HEWLETT-PACKARD



#### Users' Library Solutions

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 Program Listing I** and Program Listing I and 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.

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rogram Title DEMOGRAPHY I: Estimates of	of Parameters/Rates of Inc	rease
Hewlett-Packard Cor	<b>ND 0 D I</b> I	
ontributor's Name new lett-rackard con	прапу	
ddress 1000 N.E. Circle Boulevard		
;ity Corvallis	State Oreogn	Zip Code 97330
Program Description, Equations, Variables Ger	neration time is estimated	using the formula:
^ ~ <sup>ω</sup> Σx1 m		
$T = \underline{\alpha}^{-x-x}$		
R <sub>o</sub>		
where x is age, $1_x$ is the fraction m is the fecundity at age x, and the equation	nal survivorship to that a R is the net reproductiv O	ge from age clas <b>s</b> zero e rate, computed from
$R_{o} = \sum_{\alpha}^{\omega} 1_{\alpha} m_{\alpha}$		
In both equations $\alpha$ is the age of reproduction. Any number of non-r keying in a constant, k, that is a the program. This program is desi much more accurate estimates of th process. This program estimates t following approximate relationship	first reproduction, and w reproductive age classes i added to each age of repro igned for use with another ne intrinsic rate of incre the intrinsic rate of incr	is the age of last s allowed, by simply duction internally by (next), which compute ase by an iterative ease, r, using the
r ¥ log R		
<u>T</u>		
Using the estimate of r store survivorship and fecundity schedul program computes the sum $\Sigma e^{-\Sigma}$	ed in R <sub>8</sub> , and the products les stored in registers 1 <sup>-rx</sup> 1.m.	of the age-specific through 7, the
x=α	X X (Continued	on next page)
0.1		
perating Limits and Warnings Unly seven	reproductive age classes	are allowed and a
constant, k, indicates the age of	the oldest non-resproduct	tive age classes.

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Program Title		
Contributor's Name		
Address		
City	State	Zip Code

<b>Program Description Equations Variables</b> where $\alpha$ is the age of first reproduction
(1. m. is stored in $\mathbb{R}_{+}$ ) and $\omega$ 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 increased (if the sum is too small.
the estimate of r is decreased). The program then stores this new r in R <sub>o</sub> 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, $\lambda$ , which is simply e <sup>r</sup> .
If the user thinks the program is taking too long to compute r, it can be stopped
with the "CLx" button and R <sub>8</sub> recalled to see what value of r was being used in the
last_loop
Operating Limits and Warnings

This program has been verified only with respect to the numerical example given in *Program Description II*. User accepts and uses this program material AT HIS OWN RISK, in reliance solely upon his own inspection of the program material and without reliance upon any representation or description concerning the program material.

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## **User Instructions**

$\hat{\mathbf{r}} \neq \mathbf{r} \qquad \lambda$		
<b>1</b> DEMOGRAPHY I:	ESTIMATE PARAMETERS/RATES	OF INCREASE <b>Z</b>
$[] 1_1, m_1 1_2$	• ma lev me 1	
$\underbrace{\mathbb{D}}_{1_2}, \mathbf{m}_2 = 14$	$m_4 = 1_6, m_6 = 1_7, m_7$	K 1, I

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
1	Load side 1 and side 2			
2	Enter data as shown for Survivorship/Fecundity	11	ENT	
		ml	ENT	
		12	ENT	
		m <sub>2</sub>	Α	
		13	ENT	
		m <sub>3</sub>	ENT	
		14	ENT	
		m4	В	
		1 <sub>5</sub>	ENT	
		m5	ENT	
		16	ENT	
		m <sub>6</sub>	C	
		17	ENT	
		1 <sup>22</sup> 7	ENT	
	Enter age constant k	k	D	
3	Compute Î		E	Î
4	Compute r		R/S	ŕ
5	Recall R from R		RCL 9	R
	0 9			Q
6	Iterate the solution of r		f A	r
7	Compute the finite rate of increasing $\lambda$		f B	λ
				-

### 97 Program Listing I

STEP	KE۱	ENTRY	к	EY CODE		сомм	ENTS	STEP	KE	Y ENTRY	KEY	CODE		CON	MENTS	
0	101	*LBLA		21 -					057	3		03				
0	02	Х		-35	Da	ta entr	У		<b>8</b> 58	RCI 8	3	6 08				
0	103	ST02		35 82					<b>A</b> 59	+		-55				
0	04	R↓		-31					868	· ×		-75				
8	05	X		-35					DC1	Â		-55				
0	106	ST01		35 01					001	T DCLA	7	-33				
8	07	RTN		24					002	RUL4	3	0.04				
Ø	08	*LELE		21 12					003	4	-	<b>0</b> 4				
A	199	X		-35					064	KULB	3	508				
Ā	16	ST04		35 04					065	+		-55				
Â	111	P.L		-71					<b>U</b> 66	X		-35				
0 0	11 2	×		-75					067	+	_	-55				
6	17	ст <b>л</b> 7		75 07					<b>0</b> 68	RCL5	3	5 <b>0</b> 5				
0 0	111	5705		00 00					<b>0</b> 69	5		<b>0</b> 5				
	14	KIN TOLO		21					070	RCL8	3	5 <b>0</b> 8				
	13	#LDLU		21 13					071	+		-55				
e e	16	X OTOC		-30					072	x		-35				
U	17	5106		33 80	÷				073	+		-55				
6	18	K↓		-31					074	RCL6	3	5 06				
0	19	Х		-35					075	6		06				
0	20	ST05		35 05					076	RCL8	3	5 08				
0	21	RTN		24					Ø77	+		-55				
0	22	<b>*</b> LBLD		21 14					A78	×		-35				
0	23	STO8		35 08					Ø79	+		-55				
0	24	STOØ		35 00					<b>8</b> 8 <b>0</b>	PCIZ	3	5 <b>8</b> 7				
0	25	R↓		-31					000 001	7	0.	07 07				
0	26	x		-35					001	PCI 0	7	C 00				
0	27	ST07		35 07					002	KULD		-55				
0	28	RTN		24					000	т v		-33				
0	29	*LBLE		21 15					004	×		-33				
Ø	130	DSP4	-	-63 04					000		7	-33				
Ø	31	RCL1		36 01					086	RULS	3	5 <b>0</b> 7				
Â	132	RCL2		36 N2					087	÷		-24	Dia	. 1	ŵ	
A	177	RCL3		36 03					088	R/S	-	51		ртау	T	
0 0	174	DCI 4		76 04					089	RCL9	3	5 69				
6	175	+		-55					090	LN		32				
	172	, ,		-55					091	X₽Y		-41				
0	130	т ⊥		-55					092	÷		-24	Char	<u>^</u>	da D	
0	137	DOLE		-JJ 76 BE					<b>0</b> 93	ST08	3:	508	Stol	rer	in K8	
0	130	DOLG		30 0J 72 02					094	RTN		24		piay	r	
0	137	RULD		30 80					<b>09</b> 5	*LBLa	21 1	5 11				
0	40	RULT		30 UI EE					<b>0</b> 96	1		01				
U	141	+		-35					<b>8</b> 97	esb0	2	3 00				
U	142	+		-33					098	RCL 1	3	5 01				
6	143	+		-55					<b>0</b> 99	х		-35				
0	144	ST09		35 69					100	2		<b>8</b> 2				
0	45	RCLI		36 01					101	6SB0	2	3 00				
0	146	1		01					102	RCL2	3	5 02				
0	47	RCL8		36 03					103	x		-35				
0	48	÷		-55					104	+		-55				
0	49	х		-35					105	3		<b>A</b> 3				
0	150	RCL2		36 02					106	6SR0	2	7 00				
0	951	2		Ø2					107	PCI 3	3	6 83				
0	952	RCL8		36 08					188	X		-75				
0	153	÷		-55					109	- -		-55				
0	)54	х		-35					110	г А		94				
0	55	+		-55					111	7 0923	0	7 00				
	956	RCL3		36 03					112	6300 DCI 4	2	5 00 5 04				
				0	1.		REGI		112	RUL4	اق حا	0 04	18		9	
U	ľ	່ <b>1 m</b> ~		1~+1m~-	$_{-1}$ $ ^{3}$	$x+2^{m}\alpha+2$	$1_{\alpha+3}m_{\alpha+3}$	° <b>1</b> _,,п	ı/	1 <sub>0</sub> m~	, <b>↓</b> _  ′	$1_{\omega}\mathbf{m}_{\omega}$	ľk,	ŕ	Ř	
50		<u>, u</u>		S2	- 02		54	S5	$\alpha + 4$	S6	57 S7	~ ~	S8		S9	
30	ľ			52												
Δ			в				L	D			E			I		
~			ľ			Ĭ		-			_					

### 97 Program Listing II

STEP	KEY	ENTRY	KEY	CODE		COMMENTS		STEP	KEY ENTRY	KEY CODE	СОММ	ENTS
i	113	X	-	35								
i	114	+	-	55				170				
1	115	5		Ø5							_	
i	116	GSB0	23	00								
1	117	RCL5	36	Ø5								
1	118	Х	-	35								
i	119	÷	-	55								
1	120	6		<i>06</i>								
1	121	GSBØ	23	00							_	
1	122	RCL6	36	06							_	
1	123	X	-	35				100			4	
1	124	+	-	55				180			_	
1	125			67								
1	126	6SB0	25	00 07							4	
1	127	KULT	36	07							-	
1	128	×	-	30 55			~				_	
1	129	+	-	-33 	Note	insertion	ot				4	
	130	ENIT	-	21	an	'R/S" here w	i11				-	
1	131	ENIT	-	21	stor	each loop						
1	132	1		01 20	and	display the						
1	133	0		00 60	sum	for user's		190			-	
1	134 175	U ENTA		00 01	insp	pection (hit		100			-	
1	172	Di		21	R/S	to continue	)				-	
1	130	<b>∧</b> *	_	31 75							-	
1	170	TNT	15	33 74							-	
	170	P†	16-	71							-	
1	1 J B 1 A B	X=Y2	16-	77							-	
1	140	ETO1	22	а1 А1							-1	
<b>د</b>	142	BIOI R1		31							-	
1	143	R.	-	31								
1	144	1		01 01				200			-	
1	145		-	45							-	
-	146	_	-	52							-	
-	147	2		02								
-	148	×	-	35								
j	149	RCL8	36	08								
1	150	÷	-	55								
j	151	ST08	35	08								
1	152	GTŨa	22-16	11								
1	153 -	*LBL1	21	01								
1	154	RCL8	36	<i>08</i>				210				
t	155	RTN		24								
1	156 👘	¥LBL0	21	00								
i	157	RCLØ	36	88	Age c	onstant k						
1	158	÷	-	55							_	
1	159	RCL8	36	08							4	
1	160	Х	-	-35							-	
i	161	CHS	-	22							_	
1	162	e <sup>x</sup>		33							-	
1	163	RTN		24				220			-1	
]	164	¥LBLb ÿ	21 16	12		•					4	
1	165	e* ntu		<b>33</b> 37	Disp1	ay λ					-1	
1	100	KIN E 20		24 51		-					1	
	167	K/5		JI	~						1	
					LAE	BELS			FLAGS		SET STATUS	
$A_{1_1}$	` m 1↓	в13	↑ m <sub>3</sub> ↑		m <sub>5</sub> ↑	$^{\cup}$ 1 <sub>7</sub> $\uparrow$ m <sub>7</sub> $\uparrow$ E	Ť	, r	o	FLAGS	TRIG	DISP
$\frac{1_2}{1_2}$	<b>m<sub>2</sub>+</b>	$1_{4}$	<b>↑</b> m <sub>4</sub> ↑	16	• m <sub>6</sub> •	k			1,	ON OFF		
$r \rightarrow 0$	_ <u>r</u>	<u>h</u> Λ 1		<u>с</u> 2			<u>&gt;</u>		2			
-		<u>use</u>	ed	<u></u>					Į			
5		6		7		8 9	)		3			n_2

Program Title DEMOGRAPHI 11: Expectation	of Life and Reproductiv	ve Value
Contributor's Name Hewlett-Packard Compa	iny	
Address 1000 N.E. Circle Boulevard		
City Corvallis	State Oregon	Zip Code 97330
Program Description, Equations, Variables After	(x) age-specific surv	rate of increase $r$ ,

Fisher's reproductive value is computed from the equation:

 $\mathbf{v}_{\mathbf{x}} = \frac{\mathbf{e}^{\mathbf{r}\mathbf{x}}}{\mathbf{l}_{\mathbf{x}}} \sum_{\mathbf{t}=\mathbf{x}}^{\infty} \mathbf{e}^{-\mathbf{r}\mathbf{t}} \mathbf{l}_{\mathbf{t}} \mathbf{m}_{\mathbf{t}}$ 

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,  $R_0$ , and the finite rate of increase,  $\lambda$ , from the equations

$$R_o = \sum_{\alpha}^{\omega} \mathbf{1}_x m_x \text{ and } \lambda = e^r$$

Generation time is computed with the approximate formula:

$$\hat{\mathbf{T}} = \frac{\overset{\boldsymbol{\omega}}{\Sigma} \mathbf{x} \mathbf{1} \mathbf{x}^{\mathbf{m}} \mathbf{x}}{\mathbf{R}}$$

( $\alpha$  is age of first reproduction and  $\omega$  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.

This program has been verified only with respect to the numerical example given in *Program Description II*. User accepts and uses this program material AT HIS OWN RISK, in reliance solely upon his own inspection of the program material and without reliance upon any representation or description concerning the program material.

