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ON THE HARDY-WEINBERG EQUILIBRIUM IN GENERALIZED

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SUMMARY

We propose a constraint formulation for the Hardy-Weinberg model in generalized ABO-like systems which lends itself to the construction of Wald tests for the corresponding equilibrium hypothesis. We illustrate the testing procedure with practical examples and provide indication for the use of a categorical data computer program (GENCAT) to perform the required calculations. We also demonstrate that as in many other settings, the Wald statistic may have an aberrant behaviour for fixed sample sizes, although it possesses optimal asymptotic properties.

Key words: ABO blood groups, Hardy-Weinberg models, Wald tests.

1. INTRODUCTION

Consider a genetic system with m codominant alleles, A_1, \dots, A_m and one recessive allele, O , in a single locus and let q_1, \dots, q_m and q_0 , $\sum_{j=0}^m q_j = 1$ denote the corresponding probabilities of occurrence in a given population. Also let the probabilities of occurrence of the $f = (m^2 + m + 2)/2$ possible phenotypes be given by:

| Phenotype | Genotype | Probability of occurrence |
|--------------|----------------|---------------------------|
| O | OO | p_0 |
| A_1 | A_1A_1, A_1O | p_1 |
| \vdots | \vdots | \vdots |
| A_m | A_mA_m, A_mO | p_m |
| A_1A_2 | A_1A_2 | p_{12} |
| \vdots | \vdots | \vdots |
| $A_{m-1}A_m$ | $A_{m-1}A_m$ | $p_{m-1,m}$ |

where $\sum_{i=0}^m p_i + \sum_{\substack{i,j=1 \\ j>i}}^m p_{ij} = 1$. Genetic systems of this type, of which the well known ABO blood group classification system constitutes a special case ($m=2$), are important in many practical situations and have been studied by a host of workers, among which we mention Cavalli-Sforza and Bodmer (1971), Elandt-Johnson (1971) and Nam and Gart (1976).

The system is said to follow the Hardy-Weinberg (HW) model (equilibrium) if there exist q_i , $i=0, \dots, m$ $\sum_{i=0}^m q_i = 1$ such that the following relations hold:

$$\begin{aligned}
 \text{a) } p_0 &= q_0^2 \\
 \text{b) } p_1 &= q_1^2 + 2q_1q_0, \quad i = 1, \dots, m \\
 \text{c) } p_{1j} &= 2q_1q_j, \quad i = 1, \dots, m, \quad j > 1
 \end{aligned} \tag{1}$$

A similar model may be considered for situations where there are no recessive alleles; an important special case is the MN blood classification system ($m=2$), discussed in Elandt-Johnson (1971, ch 14) among other authors. In such cases the relations (1) reduce to:

$$\begin{aligned}
 \text{a) } p_1 &= q_1^2, \quad i = 1, \dots, m \\
 \text{b) } p_{1j} &= 2q_1q_j, \quad i, j = 1, \dots, m, \quad j > 1.
 \end{aligned} \tag{2}$$

A problem of general concern to geneticists is to test whether a given population satisfies the HW equilibrium relations [(1) or (2)] based on the evidence provided by a sample of n observational units for which the phenotype frequencies are n_i , $i = 0, \dots, m$ and n_{1j} , $i, j = 1, \dots, m$, $j > 1$, respectively. $\sum_{i=0}^m n_i + \sum_{\substack{i,j=1 \\ j>1}}^m n_{1j} = n$. In this paper we address this problem via an alternative formulation of the HW model, based on the restrictions that (1) or (2) impose on the space of the phenotype population proportions $p_0, p_1, \dots, p_{m-1, m}$. In Section 2 we show the equivalence between the two formulations; in Section 3 we indicate how the constraint formulation may be employed to produce Wald tests for the HW equilibrium hypotheses and consider related computational aspects; finally in Section 4 we discuss statistical properties associated with the proposed tests.

