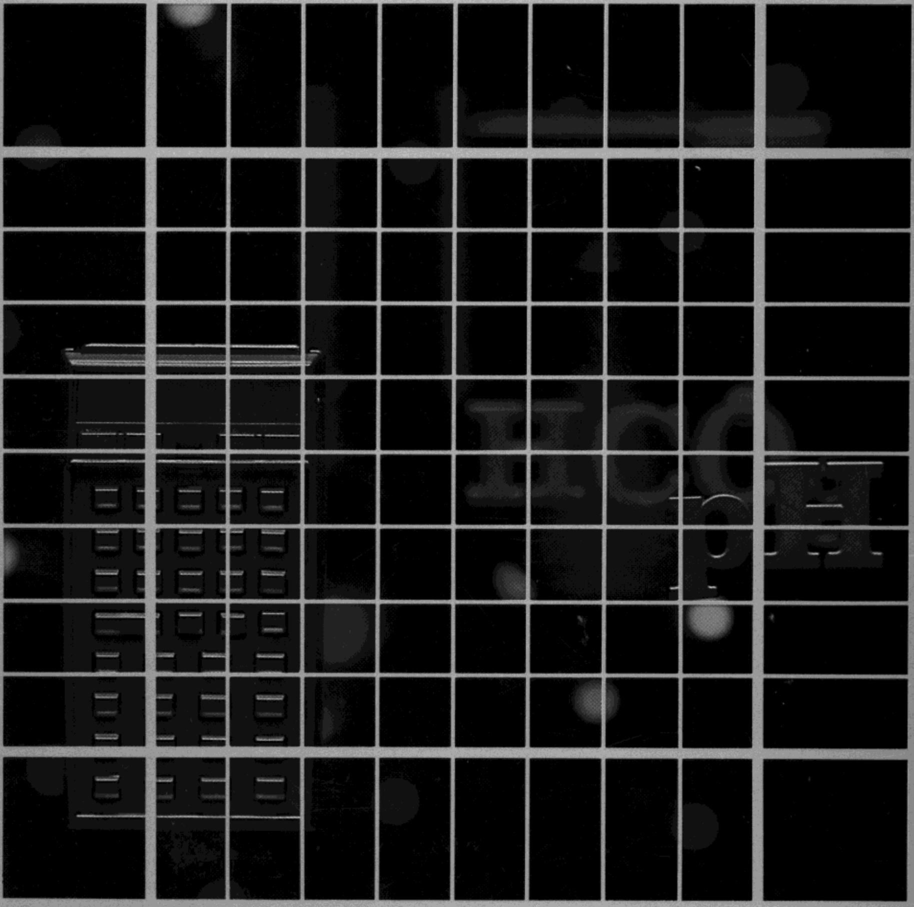
HEWLETT-PACKARD

HP-41C
CLINICAL LAB AND NUCLEAR MEDICINE PAC



INTRODUCTION

The programs in this Clinical Laboratory and Nuclear Medicine Pac have been chosen to aid you in calculations used in a number of common clinical lab procedures.

Each program in this pac represents a program in the Application Module 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 keystrokes required for its solution.

Before plugging in your Application Module, *turn the calculator off,* and be sure you understand the section *Inserting and Removing Application Modules*. And before using a particular program, take a few minutes to read *Format of User Instructions* and *A Word About Program Usage*.

You should first familiarize yourself with a program by running it once or twice while following the complete User Instructions in the manual. Thereafter, the program's prompting or the mnemonics on the overlay should provide the necessary instructions, including which variables are to be input, which keys are to be pressed, and which values will be output. A quick-reference card with a brief description of each program's operating instructions has been provided for your convenience.

We hope that this Clinical Lab and Nuclear Medicine Pac will assist you in the solution of numerous problems in your discipline. We would 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 from your comments that we learn how to increase the usefulness of our application pacs.

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INSERTING AND REMOVING APPLICATION MODULES

Before you insert an application module for the first time, familiarize yourself with the following information.

Up to four application modules can be plugged into the ports on the HP-41C. While plugged in, the names of all programs contained in the module can be displayed by pressing ■ CATALOG 2.

CAUTION

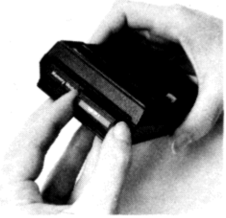
Always turn the HP-41C off before inserting or removing any plug-in extensions or accessories. Failure to turn the HP-41C off could damage both the calculator and the accessory.

Here is how you should insert application modules:

1. Turn the HP-41C off! Failure to turn the calculator off could damage both the module and the calculator.

2. Remove the port covers. Remember to save the port covers, they should be inserted into the empty ports when no extensions are inserted.

3. With the application module label facing downward as shown, insert the application module into any port **after** the last memory module presently inserted.



4. If you have additional application modules to insert, plug them into any port after the last memory module. For example, if you have a memory module inserted in port 1, you can insert application modules in any of ports 2, 3, or 4. **Never insert an application module into a lower numbered port than a memory module.** Be sure to place port covers over unused ports.

5. Turn the calculator on and follow the instructions given in this book for the desired application functions.

To remove application modules:

1. Turn the HP-41C off! Failure to do so could damage both the calculator and the module.

2. Grasp the desired module handle and pull it out as shown.

3. Place a port cap into the empty ports.

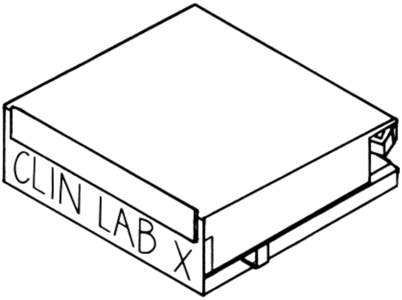
Mixing Memory Modules and Application Modules

Any time you wish to insert other extensions (such as the HP-82104A Card Reader, or the HP-82143A Printer) the HP-41C has been designed so that the memory modules are in lower numbered ports.

So, when you are using both memory modules and application modules, the memory modules must always be inserted into the lower numbered ports and the application module into any port after the last memory module. When mixing memory and application modules, the HP-41C allows you to leave gaps in the port sequence. For example, you can plug a memory module into port 1 and an application module into port 4, leaving ports 2 and 3 empty.

Incompatible Application Module

This pac contains a type X application module. Type X modules have incompatible XROM instructions. You should never plug two type X application modules into your HP-41C at the same time. Type X application modules may be identified by an "X" on the application module label:



Type X Application Module

FORMAT OF USER INSTRUCTIONS

The completed User Instruction Form accompanying 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 column specifies the input data, the units of data if applicable, or the applicable alpha response to a prompted question. Data Input keys consist of 0 to 9 and the decimal point (the numeric keys), EEX (enter exponent), and CHS (change sign).

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

Whenever a statement in the FUNCTION column is printed in gold the ALPHA must be pressed before the statement can be keyed in. After the statement is keyed in, press ALPHA again to return the calculator to its normal operating mode, or to begin program execution. For example, XEQ CREAT means press the following keys: XEQ ALPHA CREAT ALPHA .

The DISPLAY column specifies prompts and intermediate and final answers as shown in the calculator display, and their units where applicable.

Above the DISPLAY column is a box, SIZE: XXX, which specifies the minimum number of registers necessary to execute the program. Refer to pages 73 and 117 in the Owner's Handbook for a complete description of how to size calculator memory.

The following illustrates a portion of the User Instruction Form for *Body Surface Area:*

SIZE: 014

STEP	INSTRUCTIONS	INPUT	FUNCTION	DISPLAY
1	Begin Body Surface Area program.		XEQ BSA	PTNT ≠ = ?
2	Input patient number.	PTNT #	R/S	
2a	If printer is used, patient number and program name are printed.			PTNT ≠ = BSA HT=?
3	Input patient height (+cm, −in.) and weight (+kg, −lb.).	±HT ±WT	R/S R/S	WT=? DUBOIS/BOYD?
4	For BSA by the Du Bois method or,	D	R/S	DUBOIS BSA=(m^2)
5	For BSA by the Boyd method	B	R/S	BOYD BSA=(m^2)
6	To calculate BSA by the alternate method:			
	Boyd		B	BOYD BSA=(m^2)
	Du Bois		D	DUBOIS BSA=(m^2)

The user should first allocate (at least) 14 data storage registers (***SIZE: 014***) for use during program execution. To do this, press the keys [XEQ] [ALPHA] SIZE [ALPHA] 014.

Program execution is begun by pressing [XEQ] [ALPHA] BSA [ALPHA] . The calculator displays ***PTNT≠=?***, prompting for input of the patient number. The user responds by inputting the patient number and pressing [R/S]. The calculator then displays the prompt: ***HT=?*** asking for the input of the patient height. The user keys in the height in centimeters (or in inches, followed by [CHS]), presses [R/S] and sees the prompt ***WT=?***. After inputting the weight in kilograms (or in pounds, followed by [CHS]) and pressing [R/S] the user sees the display: ***DUBOIS/BOYD?***. To calculate the body surface area by the Du Bois method press ***D*** [R/S] and the body surface area is calculated and displayed: ***DUBOIS BSA=*** . Similarly, press ***B*** [R/S] for the Boyd calculation.

When these programs are run with the HP 82143A printer attached to the calculator and turned on, the calculated results will be printed automatically. In addition, when the patient number is input the printer will automatically print the patient number and the program name to identify the data and results of the calculations which follow. The use of the patient number is optional and may be ignored.

The Reprint routine, present in a number of the programs, is also optional. It allows for an additional printout of data and results after the calculations have been completed. If the tests must be reported to several departments this feature allows you to obtain additional copies of the data and results directly from the program.

A WORD ABOUT PROGRAM USAGE

Catalog

When an Application Module is plugged into a port of the HP-41C, the contents of the Module can be reviewed by pressing ■ CATALOG 2 (the Extension Catalog). Executing the CATALOG function lists the name of each program or function in the module, as well as functions of any other extensions which might be plugged in.

Overlays

An overlay has been included for some of the programs in this pac. To run these programs, place the overlay on the calculator. The mnemonics on the overlay are provided to help you run the program. The program's name is given vertically on the left side. Blue mnemonics are associated with the key they are directly below when the overlay is in place and the calculator is in USER mode. Gold mnemonics are similar to blue mnemonics, except that they are above the appropriate key and the shift (gold) key must be pressed before the re-defined key. Once again, USER mode must be set.

ALPHA and USER Mode Notation

This manual uses a special notation to signify ALPHA mode. Whenever a statement on the User Instruction Form is printed in gold, the ALPHA key must be pressed before the statement can be keyed in. After the statement is input, press ALPHA again to return the calculator to its normal operating mode or to begin program execution. For example, XEQ CREAT means press the following keys: XEQ ALPHA CREAT ALPHA .

