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APPENDIX
5

Calculating Inbreeding Coefficients from Pedigrees

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Inbreeding can be loosely defined as any mating between relatives. However, this definition needs to be put in some perspective, since any two individuals in a population can probably be traced back to a common relative—providing their lineages are traced back far enough. We then must be careful to define inbreeding relative to either some point in time or to some "base" population—that is, a population that consists of individuals assumed to be unrelated to each other. Exactly what constitutes the "base" population is important in defining the level of inbreeding in any population.

Determining the base population is usually dependent on how much information is available on the population we are interested in. In the best of cases, the field or zoo manager will have pedigree information available only as far back as the founding of his population. Often times this information is unavailable, and only data on the most recent generations are available. For this reason it is often convenient to define the base population as those individuals in a pedigree beyond which no further information is available. These may be wild-caught founders or those individuals existing in a population when the first pedigree information was recorded. These individuals are assumed to be unrelated (unless it is known otherwise), and any inbreeding occurring in the population is relative to this group of individuals.

The genetic effect of inbreeding is to increase the average homozygosity of the population, and inbred offspring (offspring resulting from consanguineous matings) have a higher probability of being homozygous for more loci than noninbred offspring. This genetic effect is measured by the "inbreeding coefficient," designated as F, and defined as the probability that the two alleles present at a given locus are "identical by descent"—that is to say, are derived by replication of a single allele from a common ancestor. The F value ranges from 0 (for noninbred individuals) to 1 (for totally homozygous individuals), and the degree of inbreeding is dependent on how closely related the parents of the individual are. (For a full discussion of inbreeding, see Hartl, 1980; Crow and Kimura, 1970; Lasley, 1978; or Falconer, 1981.)

Various methods have been used to calculate inbreeding coefficients (for examples, see the above references). We shall present two common methods: One using Path Analysis techniques and the other using an Additive Relationship method.

Path Analysis Technique

Once a pedigree of an individual (say X) is obtained, we can calculate its inbreeding coefficient, F_X. The steps involved can be summarized as follows:

Step 1: *Draw the pedigree so that common ancestors appear only once.* A common ancestor is any individual related to both parents of X, the individual for whom we wish to determine F_X. If there are no common ancestors, then $F_X = 0$, and X is noninbred.

Step 2: *Determine the inbreeding coefficients of all common ancestors.* If there is no pedigree information on the common ancestor, it is often assumed to be noninbred. If the common ancestor is inbred, then its inbreeding coefficient, F_{CA}, must be calculated before calculating F_X. Calculate F_{CA} as you would F_X as described in the following steps. Once F_{CA} is determined, F_X can then be calculated by returning to step 3 (see example 4 below).

Step 3: *Look for loops in the pedigree.* A loop is a path that runs from X, through one parent, to the common ancestor, through the other parent, and back to X without going through any individual more than once. Determine the number of steps in each loop.

Step 4: *Calculate the contribution of each loop to the inbreeding coefficient.* The contribution of each loop to the F_X is determined by using the following formula:

