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PBDAT — A Program for Reduction of Pb-U-Th Isotope Data, for Use with HP-86/87 Microcomputers

by

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INTRODUCTION

PBDAT is a computer program in HP Series-80 BASIC that converts raw laboratory and mass-spectrometer data for Pb-U-Th studies into blank- and fractionation-corrected isotope ratios and concentrations, together with all associated errors and error-correlations. The algorithms used for error and error-correlation estimates are those given in Ludwig (1980), and are generally more accurate than those commonly used.

Raw data for PBDAT may be entered either from the computer keyboard and reduced one sample at a time, or can be reduced in batches from VISICALC-created datafiles of the raw data. Batch-reduced files can either be converted into a VISICALC-compatible format, and stored as VISICALC-readable reduced-data files, or stored as simple numeric files. These reduced-data files can then be used as direct input to the isotope-oriented plotting programs ISOPLOT, CPLOT, and PBPLOT (Ludwig, 1983).

PBDAT is flexible in its requirements for input-data format (for example, whether the samples were aliquoted after dissolution or total-spiked for one or more elements, and whether a Pb-208,Pb-206, or Pb-205 spike was used), so that it is suitable for a variety of isotopic procedures. Data for spikes, fractionation, and some basic uncertainties are created by the program and stored on a disk, so that different users can easily use different spike, fractionation, and error data without editing the program itself. The format of the output of the program is designed to be readable (without excess significant figures or unnecessary scientific notation) and compact, without sacrificing useful parameters.

Except for structuring the VISICALC data files, the program can be used without extensive reference to this documentation, as HELP screens are available at several points in the program. The program itself is reasonably transparent and self-documenting, so that other users should be able to maintain and upgrade the code without an unreasonable amount of effort.

HARDWARE REQUIRED

The program requires a Hewlett-Packard HP-86 or HP-87 microcomputer with a disk drive, at least 128 kbytes of memory, and the Advanced-Programming ROM. Also, for batch-processing of data, the VISICALC PLUS program from Hewlett-Packard is necessary.

USING THE COMPUTER and DATA-INPUT CONVENTIONS

Two peculiarities of the HP-86/87 computers must be understood. First, if you touch a key on the keyboard while the program is running (but not while it is waiting for you to type in a reponse), the computer will beep and stop running. To resume operation, just press the CONT key. Second, after starting the program by pressing the RUN key, the calculations will be significantly slower the first time the computer performs a given part of the program. After a given routine has been done once, it will be accomplished much faster during subsequent passes.

When the CRT requests input of several values, a typical prompt format might look like,

variable# 1, variable# 2 [,variable #3 [,variable #4]]

Commas separate different parameters for input, and brackets enclose parameters whose input is optional. The above example requests you to type in an least 2, but up to 4, values, separated by commas. Variables 1 and 2 must be entered (you enter a response by pressing the END LINE key after typing it in), whereas variables 3 and 4 are optional. If you enter 3 values, the third value will be assigned to variable #3, as variable #4 is the most-deeply "nested" in brackets.

STARTING UP

Put the disk containing the PBDAT program in one of the disk drives and start the program by typing in CHAIN PBDAT (assuming the disk is in the default drive). After loading the program, about 10 seconds is required for the pre-run initialization. Before you can start reducing your own data, you'll have to define a "LabData File" containing information on your spikes, blanks, and expected mass-discrimination, but for just getting familiar with the program, you can use the

default LabData File that should be stored along with the program.

The first display that will appear on the CRT will be a row of boxes with the labels listed below. These boxes indicate the functions of the 14 "Special Function Keys" (k1 - k14) that are positioned just below the CRT. During this initial display, the Special Function Keys are defined as follows (note that the default options are enclosed in asterisks):

KEY#	LABEL	FUNCTION
k1	*CRT*	(Default) Use the CRT as the printing device, rather than the printer.
k2	PRINT	Use the printer as the printing device.
k3	*KEYBOARD*	(Default) Input data from the keyboard rather than a VISICALC file.
k4	DATAFILE	Input data from a VISICALC data-file rather than from the keyboard.
k5	CHANGE Pb0	Enter new values for the initial-Pb isotopic composition (radiogenic leads only).
k6	VISICALC	Load and invoke the VISICALC program.
k7	*Pb-208*	(Default) Assume a Pb-208 or Pb-206 spike, rather than a Pb-205 spike.
k14	Pb-205	Assume a mixed Pb-205/U-235/Th-230 spike rather than a Pb-208 spike.
k11	MORE DFRED	(Appears only if you have just completed reduction of some data-file data) Continue reduction of more data from a data file.
k12	LABDATA	Edit, redefine, or replace the LabData File in memory (the LabData File contains the information on spike isotopes, blanks, and mass-discrimination during mass-spectrometer runs).
k13	HELP	Display a HELP screen with information

about how the program is used, including definitions of these special-function keys.

Before starting to enter data (again, I'll discuss defining your own Lab Datafile later), you'll need to check that the default options (those enclosed in asterisks) are the ones you want: CRT output only (that is, no printer output), and a Pb-208 spiked sample. To request a printed output, just press the PRINT key (k2), and to specify a sample spiked with a mixed Pb-205/U-235/Th-230 spike just press the Pb-205 key (k14). Then, to start entering your raw data, press the *KEYBOARD* key (k3).

ENTERING DATA FROM THE KEYBOARD

Pb-208 Spiked Samples:

For samples spiked with a Pb-208 spike (or Pb-206 spike - both are suitable), the following queries will appear after pressing the *KEYBOARD* key. First, after the CRT clears, the query will be,

(Brackets indicate optional input)
(enter H for help with any query)

SAMPLE NAME (<= 18 CHAR.)?

Type in a name for the sample, using no more than 18 characters, and press END LINE to enter the name.

The next query will be,

[GRAMS OF SAMPLE [, TOTAL ALIQUOT]]?

The total-aliquot weight is the weight of the total dissolved solution of the sample. You only need to enter a value for the total-aliquot weight if you did't use all of the dissolved solution for the Pb-spiked plus Pb-unspiked aliquots. For example, if the total-aliquot were 5 grams, the Pb-spiked aliquot 2 grams and the Pb-unspiked aliquot 3 grams, you needn't enter a value for the total-aliquot weight. Also, if the sample were

total-spiked for Pb and U(Th), a total-aliquot weight would not be required. However, if only part of the total aliquot were used - for example, a total aliquot of 50 grams, a Pb-spiked aliquot of 1 gram and a Pb-unspiked aliquot of 2 grams - then you would need to enter the total-aliquot weight.

The GRAMS OF SAMPLE value can also be omitted (just press END LINE) if the sample were unweighed or if a weight were irrelevant (for example, a loading blank).

The next query will be,

(if total-spiked for U-[Th] but not Pb, enter latter value as negative)

GRAMS OF [[UNSPIKED ALIQUOT,] SPIKED ALIQUOT]?

If the sample were total-spiked for Pb and U(Th), no values need be entered (just press END LINE). Usually, you will need to enter 2 values corresponding to the weights of the Pb-unspiked aliquot and the Pb-spiked aliquot. If the Pb-spiked aliquot weight is entered as a positive value, the program will assume that the Pb-spiked aliquot was also spiked for U (and Th, if used). If the Pb-spiked aliquot weight is entered as a negative value, the absolute value of that number will be used as the Pb-spike weight, and the program will assume that the sample were total-spiked for U(Th). If you enter only 1 value in response to the above query, the program will take it to be the spiked-aliquot weight, and assume that no Pb-unspiked aliquot exists.

The next query will be,

GRAMS SPIKED OF: Pb-208 [, U-235 [, Th-230]]?

Enter the weights of the spike(s) added to the aliquots. If you enter only 1 value, it will be taken as the Pb-208 spike weight; 2 values will be taken as the Pb-208 and U-235 spike weights; and 3 values will be taken as the Pb-208, U-235, and Th-230 spike weights. If your U and Th spikes are mixed, you will still need to include a separate spike weight for Th, even though it will be the same as the U-spike weight. Similarly, if your spike is a mixed Pb-U(-Th) spike, you'll have to

include at least 2 values.

The next query will be,

Pb-UNSPIKED ALIQUOT:
[206/204,%err, 206/207,%err,] 206/208,%err?

Normally, you'll need to enter 6 values, corresponding to the 3 ratios and their uncertainties. The "%err" values must be the uncertainty in the ratio from the mass-spectrometer run alone, in percent and at the 2-sigma/95%-confidence level. The ratios must not be corrected for mass-discrimination, and their uncertainties must not include the uncertainty due to the imperfectly known mass-discrimination of the mass-spectrometer run.

If you have useable 206/204 and 206/207 (as well as 206/208) data from the Pb-spiked aliquot, but no useable 206/207 and/or 206/204 from the Pb-unspiked aliquot, enter only 2 values - the estimated 206/208 ratio of the unspiked sample (not including effects of blank-Pb or mass-discrimination), and the estimated uncertainty in the estimate. This is, of course, the usual situation for blanks, and occasionally the situation for samples where the Pb-unspiked run failed for some reason. If the sample were not under-spiked, and if your estimate of the unspiked 206/208 ratio were not too far off, you should still be able to get adequate Pb concentrations and isotope ratios from this type of input.

The next query will be,

Pb-SPIKED ALIQUOT:
[[206/204,%err,] 206/207,%err,] 206/208,%err?

If you entered only the estimated 206/208 ratio of the Pb-unspiked aliquot, you must enter all 6 values for this query. Otherwise, only the 2 values for the 206/208 and its uncertainty are required. This is adequate and appropriate, for example, if the Pb of the sample were a common-Pb. If the Pb of the sample were a radiogenic Pb, however, you should always include data for the observed 206/207 of the Pb-spiked aliquot. If this is done (4 values entered), the program will use the difference between the Pb-spiked and Pb-unspiked 206/207 ratios as an index of the common-Pb contamination in the Pb-spiked run. At the least, this approach gives a more accurate estimate of the Pb

concentration of the sample, since the ratio of contamination to sample Pb for the Pb-spiked aliquot is generally greater than for the Pb-unspiked aliquot. Also, because the output will show the calculated amount of contaminant common-Pb in the Pb-spiked run, any spot contamination or inaccurate estimates of contamination will be effectively monitored.

If complete Pb-unspiked data (206/204, 206/207, and 206/208) were entered, the Pb-spiked 206/204 data would not be used for calculations (though it would appear on the printout).

The next query will be,

BLANKS (in nanograms): Pb [,U [,Th]]?

Enter 1, 2, or 3 values corresponding to the blanks for each element. The Pb-blank pertains to the Pb-unspiked aliquot only, and the U and Th blanks to the U(-Th)-spiked aliquot only.

The final query will be,

(Note that errors are to be entered as absolute, not percent)

(enter H for help)

INITIAL-Pb: [206/204 [,err] 207/204 [,err] 208/204 [,err] Rho(6/4-7/4)]?

This query will appear only for the first set of data that you enter; The program assumes that any subsequent samples share the last-entered initial-Pb ratios. If for any sample (after the first one that was reduced) you wish to use a new initial-Pb, press the CHANGEPbO key during the initial display.

If the sample contained only common-Pb, or if you are not interested in the U-Th-Pb or Pb-Pb apparent ages of the sample, just press END LINE . Otherwise, enter all 7 values of your estimate of the initial-Pb of the sample (the initial-Pb is the Pb that the sample was "born" with). Enter the errors as absolute values, not as percent values. "Rho(6/4-7/4)" is the error correlation between the 206/204 and 207/204 values. You can calculate Rho if you can estimate the 206/207 error, from the equation,

$$Rho = (Ex^2 + Ey^2 - Ez^2)/(2ExEy)$$

where Ex is the percent 206/204 error, Ey is the percent 207/204 error, and Ez is the percent 206/207 error.

I M P O R T A N T	You should assign nonzero estimated errors to the initial-Pb ratios if you wish to know the propagated uncertainty in the apparent ages for each sample. However, if you intend to use the reduced data for several samples to calculate concordia-intercept ages, and if you expect that all of the samples used for a given regression had the same initial-Pb ratios, then you should assign zero uncertainties and error correllations to the initial-Pb ratios.

The program will start reduction of your data after your response to the INITIAL-Pb query. Remember that the first data-reduction after pressing the RUN key will take about 5 times longer than subsequent data-reductions.

Pb-205 Spiked Samples:

First, of course, indicate that the sample is a Pb-205 spiked sample by pressing the Pb-205 key during the initial display. Then press the *KEYBOARD* key. The first CRT-query after entering the sample name will be,

GRAMS OF SAMPLE [, PERCENT OF DISSOLVED SAMPLE (EXTRACTED &) LOADED]?

If all of the dissolved sample were loaded onto the filament (whether extracted for Pb or not), just enter 1 value - the weight of the sample in grams. The sample is assumed to have been spiked before dissolution. If only a fraction of the dissolved sample were loaded onto the filament, enter 2 values - the sample weight, and the percent of the total solution that was actually (extracted for Pb and) loaded. This second parameter is used to calculate the appropriate sample-Pb/blank-Pb ratio.

The next query will be,

GRAMS SPIKED OF Pb-205/U-235/Th-230?

Enter the weight of the mixed Pb205-U-Th spike added to the sample. The next query will be,

206/205, %err?

Enter the observed 206/205 ratio and its 2-sigma uncertainty, not including the mass discrimination correction or error. The next query will be,

Pb-SPIKED ALIQUOT:
[[206/204,%err,] 206/207,%err,] 206/208,%err?

This and the succeeding queries are identical to those used for Pb-208 spiked samples. No unspiked aliquot is assumed to exist.

THE LABDATA FILES

The LabData Files contain information on

a) spike isotope ratios and abundances,
b) blank-Pb isotope ratios and ratio-uncertainties,
c) Uncertainties in the amounts of Pb, U, and Th blank amounts, and
d) Uncertainties in the mass-discrimination for Pb, U, and Th during the mass-spectrometer runs

for various users. A default LabData File is loaded each time the program is started from the RUN command, but can only be valid for one particular laboratory. Thus each user should either

a) define a new default LabData File for his/her personal disk, or

b) define a new LabData File at some point, store it on a disk, and request that file (using the LABDATA key) each time the program is run.

To redefine, edit, or print out the contents of a LabData File, press the LABDATA key during the initial display. The CRT will clear, and display the following special-function key labels:

KEY#	LABEL	FUNCTION
1	ALL	Define a completely new LabData File.
3	Pb208Spike	Define data for the Pb-208 spike.
4	Pb205Spike	Define data for the mixed Pb205-U235-Th230 spike.
5	U235 Spike	Define data for the U-235 spike.
6	Th230Spike	Define data for the Th-230 spike.
7	Mass Discr.	Define data for the Pb, U, and Th mass-discrimination during the mass-spectrometer runs.
8	Blanks	Define data for isotope ratios of the Pb blanks, and for the uncertainties in amounts of the Pb, U, and Th blanks.
9	Store File	Store the current LabData File in memory on a disk.
10	Print File	Printout the contents of the current LabData File in memory.
11	ESCAPE	Exit the LabData File part of the program and return to the initial display.
12	NEW FILE	Bring a different LabData File into memory from a disk.
13	CHANGENAME	Change the name of the current Labdata File in memory.
14	HELP	Invoke a HELP screen explaining the functions of the keys defined in this display.

The default LabData File is named "DefLab". At the start of the program, the computer searches the contents of drive 0, then drive 1, for a "DefLab" file, and load it into memory. To define a new DefLab file, press the ALL key and press the Y key in response to the query,

Is this new LabData File to be the new Default LabData File (Y/N)?

To edit any part of a LabData File, first load it into memory from a disk, if it is not already in memory, then press the special-function key for that part of the file that you wish to edit. You must specifically request that an edited file be stored on a disk (using the Store File key) if you wish to permanently save the file. To make sure that the file is stored on the proper disk, you should add the mass-storage specifier to the name of the file - :D700 for drive 0, or :D701 for drive 1. For example, if you wished a LabData File named "SallyLab" to be stored on the disk in drive 1, you would define the name of the file to be "SallyLab:D701" (without the quotation marks).

If you wish to check the contents of a LabData File, first make sure that it's in memory (load the file from a disk if necessary, using the NEW FILE key), then press the Print File key during the main LabData File display.

I should mention that the values used for the spike-concentration errors in the LabData File should in most cases really correspond to the precision of the delivered amounts of spike isotopes, and not usually to the accuracy. This is because sets of isotope data are most often used for regression analyses, so that any constant error in the spike concentrations will be present for all of the samples of a suite. Because the goodness-of-fit of any regression line (such as an isochron or a concordia chord) will not be affected by such a common bias, you generally don't want the spike-concentration error propagated for the reduced data of a suite of samples. If you won't be using the data for some sort of pooled suite of samples, however, then it might be appropriate to assign the true spike-concentration uncertainties.

REDUCING DATA FROM VISICALC FILES

Structuring the VISICALC Raw-Data File:

VISICALC is a very widely-used, commercially available program for creating, manipulating, and storing arrays of data, and is well-suited for use with both large and small files of both raw and reduced Pb-U-Th isotope data. Briefly, the program allows either numeric of alphanumeric data to be displayed as a 2-dimensional array of rows and columns of arbitrary size, and stored as individual character-strings for each element in the array. The advantage of this format is its flexibility of display and ease of manipulation - for example, moving, adding, or deleting columns or rows of data.

PBDAT is designed to use VISICALC data files, both for raw-data input of many samples in a sequence, and for reduced-data output of such samples. In other words, PBDAT can take a VISICALC file of raw data, and automatically transform all or part of the raw-data file to a reduced-data VISICALC file. The raw-data VISICALC files must conform to a certain format for the program to accurately recover its data, however. This format is as follows:

1) the column-width of the VISICALC cells must be 9 characters wide (type in /GC9 when in VISICALC),

2) the column-headings must be separated from the data cells by a double-underline (=========),

3) the sample names must be in the first 2 columns (A and B),

4) all uncertainties (errors) must be in percent and at the 2-sigma/95%-confidence level, and,

5) the following data must be in specified columns, as outlined below.

For Pb-208 spiked samples, the VISICALC columns must be defined as:

COLUMN#	PARAMETER (Pb-208 spiked)
A	Sample Name (first 9 characters).
B	Sample Name (last 9 characters).
C	Gross Sample-Weight, in grams. This is the weight of the powdered sample before any solid aliquoting or splitting. Zero if irrelevant.
D	Sample Weight, in grams. This is the weight of the sample that was actually dissolved.
E	Total-Aliquot, weight in grams. The total aliquot is the total solution of the dissolved sample.
F	Pb-Unspiked Aliquot, weight in grams (the part of the total aliquot that was left unspiked).
G	Pb-spiked Aliquot, weight in grams (the part of the total aliquot that was spiked with Pb-208). If the sample were total-spiked for U(Th), this entry should be its negative value.
H	Pb-208 Spiked (grams Pb-spike delivered to the Pb-spiked aliquot).
I	U-235 Spiked (grams U-235 spike delivered either to the Pb-spiked aliquot or to the total sample).
J	Th-230 Spiked (grams Th-230 spike delivered with the U-235 spike).
K	206/204 (raw) of Pb-unspiked aliquot.
L	Percent uncertainty in K.
M	206/207 (raw) of Pb-unspiked aliquot.
N	Percent uncertainty in M.

O	206/208 (raw) of Pb-unspiked aliquot.
P	Percent uncertainty in O.
Q	206/204 (raw) of Pb-spiked aliquot.
R	Percent uncertainty in Q.
S	206/207 (raw) of Pb-spiked aliquot.
T	Percent uncertainty in S.
U	206/208 (raw) of Pb-spiked aliquot.
V	Percent uncertainty in U.
W	238/235 (raw) of U-spiked aliquot.
X	Percent uncertainty in V.
Y	232/230 (raw) of Th-spiked aliquot.
Z	Percent uncertainty (raw) in Y.
AA	Pb-blank of Pb-unspiked aliquot, in nanograms.
AB	U-blank of U-spiked aliquot, in nanograms.
AC	Th-blank of Th-spiked aliquot, in nanograms.

