

HEWLETT-PACKARD

# HP-67/HP-97

Clinical Lab and Nuclear Medicine Pac





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# Introduction

The 19 programs of Clinical Lab and Nuclear Medicine Pac have been drawn from the fields of clinical chemistry, nuclear medicine, radioimmunoassay, and statistics.

Each program in the pac is represented by a magnetic program card and a section in this manual. The manual provides a description of the program with relevant equations, a set of instructions for using the program, and one or more example problems, each of which includes a list of the actual keystrokes required for its solution. Program listings for all the programs in the pac appear at the back of this manual. Explanatory comments have been incorporated in the listings to assist you should you want to study the actual workings of the program.

No knowledge of programming is required to use the programs in this pac. However, some familiarity with keyboard operations, as described in Sections 1 through 5 of the Owner's Handbook, is assumed. If you have already run a number of programs from Standard Pac or another applications pac, you will be able to use these programs with very little additional instruction. We recommend that you read only "A Word about these Programs" on pages iv and v of this manual. If, on the other hand, this is your first exposure to running pre-recorded programs, be sure to read the entire introductory section on pages iv to xii.

We hope that Clinical Lab and Nuclear Medicine Pac will assist you in the solution of numerous problems around the laboratory. We have tried to provide you with the most commonly used statistics programs as well, but should you find the need for more, there is another pac, Stat Pac I, exclusively for statistics.

We would very much appreciate knowing your reactions to the programs in this pac, and to this end we have provided a questionnaire inside the front cover of this manual. Would you please take a few minutes to give us your comments on these programs? It is in the comments we receive from you that we learn how best to increase the usefulness of programs like these.

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## A WORD ABOUT THESE PROGRAMS

This application pac has been designed for both the HP-97 Programmable Printing Calculator and the HP-67 Programmable Pocket Calculator. The most significant difference between the HP-67 and the HP-97 calculators is the printing capability of the HP-97. Most of the computed results in this pac are output by the command PRINTx. On the HP-97 these results will be output on the printer. On the HP-67 each PRINTx command will be interpreted as a PAUSE: the program will halt, display the result for about five seconds, then continue execution.

If you use an HP-67, you may want more time to copy down the number displayed by a PRINTx command. All you need to do is press any key on the keyboard during the pause interval in which the result is displayed. This action will cause the program to halt; execution of the halted program may be re-initiated by pressing **R/S**. Values that are output by a PRINTx command are marked by three asterisks (\*\*\*) in the keystroke solutions to example problems. The keystroke solutions reflect another slight difference between the HP-67 and the HP-97. It is sometimes necessary in these solutions to include operations that involve prefix keys, namely, **f** on the HP-97 and **f**, **g**, and **h** on the HP-67. For example, the operation ( $10^x$ ) is performed on the HP-97 as **f**  $10^x$  and on the HP-67 as **g**  $10^x$ . In such cases, the keystroke solution omits the prefix key and indicates only the operation (as here,  $10^x$ ). As you work through the example problems, take care to press the appropriate prefix keys (if any) for your calculator.

Programs 1 through 13 of this pac are alike in that many of the same operations are available in each of these programs. A look at the magnetic cards for these programs will show three instructions repeated in gold on every card of these thirteen: PTNT #, P OFF?, and REPRINT. These three operations are intended primarily for use on the HP-97. In addition, either CLEAR or START appears on all of the first thirteen cards. Some discussion of these common operations may be helpful.

The instruction PTNT # allows you to key in a patient number which will be immediately printed in order to identify the data and results of the following calculations. The patient number used should be a whole number; the program will append two digits after the decimal point to identify the program being used, 01 to 13. For example, if the patient number 1234 is used in program 7, the program would print the identification 1234.07, which serves to identify the entire context of the calculations which are to follow. The use of the patient number for identification purposes is entirely optional and may be omitted.

The interrogative P OFF? asks the question: do you want to turn the print function off? When the program is loaded, a flag is set that causes all inputs and outputs of the program to be printed. If this information is not all desired, you may eliminate some or all of it, depending on the program, by turning the print

function off. It may later be turned back on at any time without affecting the operation of the program.

The instruction REPRINT allows for an additional printout of all data and results after a calculation has been completed. Frequently in the clinical lab, the results of a test must be reported to several different departments. The REPRINT feature allows you to obtain additional copies of the data and results directly from the program.

The instructions CLEAR and START are similar in that both have to do with initialization of the program and should be executed before any other operation in the program. They differ in that CLEAR is an optional instruction and START is mandatory. Basically, CLEAR simply sets certain registers to zero to insure that meaningless information is not output during a REPRINT. On the other hand, START loads registers with necessary initial values without which the program would fail to function properly.

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Select the *Protein Electrophoresis* card, CL1-02A, from the card case supplied with this application pac.

If you are using the HP-97, set the printer switch to MAN. All the programs in this pac are designed for manual printer setting.

Gently insert either end of the card (printed side up) in the reader slot of your calculator as shown in figure 1a or 1b.



When the card is part way in, a motor engages and passes it out the other side of the calculator. Sometimes the motor engages but does not pull the card in. If this happens, push the card a little farther into the machine. Do not impede or force the card; let it move freely.

The display will show “Error” if the card reads improperly. In this case, press **CLx** and reinsert the card.

Since *Protein Electrophoresis* is longer than 112 steps (the capacity of one side of a magnetic card), the display now shows "Crd" indicating that a



second card pass is necessary to load the remaining steps. With the writing still visible to you, insert the *opposite* end of the card (figures 2a and 2b) and pass the card through the card reader again.

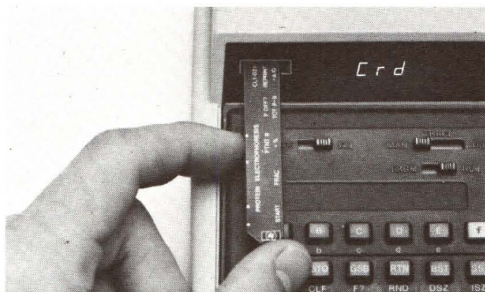


Figure 2a. HP-97



Figure 2b. HP-67

When the motor stops, remove the card from the other side of the calculator and insert it in the “window slot” of the calculator (figures 3a and 3b).



Figure 3a. HP-97



Figure 3b. HP-67

The program has now been stored in the calculator. It will remain stored until another program is loaded or the calculator is turned off.

### The Magnetic Card

Complete instructions for running the program are found in the User Instructions form for that program. The first few times you run the program, you should refer to these instructions at each step of the operation. Thereafter, mnemonic symbols on the magnetic card itself will provide shorthand instructions to the program's operation.

Take a look at the card that you have inserted in the window slot of the calculator. Notice that the mnemonic symbols on the card are grouped above the user-definable keys **A** through **E**. For example, the symbols “→%” and “PTNT #” are associated with key **C**. Symbols in gold are associated with the shifted keys **f A** through **f E**.

Below is a table of the important symbols and conventions you will find on magnetic cards.

SYMBOL OR CONVENTION	INDICATED MEANING
White mnemonic: x <b>A</b>	White mnemonics are associated with the user-definable key they are above when the card is inserted in the calculator's window slot. In this case the value of x could be input by keying it in and pressing <b>A</b> .
Gold mnemonic: y x <b>f E</b>	Gold mnemonics are similar to white mnemonics except that the gold <b>f</b> key must be pressed before the user-definable key. In this case y could be input by pressing <b>f E</b> .
x $\uparrow$ y <b>A</b>	$\uparrow$ is the symbol for <b>ENTER</b> . In this case <b>ENTER</b> is used to separate the input variables x and y. To input both x and y you would key in x, press <b>ENTER</b> , key in y and press <b>A</b> .

## SYMBOLS AND CONVENTIONS (Continued)

SYMBOL OR CONVENTION	INDICATED MEANING
$\boxed{x}$ <b>A</b>	The box around the variable $x$ indicates input by pressing <b>STO</b> <b>A</b> .
$(x)$ <b>A</b>	Parentheses indicate an option. In this case, $x$ is not a required input but could be input in special cases.
$\rightarrow x$ <b>A</b>	$\rightarrow$ is the symbol for calculate. This indicates that you may calculate $x$ by pressing key <b>A</b> .
$\rightarrow x, y, z$ <b>A</b>	This indicates that $x$ , $y$ , and $z$ are calculated by pressing <b>A</b> once. The values would be printed in $x, y, z$ order.
$\rightarrow x; y; z$ <b>A</b>	The semi-colons indicate that after $x$ has been calculated using <b>A</b> , $y$ and $z$ may be calculated by pressing <b>R/S</b> .
$\rightarrow "x," y$ <b>A</b>	The quote marks indicate that the $x$ value will be "paused" or held in the display for one second. The pause will be followed by the display of $y$ .
$\diamond x$ <b>A</b>	The two-way arrow $\diamond$ indicates that $x$ may be either output or input when the associated user-definable key is pressed. If numeric keys have been pressed between user-definable keys, $x$ is stored. If numeric keys have not been pressed, the program will calculate $x$ .
$P?$ <b>A</b>	The question mark indicates that this is a mode setting, while the mnemonic indicates the type of mode being set. In this case a print mode is controlled. Mode settings typically have a 1.00 or 0.00 indicator displayed after they are executed. If 1.00 is displayed, the mode is on. If 0.00 is displayed, it is off.
START <b>A</b>	The word START is an example of a command. The start function should be performed to begin or start a program. It is included when initialization is necessary.
DEL <b>A</b>	This special command indicates that the last value or set of values input may be deleted by pressing <b>A</b> .



## FORMAT OF USER INSTRUCTIONS

The completed User Instructions Form—which accompanies each program—is your guide to operating the programs in this Pac.

The form is composed of five labeled columns. Reading from left to right, the first column, labeled STEP, gives the instruction step number.

The INSTRUCTIONS column gives instructions and comments concerning the operations to be performed.

The INPUT DATA/UNITS column specifies the input data, and the units of data if applicable. Data input keys consist of [0] to [9] and decimal point (the numeric keys), [EEX] (enter exponent), and [CHS] (change sign).

The KEYS column specifies the keys to be pressed after keying in the corresponding input data.

The OUTPUT DATA/UNITS column specifies intermediate and final outputs and their units, where applicable.

The following illustrates the User Instruction Form for *Protein Electrophoresis*, CL1-02A.

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
1	Load side 1 and side 2.			
2	Initialize.		<b>A</b>	0.00
3	(optional) Key in patient number.	Ptnt #	<b>f C</b>	Ptnt # .02
4	To suppress output of data, turn print function off.		<b>f D</b>	0.00
5	To turn print back on later.		<b>f D</b>	1.00
6	Key in the counts of the first protein fraction.	Fract <sub>1</sub>	<b>B</b>	1.00
7	Repeat this step for the rest of the fractions.	Fract <sub>i</sub>	<b>B</b>	i
8	Calculate the percentage each fraction is of the whole.		<b>C</b>	%
9	(optional) Key in the total grams of protein and find the grams in each fraction.	Total Protein	<b>D</b>	grams
10	(optional) Find the albumin/globulin ratio.		<b>E</b>	A/G
11	(optional) Obtain a reprint of all			

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
	data and results (Total Protein			
	and grams omitted if Total			
	Protein not input).		<b>f</b> <b>E</b>	Ptnt # .02
				Fract <sub>1</sub> ...
				Fract <sub>n</sub>
				(%) <sub>1</sub> ...
				(%) <sub>n</sub>
				Total Protein
				grams <sub>1</sub> ...
				grams <sub>n</sub>
				A/G
12	For a new case, go to step 2.			

Since you loaded this program in "Loading a Program" on page vi, step 1 is already done and we can move to step 2. (If you turned your calculator off, you must reload the program.) Leave the magnetic card in the window slot above keys **A** through **E**.

Step 2 is an initialization procedure, marked START on the magnetic card. Press **A** now to perform the initialization, as shown in the KEYS column. You should see a display of 0.00.

Step 3 is optional and allows for input of the patient number if identification of the output is desired. The number output at this step is the patient number followed by ".02", which marks the second program of the pac, CL1-02A. Key in the patient number 1234 and see an output of 1234.02.

Steps 4 and 5 have to do with the optional print mode, which may be turned off or on through the keystrokes **f** **D**. When the program is loaded, the print function is on; pressing **f** **D** will turn it off and display 0.00. Try it. Successive presses of **f** **D** will turn the print function on, then off, alternately displaying 1.00 (on) and 0.00 (off). Try this, but leave 1.00 displayed (print function on) when you are finished. This will allow the input data to be output through PRINTx commands.

Step 6 begins the actual input of the fractionation data. You are to key in the counts for the first protein fraction (Fract<sub>1</sub> under INPUT DATA/UNITS) and press **B**. This value will be output and a 1.00 will be displayed to mark the input of the first fraction. Step 7 instructs you to input the remaining protein fractionation counts in a like manner, keying in each value and pressing **B**.

The number displayed after each value is input indicates the number of functions input so far. Try this sequence with the values from the table below.

Fraction	Substance	Counts
1	Albumin	67
2	$\alpha_1$ -globulin	4
3	$\alpha_2$ -globulin	10
4	$\beta$ -globulin	14
5	$\gamma$ -globulin	13

Use the keystrokes 67 **B** 4 **B** 10 **B** 14 **B** 13 **B**. At the end of this sequence the display should show 5.00.

Now that all fractions have been input, step 8 instructs you to find the percentages for the fractions input by pressing **C**. Each percentage is output by a PRINTx command, and the percentages will be output in the order the fractions were input. Press **C** now. The outputs you should see are, in this order, 62.04, 3.70, 9.26, 12.96, and 12.04.

Step 9 is optional. Here you may key in the total grams of protein and press **D** to find the number of grams in each fraction. Key in 7, press **D**, and you should see these outputs: 4.34, 0.26, 0.65, 0.91, and 0.84.

Step 10 is optional. You may press **E** to compute the albumin/globulin ratio. Press **E** now and find an A/G value of 1.63.

Step 11 is also optional. This is the REPRINT feature described on page v. If **F** **E** is pressed, the entire set of data and results will be output through PRINTx commands in the order shown in the OUTPUT DATA/UNITS column. You may do this now and check that the values returned by the REPRINT function are the same as those you keyed in or calculated earlier.

If your answers agree with ours, you are ready to try other programs in this pac. Otherwise, go back to the start of this section and try the procedure again.



## Notes

## BEER'S LAW



This program combines two independent routines in the area of spectrophotometry. The first routine, on keys **A** and **B**, solves Beer's law interchangeably to find either absorbance (optical density) or percent transmittance (%T). To find %T, key in absorbance and press key **A**. The output will be %T. To find absorbance, key in %T and press key **B**. Absorbance will be output.

The second routine, on keys **C**, **D**, and **E**, allows calculation of the concentration of an unknown given the concentration of a standard and the absorbance of %T of the standard and unknown. If the percent transmittance of the standard (%T<sub>s</sub>) is known, it may be keyed in to key **C**. If the absorbance of the standard (A<sub>s</sub>) is known instead, it may be keyed in as a *negative number* to key **C**. Similarly, for the unknown, percent transmittance (%T<sub>u</sub>) may be keyed in as a positive number or absorbance (A<sub>u</sub>) as a *negative number* to key **D**. Then the concentration of the standard (c<sub>s</sub>) should be keyed in to key **E**. This will allow output of the concentration of the unknown (c<sub>u</sub>).

### Equations:

$$A = 2 - \log \%T$$

$$\%T = 10^{2-A}$$

$$c_u = c_s \times \frac{A_u}{A_s}$$

### Reference:

*Clinical Chemistry*, ed. Henry, Cannon, and Winkelman, Harper and Row, 1974.

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
1	Load side 1 and side 2.			
2	(optional) Initialize for reprint.		<b>f</b> <b>A</b>	0.00
3	(optional) Key in patient number.	Ptnt #	<b>f</b> <b>C</b>	Ptnt # .01
4	To suppress printing of data and results, turn print function off.		<b>f</b> <b>D</b>	0.00
5	To turn print function back on.		<b>f</b> <b>D</b>	1.00
6	To solve interchangeably for A and %T, go to step 7; to find an unknown concentration, go to step 9.			
	<b>A<math>\rightleftharpoons</math>%T</b>			
7	To find percent transmittance, key in absorbance.	A	<b>A</b>	%T
8	To find absorbance, key in percent transmittance.	%T	<b>B</b>	A
	<b>Unknown concentration</b>			
9	Key in A or %T for the standard and the unknown (follow A by <b>CHS</b> ):			
	• Standard	$+ \%T_s(-A_s)$	<b>C</b>	$+ \%T_s(-A_s)$
	• Unknown	$+ \%T_u(-A_u)$	<b>D</b>	$+ \%T_u(-A_u)$
10	Key in concentration of standard and compute concentration of unknown.	$C_s$	<b>E</b>	$C_u$

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
	<b>Reprint</b>			
11	Reprint all data and results.		<b>f E</b>	Ptnt # .01
				A
				%T
				$+ \%T_s(-A_s)$
				$+ \%T_u(-A_u)$
				$c_s$
				$c_u$

**Example:**

A standard solution with a solute concentration of 2 mg/ml is found to have an absorbance of 0.41 at 550 nm. An unknown from patient number 10183 is found to show 46% transmittance at the same wavelength. Convert this %T to absorbance. Also find the solute concentration in the unknown. After all calculations obtain a reprint.

**Keystrokes:**

**f A** →  
 10183 **f C** →  
 46 **B** →  
  
 .41 **CHS C** →  
 46 **D** →  
 2 **E** →  
  
**f E** →

**Outputs:**

0.00 (Clear)  
 10183.01 \*\*\* (Ptnt ID)  
 46.00 \*\*\* (%T)  
 0.34 \*\*\* (A)  
 -0.41 \*\*\* ( $-A_s$ )  
 46.00 \*\*\* ( $\%T_u$ )  
 2.00 \*\*\* ( $c_s$ )  
 1.65 \*\*\* ( $c_u$ )  
 10183.01 \*\*\* (Ptnt ID)  
 0.34 \*\*\* (A)  
 46.00 \*\*\* (%T)  
 -0.41 \*\*\* ( $-A_s$ )  
 46.00 \*\*\* ( $\%T_u$ )  
 2.00 \*\*\* ( $c_s$ )  
 1.65 \*\*\* ( $c_u$ )



Notes

## PROTEIN ELECTROPHORESIS



This program is designed to aid in the calculations of protein fractionation. The required data for the program are the integration counts for each protein fraction and, optionally, the total protein. The results calculated by the program are the percentage of the total for each fraction and, if total protein has been input, the number of grams of each protein fraction. An optional output is the albumin/globulin ratio.

To operate the program, press key **A** to initialize. Then for each fraction, key in its integration counts and press key **B**. After the counts have been keyed in for every fraction, you may press key **C** to find the percentage that each fraction is of the total. A single press of **C** will cause all the percentages to be output in the same order as the counts were input. You may then, if you wish, key in the total protein in grams, press key **D**, and output the grams of protein for each fraction.

The albumin/globulin ratio (A/G) may be calculated by pressing key **E**. If A/G is to be found, albumin should be the first fraction input, followed by the four globulin counts.

### Equations:

Let  $\text{Fract}_i$  be the counts for the  $i^{\text{th}}$  fraction, and  $(\%)_i$  the percentage of the total for the  $i^{\text{th}}$  fraction.

$$(\%)_i = \frac{\text{Fract}_i}{\sum_{j=1}^n \text{Fract}_j} \times 100$$

Let  $\text{TPr}$  be the total protein in grams and  $g_i$  be the number of grams of the  $i^{\text{th}}$  fraction.

$$g_i = \frac{\text{Fract}_i}{\sum_{j=1}^n \text{Fract}_j} \times \text{TPr}$$

$$\text{A/G} = \frac{\text{Fract}_1}{\sum_{j=2}^5 \text{Fract}_j}$$

**Remarks:**

1. If the print function is turned off, input data will not be printed. Calculated results will still be printed regardless of the status of the print function.
2. If a reprint is called for by pressing **f E**, all possible inputs and outputs will be printed except that if no value was keyed in for total protein, neither it nor the grams of each fraction will be output.
3. The use of this program need not be restricted to protein fractionation. It may be used as a general-purpose total and percent-of-total program. The only restriction is that the number of inputs (fractions) is limited to 21.

**Reference:**

*Clinical Chemistry*, ed. Henry *et. al.*, Harper and Row, 1974.

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
1	Load side 1 and side 2.			
2	Initialize.		<b>A</b>	0.00
3	(optional) Key in patient number.	Ptnt #	<b>f C</b>	Ptnt # .02
4	To suppress output of data, turn print function off.		<b>f D</b>	0.00
5	To turn print back on later.		<b>f D</b>	1.00
6	Key in the counts of the first protein fraction.	Fract <sub>1</sub>	<b>B</b>	1.00
7	Repeat this step for the rest of the fractions.	Fract <sub>i</sub>	<b>B</b>	i
8	Calculate the percentage each fraction is of the whole.		<b>C</b>	%
9	(optional) Key in the total grams of protein and find the grams in each fraction.	Total Protein	<b>D</b>	grams
10	(optional) Find the albumin/globulin ratio.		<b>E</b>	A/G

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
11	(optional) Obtain a reprint of			
	all data and results (Total			
	Protein and grams omitted if			
	Total Protein not input).		<b>f</b> <b>E</b>	Ptnt # .02
				Fract <sub>1</sub> ...
				Fract <sub>n</sub>
				(%) <sub>1</sub> ...
				(%) <sub>n</sub>
				Total Protein
				grams <sub>1</sub> ...
				grams <sub>n</sub>
				A/G
12	For a new case, go to step 2.			

Example:

The following integration counts are determined electrophoretically for serum proteins:

Albumin	67
$\alpha_1$ -globulin	4
$\alpha_2$ -globulin	10
$\beta$ -globulin	14
$\gamma$ -globulin	13

If the total amount of protein is 7.0 grams, find the percentage of the total and the number of grams for each protein fraction. Also find the albumin/globulin ratio. The patient number is 10183.

Keystrokes:

<b>A</b>	_____→
10183	<b>f</b> <b>C</b> _____→
67	<b>B</b> _____→
4	<b>B</b> _____→
10	<b>B</b> _____→
14	<b>B</b> _____→
13	<b>B</b> _____→

Outputs:

0.00
10183.02 *** (Ptnt ID)
1.00
2.00
3.00
4.00
5.00



**C** →

62.04 \*\*\* (% albumin)

3.70 \*\*\* (%  $\alpha_1$ )9.26 \*\*\* (%  $\alpha_2$ )12.96 \*\*\* (%  $\beta$ )12.04 \*\*\* (%  $\gamma$ )7 **D** →

7.00 \*\*\* (Total Protein)

4.34 \*\*\* (g albumin)

0.26 \*\*\* (g  $\alpha_1$ )0.65 \*\*\* (g  $\alpha_2$ )0.91 \*\*\* (g  $\beta$ )0.84 \*\*\* (g  $\gamma$ )**E** →

1.63 \*\*\* (A/G)

## LDH ISOENZYMES



This program analyzes the results of the fractionation of lactic dehydrogenase isoenzymes and computes for each isoenzyme (LDH<sub>1</sub> through LDH<sub>5</sub>) the percentage it represents of the whole. After key **A** is pressed to initialize the program, each enzyme value is input by keying in the value and pressing **B**. After all five LDH fractions have been input, key **C** may be pressed to find the percentage each enzyme is of the whole.

An additional feature of the program is the checking of the computed percentage of each enzyme against its accepted normal value. All five percentages are computed and output; if one or more of these values lie outside the accepted normal range, the word "Error" will be displayed at the end of all calculations. (This indicates only that a value is abnormal; the answers calculated are accurate.)

The abnormal value or values should then be determined by inspection. The normal values used by the program are shown below.

Enzyme	Normal Range
LDH <sub>1</sub>	18%—33%
LDH <sub>2</sub>	28%—40%
LDH <sub>3</sub>	18%—30%
LDH <sub>4</sub>	6%—16%
LDH <sub>5</sub>	2%—13%

These values for normal ranges may be changed easily within the program if you so desire. Simply look at the program listing and find the value you want to change by referring to the program comments. Delete the number as it now exists in the program and key in your own value. Do not forget to record the modified program on a blank magnetic card if you want to preserve it.