In USER mode, when referring to the top two rows of keys (the keys having been re-defined), this manual will use the symbols A - J and ■ A - ■ E on the User Instruction Form and in the keystroke solutions to sample problems.

Using Optional Printer

When the optional printer is plugged into the HP-41C along with the Clinical Lab Pac Applications Module, all results will be printed automatically. You may also want to keep a permanent record of the values input to a certain program. A convenient way to do this is to set the Print Mode switch to NORMAL before running the program. In this mode, all input values and the corresponding keystrokes will be listed on the printer, thus providing a record of the entire operation of the program.

Downloading Module Programs

If you wish to trace execution, to modify, to record on magnetic cards, or to print a program in this Applications Module, it must first be copied into the

HP-41C's program memory. For information concerning the HP-41C COPY function, see the Owner's Handbook. It is *not* necessary to copy a program in order to run it.

Program Interruption

These programs have been designed to operate properly when run from beginning to end, without turning the calculator off (remember, the calculator may turn itself off). If the HP-41C is turned off, it may be necessary to set flag 21 (SF 21) to continue proper execution.

Use of Labels

The user should be aware of possible problems when writing programs into calculator memory using Alpha labels identical with those in an Application Module.

Clinical Chemistry

BEER'S LAW

This program provides several useful calculations in the field of spectrophotometry. Short routines convert absorbance (optical density) to percent transmittance or vice versa. A third routine uses Beer's law to calculate the concentration of an unknown, given the concentration of a standard and the absorbance (or percent transmittance) of the standard and unknown.

To find the concentration of an unknown sample follow the input prompting, inputting the absorbance or the percent transmittance, %T, of the standard and unknown samples, and the concentration of the standard sample. The concentration of the unknown is then automatically calculated. (Note that the user may input either absorbances or %T interchangeably, by selecting the appropriate prompting.)

To convert absorbance, A, to %T, press [A] and input the absorbance. Pressing [R/S] calculates %T. To convert %T to absorbance press [B] and input %T. Pressing [R/S] calculates the absorbance.

Equations:

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

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

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

where

A = absorbance

%T = Percent transmittance

c_u = concentration of the unknown

c_s = concentration of the standard

Reference:

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

SIZE: 015

STEP	INSTRUCTIONS	INPUT	FUNCTION	DISPLAY
1	Begin Beer's Law program.		XEQ BEERS	PTNT≠=?
2	Input the patient number.	Patient #	R/S	PTNT≠=
2a	If printer is used patient number and program name will be printed.			BEERS LAW
3	Input the absorbance or % transmittance of the standard solution. (The %T prompt may be obtained by pressing R/S without prior data entry.)	 A_{STD} $\%T_{STD}$	 R/S (or,) R/S R/S	A STD=? A UNKN=? %T STD=? %T UNKN=?
4	Input the absorbance or the % transmittance of the unkown solution. (Again, the %T prompt may be obtained by pressing R/S without prior data entry.)	A_{UNKN} $\%T_{UNKN}$	R/S (or,) R/S R/S	C STD=? %T UNKN=? C STD=?
5	Input the concentration of the standard solution and calculate the concentration of the unknown solution.	C_{STD}	R/S	C UNKN=
6	For a new calculation press C and go to step 3.		C	A STD=?
7	To convert absorbance to % transmittance; press A and input absorbance.	 A	A R/S	A=? %T=
8	To convert % transmittance to absorbance, press B and input % transmittance.	 %	B R/S	%T=? A=
9	For a reprint of data and results:		■ E R/S * R/S * R/S * R/S * R/S *	PTNT≠= BEERS LAW A (or %T) STD= A (or %T) UNKN= C STD= C UNKN=
10	For a new case, press E and go to step 2. * This R/S not required when calculator is operated with printer.		E	PTNT≠=?

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. Find the solute concentration in the unknown. What is the absorbance of a solution with %T=46? After all calculations obtain a reprint.

Keystrokes:	**Display:**	
XEQ ALPHA SIZE ALPHA 015	***SIZE 015***	
XEQ ALPHA BEERS ALPHA	***PTNT≠=?***	
10183 R/S	***(PTNT≠=10,183.00)****	
	(BEERS LAW)	
	A STD=?	
.41 R/S	***A UNKN=?***	A_{UNKN} is not known
R/S	***%T UNKN=?***	
46 R/S	***C STD=?***	
2 R/S	***C UNKN=1.65***	
B	***%T=?***	
46 R/S	***A=0.34***	
■ E	***PTNT≠=10,183.00***	
R/S	***BEERS LAW***	
R/S	***A STD=0.41***	
R/S	***%T UNKN=46.00***	
R/S	***C STD=2.00***	
R/S	***C UNKN=1.65***	

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* Displays in parentheses appear only if printer is used.

BODY SURFACE AREA

This program calculates body surface area, BSA, by either the Boyd or Du Bois method. 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, input height in either cm or inches and the weight in either kg or pounds. Then inputting **B** R/S calculates body surface area in m^2 by the method of Boyd; inputting **D** R/S calculates BSA in m^2 by the Du Bois formula. 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 input again.

Equations:

Let Ht be height, Wt be weight, and BSA be the body surface area in m^2.

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

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

Du Bois:

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

Boyd:

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

Remarks:

The Du Bois formula for BSA is undefined for children with a BSA less than $0.6\ m^2$. In such cases BSA should be calculated by the Boyd formula.

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.

SIZE: 014

STEP	INSTRUCTIONS	INPUT	FUNCTION	DISPLAY
1	Begin Body Surface Area program.		XEQ BSA	PTNT≠=?
2	Input patient number.	Patient #	R/S	
2a	If printer is used patient number and program name are printed.			PTNT≠= BSA HT=?
3	Input patient height (+cm, −in.) and weight (+kg, −lb.).	±HT ±WT	R/S R/S	WT=? DUBOIS/BOYD?
4	For BSA by the Du Bois method or,	D	R/S	DUBOIS BSA=(m^2)
5	For BSA by the Boyd Method	B	R/S	BOYD BSA=(m^2)
6	To calculate BSA by the alternate method: Boyd Du Bois		B D	BOYD BSA=(m^2) DUBOIS BSA=(m^2)
7	For reprint of data and results		■ E R/S * R/S * R/S * R/S *	PTNT≠= BSA HT=(units) WT=(units) (DUBOIS)(BOYD) BSA=
8	For new inputs press A and go to step 3.		A	HT=?
9	For a new case press E and go to step 2.		E	PTNT≠=?
	* This R/S not required when calculator is operated with printer.			

Example 1:

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

Keystrokes:	**Display:**
XEQ ALPHA SIZE ALPHA 014	***SIZE 014***
XEQ ALPHA BSA ALPHA	***PTNT≠=?***
10183 R/S	***(PTNT≠=10,183.00)****
	(BSA)
	HT=?
176 R/S	***WT=?***
63.5 R/S	***DUBOIS/BOYD?***
D R/S	***DUBOIS BSA=1.78*** (m^2)
B	***BOYD BSA=1.76*** (m^2)

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:	Display:	
[E]	*PTNT≠=?*	
10070 [R/S]	*(PTNT≠=10,070.00)*	
	(BSA)	
	HT=?	
64 [CHS] [R/S]	*WT=?*	
112 [CHS] [R/S]	*DUBOIS/BOYD?*	
B [R/S]	*BOYD BSA=1.52*	
■ [E]	*PTNT≠=10,070.00*	
[R/S]	*BSA*	
[R/S]	*HT=64.00IN*	
[R/S]	*WT=112.00LB*	
[R/S]	*BOYD BSA=1.52*	(m^2)

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* Displays in parentheses appear only when printer is used.

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.

If the urine flow rate is to be corrected for body surface area and the BSA is unknown answer the question ***"BSA CALC?"*** by inputting ***Y*** and pressing [R/S]. You may then calculate BSA by inputting the patient's height and weight. If BSA is already known answer ***N*** and input BSA after the prompt ***"BSA=?"***

If the urine flow is not to be corrected for BSA answer ***"BSA CALC?"*** with ***N***, and press [R/S] *without prior data entry* at the prompt ***BSA=?***.

When inputting the urine flow rate you may either input the urine volume in ml and the time in minutes or input the flow rate itself. If the flow rate is being corrected for BSA the corrected flow rate is displayed.

Urea Clearance

Calculation of maximum urea clearance may also be made using this program. Simply input the concentration of urea in the urine in place of the creatinine concentration (U_{CREAT}) and input the urea concentration in the blood in place of the creatinine concentration in the plasma (P_{CREAT}). Note, however, that these calculations result in the *maximum urea clearance* even if the corrected flow is less than 2 ml/min.

Equations:

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

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

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

where

$\dot{V}$ = flow rate, ml/min.

C_{creat} = creatinine clearance

U_{creat} = concentration of creatinine in urine

P_{creat} = concentration of creatinine in plasma

Remark:

Any units may be used for U_{creat} and P_{creat} as long as they are consistent.

Reference:

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

SIZE: 015

STEP	INSTRUCTIONS	INPUT	FUNCTION	DISPLAY
1	Begin Creatinine Clearance program.		XEQ CREAT	PTNT≠=?
2	Input patient number.	patient #	R/S	
2a	If printer is used patient number and program name are printed.			PTNT≠= CREAT CLEAR
3	If correction for BSA is required but BSA has not yet been calculated answer "Y" and go to step 4 or, if BSA is not to be calculated answer "N" and go to step 5.			BSA CALC?
		Y	R/S	HT=?
		N	R/S	BSA?
4	Calculate BSA:			HT=?
	Input height (+cm, −in.) and weight (+kg, −lb) and calculate BSA by Du Bois method or Boyd method. Then go to step 6.	±HT	R/S	WT=?
		±WT	R/S	DUBOIS/BOYD?
		D or	R/S	DUBOIS BSA=
		B	R/S	BOYD BSA=
5	If BSA is known and if the urine flow rate is to be corrected for BSA, input the BSA, or, if no BSA is required press R/S without prior data entry.			BSA?
		BSA	R/S	FLOW=?
			R/S	FLOW=?
6	Input urine flow rate, if known, and go to step 7.	FLOW (ml/min)	R/S	(see step 7)
6a	Or, if flow rate is not known press R/S without prior data entry, input urine volume and time, and go to step 7.		R/S	VOL=?
		VOL (ml)	R/S	T=?
		TIME (min)	R/S	(see step 7)
7	(If urine flow is being corrected for BSA the corrected flow is displayed)			FLOW CORR=
7a	Go to prompting for inputs of urea concentrations.		R/S *	U CREAT=?
8	Input the concentration of creatinine in the urine and the concentration of creatinine in the plasma. The creatinine clearance is calculated and displayed.	U creat (mg/100 ml)	R/S	P CREAT=?
		P creat (mg/100 ml)	R/S	CREAT CLEAR=
9	For a reprint of data and results		■ E	PTNT≠=
			R/S *	CREAT CLEAR
			R/S *	FLOW= or, FLOW CORR=

STEP	INSTRUCTIONS	INPUT	FUNCTION	DISPLAY
			R/S *	U CREAT=
			R/S *	P CREAT=
			R/S *	CREAT CLEAR=
10	For new clearance data, press A and go to step 6.		A	FLOW=?
11	For a new case, press E and go to step 2. * This R/S not required when calculator is operated with printer.		E	PTNT≠=?

