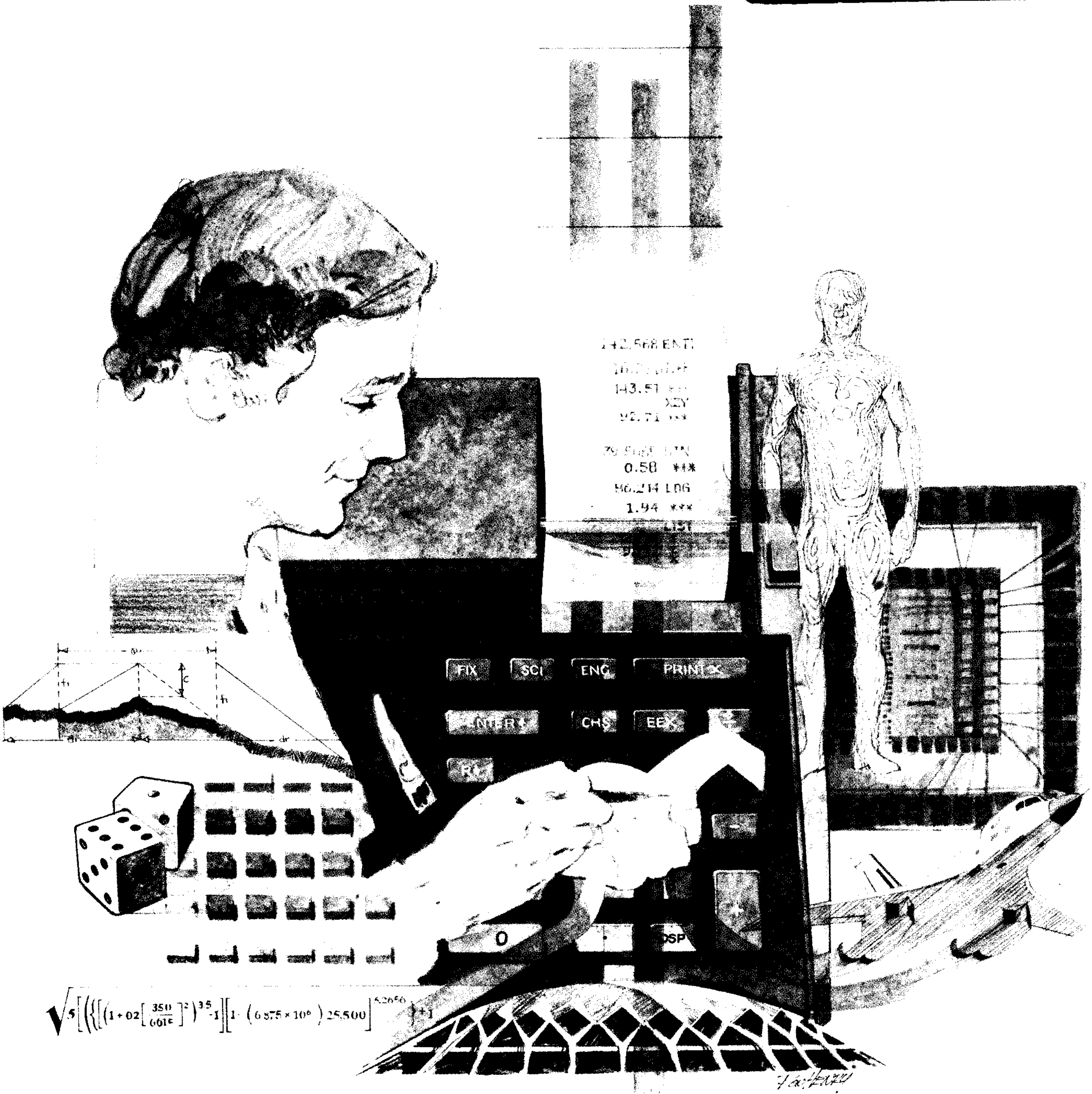
HEWLETT-PACKARD

HP-67/HP-97

Users' Library Solutions

[redacted]

Biology



INTRODUCTION

In an effort to provide continued value to it's customers, Hewlett-Packard is introducing a unique service for the HP fully programmable calculator user. This service is designed to save you time and programming effort. As users are aware, Programmable Calculators are capable of delivering tremendous problem solving potential in terms of power and flexibility, but the real genie in the bottle is program solutions. HP's introduction of the first handheld programmable calculator in 1974 immediately led to a request for program **solutions** — hence the beginning of the HP-65 Users' Library. In order to save HP calculator customers time, users wrote their own programs and sent them to the Library for the benefit of other program users. In a short period of time over 5,000 programs were accepted and made available. This overwhelming response indicated the value of the program library and a Users' Library was then established for the HP-67/97 users.

To extend the value of the Users' Library, Hewlett-Packard is introducing a unique service—a service designed to save you time and money. The Users' Library has collected the best programs in the most popular categories from the HP-67/97 and HP-65 Libraries. These programs have been packaged into a series of low-cost books, resulting in substantial savings for our valued HP-67/97 users.

We feel this new software service will extend the capabilities of our programmable calculators and provide a great benefit to our HP-67/97 users.

A WORD ABOUT PROGRAM USAGE

Each program contained herein is reproduced on the standard forms used by the Users' Library. Magnetic cards are not included. The Program Description I page gives a basic description of the program. The Program Description II page provides a sample problem and the keystrokes used to solve it. The User Instructions page contains a description of the keystrokes used to solve problems in general and the options which are available to the user. The Program Listing I and Program Listing II pages list the program steps necessary to operate the calculator. The comments, listed next to the steps, describe the reason for a step or group of steps. Other pertinent information about data register contents, uses of labels and flags and the initial calculator status mode is also found on these pages. Following the directions in your HP-67 or HP-97 **Owners' Handbook and Programming Guide,** "Loading a Program" (page 134, HP-67; page 119, HP-97), key in the program from the Program Listing I and Program Listing II pages. A number at the top of the Program Listing indicates on which calculator the program was written (HP-67 or HP-97). If the calculator indicated differs from the calculator you will be using, consult Appendix E of your **Owner's Handbook** for the corresponding keycodes and keystrokes converting HP-67 to HP-97 keycodes and vice versa. No program conversion is necessary. The HP-67 and HP-97 are totally compatible, but some differences do occur in the keycodes used to represent some of the functions.

A program loaded into the HP-67 or HP-97 is not permanent—once the calculator is turned off, the program will not be retained. You can, however, permanently save any program by recording it on a blank magnetic card, several of which were provided in the Standard Pac that was shipped with your calculator. Consult your **Owner's Handbook** for full instructions. A few points to remember:

> The Set Status section indicates the status of flags, angular mode, and display setting. After keying in your program, review the status section and set the conditions as indicated before using or permanently recording the program.
>
> REMEMBER! To save the program permanently, **clip** the corners of the magnetic card once you have recorded the program. This simple step will protect the magnetic card and keep the program from being inadvertently erased.

As a part of HP's continuing effort to provide value to our customers, we hope you will enjoy our newest concept.

TABLE OF CONTENTS

DEMOGRAPHY I: ESTIMATES OF PARAMETERS/RATES OF INCREASE 1

Computes estimates of generation time and the intrinsic rate of natural increase, r, for up to seven reproductive age classes.

DEMOGRAPHY II: EXPECTATION OF LIFE AND REPRODUCTIVE VALUE 7

Computes expectation of life, age-specific reproductive value, net reproductive rate, finite rate of increase, and generation time.

DIVERSITY AND EQUITABILITY INDICES 11

Computes diversity index as described by Wilhm and Dorris (1968) and the equitability index as described by Peet (1974).

NICHE BREADTH AND OVERLAP/SHANNON'S H AND HORN'S RO. 15

Computes niche breadths from Simpson's diversity index, niche overlap from Pianka's overlap index, Shannon's information theoretic index of diversity for two communities, and Horn's overlap index.

POPULATION SIZE ESTIMATE (JOLLY'S ESTIMATE). 22

Computes estimated population size, N, and the standard error of this estimate from capture-recapture data by Jolly's (1965) method.

CELL PHASE AND CYCLE TIMES 26

Computes the amount of time spent by randomly dividing cells in G1,S, G2, and M phases and the cell cycle time (doubling time).

CROSSOVER: LOCATION/PRODUCTS 31

Computes the number and location of crossovers which must occur to produce a given progeny chromatid and also the progeny chromatid resulting from single or multiple crossovers of the given parental chromatid.

CHROMOSOME CLEAVAGE. 37

Simulates chromosomal cleavage to analyze chromosome models.

RECESSIVE GENE FREQUENCY AFTER SELECTION, MUTATION, AND INBREEDING 41

Two models: one computes recessive gene frequency after selection & mutation; the other computes recessive gene frequency after selection, mutation, & inbreeding.

SELECTION AND GENE FREQUENCY 47

Calculates the equilibrium recessive gene frequency and the recessive gene frequency after the desired number of generations.

GENETIC INFERENCE FROM TRUNCATE DATA 51

Computes the proportion of affected offspring, the goodness of fit of the assumption made, and the probability that any deviation between observed and expected values of affected offspring would arise by chance alone.

POSITIVE ASSORTATIVE MATING FOR A RECESSIVE PHENOTYPE 55

Computes recessive phenotype frequency and positive assortative mating equilibrium values.

Program Description I

Program Title DEMOGRAPHY: Estimates of Parameters/Rates of Increase

Contributor's Name Hewlett-Packard Company

Address 1000 N.E. Circle Boulevard

City Corvallis **State** Oreogn **Zip Code** 97330

Program Description, Equations, Variables Generation time is estimated using the formula:

$$\hat{T} \cong \frac{\sum_{\alpha}^{\omega} x l_x m_x}{R_o}$$

where x is age, l_x is the fractional survivorship to that age from age class zero, m_x is the fecundity at age x, and R_o is the net reproductive rate, computed from the equation

$$R_o = \sum_{\alpha}^{\omega} l_x m_x$$

In both equations α is the age of first reproduction, and ω is the age of last reproduction. Any number of non-reproductive age classes is allowed, by simply keying in a constant, k, that is added to each age of reproduction internally by the program. This program is designed for use with another (next), which computes much more accurate estimates of the intrinsic rate of increase by an iterative process. This program estimates the intrinsic rate of increase, r, using the following approximate relationship:

$$\hat{r} \cong \frac{\log_e R_o}{T}$$

Using the estimate of r stored in R_8, and the products of the age-specific survivorship and fecundity schedules stored in registers 1 through 7, the program computes the sum

$$\sum_{x=\alpha}^{\omega} e^{-rx} l_x m_x$$

(Continued on next page)

Operating Limits and Warnings Only seven reproductive age classes are allowed and a constant, k, indicates the number of non-reproductive age classes.

Program Description I

Program Title

Contributor's Name

Address

City **State** **Zip Code**

Program Description, Equations, Variables where α is the age of first reproduction ($l_\alpha m_\alpha$ is stored in R_1) and ω is the age of last reproduction. This sum should be unity if the estimate of r is good. The program compares the sum with 1.00 and if it is too large the estimate of r is decreased (if the sum is too small, the estimate of r is increased). The program then stores this new r in R_8 and recalculates the new sum, which is compared with 1.00 again as before. The process is continued until the sum is unity (to two decimal places) and then the program terminates and displays the intrinsic rate of increase. Each loop requires about 10 seconds of calculator (computer?) time, and some parameter sets may take up to about 2 minutes before r is displayed.

The program also displays the finite rate of increase, λ, which is simply e^r.

If the user thinks the program is taking too long to compute r, it can be stopped with the "CLx" button and R_8 recalled to see what value of r was being used in the last loop.

Operating Limits and Warnings

Program Description II

SAMPLE PROBLEM: A population has the following schedules of age-specific survivorship and fecundity:

Age (x)	Survivorship (l_x)	Fecundity (m_x)
0	1.0	0.0
1	.9	0.0
2	.7	0.0
3	.5	0.0
4 (α)	.4	1.0
5	.3	1.0
6	.2	1.5
7	.2	1.0
8	.1	1.0
9	.1	0.5
10 (ω)	.01	1.0

1. Compute the net reproductive rate, R_o, of this population and estimate its mean generation time, $\hat{T}$, and intrinsic rate of natural increase, $\hat{r}$.

   Note that the data needed to compute these demographic parameters are contained entirely in the last seven (reproductive) age classes. Therefore, data are keyed in beginning with age class 4, which is the age of first reproduction. In this example k = 3. Data above the dashed line may be used with the next program in this series to compute demographic parameters for non-reproductive age classes, such as expectation of life and reproductive value.

2. Calculate the intrinsic rate of increase and the finite rate of increase for the same population.

Solution(s)

$R_o = 1.36$

$\hat{T} = 5.625$

$\hat{r} = .3594$ (an overestimate)

```
1.  .4[ENTER ↑] 1 [ENTER ↑] .3 [ENTER ↑] 1 [A]
    .2[ENTER ↑] 1.5[ENTER ↑] .2 [ENTER ↑] 1 [B]
    .1[ENTER ↑] 1 [ENTER ↑] .1 [ENTER ↑] .5 [C]
    .01[ENTER ↑] 1 [ENTER ↑] 3 [D] [E]  → 5.6250
                               [R/S]  → 0.3594
                           [RCL] [9]  → 1.3600

2.  [f] [A]  →  .0552 (r)
    [f] [B]  → 1.0568 (λ)
```

Reference(s)

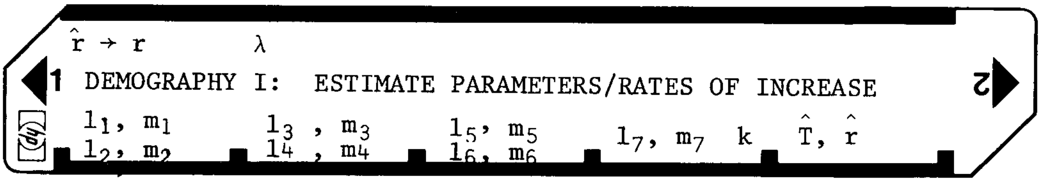
Mertz, D.B. 1970. Notes on methods used in life-history studies. pp.4-17 in Connell, Mertz, and Murdoch's "Readings in ecology and ecological genetics." Harper & Row, New York, 397 p.

Pianka, E.R. 1974. Evolutionary ecology. Harper & Row. 356 pp.

Poole, R.W. 1974. An introduction to quantitative ecology. McGraw-Hill.

This program is a modification of the Users' Library Programs #03637A and #03638A submitted by Eric R. Pianka.

