# |||-(67 || ${ }^{(1)}$ 

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 Programming Guide, "Loading a Program" (page 134, HP-67; page 119, HP-97), key in the program from the Program Listing I and Program Listing II pages. A number at the top of the Program Listing indicates on which calculator the program was written (HP-67 or HP-97). If the calculator indicated differs from the calculator you will be using, consult Appendix E of your Owner's Handbook for the corresponding keycodes and keystrokes converting HP-67 to HP-97 keycodes and vice versa. No program conversion is necessary. The HP-67 and HP-97 are totally compatible, but some differences do occur in the keycodes used to represent some of the functions.

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

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

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

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# Program Description 



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

$$
\hat{T} \cong \frac{\sum_{\alpha}^{\omega} x 1_{x} m_{x}}{R_{o}}
$$

where $x$ is age, $I_{x}$ is the fractional survivorship to that age from age class zero, $m$ is the fecundity at age $x$, and $R_{0}$ is the net reproductive rate, computed from the equation

$$
R_{0}=\sum_{\alpha}^{W} 1_{x} m_{x}
$$

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

$$
\hat{\boldsymbol{r}} \cong \log _{e} R_{0}
$$

Using the estimate of $r$ stored in $R_{8}$, and the products of the age-specific survivorship and fecundity schedules stored in registers 1 through 7 , the program computes the sum

$$
\sum_{x=\alpha}^{\omega} e^{-r x} 1_{x} m_{x}
$$

(Continued on next page)

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

[^0]
## Program Description

| Program Title |  |  |
| :--- | :--- | :--- |
| Contributor's Name |  |  |
| Address | State |  |
| City | Zip Code |  |

```
Program Description, Equations, Variables where \alpha is the age of first reproduction
    ( }\mp@subsup{1}{\alpha}{}\mp@subsup{m}{\alpha}{}\mathrm{ is stored in }\mp@subsup{R}{1}{}\mathrm{ ) and }\omega\mathrm{ 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 R and
    recalculates the new sum, wh1ch is compared with }1.00\mathrm{ 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\mathrm{ , which is simply e r}\mathrm{ .
    If the user thinks the program is taking too long to compute r, it can be stopped
    with the "CLx" button and R8 recalled to see what value of r was being used in the
    last loop.
```

|  |
| :--- | :--- | :--- |
| Operating Limits and Warnings |
|  |
|  |
|  |

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## Progiram IDescription II

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

| Age (x) | Survivorship $\left(1_{x}\right)$ | Fecundity $\left(m_{x}\right)$ |
| ---: | :---: | :---: |
| 0 | 1.0 | 0.0 |
| 1 | .9 | 0.0 |
| 2 | .7 | 0.0 |
| $-\frac{.5}{4}-(\alpha)$ | 0.0 |  |
| 5 | .4 | 1.0 |
| 6 | .3 | 1.0 |
| 7 | .2 | 1.5 |
| 8 | .1 | 1.0 |
| 9 | .1 | 1.0 |
| $10(\omega)$ | .01 | 0.5 |
|  |  | 1.0 |

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

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

Solution(s)

$$
\begin{aligned}
& \mathrm{R}=1.36 \\
& \hat{T}^{0}=5.625 \\
& \hat{\mathbf{r}}=0.0547 \text { (a slight underestimate). }
\end{aligned}
$$

1. . 4 [ENTER $\uparrow$ ] 1 [ENTER $\uparrow$ ] . 3 [ENTER $\uparrow$ ] 1 [A]
. 2 [ENTER $\uparrow$ ] 1.5 [ENTER $\uparrow$ ] . 2 [ENTER $\uparrow$ ] 1 [B]
. 1 [ENTER $\uparrow$ ] 1 [ENTER $\uparrow$ ] . 1 [ENTER $\uparrow$ ] . 5 [C]
.01 [ENTER $\uparrow$ ] 1 [ENTER $\uparrow$ ] 3 [D] [E] $\rightarrow 5.625$
$[R / S] \rightarrow 0.0547$
[RCL] [9] $\rightarrow 1.3600$
2. [f] [A] $\rightarrow .0552(r)$
[f] [B] $\rightarrow 1.0568(\lambda)$

Reference(s) Mertz, D.B. 1970. Notes on methods used in life-history studies. pp.4-17 in Connell, Mertz, and Murdoch's'Readings in ecology and ecological genetics!' Harper \& Row, New York, 397 p.
Pianka, E.R. 1974. Evolutionary ecology. Harper \& Row. 356 pp. Poole, R.W. 1974. An introduction to quantitative ecology. McGraw-Hill. This program is a modification of the Users' Library Programs \#03637A and $\#^{0} 03638$ A submitted by Eric R. Pianka.


$6$


## Program Description



Program Description, Equations, Variables After storing the intrinsic rate of increase r, in register 1, the user enters age (x), age-specific survivorship ( $1_{x}$ ), and age-specific fecundity ( $m_{x}$ ) sequentially, beginning with the oldest age class and working toward the youngest age class. User-defined key "C" is punched for each age class and the expectation of further life, $\mathrm{E}_{\mathrm{X}}$, is displayed as computed from the equation:

$$
E_{x}=\frac{\sum_{y=x}^{\infty} 1 y}{1_{x}}
$$

Fisher's reproductive value is computed from the equation:

$$
v_{x}=\frac{e^{r x}}{1_{x}} \sum_{t=x}^{\infty} e^{-r t} 1_{t} m_{t}
$$

After all age classes have been entered and $E_{x}$ and $v_{x}$ for each has been computed and recorded, User-defined key $D$ computes the net reproductive rate, $R_{0}$, and the finite rate of increase, $\lambda$, from the equations

$$
R_{0}=\sum_{\alpha}^{\mu} 1_{x} m_{x} \quad \text { and } \quad \lambda=e^{r}
$$

Generation time is computed with the approximate formula:

$$
\hat{\mathrm{T}}=\frac{\sum_{\alpha}^{\omega} \mathrm{x} 1_{\mathrm{x}} \mathrm{~m}_{\mathrm{x}}}{\mathrm{R}_{\mathrm{o}}}
$$

( $\alpha$ 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 $\mathrm{v}_{\mathrm{x}}$; hence an error in data entry at any age will throw off all subsequent computations for younger age groups.