For samples spiked with a mixed Pb-205/U-235/Th-230 spike, the format of the raw-data VISICALC file is somewhat different, with the VISICALC columns defined as follows:

COLUMN#	PARAMETER (Pb-205 spiked)
A	Sample Name (1st 9 characters).
B	Sample Name (last 9 characters).
C	Sample weight, in grams (assumed total-spiked).
D	Grams Pb-205/U-235/Th-230 spiked.
E	Percent of the total dissolved sample that was actually (extracted and) loaded.
F	Observed 206/204 ratio.
G	Uncertainty (%) in observed 206/204.
H	Observed 206/207 ratio.
I	Uncertainty (%) in observed 206/207.
J	Observed 206/208 ratio.
K	Uncertainty (%) in observed 206/208.
L	Observed 206/205 ratio.
M	Uncertainty (%) in observed 206/205.
N	Observed 238/235 ratio.
O	Uncertainty (%) in observed 238/235.
P	Observed 232/230 ratio.
Q	Uncertainty (%) in observed 232/230.
R	Pb blank for Pb run, in nanograms.
S	U blank for U run, in nanograms.
T	Th blank for Th run, in nanograms.

For more detailed information on these parameters, refer to the section on entering data from the keyboard.

Processing VISICALC Raw-Data Files:

To start reducing raw data from a VISICALC file, press the DATAFILE special-function key (k4) during the initial CRT-display. If the Pb-205 key were pressed during the initial CRT-display, the program will assume that the VISICALC data is for a suite of Pb-205 spiked samples. Otherwise, Pb-208 spiked samples will be assumed. The contents of the VISICALC datafile themselves can override these assumptions, however, if either of the characters *8* or *5* occurs in a sample name. If *5* is present in a sample name, then that sample and any following samples will be assumed to be Pb-205 spiked. If *8* occurs in a sample name, then data for Pb-208 spiked samples will be assumed.

After pressing the DATAFILE key, the CRT will query,

Name of the VISICALC file containing the raw data?
(enter * to escape)

Enter the name of the raw-data VISICALC file, including the mass-storage specifier if the file isn't on the disk in the default drive. In other words, if the disk with the raw-data VISICALC file is in drive 1 and the name of the VISICALC file is GEORGE, you would enter GEORGE:D701. The CRT will clear and display the message "Converting raw-data VISICALC file...". Depending on how many samples exist in the VISICALC file, it may take from about 1 to several minutes to bring the VISICALC file into memory and convert it into a numeric array. When the VISICALC file is converted, the computer will display or print out (depending on whether the printer or CRT was designated as the output device) a list of the sample-names in the VISICALC file, make some happy-sounding beeps, and display "VISICALC FILE GEORGE:D701 CONVERTED." (for the sample-file mentioned above).

The next CRT query will be,

SAMPLES TO BE REDUCED: FIRST [, LAST] (ALL)?

If you want to reduce all of the data in the raw-data VISICALC file to be reduced, just enter the word ALL. If you want to reduce the data for several samples in sequence, enter two numbers: the number of the first

sample in the sequence and the number of the last sample in the sequence. For example, a reponse of 9,14 indicates that you want samples 9 through 14, inclusive, to be reduced. If you want to reduce only 1 sample, just enter the number of that sample (the sample numbers were displayed or printed out just after the VISICALC file was converted).

Before starting data reduction, the CRT will request the initial-Pb isotope ratios; as before, just press END LINE if you don't want any radiogenic-Pb isotope data. You can't mix samples that require different initial-Pb ratios in one sequence, so if you wanted to reduce samples 1 through 12 with one initial-Pb and samples 13 through 34 with another, you would have to do the following: first, enter 1,12 as the "SAMPLES TO BE REDUCED", and enter the appropriate initial-Pb when requested. Wait for the computer to reduce the data for samples 1 through 12. Then, enter 13,34 as the next "SAMPLES TO BE REDUCED", and enter the second initial-Pb when requested.

The computer will then reduce the data for all of the samples that you requested, printing out the results either on the CRT or the printer, depending on which output device you selected during the initial CRT-display. When finished, the computer will make some happy-sounding beeps, and display the query,

TYPE OF DATAFILE FOR REDUCED DATA?

and label three of the special-function keys as VISICALC, NUMERIC, and ESCAPE.

STORING REDUCED DATA AS VISICALC OR NUMERIC FILES

If you don't want to store the data on a disk, press the ESCAPE key. But if you do want to store the reduced data on a disk, you'll have to choose which type of file-structure to use. If you choose VISICALC ,the computer will create a VISICALC file of the reduced data, complete with title and column-headings; in other words, the reduced-data VISICALC file will be a transformed version of the raw-data VISICALC file (the raw-data file will remain intact). If you choose NUMERIC, the computer will create a file consisting of a string-array of sample names plus a numeric array of the reduced-data values. The VISICALC reduced-data file is

by far the more flexible and convenient, but it takes more time to create and store, and more time for other programs to retrieve from the disk.

Retrieving data from numeric reduced-data files:

If you intend to use the numeric-data files only with the ISOPLOT, CPLOT, or PBPLOT programs (Ludwig, 1983), you can skip this part of the user's guide because these programs can directly retrieve PBDAT-created numeric files.

But if you want to access these numeric-data files from some other program, you'll need to know the following: for an n-sample file, the data are stored as n pairs of 18-character strings (the sample names) plus 45-element, short-precision vectors. So to retrieve the data, you must

1) dimension an 18-character string or string-array and a 45-element short-precision vector (DIM Name$[18]... SHORT X(45)),

2) assign a buffer to the file (ASSIGN# 1 TO GEORGE:D701),

3) read the data from the file 1 sample at a time; for example,

```
1000 READ# 1,I ; Name$,X() !  Ith sample
```

Structure of Reduced-Data Files:

The VISICALC and numeric reduced-data files have the following structure:

VISICALC COLUMN	NUMERIC COLUMN	PARAMETER
C	1	The larger of Sample-Weight or Gross-Weight.
D	2	Uranium concentration (ppm).
E	3	Thorium concentration (ppm).
F	4	Lead concentration (ppm).
G	5	Common-lead concentration (ppm).
H	6	Nanomoles of Pb-206 per gram.
I	7	Raw (blank and mass-discrimination uncorrected) 206/204.
J	8	Corrected (for blank and mass-discrimination) 206/204.
K	9	Corrected 207/204.
L	10	Corrected 208/204.
M	11	radiogenic (corrected for blank- and initial-Pb) Pb-206/U-238.
N	12	radiogenic Pb-207/U-235.
O	13	radiogenic Pb-207/Pb-206.
P	14	radiogenic Pb-208/Th-232.
Q	15	Pb-206/U-238 apparent age (Ma).
R	16	Pb-207/U-235 apparent age (Ma).
S	17	Pb-207/Pb-206 apparent age (Ma).
T	18	Pb-208/Th-232 apparent age (Ma).
U	19	Mu (U-238/Pb-204).
V	20	Nu (U-235/Pb-204).
W	21	Th-232/Pb-204.
X	22	Beta eU/U (ratio of estimated [U]

		from beta activity to isotope-dilution [U]).
Y	23	Gamma eU/U (ratio of estimated [U] from gamma activity to isotope-dilution [U]).
Z	24	Beta/Gamma activity ratio.
AA	25	Uncertainty in [U].
AB	26	Uncertainty in [Th].
AC	27	Uncertainty in [Pb-204].
AD	28	Uncertainty in [Pb-206].
AE	29	Uncertainty in corrected 206/204.
AF	30	Uncertainty in corrected 207/204.
AG	31	Uncertainty in corrected 208/204.
AH	32	Error-correlation for corrected 206/204 - 207/204.
AI	33	Error-correlation for corrected 206/204 - 208/204.
AJ	34	Uncertainty in radiogenic Pb-206/U-238 (& 206/238 age).
AK	35	Uncertainty in radiogenic Pb-207/U-235 (& 207/235 age).
AL	36	Uncertainty in radiogenic Pb-207/Pb-207 (& 207/206 age).
AM	37	Error-correlation for radiogenic Pb-206/U-238 - Pb-207/U-235.
AN	38	Uncertainty in radiogenic Pb-208/Th-232.
AO	39	Uncertainty in Mu and Nu.
AP	40	Uncertainty in Pb-208/Th-232.
AQ	41	Error-correlation for 206/204 - Mu.

AR	42	Error-correlation for 207/204 - Nu.
AS	43	Error-correlation for 208/204 - Th-232/Pb-204.

Note that all of the uncertainty parameters are in percent and at the 2-sigma/95%-confidence level.

REFERENCES

Ludwig, K.R., 1980, Calculation of uncertainties of U-Pb isotope data; Earth Planetary Science Letters, v. 46, p. 212-220.

Ludwig , K.R., 1983, Programs for plotting and regression of isotope geochemical data, written for HP-86/87 microcomputers; U.S. Geological Survey Open-File Report 83-849, 94 p.

SAMPLE: Figure 1: Example of Reduced Data for a Pb-208 Spiked Sample

	206/204	%err	206/207	%err	206/208	%err
UNSPKD	1001.2	.94	10.032	.022	15.321	.021
SPIKED			9.9784	.011	.9432	.009
SPIKE	16.2		.3128		.0000931	

BLANK: 6/4=18.900+/-2.00 7/4=15.550+/- .20 8/4=37.900+/-1.80
.07319 G Pb-208III spiked, @9.7922E-009 +/- .05% moles 208/G
.06138 G U-235III spiked, @5.9419E-008 +/- .05% moles 235/G
.06138 G Th-230II spiked, @7.9810E-008 +/- 2.00% moles 230/G

SAMPLE WT.	TOTAL-AL.	Pb-UNSPKD AL.	Pb-SPKD AL.
.01234	.6666	.5432	.1234

Pb-Unspiked Aliquot, Corrected for .14+/-.084 nG Pb-Blank,
and .14+/-.05 %/a.m.u. Mass-Discrimination

206/207	206/208	206/204	207/204	208/204
10.021	15.303	1006.9	100.47	65.797
+/-.0598%	+/-.142%	+/-.964%	+/-.966%	+/-.967%

Error-Correls: 207/204-206/204=.99808 208/204-206/204=.98913

Moles Pb Per Gram:

206	207	208	204	TOTAL
3.14501E-007	3.13812E-008	2.05515E-008	3.12348E-010	3.66746E-007
+/-.12%				

44 nG Common-Pb in Unspkd Al. ——— (4.41 PPM)

PPM Total Pb = 75.612 Pb-Spiked Aliquot Blank = .23 nG

238/235= 1.2543 +/- .21 % 232/230= .05321 +/- .32 %
.32 nG U-Blank, .11 nG Th-Blank U-Th SPIKED-AL.= .1234 Grams

	238	235	232
Moles Per Gram:	2.0381E-006	1.4781E-008	1.1181E-007

488.63 PPM Uranium (+/-.499%)
25.94 PPM Thorium (+/-2.08%) Th/U= .05309

238/204= 6525 235/204= 47.323 (+/-1.09%)
232/204= 357.98 (+/-2.3%)

Rho(U/4-6/4)= .87773 Rho(U/4-7/4)= .87918 Rho(Th/4-8/4)= .41365

Radiogenic-Pb	206*	207*	208*
Moles Per Gram:	3.0944E-007	2.6602E-008	9.4007E-009

Initial-Pb: 6/4=16.2 +/- 0 7/4=15.3 +/- 0
8/4=35.7 +/- 0 RHO(6/4-7/4) = 0

	206/238	207/235	207/206	208/232
RATIOS:	.15183	1.7997	.085969	.084075
ERRORS:	.514%	.545%	.167%	2.38%
AGES (Ma):	911.22	1045.4	1337.5	1631.7

Rho (207/235-206/238) = .9516

****

SAMPLE: Figure 2: Example of Reduced Data for a Pb-205 Spiked Sample

	206/204	%err	206/207	%err	206/208	%err
SPIKED	1001.2	.54	10.032	.13	5.0711	.085
SPIKE	20.3		1.21		.4846	

SPIKED-SAMPLE 206/205 = .5402 +/-.12% SPIKE 206/205 = .001128

BLANK: 6/4=18.900+/-2.00 7/4=15.550+/- .20 8/4=37.900+/-1.80
.05321 G Pb-205a spiked, @3.9485E-011 +/- .50% moles 205/G
.05321 G Pb-205a spiked, @1.7055E-009 +/- .50% moles 235/G
.05321 G Pb-205a spiked, @7.9810E-008 +/- 2.00% moles 230/G

SAMPLE WT. (mG)	PERCENT LOADED
.0203	70

Pb-Unspiked Aliquot, Corrected for .0062+/-.0037 nG Pb-Blank,
and .14+/-.05 %/a.m.u. Mass-Discrimination

206/207	206/208	206/204	207/204	208/204
10.965	5.679	2597.1	236.85	457.31
+/-4.8%	+/-6.17%	+/-81.5%	+/-76.7%	+/-75.3%

Error-Correls: 207/204-206/204=1 208/204-206/204=.99998

Moles Pb Per Gram:

206	207	208	204	TOTAL
5.53282E-008 +/-.781%	5.04581E-009	9.74253E-009	2.13042E-011	7.01379E-008

.0061 nG Common-Pb in Unspkd Al. ——— (.301 PPM)

PPM Total Pb = 14.471

238/235= 5.321 +/- .32 % 232/230= 3.097 +/- .45 %
.015 nG U-Blank, .009 nG Th-Blank

	238	235	232
Moles Per Gram:	2.4966E-005	1.8107E-007	6.5150E-004

5985.8 PPM Uranium (+/-.75%)
15.11 % Thorium (+/-2.08%) Th/U= 25.25

238/204= 1171900 235/204= 8499.4 (+/-82.1%)
232/204= 30581000 (+/-82.1%)

Rho(U/4-6/4)= .99991 Rho(U/4-7/4)= .93926 Rho(Th/4-8/4)= .93767

Radiogenic-Pb	206*	207*	208*
Moles Per Gram:	5.4983E-008	4.7194E-009	8.9818E-009

Initial-Pb: 6/4=16.2 +/- .25 7/4=15.32 +/- .031
8/4=35.71 +/- .42 RHO(6/4-7/4) = .925

	206/238	207/235	207/206	208/232
RATIOS:	.0022023	.026064	.085834	.000013786
ERRORS:	1.09%	1.1%	.201%	2.34%
AGES (Ma):	14.181	26.126	1334.5	.27865

Rho (207/235-206/238) = .98327

****

Figure 3

```
DATA FROM LABDATA FILE  "DefLab":

Pb-208 Spike  (Pb-208III):

[208] = 9.7922E-009  +/-  .05% moles/g
(not a mixed Pb/U spike)
206/204= 16.2          206/207= .5             206/208= .0000931


Pb-205 mixed spike   (Pb-205a):

[205] = 3.9485E-011  +/-  .50% moles/g
[235] = 1.7055E-009  +/-  .50% moles/g
[230] = 1.2774E-009  +/-  .50% moles/g

206/205 = .001128                  238/235 = .0006119951
206/204 = 20.3                     232/230 = .0003921569
206/207 = 1.21
206/208 = .4846


U-spike  (U-235III):

[235] = 5.9419E-008  +/-  .05% moles/g
238/235 = .00041841


Th-spike  (Th-230II):

[230] = 7.9810E-008  +/- 2.00% moles/g
232/230 = .001292


Average mass-discrimination during mass-spectrometer runs, in %/a.m.u. --

Pb:   .14 +/- .05       U:  .3 +/- .15           Th:  .3 +/- .3


Average Blanks:

Uncertainty in assigned amount:  Pb - 60%      U - 100%       Th - 100%

Pb blank ratios and uncertainties:

206/204 = 18.9+/-2       207/204 = 15.55+/-.2      208/204 = 37.9+/-1.8
Error-Correlations: 206/204-207/204= .7     206/204-208/204= .7
```

Figure 4

SAMPLE VISICALC RAW-DATA FILE FOR Pb-208 SPIKED SAMPLES

A	B	C	D	E	F	G	H	I	J	K	L	M	N
SAMPLE	NAME	GROSS WT. (G)	WEIGHT (G)	TOT. AL. (G)	UNSPKD AL (G)	SPKD AL (G)	Pb SPIKE (G)	U SPIKE (G)	Th SPIKE (G)	206/204 UNSPKD	%err	206/207 UNSPKD	%err
C1-1	LEACH	32.53	1.14	68.62	.2595	.137	.2136	.2142	.0787	42.34	.055	2.4833	.004
C1-1	RESIDUE	17.04	1.14	26.46	3.3946	1.1352	.2105	.2136	.0797	190.22	.0044	8.6466	.0044
C1-2	LEACH	2.305	.66	63.42	.2797	.1076	.2128	.2126	.0799	45.594	.044	2.6432	.016
C1-2		36.79	.73	53.77	3.3391	.2333	.2126	.2072	.0842	46.069	.03	2.6705	.024
C1-3	T	2.019	.83	51.68	3.2732	.2163	.2161	.2138	.0841	48.588	.039	2.7911	.028
C1-4	I	3.004	1.16	56.58	.3321	.2204	.2119	.214	.0799	49.63	.105	2.8465	.02
C1-5	T	.91	.91	55.03	.3047	.2211	.2132	.2125	.0643	48.232	.043	2.7795	.027
C1-6	A	21.45	.63	57.11	.3967	.2204	.2125	.2124	.0784	46.33	.01	2.6809	.014
C1-7	N	27.98	1.24	62.45	.3215	.2313	.2132	.2123	.0798	46.529	.009	2.6928	.008
C1-8		104.32	.74	58.91	.2301	.1261	.2146	.2129	.0804	44.935	.047	2.6123	.01

O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB
206/208 UNSPKD	%err	206/204 SPIKED	%err	206/207 SPKD	%err	206/208 SPKD	%err	238/235	%err	232/230	%err	Pb-BLANK (nG)	U-BLANK (nG)
1.0562	.003			2.4865	.01	.58145	.01	7.1174	.31	.00924	1.8	.66	.052
4.7922	.003			8.5016	.01	.41067	.01	1.2394	.06	.00804	.359	.66	.052
1.1267	.01	45.532	.426	2.6415	.087	.48263	.054	5.1504	.006	.00607	.042	.66	.052
1.1398	.033			2.6704	.011	.77951	.017	14.211	.172	.00502	.104	.66	.052
1.1952	.04			2.7897	.026	.85566	.041	17.869	.157	.00401	.347	.54	.037
1.2229	.028			2.8461	.04	.921	.028	21.519	.025	.00397	.109	.54	.037
1.1954	.043			2.779	.007	.87381	.032	19.362	.019	.00233	.543	.54	.037
1.1445	.015			2.6792	.023	.76792	.049	13.429	.19	.0104	.104	.66	.052
1.1502	.017			2.6923	.004	.93693	.023	26.614	.128	.00109	.684	.66	.052
1.1127	.013	45.048	.01	2.6123	.021	.65049	.042	8.5994	.16	.00056	3.42	.66	.052

