Random Genetic Drift Effective Population Size

- Hardy-Weinberg equilibrium predicts:
 - 1) Allele frequencies remain constant
 - 2) Genotype frequencies predicted by allele frequencies
- HW model assumes infinite population size
- With finite population size, allele frequencies change over time due to sampling
- Random genetic drift: stochastic change in allele frequencies due to finite sampling of gametes

- Haploid population of size N
- Two alleles: A, a
- At generation t
 - Frequency of A is p
- Frequency of a is q = (1-p)

What is frequency of A at generation t + 1?

Probability(X) = # ways X can happen/Total Possible Outcomes

1. You roll a die. What is the probability that you roll a 4?

2. You roll a die. What is the probability that you roll an even number?

3. You roll a die twice. What is the probability that you roll a 4 twice?

4. You flip a fair coin. What is the probability you flip a head?

5. You flip a fair coin twice. What is the probability you flip a head twice?

6. You flip a fair coin and it flips heads. What is the probability if you flip it again, it will flip heads?

7. You flip a fair coin twice. What is the probability you flip at least one head?

8. A bag of marbles contains 36 blue marbles and 14 red marbles. If you pull out one marble, what is the probability that it is blue?

9. A bag of marbles contains 36 blue marbles and 14 red marbles. If you pull out one marble, what is the probability that it is NOT blue?

10. A population contains 36 AA individuals and 14 aa individuals. If you pull out genotype at random, what is the probability that it is AA?

11. A randomly mating population contains 36 AA individuals, 50 Aa individuals and 14 aa individuals. These individuals each produce an infinite number of gametes. If you reach into the gamete pool and pull out a single allele, what is the probability that it is A?

In generation t, freq(A) = p, freq(a) = (1-p)

Randomly select 1 individual to be parent

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$$-\Pr(2A) = p^2$$

$$- Pr(1A) =$$

$$- Pr(0A) = (1 - p)^2$$



$$a$$
 $Pr = (1 - p)p$

- Randomly select 1 individual to be parent
 - Pr(1A) = p
 - Pr(0A) = (1 p)
- Randomly select 2 individuals to be parents

$$-\Pr(2A) = p^2$$

$$- Pr(1A) = 2p(1-p)$$

$$- Pr(0A) = (1 - p)^2$$





- Randomly select 1 individual to be parent
 - Pr(1A) = p
 - Pr(0A) = (1 p)
- Randomly select 2 individuals to be parents
 - $-\Pr(2A) = p^2$
 - Pr(1A) = 2p(1-p)
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- Randomly select 3 individuals to be parents

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 - Pr(1A) = p
 - Pr(0A) = (1 p)
- Randomly select 2 individuals to be parents
 - $Pr(2A) = p^2$
 - Pr(1A) = 2p(1-p)
 - $Pr(0A) = (1 p)^2$
- Randomly select 3 individuals to be parents
 - Pr(3A) =
 - -Pr(2A) =
 - -Pr(1A) =
 - Pr(0A) =

- Randomly select 1 individual to be parent
 - Pr(1A) = p
 - Pr(0A) = (1 p)
- Randomly select 2 individuals to be parents
 - $-\Pr(2A) = p^2$
 - Pr(1A) = 2p(1-p)
 - $Pr(0A) = (1 p)^2$
- Randomly select 3 individuals to be parents
 - $Pr(3A) = p^3$
 - $-\Pr(2A) = 3p^2(1-p)$
 - $Pr(1A) = 3p(1-p)^2$
 - $Pr(0A) = (1 p)^3$

In generation t, freq(A) = p, freq(a) = (1-p)

Randomly select N individuals to be parents

$$Pr(j \text{ alleles of type } A) = \binom{N}{j} p^{j} (1-p)^{N-j}$$

What is frequency of A at generation t + 1?

