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Distributions of Genotypes after a Panmixia

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1. Introduction.

Consider a population of size $2N$ consisting of N females and N males. We observe a single inherited character which consists of m multiple alleles at one diploid locus denoted by

$$A_i \qquad (i=1, \cdots, m)$$

and of which the inheritance is subject to Mendelian law.

There are $m(m+1)/2$ possible genotypes A_aA_b $(a, b=1, \cdots, m; a\leqq b)$ among which m types A_bA_b $(b=1, \cdots, m)$ are homozygous and $m(m-1)/2$ types A_aA_b $(a, b=1, \cdots, m; a<b)$ are heterozygous. Let the distributions of these $m(m+1)/2$ genotypes A_aA_b $(a\leqq b)$ in females and in males be designated by

$$F_{ab} \text{ and } M_{ab} \qquad (a, b=1, \cdots, m; a\leqq b)$$

or, as the aggregates, by

$$\mathfrak{F}=(F_{11}, \cdots, F_{mm}, F_{12}, \cdots, F_{m-1,m})$$

and

$$\mathfrak{M}=(M_{11}, \cdots, M_{mm}, M_{12}, \cdots, M_{m-1,m})$$

respectively, so that

$$\sum_{a\leqq b} F_{ab}=\sum_{a\leqq b} M_{ab}=N.$$

The order of genes in a genotype being immaterial, both genotypes A_aA_b and A_bA_a are regarded as identical each other even when the suffices a and b are distinct. Accordingly, we put $F_{ab}=F_{ba}$ and $M_{ab}=M_{ba}$.

We now introduce a set of stochastic variables

$$\mathfrak{C}=(C_{11}, \cdots, C_{mm}, C_{12}, \cdots, C_{m-1,m})$$