

Bernoulli **16**(2), 2010, 585–603
DOI: [10.3150/09-BEJ210](https://doi.org/10.3150/09-BEJ210)

A semiparametric efficient estimator in case-control studies

YANYUAN MA

*Department of Statistics, Texas A&M University, College Station, TX 77843, USA.
E-mail: ma@stat.tamu.edu*

We construct a semiparametric estimator in case-control studies where the gene and the environment are assumed to be independent. A discrete or continuous parametric distribution of the genes is assumed in the model. A discrete distribution of the genes can be used to model the mutation or presence of certain group of genes. A continuous distribution allows the distribution of the gene effects to be in a finite-dimensional parametric family and can hence be used to model the gene expression levels. We leave the distribution of the environment totally unspecified. The estimator is derived through calculating the efficiency score function in a hypothetical setting where a close approximation to the samples is random. The resulting estimator is proved to be efficient in the hypothetical situation. The efficiency of the estimator is further demonstrated to hold in the case-control setting as well.

Keywords: case-control study; gene-environment interaction; logistic regression; semiparametric efficiency

1. Introduction

Case-control designs are frequently implemented in clinical studies where, instead of taking a random sample of a mixed population of both cases and non-cases, a fixed number of cases and a fixed number of controls are randomly sampled from the respective populations of cases and non-cases. Because the resulting samples are no longer random or independently and identically distributed (i.i.d.), the classical large-sample asymptotic theories could fail to apply. In the literature, two main approaches are taken in order to adapt the large-sample theory to the case-control setting. The first approach is highlighted in Breslow *et al.* (2000), where a modified design of the usual case-control study is proposed. The resulting random sample is then linked to the true case-control sample through using results from McNeney (1998), where the similarity between random and non-random sample asymptotic properties is developed by almost establishing the whole asymptotic theory under non-i.i.d. samples. The second approach is somewhat more direct and is implicitly used by Rabinowitz (2000). Instead of treating the indicator (D)

This is an electronic reprint of the original article published by the ISI/BS in <i>Bernoulli</i> , 2010, Vol. 16, No. 2, 585–603. This reprint differs from the original in pagination and typographic detail.

of case/control as a random variable, D is assumed to be known and all the calculations are performed conditionally on D . Although it does result in the conditional randomness of the case-control samples, the resulting data is not really identically distributed. Specifically, two different distributions are involved and the large-sample theory is still not available. Strictly speaking, the asymptotic theory for non-i.i.d. data rederived in McNeney (1998) also needs to be applied in order to treat such a combination of two sample cases.

In addition to the complexity arising from a case-control design, the problem considered in this article is also a semiparametric model problem, whose efficient estimator has not yet been explored even in the i.i.d. data situation. Specifically, the problem is as follows. Suppose that in the general population, the occurrence of a disease ($D = 1$) follows a logistic model $\text{logit}\{\Pr(D = 1)\} = m(G, E)$, where G represents a person's genetic character and E represents the environmental elements. Further, suppose that G and E are independent of each other and that we are interested in the effect of gene, environment and their interaction on the disease status. Thus, $m(g, e) = \beta_c + \beta_1 g + \beta_2 e + \beta_3 ge$. The parametric form of the distribution of gene g is assumed to be known as $q(g, \beta_4)$, where β_4 is an unknown finite-dimensional parameter. The distribution of the environment, $\eta(e)$, is unspecified. A special version of this problem is considered in Chatterjee and Carroll (2005), where $q(g, \beta_4)$ is assumed to be a discrete distribution. There, the authors derived a profile maximum likelihood estimator for $\beta = (\beta_c, \beta_1, \beta_2, \beta_3, \beta_4)^T$ and showed that it is root- N consistent, where N is the size of the combined samples. The estimator is later extended to a more general framework in Spinka *et al.* (2005). However, it is not investigated whether the estimator achieves the optimal semiparametric efficiency.

In this paper, we first establish in Section 2 that the classical semiparametric theory of Bickel *et al.* (1993) is applicable in general case-control studies, without having to rederive the theory in parallel or having to resort to the results from McNeney (1998). Such first order asymptotic equivalence between case-control sampling and random sampling is a new result. We then proceed to compute the semiparametric efficient score and construct a semiparametric estimator for β in Section 3. The computation is carried out in a hypothetical population described in Section 2. This differs from the real population from which the cases and controls are drawn. Hence, the derivation has its own interest and novelty. In this section, we also prove that although the estimation of the nuisance parameter η is bypassed in our estimator, the resulting semiparametric estimator still achieves the optimal efficiency. The proof and treatment is rather non-standard. Numerical examples are included in Section 4 to demonstrate the performance of the proposed estimator. The performance of the method in the discrete gene model is close to that of the method in Chatterjee and Carroll (2005) and we pointed out the possible equivalence between the two methods in Section 5. Some analytical derivations and technical details are included in the Appendix.

2. Case-control data versus i.i.d. data

The samples from a case control study are not random because the disease status is not random. In general, the design randomly samples N_1 individuals from the case population and N_0 from the non-case population. However, let us consider a hypothetical population of interest with infinite population size, in which the disease to non-disease ratio is fixed at $\pi = N_1/N_0$. Here, the reason for introducing the notion of hypothetical population is to be able to use the classical semiparametric theory for i.i.d. data, developed in Bickel *et al.* (1993). If the sample of size $N = N_0 + N_1$ from a case-control study happens to be a random sample from the hypothetical population of interest, then we have a size- N i.i.d. random sample and the usual semiparametric analysis will apply. The asymptotic results hold when $N \rightarrow \infty$ and π stays fixed.

Of course, the problem is that a random sample of size N from the hypothetical population of interest does not have to have exactly N_0 controls and N_1 cases, hence we cannot immediately equate a case-control sample and a random sample from the hypothetical population. In general, the number of controls/cases of a random sample from the hypothetical population will have a binomial distribution $N_d^r \sim \text{Binomial}(N, N_d/N)$, $d = 0, 1$, which is very close to a normal distribution when N is large, that is, $(N_d^r - N_d)/\sqrt{N\pi(1-\pi)} \rightarrow \text{Normal}(0, 1)$ in distribution when $N \rightarrow \infty$. Here, the superscript r stands for ‘random.’ Furthermore, the probability of having $|N_d^r - N_d| > N^{2/3}$ goes to zero when $N \rightarrow \infty$. Thus, we could think of the case-control sample as obtained by randomly picking a size- N sample from the hypothetical population of interest, then deleting a random $o_p(N^{2/3})$ cases (controls) and adding a random $o_p(N^{2/3})$ controls (cases). Or, alternatively, we can think of the case-control sample as a random sample of size N , but with a randomly chosen $o_p(N^{2/3})$ data contaminated in a particular way. This “particular” contamination implies the following three properties: (i) the contamination happens only to $o_p(N)$ of the observations (in the case-control samples, the contamination in fact only happens to $o_p(N^{2/3})$ observations, but, in general, $o_p(N)$ is already sufficient for our further analysis); (ii) the contaminated data is still of order $O(1)$, that is, $|X_i^c - X_i|$ is bounded in probability for $i = 1, \dots, N$; (iii) the zero expectation holds for the contaminated observations, that is, if an estimating equation for β of the form $\sum_{i=1}^N f(X_i; \beta) = 0$ satisfies $E\{f(X_i; \beta_0)\} = 0$, then $E\{f(X_i^c; \beta_0)\} = 0$ as well. Here, $X_i, i = 1, \dots, N$, are i.i.d. random samples, the superscript c stands for ‘contaminated’ and the subscript 0 represents the true parameter value.

When the case-control sample is viewed as a contaminated random sample from the hypothetical population of interest, the first two “particular” properties certainly hold. For the estimator we will construct, we shall demonstrate that the third property also holds. Thus, if we can show that the same first order asymptotics apply to both the i.i.d. sample of size N and its contaminated version as long as the three properties hold, then we can treat the case-control sample as an i.i.d. sample.