User Instructions



STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS		OUTPUT DATA/UNITS
1	Load side 1 and side 2				
2	Enter data as shown for Survivorship/Fecundity	l_1	ENT		
		m_1	ENT		
		l_2	ENT		
		m_2	A		
		l_3	ENT		
		m_3	ENT		
		l_4	ENT		
		m_4	B		
		l_5	ENT		
		m_5	ENT		
		l_6	ENT		
		m_6	C		
		l_7	ENT		
		m_7	ENT		
	Enter age constant k	k	D		
3	Compute $\hat{T}$		E		$\hat{T}$
4	Compute $\hat{r}$		R/S		$\hat{r}$
5	Recall R_o from R_9		RCL	9	R_o
6	Iterate the solution of r		f	A	r
7	Compute the finite rate of increasing λ		f	B	λ

97 Program Listing I

STEP	KEY ENTRY	KEY CODE	COMMENTS
001	*LBLA	21 11	Data entry
002	×	-35	
003	STO2	35 02	
004	R↓	-31	
005	×	-35	
006	STO1	35 01	
007	RTN	24	
008	*LBLB	21 12	
009	×	-35	
010	STO4	35 04	
011	R↓	-31	
012	×	-35	
013	STO3	35 03	
014	RTN	24	
015	*LBLC	21 13	
016	×	-35	
017	STO6	35 06	
018	R↓	-31	
019	×	-35	
020	STO5	35 05	
021	RTN	24	
022	*LBLD	21 14	
023	STO8	35 08	
024	STO0	35 00	
025	R↓	-31	
026	×	-35	
027	STO7	35 07	
028	RTN	24	
029	*LBLE	21 15	
030	DSP4	-63 04	
031	RCL1	36 01	
032	RCL2	36 02	
033	RCL3	36 03	
034	RCL4	36 04	
035	+	-55	
036	+	-55	
037	+	-55	
038	RCL5	36 05	
039	RCL6	36 06	
040	RCL7	36 07	
041	+	-55	
042	+	-55	
043	+	-55	
044	STO9	35 09	
045	RCL1	36 01	
046	1	01	
047	RCL8	36 08	
048	+	-55	
049	×	-35	
050	RCL2	36 02	
051	2	02	
052	RCL8	36 08	
053	+	-55	
054	×	-35	
055	+	-55	
056	RCL3	36 03	

STEP	KEY ENTRY	KEY CODE	COMMENTS
057	3	03	
058	RCL8	36 08	
059	+	-55	
060	×	-35	
061	+	-55	
062	RCL4	36 04	
063	4	04	
064	RCL8	36 08	
065	+	-55	
066	×	-35	
067	+	-55	
068	RCL5	36 05	
069	5	05	
070	RCL8	36 08	
071	+	-55	
072	×	-35	
073	+	-55	
074	RCL6	36 06	
075	6	06	
076	RCL8	36 08	
077	+	-55	
078	×	-35	
079	+	-55	
080	RCL7	36 07	
081	7	07	
082	RCL8	36 08	
083	+	-55	
084	×	-35	
085	+	-55	
086	RCL9	36 09	
087	÷	-24	
088	R/S	51	Display $\hat{T}$
089	X⇄Y	-41	
090	LN	32	
091	X⇄Y	-41	
092	÷	-24	
093	STO8	35 08	Store $\hat{r}$ in R_8
094	RTN	24	Display $\hat{r}$
095	*LBLa	21 16 11	
096	1	01	
097	GSB0	23 00	
098	RCL1	36 01	
099	×	-35	
100	2	02	
101	GSB0	23 00	
102	RCL2	36 02	
103	×	-35	
104	+	-55	
105	3	03	
106	GSB0	23 00	
107	RCL3	36 03	
108	×	-35	
109	+	-55	
110	4	04	
111	GSB0	23 00	
112	RCL4	36 04	

REGISTERS

0	1	2	3	4	5	6	7	8	9
	$l_\alpha m_\alpha$	$l_{\alpha+1}m_{\alpha+1}$	$l_{\alpha+2}m_{\alpha+2}$	$l_{\alpha+3}m_{\alpha+3}$	$l_{\alpha+4}m_{\alpha+4}$	$l_{\alpha+5}m_{\alpha+5}$	$l_\omega m_\omega$	k, $\hat{r}$	R_o

S0	S1	S2	S3	S4	S5	S6	S7	S8	S9

A	B	C	D	E	I

97 Program Listing II

STEP	KEY ENTRY	KEY CODE	COMMENTS
113	×	-35	
114	+	-55	
115	5	05	
116	GSB0	23 00	
117	RCL5	36 05	
118	×	-35	
119	+	-55	
120	6	06	
121	GSB0	23 00	
122	RCL6	36 06	
123	×	-35	
124	+	-55	
125	7	07	
126	GSB0	23 00	
127	RCL7	36 07	
128	×	-35	
129	+	-55	Note: insertion of an "R/S" here will stop each loop and display the sum for user's inspection (hit R/S to continue)
130	ENT↑	-21	
131	ENT↑	-21	
132	1	01	
133	0	00	
134	0	00	
135	ENT↑	-21	
136	R↓	-31	
137	×	-35	
138	INT	16 34	
139	R↑	16-31	
140	X=Y?	16-33	
141	GTO1	22 01	
142	R↓	-31	
143	R↓	-31	
144	1	01	
145	-	-45	
146	.	-62	
147	2	02	
148	×	-35	
149	RCL8	36 08	
150	+	-55	
151	STO8	35 08	
152	GTOa	22 16 11	
153	*LBL1	21 01	
154	RCL8	36 08	
155	RTN	24	
156	*LBL0	21 00	
157	RCL0	36 00	Age constant k
158	+	-55	
159	RCL8	36 08	
160	×	-35	
161	CHS	-22	
162	e^x	33	
163	RTN	24	
164	*LBLb	21 16 12	
165	e^x	33	
166	RTN	24	Display $\hat{\lambda}$
167	R/S	51	

STEP	KEY ENTRY	KEY CODE	COMMENTS
170			
180			
190			
200			
210			
220			

LABELS

A l_1 ↑ m_1↑ l_2 ↑ m_2↑	B l_3 ↑ m_3 ↑ l_4 ↑ m_4 ↑	C l_5 ↑ m_5 ↑ l_6 ↑ m_6 ↑	D l_7 ↑ m_7 ↑ k	E $\hat{T}$, $\hat{r}$
a $r \to r$	b λ	c	d	e
0	1 used	2	3	4
5	6	7	8	9

FLAGS

0
1
2
3

SET STATUS

FLAGS	ON	OFF	TRIG		DISP	
0	☐	☒	DEG	☒	FIX	☒
1	☐	☒	GRAD	☐	SCI	☐
2	☐	☒	RAD	☐	ENG	☐
3	☐	☒			n 2	

Program Description I

Program Title DEMOGRAPHY: Expectation of Life and Reproductive Value

Contributor's Name Hewlett-Packard Company

Address 1000 N.E. Circle Boulevard

City Corvallis **State** Oregon **Zip Code** 97330

Program Description, Equations, Variables After storing the intrinsic rate of increase r, in register 1, the user enters age (x), age-specific survivorship (l_x), and age-specific fecundity (m_x) sequentially, beginning with the <u>oldest</u> age class and working toward the youngest age class. User-defined key "C" is punched for each age class and the expectation of further life, E_x, is displayed as computed from the equation:

$$E_x = \frac{\sum_{y=x}^{\infty} l_y}{l_x}$$

Fisher's reproductive value is computed from the equation:

$$v_x = \frac{e^{rx}}{l_x} \sum_{t=x}^{\infty} e^{-rt} l_t \, m_t$$

After all age classes have been entered and E_x and v_x for each has been computed and recorded, User-defined key D computes the net reproductive rate, R_o, and the finite rate of increase, λ, from the equations

$$R_o = \sum_{\alpha}^{\omega} l_x m_x \quad \text{and} \quad \lambda = e^r$$

Generation time is computed with the approximate formula:

$$\hat{T} = \frac{\sum_{\alpha}^{\omega} x l_x m_x}{R_o}$$

(α is age of first reproduction and ω is the age of last reproduction.)

Operating Limits and Warnings Register 8 stores a sum that is used in each computation of v_x; hence an error in data entry at any age will throw off all subsequent computations for younger age groups.

Program Description II

Sketch(es)

Sample Problem(s) Compute expectation of life and Fisher's reproductive value for each age group in a population with the following schedules of age-specific survivorship and fecundity:

{the intrinsic rate of natural increase is known to be .0552}

Age (x)	Survivorship (l_x)	Fecundity (m_x)
0	1.0	0
1	.9	0
2	.7	0
3	.5	0
4	.4	1
5	.3	1
6	.2	1.5
7	.2	1
8	.1	1
9	.1	0.5
10	.01	1

Also calculate net reproductive rate, the finite rate of increase and mean generation time.

Solution(s) .0552 [A] 10 [ENTER ↑] .01 [ENTER ↑] 1 [B] → 10; [C]→1.000;[R/S]→1.000
9[ENTER ↑] .1[ENTER ↑] .5[B] → 9; [C] → 1.100; [R/S] → 0.595
Repeat for 8 thru 0 to obtain values in table

$E_0 = 4.41$, $v_0 = 1.000$
$E_1 = 3.79$, $v_1 = 1.174$
$E_2 = 3.59$, $v_2 = 1.595$
$E_3 = 3.62$, $v_3 = 2.361$
$E_4 = 3.28$, $v_4 = 3.118$
$E_5 = 3.03$, $v_5 = 2.985$
$E_6 = 3.05$, $v_6 = 3.146$
$E_7 = 2.05$, $v_7 = 1.739$
$E_8 = 2.10$, $v_8 = 1.563$
$E_9 = 1.10$, $v_9 = 0.595$
$E_{10} = 1.00$, $v_{10} = 1.000$

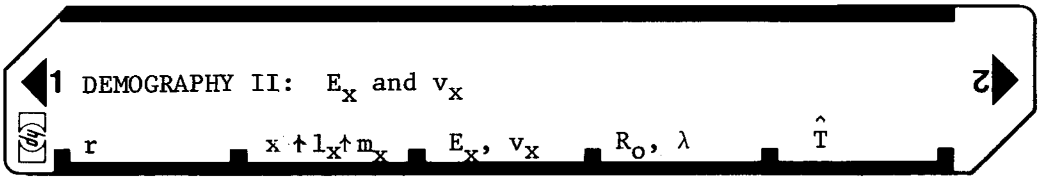
[D] → 1.3600 (R_o)
[R/S] → 1.0568 (λ)
[E] → 5.625 ($\hat{T}$)

Reference(s)

Fisher, R.A. 1930. The genetical theory of natural selection. Oxford.
Mertz, D.B. 1970. Notes on methods used in life-history studies, pp 4-17 in Connell, Mertz, and Murdoch's "Readings in ecology and ecological genetics." Harper & Row.
Pianka, E.R. 1974. Evolutionary ecology. Harper & Row.
Poole, R.W. 1974. An introduction to quantitative ecology. McGraw-Hill.
Wilson, E.O. and W. Bossert. 1971. A primer of population biology. Sinauer.

This program is a translation of the HP-65 Users' Library Program #03639A submitted by Eric R. Pianka.

User Instructions



STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS		OUTPUT DATA/UNITS
1	Read program (in "run" mode!)				
2	Enter intrinsic rate of increase in R_1	r	A		
3	Key in age (x) of oldest age group first	x	↑		
4	Key in survivorship of oldest age group, (l_x) first	l_x	↑		
5	Key in fecundity of oldest age group (m_x) first	m_x	B		(x)
6	Compute and record expectation of life, E_x		C		E_x
7	Compute and record reproductive value, v_x		R/S		v_x
8	Repeat steps 3 through 7 for next oldest age until all age classes have been entered and a complete sequence of values have been obtained for E_x and v_x for all ages.				x E_x v_x
9	Calculate net reproductive rate, R_o		D		R_o
10	Calculate finite rate of increase, λ		R/S		λ
11	Compute estimate of mean generation time, $\hat{T}$		E		$\hat{T}$

97 Program Listing I

STEP	KEY ENTRY	KEY CODE	COMMENTS
001	*LBLA	21 11	
002	CLRG	16-53	Clear registers
003	STO1	35 01	Store r in R_1
004	RTN	24	
005	*LBLB	21 12	
006	DSP3	-63 03	
007	STO4	35 04	Store m_x in R_4
008	X⇄Y	-41	
009	STO3	35 03	Store l_x in R_3
010	×	-35	
011	RCL7	36 07	
012	+	-55	
013	STO7	35 07	
014	R↓	-31	
015	STO2	35 02	Store x in R_2
016	RCL1	36 01	
017	×	-35	
018	STO5	35 05	
019	RCL6	36 06	
020	RCL3	36 03	
021	+	-55	
022	STO6	35 06	
023	RCL2	36 02	
024	RCL3	36 03	
025	RCL4	36 04	
026	×	-35	
027	×	-35	
028	RCL9	36 09	
029	+	-55	
030	STO9	35 09	
031	RCL2	36 02	Display age x
032	RTN	24	
033	*LBLC	21 13	
034	RCL6	36 06	
035	RCL3	36 03	
036	÷	-24	
037	R/S	51	Display E_x
038	RCL5	36 05	
039	CHS	-22	
040	e^x	33	
041	RCL3	36 03	
042	×	-35	
043	RCL4	36 04	
044	×	-35	
045	RCL8	36 08	
046	+	-55	
047	STO8	35 08	
048	RCL5	36 05	
049	e^x	33	
050	RCL3	36 03	
051	÷	-24	
052	×	-35	
053	RTN	24	Display v_x
054	*LBLD	21 14	
055	DSP4	-63 04	
056	RCL7	36 07	
057	R/S	51	Display R_o
058	RCL1	36 01	
059	e^x	33	
060	RTN	24	Display λ
061	*LBLE	21 15	
062	RCL9	36 09	
063	RCL7	36 07	
064	÷	-24	
065	R/S	51	Display $\hat{T}$
066	RCL7	36 07	
067	LN	32	
068	RCL1	36 01	
069	÷	-24	
070	RTN	24	Display T
071	R/S	51	
080			
090			
100			
110			

SET STATUS

FLAGS	ON	OFF	TRIG		DISP	
0	☐	☒	DEG	☒	FIX	☒
1	☐	☒	GRAD	☐	SCI	☐
2	☐	☒	RAD	☐	ENG	☐
3	☐	☒			n 2	

REGISTERS

0	1	2	3	4	5	6	7	8	9
	r	x	l_x	m_x	rx	Σl_x	$\Sigma l_x m_x$	$\Sigma^{-rx} l_x m_x$	$\Sigma x l_x m_x$
S0	S1	S2	S3	S4	S5	S6	S7	S8	S9

A	B	C	D	E	I

Program Description I

Program Title DIVERSITY AND EQUITABILITY INDICES

Contributor's Name Hewlett-Packard Company

Address 1000 N.E. Circle Boulevard

City Corvallis **State** Oregon **Zip Code** 97330

Program Description, Equations, Variables

Given a data set:

$$\{n_1, n_2, n_3, \ldots n_i\}$$

The program computes the following:

$$\text{Diversity} = 3.3219 \left(\log_{10} N - \frac{1}{N} \Sigma n_i \log_{10} n_i\right)$$

$$\text{Equitability} = \frac{\text{Diversity}}{3.3219 (\log_{10} N)}$$

Where:

n_i = number of individuals of the i th group

N = total number of individuals in the collection

3.3219 = conversion factor $\log_{10}$ to $\log_2$

Operating Limits and Warnings

n is a positive interger and $n \geq 1$.