2. A CONSTRAINT FORMULATION FOR THE HARDY-WEINBERG MODEL

Here we show that the ABO-like genetic system described in the previous section is in HW equilibrium if and only if the phenotype parameters, p_i , $i = 0, \dots, m$, p_{ij} , $i, j = 1, \dots, m$, $j > i$, $\sum_{i=0}^m p_i + \sum_{\substack{i,j=1 \\ j>i}}^m p_{ij} = 1$, satisfy the $m(m-1)/2$ relations:

$$p_{ij} = 2(\sqrt{p_i + p_0} - \sqrt{p_0})(\sqrt{p_j + p_0} - \sqrt{p_0}), \quad i, j = 1, \dots, m, \quad j > i \quad (3)$$

First suppose that there exist q_i , $i = 0, \dots, m$, $\sum_{i=0}^m q_i = 1$ such that (1) holds. This clearly implies that $\sum_{i=0}^m p_i + \sum_{j>i} p_{ij} = 1$. Then, using (1a) and (1b) we may write:

$$q_0 = \sqrt{p_0}, \quad q_i = \sqrt{p_i + p_0} - \sqrt{p_0}, \quad i = 1, \dots, m \quad (4)$$

and substituting (4) in (1c) it follows that (3) holds.

Now suppose that the phenotype parameters satisfy (3). Letting q_0, q_i , $i = 1, \dots, m$ be defined by (4) it follows that (1a) - (1c) hold. It remains to show that $\sum_{i=0}^m q_i = 1$. In this direction, let:

$$x = \sum_{i=0}^m q_i = \sum_{i=1}^m \sqrt{p_i + p_0} - (m-1) \sqrt{p_0} \quad (5)$$

which implies:

$$(x + (m-1) \sqrt{p_0})^2 = mp_0 + \sum_{i=1}^m p_i + 2 \sum_{\substack{i=1 \\ j>i}}^m \sqrt{(p_i + p_0)(p_j + p_0)} \quad (6)$$

Now, adding the $m(m-1)/2$ relations (3) memberwise we get:

$$\sum_{i=1}^m \sum_{j>1} p_{ij} = 2 \sum_{i=1}^m \sum_{j>1} \sqrt{(p_i + p_0)(p_j + p_0)} - 2(m-1)\sqrt{p_0} \sum_{i=1}^m \sqrt{p_i + p_0} + m(m-1)p_0 \quad (7)$$

From (7) and the fact that $\sum_{i=0}^m p_i + \sum_{i,j=1}^m \sum_{j>i} p_{ij} = 1$, it follows that:

$$\sum_{i=1}^m p_{i+2} + \sum_{i,j=1}^m \sum_{j>1} \sqrt{(p_i + p_0)(p_j + p_0)} = 1 + 2(m-1)\sqrt{p_0} \left\{ \sum_{i=1}^m \sqrt{p_i + p_0} - (m-1)\sqrt{p_0} \right\} + (m^2 - 3m + 1)p_0 \quad (8)$$

Substituting (5) into (8) and using (6) we obtain the second degree equation:

$$(x + (m-1)\sqrt{p_0})^2 = 1 + 2(m-1)\sqrt{p_0}x + (m^2 - 2m + 1)p_0$$

which has $x = 1$ as the only positive root and the result follows.

Note that when there are no recessive alleles, the relations (3) reduce to:

$$p_{ij} = 2\sqrt{p_i p_j}, \quad i, j = 1, \dots, m, \quad j > 1 \quad (9)$$

which have been considered in the literature (see Pereira and Rogatko (1984), for example). Also note that the set of parameters $\theta_{ij} = p_{ij} / (2(\sqrt{p_i + p_0} - \sqrt{p_0})(\sqrt{p_j + p_0} - \sqrt{p_0}))$, $i, j = 1, \dots, m$, $j > 1$ (or alternatively a set of monotone functions of the θ_{ij} , like $\log \theta_{ij}$) may be employed as a measure of departure from the HW equilibrium; in view of (3), $\theta_{ij} \neq 1$ (or $\log \theta_{ij} \neq 0$) for some (i, j) corresponds to a lack of equilibrium. In the next section we indicate how such ideas may be employed to construct a test of the HW hypothesis.