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ketch(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:

	<u>Age</u> (x)	Survivorship $(1_x)$	Fecundity $(m_{\chi})$
	0	1.0	0
	1	.9	_0
	2	.7	0
the intrinsic rate	3	• 5	0
$\langle of natural increase \langle e \rangle$	4	. 4	1
is known to be .0552)	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 $\uparrow$ ] 9[ENTER $\uparrow$ ] .1[ENTER $\uparrow$ ] Repeat for 8 thru 0 to E <sub>0</sub> = 4.41, v <sub>0</sub> = 1.000	.01 [ENTER ↑] 1 [B] → 10; [C]→1.000;[R/S]→1.000 .5[B] → 9; [C] → 1.100; [R/S] → 0.595 obtain values in table
	$E_1 = 3.79, v_1 = 1.174$	
	$E_2 = 3.59$ , $v_2 = 1.595$ $E_3 = 3.62$ , $v_3 = 2.361$	$[D] \rightarrow 1.3600 (R_0)$
	$E_4 = 3.28, v_4 = 3.118$	$[R/S] \rightarrow 1.0568 (\lambda)$
	$E_5 = 3.03, v_5 = 2.985$ $E_6 = 3.05, v_6 = 3.146$	$[E] \rightarrow 5.625$ (T)
	$E_7 = 2.05, v_7 = 1.739$	
	$E_8 = 2.10, v_8 = 1.563$	
	$E_9 = 1.10, v_9 = 0.595$	
-	$E_{10}$ = 1.00, $v_{10}$ = 1.000	

Reference(s)	Fisher, R.A. 1930. The genetical theory of natural selection. Oxford.
Mar da - Mar - 14	Mertz, D.B. 1970. Notes on methods used in life-history studies, pp 4-17
an a same an analysis a same same same same	in Connell, Mertz, and Murdoch's "Readings in ecology and
	ecological genetics." Harper & Row.
	Pianka, E.R. 1974. Evolutionary ecology. Harper & Row.
The state of the s	Poole, R.W. 1974. An introduction to quantitative ecology. McGraw-Hill.
	Wilson, E.O. and W. Bossert. 1971. A primer of population biology Singue
This prog	ram is a translation of the HP-65 Users' Library Program #03639A
submitted	by Eric R. Pianka.

## **User Instructions**

<b>1</b> DEMOGRAPHY II: E <sub>x</sub> and v <sub>x</sub>		5
$S = r = x \uparrow 1_{y} \uparrow m = E_{y}, v_{y} = R_{0}, \lambda$	_	_ /

1       Read program (in "run" mode!)	PUT UNITS
2 Enter intrinsic rate of increase in R1   3 Key in age (x) of oldest age group first   4 Key in survivorship of oldest age group, (1x)   1 1   4 Key in fecundity of oldest age group (mx)   5 Key in fecundity of oldest age group (mx)   6 Compute and record expectation of life. Exp	
2       Enter intrinsic rate of increase in R1       r       A       A         3       Key in age (x) of oldest age group first       x       A       A         3       Key in age (x) of oldest age group first       x       A       A         4       Key in survivorship of oldest age group, (1x)       1x       A       A         5       Key in fecundity of oldest age group (mx)       mx       B       (x)         6       Compute and record expectation of life. Ex       C       Ex	
3       Key in age (x) of oldest age group first       x       1         4       Key in survivorship of oldest age group, (l <sub>x</sub> )       l <sub>x</sub> 1         4       Key in fecundity of oldest age group, (l <sub>x</sub> )       l <sub>x</sub> 1         5       Key in fecundity of oldest age group (m <sub>x</sub> )       m <sub>x</sub> B       (x)         first       Image (x)       Image (x)       Image (x)       Image (x)         6       Compute and record expectation of life. Employee       C       Employee	
3       Key in age (x) of oldest age group first       x       +	
4       Key in survivorship of oldest age group, (l <sub>x</sub> )       l <sub>x</sub> 1         first       Image: state sta	
4       Key in survivorship of oldest age group, $(1_x)$ $1_x$ $\uparrow$ first       Image: Stress	
first       B       (x)         5       Key in fecundity of oldest age group (m <sub>x</sub> )       m <sub>x</sub> B       (x)         first       C       Ex       C       Ex	
5       Key in fecundity of oldest age group (mx)       mx       B       (x)         first	
first     C       6     Compute and record expectation of life. Exp	
6 Compute and record expectation of life. E.	
7 Compute and record reproductive value, v <sub>x</sub> R/S V <sub>x</sub>	
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 <sub>x</sub> and v <sub>x</sub> for all ages.	
9 Calculate net reproductive rate, R <sub>o</sub>	)
10 Calculate finite rate of increase, $\lambda$ [R/S] $\lambda$	
11   Compute estimate of mean generation time, T   E   T	

## 97 Program Listing I

STEP	KE	Y ENTRY	KEY CODE	COMMENTS	STEP	KE	Y ENTRY	κ	EY CODE	СОММ	ENTS
	001	*LBLA				<b>0</b> 57	R∕S		51	Display R	·0
	002	CLRG	16-53 75 01	Clear registers		058	RCL1		36 81		
	003 BBA	5101 PT4	30 UI 94	Store r in R <sub>1</sub>		059	e^ DTU		33 57	Dissian )	
	004 005	*IELE	21 12			050	KIN + DIE		24	Display A	
	006	DSP3	-63 03			001 062	FC: 9		76 89		
	007	ST04	35 04	Store m <sub>w</sub> in R/		062 063	RCL7		36 67		
	008	X≠Y	-41	x 4		<i>064</i>	÷		-24		
	009	ST03	<b>3</b> 5 03	Store $l_x$ in $R_3$		065	R∕S		51	Display Î	
	010	Х	-35			066	RCL7		36 07		
	011	RCL7	36 07			067	LN		32		
	012	÷ otot	-55			<b>0</b> 68	RCL1		36 01		
	013	5107	33 67			069	÷		-24		
	014	<b>R∳</b> 0700	-31 75 80	Store w in De		070	RTN		24	Dispiay I	
	015 016	9102 RCL1	35 82 36 81	Store x in K2		071	K/S		51		
	017	X	-35								
	018	ST05	35 05								
	019	RCL6	36 06								
	020	RCL3	36 03								
	021	+	-55								
	<b>0</b> 22	ST06	35 06								
	023	RCL2	36 02		080						
	024	RULS	36 U3 76 01		080						
	023 026	KUL4 V	30 04 -75								
	020 й27	X	-35								
	028	RCLS	36 39								
	029	÷	-55								
	030	ST09	35 09								
	031	RCL2	36 02	Display age x							
	032	RTN	24								
	033	*LBLC	21 13		090						
	034 075	RULD	36 Ø5 76 97			+					
	035 076	- KULU	-24			1					
	037	R∕S	51	Display E.		1					
	038	RCL5	36 05								
	<b>0</b> 39	CHS	-22								
	040	e×	33								
	<b>0</b> 41	RCL3	36 03			+					
	042	X DOLA	-33 77 94			+					
	043 044	KUL4 X	JD 84 -75	1	100			-			
	<b>0</b> 45	RCLS	36 08	1							
	046	+	-55	]							
	047	ST08	35 08	1							
	<b>0</b> 48	RCL5	36 05	4		+					
	049	e×	33	4		+				SET STATUS	
	050	RCL3	36 03	1			1		=	TRIO	
	031 052	÷ x	-24 -75	1					ON OFF		
	053	RTN	24	Display v <sub>x</sub>					$0 \square \mathbf{X}$	DEG 🛛	FIX 🗓
	054	*LBLD	21 14		110				1 🗆 🕅		
,	<b>0</b> 55	DSP4	-63 04	4					$2 \square X$ $3 \square X$		n_2
	056	RCL7	36 07	<u> </u>	EGISTERS			L		Å	·
0		1 r	2	3 1 4	5		6 51		7	8 - rx1	9
		<u> </u>	A				<u>x<sup>1</sup> 2</u>		$\frac{L \mathbf{x}^{\mathrm{m}} \mathbf{x}}{\mathbf{x}^{\mathrm{m}}}$	S8	<sup>∠</sup> x⊥ <sub>x</sub> m <sub>x</sub>
50		51	52	53 54	55		30				~~
A			В	c	D			E		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:
$\{n_1, n_2, n_3, \dots, n_i\}$
The program computes the following:
Diversity = 3.3219 $(\log_{10} N - \frac{1}{N} \Sigma n_i \log_{10} n_i)$
Diversity
Equitability = $3.3219 (\log_{10}N)$
Where:
$n_i = number$ of individuals of the i th group
N = total number of individuals in the collection
$3.3219 = \text{conversion factor } \log_{10} \text{ to } \log_2$
Operating Limits and Warnings
n is a positive interger and $n > 1$ .

This program has been verified only with respect to the numerical example given in *Program Description II*. User accepts and uses this program material AT HIS OWN RISK, in reliance solely upon his own inspection of the program material and without reliance upon any representation or description concerning the program material.

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Sketch(es)		
Sample Proble	em(s)	
	$\int 7/0.11 000.020.180.180.7/0.180$	
	ι /40; II,000; 920; IOU; IOU, /40, IOU]	
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**

	DIVERSITY AND	EQUITABILITY INDEX		5
Initi	al data	correct div	er equit	_ /

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

## 97 Program Listing I

14			77 i rugi am		ning i		
STEP	KEY ENTR	Y KEY CODE	COMMENTS	STEP	KEY ENTRY	KEY CODE	COMMENTS
6	101 <b>*</b> LBLA	2i 11	Initialize, press A				
Ø	102 CLRG	16-53					
e	103 RTN	24					
8	004 *LBLB	21 12	No, individuals in	060			
8	<b>10</b> 5 STO6	35 <b>0</b> 6	ith group,				
8	106 ST+2	35-55 <b>8</b> 2	N = S + N				
9	107 LOG	16 <b>3</b> 2					
0	108 RCL6	36 06					
0	109 X	-35	X = S * log(s)				
8	10 ST+3	35-55 03	Z = X + Z				
8	)11 i	01					
8	112 ST+9	35-55 <i>09</i>					
8	113 RCL9	36 09					
8	14 RTN	24		070			
0	15 ¥LBLD	21-14	Diversity				
0	16 RCL3	36 03	Z/N				
8	17 RCL2	36 02					
0	18 ÷	-24					
Ø	119 ST04	35 04					
A	20 RCL2	36 02					
Ā	21 106	16 32					
ค	22 RCL4	36 84					
Â	123 -	-45	Log (N) - (Z/N)				
ด	24 3	N3		080			
a a	25	-62					
a a	26 7	02 03					
a a	27 2	82 82					
A	128 1	61					
a a	129 9	01 99					
a a	20 STO1	75 Ø1					
0	100 0701 171 v	-75	$3 3219 \times [1 \circ \alpha(N) - (7/N)]$				
0	от ^ 179 рты	-55	5.5219 [10g(N) – (2) N	' <b> </b>			
0	132 KIN 177 VIDIE	21 15	Fauitability				
0	133 <b>FEDEE</b> 174 STO7	75 67	Equicability	090			
0	175 DCI 2	76 89					
0	5J KULZ 172 INC	16 72					
0	136 LUG 177 Drii	10 32 76 Ai					
0	57 KULI 70 V	-75					
0 0	30 ^ 70 CTNO	-33 75 AC					
0	37 3100 40 pri7	33 00 76 07					
0	40 RULI Mi delo	30 07 72 00					
0	41 KULO	30 00					
0	42 <del>-</del> 47 рти	-24					
0		24	Correct	100	1		
0	45 CTOC	21 13 75 82					
0	4J 5106 4C CT-2	33 00 75-45 00					
0	40 31-2	3J-4J 02 12 79					
0	47 LU5	16 32					
0	40 KULD	30 00					
	77 X 50 CT_7	-33 75_45 A7					SET STATUS
	JU 31-3 51 1	3 <b>3-4</b> 3 <b>0</b> 3 At				FL A C C	
8	Ы I Басто	01 75-45 00					
	שב אב ביי הדיי	3 <b>3-43 0</b> 9 04					
U 0	JO KIN EA DZO	24 E 1		110			GRAD 🗌 SCI 🗍
ש ש	34 K/S	. 51				2 🗆 🕱	RAD 🗆 ENG 🗆
			]			3 🗆 🖾	n
			REGI	STERS			
0	1	2 70	3	5	6	7	8 9
	Use	α ΣS	ΣSlogS Used	L	S	Used	Used i
S0	S1	S2	S3 S4	S5	S6	S7	58 59
					I		
А		В	С	D		E	l'
1		1		1			

NICHE BREADTH AND OVERLAP AND SHANNON'S H AND HORN'S R **Program Title** Hewlett-Packard Company Contributor's Name 1000 N.E. Circle Boulevard Address Corvallis City 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:  $B = \frac{1}{\sum_{i=1}^{n} p_i^2}$  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:  $0 = \frac{\Sigma p_i q_i}{\sqrt{\Sigma p_i^2 \Sigma q_i^2}}$ 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.

This program has been verified only with respect to the numerical example given in *Program Description II*. User accepts and uses this program material AT HIS OWN RISK, in reliance solely upon his own inspection of the program material and without reliance upon any representation or description concerning the program material.

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Program Title		
Contributor's Name		
Address		
City	State	Zip Code
Program Description, Equations, Variables		
to the formula:		
$H_{p} = -\Sigma p_{i} Ln p_{j}$	i or -Σq <sub>i</sub> LN q <sub>i</sub> .	= H <sub>q</sub>
Each H is expressed both as an absolute fraction of the maximal possible H value	e value and as a le, H <sub>max</sub> .	"J" value, which is a
The program also computes Horn's (1966 simplified computational formula:	) measure of ove	rlap, R <sub>o</sub> , from a
Overlap =	$R = \frac{((H_p + H_q))}{(H_p + H_q)}$	$\frac{2}{2} - \frac{H_r}{r} + 1$
-	o Ln 2	
where H <sub>r</sub> is computed from the p <sub>i</sub> and q according to Shannon's formula (above)	i vectors, with • H <sub>r</sub> is stored	$r_i = (p_i + q_i)/2$ in register 6.
Operating Limits and Warnings		

This program has been verified only with respect to the numerical example given in *Program Description II*. User accepts and uses this program material AT HIS OWN RISK, in reliance solely upon his own inspection of the program material and without reliance upon any representation or description concerning the program material.