Program Description II

Sketch(es)

Sample Problem(s)

Compute diversity and equitability for the following data:

{ 740; 11,000; 920; 180; 180; 740; 180}

Solution(s)

[A] 740 [B] 11,000 [B] 920 [B] 180 [B] 180 [B]740 [B] 180 [B]

[D] 1.22

[E] 0.09

Reference(s)

Wilhm, J.L. and Dorris, T.C., 1968, Biological parameters for water quality criteria: Bioscience, v. 18, p. 477-481.

Peet, R.K., 1974, The measurement of species diversity: Annual Review of Ecology and Systematics, v. 5, p. 285-307.

This program is a modification of the Users' Library Program # 04754A submitted by W. Thomas Shoaf.

User Instructions

1 DIVERSITY AND EQUITABILITY INDEX 2

A	B	C	D	E
Initial	data	correct	diver	equit

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS		OUTPUT DATA/UNITS
1	Enter program				
2	Initialize		A		
3	Perform step 3 for i = 1, 2, ...x	n_i	B		i
	(number of individuals of the i th group)				
4	To correct entry	n_i	C		i-1
5	Compute diversity		D		diversity
6	Compute equitability		E		equitabiity
	(For a new case go to step 2)				

97 Program Listing I

STEP	KEY ENTRY	KEY CODE	COMMENTS	STEP	KEY ENTRY	KEY CODE	COMMENTS
001	*LBLA	21 11	Initialize, press A				
002	CLRG	16-53					
003	RTN	24					
004	*LBLB	21 12	No. individuals in	060			
005	STO6	35 06	ith group,				
006	ST+2	35-55 02	N = S + N				
007	LOG	16 32					
008	RCL6	36 06					
009	x	-35	X = S * log(s)				
010	ST+3	35-55 03	Z = X + Z				
011	1	01					
012	ST+9	35-55 09					
013	RCL9	36 09					
014	RTN	24		070			
015	*LBLD	21 14	Diversity				
016	RCL3	36 03	Z/N				
017	RCL2	36 02					
018	÷	-24					
019	STO4	35 04					
020	RCL2	36 02					
021	LOG	16 32					
022	RCL4	36 04					
023	-	-45	Log (N)-(Z/N)				
024	3	03		080			
025	.	-62					
026	3	03					
027	2	02					
028	1	01					
029	9	09					
030	STO1	35 01					
031	x	-35	3.3219*[log(N)-(Z/N)				
032	RTN	24					
033	*LBLE	21 15	Equitability				
034	STO7	35 07		090			
035	RCL2	36 02					
036	LOG	16 32					
037	RCL1	36 01					
038	x	-35					
039	STO8	35 08					
040	RCL7	36 07					
041	RCL8	36 08					
042	÷	-24					
043	RTN	24					
044	*LBLC	21 13	Correct	100			
045	STO6	35 06					
046	ST-2	35-45 02					
047	LOG	16 32					
048	RCL6	36 06					
049	x	-35					
050	ST-3	35-45 03					
051	1	01					
052	ST-9	35-45 09					
053	RTN	24					
054	R/S	51		110			

SET STATUS

FLAGS	ON	OFF	TRIG		DISP	
0	☐	☒	DEG	☒	FIX	☒
1	☐	☒	GRAD	☐	SCI	☐
2	☐	☒	RAD	☐	ENG	☐
3	☐	☒			n 2	

REGISTERS

0	1	2	3	4	5	6	7	8	9
	Used	ΣS	ΣSlogS	Used		S	Used	Used	i

S0	S1	S2	S3	S4	S5	S6	S7	S8	S9

A	B	C	D	E	I

Program Description I

Program Title NICHE BREADTH AND OVERLAP AND SHANNON'S H AND HORN'S R_o

Contributor's Name Hewlett-Packard Company

Address 1000 N.E. Circle Boulevard

City Corvallis **State** Oregon **Zip Code** 97330

Program Description, Equations, Variables Given resource utilization vectors for two species, this program computes niche breadths for both species using Simpson's diversity equation:

$$B = \frac{1}{\sum_{i}^{n} p_i^2}$$

where the p_i are the proportion of the ith resource used and n is the total number of resources.

Thus computed, B varies from 1/n to n, and can be standardized as a fraction of the maximal possible value, B_{max}, which is equal to n, by dividing by n.

Overlap is computed using Pianka's (1974) formula:

$$O = \frac{\Sigma\, p_i\, q_i}{\sqrt{\Sigma p_i^2\ \Sigma q_i^2}}$$

where the sums are over all i from one to n, p_i and q_i are the proportional use values of resource i by species A and B, respectively. Thus computed, overlap varies from zero to one. For some purposes, the Arc sine of this value, which varies from 0° to 90°, is useful.

Given two vectors of proportional relative importance, p_i and q_i, this program computes Shannon's information theoretic index of diversity for each, according

(Continued on next page)

Operating Limits and Warnings None; zero entries are permitted.

Program Description I

Program Title

Contributor's Name

Address

City **State** **Zip Code**

Program Description, Equations, Variables

to the formula:

$$H_p = -\Sigma p_i \mathrm{Ln} p_i \text{ or } -\Sigma q_i \text{ LN } q_i. = H_q$$

Each H is expressed both as an absolute value and as a "J" value, which is a fraction of the maximal possible H value, H_{max}.

The program also computes Horn's (1966) measure of overlap, R_o, from a simplified computational formula:

$$\text{Overlap} = R_o = \frac{((H_p + H_q)/2) - H_r}{\text{Ln } 2} + 1$$

where H_r is computed from the p_i and q_i vectors, with $r_i = (p_i + q_i)/2$ according to Shannon's formula (above). H_r is stored in register 6.

Operating Limits and Warnings

Program Description II

Sketch(es)

Sample Problem(s) 1. Two species (or individuals or populations or other organismic units) use four resources (microhabitats, foods, or whatever) in the following proportions:

	Resource 1	Resource 2	Resource 3	Resource 4
Species A	0.2	0.5	0.1	0.2
Species B	0.3	0.1	0.4	0.2

2. Two communities have a total of five species in the following proportional relative abundances (or importances);

	Community A	Community B
Species 1	.1	0.00
Species 2	.2	.4
Species 3	0.0	.2
Species 4	.5	.1
Species 5	.2	.3

What is the diversity of each and how much do they overlap?

Solution(s) 1. a. Initialize (zero all registers): [CL REG]

b. Key in p_i, q_i data as follows:

0.2 [↑] 0.3 [A]
0.5 [↑] 0.1 [A]
0.1 [↑] 0.4 [A]
0.2 [↑] 0.2 [A]

c. Compute niche breadths: [B] 2.94 [R/S] 0.74 (B_p/n)
[R/S] 3.33 [R/S] 0.83 (B_q/n)

d. Compute niche overlap: [C] 0.59, Arc sine: [R/S] 36.2

e. Check Sums of p_i, q_i: [D] 1.00, [R/S] 1.00

(Continued on next page)

Reference(s)

Simpson, E.H. 1949. Measurement of diversity. Nature 163: 688.
Pianka, E.R. 1974. Niche overlap and diffuse competition. Proc. Nat. Acad. Sci., USA 71: 2141-2145.
May, R.M. 1975. Some notes on measurements of the competition matix, α. Ecology 56: in press.

Program Description II

Sketch(es)

Sample Problem(s)

Solution(s) 2. a. Initialize (zero all registers): [CL REG]

b. Key in the five sets of p_i and q_i data, letting i run from 1 to 5:

0.1 [↑] 0.0 [f] [A]
0.2 [↑] 0.4 [f] [A]
0.0 [↑] 0.2 [f] [A]
0.5 [↑] 0.1 [f] [A]
0.2 [↑] 0.3 [f] [A]

c, Compute diversity of community A (H_p) : [f][B] 1.28, [R/S] 0.80(H/H_{max})
d. Compute diversity of community B (H_q): [f][C] 1.22, [R/S] 0.76(H/H_{max})
e. Compute community overlap, R_o [f][D] 0.71

Reference(s)

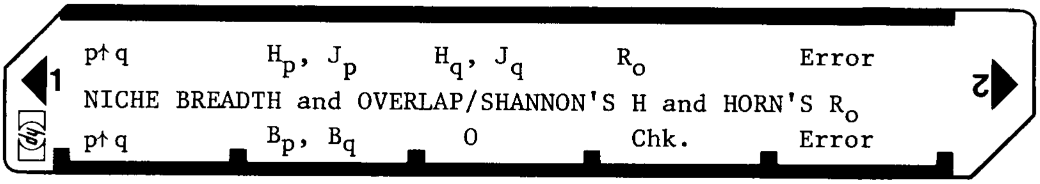
Shannon, C.E. and W. Weaver, 1949. The mathematical theory of communicatio Univ. Illinois Press, Urbana.

Horn, H.S., 1966. Measurement of "overlap" in comparative ecological studies. Amer. Naturalist 100: 419-424.

Lloyd, M.J.H.Zar, and J. Karr. 1968. On the calculation of information theoretical measures of diversity. Amer. Midlan Naturalist 79: 257-272.

This program is a modification of the Users' Library Programs # 02158A & #03150A submitted by Eric R. Pianka.

User Instructions



STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS		OUTPUT DATA/UNITS
1	Enter program				
2	Initialize (zero registers)			CL REG	
3	For niche breadth and overlap, go to step 4.				
	For Shannon's H and Horn's R_o, to to step 9.				
4	Enter pairs of data, p_i, [ENTER↑] ↕ repeat til	p_i	↑		
	then q_i finished	q_i	A		
5	To remove erroneous data pairs, p_i [ENTER↑]	p_i	↑		
	q_i	q_i	E		
6	After all n data pairs have been entered,				
	compute niche breadth for first species		B		B_p
	compute its standardized niche breadth		R/S		B_p/n
	compute niche breadth for second species		R/S		B_q
	compute its standardized niche breadth		R/S		B_q/n
7	Compute niche overlap		C		0
	compute Arc sin of overlap		R/S		Arc sin(0)
8	Check sum of p_i to see if it is unity		D		Σp_i
	check sum of q_i to see if it is unity		R/S		Σq_i
9	Enter data pairs	p_i		↑	
		q_i	f	A	
	repeat 9 until all pairs of data are entered				
10	To remove erroneous data pairs, p_i [ENTER↑]	p_i	ENT↑		
	q_i	q_i	f	E	
11	Compute diviersity H_p		f	B	$-\Sigma p_i LNp_i$
12	Compute J (H/H_{max})			R/S	H_p/H_{max}
13	Compute diversity H_q		f	C	$-\Sigma q_i LNq_i$
14	Compute J (H/H_{max})			R/S	H_q/H_{max}
15	Calculate overlap R_o		f	D	R_o

97 Program Listing I

STEP	KEY ENTRY	KEY CODE	COMMENTS
001	*LBLA	21 11	p ↑ q
002	STO7	35 07	
003	ST+4	35-55 04	
004	X²	53	
005	ST+5	35-55 05	
006	X⇄Y	-41	
007	ST+2	35-55 02	
008	X²	53	
009	ST+3	35-55 03	
010	LSTX	16-63	
011	RCL7	36 07	
012	×	-35	
013	ST+6	35-55 06	
014	1	01	
015	ST+1	35-55 01	
016	RCL1	36 01	
017	RTN	24	
018	*LBLB	21 12	B_p, B_q
019	RCL3	36 03	
020	1/X	52	
021	R/S	51	
022	RCL1	36 01	
023	÷	-24	
024	R/S	51	
025	RCL5	36 05	
026	1/X	52	
027	R/S	51	
028	RCL1	36 01	
029	÷	-24	
030	RTN	24	
031	*LBLC	21 13	0
032	RCL3	36 03	
033	RCL5	36 05	
034	×	-35	
035	√X	54	
036	RCL6	36 06	
037	X⇄Y	-41	
038	÷	-24	
039	R/S	51	
040	SIN⁻¹	16 41	Takes Arc sin of 0
041	RTN	24	
042	*LBLE	21 15	Error
043	STO7	35 07	
044	ST-4	35-45 04	
045	X²	53	
046	ST-5	35-45 05	
047	X⇄Y	-41	
048	ST-2	35-45 02	
049	X²	53	
050	ST-3	35-45 03	
051	LSTX	16-63	
052	RCL7	36 07	
053	×	-35	
054	ST-6	35-45 06	
055	1	01	
056	ST-1	35-45 01	

STEP	KEY ENTRY	KEY CODE	COMMENTS
057	RCL1	36 01	
058	RTN	24	
059	*LBLD	21 14	Chk.
060	RCL2	36 02	
061	R/S	51	
062	RCL4	36 04	
063	RTN	24	
064	*LBLa	21 16 11	p ↑ q
065	STO7	35 07	
066	X⇄Y	-41	
067	STO8	35 08	
068	ST+4	35-55 04	
069	0	00	
070	X=Y?	16-33	
071	GTO1	22 01	
072	R↓	-31	
073	ENT↑	-21	
074	LN	32	
075	×	-35	
076	ST-5	35-45 05	
077	*LBL1	21 01	
078	RCL7	36 07	
079	ST+2	35-55 02	
080	0	00	
081	X=Y?	16-33	
082	GTO2	22 02	
083	R↓	-31	
084	ENT↑	-21	
085	LN	32	
086	×	-35	
087	ST-3	35-45 03	
088	*LBL2	21 02	
089	RCL8	36 08	
090	RCL7	36 07	
091	+	-55	
092	2	02	
093	÷	-24	
094	0	00	
095	X=Y?	16-33	
096	GTO3	22 03	
097	R↓	-31	
098	ENT↑	-21	
099	LN	32	
100	×	-35	
101	ST-6	35-45 06	
102	*LBL3	21 03	
103	1	01	
104	ST+1	35-55 01	
105	RCL1	36 01	
106	RTN	24	
107	*LBLb	21 16 12	H_p, J_p
108	RCL3	36 03	
109	R/S	51	
110	RCL1	36 01	
111	LN	32	
112	STO7	35 07	

REGISTERS

0	1 n n	2 Σp_i Σq_i	3 Σp_i^2 $-\Sigma q_i LNq_i$	4 Σq_i Σp_i	5 Σq_i^2 $-\Sigma p_i LNp_i$	6 $\Sigma p_i q_i$ $-\Sigma r_i LNr_i$	7 Used last q_i	8 last p_i	9
S0	S1	S2	S3	S4	S5	S6	S7	S8	S9

