Let P be a stochastic matrix and F (x), G (x) be vectors of distribution  $n \times 1$   $k \times 1$ functions. The Mendelian inheritance model of genetic experiments is

$$F(x) = P \quad G(x), \qquad k \leq n$$

$$n \times 1 \qquad n \times k \quad k \times 1$$

where P then represents a matrix of Mendelian segregation probabilities specified by the genetic hypothesis for n different crosses,  $G_j(x)$  is the probability distribution of phenotypes for progeny having the j<sup>th</sup> genotype,  $j = 1, \dots, k$ , and  $F_i(x)$ is the mixed distribution formed when the distributions  $G_j(x)$  are compounded with the i<sup>th</sup> row of P,

$$F_{i}(x) = p_{i1}G_{1}(x) + \cdots + p_{ik}G_{k}(x)$$
.

The genetic experiment produces  $m_i$  independent observations  $X_{i1}$ ,  $\cdots$ ,  $X_{i2}$  from the distribution  $F_i(x)$ ,  $i = 1, \cdots$ , n, and the observations from the n different crosses are independent.

The genetic hypothesis specifies P but not G (and hence not F), and the statistical problem is to test the "goodness of fit" of the specified P. Equivalently, if P is of rank r,  $r \leq k$ , the problem is to test goodness of fit for r linearly independent rows of

$$(I - P(P'P)^{-}P')F(x) \equiv O_{x}$$

where  $(P'P)^{-}$  is a generalized inverse of P.

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