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:	**Display:**
XEQ ALPHA SIZE ALPHA 015	*SIZE 015*
XEQ ALPHA CREAT ALPHA	*PTNT≠=?*
10095 R/S	*BSA CALC?*
N R/S	*BSA?*
R/S	*FLOW=?*
R/S	*VOL=?*
506 R/S	*T=?*
240 R/S	*U CREAT=?*
43.4 R/S	*P CREAT=?*
.91 R/S	*CREAT CLEAR=100.55*
■ E	*PTNT≠=10,095.00*
R/S	*CREAT CLEAR*
R/S	*FLOW=2.11*
R/S	*U CREAT=43.40*
R/S	*P CREAT=0.91*
R/S	*CREAT CLEAR=100.55*

Example 2:

Patient number 10124 is a female with a body surface area of 1.56 m^2. 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:	**Display:**
[E]	***PTNT≠=?***
10124 [R/S]	***BSA CALC?***
N [R/S]	***BSA?***
1.56 [R/S]	***FLOW=?***
1.81 [R/S]	***FLOW CORR=2.01***
[R/S]	***U CREAT=?***
46.5 [R/S]	***P CREAT=?***
1.03 [R/S]	***CREAT CLEAR=90.62***

BLOOD ACID-BASE STATUS

The program calculates total plasma CO_2 (TCO_2) and base excess (BE) from the partial pressure of CO_2 (PCO_2), pH, and hemoglobin concentration (Hgb). The PCO_2 and pH values used should be found at 37°C. If they are found at a body temperature (BT) other than 37°C, the program will correct them to 37°C values if BT is also input. An additional, optional output of the program is the concentration of plasma bicarbonate ($[HCO_3^-]$).

Following input of the body temperature (in °C) the user chooses whether or not PCO_2 and pH are to be corrected to 37°C by answering the question ***BT CORR?*** (***Y*** if correction is desired, ***N*** if not). PCO_2 and pH are then input (if they are corrected to 37°C the corrected values are displayed) and the total plasma CO_2 (TCO_2) is calculated and displayed.

The user may now calculate base excess (BE) and plasma bicarbonate concentration if desired, by pressing [R/S] and inputting the hemoglobin concentration.

If a second calculation is to be made with only a few of the data values differing from the previous run, press [A] and input the new data at the appropriate prompt. Press [R/S] *without prior data entry* for any values which remain unchanged.

If Oxygen Saturation and Content has just been run and you now wish to run Blood Acid-Base Status you may do so without reinputting the data. Press [XEQ] *BLOOD*, input the patient number, then press [R/S] *without prior data entry* until TCO_2 is output.

Equations:

$$PCO_2\ (37°C) = PCO_2\ (BT) \cdot 10^{0.019\ (37-BT)}$$

$$pH\ (37°C) = pH\ (BT) - 0.0146\ (37 - BT)$$

$$TCO_2 = s \cdot PCO_2 \left[1 + 10^{pH-pK}\right]$$

where

s = solubility of CO_2 in plasma, mmol/l (taken to be 0.0307)

$pK = 6.11$

$$[BE]_b = (1 - 0.0143\ Hgb)\left([HCO_3^-] - (9.5 + 1.63\ Hgb)(7.4 - pH) - 24\right)$$

where

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

Hgb = hemoglobin concentration in g/100 ml

$$[\mathrm{HCO_3}^-] = s \cdot \mathrm{PCO_2} \cdot 10^{\mathrm{pH-pK}}$$

where

$[\mathrm{HCO_3}^-]$ = concentration of plasma bicarbonate in mmol/*l*.

Remarks:

1. This program can also be used to correct $\mathrm{PCO_2}$ and pH values from 37°C to body temperature. To do this, let x = (74 − BT) °C. Input x in place of BT and set the program to correct for BT. Then input $\mathrm{PCO_2}$ and pH 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 at 37°C a $\mathrm{PCO_2}$ value of 45 mm Hg to a body temperature value with BT = 40°C, let x = 34. At the prompt, BT=?, input 34, press R/S and at BT CORR? input **Y**. Then at $\mathrm{PCO_2}$=? input 45. The corrected $\mathrm{PCO_2}$ is found to be 51.31 mm Hg.
2. The equation to correct pH to 37°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 °C.

References:

Severinghaus, John W., ''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.

Thomas, L. J. Jr., ''Algorithms for Selected Blood Acid-Base and Blood Gas Calculation,'' *J. Appl. Physiol.,* **33:** 154-148, 1972.

				SIZE: 016
STEP	**INSTRUCTIONS**	**INPUT**	**FUNCTION**	**DISPLAY**
1	Begin Blood Acid-Base Status program.		XEQ BLOOD	PTNT≠=?
2	Input patient number.	patient #	R/S	
2a	If printer is used patient number and program name are printed.			PTNT≠= BLOOD STATUS BT=?

STEP	INSTRUCTIONS	INPUT	FUNCTION	DISPLAY
	(NOTE: If data has already been stored by running "Oxygen Saturation and Content" it is not necessary to reenter it at this point. Merely press [R/S] without prior data entry after each prompt.)			
3	Input patient's body temperature in °C. (Not required if PCO$_2$ and pH are not to be corrected to 37°C.)	BT(°C)	[R/S]	BT CORR?
4	To correct PCO$_2$ and pH to 37°C, answer ***Y*** to question, BT CORR? or, if no correction is desired; answer ***N***.	Y N	[R/S] [R/S]	PCO2=? PCO2=?
5	Input partial pressure of CO$_2$ (in mm of Hg). (If PCO$_2$ is corrected to 37°C, the corrected value is displayed.)	PCO$_2$(mmHg)	[R/S] [R/S] *	(PCO$_2$ 37°) PH=?
6	Input pH (If pH is corrected to 37°C, the corrected value is displayed.) Calculate total plasma CO$_2$ in mmol/l.	pH	[R/S] [R/S] *	(pH 37°) TCO2=(mmol/l)
7	(OPTIONAL) To calculate base excess and $[HCO_3^-]$: Input hemoglobin concentration.	Hgb (g/100ml)	[R/S] [R/S] [R/S] *	HGB=? BE=(mEq/l) HCO3$^-$=(mmol/l)
8	For reprint of data and results.		■ [E] [R/S] * [R/S] * [R/S] * [R/S] * [R/S] * [R/S] * [R/S] * [R/S] *	PTNT≠= BLOOD STATUS BT= PCO2= PH= TCO$_2$= HGB= BE= HCO3$^-$=
9	For new data, press [A] and go to step 3. Enter only the data which is to be changed, press [R/S] without prior data entry for any values which remain unchanged.		[A]	BT=?
10	For a new case, press [E] and go to step 2.		[E]	PTNT≠=?
	* This [R/S] is not required when calculator is operated with printer.			

Example:

Patient number 10183 has a body temperature of 40°C. His PCO_2 at 40°C is found to be 51 mm Hg, his pH at the same temperature is 7.31. His hemoglobin concentration is 16 g/100 ml. Find his total plasma CO_2, base excess and plasma bicarbonate concentration. Review the data and results.

Keystrokes:	Display:	
[XEQ] [ALPHA] SIZE [ALPHA] 016	*SIZE 016*	
[XEQ] [ALPHA] BLOOD [ALPHA]	*PTNT≠=?*	
10183 [R/S]	*BT=?*	
40 [R/S]	*BT CORR?*	
Y [R/S]	*PCO2=?*	
51 [R/S]	*44.73*	(PCO_2 corr. to 37°C)
[R/S]	*PH=?*	
7.31 [R/S]	*7.35*	(pH corr. to 37°C)
[R/S]	*TCO2=25.44*	
[R/S]	*HGB=?*	
16 [R/S]	*BE=-1.21*	
[R/S]	*HCO3-=24.07*	
■ [E]	*PTNT≠=10,183.00*	
[R/S]	*BLOOD STATUS*	
[R/S]	*BT=40.00*	
[R/S]	*BT CORR*	
[R/S]	*PCO2=51.00*	
[R/S]	*PH=7.31*	
[R/S]	*TCO2=25.44*	
[R/S]	*HGB=16.00*	
[R/S]	*BE=-1.21*	
[R/S]	*HCO3-=24.07*	

OXYGEN SATURATION AND CONTENT

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

Estimated saturation

Typically, the input parameters to the program are PCO_2, pH, and PO_2 *measured at 37°C,* and the body temperature in °C. If the parameters PCO_2 and pH are known only at body temperature, they may be corrected to 37°C. (PO_2 is not corrected to 37°C by this routine.)

Following input of the body temperature (in °C) the user chooses whether or not PCO_2 and pH are to be corrected to 37°C by answering the question ***BT CORR?*** (***Y*** if correction is desired, ***N*** if not). PCO_2 and pH are then input (if they are corrected to 37°C the corrected values are displayed) followed by the PO_2. Percent oxygen saturation is then calculated and displayed.

If a second calculation is to be made with only a few of the data values differing from the previous run, press [A] and input the new data at the appropriate prompt. Press [R/S] *without prior data entry* for any values which remain unchanged.

If only the PO_2 data is to be changed, press [B] and input the new PO_2 to obtain a new % saturation.

If Blood Acid-Base Status has just been run and you now wish to run Oxygen Saturation and Content you may do so without reinputting the data. Press [XEQ] 02SAT, input the patient number, then press [R/S] *without prior data entry* until the prompt ***PO2=?*** appears. Input PO_2 and % oxygen saturation will be calculated.

After the input of PO_2 an intermediate value of virtual PO_2 (VPO_2) will be calculated prior to the calculation of estimated saturation. The value found for VPO_2 will not be output but may be displayed after the calculation of saturation by pressing [RCL] 11. VPO_2 is not a real physiologic PO_2. Its only use is in estimating O_2 saturation.