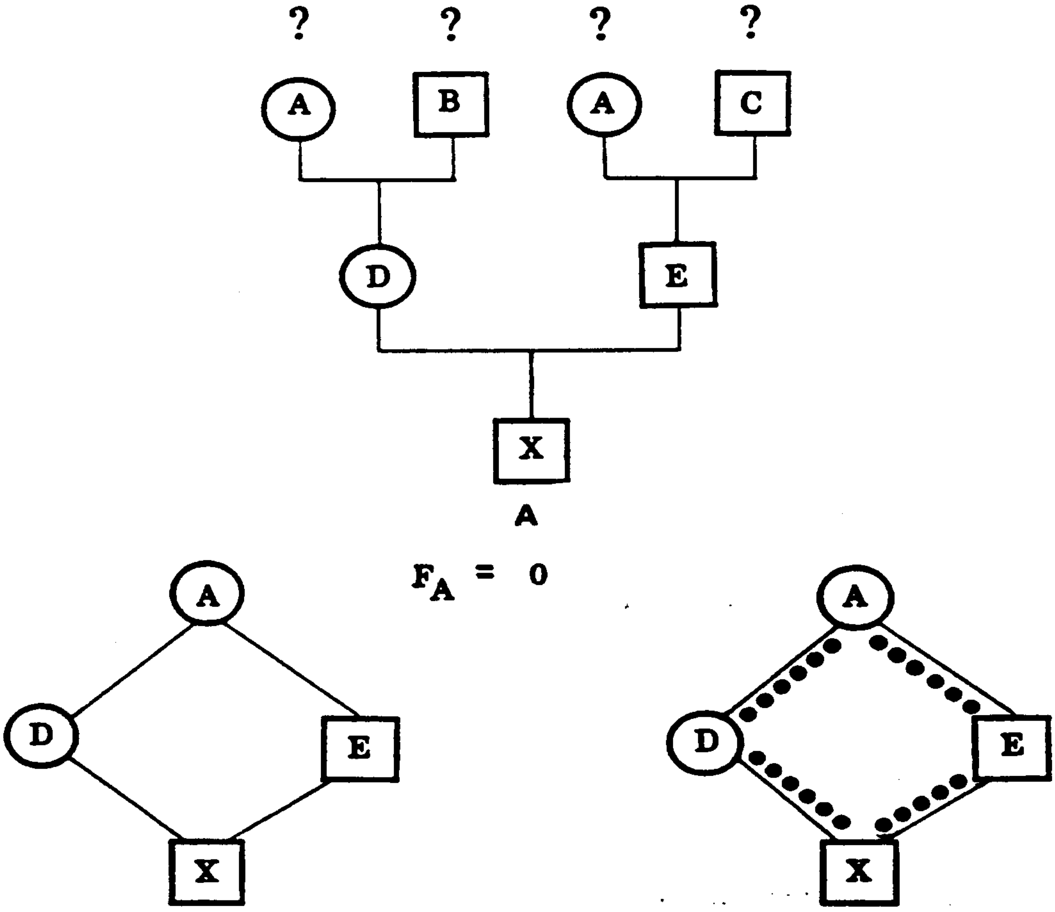
$$\left(\frac{1}{2}\right)^{i-1} \times (1 + F_{CA})$$

where: F_{CA} = inbreeding coefficient of the common ancestor,
i = number of steps in each loop as defined in step 3.

Step 5: *Sum the contributions of each loop.* The summation of all the contributions will be the inbreeding coefficient of individual X.

Several examples follow to illustrate the principles involved.

Example 1: Half-sib mating
The pedigree of individual X is shown in Figure 1A. X's mother and father are D and E, respectively, and they share the same mother, A, but have



B Figure 1. C

different fathers. We wish to calculate the inbreeding coefficient of X, the offspring of two half-sibs. In this example, A is the common ancestor, since it is related to both parents of X.

Step 1: Figure 1B shows the pedigree redrawn so that the common ancestor, A, appears only once.
Step 2: Since the pedigree of A is unknown, we assume that it is noninbred and let F_A, the inbreeding coefficient of A, equal 0.
Step 3: After examining the pedigree, it is seen that there is only one four-step loop, shown in Figure 1C (dotted line). Therefore, $i = 4$.
Step 4: The contribution of this loop is calculated:

Loop	F_{CA}	i	Contribution to F_X
$X-D-\underline{A}-E-X$	0.0	4	$(1/2)^3 \times (1 + 0.0) = 0.125$

Step 5: Since only one loop is involved: $F_X = 0.125$
Individual X therefore has an inbreeding coefficient of 0.125.

Example 2: Multiple-loop pedigree
The pedigree of individual X is shown in Figure 2A. H and G are the parents of X; E and F are the parents of H. A is the mother of E, F, and G; however, they all have different fathers. We wish to calculate the inbreeding coefficient of X.