Figure 5

SAMPLE VISICALC RAW-DATA FILE FOR Pb-205 SPIKED SAMPLES

A	B	C	D	E	F	G	H	I	J	K	L
SAMPLE	NAME	WEIGHT (mG)	IPb LOADED	Pb-U-Th SPIKED-G	206/204	%err	206/207	%err	206/208	%err	206/205
M	200-270,5D,1-1.5	.127	67	.074	2375(D)	1	9.5101(D	.06	.4399(C)	.06	12.680(D
	200-270,M2.5D	.104	67	.076	1635.23	.4	8.1571(C	.08	10.427(M	.1	6.980(M)
	200-270,1-2.5D	.0052	67	.073	863.0(M)	.4	8.6815(C	.08	13.888(M	.1	8.732(M)
	200-270,NM1D	.084	80	.074	957.9(D)	.4	8.3606(D	.06	13.183(D	.06	5.3345(D
	270-425,NM1D	.117	80	.074	914.1(M)	.32	8.686(C)	.06	14.0168(	.1	5.227(M)
	+200,NM1.5A	.018	90	.076	3545	2	7.517	.34	.63071	.3	12.154
	+200,.NM1.5A	.015	67	.073	2129	1.5	4.835	.15	2.926	.07	4.523
	+200NM1.5 10GR	.018	67	.074	541.5 M	2	7.532	.1	.6307 D	.2	12.161 D
	+200NM 1.5 40 GLIR	.137	50	.078	15480	2.8	9.0956	.1	22.238 M	.3	86.97 M
	+200M 1.5 19 MON	.053	67	.089	8160 M	.8	9.873	.04	.8538	.1	256.8 M
	-200+270 M1.5 MON	.084	67	.062	11959 M	1	9.941	.1	.4092	.2	307.3 M
	-270+425 M1D	.0084	67	.074	2893. D	1.8	9.630 D	.6	25.81 D	1.2	228.51 D
	-200+270 M2.5D	.0067	67	.072	1350. D	.54	9.253 D	.06	19.441 D	.14	69.98 D

M	N	O	P	Q	R	S	T
%err	238/235	%err	232/230	%err	Pb-BLANK nG	U-BLANK nG	Th-BLANK nG
.1	.9901(D)	.04			.054	.005	.004
.12	.6943(D)	.16	.4680(D)	.14	.054	.005	.004
.12	.8191(D)	.06	.2322(D)	.12	.54	.005	.004
.04	.4407(D)	.08	.08430(D	.1	.012	.005	.004
.1	.4438(D)	1	.08223(D	.42	.012	.005	.004
.4	.9426(D)	.5	7.028(D)	.51	.012	.005	.004
.07	.3315(D)	.1	.0971(D)	.49	.012	.005	.004
.2	.9511 D	.3	7.07 D	.32	.054	.005	.004
.6	6.403 D	.1	1.326 D	.38	.054	.005	.004
.14	17.84 D	.2	111.4 D	.42	.054	.005	.004
.5	20.53 D	.4	274.4 D	.31	.012	.005	.004
2	13.34 D	.4	4.270 D	.51	.054	.005	.004

Figure 6

SAMPLE VISICALC REDUCED-DATA FILE

A	B	C	D	E	F	G	H	I	J	K	L
SAMPLE NAME		SAMPLE-WT (G)	U(ppm)	Th(ppm)	Pb(ppm)	COMMON Pb(ppm)	Pb-206 nMOLES/G	206/204 RAW	206/204 CORR.	207/204 CORR.	208/204 CORR.
RA 3/83-	400.8 TA	36	32.241	15.999	4.2666	.756	14.302	206.32	264.01	35.281	81.128
RA 3/83-	400.8 L	36	30.685	14.715	2.8472	.2388	10.341	556.15	604.37	59.699	141.16
RA 3/83-	224.6 L	26	3.428	15.093	2.289	.2191	7.8679	455.29	501.06	31.862	171.99
RA 3/83-	182.1 TA	52	266.57	19.398	46.327	.642	205.24	3632.4	4461.5	299.79	124.23
RA 3/83-	246.0 TA	32	7582.8	18.57	1006.9	3.384	4467.7	17379	18422	1646.2	79.149
RA 3/83-	273.8 TA	25	1759.2	16.446	854.5	29.63	3589.6	1666.5	1690.6	204.7	56.027
RA 3/83-	291.7 TA	23	2008.5	21.176	985.83	6.964	4267.3	8294.1	8550.9	971.94	61.581

M	N	O	P	Q	R	S	T	U	V	W	X
206/238 RAD.	207/235 RAD.	207/206 RAD.	206/232 RAD.	206/238 AGE(my)	207/235 AGE(my)	207/206 AGE(my)	208/232 AGE (my)	238/204	235/204	232/204	BETA eU/U
.10003	1.1092	.080421	.035976	614.6	737.79	1207.3	714.39	2482.3	18.004	1272.8	
.078699	.81822	.075404	.028552	488.36	607.05	1079.3	569.01	7479.9	54.249	3706.4	
.53303	2.5062	.0341	.032988	2754.2	1273.8	-781.67	656.01	910.56	6.604	4142.4	
.18395	1.6229	.063987	.048913	1088.5	979.1	741.2	965.21	24169	175.29	1817.3	1.0729
.14114	1.7244	.088607	.13276	851.12	1017.6	1395.7	2519.6	130410	945.83	329.99	.95875
.48466	7.556	.11307	.01974	2547.5	2179.7	1849.3		3455.9	25.064	33.382	.85266
.50845	7.8574	.11208	.1435	2650	2214.8	1833.4	2710.4	16787	121.75	182.87	.76674

Y	Z	AA	AB	AC	AD	AE	AF	AG	AH	AI	AJ
GAMMA eU/U	BETA/ GAMMA	[U] Zerr	[Th] Zerr	COMM.-Pb Zerr	[Pb-206] Zerr	206/204 Zerr	207/204 Zerr	208/204 Zerr	RHO 6/4-7/4	RHO 6/4-8/4	206/238 Zerr
		.417	.529	17.2	.113	17.2	10.3	9.97	.99982	.99804	.666
		1.09	.721	5.12	.115	5.11	3.91	3.88	.99965	.99909	1.11
		.405	.611	5.97	.129	5.97	3.18	4.84	.99919	.9995	.473
2.3746	.929	.405	.515	13.7	.114	13.7	13	9.62	.99998	.99921	.418
1.4111	1.4	.421	.535	3.74	.117	3.74	3.72	2.31	.99988	.96041	.434
1.4836	1.19	.512	.767	.736	.123	.726	.699	.338	.98398	.8263	.528
1.414	1.12	.428	.541	1.85	.114	1.65	1.83	.999	.99953	.89975	.44

AK	AL	AM	AN	AO	AP	AQ	AR	AS
207/235 Zerr	207/206 Zerr	RHO 6/8-7/5	208/232 Zerr	238/204 Zerr	232/204 Zerr	RHO Mu-Alpha	RHO Mu-Beta	RHO Th/4-8/4
1.17	.734	.81801	4.65	18.5	18.5	.99961	.93529	.92102
1.19	.329	.96196	2.03	5.39	5.32	.97854	.91779	.92333
1.3	1.04	.665	1.6	6.21	6.22	.99744	.93197	.92927
.432	.0997	.97311	2.39	13.7	13.7	.99949	.93899	.93028
.439	.0591	.99089	4.74	3.77	3.79	.99284	.94161	.89426
.551	.144	.9652	9.7	.904	1.06	.80415	.75334	.52051
.444	.0576	.99157	7.7	1.91	1.93	.97116	.9224	.80909

