More Effective Population Size Concepts

- Inbreeding effective population size
  - the size of an ideal population with the same probability of randomly sampled alleles being IBD as the real population
- Variance effective population size
  - the size of an ideal population with the same sampling variance in allele frequency as the real population

Inbreeding effective population size

- observed change in heterozygosity (IBD) over time can be used to estimate N_e

$$P(IBD) = \frac{1}{2N_e}$$

$$N_e^i = \frac{1}{2P(IBD)}$$

$$N_e^i \approx -\frac{t}{2\ln(H_t / H_0)}$$

Variance effective population size

- observed changes in allele frequencies over time can be used to estimate N_e

$$\mathrm{var}(\Delta p) = \frac{p_{t-1}q_{t-1}}{2N_e}$$

$$N_e^v = \frac{pq}{2x\,\mathrm{var}(\Delta p)}$$

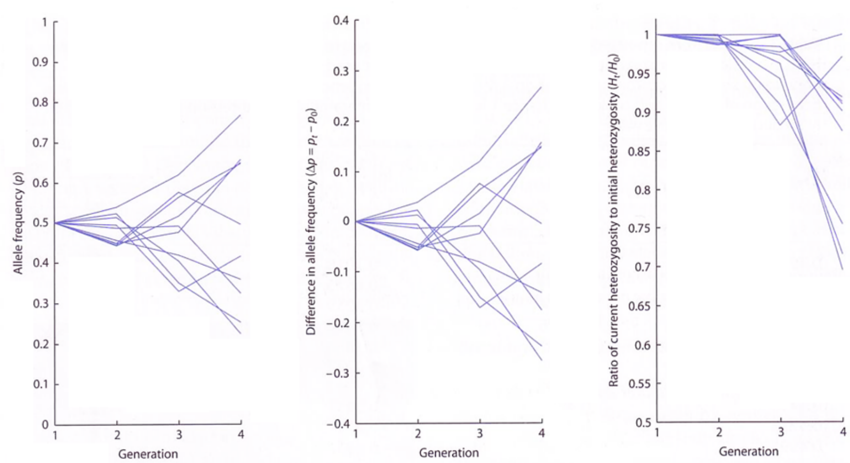


Figure 3.20 Simulated allele frequencies in 10 replicate populations that experienced effective population sizes of 100, 10, 50, and 100 individuals across four generations. The variance in the change in allele frequency (Δp) can be used to estimate the variance effective population size. The inbreeding effective population size can be estimated from the change in heterozygosity through time.

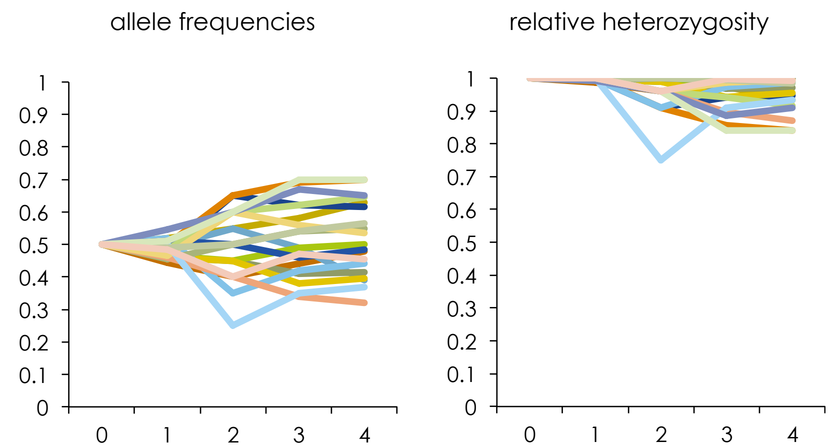


Table 3.4 Data from simulated allele frequencies in Fig. 3.20 used to estimate the effective population size. Here, the ratio of heterozygosity in generations three and four is used to estimate inbreeding effective population size ($\hat{N}_e^i$) according to equation 3.59. Initial allele frequencies were $p = q = 0.5$, so $H_{t=1} = 0.5$. One generation of genetic drift took place, hence 1 is used in the numerator of the expression for N_e^i. The average N_e^i excludes the negative values.

