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Genetic Screening and Price Discrimination in Insurance Markets

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Abstract

Basing insurance prices on the results of an imperfect screening test to identify risk types can reduce or increase aggregate discrimination across insureds. We present a powerful and general new framework of analysis to examine this issue, drawing upon recent work which uses decomposable inequality indices to measure vertical and horizontal inequity in taxation. We find that, whilst improved test performance inevitably reduces vertical discrimination (in the average prices faced by different risk types), even very accurate tests can lead to substantial horizontal discrimination (within risk types) and enhanced overall discrimination. These conclusions are shown to be robust to a range of different value judgements about how to aggregate individual discriminatory effects and to be particularly relevant to the case of genetic screening.

Key words: insurance, genetic information, discrimination

1. Introduction

There is substantial debate about the fairness of insurance companies using results from genetic screening tests to determine the price of insurance. On the one hand are those who feel individuals should not be charged different rates for health, life or disability insurance on the basis of unalterable and inherited genes,[1] while others note that insurers should not be required to carry substantially higher risks at what would effectively be subsidized rates. If one adopts a standard economic view of price discrimination, it may seem clear that prices should reflect differences in expected costs of insureds. For example, consider the following standard definition of price discrimination:

> "Discrimination may be said to occur in a market where individuals face terms of trade that are determined by personal characteristics *which do not appear directly relevant to the transaction.*"
>
> (our italics)... Mueser, (1989, p. 856)

Since insurance prices are based on actuarial principles the following definition seems natural:

> "An insurance rate structure will be considered to be unfairly discriminatory ... if, allowing for practical limitations, there are premium differences that do not correspond to expected losses and average expenses or *if there are expected average cost differences that are not reflected in premium differences.*"
>
> (our italics)... Williams (1969, pp. 211–212)

Thus, it might seem that the use of genetic testing, which provides finer information on expected cost differences for providing insurance to different individuals, would be clearly justified on the grounds of reducing *unfair* price discrimination.

We will argue in this paper that such a conclusion is not obvious if one considers carefully how to measure the impact on discrimination from using imperfect information to classify insureds. By adapting standard indices of inequality to measure the dispersion in price-cost differentials and applying recent concepts from the literature on vertical and horizontal equity within taxation,[2] we show that an improvement in the quality of information used to assign individuals to risk classes does not necessarily reduce the aggregate amount of discrimination. As we shall show, if one presumes that the elemental measure of the degree of discrimination resulting from charging a price different from (expected) cost should be convex in the price/cost ratio, then a more informative signal of risk type may increase the aggregate amount of price discrimination.

The essence of the analysis in this paper stems from the fact that, although using a more informative (yet not perfect) signal to assign individuals to their true risk classes improves the accuracy of the assignments, it also means that those who are misclassified face a greater price-cost differential in insurance. Average price differences between different risk classes better reflect actual expected cost differences when a more informative signal is used. However, since a more informative signal leads to a greater price differential between risk classes, those individuals who are assigned to inappropriate risk classes face a higher degree of price discrimination than they would if a less informative signal were used. There is some previous research that has addressed the relationship between imperfect classification and price discrimination.[3] Our contribution to this research stems from the way we separate horizontal and vertical components of fairness and treat more explicitly the issue of how to aggregate over individuals to obtain an overall measure of price discrimination.

2. The anatomy of price discrimination: A general model

First we present our general characterization for measuring and decomposing the extent of price discrimination under imperfect categorization. In the following sections we will apply this general theory to the particular case of a genetic screening test for a single disease gene.

According to our basic concept of price discrimination, as outlined in the introduction of the paper, the elemental measure of price discrimination faced by an individual of a given risk type is founded on the relationship between the price that person is charged and the expected cost of coverage the person imposes on the insurer. Let C_i be the expected cost to the insurance company from insuring individuals of risk type i. In particular, this will reflect the cost of standard health care for an individual and will be higher for those who possess a

particular disease gene. Let test outcomes be indexed by j and let P_{ij} be the prices charged to persons whose true type is i and who receive test result j and let N_{ij} be the number of individuals in each of these scenarios. We will assume a competitive insurance market in which firms charge actuarially fair prices conditional on the information available.[4] Thus, summing over individuals of each risk type i as they are assigned to each risk category j, the following overall constraint is ensured by actuarial fairness of premiums across test outcomes:

$$\sum_i \sum_j N_{ij} P_{ij} = \sum_i N_i C_i \tag{1}$$

where N_i is the number of persons of type i in the population.

Our elemental measure of price discrimination is the extent to which price differs from expected cost to the insurer in ratio form. Thus we use the variable $r_{ij} = P_{ij}/C_i$ to capture the extent of price discrimination when an individual of type i is assigned to risk category j and charged the relevant price. In these terms Eq. (1) can be expressed as:

$$\sum_i \left\{ \sum_j N_{ij} r_{ij} - N_i \right\} C_i = 0 \tag{2}$$

Under actuarially fair risk-type specific pricing, we have $r_{ij} = 1$, $\forall i$, $\forall j$. This is the condition for zero total price discrimination:

$$TD = 0 : r_{ij} = 1, \quad \forall i, \forall j \tag{3}$$

Horizontal discrimination (henceforth *HD*) occurs if like individuals are treated differently. For horizontal discrimination to be zero, we require that

$$HD = 0 : r_{ij} \text{ independent of } j, \quad \forall i \tag{4}$$

Vertical discrimination (henceforth *VD*) occurs between groups if the average price charged to members of a particular risk type i deviates from the expected cost of insuring members of that group. For vertical discrimination to be zero, we require that

$$VD = 0 : \sum_j N_{ij} r_{ij} = N_i, \quad \forall i \tag{5}$$

Note that if (3) is true, so are (4) and (5): that is; $TD = 0$ implies both $VD = 0$ and $HD = 0$. However, it is possible for one of $VD = 0$ or $HD = 0$ without $TD = 0$. For example, charging everyone the same price for insurance in an environment with different risk types implies that $HD = 0$, but neither $VD = 0$ nor $TD = 0$.

The variable r_{ij} is the ratio of price to expected cost to the insurer for an individual who is of risk type i with test result j. This is a sensible value in terms of which to measure the extent to which an individual is assessed a fair or nondiscriminatory price.[5] However, it is less clear how one ought to aggregate over individuals to determine an overall measure of

price discrimination. Taking an intuition from the measurement of income inequality, one may wish to apply increasing weight to greater differences in this ratio.[6] In general terms then, defining $\mathbf{r}_{ij}$ as the vector of all r_{ij} values for all individuals in the population, we can aggregate the extent to which the P_{ij}/C_i values vary (from 1) by using an inequality index $I[\mathbf{r}_{ij}]$ which is convex in the arguments $\mathbf{r}_{ij}$.

Let $\mathbf{r}_{ij} \mid i$ represent the vector of price/cost ratios faced by individuals of a given type but assigned (possibly) to different risk categories. So, for example, if there were five individuals of a given risk type (say type #1), with three of them assigned to risk category one and the remaining two assigned to risk category two, then the vector $\mathbf{r}_{ij}|i, i = 1$, would be the vector $(r_{11}, r_{11}, r_{11}, r_{12}, r_{12})$. $\sum_j \mathbf{r}_{ij}/N_i$ is the vector formed by averaging price/cost ratios for a given risk type i over the various risk categories to which they are assigned. This vector will then be composed of the average price-cost ratios for each risk type. Thus, following the intuition from the inequality measurement literature, it is natural to define total and vertical price discrimination as

$$TD = I[\mathbf{r}_{ij}] \tag{6}$$

and

$$VD = I\left[\sum_j \mathbf{r}_{ij}/N_i\right] \tag{7}$$

respectively. Horizontal discrimination locally (within type i) is defined as

$$HD_i = I[\mathbf{r}_{ij} \mid i] \tag{8}$$

and horizontal discrimination globally as

$$HD = \sum_i w_i HD_i \tag{9}$$

where w_i is the proportion of the population which is of type i ($w_i = N_i/N$ where $N = \sum_i N_i = \sum_i \sum_j N_{ij}$).

The natural inequality indices $I[\cdot]$ to use in such an analysis come from the so-called generalized entropy (GE) family, because of their decomposability properties [Bourguignon, 1979; Cowell, 1980; Shorrocks, 1980, 1984]. In fact these—and monotonic transformations of them—are the only indices of relative inequality to enjoy a 'subgroup consistency' property, according to which overall inequality necessarily falls if it does so in a subgroup [Shorrocks, 1984], and this will be an essential property for our analysis. All such transformations satisfy the principle of transfers and scale invariance. The GE family itself, uniquely, has the decomposability property according to which overall inequality can be decomposed additively into between-groups inequality and a weighted sum of within-group inequalities. The weights are independent of group income levels, or price/cost ratios in our case, only in the case of the mean logarithmic deviation. First, however, we argue that

all of the above mentioned properties of an inequality measure are desirable for a measure of price discrimination.

The principle of transfers requires that, for any pair of values u,v where $u < v$, if u (the lower value) is reduced by some amount while v (the higher value) is increased by an equal amount, then the index $I[\cdot]$ must increase.[7] In fact, any convex function $I[\cdot]$ would satisfy this property, not only the decomposable indices we are interested in. This is an intuitively pleasing property when measuring the dispersion of price/cost ratios since it seems natural that an individual's perceived cost or harm from facing a higher price than is actuarially fair would be increasing at an increasing rate in this ratio much as it is generally accepted within inequality analysis that the cost of inequality should be a convex function of the analogous quantities. Scale invariance requires that the relative degree of dispersion in price/cost ratios is not changed if one multiplies the entries of the vector by any positive constant. This implies, for example, that if the price faced by all individuals were to rise by the same percent, the aggregate relative dispersion in price/cost ratios would remain unchanged.[8] Subgroup consistency would record a higher total discrimination if, hypothetically, for one type the degree of discrimination were increased and no change were made elsewhere.