Frequency of A

Generation(t+1)

0/N

$$\binom{N}{0} (p_t)^0 (1-p_t)^{N-0}$$

1/N

$$\binom{N}{1} (p_t)^1 (1-p_t)^{N-1}$$

2/N

$$\binom{N}{2} (p_t)^2 (1-p_t)^{N-2}$$

•

1

N/N

$$\binom{N}{N}(p_t)^N(1-p_t)^0$$

Frequency of A

Generation(t+1)

Generation (t+2)

0/N

$$\binom{\mathsf{N}}{\mathsf{O}}(p_t)^{\mathsf{O}}(1-p_t)^{\mathsf{N}-\mathsf{O}}$$

$$\binom{N}{0}(p_{t+1})^0(1-p_{t+1})^{N-0}$$

1/N

$$\binom{N}{1} (p_t)^1 (1-p_t)^{N-1}$$

$$\binom{N}{1} (p_{t+1})^1 (1-p_{t+1})^{N-1}$$

2/N

$$\binom{N}{2}(p_t)^2(1-p_t)^{N-2}$$

$$\binom{N}{2} (p_{t+1})^2 (1 - p_{t+1})^{N-2}$$

•

•

N/N

$$\binom{N}{N}(p_t)^N(1-p_t)^0$$

$$\binom{N}{N} (p_{t+1})^N (1-p_{t+1})^0$$

Generation(t+1)

Generation (t+2)

Generation(t+3)

$$\binom{\mathsf{N}}{\mathsf{O}}(p_t)^{\mathsf{O}}(1-p_t)^{\mathsf{N}-\mathsf{O}}$$

$$\binom{N}{0} (p_{t+1})^0 (1-p_{t+1})^{N-0}$$

$$\binom{N}{0}(p_{t+1})^0(1-p_{t+1})^{N-0} \qquad \binom{N}{0}(p_{t+2})^0(1-p_{t+2})^{N-0}$$

$$\binom{N}{1} (p_t)^1 (1-p_t)^{N-1}$$

$$\binom{N}{1}(p_{t+1})^{1}(1-p_{t+1})^{N-1} \qquad \binom{N}{1}(p_{t+2})^{1}(1-p_{t+2})^{N-1}$$

$$\binom{N}{1}(p_{t+2})^1(1-p_{t+2})^{N-1}$$

$$\binom{N}{2}(p_t)^2(1-p_t)^{N-2}$$

$$\binom{N}{2}(p_{t+1})^2(1-p_{t+1})^{N-2}$$

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 $\binom{N}{2}(p_{t+2})^2(1-p_{t+2})^{N-2}$

N/N

$$\binom{N}{N}(p_t)^N(1-p_t)^0$$

$$\binom{N}{N} (p_{t+1})^N (1-p_{t+1})^C$$

$$\binom{N}{N}(p_{t+1})^{N}(1-p_{t+1})^{0} \qquad \binom{N}{N}(p_{t+2})^{N}(1-p_{t+2})^{0}$$

Transitions between states are random, but defined by a probability

Transitions have no memory beyond previous step

Frequency of A	Generation(t+1)	Generation (t+2)	Generation(t+3)
0/N	$\binom{N}{O} (p_t)^{O} (1-p_t)^{N-O}$	$\binom{N}{0} (p_{t+1})^0 (1-p_{t+1})^{N-0}$	$\binom{N}{0} (p_{t+2})^0 (1-p_{t+2})^{N-0}$
1/N	$\binom{N}{1}(p_t)^1(1-p_t)^{N-1}$	$\binom{N}{1}(p_{t+1})^1(1-p_{t+1})^{N-1}$	$\binom{N}{1} (p_{t+2})^1 (1-p_{t+2})^{N-1}$
2/N	$\binom{N}{2}(p_t)^2(1-p_t)^{N-2}$	$\binom{N}{2}(p_{t+1})^2(1-p_{t+1})^{N-2}$	$\binom{N}{2} (p_{t+2})^2 (1-p_{t+2})^{N-2}$
•			
N/N	$\binom{N}{N} (p_t)^{N} (1-p_t)^{O}$	$\binom{N}{N} (p_{t+1})^N (1 - p_{t+1})^0$	$\binom{N}{N} (p_{t+2})^N (1 - p_{t+2})^0$

Transitions between states are random, but defined by a probability

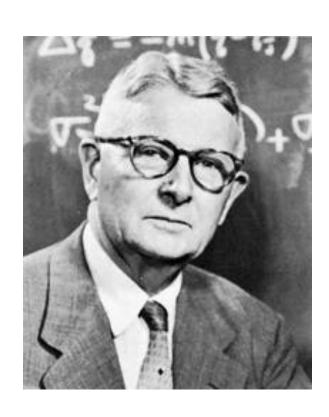
Transitions have no memory beyond previous step