The argument is as follows. Assume that we mistakenly treated the contaminated data as i.i.d. and obtained an efficient estimator:

$$\sum_{i=1}^N S_{\text{eff}}(X_i^c; \beta) = 0. \quad (2.1)$$

Here, S_{eff} is the efficient score function and its derivation is model-dependent. One obvious aspect of S_{eff} worth emphasizing is that the construction of S_{eff} does not depend on the observations. Regardless of the method of derivation, the efficient score function S_{eff} has the property $E\{S_{\text{eff}}(X_i; \beta_0)\} = 0$. If we had the uncontaminated data, our subsequent estimator for β would have been $\sum_{i=1}^N S_{\text{eff}}(X_i; \beta) = 0$. Working with the contaminated data, (2.1) is the estimating equation we really have. Suppose that $\hat{\beta}$ solves (2.1). We then have

$$0 = \sum_{i=1}^N S_{\text{eff}}(X_i^c; \hat{\beta}) = \sum_{i=1}^N S_{\text{eff}}(X_i^c; \beta_0) + \sum_{i=1}^N \frac{\partial S_{\text{eff}}(X_i^c; \beta^*)}{\partial \beta^T} (\hat{\beta} - \beta_0),$$

therefore,

$$-N^{-1} \left\{ \sum_{i=1}^N \frac{\partial S_{\text{eff}}(X_i^c; \beta^*)}{\partial \beta^T} \right\} \sqrt{N} (\hat{\beta} - \beta_0) = N^{-1/2} \sum_{i=1}^N S_{\text{eff}}(X_i^c; \beta_0), \quad (2.2)$$

where β^* lies on the line connecting β_0 and $\hat{\beta}$. Note that in our “particular” contamination requirement, only $o_p(N)$ terms yield a different X_i from X_i^c (requirement (i)) and, for each $X_i^c \neq X_i$, the difference is $O_p(1)$ (requirement (ii)), so we have

$$\begin{aligned} N^{-1} \left\{ \sum_{i=1}^N \frac{\partial S_{\text{eff}}(X_i^c; \beta^*)}{\partial \beta^T} \right\} &= N^{-1} \left\{ \sum_{i=1}^N \frac{\partial S_{\text{eff}}(X_i; \beta^*)}{\partial \beta^T} \right\} + o_p(1) \\ &= E \left\{ \frac{\partial S_{\text{eff}}(X_i; \beta_0)}{\partial \beta^T} \right\} + o_p(1). \end{aligned} \quad (2.3)$$

From the third “particular” property, we have $E\{S_{\text{eff}}(X_i^c; \beta_0)\} = 0$ (we will prove that this property holds for the case-control data in Section 3). In conjunction with the fact that only $o_p(N)$ of the terms $S_{\text{eff}}(X_i^c; \beta_0) - S_{\text{eff}}(X_i; \beta_0)$ are non-zero, we can further obtain

$$N^{-1/2} \sum_{i=1}^N S_{\text{eff}}(X_i^c; \beta_0) = N^{-1/2} \sum_{i=1}^N S_{\text{eff}}(X_i; \beta_0) + o_p(1). \quad (2.4)$$

The detailed argument of (2.4) is the following. Suppose for the first $l = o_p(N)$ observations, $X_i^c \neq X_i$. Then we have

$$\begin{aligned} &N^{-1/2} \sum_{i=1}^N S_{\text{eff}}(X_i^c; \beta_0) \\ &= N^{-1/2} \sum_{i=1}^N S_{\text{eff}}(X_i; \beta_0) + N^{-1/2} \sum_{i=1}^l \{S_{\text{eff}}(X_i^c; \beta_0) - S_{\text{eff}}(X_i; \beta_0)\} \end{aligned}$$

$$= N^{-1/2} \sum_{i=1}^N S_{\text{eff}}(X_i; \beta_0) + (N/l)^{-1/2} l^{-1/2} \sum_{i=1}^l \{S_{\text{eff}}(X_i^c; \beta_0) - S_{\text{eff}}(X_i; \beta_0)\}.$$

Note that $S_{\text{eff}}(X_i^c; \beta_0) - S_{\text{eff}}(X_i; \beta_0)$ has mean zero, hence $l^{-1/2} \sum_{i=1}^l \{S_{\text{eff}}(X_i^c; \beta_0) - S_{\text{eff}}(X_i; \beta_0)\} = O_p(1)$. From $l = o_p(N)$, we obtain the result in (2.4) immediately. Thus, plugging (2.3) and (2.4) into (2.2), we obtain

$$-E \left\{ \frac{\partial S_{\text{eff}}(X_i; \beta_0)}{\partial \beta^T} \right\} \sqrt{N}(\hat{\beta} - \beta_0) = N^{-1/2} \sum_{i=1}^N S_{\text{eff}}(X_i; \beta_0) + o_p(1).$$

The above display is exactly the first order asymptotic expansion of the estimator for β if we had performed the estimation procedure on the uncontaminated data. Thus, we have demonstrated that the estimator obtained from contaminated data performs as well as the one obtained from uncontaminated data in terms of first order asymptotic properties. Note that the efficient estimator can be replaced by a consistent estimator, say, a general S instead of S_{eff} , as long as $E(S|D = d) = 0$ holds for $d = 0, 1$. This ensures that $E\{S(X_i^c)\} = 0$ as long as $E\{S(X_i)\} = 0$ (shown in Section 3), so the above derivation will still carry through. Hence, the asymptotic property of the estimator using the contaminated data is indeed the same as if we had the uncontaminated data. Thus, the case-control data can be treated as i.i.d. data and we can achieve the same efficiency as when the data was indeed i.i.d. In other words, a semiparametric estimator using contaminated data is at least as efficient as one using the uncontaminated data.

One question still remains: can we do even better than in the i.i.d. data case? In fact, since case-control sampling is designed to be an efficient way to collect covariate information, it seems to contain more information than a random sample. However, we claim that for asymptotically linear estimators of the form

$$\sqrt{N}(\hat{\beta} - \beta_0) = \frac{1}{\sqrt{N}} \sum_{i=1}^N \psi(X_i^c; \beta_0) + o_p(1),$$

where $E\{\psi(X_i^c; \beta_0)|d\} = 0$, the efficiency in parameter estimation cannot be further improved by taking into account the special sampling procedure. This is because otherwise, we could have obtained a better estimator for the i.i.d. sample as well, by replacing X_i^c with X_i . The detailed derivation is the same as in the above paragraph, where the condition $E\{\psi(X_i^c; \beta_0)|d\} = 0$ implies $E\{\psi(X_i; \beta_0)|d\} = 0$ for case-control data, which ensures $E\{\psi(X_i^c; \beta_0)\} = E\{\psi(X_i; \beta_0)\} = 0$. Of course, if the condition $E\{\psi|d\} = 0$ is not satisfied, the argument does not work. However, we now show that if ψ achieves the optimal variance for the case-control data X_i^c , then it has to satisfy $E\{\psi(X_i^c; \beta_0)|d\} = 0$.

First, $E\{\partial E(\psi|D)/\partial \beta\} = \partial E(\psi)/\partial \beta = 0$ because the probability density function (p.d.f.) of D does not contain β . If we let $\tilde{\psi}(X_i^c) = \psi(X_i^c) - E\{\psi(X_i^c)|d\}$, then $E\{\tilde{\psi}(X_i^c)\} = 0$ and $E\{\partial \tilde{\psi}(X_i^c)/\partial \beta\} = E\{\partial \psi(X_i^c)/\partial \beta\}$. If $E\{\psi(X_i^c)|d\} \neq 0$, then we can obtain

$$\text{var}\{\psi(X_i^c)\} = E[\text{var}\{\psi(X_i^c)|D\}] + \text{var}[E\{\psi(X_i^c)|D\}] = \text{var}\{\tilde{\psi}(X_i^c)\} + \text{var}[E\{\psi(X_i^c)|D\}]$$

$$> \text{var}\{\tilde{\psi}(X_i^c)\},$$

which, together with $E\{\partial\tilde{\psi}(X_i^c)/\partial\beta\} = E\{\partial\psi(X_i^c)/\partial\beta\}$, contradicts the fact that $\psi(X_i^c)$ is optimal.