The advantage of full decomposability is that it permits an additional subdivision of overall discrimination into vertical and aggregate (global) horizontal components, the latter itself a weighted sum of local horizontal discriminations. To see this, just note that inequality in the vector $\mathbf{r}_{ij}$ used to measure discrimination is made up of the inequalities in the vectors $\mathbf{r}_{ij} \mid i$ and $\sum_j \mathbf{r}_{ij}/N_i$, when the groups are defined by the index i, and that the between groups contribution is defined by inequality in the distribution of within-group averages. For the GE family, then, a decomposition of total discrimination of the form $TD = VD + \sum_i \theta_i HD_i$ is achieved, where the θ_i values are aggregation weights. We state these results formally below.[9]

Theorem 1: *A continuous inequality measure $I[\mathbf{r}_{ij}]$ satisfies the principle of transfers, scale invariance and decomposability, if and only if it is a member of the generalized entropy family; i.e.,*

$$I[\mathbf{r}_{ij}] = \left(\frac{1}{\alpha^2 - \alpha}\right)\left(\frac{1}{N}\right)\left[\sum_i \sum_j r_{ij}^{\alpha} - 1\right]$$

for some $\alpha \in (-\infty, +\infty), \alpha \neq 1, 0$ (see on for other formulae for $\alpha = 1, 0$). The formulae for decomposing the measures into horizontal and vertical components is $TD = VD + HD = VD + \Sigma_i \theta_i HD_i$ where

$$VD = I\left[\sum_j \mathbf{r}_{ij}/N_i\right] = \left(\frac{1}{\alpha^2 - \alpha}\right)\left[\sum_i \frac{1}{N_i}\overline{r_i}^{\alpha} - 1\right]$$

$$HD_i = I[\mathbf{r}_{ij} \mid i] = \left(\frac{1}{\alpha^2 - \alpha}\right)\left(\frac{1}{N_i}\right)\left[\sum_j r_{ij}^{\alpha} - 1\right], \forall i$$

$$\theta_i = \left(w_i^{\alpha}\right)\left(v_i^{1-\alpha}\right)$$

where $\bar{r}_i$ *is the average price/cost ratio faced by individuals of risk type* i, $w_i = \frac{N_i}{N}$, *and* $v_i = \frac{\sum_j r_{ij}}{\sum_i \sum_j r ij}$. *In the case of* $\alpha = 1$ *the functional form for* $I[\mathbf{r}_{ij}]$ *becomes*

$$I[\mathbf{r}_{ij}] = \left(\frac{1}{N}\right) \sum_i \sum_j \ln\left(\frac{1}{r_{ij}}\right)$$

and aggregation for HD is performed using population weights $\theta_i = w_i$. *In the case of* $\alpha = 0$ *the functional form for* $I[\mathbf{r}_{ij}]$ *becomes*

$$I[\mathbf{r}_{ij}] = \left(\frac{1}{N}\right) \sum_i \sum_j r_{ij} \ln\left(r_{ij}\right)$$

and aggregation for HD is performed using the weights $\theta_i = v_i$ (*i.e., the average rate of the price/cost ratios within each group*).[10]

Aggregation using population weights is perhaps the most appealing on intuitive grounds. However, by insisting on such a weighting scheme, along with the other requirements mentioned in the theorem, we effectively adopt the logarithmic function as our particular normative standard for comparing deviations of price/cost ratios among individuals. By admitting weights which are not the population weights, we allow ourselves a wider range of relative sensitivities concerning the impact of deviations of price/cost ratios on our aggregate assessment of price discrimination. In particular, a choice of $\alpha < 2$ places more emphasis on lower values of price/cost ratios while $\alpha > 2$ places more emphasis on higher values of price/cost ratios.[11] When measuring the overall inequality of incomes it is natural to place more emphasis on lower incomes. However, it is perhaps more compelling in the present context to express increasing concern with higher price/cost ratios since the higher is the ratio $r_{ij} = P_{ij}/C_i$, the greater is the degree of *unfavourable* price discrimination. We will explore this issue in Section 6.

3. An application to genetic testing

Consider the implications of genetic testing for a simple, single gene disorder. We will model a stylized view of the relationship between genes and a disease, or risk of a person incurring the disease, which applies in a strict sense to only a few diseases.[12] However, expanding the perspective on the relationship between genes and susceptibility to disease to better reflect the reality of many diseases will only strengthen our argument; we discuss this aspect later in the paper.

Let $i = h, l$ indicate the true risk type of a person, with a person of type h (high risk) possessing the disease gene and a person of type l (low risk) having the "normal or healthy" gene. Let $j = p, n$ denote the test result: p for a positive result and n for a negative result. A person who tests positive for the gene is placed into the high risk category and charged price P_p and a person who tests negative is placed into the low risk category and charged price P_n. We presume that the expected cost imposed on an insurer by a person of risk

type i is C_i, with $C_h > C_l$, and so with actuarially fair pricing based on test results we have $P_p > P_n$. Imperfect testing (i.e., the presence of false negative and false positive test results) implies $C_h > P_p > P_n > C_l$. Thus, we need to consider four situations for individuals: (i) high risk types who test positive and face price/cost ratio P_p/C_h, ii) high risk types who test (false) negative and face price/cost ratio P_n/C_h, iii) low risk types who test (false) positive and face price/cost ratio P_p/C_l, and iv) low risk types who test negative and face price/cost ratio P_n/C_l, where $P_p/C_l > P_n/C_l > 1 > P_p/C_h > P_n/C_h$. Recall that zero price discrimination would require $P_i/C_j = 1$ for each i and j.

If an individual possesses the disease gene then her probability of incurring the disease in the insurance period is higher than it otherwise would be. For now, we presume that the only determinant of the disease, given current knowledge, is whether the individual possesses the gene or not. A genetic test provides imperfect information. The degree of informativeness of the test can be summarized by the false positive and false negative rates inherent in the test. The higher either the false positive or false negative rate, the less is the information value of the test. The following variables describe the relevant parameters in the population and for the genetic test:

$\varepsilon_{fn}, \varepsilon_{fp}$ are the rates of false negatives and positives, respectively, associated with the test;

π_{ji} is the probability that a person of risk type $i = h, l$ would receive test result $j = p, n$;

π^{ij} is the probability that a person who receives test result $j = p, n$ is of risk type $i = h, l$;[13]

q_h, q_l are the proportions of the population that are of risk types h, l respectively.

It is presumed that high risk types impose higher average or expected costs on the insurance company than do low risk types. Depending on the disease, this cost differential could exist for one or all of the areas of health, life and disability insurance. We will assume, for the sake of discussion, that the application concerns health insurance.

As noted earlier, we assume that the insurance industry is competitive and that insurers are risk neutral: they price according to the actuarial costs of providing insurance.

Thus, we have the following relationships among these variables:

$$\pi_{ph} = 1 - \varepsilon_{fn}, \quad \pi_{nh} = \varepsilon_{fn}, \quad \pi_{pl} = \varepsilon_{fp}, \quad \pi_{nl} = 1 - \varepsilon_{fp} \tag{10}$$

and since the π^{ij}'s are the complementary probabilities of the π_{ji}'s, we can use Bayes' theorem to derive:

$$\pi^{hp} = \frac{q_h \pi_{ph}}{q_h \pi_{ph} + q_l \pi_{pl}} \tag{11}$$

$$\pi^{hn} = \frac{q_h \pi_{nh}}{q_h \pi_{nh} + q_l \pi_{nl}} \tag{12}$$

$$\pi^{lp} = \frac{q_l \pi_{pl}}{q_h \pi_{ph} + q_l \pi_{pl}} \tag{13}$$

$$\pi^{ln} = \frac{q_l \pi_{nl}}{q_h \pi_{nh} + q_l \pi_{nl}} \tag{14}$$

In generating our pricing equations we assume all individuals purchase the same amount of insurance regardless of whether genetic testing is used in setting prices. If individuals

have better information concerning their risk type than do insurers, then one would expect adverse selection to arise, with high risk types purchasing more insurance than low risk types.[14] For now, we assume all individuals purchase full insurance coverage regardless of their information set and the price they face. In a pooling equilibrium, in which individuals with different information sets facing the same price purchase different amounts of insurance, the same qualitative aspects of our results would still apply. We return to this issue in Section 6 also. Under the condition of equal insurance purchases, the actuarially fair price of insurance with no ratemaking using results from genetic testing will be P_0 where

$$P_0 = q_h C_h + q_l C_l \tag{15}$$

If genetic testing prevails and insurers are allowed to charge prices according to test results, then (pooled) actuarially fair pricing leads to

$$P_p = \pi^{hp} C_h + \pi^{lp} C_l \tag{16}$$
$$P_n = \pi^{hn} C_h + \pi^{ln} C_l \tag{17}$$

where P_p and P_n are the prices for those who test positive and negative respectively.