Diploid Model

- N diploid individuals
 - 2N alleles in population
- Two alleles: A, a (frequencies p, q)
- Randomly draw 2N gametes to found next generation

$$Pr(j \text{ alleles of type } A) = {2N \choose j} p^{j} (1-p)^{2N-j}$$

Wright-Fisher Model





Wright-Fisher Model

Assumptions:

- N diploid organisms (2N alleles)
- Infinite gametes
- Discrete Generations
- Random mating
- No mutation
- No selection

$$P_{ij} = {2N \choose j} \left(\frac{i}{2N}\right)^j \left(1 - \frac{i}{2N}\right)^{2N-j} = {2N \choose j} p^j q^{2N-j}$$

- Alleles are eventually fixed or lost
- 2N alleles
 - Each equally likely to fix (selectively equivalent)
 - Pr(fixation) =

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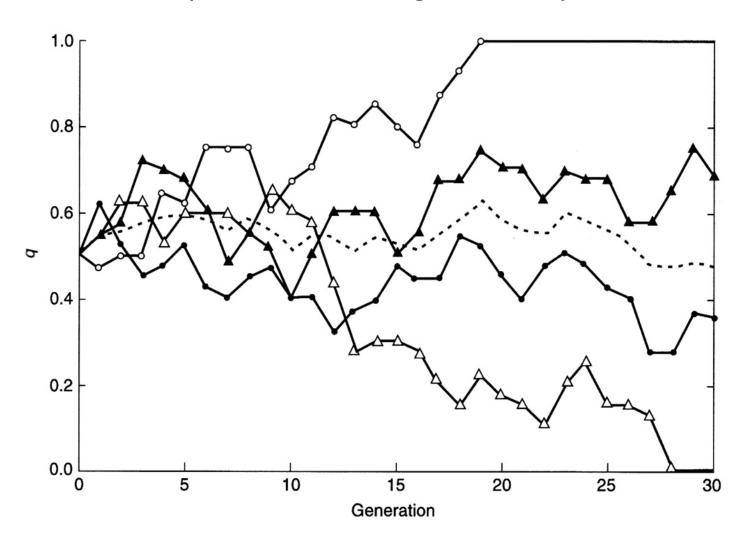
- Alleles are eventually fixed or lost
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 - Each equally likely to fix (selectively equivalent)
 - Pr(fixation) = 1/2N
 - If *i* copies of allele, Pr(fixation) = i/2N

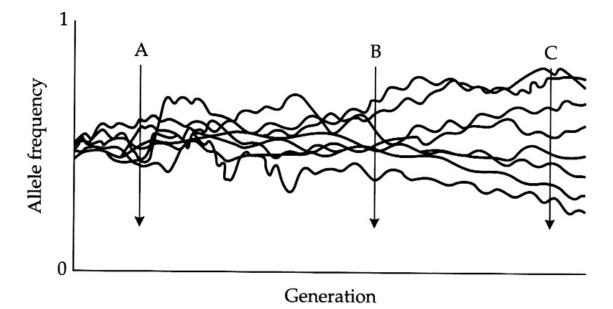
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 - Each equally likely to fix (selectively equivalent)
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 - If *i* copies of allele, Pr(fixation) = i/2N
- Pr(fixation) = p

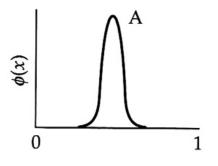
Probabilities of fixation, loss

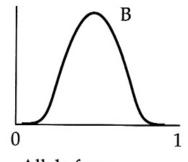
- Alleles are eventually fixed or lost
- 2N alleles
 - Each equally likely to fix (selectively equivalent)
 - Pr(fixation) = 1/2N
 - If *i* copies of allele, Pr(fixation) = i/2N
- Pr(fixation) = p
- Pr(loss) = 1-p

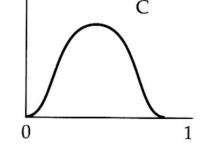
Allele frequencies will change randomly over time