Step 1: The abbreviated pedigree is shown in Figure 2B, with A, the only common ancestor, appearing once. Only individuals involved in the pathways from the common ancestor to X are shown (that is, B, C, and D need not be included).
Step 2: Since the pedigree of A is unknown, we assume that A is noninbred and let $F_A = 0$.
Step 3: Two separate five-step loops can be drawn through the pedigree as shown by the dashed and dotted lines in Figure 2C.
Step 4: The contribution of each loop to F_X is calculated:

Loop	F_{CA}	i	Contributions to F_X
$X-H-E-\underline{A}-G-X$	0.0	5	$(1/2)^4 \times (1 + 0.0) = 0.0625$
$X-H-F-\underline{A}-G-X$	0.0	5	$(1/2)^4 \times (1 + 0.0) = 0.0625$

Step 5: Summing over all loops: $F_X = 0.125$
The inbreeding coefficient of X is 0.125.

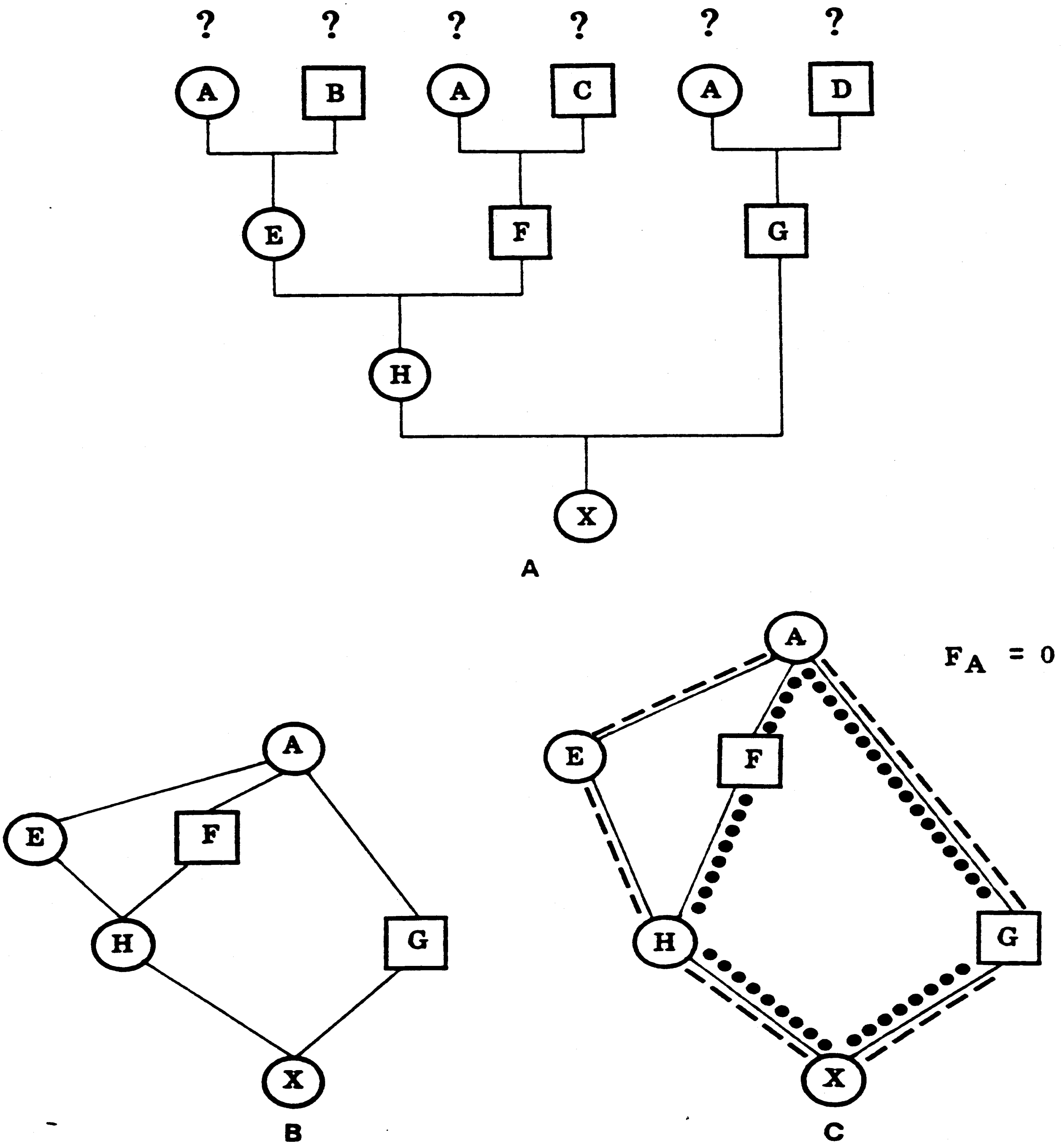


Figure 2.

Example 3: Full-sib mating
The complete pedigree of *X* is shown in Figure 3A. *X* is the offspring of two full sibs, *C* and *D*, who are offspring of *A* and *B*. The parents of *A* and *B* are unknown. We wish to calculate the inbreeding coefficient of *X*.