APPENDIX: PROGRAM LIST FOR PBDAT

```
8 ! ****************************** PBDAT ****************************************
12 ! HP-87 program to reduce raw Pb-U-Th isotope ratios and lab-data to blank-
16 !  and discrimination-corrected ratios and concentrations, together with
20 !  errors and error-correlations.
24 ! Error and error-correlation calculations follow EPSL V.46, P.212-220,1980
28 !
32 ! K.R. Ludwig, U.S. Geological Survey Open-File Report 84-***.
36 ! Requires 120 kbytes, Adv. Progr. & Matrix ROMS
40 !
44 ALPHALL @ PAGESIZE 24 @ CLEAR @ DISP "Please wait about 10 seconds..." @ DISP @ GOTO BEGIN
48 !
52 ! Variables from LabData File:
56 !
60 !  Mixed_spike              mixed Pb-208/U(/Th) spike? (0/1)
64 !  Pbdisc                   %/a.m.u. mass-discr. for Pb
68 !  Udisc                      "        "       " U
72 !  Thdisc                     "        "       " Th
76 !  Blank64                  206/204 of blank-Pb
80 !  Blank74                  207/204      "
84 !  Blank84                  208/204      "
88 !  Blank64err               absolute uncertainty in blank 206/204
92 !  Blank74err                  "        "          "   207/204
96 !  Blank84err                  "        "          "   208/204
100 !  Blank6474_rho            error-correlation for blank 6/4-7/4
104 !  Blank6484_rho                 "               "   6/4-8/4
108 !  Pbblank_perr             %uncertainty in ng of Pb blank
112 !  Pbdisc_err               uncertainty in Pb mass-discr./amu
116 !  Udisc_err                    "      " U        "
120 !  Thdisc_err                   "      " Th       "
124 !  Spike64                  Pb-spike 206/204 ratio
128 !  Spike67                   "    "   206/207   "
132 !  Spike68                   "    "   206/208   "
136 !  Spike65                  Pb-205 spike 206/205 ratio
140 !  Spike238235              U-spike 238/235 ratio
144 !  Spike232230              Th "    232/230   "
148 !  Spike208pg               moles/g of Pb-208 in spike
152 !  Spike205pg               moles/g of Pb-205 in spike
156 !  Pbspike_conc_perr        % +/- in Pb-spike concentration
160 !  Spike205pg_perr          % +/- in Pb-205 spike concentration
164 !  Spike235pg               moles/g of U-235 in U-spike
168 !  Spike230pg                 "       Th-230 in Th-spike
172 !  Spike235pg_err           % uncertainty in U-spike concentration
176 !  Spike230pg_perr           "    "          Th  "       "
180 !
184 ! DEFINITIONS OF INPUT (RAW-DATA) DATAFILE VARIABLES
188 ! ARRAY R(I,J) & VISICALC COLUMN VCcol
192 !
196 ! ************ FOR SAMPLES SPIKED WITH Pb-208 OR Pb-206 ONLY ****************
200 !
```

```
204 !  J  VCcol            SIGNIFICANCE
208 !
212 !
216 !  1    C    gross sample-weight (g) - i.e., before solid aliquoting
220 !  2    D    sample-weight (g)  -  actually dissolved
224 !  3    E    weight of solution of dissolved sample before aliquoting
228 !  4    F    weight of Pb-unspiked liquid aliquot of dissolved sample
232 !  5    G    weight of Pb-spiked liquid aliquot   "     "       "
236 !  6    H    grams Pb-spike delivered to 5
240 !  7    I    grams uranium spike delivered either to 3 or 5
244 !  8    J      "   thorium  "       "       "       "     "
248 !  9    K    unspiked-aliquot 206/204
252 !  10   L    %uncertainty in 9 (not incl. mass-discr. err)
256 !  11   M    unspiked-aliquot 206/207
260 !  12   N    %uncertainty in 11 (not incl. mass-discr. err)
264 !  13   O    unspiked-aliquot 206/208
268 !  14   P    %uncertainty in 13 (not incl. ...)
272 !  15   Q    Pb-spiked aliquot 206/204
276 !  16   R    % uncertainty in 15 (not incl....)
280 !  17   S    Pb-spiked aliquot 206/207
284 !  18   T    % uncertainty in 17 (not incl....)
288 !  19   U    Pb-spiked aliquot 206/208
292 !  20   V    % uncertainty in 19 (not incl....)
296 !  21   W    238/235 of U-spiked aliquot
300 !  22   X    %uncertainty in 21 (not incl...)
304 !  23   Y    232/230 of Th-spiked aliquot
308 !  24   Z    %uncertainty in 23 (not incl...)
312 !  25   AA   Pb blank of Pb-unspiked aliquot, in nanograms
316 !  26   AB   U blank of U-spiked aliquot, in nanograms
320 !  27   AC   Th blank of Th-spiked aliquot, in nanograms
324 !  28   AD   Beta-eU [Est. U-content from beta-activity] (percent)
328 !  29   AE   gamma-eU [est. U-content from gamma-activity] (percent)
332 !  30   AF   Beta/Gamma activity-ratio
336 !
340 ! $$$$$$$$$$$ FOR MIXED Pb205/U235/Th230 SPIKED SAMPLES ONLY $$$$$$$$$$$$$
344 !  1    C    sample weight (g)
348 !  2    D    weight (g) of mixed Pb205-U235-Th230 spike delivered
352 !  3    E    Percent of total dissolved sample (extracted and) loaded
356 !  4    F    observed 206/204 ratio
360 !  5    G    %uncertainty in 206/204, not incl. mass-discr. err
364 !  6    H    observed 206/207 ratio
368 !  7    I    %uncertainty in 206/207, not incl. mass-discr. err
372 !  8    J    observed 206/208 ratio
376 !  9    K    %uncertainty in 206/208, not incl. mass-discr. err
380 !  10   L    observed 206/205 ratio
384 !  11   M    %uncertainty in 206/205, not incl. mass-discr. err
388 !  12   N    observed 238/235 ratio
392 !  13   O    %uncertainty in 238/235, not incl. mass-discr. err
396 !  14   P    observed 232/230 ratio
400 !  15   Q    %uncertainty in 232/230, not incl. mass-discr. err
404 !  16   R    Pb blank for Pb run, in nanograms
408 !  17   S    U blank for U run, in nanograms
412 !  18   T    Th blank for Th run, in nanograms
416 ! 19-43      not used for Pb-205 spiked samples
420 !
424 !
428 ! DEFINITIONS OF OUTPUT (PROCESSED-DATA) VARIABLES:  ARRAY P(I,J)
432 ! ARRAY P(I,J); NUMERIC-FILE COLUMN# J, VISICALC COLUMN VCcol
436 !
440 !  J   VCcoL           SIGNIFICANCE
```

```
444 !  1   C   sample-weight (g) or, if one exists, gross-weight
448 !          (gross-wt is weight of total ground sample before splitting)
452 !  2   D   ppm U
456 !  3   E   ppm Th
460 !  4   F   ppm Pb
464 !  5   G   ppm common-Pb
468 !  6   H   nanomoles Pb-206 per gram
472 !  7   I   raw (uncorrected) 206/204 of unspiked-aliquot
476 !  8   J   blank & discr.-corrected sample 206/204
480 !  9   K     "          "          "    207/204
484 !  10  L     "          "          "    208/204
488 !  11  M   radiogenic Pb-206/U-238
492 !  12  N   radiogenic Pb-207/U-235
496 !  13  O   radiogenic Pb-207/Pb-206
500 !  14  P   radiogenic Pb-208/Th-232
504 !  15  Q   206/238 age (Ma)
508 !  16  R   207/235    "
512 !  17  S   207/206    "
516 !  18  T   208/232    "
520 !  19  U   Mu (238/204)
524 !  20  V   Nu (235/204)
528 !  21  W   232/204
532 !  22  X   Beta eU/U
536 !  23  Y   Gamma eU/U
540 !  24  Z   Beta/Gamma (cps)
544 !  25  AA  %uncertainty in [U]
548 !  26  AB        "        [Th]
552 !  27  AC        "        [Pb-204]
556 !  28  AD        "        [Pb-206]
560 !  29  AE        "        206/204
564 !  30  AF        "        206/207
568 !  31  AG        "        208/204
572 !  32  AH  error-correlation for 206/204-207/204
576 !  33  AI        "             206/204-208/204
580 !  34  AJ  %uncertainty in radiogenic 206/238
584 !  35  AK        "           "     207/235
588 !  36  AL        "           "     207/206
592 !  37  AM  error-correlation for 206/238-207/235
596 !  38  AN  %uncertainty in radiogenic 208/232
600 !  39  AO  %uncertainty in Mu and Nu (238/204 & 235/204)
604 !  40  AP  %uncertainty in 232/204
608 !  41  AQ  error-correlation for Alpha-Mu
612 !  42  AR        "             Beta-Nu
616 !  43  AS        "             Gamma-232/204
620 !
624 !  VAR  in a variable name indicates a variance, PVAR  indicates a variance in percent-squared, err usually indicate
s an absolute error, perr a % error.
628 !
632 BEGIN: OPTION BASE 1
636 SHORT R(100,30),P(100,45),X(45),C(30)
640 DIM N$(100)[18],F$(3)[3],TABLE$[80],A(7),A$[80],AA$[80],ALLKEY$[256]
644 DIM Pb208(6),Pb205(12),U235(3),Th230(3),Discr(6),Blanks(11),Trialname$[80]
648 DIM Labdata$[15],Pb208$[15],Pb205$[15],U235$[15],Th230$[15],CT$[8]
652 DIM Pbspike$[15],Uspike$[15],Thspike$[15],Q$[1],S1$[10],S2$[10],S3$[10]
656 !
660 ! Default settings are for CRT output, keyboard data-entry, Pb-208 spiked.  Q$ is "
664 Printer,Datafile,Pb_205spiked=0 @ PRINTER IS 1 @ Q$=CHR$ (34) @ CT$=HGL$ (" CONT ") @ EL$=HGL$ (" END LINE ")
668 NE9=1000000000 @ NE6=1000000 @ KYBRD,Datafile,New_default_labdata,Init64,Newfile=0 @ Blank_mult=1
672 AW204=203.973 @ AW206=205.974 @ AW207=206.976 @ AW208=207.977 @ AtWt_U=238.029 @ AtWt_Th=232.038 ! atomic wts of Pb
isotopes, natural U & natural Th
```

```
676 Lambda238=.000155125 @ Lambda235=.00098485 @ Lambda232=.000049475 ! decay constants of U-238, U-235, Th-232, in deca
ys/m.y.
680 Nat_Uratio=137.88 ! 238/235 of natural uranium
684 !
688 ALLKEY$=RPT$ (" ",256) ! build string for keyboard-interrupt procedures
692 !
696 FOR I=1 TO 256
700  IF I<128 OR I>172 THEN ALLKEY$[I,I]=CHR$ (I)
704 NEXT I
708 !
712 Labdata$="DefLab" @ GOSUB Read_labdatafile  @ GOSUB Transfer_labdata_variables  ! load default Labdata File ("DefLab
") into memory
716 CHOOSE: ALPHA 1 @ CLEAR @ ALPHA 21,24 @ AWRIT "ASTERISKS INDICATE DEFAULT OPTIONS" @ GOSUB CLEARKEY
720                   ON KEY# 1,"  *CRT*" GOTO DISPLAY
724                   ON KEY# 2,"  PRINT" GOTO HARDCOPY
728                   ON KEY# 3,"*KEYBOARD*" GOTO KEYBOARD
732                   ON KEY# 4," DATAFILE" GOTO DATAFILE
736     IF Init64 THEN ON KEY# 5,"CHANGE PBO" GOTO CHANGEPBO
740                   ON KEY# 6," VISICALC" GOTO VISICALC
744                   ON KEY# 7," *Pb-208*" GOSUB Pb_208
748                   ON KEY# 8,"  LABDATA" GOTO Labdatafile
752   IF Datafile THEN ON KEY# 11,"MORE DFRED" GOTO DATAFILEINPUT
756                   ON KEY# 13,"  HELP" GOTO HELP_1
760                   ON KEY# 14,"  Pb-205" GOSUB Pb_205
764 KLABEL: KEY LABEL
768 GOTO 768
772 !
776 ! Utility Subroutines:
780 !
784 CLEARKEY: ! Clears all special-function-key functions & labels
788           FOR i=1 TO 14 @ ON KEY# i,"" GOSUB RETRN  @ NEXT i @ RETURN
792 !
796 RETRN: RETURN ! Dummy return
800 !
804 YESNO: ! Return 1 if Y-key pressed, 0 if N-key pressed, clunk if any other
808          ON KYBD k,ALLKEY$ GOTO Key_pressed
812          GOTO 812
816    Key_pressed: KEY$=UPC$ (CHR$ (k))
820                 IF KEY$#"N" AND KEY$#"Y" THEN GOSUB CLUNK  @ GOTO YESNO
824                 IF KEY$="Y" THEN YES=1 ELSE YES=0
828                 OFF KYBD @ RETURN
832 !
836  DEF FNAliq(Pbunspkd_al_equiv,Pbspkd_al_equiv)
840 !    Returns Pb-unspiked aliquot equivalent sample-wt if an unspiked aliquot exists, otherwise returns Pb-spiked ali
quot equivalent wt.
844      IF Pbunspkd_al_equiv THEN FNAliq=Pbunspkd_al_equiv
848      IF NOT Pbunspkd_al_equiv THEN FNAliq=Pbspkd_al_equiv
852      FN END
856 !
860  DEF FNDr(N,D) ! Returns N rounded to D significant figures (HP9845 Dround)
864      IF N THEN Mu=10^(D-INT (LGT (ABS (N)))-1) ELSE Mu=1
868      FNDr=IP (N*Mu)/Mu
872      FN END
876 !
880  RETRIEVE: ! Retrieve up to 7 numeric values from string, separated by a comma. If less than 7
884 !            values are entered, the unused elements of the 7-element A-vector remain zero.
888      LINPUT A$ @ Ninputs=0 @ MAT A=ZER
892      AA$=A$ @ ON ERROR GOTO 904
896      A(1+Ninputs)=VAL (A$) @ Ninputs=1+Ninputs
900      Comma=POS (A$,",") @ IF Comma=0 THEN 904 ELSE A$=A$[Comma+1] @ GOTO 896
```

```
904      OFF ERROR @ RETURN
908 !
912  BAD_INPUT: GOSUB CLUNK  @ DISP @ DISP AA$;"  IS NOT A LEGAL RESPONSE  !!!!" @ DISP @ RETURN
916 !
920  DEF FNERR$(X) = "+/-"&VAL$ (FNDr(SQR (X),3))&"%"
924 !               e.g. for X=3.141592, output is  +/-1.77%
928 !
932  DEF FNER$(X) = "+/-"&VAL$ (X)&"%"
936 !               e.g. for X=3.141592 output is  +/-3.141592%
940 !
944 !
948  DEF FNM(X) = X!((X<1/NE6)!NE9+(X>= 1/NE6)!(X<.01)!NE6+(X>= .01)!100) ! MULTIPLY BY 1E9, 1E6, OR 100
952 !
956  DEF FNL$(X) ! Return appropriate units  (PPB,  PPM,  or %)
960   F$(1)="PPB" @ F$(2)="PPM" @ F$(3)="%"
964   FNL$=F$((X<1/NE6)+2!(X>= 1/NE6)!(X<.01)+3!(X>= .01))
968   FN END
972 !
976 !
980 ! !!!!!!!!!!!!! Input data from the keyboard !!!!!!!!!!!!!!!!!!!!!!!
984 !
988 KYBRDINPUT: OFF KEY$ @ CLEAR @ DISP "(Brackets indicate optional input)" @ DISP @ DISP "(enter  H  for help with any
 query)" @ DISP @ DISP
992 LINPUT "SAMPLE NAME",Trialname$
996  IF UPC$ (Trialname$)="H" THEN GOSUB NOHELP  @ GOTO 992
1000  IF Trialname$="" THEN Trialname$=" "
1004  N$(I)=Trialname$[1,MIN (LEN (Trialname$),18)] @ GOTO 1008
1008  FOR J=1 TO 30 @ R(I,J)=0 @ NEXT J
1012 IF NOT Pb_205spiked THEN 1056
1016 !
1020  DISP @ DISP "GRAMS OF SAMPLE [,PERCENT OF DISSOLVED SAMPLE (EXTRACTED &) LOADED]";@ GOSUB RETRIEVE
1024  IF UPC$ (AA$)="H" THEN GOSUB HELP_4  @ GOTO 1020
1028  R(I,4)=0 @ R(I,3),R(I,5)=1 @ IF A(1) THEN R(I,2)=A(1) ELSE R(I,2)=1
1032  IF A(2) THEN Blank_mult=100/A(2) ELSE Blank_mult=1
1036  DISP @ DISP "GRAMS SPIKED OF Pb-205/U-235/Th-230";@ GOSUB RETRIEVE
1040  IF UPC$ (AA$)="H" THEN GOSUB HELP_5  @ GOTO 1036
1044  R(I,6),R(I,7),R(I,8)=A(1) @ R(I,9),R(I,10),R(I,11),R(I,12),R(I,13),R(I,14)=0
1048 GOTO 1132
1052 !
1056 DISP @ DISP "[GRAMS OF SAMPLE [, TOTAL-ALIQUOT]]";@ GOSUB RETRIEVE
1060  IF UPC$ (AA$)="H" THEN GOSUB HELP_3  @ GOTO 1044
1064  R(I,2)=A(1) @ R(I,3)=A(2) @ IF R(I,2)=0 THEN R(I,2)=1
1068 !
1072 IF R(I,2)=1 AND R(I,3)=0 THEN R(I,4)=0 @ R(I,5)=1 @ GOTO 1092 ! IF no sample or total-aliquot weights entered
1076 DISP @ DISP "(If total-spiked for U[Th] but not for Pb, enter" @ DISP "Spiked Aliquot weight as its negative value)
" @ DISP
1080 DISP "GRAMS OF [[UNSPIKED-ALIQUOT,]  SPIKED-ALIQUOT]";@ GOSUB RETRIEVE
1084 IF UPC$ (AA$)="H" THEN GOSUB HELP_7  @ GOTO 1076
1088  IF A(2) THEN R(I,4)=A(1) @ R(I,5)=A(2) ELSE R(I,4)=0 @ R(I,5)=A(1)
1092 IF R(I,3)=0 THEN R(I,3)=R(I,4)+R(I,5)
1096 DISP @ DISP "GRAMS SPIKED OF: Pb-208  [, U-235] [, Th-230]]";@ GOSUB RETRIEVE
1100 IF UPC$ (AA$)="H" THEN GOSUB HELP_8  @ GOTO 1096
1104  R(I,6)=A(1) @ R(I,7)=A(2) @ R(I,8)=A(3) @ IF R(I,6)=0 THEN 1172
