclide for each of the peaks encountered in the scan. At this point, ANALYST will take a minute or so to find the half-peak magnet-offset for the peaks, center all of the peaks, and calculate a least-squares quadratic curve for the magnet-settings as a function of the mass of the peak.

You'll probably want your new ELEMENT to include information about peaks that weren't present during the scan, so ANALYST will now query,

MASS, NUCLIDE OF PEAKS THAT WEREN'T FOUND
DURING SCAN? (e.g. 85,Rb)

(6 chars. max., no commas)

(press CONTINUE when done)

Enter the mass and nuclide as before, and continue answering the query until all of the desired nuclides have been entered. You should include all of the nuclides that you may want to either take data on, monitor for interferences, or just look at occasionally. No more that 24 nuclides may be defined, however, so you may need to prune your list a bit.

Remember that ^{187}Re will also be included in your list of defined nuclides for the ELEMENT as an additional nuclide, so long as the Re ELEMENT defined on the SYSTEM disk was defined at about the high voltage that you are now using.

Defining RUNNING DATA...

The first query that ANALYST will give you is the number and name of the new ELEMENT that you're defining (or modifying). A list of ELEMENTs that are currently defined on the SYSTEM disk will be shown above the query. The maximum number of ELEMENTs is 20. You can replace an existing ELEMENT with the new one, but of course make sure that this won't affect someone else who might want to use the ELEMENT that you're replacing.

ANALYST will then ask you to enter the reference-isotope. The reference isotope is the isotope to which all others will be ratioed, and is important mainly for fractionation-normalizable ELEMENTs.

ANALYST will then ask whether you want your ratios calculated with the reference isotope in the numerator or denominator. This is purely a stylistic preference on your part.

The next query asks if you can control mass-fractionation by normalizing each ratio to some internal ratio with a constant natural value, and if so, what ratio to use. The actual query is,

WHAT ISOTOPE, IF ANY DO YOU WANT TO USE TOGETHER
WITH 86 FOR FRACTIONATION NORMALIZATION?

(EXAMPLE: 88 FOR Sr)
(press CONTINUE if fractionation-normalization isn't possible)

The "86", of course, is just an example. The actual isotope that will appear here will be whatever reference isotope that you chose above.

If you entered an isotope, ANALYST will ask you to enter the "standard" value for the normalizing ratio. Enter whatever value you wish to accept as standard for the natural element (such as 0.1194 for 86/88 or 0.7219 for 146/144).

ANALYST will now query,

ENTER THE NUMBER (UP TO 4) OF ISOBARIC INTERFERENCES
FOR THE DATA-DATING ISOTOPES:

One isotope can have more than one isobaric interference, but no more than 4 interferences can be corrected for. For example, for neodymium, there can be a Ce-142 interference on Nd-142 monitored with Ce-140, and Sm interferences on Nd-144, Nd-148, and Nd-150 all monitored with Sm-147. You can't have interferences on monitor isotopes corrected by other monitor isotopes, though.

The next query will ask you to enter, for each isobaric interence, the monitor isotope and the interfering isotope. The monitor isotope is an isotope of the interfering element that will be used to estimate the intensity of the interfering isotope. An example would be Rb-85 for a strontium run. The interfering isotope is the isotope that is actually causing interference (and also the isotope being interfered with), such as 87 for a strontium run.

After you've answered the above query, **ANALYST** will ask you to enter, for each isobaric interference, the ratios for the natural interfering element of the monitor isotope to the interfering isotope (example: 85/87 for strontium runs). For the most precise corrections, you should enter the ratio that the interfering element would actually give under the expected running conditions, rather than the true natural ratio. In other words, take some typical amount of mass-fractionation into account for the ratios.

How the Isotope Ratios and their Errors are Calculated by ANALYST

This subject has been covered to some degree in the **TUTORIAL - MANUAL RUNNING** section, but is given here again in somewhat more detail.

After the appropriate backgrounds values (zeroes) have been subtracted from the raw peak heights collected during the peaktop-jumping part of the block, any calculated isobaric interferences are subtracted from the peaks. If the interference-monitor peaks were measured only before and after the peaktop-jumping, a linear interpolation of the interference-monitor peaks is used to estimate the amount of interference at the time that each interfered-with peak was measured. If the interference-monitor peaks were measured during the peaktop-jumping sequence (as is done for relatively large interferences), the size of the interference-monitor peaks is estimated for the time of each interfered-with peak by fitting a least-squares cubic polynomial to the intensities of the interference-monitor peaks with time.

The raw ratios of the isotopes are then calculated, using the linear-interpolation method of Dodson (1978), which corrects for any second-order curvature of the ion-beam with time. The effect of the time constants of the amplifier system on the ratios is then calculated, and the resulting small correction applied to the raw ratios.

If the **ELEMENT** were one that requires normalization of mass-fractionation using an internal ratio (such as Sr, Nd...), the normalizing ratio is calculated first, and a linear regression of this ratio with time is calculated. Using this regression, the amount of fractionation (using the exponential law of Russell and others, 1978) is estimated for the time of each individual set in the block.

If the run were for a spiked sample and a fractionation-normalizable ELEMENT, the double-spike algorithm of Dodson (1970) is used to calculate the sample/spike ratio and the fractionation-corrected radiogenic-isotope ratio. This algorithm assumes a linear fractionation law.

Outlying ratio-values (one value for each isotope ratio per set) are rejected by a multi-pass procedure that starts out rejecting at the 2-sigma level, and increases by 0.3 sigma for each pass. This method avoids the rejection of too many valid ratios for blocks with a large number of sets. No more than 30% of the set ratios can be rejected.

The calculated errors for the ratios of each block are calculated from the sum of the following variances:

1) the set-to-set variance (that is, just the square of the standard deviation of the ratios of each set);

2) the background variance, calculated from either the observed background noise (long background counts) or the know dark noise of the particular collector (short background counts);

3) the variance from the isobaric-interference corrections, if any. This is calculated from a combination of the theoretical noise for the interference-monitor peaks plus the background uncertainty of the interference-monitor peaks plus as assigned 2% uncertainty in the assumed ratio of the (interfering isotope)/(monitor isotope);

4) the variance from the fractionation-correction (if any), calculated from the uncertainty in the normalizing ratio;

5) The theoretical variance of the ratio, as calculated from a combination of the dark noise of the collector and the counting statistics from the number of ions arriving at the collector. If the observed variance is greater that this theoretical variance, the observed variance is the one that is used; otherwise, the theoretical variance is used.

6) If the run were a spiked run of a fractionation-normalizable ELEMENT, the propagated uncertainties of the double-spike calculation (Dodson, 1970) are included in the errors of the spike-corrected ratios.

Locating Isotope-Ratio Data on the DATA Disk

Though ANALYST's DATA disk retains data for the last 500 blocks of isotope-ratio data, the directory to this data only contains information for run-numbers 1 through 32. Moreover, since the assigned number of the runs is reset to 1 each time a new automatic-run sequence is initiated, the next person to do automatic running will probably overwrite the run-directory for at least the first several runs of the last runs you initiated. So if you tried to have a run-summary printed out for these runs, or to average the data in these runs, you would get someone else's data when you requested the data by run number.

All is not lost, however. The first 10 characters of the names for each run are stored along with the data for each block, and you can use this fragment of the run name as a key to locate the data you want. The procedure is as follows:

First, from the bmc, press SHIFT k4 to obtain the menu for ISOTOPE-RATIO DATA, Then k5 to invoke the Locate Isotope-Ratio Data function (or you can just press CTRL L from the bmc). The CRT will clear and display:

KEY# FUNCTION

0 --- SEARCH THE DISK FOR A RUN WITH A PARTICULAR SAMPLE-NAME
1 --- SHOW THE DISK-DIRECTORY OF THE LAST GROUP OF RUNS
3 --- DISPLAY ON CRT ONLY (DEFAULT)
4 --- PRINTOUT ON THE PRINTER
9 --- RETURN TO THE BMC

Press k0, and when asked, enter the characters in the sample-name of interest to be used as the search-key (I'm using sample name and run name interchangeably here). ANALYST will then search the DATA disk for blocks with characters in the first 10 characters of the sample name that match. When a consecutive number of blocks that provide a match is found, the sample name (first 10 characters) for these blocks and the file numbers of these blocks will be displayed or printed out.

Copy down the file numbers for the run of interest. You can then use these file numbers instead of a run number to specify a Run-Summary printout or to do weighted averages. ANALYST will tell you how to do this in the run-number query for the particular operation desired.