In summary, we have shown that the case control samples can be treated as if they were i.i.d. and all the first order asymptotic results for i.i.d. data will be inherited for case-control data as well. We can see that the above establishment is similar to the development in Breslow *et al.* (2000). However, one prominent difference is that in Breslow *et al.* (2000), the case-control sample is viewed as the result of a biased sampling procedure with fixed subsample size, hence they cannot use the classical semiparametric theory for i.i.d. data, but have to refer to McNeney (1998) for the theoretical properties, where the whole semiparametric theory for fixed-size subsamples is established in parallel to the i.i.d. framework. Here, through introducing the notion of hypothetical population and by analyzing the first order equivalence between a random sample and a sample with fixed-size subsamples, we can easily contain the case-control problem in the usual i.i.d. model framework. The derivation is much simpler and more elegant. Thus, in the remainder of the paper, we ignore the case-control nature of the data and proceed with our analysis by pretending the data is i.i.d. from the aforementioned hypothetical population of interest.

3. A semiparametric efficient estimator

3.1. Geometric approach

A random sample from the hypothetical population of interest has p.d.f.

$$\begin{aligned} p(g, e, d; \beta, \eta) &= p_D(d)p_{G,E|D}(g, e|d) = p_D(d)p_{G,E|D}^t(g, e|d) \\ &= p_D(d)p_G^t(g)p_E^t(e)p_{D|G,E}^t(d|g, e)/p_D^t(d) \\ &= \frac{N_d}{N} \frac{q(g)\eta(e)H(d, g, e)}{p_D^t(d)}. \end{aligned} \quad (3.1)$$

Here, the superscript t stands for the p.d.f. in the true population, whereas expressions without superscripts, including various p.d.f.'s and expectation E , are quantities in the hypothetical population of interest; $\eta(e) = p_E^t(e)$ is the unknown infinite-dimensional parameter and

$$\begin{aligned} H(d, g, e; \beta) &= \exp[d\{m(g, e)\}]/[1 + \exp\{m(g, e)\}] \\ &= \exp\{d(\beta_c + \beta_1g + \beta_2e + \beta_3ge)\}/\{1 + \exp(\beta_c + \beta_1g + \beta_2e + \beta_3ge)\}; \\ p_D^t(d; \beta, \eta) &= \int q(g, \beta_4)\eta(e)H(d, g, e; \beta) d\mu(g) d\mu(e). \end{aligned}$$

We recognize that estimating the finite-dimensional parameter β in the presence of an infinite-dimensional nuisance parameter η , using an i.i.d. sample of size $N = N_0 + N_1$ from

a hypothetical population of interest, with the p.d.f. of a random observation given by (3.1), is a classical semiparametric problem. Therefore, we implement the semiparametric estimation methods to derive the semiparametric efficient estimator. The approach we take is geometric, first introduced in Bickel *et al.* (1993). Because the general approach and related concepts have been nicely described in several recent papers including Tsiatis and Ma (2004), Allen *et al.* (2005), Ma *et al.* (2005) and Ma and Tsiatis (2006), here, we only briefly outline the general approach and the definition of the relevant concepts, referring the reader to these papers for more detailed descriptions.

In general semiparametric problems, one approach to construct estimators for β is to obtain some influence function $\phi(X_i; \beta, \eta)$ which is subsequently used to form estimating equations for β in the form of $\sum_{i=1}^N \phi(X_i; \beta, \eta) = 0$. Here, $X_i = (G_i, E_i, D_i)$, $i = 1, \dots, N$, are i.i.d. observations. The solution of the estimating equation, $\hat{\beta}$, is subsequently a semiparametric estimator and its variance has been established to be equal to the variance of $\phi(X_i; \beta, \eta)$. Consequently, the optimal estimator among the class of all such estimators is the one whose influence function has the smallest variance. This is usually referred to as the *semiparametric efficient estimator*.

The geometric approach considers the space in which all influence functions belong. Specifically, one considers a Hilbert space \mathcal{H} which consists of all zero-mean measurable functions with finite variance and the same dimension as β . The inner product in \mathcal{H} is defined as the covariance. The Hilbert space \mathcal{H} is further decomposed into two spaces, the nuisance tangent space Λ and its orthogonal complement Λ^\perp .

To understand the nuisance tangent space Λ , consider first the case where the nuisance parameter, denoted γ , is finite-dimensional. Then, the nuisance score function, $S_\gamma = \partial \log p(X_i; \beta, \gamma) / \partial \gamma$, spans a linear space, which is denoted Λ . In the case of the infinite-dimensional nuisance parameter η , the corresponding Λ is defined as the mean squared closure of the span of all the nuisance score functions S_γ , where $p(X_i; \beta, \gamma)$ is any parametric submodel of $p(X_i; \beta, \eta)$. The orthogonal complement of Λ in \mathcal{H} is subsequently defined as Λ^\perp .

Any function in Λ^\perp can be properly normalized to obtain a valid influence function. On the other hand, every influence function is a function in Λ^\perp . Among all these functions, the projection of the score function $S_\beta = \partial \log p(X_i; \beta, \gamma) / \partial \beta$ results in the efficient influence function. If we denote the projection by S_{eff} , then the corresponding optimal variance is $\text{var}(S_{\text{eff}})^{-1}$. The projection S_{eff} is usually called the *efficient score function*.

Hence, the geometric approach converts the problem of searching for efficient semiparametric estimators to the problem of calculating S_{eff} .

3.2. Construction of the estimator

Following the description in Section 3.1, we obtain the efficient score function S_{eff} . Viewing the sample as random from the hypothetical population, the p.d.f. in (3.1) is no longer in a simple multiplicative form, in that the nuisance parameter appears both in the numerator and in the integral in the denominator. Since this implies that the nuisance tangent space is not automatically orthogonal to the score functions, the related

computation for the nuisance tangent space and associated objects is more involved. In addition, one needs to be aware that the calculation should be carried out with respect to the hypothetical population, hence quantities such as p_G^t, p_E^t, p_D^t need to be treated with extra care and not confused with p_G, p_E, p_D . The main steps of the derivation are as follows. We first calculate the score function S_β by taking the derivative of $\log p(g, e, d; \beta, \eta)$ with respect to β . This results in $S_\beta = S - E(S|d)$, where

$$S = \left\{ (m'_{\beta_c} \ m'_{\beta_1} \ m'_{\beta_2} \ m'_{\beta_3}) \left(d - 1 + \frac{1}{1 + e^m} \right) \ \frac{q'_{\beta_4}(g, \beta_4)^T}{q(g, \beta_4)} \right\}^T.$$

We then calculate the two spaces Λ, Λ^\perp by replacing η in (3.1) with a finite-dimensional parameter γ , taking the derivative of $\log p(g, e, d; \beta, \gamma)$ with respect to γ to obtain S_γ , hypothesizing a space of all such S_γ and proving that Λ is equivalent to this space. The results are

$$\begin{aligned} \Lambda &= [h(e) - E\{h(e)|d\}: \forall h(e) \text{ such that } E^t(h) = 0] = [h(e) - E\{h(e)|d\}: \forall h(e)], \\ \Lambda^\perp &= [h(g, e, d): E(h|e) = E\{E(h|d)|e\}]. \end{aligned}$$

We finally project the score vector S_β onto Λ^\perp to obtain $S_{\text{eff}} = S_\beta - f(e) + E(f|d) = S - E(S|d) - f(e) + E(f|d)$, where $f(e) - E(f|d)$ represents the projection of S_β onto Λ . The details of the derivation can be found in the Appendix. Note that this form of S_{eff} implies that $E\{S_{\text{eff}}(X)|d\} = 0$. When X is replaced by X^c , the non-random case-control sample, we still have $E\{S_{\text{eff}}(X^c)|d\} = 0$ because the design itself guarantees that the only non-random component is d , which is held constant. Thus, viewing X^c as a special contaminated version of X , we still have $E\{S_{\text{eff}}(X^c)\} = 0$, which is required in Section 2.