3. WALD TESTS FOR THE HARDY-WEINBERG EQUILIBRIUM

Let $p = (p_0, \dots, p_m, p_{12}, \dots, p_{m-1,m})'$ denote the $(m^2+m+2)/2$ vector of phenotype population proportions and note that the HW equilibrium corresponds to:

$$\underline{F}(p) = \underline{0} \quad (10)$$

where $\underline{F}(\cdot)$ is a vector-valued function with elements $F_{1j} = \theta_{1j} - 1$ (or $F_{1j} = \log \theta_{1j}$), $i, j = 1, \dots, m, j > i$. Assume that the vector of observed phenotype frequencies $\underline{n} = (n_0, \dots, n_m, n_{12}, \dots, n_{m-1,m})'$ has a multinomial distribution with parameters n and p ; then, if n is sufficiently large, it follows by Central Limit theory that $\hat{p} = \underline{n}/n$ has an asymptotic multinormal distribution with mean vector p and covariance matrix $\underline{V}(p) = n^{-1}(\underline{D}_p - p p')$ where \underline{D}_p denotes a diagonal matrix with the elements of p along the main diagonal. As indicated in Bhapkar (1966), a Wald statistic to test (10) is given by:

$$Q = \underline{F}(\hat{p})' (\underline{V}_F(\hat{p}))^{-1} \underline{F}(\hat{p}) \quad (11)$$

where $\underline{V}_F(\hat{p}) = \underline{H}(\hat{p}) \underline{V}(\hat{p}) \underline{H}'(\hat{p})$ with $\underline{V}(\hat{p}) = n^{-1}(\underline{D}_{\hat{p}} - \hat{p} \hat{p}')$ and

$$\underline{H}(\hat{p}) = \left[\frac{\partial \underline{F}(\underline{z})}{\partial \underline{z}} \right]_{\underline{z}=\hat{p}}. \quad \text{Under the hypothesis (10), the statistic}$$

Q follows an asymptotic chi-squared distribution with $m(m-1)/2$ degrees of freedom. Bhapkar (1966) demonstrated that Q is algebraically identical to Neyman's minimum chi-squared statistic and thus shares the same asymptotic optimality properties of Pearson's chi-squared or Wilks' likelihood ratio criteria.

Letting $F_{1j} = \theta_{1j}^{-1}$, the elements of the matrix of partial derivatives $H(\hat{p})$ are given by:

$$\begin{aligned} \frac{\partial F_{1j}}{\partial \hat{p}_0} &= \frac{\hat{\theta}_{1j}}{2} ([\hat{p}_0(\hat{p}_1 + \hat{p}_0)]^{-1/2} + [\hat{p}_0(\hat{p}_j + \hat{p}_0)]^{-1/2}) \\ \frac{\partial F_{1j}}{\partial \hat{p}_k} &= \begin{cases} -\frac{\hat{\theta}_{1j}}{2} (\sqrt{\hat{p}_1 + \hat{p}_0} \sqrt{\hat{p}_j + \hat{p}_0} - \sqrt{\hat{p}_0})^{-1}, & k=1, j \\ 0 & k \neq 1, j \end{cases} \quad (12) \\ \frac{\partial F_{1j}}{\partial \hat{p}_{k_1}} &= \begin{cases} \frac{\hat{\theta}_{1j}}{\hat{p}_{1j}} & (k_1) = (1, j) \\ 0 & (k_1) \neq (1, j) \end{cases} \end{aligned}$$