Manual Beam-Tuneup Functions

If you'd rather assume complete and specific control of the beam-tuneup, rather than rely on the automatic beam-tuneup functions of ANALYST, you can do so from within ANALYST rather than use the hardware controls on the mass spectrometer. These manual beam-tuneup functions are described below.

Manual Focus:

The best way to manually focus a beam is to first invoke the CRT beam-chart function (**k3**) so that you can graphically see the effect of changing the focus potentials on the beam. Make sure that you have enough "headroom" in case the beamsize increases significantly. Then, invoke the **ION OPTICS** menu with **SHIFT-k2** and press the **MANUAL FOC.** key (**k1**) (or you can simply press **CTRL-F** during the **bmc**). The beam-chart graphics will appear on the CRT, and the lowest line of the CRT will show the settings of each of the focus "plates".

You can change the focus settings continuously by rotating the KNOB, or in 1-unit increments by pressing the plus or minus keys, or by pressing the up- or down-arrows. The "plate" number that you will be changing will be shown as a blinking number in the bottom line of the CRT. To change "plates", either press the softkey corresponding to the plate, or the number-key in the numeric keypad corresponding to the plate. Maximize the beam by watching the CRT (if the beam-chart weren't invoked before you called up the manual focus function, there will be a line at the bottom of the CRT showing you the beamsize as you change the focus settings). This method is entirely equivalent to focusing the beam using the hardware on the focus-panels, but is much more simple and rapid.

Manual Magnet-Scan:

You can scan the magnet with the KNOB by pressing the **MAGNET KNOB** key (**k1**) from the **MAGNET** menu (**SHIFT-k0** from the **bmc**). Using the softkeys, you can then change the "speed" of the knob response with the softkeys, or switch magnet coarse-ranges. No CRT beam-chart graphics are provided, so you'll have to use an external chart-recorder or just use the numeric beamsize display on the CRT.

Manual Barrel-Scan:

To rotate the barrel "manually" using the KNOB, press the **MAN.-ADJUST** softkey (k1) from the **BARREL** menu (**SHIFT-k2** from the bmc). Normally, **ANALYST** won't let you rotate the barrel beyond the region where filament-contact can be maintained. If you want to override this protection, you must press the **SHIFT** key at the same time you rotate the KNOB. Note that the barrel mechanism has a nonzero amount of free play (7-12 barrel-units) so that to reproducibly arrive at the same physical barrel position, you'll need to approach that position from the same rotational direction each time.

Miscellaneous Other Functions Available within ANALYST

Scanning the Focus Potentials:

For troubleshooting ion-optics problems, or just for getting a feel for the effect of varying the various focus potentials, you can scan the focus potential for any "plate" and graphically see the effect on the beam. Press the **SCAN FOCUS** softkey (k2) from the **ION OPTICS** menu (**SHIFT-k1** from the bmc), and then select the plate that you wish to scan and the scanning step-interval from the **FORM** that follows.

Defining or Storing Standard (Default) Focus-Values:

Occasionally, you may decide that the focus settings in use are so far away from the best settings that **ANALYST** won't be able to "find" its way back to the optimum focus conditions. In this case, it can be useful to just restore the default focus-settings (the ones that are invoked at each sample-change) and go from there. To do this, press the **USE STD** softkey (k4) from the **ION OPTICS** menu (**SHIFT-k1** from the bmc). The standard (default) focus-settings will then be recovered from the **SYSTEM** disk and restored as the focus-settings.

If the physical state of the ion optics shifts for some reason (for example, each time the source is changed or cleaned), you'll probably want to change the default focus-settings. To do this, first make sure that you have a well-focused beam and that you're satisfied that the current focus-settings are appropriate as default focus-settings. Then press the **DEFINE STD** softkey (k5) from the **ION OPTICS** menu (**SHIFT-k1** from the bmc). **ANALYST** will then store the current focus-settings on the **SYSTEM** disk as the default ones.

There are 2 default (standard) focus-settings stored on the disk: one for single-filament samples, and one for triple-filament samples. So you'll need to do the above procedure for each type of filament-assembly to completely redefine the default focus-settings.

Graphics Pressure-Monitor:

To use the computer as a logarithmic stripchart-recorder for the pressure in both the source can and the flight tube (fig. 13), press the PRESSURE-GRAPH softkey (k1) from the MASS-SPEC. STATUS menu (SHIFT-k6 from the bmc). You can then define the time-interval of the chart, the maximum pressure to be shown, and whether or not to dump the chart to the printer each time it reaches the time-interval.

Taking Collector Zeroes:

Normally, ANALYST only takes collector zeroes at the time you request a sample change. But if you want to re-check the zeroes (perhaps due to a pressure rise or change in the hardware zero-settings), you can do this by pressing the ZEROES softkey (k1) from the COLLECTOR menu (SHIFT-k3 from the bmc). ANALYST will search for the magnet-position with the lowest apparent beamsize, and take zeroes for both collectors.

Calibrating the Daly Gain:

The Daly gain will vary significantly (10-30%) from element to element, or even over a time interval of a few weeks. To calibrate the gain, so that the apparent Daly beamsize exactly matches the Faraday Cup beamsize, you will need to invoke the Daly Gain Calibration function.

First, get a beam of between 5 and 45 millivolts. Then, press the DALYCAL softkey (k2) from the COLLECTOR menu (SHIFT-k3 from the bmc). ANALYST will then center the peak, take fresh collector zeroes, and determine the current Daly gain by monitoring the peak on the Cup, Daly, then Cup again.

Summary of Functions Available from the BMC

(Note: in the table below, the carat symbol (^) is used to indicate that the SHIFT key is to be depressed before the key following; for example, ^k4 k2 indicates that SHIFT-k4 is to be pressed, followed by UNSHIFTED k2)

Unshifted-Softkey Functions:

PRESS	TO
k0	Center the peak for the current isotope.
k1	Focus the ion optics (automatic).
k2	Optimize the barrel-position (figure 4).
k3	Start a real-time graphics beam-chart (figure 1).
k4	Change filament-currents semi-automatically.
k5	Change collector from Faraday cup to Daly or vice-versa.
k6	Scan magnet semi-automatically (figures 2-3).
k7	Change the ELEMENT.
k8	Rotate the barrel to a new sample.
k9	Take isotope-ratio data in the "manual" mode.

Shifted Softkey Functions:

(the "shortcut" keys indicate how to access the same function directly from the BMC)

MAGNET menu functions...

PRESS	TO
^k0 k0	Scan magnet semi-automatically. (shortcut: k0)
^k0 k1	Scan magnet manually, using KNOB.
^k0 k2	Do a graphics peakshape-check (figure 12). (shortcut: CTRL P)
^k0 k3	Display magnet and running data for the current ELEMENT.
^k0 k4	Change the ELEMENT. (shortcut: k7)
^k0 k5	Define a new ELEMENT.

ION OPTICS menu functions...

PRESS	TO
^k1 k0	Focus the ion-optics (automatic). (shortcut: k1)
^k1 k1	Focus the ion-optics manually, using the KNOB. (shortcut: CTRL F)
^k1 k2	Do a graphics scan of the focus-settings for any plate.
^k1 k3	Display the current focus-settings.
^k1 k4	Restore the default (standard) focus set-tings.
^k1 k5	Define the current focus-settings as the default focus settings and store on the SYSTEM disk. The default focus-settings (one for single filaments, another for triple filaments) are invoked each time a sample is changed.

^k6	Query the current high-voltage. (shortcut: CTRL V)
^k1 k7	Type in new focus-settings for any or all plates.
^k1 k8	Do a complete beam-tuneup, in the sequence: center peak, focus ion-optics, center peak, optimize barrel, focus ion-optics. (shortcut: CTRL *)

BARREL menu functions...

PRESS	TO
^k2 k0	Optimize barrel-position for best beam. (shortcut: k2)
^k2 k1	Adjust barrel-position manually, using KNOB.
^k2 k2	Test contacts for all samples in barrel (turns all filaments off). (shortcut: CTRL B)

COLLECTORS menu functions...

PRESS	TO
^k3 k0 (or k5)	Use Daly detector as the collector. (shortcut: k5)
^k3 k1	Use Faraday cup as the collector. (shortcut: k5)
^k3 k2	Calibrate the gain of the Daly detector for the nuclide currently arriving at the collector.
^k3 k3	Change the enable/disable status of the Daly. (shortcut: CTRL D)

ISOTOPE-RATIO DATA menu functions...