From the Appendix, we can further write

$$S_{\text{eff}} = S - E(S|e) + (-1)^d \{a(0) - a(1)\} w(e, 1 - d), \tag{3.2}$$

where $a(0) - a(1) = E(f|D = 0) - E(S|D = 0) - E(f|D = 1) + E(S|D = 1)$.

In terms of the calculation of S_{eff} , note that $S, E(S|e)$ and w , as given in (A.1), are all functions with parameters β and $p_D^t(d)$ only. Hence, as long as we can calculate $p_D^t(d)$, we will have the ability to evaluate $S, E(S|e)$ and w . The computation of $a(0) - a(1)$ requires further arguments.

In the following, we first obtain an approximation of $p_D^t(d)$, then pursue the estimation of $a(0) - a(1)$. To estimate $p_D^t(d)$, using $p_E(e)$ to denote the probability density function of e in the hypothetical population, we observe that

$$\begin{aligned} N_d &= N p_D(d) = \int N p_{D,E}(d, e) \, d\mu(e) = \int N p_E(e) p_{D,G|E}(d, g|e) \, d\mu(g) \, d\mu(e) \\ &= \int N p_E(e) \frac{\int N_d q(g, \beta_4) H(d, g, e) \, d\mu(g) / p_D^t(d)}{\sum_d \int N_d q(g, \beta_4) H(d, g, e) \, d\mu(g) / p_D^t(d)} \, d\mu(e) \\ &= E_e \left\{ \frac{N \int N_d q(g, \beta_4) H(d, g, e) \, d\mu(g) / p_D^t(d)}{\sum_d \int N_d q(g, \beta_4) H(d, g, e) \, d\mu(g) / p_D^t(d)} \right\}. \end{aligned}$$

Replacing the moment E_e with its sample moment through averaging across different observed e_i 's, we obtain

$$N_d \approx \sum_{i=1}^N \frac{\int N_d q(g, \beta_4) H(d, g, e_i) d\mu(g) / p_D^t(d)}{\sum_d \int N_d q(g, \beta_4) H(d, g, e_i) d\mu(g) / p_D^t(d)} \quad \text{for } d = 0, 1. \quad (3.3)$$

Note that the above two equations are not independent – one determines the other. But, in combination with $p_D^t(0) + p_D^t(1) = 1$, we can estimate $p_D^t(d)$ completely. Because the only approximation involved in estimating $p_D^t(d)$ is replacing the mean with a sample mean, the calculation will produce a root- N -consistent estimator for $p_D^t(0)$ and $p_D^t(1)$. We denote the estimators by $\hat{p}_D^t(0)$ and $\hat{p}_D^t(1)$. In calculating N_d , we write $p(g, e, d)$ as $p_E(e)p_{D,G|E}(d, g|e)$, instead of directly using the form in (3.1). Since $p_E(e)$ is the p.d.f. of the environment variable in the hypothetical population, this enables us to replace the expectation E_e with the average of the samples.

The estimation of $a(0) - a(1)$ is much more tedious, and involves an almost brute force calculation of $E(S|d)$ and $E(f|d)$. If we let $b_0 = E(S|D = 0)$, $b_1 = E(S|D = 1)$, $c_0 = E(f|D = 0)$ and $c_1 = E(f|D = 1)$, then $a(0) - a(1) = b_1 - b_0 + c_0 - c_1$. The calculation of b_0 and b_1 follows from

$$\begin{aligned} b_d &= \frac{\int S p_{D,G,E}(d, g, e) d\mu(g) d\mu(e)}{\int p_{D,G,E}(d, g, e) d\mu(g) d\mu(e)} = \frac{\int S p_E(e) p_{D,G|E}(d, g|e) d\mu(g) d\mu(e)}{\int p_E(e) p_{D,G|E}(d, g|e) d\mu(g) d\mu(e)} \\ &= \int p_E(e) \frac{\int S N_d q(g) H(d, g, e) d\mu(g) / p_D^t(d)}{\sum_d \int N_d q(g) H(d, g, e) d\mu(g) / p_D^t(d)} d\mu(e) \\ &\quad / \int p_E(e) \frac{\int N_d q(g) H(d, g, e) d\mu(g) / p_D^t(d)}{\sum_d \int N_d q(g) H(d, g, e) d\mu(g) / p_D^t(d)} d\mu(e). \end{aligned}$$

Since S can be calculated directly, we simply obtain the approximation of $b_d, d = 0, 1$, by replacing the mean with sample mean and plugging in the estimated $p_D^t(d)$:

$$\begin{aligned} \hat{b}_0 &= \sum_{i=1}^N \frac{\int S(0, g, e_i) q(g) H(0, g, e_i) d\mu(g)}{\sum_d \int N_d q(g) H(d, g, e_i) d\mu(g) / \hat{p}_D^t(d)} \\ &\quad / \sum_{i=1}^N \frac{\int q(g) H(0, g, e_i) d\mu(g)}{\sum_d \int N_d q(g) H(d, g, e_i) d\mu(g) / \hat{p}_D^t(d)}, \end{aligned} \quad (3.4)$$

$$\begin{aligned} \hat{b}_1 &= \sum_{i=1}^N \frac{\int S(1, g, e_i) q(g) H(1, g, e_i) d\mu(g)}{\sum_d \int N_d q(g) H(d, g, e_i) d\mu(g) / \hat{p}_D^t(d)} \\ &\quad / \sum_{i=1}^N \frac{\int q(g) H(1, g, e_i) d\mu(g)}{\sum_d \int N_d q(g) H(d, g, e_i) d\mu(g) / \hat{p}_D^t(d)}. \end{aligned} \quad (3.5)$$

The calculations of c_0 and c_1 are a bit more tricky. Since

$$f = E(S|e) + (c_0 - b_0)w(e, 0) + (c_1 - b_1)\{1 - w(e, 0)\},$$

taking expectation conditional on, say $D = 0$, we have

$$c_0 = E\{E(S|e)|D = 0\} + (c_0 - b_0)E\{w(e, 0)|D = 0\} \\ + (c_1 - b_1)[1 - E\{w(e, 0)|D = 0\}]$$

or, equivalently, we obtain

$$c_0 - c_1 = \frac{E\{E(S|e)|D = 0\} - b_0E\{w(e, 0)|D = 0\} - b_1[1 - E\{w(e, 0)|D = 0\}]}{1 - E\{w(e, 0)|D = 0\}}.$$

Hence, replacing mean by sample mean and using $\hat{p}_D^t(d)$, $c_0 - c_1$ is estimated by

$$\hat{c}_0 - \hat{c}_1 = \frac{\hat{E}\{E(S|e)|D = 0\} - \hat{b}_0\hat{E}\{w(e, 0)|D = 0\} - \hat{b}_1[1 - \hat{E}\{w(e, 0)|D = 0\}]}{1 - \hat{E}\{w(e, 0)|D = 0\}}, \quad (3.6)$$

where

$$\hat{E}\{w(e, 0)|D = 0\} = \frac{\sum_{i=1}^N \frac{w(e_i, 0) \int q(g)H(0, g, e_i) d\mu(g)}{\sum_d \int N_d q(g)H(d, g, e_i) d\mu(g) / \hat{p}_D^t(d)}}{\sum_{i=1}^N \frac{\int q(g)H(0, g, e_i) d\mu(g)}{\sum_d \int N_d q(g)H(d, g, e_i) d\mu(g) / \hat{p}_D^t(d)}} \quad (3.7)$$

and

$$\hat{E}\{E(S|e)|D = 0\} = \frac{\sum_{i=1}^N \frac{E(S|e_i) \int q(g)H(0, g, e_i) d\mu(g)}{\sum_d \int N_d q(g)H(d, g, e_i) d\mu(g) / \hat{p}_D^t(d)}}{\sum_{i=1}^N \frac{\int q(g)H(0, g, e_i) d\mu(g)}{\sum_d \int N_d q(g)H(d, g, e_i) d\mu(g) / \hat{p}_D^t(d)}}. \quad (3.8)$$

Similarly to the estimation of $p_D^t(d)$, the only approximation involved in obtaining $b(0), b(1)$ and $c(0) - c(1)$ is replacing mean by sample mean, so $a(0) - a(1)$ is estimated using $\hat{a}(0) - \hat{a}(1) = \hat{b}_1 - \hat{b}_0 + \hat{c}_0 - \hat{c}_1$ at the root- N rate.