where $\hat{\theta}_{1j} = \hat{p}_{1j} / 2(\sqrt{\hat{p}_1 + \hat{p}_0} - \sqrt{\hat{p}_0})(\sqrt{\hat{p}_j + \hat{p}_0} - \sqrt{\hat{p}_0})$. In the case $F_{1j} = \log \theta_{1j}$ the derivatives are obtained by dividing the above expressions by $\hat{\theta}_{1j}$. In general, computation of the Wald statistic (11) must be carried out by appropriate statistical software since it involves the inversion of the matrix $V_F(\hat{p})$. In this direction, a convenient computer program is GENCAT (Landis et al. (1976)). Among other capabilities related to the analysis of categorical data, it computes Wald statistics for testing that certain classes of functions of the parameters of multinomial distributions are zero. They include functions obtained from compositions of linear, logarithmic and exponential operations along the lines indicated in Forthofer and Koch (1973) or Koch et al. (1977). In particular, For $F_{1j} = \theta_{1j}^{-1}$, the

compound function expression for $F(p)$ in (10) may be given by $F(p) = \exp A_4 \log A_3 \exp A_2 \log A_1 p - c$ where $\log(\cdot)$ and $\exp(\cdot)$ are the elementwise vector logarithmic and exponential operators, respectively (i.e. the i^{th} element of $\log x$ is $\log x_i$ and that of $\exp x$ is $\exp x_i$).

$$A_1 = (f \times f) \begin{bmatrix} \overbrace{1 \ 0 \ \dots \ 0}^{m+1} & \overbrace{0 \ 0 \ \dots \ 0}^{m(m-1)/2} \\ 1 \ 1 \ \dots \ 0 & 0 \ 0 \ \dots \ 0 \\ \vdots & \vdots \\ 1 \ 0 \ \dots \ 1 & 0 \ 0 \ \dots \ 0 \\ 0 \ 0 \ \dots \ 0 & 1/2 \ 0 \ \dots \ 0 \\ 0 \ 0 \ \dots \ 0 & 0 \ 1/2 \ \dots \ 0 \\ \vdots & \vdots \\ 0 \ 0 \ \dots \ 0 & 0 \ 0 \ \dots \ 1/2 \end{bmatrix}$$

$$A_2 = (f \times f) \begin{bmatrix} \overbrace{1/2 \ 0 \ \dots \ 0}^{m+1} & \overbrace{0 \ 0 \ \dots \ 0}^{m(m-1)/2} \\ 0 \ 1/2 \ \dots \ 0 & 0 \ 0 \ \dots \ 0 \\ \vdots & \vdots \\ 0 \ 0 \ \dots \ 1/2 & 0 \ 0 \ \dots \ 0 \\ 0 \ 0 \ \dots \ 0 & 1 \ 0 \ \dots \ 0 \\ 0 \ 0 \ \dots \ 0 & 0 \ 1 \ \dots \ 0 \\ \vdots & \vdots \\ 0 \ 0 \ \dots \ 0 & 0 \ 0 \ \dots \ 1 \end{bmatrix}$$

$$A_3 = (f-1 \times f) \begin{bmatrix} \overbrace{-1 \ 1 \ \dots \ 0}^{m+1} & \overbrace{0 \ 0 \ \dots \ 0}^{m(m-1)/2} \\ \vdots & \vdots \\ -1 \ 0 \ \dots \ 1 & 0 \ 0 \ \dots \ 0 \\ 0 \ 0 \ \dots \ 0 & 1 \ 0 \ \dots \ 0 \\ 0 \ 0 \ \dots \ 0 & 0 \ 1 \ \dots \ 0 \\ \vdots & \vdots \\ 0 \ 0 & 0 \ 0 \ 0 \ \dots \ 1 \end{bmatrix}$$