To examine the issue of vertical price discrimination we need to determine the average price faced by individuals of each risk type, which includes both individuals who are properly classified and those who are not. The average prices faced by individuals of risk types $i = h, l$,$\bar{P}_i$, are given in the two equations below:

$$\bar{P}_h = \pi_{ph} P_p + \pi_{nh} P_n \tag{18}$$
$$\bar{P}_l = \pi_{pl} P_p + \pi_{nl} P_n \tag{19}$$

Turning to the measurement of discrimination, for the mean logarithmic deviation (henceforth MLD), which is the case of $\alpha = 1$ in Theorem 1, total discrimination (or inequality in price/cost ratios) is:

$$TD = \ln(E[r]) - E[\ln(r)] \tag{20}$$

where r refers to a generic price/cost ratio and expectations are taken over the entire population. Since the joint probability that a person is of risk type i $(i = h, l)$ and assigned to risk category j (i.e., receives test result $j = p, n$) is $q_i \cdot \pi_{ji}$, we have

$$E[r] = q_h \pi_{ph} r_{hp} + q_h \pi_{nh} r_{hn} + q_l \pi_{pl} r_{lp} + q_l \pi_{nl} r_{ln} \tag{21}$$

and

$$E[\ln(r)] = q_h \pi_{ph} \ln(r_{hp}) + q_h \pi_{nh} \ln(r_{hn}) + q_l \pi_{pl} \ln(r_{lp}) + q_l \pi_{nl} \ln(r_{ln}) \tag{22}$$

Vertical discrimination measures the extent to which the average price to cost ratio varies between groups:

$$VD = \ln E[\bar{r_i}] - E[\ln(\bar{r_i})] \tag{23}$$

where $\bar{r_i}$ is the average price/cost ratio for individuals of type i. We have

$$E[\bar{r_i}] = q_h \frac{\bar{P_h}}{C_h} + q_l \frac{\bar{P_l}}{C_l} \tag{24}$$

and

$$E[\ln(\bar{r_i})] = q_h \ln\left(\frac{\bar{P_h}}{C_h}\right) + q_l \ln\left(\frac{\bar{P_l}}{C_l}\right) \tag{25}$$

Horizontal discrimination for risk type i is the amount of discrimination for that population subgroup; one measures it just as one measures total discrimination:

$$HD_i = \ln(E[r_i]) - E[\ln(r_i)], \quad i = h, l \tag{26}$$

where r_i is the price faced by risk type i individuals (depending on which risk category they are assigned to), hence:

$$E[r_i] = \pi_{pi} \frac{P_p}{C_i} + \pi_{ni} \frac{P_n}{C_i}, \quad i = h, l \tag{27}$$

and

$$E[\ln(r_i)] = \pi_{pi} \ln\left(\frac{P_p}{C_i}\right) + \pi_{ni} \ln\left(\frac{P_n}{C_i}\right), \quad i = h, l \tag{28}$$

Globally, horizontal discrimination is the population weighted average of horizontal discrimination within each risk group:

$$HD = q_h HD_h + q_l HD_l \tag{29}$$

From Theorem 1 we know that

$$TD = VD + HD \tag{30}$$

We are interested to explore how all components of total discrimination (i.e., *VD*, *HD* and its constituents HD_h and HD_l), as well as the total itself, are affected by changing the quality of the screening test. We do this in the next section, where, first, we show that for any of the family of measures that appear in Theorem 1, a higher quality test (i.e., a test with a lower false positive and/or false negative rate) always reduces vertical discrimination. Then we

examine the question of the effect of the quality of the test on horizontal discrimination, which is more complex.

For the other measures of the GE family specified in Theorem 1, expressions corresponding to (20), (23) and (26) (for $\alpha \neq 1$) generate *TD*, *VD* and the $HD_i, i = h, l$ whilst (29) needs modified weights, and then (30) again holds. The same questions as for the MLD can be explored in this more general context, concerning the effect of test quality changes.

4. Test quality and price discrimination

From Eqs. (16) through (19) it is straightforward to see that $C_h > \bar{P}_h > \bar{P}_l > C_l$. That is, on average high risk types pay a price which is less than the expected cost they impose on the insurer but more than do low risk types who in turn pay a price which is greater than the price they impose on the insurer. So vertical discrimination occurs due to the fact that $\frac{\bar{P}_h}{C_h} < 1$ and $\frac{\bar{P}_l}{C_l} > 1$. If a higher quality test (i.e., lower value of ε_{fn} and/or ε_{fp}) leads to an increase in $\bar{P}_h$ and a decrease in $\bar{P}_l$ then vertical discrimination will be reduced for any of the inequality measures with properties as described in Theorem 1.[15] To show that this is indeed the case, we need to investigate how the values of the probabilities π^{ij} and π_{ji} and the prices P_p and P_n are affected by changes in the false positive and false negative rates ε_{fn} and ε_{fp}.

From Eq. (10) the following are obvious:

$$\frac{\partial \pi_{ph}}{\partial \varepsilon_{fn}} = \frac{\partial \pi_{nl}}{\partial \varepsilon_{fp}} = -1, \quad \frac{\partial \pi_{nh}}{\partial \varepsilon_{fn}} = \frac{\partial \pi_{pl}}{\partial \varepsilon_{fp}} = 1, \quad \frac{\partial \pi_{nl}}{\partial \varepsilon_{fn}} = \frac{\partial \pi_{pl}}{\partial \varepsilon_{fn}} = \frac{\partial \pi_{ph}}{\partial \varepsilon_{fp}} = \frac{\partial \pi_{nh}}{\partial \varepsilon_{fp}} = 0 \tag{31}$$

Using these results and Eqs. (11) through (14), a little algebra gives the following comparative statics results for the complementary probabilities π^{ij} (actual values of the derivatives appear in the Appendix):

$$\frac{\partial \pi^{hp}}{\partial \varepsilon_{fn}}, \frac{\partial \pi^{hp}}{\partial \varepsilon_{fp}}, \frac{\partial \pi^{ln}}{\partial \varepsilon_{fn}}, \frac{\partial \pi^{ln}}{\partial \varepsilon_{fp}} < 0; \quad \frac{\partial \pi^{hn}}{\partial \varepsilon_{fn}}, \frac{\partial \pi^{hn}}{\partial \varepsilon_{fp}}, \frac{\partial \pi^{lp}}{\partial \varepsilon_{fn}}, \frac{\partial \pi^{lp}}{\partial \varepsilon_{fp}} > 0 \tag{32}$$

The comparative statics results for the effects of changes of the false positive and false negative rates on the prices paid by those who test positive and negative for the disease gene can also be derived. Again, see the Appendix for the values of these partial derivatives. These results are required to understand the effects of changes in the accuracy of the screening test on average prices paid by members of each risk type, but also they will be of use later in the paper when we consider horizontal discrimination:

$$\frac{\partial P_p}{\partial \varepsilon_{fn}}, \frac{\partial P_p}{\partial \varepsilon_{fp}} < 0, \quad \frac{\partial P_n}{\partial \varepsilon_{fn}}, \frac{\partial P_n}{\partial \varepsilon_{fp}} > 0 \tag{33}$$

These results indicate that a test with a higher rate of false negatives leads to (i) an increase in the price paid by those who test negative, since that group will have a higher proportion

of individuals who are actually high risk types, and (ii) a decrease in the price paid by those who do test positive since more individuals who are high risk types are in fact being placed in the other category (i.e., the "negative" category).[16] Also, a test with a higher rate of false positives leads to (i) a decrease in the price paid by those who test positive, since that group will have a higher proportion of individuals who are actually low risk types, and (ii) an increase in the price paid by those who test negative since more individuals who are low risk types are in fact being placed in the other category (i.e., the "positive" category).[17]

The relationships between the rates of false negatives and false positives and the average price paid by individuals of a given risk type, however, are less clear intuitively. Consider, for example, the impact of an increased rate of false negatives on the average price paid by high risk types. Since $P_p > P_n$, the fact that more h-types are assigned to the "negative category" and fewer to the "positive category" implies a reduction in the average price paid by h-types. Similarly, an increased rate of false positives implies a reduction in the average price paid by those who are assigned to the "positive category." However, there is also an increase in the price of insurance paid by those in the "negative category" and this, in conjunction with the fact that the likelihood of being assigned to this category is higher, has an opposite effect on $\bar{P}_h$.

It turns out, though, that the overall effect of an increase in the rate of false negatives is a reduction in the average price of insurance paid by high risk types, which implies a greater degree of price discrimination for this group. Similar results apply with respect to the relationships between the average price paid by individuals of either risk group and the rates of false positives and negatives. All of these results are stated in the following theorem. Due to the amount of algebra required, they are proved in the Appendix.

Theorem 2: *A more accurate screening test reduces the average price paid by members of the low risk group and increases the average price paid by members of the high risk group, thus reducing the overall degree of vertical price discrimination.*

We now turn our attention to the relationship between the accuracy of the screening test and the degree of horizontal discrimination. If no screening test or equivalently a completely uninformative one is used, then all individuals are treated the same and so there is no horizontal discrimination. Alternatively, if a perfectly informative screening test is available and used for pricing insurance, then individuals of any risk type i are charged the same price (i.e., their risk-type specific actuarially fair price, $P_i = C_i$) and so in this case again there is no horizontal discrimination. Hence, in between, any imperfect screening test leads to some horizontal discrimination even if the test is almost perfectly accurate. An improvement in the accuracy of an imperfect screening test will in some cases increase and in other cases decrease the degree of horizontal discrimination. The effects of increased accuracy of a screening test on the components affecting the degree of horizontal discrimination are multifaceted and so, not surprisingly, the overall directional effect on *HD* cannot be predicted unambiguously.