[^1]
## Program Description II

## Sketch(es)

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

|  | Age (x) | Survivorship ( $1_{\mathrm{x}}$ ) | Fecundity ( $\mathrm{m}_{\mathrm{x}}$ ) |
| :---: | :---: | :---: | :---: |
| $\left\{\begin{array}{l}\text { the intrinsic rate } \\ \text { of natural increase } \\ \text { is known to be . } 0552\end{array}\right\}$ | 0 | 1.0 | 0 |
|  | 1 | . 9 | 0 |
|  | 2 | . 7 | 0 |
|  | 3 | . 5 | 0 |
|  | 4 | . 4 | 1 |
|  | 5 | . 3 | 1 |
|  | 6 | . 2 | 1.5 |
|  | 7 | . 2 | 1 |
|  | 8 | . 1 | 1 |
|  | 9 | . 1 | 0.5 |
|  | 10 | . 01 | 1 |

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

Solution(s) .0552 [A] 10 [ENTER $\uparrow$ ] . 01 [ENTER $\uparrow$ ] 1 [B] $\rightarrow 10$; [C] $\rightarrow 1.000 ;[R / S] \rightarrow 1.000$

```
    9[ENTER \uparrow] . 1[ENTER \uparrow] .5[B] -> 9; [C] -> 1.100; [R/S] -> 0.595
```

    Repeat for 8 thru 0 to obtain values in table
    \(\mathrm{E}_{\mathrm{O}}=4.41, \mathrm{v}_{0}=1.000\)
    \(\mathrm{E}_{1}=3.79, \mathrm{v}_{1}=1.174\)
    \(E_{2}=3.59, v_{2}=1.595\)
    \(E_{3}=3.62, v_{3}=2.361\)
    \([D] \rightarrow 1.3600\left(R_{o}\right)\)
    \(\mathrm{E}_{4}=3.28, \mathrm{v}_{4}=3.118 \quad[\mathrm{R} / \mathrm{S}] \rightarrow 1.0568(\lambda)\)
    \(E_{5}=3.03, v_{5}=2.985 \quad[E] \rightarrow 5.625 \quad(\hat{T})\)
    \(\mathrm{E}_{6}=3.05, \mathrm{v}_{6}=3.146\)
    \(E_{7}=2.05, v_{7}=1.739\)
    \(E_{8}=2.10, v_{8}=1.563\)
    \(\mathrm{E}_{\mathrm{g}}=1.10, \mathrm{v}_{9}=0.595\)
    \(\mathrm{E}_{10}=1.00, \mathrm{v}_{10}=1.000\)
    Reference(s) Fisher, R.A. 1930. The genetical theory of natural selection. Oxford.
Mertz, D.B. 1970. Notes on methods used in life-history studies, pp 4-17 in Connell, Mertz, and Murdoch's 'Readings in ecology and ecological genetics." Harper \& Row.
Pianka, E.R. 1974. Evolutionary ecology. Harper \& Row.
Poole, R.W. 1974. An introduction to quantitative ecology. McGraw-Hill. Wilson, E.O. and W. Bossert. 1971. A primer of population biglggy. Sinaue
 submitted by Eric R, Pianka.

## User Instructions



| STEP | INSTRUCTIONS | INPUT DATA/UNITS |  | KEYS | OUTPUT DATA/UNITS |
| :---: | :---: | :---: | :---: | :---: | :---: |
| 1 | Read program (in "run" mode!) |  |  |  |  |
|  |  |  |  |  |  |
| 2 | Enter intrinsic rate of increase in $\mathrm{R}_{1}$ | r | A |  |  |
|  |  |  |  | - |  |
| 3 | Key in age (x) of oldest age group first | x | $\uparrow$ |  |  |
|  |  |  |  | -- |  |
| 4 | Key in survivorship of oldest age group, ( $\mathrm{l}_{\mathrm{x}}$ ) | $1_{x}$ | $\uparrow$ | $\square$ |  |
|  | first |  |  |  |  |
| 5 | Key in fecundity of oldest age group ( $\mathrm{m}_{\mathrm{x}}$ ) | $\mathrm{m}_{\mathrm{x}}$ | B |  | (x) |
|  | first |  |  |  |  |
| 6 | Compute and record expectation of life, $E_{X}$ |  | C |  | $\mathrm{E}_{\mathrm{x}}$ |
|  |  |  |  |  |  |
| 7 | Compute and record reproductive value, $\mathrm{v}_{\mathrm{x}}$ |  | R/S |  | $\mathrm{v}_{\mathrm{x}}$ |
|  |  |  |  | - $]$ |  |
| 8 | Repeat steps 3 through 7 for next oldest age |  |  | , | x |
|  | until all age classes have been entered and |  |  |  | $\mathrm{E}_{\mathrm{x}}$ |
|  | a complete sequence of values have been |  |  |  |  |
|  | obtained for $\mathrm{E}_{\mathrm{X}}$ and $\mathrm{v}_{\mathbf{X}}$ for all ages. |  |  |  |  |
|  |  |  |  | - |  |
| 9 | Calculate net reproductive rate, $\mathrm{R}_{\mathrm{O}}$ |  | D | - | $\mathrm{R}_{0}$ |
|  |  |  |  | [ ] |  |
| 10 | Calculate finite rate of increase, $\lambda$ |  | R/S |  | $\lambda$ |
|  |  |  |  | I |  |
| 11 | Compute estimate of mean generation time, $\hat{\mathrm{T}}$ |  | E | $\square]$ | $\hat{T}$ |
|  |  |  |  | 1 |  |
|  |  |  |  | [ - ] |  |
|  |  |  |  | 1 |  |
|  |  |  |  |  |  |
|  |  |  |  | \| |  |
|  |  |  |  | I |  |
|  |  |  |  | 1 - 1 |  |
|  |  |  |  | I |  |
|  |  |  |  | I |  |
|  |  |  |  | 1 |  |
|  |  |  |  | 1 |  |
|  |  |  |  |  |  |
|  |  |  |  | 1 |  |
|  |  |  |  |  |  |
|  |  |  |  |  |  |