$$A_4 = \frac{m(m-1)}{2} \times (f-1) \begin{bmatrix} \overbrace{-1 \ -1 \ 0 \ \dots \ 0 \ 0}^m & \overbrace{1 \ 0 \ \dots \ 0 \ 0 \ \dots \ 0 \ \dots \ 0}^{m(m-1)/2} \\ -1 \ 0 \ -1 \ \dots \ 0 \ 0 & 0 \ 1 \ \dots \ 0 \ 0 \ \dots \ 0 \ \dots \ 0 \\ \vdots & \vdots \\ -1 \ 0 \ 0 \ \dots \ 0 \ -1 \ 0 \ 0 \ \dots \ 1 \ 0 \ \dots \ 0 \ \dots \ 0 \\ 0 \ -1 \ -1 \ \dots \ 0 \ 0 & 0 \ 0 \ \dots \ 0 \ 1 \ \dots \ 0 \ \dots \ 0 \\ \vdots & \vdots \\ 0 \ -1 \ 0 \ \dots \ 0 \ -1 \ 0 \ 0 \ \dots \ 0 \ 0 \ \dots \ 1 \ \dots \ 0 \\ \vdots & \vdots \\ 0 \ 0 \ 0 \ \dots \ -1 \ -1 \ 0 \ 0 \ \dots \ 0 \ 0 \ \dots \ 0 \ \dots \ 1 \end{bmatrix}$$

and $\underline{c} = \frac{1}{2} \underline{1}_{m(m-1)/2}$, a vector with $m(m-1)/2$ elements equal to 1. For

$F_{1j} = \log e_{1j}$ we have $F(p) = A_4 \log A_3 \exp A_2 \log A_1 p$.

We present the details for the two special cases discussed above. First consider the MN blood group classification system. From (9), it follows that the HW equilibrium corresponds to $\theta = p_{MN}/2\sqrt{p_M p_N} = 1$, where p_M, p_N and p_{MN} denote the population proportions of the M, N and MN phenotypes, respectively. Taking $F(p) = \theta - 1$ we obtain $H(\hat{p}) = \frac{\hat{\theta}}{2} (-\hat{p}_M^{-1}, -\hat{p}_N^{-1}, 2\hat{p}_{MN}^{-1})$ and the Wald statistic (11) reduces to:

$$Q = n(1 - \frac{1}{\hat{\theta}})^2 (\frac{1}{4\hat{p}_M} + \frac{1}{4\hat{p}_N} + \frac{1}{\hat{p}_{MN}})^{-1} \quad (13)$$

where \hat{p}_M , \hat{p}_N and \hat{p}_{MN} correspond to the observed proportions of the M, N and MN phenotypes, respectively and $\hat{\theta} = \hat{p}_{MN}/2\sqrt{\hat{p}_M\hat{p}_N}$. Alternatively, taking $F(p) = \log \theta$, we obtain $H(\hat{p}) = \frac{1}{2} (-\hat{p}_M^{-1}, -\hat{p}_N^{-1}, 2\hat{p}_{MN}^{-1})$ and the Wald statistic (11) reduces to:

$$Q_L = n \log^2 \hat{\theta} (\frac{1}{4\hat{p}_M} + \frac{1}{4\hat{p}_N} + \frac{1}{\hat{p}_{MN}})^{-1} \quad (14)$$

If the system is in HW equilibrium, both (13) and (14) follow asymptotic chi-squared distributions with 1 degree of freedom.

Consider now, the ABO blood group classification system. From (3), it follows that the HW equilibrium corresponds to $\theta = p_{AB}/2(\sqrt{p_A+p_O} - \sqrt{p_O})(\sqrt{p_B+p_O} - \sqrt{p_O}) = 1$, where p_O , p_A , p_B and p_{AB} denote the population proportions of the O, A, B and AB phenotypes, respectively. Taking $F(p) = \theta - 1$, relations (11) and (12) yield, after some algebraic manipulation:

$$Q = n(1 - \frac{1}{\hat{\theta}})^2 (O^2 \hat{p}_O + A^2 \hat{p}_A + B^2 \hat{p}_B + \hat{p}_{AB}^{-1})^{-1} \quad (15)$$

where $O = \{[\hat{p}_O(\hat{p}_A + \hat{p}_O)]^{-1/2} + [\hat{p}_O(\hat{p}_B + \hat{p}_O)]^{-1/2}\}/2$,