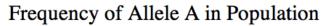


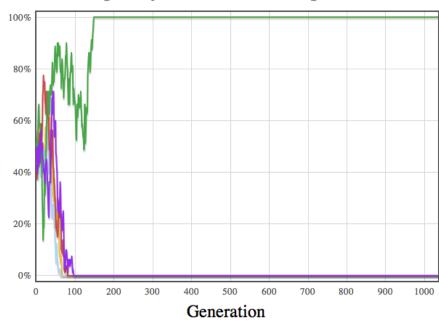




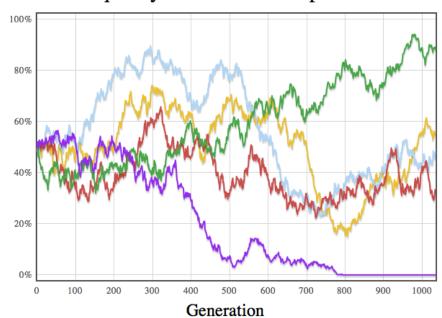


Allele frequency, x





Frequency of Allele A in Population



N = 2000

N = 40

Times to fixation, loss

$$t_{fix} = \frac{-4N(1-p)\ln(1-p)}{p}$$

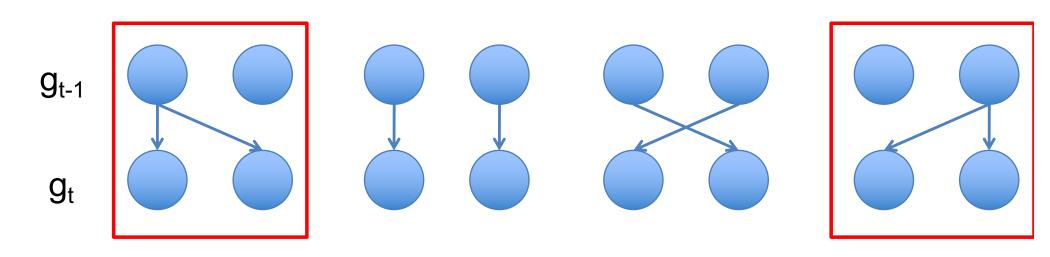
For p =
$$1/2N$$
, $t_{fix} \approx 4N$

$$t_{oss} = \frac{-4N(p)ln(p)}{1-p}$$

For p =
$$1/2N$$
, $t_{loss} \approx 2ln(2N)$

Fixation index

2N=2



$$Pr(IBD) = 2/4 = 1/2$$

$$Pr(IBD) = 1/2N$$

Pr(not IBD) = 1 - 1/2N
Pr(IBD_t) =
$$F_t = \frac{1}{2N} + (1 - \frac{1}{2N})F_{t-1}$$

If $F_0 = 0$, $F_t = 1 - (1 - \frac{1}{2N})^t$

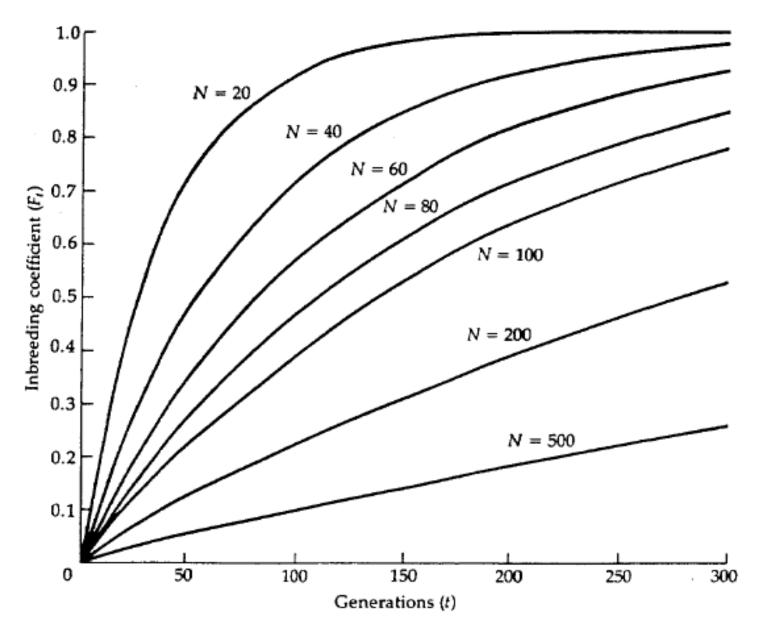


Figure 9. Increase of F_t in ideal populations as a function of time and effective population size N.