A	B	C	D	E	I

97 Program Listing II

STEP	KEY ENTRY	KEY CODE	COMMENTS
113	÷	-24	
114	RTN	24	
115	*LBLc	21 16 13	H_q, J_q
116	RCL5	36 05	
117	R/S	51	
118	RCL7	36 07	
119	÷	-24	
120	RTN	24	
121	*LBLd	21 16 14	R_o
122	RCL3	36 03	
123	RCL5	36 05	
124	+	-55	
125	2	02	
126	÷	-24	
127	RCL6	36 06	
128	-	-45	
129	2	02	
130	LN	32	
131	÷	-24	
132	1	01	
133	+	-55	
134	RTN	24	
135	*LBLe	21 16 15	Error
136	STO7	35 07	
137	X⇄Y	-41	
138	STO8	35 08	
139	ST-4	35-45 04	
140	0	00	
141	X=Y?	16-33	
142	GTO4	22 04	
143	R↓	-31	
144	ENT↑	-21	
145	LN	32	
146	×	-35	
147	ST+5	35-55 05	
148	*LBL4	21 04	
149	RCL7	36 07	
150	ST-2	35-45 02	
151	0	00	
152	X=Y?	16-33	
153	GTO5	22 05	
154	R↓	-31	
155	ENT↑	-21	
156	LN	32	
157	×	-35	
158	ST+3	35-55 03	
159	*LBL5	21 05	
160	RCL8	36 08	
161	RCL7	36 07	
162	+	-55	
163	2	02	
164	÷	-24	
165	0	00	
166	X=Y?	16-33	
167	GTO6	22 06	
168	R↓	-31	
169	ENT↑	-21	
170	LN	32	
171	×	-35	
172	ST+6	35-55 06	
173	*LBL6	21 06	
174	1	01	
175	ST-1	35-45 01	
176	RCL1	36 01	
177	RTN	24	
178	R/S	51	

LABELS

A $p_i \uparrow q_i$	B B_p, B_q	C 0,Arc sin	D Σp_i, Σq_i	E $p_i \uparrow q_i$
a p_i, q_i	b H_p, J_p	c H_q, J_q	d R_o	e Error
0	1 Used	2 Used	3 Used	4 Used
5 Used	6 Used	7	8	9

FLAGS

0	
1	
2	
3	

SET STATUS

FLAGS	ON	OFF
0	☐	☒
1	☐	☒
2	☐	☒
3	☐	☒

TRIG	
DEG	☒
GRAD	☐
RAD	☐

DISP	
FIX	☒
SCI	☐
ENG	☐
n	2

Program Description I

Program Title POPULATION SIZE ESTIMATE (JOLLY'S METHOD)

Contributor's Name Hewlett-Packard Company

Address 1000 N.E. Circle Boulevard

City Corvallis **State** Oregon **Zip Code** 97330

Program Description, Equations, Variables Using Jolly's (1965) symbols, let

n = number in sample (at time t)

m = number of marked individuals in sample at time t (recaptures)

s = number of marked individuals released from sample (need not be all)

r = number of marked individuals released from sample which are subsequently captured again at least once (known to be alive later)

z = number of individuals marked prior to sample, but <u>not</u> captured in sample, and which are subsequently captured in later samples (hence the individuals known to be alive at time of sample).

The estimated size of the marked portion of the population at time t is given by

$$\hat{M} = m + z\frac{s}{r}$$

Estimated population size, $\hat{N}$, is simply $\hat{M}$ times the ratio of marked plus unmarked individuals in the sample (n) to marked individuals in the sample (m):

$$\hat{N} = \hat{M} \cdot \frac{n}{m}$$

Jolly's formula for the standard error of the population size is as follows:

$$\text{S. E.}_{\hat{N}} = \sqrt{\hat{N}(\hat{N} - r)\left\{\frac{\hat{M}-m+s}{\hat{M}}\left(\frac{1}{r} - \frac{1}{s}\right) + \left(\frac{1}{m} - \frac{1}{n}\right)\right\}}$$

Operating Limits and Warnings The following inequalities must be met:

$$n \geqslant m \geqslant s \geqslant r$$

Program Description II

Sketch(es)

Sample Problem(s) Suppose you collect a sample of 100 isopods from a marked population and recover 64 marked animals. Of these 64 you retain 16 gravid females for further observation of fecundity-size relationships (this means that 48 are released). Subsequent sampling of the population produces 28 recaptures of these 48 animals. Lastly, you knew that you had only 80 marked animals in the study plot, so that you collected all but 16 of the marked individuals. Hence Jolly's input values are

$n = 100$

$m = 64$

$s = 48$

$r = 28$

$z = 16$

Estimate the population size and its standard error.

Solution(s)

100 [ENTER ↑] 64 [A] 48 [ENTER ↑] 28 [ENTER ↑] 16 [B]

[C] → 142.86 ($\hat{N}$)

[R/S] → 10.47 (SE)

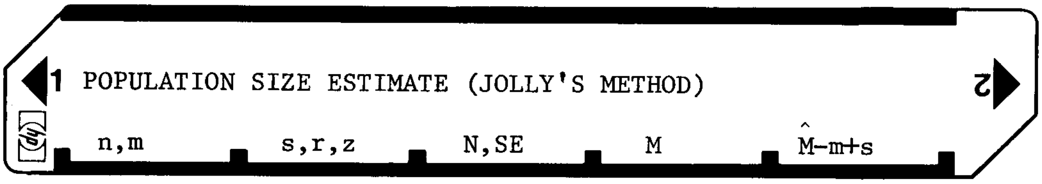
[D] → 91.43 ($\hat{M}$)

Reference(s) Jolly, G.M. 1965. Explicit estimates from capture-recapture data with both death and dilution -- stochastic model. Biometrika 52: 225-247.

Poole, R.W. 1974. An introduction to quantitative ecology. McGraw-Hill. (pp. 307-312.)

This program is a translation of the HP-65 Users' Library Program # 03257A submitted by Eric R. Pianka.

User Instructions



STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
1	Load side 1			
2	Enter n	n	ENT↑	
3	Enter m	m	A	
4	Enter s	s	ENT↑	
5	Enter r	r	ENT↑	
6	Enter z	z	B	
7	Compute $\hat{N}$		C	$\hat{N}$
8	Compute SE		R/S	SE
9	Display $\hat{M}$		D	$\hat{M}$
10	Display $\hat{M}$ - m + s (if desired)		E	$\hat{M}$-m+s

97 Program Listing I

STEP	KEY ENTRY	KEY CODE	COMMENTS
001	*LBLA	21 11	
002	STO2	35 02	
003	R↓	-31	
004	STO1	35 01	
005	RTN	24	
006	*LBLB	21 12	
007	STO5	35 05	
008	R↓	-31	
009	STO4	35 04	
010	R↓	-31	
011	STO3	35 03	
012	RTN	24	
013	*LBLC	21 13	
014	RCL2	36 02	
015	RCL5	36 05	
016	RCL3	36 03	
017	RCL4	36 04	
018	÷	-24	
019	×	-35	
020	+	-55	
021	STO7	35 07	Store $\hat{M}$
022	RCL1	36 01	
023	×	-35	
024	RCL2	36 02	
025	÷	-24	
026	STO8	35 08	Store $\hat{N}$
027	R/S	51	
028	RCL1	36 01	
029	-	-45	
030	RCL8	36 08	
031	×	-35	
032	RCL7	36 07	
033	RCL2	36 02	
034	-	-45	
035	RCL3	36 03	
036	+	-55	
037	RCL7	36 07	
038	÷	-24	
039	RCL4	36 04	
040	1/X	52	
041	RCL3	36 03	
042	1/X	52	
043	-	-45	
044	×	-35	
045	RCL2	36 02	
046	1/X	52	
047	RCL1	36 01	
048	1/X	52	
049	-	-45	
050	+	-55	
051	×	-35	
052	√X	54	
053	RTN	24	
054	*LBLD	21 14	
055	RCL7	36 07	Display $\hat{M}$
056	RTN	24	

STEP	KEY ENTRY	KEY CODE	COMMENTS
057	*LBLE	21 15	
058	RCL7	36 07	
059	RCL2	36 02	
060	-	-45	
061	RCL3	36 03	
062	+	-55	
063	RTN	24	
064	R/S	51	
070			
080			
090			
100			
110			

SET STATUS

FLAGS	ON	OFF	TRIG		DISP	
0	☐	☒	DEG	☒	FIX	☒
1	☐	☒	GRAD	☐	SCI	☐
2	☐	☒	RAD	☐	ENG	☐
3	☐	☒			n 2	

REGISTERS

0	1	2	3	4	5	6	7	8	9
	n	m	s	r	z		$\hat{M}$	$\hat{N}$	

S0	S1	S2	S3	S4	S5	S6	S7	S8	S9

A	B	C	D	E	I

Program Description I

Program Title CELL PHASE AND CYCLE TIMES

Contributor's Name Hewlett-Packard Company

Address 1000 N.E. Circle Boulevard

City Corvallis **State** Oregon **Zip Code** 97330

Program Description, Equations, Variables

Where n_{G1} = the number of cells in G1 phase
n_S = the number of cells in S phase
n_{G2} = the number of cells in G2 phase
n_M = the number of cells in M phase
$n = n_{G1} + n_{G2} + n_M$ = total number of cells.

The proportion of cells in each phase $N_x = \frac{x}{n}$ is computed. The proportion of cells in each stage is related to the time required for completion of that phase:

$$N_x = 2^{\frac{T_x}{T}} - 1$$

where T_x is the phase time and T is the cell cycle time.

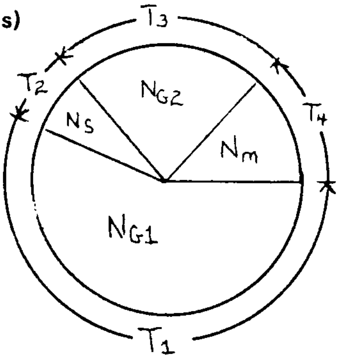
Given a starting concentration of cells, n_o, and a subsequent concentration of cells, n, after a measured amount of time, t, has elapsed, the program computes the cell cycle time, T, from the equation:

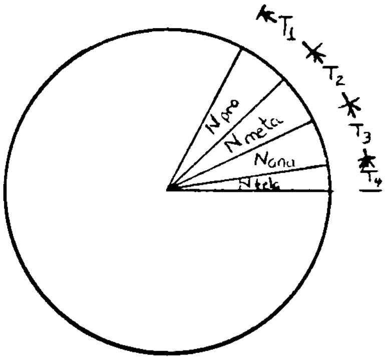
$$n = n_o 2^{\frac{t}{T}}$$

Operating Limits and Warnings Date must be obtained from cells growing in the logarithmic growth phase. Viability of the cells should be confirmed as no adjustment is made for cell death. Please note that the sketches drawn employing circles to represent cell cycles are used for simplicity of expression. However, the relationship between the proportion of cells in a given phase and the amount of the cell cycle time used is not linear.

Program Description II

Sketch(es)





Sample Problem(s)

1. In a randomly dividing cell culture with a cell cycle time of 24 hours, a sample is evaluated and 500 cells are found in M, 1000 in G2, 500 in S, and 1500 in G1 phase. Calculate the time spent in each phase:

   T_{G1}, T_S, T_{G2}, and T_M.

2. In this culture the cells in mitosis were examined, and it was found that 30 cells were in telophase, 50 in anaphase, 70 in metaphase, and 350 in prophase. As above, the cell cycle time is 24 hours and the total number of cells counted is 3500. Calculate the time spent in each phase of mitosis:

   T_{pro}, T_{meta}, T_{ana}, and T_{telo}.

(Continued on next page)

Solution(s)

1. 24 [ENTER↑] 3500 [f][A]
   1500[ENTER↑] 500[ENTER↑] 1000[ENTER↑] 500[A] → 3500
   [B] → 8.35 hours
   [C] → 3.30 hours
   [D] → 7.73 hours
   [E] → 4.62 hours

2. 350 [ENTER↑] 70[ENTER↑] 50[ENTER↑] 30[A] → 500
   [B] → 3.17 hours
   [C] → 0.67 hours
   [D] → 0.49 hours
   [E] → 0.30 hours

1. T_{G1} = 8.35 hours
   T_S = 3.30 hours
   T_{G2} = 7.73 hours
   T_M = 4.62 hours

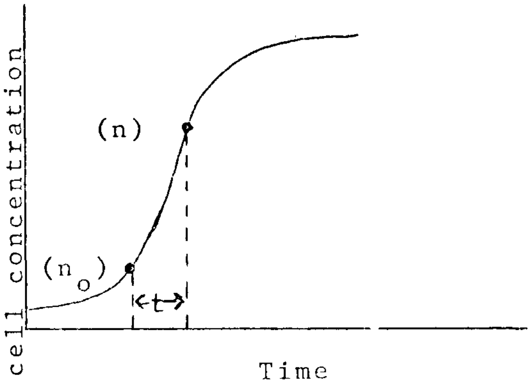
2. T_{pro} = 3.17 hours
   T_{meta} = 0.67 hours
   T_{ana} = 0.49 hours
   T_{telo} = 0.30 hours

Reference(s) Puck, Theodore T., and Steffen, Jan. Life cycle analysis of mammalian cells. I. Biophysical Journal 3: 379-397. 1963

This program is a modification of the Users' Library Programs #01522A and #01630A submitted by James M. Mason.

Program Description II

Sketch(es)



Sample Problem(s)

3. Find the cell cycle time, T, of cultured cells (represented above) where a starting concentration of cells, n_o, a subsequent concentration of cells, n, and the elapsed time, t, are given:

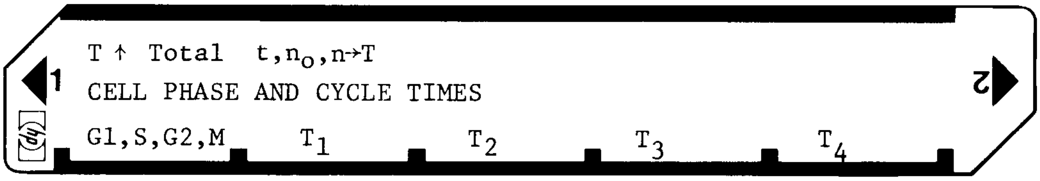
n_o = 100,000 cells/ml
n = 500,000 cells/ml
t = 48 hours

Solution(s)

3. T = 20.67 hours
48[ENTER↑] 1[EEX] 5[ENTER↑] 5[EEX] 5[f][B] → 20.67 hours

Reference(s)

User Instructions



STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS		OUTPUT DATA/UNITS
1	Load side 1				
2	If cell cycle time is known go to step 3				
	If cell cycle time is to be calculate				
	go to step 5				
3	Enter cell cycle time	T	↑		
	Enter total number of cells	total	f	A	T
4	Go to step 7				
5	Enter total number of cells	n total	f	A	
6	Enter elapsed time	t	↑		
	Enter starting concentration of cells	n_o	↑		
	Enter subsequent concentration of cells	n	f	B	T
7	Enter number of cells in four phases:				
	# cells in G1 phase or prophase	n_{G1} or n pro	↑		
	# cells in S phase or metaphase	n_S or n meta	↑		
	# cells in G2 phase or anaphase	n_{G2} or n ana	↑		
	# cells in M phase or telophase	n_M or n telo	A		total 4 phase
8	Compute time for G1 or prophase		B		T_1
9	Compute time for S or metaphase		C		T_2
10	Compute time for G2 or anaphase		D		T_3
11	Compute time for M or telophase		E		T_4
12	Find $T_1 + T_2 + T_3 + T_4$		RCL	7	ΣT_{1-4}