1108 DISP @ DISP "Pb-UNSPIKED-ALIQUOT:  [206/204,%err, 206/207,%err,]  206/208,%err";@ GOSUB RETRIEVE
1112  IF UPC$ (AA$)="H" THEN GOSUB HELP_9  @ GOTO 1108
1116  IF Ninputs=1 OR Ninputs=2 THEN R(I,13)=A(1) @ R(I,14)=A(2) @ GOTO 1124
1120  IF Ninputs=6 THEN R(I,9)=A(1) @ R(I,10)=A(2) @ R(I,11)=A(3) @ R(I,12)=A(4) @ R(I,13)=A(5) @ R(I,14)=A(6) @ GOTO 11
24 ELSE GOSUB BAD_INPUT  @ GOTO 1108
1124 GOTO 1152
1128 !
```

```
1132  DISP @ DISP "206/205, Zerr";@ GOSUB RETRIEVE
1136  IF UPC$ (AA$)="H" THEN GOSUB HELP_6  @ GOTO 1132
1140  R(I,10)=A(1) @ R(I,11)=A(2)
1144  IF A(1) THEN 1124 ELSE R(I,6)=0 @ GOTO 1176
1148 !
1152 DISP @ DISP "Pb-SPIKED ALIQUOT: [[206/204,Zerr,] 206/207,Zerr,] 206/208,Zerr";@ GOSUB RETRIEVE
1156 IF UPC$ (AA$)="H" THEN GOSUB HELP_10  @ GOTO 1124
1160  IF Ninputs=1 OR Ninputs=2 THEN R(I,19)=A(1) @ R(I,20)=A(2) @ GOTO 1172
1164  IF Ninputs=4 THEN R(I,17)=A(1) @ R(I,18)=A(2) @ R(I,19)=A(3) @ R(I,20)=A(4) @ GOTO 1172
1168  IF Ninputs=6 THEN R(I,15)=A(1) @ R(I,16)=A(2) @ R(I,17)=A(3) @ R(I,18)=A(4) @ R(I,19)=A(5) @ R(I,20)=A(6) @ GOTO 1
172 ELSE GOSUB BAD_INPUT  @ GOTO 1124
1172 IF R(I,7)=0 AND R(I,8)=0 THEN 1188
1176 DISP @ DISP "U-SPIKED-ALIQUOT: 238/235, Zerr  [,232/230, Zerr]";@ GOSUB RETRIEVE
1180 IF UPC$ (AA$)="H" THEN GOSUB HELP_11  @ GOTO 1176
1184  R(I,21)=A(1) @ R(I,22)=A(2) @ R(I,23)=A(3) @ R(I,24)=A(4)
1188 DISP @ DISP "BLANKS (in nanograms):  Pb  [,U  [,Th]]";@ GOSUB RETRIEVE
1192 IF UPC$ (AA$)="H" THEN GOSUB HELP_12  @ GOTO 1188
1196  R(I,25)=A(1) @ R(I,26)=A(2) @ R(I,27)=A(3)
1200 IF R(I,7) AND R(I,21) AND R(I,6) THEN GOSUB INPUTPBO  ELSE Init64,Init74,Init84,Init64err,Init74err,Init84err=0
1204 !
1208 !
1212 ! ################ Printout Raw Data for This Sample ####################
1216 !
1220 GO:
1224 IF KYBRD THEN CLEAR ELSE DISP @ DISP "SAMPLE# ";I,N$(I)
1228 PRINT RPT$ ("-",80) @ PRINT "SAMPLE:    ";Trialname$ @ PRINT
1232 IF R(I,6)=0 THEN 1292
1236 PRINT TAB (11);"206/204   Zerr";TAB (33);"206/207   Zerr";TAB (55);"206/208   Zerr" @ PRINT
1240 IF NOT (R(I,9)#R(I,11)) THEN 1252
1244 PRINT "UNSPKD";TAB (10);R(I,9);TAB (20);R(I,10);TAB (32);R(I,11);TAB (42);
1248 PRINT R(I,12);TAB (54);R(I,13);TAB (64);R(I,14)
1252 PRINT "SPIKED";
1256 IF R(I,15) THEN PRINT TAB (10);R(I,15);TAB (20);R(I,16);
1260 IF R(I,17) THEN PRINT TAB (32);R(I,17);TAB (42);R(I,18);
1264 PRINT TAB (54);R(I,19);TAB (64);R(I,20)
1268 PRINT "SPIKE";TAB (10);Spike64;TAB (32);Spike67;TAB (54);Spike68 @ PRINT
1272 IF Pb_205spiked THEN PRINT "SPIKED-SAMPLE 206/205 =";R(I,10);FNER$(R(I,11)),"SPIKE 206/205 =";Spike65 @ PRINT
1276 IMAGE "BLANK:  6/4=",DD.3D,"+/-",D.DD,5X,"7/4=",DD.3D,"+/-",D.DD,5X,"8/4=",DD.3D,"+/-",D.DD,/
1280 PRINT USING 1276 ; Blank64,Blank64err,Blank74,Blank74err,Blank84,Blank84err
1284 IMAGE 3D.5D," G ",10A," spiked, @",D.4DE,"  +/-",DD.DD,"% moles ",3D,"/G"
1288 IF NOT Pb_205spiked THEN S1$=Pb208$ @ S2$=U235$ @ S3$=Th230$ ELSE S1$,S2$,S3$=Pb205$
1292 IF R(I,6)+R(I,7)=0 THEN GOSUB CLUNK  @ PRINT @ PRINT "##### MUST BE SPIKED FOR AT LEAST ONE OF Pb OR U SPIKES #####
" @ GOTO DONE
1296 IF R(I,6) AND NOT Pb_205spiked THEN PRINT USING 1284 ; R(I,6),S1$,Spike208pg,Pbspike_conc_perr,208
1300 IF Pb_205spiked THEN PRINT USING 1284 ; R(I,6),S1$,Spike205pg,Pbspike_conc_perr,205
1304 IF R(I,7) THEN PRINT USING 1284 ; R(I,7),S2$,Spike235pg,Spike235pg_perr,235
1308 IF R(I,8) THEN PRINT USING 1284 ; R(I,8),S3$,Spike230pg,Spike230pg_perr,230
1312 IF NOT Pb_205spiked THEN PRINT @ PRINT TAB (6);"SAMPLE WT.";TAB (21);"TOTAL-AL.";TAB (34);"Pb-UNSPKD AL.";TAB (51);
"Pb-SPKD AL."
1316 IF Pb_205spiked THEN PRINT @ PRINT TAB (19);"SAMPLE WT. (mG)";TAB (40);"PERCENT LOADED"
1320 IF NOT Pb_205spiked THEN PRINT TAB (6);R(I,2);TAB (21);R(I,3);TAB (35);R(I,4);TAB (51);R(I,5)
1324 IF Pb_205spiked THEN PRINT TAB (22);R(I,2)#1000;TAB (43);FNDr(100/Blank_mult,4)
1328 PRINT RPT$ ("-",80)
1332 IF R(I,2)=0 THEN GOSUB CLUNK  @ PRINT @ PRINT "????? NO SAMPLE-WEIGHT FOR THIS SAMPLE ?????" @ GOTO DONE
1336 IF R(I,3)=0 OR R(I,5)=0 THEN GOSUB CLUNK  @ PRINT @ PRINT "##### NEED VALUES FOR TOTAL AND SPIKED ALIQUOT-WEIGHTS #
#### @ GOTO DONE
1340 !
1344 !
1348 ! ###################### Start Calculations for this Sample ##############
1352 !
```

```
1356 IF NOT KYBRD THEN GOSUB Transfer_labdata_variables
1360 Pbspkd_al_equiv=ABS (R(I,5)*R(I,2)/R(I,3)) ! grams of solid-sample equivalent in Pb-spiked aliquot
1364 IF R(I,6)=0 OR (Pb_205spiked=0)*(R(I,13)=0)+(R(I,19)=0) THEN U_Th_CONC
1368 FOR J=1 TO 45 @ P(I,J)=0 @ NEXT J ! zero the appropriate row in P(i,j)
1372 IF NOT Pb_205spiked THEN P(I,7)=R(I,9) ELSE P(I,7)=R(I,17) ! Raw 206/204
1376 P(I,1)=MAX (R(I,1),R(I,2)) ! Use gross-weight for sample weight if gross weight exists, otherwise use sample-weight

1380 Blank64perr=100*Blank64err/Blank64 @ Blank74perr=100*Blank74err/Blank74 @ Blank84perr=100*Blank84err/Blank84
1384 Init64perr=100*Init64err/(Init64+(Init64=0)) @ Init74perr=100*Init74err/(Init74+(Init74=0)) @ Init84perr=100*Init84
err/(Init84+(Init84=0))
1388 !
1392 ! Test to see if Pb-data should be reduced using 206/208 ratios only, or with both 206/207 & 206/208 ratios
1396 IF NOT Pb_205spiked AND ABS (R(I,11)-R(I,17))<2*SQR (2*Pbdisc_err^2+(R(I,12)*R(I,11))^2+(R(I,18)*R(I,17))^2)/100 TH
EN Pb68_only=1 ELSE Pb68_only=0
1400 IF R(I,17)=0 OR R(I,9)<22 THEN Pb68_only=1
1404 ! If either 206/204<22 or the difference between the unspiked 6/7 & spiked 6/7 is not statistically significant, us
e only the 6/8 ratios
1408 IF R(I,9)=0 OR R(I,11)=0 THEN NOCOMP=1 ELSE NOCOMP=0
1412 !
1416 ! <<<<<<<<<< Correct Pb-isotope ratios for mass-discrimination >>>>>>>>>>
1420  IF Pb_205spiked THEN DCcorr_spkd65=R(I,10)*(1+Pbdisc/100) ELSE DCcorr_unsp64=R(I,9)*(1+2*Pbdisc/100)
1424  DCcorr_unsp67=R(I,11)*(1-Pbdisc/100)
1428  IF R(I,9) AND R(I,11) THEN DCcorr_unsp68=R(I,13)*(1-2*Pbdisc/100) ELSE DCcorr_unsp68=R(I,13)
1432  DCcorr_spkd68=R(I,19)*(1-2*Pbdisc/100)
1436  DCcorr_spkd64=R(I,15)*(1+2*Pbdisc/100)
1440  DCcorr_spkd67=R(I,17)*(1-Pbdisc/100)
1444 !
1448 ! <<<<<<<<<< Calculate blank and spike ratios & abundances >>>>>>>>>>>>>>>
1452 Blank67=Blank64/Blank74 @ Blank68=Blank64/Blank84 @ Pbblank_ng=R(I,25) ! BLANK-Pb 6/7, 6/8, amount in nanograms
1456 IF Pb_205spiked THEN Pbblank_ng=Pbblank_ng*Blank_mult
1460 Pbunspkd_al_equiv=R(I,4)*R(I,2)*(R(I,9)*R(I,11)*R(I,13)*0)/R(I,3) ! equivalnet solid-sample weight, in grams, for P
b-unspiked aliquot
1464 Blank_mf204=1/(1+Blank64+Blank74+Blank84) ! Mole-fraction 204 in Pb blank
1468 IF Init64=0 THEN CPb_mf204=Blank_mf204 ELSE CPb_mf204=1/(Init64+Init74+Init84+1) ! Mole-fraction 204 for "common-Pb
"
1472 AtWt_BlankPb=(AW204+AW206*Blank64+AW207*Blank74+AW208*Blank84)/(1+Blank64+Blank74+Blank84) ! atomic weight of blank
-Pb
1476 IF Init64 THEN AtWt_CPb=(AW204+AW206*Init64+AW207*Init74+AW208*Init84)/(1+Init64+Init74+Init84) ELSE AtWt_CPb=AtWt_
BlankPb
1480 Blank204=Pbblank_ng*Blank_mf204/AtWt_BlankPb/NE9 ! Moles blank-204
1484 Blank206=Blank64*Blank204 @ Blank207=Blank206/Blank67 @ Blank208=Blank206/Blank68 ! Moles blank 206,207,208
1488 IF Pb_205spiked THEN Calculate_205spiked_Pb_conc
1492 !
1496 ! <<<<<<<< [Pb] calculation for Pb-208 or Pb-206 spiked aliquot >>>>>>>>
1500 Spike208=Spike208pg*R(I,6) @ Spike206=Spike208*Spike68 @ Spike207=Spike206/Spike67 @ Spike204=Spike206/Spike64 ! Mo
les spike 208,206,207,204
1504 Corr64=DCcorr_unsp64 @ Corr67=DCcorr_unsp67 @ Corr68=DCcorr_unsp68 ! Trial blank-corr. 6/4,6/7,6/8 of sample
1508 IF R(I,9)=0 OR R(I,11)=0 OR Pb68_only=1 THEN Pb_206208_only
1512 !
1516 ! <<<< Calculate [Pb] using both 206/207 and 206/208 of both Pb-spiked & Pb-unspiked aliquots >>>>>>
1520 Numer=(DCcorr_spkd67*Spike207-Spike206)/(1-DCcorr_spkd67/Corr67)-(DCcorr_spkd68*Spike208-Spike206)/(1-DCcorr_spkd68
/Corr68)
1524 Denom=(DCcorr_spkd68/Blank68-1)/(1-DCcorr_spkd68/Corr68)-(DCcorr_spkd67/Blank67-1)/(1-DCcorr_spkd67/Corr67)
1528 Pbspkd_blank206=Numer/Denom ! Moles blank-206 in spiked-aliquot required to explain the difference in unspiked & sp
iked 206/207 ratios
1532 Pb206_compal=(DCcorr_spkd68*(Pbspkd_blank206/Blank68+Spike208)-Spike206-Pbspkd_blank206)/(1-DCcorr_spkd68/Corr68)*P
bunspkd_al_equiv/Pbspkd_al_equiv
1536 ! moles sample Pb-206 in Pb-unspiked aliquot
1540 Test64=Corr64 @ GOSUB SUBTRACT_BLANK  @ IF Corr64<0 THEN BLANK_TOO_HIGH
1544 IF ABS (Corr64-Test64)>Test64/NE9 THEN 1520 ! 6/4 Convergence?
```

```
1548 Ng_blnk_Pbspkd=AtWt_BlankPb*NE9*Pbspkd_blank206/Blank64/Blank_af204 @ GOTO 1688 ! Ng_blnk_Pbspkd is nanograms blank
-Pb in Pb-spiked aliquot
1552 !
1556 SUBTRACT_BLANK: ! Remove blank-Pb contribution to observed ratios
1560   Corr64=Pb206_compal/((Pb206_compal+Blank206)/DCcorr_unsp64-Blank204)
1564   Corr67=Pb206_compal/((Pb206_compal+Blank206)/DCcorr_unsp67-Blank207)
1568   Corr68=Pb206_compal/((Pb206_compal+Blank206)/DCcorr_unsp68-Blank208)
1572   RETURN
1576 !
1580 BLANK_TOO_HIGH: BEEP @ PRINT "*** Pb-BLANK MUST BE <";VAL$ (FNDr(R(I,25),3));" nG ***" @ PRINT
1584 Pbblank_ng=Pbblank_ng/2 @ R(I,25)=R(I,25)/2 @ GOTO 1480 !  Reduce blank-amount by 1/2
1588 !
1592 Pb_206208_only: ! <<<< Calculate [Pb] using only 206/208 ratios >>>>
1596 IF NOCOMP AND R(I,13)=0 THEN GOSUB CLUNK  @ PRINT @ PRINT "**** ESTIMATED UNSPIKED 206/208 MUST BE ENTERED ****" @
PRINT @ PRINT @ GOTO 1108
1600 IF NOCOMP THEN R(I,10)=R(I,16) @ R(I,12)=R(I,18)
1604 Corr68=ABS (DCcorr_unsp68)
1608 ! Pb206_compal=Estimated moles of sample 206 in Pb-unspiked aliquot (or spiked aliquot if there is no unspiked sali
quot)
1612 Pb206_compal=(Pbunspkd_al_equiv/Pbspkd_al_equiv+(Pbunspkd_al_equiv=0))*(DCcorr_spkd68*(Spike208+Blank208)-Spike206-
Blank206)/(1-DCcorr_spkd68/Corr68)
1616 Test68=Corr68
1620 IF NOCOMP THEN 1632 ELSE GOSUB SUBTRACT_BLANK
1624 IF ABS (Test68/Corr68-1)>1/NE9 THEN 1612 ! Convergence test on 6/8
1628 IF Corr64<= 0 THEN 1580 ELSE PBERRORS
1632 Corr67=Pb206_compal/((Pb206_compal+Blank206+Spike206)/DCcorr_spkd67-Blank207-Spike207) ! Corrected sample 206/207 (
no Pb-unspiked data)
1636 Corr64=Pb206_compal/((Pb206_compal+Blank206+Spike206)/DCcorr_spkd64-Blank204-Spike204) ! same for 206/204
1640 GOTO 1628
1644 !
1648 Calculate_205spiked_Pb_conc: ! calculate [Pb] for Pb-205 spiked aliquot
1652 Sample206=Spike205pg*R(I,6) @ Pb206_compal=Sample206*(DCcorr_spkd65-Spike65)-Blank206 ! Pb-205 spiked concentration
 calculation - [206] in Pbspiked-al
1656 Corr68=Pb206_compal/(Sample206*(DCcorr_spkd65/DCcorr_spkd68-Spike65/Spike68)-Blank208) ! BLANK-CORR 6/8
1660 Corr67=Pb206_compal/(Sample206*(DCcorr_spkd65/DCcorr_spkd67-Spike65/Spike67)-Blank207) !   "    "   6/7
1664 Corr64=Pb206_compal/(Sample206*(DCcorr_spkd65/DCcorr_spkd64-Spike65/Spike64)-Blank204) !   "    "   6/4
1668 IF Corr64<= 0 THEN BLANK_TOO_HIGH
1672 PVAR_206=(DCcorr_spkd65*Sample206/Pb206_compal*R(I,11))^2+(Blank206/Pb206_compal*Pbblank_perr)^2+Pbspike_conc_perr^
2 ! VARZ for Pb-206 concentration
1676 R(I,10)=R(I,16) @ R(I,12)=R(I,18) @ R(I,14)=R(I,20)
1680 !
1684 ! <<<<< Error & error-correlation calculation for Pb ratios & concentrations >>>>>
1688 PBERRORS: D=Blank206/Pb206_compal @ F=Blank207*Corr67/Pb206_compal @ E=Blank204*Corr64/Pb206_compal @ G=Blank208*Co
rr68/Pb206_compal
1692 ! D=blank-206/sample-206       E=blank-204/sample-204
1696 ! F=blank-207/sample-207       G=blank-208/sample-208
1700 PVAR_spkd68=R(I,14)^2+4*Pbdisc_err^2 !      VARZ of spiked 6/8
1704 PVAR_unspkd68=R(I,20)^2+4*Pbdisc_err^2 !     "   "  unspiked "
1708 IF Pb_205spiked THEN 1748
1712 Total208=Spike208+Blank208 @ Total68=(Spike206+Blank206)/Total208
1716 VAR_Blank206=(.01*Pbblank_perr*Blank206)^2 ! VAR of blank 206 amount
1720 VAR_Blank68=((Blank64err/Blank64)^2+(Blank84err/Blank84)^2-2*Blank6484_rho*Blank64err/Blank64*Blank84err/Blank84)*B
lank68^2 ! VAR of blank 206/208
1724 V6=((Corr68-Total68)*DCcorr_spkd68/((Corr68-DCcorr_spkd68)*(DCcorr_spkd68-Total68)))^2*PVAR_spkd68+(DCcorr_spkd68/(
Corr68-DCcorr_spkd68))^2*PVAR_unspkd68
1728 ! V6 is [206] VARZ, not including contr. from blank-Pb or Spike uncertainties
1732 A=(Corr68/(Corr68-DCcorr_spkd68))^2
1736 Vb=A*(VAR_Blank206/Total208^2+(Blank206/Total208^2/Blank68)^2*(VAR_Blank206+Blank206^2*VAR_Blank68))*10000/Pb206_co
mpal*Spike208^2
1740 ! Vb is [206] VARZ contribution from blank-Pb uncertainties
```

```
1744 PVAR_206=V6+Vb+Pbspike_conc_perr^2 !   VARZ of Pb-206 concentration
1748 V64=R(I,10)^2 !      "   of raw 6/4  (uncorr. for blank or discrimination)
1752 V67=R(I,12)^2 !      "   "   "  6/7     "
1756 V68=R(I,14)^2 !      "   "   "  6/8     "
1760 PVAR_64=(1+E)^2*V64+(E*Blank64perr)^2+(D-E)^2*PVAR_206+((E-D)*Pbblank_perr)^2+((2+2*E)*Pbdisc_err)^2 ! VARZ of blan
k & discrim.-corr. sample 206/204
1764 A=(1+E)^2*V64+(1+F)^2*V67+((F-E)*Blank64perr)^2+(F*Blank74perr)^2+(F-E)^2*PVAR_206
1768 PVAR_74=A+((E-F)*Pbblank_perr)^2-2*F*(F-E)*Blank6474_rho*Blank64perr*Blank74perr+((3+2*E+F)*Pbdisc_err)^2 ! ditto,
207/204
1772 A=(1+E)^2*V64+(1+G)^2*V68+((E-G)*Blank64perr)^2+(G*Blank84perr)^2+(E-G)^2*PVAR_206
1776 PVAR_84=A+((E-G)*Pbblank_perr)^2-2*G*(G-E)*Blank64perr*Blank84perr*Blank6484_rho+((4+2*E+2*G)*Pbdisc_err)^2 ! ditto
, 208/204
1780 A=(1+E)^2*V64-E*(F-E)*Blank64perr^2+(D-E)*(F-E)*PVAR_206+(E-D)*(E-F)*Pbblank_perr^2
1784 Rho_BetaAlpha=(A+(3+2*E+F)*(2+2*E)*Pbdisc_err^2+E*F*Blank6474_rho*Blank64perr*Blank74perr)/SQR (PVAR_64*PVAR_74) !
Rho for true sample 207/204-206/204
1788 A=(1+E)^2*V64+E*(E-G)*Blank64perr^2+(D-E)*(G-E)*PVAR_206+(D-E)*(G-E)*Pbblank_perr^2
1792 Rho_GammaAlpha=(A+(2+2*E)*(4+2*E+2*G)*Pbdisc_err^2+E*G*Blank64perr*Blank84perr*Blank6484_rho)/SQR (PVAR_64*PVAR_84)
 ! ditto, 208/204-206/204
1796 Molespg_206=Pb206_compal/FNAliq(Pbunspkd_al_equiv,Pbspkd_al_equiv) !  moles 206 per gram
1800 P=Molespg_206
1804 Pbgrams_per_gram=AW206*P+AW207*P/Corr67+AW208*P/Corr68+AW204*P/Corr64
1808 CPb_ppm=AtWt_CPb*NE6*Pb206_compal/(CPb_af204*Corr64*FNAliq(Pbunspkd_al_equiv,Pbspkd_al_equiv)) ! ppm common Pb
1812 PVAR_67=PVAR_64+PVAR_74-2*Rho_BetaAlpha*SQR (PVAR_64*PVAR_74) ! 6/7 VARZ
1816 PVAR_68=PVAR_64+PVAR_84-2*Rho_GammaAlpha*SQR (PVAR_64*PVAR_84) ! 6/8 VARZ