We would like to emphasize that in all of the above calculations, when we replace the expectation with the sample average, we use the result that the case-control sample can be treated as a random sample from the hypothetical population. Hence, for any function $u(e)$, the approximation $N^{-1} \sum_{i=1}^N u(e_i)$ can only be used to replace $\int u(e)p_E(e) d\mu(e)$, not $\int u(e)\eta(e) d\mu(e)$.

We omitted the parameter β in all of the above expressions, in fact, $p_D^t(0), p_D^t(1), a(0) - a(1)$ are all functions of β . However, if we replace β with $\tilde{\beta}$, an initial estimator of β , we will still obtain $\hat{p}_D^t(d; \tilde{\beta}), \hat{a}(0; \tilde{\beta}) - \hat{a}(1; \tilde{\beta})$ that are root- N -consistent, as long as $\tilde{\beta} - \beta = O_p(N^{-1/2})$. The final estimating equation of β has the form

$$\sum_{i=1}^N \hat{S}_{\text{eff}}(x_i; \beta) = \sum_{i=1}^N S_{\text{eff}}\{x_i; \beta, \hat{p}_D^t(d; \tilde{\beta}), \hat{a}(0; \hat{p}_D^t, \tilde{\beta}) - \hat{a}(1; \hat{p}_D^t, \tilde{\beta})\} = 0, \quad (3.9)$$

where x_i denotes the i th observation (d_i, g_i, e_i) .

To summarize the description of the estimator, we outline the algorithm here:

- Step 1. Pick a starting value $\tilde{\beta}$ that is root- N consistent.
- Step 2. Solve for $\hat{p}_D^t(0)$ and $\hat{p}_D^t(1) = 1 - \hat{p}_D^t(0)$ from (3.3).
- Step 3. Obtain \hat{b}_0 and \hat{b}_1 from (3.4) and (3.5).
- Step 4. Obtain $\hat{c}_0 - \hat{c}_1$ from (3.6) and (3.7), (3.8).
- Step 5. Calculate S_{eff} using (3.2) and obtain $\hat{\beta}$ from solving (3.9).

It is worth pointing out that in order to carry out Step 1, we have used a vital assumption that a root- N starting value $\tilde{\beta}$ exists. Fortunately, the existence of $\tilde{\beta}$ is equivalent to the identifiability of β and is already well established in Chatterjee and Carroll (2005). The starting value used there, or in Spinka *et al.* (2005), can be used to obtain the initial estimator $\tilde{\beta}$. Our algorithm here does not require an iteration of Steps 2–5 upon each update of β . However, in practice, a more accurate $\tilde{\beta}$ can improve the final estimation $\hat{\beta}$ significantly, hence iterations are almost always implemented.

3.3. Semiparametric efficiency

If we could use the exact $p_D^t(d; \beta)$ and $a(0; \beta) - a(1; \beta)$ in (3.9), then, according to Section 3.1, the resulting estimator for β would be an efficient estimator, with estimation variance $V = E(S_{\text{eff}} S_{\text{eff}}^T)^{-1}$. To first order, V can be approximated using $N\{\sum_{i=1}^N \hat{S}_{\text{eff}}(x_i; \hat{\beta}) \hat{S}_{\text{eff}}^T(x_i; \hat{\beta})\}^{-1}$, where $\hat{\beta}$ solves (3.9).

We claim that using the estimated \hat{S}_{eff} as in (3.9), we obtain an estimating equation that yields the same estimator for β as using S_{eff} , in terms of its first order asymptotic properties.

Theorem 1. *The algorithm in Section 3.2 yields a semiparametric efficient estimator for β . That is,*

$$\sqrt{N}(\hat{\beta} - \beta_0) \rightarrow \text{Normal}\{0, \text{var}(S_{\text{eff}})^{-1}\}$$

in distribution when $N \rightarrow \infty$ and N_1/N_0 is fixed.

The proof of the theorem contains two main steps. In the first step, we show the semiparametric efficiency of the estimator if the observations had been i.i.d. In the second

Table 1. Simulation results for the two experiments, each with two different sets of parameter values, representing uncommon (upper-left) and common (upper-right) gene mutation, and homogeneous (lower-left) and diversified (lower-right) gene expression levels. ‘true’ is the true value of β , ‘est’ is the average of the estimated β , ‘sd’ is the sample standard deviation and ‘ $\widehat{\text{sd}}$ ’ is the average of the estimated standard deviation

	β_c	β_1	β_2	β_3	β_4	β_c	β_1	β_2	β_3	β_4
Experiment 1										
true	-3.2000	0.2600	0.1000	0.3000	0.0650	-3.4500	0.2600	0.1000	0.3000	0.2600
est	-3.8925	0.2498	0.0995	0.3101	0.0649	-3.9263	0.2618	0.0994	0.2998	0.2610
sd	1.6390	0.3110	0.0359	0.1226	0.0111	1.3958	0.2196	0.0445	0.0783	0.0229
$\widehat{\text{sd}}$	1.6285	0.3236	0.0364	0.1192	0.0116	1.2534	0.1956	0.0422	0.0723	0.0207
Experiment 2										
true	-3.2000	0.2600	0.1000	0.3000	0.3000	-3.7300	0.2600	0.1000	0.3000	1.0000
est	-3.3128	0.2553	0.0993	0.3126	0.2999	-3.7442	0.2589	0.0995	0.3053	0.9986
sd	0.7815	0.1624	0.0352	0.0750	0.0101	0.2906	0.0685	0.0442	0.0405	0.0378
$\widehat{\text{sd}}$	0.7969	0.1663	0.0358	0.0789	0.0101	0.2859	0.0676	0.0439	0.0402	0.0373

step, we proceed to show the efficiency in the case-control study using results in Section 2. Rather complex algebra needs to be employed in the first step. The proof also involves a split of the data in the final estimation of β , and in estimating $p_D^t(d)$ and $a(0) - a(1)$, mainly for technical convenience. The details of the proof appear in the [Appendix](#).

4. Numerical examples

We conducted a small simulation study to demonstrate the performance of the estimator. In the first experiment, we generated 500 cases and 500 controls, where the true environment element E is $\min(10, X)$ and X is generated from a log-normal distribution with mean 0 and variance 1. A dichotomous model of the gene is used, where $G = 1$ with probability β_4 and $G = 0$ with probability $1 - \beta_4$. This kind of model for $q(g, \beta_4)$ can represent the presence/absence of a certain gene mutation. We used two different sets of values for β : the first set is $\beta = (-3.45, 0.26, 0.1, 0.3, 0.26)^T$, where $\beta_4 = 0.26$ represents a relatively common mutation; the second set is $\beta = (-3.2, 0.26, 0.1, 0.3, 0.065)^T$, where $\beta_4 = 0.065$ represents a very rare mutation. In both sets, the true parameters are chosen so that the model results in a population disease rate $p_D^t(1) \approx 5\%$. The simulation results are presented in the upper half of Table 1.

The second experiment differs from the first one in its assumption on $q(g, \beta_4)$. Here, we model $q(g, \beta_4)$ with a Laplace distribution with variance β_4 . This kind of model is typically used to model the gene expression level. To maintain an approximate 5% disease rate in the population, we used $\beta = (-3.2, 0.26, 0.1, 0.3, 0.3)^T$ and $\beta = (-3.73, 0.26, 0.1, 0.3, 1)^T$ as the true parameter values. Again, in the first set, $\beta_4 = 0.3$ represents a small variation

in the population distribution for the gene expression levels, resulting in a more homogeneous population in terms of this gene. In the second set, $\beta_4 = 1$ represents a larger variation, so the population is more diversified. The simulation results are presented in the lower half of Table 1. In both experiments, 1000 simulations are implemented.

