

Inbreeding coefficients in diploids

In diploids, one can speak of *the* inbreeding coefficient F of an individual, defined as the probability that two distinct genes at a locus are identical by descent. This probability is relevant, in that the pedigree of an individual with respect to some *base generation* is sufficient to compute it. Note that it is a probability, and hence a measure of uncertainty or degree of belief. Specifically, F measures the degree of belief we have that two gene copies are identical by descent *on the supposition of Mendelian segregation*.

The inbreeding coefficient in diploids is well-studied. For various population models, e.g. the WF model, its expected value across the population has a well-defined law. Note that the inbreeding coefficient of each *individual* in such a population is still determined by the pedigree and not such a law. However, to track the inbreeding coefficients of a diploid population, one does not need to track the pedigree explicitly, as the latter can be adequately represented by a matrix of coancestry coefficients (I think that is the right term, but I am not completely sure). This is for instance used in @barton2017 (where they term the matrix of these coefficients the pedigree matrix). Let $F_{i,j}$ be the coancestry coefficient for individual i and j , i.e. the probability that a random gene pair from i and j at a homologous locus is IBD. $F_{i,i}$ is the usual inbreeding coefficient for individual i . Let P be the pedigree matrix, with entry $P_{i,k}$ be the probability that a gene from individual i came from individual k in the *previous* generation.

$$F'_{i,j} = \sum_k \sum_l P_{i,k} P_{j,l} F_{k,l}$$

and

$$F'_{i,i} = \begin{cases} F_{k,l} & k \neq l \\ \frac{1}{2}(1 + F_{k,k}) & k = l \end{cases}$$

where k and l are the parents of i .¹

Inbreeding coefficients in tetraploids

In tetraploids there are five different degrees of homozygosity possible at any locus. Symbolically: $abcd$, $aabc$, $aabb$, $aaab$, $aaaa$ (what's the law?). There are, concomitantly, four inbreeding coefficients².

¹ @barton2017 gave for diploids

$$F'_{i,j} = \sum_k \sum_l P_{i,k} P_{j,l} \begin{cases} F_{k,l} & \text{if } k \neq l \\ \frac{1}{2}(1 + F_{k,k}) & \text{if } k = l \end{cases}$$

However, this appears to be wrong. Consider an individual i which is an offspring from k and l , with $k \neq l$. There will be a term $P_{i,k}^2 \frac{1}{2}(1 + F_{k,k}) = \frac{1}{8}(1 + F_{k,k})$ as well as a term $P_{i,l}^2(1 + F_{l,l})$ in the sum for $F_{i,i}$, both of which are spurious since $F_{i,i}$ is the probability that two distinct genes are IBD, and the probability that two *distinct* genes come from parent k is not $P_{i,k}^2$ but 0.

²In hexaploids, we have 11 states, and 10 coefficients: $abcdef$, $aabcde$, $aabbcd$, $aabbcc$, $aaabcd$, $aaabbc$, $aaabbb$, $aaaabc$, $aaaabb$, $aaaaab$, $aaaaaa$.

Segregation variance in autotetraploids

The segregation variance, here defined as the variance of *gametic values*, in autotetraploids conditional on any of the five IBD states is given in the following table

state	probability	segregation variance
<i>abcd</i>	f_1	V_0
<i>aabc</i>	f_2	$(1 - \frac{1}{6})V_0$
<i>aabb</i>	f_3	$(1 - \frac{1}{3})V_0$
<i>aaab</i>	f_4	$(1 - \frac{1}{2})V_0$
<i>aaaa</i>	f_5	0

This is easily verified by Monte Carlo experiments.

When double reduction happens with probability α , the segregation variance is increased by a factor $(1+2\alpha)$ in my experiments. However, it should be $(1+\alpha)$: $(1-\alpha)V[X+X]+\alpha V[2X] = (1-\alpha)v_0 + 4\alpha\frac{v_0}{2} = v_0(1+\alpha)$? (this is for the total variance!) Note that double reduction accelerates inbreeding, and hence the decline of the segregation variance over time, but increases the segregation variance within any given generation with respect to the segregation variance in the absence of double reduction.