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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: <u>Resource 1</u> 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);	
Species 1 .1 Community A Community B	
Species 2 .2 .4	
Species 4 0.0 .2	
Species 5 .2 .3	
What is the diversity of each and how much do they overlap?	
Solution(s) l. a. Initialize (zero all registers): [CL REG] b. Key in P <sub>i</sub> , q <sub>i</sub> data as follows:	
0.2 [↑] 0.3 [A]	
$0.5$ [ $\uparrow$ ] $0.1$ [A]	
0.1 [T] 0.4 [A] 0.2 [A]	
c. Compute niche breadths: [B] 2.94 [R/S] 0.74 $(B_p/n)$	
$[R/S] 3.33 [R/S] 0.83 (B'_q/n)$	
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.	

Acad. Sci., USA 71: 2141-2145. May, R.M. 1975. Some notes on measurements of the competition matix, α. Ecology 56: in press.

Sketch(es)

C Sample Problem(s)	
Solution(s) 2. a. Initialize (zero all registers): [CL REG] b. Key in the five sets of p <sub>i</sub> and q <sub>i</sub> data, letting i run from 1	to 5:
0.1 [†] 0.0 [f] [A] 0.2 [†] 0.4 [f] [A]	
$0.0 [\uparrow] 0.2 [f] [A] 0.5 [A] 0.1 [f] [A]$	
0.2 [↑] 0.3 [f] [A]	
c. Compute diversity of community A (H <sub>p</sub> ) : [f][B] 1.28, [R/S] 0. d. Compute diversity of community B (H <sub>q</sub> ): [f][C] 1.22, [R/S] 0.7 e. Compute community overlap, R <sub>o</sub> [f][D] 0.71	80(H/H <sub>ma</sub> '6(H/H <sub>max</sub>
Reference(s) Shannon, C.E. and W. Weaver, 1949. The mathematical theory of commu Univ. Illinois Press, Urbana.	nication
Horn, H.S., 1966. Measurement of "overlap" in compar <b>a</b> tive ecologica studies. Amer. Naturalist 100: 419-424.	1
Lloyd, M.J.H.Zar, and J. Karr. 1968. On the calculation of informat theoretical measures of diversity. Amer. Midlan Naturalist 79:	ion 257 <b>-</b> 272.
submitted by Eric R. Pianka.	.50A

## **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 <sub>o</sub> , to to step 9.			
4	Enter pairs of data, p <sub>i</sub> , [ENTER <sup>†</sup> ] <b>↑</b> repeat til	Pi	<b>↑</b>	
	then q <sub>i</sub> 🗸 finished	qi	Α	
5	To remove erroneous data pairs, p <sub>i</sub> [ENTER†]	Pi		
	qi	qi	E	
6	After all n data pairs have been entered,			
	compute niche breadth for first species		В	Bp
	compute its standardized niche breadth		R/S	$B_n/n$
	compute niche breadth for second species		R/S	B <sub>q</sub>
	compute its standardized niche breadth		R/S	B <sub>q</sub> /n
7	Compute niche overlap		C ] [ ]	0
	compute Arc sin of overlap		R/S	Arc sin(O
8	Check sum of p <sub>i</sub> to see if it is unity		D ]	ΣPi
	check sum of q <sub>i</sub> to see if it is unity		R/S	Σqi
9	Enter data pairs	Pi		
		٩ <sub>i</sub>	f A	
	repeat 9 until all pairs of data are entered			
10	To remove erroneous data pairs, p <sub>i</sub> [ENTER <sup>†</sup> ]	<sup>p</sup> i		
	qi	٩i	f E	
11	Compute diviersity H <sub>p</sub>		<b>f B</b>	-SpilNpi
12	Compute J (H/H <sub>max</sub> )		[R/S ]	H <sub>p</sub> /H <sub>max</sub>
13	Compute diversity H <sub>q</sub>		f ] [ C ]	$-\Sigma q_i LNq_i$
14	Compute J (H/H <sub>max</sub> )			Ha/Hmax
15	Calculate overlap R <sub>o</sub>		f   D	R <sub>o</sub>

## 97 Program Listing I

STEP	KE	EY ENTRY	KEY CODE	COMMENTS	STEP	KE	Y ENTRY	KEY CODE	COM	MENTS
	001	*LBLA	21 11	p † q		957	RCL1	36 01		
	002	ST07	35 07	k · · · · ·	6	958	RTN	24		
	<b>0</b> 03	ST+4	35-55 04			959	*LBLD	21 14	Chk.	
	004	X2	53		ŧ	960	RCL2	36 02		
	005	ST+5	35-55 05		ł	961	R∕S	51		
	006	XŦY	-41		l	962	RCL4	36 <b>04</b>		
	007	ST+2	35-55 02		6	963	RTN	24		
	008	χ2	53			964	<b>≭LB</b> La	21 16 11	p ↑ q	
	009	51+3	35-55 03			965	ST07	35 07		
	010	LSIX	16-63		l	966	X≠Y	-41		
	U11 040	RUL7	36 07		(	967	ST08	35 08		
	012	X 07.0	-33		e e	968	ST+4	35-55 04		
	013	51+6	30-00 06		l	969	6	00		
	014	1 67.1	01 75 55 01		l. l	970	X=Y?	16-33		
	010	51+1	33-33 <b>0</b> 1 76 Bi			971	6101	22 01		
	010	RULI	30 01		ŧ	972	K∔ EUT+	-31		
	017		<b>24</b> 03 40		(	973	ENIT	-21		
	010	RCL7	21 12 76 07	<sup>B</sup> p, <sup>B</sup> q		874	LN	32		
	017	KULS 170	30 03 50		ł	975	X of F	-35		
	020 021	1/A D/C	J2 51		l	9/6	51-5	33-43 05		
	021	R/D PCI1	JI 76 Q1		ł	977	#LBL1	21 01		
	022	KULI ÷	-24		1	978 970	KUL7	36 07 75 55 00		
	023 024	₽/9	51		e	9/3 200	51+2	33-33 02		
	02 <del>-</del> 025	RCI 5	31 36 05		e	280 201	0 v_vo	00 17 77		
	025 026	1/8	50 65			901 902	A=1? CTO2	10-33		
	020 027	R/S	51		, ,	002 907	6102 Di	-71		
	<u>я28</u>	RCI 1	36 01			903 904	K∳ ENTA	-31		
	R29	÷	-24			204		72		
	030	RTN	24			986	X	-75		
	031	*LBLC	21 13	0		900 <b>9</b> 87	ST-7	75-45 07		
	032	RCL3	36 03	0		888	*1 Ri 2	21 <b>0</b> 2		
	033	RCL5	36 05			989	Pris	76 88		
	034	X	-35			1902 1908	RCL 7	36 07		
	035	<b>1</b> X	54		Ĩ	991	+	-55		
	036	RCL6	36 06		Ĩ	192	2	Ø2		
	037	X≠Y	-41		í	93	÷	-24		
	038	÷	-24		i	394	0	00		
	039	R∕S	51		Ĩ	995	X=Y?	16-33		
	040	SIN-	16 41	Takes Arc sin of O	l	396	GT03	22 03		
	041	RTN	24		í	97	R↓	-31		
	042	<b>≭LBLE</b>	21 15	Error	6	898	ENTT	-21		
	043	ST07	35 <b>0</b> 7		6	999	LN	32		
	044	ST-4	35-45 04		t	100	х	-35		
	045	X2	53		1	101	ST-6	35-45 06		
	046	ST-5	35-45 05		i	102	*LBL3	21 03		
	047	XZY	-41		נ	103	1	01		
	048	51-2	35-45 02		1	104	ST+1	35-55 01		
	049	<u>~</u> ~	33 75 45 07		i	105	RCL1	36 01		
	050	51-3	30-40 03		1	06	RTN	24	и т	
	051	LSIA	16-63	1	1	107	*LBL6	21 16 12	<sup>n</sup> p' <sup>j</sup> p	
	052	KULT	30 U/ -75		1	08	RCL3	36 03		
	033 051	л Ст_2	-33 75-85 pc		1	109	R/S	51		
	034	31-6	33-43 00		1	10	RCL1	36 <b>U</b> I		
	033 052	1 ST_1	01 75-d5 Di		1	11	LN	32		
	010	51-1	JJ=4J 01	REGIS	<u></u> 1	12	5107	35 107		
0		1 n	<sup>2</sup> Σp;	$3 \Sigma p_i^2$ $4 \Sigma q_i$	<sup>5</sup> Σα.2		<sup>6</sup> Σ <b>Did</b> ;	<sup>7</sup> Used	8	9
		n	Σαι	$-\Sigma q_i LNq_i \Sigma p_i$	-SpiL	Npil	-Xr;LN	r; last q;	last p₁	
SO		IS1	S2	S3 S4	S5	<u> + +</u>	<u></u>	S7	58	59
Δ		L	I B		D			F	100	
<b>^</b>				Ŭ I	2				ľ	

## 97 Program Listing II

STEP KE		KEY CO	DE	COMMENTS		STEP	KE	EY ENTRY	KEY CODE	COMM	IENTS
113	÷	-24				1	169	ENTT	-21		
114	RTN	24	1				170	LN	32		
115	<b>#LBL</b> c	21 16 13	H <sub>q</sub> ,	Ja			171	Х	-35		
116	RCL5	36 05	•	4			172	ST+6	35-55 <b>0</b> 6		
117	R/S	51					173	<b>≢LB</b> L6	21 <b>0</b> 6		
118	RCL7	36 07					174	1	<b>0</b> 1		
119	÷	-24					175	ST-1	35-45 01		
120	RTN	24					176	RCL1	36 01		
121	#LBLd	21 16 14	Ro				177	RTN	24		
122	RCL3	36 03					178	R∕S	51		
123	RCL5	36 85									
124	+	-55				180				1	
125	2	02								7	
126	÷	-24								1	
127	RCL6	36 06								]	
128	-	-45								7	
129	2	02								7	
130	LN	32								7	
131	÷	-24								1	
132	1	01								1	
133	+	-55								1	
134	RTN	24				190					
135	<b>≭</b> L₿Le	21 16 15	Err	or							
136	ST07	35 <b>0</b> 7									
137	X≓Y	-41									
138	ST08	35 08								1	
139	ST-4	35-45 04								1	
140	0	00								1	
1 <b>41</b>	X=Y?	16-33								1	
142	GT04	22 <b>0</b> 4								1	
143	R∔	-31							1		
144	ENTT	-21				200			1	1	
145	LN	32								-	
146	Х	-35									
147	ST+5	35-55 05							1	1	
148	*LBL4	21 04								1	
149	RCL7	<b>36 0</b> 7					1			1	
150	ST-2	35-45 02					1			1	
151	0	00									
152	X=Y?	16-33								1	
153	GT05	22 05					1			1	
154	Rŧ	-31				210				1	
155	ENTŤ	-21								1	
156	LN	32								]	
157	Х	-35									
158	ST+3	35-55 03									
159	<b>≭LBL5</b>	21 05									
160	RCLS	36 <b>0</b> 8									
161	RCL7	36 07									
162	+	-55									
163	2	<b>8</b> 2									
164	÷	-24				220					
165	0	00								4	
166	X=Y?	16-33							l	4	
167	GT06	22 <b>0</b> 6								4	
168	R↓	-31					4	EL ACC	L	ET STATUS	
A	В	Ic	L		IF			FLAGS		SEISTATUS	
Pitqi	ĔΒp,	Bq	0,Arc s:	in Σp <sub>i</sub> , Σq <sub>i</sub>	Pj	tqi			FLAGS	TRIG	DISP
	р <sup>ц</sup>	,T C	н.т	d R	е г	ror	1		ON OFF		
0 Pi, 41	1 <sup>11</sup> p,	<u>p</u> 2	<u>., d</u>	3	4	.101	2				
5	Use	d fi	Used	Used	Us	sed				RAD 🗆	
<sup>5</sup> Used	<sup>6</sup> Use	d 7		8	9		3		$3 \square \mathbf{v}$		n_2

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, VariablesUsing Jolly's (1965) symbols, letn = 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<br/>captured again at least once (known to be alive later)z = number of individuals marked prior to sample, but <u>not</u> captured in<br/>sample, and which are subsequently captured in later samples (hence<br/>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<br/> $\hat{M} = m + z \frac{s}{r}$ Estimated population size,  $\hat{N}$ , is simply  $\hat{M}$  times the ratio of marked plus<br/>unmarked individuals in the sample (n) to marked individuals in the sample (m):<br/> $\hat{N} = \hat{M} \cdot \frac{n}{m}$ Jolly's formula for the standard error of the population size is as follows:

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

**Operating Limits and Warnings** The following inequalities must be met:

n > m > s > r

This program has been verified only with respect to the numerical example given in *Program Description II*. User accepts and uses this program material AT HIS OWN RISK, in reliance solely upon his own inspection of the program material and without reliance upon any representation or description concerning the program material.