Suppose as an alternate case that BT, PCO_2, and pH are not known, but virtual PO_2, or alveolar PO_2 (P_AO_2) is known. In this case, only the known VPO_2 or P_AO_2 need be input in order to compute estimated saturation. Press [B] and input VPO_2 or P_AO_2 as *negative* numbers, i.e., key in the value followed by [CHS], then press [R/S]. The output, as before, will be estimated oxygen saturation.

After computing saturation, the hemoglobin concentration (in g/100 ml) may be input and the oxygen content calculated as a volume percent.

Known saturation

If the actual percent O_2 saturation is known, the oxygen content may be computed directly. Press `C`, key in the O_2 saturation, press `R/S`, then key in hemoglobin concentration and press `R/S` again for the oxygen content.

Equations:

$$VPO_2 = PO_2 \cdot 10^{\left[0.024(37-BT) + 0.48(pH-7.4) + 0.06\log(40/PCO_2)\right]}$$

O_2 Sat =

$$\frac{(VPO_2)^4 - 15(VPO_2)^3 + 2045(VPO_2)^2 + 2000(VPO_2)}{(VPO_2)^4 - 15(VPO_2)^3 + 2400(VPO_2)^2 - 31{,}100(VPO_2) + 2{,}400{,}000}$$

$$O_2\,\text{content} = 1.34 \cdot \frac{\text{Sat }(\%)}{100} \cdot \text{Hgb} + 0.0031\ VPO_2$$

Remarks:

1. In the computation of VPO_2, it is important to input the values for pH and BT exactly, as these have a great influence on the value of VPO_2. PCO_2 has relatively little influence.

2. The equation for 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 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 PO_2 and O_2 saturation are measured, the program may be used as a convenient means to check for the normality of the dissociation curve.

References:

Thomas, L. J. Jr., "Algorithms for Selected Blood Acid-Base and Blood Gas Calculation," *J. Appl. Physiol.,* **33:** 154-158, 1972.

Kelman, G. Richard, "Digital Computer Subroutine for the Conversion of Oxygen Tension into Saturation," *J. Appl. Physiol.,* **21:** 1375-1376, 1966.

SIZE: 016

STEP	INSTRUCTIONS	INPUT	FUNCTION	DISPLAY
1	Begin Oxygen Saturation and Content program.		XEQ 02SAT	PTNT≠=?
2	Input patient number.	patient#	R/S	
2a	If printer is used patient number and program name are printed. NOTE: If data has already been stored by running "Blood Acid-Base Status" it is not necessary to reenter it at this point. Merely press R/S without prior data entry after each prompt until step 7 is reached.			PTNT≠= 02SAT BT=?
3	Input patient's body temperature in °C. (Not required if PCO_2 and pH are not to be corrected to 37°C).	BT (°C)	R/S	BT CORR?
4	To correct PCO_2 and pH to 37°C, answer ***Y*** to question, BT CORR? or if no correction is desired, answer ***N***.	Y N	R/S R/S	PCO2=? PCO2=?
5	Input partial pressure of PCO2 (in mm of Hg.) (If PCO2 is corrected to 37°C, the corrected value is displayed.)	PCO_2 (mm Hg)	R/S	(PCO_2 37°) PH=?
6	Input pH. (If pH is corrected to 37°C, the corrected value is displayed.)	pH	R/S	(pH 37°) PO2=?
7	Input PO_2 in mm Hg. (CHS for VPO_2 or P_AO_2) and find oxygen saturation.	PO_2 (mmHg)	R/S	%SAT=
8	To calculate oxygen content as a volume percent: Input hemoglobin concentration	Hgb(g/100ml)	R/S R/S	HGB=? 02 CONT.=
	Virtual or Alveolar PO_2 Known: If virtual PO_2 (VPO_2) or alveolar PO_2(P_AO_2) are known, you may calculate estimated O_2 saturation. (It is unnecessary to know BT, PCO_2 and pH in this case):			
9	Press B and input VPO_2 or P_AO_2 in mm Hg.	VPO_2 or P_AO_2	B CHS R/S	PO2=? %SAT=
9a	Optional: Go to step 8 to calculate oxygen content or a volume percent.			
	Known Saturation:			
10	Input % O_2 saturation and hemoglobin concentration.	SAT (%) Hgb(g/100ml)	C R/S R/S	%SAT=? HGB=? 02 CONT.=

STEP	INSTRUCTIONS	INPUT	FUNCTION	DISPLAY
11	For a reprint.		■ E R/S * R/S * R/S * R/S * R/S * R/S * R/S * R/S *	PTNT≠= 02SAT BT= PCO2= PH= PO2= %SAT= HGB= 02 CONT.=
12	For new data, press A and go to step 3. Enter only the data which is to be changed, press R/S without prior data entry for any values which remain unchanged.		A	BT=?
13	For a new case, press E and go to step 2. * This R/S is not required when calculator is operated with printer.		E	PTNT≠=?

Example 1:

Patient number 10183 has a body temperature of 40°C. The following parameters are measured at 37°C: PCO_2 = 45 mm Hg, pH = 7.35, and PO_2 = 75 mm Hg. Find the estimated O_2 saturation. Given a hemoglobin concentration of 16 g/100 ml, find oxygen content.

Keystrokes:	Display:
XEQ ALPHA SIZE ALPHA 016	***SIZE 016***
XEQ ALPHA 02SAT ALPHA	***PTNT≠=?***
10183 R/S	***BT=?***
40 R/S	***BT CORR?***
N R/S	***PCO2=?***
45 R/S	***PH=?***
7.35 R/S	***PO2=?***
75 R/S	***%SAT=90.92***
R/S	***HGB=?***
16 R/S	***02 CONT.=19.68***

Example 2:

Subsequent tests on patient 10183 show alveolar PO_2 (P_AO_2) is known to be 103 mm Hg. Find the estimated O_2 saturation. Given a hemoglobin concentration of 14.5 g/100 ml, find the oxygen content.

Keystrokes:	**Display:**
B	***PO2=?***
103 CHS R/S	***%SAT=97.72***
R/S	***HGB=?***
14.5 R/S	***02 CONT.=19.31***

Example 3:

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

Keystrokes:	**Display:**
C	***%SAT=?***
92 R/S	***HGB=?***
16 R/S	***02 CONT.=20.04***

RED CELL INDICES

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

The red cell count in millions per mm^3 is input, followed by the hematocrit (HCT) as a percent. The hemoglobin (HGB) in g/dl (g/100ml) is then input and MCV in cubic microns (μ^3) is calculated and displayed. Pressing R/S consecutively calculates and displays MCH in picograms (pg or micromicrograms, $\mu\mu$g) and MCHC in g/dl (g/100ml).

Equations:

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

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

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

Reference:

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

				SIZE: 014
STEP	**INSTRUCTIONS**	**INPUT**	**FUNCTION**	**DISPLAY**
1	Begin Red Cell Indices program.		XEQ RCI	PTNT≠=?
2	Input the patient number.	patient#	R/S	
2a	If printer is used patient number and program name are printed.			PTNT≠= RED CELL IND COUNT=?
3	Input the red cell count in millions per mm^3.	(10 /mm^3)	R/S	HCT=?
4	Input the hematocrit.	Hct (%)	R/S	HGB=?
5	Input the hemoglobin and calculate the mean corpuscular volume in μ^3.	Hgb (g/dl)	R/S	MCV=(μ^3)
6	Calculate the mean corpuscular hemoglobin in pg ($\mu\mu$g).		R/S *	MCH=(pg)
7	Calculate the mean corpuscular hemoglobin concentration in g/dl (g/100ml).		R/S *	MCHC=(g/dl)
8	To obtain a reprint.		■ E R/S * R/S * R/S * R/S * R/S * R/S *	PTNT≠= RED CELL IND COUNT= HCT= MCV= MCH= MCHC=
9	For a new set of data, press A and go to step 3.		A	COUNT=?
10	For a new case, press E and go to step 2.		E	PTNT≠=?
	* This R/S not required when calculator is operated with printer.			

Example:

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

Keystrokes:	**Display:**
XEQ ALPHA SIZE ALPHA 014	***SIZE 014***
XEQ ALPHA RCI ALPHA	***PTNT≠=?***
10183 R/S	***COUNT=?***
2.25 R/S	***HCT=?***
21 R/S	***HGB=?***
7.2 R/S	***MCV=93.33***
R/S	***MCH=32.00***
R/S	***MCHC=34.29***

Nuclear Medicine

TOTAL BLOOD VOLUME

This program computes total blood volume by the radioisotope dilution technique. The inputs to the program are the background counts per minute (BCK COUNT), the volume of radioactive solution injected (VOL 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 (BLOOD CPM). From these values the program will compute total blood volume (TBV).

Equation:

$$\text{TBV} = (\text{STD DIL}) \times (\text{VOL INJ}) \times \left(\frac{\text{STD CPM} - \text{BCK COUNTS}}{\text{BLOOD CPM} - \text{BCK COUNTS}} \right)$$

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

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

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.

Reference:

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

SIZE: 014

STEP	INSTRUCTIONS	INPUT	FUNCTION	DISPLAY
1	Begin Total Blood Volume program.		XEQ TBV	PTNT≠=?
2	Input the patient number.	patient#	R/S	
2a	If printer is used patient number and program name are printed.			PTNT≠= BLOOD VOL BCK COUNT=?
3	Input background counts.	Bck. Count	R/S	VOL INJ=?
4	Input the volume of fluid injected.	Vol. inj.	R/S	STD DIL=?
5	Input the dilution of the standard.	Std. dil.	R/S	STD CPM=?
6	Input standard counts.	Std. CPM	R/S	BLOOD CPM=?
7	Input whole blood counts and calculate the total blood volume.	Blood CPM	R/S	TBV=
8	To obtain a reprint.		■ E	PTNT≠=
			R/S *	BLOOD VOL
			R/S *	BCK COUNT=
			R/S *	VOL INJ=
			R/S *	STD DIL=
			R/S *	STD CPM=
			R/S *	BLOOD CPM=
			R/S *	TBV=
9	For a new set of data, press A and go to step 3.		A	BCK COUNT=?
10	For a new case, press E and go to step 2.		E	PTNT≠=?
	* This R/S not required when calculator is operated with printer.			

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? Obtain a reprint of the data and results.