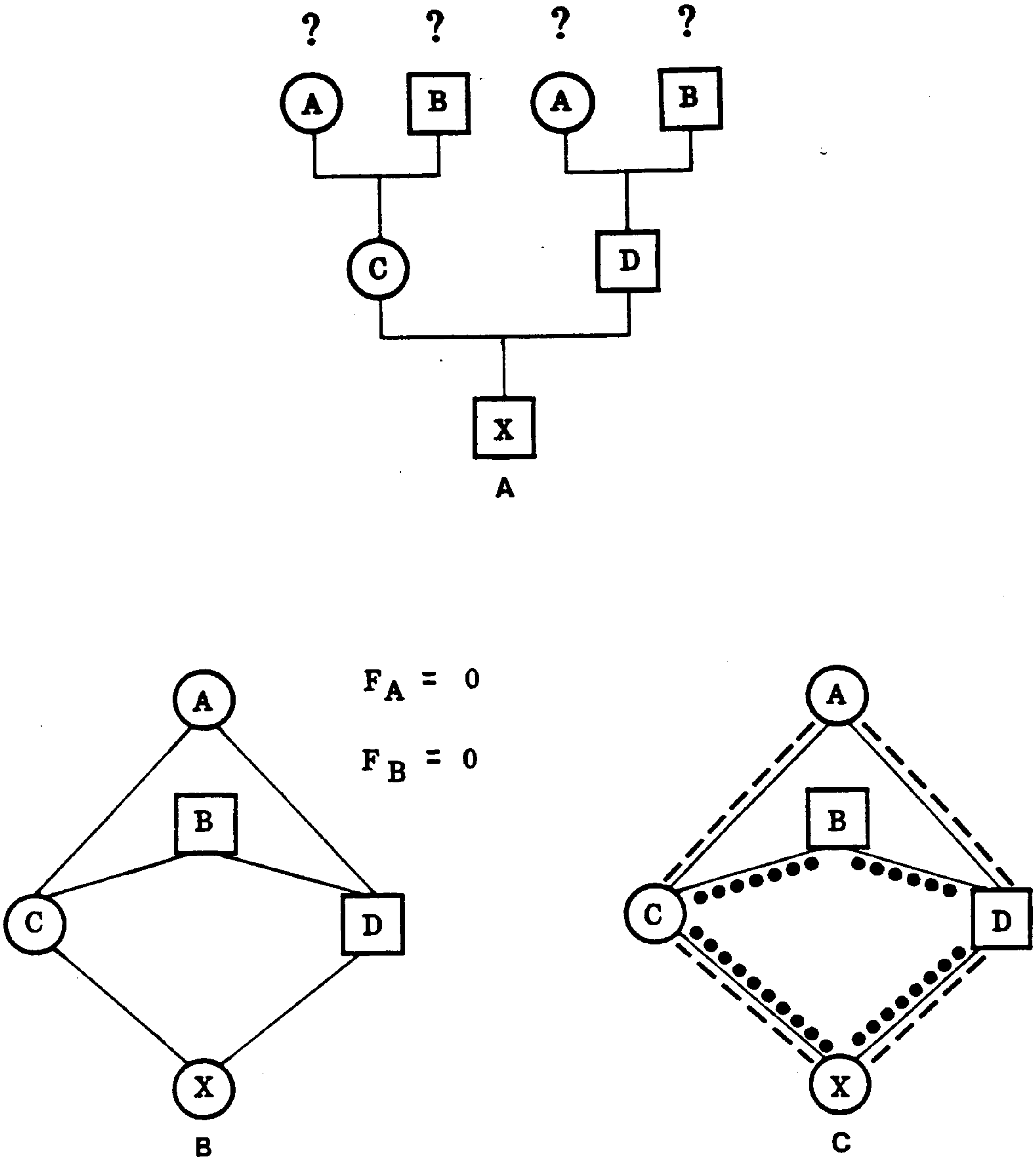


Figure 3.

Step 1: A and B are both common ancestors, since they are related to both parents of X. The abbreviated pedigree is shown in Figure 3B, with A and B appearing only once.

Step 2: Since neither of the common ancestor's pedigrees is known, they are assumed to be noninbred, and F_A and F_B are 0.

Step 3: Only one loop can be traced through each of the common ancestors, as shown in Figure 3C (dashed and dotted lines).

Step 4: The contribution of each loop to F_X is calculated:

Loop	F_{CA}	i	Contribution to F_X
X-C-$\underline{A}$-D-X	0.0	4	$(1/2)^3 \times (1 + 0.0) = 0.125$
X-C-$\underline{B}$-D-X	0.0	4	$(1/2)^3 \times (1 + 0.0) = 0.125$

Step 5: Summing over all loops: $F_X = 0.25$
The inbreeding coefficient of *X* is 0.25.

Example 4: Complex pedigree

Step 1: Figure 4A shows the already abbreviated pedigree of individual *X*. *A*, *C*, and *E* are all common ancestors, since they are related to both *B* and *D*, the parents of *X*. We wish to determine the inbreeding coefficient of *X*.

Step 2: In calculating the inbreeding coefficient of *A*, *C*, and *E*, the common ancestors, we assume that both *A* and *E* are noninbred. However, *C* is inbred, and we must first calculate F_C before determining F_X.