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Sketch(es)

```
Suppose you collect a sample of 100 isopods from a marked
Sample Problem(s)
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] \rightarrow 142.86 (\hat{N})
          [R/S] \rightarrow 10.47 (SE)
           [D] \rightarrow 91.43 (M)
           Jolly, G.M. 1965. Explicit estimates from capture-recapture data
Reference(s)
                   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**

					$\square$
POPULATION	SIZE ESTIMATE	(JOLLY'S ME	THOD)		7
n,m	s,r,z	N,SE	М	Â−m+s	

STEP	INSTRUCTIONS	INPUT DATA/UNITS	OUTPUT DATA/UNITS	
1	Load side 1			
2	Enter n	n		
2	Patra a			
5	Enter m	m		
4	Enter s		ENTT	
		5		
5	Enter r	r	ENT	
6	Enter z	z	В	
	^			
7	Compute N		<b></b>	<u> </u>
				CE
8	Compute SE		K/ 5	<u>SE</u>
9	Display Â			М
10	Display Ḿ - m + s (if desired)		E	Ĥ-m+s
		· · ·		

#### 97 Program Listing I

STEP K		KEY CODE	COMMENTS	STEP	KEY ENT	RY KEY CODE	COMMENTS
881	*LBLA	21 11				E 21 15	
002	ST02	35 02			058 RCI	7 36 07	
003 004		-31 75 o:			059 RCI	2 36 02	
004 205	JIUI DTH	30 BI 57			060 -	45	
00J BBE	8 ( D) D	24			061 RCI	_3 36 83	
000 007	*EDED STA5	21 12 75 85			<b>0</b> 62	+ -55	
00, 008	5100 F1	-31			063 R	TN 24	
009	ST04	35 04			064 K. I	/S 51	
<b>0</b> 10	Ę↓	-31					4
011	ST03	35 03					1
012	RTN	24					1
013	*LBLC	21 13					1
<b>0</b> 14	RCL2	36 02		070			1
015	RCL5	36 05					]
016	RCL3	36 03					]
U17	RUL4	36 04					1
<b>U</b> 18 010	÷	-24					1
<b>0</b> 13 000	× .	-30					4
020 Gen	+ 6767	-38 75 87	Store M				4
021 022	Pri i	36 81	Store M				4
022 023	X	-35					4
020 024	RCL2	36 02		080			1
025 025	÷	-24					1
026	STJ8	35 08	Store Â				1
027	R∕S	51					1
<b>0</b> 28	RCL1	36 01					]
025	-	-45					]
030	RCL8	36 08					
031	Χ	-35					4
032	RCL7	36 67					4
<b>U</b> 33 674	RULZ	36 UZ		090			-
034 075	- 7 ויזם	-43 74 07		000			4
033 076	KULO 4	30 03 _55					4
030 037	RCL7	36 87					1
038	÷	-24					†
039	RCL4	36 64					]
040	1/X	52					]
841	RCL3	36 03					
042	17X	52					4
043	-	-45		100			•
044	Χ	-35		100			4
<b>U4</b> 5	RULZ	36 82					4
046 047	178 PCL1	32 72 94					4
041 049	RULI	30 81 - 50					1
040 049	1< n -	-45					
015 050	÷	-55					SET STATUS
051	X	-35				FLAGS	TRIG DISP
052	18	54 -				ON OFF	
053	RTN	24		110			DEG XX FIX XX
054	*LBLD	21 14		110			$\begin{bmatrix} GRAD \ \Box \end{bmatrix} = \begin{bmatrix} SCI \ \Box \end{bmatrix}$
<b>0</b> 55	RCL7	36 07	Dispiay M			$ 3 \square \mathbf{X}$	n_2
056 I	RTN	24 L	RE	GISTERS			<u></u>
0	1	2	3 4	5	6	7 ^	8 9
	n	m	s r	Z		M	N CO
50	51	52	53 S4	55	56	57	20 29
A	В		c	D	1	E	I

5

Program 1	itle CELL PHASE AND CYCLE T	IMES	······
Contributo Address	r's Name Hewlett-Packard Company 1000 N.E. Circle Boulevard		
City	Corvallis	State Oregon	<b>Zip Code</b> 97330

Program Description, Equations, Variables

Where  $n_{G1}$  = the number of cells in Gl 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  $n = n_{G1} + n_S + n_{G2} + n_M$  = 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  $T_{\mathbf{X}}$  is the phase time and T is the cell cycle time.

Given a starting concentration of cells, n<sub>o</sub>, 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:

$$n = n_0 2^{\frac{t}{T}}$$

**Operating Limits and Warnings** Data 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.

This program has been verified only with respect to the numerical example given in *Program Description II*. User accepts and uses this program material AT HIS OWN RISK, in reliance solely upon his own inspection of the program material and without reliance upon any representation or description concerning the program material.

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Reference(s) Puck, Theodore T., and Steffen, Jan. Life cycle analysis of mammalian cells. I. Biophysical Journal <u>3</u>: 379-397. 1963 This program is a modification of the Users' Library Programs #01522A and #01630A submitted by James M. Mason.



## **User Instructions**

T  $\uparrow$  Total t, n<sub>0</sub>, n $\rightarrow$ T CELL PHASE AND CYCLE TIMES G1, S, G2, M T<sub>1</sub> T<sub>2</sub> T<sub>3</sub> T<sub>4</sub>

STEP	INSTRUCTIONS	INPUT DATA/UNITS	к	EYS	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	Т	1		
	Enter total number of cells	tota1	f	Α	Т
4	Go to step 7				
5	Enter total number of cells	n total	f	A	
6	Enter elapsed time	t	1		
	Enter starting concentration of cells	n	1		
	Enter subsequent concentration of cells	n	f	B	T
7	Enter number of cells in four phases:				
	# cells in Gl phase or prophase	n <sub>C1</sub> or n pro			
	<pre># cells in S phase or metaphase</pre>	n <sub>S</sub> or n meta	1		
	<pre># cells in G2 phase or anaphase</pre>	n <sub>G2</sub> or n ana	↑		
	<pre># cells in M phase or telophase</pre>	n <sub>M</sub> or n telo	A		total 4 phase
8	Compute time for G1 or prophase	1	B		T <sub>1</sub>
9	Compute time for S or metaphase		C C		T <sub>2</sub>
10	Compute time for G2 or anaphase		D		T <sub>3</sub>
11	Compute time for M or telophase		E		Τ.
12	Find $T_1 + T_2 + T_3 + T_4$		RCL		$\Sigma T_1 $
					1-4

#### 97 Program Listing I

STEP	KE	Y ENTRY	KEY CODE	COMMENTS	STEP	KE	YENTRY	KEY CODE	СОМ	MENTS
	ØØ1	*LBLA	21 11	Enter cell counts		<b>Ø</b> 57	RCL5	36 05		
l	002	ST01	35 <b>0</b> 1			<b>0</b> 58	-	-45		
ł	003	÷	-55			<b>05</b> 9	RTN	24		
(	004	ST02	35 <b>0</b> 2			060	*LBLD	21 14	<sup>T</sup> 3	
l	005	+	-55			061	RCL1	36 01		
l	006	STO3	35 03			062	GSB0	23 00		
(	007	+	-55			063	ST05	35 05		
l	<b>00</b> 8	ST04	35 04			064	RCL2	36 <b>0</b> 2		
ł	989	RIN	24			065	GSB0	23 00		
6	916	*LBLa	21 16 11	Enter T and n total		066	RCL5	36 05		
	011	5108	33 08			067	-	-45		
e	012	λ÷ĭ στος	-41 75 8/			068	RIN	24	m	
e	013	5105	30 06 04			069	*LELE	21 15	<sup>T</sup> 4	
e	014		24			070	RCL1	35 81		
e (	013 012	#LDL®	21 10 12	Cell cycle time(T)		071	6560	23 80		
	010 017	£06 V+V	-41			072	KIN D/C	24		
e 1	017 010	^+1 1.0C	16 72			073	K/5	51 I		
	010 010	-	-45						ł	
c í	015 020	STOR	75 AG			+			1	
c 4	020 021	5100 P.L	-71			-			1	
í.	A22	2	01 02			+			1	
4	022	inc	16 32						1	
4	020 024	x	-35		080				1	
6	925	RCI 6	36 06						1	
í	A26	÷	-24			1			1	
i	927	ST06	35 06	Stores cycle time		1			1	
í	928	RTN	24	ÿ					1	
é	929	*LBL0	21 00	Computational loop					1	
é	030	RCL8	36 08	1					1	
ł	831	÷	-24						]	
6	032	1	01						]	
l	933	+	-55						]	
E	934	LOG	16 32		090					
6	935	2	<b>0</b> 2						1	
é	936	LOG	16 32			_				
6	937	÷	-24						ļ	
E E	938	RCL6	36 06						4	
é	939	X	-35						-	
é	940	RTN	24	-					4	
E	941	*LBLB	21 12	<sup>T</sup> 1					4	
	942	RULS	36 03			+			1	
<u>ا</u>	943	6560	23 00		100	+			4	
<u>ا</u>	044 075	5100 PCL4	30 00 76 04						1	
t (	943 982	KUL4 CCDA	30 <b>04</b> 27 <b>0</b> 0			+			1	
e f	940 947	6360 ST07	25 00 75 07	Total of $T_1, T_2, T_3, T$	<i>.</i>	-			1	
, e	348	PCI5	36 85	τ, Σ, Ξ,	4	1			1	
e e	949	-	-45						1	
Ģ	950	RTN	24						SET STATUS	
í	951	<b>#LB</b> LC	21 13	T <sub>2</sub>				FLAGS	TRIG	DISP
é	952	RCL2	36 02	-				ON OFF		
é	953	GSB0	23 00		110			0 🗆 🛣	DEG 🛛	FIX 🛛
e	954	ST05	35 <b>0</b> 5		110	+				
e	955	RCL3	36 03			+				n_2
e	956	GSB0	23 <b>0</b> 0 l	DECIG	TEPS					<b>لا</b>
0		1	2 .	$\frac{3}{2}$ n $\pm n$ $\pm 4$ n $\pm n$	5	a t - 1	6 6 11	7_	<sup>8</sup> total	9
-		<sup>n</sup> 4	$n_4 + n_3$	$14^{+113}$ + $14^{+113}$	scra for ca	atch al-	cycle	$T_{1} + T_{2}$	number	
				$n_2 + n_2 + n_1$	culat.	ions	time	13 +14	ot cells	
S0		S1	S2	S3 S4	<u>S5</u>		S6	S7	<u> </u>	I S9
А			В	С	υ			E	I I	
1			1							

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Program T	itle CROSSOVER:	LOCATIONS/PRODUCTS		
	Uselatt Da	land Carrier		
Contributo	r's Name Hewlett-Pa	ckard Company		
Address	1000 N. E. Circle	e Boulevard		
City (	Corvallis	State	Oregon	<b>Zip Code</b> 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.

This program has been verified only with respect to the numerical example given in *Program Description II*. User accepts and uses this program material AT HIS OWN RISK, in reliance solely upon his own inspection of the program material and without reliance upon any representation or description concerning the program material.

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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:  $2 \le g \le 10$ . The first digit of the parental genotype should be 1. No more than 3 crossover regions can be specified for a single calculation.

This program has been verified only with respect to the numerical example given in *Program Description II*. User accepts and uses this program material AT HIS OWN RISK, in reliance solely upon his own inspection of the program material and without reliance upon any representation or description concerning the program material.

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#### **Program Description 11** SKETCH(ES) 1 2 3 4 5 6 7 1. Regions: 2. 1 2 3 4 5 6 7 AbcdEFgh AbcdEFgh P1: a B C D e f G H ABCDefGH F1: AbcDEfGh F1: a b C D e f G H 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? 1. a) .10001100 [ENTERt] .10011010 [A] Solution(s) 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 [ENTERt] 2 [ENTERt] 3 [ENTERt] 5 [C] $\rightarrow$ 10101011(AbCdEfGH) b) 10001100 [ENTERt] 1 [ENTERt] 4 [ENTERt] 6 [C] $\rightarrow$ 11111111(ABCDEFGH) Srb, A. M., R. D. Owen and R. S. Edgar. General Genetics, 2nd Ed., Reference(s) 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.

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## **User Instructions**

CROSSOVER:	LOCATIONS/PRODUC	CTS		7
P1 + .F1	n mult	single	g	$\checkmark$

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	Α	
5	Input total crossover regions n (number of	-		
	genes $-1 = n$ ) and calculate regions	n	В	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 chromatic	l g	E	g
8	Input genotype, P1, using 1 for dominant and			
	0 for recessive.	P1	<b>↑</b>	P1
	(For multiple crossovers go to step 12)			
9	Specify desired crossover region, Xo	Хо		
10	Calculate Fl 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, Xol	Xol	<b>†</b>	
13	Specify second crossover region, Xo2			
	or 0 for none	Xo2	↑	
14	Specify third crossover region, Xo3			
	or 0 for none	Xo3		
15	Calculate Fl genotype		C	F1
16	For an additional single Xo go to 8			
	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	STEP KEY E	NTRY KEY COD	E COMMENTS
<i>00</i>	1 ¥LBLA	21 11	STO F1	057	RCL1 36 01	Get new genes