PRESS	TO GET
^k4 k0	Take isotope-ratio data in the "manual" mode. (shortcut: k9)

^k4 k1	Enter names for all of the samples in the barrel.
^k4 k2	Printout a summary of one or more runs. (shortcut: RESULT)
^k4 k3	Display " " " " " " " . (shortcut: SHIFT-RESULT)
^k4 k4	Calculate weighted averages of one or more runs. (shortcut: CTRL A)
^k4 k5	Locate isotope-ratio data for one or more runs on the DATA disk. (shortcut: CTRL L)
^k4 k6	Display a list of the currently-defined sample-names. (shortcut: CTRL N)

SPIKES menu functions...

PRESS	TO GET
^k5 k0	Display data for one or more of the normalizable-element spikes that are defined and stored on the DATA disk.
^k5 k1	Define a new normalizable-element spike and store the spike-data on the DATA disk.

MASS-SPEC STATUS menu functions...

PRESS	TO GET
^k6 k0	Query the pressure in the source-can and the flight-tube (single query).
^k6 k1	Use the CRT as a stripchart for continuous monitoring of the pressure in the source-can and the flight-tube (figure 13).
^k6 k2	Query the high-voltage setting. (shortcut: CTRL V)
^k6 k3	Query the computer clock and display the current time and date.
^k6 k4	Set the time and/or date of the computer clock.

^k6 k5	Test the contacts for the filament-assemblies currently in the running and preheat positions.
^k6 k6	Test the contacts for all of the samples in the barrel (turns filament-currents off). (shortcut: CTRL B)
^k6 k7	Display the magnet and running data for the ELEMENT currently in use.
^k6 k8	Display the current focus-settings.

Other Shifted-Softkey Functions...

^k7 k0 through k8	Access functions for Run Variables and Standard-Run Variables.
^k8	Start automatic running if in the manual running mode, revert to manual running if in the automatic running mode.
^k9	Enable the KNOB (without the CONTROL key) as the filament-current controller for the filament-assemblies in both the sample and preheat positions.

Functions of Softkeys with the CONTROL Key:

-- Press CTRL-k1 through CTRL-k9 to jump up-mass 1 through 9 isotopes (the isotopes are those defined for the current ELEMENT).

-- Press CTRL-SHIFT-k1 through CTRL-SHIFT-k9 to jump down-mass 1 through 9 defined isotopes.

Functions of NON-Softkeys During the BMC:

PRESS	TO GET
CTRL A	Weighted averages of isotope-ratio data for one or more runs.
CTRL B	Test the filament contacts for all of the

samples in the barrel.

CTRL D	Change the enable/disable status of the Daly detector.
CTRL F	Manually focus the ion-optics using the KNOB.
CTRL G	Use the CRT graphics to continuously monitor the pressure in the source-can and flight-tube.
CTRL H	Query the computer's clock/calendar.
CTRL L	Locate run-data on the DATA disk.
CTRL N	Display a list of the currently-defined sample names on the CRT.
CTRL P	Do a graphics check of the peak-shape.
CTRL X	Invoke the pretty pattern-generating program that appears at the end of every automatic run series (from the Hewlett-Packard demo disk).
CTRL Z	Take zeroes for both the Faraday cup and the Daly detector (OK if a beam is present).
? or /	Restore the shifted-softkey menu and sample-name display to the CRT.
CTRL 1	Turns off the center filament of the sample in the running position (must be pressed twice within 0.5 seconds).
CTRL 2	Turns of the side filaments of the sample in the preheat position (must be pressed twice within ...).
CTRL 3	Turns of the center filaments of the sample in the running position (must be pressed twice...).
CTRL 4	Turns of the side filaments of the sample
+	Jump to the peak-top of the next-higher defined isotope.
-	Jump to the peak-top of the next-lower defined isotope.

Jump to the lower peak-side (halfway down the peak).

) Jump to the upper peak-side (halfway down the peak).

L arrow Jump to one-half mass below the current peak-top.

R arrow Jump to one-half mass above the current peak-top.

CTRL - Jump to the ^{187}Re peak from any isotope.

CTRL + From the ^{187}Re peak accessed with **CTRL -**, return to the original peak.

CTRL k1...k9 Jump to the Nth defined isotope above the current isotope

CTRL-SHIFT k1...k9 Jump to the Nth defined isotope below the current isotope.

CTRL * Do a complete beam-tuneup (center, focus ion-optics, optimize barrel, focus again).

Up-Arrow Increase the center-filament current by 0.01 amperes (add the **CONTROL** key to change by only 0.001 amperes).

Down-Arrow Decrease the center-filament current by 0.01 amperes (add the **CONTROL** key to change by only 0.001 amperes.

SHIFT Up-Arrow Increase the side-filament current by 0.01 amperes (add the **CONTROL** key to change by only 0.001 amperes.

SHIFT Down-Arrow Decrease the side-filament current by 0.01 amperes (add the **CONTROL** key to change by only 0.001 amperes.

ALPHA Switch from graphics CRT-display to alphanumeric. One press turns the ALPHA display on, the next turns the GRAPHICS display off.

GRAPHICS Switch from alphanumeric CRT-display to graphics. One press turns the GRAPHICS display on, the next turns the ALPHA display off.

DUMP ALPHA Dump the alphanumeric CRT-display to the printer.

DUMP GRAPHICS	Dump the graphics CRT-display to the printer.
CTRL /	Use a 1-second integration time while measuring the ion-beam.
CTRL ^	Use a 0.2-second integration time (standard) while measuring the ion-beam.
RESULT	Printout a Run Summary for one or more runs.
SHIFT-RESULT	Display a Run Summary for one or more runs.
RECALL	Revert to full-automatic running from where the full-automatic run left off. Active only if you temporarily exited automatic running.
SHIFT-RECALL	Revert to full-automatic running at the start of any run (defined in the **Run Variables**, of course). Active only if you temporarily exited from automatic running.
CLR LN or **CLR SCREEN**	Clear the CRT-display.
PAUSE	Pause the program. Can restart with **CONTINUE** (from where you paused the program), or with **RUN** (to re-start at the **bmc**).
INS LN	Dump the CRT-graphics to the printer, but first request a label to be added to the bottom of the graphics.
SHIFT-STEP	Restart **ANALYST** from the power-up state of the program (requests the user to check all switch-settings, etcetera).

STANDARD SETTINGS OF THE MASS-SPECTROMETER WHEN UNDER CONTROL OF ANALYST:

ANALYST requires that the mass-spectrometer switches be set to the following standard settings:

SET	TO
Pirani Ion-Gauge Trip Level	10^{-4}
Electromagnet Supply Programme	Digital
Electromagnet Supply Control	Field
System Monitor	Auto
Digital Integrator Offset	about 5.50 (to get a Faraday-cup zero of ~500 cps)
Digital Integrator Response	.03
Digital Integrator Gain	x1
FA3 Amplifier, Amps-Full-Scale	10^{-5}
" " , Gain	1
" " , Response Time	30 milliseconds
" " , Zero	adjust for a Daly zero of 400-600 cps
Brandenburg, Mains then Reset Button	depress
" , Local/Remote	Local
*Programmable Filament Supply, Centre Fil.	RESET, then ON
* " " " , Man/Auto	Auto
* " " " , EB/TH	TH
* " " " , Side Fils.	RESET, then ON
* " " " , " "	1+2
Programmable Deflection Unit, Mode	Auto
Programmable Focus Unit, Mode	Auto
" " " , Standby/On	ON
Beam Valve (on Flight Tube)	Open
Mains or Power Switches for:	
Pirani Ion-Gauge	ON
Electromagnet Supply	ON
Multiplier Supply	ON
Barrel-Motor Control	ON
Mains Distribution Electronics	ON
Mains Distribution Vacuum	ON
Digital Integrator	ON
FA3 Amplifier	ON
Brandenburg Power Supply	ON
Programmable Focus Unit	ON
Ion-Pump Power Supply	ON

*for both Sample-Filaments and Preheat-Filaments

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I am indebted to Kathy Simmons and M. Tatsumoto for their patient tolerance of early versions of this program and its precursors DBAT1B and DBAT2B, and for their valuable suggestions on how to improve the usefulness of the program; and to Ernie Wilson, for many useful and accurate answers as to just what is going on at the hardware and I/O levels of the computer/mass-spectrometer interface.