COMMENTS


STEP KEY ENTRY KEY CODE
COMMENTS


## Program Description, Equations, Variables

Given a data set:

$$
\left\{n_{1}, n_{2}, n_{3}, \ldots n_{i}\right\}
$$

The program computes the following:

$$
\begin{aligned}
& \text { Diversity }=3.3219\left(\log _{10} N-\frac{1}{N} \Sigma n_{i} \log _{10} n_{i}\right) \\
& \text { Equitability }=\frac{\text { Diversity }}{3.3219\left(\log _{10^{N}}\right)}
\end{aligned}
$$

Where:

$$
\begin{gathered}
n_{i}=\text { number of individuals of the } i \text { th group } \\
N=\text { total number of individuals in the collection } \\
3.3219=\text { conversion factor } \log _{10} \text { to } \log _{2}
\end{gathered}
$$

## Operating Limits and Warnings

n is a positive interger and $\mathrm{n}>1$.

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 Problem(s)

Compute diversity and equitability for the following data:
$\{740 ; 11,000 ; 920 ; 180 ; 180 ; 740 ; 180\}$

Solution(s)
[A] 740
[B] 11,000
[B] 920 [B] 180
[B] 180 [B]740
[в] 180 [в]
[D]
[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 非 04754A submitted by W. Thomas Shoaf.

## User Instruetions






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

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

where the $p_{i}$ are the proportion of the ith resource used and $n$ is the total number of resources.

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

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

$$
0=\frac{\Sigma \mathrm{p}_{i} \mathrm{q}_{i}}{\sqrt{\Sigma \mathrm{p}_{i}^{2} \Sigma \mathrm{q}_{i}^{2}}}
$$

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 $0^{\circ}$ to $90^{\circ}$, 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.

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## Program Description

## Program Title

## Contributor's Name

Address
City State Zip Code

## Program Description, Equations, Variables

to the formula:

$$
\mathrm{H}_{\mathrm{p}}=-\Sigma \mathrm{p}_{\mathrm{i}} \mathrm{Ln} p_{i} \text { or }-\sum \mathrm{q}_{\mathrm{i}} \mathrm{LN} \mathrm{q}_{\mathrm{i}} \cdot=\mathrm{H}_{\mathrm{q}}
$$

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

The program also computes Horn's (1966) measure of overlap, $\mathrm{R}_{\mathrm{O}}$, from a simplified computational formula:

$$
\text { Overlap }=R_{o}=\frac{\left(\left(\mathrm{H}_{\mathrm{p}}+\mathrm{H}_{\mathrm{q}}\right) / 2\right)-\mathrm{H}_{\mathrm{r}}}{\operatorname{Ln} 2}+1
$$

where $H_{r}$ is computed from the $p_{i}$ and $q_{i}$ vectors, with $r_{i}=\left(p_{i}+q_{i}\right) / 2$ according to Shannon's formula (above). $H_{r}$ is stored in register 6 .

Operating Limits and Warnings

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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:

| Resource 1 | Resource 2 | Resource 3 | Resource 4 |
| :---: | :---: | :---: | :---: |
| 0.2 | 0.5 | 0.1 | 0.2 |
| 0.3 | 0.1 | 0.4 | 0.2 |

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

$$
\begin{array}{ll}
\text { Species } & 1 \\
\text { Species } & 2 \\
\text { Species } & 3 \\
\text { Species } & 4 \\
\text { Species } & 5
\end{array}
$$

$$
\frac{\text { Community A }}{.1}
$$

$\frac{\text { Community } \mathrm{B}}{0.00}$

- 1
. 2
0.0
.5
. 2
.4
. 2
. 1
.3

Species A
$\begin{array}{lll}0.2 & 0.5 \\ 0.3 & 0.1\end{array}$
0.1
0.4
0.2
0.2

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

Solution(s) 1. a. Initialize (zero all registers): [CL REG]
b. Key in $p_{i}, q_{i}$ data as follows:

$$
\begin{array}{llll}
0.2 & {[\uparrow]} & 0.3 & \text { [A] } \\
0.5 & {[\uparrow]} & 0.1 & \text { [A] } \\
0.1 & {[\uparrow]} & 0.4 & \text { [A] } \\
0.2 & {[\uparrow]} & 0.2 & {[\mathrm{~A}]}
\end{array}
$$

c. Compute niche breadths: [B] 2.94 [R/S] $0.74\left(\mathrm{~B}_{\mathrm{p}} / \mathrm{n}\right)$
[R/S] 3.33 [R/S] $0.83\left(\mathrm{~B}_{\mathrm{q}} / \mathrm{n}\right)$
d. Compute niche overlap: [C] 0.59, Arc sine: [R/S] 36.51
e. Check Sums of $\mathrm{p}_{\mathrm{i}}, \mathrm{q}_{\mathrm{i}}$ : [D] 1.00, [R/S] 1.00