Keystrokes:	Display:
XEQ ALPHA SIZE ALPHA 014	***SIZE 014***
XEQ ALPHA TBV ALPHA	***PTNT≠=?***
10183 R/S	***BCK COUNT=?***
152 R/S	***VOL INJ=?***
5 R/S	***STD DIL=?***

Keystrokes:	**Display:**
250 [R/S]	*STD CPM=?*
2518 [R/S]	*BLOOD CPM=?*
837 [R/S]	*TBV=4,317.52*
■ [E]	*PTNT≠=10,183.00*
[R/S]	*BLOOD VOL*
[R/S]	*BCK COUNT=152.00*
[R/S]	*VOL INJ=5.00*
[R/S]	*STD DIL=250.00*
[R/S]	*STD CPM=2,518.00*
[R/S]	*BLOOD CPM=837.00*
[R/S]	*TBV=4,317.52*

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, percent uptake is calculated.

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.

After initialization and input of the patient number, the program inquires whether there has been prior patient radioactivity (***PTNT PRERAD?***). 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. By answering ***Y*** (yes) to the above question the user initiates a routine which will calculate and store a decay factor, A, that is used by the program to adjust the predose counts to the present time. The radioisotope used in the *prior* radioactivity is selected and unity (1) is input for the initial activity. 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 [R/S]. The decay factor A will be displayed and automatically stored. Then follow the basic procedure to find the uncorrected percentage uptake. After computing percent uptake, key in the predose patient counts and the predose background counts. The corrected 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 ±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 finding the uptake, press [C] and key in the standard precount and the dose precount. The program then calculates the corrected thyroid uptake.

The two corrections to the uptake calculation operate independently of each other. If both are to be made, the correction for prior radioactivity is made first. 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 predose counts or the standard 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.

$$K = \begin{cases} 1 & \text{if no correction} \\[2ex] \dfrac{\text{NPC} - A \times (\text{Ptnt Predose Ct} - \text{Bck Predose Ct})}{\text{NPC}} & \text{if prior radioactivity} \\[2ex] \dfrac{\text{Std. Precount}}{\text{Dose Precount}} & \text{if different activities} \end{cases}$$

where

A is the radioactive decay factor.

Remark:

The counts need not be input as counts *per minute;* however, all counts should be measured over the same time interval.

Reference:

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

SIZE: 015

STEP	INSTRUCTIONS	INPUT	FUNCTION	DISPLAY
1	Begin Thyroid Uptake program.		XEQ THY	PTNT≠=?
2	Input the patient number.	Patient#	R/S	
2a	If printer is used, patient number and program name are printed.			PTNT≠= THYROID UPTAKE PTNT PRERAD?

STEP	INSTRUCTIONS	INPUT	FUNCTION	DISPLAY
3	If correction is to be made for prior patient radioactivity answer Y and go to step 4. If not, answer N and go to step 7.	Y N	[R/S] [R/S]	ISOTOPE? STD CPM=?
4	**Prior Radioactivity:** Select the radioisotope of the prior radioactivity by entering its chemical symbol (see Radioactive Decay Corrections program for details) and see half-life displayed.	symbol	[R/S]	ISOTOPE? symbol and halflife (hours)
5	Proceed to prompt for initial activity. Input 1 for the initial activity.	1	[R/S] * [R/S]	A0=? T=?
6	Input the time elapsed in the format Days.Hours (e.g., 1 day, 6 hours is keyed in as 1.06) and the decay factor, A, is automatically stored and displayed.	t(dd.hh)	[R/S]	A=(decay factor)
7	**Basic Procedure:** Proceed to prompt for thyroid uptake. Input counts for the standard.	STD CPM	[R/S] * [R/S]	STD CPM=? STD BCK=?
8	Input background counts for the standard and calculate net standard counts.	STD BCK	[R/S]	NET STD CTS=
9	Continue program. Input counts for the patient.	PTNT CPM	[R/S] * [R/S]	PTNT CPM=? PTNT BCK=?
10	Input the background counts for the patient and calculate net patient counts.	PTNT BCK	[R/S] *	NET PTNT CTS=
11	Calculate thyroid uptake as a percent.		[R/S] *	%UPTAKE=
12	**Corrections:** For corrections due to prior radioactivity go to step 13. For corrections due to differences in standard and dose, go to step 15.			
13	**Prior Radioactivity:** Press [R/S] for prompting and input predose counts.	PREDOSE CTS	[R/S] * [R/S]	PREDOSE CTS=? PREDOSE BCK=?
14	Input predose background and calculate corrected percent uptake.	PREDOSE BCK	[R/S]	PRERAD CORR %UPTAKE=
15	**Differences in Dose and Standard:** If standard and dose precounts differ by more than 3%, perform activity difference correction. Initiate corrections routine by pressing	STD PRECTS DOSE PRECTS	[C] [R/S] [R/S]	STD PRECTS=? DOSE PRECTS=? ACTIV DIFF CORR

STEP	INSTRUCTIONS	INPUT	FUNCTION	DISPLAY
	[C]. Input standard precounts and dose precounts.			%UPTAKE=
	Reprint:			
16	For a reprint of data and results		■ [E] [R/S] * [R/S] * [R/S] * [R/S] * [R/S] * [R/S] * [R/S] *	PTNT≠= THYROID UPTAKE STD CPM= STD BCK= PTNT CPM= PTNT BCK= (type of correction) %UPTAKE=
17	If you later desire to perform activity difference correction, go to step 15.			
18	For new data, press [A] and go to step 7.		[A]	STD CPM=?
19	For a new case, press [E] and go to step 2.		[E]	PTNT≠=?
	* This [R/S] not required when calculator is operated with printer.			

Example 1:

Before a dose of radioiodine (^{131}I) is administered to patient 10183, a count is made of the patient's current level of radioactivity from a prior ingestion of ^{131}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}I is measured at 1500 CPM with a background of 200 CPM. Find the percentage uptake corrected for prior radioactivity.

Keystrokes:	**Display:**
[XEQ] [ALPHA] SIZE [ALPHA] 015	***SIZE 015***
[XEQ] [ALPHA] THY [ALPHA]	***PTNT≠=?***
10183 [R/S]	***PTNT PREAD?***
Y [R/S]	***ISOTOPE?***
I ■ 1 ■ 3 ■ 1 [R/S]	***I131=193.20***
[R/S]	***A0=?***
1 [R/S]	***T=?***
0.24 [R/S]	***A=0.92***
[R/S]	***STD CPM=?***
1500 [R/S]	***STD BCK=?***
200 [R/S]	***NET STD CTS=1,300.00***
[R/S]	***PTNT CPM=?***

350 [R/S]	PTNT BCK=?	
100 [R/S]	NET PTNT CTS=250.00	
[R/S]	%UPTAKE=19.23	
[R/S]	PREDOSE CTS=?	correction for
75 [R/S]	PREDOSE BCK=?	prior radioactivity
25 [R/S]	PRERAD CORR	
	%UPTAKE=15.70	

Example 2:

For patient number 10174 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 then 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. Obtain a reprint.

Keystrokes:	**Display:**	
[XEQ] [ALPHA] THY [ALPHA]	PTNT≠=?	
10174 [R/S]	PTNT PRERAD?	
N [R/S]	STD CPM=?	
11500 [R/S]	STD BCK=?	
1000 [R/S]	NET STD CTS=	
	10,500.00	
[R/S]	PTNT CPM=?	
2650 [R/S]	PTNT BCK=?	
500 [R/S]	NET PTNT CTS=	
	2,150.00	
[R/S]	%UPTAKE=20.48	
[C]	STD PRECTS=?	correction for act-
14500 [R/S]	DOSE PRECTS=?	ivity difference
12500 [R/S]	ACTIV DIFF CORR	
	%UPTAKE=23.75	
■ [E]	PTNT≠=10,174.00	
[R/S]	THYROID UPTAKE	
[R/S]	STD CPM=11,500.00	
[R/S]	STD BCK=1,000.00	
[R/S]	PTNT CPM=2,650.00	
[R/S]	PTNT BCK=500.00	
[R/S]	ACTIV DIFF CORR	
	%UPTAKE=23.75	

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. The three variables needed to define the problem are: A_0, t, and A. This program calculates any one of the variables given the other two.

The desired isotope is selected by keying in its chemical symbol. For instance, to specify use of ^{57}CO, **CO** is keyed in. 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}Cr	667.2
^{57}Co	6480
^{99m}Tc	6
^{125}I	1440
^{131}I	193.2
^{137}Cs	262980
^{3}H	107470
^{14}C	5.058×10^7
^{18}F	1.87
^{32}P	343.2
^{75}Se	2880
^{85}Sr	1536
^{113m}In	1.73
^{133}Xe	126.5
^{197}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, input **X** followed by the half-life in hours. 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 2, this would appear as 6.24, even though 7.00 might be the preferred rounded format.

SIZE: 007

STEP	INSTRUCTIONS	INPUT	FUNCTION	DISPLAY
1	Begin Radioactive Decay Corrections program.		XEQ RADCORR	(RAD DECAY) ISOTOPE?
2a	Select one of the 15 radioisotopes to obtain its half-life (in hours):			
	• Chromium-51 (^{51}Cr)	CR	R/S	CR=667.20
	• Cobalt-57 (^{57}Co)	CO	R/S	CO=6,480.00
	• Technetium-99m (^{99m}Tc)	TC	R/S	TC=6.00
	• Iodine-125 (^{125}I)†	I125	R/S	I125=1,440.00
	• Iodine-131 (^{131}I)†	I131	R/S	I131=193.20
	• Cesium-137 (^{137}Cs)	CS	R/S	CS=262,980.00
	• Hydrogen-3 (^{3}H)	H	R/S	H=107,470.00
	• Carbon-14 (^{14}C)	C	R/S	C=50,580,000.00
	• Fluorine-18 (^{18}F)	F	R/S	F=1.87
	• Phosphorous-32 (^{32}P)	P	R/S	P=343.20
	• Selenium-75 (^{75}Se)	SE	R/S	SE=2,880.00
	• Strontium-85 (^{85}Sr)	SR	R/S	SR=1,536.00
	• Indium-113m (^{113m}In)	IN	R/S	IN=1.73
	• Xenon-133 (^{133}Xe)	XE	R/S	XE=126.50
	• Mercury-197 (^{197}Hg)	HG	R/S	HG=65.00
	then go to step 3.		R/S *	A0=?
2b	Or, for isotope other than those above, key in X, press R/S and	X	R/S	1/2 LIFE=?
	input the half-life, in hours, of the desired radioisotope. Then go to step 3.	τ½(hours)	R/S	A0=?
3	Input 2 of the three variables:			A0=?
	• Activity at time zero if known,	A_0	R/S	T=?
	or, if unknown.		R/S	T=?
	• Time elapsed (in days.hours format) if known,	T(dd.hh)	R/S	A=? or see step 4
	or if unknown.		R/S	A=?
	• Present activity.	A	R/S	see step 4
4	After input of any two values, the third, unknown quantity, will automatically be calculated.			A0=
	or,			T=(dd.hh)
	or,			A=
5	For a new set of conditions, press A and go to step 3.		A	A0=?
6	For a new isotope, press E and go to step 2.		E	ISOTOPE?
	† To distinguish between ^{125}I and ^{131}I, it is necessary to input the symbol I followed by the atomic number of the isotope. (Remember to press ■ before keying in each numeral.)			
	* This R/S not required if calculator is operated with printer.			