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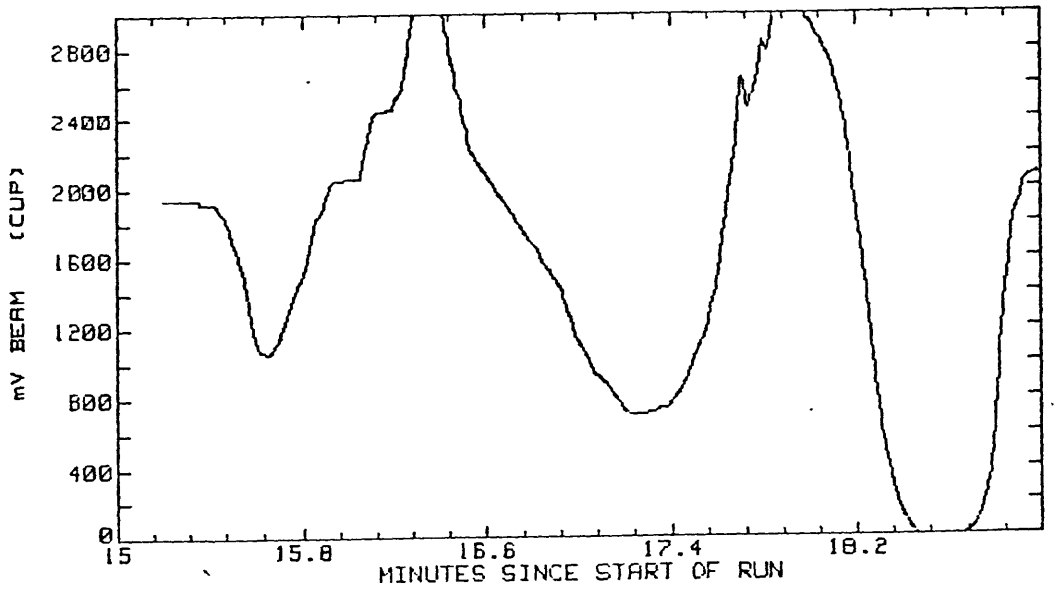