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

## Sketch(es)

## Sample Problem(s)

Solution(s) 2. a. Initialize (zero all registers): [CL REG]
b. Key in the five sets of $p_{i}$ and $q_{i}$ data, letting $i$ run from 1 to 5:
0.1 [ $\uparrow$ ] 0.0 [f] [A]
0.2 [ $\uparrow$ ] 0.4 [f] [A]
0.0 [ $\uparrow$ ] 0.2 [f] [A]
0.5 [ $\uparrow$ ] 0.1 [f] [A]
0.2 [ $\uparrow$ ] 0.3 [f] [A]
c. Compute diversity of community $A\left(H_{p}\right)$ : [f][B] $1.28,[R / S] 0.80\left(H / H_{m a x}\right)$
d. Compute diversity of community $B\left(H_{q}\right):[f][C] 1.22,[R / S] 0.76\left(H / H_{m a x}\right)$
e. Compute community overlap, $R_{o}[f][D] 0.71$

Reference(s) Shannon, C.E. and W. Weaver, 1949. The mathematical theory of communication Univ. Illinois Press, Urbana.
Horn, H.S., 1966. Measurement of "overlap" in comparative ecological studies. Amer. Naturalist 100: 419-424.
Lloyd, M.J.H.Zar, and J. Karr. 1968. On the calculation of information theoretical measures of diversity. Amer. Midlan Naturalist 79: 257-272. This program is a modification of the Users' Library Programs 非 02158A \& 非03150A submitted by Eric R. Pianka.




| Program Title POPULATION SIZE ESTIMATE | (JOLLY'S METHOD) |  |  |
| :---: | :---: | :---: | :---: |
| Contributor's Name Hewlett-Packard Company |  |  |  |
| Address 1000 N.E. Circle Boulevard |  |  |  |
| City Corvallis | State | Oregon | Zip Code 97330 |

Program Description, Equations, Variables Using Jolly's (1965) symbo1s, 1et
$\mathrm{n}=$ number in sample (at time t )
$m=$ number of marked individuals in sample at time $t$ (recaptures)
$s=$ number of marked individuals released from sample (need not be all)
$r=$ number of marked individuals released from sample which are subsequently captured again at least once (known to be alive later)
$z=$ number of individuals marked prior to sample, but not captured in sample, and which are subsequently captured in later samples (hence the individuals known to be alive at time of sample).

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

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

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

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

Jolly's formula for the standard error of the population size is as follows:
S. E. $\hat{N}=\sqrt{\hat{N}(\hat{N}-r)\left\{\frac{\hat{M}-m+s}{\hat{M}}\left(\frac{1}{r}-\frac{1}{s}\right)+\left(\frac{1}{m}-\frac{1}{n}\right)\right\}}$

Operating Limits and Warnings The following inequalities must be met:
$\mathrm{n} \geqslant \mathrm{m} \geqslant \mathrm{s} \geqslant \mathrm{r}$

[^2]
## Sketch(es)

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

$$
\begin{aligned}
& \mathrm{n}=100 \\
& \mathrm{~m}=64 \\
& \mathrm{~s}=48 \\
& \mathrm{r}=28 \\
& \mathrm{z}=16
\end{aligned}
$$

Estimate the population size and its standard error.

Solution(s)

```
100 [ENTER \uparrow] 64 [A] 48 [ENTER \uparrow] 28 [ENTER \uparrow] 16 [B]
    [C] }->142.86(\hat{N}
    [R/S] -> 10.47 (SE)
        [D] }->91.43(\hat{M}
```

Reference(s) Jolly, G.M. 1965. Explicit estimates from capture-recapture data with both death and dilution -- stochastic model. Biometrika 52: 225-247.
Poole, R.W. 1974. An introduction to quantitative ecology. McGraw-Hill. (pp. 307-312.)
This program is a translation of the HP-65 Users' Library
Program \# 03257A submitted by Eric R. Pianka,

1 POPULATION SIZE ESTIMATE (JOLLY'S METHOD)


| STEP | Instructions | INPUT DATA/UNITS | KEYS |  | OUTPUT DATA/UNITS |
| :---: | :---: | :---: | :---: | :---: | :---: |
| 1 | Load side 1 |  |  | $\square$ |  |
|  |  |  |  |  |  |
| 2 | Enter n | n | ENT $\uparrow$ |  |  |
|  |  |  |  | $\square$ |  |
| 3 | Enter m | m | A | , |  |
|  |  |  |  | $\square$ |  |
| 4 | Enter s | s | EnTt ${ }^{\text {c }}$ | ] |  |
|  |  |  |  | I |  |
| 5 | Enter r | r | ENT ${ }^{\text {f }}$ |  |  |
|  |  |  |  | $\square$ |  |
| 6 | Enter z | z | B |  |  |
|  |  |  |  | , |  |
| 7 | Compute $\hat{\mathrm{N}}$ |  | c | $\square$ | N |
|  |  |  |  | - |  |
| 8 | Compute SE |  | R/S | $\square$ | SE |
|  |  |  |  |  |  |
| 9 | Display $\hat{M}$ |  | D | $\square$ | $\hat{M}$ |
|  |  |  |  | $\square$ |  |
| 10 | Display $\hat{M}-m+s$ (if desired) |  | E | $\square$ | $\hat{M}-\mathrm{m}+\mathrm{s}$ |
|  |  |  |  | $\square$ |  |
|  |  |  |  | $\square$ |  |
|  |  |  |  | $\square$ |  |
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|  |  |  |  | $\square$ |  |
|  |  |  |  | $\square$ |  |



| m Title $\quad$ CELL PHASE AND CYCLE TIMES |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: |
| Contributor's Name | Hewlett-Packard Company |  |  |  |
| Address 1000 |  |  |  |  |
| City Corvallis | State | Oregon | Zip Code | 97330 |