### Equations:

Let LDH<sub>i</sub> be the value of the *i*<sup>th</sup> LDH isoenzyme (*i* = 1,...,5) and LDH<sub>i</sub>% be that enzyme's percentage of the whole.

$$\text{LDH}_i\% = \frac{\text{LDH}_i}{\sum_{j=1}^5 \text{LDH}_j}$$

**Remarks:**

If the print function is turned off, input data will not be printed. Calculated results will still be printed regardless of the status of the print function.

**Reference:**

*Clinical Chemistry*, ed. Henry *et. al.*, Harper and Row, 1974.

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
1	Load side 1 and side 2.			
2	Initialize.		<b>A</b>	0.00
3	(optional) Key in patient number.	Ptnt #	<b>I C</b>	Ptnt # .03
4	To suppress printing of input data, turn the print function off.		<b>I D</b>	0.00
5	To turn the print function back on.		<b>I D</b>	1.00
6	Key in the first LDH enzyme value.	LDH <sub>1</sub>	<b>B</b>	1.00
7	Repeat step 6 for LDH values 2 through 5.	LDH <sub>i</sub>	<b>B</b>	i
8	Calculate the percentage each enzyme is of the total.*		<b>C</b>	LDH <sub>1</sub> %
				...
				LDH <sub>5</sub> %

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
9	(optional) Obtain a reprint of			
	all data and results.*		<b>I E</b>	Ptnt # .03
				LDH <sub>1</sub>
				...
				LDH <sub>5</sub>
				LDH <sub>1</sub> %
				...
				LDH <sub>5</sub> %
	*A display of "Error" following			
	execution of this step			
	indicates a percentage			
	value that lies outside the			
	normal range for that			
	enzyme.			

Example:

Electrophoretic separation of the LDH isoenzymes results in the following counts:

Enzymes	Counts
LDH <sub>1</sub>	95
LDH <sub>2</sub>	120
LDH <sub>3</sub>	85
LDH <sub>4</sub>	15
LDH <sub>5</sub>	22

Find the percentage of the whole for each isoenzyme. The patient number is 10183. Obtain a reprint of the data and results.

Keystrokes:

**A** \_\_\_\_\_→  
10183 **f** **C** \_\_\_\_\_→  
95 **B** \_\_\_\_\_→  
120 **B** \_\_\_\_\_→  
85 **B** \_\_\_\_\_→  
15 **B** \_\_\_\_\_→  
22 **B** \_\_\_\_\_→

Outputs:

0.00  
10183.03 \*\*\* (Ptnt ID)  
1.00  
2.00  
3.00  
4.00  
5.00



<b>C</b> →	28.19 *** (% LDH <sub>1</sub> )
	35.61 *** (% LDH <sub>2</sub> )
	25.22 *** (% LDH <sub>3</sub> )
	4.45 *** (% LDH <sub>4</sub> )
	6.53 *** (% LDH <sub>5</sub> )
	“Error”
<b>CLx</b> (clears “Error”) →	0.00
<b>f E</b> →	10183.03 ***
	95.00 ***
	120.00 ***
	85.00 ***
	15.00 ***
	22.00 ***
	28.19 ***
	35.61 ***
	25.22 ***
	4.45 ***
	6.53 ***
	“Error”

A visual scan of the results indicates that the message “Error” resulted from the percentage value of LDH<sub>4</sub> (4.45%) being below the normal range (6%—16%).

## BODY SURFACE AREA



This program calculates body surface area by either the method of Dubois or the method of Boyd. In both cases, the required inputs are height and weight, which may be input either in metric (cm, kg) or English (in., lb.) units. Quantities in English units should be input as negative numbers; that is, **CHS** should be pressed after keying the number in.

To operate the program, the height in either cm or inches should be keyed in to **A**, and the weight in either kg or pounds keyed in to **B**. Then pressing **C** will allow the calculation of body surface area in  $\text{m}^2$  by the method of Dubois; pressing **D** computes BSA in  $\text{m}^2$  by the Boyd formula. Even if you have already found BSA by one method, you may also find it by the other method simply by pressing the appropriate key; the values of height and weight need not be re-input.

### Equations:

Let Ht be height, Wt be weight, and BSA be the body surface area in  $\text{m}^2$ .

$$\text{Ht (cm)} = 2.54 \text{ Ht (in.)}$$

$$\text{Wt (kg)} = 0.45359237 \text{ Wt (lb.)}$$

Dubois:

$$\text{BSA (m}^2\text{)} = \text{Ht (cm)}^{0.725} \cdot \text{Wt (kg)}^{0.425} \cdot 7.184 \times 10^{-3}$$

Boyd:

$$\text{BSA (m}^2\text{)} = \text{Wt (g)}^{(0.7285 - 0.0188 \log \text{ Wt})} \cdot \text{Ht (cm)}^{0.3} \cdot 3.207 \times 10^{-4}$$

### Remarks:

1. The Dubois formula for BSA is undefined for children with a BSA less than  $0.6 \text{ m}^2$ . In such cases BSA should be calculated by the Boyd formula.
2. Turning off the print function will suppress printing of both data and results.

**References:**

D. Du Bois and E.F. Du Bois, Clin. Cal. 10, Arch. Int. Med., **17**, 863, 1916.

Edith Boyd, *Growth of the Surface Area of the Human Body*, U. of Minnesota Press, 1935, p. 132.

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
1	Load side 1 and side 2.			
2	(optional) Initialize if reprint desired.		<b>f</b> <b>A</b>	0.00
3	(optional) Key in patient number.	Ptnt #	<b>f</b> <b>C</b>	Ptnt # .04
4	To suppress printing of data and results.		<b>f</b> <b>D</b>	0.00
5	To turn print function back on.		<b>f</b> <b>D</b>	1.00
6	Key in height (+ cm, - in.)	Ht	<b>A</b>	Ht (cm)
7	Key in weight (+ kg, - lb.)	Wt	<b>B</b>	Wt (kg)
8	Compute BSA by method of either			
	• Dubois		<b>C</b>	BSA (m <sup>2</sup> )
	• Boyd		<b>D</b>	BSA (m <sup>2</sup> )
9	(optional) Reprint all data and results.		<b>f</b> <b>E</b>	Ptnt # .04
				Ht input
				Wt input
				BSA (m <sup>2</sup> )

**Example 1:**

Patient number 10183 is a male, height 176 cm, weight 63.5 kg. What is his BSA by the Dubois formula? Compare by also finding the Boyd BSA.

**Keystrokes:**

10183 **f** **C** →  
 176 **A** →  
 63.5 **B** →  
**C** →  
**D** →

**Outputs:**

10183.04 \*\*\* (Ptnt ID)  
 176.00 (Ht (cm))  
 63.50 (Wt (kg))  
 1.78 \*\*\* (Dubois)  
 1.76 \*\*\* (Boyd)

Example 2:

Patient number 10070 is a female, height 64 inches, weight 112 pounds. Find her BSA by the Boyd formula. Obtain a reprint. Remember to input height and weight as negative numbers.

Keystrokes:

f A →  
10070 f C →  
64 CHS A →  
112 CHS B →  
D →  
f E →

Outputs:

0.00  
10070.04 \*\*\* (Ptnt ID)  
162.56 (Ht (cm))  
50.80 (Wt (kg))  
1.52 \*\*\* (Boyd)  
10070.04 \*\*\* (Ptnt ID)  
-64.00 \*\*\* (Ht)  
-112.00 \*\*\* (Wt)  
1.52 \*\*\* (BSA)



Notes

## UREA CLEARANCE



This program calculates urea clearance given the urine flow rate and the concentration of urea in urine and blood. The urine flow rate may be corrected for the patient's body surface area, if desired. The program will calculate standard or maximum clearance depending on whether the corrected urine flow rate is above or below 2 ml/min. The percent of mean normal may also be found.

If the urine flow rate is to be corrected for body surface area, key **f** **B** should be pressed to indicate that. No action is necessary if the correction is not desired. If correction is to be made, the program will need to find the patient's body surface area (BSA) in register  $R_A$ . If the program *Body Surface Area* (CL1-04A) has been run immediately before this program, BSA will already have been stored in  $R_A$ . Otherwise you will need to key in the patient's BSA and store it in  $R_A$ .

When inputting the urine flow rate, you may either key in the flow rate ( $\dot{V}$ , in ml/min.) directly to key **B**, or key in both the urine volume  $V$  in ml and the time  $t$  in min. to key **A**. If the print function is on and inputs are being printed, in both cases the printout will be of  $\dot{V}$ , the flow rate in ml/min. The number in the display at the end of routine **A** or **B** is  $\dot{V}_{\text{corr}}$ , the flow rate after correction for BSA. It is the size of this number that determines whether the standard or the maximum clearance will be calculated. This number will also be printed if the print function is on.

### Equations:

$$\dot{V}(\text{ml/min}) = \frac{V(\text{ml})}{t(\text{min})}$$

$$\dot{V}_{\text{corr}} = \begin{cases} \frac{1.73}{\text{BSA}} \dot{V} & \text{if corrected for BSA} \\ \dot{V} & \text{if no correction for BSA} \end{cases}$$

Maximum clearance ( $\dot{V}_{\text{corr}} > 2$ ):

$$C_m(\text{ml/min}) = \frac{U_{\text{urea}} \dot{V}_{\text{corr}}}{B_{\text{urea}}}$$

Standard clearance ( $\dot{V}_{\text{corr}} \leq 2$ ):

$$C_s(\text{ml/min}) = \frac{U_{\text{urea}} \sqrt{\dot{V}_{\text{corr}}}}{B_{\text{urea}}}$$

where

$U_{\text{urea}}$  = concentration of urea in urine

$B_{\text{urea}}$  = concentration of urea in blood

$$\% \text{ mean normal } C_m = 1.33 C_m$$

$$\% \text{ mean normal } C_s = 1.85 C_s$$

### Remarks:

1. Any units may be used for  $U_{\text{urea}}$  and  $B_{\text{urea}}$  as long as they are consistent.
2. Some users may prefer to ignore the distinction between standard and maximum clearance and use the maximum formula for all cases. This can be accomplished by using the program *Creatinine Clearance* (CL1-06A) and inputting  $U_{\text{urea}}$  and  $B_{\text{urea}}$  in place of  $U_{\text{creat}}$  and  $P_{\text{creat}}$ , respectively.
3. If the print function is turned off, neither inputs nor outputs will be printed.

### Reference:

*Clinical Chemistry*, ed. Henry *et al.*, Harper and Row, 1974.

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
1	Load side 1 and side 2.			
2	(optional) Initialize if reprint desired.		<b>F</b> <b>A</b>	0.00
3	(optional) Key in patient number.	Ptnt #	<b>F</b> <b>C</b>	Ptnt # .05
4	To suppress printing of data and results, turn the print function off.		<b>F</b> <b>D</b>	0.00
5	To turn the print function back on.		<b>F</b> <b>D</b>	1.00

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
6	If BSA is required and <i>Body Surface Area</i> has not been run, key in BSA.	BSA (m <sup>2</sup> )	STO A	
7	If $\dot{V}$ is to be corrected for BSA		f B	BSA (m <sup>2</sup> )
8	Perform either one of the steps below:			
	• Key in urine volume and time	V (ml)	ENTER	
		t (min)	A	$\dot{V}_{\text{corr}}$
	• Key in urine flow rate	$\dot{V}$ (ml/min)	B	$\dot{V}_{\text{corr}}$
9	Key in the concentration of urea in urine.	U <sub>urea</sub>	C	U <sub>urea</sub>
10	Key in the concentration of urea in blood and find the urea clearance.	B <sub>urea</sub>	D	C <sub>urea</sub> (ml/min)
11	Find the percent of mean normal.		E	% m.n.
12	(optional) Reprint data and results.		f E	Ptnt # .05
				$\dot{V}$
				$\dot{V}_{\text{corr}}$
				U <sub>urea</sub>
				B <sub>urea</sub>
				C <sub>s</sub> or C <sub>m</sub>
				% m.n.
13	For a new case go to step 2.			

**Example 1:**

A patient, number 10183, is to be tested for urea clearance. A volume of 204 ml of urine is collected over a period of 120 min. The concentration of urea in this urine is found to be 903 mg/100 ml. A blood sample is taken halfway through the urine collection and found to have a urea concentration of 26 mg/100 ml. Determine the urea clearance. Do not correct for body surface area.



**Keystrokes:**10183 **f** **C** →204 **ENTER** 120 **A** →903 **C** →26 **D** →**E** →**Outputs:**

10183.05 \*\*\* (Ptnt ID)

1.70 \*\*\* ( $\dot{V}$ )1.70 \*\*\* ( $\dot{V}_{\text{corr}}$ )903.00 \*\*\* ( $U_{\text{urea}}$ )26.00 \*\*\* ( $B_{\text{urea}}$ )45.28 \*\*\* ( $C_s$ , ml/min)

83.77 \*\*\* (% m.n.)

**Example 2:**

Patient number 10142 is a male, height 188 cm, weight 88.5 kg. A urine flow rate of 2.7 ml/min. is recorded. The concentration of urea is 798 mg/100 ml in urine and 21 mg/100 ml in blood. Determine the urea clearance corrected for body surface area using the Dubois formula for BSA.

**Keystrokes:****f** **D** →188 **A** →88.5 **B** →**C** →**Outputs:**

0.00 (Print off)

188.00 (Ht, cm)

88.50 (Wt, kg)

2.15 (Dubois BSA)

Load side 1 and side 2 of *Urea Clearance* (CL1-05A).10142 **f** **C** →**f** **B** →2.7 **B** →798 **C** →21 **D** →**E** →

10142.05 \*\*\* (Ptnt ID)

2.15 (BSA)

2.70 \*\*\* ( $\dot{V}$ )2.17 \*\*\* ( $\dot{V}_{\text{corr}}$ )798.00 \*\*\* ( $U_{\text{urea}}$ )21.00 \*\*\* ( $B_{\text{urea}}$ )82.53 \*\*\* ( $C_m$ , ml/min)

109.76 \*\*\* (% m.n.)

## CREATININE CLEARANCE



This program allows the calculation of creatinine clearance given the urine flow rate and the concentration of creatinine in urine and plasma. The urine flow rate may be corrected for the patient's body surface area if desired.

To indicate that a correction should be made for the body surface area, press **f B**. No action is necessary if the correction is not desired. If correction is to be made, the program will need to find the patient's body surface area (BSA, in m<sup>2</sup>) in register R<sub>A</sub>. The program *Body Surface Area* (CL1-04A) automatically leaves BSA stored in R<sub>A</sub>. If *Body Surface Area* has not been run immediately before this program, you will need to key in the BSA and press **STO A**.

When inputting the urine flow rate, you may either key in the flow rate ( $\dot{V}$ , in ml/min.) directly to key **B**, or key in both the urine volume ( $V$ , in ml) and the time ( $t$ , in minutes) to key **A**. If the print function is on and inputs are being printed, in both cases the printout will be of  $\dot{V}$ , the flow rate in ml/min. The number in the display at the end of routine **A** or **B** is  $\dot{V}_{\text{corr}}$ , the flow rate after correction for BSA. (If no correction is desired,  $\dot{V}_{\text{corr}}$  will be the same as  $\dot{V}$ .) This number will also be printed if the print function is on.

### Equations:

$$\dot{V}(\text{ml/min}) = \frac{V(\text{ml})}{t(\text{min})}$$

$$\dot{V}_{\text{corr}} = \begin{cases} \frac{1.73}{\text{BSA}} \dot{V} & \text{if corrected for BSA} \\ \dot{V} & \text{if not corrected for BSA} \end{cases}$$

$$C_{\text{creat}}(\text{ml/min}) = \frac{U_{\text{creat}} \dot{V}_{\text{corr}}}{P_{\text{creat}}}$$

where

$C_{\text{creat}}$  = creatinine clearance

$U_{\text{creat}}$  = concentration of creatinine in urine

$P_{\text{creat}}$  = concentration of creatinine in plasma

**Remarks:**

1. Any units may be used for  $U_{\text{creat}}$  and  $P_{\text{creat}}$  as long as they are consistent.
2. If the print function is turned off, neither inputs nor outputs will be printed.

**Reference:**

*Clinical Chemistry*, ed. Henry *et al.*, Harper and Row, 1974.

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
1	Load side 1 of program.			
2	(optional) Initialize if reprint desired.		<b>f A</b>	0.00
3	(optional) Key in patient number.	Ptnt #	<b>f C</b>	Ptnt # .06
4	To suppress printing of data and results, turn print function off.		<b>f D</b>	0.00
5	To turn print function back on later		<b>f D</b>	1.00
6	If BSA is required and <i>Body Surface Area</i> has not been run, key in BSA.	BSA (m <sup>2</sup> )	<b>STO A</b>	
7	If $\dot{V}$ is to be corrected for BSA.		<b>f B</b>	BSA (m <sup>2</sup> )
8	Perform either one of the steps below:			
	• Key in urine volume and time	V (ml)	<b>ENTER</b>	
		t (min)	<b>A</b>	$\dot{V}_{\text{corr}}$
	• Key in urine flow rate.	$\dot{V}$ (ml/min)	<b>B</b>	$\dot{V}_{\text{corr}}$
9	Key in the concentration of creatinine in urine.	$U_{\text{creat}}$	<b>C</b>	$U_{\text{creat}}$
10	Key in the concentration of creatinine in plasma and find the creatinine clearance.	$P_{\text{creat}}$	<b>D</b>	$C_{\text{creat}}$ (ml/min)

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
11	(optional) Reprint data and results.		<b>f E</b>	Ptnt # .06
				$\dot{V}$
				$\dot{V}_{\text{corr}}$
				$U_{\text{creat}}$
				$P_{\text{creat}}$
				$C_{\text{creat}}$
12	For a new case go to step 2.			

Example 1:

A male, patient number 10095, is tested for creatinine clearance. A urine volume of 506 ml is collected over a 4-hour (240-min.) period. The concentration of creatinine is found to be 43.4 mg/dl in urine and 0.91 mg/dl in plasma. Find the creatinine clearance. Do not correct for body surface area.

Keystrokes:

10095 **f C** \_\_\_\_\_  
506 **ENTER** **A** \_\_\_\_\_  
43.4 **C** \_\_\_\_\_  
0.91 **D** \_\_\_\_\_

Outputs:

10095.06 \*\*\* (Ptnt ID)  
2.11 \*\*\* ( $\dot{V}$ )  
2.11 \*\*\* ( $\dot{V}_{\text{corr}}$ )  
43.40 \*\*\* ( $U_{\text{creat}}$ )  
0.91 \*\*\* ( $P_{\text{creat}}$ )  
100.55 \*\*\* ( $C_{\text{creat}}$ , ml/min)

Example 2:

Patient number 10124 is a female with a body surface area of 1.56 m<sup>2</sup>. Given a urine flow rate of 1.81 ml/min., a creatinine concentration of 46.5 mg/dl in urine and 1.03 mg/dl in plasma, find the creatinine clearance.

Keystrokes:

10124 **f C** \_\_\_\_\_  
1.56 **STO** **A** \_\_\_\_\_  
**f B** \_\_\_\_\_  
1.81 **B** \_\_\_\_\_  
46.5 **C** \_\_\_\_\_  
1.03 **D** \_\_\_\_\_

Outputs:

10124.06 \*\*\* (Ptnt ID)  
1.56 (BSA)  
1.56  
1.81 \*\*\* ( $\dot{V}$ )  
2.01 \*\*\* ( $\dot{V}_{\text{corr}}$ )  
46.50 \*\*\* ( $U_{\text{creat}}$ )  
1.03 \*\*\* ( $P_{\text{creat}}$ )  
90.62 \*\*\* ( $C_{\text{creat}}$ , ml/min)

Notes



## AMNIOTIC FLUID ASSAY

AMNIOTIC FLUID ASSAY				CL1-07A
[hp]	CLEAR	PTNT #	P OFF?	REPRINT
A <sub>365</sub>	A <sub>550</sub>	A <sub>450</sub> + Δ	Wk + b	Zone

This program performs calculations for the spectrophotometric estimation of bile pigments in amniotic fluid. Measurement of absorbance changes in the fluid has been shown to be useful in determining the management of Rh-sensitized pregnancies. The absorbance of the fluid is measured at two wavelengths (typically, 365 nm and 550 nm) to form a baseline, and then at a third wavelength between these two (typically, 450 nm) to allow calculation of the difference ( $\Delta$ ) between the actual and the interpolated absorbances at the intermediate wavelength. Then, given the weeks of gestation, the "b" factor and, optionally, the Liley zone number may be found.

The inputs to the program, then, are the absorbances of the amniotic fluid at three wavelengths ( $A_{365}$ ,  $A_{550}$ , and  $A_{450}$ ). From these may be found  $\Delta A_{450}$ , the difference in absorbance at the intermediate wavelength. The final input is the week of gestation (Wk), from which may be found the "b" factor and zone. The last two outputs are the most meaningful for the obstetrician; for interpretation, see references 1 and 2 below.

### Equations:

$$\Delta A_{450} = A_{450} - e^{[.541 (\ln A_{365} - \ln A_{550}) + \ln A_{550}]}$$

$$b = \Delta A_{450} / a^{\text{Wk}}$$

where

$$a = 0.91509$$

Wk = week of gestation

Liley zones:

Zone I:  $b < 0.7$

Zone II:  $0.7 \leq b \leq 3$

Zone III:  $b > 3$

### Remarks:

1. Some users may prefer to take absorbance readings at wavelengths other than those indicated here. Burnett<sup>3</sup>, for instance, advocates readings at 350 nm, 550 nm, and 455 nm. It is quite easy to modify the program to handle such a case. The only change required is the alteration of

one constant occupying four steps of program memory, 024-027. At present in these locations the program holds the constant .541. For Burnett's values (350, 550, 455) this constant would have to be changed to .475. In general, if the three wavelengths used are x, y, and z, with  $x < z < y$ , the constant to be used is

$$\frac{y - z}{y - x}.$$

The absorbances at wavelengths x, y, and z should be input to keys **A**, **B**, and **C** respectively.

2. If the print function is turned off, neither inputs nor outputs will be printed.

### References:

1. R.C. Brown and W.J. Beckfield, "Computer-assisted spectrophotometric analysis of amniotic fluid in erythroblastosis fetalis," *Amer. J. Clin. Path.*, **57**: 659-663, 1972.
2. A.W. Liley, "Liquor amnii analysis in the management of the pregnancy complicated by rhesus sensitization," *Amer. J. Obstet. Gynecol.*, **82**: 1359-1370, 1961.
3. R. Burnett, "Instrumental and procedural sources of error in determination of bile pigments in amniotic fluid," *Clin. Chem.*, **18**: 150-154, 1972.

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
1	Load side 1 and side 2.			
2	(optional) Initialize if reprint desired.		<b>f A</b>	0.00
3	(optional) Key in patient number.	Ptnt #	<b>f C</b>	Ptnt # .07
4	To suppress printing of data and results, turn print function off.		<b>f D</b>	0.00
5	To turn print function back on later.		<b>f D</b>	1.00
6	Key in absorbance at 365 nm.	A <sub>365</sub>	<b>A</b>	A <sub>365</sub>
7	Key in absorbance at 550 nm.	A <sub>550</sub>	<b>B</b>	A <sub>550</sub>

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
8	Key in absorbance at 450 nm			
	and find $\Delta A_{450}$ .	$A_{450}$	<b>C</b>	$\Delta A_{450}$
9	Key in week of gestation and			
	find b factor.	Wk	<b>D</b>	b
10	(optional) Find Liley zone			
	number (1, 2, or 3).		<b>E</b>	Zone
11	(optional) To obtain a reprint			
	of data and results.		<b>I E</b>	Ptnt # .07
				$A_{365}$
				$A_{550}$
				$A_{450}$
				$\Delta A_{450}$
				Week
				b
				Zone

Example:

A sample of amniotic fluid from patient number 10070 is found to have absorbances of 0.43, 0.25, and 0.39 at wavelengths 365 nm, 550 nm, and 450 nm respectively. Find  $\Delta A_{450}$ , the b factor, and the Liley zone number given that it is the 35<sup>th</sup> week of gestation.