$A = -(2(\hat{p}_A + \hat{p}_O))^{1/2}[(\hat{p}_A + \hat{p}_O)^{1/2} - \hat{p}_O^{1/2}]^{-1}$

and $B = -(2(\hat{p}_B + \hat{p}_O))^{1/2}[(\hat{p}_B + \hat{p}_O)^{1/2} - \hat{p}_O^{1/2}]^{-1}$. For $F(p) = \log \theta$ the corresponding wald statistic is given by:

$$Q_L = n \log^2 \hat{\theta} (\sigma^2 \hat{p}_O + A^2 \hat{p}_A + B^2 \hat{p}_B + \hat{p}_{AB}^{-1})^{-1} \quad (16)$$

If the HW equilibrium hypothesis holds, both statistics follow asymptotic chi-squared distributions with 1 degree of freedom.

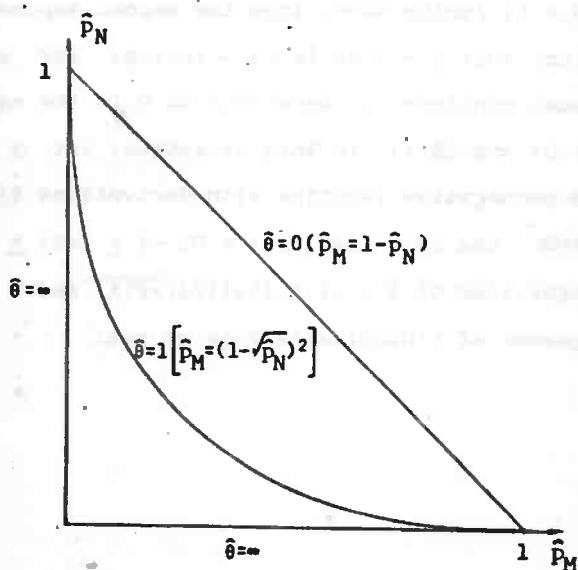
To illustrate the above procedures numerically, we first consider a set of data from the MN blood classification system presented in Crow and Kimura (1970, p.36); the observed phenotype frequencies are $n_M = 362$, $n_N = 282$ and $n_{MN} = 634$ and the Wald statistics obtained from (13) and (14) are $Q = 0.02$ and $Q_L = 0.02$ ($\hat{\theta} = 0.99$); the corresponding Pearson chi-squared statistic is $Q_P = 0.03$. In a second example (Rao (1973), p.402), the observed phenotype frequencies for the O, A, B and AB blood groups are $n_O = 121$, $n_A = 120$, $n_B = 79$ and $n_{AB} = 33$, respectively. The corresponding Wald statistics, obtained via (15) and (16) are $Q = 0.38$ and $Q_L = 0.44$, respectively ($\hat{\theta} = 1.16$), while the Pearson chi-squared statistic is $Q_P = 0.44$. Finally we consider the data for Esterase variants of *Drosophila virilis* cited by Yasuda and Kimura (1968, p.415); in this case $m = 3$ and the phenotype observed frequencies are given by $n_0 = 20$, $n_1 = 1149$, $n_2 = 36$, $n_3 = 17$, $n_{12} = 336$, $n_{13} = 25$ and $n_{23} = 17$. Here we obtain $\hat{\theta}_{12} = 0.88$, $\hat{\theta}_{13} = 1.12$ and $\hat{\theta}_{23} = 1.58$; also from (11) and (12) we get $Q = 11.79$ using $F_{ij} = \theta_{ij} - 1$ and $Q_L = 21.18$ using $F_{ij} = \log \theta_{ij}$ while the corresponding Pearson chi-squared statistic is $Q_P = 26.98$.

4. ON THE BEHAVIOUR OF THE PROPOSED WALD STATISTICS FOR FIXED SAMPLE SIZES.

Although the Wald statistics considered in Section 3 have optimal asymptotic properties, it is of interest to study their statistical behaviour for fixed sample sizes since this is the case in practical applications. Considering one-parameter exponential families, Hauck and Donner (1977) and Væth (1985) have shown that Wald statistics may decrease to zero as the parameter estimate moves away from the null value, indicating an aberrant behaviour. In this section we demonstrate that this is also true for the Wald statistics proposed above, at least in the special case $m = 2$, $p_0 = 0$.