00	2 ST02	35 82		058	6SB7 23 07	for comparison
60	3 ST06	35 68		059	ST01 35 01	
60	4 X≢Y			060	RCL2 36 02	
00	5 ST01	35 01	STO P1	<b>U</b> 61	6587 - 23 Ø7	
<b>0</b> 0	6 ST05	35 05		862	STUZ 35 02	
ÛŨ	7 RTN	24		863	DSZ1 16 25 45	
00	8 *LBLB	21 12		<b>U</b> 64	6105 22.05	
00	9 STOI	35 4 <i>6</i>	STO n, estab.counter	<b>8</b> 65	RULA 36-04	
Ø1	0 1	61		866	KIN 24	
01	1 +	-55		1067 ¥. 076	LBL6 21.05	Shift left one gene
61	2 5107	30 87		<b>86</b> 8 0.00	I 01	
01	3 U 3 TTO 3	80		002 070	ຍ ຍຍ ∀ _75	
Ø1 04	4 5104	33 84		070 071		
61	Э	60 07 05		071 072	- INI - 10-34 - DTN - 24	
UI 01	6 ¥LBLƏ Ə Dolla	21 85	Gene comparison	072 077 *	KIN 24 IBI7 31.27	
<b>U</b> 1	A KULI A AARA	36 81 57 65	algorithm	073 40 674	1 DL7 21 07	Shift left total
61 D (	6 6366 0 6010	23 60 76 00	Get PI gene 1	075 075	1 UI 0 00	genotype 1 gene
01 00	9 KULZ a conz	35 62 07 07		075	v -75	
02 00	0 6306 4 Viva	23 00 16-77	Get Fl gene 1	070 077	FPC 16 44	
02 00	1 A=12 0 0E1	10-00	Compare	071 078	PTN 24	
02 00	2 3F1 7 V2VA	10 21 61 16-72		070 079 *1	IBLC 21.17	
02 02	3 AFI: X CE1	10-32		010 #1 080	STOI 35.46	Store Xo3
20 60	4 UFI 5 DOL1	10 22 01 75 Bi	Cot Pl come 2	680 . 681	RL -31	
02 60	J KULI 2 red7	30 01 27 87	Get Fi gene 2	<b>8</b> 82 :	STO7 35.07	
02 QQ	6 6307 7 rede	23 87		883	R4 -31	Store Xo2
02 60	0 DF10	23 66 76 69	Cot Fl come 2	084 084	6SBD 23-14	
02 02	0 KCEZ 0 CSR7	23 BZ	Get fi gene 2	085	RCL7 36 07	Calculate Xol
02 07	A ESRE	23 BE		086	0 00	
03 07	1 X=Y2	16-33	Compare	087	X=Y9 16-33	Test for Xo2
00 87	2 SF2	16 21 82	oompure	088	GT09 Z2 85	TEST FOR NOL
Ø3	3 X≠Υ?	16-32		<b>8</b> 89 i	RCL5 36-05	
<b>N</b> 3	4 CE2	16 22 82		<b>0</b> 90	RCL7 36-07	
03	5 F1?	16 23 01		<b>0</b> 91 (	GSBD 23-14	Calculate Xo2
03	6 GT00	22 00		<b>0</b> 92	RCLI 36-46	
03	7 GT01	22 01		<b>0</b> 93	0 00	
03	8 *LBL0	21 00		<b>0</b> 94 1	X=Y? 16-33	Test for Xo3
03.	9 F2?	16 23 02		<b>0</b> 95 (	GTO9 22 09	
64	0 GT04	22 04		<i>096</i>	RCL5 36-05	
<b>Ø</b> 4	1 GTO3	22 03		097	RCLI 36-46	
84	2 ¥LBL1	21 01	Crossover occured	<b>0</b> 98 (	GSBD 23-14	Calculate Xo3
Ū4	3 F2?	16 23 Ø2	record; no	099	RTN 24	
84	4 GTO3	22 03	crossover get	100 #1	LBLU 21-14	Single Xo logorithm
04	5 GT04	22 04	new gene	101	KLL6 3606	Test for region
Ø4	6 ¥LBL3	21 03	Crossover occured	102	⊼≠Y =41	not to be comple-
<b>Ø</b> 4	7 RCLI	36 46		103	45 etes 75 es	mented
64	8 1	81		104 3	5102 33 02	
04	9 -	-45		103	- A+1	
65	0 10*	16 33	Calculate region	100 3	5101 53161 B BB	
65	I KÜLT A DALT	35 87	of crossover	101 100 - 1	5 50 STAZ 7567	
65	Z KULI 7	36 46 15	or crossover	100	RCI 1 74 81	
<b>U</b> 5 85	ರಿ. – ಸ	-43		110 I	RCL2 36 82	
<b>U</b> D 05	Ч А Б. СТ⊥А	-30 75_55 <i>84</i>	Store res. of cross	111	5 AS	Correct antilog
60 105	U DI <b>74</b> 6 yidix	30-33 04 21 34		112	45	error
<del>ره</del>	U #LDL4	21 87	REGIS	TERS		
0	<sup>1</sup> Used	<sup>2</sup> Used	<sup>3</sup> Used <sup>4</sup> Used	5 PL   <sup>6</sup> F	1 <sup>7</sup> Used	Counter <sup>9</sup> Used
S0	S1	S2	S3 S4	55 S6	Sed S7	S8 S9
A		В	С	D	E	I

#### 97 Program Listing II

STEP	KE		KEY	CODE		COMMENTS		STEP	KEY ENTRY	KEY CODE	сомм	ENTS
0121	113	10×	16	33	[							
	114	EEX		-23				170			1	
	115	5		05								
	116	х	-	-35							4	
	117	ST04	35	04							4	
	118	÷	-	-24							4	
	119	INT	16	34							4	
	120	RCL4	36	04 							4	
	121	X CTOE	-	-33 05	Store						4	
	122	3103 *1 PL 2	21	03 00	To de	termine if	leg.				1	
	123	RCL1	36	02 01	gene	is to be		180			1	
	125	2	00	02	comp	lemented					1	
	126	÷	-	-24							]	
	127	FRC	16	44							]	
	128	Ø		<i>00</i>							4	
	129	X≠Y?	16-	-32							4	
	130	GT08	22	Ø8	51	-					4	
	131	RCL3	36	03 05	Place	uncompleme	ente	۹ 			4	
	132	5		05 45	gene	e value in					4	
	133 -	107	- +	-43 77	stor	age		190			1	
	134	IQ~ Eev	10	33 -27							1	
	136	5		25 85							1	
	137	x	-	-35							1	
	138	ST+5	35-55	05							]	
	139	¥LBL8	21	08	Place	e complement	ted				]	
	140	1		01	gene	e value in					1	
	141	ST+3	35-55	03	stor	age					4	
	142	RCL2	36	Ø2							4	
	143	RCL3	36	03	Teet		Val	200			4	
	144	X=Y?	16-	-33	rest	completion	X0	<u> </u>			{	
	145	6109	22	69	Get n	ew gene					1	
	146	RULI	30	61 G (		80110					1	
	148	1 14		01 88							1	
	149	÷	-	-24							1	
	150	INT	16	34							]	
	151	ST01	35	81								
	152	GT02	22	02		_					4	
	153	<b>*</b> LBLE	21	15	Store	e number of		210			4	
	154	DSPØ	-63	00	gene	es in Pl and	1	210			4	
	155	ST06	35	06	set	атартау					1	
	136	KIN	<b></b>	24 00	Show	Result					1	
	137 158	FLDL9 Dris	21 72	07 85	Stop	)					1	
	159	RTN	50	24	1						1	
	160	R∕S		51								
	+		+								1	
			<b>+</b>								4	
	<u>†</u>							220			4	
	1		1								1	
											J	
	<b> </b>											
	1	579 Million (1999)	L									
A Com	arc	B 1 0	int	C 10v	dec	D	E	National States and States and	PLAGS		SET STATUS	
Mult	Xo's	Sing	le xo	Nbr	genes		-		ľ	FLAGS	TRIG	DISP
a		Ъ		с		d	е		1 Used		DEG 🕅	FIX 🔽
0		1		2		3	4		<sup>2</sup> Used	1 🗆 🗴	GRAD	SCI 📋
5		6		7		8	9		3	2 🗆 🛛	RAD 🗆	ENG 🗆
		1							1	3 🗆 🛛	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 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  $(S_{i+1} = 2S_i \text{ module P})$ , starting from any  $S_1(1 \leq S_1 \leq (P-1))$ . Permissable chromosome lengths for  $n \leq 100$  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** 

This program has been verified only with respect to the numerical example given in *Program Description II*. User accepts and uses this program material AT HIS OWN RISK, in reliance solely upon his own inspection of the program material and without reliance upon any representation or description concerning the program material.

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ketch(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, 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	к	EYS	OUTPUT DATA/UNITS
1	Load side 1 and side 2				
2	(Optional: enter random seed $0 < S < 1$ )	S	f	Α	
3	Select chromosome of desired length = no. of				
	genes, n, in linear sequence.	n	Α		
	(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 $(1 \le g_i \le n)$	81	<b>ENT</b> ↑		
	(Note: If $g_1=7$ , for example, the '7' is	82	В		
	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		С		# of genes
6	Repeat 5 as often as desired, with additional				on 1st frag
	chromosome copies, to obtain an experimental		_		
	statistical pattern for g1, g2 separation.				
7	When ready, see actual no, of genes intervening	<u> </u>			g1 g2
	between g1 and g2 for comparison with				separation
	deduced value.		D		(ienore sign
8	For another gene pair on same chromosome				
	so 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.				
					1
				SET STATU	S
			FLAGS	TRIG	DISP
			1 🗆 🖾	GRAD	SCI 🗆
			2 ∐ X 3 □ X	RAD 🖸	ENG n2

## 97 Program Listing I

STEP	KEY ENTRY	KEY CODE	COMMENTS	STEP	KE	Y ENTRY	KEY CODE	COMMENTS
00.	t #LBLa	21 16 11	STORE seed	] (	957	÷	-55	(8k+3) or
00:	2 ST07	35 07	1		958	ST06	35 06	(8k+5) for some
00	3 RTN	24		1 6	959	÷	-24	integer k]
00-	4 ¥LBLA	21 11	Store length	[ 6	960	FRC	16 44	
00	5 DSPØ	-63 00		[ 6	961	RCL6	36 <b>0</b> 6	
000	5 STO3	35 03	1		362	X	-35	
007	' RTN	24		[ 6	363		-62	for matching
001	3 *LBLB	21 12	Store gene pair	[ 6	364	1	01	purposes
00:	9 STO2	35 02		[ 6	965	+	-55	
010	9 X≠Y	-41		[ 6	366	INT	16 34	
<i>01</i> :	I ST01	35 ØI		[ 6	967	ST04	35 04	Leave S; in R4 & X
812	? RTN	24		[ ε	368	RTN	24	I I
01.	3 *LBLD	21 14	$S_0 = (n-1)$ at start	[ 6	969	<b>≭LBLC</b>	21 13	Break chrom. at Rand
01-	4 RCL3	36 03	of $S_1 \rightarrow S_n$ gene	[ 6	970	RCL7	36 07	Rand $i$ in $R_7 =$
01	5 1	61	sequence	[ ε	971	Pi	16-24	first part of
01 e	5 -	-45	-	[ 6	972	+	-55	$(R and -1 + \pi)^5$
011	7 ST04	35 04		[ 6	373	5	85	(
018	30	60	Reset gene	[ 6	374	γ×	31	
019	9 STOI	35 46	separation counter	[ 6	975	FRC	16 44	
020	3 <b>*</b> LBLØ	21 00	No g1org2 match loo	ŧ	976	ST07	35 07	
02	RCL1	36 81	When the 1st match	[ e	377	RCL3	36 03	Use Rand to obtain
022	S GSB5	23 05	is found for eithe	f é	378	1	Đi	an arbitrary
023	3 X=Y?	16-33	$g_1$ or $g_2$ in the	[ e	379	-	-45	integer from
624	4 GTO1	22 81	$S_1 \rightarrow S_n$ gene		980	ST04	35 84	$1 \pm 2 (p-1) \pm 0$
825	5 RCL2	36 02	sequence, go to	t i	781	X	-35	correspond to one
<b>R</b> 26	5 X <b>≠</b> Υ?	16-32	LBL1.	t i	182	1	ĤÍ	of the $(n-1)$
R27	, 6100	22 AA			183	+	-55	possible break-pte
R28	3 #LBL1	21 01	No. 2nd match loop	t e	784	INT	16 34	in a chromosomo of
829	RCLI	36 01	When the 2nd of	t i	185	STOT	35 46	ana langth n
036	GSB5	23 05	gi or go have been		186	R	88	
A31	X=Y9	16-33	matched in the	t i	987	ST05	35 05	Reset g <sub>1</sub> g <sub>2</sub> gene
A33	- 6T03	22 <b>R</b> 3	$S_1 \rightarrow S_n$ gene sequence		188	#1.BL2	21 82	Loop to test all
033	RCL2	36 02	display no of	ļ	189	6SB5	23 05	genes on 1st frag.
<u>яз</u> ,	x=Y?	16-33	genes between g. S.	i p	190	RCI 1	36 01	$g_1$ appears on $F_1$
035	5 6703	22 Ø3	genes between gi a		991	X=97	16-33	
A36	5 0521	16 25 46	I If 2nd cone has not		992	ESR4	27 BA	
837	, 6021 , 6T01	22 01	hoon matched inc.		997	RCI 4	36 04	а
001 079	CT05	22 05	been matched, inc.+	l a	194	PCI 2	36 82	g <sub>2</sub> appears on F <sub>1</sub>
A20		21 15	Toop for hxt gene	l a	195	X=Y9	16-33	
00- 040	RCI3	36.03	Irue sequence	l a	196	CSR4	27 04	
Ø41	STOL	35 46		l i	997	DS71	16 25 46	If break-pt has not
043 043	> 1	00 10 A1		Ē	998	CT02	22 <b>A</b> 2	hop reached tost
041 041	 7 _	-45			199	PCIS	76 <b>8</b> 5	All Er corport to stor
64. 64.	STO4	35 AA		1	AA	PTN	24	Dioploy no a c
GA <sup>r</sup>	T THE	21 BA			A1	±iRI₹	21 AZ	on F-
04C	5 6585	23 <b>R</b> 5			02	RCIT	36 46	
Q47	PRTX	-14		1	67	RTN	24	
041 041		16 25 46		1	A4		21 A4	Match counter is
DA(		22 BK		1	85	1	£1 04 Ø1	incromonted
A21	RTN	24		1	AF.	ST+5	35-55 85	Incremented
050 051	xIRI5	21 05	Obtain nort cone S.	1	87	PTN	24	
A22	P RCIA	36 04	$S_{i}=2S_{i}$ Mod $(-1)$	1	68	R/S	51	
051 051	2 2	00 04 A2	$\frac{1}{1} \frac{1}{1} \frac{1}$	í	00	Nº U		1
000 054	, <u> </u>	-75	$\frac{1}{2} \frac{1}{2} \frac{1}$	110				]
00-	דוזים ד	36 03	R <sub>C</sub> is a prime of				!	] [
050	, KOLO I	00 00 Dii	LOL					
	· · ·		REGIS	TERS				
0	<sup>1</sup> g <sub>1</sub> g	ene <sup>2</sup> g, gen	$ne^{3}n$ no. $4S_{i}$ ith	<sup>5</sup> 0,1,2	no	<sup>6</sup> (n+1)	7	<sup>8</sup> Separat. <sup>9</sup>
ł	lst ch	osen 2nd ol	of genes gene of	of g1g	21	nora = module	s Rand	brk-pt
			e chi chi chi gene chro	<u>c</u> 5		C6	27	88 50
A	191	B	<u>во 154</u> С	<b>D</b>		<u>50</u>	<u>IŞ/</u>	
			-					