Example 1:

An activity of 200 μCi is measured for a standard of ^{51}Cr. What is the activity after one week?

Keystrokes:	Display:	
XEQ ALPHA SIZE ALPHA 007	***SIZE 007***	
XEQ ALPHA RADCORR ALPHA	***ISOTOPE?***	
CR R/S	***CR=667.20***	
R/S	***A0=?***	
200 R/S	***T=?***	
7 R/S	***A=167.97***	(μCi)

Example 2:

A source of ^{131}I has an initial activity of 50 μCi. After what period of time will it have decayed to 20 μCi?

Keystrokes:	Display:	
E	***ISOTOPE=?***	
I 131 R/S *	***I131=193.20***	
R/S	***A0=?***	
50 R/S	***T=?***	
R/S	***A=?***	
20 R/S	***T=10.15***	(10 days, 15 hours)

---

* Remember when keying in alpha numerals, press ■ before pressing numeral key. (i.e., I ■ 1 ■ 3 ■ 1).

Radioimmunoassay

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 the program the user specifies whether the input data is to be printed (if a printer is attached to the calculator) and if the logit/log plot data are to be displayed. The non-specific binding (or blank) counts, NSB, are input and repeated for as many replicates as desired. After all replicates have been input the average non-specific binding count is calculated and displayed. The same procedure is repeated for counts at zero concentration.

The next step is to input the data for the standards. The counts for the first standard are input, with as many replicates as desired. After all replicates for the first standard are input, the concentration of the standard is keyed in. The calculator displays the average number of counts for the standard and the net B/B_0. Optionally the concentration, logit and log of the concentration may also be displayed at this point. This procedure is repeated for as many standards as desired.

After all standards have been input the user executes the least-squares regression portion of the program by pressing C. The correlation coefficient, r, slope, m, and intercept, b, of the least-squares logit/log regression line, calculated from the standards, are displayed. The regression performed is an unweighted regression.

Next, the counts of an unknown may be input with as many replicates as desired, and the concentration of the unknown is calculated along with the average counts and the net B/B_0. Optional outputs are the logit and log concentration values. These calculations may be repeated for as many unknowns as desired.

Upon beginning the program, if a printer is attached to the system, the user has the option of choosing to print all input data by answering ***Y*** (yes) to the question ***PRINT INPUT?*** Likewise, one may elect to display and/or print the plot values log and logit (X and Y) for standards and unknown by answering ***Y*** (yes) to the question ***DATA FOR PLOT?*** 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^{th} standard ($i = 1, 2, \ldots, n$)

C_i = concentration of i^{th} standard

Let

$$x_i = \log C_i$$

$$\begin{aligned} y_i &= \operatorname{logit}\left(\frac{B_i - NSB}{B_0 - NSB}\right) \\ &= \ln\left[\frac{(B_i - NSB)/(B_0 - NSB)}{1 - (B_i - NSB)/(B_0 - NSB)}\right] \\ &= \ln\left(\frac{B_i - NSB}{B_0 - B_i}\right) \end{aligned}$$

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

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.

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

$$b = \overline{y} - m\,\overline{x}$$

where:

$$\overline{y} = \frac{\Sigma y}{n}$$

$$\overline{x} = \frac{\Sigma x}{n}$$

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

Let

B = average of replicate counts for an unknown

C_u = concentration of unknown

$$C_u = 10^x$$

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

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_{10}, m in R_{11}, and b in R_{12}.

References:

Rodbard, Bridson, and Rayford, "Rapid Calculation of Radioimmunoassay Results," *J. Lab. Clin. Med.*, 74:770 (1969).

SIZE: 016

STEP	INSTRUCTIONS	INPUT	FUNCTION	DISPLAY
1	Begin Radioimmunoassay program		[XEQ] RIA	
2	If printer is present, see display and go to step 2a. Otherwise, go to step 3.			RIA PRINT INPUT?
2a	If you wish data inputs printed or, if you do not wish inputs printed.	Y N	[R/S] [R/S]	(see step 3) (see step 3)
3	If you wish display of data for plotting purposes (logit, log conc.) input Y or, if not, input N.	 Y N	 [R/S] [R/S]	DATA FOR PLOT? NSB=? NSB=?
4	Input non-specific binding counts, repeat for as many replicates as desired.	NSB	[R/S]	NSB=?
5	After all replicates have been entered, press [R/S] without prior data entry, to find the average NSB.		[R/S]	AVE NSB=
6	Proceed with prompting for B_0 counts.		[R/S] *	B0=?
7	Input counts for B_0, (the zero dose); repeat for as many replicates as desired.	B_0	[R/S]	B0=?

STEP	INSTRUCTIONS	INPUT	FUNCTION	DISPLAY
8	After all replicates have been entered, press R/S without prior data entry to find the average B_0.		R/S	AVE B0=?
9	Proceed with prompting for standards.		R/S *	STD B=?
10	**Standards:** Input the counts for the first standard, repeat for as many replicates as desired.	Std B	R/S	STD B=?
11	When all replicates have been input, press R/S without prior data entry, input the concentration of the first standard and obtain outputs. (optional outputs are shown in parentheses, 1.00 indicates the first standard.)	Conc.	R/S R/S R/S * R/S * R/S * R/S *	CONC=? (1.00) AVE STD B= NET B/B0= (CONC=) (LOGIT=) (LOG CONC=) STD B=?
12	Repeat steps 10 and 11 for all standards then go to step 13.			
13	**Results:** Calculate the correlation coefficient (r), slope (m) and intercept (b) of regression line.		C R/S * R/S *	R= SLOPE= INTCPT=
14	Continue with prompting for unknowns.		R/S *	UNKN B=?
15	**Unknowns:** Input the counts for an unknown; repeat for as many replicates as desired.	Unknown B	R/S	UNKN B=? UNKN B=?
16	When all replicates have been input, press R/S without prior data entry, and calculate the concentration of the unknown. (Optional outputs are shown in parentheses, 1.00 indicates the first unknown.)		R/S R/S * R/S * R/S *	(1.00) AVE UNKN B= CONC= (LOGIT=) (LOG CONC=)
17	Repeat steps 15 and 16 for any number of unknowns.		R/S *	UNKN B=?
18	**New Case:** For a new assay go to step 1.			
	* This R/S not required when calculator is used with a printer. NOTE: Results shown in parentheses are optional outputs.			

Example:

Below are the data for non-specific binding (NSB), zero concentration (B_0), and various standards for a radioimmunoassay.

Description	Counts per minute	Concentration (pg)
NSB	425, 339, 342, 369	-
B_0	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

User the ***DATA FOR PLOT*** option for complete outputs. (Parenthetical displays appear only if calculator is used with a printer.)

Keystrokes:	**Display:**	
XEQ ALPHA SIZE ALPHA 016	***SIZE 016***	
XEQ ALPHA RIA ALPHA	***RIA***	only if printer is present
	PRINT INPUT?	
N R/S *	***DATA FOR PLOT?***	
Y R/S	***NSB=?***	
425 R/S	***NSB=?***	
339 R/S	***NSB=?***	
342 R/S	***NSB=?***	
369 R/S	***NSB=?***	
R/S	***AVE NSB=368.75***	
R/S	***B0=?***	
10670 R/S	***B0=?***	
10570 R/S	***B0=?***	
10925 R/S	***B0=?***	
R/S	***AVE B0=10,721.67***	
R/S	***STD B=?***	
9176 R/S	***STD B=?***	
9850 R/S	***STD B=?***	
R/S	***CONC=?***	

* This input only necessary when calculator is operated with printer.

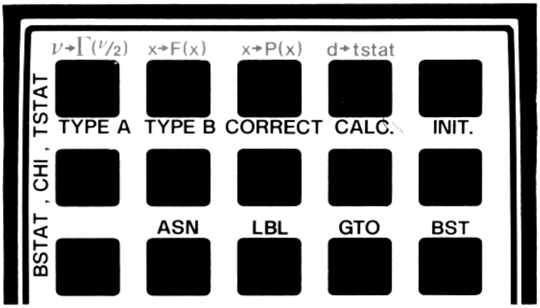
25 R/S	*(1.00)*
	AVE STD B=9,513.00
R/S	***NET B/B0=0.88***
	(CONC=25.00)
R/S	***LOGIT=2.02***
R/S	***LOG CONC=1.40***
R/S	***STD B=?***
8453 R/S	***STD B=?***
7967 R/S	***STD B=?***
R/S	***CONC=?***
50 R/S	*(2.00)*
	AVE STD B=8,210.00
R/S	***NET B/B0=0.76***
	(CONC=50.00)
R/S	***LOGIT=1.14***
R/S	***LOG CONC=1.70***
R/S	***STD B=?***
6323 R/S	***STD B=?***
6057 R/S	***STD B=?***
R/S	***CONC=?***
100 R/S	*(3.00)*
	AVE STD B=6,190.00
R/S	***NET B/B0=0.56***
	(CONC=100.00)
R/S	***LOGIT=0.25***
R/S	***LOG CONC=2.00***
R/S	***STD B=?***
3866 R/S	***STD B=?***
4088 R/S	***STD B=?***
R/S	***CONC=?***
200 R/S	*(4.00)*
	AVE STD B=3,977.00
R/S	***NET B/B0=0.35***
	(CONC=200.00)
R/S	***LOGIT=-0.63***
R/S	***LOG CONC=2.30***
R/S	***STD B=?***
2027 R/S	***STD B=?***
2221 R/S	***STD B=?***

R/S	*CONC=?*
400 R/S	*(5.00)*
	AVE STD B=2,124.00
R/S	*NET B/B0=0.17*
	(CONC=400.00)
R/S	*LOGIT=-1.59*
R/S	*LOG CONC=2.60*
R/S	*STD B=?*
1251 R/S	*STD B=?*
1462 R/S	*STD B=?*
R/S	*CONC=?*
800 R/S	*(6.00)*
	AVE STD B=1,356.50
R/S	*NET B/B0=0.10*
	(CONC=800.00)
R/S	*LOGIT=-2.25*
R/S	*LOG CONC=2.90*
	(STD B=?)
C	*R=-1.00*
R/S	*SLOPE=-2.89*
R/S	*INTCPT=6.03*
R/S	*UNKN B=?*
10230 R/S	*UNKN B=?*
10170 R/S	*UNKN B=?*
R/S	*(1.00)*
	AVE UNKN B=
	10,200.00
R/S	*NET B/B0=0.95*
R/S	*CONC=11.83*
R/S	*LOGIT=2.94*
R/S	*LOG CONC=1.07*
R/S	*UNKN B=?*
3270 R/S	*UNKN B=?*
3400 R/S	*UNKN B=?*
R/S	*(2.00)*
	AVE UNKN B=3,335.00
R/S	*NET B/B0= 0.29*

R/S	*CONC=254.57*
R/S	*LOGIT=-0.91*
R/S	*LOG CONC=2.41*
	(UNKN B=?)