## Program Description, Equations, Variables

$$
\begin{aligned}
\text { Where } \mathrm{n}_{\mathrm{G} 1} & =\text { the number of cells in } \mathrm{G} 1 \text { phase } \\
\mathrm{n}_{\mathrm{S}} & =\text { the number of cells in } \mathrm{S} \text { phase } \\
\mathrm{n}_{\mathrm{G} 2} & =\text { the number of cells in } \mathrm{G} 2 \text { phase } \\
\mathrm{n}_{\mathrm{M}} & =\text { the number of cells in } \mathrm{M} \text { phase } \\
\mathrm{n} & =\mathrm{n}_{\mathrm{G} 1}+\mathrm{n}_{\mathrm{S}}+\mathrm{n}_{\mathrm{G} 2}+\mathrm{n}_{\mathrm{M}}=\text { total number of cells. }
\end{aligned}
$$

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:

$$
N_{x}=2 \stackrel{T}{T}-1
$$

where $T_{x}$ is the phase time and $T$ is the cell cycle time.
Given a starting concentration of cells, $n_{0}$, 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:

$$
\mathrm{n}=\mathrm{n}_{\mathrm{o}} 2^{\frac{\mathrm{t}}{\mathrm{~T}}}
$$

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.

[^3]

## Sample Problem(s)

1. In a randomly dividing cell culture with a cell cycle time of 24 hours, a sample is evaluated and 500 cells are found in M, 1000 in G2, 500 in S, and 1500 in G1 phase. Calculate the time spent in each phase:
$T_{G 1}, T_{S}, T_{G 2}$, and $T_{M}$.
2. In this culture the cells in mitosis were examined, and it was found that 30 cells were in telophase, 50 in anaphase, 70 in metaphase, and 350 in prophase. As above, the cell cycle time is 24 hours and the total number of cells counted is 3500. Calculate the time spent in each phase of mitosis:

$$
\mathrm{T}_{\text {pro }}, \mathrm{T}_{\text {meta }}, \mathrm{T}_{\text {ana }}, \text { and } \mathrm{T}_{\text {telo }}
$$

(Continued on next page)

## Solution(s)

1. 24 [ENTER $\uparrow 3500$ [f][A] 1500 [ENTER $\uparrow$ ] 500[ENTER $] 1000$ [ENTER $\uparrow$ ] 500 [A] $\rightarrow 3500$
$[B] \rightarrow 8.35$ hours
$[C] \rightarrow 3.30$ hours
[D] $\rightarrow 7.73$ hours
[E] $\rightarrow 4.62$ hours
2. 350 [ENTER ] 70 [ENTER ] 50 [ENTER $] 30$ [A] $\rightarrow 500$
[B] $\rightarrow 3.17$ hours
$[\mathrm{C}] \rightarrow 0.67$ hours
[D] $\rightarrow 0.49$ hours
[E] $\rightarrow 0.30$ hours
3. $\mathrm{T}_{\mathrm{GI}}=8.35$ hours
$\mathrm{T}_{\mathrm{S}}=3.30$ hours
$\mathrm{T}_{\mathrm{G} 2}=7.73$ hours
$\mathrm{T}_{\mathrm{M}}=4.62$ hours
[E] $\rightarrow 0.30$ hours
4. $\mathrm{T}_{\mathrm{pro}}=3.17$ hours
$\mathrm{T}_{\text {meta }}=0.67$ hours
$\mathrm{T}_{\text {ana }}=0.49$ hours
$\mathrm{T}_{\text {telo }}=0.30$ hours

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


Sample Problem(s)
3. Find the cell cycle time, $T$, of cultured cells (represented above) where a starting concentration of cells, $\mathrm{n}_{\mathrm{O}}$, a subsequent concentration of cells, n , and the elapsed time, t , are given:
$\mathrm{n}_{\mathrm{o}}=100,000 \mathrm{cells} / \mathrm{ml}$
$\mathrm{n}=500,000 \mathrm{cells} / \mathrm{ml}$
$\mathrm{t}=48$ hours

Solution(s)

```
        3. T = 20.67 hours
        48[ENTER\uparrow ] 1[EEX] 5[ENTER\uparrow ] 5[EEX] 5[f][B] -> 20.67 hours
```

Reference(s)





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.

[^4]
## Program Title

## Contributor's Name

## Address

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

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

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)

1. Regions: 1234567

2. 1234567


Sample Problem(s) 1. Given the paternal chromatids, P1, observed progeny chromatids, F1, and 7 crossover regions as shown above: a) In what regions did crossovers occur producing the progeny chromatid with the genotype AbcDEfGh? b) The progeny chromatid with the genotype abCDefGH?
2. Given the parental chromatids above: a) What is the genotype of the progeny chromatid resulting from crossovers occurring in regions 2,3 and 5? b) In regions 1, 4 and 6?