Consider, for example, the low risk types. Some are misclassified (i.e., receive false positive tests) and pay the price P_p, while others are properly classified (i.e., receive true negatives) and pay the price P_n; the range of price-cost ratios for this group is $(r_{ln}, r_{lp}) =$

$(\frac{P_n}{C_l}, \frac{P_p}{C_l})$. Increasing the accuracy of the test leads to an increase in P_p and a decrease in P_n, widening this range, implying greater inequality or price discrimination for this group. However, this increase in accuracy also reduces the fraction of l-types who pay price P_p and increases the fraction who pay price P_l and reduces the average price to cost ratio for this group (i.e., $\frac{\bar{P}_l}{C_l}$) too. Thus, the net result of an increase in the accuracy of the test can be either to increase or decrease horizontal equity for the low risk group. Similar arguments apply to the high risk group. Our simulations in the next section confirm this and provide us with insight on how the accuracy of a screening test is related to the degrees of horizontal and overall discrimination. Of particular interest is the relationship between parameter values, which should reflect the reality of genetic testing and genetic diseases, and the effect of changing the parameter α, which reflects one's values about the degree of horizontal discrimination for the various groups of individuals in society.

5. Simulation results for changes in test accuracy

In our simulations we consider a number of different measures of discrimination based on the entropy family presented in Sections 2 and 3 of this paper. But first we further develop some intuition concerning the relationship between the amount of horizontal discrimination and the accuracy of genetic tests.

Consider the situation of low risk types facing an imperfect screening test. The degree of horizontal discrimination for l-types is represented by the inequality in their price-cost ratios as follows:

$$HD_l = I\left(\frac{P_n[\downarrow]}{C_l}, \frac{P_p[\uparrow]}{C_l}\right) = I\left(r_{ln}[\downarrow], r_{lp}[\uparrow]\right)$$

The arrows indicate the direction of the change in price or price-cost ratios resulting from an increase in the degree of accuracy of a screening test. This results in increased dispersion in prices paid by l-types who are properly classified versus those who are misclassified and so increases horizontal discrimination. One must remember, however, that the proportion of those l-types who are misclassified falls, while the proportion of properly classified l-types rises, with increased test accuracy (i.e., π_{pl} falls while π_{nl} rises) which can counterbalance the first effect mentioned. In the limit, as the test becomes perfectly accurate $\pi_{pl} \to 0$ and $\pi_{nl} \to 1$ and horizontal discrimination for l-types vanishes altogether.

A similar analysis applies to the high risk types, with:

$$HD_h = I\left(\frac{P_n[\downarrow]}{C_h}, \frac{P_p[\uparrow]}{C_h}\right) = I\left(r_{hn}[\downarrow], r_{hp}[\uparrow]\right)$$

As the accuracy of a test improves, the proportion of those h-types who are misclassified falls, while the proportion properly classified rises, (i.e., π_{nh} falls while π_{ph} rises) and in the limit, as the test becomes perfectly accurate $\pi_{np} \to 0$ and $\pi_{ph} \to 1$ and so horizontal discrimination for h-types vanishes.

Overall horizontal price discrimination is

$$HD = q_h HD_h + q_l HD_l$$

By noting the relative values of the price-cost ratios for both types, we can better understand the overall implications for horizontal price discrimination as it relates to the accuracy of the test and the choice of measure $I(\cdot)$; that is:

$$r_{hn}[\downarrow] < r_{hp}[\uparrow] < r_{ln}[\downarrow] < r_{lp}[\uparrow]$$

Again, the arrows indicate the direction of changes resulting from a more accurate test. A given Mendelian or purely genetic disease tends to afflict a very small fraction of the population and so q_l is generally much larger than q_h, leading to a substantially higher weight being placed on l-types. Moreover, in the context of a genetic testing scenario, the difference $r_{lp} - r_{ln}$ is likely to be large and increasing in the accuracy of the test and so it is this difference which will tend to dominate the overall horizontal equity implications of imperfect categorization. From a normative standpoint as well, it makes sense to place concern more towards individuals most heavily penalized by being misclassified. These are the low risk types who face the highest price-cost ratio. In choosing a specific member of the entropy family of inequality measures, the larger is the value of the parameter α, the greater is the emphasis on horizontal discrimination within the l-types (i.e., the more sensitive is the measure to variability in the higher end of the vector of price-cost ratios). Thus, both the facts about genetic diseases and our normative concerns about misclassification arising from imperfect categorization lead to a conclusion that, even though vertical price discrimination is always reduced by using a more accurate genetic test for pricing insurance, horizontal price discrimination generated by misclassification of low risk types will be a greater concern. This is borne out by our simulation results which we now describe.

Our first simulation result, depicted in figure 1, was computed using the MLD (mean logarithmic deviation) measure of discrimination. Recall that this is equivalent to a choice of parameter value $\alpha = 1$ for the generalized entropy family of inequality measurement and such a choice implies relatively greater emphasis on dispersion between smaller values of price-cost ratios. Thus, this represents relatively less concern with misclassification among l-types than among h-types. The parameter values chosen for population proportions are $q_h = 0.001$ and $q_l = 0.999$, also reflecting a conservative view of the relative importance of low-risk types in the population.[18] The relative expected costs of insurance are $c_h = 50{,}000$ and $c_l = 2{,}000$. In the context of health insurance this would represent a situation in which those with the genetic disease will face substantial costs for medical treatment. In the context of disability insurance these parameter values reflect a very high probability of loss of income. Since the range of genetic diseases generates a wide range of costs there is no natural choice for such parameters. In a later simulation we consider a case with much more similar costs for the two types.

To simplify the graphical analysis, we represent the accuracy of the test by a choice of false positive and negative rates which are equal (i.e., $\varepsilon_{fp} = \varepsilon_{fn}$), thus allowing us to use a two dimensional graph. A decrease in ε_{fp}, the rate of false positives, represents an increase in the accuracy of the test. As previously noted, if the test is either completely uninformative

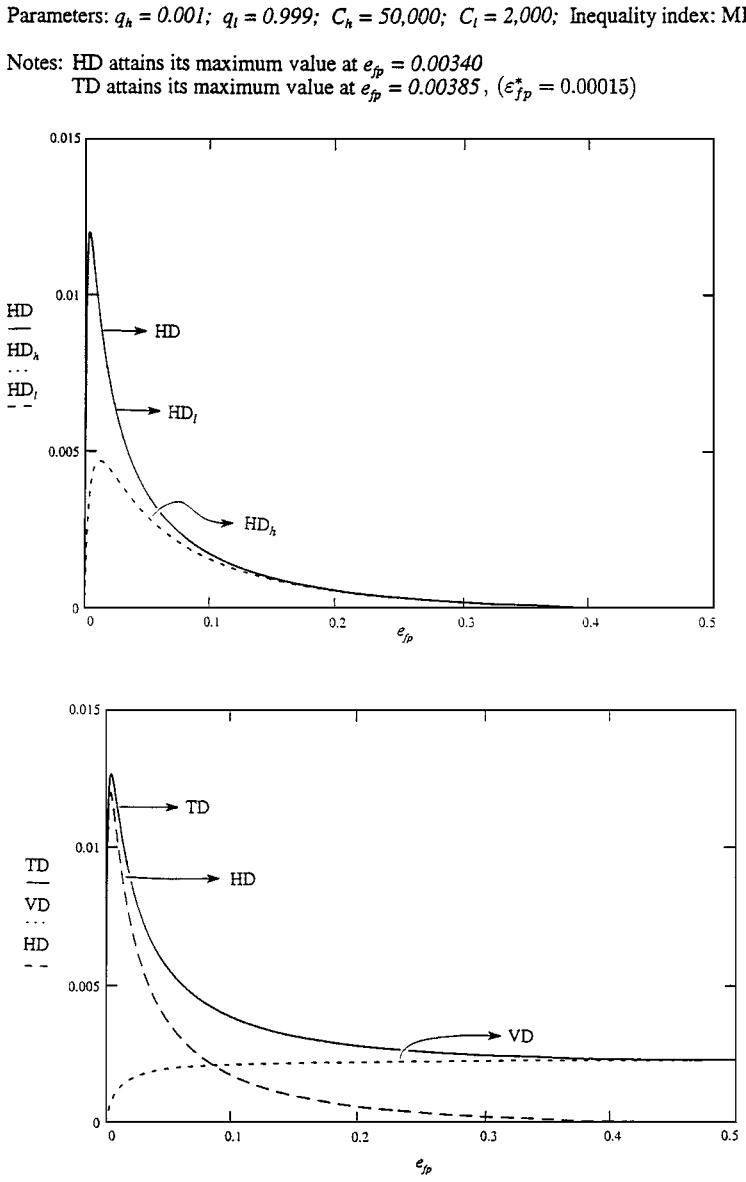

Figure 1. Base case simulation: components of discrimination.

($\varepsilon_{fp} = 0.5$) or perfectly informative ($\varepsilon_{fp} = 0$), there is zero horizontal price discrimination. Consideration of increasingly accurate genetic screening tests is represented in the graphs by movement from the value $\varepsilon_{fp} = 0.5$ to $\varepsilon_{fp} = 0$. We define ε^*_{fp} as that critical value of ε_{fp} such that using any screening test that has less information value (i.e., $\varepsilon_{fp} > \varepsilon^*_{fp}$) to

categorize risks creates more total discrimination than if no categorization at all occurs (i.e., all consumers pay the same pooled price for insurance).

The top graph in figure 1 represents the relationship between horizontal discrimination and the accuracy of the genetic test. As we can see, both groups face increasing horizontal discrimination as a result of increasing the accuracy of the test over much of the range of values for ε_{fp}. Since the relative population proportion of l-types dominates that of h-types, not surprisingly the overall amount of horizontal discrimination, *HD*, virtually coincides with HD_l in this graph (but see on for some cases where this does not happen).

