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POPGEN I: COMPUTER SIMULATION OF POPULATION GENETICS

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The availability of relatively inexpensive computers has given many people access to the devices in schools, businesses, and even homes. Creationists will be able increasingly to test aspects of both the evolution and Creation models through the use of these "smart machines". This paper describes the use of a program to simulate a population of organisms in which the processes of reproduction, mutation, and natural selection are operating.

Population Genetics

A simplified discussion of the genetic principles involved may aid in the use of POPGEN I. Population genetics is concerned with the behavior of genes in populations rather than individuals. Interest centers on the *gene pool*, all of the genes possessed by all of the creatures in a population. Usually attention is focused on a single gene, which we can symbolize as A, and studies are made of the change through time in the relative frequencies of A_1 and A_2 , the alleles of A. These frequencies are symbolized as p and q, respectively.

Three factors are most important in changing allele frequencies from generation to generation. Mutation can change A_1 to A_2 , and the relative frequency with which that occurs is expressed as a fraction, *u*. Typical mutation rates are in the range 0.00001 to 0.000001. The mutation rate for achondroplastic dwarfism in humans has been estimated at 0.000042, which means that 42 out of one million times that the A_1 (normal) allele is copied, it changes to A_2 (the allele that produces dwarfism). Mutation can also change A_2 to A_1 , but this is much less frequent and is ignored in POPGEN I.

A second factor that affects allele frequencies is natural selection. Unlike mutation, which acts on single genes, natural selection acts on the phenotype, the expression of the genotype. The amount of selection (s), is a number between 0 and 1. A phenotype with s = 1 is lethal, while s = 0 indicates that there is no selection against that phenotype. One may also speak of the fitness (w) of a particular phenotype, which is equal to 1-s. POPGEN I uses fitness values for the three possible genotypes A_1A_1 , A_1A_2 , and A_2A_2 , to simulate the effects of natural selection.

The third factor affecting allele frequencies is drift, which refers to random changes in frequencies not caused by mutation or natural selection. Drift is particularly important in small populations where, for example, the death of a few individuals may change significantly the allele frequencies.

Description of the Program

Figure 1 is the program POPGEN I, which is written in BASIC for the IBM 5100 portable computer¹. With modification to be described later, it can be run on the Radio Shack TRS-80, Level II. Other computers with BASIC and a random number generator can also use the program.

Statements 20-80 allow the user to specify all parameters of the program: population size, number of generations, initial frequencies of the alleles, mutation rate, and fitness of the three genotypes. Statements 110-180 print the parameters supplied by the user and the headings for the results of the simulation.

The rest of the program consists of two loops. Statements 190-520 loop for the number of generations specified, while statements 220-470 loop for the number of individuals in the population. Statement 200 calculates the probability (M) that an allele selected at random from the gene pool will be an A_1 , that is, the relative frequency of A_1 (p) minus the probability that A_1 mutates to A_2 (u). Statements 240-260 generate a random number between 0 and 1 and compare it to M. If M is greater, an A_1 allele is selected; if less, an A_2 .

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0101 PRINT 'ENTER MINUTES AFTER THE HOUR.' 0102 INPUT T 0103 FOR I=1 TO T 0104 X=RND 0105 NEXT I

Figure 2. Program statements to be added for RND initialization.

Figure 2 can be added to POPGEN I and will cause RND to start with different numbers later in the program.

Description of the Printout

Figure 3 illustrates the printout from one run of POPGEN I. A description of its features may aid in the use of the program. The first few lines report the parameters supplied by the user. The initial frequency of allele $A_1 = 0.6$, which means that sixty percent of the A genes in the gene pool are A_1 and forty percent are A_2 .

The mutation rate equals 1E-7, which is the computer's way of writing 1×10^{-7} or 0.0000001. This means that A_1 mutates to A_2 about once for every ten million times that it is copied.

The fitness values illustrate a situation in which A_1 is dominant, that is, both A_1A_1 and A_1A_2 have the same phenotype. In this example A_2A_2 has a fitness of 0.8 compared to the other two genotypes. This could mean that only 80% of the A_2A_2 individuals survive to