97 Program Listing I

STEP	KEY ENTRY	KEY CODE	COMMENTS
001	*LBLA	21 11	Enter cell counts
002	STO1	35 01	
003	+	-55	
004	STO2	35 02	
005	+	-55	
006	STO3	35 03	
007	+	-55	
008	STO4	35 04	
009	RTN	24	
010	*LBLa	21 16 11	Enter T and n total
011	STO8	35 08	
012	X⇄Y	-41	
013	STO6	35 06	
014	RTN	24	
015	*LBLb	21 16 12	Cell cycle time(T)
016	LOG	16 32	
017	X⇄Y	-41	
018	LOG	16 32	
019	-	-45	
020	STO6	35 06	
021	R↓	-31	
022	2	02	
023	LOG	16 32	
024	x	-35	
025	RCL6	36 06	
026	÷	-24	
027	STO6	35 06	Stores cycle time
028	RTN	24	
029	*LBL0	21 00	Computational loop
030	RCL8	36 08	
031	÷	-24	
032	1	01	
033	+	-55	
034	LOG	16 32	
035	2	02	
036	LOG	16 32	
037	÷	-24	
038	RCL6	36 06	
039	x	-35	
040	RTN	24	
041	*LBLB	21 12	T_1
042	RCL3	36 03	
043	GSB0	23 00	
044	STO5	35 05	
045	RCL4	36 04	
046	GSB0	23 00	
047	STO7	35 07	Total of T_1,T_2,T_3,T_4
048	RCL5	36 05	
049	-	-45	
050	RTN	24	
051	*LBLC	21 13	T_2
052	RCL2	36 02	
053	GSB0	23 00	
054	STO5	35 05	
055	RCL3	36 03	
056	GSB0	23 00	
057	RCL5	36 05	
058	-	-45	
059	RTN	24	
060	*LBLD	21 14	T_3
061	RCL1	36 01	
062	GSB0	23 00	
063	STO5	35 05	
064	RCL2	36 02	
065	GSB0	23 00	
066	RCL5	36 05	
067	-	-45	
068	RTN	24	
069	*LBLE	21 15	T_4
070	RCL1	36 01	
071	GSB0	23 00	
072	RTN	24	
073	R/S	51	
080			
090			
100			
110			

SET STATUS

FLAGS	ON	OFF
0	☐	☒
1	☐	☒
2	☐	☒
3	☐	☒

TRIG	
DEG	☒
GRAD	☐
RAD	☐

DISP	
FIX	☒
SCI	☐
ENG	☐
n	2

REGISTERS

0	1	2	3	4	5	6	7	8	9
	n_4	$n_4 + n_3$	$n_4+n_3 + n_2$	$n_4 + n_3 + n_2 + n_1$	scratch for calculations	cell cycle time	$T_1 + T_2 + T_3 + T_4$	total number of cells	

S0	S1	S2	S3	S4	S5	S6	S7	S8	S9

A	B	C	D	E	I

Program Description I

Program Title CROSSOVER: LOCATIONS/PRODUCTS

Contributor's Name Hewlett-Packard Company

Address 1000 N. E. Circle Boulevard

City Corvallis **State** Oregon **Zip Code** 97330

Program Description, Equations, Variables This program calculates the locations of all crossovers which must occur to produce a given progeny chromatid. Two-strand crossovers between complementary parental homologues are assumed. Following a decimal point, the presence or absence of dominant alleles are represented by '1' or '0' respectively. A chromatid with alleles AbcdEFgh is expressed as .10001100. Crossover regions are numbered consecutively 1, 2, ..., n, from left to right. Crossover region 1 is the region between the two digits nearest the decimal point; region n is between the two digits farthest from the decimal point. After entering parental genotype, progeny genotype and, the total number of crossover regions, n, the program specifies each region in which a crossover occurred to produce the progeny chromatid. The presence of a crossover in region 1 is represented by 1; a crossover in region n, by n. Absence of a crossover in a region is denoted by 0. Crossover locations are calculated by an algorithm which successively compares adjacent and progeny gene pairs and determines whether progeny genes are in parental or crossover configurations.

(Continued on next page)

Operating Limits and Warnings The maximum number of testable loci is 10. The decimal point must always be entered before the binary equivalent genotype is entered. Use only 1's and 0's. To prevent logarithmic conversion errors produced in the algorithm from appearing in the results, results must be read with calculator set to DSP 0.

Program Description I

Program Title

Contributor's Name

Address

City **State** **Zip Code**

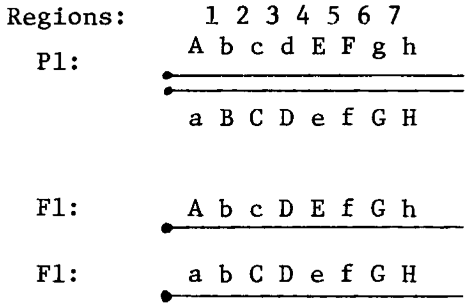
Program Description, Equations, Variables The program calculates the genotype of a chromatid produced by crossovers between specified loci of a parental chromatid and its complementary homologue. The presence or absence of a dominant parental allele is represented by '1' or '0' respectively. The parental chromatid with alleles AbcdEFgh is expressed as 10001100; its complementary homologue with alleles ABCDefGH, as 11110011. Crossover regions are numbered consecutively 1, 2, ..., n, from left to right. Crossover region 1 is the region between the leftmost two digits and crossover region n is between the rightmost two digits. After specifying crossover regions, the program provides the genotype resulting from crossovers in the designated regions. The new genotype is shown as a number consisting of 1's and 0's (a binary equivalent) with length equal to the number of parental alleles. The new genotype is calculated by means of an algorithm which successively produces binary complements of the parental strand to the right of the crossover regions specified.

Operating Limits and Warnings The number of genes, g, must be entered before calculations can be effected. Parental genes limited: $2 \leqslant g \leqslant 10$. The first digit of the parental genotype should be 1. No more than 3 crossover regions can be specified for a single calculation.

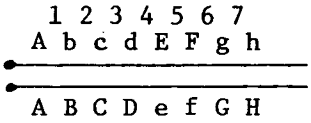
Program Description II

SKETCH(ES)

1.



2.



Sample Problem(s) 1. Given the paternal chromatids, P1, observed progeny chromatids, F1, and 7 crossover regions as shown above; a) In what regions did crossovers occur producing the progeny chromatid with the genotype AbcDEfGh? b) The progeny chromatid with the genotype abCDefGH?

2. Given the parental chromatids above; a) What is the genotype of the progeny chromatid resulting from crossovers occurring in regions 2, 3 and 5? b) In regions 1, 4 and 6?

Solution(s) 1. a) .10001100 [ENTER↑] .10011010 [A]
7 [B] → 34507
Crossovers occur in regions 3, 4, 5, and 7
b) .01110011 [ENTER↑] .00110011 [A]
7 [B] → 1200000
Crossovers occur in regions 1 and 2.

2. a) 8 [E]
10001100 [ENTER↑] 2 [ENTER↑] 3 [ENTER↑] 5 [C] → 10101011(AbCdEfGH)
b) 10001100 [ENTER↑] 1 [ENTER↑] 4 [ENTER↑] 6 [C] → 11111111(ABCDEFGH)

Reference(s)

Srb, A. M., R. D. Owen and R. S. Edgar. General Genetics, 2nd Ed., 1965. W. H. Freeman and Co., San Francisco. Chapter 6.

This program is a modification of the Users' Library Programs #01523A and #01524A submitted by James N. Adams.

User Instructions

1 CROSSOVER: LOCATIONS/PRODUCTS 2

P1 ↑ .F1 | n | mult | single | g

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS		OUTPUT DATA/UNITS
1	Load side 1 and side 2				
2	For crossover locations go to step 3.				
	For crossover products go to step 7.				
3	Input parental genotype, P1, following a				
	decimal point. Use 1 for a dominant and 0				
	for a recessive allele	.P1	ENT↑		
4	Input progeny genotype, F1	.F1	A		
5	Input total crossover regions n (number of				
	genes -1 = n) and calculate regions	n	B		Xo's
	in which crossovers occur (Xo's) (0's in				
	result are ignored. E. g. Xo's=1004067 means				
	crossovers in regions 1, 4, 6 and 7.)				
6	For new case go to step 3.				
7	Input number of genes, g, in parental chromatid	g	E		g
8	Input genotype, P1, using 1 for dominant and				
	0 for recessive.	P1	↑		P1
	(For multiple crossovers go to step 12)				
9	Specify desired crossover region, Xo	Xo			
10	Calculate F1 genotype		D		F1
11	For an additional single Xo, go to 9				
	or				
	For a new parental type, go to 8				
	or				
	For a new case go to 7				
12	Specify first crossover region, Xo1	Xo1	↑		
13	Specify second crossover region, Xo2				
	or 0 for none	Xo2	↑		
14	Specify third crossover region, Xo3				
	or 0 for none	Xo3	↑		
15	Calculate F1 genotype		C		F1
16	For an additional single Xo go to 9				
	or				
	For additional multiple Xo's go to 12				
	or				
	For a new parental type go to 8				
	or				
	For a new case go to 7				

97 Program Listing I

STEP	KEY ENTRY	KEY CODE	COMMENTS
001	*LBLA	21 11	STO F1
002	STO2	35 02	
003	STO6	35 06	
004	X⇄Y	-41	
005	STO1	35 01	STO P1
006	STO5	35 05	
007	RTN	24	
008	*LBLB	21 12	
009	STOI	35 46	STO n, estab.counte
010	1	01	
011	+	-55	
012	STO7	35 07	
013	0	00	
014	STO4	35 04	
015	6	06	
016	*LBL5	21 05	Gene comparison algorithm
017	RCL1	36 01	
018	GSB6	23 06	Get P1 gene 1
019	RCL2	36 02	
020	GSB6	23 06	Get F1 gene 1
021	X=Y?	16-33	Compare
022	SF1	16 21 01	
023	X≠Y?	16-32	
024	CF1	16 22 01	
025	RCL1	36 01	Get P1 gene 2
026	GSB7	23 07	
027	GSB6	23 06	
028	RCL2	36 02	Get F1 gene 2
029	GSB7	23 07	
030	GSB6	23 06	
031	X=Y?	16-33	Compare
032	SF2	16 21 02	
033	X≠Y?	16-32	
034	CF2	16 22 02	
035	F1?	16 23 01	
036	GTO0	22 00	
037	GTO1	22 01	
038	*LBL0	21 00	
039	F2?	16 23 02	
040	GTO4	22 04	
041	GTO3	22 03	
042	*LBL1	21 01	Crossover occured record; no crossover get new gene
043	F2?	16 23 02	
044	GTO3	22 03	
045	GTO4	22 04	
046	*LBL3	21 03	Crossover occured
047	RCLI	36 46	
048	1	01	
049	-	-45	
050	10^x	16 33	
051	RCL7	36 07	Calculate region of crossover
052	RCLI	36 46	
053	-	-45	
054	×	-35	
055	ST+4	35-55 04	Store res. of cross
056	*LBL4	21 04	
057	RCL1	36 01	Get new genes for comparison
058	GSB7	23 07	
059	STO1	35 01	
060	RCL2	36 02	
061	GSB7	23 07	
062	STO2	35 02	
063	DSZI	16 25 46	
064	GTO5	22 05	
065	RCL4	36 04	
066	RTN	24	
067	*LBL6	21 06	Shift left one gene
068	1	01	
069	0	00	
070	×	-35	
071	INT	16 34	
072	RTN	24	
073	*LBL7	21 07	Shift left total genotype 1 gene
074	1	01	
075	0	00	
076	×	-35	
077	FRC	16 44	
078	RTN	24	
079	*LBLC	21 13	Store Xo3
080	STOI	35 46	
081	R↓	-31	
082	STO7	35 07	Store Xo2
083	R↓	-31	
084	GSBD	23 14	Calculate Xo1
085	RCL7	36 07	
086	0	00	
087	X=Y?	16-33	Test for Xo2
088	GTO9	22 09	
089	RCL5	36 05	
090	RCL7	36 07	
091	GSBD	23 14	Calculate Xo2
092	RCLI	36 46	
093	0	00	
094	X=Y?	16-33	Test for Xo3
095	GTO9	22 09	
096	RCL5	36 05	
097	RCLI	36 46	
098	GSBD	23 14	Calculate Xo3
099	RTN	24	
100	*LBLD	21 14	Single Xo logorithm
101	RCL6	36 06	Test for region not to be complemented
102	X⇄Y	-41	
103	-	-45	
104	STO2	35 02	
105	X⇄Y	-41	
106	STO1	35 01	
107	0	00	
108	STO3	35 03	
109	RCL1	36 01	
110	RCL2	36 02	
111	5	05	Correct antilog error
112	-	-45	

REGISTERS

0	1 Used	2 Used	3 Used	4 Used	5 P1 F1	6 F1 Used	7 Used	8 Counter Used	9 Used
S0	S1	S2	S3	S4	S5	S6	S7	S8	S9
A	B	C	D	E	I				

97 Program Listing II

STEP	KEY ENTRY	KEY CODE	COMMENTS
113	10^x	16 33	
114	EEX	-23	
115	5	05	
116	x	-35	
117	STO4	35 04	
118	÷	-24	
119	INT	16 34	
120	RCL4	36 04	
121	x	-35	
122	STO5	35 05	Store non-comp.reg.
123	*LBL2	21 02	To determine if
124	RCL1	36 01	gene is to be
125	2	02	complemented
126	÷	-24	
127	FRC	16 44	
128	0	00	
129	X≠Y?	16-32	
130	GTO8	22 08	
131	RCL3	36 03	Place uncomplemented
132	5	05	gene value in
133	-	-45	storage
134	10^x	16 33	
135	EEX	-23	
136	5	05	
137	x	-35	
138	ST+5	35-55 05	
139	*LBL8	21 08	Place complemented
140	1	01	gene value in
141	ST+3	35-55 03	storage
142	RCL2	36 02	
143	RCL3	36 03	
144	X=Y?	16-33	Test completion Xo's
145	GTO9	22 09	
146	RCL1	36 01	Get new gene
147	1	01	
148	0	00	
149	÷	-24	
150	INT	16 34	
151	STO1	35 01	
152	GTO2	22 02	
153	*LBLE	21 15	Store number of
154	DSP0	-63 00	genes in P1 and
155	STO6	35 06	set display
156	RTN	24	
157	*LBL9	21 09	Show Result
158	RCL5	36 05	Stop
159	RTN	24	
160	R/S	51	

LABELS

A Compare Mult Xo's	B 10x int Single xo	C 10x dec. Nbr genes	D	E
a	b	c	d	e
0	1	2	3	4
5	6	7	8	9

FLAGS

0	
1	Used
2	Used
3	

SET STATUS

FLAGS	ON	OFF
0	☐	☒
1	☐	☒
2	☐	☒
3	☐	☒

TRIG	
DEG	☒
GRAD	☐
RAD	☐

DISP	
FIX	☒
SCI	☐
ENG	☐
n	2

Program Description I

Program Title CHROMOSOME CLEAVAGE

Contributor's Name Hewlett-Packard Company

Address 1000 N.E. Circle Boulevard

City Corvallis **State** Oregon **Zip Code** 97330

Program Description, Equations, Variables Chromosome cleavage is a powerful experimental genetic technique which has yielded a wealth of knowledge concerning gene loci on the chromosomal DNA code. The program simulates chromosome models consisting of even hundreds or thousands of unique individually identifiable genes in linear array. By noting what happens to any two genes after chromosomal fragmentation at arbitrary break-points, entire chromosomal gene sequences may be reconstructed experimentally.