Statistics

BASIC STATISTICS



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

The data input to the program may be either grouped or ungrouped. Ungrouped data should be input using key [A] and grouped data using key [B]. Key [C] provides error correction for both ungrouped and grouped cases. If an incorrect entry is made, it may be corrected by keying in that entry a second time and pressing [C]. 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 number 4.31 is accidently input to key [A]. To correct this mistake, simply key in 4.31 again and press [C]. At this point the error has been eliminated. Now enter the correct data, 7.31 and press [A].

Equations:

Ungrouped data: (type A data)

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

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

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

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

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

Grouped data: (type B data)

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

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

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

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

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

Remarks:

1. Grouped and ungrouped data may be mixed in the same set of data.
2. The preprogrammed functions Σ+ and Σ− may be used to input and correct **ungrouped** data in place of keys A and C. Calculation of mean and standard deviation may also be done by the preprogrammed functions "MEAN" and "SDEV" for both grouped and ungrouped data.

				SIZE: 010
STEP	**INSTRUCTIONS**	**INPUT**	**FUNCTION**	**DISPLAY**
1	Place overlay on keyboard and begin Basic Statistics program.		XEQ BSTAT	(BASIC STAT) X=?
2	For ungrouped data, go to step 3; for grouped data, go to step 6.			
	(Type A) Ungrouped Data:			
3	Input data point. Perform this step for i = 1, 2, ..., m.	X_i	A	i
4	To correct an erroneous entry.	X_k	C	i-1
5	Go to step 8.			
	(Type B) Grouped Data:			
6	Input frequency and data. Perform this step for i = 1, 2, ..., m	f_i X_i	ENTER↑ B	 i
7	To correct an erroneous entry.	f_k X_k	ENTER↑ C	 i-1
	Results:			
8	Calculate mean, standard deviation, standard error, coefficient of variation.		D R/S * R/S * R/S *	MEAN= STD DEV= STD ERROR= CV%=

STEP	INSTRUCTIONS	INPUT	FUNCTION	DISPLAY
9	For a new case, press E and go to step 2. * This R/S not needed when printer is used with the calculator.		E	(BASIC STAT) X=?

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:	Display:	
XEQ ALPHA SIZE ALPHA 010	*SIZE 010*	
XEQ ALPHA BSTAT ALPHA	*(BASIC STAT)*	
	X=?	
13.8 A	*1.000*	
16.9 A	*2.000*	
16.5 A	*3.000*	
17.7 A	*4.000*	
16 A	*5.000*	
17.4 A	*6.000*	
3.4 A	*7.000*	(Error!)
3.4 C	*6.000*	(Correction)
13.4 A	*7.000*	
17.9 A	*8.000*	
15.2 A	*9.000*	
D	*MEAN=16.089*	
R/S	*STD DEV=1.647*	
R/S	*STD ERR=0.549*	
R/S	*CV%=10.234*	

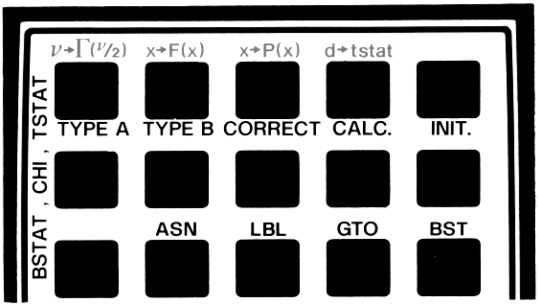
Example 2:

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:	**Display:**	
E	*(BASIC STAT)* *X=?*	
5 ENTER↑ 18 B	*1.000*	
9 ENTER↑ 19 B	*2.000*	
12 ENTER↑ 20 B	*3.000*	(Error!)
12 ENTER↑ 20 C	*2.000*	(Correction)
13 ENTER↑ 20 B	*3.000*	
7 ENTER↑ 21 B	*4.000*	
1 ENTER↑ 22 B	*5.000*	
D	*MEAN=19.714*	
R/S	*STD DEV=1.045*	
R/S	*STD ERROR=0.177*	
R/S	*CV%=5.302*	

CHI-SQUARE EVALUATION AND DISTRIBUTION



This program allows you to perform two important calculations concerning the chi-square statistic. The first of these calculates the value of the χ^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 ν.

The χ^2 statistic may be computed for the case where the expected frequencies are equal (type A data) as well as for the case where they are different (type B data). If they are equal, only the observed frequencies O_i need be input with key [A]. Error correction is provided on key [C]. After calculation of χ^2 with key [D], the expected frequency E may be calculated by pressing [R/S]. If the expected frequencies are different (type B data), both the observed and expected frequencies should be input to key [B]. Error correction is provided on key [C].

To make calculations involving the chi-square distribution, first input the degrees of freedom ν to key ■ [A]. Then key in the value of x and press ■ [B] to find the density f(x) or ■ [C] 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 (type A data)

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

then

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

Chi-square distribution:

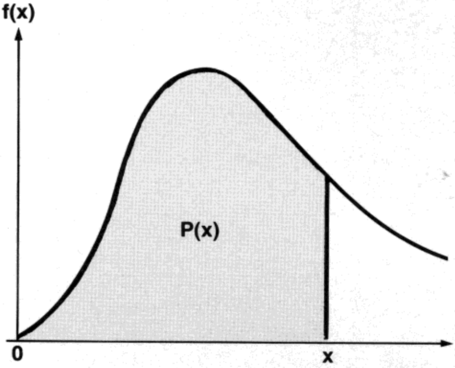
Chi-square density:

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

where:

$x \geqslant 0$

ν is the degrees of freedom.



Series approximation is used to evaluate the cumulative distribution

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

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

where:

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

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

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 $\nu \leqslant 141$. If $\nu > 141$, erroneous overflow will result.
3. If both x and ν are large, the calculation of f(x) may cause overflow.

References:

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

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

				SIZE: 007
STEP	**INSTRUCTIONS**	**INPUT**	**FUNCTION**	**DISPLAY**
1	Place overlay on keyboard and begin Chi-Square Evaluation and Distribution program.		XEQ CHI	(CHI SQ) 0=?
2	For χ^2 evaluation go to step 3, for χ^2 distribution go to step 10.			
	χ^2 Evaluation:			
3	If the expected frequencies are equal go to step 4; if they are not equal go to step 7.			
	(Type A) Expected Frequencies Equal:			
4	Input the observed value. Perform this step for i = 1, 2, ..., n.	O_i	A	i

STEP	INSTRUCTIONS	INPUT	FUNCTION	DISPLAY
5	To correct an erroneous entry.	O_k	[C]	i-1
6	Calculate the χ^2 statistic and the average expected frequency.		[D] [R/S] *	CHI SQ= E=
	(Type B) Expected Frequencies Unequal:			
7	Input the observed value and expected frequency. Perform this step for i = 1, 2, ..., n.	O_i E_i	[ENTER↑] [B]	 i
8	To correct an erroneous entry.	O_k E_k	[ENTER↑] [C]	 i-1
9	Calculate the χ^2 statistic.		[D]	CHI SQ=
	χ^2 Distribution:			
10	Input degrees of freedom.	ν	■ [A]	GAMMA=
11	Input x and calculate • Density or • Cumulative Distribution	 x x	 ■ [B] ■ [C]	 DENSITY= CUM DIST=
12	For a new case, press [E] and go to step 2.		[E]	(CHI SQ) O=?
	* This [R/S] not necessary if calculator is operated with a printer.			

Example:

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

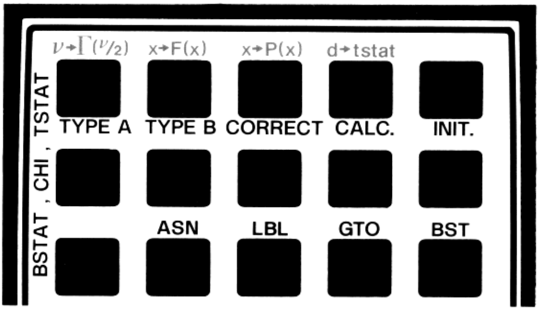
25601	25553
25546	25841
25592	25560
25820	25633
25569	25464

Keystrokes:	Display:
[XEQ] [ALPHA] SIZE [ALPHA] 007	*SIZE 007*
[XEQ] [ALPHA] CHI [ALPHA]	*(CHI SQ)*
	O=?
25601 [A]	*1.000*
25546 [A]	*2.000*
25592 [A]	*3.000*
25820 [A]	*4.000*

Keystrokes:	**Display:**
25569 [A]	***5.000***
25553 [A]	***6.000***
25841 [A]	***7.000***
25560 [A]	***8.000***
25633 [A]	***9.000***
25464 [A]	***10.000***
[D]	***CHI SQ=5.099***
[R/S]	***E=25,617.900***
9 ■ [A]	***GAMMA=11.632***
5.099 ■ [C]	***CUM DIST=0.174***

Since $P(\chi^2) = 0.174 < 0.90$, we accept the assumption that the instrument is operating correctly.

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.

Paired t Statistic (type A data):

The paired t statistic applies to a set of *paired* observations drawn from two normal populations with unknown means μ_1, μ_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 the *t Distribution Program*) then we reject the hypothesis that the population means are equal.

The x- and y-values are input with key $\boxed{\text{A}}$. Error correction is provided by key $\boxed{\text{C}}$. After the input of all x-y pairs, the t statistic may be found by pressing $\boxed{\text{D}}$.

t Statistics for two means (type B data):

The t statistic for two means applies to independent random samples $\{x_1, x_2, \ldots, x_{n1}\}$ and $\{y_1, y_2, \ldots, y_{n2}\}$ drawn from two normal populations with unknown means μ_1, μ_2 and the same unknown variance σ^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 input to key $\boxed{\text{B}}$. Error correction is available on key $\boxed{\text{C}}$. After all x-values have been input, the value of d is input. Then the y-values should be input to key $\boxed{\text{B}}$. After input of all the y-values, the t statistic may be found by pressing $\boxed{\text{D}}$.