Consider, for example, the MN blood group classification system discussed above. Write $\hat{\theta} = (1 - \hat{p}_M - \hat{p}_N) / 2\sqrt{\hat{p}_M \hat{p}_N}$ and note that the domain of $\hat{\theta}$ as a function of \hat{p}_M and \hat{p}_N corresponds to the region delimited by the triangle in Figure 1.

Figure 1: Domain of the function $\hat{\theta} = \hat{\theta}(\hat{p}_M, \hat{p}_N)$.



Let us first study the behaviour of $\hat{\theta}$ in this domain. Observe that, given $\theta_0 \geq 0$, the set of points for which $\hat{\theta} = \theta_0$ corresponds to the curve with equation $\hat{p}_M = (\sqrt{1+(\theta_0^2-1)\hat{p}_N} - \theta_0\sqrt{\hat{p}_N})^2$; in particular for the null value, $\theta_0 = 1$, we have $\hat{p}_M = (1-\sqrt{\hat{p}_N})^2$; also, for $\theta_0 = 0$, we get $\hat{p}_M = 1 - \hat{p}_N$ and as $\theta_0 \rightarrow \infty$ we must have either $\hat{p}_M \rightarrow 0$ or $\hat{p}_N \rightarrow 0$. Therefore we need to be concerned with points on the boundary of the triangular region presented in Figure 1.

For simplicity, let $\hat{p}_M = x$, $\hat{p}_N = y$ and let us examine the behaviour of the statistic (13) which may be written as:

$$Q = n \left(1 - \frac{2\sqrt{xy}}{1-x-y} \right)^2 \left(\frac{1}{4x} + \frac{1}{4y} + \frac{1}{1-x-y} \right)^{-1} =$$

$$= n \left(\frac{1-x-y}{2\sqrt{xy}} - 1 \right)^2 \left(\frac{(1-x-y)^2}{16x^2y} + \frac{(1-x-y)^2}{16xy^2} + \frac{(1-x-y)}{4xy} \right)^{-1} \quad (17)$$

Using the first expression for Q in (17) it is easy to see that $Q \rightarrow 0$ as $(x,y) \rightarrow (0,p)$ or $(x,y) \rightarrow (p,0)$ or $(x,y) \rightarrow (p,0)$ or $(x,y) \rightarrow (0,0)$ for any $0 < p < 1$; furthermore, from the second expression for Q in (17) it is clear that $Q \rightarrow \infty$ as $(x,y) \rightarrow (p,1-p)$ for any $0 < p < 1$. Finally, we must consider the behaviour of Q in the neighbourhood of the points $(1,0)$ and $(0,1)$. In this direction, let $y = f(x)$ where $f: [0,1]$ is a nonnegative function with derivatives $\dot{f}(x) = df(x)/dx$ and $\ddot{f}(x) = d^2f(x)/dx^2$ and such that $f(1) = 0$; $-1 \leq \dot{f}(1) \leq 0$ and let us examine the behaviour of $\hat{\theta} = (1-x-f(x))/2\sqrt{xf(x)}$ and Q as $x \rightarrow 1$. As a direct consequence of L'Hospital's rule we get:

$$\lim_{x \rightarrow 1} \frac{1-x-f(x)}{2\sqrt{xf(x)}} = \begin{cases} 0 & \text{if } \dot{f}(1) \neq 0 \\ [2\ddot{f}(1)]^{-1/2} & \text{if } \dot{f}(1) = 0 \text{ and } \ddot{f}(1) \neq 0 \\ - & \text{if } \dot{f}(1) = 0 \text{ and } \ddot{f}(1) = 0 \end{cases} \quad (18)$$