Hartl & Clark

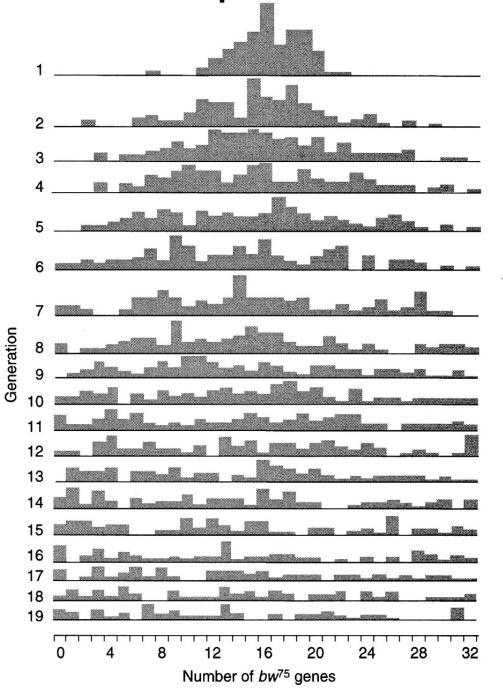
Decay of Heterozygosity

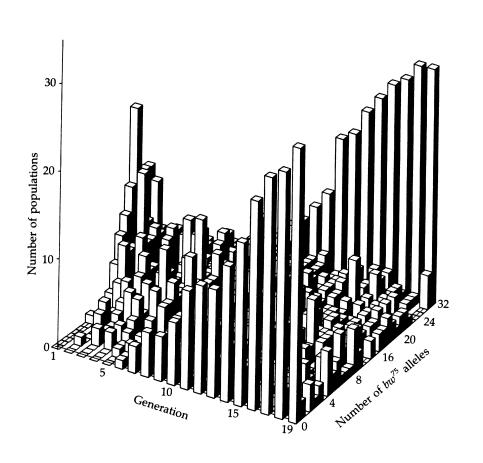
$$F_{t} = 1 - (1 - \frac{1}{2N})^{t}$$

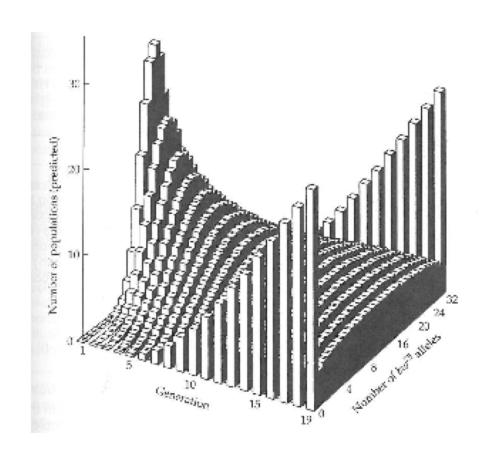
$$H_{t} = H_{0} \left(1 - \frac{1}{2N} \right)^{t} \approx H_{0} e^{-t/2N}$$

Summary of Drift

- Stochastic fluctuations in allele frequencies due to sampling in a finite population
- Described by Wright-Fisher model
- Alleles are ultimately fixed or lost from population
 - $-\Pr(\text{fix}) = p$; $\Pr(\text{loss}) = 1 p$
 - Time(fix_{1/2N}) ≈ 4N; Time(loss_{1/2N}) ≈ 2ln(2N)
- H decreases (~1/2N) over time
- Hardy-Weinberg largely still applies
 - Allele frequency changes small
 - Deviation from expected genotype frequencies ~
 1/2N







$$Var(p) = Var\left(\frac{\#A}{2N}\right) = \left(\frac{1}{2N}\right)^2 Var(\#A)$$

$$= \left(\frac{1}{2N}\right)^2 2Npq$$

$$=\frac{pq}{2N}$$

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- In reality, allele frequency changes > pq/2N
 - Fluctuations in population size, N_m≠N_f, etc.