1820 P(I,29)=FNDr(SQR (PVAR_64),3) ! 6/4 err, to 3 signif. figs
1824 P(I,30)=FNDr(SQR (PVAR_74),3) ! 7/4  "   " "  "     "
1828 P(I,31)=FNDr(SQR (PVAR_84),3) ! 8/4  "   " "  "     "
1832 P(I,32)=Rho_BetaAlpha !         Error-correlation between 6/4 & 7/4
1836 P(I,28)=FNDr(SQR (PVAR_206),3) ! [206] err, to 3 signif. figs
1840 P(I,27)=FNDr(SQR (PVAR_206+PVAR_64),3) ! ditto [204] err
1844 P(I,33)=Rho_GammaAlpha ! Error-correlation between 6/4 & 8/4
1848 P(I,4)=NE6*Pbgrams_per_gram ! ppm Pb
1852 P(I,8)=Corr64 ! Blank- & discrimination-corrected 206/204
1856 P(I,5)=FNDr(CPb_ppm,4) ! ppm common-Pb, rounded to 4 signif. figs
1860 P(I,9)=Corr64/Corr67 ! Blank & discrimination-corrected 206/207
1864 P(I,10)=Corr64/Corr68 ! ditto, 206/208
1868 P(I,6)=NE9*Molespg_206 ! nanomoles Pb-206 per gram
1872 PRINT TAB (9);"Pb-Unspiked Aliquot, Corrected for ";VAL$ (FNDr(R(I,25),2));"+/-";VAL$ (FNDr(.01*Pbblank_perr*R(I,25
),2));" nG Pb-Blank, "
1876 PRINT TAB (15);"and ";VAL$ (Pbdisc);"+/-";VAL$ (Pbdisc_err);" Z/a.m.u. Mass-Discrimination" @ PRINT
1880 PRINT "  206/207";TAB (18);"206/208";TAB (32);"206/204";TAB (47);"207/204";TAB (62);"208/204"
1884 PRINT TAB (2);FNDr(Corr67,5);TAB (17);FNDr(Corr68,5);TAB (31);P(I,8);TAB (46);P(I,9);TAB (61);P(I,10)
1888 PRINT " "&FNERR$(PVAR_67);TAB (17);FNERR$(PVAR_68);TAB (31);FNER$(P(I,29));
1892 PRINT TAB (46);FNER$(P(I,30));TAB (61);FNER$(P(I,31)) @ PRINT
1896 PRINT " Error-Correls:  207/204-206/204=";VAL$ (P(I,32));"     208/204-206/204=";VAL$ (P(I,33)) @ PRINT
1900 IMAGE 26X,"Moles Pb Per Gram:",/,4X,"206",12X,"207",12X,"208",12X,"204",11X,"TOTAL",/,5(D.5DE,3X)
1904 P=Molespg_206
1908 PRINT USING 1900 ; P,P/Corr67,P/Corr68,P/Corr64,P+P/Corr67+P/Corr68+P/Corr64
1912 PRINT " "&FNER$(P(I,28))
1916 IF Pb68_only AND NOT Pb_205spiked THEN 1924
1920 PRINT @ PRINT FNDr(1000*CPb_ppm*FNAliq(Pbunspkd_al_equiv,Pbspkd_al_equiv),2);" nG Common-Pb in Unspkd Al. ---- ("&V
AL$ (FNDr(CPb_ppm,3))&" PPM)"
1924 PRINT @ PRINT FNL$(Pbgrams_per_gram);" Total Pb =";FNDr(FNM(Pbgrams_per_gram),5);
1928 IF Pb68_only=1 THEN PRINT "       Pb-Spiked Aliquot Blank =";FNDr(Ng_blnk_Pbspkd,2);"nG";
1932 PRINT
1936 !
1940 ! ################## CALCULATE U,Th CONCENTRATIONS &ERRORS ##################
1944 U_Th_CONC: IF R(I,7)*R(I,21)=0 THEN DONE ! if not spiked for U-Th or no ratios
1948 Uspkd_equiv=Pbspkd_al_equiv*(R(I,5)>0)+(R(I,5)<= 0)*R(I,2) ! Wt of sample spiked with U & Th spike
1952 Fract_corr85=R(I,21)*(1+.03*Udisc) @ Fract_corr20=R(I,23)*(1+.02*Thdisc)
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1956 Moles238_spkdal=R(I,7)*Spike235pg*(Fract_corr85-Spike238235)/(1-Fract_corr85/Nat_Uratio)-4.171E-12*R(I,26)*Blank_mu
lt ! [238] in U-spiked aliquot
1960 NanogramsU_spkdal=Moles238_spkdal*(1+1/Nat_Uratio)*AtWt_U*NE9
1964 Moles232_spkdal=(R(I,23)#0)*(R(I,8)*Spike230pg*(Fract_corr20-(Spike232230+(Spike232230=0)))-R(I,27)/NE9/232*Blank_m
ult) ! [Th] in U/Th-spiked aliquot
1968 NanogramsTh_spkdal=Moles232_spkdal*AtWt_Th*NE9
1972 P(I,3),PpmTh=NE6*(Moles232_spkdal#0)*AtWt_Th*Moles232_spkdal/Uspkd_equiv
1976 P(I,2),PpmU=NE6*AtWt_U*(Moles238_spkdal+Moles238_spkdal/Nat_Uratio)/Uspkd_equiv
1980 ! Errors & error-correlations - U-Th concs & U-Th/Pb-204 ratios
1984 IF Pb_205spiked THEN Pbspike_perr=Pbspike_conc_perr ELSE Pbspike_perr=Pbspike_conc_perr
1988 PVAR_U=(Nat_Uratio/(Nat_Uratio-R(I,21)))^2*R(I,22)^2+(3*Udisc_err)^2+Spike235pg_perr^2+(.01*Ublank_perr*R(I,26)/NE9
/NanogramsU_spkdal)^2 ! VAR% of [U]
1992 IF PpmTh=0 THEN PVAR_Th=0 @ GOTO 2004
1996   PVAR_Th=R(I,23)/(R(I,23)-1/(Spike232230+(Spike232230=0)))^2*R(I,24)^2+(2*Thdisc_err)^2+Spike230pg_perr^2 ! Ditto,
 [Th]
2000   PVAR_Th=PVAR_Th+(.01*Thblank_perr*R(I,27)/NE9/NanogramsTh_spkdal)^2
2004 IF R(I,6)=0 THEN 2076
2008 P(I,21)=Moles232_spkdal*Corr64/Uspkd_equiv/Molespg_206 ! 232/204
2012 PVAR1_206=PVAR_206-Mixed_spike*Pbspike_conc_perr^2 ! don't include spike-concentration uncertainty for Pb/U ratios
if a mixed Pb-U-Th spike
2016 PVAR1_U=PVAR_U-Mixed_spike*Spike235pg_perr^2 !    ditto
2020 PVAR1_Th=PVAR_Th-Mixed_spike*Spike230pg_perr^2 !  ditto
2024 PVAR_Mu=V64*(1+E)^2+(E*Blank64perr)^2+PVAR1_206*(1+E)^2+(E*Pbblank_perr)^2+((2+2*E)*Pbdisc_err)^2+PVAR1_U ! var% in
 238/204
2028 P(I,39)=FNDr(SQR (PVAR_Mu),3) ! %error in Mu
2032 A=V64*(1+E)^2+(E*Blank64perr)^2-(1+E)*(D-E)*PVAR1_206+E*(E-D)*Pbblank_perr^2
2036 P(I,41)=(A+2*(1+E)*Pbdisc_err^2)/SQR (PVAR_64*PVAR_Mu) ! error-correl. 206/204-238/204
2040 A=V64*(1+E)^2+E*(F-E)*Blank64perr^2-(1+E)*(F-E)*PVAR1_206+E*(E-F)*Pbblank_perr^2
2044 P(I,42)=(A+2*(3+2*E+F)*(1+E)*Pbdisc_err^2-E*F*Blank6474_rho*Blank64perr*Blank74perr)/SQR (PVAR_74*PVAR_Mu) ! error-
correl. 207/204-235/204
2048 IF PpmTh=0 THEN 2068
2052  PVAR_Th204=V64*(1+E)^2+(E*Blank64perr)^2+(1+E)^2*PVAR1_206+(E*Pbblank_perr)^2+((2+2*E)*Pbdisc_err)^2+PVAR1_Th ! va
r% in 232/204
2056  P(I,40)=FNDr(SQR (PVAR_Th204),3) ! %error in 232/204
2060  A=(1+E)^2*V64+E*(G-E)*Blank64perr^2-(1+E)*(G-E)*PVAR1_206+E*(E-G)*Pbblank_perr^2
2064  P(I,43)=(A+(4+2*E+2*G)*(2+2*E)*Pbdisc_err^2-E*G*Blank6474_rho*Blank64perr*Blank84perr)/SQR (PVAR_Th204*PVAR_84) !
error-corr. 208/204-232/204
2068 P(I,19),Mu=Moles238_spkdal*Corr64/Uspkd_equiv/Molespg_206 @ P(I,20)=Mu/Nat_Uratio !    238/204,235/204
2072 !
2076 PRINT RPT$ ("-",80) @ PRINT "238/235=";R(I,21);"+/-";R(I,22);"%";
2080 IF PpmTh THEN PRINT TAB (37);"232/230=";R(I,23);"+/-";R(I,24);"%";
2084 PRINT @ PRINT R(I,26);"nG U-Blank,  ";@ IF PpmTh THEN PRINT R(I,27);"nG Th-Blank";
2088 A=R(I,3)*(R(I,5)<= 0)+R(I,5)*(R(I,5)>0)
2092 IF A#1 THEN PRINT USING "8X,3(K),2/" ; "U-Th SPIKED-AL.= ",A," Grams" ELSE PRINT USING "2/"
2096 IMAGE 23X,"238",12X,"235",12X,"232",/,"Moles Per Gram:",5X,3(D.4DE,4X),/
2100 PRINT USING 2096 ; Moles238_spkdal/Uspkd_equiv,Moles238_spkdal/Uspkd_equiv/Nat_Uratio,Moles232_spkdal/Uspkd_equiv
2104 P(I,25)=FNDr(SQR (PVAR_U),3) ! %error in [U]
2108 PRINT TAB (4);FNDr(FNM(PpmU/NE6),5);TAB (12);FNL$(PpmU/NE6);TAB (16);"Uranium";TAB (30);"("%FNER$(P(I,25))&")"
2112 IF NOT PpmTh THEN 2128
2116  P(I,26)=FNDr(SQR (PVAR_Th),3) ! %error in [Th]
2120  PRINT TAB (4);FNDr(FNM(PpmTh/NE6),4);TAB (12);FNL$(PpmTh/NE6);TAB (16);"Thorium";TAB (30);"("%FNER$(P(I,26))&")";
2124  IF PpmU AND PpmTh THEN PRINT TAB (51);"Th/U=";FNDr(PpmTh/PpmU,4) @ PRINT ELSE PRINT
2128 IF R(I,6)=0 THEN 2148
2132 PRINT "238/204=";P(I,19),"    235/204=";P(I,20);TAB (51);"("%FNER$(P(I,39))&")"
2136 IF PpmTh THEN PRINT "232/204=";P(I,21);TAB (51);"("%FNER$(P(I,40))&")"
2140 PRINT @ PRINT "Rho(U/4-6/4)=";P(I,41);"    Rho(U/4-7/4)=";P(I,42);
2144 IF PpmTh THEN PRINT "    Rho(Th/4-8/4)=";P(I,43);
2148 PRINT @ PRINT RPT$ ("-",80)
2152 IF NOT Init64 THEN DONE
2156 !
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2160 ! ******* Calculate radiogenic-Pb isotope ratios and errors **************
2164 !
2168 !
2172 Rad206=Molespg_206*(Corr64-Init64)/Corr64 @ Rad207=Molespg_206*(1/Corr67-Init74/Corr64) @ Rad208=Molespg_206*(1/Cor
r68-Init84/Corr64)
2176 Radsample_wt=FNAliq(Pbunspkd_al_equiv,Pbspkd_al_equiv)
2180 !
2184 ! D1=init-206/rad-206    D2=total-206/rad-206   D3=blank-206/rad-206
2188 ! E1=total-204/initial-204                      E2=blank-204/initial-204
2192 ! F1=init-207/rad-207    F2=total-207/rad-207   F3=blank-207/rad-207
2196 ! G1=init-208/rad-208    G2=total-208/rad-208   G3=blank-208/rad-208
2200 !
2204 D1=Pb206_compal*Init64/(Corr64*Rad206*Radsample_wt) @ D2=(Pb206_compal+Blank206)/(Rad206*Radsample_wt) @ D3=Blank20
6/(Rad206*Radsample_wt)
2208 F1=Init74*Pb206_compal/(Corr64*Rad207*Radsample_wt) @ F2=(Pb206_compal/Corr67+Blank207)/(Rad207*Radsample_wt) @ F3=
Blank207/(Rad207*Radsample_wt)
2212 E1=(Pb206_compal+Blank204*Corr64)/Pb206_compal @ E2=Corr64*Blank204/Pb206_compal
2216 G1=Init84*Pb206_compal/(Corr64*Rad208*Radsample_wt)
2220 G2=(Pb206_compal/Corr68+Blank208)/(Rad208*Radsample_wt) @ G3=Blank208/(Rad208*Radsample_wt) @ PVAR_208232=0
2224 V64=R(I,10)^2+(2*Pbdisc_err)^2 @ V67=R(I,12)^2+Pbdisc_err^2 @ V68=R(I,14)^2+(2*Pbdisc_err)^2 ! %var for raw 6/4,6/7
,6/8, incl mass-disc. error
2228 PVAR_206238=(D1*E1)^2*V64+(D1*E2*Blank64perr)^2+(D1*Init64perr)^2+(D2-D1*E1)^2*PVAR1_206+((D3-D1*E2)*Pbblank_perr)^
2+PVAR1_U
2232 P(I,34)=FNDr(SQR (PVAR_206238),3) ! %error in radiogenic 206/238
2236 A=(F1*E1)^2*V64+((F3-F1*E2)*Blank64perr)^2+(F1*Init74perr)^2+F2^2*V67+(F3*Blank74perr)^2+(F2-F1*E1)^2*PVAR1_206
2240 PVAR_207235=A+((F3-F1*E2)*Pbblank_perr)^2+PVAR1_U-2*F3*(F3-F1*E2)*Blank6474_rho*Blank64perr*Blank74perr
2244 P(I,35)=FNDr(SQR (PVAR_207235),3) ! %error in radiogenic 207/235
2248 IF R(I,8)=0 OR R(I,23)=0 THEN 2264 ! if not spiked with Th or no 232/230 data
2252 A=(G1*E1)^2*V64+((G3-G1*E2)*Blank64perr)^2+(G1*Init84perr)^2+G2^2*V68+(G3*Blank84perr)^2+(G2-G1*E1)^2*PVAR1_206
2256 PVAR_208232=A+((G3-G1*E2)*Pbblank_perr)^2+PVAR1_Th-2*G3*(G3-G1*E2)*Blank6484_rho*Blank64perr*Blank84perr
2260 P(I,38)=FNDr(SQR (PVAR_208232),3) ! %error in 208/232
2264 A=D1*F1*E1^2*V64-D1*E2*(F3-F1*E2)*Blank64perr^2+(D2-D1*E1)*(F2-F1*E1)*PVAR1_206+(D3-D1*E2)*(F3-F1*E2)*Pbblank_perr^
2
2268 COV=A+PVAR1_U+D1*F1*Init6474_rho*Init64perr*Init74perr+D1*F3*E2*Blank6474_rho*Blank64perr*Blank74perr ! COV(206/238
,207/235)/((206/238)*(207/235))
2272 PVAR_207206=PVAR_206238+PVAR_207235-2*COV @ P(I,36)=FNDr(SQR (PVAR_207206),3) ! VAR% & %error in radiogenic 207/206

2276 P(I,37)=COV/SQR (PVAR_206238*PVAR_207235) ! Error-correlation for 206/238-207/235
2280 P(I,11),Rad206238=Rad206*Uspkd_equiv/Moles238_spkdal @ P(I,12),Rad207235=Rad207*Uspkd_equiv*Nat_Uratio/Moles238_spk
dal ! radiogenic 206/238,207/235
2284 P(I,13),Rad207206=Rad207/Rad206
2288 IF PpmTh THEN P(I,14),Rad208232=Uspkd_equiv*Rad208/Moles232_spkdal ELSE P(I,14),Rad208232=0
2292 ! Pb/U AND Pb/Th APPARENT-AGES
2296 IF Rad206238>-1 THEN P(I,15)=LOG (1+Rad206238)/Lambda238 ELSE P(I,15),Rad206238=0 ! Pb206/U238 age
2300 IF Rad207235>-1 THEN P(I,16)=LOG (1+Rad207235)/Lambda235 ELSE P(I,16),Rad207235=0 ! Pb207/U235 age
2304 IF Rad208232>-1 AND Rad208232<.5 THEN P(I,18)=LOG (1+Rad208232)/Lambda232 ELSE P(I,18),Rad208232=0 ! Pb208/Th232 ag
e
2308 !
2312 ! Calculate 207/206 age
2316 !
2320   IF Rad207206<.0156 THEN P(I,17),Age207206=-50000 @ GOTO 2368
2324 ! Can't calculate a 7/6 age for 7/6<.0156, so assign default age of -50000
2328   IF Rad207206>6 THEN P(I,17),Age207206=99999 @ GOTO 2368
2332   T1=3000*(SGN (-(1/2)+(Rad207206>Lambda235/(Lambda238*Nat_Uratio)))+(Rad207206>.7)) ! Choose initial estimate of a
ge- either -3000 Ma or +3000 Ma
2336   F=Lambda238/Lambda235*EXP (T1*(Lambda238-Lambda235))
2340   A=1+(EXP (T1*Lambda238)-1-F*(EXP (T1*Lambda235)-1))/(1/(Nat_Uratio*Rad207206)-F)
2344   IF A<= 0 THEN P(I,17),Age207206=0 @ GOTO 2368
2348   P(I,17),Age207206=LOG (A)/Lambda235
2352   IF ABS (Age207206-T1)<.001 THEN 2368 ELSE T1=Age207206 @ GOTO 2336
```

```
2356 !
2360 ! ------------------- Printout radiogenic-Pb results -----------------
2364 IMAGE "Radiogenic-Pb",8X,"206#",12X,"207#",12X,"208#",/,"Moles Per Gram:",3X,3(D.4DE,5X),/
2368 PRINT USING 2364 ; Rad206,Rad207,Rad208 @ PRINT
2372 PRINT "Initial-Pb:   6/4=";VAL$ (Init64);" +/- ";VAL$ (Init64err);TAB (43);"7/4=";
2376 PRINT VAL$ (Init74);" +/- ";VAL$ (Init74err) @ PRINT TAB (15);"8/4=";VAL$ (Init84);" +/- ";VAL$ (Init84err);
2380 PRINT TAB (43);"RHO(6/4-7/4) =";Init6474_rho @ PRINT
2384 PRINT TAB (16);"206/238";TAB (32);"207/235";TAB (47);"207/206";
2388 IF P(I,14) THEN PRINT TAB (61);"208/232" ELSE PRINT
2392 PRINT @ PRINT "RATIOS:";TAB (15);P(I,11);TAB (31);P(I,12);TAB (46);P(I,13);
2396 IF P(I,14) THEN PRINT TAB (60);P(I,14) ELSE PRINT
2400 PRINT "ERRORS:";TAB (17);VAL$ (P(I,34))&"%";TAB (33);VAL$ (P(I,35))&"%";TAB (48);VAL$ (P(I,36))&"%";
2404 IF P(I,14) THEN PRINT TAB (62);VAL$ (P(I,38))&"%" ELSE PRINT
2408 PRINT "AGES (Ma):";TAB (16);P(I,15);TAB (32);P(I,16);TAB (47);P(I,17);
2412 IF P(I,14) THEN PRINT TAB (61);P(I,18) ELSE PRINT
2416 PRINT @ PRINT "Rho (207/235-206/238) =";P(I,37)
2420 IF KYBRD THEN DONE
2424 IF P(I,2) THEN P(I,22)=R(I,28)/P(I,2) !   BETA eU/U
2428 IF P(I,2) THEN P(I,23)=R(I,29)/P(I,2) !  GAMMA eU/U
2432 P(I,24)=R(I,30) !                     !  BETA/GAMMA
2436 DONE: PRINT RPT$ ("#",80)
2440 !
2444 ! ########################## END CALCULATIONS ################################
2448 IF Printer THEN PRINT @ PRINT
2452 IF KYBRD=0 THEN GOTO NEXTSAMPLE  ELSE GOSUB WHOOP  @ DISP @ DISP "PRESS "&CT$&" TO CONTINUE." @ PAUSE
2456 CLEAR @ GOTO CHOOSE
2460 !
2464 HARDCOPY: BEEP @ Printer=1 @ PRINTER IS 701 @ DISP "### PRINTED OUTPUT ###" @ PRINT CHR$ (27)&"&k0S" @ GOTO KLABEL
2468 !
2472 DISPLAY: BEEP @ Printer=0 @ PRINTER IS 1 @ DISP "### CRT OUTPUT ###" @ GOTO KLABEL
2476 !
2480 KEYBOARD: BEEP @ I=1 @ KYBRD=1 @ CLEAR @ GOTO KYBRDINPUT
2484 !
2488 CHANGEPBO: BEEP @ CLEAR @ GOSUB INPUTPBO  @ CLEAR @ GOTO KLABEL
2492 !
2496 Pb_205: Pb_205spiked=1 @ BEEP @ DISP "## SAMPLES SPIKED WITH A MIXED Pb205/U235/Th230 SPIKE ##" @ GOSUB Transfer_la
bdata_variables  @ RETURN
2500 !
2504 Pb_208: Pb_205spiked=0 @ BEEP @ DISP "## SAMPLES SPIKED WITH A Pb-208 SPIKE ###" @ GOSUB Transfer_labdata_variables
  @ Blank_mult=1 @ RETURN
2508 !
2512 !
2516 DATAFILE: BEEP @ OFF KEY# @ CLEAR @ GOSUB CONVERT
2520 !
2524 DATAFILEINPUT: OFF KEY# @ DISP "SAMPLES TO BE REDUCED: FIRST  [, LAST]       (ALL)";@ GOSUB RETRIEVE
2528   IF UPC$ (AA$)="H" THEN GOSUB HELP_14  @ GOTO DATAFILEINPUT
2532   IF UPC$ (A$)="ALL" THEN FIRSTSAMPLE=1 @ LASTSAMPLE=NSAMPLES @ GOTO 2548
2536   IF Ninputs=0 THEN CLEAR @ GOTO CHOOSE
2540   IF Ninputs=1 THEN FIRSTSAMPLE,LASTSAMPLE=A(1) @ GOTO 2548
2544   FIRSTSAMPLE=A(1) @ LASTSAMPLE=A(2)
2548   GOSUB INPUTPBO  @ CLEAR @ GOTO START
2552 !
2556 CLUNK: BEEP 110,40 @ BEEP 190,40 @ RETURN
2560 !
2564 WHOOP: BEEP 100,40 @ BEEP 70,40 @ BEEP 49,40 @ RETURN
2568 !
2572 INPUTPBO: DISP USING "2/" @ DISP TAB (12);"(Note errors are to be entered as absolute, not percent)"
2576          DISP TAB (10);"(press  "&EL$&" if you don't want any radiogenic-Pb data)" @ DISP TAB (24);"(enter  H  for
 help)" @ DISP