Solution(s)

1. a) . 10001100 [ENTERt] . 10011010 [A]

7 [B] $\rightarrow 34507$
Crossovers occur in regions 3, 4, 5, and 7
b) . 01110011 [ENTERA] . 00110011 [A]
$7[\mathrm{~B}] \rightarrow 1200000$
Crossovers occur in regions 1 and 2.
2. a) 8 [E]

10001100 [ENTERA] 2 [ENTERT] 3 [ENTERA] 5 [C] $\rightarrow 10101011$ (AbCdEfGH)
b) 10001100 [ENTER ] 1 [ENTER ] 4 [ENTER ] 6 [C] $\rightarrow 11111111$ (ABCDEFGH)

Reference (s)
Srb, A. M., R. D. Owen and R. S. Edgar. General Genetics, 2nd Ed.,
1965. W. H. Freeman and Co., San Francisco. Chapter 6. This program is a modification of the Users' Library Programs非01523A and 非01524A submitted by James N. Adams.


| STEP | INSTRUCTIONS | INPUT |
| :---: | :--- | :--- | :--- | :--- |
| OUTPUT |  |  |
| DATA/UNITS |  |  |




# Program Description 



```
Program Description, Equations, Variables Chromosome cleavage is a powerful experimental genetic technique which has yielded a wealth of knowledge concerning gene loci on the chromosomal DNA code. The program simulates chromosome models consisting of even hundreds or thousands of unique individually identifiable genes in linear array. By noting what happens to any two genes after chromosomal fragmentation at arbitrary break-points, entire chromosomal gene sequences may be reconstructed experimentally.
The genetic sequences are based upon the ability of a prime \(P\), of form ( \(8 \mathrm{k}+3\) ) or ( \(8 \mathrm{k}+5\) ) for some integer \(k\), to reproduce all integers from 1 to ( \(\mathrm{P}-1\) ) in any ( \(\mathrm{P}-1\) ) consecutive passes of the formula \(\left(S_{i+1}=2 S_{i}\right.\) module \(P\) ), starting from any \(\mathrm{S}_{1}\left(1 \leqslant \mathrm{~S}_{1} \leqslant(\mathrm{P}-1)\right.\). Permissable chromosome lengths for \(\mathrm{n} \leqslant 100\) genes are \(10,12,18,28,36,42,52,58,60,66,82,100\). For example, for \(n=100\), \(\mathrm{P}=101=(8 \cdot(12)+5)\) is a prime of form \((8 k+5)\).
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 lst fragment ( \(\mathrm{F}_{1}\) ) 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

[^5]
## Sketch(es)

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

Solution(s) . 456 [f][A] 10 [A] 1 [ENTER $\uparrow 6$ [B]
Press [C] 10 times and get the sequence 2, $0,2,2,2,0,1,2,2$,
$[\mathrm{D}] \rightarrow 0$
1 [ENTER $\uparrow$ ] [B]; Press [C] 10 times $\rightarrow 1,2,1,2,2,2,2,2,1,2$
[D] $\rightarrow-2[D i s r e g a r d ~ t h e ~ s i g n] ~$
6 [ENTER ] 9 [B]; Press [C] 10 times $\rightarrow 1,0,1,1,1,1,1,0,0,0$
[D] $\rightarrow-6$ [Disregard the sign]
$[E] \rightarrow 7,3,6,1,2,4,8,5,10,9$ True Gene Sequence

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




# Progiram Description 

Program Title RECESSIVE GENE FREQUENCY AFTER SELECTION, MUTATION, AND INBREEDING
Contributor's Name Hewlett-Packard Company

Address 1000 N.E. Circle Boulevard
City Corvallis State Oregon Zip Code 97330

## Program Description, Equations, Variables The following selection and mutation model

was used:


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

$$
\mathrm{q}_{\mathrm{n}+1}=\frac{\mathrm{q}_{\mathrm{n}}^{2}(h t+\mathrm{uht}-\mathrm{t})+\mathrm{q}_{\mathrm{n}}(1-\mathrm{ht}-\mathrm{u}-\mathrm{uht})+\mathrm{u}}{1-2 h t \mathrm{q}_{\mathrm{n}}+\mathrm{q}_{\mathrm{n}}^{2}(2 h t-1)}
$$

where:

```
            u = mutation rate q = recessive or mutant gene frequency
                (1-t) = mutant homozygote fitness }n=\mp@code{no. of generations.
                (1-ht) = mutant heterozygote fitness }\mp@subsup{q}{0}{}=\mathrm{ initial gene frequency and equilibriu
                                    gene frequency
                    qe}\mathrm{ is attained when }\mp@subsup{q}{n+1}{}=\mp@subsup{q}{n}{}\mathrm{ (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.

[^6]
## Progiram Description

## Program Title

## Contributor's Name

Address
City
State
Zip Code

## Program Description, Equations, Variables Using simplifying assumptions (see below)

and the following model,

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

$$
A=\frac{(1-F)(h t-1)\left[q_{n}^{2}(2-t)-q_{n}\right]+q_{n} F(1-t)}{\left(1-q_{n} F\right)-(1-F)\left[q_{n}^{2}(2+2 h t-t)-2 q_{n} h t\right]+q_{n} F(1-t)}
$$

where:

```
(1-t) = fitness of recessive homozygote
(1-ht) = fitness of heterozygote (fitness of normal homozygote
                is assumed as unity)
                    u = mutation rate for recessive gene
            F = inbreeding coefficient
            q
            qe}=\mathrm{ equilibrium gene frequency
```

Operating Limits and Warnings The following simplifying assumptions apply:

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

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. Given the genetic parameters: $\mathrm{h}=0.1, \mathrm{t}=0.5, \mathrm{u}=10^{-4}, \mathrm{q}_{\mathrm{o}}=10^{-3}$, calculate the equilibrium gene frequency, $q_{e}$, and estimate the no. of generations to attain this frequency.
2. Given the genetic parameters: $h=0.5$, $t=1, u=q_{0}=10^{-6}$, compute the values of $\mathrm{q}_{2}$ and $\mathrm{q}_{\mathrm{e}}$.
3. Using the following values: $\mathrm{q}_{\mathrm{O}}=\mathrm{u}=1 \times 10^{-5}, \mathrm{~h}=0.1, \mathrm{~F}=0.1, \mathrm{t}=1$, calculate $\mathrm{q}_{2}, \mathrm{q}_{10}, \mathrm{q}_{\mathrm{e}}$, and estimate the value of n to attain $\mathrm{q}_{\mathrm{e}}$. (Note that when $\mathrm{q}_{\mathrm{e}}$ is computed directly after $\mathrm{q}_{10}$ was computed, the value of $\left.n=10+\left|R_{8}\right|\right)$.

Solution(s) 1. 0 [STO][8] . 1 [ 1 ]. . $[\uparrow$ ] [EEX] 4 [CHS][ $][E E X] 3$ [CHS] $[\mathrm{A}] \rightarrow \mathrm{q}_{\mathrm{e}}=1.97 \mathrm{X} 1 \sigma^{-3}$ (ca. 10 min . of running time)
[RCL] $7 \rightarrow \mathrm{n}=150$
2. 2 [STO][8] . $5[\uparrow] 1[\uparrow][E E X] 6$ [CHS][ $1[\mathrm{~A}] \div \mathrm{q}_{2}=1.75 \mathrm{X} 10^{-6}$

0 [STO][8] [R/S] $\rightarrow \mathrm{q}_{\mathbf{e}}=2.00 \times 10^{-6}$
3. [EEX] 5 [CHS][STO] 1 [STO][5] 2 [STO] [I] $1[\uparrow] .1[\uparrow] .1[E] \rightarrow \mathrm{q}_{2}=2.47 \times 10^{-5}$
8 [STO][I] [R/S] $\rightarrow \mathrm{q}_{10}=4.74 \times 10^{-5}$ 0 [STO][I] [R/S] $\rightarrow \mathrm{q}_{\mathrm{e}}=5.26 \times 10^{-5}$ (ca. 3 min . running time) [I] [ABS] $10+\rightarrow \mathrm{n}=47$ generations.

Reference (s)
Cavalli - Sforza, L.L. and Bodmer, W.F., The Genetics of Human Populations, pgs. 82-88, 365, W.H. Freeman, 1971. This program is a modification of the Users' Library Programs非04531A and 非04679A submitted by Dr. Leo S. Reich.






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

The following equations were used in the program:

$$
\mathrm{q}_{\mathrm{n}+1}=\frac{\mathrm{q}_{\mathrm{n}} \mathrm{~W}_{2}+\mathrm{q}_{\mathrm{n}}^{2}\left(\mathrm{~W}_{3}-\mathrm{W}_{2}\right)}{\mathrm{W}_{1}+2 \mathrm{q}_{\mathrm{n}}\left(\mathrm{~W}_{2}-\mathrm{W}_{1}\right)+\mathrm{q}_{\mathrm{n}}^{2}\left(\mathrm{~W}_{1}+\mathrm{W}_{3}-2 \mathrm{~W}_{2}\right)} ; \hat{\mathrm{q}}=\frac{\mathrm{W}_{1}-\mathrm{W}_{2}}{\mathrm{~W}_{1}+\mathrm{W}_{3}-2 \mathrm{~W}_{2}}
$$

Where:

$$
\left.\begin{array}{rl}
\mathrm{W}_{1}, \mathrm{~W}_{2}, \mathrm{~W}_{3} & \text { denote adaptive values for genotypes } A A, \text { Aa, aa, respectively } \\
& (A=\text { dominant and } a=\text { recessive gene) }
\end{array}\right)
$$

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

[^7]
## Sketch(es)



Reference(s) Gardner, E.J., Principles of Genetics, fifth edition, J. Wiley \& Sons, 1975.

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



Program Title GENETIC INFERENCE FROM TRUNCATE DATA

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

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

The equations employed are:

$$
\begin{aligned}
& \hat{q}=\frac{\Sigma D}{\Sigma T c} ; \quad T_{c}=\frac{A B}{1-p^{A}} ; \Sigma T_{c}(1-p)=\Sigma D \quad \text { (expected) } ; \\
& x^{2}=\frac{\left(\Sigma D-\Sigma D_{\exp }\right)^{2}}{\Sigma D_{\exp }} \rightarrow P
\end{aligned}
$$

where:

$$
\begin{array}{rlrl}
T_{c}=\text { corrected total data } & D \text { and } D_{\text {exp }}= & \text { observed and expected } \\
A & & \text { affected for one set of dat } \\
B= & \text { number of sibships, } & &
\end{array}
$$

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 $\mathrm{P}(\mathrm{ca.O.9}$ ) and at intermediate values (ca.0.5).