In the bottom graph of figure 1 we compare the size of vertical discrimination to overall horizontal discrimination. One can see that vertical discrimination always falls as the accuracy of the test improves. This conforms to the result of Theorem 2. Beginning with a completely uninformative test, *HD* rises more quickly than does *VD* fall as one considers tests of greater accuracy and so increasing the accuracy of testing increases total discrimination up to the point where the test is almost perfectly accurate.[19] This means that unless the screening test is almost perfect, there will be lower overall discrimination if all insureds are charged the same price instead of using the results of screening tests for price setting. In fact, for this case the use of any screening test with a false positive rate greater than $\varepsilon^*_{fp} = 0.00015$ (i.e., 1.5 persons per 10,000 tested) would induce a greater amount of total discrimination than if no categorization at all were allowed.

This result follows despite the fact that the choice of the MLD as inequality measure is not particularly sensitive to the dispersion of price-cost ratios for low-risk types, the group which includes those individuals most heavily discriminated against as a result of imperfect categorization (i.e., misclassified low-risk types). In figure 2 we adopt all of the same parameters as for the example in figure 1, except we choose parameter value $\alpha = 5$ for the generalized entropy inequality index. As previously discussed, any value for this index in excess of 2 places greater weight on dispersion of higher price-cost ratios than lower ones and the higher is α, the greater is such emphasis.[20] In the top graph[21] we see that the relative contribution of horizontal discrimination among the l-types completely dominates that for h-types even on a per capita basis and so, a fortiori, overall horizontal discrimination is dominated by the HD_l component. Also, the relative importance of horizontal discrimination compared to vertical discrimination is greater in this case and the accuracy of testing must be even higher before improved accuracy leads to a reduction in total discrimination.[22] In this case the use of any screening test with a false positive rate greater than $\varepsilon^*_{fp} = 1.5 \times 10^{-9}$ would induce a greater amount of total discrimination than if no categorization at all were allowed. It seems very unlikely that risks could be classified so accurately that a false positive rate on the order of only one misclassification out of a billion tested (or less) could be met.

In the example illustrated in figure 3, one can observe the important role played by the choice of the parameter α for the generalized entropy inequality index. Here we perform the simulations for the case of $\alpha = -3$, a value which implies substantially greater emphasis on the dispersion of relatively smaller price-cost ratios, which in our context means the difference in prices paid by high risk types who are properly or misproperly classified. If one's principal emphasis on discrimination is within the group who receive favourable discrimination (i.e., the values $r_{hn} < r_{hp} < 1$) then, in per capita terms, HD_h becomes the

Parameters: $q_h = 0.001$; $q_l = 0.999$; $C_h = 50{,}000$; $C_l = 2{,}000$; Inequality index: GE, $\alpha = 5$

Notes: HD attains its maximum value at $e_{fp} = 0.000271$
TD attains its maximum value at $e_{fp} = 0.000271$ (same as for HD up to 7th significant digit)
$(\varepsilon^*_{fp} = 1.5 \times 10^{-9})$

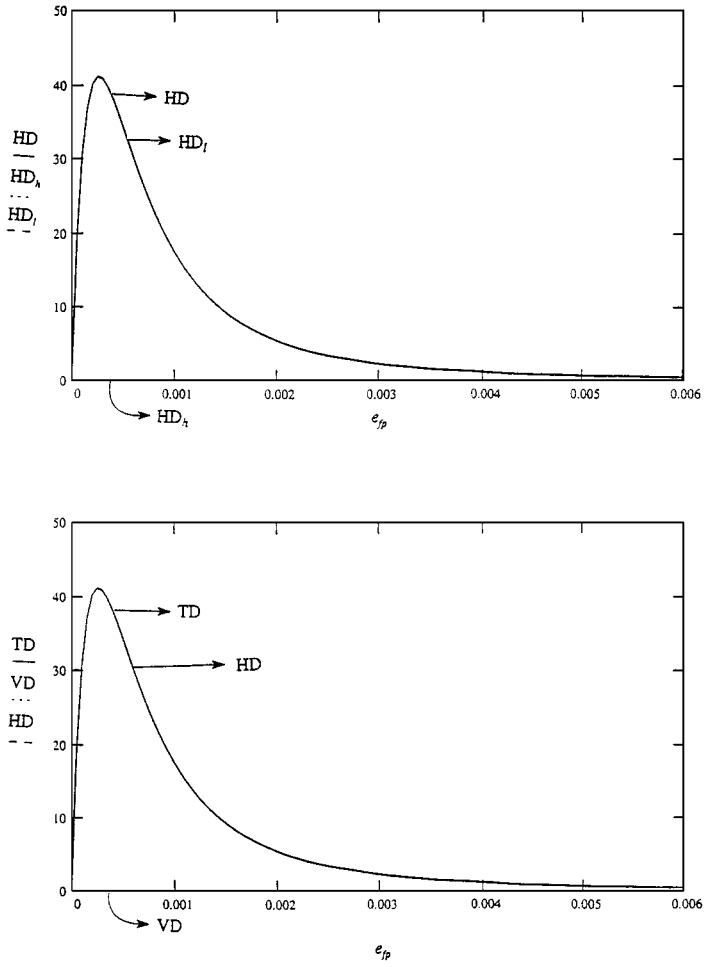

Figure 2. Case II simulation: components of discrimination.

more important term in the consideration of horizontal discrimination. Since h-types represent only a small fraction of the population, however, overall horizontal discrimination is influenced substantially by HD_l, as can be seen in figure 3. Overall discrimination, TD, is in this case dominated by vertical discrimination. It is only horizontal discrimination among h-types that is deemed very relevant according to the choice of parameter $\alpha = -3$ and with so few h-types in the population overall horizontal discrimination becomes relatively

Parameters: $q_h = 0.001$; $q_l = 0.999$; $C_h = 50{,}000$; $C_l = 2{,}000$; Inequality index: GE, $\alpha = -3$

Notes: HD attains its maximum value at $e_{fp} = 0.0389$
TD attains its maximum value at $e_{fp} = 0.50$, $(\varepsilon^*_{fp} = 0.50)$

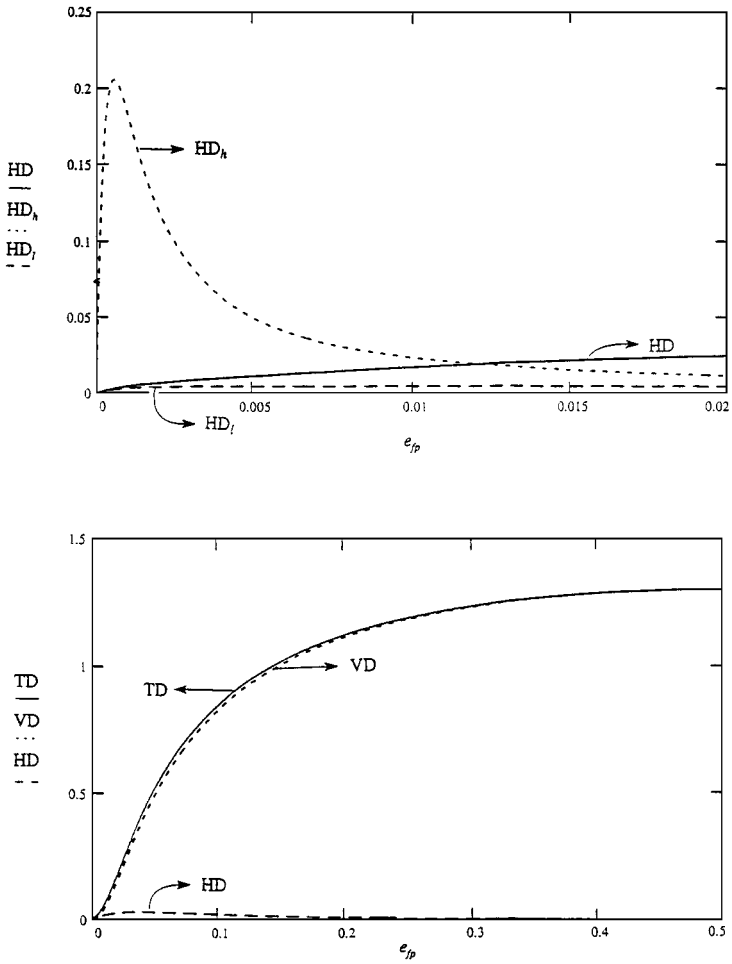

Figure 3. Case III simulation: components of discrimination.

less important. Thus, since vertical discrimination is always less when a more informative screening test is used for pricing insurance, we have that total discrimination is reduced by any increase in accuracy of the screening test. We do not, however, think that this is a relevant result from an ethical or policy perspective since it seems natural when concerned about price discrimination to focus at least as much on those who are penalized by discrimination (i.e., those facing a price greater than costs) as on those who benefit from it (i.e., those facing a price less than costs).