Keystrokes:

10070 **I C** \_\_\_\_\_→  
.43 **A** \_\_\_\_\_→  
.25 **B** \_\_\_\_\_→  
.39 **C** \_\_\_\_\_→  
  
35 **D** \_\_\_\_\_→  
  
**E** \_\_\_\_\_→

Outputs:

10070.07 \*\*\* (Ptnt ID)  
0.43 \*\*\* ( $A_{365}$ )  
0.25 \*\*\* ( $A_{550}$ )  
0.39 \*\*\* ( $A_{450}$ )  
0.05 \*\*\* ( $\Delta A_{450}$ )  
35. \*\*\* (Wk)  
1.22 \*\*\* (b)  
2. \*\*\* (Zone)

Notes

## BLOOD ACID-BASE STATUS



This program computes total plasma  $\text{CO}_2$  ( $\text{TCO}_2$ ) and base excess (BE) from the partial pressure of  $\text{CO}_2$  ( $\text{PCO}_2$ ), pH, and hemoglobin concentration (Hgb). The  $\text{PCO}_2$  and pH values used should be found at  $37^\circ\text{C}$ ; if they are found at a body temperature (BT) other than  $37^\circ\text{C}$ , the program will correct them to  $37^\circ\text{C}$  values if BT is also input. An additional, optional output of the program is the concentration of plasma bicarbonate ( $[\text{HCO}_3^-]$ ).

To operate the program, if the body temperature is different from  $37^\circ\text{C}$ , then key in BT in  $^\circ\text{C}$  and press key **A**. If  $\text{BT} = 37^\circ\text{C}$ , it need not be input; if it is, however, no harm will be done. Next key in  $\text{PCO}_2$  in mm Hg and press **B**; the number displayed at the completion of this step is the value of  $\text{PCO}_2$  corrected to  $37^\circ\text{C}$ . Then key in pH and press **C**; the result in the display at the end of this step is the pH value corrected to  $37^\circ\text{C}$ . Finally, press **D** to calculate  $\text{TCO}_2$  in mmol/l. As an optional step, hemoglobin may now be input in units of g/100 ml. Pressing **E** will allow the calculation of base excess in mEq/l using an equation suggested by Siggaard-Andersen. The last value output is  $[\text{HCO}_3^-]$ , which may be found by pressing **R/S** after the calculation of base excess.

### Equations:

$$\text{PCO}_2 (37^\circ\text{C}) = \text{PCO}_2 (\text{BT}) \cdot 10^{0.019 (37 - \text{BT})}$$

$$\text{pH} (37^\circ\text{C}) = \text{pH} (\text{BT}) - 0.0146 (37 - \text{BT})$$

$$\text{TCO}_2 = s \cdot \text{PCO}_2 [1 + 10^{\text{pH} - \text{pK}}]$$

where

$s$  = solubility of  $\text{CO}_2$  in plasma, mmol/l (taken to be 0.0307)

$\text{pK} = 6.11$

$$[\text{BE}]_b = (1 - 0.0143 \text{ Hgb}) ([\text{HCO}_3^-] - (9.5 + 1.63 \text{ Hgb}) (7.4 - \text{pH}) - 24)$$

where

$[\text{BE}]_b$  = base excess in mEq/l of blood

Hgb = hemoglobin concentration in g/100 ml

$$[\text{HCO}_3^-] = s \cdot \text{PCO}_2 \cdot 10^{\text{pH} - \text{pK}}$$

where

$[\text{HCO}_3^-]$  = concentration of plasma bicarbonate in mmol/l.



**Remarks:**

1. This program can also be used to correct  $\text{PCO}_2$  and pH values from  $37^\circ\text{C}$  to body temperature. To do this, let  $x = (74 - \text{BT})^\circ\text{C}$ . Key in  $x$  to key **A**. Then input  $\text{PCO}_2$  and pH to keys **B** and **C**, respectively. The number displayed after each of these steps is the value of the parameter corrected to body temperature. For example, if it is desired to correct a  $37^\circ\text{C}$   $\text{PCO}_2$  value of 45 mm Hg to a body temperature value with  $\text{BT} = 40^\circ\text{C}$ , let  $x = 34$ . Key in 34, press **A**, key in 45, and press **B**. The corrected  $\text{PCO}_2$  is found to be 51.31 mm Hg.
2. The equation to correct pH to  $37^\circ\text{C}$  values is a simplification of a formula from Severinghaus. It ignores the pH and BE dependent terms. This introduces a very small error except at extreme conditions of acid-base status and large temperature shifts. For example, at a pH of 7.2 or 7.6, the error is 0.0013 units per  $^\circ\text{C}$ .
3. If the print function is turned off, neither inputs nor outputs will be printed.

**References:**

- John W. Severinghaus, "Blood gas calculator," *J. Appl. Physiol.*, **21**: 1108 -- 1116, 1966.
- Siggaard-Andersen, "Titrable acid or base of body fluids," *Annals New York Academy of Science*, **133**: 41-48, 1966.
- L.J. Thomas, Jr., "Algorithms for selected blood acid-base and blood gas calculation," *J. Appl. Physiol.*, **33**: 154-158, 1972.

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
1	Load side 1 and side 2 of program.			
2	(optional) Initialize if reprint desired.		<b>f A</b>	0.00
3	(optional) Key in patient number.	Ptnt #	<b>f C</b>	Ptnt # .08
4	To suppress printing of data and results, turn print function off.		<b>f D</b>	0.00
5	To turn print function back on later.		<b>f D</b>	1.00
6	If PCO <sub>2</sub> and pH are to be corrected to 37°C, key in body temperature in °C.	BT (°C)	<b>A</b>	37 – BT
7	Key in partial pressure of CO <sub>2</sub> in mm Hg.	PCO <sub>2</sub> (mm Hg)	<b>B</b>	PCO <sub>2</sub> (37°)
8	Key in pH.	pH	<b>C</b>	pH (37°)
9	Find total plasma CO <sub>2</sub> in mmol/l.		<b>D</b>	TCO <sub>2</sub> (mmol/l)
10	(optional) Key in hemoglobin concentration and compute base excess and [HCO <sub>3</sub> <sup>-</sup> ]	Hgb(g/100ml)	<b>E</b>	BE (mEq/l)
			<b>R/S</b>	[HCO <sub>3</sub> <sup>-</sup> ](mmol/l)
11	To obtain a reprint.		<b>f E</b>	Ptnt # .08
				BT
				PCO <sub>2</sub>
				pH
				TCO <sub>2</sub>
				Hgb
				BE
				[HCO <sub>3</sub> <sup>-</sup> ]

Example :

Patient number 10183 has a body temperature of 40°C. His PCO<sub>2</sub> at 40°C is found to be 51 mm Hg, his pH at the same temperature 7.31. His hemoglobin concentration is 16 g/100 ml. Find TCO<sub>2</sub>, BE, and [HCO<sub>3</sub><sup>-</sup>].

Keystrokes:

f A →  
10183 f C →  
40 A →  
51 B →  
7.31 C →  
D →  
16 E →  
R/S →

Outputs:.

0.00  
10183.08 \*\*\* (Ptnt ID)  
40.00 \*\*\* (BT)  
-3.00 (37 - BT)  
51.00 \*\*\* (PCO<sub>2</sub>(40))  
44.73 (PCO<sub>2</sub>(37))  
7.31 \*\*\* (pH(40))  
7.35 (pH(37))  
25.44 \*\*\* (TCO<sub>2</sub>)  
16.00 \*\*\* (Hgb)  
-1.21 \*\*\* (BE)  
24.07 \*\*\* ([HCO<sub>3</sub><sup>-</sup>])

## OXYGEN SATURATION AND CONTENT



This program estimates oxygen saturation of blood from various body parameters and computes oxygen content. If the actual oxygen saturation is known, oxygen content may be computed directly.

### Estimated saturation

Typically, the input parameters to the program are  $\text{PCO}_2$ , pH, and  $\text{PO}_2$  measured at  $37^\circ\text{C}$ , and the body temperature in  $^\circ\text{C}$ . If the parameters  $\text{PCO}_2$  and pH are known only at body temperature, they may be corrected to  $37^\circ\text{C}$  through use of the program *Blood Acid-Base Status*, CL1-08A. If CL1-08A is run before this program, the values of BT,  $\text{PCO}_2$ , and pH may be recalled by this program for input to the appropriate keys. For example, pressing **f** **B** will recall the value of BT. Pressing **A** will then input the recalled value to this program and recall the value of  $\text{PCO}_2$ . Pressing **B** will input the recalled  $\text{PCO}_2$  value and recall the value of pH. If CL1-08A has not been run previously, the recalled values will be meaningless numbers or zero.

After the input of  $\text{PO}_2$  to **D**, an intermediate value of virtual  $\text{PO}_2$  ( $\text{VPO}_2$ ) will be calculated prior to the calculation of estimated saturation. The value found for  $\text{VPO}_2$  will not be output but may be displayed after the calculation of saturation by pressing **RCL C**.  $\text{VPO}_2$  is not a real physiologic  $\text{PO}_2$ . Its only use is in estimating  $\text{O}_2$  saturation.

Suppose as an alternate case that BT,  $\text{PCO}_2$ , and pH are not known, but virtual  $\text{PO}_2$ , or alveolar  $\text{PO}_2$  ( $\text{P}_{\text{A}}\text{O}_2$ ) is known. In this case, only the known  $\text{VPO}_2$  or  $\text{P}_{\text{A}}\text{O}_2$  need be input in order to compute estimated saturation. Input  $\text{VPO}_2$  or  $\text{P}_{\text{A}}\text{O}_2$  to key **D** as *negative* numbers, i.e., key in the value followed by **CHS**, then press **D**. The output, as before, will be estimated oxygen saturation.

After computing saturation, the hemoglobin concentration in g/100 ml should be keyed into **E**. Output from this sequence will be the oxygen content as a volume percent.

### Known saturation

If the actual  $\text{O}_2$  saturation is known, the oxygen content may be computed directly. Simply key in the  $\text{O}_2$  saturation, press **ENTER**, key in hemoglobin concentration and press **E**. Oxygen content will be output.

**Equations:**

$$\text{VPO}_2 = \text{PO}_2 \cdot 10^{[0.024(37-\text{BT}) + 0.48(\text{pH}-7.4) + 0.06 \log(40/\text{PCO}_2)]}$$

$$\text{O}_2 \text{ Sat} = \frac{(\text{VPO}_2)^4 - 15(\text{VPO}_2)^3 + 2045(\text{VPO}_2)^2 + 2000(\text{VPO}_2)}{(\text{VPO}_2)^4 - 15(\text{VPO}_2)^3 + 2400(\text{VPO}_2)^2 - 31,100(\text{VPO}_2) + 2,400,000}$$

$$\text{O}_2 \text{ content} = 1.34 \cdot \frac{\text{Sat} (\%)}{100} \cdot \text{Hgb} + 0.0031 \text{ VPO}_2$$

**Remarks:**

1. In the computation of  $\text{VPO}_2$ , it is important to input the values for pH and BT exactly, as these have a great influence on the value of  $\text{VPO}_2$ .  $\text{PCO}_2$  has relatively little influence.
2. The equation for  $\text{VPO}_2$  is a hybrid of the equation used by Thomas and that used by Kelman. There is some disagreement regarding the best value of the pH multiplier, 0.48 being used by most workers, but see, for example, Kelman.
3. The calculation of saturation from  $\text{PO}_2$  will give inaccurate results for fetal hemoglobin, present in babies less than six months old, and for some abnormal adult hemoglobins and certain other blood conditions. The results of the estimation and any subsequent calculations based on it, should be viewed with caution unless the dissociation curve has been previously established to be normal. If both  $\text{PO}_2$  and  $\text{O}_2$  saturation are measured, the program may be used as a convenient means to check for the normality of the dissociation curve.
4. If the print function is turned off, neither inputs nor outputs will be printed.
5. After a keystroke sequence in which **D** is pressed to find saturation, **E** should also be pressed to complete the sequence even if Hgb is not input and the calculated oxygen content is meaningless.

**References:**

- L.J. Thomas, Jr., "Algorithms for selected blood acid-base and blood gas calculation," *J. Appl. Physiol.*, **33**: 154-158, 1972.
- G. Richard Kelman, "Digital computer subroutine for the conversion of oxygen tension into saturation." *J. Appl. Physiol.*, **21**: 1375-1376, 1966.



STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
1	Load side 1 and side 2.			
2	(optional) Initialize if reprint desired.		<b>f</b> <b>A</b>	0.00
3	(optional) Key in patient number.	Ptnt #	<b>f</b> <b>C</b>	Ptnt # .09
4	To suppress printing of data and results, turn print function off.		<b>f</b> <b>D</b>	0.00
5	To turn print function back on later.		<b>f</b> <b>D</b>	1.00
6	If oxygen saturation is to be estimated, go to step 7; if it is known already, go to step 14.			
	<b>Estimated saturation</b>			
7	If BT was stored from <i>Blood Acid-Base Status</i> (CL1-08A), it may be recalled.		<b>f</b> <b>B</b>	BT (°C)
8	Input body temperature in °C.	BT (°C)	<b>A</b>	PCO <sub>2</sub> (if stored)
9	Input PCO <sub>2</sub> in mm Hg.	PCO <sub>2</sub> (mm Hg)	<b>B</b>	pH(if stored)
10	Input pH.	pH	<b>C</b>	pH
11	Input PO <sub>2</sub> in mm Hg ( <b>CHS</b> for VPO <sub>2</sub> or P <sub>A</sub> O <sub>2</sub> ) and find oxygen saturation.	PO <sub>2</sub> (mm Hg)	<b>D</b>	Sat (%)
12	Key in hemoglobin and find oxygen content as a volume percent.	Hgb (g/100ml)	<b>E</b>	O <sub>2</sub> content

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
13	To obtain a reprint.		<b>f</b> <b>E</b>	Ptnt # .09
				BT
				PCO <sub>2</sub>
				pH
				PO <sub>2</sub>
				Sat (%)
				Hgb
				O <sub>2</sub> content
	<b>Known saturation</b>			
14	Key in saturation and			
	hemoglobin concentration and			
	find oxygen content as a			
	volume percent.	Sat (%)	<b>ENTER</b> <b>Δ</b>	
		Hgb (g/100ml)	<b>E</b>	O <sub>2</sub> content

**Example 1:**

Patient number 10183 has a body temperature of 40°C. The following parameters are measured at 37°C: PCO<sub>2</sub> = 45 mm Hg, pH = 7.35, and PO<sub>2</sub> = 75 mm Hg. Find the estimated O<sub>2</sub> saturation. Given a hemoglobin concentration of 16 g/100 ml, find oxygen content.

**Keystrokes:**

10183 **f** **C** →  
 40 **A** →  
 45 **B** →  
 7.35 **C** →  
 75 **D** →  
 16 **E** →

**Outputs:**

10183.09 \*\*\* (Ptnt ID)  
 40.00 \*\*\* (BT)  
 45.00 \*\*\* (PCO<sub>2</sub>)  
 7.35 \*\*\* (pH)  
 75.00 \*\*\* (PO<sub>2</sub>)  
 90.92 \*\*\* (Sat %)  
 16.00 \*\*\* (Hgb)  
 19.68 \*\*\* (O<sub>2</sub> cont.)

**Example 2:**

Alveolar PO<sub>2</sub> (P<sub>A</sub> O<sub>2</sub>) is known to be 103 mm Hg in patient number 10184. Find the estimated O<sub>2</sub> saturation. Given a hemoglobin concentration of 14.5 g/100 ml, find the oxygen content.

**Keystrokes:**

10184 **f** **C** →

103 **CHS** **D** →

14.5 **E** →

**Outputs:**

10184.09 \*\*\* (Ptnt ID.)

-103.00 \*\*\* ( $P_{AO_2}$ )

97.72 \*\*\* (Sat %)

14.50 \*\*\* (Hgb)

19.31 \*\*\* ( $O_2$  cont.)

**Example 3:**

Oxygen saturation is measured at 92%. Hemoglobin concentration is 16 g/100 ml. What is the oxygen content?

92 **ENTER** 16 **E** →

92.00 \*\*\* (Sat %)

16.00 \*\*\* (Hgb)

20.04 \*\*\* ( $O_2$  cont.)

Notes

## RED CELL INDICES



This program computes red cell indices based on three measured values: red cell count, hematocrit, and hemoglobin. The indices computed are mean corpuscular volume (MCV), mean corpuscular hemoglobin (MCH), and mean corpuscular hemoglobin concentration (MCHC).

The red cell count in millions per  $\text{mm}^3$  should be input to key **A** and hematocrit as a percent to key **B**. Then hemoglobin in g/dl (g/100 ml) is keyed in, and **C** is pressed to allow calculation of MCV in cubic microns ( $\mu^3$ ). Pressing **D** will cause the output of MCH in picograms, pg (or micromicrograms,  $\mu\mu\text{g}$ ). Finally, key **E** is pressed to compute MCHC in g/dl (g/100 ml).

## Equations:

$$\text{MCV } (\mu^3) = \frac{\text{Hct } (\%) \times 10}{\text{Count } (10^6/\text{mm}^3)}$$

$$\text{MCH } (\text{pg}) = \frac{\text{Hgb } (\text{g/dl}) \times 10}{\text{Count } (10^6/\text{mm}^3)}$$

$$\text{MCHC } (\text{g/dl}) = \frac{\text{Hgb } (\text{g/dl}) \times 100}{\text{Hct } (\%)}$$






## Remarks:

If the print function is turned off, neither inputs nor outputs will be printed.

## Reference:

Davidson and Henry, *Todd-Sanford Clinical Diagnosis by Laboratory Methods*, W.B. Saunders Co., 1969.



STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
1	Load side 1.			
2	(optional) Initialize if reprint desired.		 <b>A</b>	0.00
3	(optional) Key in patient number.	Ptnt #	 <b>C</b>	Ptnt # .10
4	To suppress printing of data and results, turn print function off.		 <b>D</b>	0.00
5	To turn print function back on later.		 <b>D</b>	1.00
6	Key in red cell count in millions per mm <sup>3</sup> .	Count (10 <sup>6</sup> /mm <sup>3</sup> )	<b>A</b>	Count
7	Key in hematocrit.	Hct (%)	<b>B</b>	Hct (%)
8	Key in hemoglobin in g/100ml and find mean corpuscular volume in $\mu^3$ .	Hgb (g/dl)	<b>C</b>	MCV ( $\mu^3$ )
9	Compute mean corpuscular hemoglobin in pg ( $\mu\mu\text{g}$ ).		<b>D</b>	MCH (pg)
10	Compute mean corpuscular hemoglobin concentration in g/dl (g/100ml).		<b>E</b>	MCHC (g/dl)
11	To obtain a reprint of data and results.		 <b>E</b>	Ptnt # .10
				Count
				Hct (%)
				Hgb
				MCV
				MCH
				MCHC

Example:

A sample of venous blood from patient 10183 reveals a red cell count of  $2.25 \times 10^6/\text{mm}^3$ , a hematocrit of 21%, and hemoglobin of 7.2 g/dl (g/100 ml). Find the indices MCV, MCH, and MCHC.

Keystrokes:

10183 **f** **C**   
2.25 **A**   
21 **B**   
7.2 **C**   
  
**D**   
**E**

Outputs:

10183.10 \*\*\* (Ptnt ID)  
2.25 \*\*\* (Count)  
21.00 \*\*\* (Hct %)  
7.20 \*\*\* (Hgb)  
93.33 \*\*\* (MCV)  
32.00 \*\*\* (MCH)  
34.29 \*\*\* (MCHC)

## Notes

## TOTAL BLOOD VOLUME

TOTAL BLOOD VOLUME				CL1-11A	
CLEAR	PTNT #	P OFF?	REPRINT		
BCK	V INJ	STD DIL	STD CPM	CPM • TBV	

This program computes total blood volume by the radioisotope dilution technique. The inputs to the program are the background counts per minute (Bck), the volume of radioactive solution injected (V Inj), the dilution of the standard solution (Std Dil), the counts per minute of the standard (Std CPM), and the counts per minute of the sample of whole blood (WB CPM). From these values the program will compute total blood volume (TBV).

### Equations:

$$TBV = Dil \times V_{Inj} \times \frac{Std\ CPM - Bck}{WB\ CPM - Bck}$$

### Remarks:

1. Total blood volume will be computed in the same units as volume injected. Typically the units used will be milliliters (ml).
2. Equal volumes of whole blood, diluted standard solution, and distilled water should be used for the measurement of whole blood counts, standard counts, and background counts. These three counts need not be counts *per minute*; they may be counts recorded over any length of time, so long as the same time interval is used for all three counts.
3. This same program may be used to find total plasma volume provided that a sample of plasma rather than whole blood is counted for the final input. Total blood volume may be determined from total plasma volume from the equation

$$\text{Total blood volume} = \frac{\text{Total plasma volume}}{(1 - Hct \times 0.9)}$$

4. If the patient has had prior radioactivity administered, a patient background correction may be necessary. To do this, a count must be made of a blood sample before the current dose is administered. These pre-dose counts should be subtracted from the post-dose whole blood counts to give the corrected counts to be input at the final step.
5. If the print function is turned off, neither inputs nor outputs will be printed.

**Reference:**

Beierwaltes, Keyes, and Carey, *Manual of Nuclear Medicine Procedure*, Chemical Rubber Co., 1971.

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
1	Load side 1.			
2	(optional) Initialize for reprint.		<b>f</b> <b>A</b>	0.00
3	(optional) Key in patient number.	Ptnt #	<b>f</b> <b>C</b>	Ptnt # .11
4	To suppress printing of data and results, turn print function off.		<b>f</b> <b>D</b>	0.00
5	To turn print function back on later.		<b>f</b> <b>D</b>	1.00
6	Key in background counts.	Bck	<b>A</b>	Bck
7	Key in volume of fluid injected.	Vol. inj.	<b>B</b>	Vol. inj.
8	Key in dilution of standard.	Std. dil.	<b>C</b>	Std. dil.
9	Key in standard counts.	Std. CPM	<b>D</b>	Std. CPM
10	Key in whole blood counts and find total blood volume.	Blood CPM	<b>E</b>	TBV
11	To obtain a reprint.		<b>f</b> <b>E</b>	Ptnt # .11
				Bck
				Vol. inj.
				Std. dil.
				Std. CPM
				Blood CPM
				TBV

**Example:**

5 ml of radioiodinated serum albumin (RISA) are injected into patient 10183. The stock RISA is diluted by a factor of 250 and a 1 ml aliquot of this standard is found to have an activity of 2518 counts over a five-minute period. A 1 ml sample of the patient's whole blood, collected 10 minutes after injection, is found to have an activity of 837 counts over a five-minute period. A five-minute count of 1 ml distilled water yields 152 counts. What is the patient's total blood volume?



Keystrokes:

10183 **f** **C** →  
152 **A** →  
5 **B** →  
250 **C** →  
2518 **D** →  
837 **E** →

Outputs:

10183.11 \*\*\* (Ptnt ID)  
152.00 \*\*\* (Bck)  
5.00 \*\*\* (V Inj)  
250.00 \*\*\* (Dil)  
2518.00 \*\*\* (Std CPM)  
837.00 \*\*\* (WB CPM)  
4317.52 \*\*\* (TBV, ml)

Notes

## SCHILLING TEST

SCHILLING TEST				CL1-12A	
	CLEAR	PTNT #	P OFF?	REPRINT	
	BCK	STD DIL	STD CPM	U VOL	U CPM-%

This program performs the calculations involved with the Schilling test for the determination of vitamin B<sub>12</sub> absorption. The inputs to the program are the background counts per minute, the dilution and counts per minute of the standard, the volume of urine excreted, and the counts per minute of the urine. The output is the % of dose excreted.

The program is set up to handle urine volume (U Vol) in liters (l). It is assumed that if the urine volume collected was less than 1 l, the volume was brought up to 1 l by the addition of water. If the volume was a liter or more, no dilution should be made.

**Equations:**

$$\% \text{ excretion} = \frac{V}{\text{Dil}} \left[ \frac{\text{Urine CPM} - \text{Background CPM}}{\text{Standard CPM} - \text{Background CPM}} \right] \times 100$$

$$\text{where } V = \begin{cases} 1 & \text{if } U \text{ Vol} \leq 1 \text{ l} \\ U \text{ Vol} & \text{if } U \text{ Vol} > 1 \text{ l} \end{cases}$$






Dil = Dilution of the standard

**Remarks:**

1. The background, standard, and urine counts should be of equal volumes counted over equal time intervals (which need not be one minute).
2. The patient should not have had recent prior radioactivity.
3. If the print function is turned off, neither data nor results will be printed.

**Reference:**

Beierwaltes, Keyes, and Carey, *Manual of Nuclear Medicine Procedures*, Chemical Rubber Co., 1971.