```
RECESSIVE GENE FREQUENCY AFTER SELECTION, MUTATION, AND INBREEDING
Program Title
Contributor's Name
                    Hewlett-Packard Company
           1000 N.E. Circle Boulevard
Address
City
       Corvallis
                                                State Oregon
                                                                            Zip Code 97330
Program Description, Equations, Variables The following selection and mutation model
 was used:
      production of gametes 

mating production of zygotes

selection

mutation may occur surviving individuals
                                           reach maturity
  From this model (see Operating Limits & Warnings) can be derived:
           q_{n+1} = \frac{q_n^2 (ht+uht-t) + q_n (1-ht-u-uht) + u}{1 - 2ht q_n + q_n^2 (2ht-1)}
  where:
                                                  q = recessive or mutant gene frequency
           u = mutation rate
       (1-t) = mutant homozygote fitness n = no. of generations.
      (1-ht) = mutant heterozygote fitness q<sub>0</sub> = initial gene frequency and equilibrium
                                                      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.
```

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Program Title		
Contributor's Name		
Address		
City	State	Zip Code

and the f	ollowing model,
	production of gametes mutation
inbre	eding and random mating may occur
	production of zygotes selection surviving individuals reach maturity
the follo	wing equation may be derived, $\underline{q_{n+1}} = A(1-u) + u$ , where
	$A \Rightarrow \frac{(1-F)(ht-1)[q_n^2(2-t) - q_n] + q_n F(1-t)}{2}$
	$(1-q_nF) - (1-F)[q_n^2(2+2ht-t) - 2q_nht] + q_nF(1-t)$
where:	
(1- (1-h	<pre>t) = fitness of recessive homozygote t) = fitness of heterozygote (fitness of normal homozygote</pre>
	q <sub>e</sub> = equilibrium gene frequency
Operating Limit	s 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.

This program has been verified only with respect to the numerical example given in *Program Description II*. User accepts and uses this program material AT HIS OWN RISK, in reliance solely upon his own inspection of the program material and without reliance upon any representation or description concerning the program material.

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Sketch(es)												
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AN INC. 1994 - 1 - 1994											•	
ana ana ang ang ang ang ang ang ang ang												
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	 and A shares a second second second							×	i akon oran		1	

Sample Problem(s)	
1. Given the e to at	the genetic parameters: h=0.1, t=0.5, u= $10^{-4}$ , $q_0 = 10^{-3}$ , calculate quilibrium gene frequency, $q_e$ , and estimate the no. of generations tain this frequency.
2. Given value	the genetic parameters: h=0.5, t=1, u=q $_0$ =10 <sup>-6</sup> , compute the s of q <sub>2</sub> and q <sub>e</sub> .
3. Using calcu (Note the v	the following values: $q_0 = u = 1 \times 10^{-5}$ , $h = 0.1$ , $F = 0.1$ , $t = 1$ , late $q_2$ , $q_{10}$ , $q_e$ , and estimate the value of n to attain $q_e$ . that when $q_e$ is computed directly after $q_{10}$ was computed, alue of $n = 10 +  R_8 $ .
Solution(s) <sup>1</sup> • [	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] $\Rightarrow$ q <sub>2</sub> =1.75 X 10 <sup>-6</sup> 0 [STO][8] [R/S] $\rightarrow$ q <sub>e</sub> = 2.00 X 10 <sup>-6</sup>
3.	[EEX] 5 [CHS][STO] 1 [STO][5] 2 [STO] [I] 1[ $\uparrow$ ] .1[ $\uparrow$ ] .1 [E] $\rightarrow$ q <sub>2</sub> = 2.47 X 10 <sup>-5</sup> 8 [STO][I] [R/S] $\rightarrow$ q <sub>10</sub> = 4.74 X 10 <sup>-5</sup> 0 [STO][I] [R/S] $\rightarrow$ q <sub>e</sub> = 5.26 X 10 <sup>-5</sup> (ca. 3 min. running time) [I] [ABS] 10 + $\rightarrow$ n = 47 generations.

Reference(s) Cavalli - Sforza, L.L. and Bodmer, W.F., <u>The Genetics of Human</u> <u>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 ste	o 3		
	For freq, after sel., mut., and inbreed, go to	step 7		
3	If equilibrium recessive gene frequency, q <sub>e</sub> ,	0		
	is desired outright, enter $0 \rightarrow R_8$ , otherwise	or	STO 8	
	if $q_n$ is desired, enter $n \rightarrow R_0$	n		
4	Enter in stack in the following order:	h		
	h, t, u, q	t		
		11		
		а а.		
5	Propa koy A to obtain desired $a = y_0   y_0$	40		
6	Press RCL 7 to obtain value of n required			qe or qn
	to obtain displayed a			
·	Noto:			n
	Note:			
	Ine value of n corresponding to q <sub>e</sub> is based			
	displayed q and preceding calcd. value of			
	q <sub>e</sub> of 0.001 or less.]			
	[After $q_n$ is calculated and $q_n$ , is next			
	desired (n'>n), enter $n' \rightarrow R_8$ and press			
	R/S. If $q_e$ is desired after $q_n$ is displayed	l,		
7	enter $0 \rightarrow Rg$ and press $R/S$ ,			
/	$q_0 \rightarrow R_1$ ; $u \rightarrow R_5$ ; 11 $q_e$ desired, enter	oP		
	$0 \neq \mathbf{k}_{\mathbf{g}}$ while if $q_{\mathbf{n}}$ desired	u	STO 5	
	enter $n \rightarrow R$ I	0 or n	STO I	
8	Enter in stack in order:	t		
	t, h, and F	h		
		F		
9	Press [E] to obtain q <sub>e</sub> or q <sub>n</sub>		E	q <sub>e</sub> or q <sub>n</sub>
	[After $q_n$ has been computed, $q_n$ ' may next be			
	calculated by entering $(n^{+}-n) \rightarrow R_{1}$ , where			
	n'>n, and pressing R/S. If q <sub>e</sub> is desired			
	after $q_n$ has been computed, enter $0 \rightarrow R_1$			
	anu press K/SJ.			
	[When $q_{\rho}$ is computed directly ( $0 \rightarrow R_{\tau}$ ), the			
	value of n may be obtained by using the			
	absolute value of $R_{I}$ . When $q_{e}$ is estimated			
	after calculating $q_n$ , then n is equal to			
	R <sub>I</sub>   + n'. The value of q <sub>e</sub> computed is			
	Dased upon a percentage deviation from a			
	preceding value of qe of 0.001 or less].			

### Program Listing I

STEP I	KEY ENTRY	KEY CODE	COMMENTS	STEP		KEY CODE	COMMENTS
001	*LBLA	21 11	Clear $R_7$ and store	057	' X≠Y	-41	
002	501	-12	various parameters	058	÷	-24	
003	USP2	-63 02 75 05		059	) STO€	35 <b>0</b> 6	
<i>UU4</i>	\$105	35 85		066	1	01	
005	K∔	-31		06)	ST+7	35-55 07	Counter for no. of
886	STUI	35 01		062	RCL7	36 07	generations, n
887	K+	-31		063	RCL8	36 <b>0</b> 8	
008	ST02	35 UZ		864	6	00	
669	Х	-35		065	5 X=Y?	16-33	
616	S103	35 US		066	S 6702	22 <b>8</b> 2	
011	RCLI	36 01		067	' R∔	-31	
012	Х	-35		068	X≠Y?	16-32	
013	ST04	35 04		069	GT03	22 <b>8</b> 3	
014	0	00		676	RCL6	36 <b>8</b> 6	Display q <sub>n</sub>
015	ST07	35 67		<b>0</b> 71	R∕S	51	
016	*LBL1	21 01	Calculate various	672	GT03	22 <b>0</b> 3	
017	RCL3	36 03	values for q	<b>0</b> 73	*LBL2	21 02	Calculate value
<b>0</b> 18	RCL4	36 04		874	RCL6	36 <b>0</b> 6	of q <sub>e</sub>
019	÷	-55		875	RCL5	36 <b>8</b> 5	-6
020	RCL2	36 Ø2		876	-	-45	
021	-	-45		877	RCL5	36 05	
822	RCL5	36 Ø5		078	÷	-24	
023	ENTŤ	-21		879	ABS	16 31	
024	Х	-35		086	EEX	-23	
<b>0</b> 25	Х	-35		081	5	<b>8</b> 5	
026	1	01		082	CHS	-22	
<b>0</b> 27	RCL3	36 03		083	XZY?	16-35	
028	-	-45		084	ET03	22 <b>0</b> 3	
029	RCL1	36 01		085	RCL6	36 <b>0</b> 6	Display q <sub>o</sub>
030	-	-45		086	R/S	51	
031	RCL4	36 04		087	*LBL3	21 03	
032	-	-45		688	RCL6	36 86	
033	RCL5	36 05		089	ST05	35 <b>8</b> 5	
034	Х	-35		096	GT01	22 01	
035	+	-55		091	<b>\$LBLE</b>	21 15	Store F. h. and t
<b>0</b> 36	RCL1	36 01		092	SCI	-12	
<b>8</b> 37	+	-55		093	DSP2	-63 82	
038	ST06	35 06		094	ST02	35 <b>0</b> 2	
<b>0</b> 39	1	ē1		095	R↓	-31	
040	RCL3	36 03		096	ST03	35 <b>8</b> 3	
041	2	02		<b>0</b> 97	' R↓	-31	
042	Х	-35		098	STŪ4	35 04	
<b>04</b> 3	RCL5	36 05		099	*LBL4	21 04	
044	Х	-35		100	1	01	
045	-	-45		10)	RCL1	36 <b>0</b> 1	
046	RCL3	36 03		102	RCL2	36 82	
047	2	02		103	X	-35	
048	Х	-35		104	-	-45	
049	RCL2	36 <b>0</b> 2		105	i 1	01	
050	-	-45		106	RCL4	36 04	
051	RCL5	36 05		107	- '	-45	
052	ENTT	-21		108	RCL1	36 01	
053	X	-35		109	X	-35	
054	X	-35		116	RCL2	36 <b>0</b> 2	
055	+	-55		11	X	-35	
056 I	RCL6	36 <b>0</b> 6	DECIG	112	ST06	35 <b>0</b> 6	
0	1	2	3 4	5	6	7	8 9
-	Р	F	h t	u	Used	i Used	Used
S0	S1	S2	S3 S4	S5	S6	S7	58 59
				D	1		
A		в	U				ŀ

## Program Listing II

STEP	KEY	ENTRY	KEY CODE	COMMENTS		STEP	K	EY ENTRY	KEY CODE	COMM	IENTS
1	13	+	-55				169	GTO5	22 05		
1	14	2 DCLA	U2 72 04				170	RCL6	36 06	q <sub>n</sub> - valu	e
1	15	KUL4 -	-45				171	K/S ≠1015	31 21 85	displaye	d T
1	17	2	43 02	ł			172 -	RCL1	21 0J 36 01	Calculate	q <sub>e</sub> or
1	18	RCL3	36 03				174	-	-45	$q_n$ depend	
1	19	RCL4	36 04				175	RCL1	36 01	Kg - Val	ue
1	20	Х	-35				176	÷	-24		
1	21	Х	-35				177	ABS	16 31		
1	22	ST07	35 07				178	EEX	-23		
1	23	+	-55				179	5	05		
1	24	RCL1	36 81				180	CHS	-22		
1	25	ENIT	-21				181	X¥Y?	16-35		
1	26	X	-35				182	GTO6	22 06		
1	21 20	x PCL7	-30 76 07				183	RCL6	36 06 E1	q <sub>e</sub> - valu	e
1	20 29	RULI PCI1	36 01 76 01				184	#/5 #/D/2	31 31 BZ	displaye	d
1	30	X	-35				10J 10Z	ALDLO Drig	21 00 76 06		
1	31	-	-45				187	STOI	35 ØJ		
1	32	1	61				188	6101	22 04		
1	33	RCL2	36 02				189	R∕S	51		
1	34	-	-45			190	1	1		1	
1	35	X	-35							1	
1	36	-	-45								
1	37	ST07	35 07								
1	38	RULI	36 UI								
1	39 10	ENIT	-21				<b> </b>				
1	40 11	~ ~	-35				<b>-</b>			1	
1	41 42	Prid	02 76 84							4	
1	43	-	-45				+			ł	
1	44	х	-35			200				4	
1	45	RCL1	36 01							4	
1	46	-	-45								
1	47	1	01				1			1	
1	48	RCL2	36 <b>0</b> 2								
1	49	-	-45								
1	50	X	-35							1	
1	51	RULS	36 Ø3 76 01								
1	JZ 57	RUL4	30 04 -75								
1	53 54	1	-33 Gi			210					
1	55		-45							4	
1	56	х	-35				-				
1	57	RCL6	36 <b>0</b> 6				1				
1	58	+	-55								
1	59	RCL7	36 07								
1	60	÷	-24	Value of A cal	culat	e					
1	61	1	61 76 65								
1	62 77	KULS	36 85								
1	03 [/	~	-40			220	<b> </b>				
1	64 65	RCIS	-33 36 05			220					
1	66	+	-55	<b>g</b> <sub>n</sub> - value cal	culat	e					
1	67	STO6	35 06	-11			1				
1	68	DSZI	16 25 46								
Δ		B	-				-	FLAGS		SET STATUS	
S - M	1	0	C		Ľs ·	- M -	I		FLAGS	TRIG	DISP
а		b	с	d	е		1				
0		1	2	3	4		2				SCI
5		6		8					$2 \square \overline{\mathbf{X}}$	RAD 🗆	ENG,
-		Ĩ	1	<b>N</b>	Ĩ.		ľ		3 🗆 🖾		n <u> </u>

rogram Title SELECTION AND GENE FI	REQUENCY	
ontributor's Name Hewlett-Packard Co	ompany	
ddress 1000 N.E. Circle Bouleva	ard	07000
ity Corvailis	State Oregon	Zip Code 97330
number of generations (n), and equilibrium recessive gene fro after n-generations may be con frequency (q') may be calculat	initial recessive gene equency $(\hat{q})$ and the reces mputed. Conversely, from ted n (see Operating Limi	frequency $(q_0)$ , the sive gene frequency the recessive gene ts and Warnings).
The following equations were u	used in the program:	
$q_{n+1} = \frac{q_n W_2 + q_n^2}{W_1 + 2q_n (W_2 - W_1)}$	$\frac{W_3 - W_2}{W_1 + W_3 - 2W_2}$ ; $\hat{q} =$	$\frac{W_1 - W_2}{W_1 + W_3 - 2W_2}$
Where:		
$W_1, W_2, W_3$ denote adaptive (A = dominant	ve values for genotypes A and a = recessive gene)	A, Aa, aa, respectively
$\hat{\mathbf{q}}$ = equilibrium fr	requency for the recessiv	e gene
$q_n = recessive generation (q_n = initial)$	e frequency after n-gener recessive gene frequency	ations )