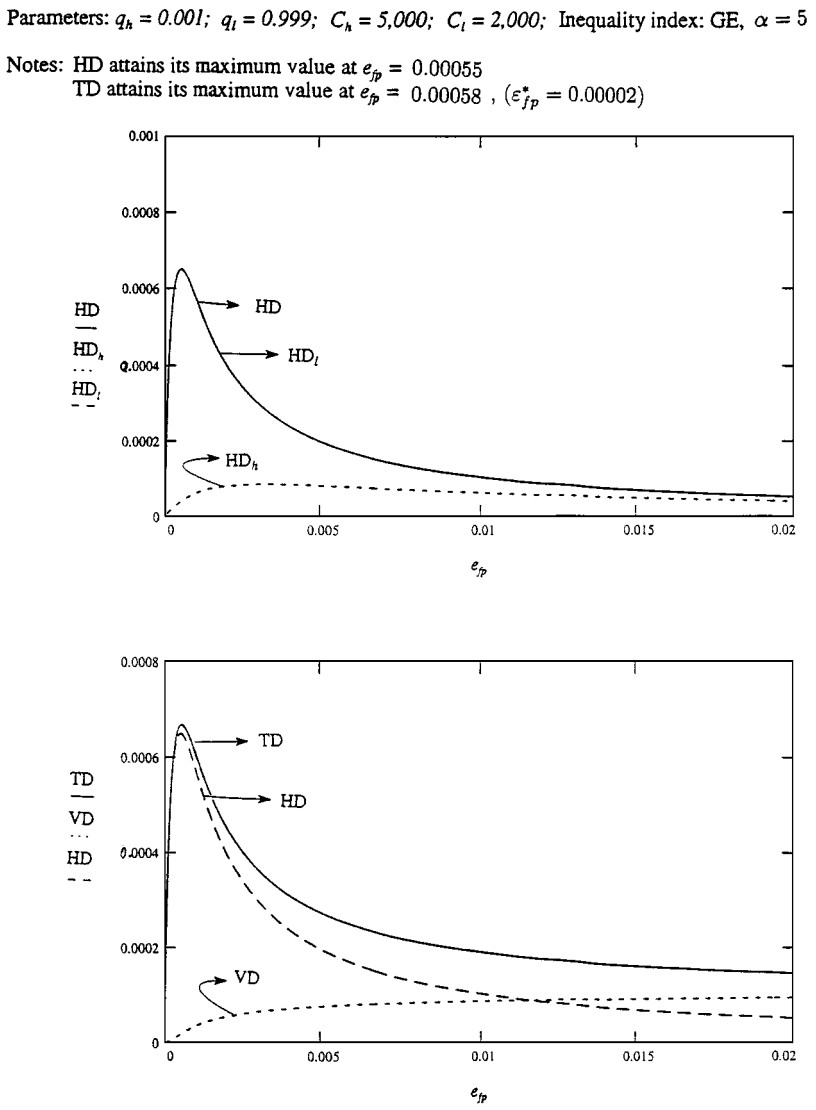

Figure 4. Case IV simulation: components of discrimination.

In figure 4 we illustrate the results of simulations which are based on a case with less difference in costs between high and low risk types. Results similar to the first two cases are obtained. In figure 5 we illustrate a case in which the population proportions are more balanced relative to scenarios consistent with genetic screening. In this case 25% of the population is of the high risk type. The importance of horizontal discrimination in the two types is similar and the contribution of vertical discrimination to total discrimination is similar to that of overall horizontal discrimination. The result is that total discrimination is

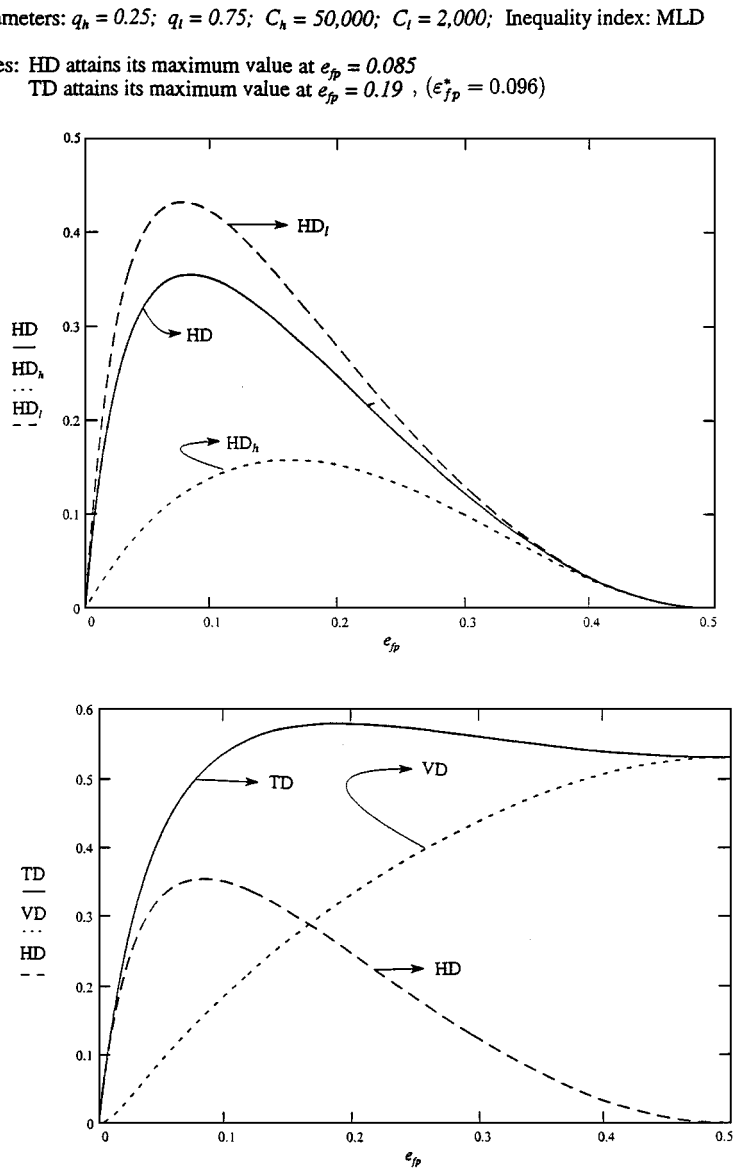

Figure 5. Case V simulation: components of discrimination.

falling in the accuracy of the test for any initial test with accuracy $\varepsilon_{fp} < 0.19$ and any test with accuracy reflected by a false positive rate $\varepsilon_{fp} < \varepsilon^*_{fp} = 0.096$ delivers a categorization scheme with less total discrimination than if no categorization were allowed. This case illustrates the importance of the context in which one considers the issue of price discrimination and the degree of misclassification associated with imperfect categorization. In a case, unlike

genetic diseases, in which the relative proportion of high risk types in the population is not *so small*, using imperfect screening to assign individuals to risk categories can more easily be justified on the grounds of reducing overall price discrimination.

6. Generalizations

In our formal analysis in Sections 3 and 4 we have taken a simplistic view of the relationship between genes and health risks. Although a few genetic diseases are quite well represented by the straightforward mapping between geno-type and risk-type,[23] that we have employed, most relationships between genes and health risks are more complex. For the majority of genetic diseases, the propensity to sustain the disease depends on a combination of several genetic determinants as well as environmental influences.[24] These cases are referred to as multifactorial genetic diseases. Recognizing this aspect of genetic diseases strengthens the conclusion that basing insurance prices on genetic screening tests is likely to increase, rather than reduce, the extent of price discrimination.

In the case of multifactorial genetic diseases, knowing whether an individual possesses a given gene does not provide a precise assessment of risk type and so the link between a given, identified gene and its associated disease(s) may be quite weak. This implies that even if a particular gene of interest is always correctly identified by the screening test, there will be substantial misclassification of individuals to risk categories. Not only must one know that a given gene is "*defective*" in order to correctly ascertain an individuals future health risks, one must also know the particular mutation for that gene, the status of other related genes, and also the environmental factors involved with that disease for the particular individual. The last of these factors would include life-style choices, not all of which are likely to be perfectly observable to the insurer.

Not only is accurate classification of risks by genetic screening tests unlikely in the context of multifactorial genetic diseases, the use of only two risk classes does not properly reflect the true degree of complexity. As our analysis in Section 2 of this paper readily demonstrates, however, one can introduce as many risk factors and classification groups as one likes without changing the nature of the analysis. The importance of being able to do so is even more evident when one considers that it is not possible to treat in a dichotomous fashion even those diseases which appear to be entirely dependent on a single gene and no other genetic or environmental factors. The disease cystic fibrosis, for example, has been identified with a single gene. However, as of 1997, more than six hundred different mutations of the gene responsible for this disease had been discovered [see Casey, 1997]. The severity of the disease depends on which of the mutations is responsible and testing for these is imperfect. Other illustrative examples are represented by the so-called breast cancer genes (BRCA-1, 2), which are contributors to the multifactorial genetic diseases of breast cancer, ovarian cancer, and others. BRCA-1, 2 are very long genes with many possible different variations/mutations creating many different scenarios concerning penetrance of the diseases and, hence, relative health risks.[25] Such complexities represent the standard, rather than the exception, and so scientific or technological accuracy in relating genes to health risks is likely to remain less than perfect.

Besides generalizing the context of genetic diseases, we can also apply our analysis to study insurance pricing environments which are more complex. In our analysis we base the price of insurance, as determined by test results (i.e., positive or negative), on the implicit assumption that both risk types purchase the same amount of insurance. Thus, recalling Eqs. (16) and (17), the unit price for those receiving test result $j = p, n$, is

$$P_j = \pi^{hj} C_h + \pi^{lj} C_l$$

As noted earlier, many models of the insurance market take account of the fact that, in the presence of asymmetric information, high risk types will typically purchase greater amounts of insurance than will low risk types when the two types are faced with the same price of insurance. Thus, the actual price of insurance will be a demand-weighted average of the risk-type specific actuarial costs. If we let L_{ij} represent the demand for insurance by an individual of risk type i with test result j, and let $\bar{L}_j$ be the average amount of insurance purchased by individuals with test result j, then the pooled actuarially fair price of insurance would be[26]

$$P_j = \pi^{hj} \frac{L_{hj}}{\bar{L}_j} C_h + \pi^{lj} \frac{L_{lj}}{\bar{L}_j} C_l$$

The qualitative nature of our results concerning price discrimination and the accuracy of the screening test would persist under these conditions. In fact, the extent of horizontal price discrimination faced by misclassified low risk types, which we saw in the previous section tends to dominate the overall degree of price discrimination in the context of genetic screening, is even greater given this consideration, while discrimination for high risk types falls as before, but this has a negligible effect on overall horizontal discrimination due to the insignificant weight attached to HD_h. This follows because, with $L_{hp} > \bar{L}_p > L_{lp}$, the extent to which low risk types who are misclassified face unfavourable discrimination is exacerbated by adverse selection considerations.