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
1	Load side 1.			
2	(optional) Initialize if reprint is desired.		 <b>A</b>	0.00
3	(optional) Key in patient number.	Ptnt #	 <b>C</b>	Ptnt # .12
4	To suppress printing of data and results, turn print function off.		 <b>D</b>	0.00
5	To turn print function back on later.		 <b>D</b>	1.00
6	Key in background counts.	Bck	<b>A</b>	Bck
7	Key in dilution of the standard.	Std Dil	<b>B</b>	Std Dil
8	Key in standard counts.	Std CPM	<b>C</b>	Std CPM
9	Key in volume of urine collected.	U Vol (l)	<b>D</b>	U Vol
10	Key in the urine counts and calculate percentage of dose excreted.	U CPM	<b>E</b>	%
11	To obtain a reprint of data and results.		 <b>E</b>	Ptnt # .12
				Bck
				Std Dil
				Std CPM
				U Vol
				U CPM
				%

**Example:**

A capsule of radioactive  $B_{12}$  is administered orally to patient 10183. Over the following 24 hours, a volume of 2.54 l of urine is collected. A 20 ml aliquot of the urine is counted for 10 minutes to give 1923 counts. A 1 ml sample of the standard is diluted to 20 ml and counted for 10 minutes, giving 1757 counts. 20 ml of tap water is used for a background count; over a ten-minute interval, 127 counts are recorded. Find the percent of dose excreted.

Keystrokes:

10183 **f** **C** →  
127 **A** →  
20 **B** →  
1757 **C** →  
2.54 **D** →  
1923 **E** →

Outputs:

10183.12 \*\*\* (Ptnt ID)  
127.00 \*\*\* (Bck)  
20.00 \*\*\* (Std Dil)  
1757.00 \*\*\* (Std CPM)  
2.54 \*\*\* (U Vol)  
1923.00 \*\*\* (U CPM)  
13.99 \*\*\* (% excreted)



Notes

## THYROID UPTAKE



This program computes thyroid uptake as a percentage of an administered dose of radioiodine. The inputs to the program are the counts per minute for the standard, the standard background, the patient counts (after ingestion of the dose), and the patient background. After these variables have been input, pressing **E** will allow computation of the percent uptake.

After calculation of the uptake, two corrections may be made to the computed value. The first correction involves recent prior radioactivity in the patient. The second correction involves a significant difference in activity between the standard and the dose. These are discussed in more detail below.

If the patient has had recent prior radioactivity, the computed uptake must be corrected to account for this. In such a case the patient counts and the background counts *before* ingestion of the present dose must be known. In addition, it will be necessary to correct these predose counts for radioactive decay over the elapsed time between the measurements of the predose counts and of the counts after ingestion of the dose. The program *Radioactive Decay Corrections* (CL1-14A) may be used to account for this decay. *Radioactive Decay Corrections* will compute and store a decay factor D that will be used by this program, *Thyroid Uptake*, to adjust the predose counts to the present time.

To correct for prior radioactivity, then, you should first load side 1 and side 2 of *Radioactive Decay Corrections* (CL1-14A). Select the radioisotope of the *prior* radioactivity. Key in 1, press **A**, then key in the time interval over which the decay has occurred, in the format DD.HH (days.hours), remembering always to allow 2 places for hours. (For example, a period of 1 day 6 hours should be keyed in as 1.06.) After keying in the elapsed time, press **B**, then press **C**. The decay factor D will be displayed and automatically stored. Now load side 1 and side 2 of *Thyroid Uptake* and follow the basic procedure to find the uncorrected percentage uptake. After computing % uptake from key **E**, key in the predose patient counts, press **ENTER**, key in the predose background counts and press **f A**. The corrected percentage uptake will be computed.

The second possible correction to be made is to account for a significant difference in the activities of the standard and the dose. These activities should be measured before the dose is administered. The counts at this point are referred to as precounts. If the standard and dose precounts agree within  $\pm 3\%$ , no correction is necessary. If the precounts differ by more than 3%, however, then the computed thyroid uptake should be corrected. To make the correction, after pressing **E** to find the uptake, key in the standard precount,

press **ENTER**, key in the dose precount, and press **f B**. The program will compute the corrected thyroid uptake.

The two corrections to computed uptake operate independently of each other. Either, both, or neither correction may be made. If both are to be made, they may be made in either order. If a reprint is called for after a correction is made, the reprint will show the corrected value of uptake but will not show the inputs that went into the correction (i.e., the patient and background pre-dose counts or the standard and dose precounts).

### Equations:

$$\% \text{ uptake} = K \times \frac{\text{NPC}}{\text{Std CPM} - \text{Std Bck}} \times 100$$

where

$$\begin{aligned} \text{NPC} &= \text{Net Ptnt Cts} \\ &= \text{Ptnt CPM} - \text{Ptnt Bck} \end{aligned}$$

and K is a correction factor.

$$K = \begin{cases} 1 & \text{if no correction} \\ \frac{\text{NPC} - D \times (\text{Ptnt Predose Ct} - \text{Bck Predose Ct})}{\text{NPC}} & \text{if prior radioactivity} \\ \frac{\text{Std. Precount}}{\text{Dose Precount}} & \text{if different activities} \end{cases}$$

where

D is the radioactive decay factor.

### Remarks:

1. The counts need not be input as counts *per minute*; however, all counts should be measured over the same time interval.
2. If the print function is turned off, neither inputs nor outputs will be printed.

### Reference:

Beierwaltes, Keyes, and Carey, *Manual of Nuclear Medicine Procedures*, Chemical Rubber Co., 1971.

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
1	If correction is to be made for prior patient radio- activity, go to step 2. Otherwise go to step 6.			
2	Load side 1 and side 2 of <i>Radioactive Decay Cor-</i> <i>rections</i> (CL1-14A) and select the radioisotope of the prior radioactivity.			
3	Key in a 1 for the initial activity.	1	<b>A</b>	1.00
4	Key in time elapsed in format Days.Hours (e.g., 1 day 6 hours is keyed in as 1.06).	t(dd.hh)	<b>B</b>	t(dd.hh)
5	Compute the decay factor (will be stored automatically).		<b>C</b>	D
	<b>Basic Procedure</b>			
6	Load side 1 and side 2 of <i>Thyroid Uptake</i> (CL1-13A).			
7	(optional) Key in patient number.	Ptnt #	<b>f C</b>	Ptnt # .13
8	To suppress printing of data and results, turn print function off.		<b>f D</b>	0.00
9	To turn print function back on later.		<b>f D</b>	1.00
10	Key in counts for the standard.	Std. CPM	<b>A</b>	Std. CPM
11	Key in background counts for the standard.	Std. Bck.	<b>B</b>	Net Std. Cts.
12	Key in counts for the patient.	Ptnt. CPM	<b>C</b>	Ptnt. CPM

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
13	Key in background counts for the patient.	Ptnt. Bck.	<b>D</b>	Net Ptnt. Cts.
14	Compute thyroid uptake as a percent.		<b>E</b>	% Uptake
	<b>Corrections</b>			
15	For prior radioactivity, go to step 16, for differences in standard and dose, go to step 19. For no correction, go to step 20.			
	<b>Prior Radioactivity</b>			
16	For prior radioactivity, CL1-14A should have been run at step 2.			
17	Now key in patient predose counts and predose background and compute the corrected percent uptake.	Predose Cts.	<b>ENTER</b> <b>+</b>	
		Predose Bck.	<b>I</b> <b>A</b>	% Uptake
18	For differences in dose and standard, go to step 19. Otherwise go to step 20.			
	<b>Differences in dose and standard</b>			
19	Key in standard and dose precounts and find the corrected percent uptake.	Std. Prec.	<b>ENTER</b> <b>+</b>	
		Dose Prec.	<b>I</b> <b>B</b>	% Uptake



STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
	<b>Reprint</b>			
20	To obtain a reprint of data			
	and results.		<b>f E</b>	Ptnt # .13
				Std. CPM
				Std. Bck.
				Ptnt. CPM
				Ptnt. Bck.
				% Uptake

**Example 1:**

Before a dose of radioiodine ( $^{131}\text{I}$ ) is administered to patient 10183, a count is made of the patient's current level of radioactivity from a prior ingestion of  $^{131}\text{I}$ . The patient's predose activity is found to be 75 counts per minute (CPM) and the background predose activity 25 CPM. Twenty-four hours after ingestion of the dose, the patient's activity is measured as 350 CPM with a background of 100 CPM. The activity of a standard of  $^{131}\text{I}$  is measured at 1500 CPM with a background of 200 CPM. Find the percentage uptake corrected for prior radioactivity.

**Keystrokes:****Outputs:**

Load side 1 and side 2 of *Radioactive Decay Corrections* (CL1-14A).

Select  $^{131}\text{I}$  as prior radioisotope.

<b>f E</b> →	193.20	( $^{131}\text{I}$ half-life)
<b>1 A</b> →	1.00	
<b>0.24 B</b> →	0.24	(24 hours)
<b>C</b> →	0.92	(Decay factor)

Load side 1 and side 2 of *Thyroid Uptake* (CL1-13A).

10183 <b>f C</b> →	10183.13 ***	(Ptnt ID)
1500 <b>A</b> →	1500.00 ***	(Std CPM)
200 <b>B</b> →	200.00 ***	(Std Bck)
	1300.00	(Net Std CPM)
350 <b>C</b> →	350.00 ***	(Ptnt CPM)
100 <b>D</b> →	100.00 ***	(Ptnt Bck)
	250.00	(Net Ptnt CPM)
<b>E</b> →	19.23 ***	(% uptake)
75 <b>ENTER</b> <b>f A</b> →	75.00 ***	(Ptnt Predose)
	25.00 ***	(Bck Predose)
	15.70 ***	(Corrected uptake)



**Example 2:**

A standard and a dose are measured (before ingestion of the dose) at activities of 14,500 and 12,500 counts. Since the activities differ by more than 3%, a correction will have to be made to the computed percentage uptake. After ingestion of the dose, the standard activity is found to be 11,500 counts with a background count of 1000. The patient's activity is found as 2650 counts with a background of 500 counts. Find the corrected uptake.

**Keystrokes:**

11500 **A** →  
 1000 **B** →  
 2650 **C** →  
 500 **D** →  
**E** →  
 14500 **ENTER** 12500 **f** **B** →

**Outputs:**

11500.00 \*\*\* (Std Cts)  
 1000.00 \*\*\* (Std Bck)  
 10500.00 (Net Std Cts)  
 2650.00 \*\*\* (Ptnt CPM)  
 500.00 \*\*\* (Ptnt Bck)  
 2150.00 (Net Ptnt Cts)  
 20.48 \*\*\* (% Uptake)  
 14500.00 \*\*\* (Std Prects)  
 12500.00 \*\*\* (Dose Prects)  
 23.75 \*\*\* (Corrected uptake)

## RADIOACTIVE DECAY CORRECTIONS



This program is designed to allow calculation of the decay in radioactivity of an isotope over a specified time interval. The half-lives of 15 different radioisotopes are stored by the program and may be used in calculating the decay. Generally, to use the program you will select an isotope, key in the activity  $A_0$  at the initial time, then key in the elapsed time  $t$  and calculate the present activity  $A$ . There are thus three variables needed to define the problem entirely:  $A_0$ ,  $t$ , and  $A$ .

An additional feature of the program is its ability to calculate *any* one of these variables given the other two. Thus you are not restricted to finding the present activity given the initial activity and time; you may also solve for initial activity given time and present activity, or for time given initial activity and present activity.

The radioisotope to be selected must be specified in one of two ways. Six isotopes are available directly by pressing user-definable keys **E** and **f A** through **f E**. Nine additional isotopes are available by keying in a digit, 1 through 9, and pressing **D**. For instance, to specify use of the radioisotope  $^{57}\text{Co}$ , simply press **f B**. To specify the isotope  $^{14}\text{C}$ , key in the number 2 and press **D**. A table of the correspondence between the isotopes and the numbers 1-9 may be found in the User Instructions. A list of available isotopes and their assumed half-lives is shown below.

You may use any units for the initial and present radioactivity, so long as they are consistent. The elapsed time must be input in the units Days. Hours (DD.HH), where two full decimal places must be allotted to the hours. For instance, an elapsed time of 5 days 18 hours would be keyed in and displayed as 5.18; a time of 1 day 6 hours as 1.06; and a time of 12 hours as 0.12.

### Equations:

$$A = A_0 \left( \frac{1}{2} \right)^{t/\tau_{1/2}}$$

$$t = \frac{\tau_{1/2} \ln (A/A_0)}{\ln (1/2)}$$

where:

$A_0$  = initial radioactivity

$A$  = present radioactivity

$t$  = time elapsed, in hours

$\tau_{1/2}$  = half-life of radioisotope, in hours

Isotope	$\tau_{1/2}$ (hrs)
$^{51}\text{Cr}$	667.2
$^{57}\text{Co}$	6480
$^{99\text{m}}\text{Tc}$	6
$^{125}\text{I}$	1440
$^{131}\text{I}$	193.2
$^{137}\text{Cs}$	262980
$^3\text{H}$	107470
$^{14}\text{C}$	$5.058 \times 10^7$
$^{18}\text{F}$	1.87
$^{32}\text{P}$	343.2
$^{75}\text{Se}$	2880
$^{85}\text{Sr}$	1536
$^{113\text{m}}\text{In}$	1.73
$^{133}\text{Xe}$	126.5
$^{197}\text{Hg}$	65

### Remarks:

1. It is also possible to use this program for isotopes other than those provided by the program. In such a case, instead of selecting a radioisotope by the usual means, simply key in half-life in hours of the new isotope and press **STO** **B**. Then execute the rest of the program in the same fashion as usual.
2. Hours are not always rounded nicely to days for output. For example, a time of 6 days 23.8 hours would be computed in days. hours format as 6.238. In display mode FIX DSP 2, this would appear as 6.24, even though 7.00 might be the preferred rounded format.
3. Neither inputs nor outputs will be printed by the program.

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
1	Load side 1 and side 2.			
2	Select one of the fifteen radio-			
	isotopes and display half-life			
	in hours:			
	● Chromium—51 ( $^{51}\text{Cr}$ )		<b>f A</b>	667.20
	● Cobalt—57 ( $^{57}\text{Co}$ )		<b>f B</b>	6480.00
	● Technetium—99m ( $^{99\text{m}}\text{Tc}$ )		<b>f C</b>	6.00
	● Iodine—125 ( $^{125}\text{I}$ )		<b>f D</b>	1440.00
	● Iodine—131 ( $^{131}\text{I}$ )		<b>f E</b>	193.20
	● Cesium—137 ( $^{137}\text{Cs}$ )		<b>E</b>	262980.00
	● Hydrogen—3 ( $^3\text{H}$ )	1	<b>D</b>	107470.00
	● Carbon—14 ( $^{14}\text{C}$ )	2	<b>D</b>	50580000.00
	● Flourine—18 ( $^{18}\text{F}$ )	3	<b>D</b>	1.87
	● Phosphorus—32 ( $^{32}\text{P}$ )	4	<b>D</b>	343.20
	● Selenium—75 ( $^{75}\text{Se}$ )	5	<b>D</b>	2880.00
	● Strontium—85 ( $^{85}\text{Sr}$ )	6	<b>D</b>	1536.00
	● Indium—113m ( $^{113\text{m}}\text{In}$ )	7	<b>D</b>	1.73
	● Xenon—133 ( $^{133}\text{Xe}$ )	8	<b>D</b>	126.50
	● Mercury—197 ( $^{197}\text{Hg}$ )	9	<b>D</b>	65.00
3	Key in two of the following			
	three quantities:			
	● Activity at time zero	$A_0$	<b>A</b>	$A_0$
	● Time elapsed in days.hours			
	format*	t (dd.hh)	<b>B</b>	t (dd.hh)
	● Present activity	A	<b>C</b>	A
4	Compute remaining variable:			
	● Activity at time zero		<b>A</b>	$A_0$
	● Time elapsed in days.hours			
	format		<b>B</b>	t (dd.hh)
	● Present activity		<b>C</b>	A

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
5	For a new isotope, go to step 2;			
	to change one or both input			
	parameters, go to step 3.			
	*Recall that two digits must			
	always be allocated for hours.			
	For example, 1 day 6 hours is			
	keyed in as 1.06.			

**Example:**

An activity of 200  $\mu\text{Ci}$  is measured for a standard of  $^{51}\text{Cr}$ . What is the activity after a week?

**Keystrokes:**

**f** **A**  $\longrightarrow$   
200 **A**  $\longrightarrow$   
7 **B**  $\longrightarrow$   
**C**  $\longrightarrow$

**Outputs:**

667.20 ( $\tau_{1/2}$  for  $^{51}\text{Cr}$ )  
200.00 ( $A_0$ )  
7.00 ( $t = 7$  days)  
167.97 ( $A$ ,  $\mu\text{Ci}$ )



## RADIOIMMUNOASSAY



This program performs the calculations for a logit/log plot of radioimmunoassay data. The program allows for any number of replicates in the counts input and for any number of standards. Outputs include correlation coefficient  $r$ , slope  $m$ , and intercept  $b$  of the least-squares regression line computed. Then, given counts for an unknown, the program will compute the corresponding concentration.

To run this program, first press **A** to initialize. Then key in the non-specific binding (or blank) counts, NSB, and press **B**; repeat for as many replicates as desired. After all replicates have been keyed in, press **R/S** to compute the average non-specific binding count. (This step is *not* optional; do not omit it.) The same procedure is repeated for the counts at zero concentration,  $B_0$ , which are input to key **C**. After input of all replicates **R/S** is pressed to compute the average  $B_0$ .

The next step in the operation of the program is the input of the data for the standards. The counts for the first standard are input to key **D**; as many replicates as desired may be keyed in. After all replicates for the first standard have been keyed in, the concentration of the standard is input to key **E**. This procedure (replicates to key **D**, concentration to key **E**) is repeated for as many standards as desired. Pressing key **f A** will then cause the output of the correlation coefficient  $r$ , the slope  $m$ , and the intercept  $b$  of the least-squares logit/log regression line computed from the standards. (The values of  $r$ ,  $m$ , and  $b$  must be found before going to the next step, which is the calculation of the concentration of an unknown.) The regression performed is an unweighted regression.

At this point, the counts of an unknown may be keyed into **f B**; repeat for any number of replicates. After all replicates have been keyed in, **f C** may be pressed to find the concentration of that unknown. Repeat for as many unknowns as desired.

Two output options are available in this program. If neither option is selected, the only values output will be  $r$ ,  $m$ ,  $b$ , and the concentration of each unknown. Selection of the PRINT mode on key **f D** allows output of the following values as well: all input values (counts and standard concentrations) and the average of each set of counts input (assuming replicates). The second option, on key **f E**, is called PLOT. If this option is selected, the net  $B/B_0$  and the log and logit ( $x$  and  $y$ ) values for standards and unknowns will also be output. This information is intended to assist those who wish to make a plot by hand of the logit-log relationship.



**Equations:**

Let

NSB = average of replicate counts for non-specific binding

 $B_0$  = average of replicate counts for zero concentration $B_i$  = average of replicate counts for  $i^{\text{th}}$  standard ( $i = 1, 2, \dots, n$ ) $C_i$  = concentration of  $i^{\text{th}}$  standard

Let

$$x_i = \log C_i$$

$$y_i = \text{logit} \left( \frac{B_i - \text{NSB}}{B_0 - \text{NSB}} \right)$$

$$= \ln \left[ \frac{(B_i - \text{NSB})/(B_0 - \text{NSB})}{1 - (B_i - \text{NSB})/(B_0 - \text{NSB})} \right]$$

$$= \ln \left( \frac{B_i - \text{NSB}}{B_0 - B_i} \right)$$

$$\text{net } B_i/B_0 = \frac{B_i - \text{NSB}}{B_0 - \text{NSB}}$$

The program fits a line of the form  $y = mx + b$  to the  $(x_i, y_i)$  pairs. All sums below are from 1 to  $n$ .

$$m = \frac{\frac{\sum xy}{n} - \frac{\sum x \sum y}{n^2}}{\frac{\sum x^2}{n} - \frac{(\sum x)^2}{n^2}}$$

$$b = \bar{y} - m \bar{x}$$

where:

$$\bar{y} = \frac{\sum y}{n}$$

$$\bar{x} = \frac{\sum x}{n}$$

$$r = \frac{\frac{\sum xy}{n} - \frac{\sum x \sum y}{n^2}}{\left[ \frac{\sum x^2}{n} - \frac{(\sum x)^2}{n^2} \right]^{1/2} \left[ \frac{\sum y^2}{n} - \frac{(\sum y)^2}{n^2} \right]^{1/2}}$$

Let

$B$  = average of replicate counts for an unknown

$C_u$  = concentration of unknown

$$C_u = 10^x$$

$$\text{where } x = \frac{1}{m} \left[ \ln \left( \frac{B - \text{NSB}}{B_0 - B} \right) - b \right]$$

### Remarks:



1. The term "intercept" is used in this program to refer to the point on the logit axis (the y-axis) where it is intersected by the regression line. It does not mean, as it is sometimes used in RIA documents, the concentration for which the value of the logit function is zero.
2. After computation of  $r$ ,  $m$ , and  $b$ , these values may be found in the following registers:  $r$  in  $R_C$  and  $Z$ ,  $m$  in  $R_B$  and  $Y$ , and  $b$  in  $R_A$  and  $X$ .

### References:

Rodbard, Bridson, and Rayford, "Rapid calculation of radioimmunoassay results", *J. Lab. Clin. Med.*, 74:770 (1969).

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
1	Load side 1 and side 2.			
2	To allow output of input data			
	and intermediate results, turn			
	print function on.		<b>f D</b>	1.00
3	To turn print function off later.		<b>f D</b>	0.00
4	To allow output of (log conc.,			
	logit) values, turn plot			
	function on.		<b>f E</b>	1.00
5	To suppress further output of			
	plot data.		<b>f E</b>	0.00
	<b>Setup</b>			
6	Initialize.		<b>A</b>	
7	Key in non-specific binding			
	counts; repeat for as many			
	replicates as desired.	NSB	<b>B</b>	i
8	After all replicates, find			
	average NSB.		<b>R/S</b>	$\overline{\text{NSB}}$

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
9	Key in counts for zero dose;			
	repeat for as many replicates			
	as desired.	$B_0$	<b>C</b>	i
10	After all replicates, find			
	average $B_0$ .		<b>R/S</b>	$\bar{B}_0$
	<b>Standards</b>			
11	Key in counts for first standard;			
	repeat for as many replicates			
	as desired.	B	<b>D</b>	i
12	Key in concentration of first			
	standard; optional outputs			
	are shown in parentheses;			
	1.00 indicates first standard.	Conc.	<b>E</b>	( $\bar{B}$ )
				(net $B/B_0$ )
				(Conc.)
				(Logit)
				(Log conc.)
				1.00
13	Repeat steps 11 and 12 for			
	all standards.			
	<b>Results</b>			
14	Calculate correlation coef-			
	ficient (r), slope (m), and			
	intercept (b) of regression line.		<b>f A</b>	r
				m
				b
	<b>Unknowns</b>			
15	Key in counts for an unknown;			
	repeat for as many replicates			
	as desired.	B	<b>f B</b>	i

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
16	Find concentration of unknown; optional outputs are shown in parentheses.		 	( $\bar{B}$ ) (net B/B <sub>0</sub> ) Conc. (Logit) (Log)
17	Repeat steps 15 and 16 for any number of unknowns. <b>New Case</b>			
18	For a new assay, go to step 6.			

Example:

Below are the data for non-specific binding (NSB), zero concentration (B<sub>0</sub>), and various standards for a radioimmunoassay.

Description	Counts per minute	Concentration (pg)
NSB	425, 339, 342, 369	-
B <sub>0</sub>	10670, 10570, 10925	-
Standard 1	9176, 9850	25
Standard 2	8453, 7967	50
Standard 3	6323, 6057	100
Standard 4	3866, 4088	200
Standard 5	2027, 2221	400
Standard 6	1251, 1462	800

Find r, m, and b for the regression line. Find the concentrations corresponding to the unknown counts below.

Unknown	Counts per minute
1	10230, 10170
2	3270, 3400

Use the PRINT and PLOT options for complete outputs.