The genetic sequences are based upon the ability of a prime P, of form (8k+3) or (8k+5) for some integer k, to reproduce all integers from 1 to (P-1) in any (P-1) consecutive passes of the formula ($S_{i+1} = 2S_i$ module P), starting from any $S_1 (1 \leqslant S_1 \leqslant (P-1)$. Permissable chromosome lengths for $n \leqslant 100$ genes are 10, 12, 18, 28, 36, 42, 52, 58, 60, 66, 82, 100. For example, for n=100, $P=101 = (8 \cdot (12) + 5)$ is a prime of form (8k + 5).

Copies of particular chromosomes are repeatedly split (each copy once) to build a statistical experimental pattern for any two genes on a chromosome. The program assumes that the 1st fragment (F_1) is identifiable - e.g. by end point radioisotope labeling - and computes how many (0, 1, 2) but not necessarily which of the two genes g_1 and g_2 are contained in F_1 for each cleavage. Powerful statistical inferences (see examples) are possible, and ultimately the whole chromosomal genes sequence may be reconstructed.

Operating Limits and Warnings

Program Description II

Sketch(es)

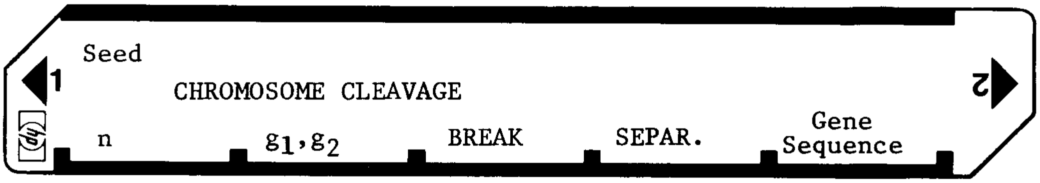
Sample Problem(s) Do a gene-pair analysis for a chromosome of length 10 in a chromosomal DNA chain in an unknown sequence. Use .456 as the initial seed and do 10 consecutive chromosomal cleavages for each of the pairs (1,6), (1,8), and (6,9). Obtain the true gene separation for each pair and finally the true gene sequence.

Solution(s) .456 [f][A] 10 [A] 1 [ENTER↑] 6 [B]

Press [C] 10 times and get the sequence 2, 0, 2, 2, 2, 0, 1, 2, 2,
[D] → 0
1 [ENTER↑] 8 [B]; Press [C] 10 times → 1, 2, 1, 2, 2, 2, 2, 2, 1, 2
[D] → -2[Disregard the sign]
6 [ENTER↑] 9 [B]; Press [C] 10 times → 1, 0, 1, 1, 1, 1, 1, 0, 0, 0
[D] → -6 [Disregard the sign]
[E] → 7, 3, 6, 1, 2, 4, 8, 5, 10, 9 True Gene Sequence

Reference(s) This program is a modification of the Users' Library Program #04138A submitted by Mordecai Schwartz, M.D.

User Instructions



STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
1	Load side 1 and side 2			
2	(Optional: enter random seed $0 < S < 1$)	S	f A	
3	Select chromosome of desired length = no. of			
	genes, n, in linear sequence.	n	A	
	(Note: (n+1) must be a prime of form (8k+3)			
	or (8k+5) for some integer k. The valid			
	chromosome lengths for n<100 are n = 10, 12			
	18, 28, 36, 42, 52, 58, 60, 66, 82, and 100)			
4	Select 2 genes, g_1 and g_2, for study($1 \leq g_i \leq n$)	g_1	ENT↑	
	(Note: If $g_1=7$, for example, the '7' is	g_2	B	
	simply an identifying label (think of it as			
	the 7th gene discovered in that chromosome)			
	and does not necessarily indicate its			
	position in the chromosome's gene sequence.			
5	Cleave the chromosome at an arbitrary break-			0, 1, 2 =
	point.		C	# of genes
6	Repeat 5 as often as desired, with additional			on 1st frag.
	chromosome copies, to obtain an experimental			
	statistical pattern for g_1, g_2 separation.			
7	When ready, see actual no. of genes intervening			g_1 g_2
	between g_1 and g_2 for comparison with			separation
	deduced value.		D	(ignore sign)
8	For another gene pair on same chromosome,			
	go to step 4.			
9	When experimentation is complete - ideally			
	with step 7 omitted - For all desired gene			
	pairs, compare complete chromosome with			
	your reconstruction.		E	
10	For a chromosome of different length go			
	to step 3.			

SET STATUS

FLAGS	ON	OFF	TRIG		DISP	
0	☐	☒	DEG	☒	FIX	☒
1	☐	☒	GRAD	○	SCI	☐
2	☐	☒	RAD	○	ENG	☐
3	☐	☒			n 2	

97 Program Listing I

STEP	KEY ENTRY	KEY CODE	COMMENTS
001	*LBLa	21 16 11	STORE seed
002	STO7	35 07	
003	RTN	24	
004	*LBLA	21 11	Store length
005	DSP0	-63 00	
006	STO3	35 03	
007	RTN	24	
008	*LBLB	21 12	Store gene pair
009	STO2	35 02	
010	X⇄Y	-41	
011	STO1	35 01	
012	RTN	24	
013	*LBLD	21 14	S_0=(n-1) at start
014	RCL3	36 03	of $S_1 \to S_n$ gene
015	1	01	sequence
016	-	-45	
017	STO4	35 04	
018	0	00	Reset gene
019	STOI	35 46	separation counter
020	*LBL0	21 00	No $g_1$org_2 match loo
021	RCL1	36 01	When the 1st match
022	GSB5	23 05	is found for eithe
023	X=Y?	16-33	g_1 or g_2 in the
024	GTO1	22 01	$S_1 \to S_n$ gene
025	RCL2	36 02	sequence, go to
026	X≠Y?	16-32	LBL1.
027	GTO0	22 00	
028	*LBL1	21 01	No. 2nd match loop
029	RCL1	36 01	When the 2nd of
030	GSB5	23 05	g_1 or g_2 have been
031	X=Y?	16-33	matched in the
032	GTO3	22 03	$S_1 \to S_n$ gene sequenc
033	RCL2	36 02	display no. of
034	X=Y?	16-33	genes between g_1 &
035	GTO3	22 03	g_2 (ignore sign)
036	DSZI	16 25 46	If 2nd gene has not
037	GTO1	22 01	been matched, inc.+
038	GTO5	22 05	loop for nxt gene
039	*LBLE	21 15	True sequence
040	RCL3	36 03	
041	STOI	35 46	
042	1	01	
043	-	-45	
044	STO4	35 04	
045	*LBL6	21 06	
046	GSB5	23 05	
047	PRTX	-14	
048	DSZI	16 25 46	
049	GTO6	22 06	
050	RTN	24	
051	*LBL5	21 05	Obtain next gene,S_i
052	RCL4	36 04	$S_i=2S_{i-1}$ Mod.(n+1)
053	2	02	[When (n+1) in
054	×	-35	R_c is a prime of
055	RCL3	36 03	form
056	1	01	
057	+	-55	(8k+3) or
058	STO6	35 06	(8k+5) for some
059	÷	-24	integer k]...
060	FRC	16 44	
061	RCL6	36 06	
062	×	-35	
063	.	-62	... for matching
064	1	01	purposes
065	+	-55	
066	INT	16 34	
067	STO4	35 04	Leave S_i in R_4 & X
068	RTN	24	
069	*LBLC	21 13	Break chrom. at Rand pt
070	RCL7	36 07	Rand $_i$ in R_7 =
071	Pi	16-24	first part of
072	+	-55	$(R\ and_{i-1} + \pi)^5$
073	5	05	
074	Y^X	31	
075	FRC	16 44	
076	STO7	35 07	
077	RCL3	36 03	Use Rand to obtain
078	1	01	an arbitrary
079	-	-45	integer from
080	STO4	35 04	1 to (n-1) to
081	×	-35	correspond to one
082	1	01	of the (n-1)
083	+	-55	possible break-pts.
084	INT	16 34	in a chromosome of
085	STOI	35 46	gene length n
086	0	00	Reset g_1g_2 gene
087	STO5	35 05	match counter
088	*LBL2	21 02	Loop to test all
089	GSB5	23 05	genes on 1st frag.F_1
090	RCL1	36 01	g_1 appears on F_1
091	X=Y?	16-33	
092	GSB4	23 04	
093	RCL4	36 04	g_2 appears on F_1
094	RCL2	36 02	
095	X=Y?	16-33	
096	GSB4	23 04	
097	DSZI	16 25 46	If break-pt has not
098	GTO2	22 02	been reached, test next
099	RCL5	36 05	All F_1 genes tested.
100	RTN	24	Display no. g_1g_2
101	*LBL3	21 03	on F_1
102	RCLI	36 46	
103	RTN	24	
104	*LBL4	21 04	Match counter is
105	1	01	incremented
106	ST+5	35-55 05	
107	RTN	24	
108	R/S	51	
110			

REGISTERS

0	1	2	3	4	5	6	7	8	9
	g_1 gene 1st chosen	g_2 gene 2nd ch.	n no. of genes on chrom.	S_i ith gene of gene chro	0,1,2 no of g_1g_2 mtch. F_1	(n+1) hold = modules	Rand	Separat. brk-pt counts	
S0	S1	S2	S3	S4	S5	S6	S7	S8	S9

A	B	C	D	E	I

Program Description I

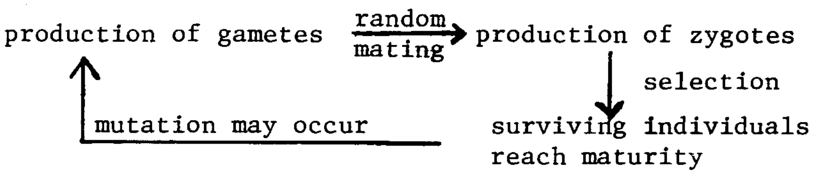
Program Title RECESSIVE GENE FREQUENCY AFTER SELECTION, MUTATION, AND INBREEDING

Contributor's Name Hewlett-Packard Company

Address 1000 N.E. Circle Boulevard

City Corvallis **State** Oregon **Zip Code** 97330

Program Description, Equations, Variables The following selection and mutation model was used:



From this model (see Operating Limits & Warnings) can be derived:

$$q_{n+1} = \frac{q_n^2\,(ht+wht-t) + q_n\,(1-ht-u-wht) + u}{1 - 2ht\,q_n + q_n^2\,(2ht-1)}$$

where:

u = mutation rate

$(1-t)$ = mutant homozygote fitness

$(1-ht)$ = mutant heterozygote fitness

q = recessive or mutant gene frequency

n = no. of generations.

q_o = initial gene frequency and equilibriu gene frequency

q_e is attained when $q_{n+1} = q_n$ (see pg 4, step 6 comment).

(Continued on next page)

Operating Limits and Warnings The following simplifying assumptions were made:

a) infinite population size

b) no. inbreeding, and random mating

c) mutational effects are irreversible

d) only autosomal genes are involved.

Program Description I

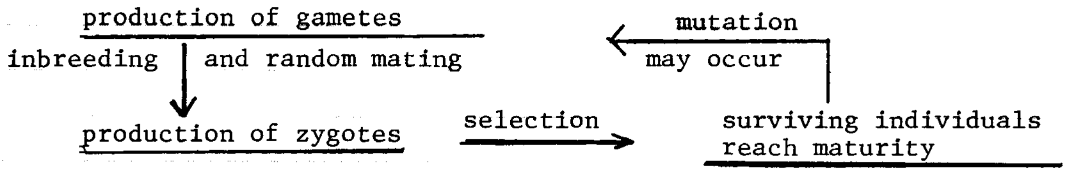
Program Title

Contributor's Name

Address

City **State** **Zip Code**

Program Description, Equations, Variables Using simplifying assumptions (see below) and the following model,



the following equation may be derived, $\underline{q_{n+1} = A(1-u) + u}$, where

$$A = \frac{(1-F)(ht-1)[q_n^2(2-t) - q_n] + q_n F(1-t)}{(1-q_nF) - (1-F)[q_n^2(2+2ht-t) - 2q_nht] + q_nF(1-t)}$$

where:

$(1-t)$ = fitness of recessive homozygote
$(1-ht)$ = fitness of heterozygote (fitness of normal homozygote is assumed as unity)
u = mutation rate for recessive gene
F = inbreeding coefficient
q_n = recessive gene frequency after n-generations (q_o=initial frequency)
q_e = equilibrium gene frequency

Operating Limits and Warnings The following simplifying assumptions apply:

1) infinite population size
2) only autosomal genes involved
3) mutation is irreversible
4) only two alleles per locus.

Program Description II

Sketch(es)

Sample Problem(s)

1. Given the genetic parameters: h=0.1, t=0.5, u=10^{-4}, $q_o=10^{-3}$, calculate the equilibrium gene frequency, q_e, and estimate the no. of generations to attain this frequency.

2. Given the genetic parameters: h=0.5, t=1, $u=q_o=10^{-6}$, compute the values of q_2 and q_e.

3. Using the following values: $q_o=u=1 \times 10^{-5}$, h=0.1, F=0.1, t=1, calculate q_2, q_{10}, q_e, and estimate the value of n to attain q_e. (Note that when q_e is computed directly after q_{10} was computed, the value of n = 10 + $|R_8|$).

Solution(s)

1. 0 [STO][8] .1 [↑] .5[↑] [EEX] 4 [CHS][↑][EEX] 3 [CHS]
[A]→ $q_e = 1.97 \times 10^{-3}$ (ca. 10 min. of running time)
[RCL] 7 → n=150

2. 2 [STO][8] .5 [↑] 1 [↑][EEX] 6 [CHS][↑][A] → $q_2=1.75 \times 10^{-6}$
0 [STO][8] [R/S] → $q_e = 2.00 \times 10^{-6}$

3. [EEX] 5 [CHS][STO] 1 [STO][5] 2 [STO] [I]
1[↑] .1[↑] .1 [E] → $q_2 = 2.47 \times 10^{-5}$
8 [STO][I] [R/S] → $q_{10} = 4.74 \times 10^{-5}$
0 [STO][I] [R/S] → $q_e = 5.26 \times 10^{-5}$ (ca. 3 min. running time)
[I] [ABS] 10 + → n = 47 generations.

Reference(s)

Cavalli - Sforza, L.L. and Bodmer, W.F., <u>The Genetics of Human Populations</u>, pgs. 82-88, 365, W.H. Freeman, 1971.

This program is a modification of the Users' Library Programs #04531A and #04679A submitted by Dr. Leo S. Reich.