Under conditions of asymmetric information, adverse selection may also lead to a separating equilibrium as described in Rothschild and Stiglitz [1976]. In this case high risk types purchase full coverage insurance at their actuarially fair price while low risk types purchase less than full coverage at their actuarially fair price. The contracts are self-selecting in that the high risk types do not purchase the contract designed for low risk types despite the lower per unit price because of the fact that high risk types prefer a higher level of coverage. In this scenario, the presence of unidentifiable high risk types creates an externality for low risk types but this is not reflected in a higher than actuarially fair price for the low risks but rather a rationing of the amount of insurance that they end up with relative to what they would purchase if there were no high risk typesin the market. Thus, this scenario is not amenable to an analysis of price discrimination. This outcome, however, requires that there be a sufficiently large fraction of high risks in the population that low risk types prefer the separating contract, which offers them a relatively low level of coverage, to a pooling equilibrium, which offers higher coverage but at an actuarially unfair (higher) price. In the context of genetic information, the fraction of high risk types in the population is very small and so a separating equilibrium is not plausible for the

case of no categorical information allowed and so our analysis of price discrimination is appropriate.[27]

Thus, natural generalizations in regards to the reality of both genetic diseases and insurance market pricing reinforces our conclusions that improved accuracy of genetic screening is likely to lead to an *increase* in the overall amount of price discrimination.

7. Conclusions

In this paper we have exploited the relationship between decomposable inequality measures and the concepts of horizontal and vertical equity in order to provide a powerful and general framework within which to address the issue of price discrimination arising from the use of imperfect categorization in insurance pricing. We developed a particular application to determine whether using results from screening tests for geno-type to risk-rate insurance premiums is more or less discriminatory than charging all heterogeneous individuals the same *average* price. We conclude that the use of such information leads to *more*, rather than less, aggregate discrimination. The reasons for this conclusion revolve around the realities associated with genetic diseases as well as compelling normative concerns.

Any single Mendelian disease affects only a small fraction of the population but many such diseases have extremely detrimental health implications. Even very accurate genetic tests, which lead to a small fraction of individuals being misclassified, can generate substantial horizontal inequity within either risk class due to the significant differences in the costs of insurance provision. Although vertical discrimination is always reduced by the introduction of a more accurate screening test, the fact that most individuals are of the low risk type means that use of population weights by risk type de-emphasizes the importance of vertical discrimination relative to horizontal discrimination.

Price discrimination persists when individuals face different price-cost ratios for a product. From a normative perspective, it is compelling to place increased concern on the dispersion in price-cost ratios between individuals for whom the levels of those ratios are higher. The reason for doing so is that those with the highest price-cost ratios resulting from imperfect categorization are those who are most heavily discriminated against. Using simulations we found that, even with a conservative value judgement regarding the relative importance of price-cost ratios across different groups, increased accuracy of a screening test leads to an overall increase in price discrimination up to very high degrees of accuracy. This conclusion follows because, even though increased accuracy in screening reduces the number of individuals who are misclassified, at the same time improved test accuracy increases the dispersion in price-cost ratios between individuals properly classified and misclassified.

Two further considerations reinforce our conclusions. Firstly, the fact that most genetic diseases are multifactoral weakens the potential to use genetic testing to predict health risks with perfect accuracy. Thus, the limiting case of perfect testing, in which discrimination would be eliminated, is unlikely for most genetic diseases. Second, adverse selection considerations exacerbate the importance of penalizing those low risk types who are misclassified and it is this aspect of imperfect testing which naturally arises as the most prominent one in our analysis and conclusions.

The consideration of asymmetric versus symmetric information also raises an interesting question about the interpretation of the measures of price discrimination. In the case of asymmetric information, each individual knows her risk type and so under any scheme of imperfect categorization each person knows with certainty the extent of price discrimination she faces. In the case of symmetric information we presume that individuals know that within the population there are high risk types (i.e., unlucky genomes) and low risk types (i.e., lucky genomes) and also know the population parameters that apply (e.g., the proportions of risk types, the rate of false positives and negatives of the screening test), but no individual knows who are the high and low risk types.[28] Thus, in an environment of asymmetric information the weights used to aggregate discrimination reflect relative frequencies of the various groups of properly and improperly classified individuals, while under symmetric information the weights reflect the probabilities that people hold regarding their classification status. For our application to genetic screening, it is the latter case that is relevant. In general, intermediate cases are also possible; that is, individuals may have better information than insurers but not perfect information about their true risk type, in which case a mixture of the above two arguments would be needed for the interpretation of the weights.

Finally, we emphasize that considerations of discrimination from using, or not using, available imperfect information to categorize risks in an insurance market is not the only relevant issue when deciding on whether or not insurers should be allowed to use such information.[29] It is also important to address efficiency and distributional implications. However, concern over equity in the context of discriminatory pricing will undoubtedly remain a legal and regulatory concern for policy-makers and so having a firm foundation for measurement of discrimination is and will remain important.

8. Appendix

8.1. Values of Partial Derivatives

$$\frac{\partial \pi^{hp}}{\partial \varepsilon_{fn}} = \frac{-q_h q_l \pi_{pl}}{[q_h \pi_{ph} + q_l \pi_{pl}]^2} < 0$$

$$\frac{\partial \pi^{hp}}{\partial \varepsilon_{fp}} = \frac{-q_h q_l \pi_{ph}}{[q_h \pi_{ph} + q_l \pi_{pl}]^2} < 0$$

$$\frac{\partial \pi^{hn}}{\partial \varepsilon_{fn}} = \frac{q_h q_l \pi_{nl}}{[q_h \pi_{nh} + q_l \pi_{nl}]^2} > 0$$

$$\frac{\partial \pi^{hn}}{\partial \varepsilon_{fp}} = \frac{q_h q_l \pi_{nh}}{[q_h \pi_{nh} + q_l \pi_{nl}]^2} > 0$$

$$\frac{\partial \pi^{lp}}{\partial \varepsilon_{fn}} = \frac{q_h q_l \pi_{pl}}{[q_h \pi_{ph} + q_l \pi_{pl}]^2} > 0$$

$$\frac{\partial \pi^{lp}}{\partial \varepsilon_{fp}} = \frac{q_h q_l \pi_{ph}}{[q_h \pi_{ph} + q_l \pi_{pl}]^2} > 0$$

$$\frac{\partial \pi^{ln}}{\partial \varepsilon_{fn}} = \frac{-q_h q_l \pi_{nl}}{[q_h \pi_{nh} + q_l \pi_{nl}]^2} < 0$$
$$\frac{\partial \pi^{ln}}{\partial \varepsilon_{fp}} = \frac{-q_h q_l \pi_{nh}}{[q_h \pi_{nh} + q_l \pi_{nl}]^2} < 0$$
$$\frac{\partial P_p}{\partial \varepsilon_{fn}} = \frac{q_h q_l \pi_{pl}}{[q_h \pi_{ph} + q_l \pi_{pl}]^2}(C_l - C_h) < 0$$
$$\frac{\partial P_p}{\partial \varepsilon_{fp}} = \frac{q_h q_l \pi_{ph}}{[q_h \pi_{ph} + q_l \pi_{pl}]^2}(C_l - C_h) < 0$$
$$\frac{\partial P_n}{\partial \varepsilon_{fn}} = \frac{q_h q_l \pi_{nl}}{[q_h \pi_{nh} + q_l \pi_{pl}]^2}(C_h - C_l) > 0$$
$$\frac{\partial P_n}{\partial \varepsilon_{fp}} = \frac{q_h q_l \pi_{nh}}{[q_h \pi_{nh} + q_l \pi_{nl}]^2}(C_h - C_l) > 0$$

8.2. Proof of Theorem 2

By a more accurate screening test we mean one in which either the rate of false negatives or positives (or both) is lower. We show that a *higher* rate of either false negatives or positives implies a higher average price for low risk types and a lower average price for higher risk types. This implies an increase in the ratio $\frac{\bar{P}_l}{C_l}$ and a decrease in the ratio $\frac{\bar{P}_h}{C_h}$ which means an unambiguous *increase* in the overall degree of price discrimination.