## Keystrokes:

A f D →

f E →

425 B →

339 B →

342 B →

369 B →

R/S →

10670 C →

10570 C →

10925 C →

R/S →

9176 D →

9850 D →

25 E →

8453 D →

## Outputs:

1.00 (Print on)

1.00 (Plot on)

425.00 \*\*\* (1<sup>st</sup> NSB)

1.00

339.00 \*\*\*

2.00

342.00 \*\*\*

3.00

369.00 \*\*\*

4.00

368.75 \*\*\* (Avg. NSB)

10670.00 \*\*\* (1<sup>st</sup> B<sub>0</sub>)

1.00

10570.00 \*\*\*

2.00

10925.00 \*\*\*

3.00

10721.67 \*\*\* (Avg. B<sub>0</sub>)9176.00 \*\*\* (1<sup>st</sup> of std. 1)

1.00

9850.00 \*\*\*

2.00

9513.00 \*\*\* (Avg. for std. 1)

0.88 \*\*\* (net B<sub>1</sub>/B<sub>0</sub>)

25.00 \*\*\* (Conc. of std. 1)

2.02 \*\*\* (Logit = y<sub>1</sub>)1.40 \*\*\* (Log = x<sub>1</sub>)

1.00 (Std. 1)

8453.00 \*\*\* (1<sup>st</sup> of std. 2)

1.00

7967 **D** →

7967.00 \*\*\*  
2.00

50 **E** →

8210.00 \*\*\* (Avg. for std. 2)  
0.76 \*\*\* (net  $B_2/B_0$ )  
50.00 \*\*\* (Conc. of std. 2)  
1.14 \*\*\* ( $y_2$ )  
1.70 \*\*\* ( $x_2$ )  
2.00 (Std. 2)

6323 **D** →

6323.00 \*\*\* (1<sup>st</sup> of std. 3)  
1.00

6057 **D** →

6057.00 \*\*\*  
2.00

100 **E** →

6190.00 \*\*\* (Avg. for std. 3)  
0.56 \*\*\* (net  $B_3/B_0$ )  
100.00 \*\*\* (Conc. of std. 3)  
0.25 \*\*\* ( $y_3$ )  
2.00 \*\*\* ( $x_3$ )  
3.00 (Std. 3)

3866 **D** →

3866.00 \*\*\* (1<sup>st</sup> of std. 4)  
1.00

4088 **D** →

4088.00 \*\*\*  
2.00

200 **E** →

3977.00 \*\*\* (Avg. for std. 4)  
0.35 \*\*\* (net  $B_4/B_0$ )  
200.00 \*\*\* (Conc. of std. 4)  
-0.63 \*\*\* ( $y_4$ )  
2.30 \*\*\* ( $x_4$ )  
4.00 (Std. 4)

2027 **D** →

2027.00 \*\*\* (1<sup>st</sup> of std. 5)  
1.00

2221 **D** →

2221.00 \*\*\*  
2.00



400 **E** →

2124.00 \*\*\* (Avg. for std. 5)  
 0.17 \*\*\* (net  $B_5/B_0$ )  
 400.00 \*\*\* (Conc. of std. 5)  
 -1.59 \*\*\* ( $y_5$ )  
 2.60 \*\*\* ( $x_5$ )  
 5.00 (Std. 5)

1251 **D** →

1251.00 \*\*\* (1<sup>st</sup> of std. 6)  
 1.00

1462 **D** →

1462.00 \*\*\*  
 2.00

800 **E** →

1356.50 \*\*\* (Avg. for std. 6)  
 0.10 \*\*\* (net  $B_6/B_0$ )  
 800.00 \*\*\* (Conc. of std. 6)  
 -2.25 \*\*\* ( $y_6$ )  
 2.90 \*\*\* ( $x_6$ )  
 6.00 (Std. 6)

**f** **A** →

-1.00 \*\*\* (r)  
 -2.89 \*\*\* (Slope m)  
 6.03 \*\*\* (Intercept b)

10230 **f** **B** →

10230.00 \*\*\* (1<sup>st</sup> of unkn. 1)  
 1.00

10170 **f** **B** →

10170.00 \*\*\*  
 2.00

**f** **C** →

10200.00 \*\*\* (Avg. of unkn. 1)  
 0.95 \*\*\* (net  $B/B_0$ )  
 11.83 \*\*\* (Conc. of unkn. 1)  
 2.94 \*\*\* (Unkn. y)  
 1.07 \*\*\* (Unkn. x)  
 11.83

3270 **f** **B** →

3270.00 \*\*\* (1<sup>st</sup> of unkn. 2)  
 1.00

3400 **f** **B** →

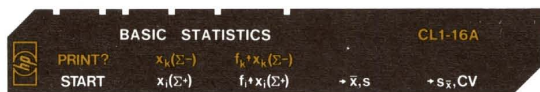
3400.00 \*\*\*  
2.00

**f** **C** →

3335.00 \*\*\* (Avg. of unkn. 2)  
0.29 \*\*\* (net B/B<sub>0</sub>)  
254.57 \*\*\* (Conc. of unkn. 2)  
-0.91 \*\*\* (Unkn. y)  
2.41 \*\*\* (Unkn. x)  
254.57

Notes

## BASIC STATISTICS



This program computes the basic statistics of one variable: mean ( $\bar{x}$ ), standard deviation ( $s$ ), standard error ( $s_{\bar{x}}$ ), and coefficient of variation (C.V. %).

The input data to the program may be either grouped or ungrouped. Ungrouped data should be input to key **B** and grouped data to key **C**; keys **f B** and **f C** provide error correction for the ungrouped and grouped cases, respectively. If an incorrect entry is made, it may be corrected by keying in that entry a second time and pressing the appropriate error correction key. Suppose, for example, that 7.31 is one data point in a set of ungrouped data, but that a mistake is made in entering it. Instead of 7.31, the value 4.31 is input to key **B**. To correct this mistake, you would simply key in 4.31 and press **f B**. At this point the error has been eliminated. Now enter the correct data, 7.31, and press **B**.

## Equations:

Ungrouped data:

Let  $\{x_1, x_2, \dots, x_n\}$  be the set of data points.

$$\text{Mean } \bar{x} = \frac{1}{n} \sum_{i=1}^n x_i$$

$$s = \sqrt{\frac{\sum x_i^2 - \frac{(\sum x_i)^2}{n}}{n - 1}}$$

$$\text{Standard error } s_{\bar{x}} = \frac{s}{\sqrt{n}}$$

$$\text{Coefficient of variation C.V. \%} = \frac{s}{\bar{x}} \times 100$$

Grouped data:

Let  $\{x_1, x_2, \dots, x_n\}$  be a set of data points occurring with the respective frequencies  $f_1, f_2, \dots, f_n$ .

$$\text{Mean } \bar{x} = \frac{\sum f_i x_i}{\sum f_i}$$

$$\text{Standard deviation } s = \sqrt{\frac{\sum f_i x_i^2 - \frac{(\sum f_i x_i)^2}{\sum f_i}}{\sum f_i - 1}}$$

$$\text{Standard error } s_{\bar{x}} = \frac{s}{\sqrt{\sum f_i}}$$

$$\text{Coefficient of variation C. V. } \% = \frac{s}{\bar{x}} \times 100$$

**Remarks:**

1. Grouped and ungrouped data may be mixed in the same set of data.
2. The preprogrammed  $\Sigma+$  and  $\Sigma-$  keys may be used to input and correct ungrouped data in place of keys **B** and **f B**. Calculation of mean and standard deviation may also be done by the preprogrammed keys  $\bar{x}$  and **S** for both grouped and ungrouped data.

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
1	Load side 1.			
2	Initialize.		<b>A</b>	0.00
3	To allow printing of input data, turn print function on.		<b>f A</b>	1.00
4	To turn print function off later.		<b>f A</b>	0.00
5	For ungrouped data, go to step 6; for grouped data, go to step 9.			
	<b>Ungrouped data</b>			
6	Perform this step for $i = 1,$ $2, \dots, n:$			
	Input data point.	$x_i$	<b>B</b>	$i$
7	To correct an erroneous entry.	$x_k$	<b>f B</b>	$i$
8	Go to step 11.			
	<b>Grouped data</b>			
9	Perform this step for $i = 1,$ $2, \dots, n:$			
	Input frequency and data.	$f_i$	<b>ENTER</b>	
		$x_i$	<b>C</b>	$i$

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
10	To correct an erroneous entry.	$f_k$	ENTER	
		$x_k$	f C	i
	Results			
11	Compute mean and standard deviation.			
			D	$\bar{x}$
				s
12	Compute standard error and coefficient of variation.			
			E	$s_{\bar{x}}$
				C.V. %
13	For a new set of data, go to step 2.			

Example 1:

Hemoglobin concentration was measured for nine male patients. Compute the basic statistics for these data.

Hemoglobin concentration (g/dl)

13.8	17.4
16.9	13.4
16.5	17.9
17.7	15.2
16.0	

Keystrokes:

A	→
f A	→
13.8 B	→
16.9 B	→
16.5 B	→
17.7 B	→

Outputs:

0.00
1.00 (Print on)
13.80 *** ( $x_i$ )
1.00 (i)
16.90 ***
2.00
16.50 ***
3.00
17.70 ***
4.00



16	B	→	16.00 ***
			5.00
17.4	B	→	17.40 ***
			6.00
3.4	B	→	3.40 *** (Error!)
			7.00 (k = 7)
3.4	f B	→	3.40 *** (Correction)
			6.00
13.4	B	→	13.40 *** ( $\bar{x}_7$ )
			7.00
17.9	B	→	17.90 ***
			8.00
15.2	B	→	15.20 ***
			9.00
D		→	16.09 *** (Mean)
			1.65 *** (Std. dev.)
E		→	0.55 *** ( $s_{\bar{x}}$ )
			10.23 *** (C.V. %)

Example 2:

A certain test was performed on college students ranging in age from 18 to 22 years. The number of subjects of each age is shown in the table. Compute the mean age of the students in the test.

Age	18	19	20	21	22
# Subjects	5	9	13	7	1

Keystrokes:

A	→
If Example 1 has just been run, turn print off:	
f A	→
5 ENTER	18 C →
9 ENTER	19 C →
13 ENTER	20 C →
7 ENTER	21 C →
1 ENTER	22 C →
D	→

Outputs:

0.00
(Print off)
1.00
2.00
3.00
4.00
5.00
19.71 *** (Mean)
1.05 *** (Std. dev.)

## CHI-SQUARE EVALUATION AND DISTRIBUTION

CHI-SQUARE TEST AND DISTRIBUTION				CL1-17A
PRINT?	$O_i(\Sigma^-)$	$O_i \cdot E_i(\Sigma^-)$	$x \cdot f(x)$	$x \cdot P(x)$
START	$O_i(\Sigma^+)$	$O_i \cdot E_i(\Sigma^+)$	$\rightarrow x^2; E$	$\nu \cdot \Gamma(\nu/2)$

This program allows you to perform two important calculations concerning the chi-square statistic. The first of these calculates the value of the  $\chi^2$  statistic for the goodness of fit test. The second evaluates the chi-square density  $f(x)$  and the cumulative distribution  $P(x)$  given  $x$  and the degrees of freedom  $\nu$ .

The  $\chi^2$  statistic may be computed for the case where the expected frequencies are equal as well as for the case where they are different. If they are equal, only the observed frequencies  $O_i$  need be input to key **B**; error correction is available on key **f B**. After calculation of  $\chi^2$  from key **D**, the expected frequency  $E$  may be calculated. If the expected frequencies are different, both the observed and expected frequencies should be input to key **C**. Error correction is provided on key **f C**.

To make calculations involving the chi-square distribution, first input the degrees of freedom  $\nu$  to key **E**. Then key in the value of  $x$  and press **f D** to find the density  $f(x)$  or **f E** to find the cumulative distribution  $P(x)$ .

### Equations:

Chi-square evaluation:

$$\chi^2 = \sum_{i=1}^n \frac{(O_i - E_i)^2}{E_i}$$

where:

$O_i$  = observed frequency

$E_i$  = expected frequency

If the expected values are equal

$$\left( E = E_i = \frac{\Sigma O_i}{n} \text{ for all } i \right)$$

then

$$\chi^2 = \frac{n \Sigma O_i^2}{\Sigma O_i} - \Sigma O_i$$

Chi-square distribution:

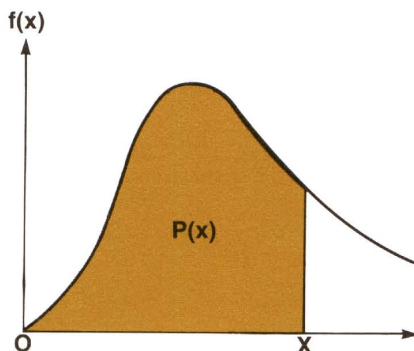
Chi-square density:

$$f(x) = \frac{1}{2^{\frac{\nu}{2}} \Gamma\left(\frac{\nu}{2}\right)} x^{\frac{\nu}{2}-1} e^{-\frac{x}{2}}$$

where:

$$x \geq 0$$

$\nu$  is the degrees of freedom.



Series approximation is used to evaluate the cumulative distribution

$$P(x) = \int_0^x f(t) dt$$

$$= \left(\frac{x}{2}\right)^{\frac{\nu}{2}} \frac{e^{-\frac{x}{2}}}{\Gamma\left(\frac{\nu+2}{2}\right)} \left[ 1 + \sum_{k=1}^{\infty} \frac{x^k}{(\nu+2)(\nu+4) \dots (\nu+2k)} \right]$$

where:

$$\Gamma\left(\frac{\nu}{2}\right) = \begin{cases} \left(\frac{\nu}{2} - 1\right)!, & \nu \text{ even} \\ \left(\frac{\nu}{2} - 1\right)\left(\frac{\nu}{2} - 2\right) \dots \left(\frac{1}{2}\right) \Gamma\left(\frac{1}{2}\right), & \nu \text{ odd} \end{cases}$$

$$\Gamma\left(\frac{1}{2}\right) = \sqrt{\pi}$$

The program computes successive partial sums of the above series. When two consecutive partial sums are equal, the value is used as the sum of the series.

### Remarks:

1. In order to apply the goodness of fit test to a set of given data, it may be necessary to combine some classes to ensure that each expected frequency is not too small (not less than, say, 5).
2. The program for distribution requires that  $\nu \leq 141$ . If  $\nu > 141$ , erroneous overflow will result.
3. If both  $x$  and  $\nu$  are large, the calculation of  $f(x)$  may cause overflow.

### References:

(Evaluation) J.E. Freund, *Mathematical Statistics*, Prentice Hall, 1962.

(Distribution) Abramowitz and Stegun, *Handbook of Mathematical Functions*, National Bureau of Standards, 1968.

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
1	Load side 1 and side 2.			
2	Initialize.		A	20.00
3	To allow printing of data and results, turn the print function on.		f A	1.00
4	To turn the print function off later.		f A	0.00
5	For $\chi^2$ evaluation, go to step 6; for $\chi^2$ distribution, go to step 15.			
	<b><math>\chi^2</math> evaluation</b>			
6	If the expected frequencies are equal, go to step 7; if they are not equal, go to step 11.			
	<b>Expected frequencies equal</b>			
7	Perform this step for $i = 1, 2, \dots, n$ :			
	Key in observed value.	$O_i$	B	$i$

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
8	To correct an erroneous entry.	$O_k$	<b>f B</b>	i
9	Calculate the $\chi^2$ statistic and (optionally) the average expected frequency.		<b>D</b> <b>R/S</b>	$\chi^2$ E
10	For a new case, go to step 2. <b>Expected frequencies</b> <b>unequal</b>			
11	Perform this step for $i = 1$ , 2, ..., n: Key in observed and expected frequency.	$O_i$ $E_i$	<b>ENTER</b> <b>C</b>	i
12	To correct an erroneous entry.	$O_k$ $E_k$	<b>ENTER</b> <b>f C</b>	i
13	Calculate the $\chi^2$ statistic.		<b>D</b>	$\chi^2$
14	For a new case, go to step 2. <b><math>\chi^2</math> distribution</b>			
15	Key in degrees of freedom.	$\nu$	<b>E</b>	$\Gamma(\nu/2)$
16	Key in x and compute either • Density or • Cumulative distribution	x x	<b>f D</b> <b>f E</b>	f(x) P(x)
17	For a new case, go to step 2.			

**Example:**

Ten one-minute counts of a Cesium-137 check source yielded the following results. Use this program to evaluate the counting instrument. (Note that with 10 data points, the degrees of freedom  $\nu = 9$ .)

25601	25553
25546	25841
25592	25560
25820	25633
25569	25464

Keystrokes:

**A** **f** **A** →  
25601 **B** →  
25546 **B** →  
25592 **B** →  
25820 **B** →  
25569 **B** →  
25553 **B** →  
25841 **B** →  
25560 **B** →  
25633 **B** →  
25464 **B** →  
**D** →  
**R/S** →  
9 **E** →  
5.10 **f** **E** →

Outputs:

1.00 (Print on)  
25601.00 \*\*\*  
1.00  
25546.00 \*\*\*  
2.00  
25592.00 \*\*\*  
3.00  
25820.00 \*\*\*  
4.00  
25569.00 \*\*\*  
5.00  
25553.00 \*\*\*  
6.00  
25841.00 \*\*\*  
7.00  
25560.00 \*\*\*  
8.00  
25633.00 \*\*\*  
9.00  
25464.00 \*\*\*  
10.00  
5.10 \*\*\* ( $\chi^2$ )  
25617.90 \*\*\* (E)  
9.00 \*\*\* ( $\nu$ )  
11.63 \*\*\* ( $\Gamma (\nu/2)$ )  
5.10 \*\*\*  
0.17 \*\*\* (P ( $\chi^2$ ))

Since P ( $\chi^2$ ) is between 0.1 and 0.9, the counting instrument is assumed to be operating properly.



Notes

# t STATISTICS



This program will compute either of two test statistics which are used to compare population means: the paired t statistic or the t statistic for two means. The paired t statistic applies to a set of *paired* observations drawn from two normal populations with unknown means  $\mu_1, \mu_2$ :

$x_i$	$x_1$	$x_2$	...	$x_n$
$y_i$	$y_1$	$y_2$	...	$y_n$

The paired t statistic can be used to test the validity of the hypothesis that the means are equal. If the computed value of t is significant (as determined by *t Distribution*, CL1-19A), then we reject the hypothesis that the population means are equal.

The x- and y-values are input to key **B**. Error correction is provided by key **f B**. After the input of all x-y pairs, the t statistic may be found by pressing **C**.

The t statistic for two means applies to independent random samples  $\{x_1, x_2, \dots, x_{n_1}\}$  and  $\{y_1, y_2, \dots, y_{n_2}\}$  drawn from two normal populations with unknown means  $\mu_1, \mu_2$  and the same unknown variance  $\sigma^2$ . The t statistic is used to test the validity of the hypothesis that the populations means differ by some amount d (i.e., that  $\mu_1 - \mu_2 = d$ ). Note that d may be chosen to be zero.

To operate this routine, the x-values should first be keyed in to key **D**. Error correction is available on key **f D**. After all x-values have been input, the value of d should be input to key **f E**. Then the y-values should be keyed in to key **D**. After input of all the y-values, the t statistic may be found by pressing **E**.

**Equations:***Paired t statistic*

let

$$D_i = x_i - y_i$$

$$\bar{D} = \frac{1}{n} \sum_{i=1}^n D_i$$

$$s_D = \sqrt{\frac{\sum D_i^2 - \frac{1}{n} (\sum D_i)^2}{n - 1}}$$

$$s_{\bar{D}} = \frac{s_D}{\sqrt{n}}$$

The test statistic

$$t = \frac{\bar{D}}{s_{\bar{D}}}$$

which has  $n - 1$  degrees of freedom (df) can be used to test the null hypothesis

$$H_0: \mu_1 = \mu_2$$

*t statistic for two means*

Define

$$\bar{x} = \frac{1}{n_1} \sum_{i=1}^{n_1} x_i$$

$$\bar{y} = \frac{1}{n_2} \sum_{i=1}^{n_2} y_i$$

$$t = \frac{\bar{x} - \bar{y} - d}{\sqrt{\frac{1}{n_1} + \frac{1}{n_2}} \sqrt{\frac{\sum x_i^2 - n_1 \bar{x}^2 + \sum y_i^2 - n_2 \bar{y}^2}{n_1 + n_2 - 2}}}$$

We can use this t statistic which has the t distribution with  $n_1 + n_2 - 2$  degrees of freedom (df) to test the null hypothesis

$$H_0: \mu_1 - \mu_2 = d$$

References:

(Paired t) B. Ostle, *Statistics in Research*, Iowa State University Press, 1963.  
(t for two means) K.A. Brownlee, *Statistical Theory and Methodology in Science and Engineering*, John Wiley and Sons, 1965.

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
1	Load side 1 and 2 of program.			
2	Initialize.		A	
3	To allow output of data and results, turn print function on.		f A	1.00
4	To turn print function off later.		f A	0.00
5	For t statistic for two means, go to step 11; for paired t statistic, go to step 6.			
	<b>Paired t statistic</b>			
6	Repeat this step for all data pairs (i = 1, 2, ..., n):			
	Key in x- and y-values.	$x_i$	ENTER+	
		$y_i$	B	i
7	To correct an erroneous entry.	$x_k$	ENTER+	
		$y_k$	f B	i
8	Compute paired t statistic.		C	t
9	(optional) Compute degrees of freedom, mean difference, and standard deviation of D.			
			R/S	df
				$\bar{D}$ .
				$s_D$
10	For a new case, go to step 2.			
	<b>t statistic for two means</b>			
11	Repeat this step for all x-values (i = 1, 2, ..., $n_1$ ):			
	Key in x-value.	$x_i$	D	i
12	To correct an erroneous entry.	$x_k$	f D	i

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
13	Key in difference to be tested.	d	<b>f</b> <b>E</b>	d
14	Repeat this step for all y-values ( $i = 1, 2, \dots, n_2$ ):			
	Key in y-value.	$y_i$	<b>D</b>	i
15	To correct an erroneous entry.	$y_k$	<b>f</b> <b>D</b>	i
16	Compute t statistic for two means.		<b>E</b>	t
17	(optional) Compute degrees of freedom.		<b>R/S</b>	df
18	(optional) Change value of d and repeat step 16.	d	<b>STO</b> <b>7</b>	
19	For a new case go to step 2.			

**Example 1:**

The hemoglobin concentration in blood samples from six patients was measured by two different methods. Use the paired t-statistic to determine if there is a significant difference between the two methods of measurement.

Sample	Method	
	1 (g/dl)	2 (g/dl)
1	17.6	17.4
2	13.0	12.9
3	15.3	15.3
4	15.0	15.2
5	15.0	15.0
6	14.6	14.5

**Keystrokes:**

**A**  $\longrightarrow$   
**f** **A**  $\longrightarrow$   
 17.6 **ENTER** 17.4 **B**  $\longrightarrow$

**Outputs:**

0.00  
 1.00 (Print on)  
 17.60 \*\*\* ( $x_1$ )  
 17.40 \*\*\* ( $y_1$ )  
 1.00 ( $i = 1$ )

13 **ENTER** 12.9 **B** →

15.3 **ENTER** 15.2 **B** →

15.3 **ENTER** 15.2 **f** **B** →

15.3 **ENTER** 15.3 **B** →

15 **ENTER** 15.2 **B** →

15 **ENTER** 15 **B** →

14.6 **ENTER** 14.5 **B** →

**C** →

**R/S** →

13.00 \*\*\*

12.90 \*\*\*

2.00

15.30 \*\*\*

15.20 \*\*\* (Error!)

3.00

15.30 \*\*\*

15.20 \*\*\* (Corrected)

2.00

15.30 \*\*\*

15.30 \*\*\*

3.00

15.00 \*\*\*

15.20 \*\*\*

4.00

15.00 \*\*\*

15.00 \*\*\*

5.00

14.60 \*\*\*

14.50 \*\*\*

6.00

0.60 \*\*\* (t)

5.00 \*\*\* (df)

0.03 \*\*\* ( $\bar{D}$ )

0.14 \*\*\* ( $S_D$ )

To interpret these results, load *t Distribution* (CL1-19A) and find the cumulative distribution  $I(x)$  for  $x = 0.60$  and 5 degrees of freedom.

**Keystrokes:**

5 **A** .60 **D** →

**Outputs:**

0.43 \*\*\* (I (0.60))

The probability of  $|t| > 0.60$  is thus 57%. We conclude that the hypothesis that the means are equal cannot be rejected.