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'.

This program has been verified only with respect to the numerical example given in *Program Description II*. User accepts and uses this program material AT HIS OWN RISK, in reliance solely upon his own inspection of the program material and without reliance upon any representation or description concerning the program material.

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Sketch(es)

Sample Problem(s)	(A) (B) (C)	Given: $q_0 = 0.90$ , $W_1 = 0.5$ , $W_2 = 1$ , $W_3 = 0.4$ , calculate $q_n$ for $n = 5$ , and $\hat{q}$ . Given: $q_0 = 0.90$ , $W_1 = 0.5$ , $W_2 = 1$ , $W_3 = 0.4$ , calculate n for $q' = 0.48$ , and $\hat{q}$ . Given: $W_1 = 0.5$ , $W_2 = 1$ , $W_3 = 0.4$ , calculate $\hat{q}$ only.
Solution(s)	(A) (B) (C)	5 [E] 0.9 [ $\uparrow$ ] 0.5 [ $\uparrow$ ] 1 [ $\uparrow$ ] 0.4 [A] $\rightarrow$ q <sub>5</sub> = 0.520 [C] $\rightarrow$ $\hat{q}$ = 0.455 0.48 [E] 0.9 [ $\uparrow$ ] 0.5 [ $\uparrow$ ] 1 [ $\uparrow$ ] 0.4 [B] $\rightarrow$ n = 7 [C] $\rightarrow$ $\hat{q}$ = 0.455 0.5 [ $\uparrow$ ] 0.5 [ $\uparrow$ ] 1 [ $\uparrow$ ] 0.4 [A][C] $\rightarrow$ $\hat{q}$ = 0.455 0.5 [ $\uparrow$ ] 0.5 [ $\uparrow$ ] 1 [ $\uparrow$ ] 0.4 [B][C] $\rightarrow$ q = 0.455

Reference(s) Gardner, E.J., <u>Principles of Genetics</u>, 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		7
(dd)	q <sub>n</sub> ∎	n	ĝ	 Clear	. /

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
1	Enter program			
2	Enter n or q'	n		
	whichever is available	or a'		
		UT Y		
3	Press E to clear registers and store n		E	n or a'
	or q' in R <sub>7</sub>			
4	Enter in order: $q_0$ , $W_1$ , $W_2$ , $W_3$	qo		
		W <sub>1</sub>		
		$W_2$		
		W <sub>3</sub>		
5	If n is given and q <sub>n</sub> is to be computed, press			
	A; if q' is given and n is to be calculated,		A	۹ <sub>D</sub>
	press B		B	n
6	After n or q <sub>n</sub> has been computed, calculate			
	q by pressing C		C	D
7	If g alone is desired, enter in order:	W <sub>1</sub>		
	$W_1$ , $W_1$ , $W_2$ , $W_3$ and press A C (or B C)	W,		
	(Note: if the machine runs unduly long	$W_2$		
	after pressing A (or B), press R/S and	W <sub>2</sub>	AC	ĝ
	C to obtain q̂).	or	BC	ĝ
			the second se	

## 97 Program Listing I

STEP	KEY ENTRY	KEY CODE	COMMENTS	STEP	KEY ENTR	Y I	KEY CODE	COMM	ENTS	
61	01 *L6LE 92 - CLDC	21 15 16-57	Clear registers	- 0	57 RCL8		36 08			1
0 0	92 CERG 93 STO7	35 AZ	and store n or	10 10	58 X212 50 CTO1		16-34 22 Bi			
0	94 RTN	24	q III K7	А	60 RCL6		22 01 36 06			
8	95 ¥LBLA	21 11	Given n, calculate	Ø	61 R/S		51			
0	96 DSP3	-63 03	q' (q <sub>n</sub> )	0	62 GT01		22 01			
00	97 SF1	16 21 01		0	63 <b>*</b> LBL0		21 00	]		
6	98 *LBL2	21 U2 75 oz		0	64 RCL6		36 06			
01 D	19 5103 IQ DI	33 03 -71		6	65 RCL7		36 07			
A:		-51 35 02		8	66 X21? VZ CTOZ		16-34			
0	12 R4	-31		0 A	67 6103 68 PCIS		22 03 76 08			
0	13 ST01	35 01		6	69 R/S		51			
0:	l4 R↓	-31			70 *LBL3		21 03			
0	15 *LBL1	21 01		0	71 RCL8		36 08			
0.	16 ST04	35 04		0	72 GTO1		22 01			
ម.	IT KULI IO DEIT	36 01 76 07		0	73 <b>*</b> LBLB		21 12	Given q',	calculate	n
01 A1	10 KULJ 19 +	30 03 -55		6	74 USPU 75 CEA	10	-63 UU 22 Ai			
02	20 RCL2	36 Ø2		0 0	73 UFI 176 CTO2	10	22 01 22 82			
0:	21 2	02		A	77 <b>*</b> LBLC		21 13	Calculate	â	
02	22 x	-35		ë	78 DSP3		-63 03	Carcurace	ч	
02	23 -	-45		0	79 RCL1		36 01			
02	24 ST05	35 05		0	80 RCL2		36 02			
U2 01	20 X DE DEIA	-30 76 84		0	81 -		-45			
02 02	20 KUL4 27 X	30 04 -75		E C	82 RUL5		36 85 34			
82	28 RCL4	36 64		0 0	83 <del>-</del> 94 PTN		-24 24			
02	29 2	62		A	85 R/S		51			
03	30 X	-35		ĬĬ	00 1.0	I.				
03	31 RCL2	36 02								l
03	S2 RCL1	36 01								
03 03	33 - 74 v	-45		000						
ยะ คว	74 ^ 75 +	-55		090						
03	NG RCL1	36 81								
03	17 +	-55								
03	8 RCL3	36 Ø3								
03	19 RCL2	36 02								
U4 04	10 - 11 DOLA	-45								
04 04	1 KUL4 2 ENTA	30 84				_				
0- Й4	13 X	-35								
04	4 x	-35		100		-				
04	5 RCL2	36 02								
04	6 RCL4	36 04								
64	17 X	-35								
04 Ø4	να τ 19 ¥≓Υ	-33 -41								
05	i0 ÷	-24				+		SET STATUS		l I
05	1 STO8	35 08						TRIC		
05	2 1	Ũĺ					ON OFF		DISF	
05	3 ST+6	35-55 06		110		$\square$	0 🗌 🖾	DEG 🛛	FIX 🛛	
05	4 F1?	16 23 01		110					SCI ∐ ENG □	
U5 05	G GIUU G Drif	22 <b>00</b> 76 87				+	∠ ⊔ \ <b>X</b> 3 □ \ <b>X</b>		n_2	
63	U RULI	30 UT	REGI	STERS						ļ
0	1 W	2 1.1	3 Wo 4	5 Head	6 Count	or	7 noral	8 Used	9	
50	<u></u>	<mark>%2</mark>	<u> </u>	S5	S6		S7	S8	S9	
A		В	С	D		E		I		
		1		1		1		1		4

50

Program Title GENETIC INFERENCE F	ROM TRUNCATE DATA
Contributor's Name Hewlett-Packar	d Company
Address 1000 N.E. Circle Boul	.evard
City Corvallis	State Oregon Zip Code 97330
Program Description, Equations, Variables attempting a complete asce an inability to identify to affected offspring are onl resulting truncate data by (the parental genotypes ar the proportion of affected assumption made, e.g., for chi-square), and the proba and expected values of aff (P) [see Operating Limits The equations employed are $\hat{q} = \frac{\Sigma D}{\pi r}$ ; $T_c = \frac{AB}{r}$	A problem often encountered by geneticists in rtainment for a recessive trait stems from the sibships with all normal offspring (the y identifiable). This program corrects the r the so-called direct "A priori" method re assumed). In this manner are calculated: l offspring ( $\hat{q}$ ), the goodness of fit of the r the existence of heterozygous parents ( $\chi^2$ , ability that any deviation between observed fected offspring would arise by chance alone and Warnings]. e: $\sum \Sigma_{C}(1-p) = \Sigma D$ (expected) ;
$\chi^{2} = \frac{(\Sigma D - \Sigma D_{exp})^{2}}{\Sigma D_{exp}}$ where: T <sub>c</sub> = corrected tota	→ P al data D and D <sub>exp</sub> . = observed and expected affected for one set of da

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

This program has been verified only with respect to the numerical example given in *Program Description II*. User accepts and uses this program material AT HIS OWN RISK, in reliance solely upon his own inspection of the program material and without reliance upon any representation or description concerning the program material.

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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							
and a subscription of the state	parental heteroz	ygotes ex	ist for (	this rece	ssive trait (p=0.75,			
	q=1-p = 0.25)	compute $\hat{c}$	, χ <sup>2</sup> , Ρ.					
1011 - 10	Data Sot No	1 7	2	2				
	Dala Sel NO.		2					
	Total affected	3	4	2				
	No. Sibships	3	2	1				
	Sibship size	2	4	7				
Solut	ion(s)							
	.75 [E]	3 [†] 3	[†] 2 [A]	] 4 [† ] 2	[^] 4 [A] 2 [^] 1 [^] 7 [A]			
	[B] →	q = 0.26	59, [C]	$\rightarrow \chi^2 = 0$	.047,			
	[D] →	P~ 0.85	53					

Reference(s) Levitan, M. and Montagu, A., <u>Textbook of Human Genetics</u>, 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**

Cilc.       q $\chi^2$ P       Clear         STEP       INSTRUCTIONS       DATAUNITS       Revs       OUTPUT         1       Enter program		<b>1</b> GENETIC INFERENCE FROM TRUNCATE DAT	ГА	5	
INSTRUCTIONS     INFUT DATAUNITS     NETS     OUTPUT DATAUNITS       1     Enter program     Image: Constraint of the set of data stree p (assumed proportion of normal offspring) in R1 P     P     E     Image: Constraint of the set of data, enter D (totally p     Image: Constraint of the set of data, enter D (totally p     Image: Constraint of the set of data, enter D (totally p     Image: Constraint of the set of data until the sets of data which are to be entered     Image: Constraint of the sets of data which are to be entered     Image: Constraint of the set of data which are to be entered     Image: Constraint of the sets of affected on the sets of affected of fispring (q) by pressing B     Image: Constraint of the set of affected (x <sup>2</sup> ) by press C     Image: Constraint of the set of affected (x <sup>2</sup> ) by press C     Image: Constraint of the set of affected (x <sup>2</sup> ) by press C     Image: Constraint of the set of the se		$\Sigma$ Calc. $q \chi^2$	P (	Clear	
1       Enter program       Image: Constraint of a source of a s	STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
2       Clear registers and store p (assumed         2       Clear registers and store p (assumed         3       For each set of data, enter D (totally       p         affected), B (number of sibships),       B       +         and A (sibship size) and press key A       A       A         4       Repeat step 3 for each set of data until the	1	Enter program			
2       Clear registers and store p (assumed proportion of normal offspring) in R1 P       P         3       For each set of data, enter D (totally p       t         affected), B (number of sibships), B       A       A         and A (sibship size) and press key A       A       A         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       Image: Clear counter (n) is equal to all for each set of fit between the counter (q) by pressing B       Image: Clear counter (q) counter (q) by pressing C         5       Calculate the corrected proportion of the expected total of affected and the expected total of affected (x <sup>2</sup> ) by press C       Image: Clear counter (q) counter (q) by press C         7       Calculate the value of P corresponding to x <sup>2</sup> Image: Clear counter c					
proportion of normal offspring) in R1 p   3 For each set of data, enter D (totally p   affected), B (number of sibships), p   and A (sibship size) and press key A A   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 (q̂) by pressing B   6 Calculate the goodness of fit between the   observed total of affected and the   expected total of affected (x²) by press C   7 Calculate the value of P corresponding to x²   (probability that any deviation is due to   (Note: the value of P is approximate at high   P-values, - see Operating Limits and Warnings)   1    1    1 </td <td>2</td> <td>Clear registers and store p (assumed</td> <td></td> <td></td> <td></td>	2	Clear registers and store p (assumed			
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and A (sibship size) and press key A       A       A       A       Pero data         4       Repeat step 3 for each set of data until the       Image: Constraint of the counter (n) is equal to all       Image: Constraint of the constread of the constraint of the constraint of the constre		affected), B (number of sibships),	В	$\uparrow$	
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 (q) by pressing B         6         Calculate the goodness of fit between the         observed total of affected and the         expected total of affected (x²) by press C         C         (probability that any deviation is due to         chance alone)         p         (Note: the value of P is approximate at high         P-values, - see Operating Limits and Warnings)         Image: Construct of the construct of		and A (sibship size) and press key A	A	A	n=no data sets entere