User Instructions

RECESSIVE GENE FREQUENCY

S - M

S-M-I

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS		OUTPUT DATA/UNITS
1	Load side 1 and side 2				
2	For freq. after selection and muta., go to step 3				
	For freq, after sel.,mut., and inbreed, go to step 7				
3	If equilibrium recessive gene frequency, q_e,	0			
	is desired outright, enter 0 → R_8, otherwise	or	STO	8	
	if q_n is desired, enter n → R_8	n			
4	Enter in stack in the following order:	h	↑		
	h, t, u, q_o	t	↑		
		u	↑		
		q_o			
5	Press key A to obtain desired q - value		A		q_e or q_n
6	Press RCL 7 to obtain value of n required				
	to obtain displayed q_e		RCL	7	n
	Note:				
	[The value of n corresponding to q_e is based				
	on a percentage deviation between the				
	displayed q_e and preceding calcd. value of				
	q_e of 0.001 or less.]				
	[After q_n is calculated and q_n', is next				
	desired (n'>n), enter n' → R_8 and press				
	R/S. If q_e is desired after q_n is displayed,				
	enter 0 → R_8 and press R/S.]				
7	q_o → R_1; u → R_5; if q_e desired, enter	q_o	STO	1	
	0 → R_8 while if q_n desired	u	STO	5	
	enter n → R_8	0 or n	STO	8	
8	Enter in stack in order:	t	↑		
	t, h, and F	h	↑		
		F			
9	Press [E] to obtain q_e or q_n		E		q_e or q_n
	[After q_n has been computed, q_n' may next be				
	calculated by entering (n'−n) → R_8, where				
	n'>n, and pressing R/S. If q_e is desired				
	after q_n has been computed, enter 0 → R_8				
	and press R/S].				
	[When q_e is computed directly (0 → R_8), the				
	value of n may be obtained by using the				
	absolute value of R_8. When q_e is estimated				
	after calculating q_n', then n is equal to				
	$\lvert R_8 \rvert$ + n'. The value of q_e computed is				
	based upon a percentage deviation from a				
	preceding value of q_e of about 0.001 or less].				

97 Program Listing I

STEP	KEY ENTRY	KEY CODE	COMMENTS
001	*LBLA	21 11	Clear R_7 and store various parameters
002	SCI	-12	
003	DSP2	-63 02	
004	STO5	35 05	
005	R↓	-31	
006	STO1	35 01	
007	R↓	-31	
008	STO2	35 02	
009	×	-35	
010	STO3	35 03	
011	RCL1	36 01	
012	×	-35	
013	STO4	35 04	
014	0	00	
015	STO7	35 07	
016	*LBL1	21 01	Calculate various values for q
017	RCL3	36 03	
018	RCL4	36 04	
019	+	-55	
020	RCL2	36 02	
021	-	-45	
022	RCL5	36 05	
023	ENT↑	-21	
024	×	-35	
025	×	-35	
026	1	01	
027	RCL3	36 03	
028	-	-45	
029	RCL1	36 01	
030	-	-45	
031	RCL4	36 04	
032	-	-45	
033	RCL5	36 05	
034	×	-35	
035	+	-55	
036	RCL1	36 01	
037	+	-55	
038	STO6	35 06	
039	1	01	
040	RCL3	36 03	
041	2	02	
042	×	-35	
043	RCL5	36 05	
044	×	-35	
045	-	-45	
046	RCL3	36 03	
047	2	02	
048	×	-35	
049	RCL2	36 02	
050	-	-45	
051	RCL5	36 05	
052	ENT↑	-21	
053	×	-35	
054	×	-35	
055	+	-55	
056	RCL6	36 06	

STEP	KEY ENTRY	KEY CODE	COMMENTS
057	X⇄Y	-41	
058	÷	-24	
059	STO6	35 06	
060	1	01	
061	ST+7	35-55 07	Counter for no. of generations, n
062	RCL7	36 07	
063	RCL8	36 08	
064	0	00	
065	X=Y?	16-33	
066	GTO2	22 02	
067	R↓	-31	
068	X≠Y?	16-32	
069	GTO3	22 03	
070	RCL6	36 06	Display q_n
071	R/S	51	
072	GTO3	22 03	
073	*LBL2	21 02	Calculate value of q_e
074	RCL6	36 06	
075	RCL5	36 05	
076	-	-45	
077	RCL5	36 05	
078	÷	-24	
079	ABS	16 31	
080	EEX	-23	
081	5	05	
082	CHS	-22	
083	X≤Y?	16-35	
084	GTO3	22 03	
085	RCL6	36 06	Display q_e
086	R/S	51	
087	*LBL3	21 03	
088	RCL6	36 06	
089	STO5	35 05	
090	GTO1	22 01	
091	*LBLE	21 15	Store F, h, and t
092	SCI	-12	
093	DSP2	-63 02	
094	STO2	35 02	
095	R↓	-31	
096	STO3	35 03	
097	R↓	-31	
098	STO4	35 04	
099	*LBL4	21 04	
100	1	01	
101	RCL1	36 01	
102	RCL2	36 02	
103	×	-35	
104	-	-45	
105	1	01	
106	RCL4	36 04	
107	-	-45	
108	RCL1	36 01	
109	×	-35	
110	RCL2	36 02	
111	×	-35	
112	STO6	35 06	

REGISTERS

0	1 q	2 F	3 h	4 t	5 u	6 Used	7 Used	8 Used	9
S0	S1	S2	S3	S4	S5	S6	S7	S8	S9

A	B	C	D	E	I

97 Program Listing II

STEP	KEY ENTRY	KEY CODE	COMMENTS
113	+	-55	
114	2	02	
115	RCL4	36 04	
116	-	-45	
117	2	02	
118	RCL3	36 03	
119	RCL4	36 04	
120	x	-35	
121	x	-35	
122	ST07	35 07	
123	+	-55	
124	RCL1	36 01	
125	ENT↑	-21	
126	x	-35	
127	x	-35	
128	RCL7	36 07	
129	RCL1	36 01	
130	x	-35	
131	-	-45	
132	1	01	
133	RCL2	36 02	
134	-	-45	
135	x	-35	
136	-	-45	
137	ST07	35 07	
138	RCL1	36 01	
139	ENT↑	-21	
140	x	-35	
141	2	02	
142	RCL4	36 04	
143	-	-45	
144	x	-35	
145	RCL1	36 01	
146	-	-45	
147	1	01	
148	RCL2	36 02	
149	-	-45	
150	x	-35	
151	RCL3	36 03	
152	RCL4	36 04	
153	x	-35	
154	1	01	
155	-	-45	
156	x	-35	
157	RCL6	36 06	
158	+	-55	
159	RCL7	36 07	
160	÷	-24	Value of A calculate
161	1	01	
162	RCL5	36 05	
163	-	-45	
164	x	-35	
165	RCL5	36 05	
166	+	-55	q_n - value calculate
167	ST06	35 06	
168	DSZI	16 25 46	

STEP	KEY ENTRY	KEY CODE	COMMENTS
169	GT05	22 05	
170	RCL6	36 06	q_n - value
171	R/S	51	displayed
172	*LBL5	21 05	Calculate q_e or
173	RCL1	36 01	q_n depending on
174	-	-45	R_8 - value
175	RCL1	36 01	
176	÷	-24	
177	ABS	16 31	
178	EEX	-23	
179	5	05	
180	CHS	-22	
181	X≤Y?	16-35	
182	GT06	22 06	
183	RCL6	36 06	q_e - value
184	R/S	51	displayed
185	*LBL6	21 06	
186	RCL6	36 06	
187	ST01	35 01	
188	GT04	22 04	
189	R/S	51	
190			
200			
210			
220			

LABELS

A S - M	B	C	D	E S - M - I
a	b	c	d	e
0	1	2	3	4
5	6	7	8	9

FLAGS

0
1
2
3

SET STATUS

FLAGS	ON	OFF
0	☐	☒
1	☐	☒
2	☐	☒
3	☐	☒

TRIG	
DEG	☒
GRAD	☐
RAD	☐

DISP	
FIX	☒
SCI	☐
ENG	☐
n	2

Program Description I

Program Title SELECTION AND GENE FREQUENCY

Contributor's Name Hewlett-Packard Company
Address 1000 N.E. Circle Boulevard
City Corvallis **State** Oregon **Zip Code** 97330

Program Description, Equations, Variables From adaptive values (W) of various genotypes, number of generations (n), and initial recessive gene frequency (q_o), the equilibrium recessive gene frequency ($\hat{q}$) and the recessive gene frequency after n-generations may be computed. Conversely, from the recessive gene frequency (q') may be calculated n (see Operating Limits and Warnings).

The following equations were used in the program:

$$q_{n+1} = \frac{q_n W_2 + q_n^2 (W_3 - W_2)}{W_1 + 2q_n(W_2 - W_1) + q_n^2(W_1 + W_3 - 2W_2)} \; ; \quad \hat{q} = \frac{W_1 - W_2}{W_1 + W_3 - 2W_2}$$

Where:

W_1, W_2, W_3 denote adaptive values for genotypes AA, Aa, aa, respectively (A = dominant and a = recessive gene)
$\hat{q}$ = equilibrium frequency for the recessive gene
q_n = recessive gene frequency after n-generations (q_o = initial recessive gene frequency)

Operating Limits and Warnings When it is desired to compute the number of generations (n) required to attain a given recessive gene frequency (q'), the value of n denotes the nearest whole number of generations which will yield a gene frequency equal to or less than q'.

Program Description II

Sketch(es)

Sample Problem(s)

(A) Given: $q_o = 0.90$, $W_1 = 0.5$, $W_2 = 1$, $W_3 = 0.4$, calculate q_n for n = 5, and $\hat{q}$.

(B) Given: $q_o = 0.90$, $W_1 = 0.5$, $W_2 = 1$, $W_3 = 0.4$, calculate n for $q' = 0.48$, and $\hat{q}$.

(C) Given: $W_1 = 0.5$, $W_2 = 1$, $W_3 = 0.4$, calculate $\hat{q}$ only.

Solution(s)

(A) 5 [E] 0.9 [↑] 0.5 [↑] 1 [↑] 0.4 [A] → $q_5 = 0.520$
[C] → $\hat{q} = 0.455$

(B) 0.48 [E] 0.9 [↑] 0.5 [↑] 1 [↑] 0.4 [B] → n = 7
[C] → $\hat{q} = 0.455$

(C) 0.5 [↑] 0.5 [↑] 1 [↑] 0.4 [A][C] → $\hat{q} = 0.455$
0.5 [↑] 0.5 [↑] 1 [↑] 0.4 [B][C] → $\hat{q} = 0.455$

Reference(s)

Gardner, E.J., Principles of Genetics, fifth edition, J. Wiley & Sons, 1975.

This program is a translation of the HP-65 Users' Library Program # 04332A submitted by Dr. Leo S. Reich.

User Instructions

SELECTION AND GENE FREQUENCY				
q_n	n	$\hat{q}$		Clear

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS		OUTPUT DATA/UNITS
1	Enter program				
2	Enter n or q'	n			
	whichever is available	or q'			
3	Press E to clear registers and store n		E		n or q'
	or q' in R_7				
4	Enter in order: q_o, W_1, W_2, W_3	q_o	↑		
		W_1	↑		
		W_2	↑		
		W_3			
5	If n is given and q_n is to be computed, press				
	A; if q' is given and n is to be calculated,		A		q_n
	press B		B		n
6	After n or q_n has been computed, calculate				
	$\hat{q}$ by pressing C		C		$\hat{q}$
7	If $\hat{q}$ alone is desired, enter in order:	W_1	↑		
	W_1, W_1, W_2, W_3 and press A C (or B C)	W_1	↑		
	(Note: if the machine runs unduly long	W_2	↑		
	after pressing A (or B), press R/S and	W_3	A	C	$\hat{q}$
	C to obtain $\hat{q}$).	or	B	C	$\hat{q}$

97 Program Listing I

STEP	KEY ENTRY	KEY CODE	COMMENTS
001	*LBLE	21 15	Clear registers and store n or q' in R_7
002	CLRG	16-53	
003	STO7	35 07	
004	RTN	24	
005	*LBLA	21 11	Given n, calculate q' (q_n)
006	DSP3	-63 03	
007	SF1	16 21 01	
008	*LBL2	21 02	
009	STO3	35 03	
010	R↓	-31	
011	STO2	35 02	
012	R↓	-31	
013	STO1	35 01	
014	R↓	-31	
015	*LBL1	21 01	
016	STO4	35 04	
017	RCL1	36 01	
018	RCL3	36 03	
019	+	-55	
020	RCL2	36 02	
021	2	02	
022	×	-35	
023	-	-45	
024	STO5	35 05	
025	×	-35	
026	RCL4	36 04	
027	×	-35	
028	RCL4	36 04	
029	2	02	
030	×	-35	
031	RCL2	36 02	
032	RCL1	36 01	
033	-	-45	
034	×	-35	
035	+	-55	
036	RCL1	36 01	
037	+	-55	
038	RCL3	36 03	
039	RCL2	36 02	
040	-	-45	
041	RCL4	36 04	
042	ENT↑	-21	
043	×	-35	
044	×	-35	
045	RCL2	36 02	
046	RCL4	36 04	
047	×	-35	
048	+	-55	
049	X⇄Y	-41	
050	÷	-24	
051	STO8	35 08	
052	1	01	
053	ST+6	35-55 06	
054	F1?	16 23 01	
055	GTO0	22 00	
056	RCL7	36 07	
057	RCL8	36 08	
058	X>Y?	16-34	
059	GTO1	22 01	
060	RCL6	36 06	
061	R/S	51	
062	GTO1	22 01	
063	*LBL0	21 00	
064	RCL6	36 06	
065	RCL7	36 07	
066	X>Y?	16-34	
067	GTO3	22 03	
068	RCL8	36 08	
069	R/S	51	
070	*LBL3	21 03	
071	RCL8	36 08	
072	GTO1	22 01	
073	*LBLB	21 12	Given q', calculate n
074	DSP0	-63 00	
075	CF1	16 22 01	
076	GTO2	22 02	
077	*LBLC	21 13	Calculate $\hat{q}$
078	DSP3	-63 03	
079	RCL1	36 01	
080	RCL2	36 02	
081	-	-45	
082	RCL5	36 05	
083	÷	-24	
084	RTN	24	
085	R/S	51	
090			
100			
110			

SET STATUS

FLAGS	ON	OFF
0	☐	☒
1	☐	☒
2	☐	☒
3	☐	☒

TRIG	
DEG	☒
GRAD	☐
RAD	☐

DISP	
FIX	☒
SCI	☐
ENG	☐
n	2

REGISTERS

0	1	2	3	4	5	6	7	8	9
	W_1	W_2	W_3	q_o	Used	Counter	n or q'	Used	

S0	S1	S2	S3	S4	S5	S6	S7	S8	S9

A	B	C	D	E	I

Program Description I

Program Title GENETIC INFERENCE FROM TRUNCATE DATA

Contributor's Name Hewlett-Packard Company

Address 1000 N.E. Circle Boulevard

City Corvallis **State** Oregon **Zip Code** 97330

Program Description, Equations, Variables A problem often encountered by geneticists in attempting a complete ascertainment for a recessive trait stems from an inability to identify the sibships with all normal offspring (the affected offspring are only identifiable). This program corrects the resulting truncate data by the so-called direct "A priori" method (the parental genotypes are assumed). In this manner are calculated: the proportion of affected offspring ($\hat{q}$), the goodness of fit of the assumption made, e.g., for the existence of heterozygous parents (χ^2, chi-square), and the probability that any deviation between observed and expected values of affected offspring would arise by chance alone (P) [see Operating Limits and Warnings].