2580          DISP "INITIAL-Pb:  206/204 [, err],  207/204 [, err],  208/204 [, err,  Rho(6/4-7/4)]";@ GOSUB RETRIEVE
```

```
2584 IF UPC$ (AA$)="H" THEN GOSUB HELP_13  @ GOTO 2572
2588  IF Ninputs#0 AND Ninputs#3 AND Ninputs#7 THEN GOSUB BAD_INPUT  @ GOTO INPUTPB0
2592  IF Ninputs=0 THEN Init64,Init74,Init84,Init64err,Init74err,Init84err,Init6474_rho=0
2596  IF Ninputs=3 THEN Init64=A(1) @ Init64err=0 @ Init74=A(2) @ Init74err=0 @ Init84=A(3) @ Init84err,Init6474_rho=0
2600  IF Ninputs=7 THEN Init64=A(1) @ Init64err=A(2) @ Init74=A(3) @ Init74err=A(4) @ Init84=A(5) @ Init84err=A(6) @ Ini
t6474_rho=A(7)
2604 IF Init6474_rho<0 OR Init6474_rho>1 THEN GOSUB CLUNK  @ DISP @ DISP "#### CORRELATION MUST BE BETWEEN 0 AND 1 ####"
 @ DISP @ GOTO INPUTPB0
2608 RETURN
2612 !
2616 START: FOR I=FIRSTSAMPLE TO LASTSAMPLE
2620         IF R(I,2)=0 THEN NEXTSAMPLE ! if no sample weight, skip to next
2624          Trialname$=N$(I)
2628 !
2632 !        Look for indicator of spike type in sample-name.
2636 IF POS (N$(I),"#8#") THEN Pb_205spiked=0 @ GOSUB Transfer_labdata_variables
2640 IF POS (N$(I),"#5#") THEN Pb_205spiked=1 @ GOSUB Transfer_labdata_variables
2644 !
2648         IF NOT Pb_205spiked THEN GO
2652 !
2656 ! ###### table conversion for Pb-205 spiked samples ########
2660         FOR J=1 TO 30 @ C(J)=R(I,J) @ R(I,J)=0 @ NEXT J
2664 !       Transfer Ith row of R-array to C-vector & zero the Ith row
2668 !
2672         R(I,2)=C(1) @ R(I,6),R(I,7),R(I,8)=C(2)
2676 !       sample wt = col. 1, set U-Th spike wts = Pb spike wts
2680 !
2684         IF C(3) THEN Blank_mult=100/C(3) ELSE Blank_mult=1
2688 !       increase blanks according to % loaded
2692 !
2696         R(I,3),R(I,5)=1 @ R(I,4)=0
2700 !       set total & spiked-al wts to 1, unspiked-al wt to zero
2704 !
2708         FOR J=15 TO 20 @ R(I,J)=C(J-11) @ NEXT J @ R(I,10)=C(10)
2712 !       Shift the Pb ratios up 11 columns, put 6/5 data in columns 10-11
2716 !
2720         FOR J=21 TO 27 @ R(I,J)=C(J-9) @ NEXT J @ R(I,11)=C(11) @ GOTO GO
2724 !       shift the U-Th ratios & all blanks up 9 columns
2728 !
2732        NEXTSAMPLE: NEXT I
2736        GOSUB WHOOP  @ GOTO STOR
2740 !
2744 ! !!!!!!!!!!! STORE VISICALC STRINGS CONTAINING REDUCED DATA !!!!!!!!!!!!
2748 !
2752 STOR: ALPHA 1 @ CLEAR @ GOSUB CLEARKEY  @ DISP USING "3/" @ ALPHA 21,44
2756       DISP "TYPE OF DATAFILE FOR REDUCED DATA?"
2760       ON KEY# 5," VISICALC" GOTO 2788
2764       ON KEY# 6," NUMERIC" GOTO 2792
2768       ON KEY# 7,"  ESCAPE" GOTO CHOOSE
2772 KEY LABEL
2776 !
2780 GOTO 2780
2784 !
2788 VISICALC=1 @ GOSUB 2796 @ GOTO 2804
2792 VISICALC=0 @ GOSUB 2796 @ GOTO NUMERIC_FILE
2796 OFF KEY# @ DISP "FILE-NAME FOR REDUCED-DATA FILE";@ INPUT FILE$
2800 RETURN
2804 DISP "TITLE FOR REDUCED-DATA VISICALC TABLE";@ LINPUT TABLE$
2808 PURG=0 @ ON ERROR GOTO PURG
2812 CREATE FILE$,CEIL ((2300+NSAMPLES#850)/256)
```

```
2816 OFF ERROR
2820 ASSIGN# 1 TO  FILE$
2824 CLEAR @ DISP "CREATING VISICALC FILE...." @ GOTO 2848
2828 !
2832 DEF FNCLM$(COLUMN) ! RETURNS VISICALC COLUMN-DESIGNATOR
2836  IF COLUMN<27 THEN FNCLM$=CHR$ (64+COLUMN) ELSE FNCLM$="A"&CHR$ (38+COLUMN)
2840  FN END
2844 !
2848 FOR I=NSAMPLES TO 1 STEP -1 !  CREATE & STORE DATA-CELLS
2852   ON ERROR GOTO 2888 @ L=LEN (N$(I)) @ IF L=0 THEN 2888
2856   ON ERROR GOTO 2872
2860   FOR J=43 TO 1 STEP -1
2864    P=P(I,J)
2868    IF P THEN PRINT# 1 ; ">"&FNCLM$(J+2)&VAL$ (I+5)&":"&VAL$ (P)&CHR$ (13)
2872   NEXT J
2876  IF L>8 THEN L0=9 ELSE L0=L
2880  IF L>9 THEN PRINT# 1 ; ">B"&VAL$ (I+5)&":"&CHR$ (34)&N$(I)[10,L]&CHR$ (13)
2884  PRINT# 1 ; ">A"&VAL$ (I+5)&":"&CHR$ (34)&N$(I)[1,L0]&CHR$ (13)
2888 NEXT I
2892 GOSUB HEADINGS
2896  L=LEN (TABLE$) ! CREATE & STORE TITLE CELLS
2900  FOR I=CEIL (L/9) TO 1 STEP -1
2904   T1=(I-1)*9+1 @ T2=T1+8 @ IF T2>= L THEN T2=L
2908   PRINT# 1 ; ">"&CHR$ (65+I)&"1:"&CHR$ (34)&TABLE$[T1,T2]&CHR$ (13)
2912  NEXT I
2916 RESTORE 2996
2920 ! CREATE & STORE VISICALC-STRUCTURE CELLS
2924 FOR I=1 TO 5 @ READ V$@ PRINT# 1 ; V$&CHR$ (13) @ NEXT I
2928 PRINT# 1 ; "/X"&CHR$ (170)&"/X>A1:>A1:/GP"&CHR$ (13)
2932 ASSIGN# 1 TO  * @ GOSUB WHOOP  @ DISP @ DISP "FILE CONVERTED AND STORED." @ GOTO STOR
2936 !
2940 PURG: IF ERRN #63 THEN 2960 ! PURGE FILE&PACK DISK
2944       PURG=1+PURG @ IF PURG>1 THEN 2964
2948       PURGE FILE$ @ A=POS (FILE$,":")+POS (FILE$,".")
2952       DISP "PACKING DISK..." @ IF A THEN PACK FILE$[A] ELSE PACK
2956       IF VISICALC THEN 2812 ELSE 3344
2960       IF ERRN #128 THEN 2972
2964       GOSUB CLUNK  @ DISP @ DISP "DISK DOESN'T HAVE ENOUGH FREE SPACE TO STORE THIS FILE." @ DISP @ DISP "REPLACE D
ISK AND PRESS "&CT$ @ PAUSE
2968       GOTO STOR
2972       IF ERRN #126 AND ERRN #89 THEN 2984
2976        DISP @ BEEP @ DISP "INVALID FILENAME" @ DISP
2980        IF VISICALC THEN 2788 ELSE 2792
2984       BEEP @ DISP "ERROR# ";ERRN ;" IN LINE";ERRL  @ PAUSE
2988 !
2992 !    DATA-LINE SPECIFIES PAGESIZE 24, 9-CHAR. COLUMN-WIDTH, LEFT-JUSTIFIED
2996 DATA "/W1","/GOC","/GRA","/GFL","/GC9"
3000 HEADINGS: ! CREATE V& STORE COLUMN-HEADING CELLS
3004   DATA "Th/4-8/4","Nu-Beta","Mu-Alpha","  Zerr","  Zerr","  Zerr"," 6/8-7/5","  Zerr","  Zerr","  Zerr"," 6/4-8/4",
" 6/4-7/4","  Zerr","  Zerr"
3008   DATA "  Zerr","  Zerr","  Zerr","  Zerr","  Zerr"," GAMMA"," eU/U"," eU/U"," 232/204"," 235/204"," 238/204"," AGE
 (my)"," AGE(my)"," AGE(my)"
3012   DATA " AGE(my)","  RAD.","  RAD.","  RAD.","  RAD."," CORR."," CORR."," CORR."," RAW","nMOLES/G"," Pb(ppm)"," Pb
(ppm)"," Th(ppm)"," U(ppm)"
3016   DATA "  (G)","AME"," SAMPLE N","  RHO","  RHO","  RHO"," 232/204"," 238/204"," 208/232","  RHO"," 207/206"," 207/
235"," 206/238","  RHO","  RHO"
3020   DATA " 208/204"," 207/204"," 206/204","[Pb-206]","COMM.-Pb","  [Th]","  [U]"," BETA/"," GAMMA"," BETA","","","","
 208/232"," 207/206"," 207/235"
3024  DATA " 206/238"," 208/232"," 207/206"," 207/235"," 206/238","208/204","207/204","206/204","206/204"," Pb-206"," CO
MMON","","","","SAMPLE-WT","",""
```

```
3028  RESTORE 3004
3032  FOR J=45 TO 1 STEP -1
3036   PRINT# 1 ; ">"&FNCLM$(J)&"5:/-="&CHR$ (13)
3040  NEXT J
3044  FOR K=4 TO 3 STEP -1
3048   FOR J=45 TO 1 STEP -1
3052    READ V$@ IF V$="" THEN 3060
3056    PRINT# 1 ; ">"&FNCLM$(J)&VAL$ (K)&":"&CHR$ (34)&V$&CHR$ (13)
3060   NEXT J
3064  NEXT K
3068 RETURN
3072 END
3076 !
3080 ! ########## CONVERT VISICALC RAW-DATA FILE TO NUMERIC ARRAY ##############
3084 !
3088 CONVERT: DISP "Name of the VISICALC file containing the raw data? (enter ! to escape)";@ INPUT FILE$
3092  IF FILE$="!" THEN CHOOSE
3096 ON ERROR GOTO WRONGFILE  @ ASSIGN# 1 TO  FILE$ @ OFF ERROR
3100 CLEAR @ DISP "Converting raw-data VISICALC file..." @ NSAMPLES=0
3104 FOR I=1 TO 3150
3108  ON ERROR GOTO FINISH  !             END SEARCH WHEN NO MORE STRINGS FOUND
3112  READ# 1 ; V$@ OFF ERROR
3116  IF POS (V$,"/-=") OR V$[1,2]="/X" THEN FINISH
3120  IF V$[1,1]#">" THEN NEXTI
3124  A=1+POS (V$,":") @ ASCII=NUM (V$[A,A])
3128  IF ASCII=34 OR ASCII=39 THEN A=1+A ! If 1st label-char is " or '
3132  G=LEN (V$[A])-1 @ D=NUM (V$[3,3]) !   D=45 to 57 (0-9) OR 65 to 90 (A-Z)
3136  IF D>64 AND D<91 THEN F=1 ELSE F=0 !  F=1 IF 3rd CHAR IS A THRU Z
3140  IF F=0 THEN COLUMN=NUM (V$[2,2])-66 ELSE COLUMN=D-40
3144  IF F=0 THEN ROWN=VAL (V$[3])-5 ELSE ROWN=VAL (V$[4])-5
3148  IF ROWN<1 THEN NEXTI !               PASS IF PART OF TABLE-HEADINGS
3152  IF COLUMN>0 THEN EXTRACT_VALUE
3156  IF COLUMN=0 THEN H=9 ELSE H=0
3160  N$(ROWN)[1+H,9+H]=V$[A,A+G-1] !             EXTRACT SAMPLE-NAME
3164  GOTO NEXTI
3168  EXTRACT_VALUE: ON ERROR GOTO NEXTI  !       EXTRACT NUMERIC VALUE OF CELL
3172  R(ROWN,COLUMN)=VAL (V$[A])
3176 NEXTI: NEXT I
3180 OFF ERROR
3184 FINISH: CLEAR @ ON ERROR GOTO 3236
3188 FOR I=1 TO 100
3192  ON ERROR GOTO 3236
3196  IF N$(I)="" THEN 3236
3200  DISP "#";I;TAB (8);N$(I)
3204  ON ERROR GOTO 3232 !             ZERO UNDEFINED ELEMENTS OF ARRAY
3208  FOR J=1 TO 30
3212   A=R(I,J)
3216  NEXT J
3220  OFF ERROR
3224 NEXT I
3228 GOTO 3236
3232 R(I,J)=0 @ GOTO 3216
3236 IF I<10 THEN N$(I)="" @ GOTO 3200 ELSE NSAMPLES=I-1
3240 IF NSAMPLES=0 THEN ILLEGALFILE
3244 OFF ERROR @ GOSUB WHOOP  @ DISP @ DISP "VISICALC FILE ";FILE$;" CONVERTED." @ DISP @ DISP @ Datafile=1
3248 RETURN
3252 !
3256 WRONGFILE: GOSUB CLUNK  @ CLEAR @ DISP "File "&Q$&FILE$&Q$&" isn't on the specified disk." @ DISP
3260  DISP "Put in the correct disk if necessary, and enter the file name again." @ DISP @ DISP @ GOTO CONVERT
3264 !
```

```
3268 ILLEGALFILE: CLEAR @ GOSUB CLUNK  @ DISP "There isn't any data in file "&Q$&FILE$&Q$ @ DISP
3272  DISP "Press "&CT$&" when you are ready to retry." @ PAUSE @ GOTO CONVERT
3276 !
3280 VISICALC: BEEP @ CLEAR @ DISP "LOADING VISICALC..."
3284           ON ERROR GOTO 3292
3288           LOADBIN "VZCALC:D700" @ VC
3292           OFF ERROR @ IF ERRN =19 THEN VC ELSE ON ERROR GOTO 3300
3296           LOADBIN "VZCALC:D701" @ VC
3300           OFF ERROR @ CLEAR @ GOSUB CLUNK
3304           DISP "Neither disk drive contains the VISICALC program." @ DISP @ DISP "Press "&CT$&" when a VISICALC-con
taining disk is in one of the drives."
3308           PAUSE @ GOTO VISICALC
3312 !
3316 NUMERIC_FILE: NS=0 ! CREATE NUMERIC DATA-FILE FOR REDUCED DATA
3320    CLEAR @ DISP "CREATING NUMERIC DATA-FILE '"&FILE$&"' ...." @ DISP
3324    ON ERROR GOSUB 3380
3328    FOR I=1 TO NSAMPLES
3332     IF P(I,1) THEN NS=NS+1
3336    NEXT I
3340    PUR6=0 @ ON ERROR GOTO PUR6  @ CREATE FILE$,NS,390 @ OFF ERROR
3344    CREATE FILE$,NS,390 @ OFF ERROR
3348    ASSIGN# 1 TO  FILE$ @ J=0 @ ON ERROR GOSUB 3380
3352    FOR I=1 TO NSAMPLES
3356     IF P(I,1)=0 THEN 3364 ELSE J=J+1
3360     MAT X=P(I,)@ PRINT# 1,J ; N$(I),X()
3364    NEXT I
3368    OFF ERROR
3372    CLEAR @ GOSUB WHOOP  @ DISP "NUMERIC DATA-FILE '"&FILE$&"' STORED.    PRESS "&CT$&" TO CONTINUE." @ ASSIGN# 1 TO
  # @ PAUSE
3376    GOTO STOR
3380    RETURN
3384 !
3388 ! ##########################################################################
3392 !
3396 Labdatafile: ! Access/edit/redefine datafile containing
3400 !              spike, blank, & mass-discr. data
3404 CLEAR @ GOSUB CLEARKEY  @ DISP "PRESS KEY TO CHOOSE WHICH PART OF THE LABDATA FILE TO DEFINE/EDIT." @ DISP @ DISP @
 Newfile=0
3408 !
3412  ON KEY# 1,"  ALL" GOTO ALL
3416  ON KEY# 3,"Pb208Spike" GOTO 3572
3420  ON KEY# 4,"Pb205Spike" GOTO 3576
3424  ON KEY# 5,"U235 Spike" GOTO 3580
3428  ON KEY# 6,"Th230Spike" GOTO 3584
3432  ON KEY# 7,"Mass Discr" GOTO 3588
3436  ON KEY# 8,"  Blanks" GOTO 3592
3440  ON KEY# 9,"Store File" GOTO 3560
3444  ON KEY# 10,"Print File" GOTO Print_labdatafile
3448  ON KEY# 11,"  ESCAPE" GOTO CHOOSE
3452  ON KEY# 12," NEW FILE" GOTO NEWFILE
3456  ON KEY# 13,"CHANGENAME" GOTO 3600
3460  ON KEY# 14,"  HELP" GOTO HELP_2
3464  KEY LABEL
3468  GOTO 3468
3472 !
3476 ALL: ! define a complete new Labdata file
3480  OFF KEY# @ CLEAR
3484  DISP @ DISP "Is this new Labdata File to be the new Default Labdata File (Y/N)?" @ GOSUB YESNO
3488  IF YES THEN New_default_labdata=1 @ Labdata$="DefLab" ELSE New_default_labdata=0
3492  Pb208$="" @ MAT Pb208=ZER
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```
3496  DISP @ DISP "Do you want to define a Pb-208 spike (Y/N)?" @ GOSUB YESNO
3500  IF YES THEN GOSUB Pb208_spike
3504  Pb205$="" @ MAT Pb205=ZER
3508  DISP @ DISP "Do you want to define a Pb-205/U-235/Th-230 spike (Y/N)?" @ GOSUB YESNO
3512  IF YES THEN GOSUB Pb205_spike
3516  U235$="" @ MAT U235=ZER
3520  GOSUB U235_spike
3524  DISP @ DISP "Do you want to define a Th-230 spike? (Y/N)" @ GOSUB YESNO
3528  Th230$="" @ MAT Th230=ZER
3532  IF YES THEN GOSUB Th230_spike
3536  GOSUB Mass_discrimination
3540  GOSUB Blanks
3544  IF NOT New_default_labdata THEN GOSUB Labdata_name
3548  GOSUB Store_labdatafile
3552  GOTO Labdatafile
3556 !
3560  GOSUB Store_labdatafile  @ GOTO Labdatafile
3564 NEWFILE: Newfile=1 @ GOTO 3596
3568 ! ON KEY# branches
3572  GOSUB Pb208_spike  @ GOTO Labdatafile
3576  GOSUB Pb205_spike  @ GOTO Labdatafile
3580  GOSUB U235_spike  @ GOTO Labdatafile
3584  GOSUB Th230_spike  @ GOTO Labdatafile
3588  GOSUB Mass_discrimination  @ GOTO Labdatafile
3592  GOSUB Blanks  @ GOTO Labdatafile
3596  GOSUB Read_labdatafile  @ GOTO Labdatafile
3600  GOSUB Labdata_name  @ GOTO Labdatafile
3604 !
3608 Labdata_name: ! edit name of labdata file
3612   DISP @ DISP "Name for this Labdata File? (<=10 characters, use ";@$;"$";@$;" for Default LabdataFile)";@ INPUT La
bdata$
3616   IF Labdata$="$" THEN Labdata$="DefLab"
3620   BEEP @ RETURN
3624 !
3628 Pb208_spike: OFF KEY# ! Enter data for a Pb-208 or Pb-206 spike
3632   CLEAR @ DISP "Name for Pb-208 spike";@ INPUT Pb208$
3636   DISP @ DISP "Is this spike mixed with a U-235 spike? (Y/N)" @ GOSUB YESNO
3640   IF YES THEN Pb208(1)=1 ELSE Pb208(1)=0
3644   DISP @ DISP "Moles Pb-208 per gram of spike";@ INPUT Pb208(2)
3648   DISP @ DISP "Uncertainty, in percent, of the Pb-208 concentration";@ INPUT Pb208(3)
3652   DISP @ DISP "Spike 206/204, 206/207, 206/208";@ INPUT Pb208(4),Pb208(5),Pb208(6)
3656   RETURN
3660 !
3664 Pb205_spike: OFF KEY# ! Enter data for a mixed Pb-205/U-235/Th-230 spike
3668   CLEAR @ DISP "Name for Pb-205 spike";@ INPUT Pb205$
3672   DISP @ DISP "Moles Pb-205 per gram of spike";@ INPUT Pb205(1)
3676   DISP @ DISP "Moles U-235 per gram of spike";@ INPUT Pb205(2)
3680   DISP @ DISP "Moles Th-230 per gram of spike";@ INPUT Pb205(3)
3684   DISP @ DISP "% uncertainty in Pb-205, U-235, Th-230 concentrations";@ INPUT Pb205(4),Pb205(5),Pb205(6)
3688   DISP @ DISP "Isotope ratios: 206/205, 206/204, 206/207, 206/208";@ INPUT Pb205(7),Pb205(8),Pb205(9),Pb205(10)
3692   DISP @ DISP "Isotope ratios:  238/235, 232/230";@ INPUT Pb205(11),Pb205(12)
3696   RETURN
3700 !
3704 U235_spike: OFF KEY# ! Enter data for a U-235 spike
3708   CLEAR @ DISP "Name for U-235 spike";@ INPUT U235$
3712   DISP @ DISP "Moles U-235 per gram of spike";@ INPUT U235(1)
3716   DISP @ DISP "% uncertainty in U-235 concentration";@ INPUT U235(2)
3720   DISP @ DISP "238/235 ratio of spike";@ INPUT U235(3)
3724   RETURN
3728 !
```