From Table 1, it is clear that the estimator for β is consistent in all four situations and the estimated standard deviation approximates the true one rather well. It is worth noting that the first experiment is a repetition of the same setting as in Chatterjee and Carroll (2005) and we observe very similar results. Specifically, for $\beta_1, \beta_2, \beta_3, \beta_4$ in the upper-left table, their results for “sd” are 0.322, 0.037, 0.128, 0.0122, respectively, and those in the upper-right table are 0.198, 0.043, 0.075 and 0.0273, respectively. Although some numerical improvement can be observed in certain parameters (for example β_4), it can be a result of finite-sample performance and numerical issues. We conjecture that the estimator in Chatterjee and Carroll (2005) is equivalent to the method proposed here, hence is also efficient, although a rigorous proof is beyond the scope of this paper. It is also worth noting that the estimation of β_c is more difficult than the remaining components of β , in that the estimation has large variability. This is especially prominent in the discrete model setting for $q(g)$. Indeed, the estimation result for β_c has not been reported elsewhere and, without the gene-environment independence, β_c is known to be unidentifiable (Prentice and Pyke (1979)). This provides an intuitive explanation for the performance of $\hat{\beta}_c$ we observe. The set of estimating equations is solved using a standard Newton–Raphson algorithm.

5. Conclusion

Semiparametric modeling and estimation to study the occurrence of a disease in relation to gene and environment has attracted much interest recently. However, despite the various estimators proposed in the literature, very little is understood in terms of the efficiency of the estimators. This is partly due to the fact that most estimators are constructed in rather ingenious ways, instead of following the standard lines of semiparametric theory. The other reason is that most such problems are set in a case-control design, which violates the i.i.d. assumption for standard semiparametric theory.

Instead of rederiving the whole semiparametric theory under non-i.i.d. samples, we argue that case-control data can be treated as if they were i.i.d. data and the standard semiparametric efficiency theory will still apply. The equivalence of the first order asymptotic theory shown in this article is a new contribution. The argument is based on rather elementary statistics without involving advanced knowledge or highly specialized techniques.

The establishment of the equivalence of the semiparametric efficiency between i.i.d. data and case-control data allows us to carry out the estimation using standard, well-established semiparametric theory. However, these standard analyses are performed under a hypothetical population of interest, hence the detailed derivation often requires special treatment, something which has not previously appeared in the literature. Under the gene-environment independence assumption, we are able to explicitly construct a

novel semiparametric estimator and show its efficiency. A special feature of this estimator is that we never attempted to estimate the infinite-dimensional nuisance parameter η itself, neither did we posit a model, true or false, for it. Rather, we avoided its estimation and instead approximated quantities that rely on it. On the one hand, this enables us to carry out the estimation rather easily; on the other hand, some asymptotic properties have to be rederived because any result that relies on the convergence properties of the nuisance parameter itself can no longer be used.

Finally, our simulation results support the theory we developed, in both discrete and continuous gene distribution cases. Our simulation results in the discrete gene model are very similar to those of Chatterjee and Carroll (2005), which leads us to believe that their estimator is also efficient. A demonstration of this aspect would be an interesting direction for future work. The programming of the method in Chatterjee and Carroll may seem easier. However, if the two methods are indeed equivalent, then the projection step in the current method should be equivalent to the profiling step in Chatterjee and Carroll, hence the computational effort and intensity should be equivalent. Although we did not further expand our estimator to stratified case-control data, the method is clearly applicable there as well.

Appendix

The derivation of S_{eff}

We will use S_{eff} to construct our estimating equation. We calculate S_{eff} by projecting the score functions with respect to the parameters of interest $\beta_c, \beta_1, \beta_2, \beta_3, \beta_4$ onto the orthogonal complement of the nuisance tangent space. We first derive the score functions $S_\beta \equiv \partial \log p(g, e, d; \beta, \eta) / \partial \beta$. Straightforward calculation shows that the score function $S_\beta = (S_1^T, S_2^T)^T$, where

$$S_1^T = (m'_{\beta_c} \ m'_{\beta_1} \ m'_{\beta_2} \ m'_{\beta_3}) \left(d - 1 + \frac{1}{1 + e^m} \right) - E \left\{ (m'_{\beta_c} \ m'_{\beta_1} \ m'_{\beta_2} \ m'_{\beta_3}) \left(d - 1 + \frac{1}{1 + e^m} \right) \middle| d \right\},$$

$$S_2 = \frac{q'_{\beta_4}(g, \beta_4)}{q(g, \beta_4)} - E \left\{ \frac{q'_{\beta_4}(g, \beta_4)}{q(g, \beta_4)} \middle| d \right\}.$$

Here, m'_* and q'_* represent partial derivatives with respect to $*$. Note that, in general, S_β can be written as $S_\beta = S - E(S|d)$.

We next derive the nuisance tangent space Λ and its orthogonal complement Λ^\perp . Inserting the form of $p_D^t(d; \beta, \eta)$ into (3.1), replacing $\eta(e)$ by an arbitrary submodel $p_E^t(e; \gamma)$ and taking the derivative of $\log p(g, e, d; \beta, \gamma)$ with respect to γ , we obtain $\partial \log p(g, e, d; \beta, \gamma) / \partial \gamma = \partial \log p_E^t(e; \gamma) / \partial \gamma - E\{\partial \log p_E^t(e; \gamma) / \partial \gamma | d\}$. Now, recognizing that $\partial \log p_E^t(e; \gamma) / \partial \gamma$ for an arbitrary submodel can yield an arbitrary function of e with mean zero calculated under the true $\eta(e)$, we obtain the nuisance tangent space:

$$\Lambda = [h(e) - E\{h(e)|d\}: \forall h(e) \text{ such that } E^t(h) = 0] = [h(e) - E\{h(e)|d\}: \forall h(e)],$$

$$\Lambda^\perp = [h(g, e, d): E(h|e) = E\{E(h|d)|e\}].$$

Here, E^t stands for an expectation calculated with respect to the true population distribution. The second expression for Λ is more convenient because it allows $h(e)$ to be an arbitrary function of e , hence this is the form of Λ that we will use.

Having obtained S_β and the spaces Λ and Λ^\perp , we can proceed to derive the efficient score function $S_{\text{eff}} \equiv \Pi(S_\beta|\Lambda^\perp)$. If we let $\Pi(S_\beta|\Lambda) = f(e) - E(f|d)$, then $S_{\text{eff}} = S_\beta - f(e) + E(f|d) = S - E(S|d) - f(e) + E(f|d)$.

We now modify the expression of S_{eff} to facilitate its actual computation. Letting $a(d) = E(f|d) - E(S|d)$, we can thus write $S_{\text{eff}} = S - f + a(d)$. Note that S does not depend on η and $a(d)$ is either $a(1)$ or $a(0)$. In addition, we have $E(S_{\text{eff}}|e) = E\{E(S_{\text{eff}}|d)|e\}$. This is equivalent to

$$E(S_\beta|e) - f(e) + E\{E(f|d)|e\} = E[E\{S - E(S|d)|d\} - E\{f - E(f|d)|d\}|e] = 0,$$

which, in turn, is equivalent to

$$\begin{aligned} E(S|e) &= f + E\{E(S|d)|e\} - E\{E(f|d)|e\} = f - E\{a(d)|e\} \\ &= f - \frac{\sum_d \int a(d) N_d q(g, \beta_4) H(d, g, e) d\mu(g) / p_D^t(d)}{\sum_d \int N_d q(g, \beta_4) H(d, g, e) d\mu(g) / p_D^t(d)}. \end{aligned}$$

Let

$$v(e, d) = N_d \int q(g, \beta_4) H(d, g, e) d\mu(g) / p_D^t(d) = p_{E,D}(e, d) N \eta^{-1}(e)$$

and

$$w(e, d) = v(e, d) / \{v(e, 0) + v(e, 1)\}. \quad (\text{A.1})$$

We have

$$\begin{aligned} E(S|e) &= f - a(0)v(e, 0) / \{v(e, 0) + v(e, 1)\} - a(1)v(e, 1) / \{v(e, 0) + v(e, 1)\} \\ &= f - a(0)w(e, 0) - a(1)w(e, 1) \end{aligned}$$

or $f = E(S|e) + a(0)w(e, 0) + a(1)w(e, 1)$. Consequently,

$$\begin{aligned} S_{\text{eff}} &= S - E(S|e) - a(0)w(e, 0) - a(1)w(e, 1) + a(d) \\ &= S - E(S|e) + (-1)^d \{a(0) - a(1)\} w(e, 1 - d). \end{aligned}$$

Proof of Theorem 1

To simplify notation, we denote $\alpha = p_D^t(0)/p_D^t(1)$, $\hat{\alpha} = \hat{p}_D^t(0)/\hat{p}_D^t(1)$, $\delta(\alpha) = \alpha\{0; p_D^t(d)\} - \alpha\{1; p_D^t(d)\}$, $\delta(\hat{\alpha}) = \hat{\alpha}\{0; \hat{p}_D^t(d)\} - \hat{\alpha}\{1; \hat{p}_D^t(d)\}$.