Figure 1

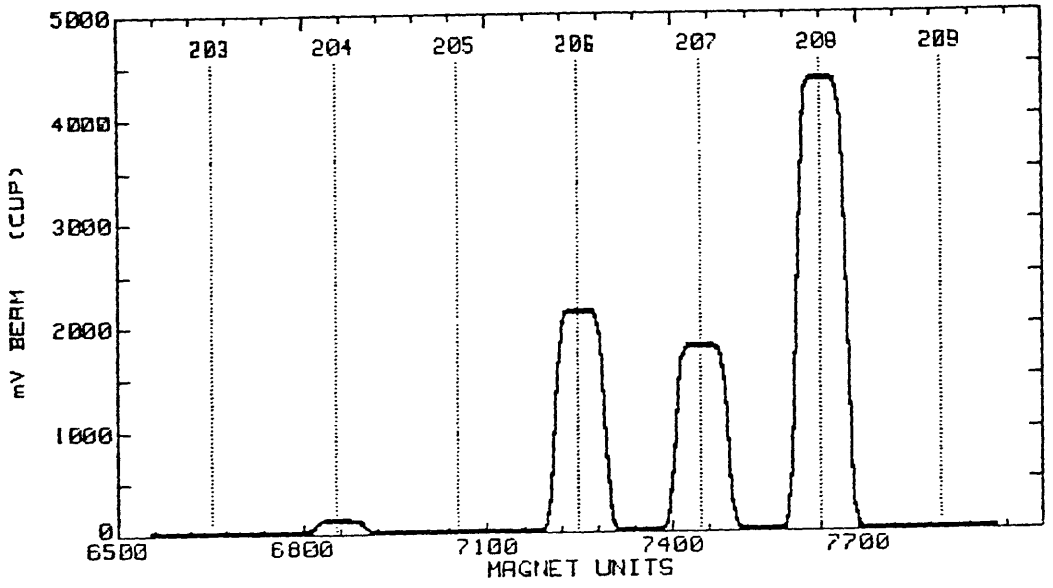


Figure 2

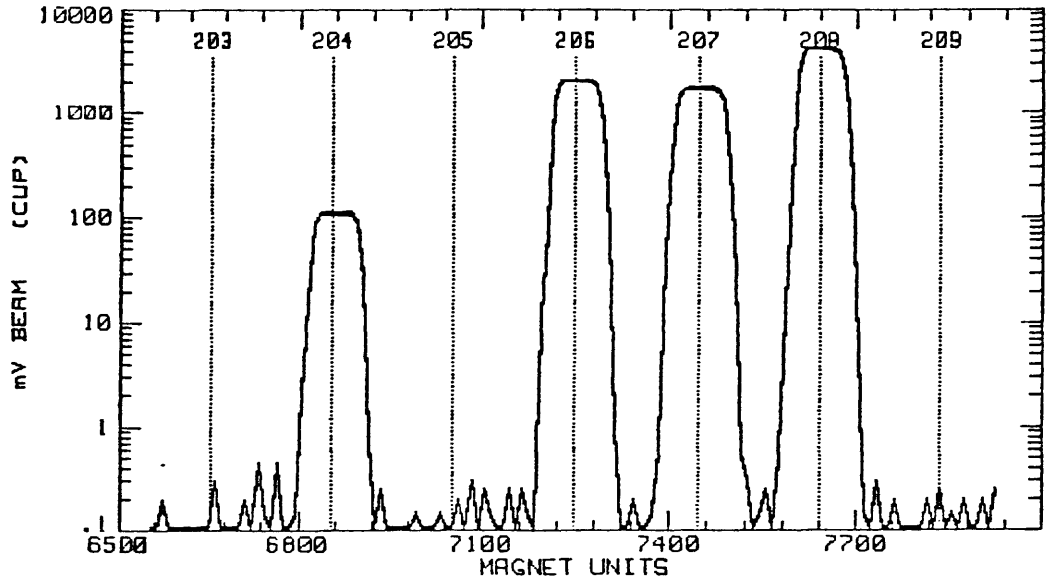


Figure 3

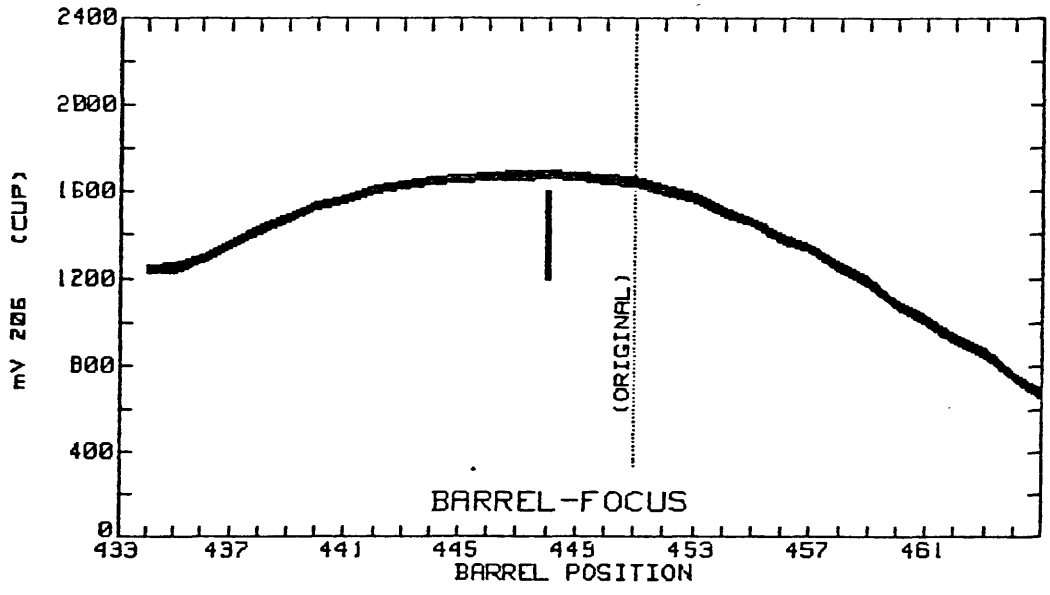


Figure 4

OTHER KEY-FUNCTIONS DEFINED DURING THE BMC

KEY	FUNCTION
? or /	-- SHOW DEFINITIONS OF SHIFTED SOFTKEYS (k0-k9) ON CRT
+	-- SWITCH MAGNET TO NEXT-HIGHER ISOTOPE
−	-- SWITCH MAGNET TO NEXT-LOWER ISOTOPE
←	-- SWITCH MAGNET 1/2 MASS LOWER (below-background)
→	-- SWITCH MAGNET 1/2 MASS HIGHER (above-background)
(	-- SWITCH MAGNET TO HALF-PEAK POSITION ABOVE PEAK-CENTER
)	-- SWITCH MAGNET TO HALF-PEAK POSITION BELOW PEAK-CENTER
^	- SWITCH MAGNET TO PEAK-TOP
CTL t	-- DO A COMPLETE BEAM TUNE-UP (center, focus, barrel)
RECALL	-- RESUME AUTOMATIC RUNNING WHERE YOU LEFT OFF
CTL−	-- SWITCH MAGNET TO Re-187
CTL+	-- SWITCH MAGNET FROM Re-187 TO PREVIOUS ISOTOPE
CTL 1	-- TURN OFF SAMPLE CENTER-FILAMENT (must press twice)
CTL 2	-- TURN OFF SAMPLE SIDE-FILAMENT
CTL 3	-- TURN OFF PREHEAT CENTER-FILAMENT
CTL 4	-- TURN OFF PREHEAT SIDE-FILAMENT

figure 5

```
XXXXXXXXXXXXXXXXXXXXXXXXX 09:57 A.M.   5 Nov 1984 XXXXXXXXXXXXXXXXXXXXXXXXX
SOURCE PRESSURE = 2.4E-9                    TUBE PRESSURE = 2.45E-9
BARREL# 1              BLOCK# 4 (of 4)        **CUP**          RUN#19
CENT. FIL.=2.134 AMPS                                        15 SETS
SAMPLE: AR-242-A-C82 Pb-COMP

ISOTOPES:              206   204
INTEGRATION-TIMES:       2    14
WAIT-TIMES:              1     3

FOCUS:   1-89  2-1  3-599  4-533  5-224  6-70  7-225
MAGNET:  (8)  206-7219  204-6823

 206     204     BACKGROUNDS: (cts per sec./std. dev.)
 171/3   171/6   below, before pk-tops
 175/4   172/5   above, before pk-tops
 173/5   171/6   below, after pk-tops
 173/6   171/6   above, after pk-tops
  1770 mV 206    46.6 mV 204
-------------------------------------------------------------------------------
(partial-block 206/204 = 37.9732 , sigma% obs. = .00999 %)
REJECTED 2 RATIO(S) OUT OF 10          TIME-CONSTANT CORRECTION = 57.5 PPM     BEAM-DECAY = .98 %/minute
-------------------------------------------------------------------------------
ISOTOPES:              208   206   207
INTEGRATION-TIMES:       3     3     5
WAIT-TIMES:              1     1     1

MAGNET:  (8)  208-7612  206-7220  207-7416

 208     206     207     BACKGROUNDS: (cts per sec./std. dev.)
 174/2   173/5   174/3   below, before pk-tops
 172/5   174/3   174/2   above, before pk-tops
 174/5   173/3   170/8   below, after pk-tops
 176/5   170/8   174/5   above, after pk-tops
  1670 mV 206    1710 mV 208     729 mV 207
-------------------------------------------------------------------------------
REJECTED 0 RATIO(S) OUT OF 14          TIME-CONSTANT CORRECTION =-4.39 PPM     BEAM-DECAY = .93 %/minute

  AVERAGE     AVERAGE     SIGMA%      SIGMA%      SIGMA%      SIGMA
  206/208     208/206      OBS.       THEOR.      MEAN        MEAN        DELTA%
  .97902      1.02143     (.0046)     .0082       .0025       2.5E-5      -.013
-------------------------------------------------------------------------------
REJECTED 3 RATIO(S) OUT OF 14          TIME-CONSTANT CORRECTION = 12.1 PPM     BEAM-DECAY = .93 %/minute

  AVERAGE     AVERAGE     SIGMA%      SIGMA%      SIGMA%      SIGMA
  206/207     207/206      OBS.       THEOR.      MEAN        MEAN        DELTA%
  2.29455     .435815     (.0035)     .0091       .0035       8.1E-5      (-.0053)
-------------------------------------------------------------------------------
ISOTOPES:              206   204
INTEGRATION-TIMES:       2    14
WAIT-TIMES:              1     3

MAGNET:  (8)  206-7222  204-6829

 206     204     BACKGROUNDS: (cts per sec./std. dev.)
 173/3   172/5   below, before pk-tops
 170/8   171/5   above, before pk-tops
 172/4   171/5   below, after pk-tops
 167/7   172/5   above, after pk-tops
  1590 mV 206    41.9 mV 204
-------------------------------------------------------------------------------
(partial-block 206/204 = 37.9893 , sigma% obs. = .0398 %)
REJECTED 0 RATIO(S) OUT OF 10          TIME-CONSTANT CORRECTION = 57.3 PPM     BEAM-DECAY = .87 %/minute

  AVERAGE     AVERAGE     SIGMA%      SIGMA%      SIGMA%      SIGMA
  206/204     204/206      OBS.       THEOR.      MEAN        MEAN        DELTA%
  37.9799     .0263297    (.014)      .028        .013        .005        (+.006)
-------------------------------------------------------------------------------
XXXXXXXXXXXXXXXXXXXXXXXXX 10:15 A.M.   5 Nov 1984 XXXXXXXXXXXXXXXXXXXXXXXXX
```

Figure 6

XXXXXXXXXXXXXXXXXXXXXXXXXX 11:55 P.M. 24 Nov 1984 XXXXXXXXXXXXXXXXXXXXXXXXXX
SOURCE PRESSURE = 7.91E-9 TUBE PRESSURE = 6.09E-9
BARREL# 8 BLOCK# 8 (of 20) **CUP** RUN# 2
CENT. FIL.=4.284 AMPS SIDE-FIL.=2.15 AMPS 20 SETS
SAMPLE: CIT nNdB COMP STD 200 nG

ISOTOPES:	144	146	143	145	150
INTEGRATION-TIMES:	3	3	4	5	5
WAIT-TIMES:	1	1	1	1	1

FOCUS: 1-128 2-0 3-574 4-545 5-194 6-139 7-335 8-466
MAGNET: (7) 144-3085 146-3546 143-2856 145-3318 150-4454 147-3773 147-3773

144	146	143	145	150	147	BACKGROUNDS: (cts per sec./std. dev.)
496/4	494/3	491/3	493/5	492/6	489/4	below, before pk-tops
493/5	489/4	496/4	494/3	491/3	493/3	above, before pk-tops
496/4	493/5	493/4	494/6	493/6	491/3	below, after pk-tops
494/6	491/3	496/4	493/5	493/6	493/4	above, after pk-tops

Average 147 peak was .00698 mV Correction on 144 = 6.5E-5 %
Average 147 peak was .00639 mV Correction on 150 = .00059 %
2140 mV 144 1550 mV 146 1100 mV 143 747 mV 145 507 mV 150

REJECTED 0 RATIO(S) OUT OF 19 TIME-CONSTANT CORRECTION =-9.76 PPM BEAM-GROWTH = .46 %/minute

AVERAGE 146/144	AVERAGE 144/146	SIGMA% OBS.	SIGMA% THEOR.	SIGMA% MEAN	SIGMA MEAN	DELTA%
.722405	1.38427	.013	.008	.0033	2.4E-5	+.047

REJECTED 1 RATIO(S) OUT OF 19 TIME-CONSTANT CORRECTION =-12.8 PPM BEAM-GROWTH = .46 %/minute
MASS-DISCRIMINATION CORRECTION WAS -.0352 %/A.M.U. (discr.-raw ratio was .511731)

AVERAGE 143/144	AVERAGE 144/143	SIGMA% OBS.	SIGMA% THEOR.	SIGMA% MEAN	SIGMA MEAN	DELTA%
.511912	1.95346	(.01)	.0082	.0035	1.8E-5	(+.00068)

REJECTED 2 RATIO(S) OUT OF 19 TIME-CONSTANT CORRECTION =-14.5 PPM BEAM-GROWTH = .46 %/minute
MASS-DISCRIMINATION CORRECTION WAS -.0352 %/A.M.U. (discr.-raw ratio was .348517)