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3732 Th230_spike: OFF KEY# ! Enter data for a Th-230 spike
3736   CLEAR @ DISP "Name for Th-230 spike";@ INPUT Th230$
3740   DISP @ DISP "Moles Th-230 per gram of spike";@ INPUT Th230(1)
3744   DISP @ DISP "% uncertainty in Th-230 concentration";@ INPUT Th230(2)
3748   DISP @ DISP "232/230 ratio of spike";@ INPUT Th230(3)
3752   RETURN
3756 !
3760 Mass_discrimination: OFF KEY# ! enter data for standard mass-discrimination for mss-spectrometer runs
3764    CLEAR @ DISP TAB (7);"(enter mass-discrimination values in percent per a.m.u.)" @ DISP @ DISP
3768    DISP @ DISP "Mass-discrimination & mass-discrimination uncertainty for Pb runs";@ INPUT Discr(1),Discr(2)
3772    DISP @ DISP "Mass-discrimination & mass-discrimination uncertainty for U runs";@ INPUT Discr(3),Discr(4)
3776    DISP @ DISP "Mass-discrimination & mass-discrimination uncertainty for Th runs";@ INPUT Discr(5),Discr(6)
3780    RETURN
3784 !
3788 Blanks: OFF KEY# ! Enter data for Pb-U-Th blanks
3792   CLEAR @ DISP "% uncertainties in assigned amounts of Pb, U, and Th blanks";
3796   INPUT Blanks(1),Blanks(2),Blanks(3)
3800   DISP @ DISP "Pb-blank:  206/204, 207/204, 208/204";@ INPUT Blanks(4),Blanks(5),Blanks(6)
3804   DISP @ DISP "Pb-blank:  absolute (not percent) uncertainty in 206/204, 207/204, 208/204";@ INPUT Blanks(7),Blanks
(8),Blanks(9)
3808   DISP @ DISP "Pb-blank:  correlation between 206/204 and 207/204 uncertainties";@ INPUT Blanks(10)
3812   DISP @ DISP "Pb-blank:  correlation between 206/204 and 208/204 uncertainties";@ INPUT Blanks(11)
3816   RETURN
3820 !
3824 Print_labdatafile: OFF KEY# ! print out or display contents of a labdata file
3828   CLEAR @ DISP "Do you want a hard-copy of this  ";Q$&Labdata$&Q$;"  labdata-file printout (Y/N)?" @ GOSUB YESNO
3832   IF YES THEN PRINTER IS 701 @ PRINT USING "5/" ELSE PRINTER IS 1
3836   PRINT @ PRINT RPT$ ("-",80);"DATA FROM LABDATA FILE  "&Q$&Labdata$&Q$&":" @ PRINT @ PRINT
3840   IMAGE "[",3A,"] = ",D.4DE,"  +/-",DD.DD,"% moles/g"
3844   PRINT "Pb-208 Spike  ("&Pb208$&"):" @ PRINT
3848   PRINT USING 3840 ; VAL$ (208),Pb208(2),Pb208(3)
3852   IF Pb208(1) THEN PRINT "(this is a Pb-U-[Th] mixed spike)" ELSE PRINT "(not a mixed Pb/U spike)"
3856   PRINT "206/204=";Pb208(4);TAB (23);"206/207=";Pb205(5);TAB (46);"206/208=";Pb208(6)
3860  PRINT USING "2/"
3864  IF Pb205(1)=0 THEN 3896
3868   PRINT "Pb-205 mixed spike   ("&Pb205$&"):" @ PRINT
3872   PRINT USING 3840 ; VAL$ (205),Pb205(1),Pb205(4)
3876   PRINT USING 3840 ; VAL$ (235),Pb205(2),Pb205(5)
3880   PRINT USING 3840 ; VAL$ (230),Pb205(3),Pb205(6)
3884   PRINT @ PRINT "206/205 =";Pb205(7);TAB (35);"238/235 =";Pb205(11)
3888   PRINT "206/204 =";Pb205(8);TAB (35);"232/230 =";Pb205(12)
3892   PRINT "206/207 =";Pb205(9) @ PRINT "206/208 =";Pb205(10)
3896 IF U235(1)=0 THEN 3932 ELSE PRINT USING "2/"
3900 PRINT "U-spike  ("&U235$&"):" @ PRINT
3904 PRINT USING 3840 ; VAL$ (235),U235(1),U235(2)
3908 PRINT "238/235 =";U235(3) @ PRINT USING "2/"
3912 IF Th230(1)=0 THEN 3932
3916 PRINT "Th-spike  ("&Th230$&"):" @ PRINT
3920   PRINT USING 3840 ; VAL$ (230),Th230(1),Th230(2)
3924 PRINT "232/230 =";Th230(3)
3928 !
3932 PRINT USING "2/"
3936 PRINT "Average mass-discrimination during mass-spectrometer runs, in %/a.m.u. --" @ PRINT
3940 PRINT "Pb:  ";Discr(1);"+/-";Discr(2);TAB (25);"U: ";Discr(3);"+/-";Discr(4);TAB (50);"Th: ";Discr(5);"+/-";Discr(6
) @ PRINT @ PRINT
3944 PRINT "Average Blanks:" @ PRINT
3948 PRINT "Uncertainty in assigned amount:  Pb - "&VAL$ (Blanks(1))&"%";TAB (48);"U - "&VAL$ (Blanks(2))&"%";TAB (63);"
Th - "&VAL$ (Blanks(3))&"%" @ PRINT
3952 PRINT "Pb blank ratios and uncertainties:" @ PRINT
3956 PRINT "206/204 = "&VAL$ (Blanks(4))&"+/-"&VAL$ (Blanks(7));TAB (26);
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3960 PRINT "207/204 = "&VAL$ (Blanks(5))&"+/-"&VAL$ (Blanks(8));TAB (52);
3964 PRINT "208/204 = "&VAL$ (Blanks(6))&"+/-"&VAL$ (Blanks(9))
3968 PRINT "Error-Correlations: 206/204-207/204=";Blanks(10);TAB (45);"206/204-208/204=";Blanks(11) @ PRINT RPT$ ("-",80
)
3972 IF Printer THEN PRINT USING "5/" ELSE PRINTER IS 1
3976 IF NOT YES THEN DISP "Press  "&CT$&" to continue, use "&HGL$ (" ROLL ")&" key to scroll display." @ PAUSE
3980 GOTO Labdatafile
3984 !
3988 Store_labdatafile: OFF KEY#
3992  DISP "Name of labdata file";@ INPUT Labdata$
3996  ON ERROR GOTO Bad_write
4000  ASSIGN# 1 TO  Labdata$
4004  PRINT# 1 ; Pb208$,Pb208(),Pb205$,Pb205(),U235$,U235(),Th230$,Th230(),Blanks(),Discr()
4008  OFF ERROR
4012  ASSIGN# 1 TO  *
4016  P=POS (Labdata$,":")+POS (Labdata$,".")
4020  IF P THEN Labdata$=Labdata$[1,P-1]
4024  GOSUB WHOOP  @ DISP @ DISP "STORED." @ DISP @ RETURN
4028 !
4032 Read_labdatafile: OFF KEY#
4036  IF Labdata$#"DefLab" OR Newfile THEN DISP @ DISP "Name of LabData file";@ INPUT Labdata$
4040  ON ERROR GOTO Bad_read
4044  ASSIGN# 1 TO  Labdata$
4048  READ# 1 ; Pb208$,Pb208(),Pb205$,Pb205(),U235$,U235(),Th230$,Th230(),Blanks(),Discr()
4052  OFF ERROR
4056  RETURN
4060 !
4064 Bad_read: ! can't read specified Labdata file
4068  ON ERROR GOTO 4080
4072  ASSIGN# 1 TO  Labdata$&":d700"
4076  READ# 1 ; Pb208$,Pb208(),Pb205$,Pb205(),U235$,U235(),Th230$,Th230(),Blanks(),Discr()@ OFF ERROR @ RETURN
4080  ON ERROR GOTO 4092
4084  ASSIGN# 1 TO  Labdata$&":d701"
4088  READ# 1 ; Pb208$,Pb208(),Pb205$,Pb205(),U235$,U235(),Th230$,Th230(),Blanks(),Discr()@ OFF ERROR @ RETURN
4092  GOSUB CLUNK  @ IF Labdata$#"DefLab" THEN 4116
4096  CLEAR @ DISP "### There isn't a default labdata file defined on either disk." @ DISP
4100  DISP "Either put in a disk with a default labdata file (1), or define a new default" @ DISP "labdata file (2)." @
DISP @ INPUT A
4104  IF A#1 AND A#2 THEN GOSUB CLUNK  @ GOTO 4100
4108  IF A=1 THEN DISP "Press "&CT$&" when proper disk is in drive." @ PAUSE @ GOTO Read_labdatafile
4112  Labdata$="DefLab" @ New_default_labdata=1 @ GOTO ALL
4116  DISP @ DISP "CAN'T READ FILE  "&Labdata$&"  -- CHECK NAME AND/OR DISK, PRESS "&CT$&" WHEN READY" @ DISP @ DISP @ P
AUSE @ GOTO Read_labdatafile
4120  !
4124 Bad_write: ! can't store Labdata file on disk
4128  GOSUB CLUNK  @ DISP @ DISP "CAN'T STORE LABDATA FILE.  PACK/SWITCH DISK IF FULL & TRY AGAIN." @ DISP @ DISP @ GOTO
 Store_labdatafile
4132 !
4136 Transfer_labdata_variables: ! transfer the array-variables from the labdata file to simple, mnemonically useful var
iables.
4140  IF Pb_205spiked THEN 4152
4144  Pbspike$=Pb208$
4148  Mixed_spike=Pb208(1) @ Spike208pg=Pb208(2) @ Pbspike_conc_perr=Pb208(3) @ Spike64=Pb208(4) @ Spike67=Pb208(5) @ Sp
ike68=Pb208(6) @ GOTO 4168
4152  Pbspike$,Uspike$,Thspike$=Pb205$
4156  Spike205pg=Pb205(1) @ Pbspike_conc_perr=Pb205(4) @ Spike64=Pb205(8) @ Spike65=Pb205(7) @ Spike67=Pb205(9) @ Spike6
8=Pb205(10)
4160  Spike235pg=Pb205(2) @ Spike235pg_perr=Pb205(5) @ Spike238235=Pb205(11)
4164  Spike230pg=Pb205(3) @ Spike230pg_perr=Pb205(6) @ Spike232230=Pb205(12) @ GOTO 4176
4168  Uspike$=U235$ @ Spike235pg=U235(1) @ Spike235pg_perr=U235(2) @ Spike238235=U235(3)
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4172  Thspike$=Th230$ @ Spike230pg=Th230(1) @ Spike230pg_perr=Th230(2) @ Spike232230=Th230(3)
4176  Pbdisc=Discr(1) @ Pbdisc_err=Discr(2) @ Udisc=Discr(3) @ Udisc_err=Discr(4) @ Thdisc=Discr(5) @ Thdisc_err=Discr(6
)
4180  Pbblank_perr=Blanks(1) @ Ublank_perr=Blanks(2) @ Thblank_perr=Blanks(3)
4184  Blank64=Blanks(4) @ Blank74=Blanks(5) @ Blank84=Blanks(6)
4188  Blank64err=Blanks(7) @ Blank74err=Blanks(8) @ Blank84err=Blanks(9)
4192  Blank6474_rho=Blanks(10) @ Blank6484_rho=Blanks(11)
4196  RETURN
4200 !
4204 HELP_1: CLEAR ! Help screen for initial key-functions
4208  DISP "This program takes raw Pb-U-Th data, in the form of laboratory weights and mass-"
4212  DISP "spectrometer ratios & errors, and calculates Pb, U, and Th concentrations,"
4216  DISP "Pb-isotope ratios, and appropriate errors & error-correlations." @ DISP
4220  DISP "The data may come from either a VISICALC datafile of the appropriate structure;"
4224  DISP "or you can type in the raw data from the keyboard." @ DISP @ DISP "Press "&CT$&"for more help." @ DISP @ PAU
SE
4228  DISP "You must have defined a LabData File for you own lab in order to get valid"
4232  DISP "results from the program.  You can do this by pressing the "&HGL$ (" LABDATA ")&" key." @ DISP
4236  DISP "If the sample were spiked with a Pb-208 spike but no Pb-unspiked data exist for"
4240  DISP "some reason, enter no data for the unspiked 206/204 and 206/207 ratios, but"
4244  DISP "enter your best estimate (with uncertainty) of the true unspiked 206/208 ratio."
4248  DISP "If a Pb-208 spiked sample were total-spiked for U and Th (rather than aliquoted"
4252  DISP "for U-Th spiking), enter the Pb-spiked aliquot weight as a negative value." @ DISP
4256  DISP "All isotope ratios must be entered without mass-discrimination correction, and"
4260  DISP "all uncertainties/errors must be entered at the 2-sigma/95%-confidence level." @ DISP
4264  DISP "Note that most errors are to be entered in percent, unless specifically"
4268 DISP "requested as absolute." @ DISP
4272 DISP "Brackets in a query indicate an optional input." @ DISP
4276 DISP "Press "&CT$&" for more HELP." @ PAUSE
4280  DISP @ DISP @ DISP TAB (22);"WHAT THE k1-k14 KEYS DO:" @ DISP @ DISP
4284  DISP HGL$ (" $CRT$ ");
4288  DISP TAB (15);"Display the results of the calculations on the CRT rather than"
4292  DISP TAB (15);"than printing them out (default)." @ DISP
4296  DISP HGL$ (" PRINT ");TAB (15);"Print out the calculations on the printer rather than" @ DISP TAB (15);"displaying
 them on the CRT." @ DISP
4300  DISP HGL$ (" $KEYBOARD$ ");TAB (15);"Type in the raw data from the keyboard rather than"
4304  DISP TAB (15);"using raw data from a datafile (default)." @ DISP
4308  DISP HGL$ (" DATAFILE ");TAB (15);"Get the raw data from a VISICALC datafile"
4312  DISP TAB (15);"rather than the computer keyboard." @ DISP
4316  DISP HGL$ (" CHANGE PBO ");TAB (15);"Change the initial-Pb values used for radiogenic-Pb"
4320  DISP TAB (15);"calculations (datafile input only)." @ DISP
4324  DISP HGL$ (" VISICALC ");TAB (15);"Load and run the VISICALC binary program." @ DISP
4328  DISP HGL$ (" $Pb208$ ");TAB (15);"Assume that the samples were spiked with a Pb-208 (or Pb-206)"
4332  DISP TAB (15);"spike, rather than a mixed Pb-205 spike (default)." @ DISP
4336  DISP HGL$ (" Pb-205 ");TAB (15);"Assume that the samples were spiked with a mixed"
4340  DISP TAB (15);"Pb-205/U-235/Th-230 spike." @ DISP
4344  DISP HGL$ (" LABDATA ");TAB (15);"Edit or change the Labdata File, which contains spike, blank," @ DISP TAB (15);"
and mass-discrimination data." @ DISP
4348  DISP HGL$ (" MORE DFRED ");TAB (15);"Reduce more data from a VISICALC datafile." @ DISP
4352  DISP HGL$ (" HELP ");TAB (15);"Invoke this HELP screen." @ DISP
4356  DISP @ DISP "press "&CT$&" to return to calling display, use "&HGL$ (" ROLL ")&" key to scroll display." @ DISP
4360  PAUSE @ GOTO CHOOSE
4364 HELP_2: CLEAR ! Help screen for Labdata File key-functions
4368 DISP "A Labdata File is a data file that contains the basic laboratory infor-"
4372 DISP "mation for reducing raw U-Pb-Th isotope data.  This file, which is stored"
4376 DISP "on a floppy disk, includes concentration and isotope ratio data for the "
4380 DISP "Pb, U, and Th spikes; the average mass discrimination and mass-discr. un-"
4384 DISP "certainty for typical Pb, U, and Th runs; and the isotope ratios and uncer-"
4388 DISP "tainties in amounts of the Pb, U, and Th blanks." @ DISP
4392  DISP "This part of the program allows you to edit the Labdata file in memory, to"
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4396  DISP "create a new Labdata file, and to bring a different Labdata file into memory."
4400 DISP "The default Labdata file, called "&Q$&"DefLab"&Q$&" is the one that is loaded into"
4404 DISP "memory at the start of the program after pressing the "&HGL$ (" RUN ")&" key."
4408 DISP @ DISP "- press "&CT$&" for more help -" @ DISP @ DISP @ PAUSE
4412  DISP TAB (22);"WHAT THE k1-k14 KEYS DO:" @ DISP
4416  DISP HGL$ (" ALL ");
4420  DISP TAB (15);"Define a completely new Labdata File." @ DISP
4424  DISP HGL$ (" Pb208spike ");TAB (15);"Redefine the data for the Pb-208 spike only." @ DISP
4428  DISP HGL$ (" Pb205spike ");TAB (15);"Redefine the data for the mixed Pb205/U235/Th230"
4432  DISP TAB (15);"spike only." @ DISP
4436  DISP HGL$ (" U235spike ");TAB (15);"Redefine the data for the U-235 spike only." @ DISP
4440  DISP HGL$ (" Th230spike ");TAB (15);"Redefine the data for the Th-230 spike only." @ DISP
4444  DISP HGL$ (" MassDiscr ");TAB (15);"Redefine the data for Pb, U, & Th mass-discrimination." @ DISP
4448 DISP HGL$ (" Blanks ");TAB (15);"Redefine the data for the composition amount-uncertainty"
4452 DISP TAB (15);"of the Pb, U and Th blanks." @ DISP
4456 DISP HGL$ (" Store File ");TAB (15);"Store the currently defined (or redefined) Labdata File" @ DISP TAB (15);"on a
 disk." @ DISP
4460 DISP HGL$ (" Print File ");TAB (15);"Printout or display the currently defined" @ DISP TAB (15);"(or redefined) Lab
data File" @ DISP
4464 DISP HGL$ (" New File ");TAB (15);"Get data for a different Labdata File from a disk." @ DISP
4468 DISP HGL$ (" CHANGENAME ");TAB (15);"Rename the currently-defined Labdata File." @ DISP
4472 DISP HGL$ (" ESCAPE ");TAB (15);"Exit the Labdata File edit/change routine." @ DISP @ DISP
4476 GOTO 4352
4480 END
4484 !
4488 NOHELP: GOSUB CLUNK  @ DISP "Sorry, no HELP screen for this query." @ DISP @ RETURN
4492 !
4496 HELP_3: DISP @ DISP Q$&"GRAMS OF SAMPLE"&Q$&"  is the weight of the sample that was actually dissolved."
4500 DISP Q$&"TOTAL-ALIQUOT"&Q$&"  is the weight, in grams, of the total solution of the sample."
4504 DISP "If you enter only 1 value, it will be taken as the sample weight, and the "&Q$&"TOTAL"
4508 DISP "ALIQUOT"&Q$&" weight will be assumed to be the sum of the Pb-spiked and Pb-unspiked"
4512 DISP "aliquot weights.  This is appropriate if none of the dissolved sample were kept"
4516 DISP "in reserve for some reason." @ DISP @ RETURN
4520 !
4524 HELP_4: DISP @ DISP "Enter the weight of the sample that was spiked with the mixed spike, and"
4528 DISP "(optional) the percent of the total solution of the dissolved sample that was"
4532 DISP "actually (extracted &) loaded.  If you don't enter a value for the latter,"
4536 DISP "the program will assume a value of 100% (all of the sample loaded)." @ DISP @ RETURN
4540 !
4544 HELP_5: DISP @ DISP "Enter the weight of mixed Pb205-U235-Th230 spike delivered to the sample." @ DISP @ RETURN
4548 !
4552 HELP_6: DISP @ DISP "Enter the observed (not corrected for mass-discrimination) 206/205 ratio"
4556 DISP "from the mass-spectrometer run, and its 2-sigma mean uncertainties, in percent." @ DISP @ RETURN
4560 !
4564 HELP_7: DISP @ DISP "Enter the weight(s), in grams, of the Pb-unspiked aliquot (if any), and the"
4568 DISP "Pb-spiked aliquot.  If there was no Pb-unspiked aliquot, just enter the weight"
4572 DISP "of the Pb-spiked aliquot.  If the sample were total-spiked for U [and Th] rather"
4576 DISP "than having a separate Pb-U-Th spiked aliquot, you must enter the Pb-spiked"
4580 DISP "aliquot weight as its "&HGL$ (" negative ")&" value." @ DISP @ RETURN
4584 !
4588 HELP_8: DISP @ DISP "Enter the weight, in grams, of Pb, U, and Th spikes delivered to the spiked"
4592 DISP "aliquot.  If no Th-spike was delivered, just enter 2 values; if only a Pb-spike"
4596 DISP "were delivered, just enter 1 value.  Even if the U-Th spike (or Pb-U-Th spike)"
4600 DISP "is a mixed spike, you must still enter a spike weight for each element." @ DISP @ RETURN
4604 !
4608 HELP_9: DISP @ DISP "Enter the raw ratios and uncertainties, uncorrected for mass-discrimination,"
4612 DISP "of the Pb-unspiked alqiquot run.  If you have no unspiked Pb data, just enter"
4616 DISP "your best estimate of the unspiked 206/208 ratio and uncertainty." @ DISP @ RETURN
4620 !
4624 HELP_10: DISP @ DISP "Enter the raw ratios and uncertainties, uncorrected for mass-discrimination,"
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4628 DISP "of the Pb-spiked aliquot run.  If you have no 204 data, just enter the 4 values"
4632 DISP "for 206/207, error, 206/208, error.  If you have only 206/208 data, just enter"
4636 DISP "the 206/208 ratio and uncertainty.  Uncertainties are 2-sigma mean, in percent." @ DISP @ RETURN
4640 !
4644 HELP_11: DISP @ DISP "Enter the raw U and Th ratios and uncertainties (uncorrected for mass-discrim-"
4648 DISP "ination, 2-sigma mean in percent) for the U-[Th] spiked aliquot run.  If no Th"
4652 DISP "data exist, just enter the U data." @ DISP @ RETURN
4656 !
4660 HELP_12: DISP @ DISP "Enter the Pb, U, and Th blanks corresponding to the Pb, U, and Th runs."
4664 DISP "If not run for Th, just enter the Pb and U values; if run only for Pb, just"
4668 DISP "enter the Pb blank.  Remember to apportion the blanks according to the"
4672 DISP "aliquoting scheme.  For example, consider a sample dissolved in a bomb,"
4676 DISP "aliquoted and extacted for Pb, and with 50% of the extracted sample loaded and"
4680 DISP "run.  Then the bomb-blank would be apportioned according to how much the"
4684 DISP "Pb-unspiked aliquot represents of the total sample, just half the Pb extraction"
4688 DISP "blank would be added, and all of the loading blank." @ DISP @ RETURN
4692 !
4696 HELP_13: DISP @ DISP "If you don't want any radiogenic-Pb ratios or apparent ages to be calculated,"
4700 DISP "just press "&EL$&"."
4704 DISP "If you're reducing data for several samples that must have shared exactly the"
4708 DISP "same initial-Pb (such as a zircon suite), enter the 6/4, 7/4, and 8/4 values"
4712 DISP "only. If you're reducing a single sample, or a set of samples whose initial-Pb"
4716 DISP "might be expected to vary somewhat (for example, whole-rocks of S-type"
4720 DISP "granites), enter all of the 7 values requested."
4724 DISP "The initial-Pb of a sample is the Pb that the sample was 'born' with - as dis-"
4728 DISP "tinct from the common-Pb introduced in the lab.  The 'err' values refer to the"
4732 DISP "absolute uncertainty in each ratio, not the percent uncertainty."
4736 DISP "Rho(6/4-7/4) refers to the error-correlation between the initial-Pb 206/204 and"
4740 DISP "207/204 ratios.  This is related to the 206/207 uncertainty in the initial-Pb"
4744 DISP "by the equation:" @ DISP @ DISP TAB (15);"Rho=[S(6/4)^2+S(7/4)^2-S(6/7)^2]/[2*S(6/4)*S(7/4)]" @ DISP @ DISP "
where S refers";
4748 DISP " to the percent uncertainty in the ratio." @ DISP
4752 DISP TAB (20);"-- press "&CT$&" to continue --" @ DISP @ PAUSE
4756 RETURN
4760 !
4764 HELP_14: DISP @ DISP "The computer assumes that you want to enter raw data from the VISICALC data-"
4768 DISP "file that is in memory.  If you enter 1 value, only that sample of the VISICALC"
4772 DISP "file will be reduced.  If you enter 2 values, all of the samples between those"
4776 DISP "2 values, inclusive, will be reduced.  If you enter the word  ALL, all of the"
4780 DISP "samples in the VISICALC file in memory will be reduced."
4784 DISP "If you just press  "&EL$&", the program will return to the initial menu." @ DISP @ DISP @ RETURN
4788 !
4792 END
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