Suppose we randomly partition the data into two groups: group 1 has m observations and group 2 has n observations. Here, $m = N^{0.9}$, $n = N - m$. We use the first group to obtain $\hat{\alpha}$, and $\hat{\delta}(\hat{\alpha})$, then use the second group to form the following estimating equation to estimate β :

$$\sum_{i=1}^n S_{\text{eff}}\{x_i; \hat{\beta}, \hat{\alpha}, \hat{\delta}(\hat{\alpha})\} = 0.$$

We will first show that the resulting estimator satisfies $n^{1/2}(\hat{\beta} - \beta_0) \rightarrow N(0, V)$ in distribution when $N \rightarrow \infty$.

The proof splits into several steps: First, obviously, $\hat{\alpha} - \alpha = O_p(m^{-1/2})$ and $\hat{\delta}(\hat{\alpha}) - \delta(\hat{\alpha}) = O_p(m^{-1/2})$, as long as a root- N -consistent $\tilde{\beta}$ is inserted in the calculation of these quantities. A standard expansion yields

$$\begin{aligned} 0 &= \sum_{i=1}^n S_{\text{eff}}\{x_i; \hat{\beta}, \hat{\alpha}, \hat{\delta}(\hat{\alpha})\} \\ &= \sum_{i=1}^n S_{\text{eff}}\{x_i; \beta_0, \hat{\alpha}, \hat{\delta}(\hat{\alpha})\} + \sum_{i=1}^n \frac{\partial}{\partial \beta^T} S_{\text{eff}}\{x_i; \beta^*, \hat{\alpha}, \hat{\delta}(\hat{\alpha})\}(\hat{\beta} - \beta_0) \\ &= \sum_{i=1}^n S_{\text{eff}}\{x_i; \beta_0, \hat{\alpha}, \hat{\delta}(\hat{\alpha})\} + n \left\{ E \left(\frac{\partial S_{\text{eff}}}{\partial \beta^T} \right) + o_p(1) \right\} (\hat{\beta} - \beta_0), \end{aligned}$$

which can be rewritten as

$$\begin{aligned} &\left\{ E \left(\frac{\partial S_{\text{eff}}}{\partial \beta^T} \right) + o_p(1) \right\} n^{1/2}(\hat{\beta} - \beta_0) \\ &= -n^{-1/2} \sum_{i=1}^n S_{\text{eff}}\{x_i; \beta_0, \hat{\alpha}, \hat{\delta}(\hat{\alpha})\} \\ &= -n^{-1/2} \sum_{i=1}^n [S_{\text{eff}}\{x_i; \beta_0, \hat{\alpha}, \delta(\hat{\alpha})\} + (-1)^{d_i} \{\hat{\delta}(\hat{\alpha}) - \delta(\hat{\alpha})\} w(e_i, 1 - d_i, \hat{\alpha})]. \end{aligned}$$

The last equality uses the form of S_{eff} in (3.2) and the fact that S , $E(S|e)$ and w do not depend on α . Because $\hat{\delta}(\hat{\alpha}) - \delta(\hat{\alpha}) = O_p(m^{-1/2}) = o_p(1)$ and

$$E\{(-1)^{d_i} w(e_i, 1 - d_i, \hat{\alpha})\} = \int \sum_{d=0,1} \frac{(-1)^d p_{E,D}(e, 1 - d; \hat{\alpha}) \eta^{-1}(e)}{v(e, 0; \hat{\alpha}) + v(e, 1; \hat{\alpha})} p_{E,D}(e, d; \hat{\alpha}) d\mu(e) = 0,$$

we actually have

$$\left\{ E \left(\frac{\partial S_{\text{eff}}}{\partial \beta^T} \right) + o_p(1) \right\} n^{1/2}(\hat{\beta} - \beta_0)$$

$$\begin{aligned}
 &= -n^{-1/2} \sum_{i=1}^n S_{\text{eff}}\{x_i; \beta_0, \hat{\alpha}, \delta(\hat{\alpha})\} + o_p(1) \\
 &= -n^{-1/2} \sum_{i=1}^n \left\{ S_{\text{eff}}(x_i) + \frac{\partial S_{\text{eff}}(x_i; \beta_0, \alpha)}{\partial \alpha} (\hat{\alpha} - \alpha) + \frac{\partial^2 S_{\text{eff}}(x_i; \beta_0, \alpha^*)}{\partial \alpha^2} (\hat{\alpha} - \alpha)^2 \right\} + o_p(1).
 \end{aligned}$$

In addition, $(\hat{\alpha} - \alpha)^2 = O_p(m^{-1}) = o_p(n^{-1/2})$, so

$$\left\{ E \left(\frac{\partial S_{\text{eff}}}{\partial \beta^T} \right) + o_p(1) \right\} n^{1/2} (\hat{\beta} - \beta_0) = -n^{-1/2} \sum_{i=1}^n \left\{ S_{\text{eff}}(x_i) + \frac{\partial S_{\text{eff}}(x_i)}{\partial \alpha} (\hat{\alpha} - \alpha) \right\} + o_p(1).$$

We now proceed to examine $\frac{\partial S_{\text{eff}}(x_i)}{\partial \alpha}$ by examining each term in (3.2). S is free of α . As a function of α , we already have

$$\begin{aligned}
 b_5(e; \alpha) &\equiv E(S|e; \alpha) = \frac{\sum_d \int SN_d q(g, \beta_4) H(d, g, e) d\mu(g) / p_D^t(d)}{\sum_d \int N_d q(g, \beta_4) H(d, g, e) d\mu(g) / p_D^t(d)} \\
 &= \frac{\int SN_0 q H_0 d\mu(g) + \alpha \int SN_1 q H_1 d\mu(g)}{\int N_0 q H_0 d\mu(g) + \alpha \int N_1 q H_1 d\mu(g)} = \frac{u_2(e, 0) + \alpha u_2(e, 1)}{u_1(e, 0) + \alpha u_1(e, 1)},
 \end{aligned}$$

where we define $u_1(e, d) = \int N_d q(g, \beta_4) H(d, g, e) d\mu(g)$ and $u_2(e, d) = \int SN_d q(g, \beta_4) H(d, g, e) d\mu(g)$. Using this notation,

$$\begin{aligned}
 \frac{\partial b_5}{\partial \alpha} &= \frac{u_2(e, 1)u_1(e, 0) - u_2(e, 0)u_1(e, 1)}{\{u_1(e, 0) + \alpha u_1(e, 1)\}^2}, \\
 w(e, 0) &= \frac{u_1(e, 0)}{u_1(e, 0) + \alpha u_1(e, 1)}, \\
 w(e, 1) &= \frac{\alpha u_1(e, 1)}{u_1(e, 0) + \alpha u_1(e, 1)}.
 \end{aligned}$$