	16 16 1€	2026EN 1**	· #		
	THE	POPULATION	IST7E ⇒	200	
THE	INITIAL	FREQUENCY	0F A1 =	. 6	
THE	INITIAL	FREQUENCY	0F A2 =	, kj.	
THE MUTATION RATE OF A1 TO A2 =				1E-7	
	THE	FITNESS OF	- A1A1 =	1	
	THE	FITNESS OF	- A1A2 =	1	
	THE	FITNESS OF	A2A2 =	. 8	
GEN	A1A1	A1A2	A2A2	A1	A2
1	.305	.565	.130	. 588	.413
2	.325	. 525	,150	. 588	.413
3	. 320	.515	.165	. 578	.423
4	.320	.560	.120	.600	.400
5	, 365	.525	. 1.1.0	.628	.373
6	.440	.485	.075	. 683	, 318
7	.465	.465	,070	.698	. 303
8	.375	. 550	.075	,650	.350
9	.440	.455	.105	. 668	. 333
10	.440	.450	.110	.665	.335
11	,465	.470	.065	.700	. 300
12	.475	.445	.080	. 698	, 303
13	.515	.395	.090	.713	. 288
14	.510	.440	.050	.730	.270
15	.565	.365	.070	. 748	. 253
16	. 580	. 385	.035	.773	.228
17	.615	.335	.050	.783	.218
18	.570	.395	.035	, 768	. 233
19	.600	.345	.055	.773	. 228
20	.610	.335	.055	.778	, 223
21	.605	.355	.040	.783	. 218
22	. 655	.315	.030	.813	. 188
23	. 645	.305	.050	.798	.203
24	.645	.300	.055	. 795	.205
25	.585	. 375	.040	.773	.228
26	. 635	. 325	.040	. 798	.203
27	.655	.310	.035	.810	.190
28	. 685	.300	.015	.835	.165
29	.675	.300	.020	.823	157
30	. 715	.260	.020	.848	.103
31	. 710	,280	. 0 1 0	.850	.150
32	. 710	.270	, 020	,845	.100
33	. 710	.270	.020	.843	.135
34	,630	.300	.020	.803	.175
30	.680	.300	.015	. 833	108
30	. (33	,230	,013	.000	105
31	100	,∠⊖U ⊃05	,UZU	.833	.140
38	. ((3	.203	1020	.075	125
39	. //0	.210	.020	,873	120
40	.743	.240	.015	.000	130
41	. (()	,210	.013	.080	.120
42	, 780	170	.005	.000	. 113
40	.820	.1/0	.005	.710	.070

Figure 3. Printout from execution of POPGEN I.

0010 PRINT FLP, ***POPGEN I**** 0020 PRINT 'ENTER THE FOLLOWING PARAMETERS: 0030 PRINT DESIRED POPULATION SIZE,' 0030 PRINT 0040 PRINT DESIRED POPULATION SIZE,' NO. OF GENERATIONS TO BE COMPUTED,' INITIAL FREQUENCY OF ALLELE A1, MUTATION RATE OF A1 TO A2, FITNESS OF A1A1,A1A2,A2A2. 0050 PRINT 0060 PRINT 0070 PRINT 0080 INPUT N1, J1, P,U, W2, W1, W0 0090 Q=1-P 0100 F=1/N1 THE POPULATION SIZE = THE INITIAL FREQUENCY OF A1 = THE INITIAL FREQUENCY OF A2 = 0110 PRINT FLP ';N1 ',Р ';0 0120 PRINT FLP, 0130 PRINT FLP, 0140 PRINT FLP, THE MUTATION RATE OF A1 TO A2 0150 PRINT FLP, THE MUTATION RATE OF A1 A1 ... 1.11 A1A1 = 0160 PRINT FLP, THE FITNESS OF A1A2 = ';₩1 0170 PRINT FLP, 0180 PRINT FLP, GEN THE FITNESS OF A2A2 = ; 60 A2. A1A1 A1A2 A2A2 A1 0190 FOR J=1 TO J1 0200 M=P-U 0210 G1,G2,G3,Z=0 0220 FOR T=1 TO N1 0230 N=0 0240 X=RND 0250 IF X>M GOTO 0270 0260 N=1 0270 X=RND 0280 IF X>M GOTO 0300 0290 N≕N+1 0300 GOTU 0310,0330,0350 ON N+1 0310 8=80 0310 W-W0 0320 GOTO 0360 0330 W=W1 0340 GOTO 0360 0340 GDTO 0360 0350 W=W2 0360 X=RNI 0370 IF X≤W GOTO 0400 0380 I=I-1 0390 GDTO 0470 0400 Z=Z+N 0410 GOT0 0420,0440,0460 ON N+1 0420 G3=G3+F 0430 GOTO 0470 0440 G2=G2+F 0450 GOTO 0470 0460 G1=G1+F 0470 NEXT I 0480 P=Z/(2*N1) 0490 Q=1-P 0500 PRINT USING FLP:0510;J:G1:G2:G3:P:Q 0510 :### 0520 NEXT J #.### #.### #.### #.### #.###

Figure 1. POPGEN I computer program.

Statements 270-290 repeat the process for the second allele of the individual.

Statements 300-390 simulate the effects of natural selection. A random number is generated and compared to the fitness of the particular genotype. If the random number is greater than the fitness, the genotype is eliminated. If it is not, then statements 400-460 add the genotype to the growing population.

After each generation is complete, statements 480-510 calculate the relative allele frequencies and print them along with the genotype frequencies.