Example 2:

Hemoglobin concentration was measured for nine male and seven female patients. Use the t-statistic for two means to test the hypothesis that the difference between the means is negligible (i.e.,  $d = 0$ ).

Hgb concentration (g/dl)	
Men	Women
13.8	11.9
16.9	14.4
16.5	13.7
17.7	16.8
16.0	11.7
17.4	14.9
13.4	12.3
17.9	
15.2	

Keystrokes:

**A** →  
If example 1 has not just been run:  
**f A** →  
13.8 **D** →  
16.9 **D** →  
16.5 **D** →  
17.7 **D** →  
16 **D** →  
17.4 **D** →  
13.4 **D** →  
17.9 **D** →  
15.2 **D** →  
0 **f E** →

Outputs:

0.00  
  
1.00 (Print on)  
13.80 \*\*\* ( $x_1$ )  
1.00 ( $i = 1$ )  
16.90 \*\*\*  
2.00  
16.50 \*\*\*  
3.00  
17.70 \*\*\*  
4.00  
16.00 \*\*\*  
5.00  
17.40 \*\*\*  
6.00  
13.40 \*\*\*  
7.00  
17.90 \*\*\*  
8.00  
15.20 \*\*\*  
9.00  
0.00 \*\*\* ( $d = 0$ )

11.9	D	→
14.4	D	→
13.7	D	→
16.8	D	→
11.7	D	→
14.9	D	→
12.3	D	→
E		→
R/S		→

11.90	***	(y <sub>1</sub> )
1.00		(i = 1)
14.40	***	
2.00		
13.70	***	
3.00		
16.80	***	
4.00		
11.70	***	
5.00		
14.90	***	
6.00		
12.30	***	
7.00		
2.76	***	(t)
14.00	***	(df)

Load *t* Distribution (CL1-19A).

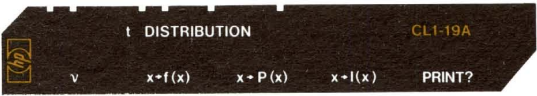
14	A	2.76	D	→
----	---	------	---	---

0.98 \*\*\* (I (2.76))

Thus the value of *t* is significant and we should reject the hypothesis that the average hemoglobin concentrations in males and females are equal.

Notes

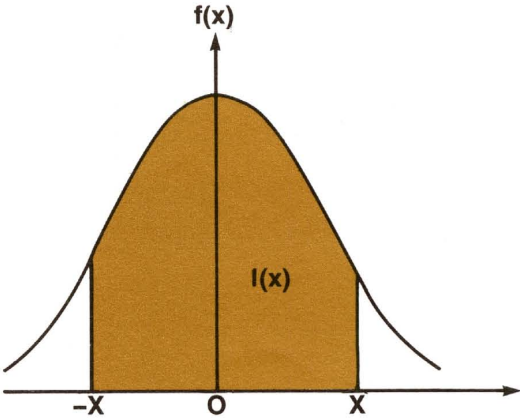
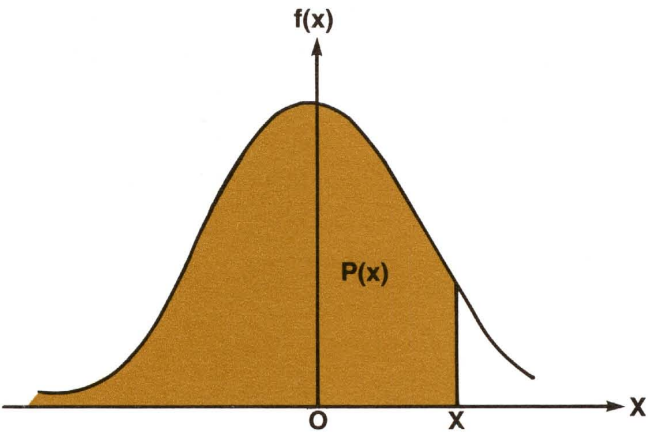
t DISTRIBUTION



This program calculates three parameters of the t distribution given  $x$  and the degrees of freedom  $\nu$ . The density function  $f(x)$  is computed as well as two measures of the area under the distribution curve,  $P(x)$  and, for  $x > 0$ ,  $I(x)$ , where

$$P(x) = \int_{-\infty}^x f(y) dy$$

and  $I(x) = \int_{-x}^x f(y) dy.$



**Equations:**

$$f(x) = \frac{\Gamma\left(\frac{\nu+1}{2}\right)}{\sqrt{\pi\nu} \Gamma\left(\frac{\nu}{2}\right)} \left(1 + \frac{x^2}{\nu}\right)^{-\frac{\nu+1}{2}}$$

(1)  $\nu$  even

$$I(x) = \sin \theta \left\{ 1 + \frac{1}{2} \cos^2 \theta + \frac{1 \cdot 3}{2 \cdot 4} \cos^4 \theta + \dots \right. \\ \left. + \frac{1 \cdot 3 \cdot 5 \dots (\nu-3)}{2 \cdot 4 \cdot 6 \dots (\nu-2)} \cos^{\nu-2} \theta \right\}$$

(2)  $\nu$  odd

$$I(x) = \begin{cases} \frac{2\theta}{\pi} \text{ if } \nu = 1 \\ \frac{2\theta}{\pi} + \frac{2}{\pi} \cos \theta \left\{ \sin \theta \left[ 1 + \frac{2}{3} \cos^2 \theta + \dots \right. \right. \\ \left. \left. + \frac{2 \cdot 4 \dots (\nu-3)}{1 \cdot 3 \dots (\nu-2)} \cos^{\nu-3} \theta \right] \right\} \text{ if } \nu > 1 \end{cases}$$

where

$$\theta = \tan^{-1} \left( \frac{x}{\sqrt{\nu}} \right)$$

$$P(x) = \begin{cases} \frac{1 + I(x)}{2} \text{ if } x > 0 \\ \frac{1 - I(x)}{2} \text{ if } x \leq 0 \end{cases}$$

**Remarks:**

The program requires  $\nu < 141$ . Otherwise an erroneous overflow will result.

**Reference:**

Abramowitz and Stegun, *Handbook of Mathematical Functions*, National Bureau of Standards, 1970.

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
1	Load side 1 and side 2			
	of program.			
2	To allow printing of inputs,			
	turn print function on.		<b>E</b>	1.00
3	To turn print function off			
	later.		<b>E</b>	0.00
4	Key in degrees of freedom.	$\nu$	<b>A</b>	$\nu$
5	Key in x and compute either			
	• Density function	x	<b>B</b>	f(x)
	or			
	• Cumulative distribution	x	<b>C</b>	P(x)
	or			
	• Integral, -x to x ( $x > 0$ ).	x	<b>D</b>	I(x)

**Example 1:**

Find the density function and P(x) for  $x = 1.6$  with 9 degrees of freedom.

**Keystrokes:**

9 **A** →  
1.6 **B** →  
1.6 **C** →

**Outputs:**

9.00 ( $\nu$ )  
0.11 \*\*\* (f (x))  
0.93 \*\*\* (P (x))

**Example 2:**

Find I(x) for  $x = 1.83$  and  $\nu = 11$ .

**Keystrokes:**

11 **A** →  
1.83 **D** →

**Outputs:**

11.00 ( $\nu$ )  
0.91 \*\*\* (I (x))



## Notes

19-05

## Notes



## PROGRAM LISTINGS

The following listings are included for your reference. A table of keycodes and keystrokes corresponding to the symbols used in the listings can be found in Appendix E of your Owner's Handbook.

<b>Program</b>	<b>Page</b>
1. Beer's Law .....	L01-01
2. Protein Electrophoresis .....	L02-01
3. LDH Isoenzymes .....	L03-01
4. Body Surface Area .....	L04-01
5. Urea Clearance .....	L05-01
6. Creatinine Clearance .....	L06-01
7. Amniotic Fluid Assay .....	L07-01
8. Blood Acid-Base Status .....	L08-01
9. Oxygen Saturation and Content .....	L09-01
10. Red Cell Indices .....	L10-01
11. Total Blood Volume .....	L11-01
12. Schilling Test .....	L12-01
13. Thyroid Uptake .....	L13-01
14. Radioactive Decay Corrections .....	L14-01
15. Radioimmunoassay .....	L15-01
16. Basic Statistics .....	L16-01
17. Chi-square Evaluation and Distribution .....	L17-01
18. t Statistics .....	L18-01
19. t Distribution .....	L19-01

Beer's Law

001 *LBLH	A → %T.	057 +	For % T <sub>u</sub> , compute A <sub>u</sub> .						
002 STOD		058 GTOD	-----						
003 F0?		059 *LBL4							
004 PRTX	A.	060 CHS							
005 2		061 *LBL0							
006 -		062 STOD	Store A <sub>u</sub> .						
007 CHS		063 RCLH	Display input.						
008 10*		064 RTN	-----						
009 STOE	%T.	065 *LBL5							
010 F0?		066 STOS							
011 FRTX		067 F0?	C <sub>s</sub> → C <sub>u</sub> .						
012 F0?		068 SPC							
013 SFC		069 F0?							
014 RTN	-----	070 PRTX							
015 *LBL5	%T → A.	071 RCL9							
016 STOE		072 *							
017 F0?		073 RCL5	C <sub>u</sub> = C <sub>s</sub> × $\frac{A_u}{A_s}$						
018 PRTX	%T.	074 +							
019 LOG		075 STOD							
020 CHS		076 F0?							
021 2		077 PRTX							
022 +		078 F0?							
023 STOD		079 SPC							
024 F0?		080 RTN							
025 PRTX	A.	081 *LBL6	-----						
026 F0?		082 0	Clear for reprint.						
027 SPC		083 STOD							
028 RTN		084 STOE							
029 *LBLC	+ % T <sub>s</sub> (-A <sub>s</sub> ).	085 STOC							
030 STOD		086 STOD							
031 F0?		087 STOE							
032 SPC		088 STOI							
033 F0?		089 RTN							
034 PRTX		090 *LBL6							
035 *X0?	For absorbance, GTO 3.	091 INT	Patient ID = Pnt# .01.						
036 GTOD		092 *							
037 LOG		093 0							
038 CHS		094 1							
039 2	For %T <sub>s</sub> , compute A <sub>s</sub> .	095 +							
040 +	-----	096 STOI							
041 GTOD		097 PRTX							
042 *LBL3		098 SPC							
043 CHS		099 RTN							
044 *LBL0		100 *LBLd							
045 STOB	Store A <sub>s</sub> .	101 F0?	Print toggle.						
046 RCLC	Display input.	102 GTOD							
047 RTN	-----	103 SFO							
048 *LBLD	+ % T <sub>u</sub> (-A <sub>u</sub> ).	104 1							
049 STOB		105 RTN							
050 F0?		106 *LBL0							
051 PRTX	For absorbance, GTO 4.	107 CF0							
052 *X0?		108 0							
053 GTOD		109 RTN							
054 LOG		110 *LBL5							
055 CHS		111 SFC	Reprint						
056 2		112 SPC	-----						
REGISTERS									
0	1	2	3	4	5	6	7 C <sub>u</sub>	8 C <sub>s</sub>	9 A <sub>u</sub>
S0	S1	S2	S3	S4	S5	S6	S7	S8	S9
A	B Input to [D]		C Input to [C]		D A		E % T		F Pnt# .01

113 RCL1			
114 INT			
115 .			
116 0			
117 1			
118 +			
119 FRTX	Patient ID.		
120 SPC			
121 RCL0	A.		
122 PRTX			
123 RCL5	%T.		
124 PRTX			
125 SPC			
126 SPC			
127 RCL0	+ % T <sub>s</sub> (-A <sub>s</sub> ).		
128 FRTX			
129 RCL4	+ % T <sub>u</sub> (-A <sub>u</sub> ).		
130 PRTX			
131 SPC			
132 RCL6	C <sub>s</sub> .		
133 PRTX			
134 RCL7	C <sub>u</sub> .		
135 PRTX			
136 RTN	-----		

LABELS					FLAGS	SET STATUS			
A A→%T	B %T→A	C +%T <sub>s</sub> (-A <sub>s</sub> )	D +%T <sub>u</sub> (-A <sub>u</sub> )	E C <sub>s</sub> →C <sub>u</sub>	0 Print	FLAGS		TRIG	DISP
a Clear	b	c Ptnt #	d P off?	e Reprint	1	0 <input checked="" type="checkbox"/> <input type="checkbox"/>	DEG <input checked="" type="checkbox"/>	FIX <input checked="" type="checkbox"/>	
0 Used	1	2	3 Store A <sub>s</sub>	4 Store A <sub>u</sub>	2	1 <input type="checkbox"/> <input checked="" type="checkbox"/>	GRAD <input type="checkbox"/>	SCI <input type="checkbox"/>	
5	6	7	8	9	3	2 <input type="checkbox"/> <input checked="" type="checkbox"/>	RAD <input type="checkbox"/>	ENG <input type="checkbox"/>	
						3 <input type="checkbox"/> <input checked="" type="checkbox"/>		n <u>2</u>	

## Protein Electrophoresis

REGISTERS									
0	1	2	3	4	5	6	7	8	9
$\Sigma$ Fract	25 - n	Tot Pr	Ptnt # .02						
S0	S1	S2	S3	S4	S5	S6	S7	S8	S9 Fract <sub>6</sub>
A Fract <sub>3</sub>	B Fract <sub>4</sub>	C Fract <sub>3</sub>	D Fract <sub>2</sub>	E Fract <sub>1</sub>	Index				



113	SPC			
114	RCL3			
115	INT			
116	.			
117	0			
118	2			
119	+			
120	PRTX	Patient ID		
121	SPC	-----		
122	#LBL7			
123	RCL1			
124	PRTX	Loop to print inputs.		
125	RCL1			
126	RCL1			
127	X=Y?			
128	GT01			
129	DSZ1			
130	GT07	-----		
131	#LBL1			
132	2			
133	4			
134	ST01			
135	SPC			
136	GSB9	Print %.		
137	SPC			
138	SPC			
139	RCL2	If total protein = 0, skip to print A/G.		
140	X=0?			
141	GT0E	Otherwise print T Pr and grams.		
142	PRTX			
143	SPC			
144	2			
145	4			
146	ST01			
147	GSB8			
148	GT0E	Print A/G.		

LABELS					FLAGS	SET STATUS		
A Start	B Fract	C →%	D T Pr→g	E →A/G	0 Print	FLAGS	TRIG	DISP
a	b	c Pnt #	d P off?	e Reprint	1	ON OFF 0 <input checked="" type="checkbox"/> <input type="checkbox"/>	DEG <input checked="" type="checkbox"/>	FIX <input checked="" type="checkbox"/>
0 Used	1 Used	2	3	4	2	1 <input type="checkbox"/> <input checked="" type="checkbox"/>	GRAD <input type="checkbox"/>	SCI <input type="checkbox"/>
5	6	7 Prt frac	8 Prt gms	9 Prt %	3	2 <input type="checkbox"/> <input checked="" type="checkbox"/>	RAD <input type="checkbox"/>	ENG <input type="checkbox"/>
						3 <input type="checkbox"/> <input checked="" type="checkbox"/>		n <u>2</u>

LDH Isoenzymes

001 *LBLA	057 RTM	-----							
002 2	058 *LBL1	Initialize.	Subroutine to find % and						
003 5	059 RCL0		test if within normal						
004 STOI	060 ÷		range.						
005 CLX	061 EEX		$(\%)_i = \frac{LDH_i}{\sum_j LDH_j} \times 100$						
006 ST00	062 2								
007 ST01	063 x								
008 ST02	064 PRTX								
009 RTM	065 XZY								
010 *LBLB	066 X>Y?	Input LDH values.							
011 DSZ?	067 SF2	LDH <sub>i</sub> → R25-i							
012 ST0i	068 R↓								
013 ST+0	069 X>Y?								
014 F0?	070 SF2	Accumulate Σ in R <sub>0</sub> .							
015 PRTX	071 RTM								
016 1	072 *LBLC								
017 ST+1	073 INT								
018 RCL1	074 .	Display i.							
019 RTM	075 0								
020 *LBLC	076 3	Calculate and print							
021 SPC	077 +	percentages.							
022 3	078 ST02								
023 3	079 PRTX	Max LDH <sub>1</sub> = 33.							
024 ENT↑	080 SPC								
025 1	081 RTM								
026 8	082 *LBLd	Min LDH <sub>1</sub> = 18.							
027 RCLF	083 F0?	LDH <sub>1</sub>							
028 GSB1	084 GT00								
029 4	085 SF0								
030 0	086 1	Max LDH <sub>2</sub> = 40.							
031 ENT↑	087 RTM								
032 2	088 *LBL0								
033 8	089 CF0	Min LDH <sub>2</sub> = 28.							
034 RCLD	090 0	LDH <sub>2</sub>							
035 GSB1	091 RTM								
036 3	092 *LBLe								
037 0	093 SPC	Max LDH <sub>3</sub> = 30.							
038 ENT↑	094 SPC								
039 1	095 RCL2								
040 0	096 INT	Min LDH <sub>3</sub> = 18.							
041 RCLC	097 .	LDH <sub>3</sub>							
042 GSB1	098 0								
043 1	099 3								
044 6	100 +	Max LDH <sub>4</sub> = 16.							
045 ENT↑	101 PRTX								
046 6	102 SPC	Min LDH <sub>4</sub> = 6.							
047 RCLB	103 RCLF	LDH <sub>4</sub>							
048 GSB1	104 PRTY								
049 1	105 RCLD								
050 3	106 PRTX	Max LDH <sub>5</sub> = 13.							
051 ENT↑	107 RCLC								
052 2	108 PRTY	Min LDH <sub>5</sub> = 2.							
053 RCL4	109 RCLB	LDH <sub>5</sub>							
054 GSB1	110 PRTY								
055 F2?	111 RCL0								
056 STOE	112 PRTX	F2 set indicates range error.							
REGISTERS									
0 Σ LDH <sub>i</sub>	1 i	2 Ptnr # .03	3	4	5	6	7	8	9
S0	S1	S2	S3	S4	S5	S6	S7	S8	S9
A LDH <sub>5</sub>	B LDH <sub>4</sub>	C LDH <sub>3</sub>	D LDH <sub>2</sub>	E LDH <sub>1</sub>	F	I	Index		



## Body Surface Area

001 #LBLA	Height (+cm, - in)	057 7	
002 STOE		058 1	
003 F0?		059 8	
004 SPC		060 4	
005 F0?		061 x	
006 PRTX		062 STOA	
007 X>0?	If height in cm, GTO 1.	063 F0?	
008 GTO1		064 PRTX	
009 CHS		065 F0?	
010 2		066 SPC	
011 .	Convert inches to cm.	067 RTN	
012 5		068 #LBLD	Boyd BSA
013 4		069 RCLD	
014 x		070 .	
015 #LBL1		071 3	
016 STOD	Store height in cm.	072 Y*	
017 RTN		073 RCLB	
018 #LBLB	Weight (+kg, - lb)	074 EEX	
019 STOC		075 3	
020 F0?		076 x	
021 PRTX		077 ENT†	
022 F0?		078 LOG	
023 SPC		079 .	
024 X>0?	If weight in kg, GTO 2.	080 0	
025 GTO2		081 1	
026 CHS		082 8	
027 .		083 8	
028 4		084 x	
029 5		085 .	
030 3	Convert pounds to kg.	086 7	
031 5		087 2	
032 9		088 E	
033 2		089 5	
034 3		090 -	
035 7		091 Y*	
036 x		092 ÷	
037 #LBL2		093 3	
038 STOB	Store weight in kg.	094 1	
039 RTN		095 1	
040 #LBLC	Dubois BSA	096 8	
041 RCLD		097 ÷	
042 .		098 STOA	
043 7		099 F0?	
044 2		100 PRTX	
045 5		101 F0?	
046 Y*		102 SPC	
047 RCLB		103 RTN	
048 .		104 #LBLc	
049 4		105 0	Clear for reprint
050 2		106 STOI	
051 5		107 RTN	
052 Y*		108 #LBLc	
053 x		109 INT	
054 .		110 .	Patient ID = Ptnt #.04
055 0		111 0	
056 0		112 4	

REGISTERS									
0	1	2	3	4	5	6	7	8	9
S0	S1	S2	S3	S4	S5	S6	S7	S8	S9
A BSA (m <sup>2</sup> )	B Wt (kg)	C Wt input	D Ht (cm)	E Ht input	F Ptnt #.04				

113	+				
114	STOI				
115	SPC				
116	PRTX				
117	RTN				
118	*LBLd	Print toggle			
119	FR?				
120	GTOR				
121	SFO				
122	1				
123	RTN				
124	*LBLd	Reprint			
125	CF0				
126	0				
127	RTN				
128	*LBLd				
129	SPC				
130	SPC				
131	RCLT				
132	INT				
133	.				
134	0				
135	4				
136	+				
137	PRTX	Patient ID			
138	SPC				
139	RCLC	Ht input			
140	PRTX				
141	RCLC	Wt input			
142	PRTX				
143	SPC				
144	RCLC	BSA (m <sup>2</sup> )			
145	PRTX				
146	SPC				
147	RTN				

LABELS					FLAGS	SET STATUS		
A	B	C	D	E	0	ON OFF		DISP
Ht (+cm)	Wt (+kg)	→ Dubois	→ Boyd		Print	0	<input checked="" type="checkbox"/> <input type="checkbox"/>	FIX <input checked="" type="checkbox"/>
a Clear	b	c Pnt #	d P off?	e Reprint	1	1	<input type="checkbox"/> <input checked="" type="checkbox"/>	SCI <input type="checkbox"/>
0 P toggle	1 Store ht	2 Store wt	3	4	2	2	<input type="checkbox"/> <input checked="" type="checkbox"/>	ENG <input type="checkbox"/>
5	6	7	8	9	3	3	<input type="checkbox"/> <input checked="" type="checkbox"/>	n <u>2</u>

Urea Clearance

001 *LEL4	V/t	057 .	Otherwise have maximum.
002 ÷	-----	058 3	
003 *LPLB	$\dot{V}$	059 3	
004 STOE		060 x	
005 F0?		061 ST08	
006 SFC		062 F0?	
007 F0?		063 PRTX	
008 PRTX		064 RTN	-----
009 F2?	If F2 set, must correct	065 *LBL0	Standard
010 GT00	for BSA.	066 RCL9	
011 GT01	-----	067 1	
012 *LBL0		068 .	
013 1		069 8	
014 .		070 5	
015 7		071 x	
016 3	$\dot{V}_{corr} = \frac{1.73}{BSA} \dot{V}$	072 ST08	
017 RCL4		073 F0?	
018 ÷		074 PRTX	
019 x	-----	075 RTN	-----
020 *LBL1		076 *LBL0	Clear for reprint.
021 ST00	Output	077 0	
022 F0?		078 ST08	
023 PRTX		079 ST01	
024 F0?		080 RTN	-----
025 SFC		081 *LBL6	
026 RTN	-----	082 SF2	Set F2 to allow correction
027 *BL0C		083 RCL4	for BSA.
028 ST0C	$U_{urea}$	084 RTN	-----
029 F0?		085 *LBL0	Patient ID = Ptnr # .05
030 PRTX		086 INT	
031 RTN	-----	087 .	
032 *BL0D		088 0	
033 ST0B	$B_{urea}$	089 5	
034 F0?		090 +	
035 PRTX		091 ST01	
036 F0?		092 SPC	
037 SFC		093 PRTX	
038 2	If $\dot{V}_{corr} \leq 2$ , take $\sqrt{\dot{V}}$ for	094 RTN	-----
039 RCLD	$C_s = \frac{U\dot{V}}{B}$	095 *LBL4	Print toggle
040 XZY?		096 F0?	
041 JY		097 GT00	
042 RCLC		098 SF0	
043 RCLB	Otherwise $C_m = \frac{U\dot{V}}{B}$	099 1	
044 ÷		100 RTN	
045 x		101 *LBL0	
046 ST09	Clearance	102 CF0	
047 F0?		103 0	
048 PRTX		104 RTN	-----
049 RTN		105 *LBL0	Reprint
050 *LBL0	% mean normal	106 SPC	
051 2		107 SPC	
052 RCLD		108 RCL1	
053 XZY?	If $\dot{V}_{corr} \leq 2$ , GTO 0 for	109 INT	
054 GT00	standard.	110 .	
055 RCL9		111 0	
056 J		112 5	

