# Homework 5: Coalescent Process (updated)
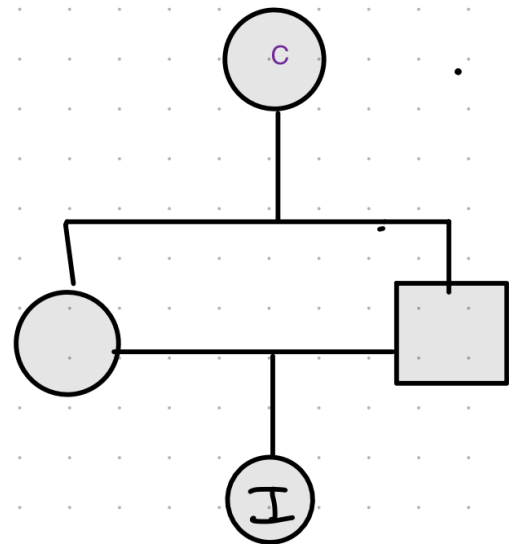
1. A full-sib half-sib breading designs

Washington State University has a state of the art Animal Disease Diagnostic Laboratory, with particular expertise in agricultural systems. Shown below are two common experimental breeding designs commonly used to detect the genetic basis of mendelian traits in cattle and other livestock.
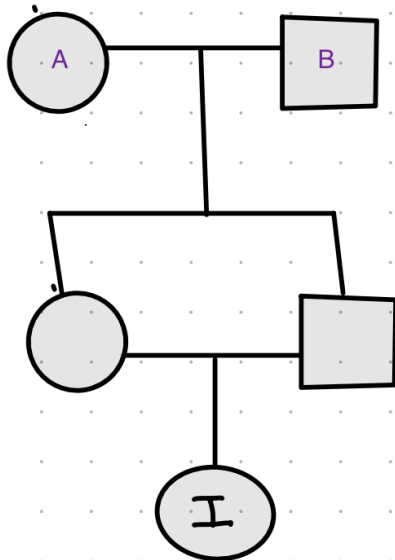
A. Calculate the inbreeding coefficient of individual I in both designs. Compare them.

B. Osteoporosis in cattle is a rare recessive mutation causing abnormal bone formation. Compare the probabilities that individual I has Osteoporosis between the designs.

C. Suppose that individuals A and B in the full sib design themselves are the result of a non-random breeding design such that the coefficient of consanguinity of A and B is $f_{AB} = f_A = f_B = 0.3$ what is the probability that individual I exhibits osteoporosis?

2. The Structured Coalescent

In class we studied the coalescent geneology in a single well mixed population. Most populations are not however well mixed. Consider two 'parapatric' populations both of diploid-size N (parapatric means that the populations exchange individuals but not at random) where the probability of moving from population 1 to population 2 (or vice versa) in a single generation is m.

A. Assuming a life cycle of migration between patches followed by random mating within a patch, what is the probability that a gene in patch 1 was in patch 1 in the previous generation? What is the probability that a gene in patch 1 was in patch 2 in the previous generation?

B. Consider two offspring genes both currently in patch 1, what is the probability that they are IBD? [Hint: They could have the same parent that stayed in patch 1, or the same parent that came from patch 2].

C. Simulate a two-patch WF model assuming $N = 10$ in each patch for 20 generations.

D. Simulate a WF model in a single patch of size $N = 20$.

E. Compare the dynamics of heterozygosity in the metapopulation (e.g., across all individuals) between the simulations in C and D. Explain why your answer makes sense.

3. Genetic diversity in a declining population

The population size of Peary caribu on the Arctic islands in Canada have been declining precipitously with a population size of 50,000 in 1960 and a population size of 100 in 2004. Assume that the population size at a constant level of 50,000 prior to 1960.

A. Assuming a generation time of 2 years, write an equation for the decline in population dynamics in units of generations.

B. Considering a sample of $n = 2$ genes sampled at the present day, what is the expected time to coalescence? What is the variance in the coalescent time? Make sure to report the units of time that you use.

C. Assuming an infinite sites model what is the expected number of segregating sites in the sample? What is the variance in the number of segregating sites.

D. Repeat parts B and D assuming a constant population size of 50,000 and compare your answers.