$H_{t=3}$	$H_{t=4}$	$\ln\left(\frac{H_{t=4}}{H_{t=3}}\right)$	$\hat{N}_e^i = -\frac{1}{2}\frac{1}{\ln\left(\frac{H_{t=4}}{H_{t=3}}\right)}$
0.4987	0.4504	−0.1018	4.91
0.4866	0.4594	−0.0575	8.69
0.4813	0.3474	−0.3259	1.53
0.4998	0.4376	−0.1329	3.76
0.4546	0.3772	−0.1864	2.68
0.4884	0.4999	0.0232	−21.58
0.4920	0.4566	−0.0747	6.69
0.4413	0.4856	0.0957	−5.22
0.4715	0.3578	−0.2761	1.81
0.4995	0.4550	−0.0932	5.36
			Average $\hat{N}_e^i$ = 4.43

1000 reps

$H_{t=3}$ = 0.466187	$H_{t=4}$ = 0.463123	-0.00659416	75.82
$H_{t=0}$ = 0.50	$H_{t=4}$ = 0.463123	-0.0766154	26.10

Table 3.5 Data from simulated allele frequencies in Fig. 3.20 used to estimate the effective population size. Here, the change in allele frequency between generations three and four is used to estimate variance effective population size ($\hat{N}_e^v$) according to equation 3.56. Allele frequencies in the third generation were used to estimate *pq*.

$p_{t=4}$	$\Delta p = p_{t=4} - p_{t=3}$	pq	$\mathrm{Var}(\Delta p) = \frac{1}{10}\sum(p_{t=4} - \bar{p})^2$	$\hat{N}_e^v = \frac{pq}{2 \times \mathrm{variance}(\Delta p)}$
0.6574	0.1825	0.2494	0.0186	6.71
0.3575	−0.0606	0.2433		6.55
0.2238	−0.1795	0.2406		6.47
0.3234	−0.1668	0.2499		6.72
0.2523	−0.0970	0.2273		6.12
0.4940	−0.0819	0.2442		6.57
0.6473	0.0842	0.2460		6.62
0.4153	0.0866	0.2207		5.94
0.7667	0.1473	0.2357		6.34
0.6499	0.1343	0.2498		6.72
				Average $\hat{N}_e^v = 6.48$

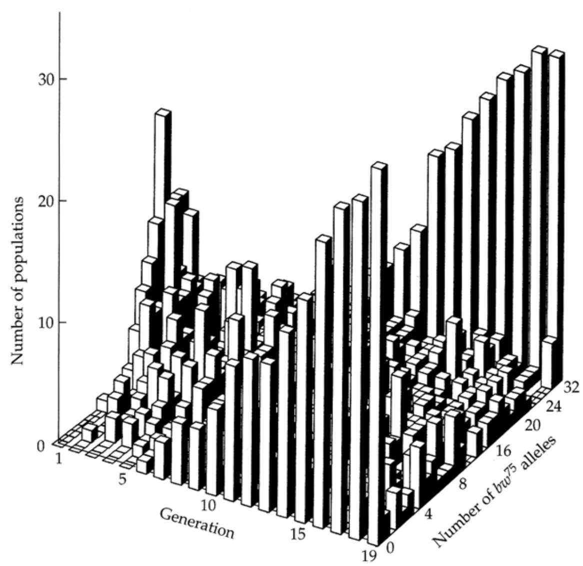
$$\mathrm{var}(\Delta p) = \frac{1}{(n-1)}\sum\left(\Delta p - \overline{\Delta p}\right)^2$$

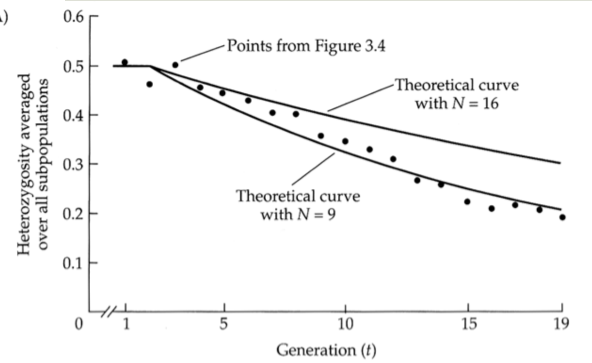
$$\equiv \mathrm{var}(p) = \frac{1}{(n-1)}\sum\left(p - \bar{p}\right)^2$$

1000 reps

0.502955	$t_{4\text{-}3}$=0.000425	0.233094	0.00112872	**103.26**
0.502955	$t_{4\text{-}0}$=0.002955	0.25	0.01844689	**27.10**

Random genetic drift in 107 *Drosophila* populations;
8 males, 8 females each generation





$$H_t = \left(1 - \frac{1}{2N_e}\right)^t H_0$$

$$\approx H_0 e^{-t/2N_e}$$

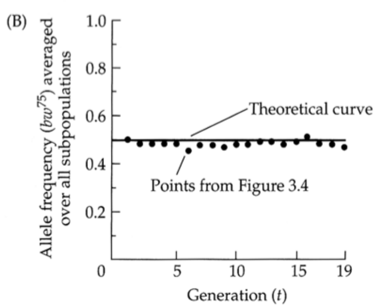


FIGURE 3.12 Theoretical curves for average heterozygosity among subpopulations (A) with $N = 9$ or $N = 16$, along with actual values (plotted as points) from the experiment in Figure 3.4. Part (B) shows the theoretically expected average allele frequency among the 107 subpopulations and the observed average. (Data from Buri 1956.)