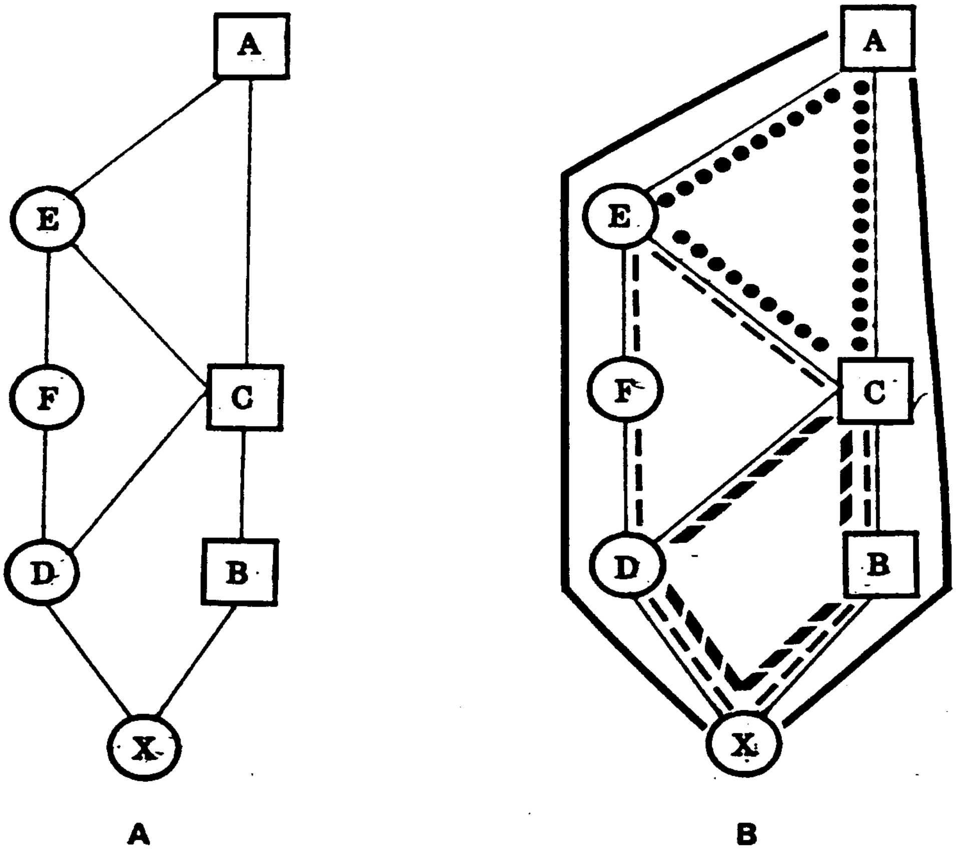


Figure 4.

Calculating F_c — Path Analysis

We determine F_C just as we would any other inbreeding coefficient. However, since the abbreviated pedigree is already drawn and we know that the inbreeding coefficient of *A*, the common ancester of *C*, is 0, we can skip steps 1 and 2. We proceed directly to step 3 and look for loops involving *A* and *C*.*

Step 3: Figure 4B shows the only three-step loop from *C* to *A* (dotted line).

Step 4: The contribution of the loop is calculated:

Loop	F_{CA}	i	Contribution of F_C
$C\text{-}E\text{-}\underline{A}\text{-}C$	0.0	3	$(1/2)^2 \times (1 + 0.0) = 0.25$
			$F_C = 0.25$

Step 5: Since there is only one loop, and we conclude that the inbreeding coefficient of the common ancestor, *C*, is 0.25.†

Proceeding with the determination of the inbreeding coefficient of *X*, starting at step 3:

Step 3: Figure 4B shows the three loops that can be traced between X and its common ancestors, *C*, *E*, and *A* (bold dashed, light dashed, and solid lines).

Step 4: The contribution of each loop to F_X is calculated:

Loop	F_{CA}	i	Contribution to F_X
$X\text{-}D\text{-}F\text{-}E\text{-}\underline{A}\text{-}C\text{-}B\text{-}X$	0.0	7	$(1/2)^6 \times (1 + 0.0) = 0.0156$
$X\text{-}D\text{-}F\text{-}\underline{E}\text{-}C\text{-}B\text{-}X$	0.0	6	$(1/2)^5 \times (1 + 0.0) = 0.0313$
$X\text{-}D\text{-}\underline{C}\text{-}B\text{-}X$	0.25	4	$(1/2)^3 \times (1 + 0.25) = 0.1563$

Step 5: Summing over all loops: $F_X = 0.2032$

The inbreeding coefficient of *X* is 0.2032.

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*Note that *A* is both a parent and a common ancestor of *C*, because *A* is related to both of *C*'s parents — it is the father of *E* and is itself the father of *C*.

† Two important points can be made here: (1) *C* is the offspring of a father-daughter mating, and all such matings, like all mother-son matings, have inbreeding coefficients of 0.25; (2) example 3 as well as the above example shows different mating patterns that result in inbreeding coefficients of 0.25. Examples 1 and 2 also show different breeding patterns that result in the same inbreeding coefficient. Different breeding schemes can obviously result in similar inbreeding coefficients; therefore one cannot draw conclusions about the mating structure based solely on the inbreeding coefficients of the offspring produced.