- Number of individuals in a theoretically ideal population having the same magnitude of drift as the actual population
- Measure 'magnitude' in 3 ways
 - Change in variance of allele frequency (variance N_e)

$$var(p) = \frac{pq}{2N}$$

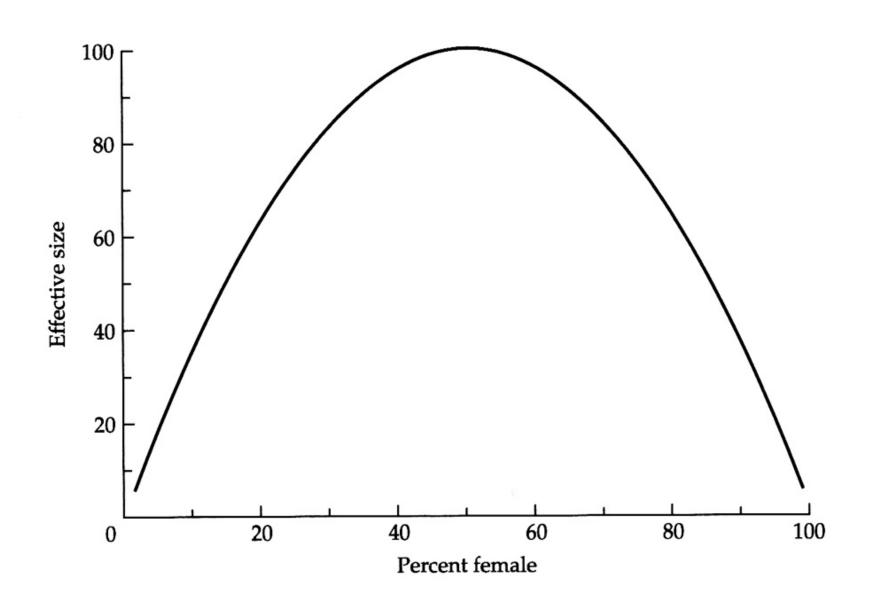
$$\overline{\text{var}}(p) = \frac{pq}{2N_e}$$

$$N_e = \frac{pq}{2\overline{\text{var}}(p)}$$

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- Measure 'magnitude' in 3 ways
 - Change in variance of allele frequency (variance N_e)
 - Change in Pr(IBD) (inbreeding $N_{\rm e}$)
 - Rate of loss of heterozygosity (eigenvalue $N_{\rm e}$)

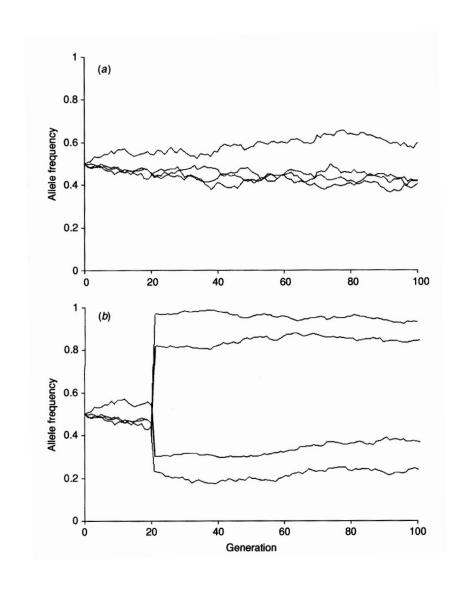
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- Typically smaller than census size N
 - Sex ratio
 - Variance in reproductive success
 - Population size changes



No bottleneck

Bottleneck at generation 20



Relating N, N_e

Population size changes

$$\frac{1}{N_e} = \frac{1}{t} \left(\frac{1}{N_0} + \frac{1}{N_1} + ... + \frac{1}{N} \right)$$

Relating N, N_e

Population size changes

$$\frac{1}{N_e} = \frac{1}{t} \left(\frac{1}{N_0} + \frac{1}{N_1} + ... + \frac{1}{N} \right)$$

Unequal males, females

$$N = N_m + N_f$$

$$N_e = \frac{4N_m N_f}{N_m + N_f}$$