AVERAGE 145/144	AVERAGE 144/145	SIGMA% OBS.	SIGMA% THEOR.	SIGMA% MEAN	SIGMA MEAN	DELTA%
.348395	2.8703	(.01)	.0088	.004	1.4E-5	(-.0078)

REJECTED 1 RATIO(S) OUT OF 19 TIME-CONSTANT CORRECTION =-15.1 PPM BEAM-GROWTH = .46 %/minute
MASS-DISCRIMINATION CORRECTION WAS -.0353 %/A.M.U. (discr.-raw ratio was .236937)

AVERAGE 150/144	AVERAGE 144/150	SIGMA% OBS.	SIGMA% THEOR.	SIGMA% MEAN	SIGMA MEAN	DELTA%
.236446	4.22929	.013	.01	.011	2.6E-5	(-.015)

XXXXXXXXXXXXXXXXXXXXXXXXXX 12:08 A.M. 25 Nov 1984 XXXXXXXXXXXXXXXXXXXXXXXXXX

Figure 7

```
XXXXXXXXXXXXXXXXXXXXXXXXXXX 4:18 P.M.  29 Oct 1984 XXXXXXXXXXXXXXXXXXXXXXXXXXX
SOURCE PRESSURE = 8.14E-9                    TUBE PRESSURE = 5.07E-9
BARREL# 14              BLOCK#  3  (of 5)      **CUP**          RUN#25
CENT. FIL.=4.268 AMPS                                        10 SETS
SAMPLE: AR-KN-A3 U-CONC

ISOTOPES:              238    235
INTEGRATION-TIMES:       2      8
WAIT-TIMES:              1      2

TUBES:   1-52  2-117  3-605  4-520  5-80  6-93  7-478
OFFSET:  (9)  238-4413  235-3856

 238      235      BACKGROUNDS: (cts per sec./std. dev.)
456/4    456/4     below, after pk-tops
467/6    467/6     above, after pk-tops
 1180 mV 238    138 mV 235
-------------------------------------------------------------------------------
REJECTED 0 RATIO(S) OUT OF 9      TIME-CONSTANT CORRECTION = 31.6 PPM      BEAM-DECAY = 3 %/minute

  AVERAGE      AVERAGE      SIGMA%       SIGMA%       SIGMA%       SIGMA
  238/235      235/238       OBS.        THEOR.       MEAN         MEAN        DELTA%
  8.5929       .116375      (.021)        .019         .011        .00097      (+.026)
-------------------------------------------------------------------------------
XXXXXXXXXXXXXXXXXXXXXXXXXXX 4:21 P.M.  29 Oct 1984 XXXXXXXXXXXXXXXXXXXXXXXXXXX
```

Figure 8

DATA SUMMARY FOR BARREL# 8 RUN# 2 25 Nov 1984
CIT nNdB COMP STD 200 n6

BLOCK	RATIO	AVERAGE	SIGMA%	SIGMAMEAN%	DELTA%	mV REF-PK	FilCurr	Minute
1	146/144	.720097	.02	.00439		1820	2.229	62.72
	143/144	.511885	.014	.00396				
	145/144	.348446	(.0092)	.00348				
	150/144	.236537	(.0096)	.0138				
2	146/144	.720566	.011	.00263	+.065	2330	2.229	75.16
	143/144	.51191	.024	.00577	(+.0049)			
	145/144	.348399	.019	.00487	-.014			
	150/144	.236484	.024	.00988	(-.022)			
3	146/144	.720989	.0091	.00238	+.059	2780	2.229	86.64
	143/144	.511925	(.0085)	.0027	(+.0029)			
	145/144	.348426	.013	.0038	(+.0077)			
	150/144	.236474	.012	.00807	(-.0041)			
4	146/144	.721434	.013	.00288	+.062	2180	2.189	99.5
	143/144	.511918	.011	.00306	(-.0013)			
	145/144	.348422	(.01)	.00318	(-.001)			
	150/144	.236464	(.0078)	.00935	(-.0046)			
5	146/144	.72161	.016	.00352	+.024	2380	2.189	111.1
	143/144	.511874	.014	.00361	(-.0088)			
	145/144	.348398	.016	.0042	(-.0069)			
	150/144	.236501	.022	.012	(+.016)			
6	146/144	.72186	(.0091)	.0021	+.035	2620	2.189	122.2
	143/144	.511925	(.0086)	.00231	+.01			
	145/144	.348418	(.0087)	.00256	(+.0057)			
	150/144	.236473	.012	.00723	(-.012)			
7	146/144	.722065	(.0078)	.00212	+.028	2890	2.189	133.7
	143/144	.511908	.0091	.00272	(-.0034)			
	145/144	.348422	.012	.00348	(+.0012)			
	150/144	.236481	.012	.00734	(+.0036)			
8	146/144	.722405	.013	.00333	+.047	2140	2.15	147.9
	143/144	.511912	(.01)	.00351	(+.00068)			
	145/144	.348395	(.01)	.00398	(-.0078)			
	150/144	.236446	.013	.0109	(-.015)			
9	146/144	.722508	.013	.00339	+.014	2280	2.15	160.7
	143/144	.511924	.014	.00417	(+.0025)			
	145/144	.348411	.013	.00452	(+.0045)			
	150/144	.236462	.016	.0113	(+.0066)			
10	146/144	.722485	.014	.00349	(-.0032)	2450	2.15	172.6
	143/144	.511888	.012	.00366	(-.007)			
	145/144	.348426	.013	.00408	(+.0045)			
	150/144	.236521	(.0091)	.0111	(+.025)			
11	146/144	.722571	.012	.00317	+.012	2620	2.15	184.5
	143/144	.511933	(.0077)	.00302	(+.0087)			
	145/144	.348405	(.0082)	.00332	(-.006)			
	150/144	.236447	(.0097)	.0101	-.031			
12	146/144	.722577	(.0057)	.00193	(+.00087)	2820	2.15	196.9
	143/144	.51191	.0098	.00291	(-.0044)			
	145/144	.348418	(.0068)	.00292	(+.0035)			
	150/144	.236484	(.01)	.00668	(+.016)			

Figure 9

Weighted Averages Printout

SAMPLE: CIT nNdB COMP STD 200 nG
BARREL# 8 RUN# 2

BLOCK#	143/144	SIGMAMEAN%
1	.511885	.00396
2	.51191	.00577
3	.511925	.0027
4	.511918	.00306
5	.511874	.00361
6	.511925	.00231
7	.511908	.00272
8	.511912	.00351
9	.511924	.00417
10	.511888	.00366
11	.511933	.00302
12	.51191	.00291
13	.511916	.00399
14	.511929	.00417
15	.511938	.00363
16	.511881	.00463
17	.511814	.00887
18	.511885	.0072
19	.511887	.00461
20	.511923	.00289

REJECTED: .511814

WTD AVERAGE 143/144 =.5119133 +/- 8.6E-6 (.0017%) (95% CONF. LIMIT)