In particular, note that if $f(x) = (\sqrt{1+(\theta_0^2-1)x} - \theta_0\sqrt{x})^2$, $\theta_0 \geq 0$ fixed, so that as $x \rightarrow 1$, $(x,y) \rightarrow (1,0)$ along the curves corresponding to $\hat{\theta} = \theta_0$, constant, we have $\lim_{x \rightarrow 1} \hat{\theta} = \theta_0$. Next write $A(x) = 1-x-f(x)$ and $B(x) = A(x)\{x+f(x)\} + 4xf(x)$ so that:

$$Q = 16n x^2 \left\{ \frac{1-x-y}{2\sqrt{xy}} - 1 \right\}^2 \left\{ \frac{f^2(x)}{A(x)B(x)} \right\} \quad (19)$$

Applying L'Hospital's rule to the last term in (19) we obtain:

$$\lim_{x \rightarrow 1} \frac{f^2(x)}{A(x)B(x)} = - \frac{\dot{f}^2(1)}{[3\dot{f}(1)-1][\dot{f}(1)+1]} \quad (20)$$

Then, from (17)-(20) we may conclude that:

$$\lim_{x \rightarrow 1} Q = \begin{cases} 0 & \text{if } \dot{f}(1) = 0 \text{ and } \ddot{f}(1) \neq 0 \\ \frac{16n \dot{f}^2(1)}{[3\dot{f}(1)-1][\dot{f}(1)+1]} & \text{if } \dot{f}(1) \neq 0 \\ - & \text{if } \dot{f}(1) = \ddot{f}(1) = 0 \end{cases} \quad (21)$$

Next, consider the statistic (14) which may be expressed

as:

$$Q_L = n \{ \log(1-x-y) - \log 2 - \frac{1}{2} \log x - \frac{1}{2} \log y \}^2 \left(\frac{1}{4x} + \frac{1}{4y} + \frac{1}{1-x-y} \right)^{-1} \quad (22)$$

An expansion of the squared term in (22) is sufficient to indicate that the limiting behaviour of Q_L is essentially determined by the behaviour of functions of the form $h(x,y) = g(x,y) \left\{ \frac{1}{4x} + \frac{1}{4y} + \frac{1}{1-x-y} \right\}^{-1}$ where $g(x,y) = \log x$, $g(x,y) = \log^2 x$ or $g(x,y) = \log x \log y$ as $(x,y) \rightarrow (0,p)$, $0 \leq p \leq 1$ or $(x,y) \rightarrow (p,1-p)$, $0 < p < 1$. Clearly $h(x,y) \rightarrow 0$ as $(x,y) \rightarrow (p,1-p)$, $0 < p < 1$. Using the fact that for $a > 0$, $x(\log x)^a \rightarrow 0$ as $x \rightarrow 0$, it is easy to see that $h(x,y) \rightarrow 0$ as $(x,y) \rightarrow (0,p)$, $0 < p < 1$. Now, using the inequality $0 \leq g(x,y) \left\{ \frac{1}{4x} + \frac{1}{4y} + \frac{1}{1-x-y} \right\}^{-1} \leq 4xg(x,y)$, it follows that $h(x,y) \rightarrow 0$ as $(x,y) \rightarrow (0,0)$ or $(x,y) \rightarrow (0,1)$ for $g(x,y) = \log x$ or $g(x,y) = \log^2 x$. Finally, note that the case $\log x \log y \left\{ \frac{1}{4x} + \frac{1}{4y} + \frac{1}{1-x-y} \right\}^{-1} \rightarrow 0$ as $(x,y) \rightarrow (0,0)$ or $(x,y) \rightarrow (0,1)$ is somewhat more elaborate, but the result may be obtained by writing $x = r \cos \phi$, $y = r \sin \phi$, $0 \leq \phi \leq \pi/2$ and letting $r \rightarrow 0$.

From the above discussion we may conclude that both Q and Q_L may converge to zero in situations which clearly violate the equilibrium hypothesis, indicating that such statistics should be used with caution; more specifically, they are not recommended in cases where the observed phenotype proportions are close to 0 or 1. Although a similar analysis for the general case is mathematically intractable, we believe that the corresponding Wald statistics have the same type of aberrant behaviour.

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