Recalling Eqs. (18) and (19), and using the results from part 1 of the Appendix, we have

$$\begin{aligned}
\frac{\partial \overline{P_l}}{\partial \varepsilon_{fn}} &= \frac{\partial \pi_{pl}}{\partial \varepsilon_{fn}} P_p + \pi_{pl} \frac{\partial P_p}{\partial \varepsilon_{fn}} + \frac{\partial \pi_{nl}}{\partial \varepsilon_{fn}} P_n + \pi_{nl} \frac{\partial P_n}{\partial \varepsilon_{fn}} \\
&= \pi_{pl} \frac{\partial P_p}{\partial \varepsilon_{fn}} + \pi_{nl} \frac{\partial P_n}{\partial \varepsilon_{fn}} \\
&= -\frac{\pi_{pl} q_h q_l \pi_{pl}}{[q_h \pi_{ph} + q_l \pi_{pl}]^2}(C_h - C_l) + \frac{\pi_{nl} q_h q_l \pi_{nl}}{[q_h \pi_{nh} + q_l \pi_{nl}]^2}(C_h - C_l) \\
&= (C_h - C_l) q_h q_l \left\{ \frac{\pi_{nl}^2}{[q_h \pi_{nh} + q_l \pi_{nl}]^2} - \frac{\pi_{pl}^2}{[q_h \pi_{ph} + q_l \pi_{pl}]^2} \right\}
\end{aligned}$$

This expression will be positive provided the term in the brackets $\{\cdot\}$ is positive; i.e., provided

$$\frac{\pi_{nl}}{[q_h \pi_{nh} + q_l \pi_{nl}]} > \frac{\pi_{pl}}{[q_h \pi_{ph} + q_l \pi_{pl}]}$$

or

$$\pi_{nl}[q_h \pi_{ph} + q_l \pi_{pl}] > \pi_{pl}[q_h \pi_{nh} + q_l \pi_{nl}]$$

or

$$\pi_{nl}\pi_{ph} > \pi_{pl}\pi_{nh}$$

and this is so since for any informative test $\varepsilon_{fp}, \varepsilon_{fn} < \frac{1}{2}$, which implies $\pi_{nl} > \pi_{nh}$ and $\pi_{ph} > \pi_{pl}$. Using similar steps, we can show that

$$\frac{\partial \bar{P}_h}{\partial \varepsilon_{fp}} = (C_h - C_l)q_h q_l \left\{ \frac{\pi_{nh}^2}{[q_h\pi_{nh} + q_l\pi_{nl}]^2} - \frac{\pi_{ph}^2}{[q_h\pi_{ph} + q_l\pi_{pl}]^2} \right\}$$

which is negative provided the term in brackets $\{\cdot\}$ is negative, which, after a few algebraic steps, is equivalent to requiring that

$$\pi_{nl}\pi_{ph} > \pi_{nh}\pi_{pl}$$

which we saw above is so for any informative test ($\varepsilon_{fp}, \varepsilon_{fn} < \frac{1}{2}$).

Thus, we have established the following two results:

$$\frac{\partial \bar{P}_l}{\partial \varepsilon_{fn}} > 0 \tag{A1}$$

$$\frac{\partial \bar{P}_h}{\partial \varepsilon_{fp}} < 0 \tag{A2}$$

Due to our assumption of pooled actuarially fair pricing we have that

$$q_h \bar{P}_h + q_l \bar{P}_l = q_h C_h + q_l C_l$$

in which the right side is independent of ε_{fn} and ε_{fp} (as are q_h and q_l). Thus, we have the following two results.

$$q_h \frac{\partial \bar{P}_h}{\partial \varepsilon_{fn}} + q_l \frac{\partial \bar{P}_l}{\partial \varepsilon_{fn}} = 0$$

$$q_h \frac{\partial \bar{P}_h}{\partial \varepsilon_{fp}} + q_l \frac{\partial \bar{P}_l}{\partial \varepsilon_{fp}} = 0$$

which, in conjunction with Eqs. (A1) and (A2) imply

$$\frac{\partial \bar{P}_l}{\partial \varepsilon_{fp}} > 0 \tag{A3}$$

$$\frac{\partial \bar{P}_h}{\partial \varepsilon_{fn}} < 0 \tag{A4}$$

Thus, an increase in either or both of the rates of false positives and negatives increases $\bar{P}_l$ and decreases $\bar{P}_h$, increasing the dispersion in the values $\frac{\bar{P}_h}{C_h} < \frac{\bar{P}_l}{C_l}$, proving Theorem 2.

Acknowledgments

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Notes

1. For a breadth of views on this controversial issue, see Hook [1992], Lapham [1996], Lowden [1992], Murray [1992], Pokorski [1995], van Leeuwen and Hertogh [1992] and the background statement on genetic testing and insurance by the ASHG Ad Hoc Committee on Genetic Testing/Insurance Issues [1995].
2. In particular, see Lambert and Ramos [1997].
3. For example, see Schmalensee [1984] and Tryfos [1987].
4. We also implicitly assume no administrative costs. However, loading factors could be included in the pricing equations without loss of generality.
5. One could use the difference $P_{ij} - C_i$ as an individual measure of price discrimination. However, this would imply, for example, that an individual charged \$10 more than the cost of providing him with either an automobile or a litre of milk would feel equally aggrieved or discriminated against in each case, which seems unlikely. Such an approach is used by Schmalensee [1984].
6. That is, the degree of discrimination created by a person facing a price which exceeds expected cost by 20% should be deemed worse by a factor somewhat greater than two than the degree of discrimination created by a person who faces a price which exceeds expected cost by 10%.
7. For example, the pair $(r_1, r_2) = (1.3, 1.7)$ should be deemed overall less discriminatory than the pair $(r_1, r_2) = (1.2, 1.8)$.
8. Thus, for example, charging every individual an equal multiplicative loading would leave overall discrimination unchanged. Alternatively, one could remove any loading factors from the price and consider discrimination in terms of the relationship between the pure premium and the actuarial cost of the indemnities.
9. For proofs see Bourguignon [1979], Cowell [1980], and Shorrocks [1980, 1984]. Since prices are actuarially fair the overall mean of the r_{ij}'s is 1; otherwise, one should divide r_{ij} by its mean in the formulae in Theorem 1.
10. If $\alpha = 1$, the inequality measure is often referred to as the mean logarithmic deviation (MLD) while if $\alpha = 0$, it is often referred to as the Theil entropy measure. In both cases, the method of computing HD_i, HD, and VD are the same as for the general case, just making the substitution of the appropriate function. The case $\alpha = 2$ provides an index which is ordinally equivalent to the coefficient of variation as the measure of inequality.
11. For more discussion on this and other properties of this family of inequality measures, see Jenkins [1991]. See Kuga [1980] for a link to the popular Gini index of inequality and Lambert and Aronson [1993] for a discussion on decomposing the Gini index.
12. Huntington's Chorea is a disease which fits this stylized view very well. If an individual possesses the "Huntington's gene" then it is effectively certain that person will eventually succumb to the disease. Many diseases, however, are multifactoral in nature in that the risk of incurring the disease depends on many environmental factors and possibly other genes as well.
13. Note that $\pi_{ji} = \Pr(j \mid i)$, the probability that a person receives test result j given that she is of risk type i, while $\pi^{ij} = \Pr(i \mid j)$, the probability that an individual is of risk type i given that she has received test result j.
14. In such circumstances differential insurance purchases by risk type are predicted under models with both linear and nonlinear pricing. For examples of the former, see Villeneuve [1996] and Hoy and Polborn [2000], while for examples of the latter, see Rothschild and Stiglitz [1976].

15. That is, if a lower value of ε_{fn} and/or ε_{fp} leads to an increase in $\bar{P}_h$ and a decrease in $\bar{P}_l$ then the dispersion in the values of $(\frac{\bar{P}_h}{c_h}, \frac{\bar{P}_l}{c_l})$ falls unambiguously.
16. This latter result, $\frac{\partial P_p}{\partial \varepsilon_{fn}} < 0$, in fact requires that there exist low risk types among those who test positive (i.e., $\pi_{pl} > 0$, see the Appendix) since otherwise an increased false negative rate would just mean fewer h-types in the group testing positive but not a smaller fraction of h-types in the group that tests positive, and then P_p would not change.
17. As in the previous footnote, a caveat is required here: $\frac{\partial P_n}{\partial \varepsilon_{fp}} < 0$ requires that there are high risk types among those who test negative ($\pi_{nh} > 0$).
18. As noted in Strachan and Reid [1997], Mendelian diseases typically affect less than 1 person in 1000.
19. Computation indicates that *HD* is increasing in the accuracy of the test up to a false negative/positive rate of 0.00340 while *TD* is increasing in accuracy up to a false negative/positive rate of 0.00385.
20. We performed the simulations for the cases of $\alpha = 2$ and $\alpha = 3$ and obtained very similar results.
21. The functions are relatively flat for values of ε_{fp} greater than 0.006 and so only that part of each function near the origin is graphed.
22. Computation indicates that *TD* is increasing in the accuracy of the test up to a false negative/positive rate of 0.000271 and essentially the same result applies to *HD*.
23. Familial retinoblastoma is such an example with a single, short gene being the indicator.
24. See Strachan and Read [1997, chapter 3] for a full discussion.
25. The BRCA-1 gene spans almost 100,000 bases of the genome and encodes a protein of 1,863 amino acids. As of 1996, 235 known sequence variations had been identified. The BRCA-2 gene is more complex and less well studied but is even longer and is known to contain a large range of sequence variations as well. [See *Science*, 1996, October issue.]
26. In Villeneuve [1996], for example, this formula is referred to as the *average clientele risk*. Other formulae would be relevant if nonlinear pricing persists but the essence of the argument remains.
27. The semi-separating, semi-pooling equilibrium possibility analyzed, for example, by Wilson [1977] involves cross-subsidization between high and low risk types and so the analysis developed in this paper could be applied with minor modifications to such cases.
28. Later in life, however, one may determine whether or not one actually was a high or low risk type and so know the extent of discrimination that one faced in the insurance market.
29. Such considerations are addressed, for example, in Crocker and Snow [1986], Doherty and Thistle [1996], Ligon and Thistle [1996], Doherty and Posey [1998], Hoy [1982, 1984], Hoy and Polborn [1998], Tabarrock [1994].

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