It should be noted that POPGEN I simulates a population in which generations do not overlap, and in which the population size remains constant.

Random Number Generator

A feature of the computer which makes possible POPGEN I and other simulations of biological systems is the random number generator (RND). In this program it provides the element of chance in the selection of alleles for the next generation (statements 240 and 270) and for the operation of natural selection (statement 360).

One property of RND is that it always generates the same list of random numbers in the same order. This may or may not be desirable, depending on the objectives of the user. To avoid this feature, the statements in

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reproduce, or that they produce only 80% as many offspring as do A_1A_1 and A_1A_2 individuals.

Following the fitness values are the results of the simulation. For each generation the relative frequencies of the three genotypes are given and then the allele frequencies. The parameter having the largest effect is the selection against A_2A_2 . This causes the frequency of A_2 to decrease rather steadily, although the effect of drift can be seen in generation 3 where the frequency of A_2 increases from 0.413 to 0.423. Drift also causes temporary increases in other generations.

Suggested Investigations

The effects of different population sizes, mutation rates, and patterns of natural selection can be evaluated with POPGEN I. A few possibilities follow.

1. A study of different population sizes as they relate to random genetic drift. Mutation rates should be set at 0 and fitness values should all equal 1. Increasing population size greatly increases computer time, so after determining the minimum population size that does not drift significantly, that parameter should be used to investigate other variables.

2. Simulate the case of sickle cell anemia in malaria-infested countries. This human mutation is recessive and usually lethal for those who carry two alleles for it (A_2A_2) . Heterozygous individuals (A_1A_2) do not suffer anemia and are resistant to malaria. To simulate this, try w $(A_1A_1) = 0.8$ (might die from malaria), w $(A_1A_2) =$ 1 (no anemia and resistant to malaria), and w $(A_2A_2) =$ 0.01 (probably dies from anemia). Give A_1 an initial frequency of 0.99.

3. After determining equilibrium frequencies for A_1 and A_2 in the preceding investigation, simulate the situation for slaves brought from Africa to America. Give A_1 the equilibrium frequency for an initial frequency and, because malaria is absent in the U.S., make $w(A_1A_1) = 1$. See what happens when the advantage of this mutation is no longer present.

Use with Radio Shack TRS-80

POPGEN I can be easily converted to use with the Radio Shack TRS-80, Level II². Although not necessary, prompting messages, such as statement 20, can be included in the INPUT statements. LPRINT is equivalent to PRINT FLP, and if the user lacks a printer, PRINT will produce the results on the video screen. LPRINT USING is equivalent to PRINT USING FLP, except that the format specification of statement 510 is included in LPRINT USING. Instead of statement 210, each variable requires a separate statement. The \geq should be written > =, and GOTO _____, ____ON____.

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PANORAMA OF SCIENCE

The Rose of Jericho

In the September-October 1980 issue of the *Biblical Archeology Review* the remarkable adaptation of the Rose of Jericho to desert conditions is described.¹ This plant is actually not a rose at all but a member of the mustard family. Its scientific name Anastatica means "not static" or maybe, from Greek, "resurrection plant". It is so named because the dried up skeleton of the plant, a ball of dried out twigs, when immersed in water gradually opens up and extends its branches like a miniature tree!

The Rose of Jericho begins to bloom in March and April, and has small spikes of white flowers set in a cluster of green oval leaves which grow close to the ground. By May or June the seeds are ripe but dormant and enclosed in tightly sealed fruits. The leaves have fallen off, and the dry, hard, twiggy skeleton has become a ball resembling a closed fist.

Now this plant has developed a special system for measuring rainfall and intermittently releasing its seeds so as to make its survival more certain. Fruits at the periphery of the skeleton have two loosely connected covers or valves. The first part of a rain causes the ball to open and if further rain falls some of the peripheral seeds will drop. Others further on down on the branches wait for a more opportune time in case the first seeds are not successful in establishing plants. Seeds at the center will wait for decades or possibly even centuries until the most propitious moment after a particularly heavy series of rains.

Laboratory tests have shown that a skeleton will open more rapidly if the soil is wet. The drier the soil the more rain it takes to open the skeleton. No seeds will be dropped unless a second shower falls before the skeleton is redried and closed. So when it rains on the *opened skeleton* drops of water hit the fruit valves and separate them. The seeds thus drop on soil sufficiently wet to insure germination. Also they drop near the parent plant thus assuring a suitable location.

When the soil is dry four millimeters of rain are needed to open the skeleton, thus exposing the fruit valves. The gradual opening of the skeleton, is a two hour process. The seeds germinate in about eight hours. This insures that the released seed will be able to root in the soil before its upper crust dries out.

Though usually found in large dense concentrations, individual plants are found along a wadi belt or runnel. By following flow channels it was found that the size and density of the plants increased downstream. But a