REGISTERS									
0	1	2	3	4	5	6	7	8 % m.n.	9 C
S0	S1	S2	S3	S4	S5	S6	S7	S8	S9
A BSA (m <sup>2</sup> )	B B <sub>urea</sub>	C U <sub>urea</sub>	D $\dot{V}_{corr}$ (ml/min)	E $\dot{V}$ (ml/min)	I Ptnr # .05				



113	+		Patient ID		
114	PRTX				
115	SPC		•		
116	RCLC		V		
117	PRTX		•		
118	RCLD		V <sub>corr</sub>		
119	PRTX				
120	SPC		U <sub>urea</sub>		
121	RCLC				
122	PRTX		B <sub>urea</sub>		
123	RCLB				
124	PRTX				
125	SPC		Clearance		
126	RCL9		% m.n.		
127	PRTX				
128	RCL8				
129	PRTX				
130	SPC				
131	RTN				

LABELS					FLAGS	SET STATUS		
A Vft	B V	C U <sub>urea</sub>	D B <sub>urea</sub> → C	E → % m.n.	0 Print	FLAGS	TRIG	DISP
<sup>a</sup> Clear	<sup>b</sup> Cor BSA?	<sup>c</sup> P <sub>tnt</sub> #	<sup>d</sup> P off?	<sup>e</sup> Reprint	1	ON OFF 0 <input checked="" type="checkbox"/> <input type="checkbox"/>	DEG <input checked="" type="checkbox"/>	FIX <input checked="" type="checkbox"/>
0 Used	1 Exit V	2	3	4	2 Cor BSA?	1 <input type="checkbox"/> <input checked="" type="checkbox"/>	GRAD <input type="checkbox"/>	SCI <input type="checkbox"/>
5	6	7	8	9	3	2 <input type="checkbox"/> <input checked="" type="checkbox"/>	RAD <input type="checkbox"/>	ENG <input type="checkbox"/>
						3 <input type="checkbox"/> <input checked="" type="checkbox"/>		n <u>2</u>

Creatinine Clearance

001 #LBLH 002 + 003 #LBLR 004 STOE 005 F0? 006 SPC 007 F0? 008 PRTX 009 F2? 010 GT00 011 GT01 012 #LBL0 013 1 014 . 015 7 016 3 017 RCLH 018 + 019 x 020 #LBL1 021 STOD 022 F0? 023 PRTX 024 F0? 025 SPC 026 RTN 027 #LBLC 028 STOC 029 F0? 030 PRTX 031 RTN 032 #LBLD 033 STOB 034 F0? 035 PRTX 036 RCLC 037 RCLD 038 x 039 RCLR 040 + 041 ST09 042 F0? 043 SPC 044 F0? 045 PRTX 046 RTN 047 #LBL0 048 0 049 ST01 050 RTN 051 #LBL0 052 SF2 053 RCLA 054 FTH 055 #LBL0 056 INT	V/t -----  V  If F2 set, must correct for BSA. -----  $\dot{V}_{corr} = \frac{1.73}{BSA} \dot{V}$  Output  -----  $U_{creat}$  -----  $P_{creat}$  $C = \frac{U \dot{V}}{P}$  -----  Clear for reprint.  -----  Set F2 to allow correction for BSA. -----	057 . 058 0 059 6 060 + 061 ST01 062 PRTX 063 SFC 064 RTN 065 #LBL0 066 F0? 067 GT00 068 SFC 069 1 070 RTN 071 #LBL0 072 CFC 073 0 074 RTN 075 #LBL0 076 SPC 077 SPC 078 RCL1 079 INT 080 . 081 0 082 6 083 + 084 PRTX 085 SPC 086 RCL0 087 PRTX 088 RCLD 089 PRTX 090 SPC 091 RCLC 092 PRTX 093 RCLR 094 PRTX 095 SPC 096 RCL9 097 PRTX 098 RTN	Patient ID = Ptn# .06  -----  Print toggle  -----  Reprint  -----  Patient ID  $\dot{V}$  $\dot{V}_{corr}$  $U_{creat}$  $P_{creat}$  C  -----							
REGISTERS										
0	1	2	3	4	5	6	7	8	9 C	
S0	S1	S2	S3	S4	S5	S6	S7	S8	S9	
A BSA (m <sup>2</sup> )		B P <sub>creat</sub>		C U <sub>creat</sub>		D V <sub>corr</sub> (ml/min)		E V (ml/min)		F Ptn# .06

LABELS					FLAGS		SET STATUS				
A V <sub>ft</sub>	B $\hat{V}$	C U <sub>creat</sub>	D P <sub>creat</sub>	E	0 Print	FLAGS		TRIG		DISP	
<sup>a</sup> Clear	<sup>b</sup> Cor BSA?	<sup>c</sup> Ptnt #	<sup>d</sup> P off?	<sup>e</sup> Reprint	1	0 <input checked="" type="checkbox"/> <input type="checkbox"/>	ON OFF	DEG <input checked="" type="checkbox"/>	FIX <input checked="" type="checkbox"/>		
<sup>0</sup> Used	<sup>1</sup> Exit $\hat{V}$	2	3	4	<sup>2</sup> Cor BSA	1 <input type="checkbox"/> <input checked="" type="checkbox"/>		GRAD <input type="checkbox"/>	SCI <input type="checkbox"/>		
5	6	7	8	9	3	2 <input type="checkbox"/> <input checked="" type="checkbox"/>		RAD <input type="checkbox"/>	ENG <input type="checkbox"/>		
						3 <input type="checkbox"/> <input checked="" type="checkbox"/>			n <u>2</u>		



[illegible]

Blood Acid-Base Status

001 *LBLA	BT	057 -		
002 F0?		058 10*		
003 PRTX		059 .		
004 F0?		060 0		
005 SPC		061 3		
006 3		062 0		
007 7		063 7		
008 XZY		064 x		s(10 <sup>PH-pK</sup> )
009 -		065 ST05		
010 ST09	37-BT	066 LSTX		
011 SF1	F1 set for BT.	067 +		
012 RTN	-----	068 RCLD		
013 *LBLB	PCO <sub>2</sub>	069 x		TCO <sub>2</sub>
014 ST0E		070 ST0A		
015 F0?		071 F0?		
016 PRTX	To correct for BT, GTO 0.	072 PRTX		Clear flag 1.
017 F1?		073 CF1		
018 GT00	For 37°, GTO 1.	074 RTN		
019 GT01	-----	075 *LBLC		
020 *LBL0		076 ST08		Hgb
021 RCL9		077 F0?		
022 .	Correct PCO <sub>2</sub> to 37°.	078 SPC		
023 0		079 F0?		
024 1		080 PRTX		
025 9		081 RCL5		
026 x		082 RCLD		
027 10*		083 x		[HCO <sub>3</sub> <sup>-</sup> ]
028 x	-----	084 ST06		
029 *LBL1		085 9		
030 ST0D	PCO <sub>2</sub> (37°C)	086 .		
031 RTN	-----	087 5		
032 *LBLC	pH	088 ENT†		
033 ST0C		089 1		
034 F0?		090 .		
035 PRTX	To correct for BT, GTO 0.	091 6		
036 F1?		092 3		
037 GT00		093 RCL8		
038 GT02	For 37°, GTO 2.	094 x		
039 *LBL0	-----	095 +		
040 RCL9		096 7		
041 .	Correct pH to 37°	097 .		
042 0		098 4		
043 1		099 RCLB		
044 4		100 -		
045 6		101 x		
046 x		102 -		
047 -	-----	103 2		
048 *LBL2		104 4		
049 ST0E	pH (37°C)	105 -		
050 RTN	-----	106 1		
051 *LBLD		107 RCL8		
052 RCLB	Compute TCO <sub>2</sub> .	108 .		
053 6		109 0		
054 .		110 1		
055 1		111 4		
056 1		112 3		
REGISTERS				
0	1	2	3	4
5	s(10 <sup>PH-pK</sup> )	6	[HCO <sub>3</sub> <sup>-</sup> ]	7
8	BE	9	Hgb	37-BT
S0	S1	S2	S3	S4
S5	S6	S7	S8	S9
A	TCO <sub>2</sub>	B	pH (37°)	C
				pH input
D	PCO <sub>2</sub> (37°)	E	PCO <sub>2</sub> input	I
				Ptnt # .08





Oxygen Saturation and Content

001 *LBLA	BT	057 GTOR	-----						
002 F0?		058 *LBL1	If input < 0, make positive						
003 PRTX		059 CHS	-----						
004 3		060 *LBL0	VPO <sub>2</sub>						
005 7		061 STOC							
006 XZY		062 ENT↑							
007 -		063 ENT↑							
008 ST09	37-BT	064 ENT↑							
009 RCLD	Rcl PCO <sub>2</sub> (if input).	065 1							
010 RTM	-----	066 5							
011 *LBLB	PCO <sub>2</sub>	067 -							
012 F0?		068 x							
013 PRTX		069 2							
014 STOD		070 0							
015 RCLB	Rcl pH (if input).	071 4							
016 RTM	-----	072 5							
017 *LBLC	pH	073 +							
018 F0?		074 x							
019 PRTX		075 2	Compute oxygen						
020 STOB		076 EEX	saturation.						
021 RTM	-----	077 3							
022 *LBLD		078 +							
023 F0?		079 x							
024 PRTX	PO <sub>2</sub> input	080 ST07							
025 STOE	If input < 0, consider as	081 CLX							
026 X<0?	VPO <sub>2</sub> .	082 1							
027 GT01	Otherwise compute VPO <sub>2</sub> .	083 5							
028 RCL9		084 -							
029 .		085 x							
030 0		086 2							
031 2		087 4							
032 4		088 0							
033 x		089 0							
034 RCLB		090 +							
035 7		091 x							
036 .		092 3							
037 4		093 1							
038 -		094 1							
039 .		095 0							
040 4		096 0							
041 0		097 -							
042 x		098 x							
043 +		099 2							
044 4		100 4							
045 0		101 EEX							
046 RCLD		102 5							
047 ÷		103 +							
048 LOG		104 EEX							
049 .		105 2							
050 0		106 ÷							
051 6		107 ST÷7							
052 x		108 RCL7							
053 +		109 SF2							
054 10*		110 F0?	O <sub>2</sub> saturation (%).						
055 RCLC		111 SPC	F2 set to indicate						
056 x		112 F0?	saturation computed.						
REGISTERS									
0	1	2	3	4	5	6	7 Sat	8 Hgb	9 37-BT
S0	S1	S2	S3	S4	S5	S6	S7	S8	S9
A. O <sub>2</sub> content	B pH(37)	C VPO <sub>2</sub>	D PCO <sub>2</sub> (37)	E PO <sub>2</sub> input	F	G	H	I Ptn# .09	



Red Cell Indices

001 *LBLA	Count.	057 +	
002 STOE		058 STOI	
003 F0?		059 PRTX	
004 PRTX		060 SPC	
005 RTN	-----	061 RTN	-----
006 *LBLB	Hematocrit (%).	062 *LBLd	Print toggle.
007 STOD		063 F0?	
008 F0?		064 STOD	
009 PRTX		065 SF0	
010 RTN	-----	066 1	
011 *LBLC	Hemoglobin.	067 RTN	
012 STOC		068 *LBL0	
013 F0?		069 CF0	
014 PRTX		070 0	
015 F0?		071 RTN	-----
016 SPC		072 *LBLc	Reprint.
017 RCLD		073 SPC	
018 1	Compute MCV.	074 SPC	
019 0		075 RCL!	
020 x		076 INT	
021 RCLE		077 .	
022 ÷		078 1	
023 STOB	MCV.	079 +	
024 F0?		080 PRTX	Patient ID.
025 PRTX		081 SPC	
026 RTN	-----	082 RCLE	Count.
027 *LBLD	Compute MCH.	083 PRTX	
028 RCLC		084 RCLD	Hct (%)
029 1		085 PRTX	
030 0		086 RCLC	Hgb
031 x		087 PRTX	
032 RCLE		088 SPC	
033 ÷		089 RCLB	MCV
034 STOA	MCH.	090 PRTX	
035 F0?		091 RCLA	MCH
036 PRTX		092 PRTX	
037 RTN	-----	093 RCL9	MCHC
038 *LBLF	Compute MCHC.	094 PRTX	
039 RCLC		095 RTN	
040 EEX			
041 2			
042 x			
043 RCLD			
044 ÷			
045 STOS	MCHC.		
046 F0?			
047 PRTX			
048 RTN	-----		
049 *LBLc	Clear.		
050 0			
051 STOI			
052 RTN	-----		
053 *LBLc	Patient ID = Pnt # .10		
054 INT			
055 .			
056 1			

REGISTERS									
0	1	2	3	4	5	6	7	8	9
S0	S1	S2	S3	S4	S5	S6	S7	S8	S9
A MCH		B MCV		C Hgb		D Hct (%)		E Count	
								F Pnt # .10	

LABELS					FLAGS		SET STATUS		
A Count	B Hct (%)	C Hgb→MCV	D →MCH	E →MCHC	F Print	0 <input checked="" type="checkbox"/> ON <input type="checkbox"/> OFF 1 <input type="checkbox"/> <input checked="" type="checkbox"/> 2 <input type="checkbox"/> <input checked="" type="checkbox"/> 3 <input type="checkbox"/> <input checked="" type="checkbox"/>		DEG <input checked="" type="checkbox"/> GRAD <input type="checkbox"/> RAD <input type="checkbox"/>	FIX <input checked="" type="checkbox"/> SCI <input type="checkbox"/> ENG <input type="checkbox"/> n <u>2</u>
a Clear	b	c Pnt #	d P off?	e Reprint	1				
f Used	1	2	3	4	2				
5	6	7	8	9	3				

Total Blood Volume

001 *LBLA 002 STOE 003 F0? 004 PRTX 005 RTN 006 *LBLB 007 STOD 008 F0? 009 PRTX 010 RTN 011 *LBLC 012 STOC 013 F0? 014 PRTX 015 RTN 016 *LBLD 017 STOE 018 F0? 019 PRTX 020 RTN 021 *LBL E 022 STOA 023 F0? 024 PRTX 025 F0? 026 SPC 027 RCLB 028 RCLC 029 - 030 XZY 031 RCL E 032 - 033 ÷ 034 RCLC 035 x 036 RCLD 037 x 038 STOA 039 F0? 040 PRTX 041 RTN 042 *LBLA 043 0 044 STOE 045 STOI 046 RTN 047 *LBL E 048 INT 049 . 050 1 051 1 052 + 053 STOI 054 PRTX 055 SPC 056 RTN	Background counts.  ----- Volume injected.  ----- Standard dilution.  ----- Standard CPM.  ----- Whole blood CPM.  Net Std. CPM = Std. CPM- Bck.  Net blood CPM = Blood CPM- Bck.  Total blood volume.  ----- Initialize.  ----- Patient ID = Ptnt # .11	057 *LBLD 058 F0? 059 STOD 060 SF0 061 1 062 RTN 063 *LBLB 064 CF0 065 0 066 RTN 067 *LBL E 068 SPC 069 SPC 070 RCL! 071 INT 072 . 073 1 074 1 075 + 076 PRTX 077 SPC 078 RCLC 079 PRTX 080 RCLD 081 PRTX 082 RCLC 083 PRTX 084 RCLB 085 PRTX 086 RCL A 087 PRTX 088 SPC 089 RCL9 090 PRTX 091 RTN	Print toggle  ----- Reprint  Patient ID  Bck  Vol. injected  Std. dilution  Std. CPM  Blood CPM  Total blood volume  -----						
REGISTERS									
0	1	2	3	4	5	6	7	8	9 TBV
S0	S1	S2	S3	S4	S5	S6	S7	S8	S9
A Blood CPM	B Std. CPM	C Std. dilution	D Vol. injected	E Bck	I Ptnt # .11				

[illegible]



## Schilling Test

001 #LBL#	Background counts.	057 .	Patient ID = Pnt # .12
002 STOE		058 1	
003 F0?		059 2	
004 PRTX		060 +	
005 RTN	-----	061 STOI	
006 #LBL#	Standard dilution.	062 PRTX	
007 STOD		063 SPC	
008 F0?		064 RTN	
009 PRTX	-----	065 #LBL#	Print toggle
010 RTN		066 F0?	
011 #BLC	Standard counts.	067 GTD	
012 STOC		068 SF0	
013 F0?		069 1	
014 PRTX	-----	070 RTN	
015 RTN		071 #LBL#	
016 #BLD	Urine volume. (V)	072 CF0	
017 STOB		073 0	
018 F0?		074 RTN	
019 PRTX	-----	075 #LBL#	Reprint
020 RTN		076 SPC	
021 #BLE	Urine counts. (U)	077 SPC	
022 STOA		078 RCL	
023 F0?		079 INT	
024 PRTX		080 .	
025 1	1 U	081 1	
026 X#Y	U 1	082 2	
027 RCLE	Bck U 1	083 +	
028 -	Net 1	084 PRTX	Patient ID
029 1	1 Net 1	085 SPC	
030 RCLB	V 1 Net 1	086 RCLE	Bck
031 X#Y?	Is V < 1?	087 PRTX	Std. dilution
032 R#	Yes, eliminate V.	088 RCLD	Std. CPM
033 x	No, V > 1, multiply by V.	089 PRTX	
034 x		090 RCLC	Urine vol.
035 RCLC		091 PRTX	Urine CPM
036 RCLE		092 RCLB	
037 -	Net std. counts.	093 PRTX	
038 ÷		094 RCL#	
039 RCLD		095 PRTX	
040 ÷		096 SPC	
041 EEX	Convert to %.	097 RCL#	% excreted
042 2		098 PRTX	
043 x	% of dose excreted.	099 RTN	
044 STOB	-----		
045 F0?	Initialize.		
046 SPC			
047 F0?	-----		
048 PRTX			
049 RTN			
050 #LBL#			
051 .0			
052 STOE			
053 STOI			
054 RTN			
055 #BLC			
056 INT			

REGISTERS										
0	1	2	3	4	5	6	7	8	9 %	
S0	S1	S2	S3	S4	S5	S6	S7	S8	S9	
A Urine CPM		B Urine Vol.		C Std. CPM		D Std. dilution		E Bck		I Pnt # .12

[illegible]

## Thyroid Uptake

001 #LELA	Standard Counts.	057 RCLC	
002 STOE		058 RCLB	
003 F0?		059 -	
004 PRTY		060 +	
005 RTN	-----	061 LSTX	
006 #LBLB	Standard Background.	062 ÷	
007 STOD		063 STX9	Corrected uptake.
008 F0?		064 RCL9	
009 PRTX		065 F0?	
010 RCLB		066 PRTX	
011 XZY		067 RTN	
012 -	Std. Cts. - Std. Bck.	068 #LBLB	Correction for different activities.
013 RTN	-----	069 F0?	
014 #LBLC	Patient Counts.	070 SPC	
015 STOC		071 XZY	Standard precounts.
016 F0?		072 F0?	
017 PRTX		073 PRTX	
018 RTN	-----	074 XZY	
019 #LBLD	Patient Background.	075 F0?	
020 STOB		076 PRTX	Dose precounts.
021 F0?		077 ÷	
022 PRTX		078 STX9	
023 RCLC		079 RCL9	Corrected uptake.
024 XZY		080 F0?	
025 -	Ptnt. Cts. - Ptnt. Bck.	081 PRTX	
026 RTN	-----	082 RTN	
027 #LBLB	Compute uptake.	083 #LBLB	Patient ID = Ptnt # .13
028 RCLC		084 INT	
029 RCLB		085 .	
030 -		086 1	
031 RCLB		087 3	
032 RCLD		088 +	
033 -		089 STOI	
034 ÷		090 PRTX	
035 EEX		091 SPC	
036 2		092 RTN	
037 x		093 #LBLB	Print toggle
038 STOD	% Uptake.	094 F0?	
039 F0?		095 STOB	
040 SPC		096 SF0	
041 F0?		097 1	
042 PRTY		098 RTN	
043 RTN		099 #LBLB	
044 #LBLB	Correction for prior radioactivity.	100 CF0	
045 F0?		101 0	
046 SPC		102 RTN	
047 XZY		103 #LBLB	Reprint
048 F0?		104 SPC	
049 PRTX	Patient predose counts.	105 SPC	
050 XZY		106 RCLB	
051 F0?		107 INT	
052 PRTX	Background predose counts.	108 .	
053 -		109 1	
054 RCLB	Decay factor.	110 3	
055 x		111 +	
056 CHS		112 PRTX	Patient ID

REGISTERS									
0	1	2	3	4	5	6	7	8	9 % Uptake
S0	S1	S2	S3	S4	S5	S6	S7	S8	S9
A Decay factor	B Ptnt. Bck	C Ptnt. Cts.	D Std. Bck	E Std. Cts.	F	G	H	I Ptnt # .13	



## Radioactive Decay Corrections

<div> <div> 001 *LBLA 002 F3? 003 GT00 004 RCLC 005 RCLA 006 ÷ 007 STOE 008 RTN 009 *LBL0 010 STOE 011 RTN 012 *LBLB 013 F3? 014 GT00 015 RCLC 016 RCLE 017 ÷ 018 STOA 019 LN 020 . 021 5 022 LN 023 ÷ 024 RCLB 025 x 026 STOD 027 2 028 4 029 ÷ 030 INT 031 ENT↑ 032 ENT↑ 033 2 034 4 035 x 036 RCLD 037 XZY 038 - 039 EEX 040 2 041 ÷ 042 + 043 RTN 044 *LBL0 045 ENT↑ 046 ENT↑ 047 INT 048 2 049 4 050 x 051 XZY 052 FRC 053 EEX 054 2 055 x 056 + </div> <div> Initial activity (A<sub>0</sub>).  Calculate: A<sub>0</sub> = A/f  ----- Store input A<sub>0</sub>. ----- Time in days, hours.   Calculate:  t = <math>\frac{\tau_{1/2} \ln f}{\ln 1/2}</math>  Store t (hours).   Convert t in hrs. to dd.hh for display.   ----- Time input.   Convert from dd.hh format to hours.   ----- </div> <div> 057 STOD 058 RCLB 059 ÷ 060 . 061 5 062 XZY 063 YX 064 STOA 065 R↑ 066 RTN 067 *LBLC 068 F3? 069 GT00 070 RCLC 071 RCLA 072 x 073 STOD 074 RTN 075 *LBL0 076 STOD 077 RTN 078 *LBLD 079 STOI 080 GSB↑ 081 STOB 082 RTN 083 *LBLc 084 6 085 6 086 7 087 . 088 2 089 STOB 090 RTN 091 *LBLb 092 6 093 4 094 6 095 0 096 STOB 097 RTN 098 *LBLc 099 6 100 STOB 101 RTN 102 *LBLd 103 1 104 4 105 4 106 0 107 STOB 108 RTN 109 *LBLc 110 1 111 9 112 3 </div> <div> Store t (hrs).  Store decay factor  <math>f = \frac{1}{2}^{t/\tau_{1/2}}</math> Display t as input. ----- Present activity (A).   Calculate: A = A<sub>0</sub> f ----- Store input A. ----- Isotopes 1–9.  Store <math>\tau_{1/2}</math>. -----  <sup>51</sup>Cr  -----  <sup>57</sup>Co  -----  99mTc  -----  <sup>125</sup>I  -----  <sup>131</sup>I </div> </div>									
REGISTERS									
0	1	2	3	4	5	6	7	8	9
S0	S1	S2	S3	S4	S5	S6	S7	S8	S9
A	Decay factor (A/A <sub>0</sub> )	B	$\tau_{1/2}$ (hours)	C	A	D	t (hours)	E	A <sub>0</sub>
							Isotope no. (1–9)		

113 .		169 .	
114 2		170 7	
115 STOP		171 3	
116 RTN		172 PTN	$^{113m}\text{In}$
117 #LBL5		173 #LBL8	
118 2		174 1	
119 6		175 2	$^{133}\text{Xe}$
120 2	$^{137}\text{Cs}$	176 6	
121 9		177 .	
122 8		178 5	
123 0		179 RTN	
124 STOP		180 #LBL9	
125 RTN		181 6	$^{197}\text{Hg}$
126 #LBL1		182 5	
127 1		183 RTN	
128 0			
129 7	$^3\text{H}$		
130 4			
131 7			
132 0			
133 RTN			
134 #LBL2			
135 5			
136 0	$^{14}\text{C}$		
137 5			
138 8			
139 EEY			
140 4			
141 RTN			
142 #LBL3			
143 1			
144 .	$^{18}\text{F}$		
145 8			
146 7			
147 RTN			
148 #LBL4			
149 3			
150 4	$^{32}\text{P}$		
151 3			
152 .			
153 2			
154 RTN			
155 #LBL5			
156 2			
157 8	$^{75}\text{Se}$		
158 8			
159 0			
160 RTN			
161 #LBL6			
162 1			
163 5	$^{85}\text{Sr}$		
164 3			
165 6			
166 RTN			
167 #LBL7			
168 1			

