

CONGEN

Inbreeding vocabulary

Inbreeding

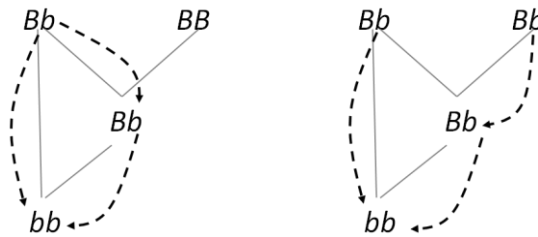
Mating between relatives.

Inbreeding depression

Reduction in fitness due to inbreeding.

Identical by descent

Alleles that are “identical by descent” are direct descendents of an allele present in an ancestor. Loci can be homozygous but not identical by descent. In the diagram below, the genotype on the left is identical by descent while the genotype on the right is not.



Inbreeding coefficient (f)

A measure of how inbred an individual is. More specifically, it is the probability that two alleles at a locus in an individual are identical by descent (or, equivalently, the proportion of an individual’s genome that is identical by descent).

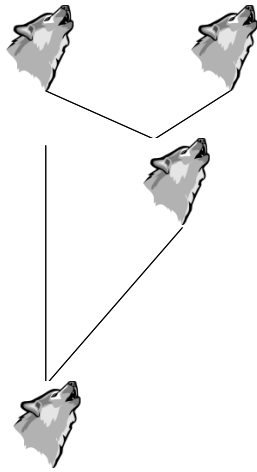
Genetic load

For our purposes now, the genetic load is the total number of deleterious recessive alleles in an individual or population. Genetic load can be measured in terms of lethal equivalents.

Lethal equivalent

An allele that is lethal when homozygous or a collection of genes that are considered to be equivalent (e.g., two alleles that each have a 50% chance of causing death if they were homozygous, or 10 alleles that each have a 10% chance of causing death if homozygous). See discussion that follows.

Reviewing the “Wolf inbreeding problem”



Allele	Frequency in population	
<i>B</i>	0.99	
<i>b</i>	0.01	
Genotype	Phenotype	Frequency in population
<i>BB</i>	Normal vision	$p^2 = \left(\frac{99}{100}\right)^2 = 0.9801$
<i>Bb</i>	Normal vision	$2pq = 2 \frac{99}{100} \frac{1}{100} = 0.0198$
<i>bb</i>	Blind	$q^2 = \left(\frac{1}{100}\right)^2 = 0.0001$

Now we note there are two types of loci in the genome of the wolf at the bottom of the pedigree: loci that are IBD and loci that are not-IBD. The alleles at this locus could either be IBD or not.

This means there are two ways a wolf could be blind:
it could be (IBD AND genotype *bb*) OR (Not-IBD and genotype *bb*)

The chance the alleles at this locus (or any) locus are IBD depends on the pedigree. Let *f* represent this probability. For this pedigree, *f* = _____.

Let $P(b|IBD)$ represent the probability the wolf at the bottom of the pedigree has genotype *bb* given that this locus is IBD. In this population, this equals _____.

Let $P(b|Not = IBD)$ represent the probability the wolf at the bottom of the pedigree has genotype *bb* given this locus is not-IBD. In this population, this equals _____.

We can put all this together to calculate the probability the wolf is blind:

$$P(bb) = f P(bb|IBD) + (1 - f) P(bb|Not = IBD)$$

Inserting all of above numbers into the above equation shows us $P(bb) = 0.002575$, which is the same result we obtained at the beginning of the course.

Inbreeding in a randomly mating population

In a randomly mating ideal population, the average inbreeding coefficient in the population at generation t (F_t) is given by the equation below

$$F_t = \frac{1}{2N} + \left(1 - \frac{1}{2N}\right)F_{t-1}$$

If the population is not ideal, replace N with N_e .

Note: If a species has two sexes, this equation is not completely accurate, but we will not worry about that in this course.

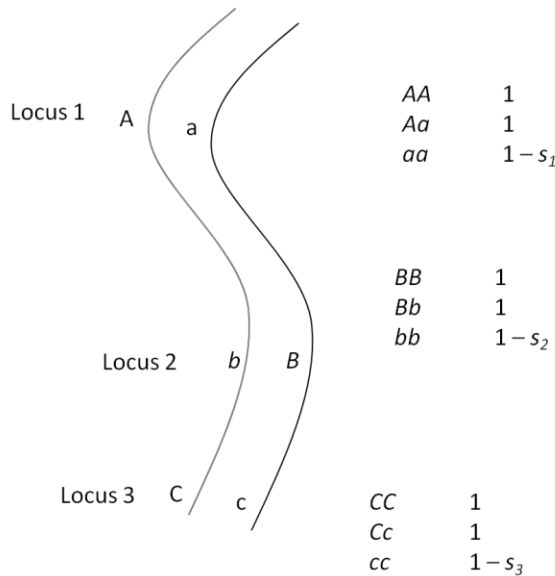
Lethal Equivalents (B) and their effect on survival

Inbreeding depression is mostly caused by deleterious recessive genes that are made homozygous by inbreeding. We can model the effect of the i^{th} locus upon an individual's probability of surviving as

Genotype	Fitness
AA	1
Aa	1
aa	$1 - s_i$

If $s_i = 1$, genotype aa is lethal. If $s_i = 0.5$, genotype aa has a 50% chance of being lethal.

The total genetic load of an individual, B , can be quantified by summing over all the loci in an individual's genome



$$B = \sum_{loci} s_i$$

where summation is done for only one set of chromosomes (half the genome). This sum is frequently called the “number of lethal equivalents” in an individual. For example, an individual with one lethal recessive allele, and 2 alleles with a 50% of causing death will have a total of two lethal equivalents.

The genetic load, B , of an average individual in a randomly mating population is approximately

$$B = \sum_{loci} q_i s_i$$

where q_i is the frequency of the detrimental allele at the i^{th} locus.

If an individual is inbred, its probability of surviving is approximately equal to

$$S = S_0 e^{-Bf}$$

where $S = S_0$ is a constant, B is the average number of lethal equivalents in a population, and f is the individual's inbreeding coefficient. Note, the above equation is expressed in a slightly different form than the textbook.

CONGEN Inbreeding quiz preparation

Quiz on Thursday Oct 24

Read Chapters 12 and 13

Be able to define inbreeding.

Be able to describe genetic consequences of inbreeding.

Be able to describe phenotypic consequences of inbreeding.

Be able to calculate the inbreeding coefficient for a simple pedigree.

Be able to describe how inbreeding and selection interact (purging)

Be able to describe lethal equivalents.

CONGEN – Inbreeding homework – Due Thursday Oct 31

Black and white lemurs are the largest lemurs living today. Unfortunately, their native habitat, the rainforests of Eastern Madagascar, have been extensively logged and the population has declined in size. A captive breeding program was established at the Smithsonian Zoo in the 1980's in order to prevent extinction. In addition, a reserve is being designed for a wild population.

You have been hired as a conservation consultant, and have been asked to answer the following questions.

1. How many lethal equivalents are there in the captive population of lemurs? There is no formula to calculate this from studbook data (available from www.montana.edu/kalinowski), so you will need to estimate B using least squares (if you are an undergraduate student) or maximum likelihood (if you are a graduate student). You can assume that the viability of non-inbred lemurs is equal to the viability of non-inbred lemurs observed in the zoo.
2. Inbreeding is a potential threat to the wild population. Assume that inbreeding affects viability according to the formula $S = S_0 e^{-Bf}$. How large would the wild population of lemurs have to be in order to prevent inbreeding from lowering the average viability by more than 5% after 25 generations?