INTERNAL SIGMAMEAN = .00079% EST. TOTAL SIGMAMEAN =.0008%
M.S.W.D. = 1.04 PROBABILITY = .41

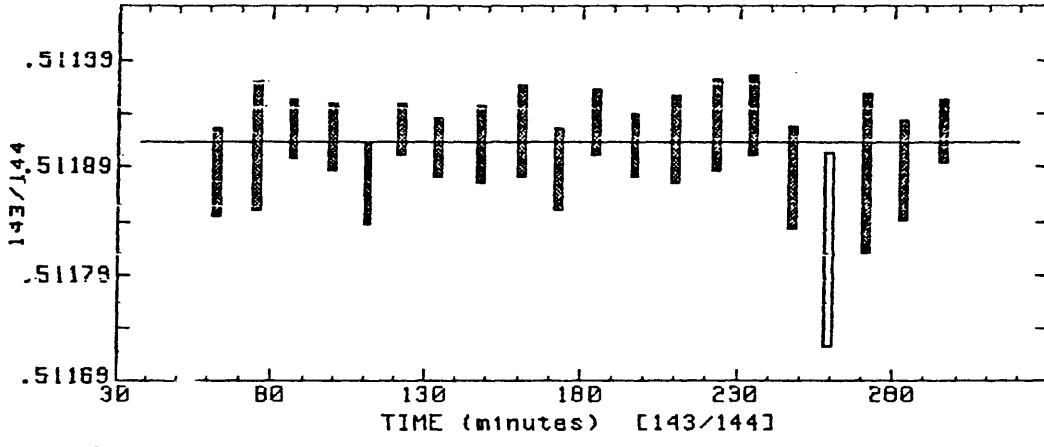


Figure 10

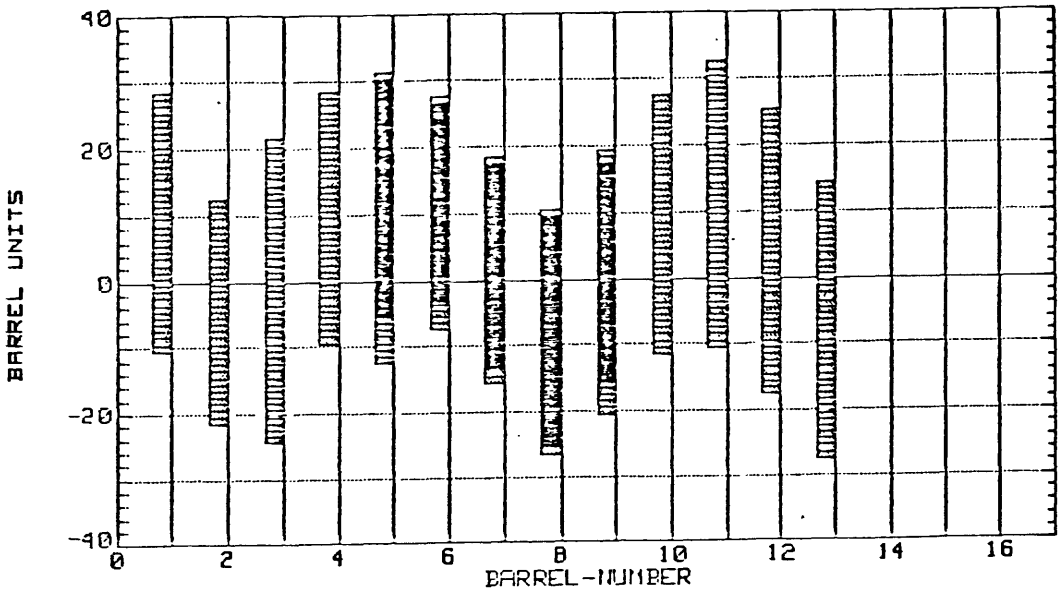


Figure 11

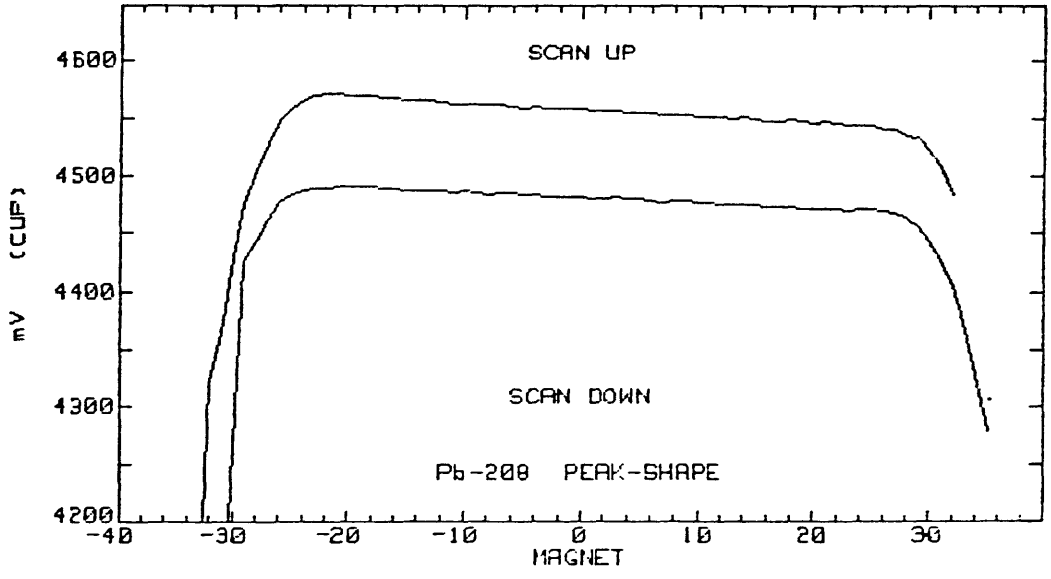
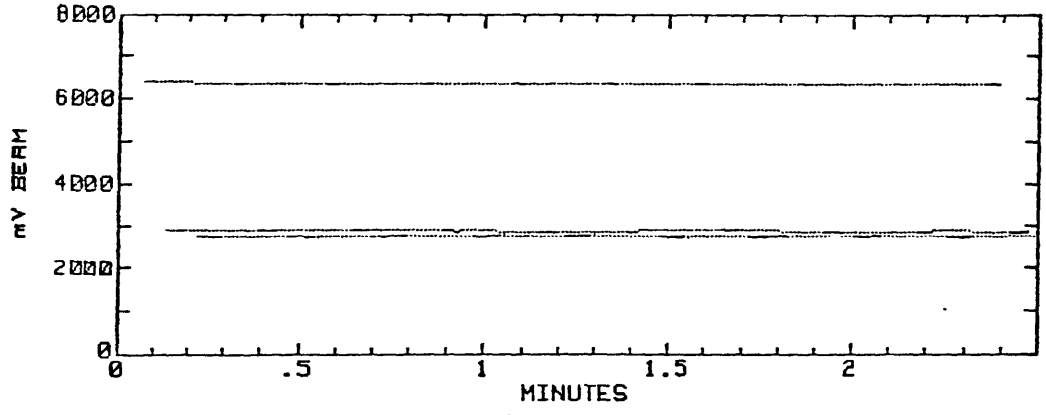


Figure 12

BARREL# 13 BLOCK# 4 (of 4) **CUP** RUN# 8
CENT. FIL.=2.033 AMPS 10 SETS
SAMPLE: JW84-20 PB-COMP



206/208 206/207
.45226-.036% 1.0489-.03%

beam-decay= .33%/min.

207 SET# 10 2722.63 mV 3

Figure 13

RUN-VARIABLES: **********

BARREL#	SAMPLE NAME	ISOTOPES				ELEMENT
1	9/21/84 #1 MOT 01 Son	206	207	208	204	Pb
2	HLR-986 MONMAG #2	206	207	208		Pb
3	HF BLANK #1, 2/4,85	206	207	208		Pb
6	NBS-987 #4a, 12/7/84	86	87	88		Sr
5	BCR-1 spike calibration, 2/16/85	86	87	88	84	Sr
8	ME/KL 1-84(-325+100) PB(U) REM OF SA	87	85			Rb
12	HUL-907 K-feldspar #1, unspiked	86	87	88		Sr
16	La Jolla Nd Standard, 100 nanograms on Ta sides					
		144	143	145	146	Nd
15	JW84-23 PB-COMP	144	143	146	150	Nd
14	HUL-089a split #3, spiked Sn	147	148	149		Sn
12	OJU-389 #4 irradiated U-ore std, double-spiked					
		238	233	236		U