LABELS					FLAGS	SET STATUS								
A	A <sub>0</sub>	B	t (dd.hh)	C	A	D	Isotope #	E	$^{137}\text{Cs}$	0	FLAGS		TRIG	DISP
a	$^{51}\text{Cr}$	b	$^{57}\text{Co}$	c	$^{99m}\text{Tc}$	d	$^{125}\text{I}$	e	$^{131}\text{I}$	1	ON OFF		DEG <input checked="" type="checkbox"/>	FIX <input checked="" type="checkbox"/>
0	Inputs	1	$^3\text{H}$	2	$^{14}\text{C}$	3	$^{18}\text{F}$	4	$^{32}\text{P}$	2	0	<input type="checkbox"/> <input checked="" type="checkbox"/>	GRAD <input type="checkbox"/>	SCI <input type="checkbox"/>
5	$^{75}\text{Se}$	6	$^{85}\text{Sr}$	7	$^{113m}\text{In}$	8	$^{133}\text{Xe}$	9	$^{197}\text{Hg}$	3	1	<input type="checkbox"/> <input checked="" type="checkbox"/>	RAD <input type="checkbox"/>	ENG <input type="checkbox"/>
											2	<input type="checkbox"/> <input checked="" type="checkbox"/>		n <u>2</u>
												3	<input type="checkbox"/> <input checked="" type="checkbox"/>	

## Radioimmunoassay

001	#LBLA	Initialize.	057	F0?	B						
002	P+S		058	PRTX							
003	CLRG		059	RCLE							
004	P+S		060	-							
005	GT02		061	RCLD							
006	#LBLB	Non-specific binding counts (NSB).	062	RCLE							
007	GSBD		063	-	net B/B <sub>0</sub>						
008	RTN		064	÷							
009	GSB1		065	F1?							
010	STOE	Average NSB.	066	PRTX							
011	RTN		067	F0?							
012	#LBLC	Zero dose counts (B <sub>0</sub> ).	068	SPC							
013	GSBD		069	R+							
014	RTN		070	F0?							
015	GSB1		071	PRTX	Concentration.						
016	STOD		072	F0?							
017	RTN	Average B <sub>0</sub> .	073	SPC							
018	#LBL1		074	LOG	log conc. (x).						
019	RCL8	Compute average counts.	075	GSB3	logit (y).						
020	RCL9		076	F1?							
021	÷		077	PRTX	Print logit.						
022	STOI	$\bar{B} = \Sigma B/n$	078	X*Y							
023	F0?		079	F1?							
024	SPC		080	PRTX	Print log conc.						
025	F0?		081	F1?							
026	PRTX	$\bar{B}$	082	SPC							
027	F0?		083	Σ+	Sum x- and y-values for regression.						
028	SPC		084	F0?							
029	F0?		085	SPC							
030	SPC		086	RTN							
031	#LBL2	Clear for n, ΣB	087	#LBLA							
032	0		088	RCLΣ	Compute r, m, b.						
033	STO8		089	x							
034	STO9		090	P+S							
035	R+		091	RCL9							
036	RTN		092	÷							
037	#LBL6	Counts for standards and unknowns.	093	RCL8							
038	#LBLD		094	X*Y							
039	F0?		095	-							
040	PRTX		096	STOB	Σxy - (Σx Σy)/n						
041	ST+8		097	ENT↑							
042	!		098	ENT↑							
043	ST+9		099	P+S							
044	RCL9		100	S							
045	RTN		101	x							
046	#LBLE		102	÷							
047	RCL8	Standard concentration.	103	P+S							
048	RCL9		104	RCL9							
049	÷		105	1							
050	STOI	$\bar{B} = \Sigma B/n$	106	-							
051	0		107	÷							
052	STOB		108	STOA							
053	STO9		109	PRTX							
054	R+		110	RCL8							
055	F0?		111	RCL5							
056	SPC		112	RCL4							
REGISTERS											
0	1	2	3	4	5	6	7	8	9		
S0	S1	S2	S3	S4	S5	S6	S7	ΣB, used	n, used		
				Σx	Σx <sup>2</sup>	Σy	Σy <sup>2</sup>	Σxy	n		
A	r	B	Used, m	C	b	D	B <sub>0</sub>	E	NSB	I	B





Basic Statistics

001 *LBLA	Clear $\Sigma$ registers	057 SPC	Print
002 P $\Sigma$ S		058 N $\Sigma$ Y	
003 0		059 PRTX	$f_k$
004 ST04		060 X $\Sigma$ Y	
005 ST05		061 PRTX	$x_k$ -----
006 ST06		062 *LBL1	
007 ST07		063 ENT $\uparrow$	
008 ST08		064 ENT $\uparrow$	
009 ST09		065 x	
010 P $\Sigma$ S		066 R $\uparrow$	
011 RTN	-----	067 ST-9	$\Sigma f_i$
012 *LBLB	$x_i (\Sigma+)$	068 x	
013 F0?		069 ST-5	$\Sigma f_i x_i^2$
014 PRTX		070 R $\downarrow$	
015 $\Sigma+$	-----	071 x	
016 RTN		072 ST-4	$\Sigma f_i x_i$
017 *LBLb	$x_k (\Sigma-)$	073 1	
018 F0?		074 ST-6	
019 SPC		075 RCL6	i
020 F0?		076 P $\Sigma$ S	
021 PRTX		077 RTN	
022 $\Sigma-$	-----	078 *LBLD	Find mean and standard deviation.
023 RTN		079 SPC	
024 *LBLC	Grouped data.	080 $\bar{x}$	
025 P $\Sigma$ S		081 PRTX	
026 F0?		082 S	
027 GT00	-----	083 PRTX	
028 GT01		084 RTN	
029 *LBL0	Print	085 *LBLB	Find standard error and coefficient of variation.
030 SPC		086 SPC	
031 X $\Sigma$ Y		087 S	
032 PRTX	$f_i$	088 P $\Sigma$ S	
033 X $\Sigma$ Y		089 RCL9	
034 PRTX	$x_i$ -----	090 P $\Sigma$ S	
035 *LBL1		091 JX	
036 ENT $\uparrow$		092 $\Sigma$	
037 ENT $\uparrow$		093 PRTX	
038 x	$x_i \quad x_i \quad x_i \quad f_i$	094 $\bar{x}$	$s_{\bar{x}}$
039 R $\uparrow$		095 S	
040 ST+9	$f_i \quad x_i^2 \quad x_i \quad f_i$	096 LSTX	
041 x	$\Sigma f_i$	097 $\Sigma$	
042 ST+5		098 EEX	
043 R $\downarrow$	$\Sigma f_i x_i^2$	099 2	
044 x		100 x	C. V. %
045 ST+4	$\Sigma f_i x_i$	101 PRTX	
046 1		102 RTN	
047 ST+6		103 *LBLa	
048 RCL6		104 F0?	Print toggle
049 P $\Sigma$ S	n	105 GT00	
050 RTN	-----	106 SFR	
051 *LBLc	Grouped data—correct error.	107 1	
052 P $\Sigma$ S		108 RTN	
053 F0?	-----	109 *LBL0	
054 GT00		110 CF0	
055 GT01		111 0	
056 *LBL0		112 RTN	

REGISTERS									
0	1	2	3	4	5	6	7	8	9
S0	S1	S2	S3	S4 $\Sigma x$	S5 $\Sigma x^2$	S6 Used	S7 Used	S8 Used	S9 n, $\Sigma f_i$
A	B	C	D	E	F	G	H	I	J



Chi-square Evaluation and Distribution

001 *LBLA	Start.	057 RTN	-----
002 CF1		058 *LBLC	Correct erroneous $O_k \uparrow E_k$
003 CLRG		059 GSB7	( $\Sigma -$ ).
004 2		060 GSB9	
005 0		061 GSB7	
006 STOI	I points to $R_A$ .	062 STOC	
007 RTN	-----	063 -	
008 *LBLB	Input $O_i$ ( $\Sigma +$ ).	064 $X^2$	
009 SF1		065 RCLC	
010 GSB4	F1 set for equal $E_i$ .	066 $\div$	
011 RCLB		067 RCLB	
012 $X^2/Y$		068 -	
013 +		069 CHS	
014 STOB	$\Sigma O_i$	070 STOB	
015 LSTX		071 !	
016 $X^2$		072 ST-i	
017 RCLC		073 RCL i	
018 +		074 RTN	-----
019 STOC	$\Sigma O_i^2$	075 *LBLD	Calculate $X^2$ .
020 1		076 F1?	
021 ST+i		077 GTOB	
022 RCL i	i	078 RCLB	If equal $E_i$ , GTO 1.
023 RTN	-----	079 GSB4	Recall $X^2$ .
024 *LBLB	Correct erroneous $O_k$ ( $\Sigma -$ ).	080 R/S	
025 GSB7		081 GTOB	"Error"
026 GSB7		082 *LBLB	-----
027 GSB8		083 RCLA	Calculate $X^2$ for equal
028 GSB7		084 RCLC	$E_i$ .
029 RCLB		085 x	
030 $X^2Y$		086 RCLB	
031 -		087 $\div$	
032 STOB		088 LSTX	
033 LSTX		089 -	
034 $X^2$		090 GSB4	$X^2$
035 RCLC		091 R/S	
036 -		092 RCLB	Calculate $E_i$ .
037 CHS		093 RCLA	
038 STOC		094 $\div$	
039 1		095 GSB8	
040 ST-i		096 GSB7	
041 RCL i		097 RTN	
042 RTN		098 *LBL9	-----
043 *LBLC	Input $O_i \uparrow E_i$ ( $\Sigma +$ ).	099 $X^2Y$	Print contents of Y- and
044 CF1		100 GSB4	X-registers if F0 set.
045 GSB9		101 $X^2Y$	
046 STOC		102 GSB8	
047 -		103 RTN	
048 $X^2$		104 *LBL4	-----
049 RCLC		105 GSB7	Space and print.
050 $\div$		106 *LBL8	-----
051 RCLB		107 F0?	
052 +		108 PRTX	Print.
053 STOB	$\Sigma \frac{(O_i - E_i)^2}{E_i}$	109 RTN	-----
054 1		110 *LBL7	Space
055 ST+i		111 F0?	
056 RCL i	i	112 SPC	

REGISTERS									
0	1	2	3	4	5	6	7	8	9
S0	S1	S2	S3	S4	S5	S6	S7	S8	S9
A	B		C		D		E		I
n	$\Sigma O_i, \Sigma (O_i - E_i)^2 / E_i$		$\Sigma O_i^2, E_i$						20

113	RTN			169	e <sup>x</sup>		
114	*LBL5	$-\mu \rightarrow \Gamma(\mu/2)$		170	x		
115	GSB8			171	2		
116	1			172	RCLA		
117	STOC			173	Y*		
118	X $\neq$ Y			174	$\div$		
119	2			175	RCLC		
120	$\div$			176	$\div$		
121	STOA			177	STOE		
122	INT			178	F1?		
123	LSTX			179	GSB8		
124	X $\neq$ Y?	If $\mu$ is odd, GTO 1.		180	F1?		
125	GT01			181	GSB7		
126	1			182	RTN		
127	-			183	*LBL5		
128	N!	$(\mu/2 - 1)!$		184	CF1		
129	GSB8			185	GSB5		
130	GSB7			186	RCLB		
131	STOC			187	RCLA		
132	R/S			188	$\div$		
133	*LBL1	$\mu$ odd.		189	RCLC		
134	.			190	x		
135	5			191	STOE		
136	X $\neq$ Y?			192	2		
137	GT02			193	RCLA		
138	X $\neq$ Y			194	x		
139	1			195	STOI		
140	-			196	1		
141	RCLC			197	STOD		
142	X $\neq$ Y			198	*LBL3		
143	x			199	RCLB		
144	STOC			200	RCLI		
145	LSTX			201	2		
146	GT01			202	+		
147	*LBL2			203	STOI		
148	Pi			204	$\div$		
149	IX			205	RCLD		
150	RCLC			206	x		
151	x			207	STOD		
152	STOC			208	+		
153	GSB8			209	X $\neq$ Y?		
154	GSB7			210	GT03		
155	R/S			211	RCLC		
156	*LBL4	$x \rightarrow f(x)$		212	x		
157	SF1			213	GSB8		
158	*LBL5			214	RTN		
159	GSB8			215	*LBL6		
160	STOB			216	F0?		
161	RCLA			217	GT00		
162	1			218	SF0		
163	-			219	!		
164	Y*			220	RTN		
165	RCLB			221	*LBL0		
166	2			222	CF0		
167	$\div$			223	0		
168	CHS			224	RTN		

LABELS					FLAGS	SET STATUS		
A Start	B $O_i(\Sigma+)$	C $O_i \uparrow E_i(\Sigma+)$	D $\rightarrow x^2; E$	E $\mu \rightarrow \Gamma(\mu/2)$	0 Print	FLAGS	TRIG	DISP
a Print?	b $O_k(\Sigma-)$	c $O_k \uparrow E_k(\Sigma-)$	d $x \rightarrow f(x)$	e $x \rightarrow P(x)$	1 Used	0 <input type="checkbox"/> ON <input checked="" type="checkbox"/> OFF	DEG <input checked="" type="checkbox"/>	FIX <input checked="" type="checkbox"/>
0 Used	1 Used	2 Used	3 Used	4 Print, spc	2	1 <input type="checkbox"/> <input checked="" type="checkbox"/>	GRAD <input type="checkbox"/>	SCI <input type="checkbox"/>
5 Used	6	7 Space	8 Print x	9 Print x, y	3	2 <input type="checkbox"/> <input checked="" type="checkbox"/>	RAD <input type="checkbox"/>	ENG <input type="checkbox"/>
						3 <input type="checkbox"/> <input checked="" type="checkbox"/>		n <u>2</u>

## t Statistics

001 #LBLA 002 0 003 ST01 004 ST02 005 ST03 006 RTN 007 #LBLA 008 F0? 009 GT00 010 SF0 011 1 012 RTN 013 #LBL0 014 CF0 015 0 016 RTN 017 #LBL0 018 F0? 019 GSB9 020 - 021 ST+2 022 X <sup>2</sup> 023 ST+3 024 RCL1 025 1 026 + 027 ST01 028 RTN 029 #LBLb 030 F0? 031 GSB9 032 - 033 ST-2 034 X <sup>2</sup> 035 ST-3 036 RCL1 037 1 038 - 039 ST01 040 RTN 041 #LBLC 042 RCL2 043 RCL1 044 ÷ 045 ST0A 046 RCL3 047 RCL2 048 X <sup>2</sup> 049 RCL1 050 ÷ 051 - 052 RCL1 053 1 054 - 055 ST0C 056 ÷	Start.   ----- Print toggle.   ----- Input $x_i, y_i$ for paired t.   ----- Correct $x_k, y_k$ for paired t.   ----- Compute paired t.   ----- $\bar{D}$   df	057 JX 058 ST0B 059 RCL1 060 JX 061 ÷ 062 ÷ 063 SPC 064 PRTX 065 R/S 066 RCLC 067 PRTX 068 RCLA 069 PRTX 070 RCLB 071 PRTX 072 RTN 073 #LBLD 074 GSB0 075 ST+2 076 X <sup>2</sup> 077 ST+3 078 RCL1 079 1 080 + 081 ST01 082 RTN 083 #LBLD 084 GSB1 085 GSB0 086 ST-2 087 X <sup>2</sup> 088 ST-3 089 RCL1 090 1 091 - 092 ST01 093 RTN 094 #LBLc 095 ST07 096 RCL1 097 ST04 098 RCL2 099 ST05 100 RCL3 101 ST06 102 0 103 ST01 104 ST02 105 ST03 106 RCL7 107 GSB1 108 GSB0 109 GSB1 110 RTN 111 #LBLc 112 RCL6	sD   t   ----- Input $x_i$ or $y_i$ for t for two means.   ----- Correct $x_k$ or $y_k$ for t for two means.   ----- Input d.   Save $n_1, \Sigma x, \Sigma x^2$ .   Clear for $\Sigma y$ .   ----- Compute t for two means.
---	--	---	---

REGISTERS								
0	1 n	2 Used	3 Used	4 $n_1$	5 $\Sigma x$	6 $\Sigma x^2$	7 d	8 df
S0	S1	S2	S3	S4	S5	S6	S7	S8
A	B	C	D	E	F	G	H	I
D		sD		df				

113	RCL5		169	Fθ°	
114	X²		170	SPC	
115	RCL4		171	RTN	
116	÷				
117	-				
118	RCL3				
119	+				
120	RCL2				
121	X²				
122	RCL1				
123	÷				
124	-				
125	RCL1				
126	RCL4				
127	+				
128	2				
129	-				
130	STO8				
131	÷				
132	IX				
133	RCL1				
134	1/X				
135	RCL4				
136	1/X				
137	+				
138	IX				
139	X				
140	RCL5				
141	RCL4				
142	÷				
143	RCL2				
144	RCL1				
145	÷				
146	-				
147	RCL7				
148	-				
149	XZY				
150	÷				
151	SPC				
152	PRTX				
153	R/S				
154	RCL8				
155	PRTX				
156	SPC				
157	RTN				
158	*LBL9				
159	XZY				
160	Fθ°				
161	SPC				
162	ESBθ				
163	XZY				
164	*LBL8				
165	Fθ°				
166	PRTX				
167	RTN				
168	*LBL1				

LABELS					FLAGS		SET STATUS		
A Start	B $x_1, y_1 (\Sigma+)$	C $\rightarrow t, \dots$	D $x_1, y_1 (\Sigma+)$	E $\rightarrow t; df$	0 Print	FLAGS		TRIG	DISP
a Print?	b $x_k, y_k (\Sigma-)$	c	d $x_k, y_k (\Sigma-)$	e d	1	0 <input type="checkbox"/> ON <input checked="" type="checkbox"/> OFF			
0 Used	1 Space	2	3	4	2	1 <input type="checkbox"/> <input checked="" type="checkbox"/>	DEG <input checked="" type="checkbox"/>	FIX <input checked="" type="checkbox"/>	
					3	2 <input type="checkbox"/> <input checked="" type="checkbox"/>	GRAD <input type="checkbox"/>	SCI <input type="checkbox"/>	
						3 <input type="checkbox"/> <input checked="" type="checkbox"/>	RAD <input type="checkbox"/>	ENG <input type="checkbox"/>	
				9 Output				n <u>2</u>	



t Distribution

001 *LBLA	Input $\nu$ .	057 ST03							
002 GSB5		058 RTN							
003 ST00		059 *LBL1	$\nu$ odd.						
004 RTN	----- $x \rightarrow f(x)$	060 .							
005 *LBLB		061 5							
006 GSB5		062 $X=Y?$							
007 ST0A		063 GT02							
008 RCLD		064 $X \neq Y$							
009 GSB0		065 1							
010 ST0B		066 -							
011 RCLD		067 ST03							
012 1		068 GT01	-----						
013 +		069 *LBL2							
014 GSB0		070 P i							
015 ST0C		071 $\sqrt{X}$							
016 RCLA		072 RCL3							
017 RCLC		073 x							
018 RCLB		074 ST03							
019 $\div$		075 RTN							
020 P i		076 *LBLC	$x \rightarrow P(x)$						
021 RCLD		077 GSB5	-----						
022 x		078 *LBLC	Enter here from LBL D.						
023 $\sqrt{X}$		079 CF1							
024 $\div$		080 ST0A							
025 1		081 ABS							
026 RCLA		082 RCLD							
027 $X^2$		083 ST00							
028 RCLD		084 RAD							
029 $\div$		085 $\sqrt{X}$							
030 +		086 $\div$							
031 RCLD		087 TAN <sup>-1</sup>							
032 1		088 ST02							
033 +		089 RCL0							
034 2		090 2							
035 $\div$		091 $\div$							
036 CHS		092 INT							
037 $Y^X$		093 LSTY							
038 x		094 $X \neq Y?$							
039 ST09		095 GT04							
040 PRTX		096 0							
041 SPC		097 ST05							
042 RTN		098 *LBL6	$\nu$ even.						
043 *LBL0	----- Compute $\Gamma(\nu/2)$ .	099 RCL2							
044 1		100 COS							
045 ST03		101 $X^2$							
046 $X \neq Y?$		102 ST03							
047 2		103 RCL2							
048 $\div$		104 SIN							
049 ST01		105 ST04							
050 INT		106 RCL0							
051 LSTX		107 2							
052 $X \neq Y?$		108 $X=Y?$							
053 GT01		109 GT08							
054 1		110 $\div$							
055 -		111 1							
056 H!		112 -							
REGISTERS									
0 $\nu, \nu - 1$	1	2 $\theta$	3 Used	4 Used	5 Used	6 Used	7 R	8 Used	9 f(x)
S0	S1	S2	S3	S4	S5	S6	S7	S8	S9
A x	B Used		C Used		D $\nu$		E	I	

112 ST01		169 GT06	-----
114 1		170 #LBL8	
115 ST06	-----	171 RCL4	
116 #LBL3		172 RCL4	-----
117 RCL3		173 #LBL6	Exit.
118 x		174 DEG	
119 RCL5		175 X>0?	
120 1		176 GT00	Compute P(x) from
121 +		177 XZ Y	R(x) for x ≤ 0.
122 x		178 1	
123 LSTX		179 -	
124 1		180 CHS	
125 +		181 2	
126 ST05		182 ÷	
127 ÷		183 GT07	-----
128 ST+6		184 #LBL0	Compute P(x) for
129 DSZ1		185 XZ Y	x > 0.
130 GT07		186 1	
131 RCL6		187 +	
132 RCL4		188 2	
133 x		189 ÷	
134 FI?		190 #LBL7	-----
135 RTN		191 F2?	If F2 set, return to
136 RCL4		192 RTN	LBL D.
137 GT06		193 PRTX	
138 #LBL4	-----	194 SPC	
139 RCL2	ν odd.	195 RTN	
140 2		196 #LBL0	-----
141 x		197 GSB5	x → I(x)
142 P i		198 SF2	
143 ÷		199 ABS	
144 ST07		200 CHS	
145 RCL0		201 GSBc	
146 1		202 2	P(-x)
147 ST05		203 x	
148 ST-0		204 1	
149 X=Y?		205 XZ Y	
150 GT09		206 -	1 - 2P(-x)
151 SF1		207 PRTX	
152 GSBc		208 SPC	I(x)
153 CF1		209 RTN	
154 RCL2		210 #LBL5	-----
155 COS		211 F0?	Print.
156 x		212 PRTX	
157 2		213 RTN	
158 x		214 #LBL6	-----
159 P i		215 F0?	Print toggle.
160 ÷		216 GT00	
161 RCL7		217 SF0	
162 +		218 1	
163 RCL4		219 RTN	
164 GT06		220 #LBL0	
165 RTN		221 CF0	
166 #LBL9	-----	222 0	
167 RCL7		223 RTN	-----
168 RCL4			

LABELS					FLAGS	SET STATUS		
A ν	B x → f(x)	C x → P(x)	D x → I(x)	E Print?	0 Print	FLAGS		
a Γ (ν/2)	b ν even	c x → P(x)	d	e	1 Call b	ON OFF		
0 Used	1 Used	2 Used	3 Used	4 Used	2 Call c	0 <input type="checkbox"/> <input checked="" type="checkbox"/>	DEG <input checked="" type="checkbox"/>	FIX <input checked="" type="checkbox"/>
5 Print	6 Exit	7 Output P	8 Used	9 Used	3	1 <input type="checkbox"/> <input checked="" type="checkbox"/>	GRAD <input type="checkbox"/>	SCI <input type="checkbox"/>
						2 <input type="checkbox"/> <input checked="" type="checkbox"/>	RAD <input type="checkbox"/>	ENG <input type="checkbox"/>
						3 <input type="checkbox"/> <input checked="" type="checkbox"/>		n <u>2</u>

## Notes



## Notes

## Notes



## Notes

## Notes





## Notes

## Notes





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