Equations:

Paired t statistic

let

$$D_i = x_i - y_i$$

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

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

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

The test statistic

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

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

$$H_o\colon \mu_1 = \mu_2$$

t statistic for two means

Define

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

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

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

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

$$H_o\colon \mu_1 - \mu_2 = d$$

References:

(Paired t) Ostle, B., *Statistics in Research,* Iowa State University Press, 1963.

(t for two means) Brownlee, K. A., *Statistical Theory and Methodology in Science and Engineering,* John Wiley and Sons, 1965.

SIZE: 012

STEP	INSTRUCTIONS	INPUT	FUNCTION	DISPLAY
1	Place overlay on keyboard and begin t Statistics program.		XEQ TSTAT	(T STAT) X=?
2	For paired t statistic go to step 3. For t statistics for two means go to step 7.			
	(Type A) Paired t Statistic:			X=?
3	Input X and Y values. Perform this step for all data pairs (i = 1, 2, ..., n).	X_i Y_i	ENTER↑ A	 i
4	To correct an erroneous entry.	X_k Y_k	ENTER↑ C	 i-1
5	Calculate paired t statistic.		D	T STAT=
6	(Optional) Calculate degrees of freedom, mean difference and standard deviation of D.		R/S * R/S * R/S *	DF= MEAN D= STD DEV=
	(Type B) t Statistic for Two Means:			X=?
7	Input the X value. Perform this step for all X values (i = 1, 2,..., n_1).	X_i	B	i
8	To correct an erroneous entry.	X_k	C	i-1
9	Input the difference to be tested.	 d	R/S R/S	DIFF=? Y=?
10	Input the Y value. Perform this step for all Y values (i = 1, 2, ..., n_2).	Y_i	B	i
11	To correct an erroneous entry.	Y_k	C	i-1
12	Calculate t statistic for two means.		D	T STAT=
13	(Optional) Calculate degrees of freedom.		R/S *	DF=
14	To change value of d, and re-calculate t statistic.	d	■ D	T STAT=
15	For a new case press E and go to step 2.		E	(T STAT) X=?
16	To interpret the results use the t Distribution program.			
	* This R/S not necessary if calculator is used with printer.			

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. Use a 10% significance level.

	Method	
Sample	**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:	**Display:**	
XEQ ALPHA SIZE ALPHA 012	*SIZE 012*	
XEQ ALPHA TSTAT ALPHA	*(T STAT)*	
	X=?	
17.6 ENTER↑ 17.4 A	*1.000*	
13 ENTER↑ 12.9 A	*2.000*	
15.3 ENTER↑ 15.2 A	*3.000*	(Error!)
15.3 ENTER↑ 15.2 C	*2.000*	(Correction)
15.3 ENTER↑ 15.3 A	*3.000*	
15 ENTER↑ 15.2 A	*4.000*	
15 ENTER↑ 15 A	*5.000*	
14.6 ENTER↑ 14.5 A	*6.000*	
D	*T STAT=0.598*	
R/S	*DF=5.000*	
R/S	*MEAN D=0.033*	
R/S	*STD DEV=0.137*	

To interpret these results, use the t Distribution program (TDIST) to find the cumulative distribution integral I(x) for X=0.598 and 5 degrees of freedom:

Keystrokes:	**Display:**
XEQ ALPHA SIZE ALPHA 015	*SIZE 015*
XEQ ALPHA TDIST ALPHA	*(T DIST)*
	DF=?
5 R/S	*X=?*
.598 R/S	*I F P*
■ A	*I ∠x∖=0.424*

Since I(.598) = 0.424<0.90, 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 and the t distribution programs for two means to test the hypothesis that the difference between the means is negligible (i.e., d = 0) at the 5% significance level.

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:	**Display:**
XEQ ALPHA SIZE ALPHA 012	***SIZE 012***
XEQ ALPHA TSTAT ALPHA	***(T STAT)***
	X=?
13.8 B 16.9 B 16.5 B	***3.000***
17.7 B 16 B 17.4 B	***6.000***
13.4 B 17.9 B 15.2 B	***9.000***
R/S	***DIFF=?***
0 R/S	***Y=?***
11.9 B 14.4 B 13.7 B	***3.000***
16.8 B 11.7 B	***5.000***
14.9 B 12.3 B	***7.000***
D	***T STAT=2.756***
R/S	***DF=14.000***
XEQ ALPHA SIZE ALPHA 015	***SIZE 015***
XEQ ALPHA TDIST ALPHA	***(T DIST)***
	DF=?
14 R/S	***X=?***
2.756 R/S	***I F P***
■ A	***I∠x∖ =0.985***

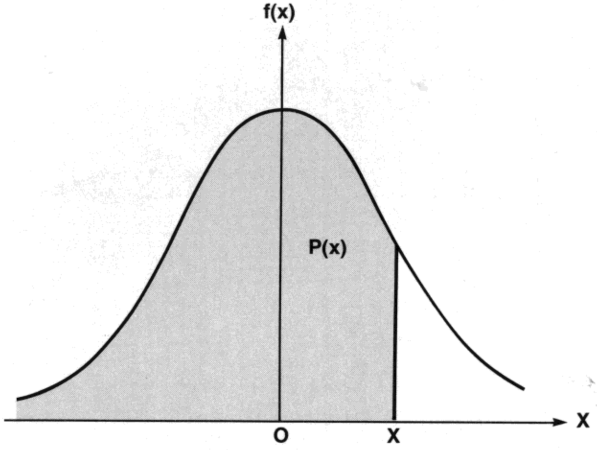
Since I(2.756) = 0.985 > 0.95, the value of t is significant and we should reject the hypothesis that the average hemoglobin concentrations in males and females are equal.

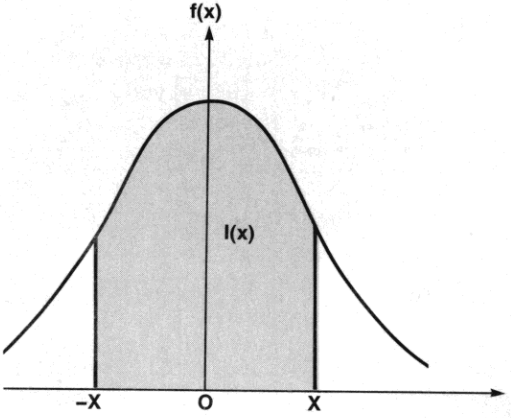
t DISTRIBUTION

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

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

$$\text{and } I(x) = \int_{-x}^{x} f(y)\,dy \text{ for } x > 0.$$





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) ν even

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

(2) ν odd

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

where

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

$$P(x) = \begin{cases} \dfrac{1+I(x)}{2} & \text{if } x > 0 \\[2ex] \dfrac{1-I(x)}{2} & \text{if } x \leq 0 \end{cases}$$

Remarks:

1. The program requires $\nu < 141$. Otherwise an erroneous overflow will result.
2. The Integral, I(x), Density function, F(x) and Cumulative distribution, P(x), are calculated using the ▨ A, ▨ B and ▨ C keys, respectively, analogous to their use in *Chi Square Evaluation and Distribution*.

Reference:

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

SIZE: 015

STEP	INSTRUCTIONS	INPUT	FUNCTION	DISPLAY
1	Begin t Distribution program.		[XEQ] TDIST	(T DIST) DF=?
2	Input degrees of freedom.	ν	[R/S]	X=?
3	Input X.	X	[R/S]	I.. F P
4	See prompt and choose desired calculation:			
	Integral, –x to x (x > 0), I(x) or,		■ [A]	I∠X⦣ =
	Density function, F(x)		■ [B]	F∠X⦣ =
	or			
	Cumulative distribution, P(x)		■ [C]	P∠X⦣ =
5	For other calculations: repeat steps 3 and 4.			
6	For a new case, press [E] and go to step 2.		[E]	(T DIST) DF=?

Example 1:

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

Keystrokes:	Display:
[XEQ] [ALPHA] SIZE [ALPHA] 015	***SIZE 015***
[XEQ] [ALPHA] TDIST [ALPHA]	***T DIST***
	DF=?
9 [R/S]	***X=?***
1.6 [R/S]	***I F P***
■ [B]	***F∠X⦣=0.111***
1.6 [R/S]	***I F P***
■ [C]	***P∠X⦣=0.928***

Example 2:

Find I(x) for x = 1.83 and ν = 11.

Keystrokes:	Display:
[E]	***T DIST***
	DF=?
11 [R/S]	***X=?***
1.83 [R/S]	***I F P***
■ [A]	***I∠X⦣=0.906***

Appendix

PROGRAM DATA

Program	# Regs. to Copy	Data Registers	Flags	Display Format	Angular Mode
Beer's Law	34	00, 02-14	00-03, 09, 10, 21, 22, 27, 29	FIX 2	N.A.
Body Surface Area	36	00-05, 07-13	00-03, 10, 21 22, 27, 29	FIX 2	N.A.
Creatinine Clearance	30	00-09, 12-14	00-03, 06, 09, 10 21, 22, 27, 29	FIX 2	N.A.
Blood Acid-Base Status Oxygen Saturation and Content	75	00-14	00-03, 05, 09, 10 21, 22, 27, 29	FIX 2	N.A.
Red Cell Indices Total Blood Volume	47	00-06, 12, 13	00-03, 05, 09, 10, 21, 22, 27, 29	FIX 2	N.A.
Thyroid Uptake	48	00-14	00-03, 09, 10, 21 22, 27, 29	FIX 2	N.A.
Radioactive Decay Corrections	59	00-06	00-03, 10, 21, 22 27, 29	FIX 2	N.A.
Radioimmunoassay	66	00-15	00-04, 09, 10, 21 22, 27, 29	FIX 2	N.A.
Basic Statistics	22	03-09	00-03, 10, 21, 22 27, 29	FIX 3	N.A.

Chi-Square Eval. and Dist.	40	01-06	00-03, 21, 22, 27, 29	FIX 3	N.A.
t Statistics	33	01-11	00-03, 21, 22 27, 29	FIX 3	N.A.
t Distribution	44	00-14	00-03, 21, 22 27, 29	FIX 3	N.A.
Utilities (∗)	34	00; 12, 14	00-03, 09, 10 21, 22, 27, 29	N.A.	N.A.

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