The equations employed are:

$$\hat{q} = \frac{\Sigma D}{\Sigma Tc} \;;\quad T_c = \frac{AB}{1-p^A} \;;\quad \Sigma T_c(1-p) = \Sigma D \text{ (expected)} \;;$$

$$\chi^2 = \frac{(\Sigma D - \Sigma D_{exp})^2}{\Sigma D_{exp}} \longrightarrow P$$

where:

T_c = corrected total data

A = sibship size

B = number of sibships,

D and $D_{exp.}$ = observed and expected affected for one set of dat

p = proportion of normal offspring

Operating Limits and Warnings The calculation of χ^2 (for one degree of freedom) is accurate; however, the value of P corresponding to χ^2 is only approximate at the high values of P(ca.0.9) and at intermediate values (ca.0.5).

Program Description II

Sketch(es)

Sample Problem(s) In six families found to have cases of spongy type polycystic kidneys of early onset, the following data was obtained. Assuming that parental heterozygotes exist for this recessive trait ($p=0.75$, $q=1-p = 0.25$) compute $\hat{q}$, χ^2, P.

Data Set No.	1	2	3
Total affected	3	4	2
No. Sibships	3	2	1
Sibship size	2	4	7

Solution(s)

.75 [E] 3 [↑] 3 [↑] 2 [A] 4 [↑] 2 [↑] 4 [A] 2 [↑] 1 [↑] 7 [A]
[B] → $q = 0.269$, [C] → $\chi^2 = 0.047$,
[D] → $P \sim 0.853$

Reference(s) Levitan, M. and Montagu, A., Textbook of Human Genetics, second printing, Oxford University Press, 1973, pages 422 ff.

This program is a translation of the HP-65 Users' Library Program #04331A submitted by Dr. Leo S. Reich.

User Instructions

1 GENETIC INFERENCE FROM TRUNCATE DATA 2

Calc. | $\hat{q}$ | χ^2 | P | Clear

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
1	Enter program			
2	Clear registers and store p (assumed			
	proportion of normal offspring) in R_1	p	E	
3	For each set of data, enter D (totally	D	↑	
	affected), B (number of sibships),	B	↑	
	and A (sibship size) and press key A	A	A	n=no data sets entered
4	Repeat step 3 for each set of data until the			
	value of the counter (n) is equal to all			
	the sets of data which are to be entered			
5	Calculate the corrected proportion of the			
	affected offspring ($\hat{q}$) by pressing B		B	$\hat{q}$
6	Calculate the goodness of fit between the			
	observed total of affected and the			
	expected total of affected (χ^2) by press C		C	χ^2
7	Calculate the value of P corresponding to χ^2			
	(probability that any deviation is due to			
	chance alone)		D	P
	(Note: the value of P is approximate at high			
	P-values, - see Operating Limits and Warnings)			

97 Program Listing I

STEP	KEY ENTRY	KEY CODE	COMMENTS
001	*LBLE	21 15	Clear registers and store p in R_1
002	DSP3	-63 03	
003	CLRG	16-53	
004	STO1	35 01	
005	RTN	24	
006	*LBLA	21 11	Calculate intermediate value
007	RCL1	36 01	
008	X⇄Y	-41	
009	STO2	35 02	
010	Y^x	31	
011	1	01	
012	-	-45	
013	CHS	-22	
014	÷	-24	
015	RCL2	36 02	
016	×	-35	
017	STO3	35 03	
018	ST+7	35-55 07	
019	X⇄Y	-41	
020	ST+6	35-55 06	
021	RCL3	36 03	
022	1	01	
023	RCL1	36 01	
024	-	-45	
025	×	-35	
026	ST+4	35-55 04	
027	1	01	
028	ST+5	35-55 05	
029	RCL5	36 05	Counter
030	R/S	51	
031	*LBLB	21 12	Calculate $\hat{q}$
032	RCL6	36 06	
033	RCL7	36 07	
034	÷	-24	
035	RTN	24	
036	*LBLC	21 13	Calculate χ^2
037	RCL6	36 06	
038	RCL4	36 04	
039	-	-45	
040	ENT↑	-21	
041	×	-35	
042	RCL4	36 04	
043	÷	-24	
044	RTN	24	
045	*LBLD	21 14	Calculate P for 1 degree of freedom
046	.	-62	
047	4	04	
048	5	05	
049	X>Y?	16-34	
050	GTO1	22 01	
051	X⇄Y	-41	
052	.	-62	
053	6	06	
054	3	03	
055	5	05	
056	×	-35	

STEP	KEY ENTRY	KEY CODE	COMMENTS
057	.	-62	
058	5	05	
059	5	05	
060	+	-55	
061	CHS	-22	
062	e^x	33	
063	RTN	24	
064	*LBL1	21 01	
065	X⇄Y	-41	
066	2	02	
067	.	-62	
068	4	04	
069	3	03	
070	×	-35	
071	.	-62	
072	0	00	
073	4	04	
074	5	05	
075	+	-55	
076	CHS	-22	
077	e^x	33	
078	RTN	24	
079	R/S	51	
080			
090			
100			
110			

SET STATUS

FLAGS	ON	OFF	TRIG		DISP	
0	☐	☒	DEG	☒	FIX	☒
1	☐	☒	GRAD	☐	SCI	☐
2	☐	☒	RAD	☐	ENG	☐
3	☐	☒			n 2	

REGISTERS

0	1	2	3	4	5	6	7	8	9
	p	A	T_c	ΣD(exp)	Counter	ΣD	ΣT_c		

S0	S1	S2	S3	S4	S5	S6	S7	S8	S9

A	B	C	D	E	I

Program Description I

Program Title POSITIVE ASSORTATIVE MATING FOR A RECESSIVE PHENOTYPE

Contributor's Name Hewlett-Packard Company

Address 1000 N.E. Circle Boulevard

City Corvallis **State** Oregon **Zip Code** 97330

Program Description, Equations, Variables Recessive phenotype frequencies may be computed after any specified number of generations of random and concurrent positive assortative mating. Equilibrium values may also be calculated. Equal viability and fertility are assumed for the two types of mating. Then, assuming a two allele locus consisting of the dominant and recessive genes, A and a, respectively, and that a proportion, r, of assortative matings are either A x A (AA x AA, AA x Aa, Aa x Aa) or a x a (aa x aa) with frequencies equal to those of the dominant and recessive phenotype, $(1-R_t)$ and R_t, respectively, at generation t, the following expression can be derived:

$$R_{t+1} = (1-r)q^2 + r\,\frac{[q^2 + R_t(1-2q)]}{1 - R_t}$$

where:

q = recessive gene frequency

(1-r) = fraction of population mating at random.

Operating Limits and Warnings

Program Description II

Sketch(es)

Sample Problem(s) Given the following values: initial recessive phenotype frequency ≡ R_0 = .01, r = 0.75, q = 0.10,

Calculate a) recessive phenotype frequency after 4 generations (t=4)

b) equilibrium recessive phenotype frequency ($\bar{R}$).

Solution(s)

a) .01 [↑] .75 [↑] .1 [↑] 4 [A] → R_4 = .0239

b) [R/S] → $\bar{R}$ = .0266

Reference(s) Cavalli-Sforza, L.L. and Bodmer, W.F., The Genetics of Human Populations, pgs. 538-540, W.H. Freeman, 1971.

This program is a translation of the HP-65 Users' Library Program #04846A submitted by Dr. Leo S. Reich.

User Instructions

1 POSITIVE ASSORTATIVE MATING FOR A RECESSIVE PHENOTYPE 2

calc.

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS		OUTPUT DATA/UNITS
1	Enter program				
2	Enter in order: R_0 (initial value),	R_0	↑		
	r, q, t	r	↑		
		q	↑		
		t			
3	Compute R_t by pressing A		A		R_t
4	Compute equilibrium value, R, by then				
	pressing R/S		R/S		$\bar{R}$
	[When $\bar{R}$ is desired outright, set t=0 in				
	step 2 and press A].				

97 Program Listing I

STEP	KEY ENTRY	KEY CODE	COMMENTS
001	*LBLA	21 11	Store values in R_5, R_1, R_2, R_3, and calculate recessive phenotype frequency
002	DSP4	-63 04	
003	STO5	35 05	
004	R↓	-31	
005	STO1	35 01	
006	R↓	-31	
007	STO2	35 02	
008	R↓	-31	
009	0	00	
010	STOI	35 46	
011	R↓	-31	
012	*LBL1	21 01	
013	DSZI	16 25 46	
014	GSB3	23 03	
015	ENT↑	-21	
016	×	-35	
017	1	01	
018	ENT↑	-21	
019	2	02	
020	RCL1	36 01	
021	×	-35	
022	-	-45	
023	RCL3	36 03	
024	×	-35	
025	+	-55	
026	1	01	
027	RCL3	36 03	
028	-	-45	
029	÷	-24	
030	RCL2	36 02	
031	×	-35	
032	1	01	
033	RCL2	36 02	
034	-	-45	
035	RCL1	36 01	
036	ENT↑	-21	
037	×	-35	
038	×	-35	
039	+	-55	
040	STO4	35 04	
041	RCLI	36 46	
042	CHS	-22	
043	RCL5	36 05	
044	X≠Y?	16-32	
045	GTO0	22 00	
046	RCL4	36 04	Display recessive phenotype frequency
047	R/S	51	
048	*LBL0	21 00	
049	RCL4	36 04	
050	RCL3	36 03	
051	-	-45	
052	RCL3	36 03	
053	÷	-24	
054	EEX	-23	
055	5	05	
056	CHS	-22	

STEP	KEY ENTRY	KEY CODE	COMMENTS
057	X≤Y?	16-35	
058	GTO2	22 02	
059	RCL4	36 04	Display recessive phenotype frequency at equilibrium
060	R/S	51	
061	*LBL2	21 02	
062	RCL4	36 04	
063	GTO1	22 01	
064	*LBL3	21 03	
065	STO3	35 03	
066	RCL1	36 01	
067	RTN	24	
068	R/S	51	
070			
080			
090			
100			
110			

SET STATUS

FLAGS	ON	OFF	TRIG		DISP	
0	☐	☒	DEG	☒	FIX	☒
1	☐	☒	GRAD	☐	SCI	☐
2	☐	☒	RAD	☐	ENG	☐
3	☐	☒			n	2

REGISTERS

0	1	2	3	4	5	6	7	8	9
	q	r	Initial R_t	Used	no. of generation				

S0	S1	S2	S3	S4	S5	S6	S7	S8	S9

A	B	C	D	E	I
					Used

Hewlett-Packard Software

In terms of power and flexibility, the problem-solving potential of the Hewlett-Packard line of fully programmable calculators is nearly limitless. And in order to see the practical side of this potential, we have several different types of software to help save you time and programming effort. Every one of our software solutions has been carefully selected to effectively increase your problem-solving potential. Chances are, we already have the solutions you're looking for.

Application Pacs

To increase the versatility of your fully programmable Hewlett-Packard calculator, HP has an extensive library of "Application Pacs". These programs transform your HP-67 and HP-97 into specialized calculators in seconds. Each program in a pac is fully documented with commented program listing, allowing the adoption of programming techniques useful to each application area. The pacs contain 20 or more programs in the form of prerecorded cards, a detailed manual, and a program card holder. Every Application Pac has been designed to extend the capabilities of our fully programmable models to increase your problem-solving potential.

You can choose from:

Statistics
Mathematics
Electrical Engineering
Business Decisions
Clinical Lab and Nuclear Medicine
Mechanical Engineering
Surveying
Civil Engineering
Navigation

Users' Library

The main objective of our Users' Library is dedicated to making selected program solutions contributed by our HP-67 and HP-97 users available to you. By subscribing to our Users' Library, you'll have at your fingertips, literally hundreds of different programs. No longer will you have to: research the application; program the solution; debug the program; or complete the documentation. Simply key your program to obtain your solution. In addition, programs from the library may be used as a source of programming techniques in your application area.

A one-year subscription to the Library costs $9.00. You receive: a catalog of contributed programs; catalog updates; and coupons for three programs of your choice (a $9.00 value).

Users' Library Solutions Books

Hewlett-Packard recently added a unique problem-solving contribution to its existing software line. The new series of software solutions are a collection of programs provided by our programmable calculator users. Hewlett-Packard has currently accepted over 6,000 programs for our Users' Libraries. The best of these programs have been compiled into 40 Library Solutions Books covering 39 application areas (including two game books).

Each of the Books, containing up to 15 programs without cards, is priced at $10.00, a savings of up to $35.00 over single copy cost.

The Users' Library Solutions Books will compliment our other applications of software and provide you with a valuable new tool for program solutions.

Options/Technical Stock Analysis
Portfolio Management/Bonds & Notes
Real Estate Investment
Taxes
Home Construction Estimating
Marketing/Sales
Home Management
Small Business
Antennas
Butterworth and Chebyshev Filters
Thermal and Transport Sciences
EE (Lab)
Industrial Engineering
Aeronautical Engineering
Control Systems
Beams and Columns
High-Level Math
Test Statistics
Geometry
Reliability/QA
Medical Practitioner
Anesthesia
Cardiac
Pulmonary
Chemistry
Optics
Physics
Earth Sciences
Energy Conservation
Space Science
Biology
Games
Games of Chance
Aircraft Operation
Avigation
Calendars
Photo Dark Room
COGO-Surveying
Astrology
Forestry

BIOLOGY

Demography, ecology, and genetics are included in these twelve programs from the biology category. Many of these programs have been formed by combining two HP-65 programs into one HP-67/97 program.

DEMOGRAPHY I: ESTIMATES OF PARAMETERS/RATES OF INCREASE

DEMOGRAPHY II: EXPECTATION OF LIFE AND REPRODUCTIVE VALUE

DIVERSITY AND EQUITABILITY INDICES

NICHE BREADTH AND OVERLAP/SHANNON'S H AND HORN'S R0

POPULATION SIZE ESTIMATE (JOLLY'S ESTIMATE)

CELL PHASE AND CYCLE TIMES

CROSSOVER: LOCATION/PRODUCTS

CHROMOSOME CLEAVAGE

RECESSIVE GENE FREQUENCY AFTER SELECTION, MUTATION, AND INBREEDING

SELECTION AND GENE FREQUENCY

GENETIC INFERENCE FROM TRUNCATE DATA

POSITIVE ASSORTATIVE MATING FOR A RECESSIVE PHENOTYPE

HEWLETT hp PACKARD

1000 N.E. Circle Blvd., Corvallis, OR 97330

Reorder No. 00097-14040 Printed in U.S.A. 00097-90215