[^8]
## Sketch（es）

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

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

Solution（s）

$$
\begin{aligned}
& .75[\mathrm{E}] 3[\uparrow] 3[\uparrow] 2[\mathrm{~A}] 4[\uparrow] 2[\uparrow] 4[\mathrm{~A}] 2[\uparrow] 1 \text { [个] } 7 \text { [A] } \\
& {[\mathrm{B}] \rightarrow \mathrm{q}=0.269,[\mathrm{C}] \rightarrow \chi^{2}=0.047 \text {, }} \\
& {[\mathrm{D}] \rightarrow \mathrm{P} \sim 0.853}
\end{aligned}
$$

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

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

1 GENETIC INFERENCE FROM TRUNCATE DATA
Calc.

$54$


| Program Title POSITIVE ASSORTATIVE MATING FOR A RECESSIVE PHENOTYPE |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: |
| Contributor's Name Hewlett-Packard Company |  |  |  |  |
| Address 1000 N.E. Circle Boulevard |  |  |  |  |
| City Corvallis | State | Oregon | Zip Code | 97330 |

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

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

where:

$$
\begin{aligned}
q & =\text { recessive gene frequency } \\
(1-r) & =\text { fraction of population mating at random. }
\end{aligned}
$$

## Operating Limits and Warnings

[^9]
## Sketch(es)

Sample Problem(s) Given the following values: initial recessive phenotype frequency $\equiv \mathrm{R}_{\mathrm{o}}=.01, \mathrm{r}=0.75, \mathrm{q}=0.10$,

Calculate a) recessive phenotype frequency after 4 generations ( $\mathrm{t}=4$ )
b) equilibrium recessive phenotype frequency ( $\overline{\mathrm{R}}$ ).

Solution(s)
a) . 01 [ $] .75[\uparrow] .1[\uparrow] 4[A] \rightarrow R_{4}=.0239$
b) $[\mathrm{R} / \mathrm{S}] \rightarrow \overline{\mathrm{R}}=.0266$

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非04846A submitted by Dr. Leo S. Reich.


| STEP | instructions | $\begin{gathered} \text { INPUT } \\ \text { DATA/UNITS } \end{gathered}$ |  | KEYS | OUTPUT DATA/UNITS |
| :---: | :---: | :---: | :---: | :---: | :---: |
| 1 | Enter program |  |  | $\square$ |  |
|  |  |  |  |  |  |
| 2 | Enter in order: $\mathrm{R}_{0}$ (initial value), | $\mathrm{R}_{\mathrm{O}}$ | $\uparrow$ |  |  |
|  | $\mathrm{r}, \mathrm{q}, \mathrm{t}$ | r | $\uparrow$ | - |  |
|  |  | q | $\uparrow$ |  |  |
|  |  | t |  |  |  |
|  |  |  |  |  |  |
| 3 | Compute $\mathrm{R}_{\mathrm{t}}$ by pressing A |  | A |  | $\mathrm{R}_{\mathrm{t}}$ |
|  |  |  |  |  |  |
| 4 | Compute equilibrium value, R , by then |  |  |  |  |
|  | pressing $\mathrm{R} / \mathrm{S}$ |  | R/S | T $\square$ | $\overline{\mathrm{R}}$ |
|  |  |  |  | 11 |  |
|  | [When $\overline{\mathrm{R}}$ is desired outright, set $\mathrm{t}=0$ in |  |  | $\square$ |  |
|  | step 2 and press A]. |  |  | $11 \square$ |  |
|  |  |  |  | \| | - |  |
|  |  |  |  | $1 \mid$ |  |
|  |  |  |  | $1 \mid$ |  |
|  |  |  |  | 1 [ |  |
|  |  |  |  | $1 \mid$ |  |
|  |  |  |  | \|| |  |
|  |  |  |  | \| [ ] |  |
|  |  |  |  | $1[$ |  |
|  |  |  |  | 1 |  |
|  |  |  |  | $11 \square$ |  |
|  |  |  |  | 11 |  |
|  |  |  |  | $11 \square$ |  |
|  |  |  |  | $11-1$ |  |
|  |  |  |  | ] - ] |  |
|  |  |  |  | $11-1$ |  |
|  |  |  |  | $11-1$ |  |
|  |  |  |  | 11.1 |  |
|  |  |  |  | 11.1 |  |
|  |  |  |  | $1 \mid$ |  |
|  |  |  |  | $1 \mid 1$ |  |
|  |  |  |  | $1 \mid-1$ |  |
|  |  |  |  | $11 \quad 1$ |  |
|  |  |  |  | \| 11 |  |
|  |  |  |  | \| 1 - |  |
|  |  |  |  | 11 |  |



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```
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                Mathematics
                Electrical Engineering
                        Business Decisions
Clinical Lab and Nuclear Medicine
```

```
Mechanical Engineering
            Surveying
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```


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EE (Lab)
Industrial Engineering
Aeronautical Engineering Control Systems
Beams and Columns
High-Level Math
Test Statistics
Geometry
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Medical Practitioner
Anesthesia
Cardiac
Pulmonary
Chemistry Optics Physics
Earth Sciences
Energy Conservation
Space Science
Biology
Games
Games of Chance
Aircraft Operation
Avigation
Calendars
Photo Dark Room
COGO-Surveying
Astrology
Forestry

## BIOLOGY

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

DEMOGRAPHY I: ESTIMATES OF PARAMETERS/RATES OF INCREASE<br>DEMOGRAPHY II: EXPECTATION OF LIFE AND REPRODUCTIVE VALUE<br>DIVERSITY AND EQUITABILITY INDICES<br>NICHE BREADTH AND OVERLAP/SHANNON'S H AND HORN'S RO<br>POPULATION SIZE ESTIMATE (JOLLY'S ESTIMATE)<br>CELL PHASE AND CYCLE TIMES<br>CROSSOVER: LOCATION/PRODUCTS<br>CHROMOSOME CLEAVAGE<br>RECESSIVE GENE FREQUENCY AFTER SELECTION, MUTATION, AND INBREEDING<br>SELECTION AND GENE FREQUENCY<br>genetic inference from truncate data<br>positive assortative mating for a recessive PHENOTYPE




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