	VARIABLE	BARREL-NUMBER										
		1	2	3	6	5	8	12	16	15	14	12
1	SINGLE(1)/TRIPLE(3)	1	1	1	1	3	3	3	3	3	3	3
2	FOCUSING ISOTOPE	--	--	--	--	88	85	88	187	187	187	187
3	CENTER-FIL BEAM (V)	--	--	--	--	.01	.01	.01	.01	.01	.01	.15
4	INITIAL CF-CURR.(A)	--	--	--	--	3.8	2.9	4.4	4.4	4.4	4.2	4.4
5	DALY (0/1/2)	1	1	1	2	2	1	2	2	2	2	2
6	CURRENT-1	1.9	1.9	1.9	2.1	2.1	.4	.4	2.1	2.1	1.4	1.5
7	RATE-1	10	10	20	10	10	10	2	5	5	5	5
8	UNIT-1 (MIN.)	1	1	0	0	0	0	0	10	10	0	5
9	CURRENT-2	2.2	2.2	2.2	2.4	2.4	.5	.5	2.3	2.3	1.6	1.7
10	RATE-2	5	5	10	.15	.15	2	.5	.2	.2	.15	1
11	UNIT-2 (MIN.)	0	0	0	0	10	5	0	5	5	5	5
12	DATA UNIT (MIN.)	10	0	0	0	5	5	0	0	0	0	0
13	ABORT-CURRENT	3.2	3.2	3.2	3.4	3.4	.9	.9	3.4	3.4	3.2	2.6
14	MIN BEAM (V)	3	6	.1	1.5	1	.5	1.5	.8	.8	.4	1
15	MAX. BEAM (V)	9	9	.3	3.5	3	9	3.5	3	3	3	4
16	DEFAULT CURRENT	2.5	2.5	2.5	2.8	2.8	.6	.7	2.5	2.5	1.9	2
17	DEFAULT BEAM (V)	.8	.05	.03	1	.5	.01	1	.4	.4	.2	.3
18	FIL. INCREASE/BLOCK	.01	.01	.03	0	0	0	0	0	0	0	.01
19	MIN. #BLOCKS	3	3	2	8	6	3	6	15	15	10	4
20	MAX. #BLOCKS	6	5	4	20	20	6	10	25	25	20	9
21	MAX SIGMAMEAN(%)	.02	.03	.2	-.012	.012	.05	-.05	.01	.01	.015	.03
22	#SETS/BLOCK	15	15	10	20	30	12	20	25	25	20	20
23	MAX. GROWTH (%/MIN)	--	--	--	2.5	2.5	3.5	2.5	3	3	3	--
24	PREHEAT CF (A)	--	--	--	--	2.2	2	3.2	4.2	4.2	--	3.7
25	PREHEAT SF (A)	--	--	--	--	1.3	.3	1.8	1.6	1.6	--	1.9
26	NORMSPIKE#	--	--	--	--	2	--	--	--	3	1	7
		1	2	3	4	5	6	7	8	9	10	11
	RUN-NUMBER											

Figure 14

STANDARD-RUN VARIABLES: **********

STANDARD-RUN#	ELEM	NAME	ISOTOPES			
1	PB	Pb-common	206	207	208	204
2	PB	PB 678	206	207	208	
3	PB	PB 6/4	206	204		
4	PB	PB blnk 1	206	207	208	
5	PB	PB blnk 2	206	207	208	204
6	U	U single	238	235		
7	TH	TH single	232	230		
8	U	U triple	238	235		
9	TH	TH triple	232	230		
10	SR	SR 678	86	87	88	
11	SR	SR spkd1	86	87	88	84
12	FREE	FREE	87	85		
13	RB	RB triple	87	85		
14	FREE	FREE	86	88	87	
15	SR	Sr triple	86	87	88	
16	SR	Sr triple	86	87	88	84
17	SM(KY)	Sm SPIKE	147	149		
18	ND(KY)	ND SPIKE	146	145		
19	ND	Nd TRIPLE	144	143	145	146
20	SM	Sm (KRS)	147	148	149	
21	U	U_33,36	238	233	236	

VARIABLE		STANDARD-RUN NUMBER															
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1	SINGLE(1)/TRIPLE(3)	1	1	1	1	1	1	1	3	3	1	1	1	3	1	3	3
2	FOCUSING ISOTOPE	--	--	--	--	--	--	--	187	187	--	--	--	85	--	88	88
3	CENTER-FIL BEAM (U)	--	--	--	--	--	--	--	.15	.15	--	--	--	.01	--	.01	.01
4	INITIAL CF-CURR.(A)	--	--	--	--	--	--	--	4.4	4.4	--	--	--	2.9	--	4.4	4.4
5	DALY (0/1/2)	1	1	1	1	1	1	1	1	1	2	2	1	1	2	2	2
6	CURRENT-1	1.9	1.9	0	1.9	1.9	3.9	4.1	1.5	1.7	2.1	2.1	.8	.4	2.1	.4	.4
7	RATE-1	10	10	5	20	20	10	100	10	100	10	10	10	10	10	2	2
8	WAIT-1 (MIN.)	1	1	0	0	0	0	0	5	0	0	0	0	0	5	0	0
9	CURRENT-2	2.2	2.2	2.2	2.2	2.2	4.1	4.5	1.7	1.9	2.4	2.4	.9	.5	2.4	.5	.5
10	RATE-2	5	5	20	10	20	10	5	.8	1	.15	.15	2	2	.15	.5	.5
11	WAIT-2 (MIN.)	0	0	0	0	0	0	0	0	0	0	0	10	5	5	0	0
12	DATA WAIT (MIN.)	10	0	0	0	0	0	0	0	0	0	0	0	5	0	0	0
13	ABORT-CURRENT	3.2	3.2	3.2	3.2	3.2	5.1	5.3	2.6	2.6	3.4	3.4	2.2	.9	3.4	.9	.9
14	MIN BEAM (U)	3	6	5	.1	1	.5	.01	2	.01	1.5	1	1	.5	1	1.5	2
15	MAX. BEAM (U)	9	9	8	.3	8	9	9	9	9	3.5	3	9	9	3	3.5	5
16	DEFAULT CURRENT	2.5	2.5	2.5	2.5	2.5	4.3	4.8	2	2.1	2.8	2.8	1.2	.6	2.8	.7	.7
17	DEFAULT BEAM (U)	.8	.05	.1	.03	.05	.05	.001	1.5	.001	1	.5	.01	.01	.5	1	1
18	FIL. INCREASE/BLOCK	.01	.01	.03	.03	.03	0	.02	0	.02	0	0	0	0	0	0	0
19	MIN. #BLOCKS	3	3	3	2	1	3	3	3	3	8	6	3	3	8	6	10
20	MAX. #BLOCKS	6	5	6	4	3	6	6	6	6	20	20	6	6	20	10	20
21	MAX SIGMA/MEAN(%)	.02	.03	.05	.2	.2	.2	.1	.06	.1	-.012	.012	.05	.05	.01	-.05	.01
22	#SETS/BLOCK	15	15	12	10	10	15	10	15	10	20	20	10	12	20	20	20
23	MAX. GROWTH (%/MIN)	--	--	--	--	--	--	--	--	--	2.5	2.5	7	3.5	2.2	2.5	2.5
24	PREHEAT CF (A)	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
25	PREHEAT SF (A)	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
26	NORMSPIKE#	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--

Figure 15

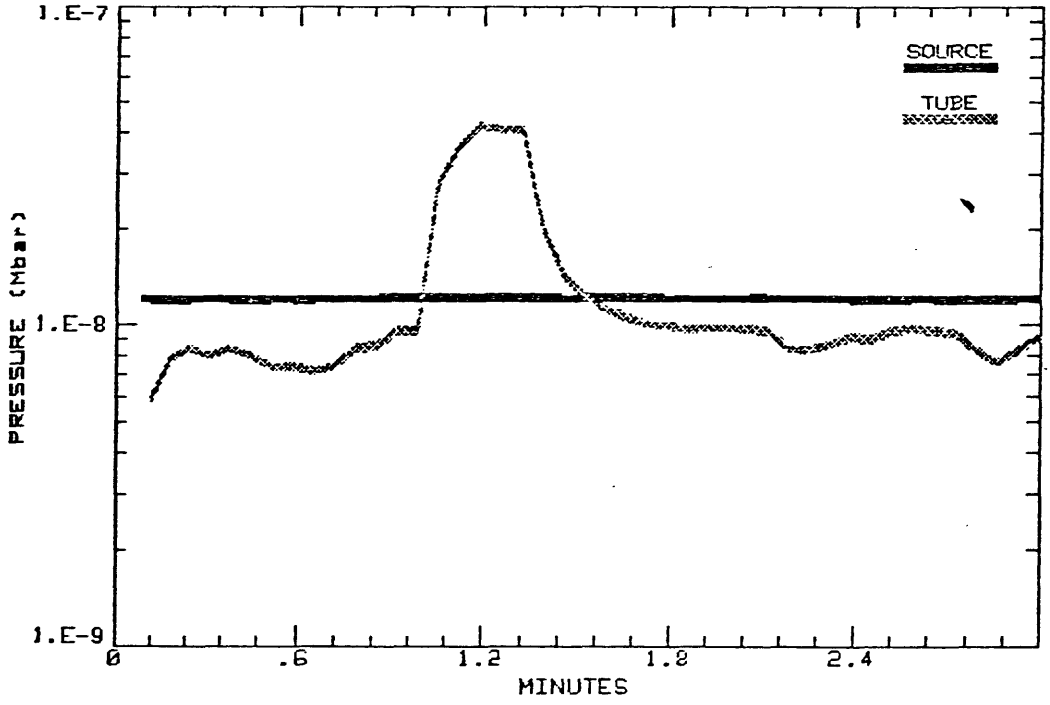


Figure 16