is post of the counter (n) is equal to all   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 (q) by pressing B   6   Calculate the goodness of fit between the   observed total of affected and the   expected total of affected (x²) by press C   7   Calculate the value of P corresponding to x²   (probability that any deviation is due to   chance alone)   P-values, - see Operating Limits and Warnings	4	Repeat step 3 for each set of data until the			
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5       Calculate the corrected proportion of the         affected offspring (\hat{q}) by pressing B       \$\hat{g}\$         6       Calculate the goodness of fit between the         observed total of affected and the       \$\hat{c}\$         expected total of affected (\chi^2) by press C       \$\mathbf{C}\$         7       Calculate the value of P corresponding to \chi^2         (probability that any deviation is due to       \$\mathbf{D}\$         (note: the value of P is approximate at high       \$\mathbf{D}\$         P-values, - see Operating Limits and Warnings       \$\mathbf{D}\$         1       \$\mathbf{D}\$         2       \$\mathbf{D}\$         2       \$\mathbf{D}\$         3       \$\mathbf{D}\$         4       \$\mathbf{D}\$         5       \$\mathbf{D}\$         5       \$\mathbf{D}\$         5       \$\mathbf{D}\$         6		the sets of data which are to be entered			
5       Calculate the corrected proportion of the affected offspring (\hfty by pressing B					
affected offspring (q̂) by pressing B       g         6       Calculate the goodness of fit between the	5	Calculate the corrected proportion of the			
6       Calculate the goodness of fit between the	-	affected offspring $(\hat{q})$ by pressing B			â
6       Calculate the goodness of fit between the         observed total of affected and the         expected total of affected ( $\chi^2$ ) by press C         7       Calculate the value of P corresponding to $\chi^2$ (probability that any deviation is due to         chance alone)         (Note: the value of P is approximate at high         P-values, - see Operating Limits and Warnings)         (Intersection of the section of the sect					
observed total of affected and the	6	Calculate the goodness of fit between the			
expected total of affected ( $\chi^2$ ) by press C       C $\chi^2$ 7       Calculate the value of P corresponding to $\chi^2$ Image: Corresponding to $\chi^2$ (probability that any deviation is due to       Image: Corresponding to $\chi^2$ Image: Corresponding to $\chi^2$ (probability that any deviation is due to       Image: Corresponding to $\chi^2$ Image: Corresponding to $\chi^2$ (probability that any deviation is due to       Image: Corresponding to $\chi^2$ Image: Corresponding to $\chi^2$ (Note: the value of P is approximate at high       Image: Corresponding to $\chi^2$ Image: Corresponding to $\chi^2$ (Note: the value of P is approximate at high       Image: Corresponding to $\chi^2$ (Note: the value of P is approximate at high       Image: Corresponding to $\chi^2$ Image: Correspon		observed total of affected and the			
7 Calculate the value of P corresponding to $\chi^2$ (probability that any deviation is due to   chance alone)   (Note: the value of P is approximate at high   P-values, - see Operating Limits and Warnings)		expected total of affected ( $\chi^2$ ) by press C		C	x <sup>2</sup>
7       Calculate the value of P corresponding to $\chi^2$					
(probability that any deviation is due to   chance alone)   (Note: the value of P is approximate at high   P-values, - see Operating Limits and Warnings)   Image: See Operating Limits and Warnings   Image: See Operating Limits and Warnin	7	Calculate the value of P corresponding to $\chi^2$			
chance alone) D   (Note: the value of P is approximate at high   P-values, - see Operating Limits and Warnings)   Image: See Operating Limits and Warnings   Image: See Operating Limits		(probability that any deviation is due to			
(Note: the value of P is approximate at high   P-values, - see Operating Limits and Warnings)		chance alone)		ם	Р
(Note: the value of P is approximate at high					
P-values, - see Operating Limits and Warnings)		(Note: the value of P is approximate at high			
		P-values, - see Operating Limits and Warnings)			
Image: Section of the sec					

#### 97 Program Listing I

STEP	KEY ENTRY	KEY CODE	COMMENTS	STEP	KE	YENTRY		KEY CODE		сом	MENTS
00 00	1 *LBLE	21 15 -63 03	Clear registers		057			-62			
00. AA	z DSFS 3 CLRG	16-53	and store p in $R_1$		058 050	5		05 85			
00	4 ST01	35 01			055 060	ن +		-55			
00	5 RTN	24			061	CHS		-22			
88	6 ¥LBLA	21-11	Calculate		062	ex		33			
00	7 RCL1	36 01	intermédiate value	2	063	RTN		24			
60	6 XZY	-41			064	<b>≭</b> LBL1		21 01			
UU 01	9 STU2 0 VX	35 62			065	X≠Y		-41			
01 Q1	0 i^ 1 1	31 13 i			066	2		02			
01 01	2 -	-45			067	•		-62 03			
01	- 3 Chs	-22			000 029	4		04 87			
01	4 ÷	-24			070	x		-35			
01	5 RCL2	36 02			071			-62			
01	6 x	-35			<b>0</b> 72	0		<b>0</b> 0			
01	7 STO3	35 03			073	4		04			
Ø1 01	8 51+7 o v→v	30-00 07			074	5		65			
01. Q2	7 AFT 0 ST46	-41 75-55 BE			075	+		-55			
02 02	1 RCL3	35 35 80 36 03			076	CHS		-22			
02	2 1	01			077	DTN		33 24			
02	3 RCL1	36 01			070 079	R/S		51			
02	4 -	-45		ບອບ	1		L		I I		
Ø2	5 ×	-35							1		
02	6 ST+4	35-55 04							]		
62		01 75-55 of		L			<b> </b>		4		
02 02	8 51+0 9 pris	30-00 <b>0</b> 0 76 05							4		
02 83	9 ROLD Ø R/S	38 83 51	Counter						4		
03	1 *LBLB	21 12	Calculate â				╂──		{		
03	2 RCL6	36 06	Calculate q				+		1		
03	3 RCL7	36 07							1		
03	4 ÷	-24		090					1		
03	5 RTN	24							]		
03	6 ¥LBLC	21 13	Calculate $\chi^2$						1		
63	T KULD O DELA	30 00 76 04					<b> </b>		4		
03 83	0 KULT 9 -	-45			-		+		-		
04	e Entt	-21					-		1		
04	1 x	-35							1		
84	2 RCL4	36 04							1		
04	3 ÷	-24									
64	4 KIN Fairin	24		100	_		_		4		
04 Ø4	J #LDLU 6	-62	Calculate P for						4		
04	74	84	I degree of freedom	1	-				$\mathbf{I}$		
04	8 5	05			-		+		1		
84	9 X>Y?	16-34							1		
05	0 GT01	22 01							SET	STATUS	
<b>8</b> 5	1 X≢Y	-41					<b> </b>	FLAGS	٦	<b>FRIG</b>	DISP
85	2 · · · · · · · · · · · · · · · · · · ·	-62 82			+		-	ON OFF			
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υ	1 D	2 A	$^{3}$ T <sub>c</sub> $^{4}$ $\Sigma$ D(exp)	Coun	ter	ΣD		ΣT <sub>C</sub>	0		3
S0	S1	S2	S3 S4	S5		S6		S7	S8		S9
										1.	L
A		В	C	D			E			ľ	

54

Program Title	POSITIVE ASSORTATIVE MATIN	IG FOR A RECESSIVE PHEN	OTYPE
Contributor's I	Name Hewlett-Packard Compan	ту	
City Cor	vallis	State Oregon	<b>Zip Code</b> 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** 

This program has been verified only with respect to the numerical example given in *Program Description II*. User accepts and uses this program material AT HIS OWN RISK, in reliance solely upon his own inspection of the program material and without reliance upon any representation or description concerning the program material.

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Sketch(es)	
ample Problem(s	) Given the following values: initial recessive phenotype
frequen	$cy \equiv R_0 = .01, r = 0.75, q = 0.10,$
	Calculate a) recessive phenotype frequency after 4 generations (t=4)
	b) equilibrium recessive phenotype frequency $(\overline{R})$ .
oration(s)	a) .01 [ $\uparrow$ ] .75 [ $\uparrow$ ] .1 [ $\uparrow$ ] 4 [A] $\rightarrow$ R <sub>4</sub> = .0239
	b) $[R/S] \rightarrow \overline{R} = .0266$

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**

POSITIVE	ASSORTATIVE	MATING	FOR A	RECESSIVE	PHENOTYPE	7
						~~~/
calc.						┛╱

STEP	INSTRUCTIONS	INPUT DATA/UNITS	KEYS	OUTPUT DATA/UNITS
1	Enter program			
		P		
2	Enter in order: R <sub>o</sub> (initial value),	<sup>K</sup> 0		
	r, q, t			
		q		
		C		
3	Compute R <sub>t</sub> by pressing A		<b>A</b>	Rt
4	Compute equilibrium value R by then			
	pressing R/S		R/S	R
	E			
	[When $\overline{R}$ is desired outright, set t=0 in			
	step 2 and press A].			

## 97 Program Listing I

STEP	KEY ENTRY	KEY CODE	COMM	ENTS	STEP	KE	EY ENTRY	ĸ	EY CODE		СОМІ	MENTS
001	*LBLA	21 11	Store valu	ies in	e	157	X¥Y?		16-35			
002	DSP4	-63 04	R5. R1. F	$R_{2}$ , $R_{2}$ ,	e	158	GT02		22 <b>0</b> 2	1		
883	ST05	35 05	and calcu	ilate	e	759	RCL4		36 04	[ Dis	play	recessive
004	<i>R↓</i>	-31	recessive	e pheno-	e	60	R∕S		51	ph	enoty	pe frequency
005	ST01	35 01	type free	luency	6	961	<b>≭LBL</b> 2		21 02	at	equi	librium
<b>00</b> 6		-31		1	e	62	RCL 4		36 04	1	-	
007	ST02	35 02			Ģ	167	ET01		22 AI	1		
008	R4	-31			Ģ	164	+I RI 7		21 07			
<b>A</b> A9	R	<u>A</u> B			5	125	¢1020		75 07			
B1B	STAT	35 46			0	163	DCLI		33 83 7/ 84			
010 Q11	5701 Pi	-71				100	RULI		30 01			
011		-31			E	167	KIN		24			
012	#LDL1	21 01 17 of 17			Ł	168	R/S		51			
013	0521	16 23 46										
614	ESB3	23 03			070							
015	ENTT	-21										
016	X X	-35						1		1		
017	1	Ū1								1		
018	ENTT	-21						1		1		
019	2	02								ł		
828	RCL1	36 01								1		
<b>R</b> 21	X	-35								1		
<b>R</b> 22	-	-45								4		
927	Priz	76 87								4		
020	KULU V	-75			000					4		
024	· .	-33			080					1		
023	· +	-33										
026	1	61										
027	RULS	36 US										
028	-	-45										
029	÷	-24								1		
030	RCL2	36 <b>0</b> 2						1		1		
031	X	-35								1		
<b>8</b> 32	1	Ū1						+		1		
033	RCL2	36 02						+		1		
R34	-	-45			090			-		1		
A35	RCL 1	36 81						+		1		
976	ENTA	-21						+		4		
030		-75								1		
037	~	-35						_		1		
038	x	-35						-		1		
039	+	-55										
U4U	5104	35 <b>U</b> 4										
041	RCLI	36 46										
042	CHS	-22						1		1		
043	RCL5	36 05								1		
044	X≠Y?	16-32			100	1		1		1		
045	GT00	22 00				1		+		1		
046	RCL4	36 84	Display r	ecessive		<u> </u>		+		1		
R47	R/S	51	nhenotun	a fraguero				+		1		
<b>R</b> 48	KI BI A	21 <b>A</b> A		c rrequenc	Y			+		1		
040 010	Pri 4	36 BA			<b> </b>	<del> </del>		+		ł		
0450 050	DCI 7	76 87						+		SET C	TATUS	
050	RULJ	30 03 - 45						╉╼┾		SET 3	TATUS	
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053	÷	-24						+	0 🗆 🔀	DE	GX	
854	EEX	-23			110	I		+		GR		
<b>8</b> 55	5	05				ļ						
056	CHS	-22							3 ∐ XJ			
L				REGIS	STERS					-16		
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	4	L	Rt		genera	110	1		07	00		60
S0	S1	S2	S3	S4	S5		56		57	58		29
		<u></u>					l,	-			T	1
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Small Business	Earth Sciences
Antennas	Energy Conservation
Butterworth and Chebyshev Filters	Space Science
Thermal and Transport Sciences	Biology
EE (Lab)	Games
Industrial Engineering	Games of Chance
Aeronautical Engineering	Aircraft Operation
Control Systems	Avigation
Beams and Columns	Calendars
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Test Statistics	COGO-Surveying
Geometry	Astrology
<b>Reliability</b> / <b>QA</b>	Forestry

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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.

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- 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



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