Similarly to the calculation of b_0, b_1 , we also have that for any function u ,

$$\begin{aligned}
 E(u|d; \alpha) &= \int \frac{p_E(e) \int u N_d q(g) H(d, g, e) d\mu(g) / p_D^t(d)}{\sum_d \int N_d q(g) H(d, g, e) d\mu(g) / p_D^t(d)} d\mu(e) \\
 &\quad / \int \frac{p_E(e) \int N_d q(g) H(d, g, e) d\mu(g) / p_D^t(d)}{\sum_d \int N_d q(g) H(d, g, e) d\mu(g) / p_D^t(d)} d\mu(e) \\
 &= \int \frac{p_E(e) \int u N_d q(g) H(d, g, e) d\mu(g) / p_D^t(d)}{\sum_d u_1(e, d) / p_D^t(d)} d\mu(e) \\
 &\quad / \int \frac{p_E(e) u_1(e, d) / p_D^t(d)}{\sum_d u_1(e, d) / p_D^t(d)} d\mu(e),
 \end{aligned}$$

thus

$$E(u|0; \alpha) = \int \frac{p_E(e) \int u N_0 q(g) H(0, g, e) d\mu(g)}{u_1(e, 0) + u_1(e, 1)\alpha} d\mu(e) / \int \frac{p_E(e) u_1(e, 0)}{u_1(e, 0) + u_1(e, 1)\alpha} d\mu(e),$$

$$E(u|1; \alpha) = \int \frac{p_E(e) \int u N_1 q(g) H(1, g, e) d\mu(g)}{u_1(e, 0) + u_1(e, 1)\alpha} d\mu(e) / \int \frac{p_E(e) u_1(e, 1)}{u_1(e, 0) + u_1(e, 1)\alpha} d\mu(e).$$

These relations lead to

$$b_0 = \int \frac{p_E(e) u_2(e, 0)}{u_1(e, 0) + u_1(e, 1)\alpha} d\mu(e) / \int \frac{p_E(e) u_1(e, 0)}{u_1(e, 0) + u_1(e, 1)\alpha} d\mu(e),$$

$$b_1 = \int \frac{p_E(e) u_2(e, 1)}{u_1(e, 0) + u_1(e, 1)\alpha} d\mu(e) / \int \frac{p_E(e) u_1(e, 1)}{u_1(e, 0) + u_1(e, 1)\alpha} d\mu(e),$$

$$b_2 \equiv E\{E(S|e)|0; \alpha\}$$

$$= \int \frac{p_E(e) \int E(S|e) N_0 q(g) H(0, g, e) d\mu(g)}{u_1(e, 0) + u_1(e, 1)\alpha} d\mu(e) / \int \frac{p_E(e) u_1(e, 0)}{u_1(e, 0) + u_1(e, 1)\alpha} d\mu(e)$$

$$= \int \frac{p_E(e) E(S|e) u_1(e, 0)}{u_1(e, 0) + u_1(e, 1)\alpha} d\mu(e) / \int \frac{p_E(e) u_1(e, 0)}{u_1(e, 0) + u_1(e, 1)\alpha} d\mu(e)$$

$$= \int \frac{p_E(e) u_1(e, 0) \{u_2(e, 0) + u_2(e, 1)\alpha\}}{\{u_1(e, 0) + u_1(e, 1)\alpha\}^2} d\mu(e) / \int \frac{p_E(e) u_1(e, 0)}{u_1(e, 0) + u_1(e, 1)\alpha} d\mu(e),$$

$$b_3 \equiv E\{w(e, 0)|D = 0\}$$

$$= \int \frac{p_E(e) \int w(e, 0) N_0 q(g) H(0, g, e) d\mu(g)}{u_1(e, 0) + u_1(e, 1)\alpha} d\mu(e) / \int \frac{p_E(e) u_1(e, 0)}{u_1(e, 0) + u_1(e, 1)\alpha} d\mu(e)$$

$$= \int \frac{p_E(e) u_1^2(e, 0)}{\{u_1(e, 0) + u_1(e, 1)\alpha\}^2} d\mu(e) / \int \frac{p_E(e) u_1(e, 0)}{u_1(e, 0) + u_1(e, 1)\alpha} d\mu(e).$$

Consequently, we obtain

$$S_{\text{eff}}(0) = S - b_5(e) + \left\{ b_1 - b_0 + \frac{b_2 - b_0 b_3 - b_1(1 - b_3)}{1 - b_3} \right\} \frac{\alpha u_1(e, 1)}{u_1(e, 0) + \alpha u_1(e, 1)}$$

$$= S - b_5(e) + \left(\frac{b_2 - b_0}{1 - b_3} \right) \frac{\alpha u_1(e, 1)}{u_1(e, 0) + \alpha u_1(e, 1)},$$

$$S_{\text{eff}}(1) = S - b_5(e) - \left(\frac{b_2 - b_0}{1 - b_3} \right) \frac{u_1(e, 0)}{u_1(e, 0) + \alpha u_1(e, 1)},$$

$$\frac{\partial S_{\text{eff}}(0)}{\partial \alpha} = -b_5'(e) + \left(\frac{b_2 - b_0}{1 - b_3} \right)' \frac{\alpha u_1(e, 1)}{u_1(e, 0) + \alpha u_1(e, 1)} + \left(\frac{b_2 - b_0}{1 - b_3} \right) \frac{u_1(e, 0) u_1(e, 1)}{\{u_1(e, 0) + \alpha u_1(e, 1)\}^2},$$

$$\frac{\partial S_{\text{eff}}(1)}{\partial \alpha} = -b_5'(e) - \left(\frac{b_2 - b_0}{1 - b_3} \right)' \frac{u_1(e, 0)}{u_1(e, 0) + \alpha u_1(e, 1)} + \left(\frac{b_2 - b_0}{1 - b_3} \right) \frac{u_1(e, 0) u_1(e, 1)}{\{u_1(e, 0) + \alpha u_1(e, 1)\}^2}.$$

Since S does not contain α , $\frac{\partial S_{\text{eff}}}{\partial \alpha}$ is a function of (e, d) only. Because $p_{E,D}(e, d) = \eta(e)u_1(e, d)/\{Np_D^t(d)\}$, we have $p_{E,D}(e, 0) = (1 + \alpha)\eta(e)u_1(e, 0)/(N\alpha)$, $p_{E,D}(e, 1) = (1 + \alpha)\eta(e)u_1(e, 1)/N$ and $p_E(e) = (1 + \alpha)\eta(e)\{u_1(e, 0) + \alpha u_1(e, 1)\}/(N\alpha)$. Combining these results, we have

$$\begin{aligned} E\left(\frac{\partial S_{\text{eff}}}{\partial \alpha}\right) &= E\left[-b'_5(e) + \left(\frac{b_2 - b_0}{1 - b_3}\right) \frac{u_1(e, 0)u_1(e, 1)}{\{u_1(e, 0) + \alpha u_1(e, 1)\}^2}\right] \\ &= E\left[\frac{-u_2(e, 1)u_1(e, 0) + u_2(e, 0)u_1(e, 1)}{\{u_1(e, 0) + \alpha u_1(e, 1)\}^2}\right] \\ &\quad + \left(\frac{b_2 - b_0}{1 - b_3}\right) E\left[\frac{u_1(e, 0)u_1(e, 1)}{\{u_1(e, 0) + \alpha u_1(e, 1)\}^2}\right]. \end{aligned}$$

Plugging in the expressions for b_0, b_2, b_3 , we obtain

$$\begin{aligned} \frac{b_2 - b_0}{1 - b_3} &= \left[\int \frac{p_E(e)u_1(e, 0)\{u_2(e, 0) + u_2(e, 1)\alpha\}}{\{u_1(e, 0) + u_1(e, 1)\alpha\}^2} d\mu(e) - \int \frac{p_E(e)u_2(e, 0)}{u_1(e, 0) + u_1(e, 1)\alpha} d\mu(e)\right] \\ &\quad / \left[\int \frac{p_E(e)u_1(e, 0)}{u_1(e, 0) + u_1(e, 1)\alpha} d\mu(e) - \int \frac{p_E(e)u_1^2(e, 0)}{\{u_1(e, 0) + u_1(e, 1)\alpha\}^2} d\mu(e)\right] \\ &= \int \frac{\alpha p_E(e)\{u_1(e, 0)u_2(e, 1) - u_1(e, 1)u_2(e, 0)\}}{\{u_1(e, 0) + u_1(e, 1)\alpha\}^2} d\mu(e) \\ &\quad / \left[\int \frac{\alpha p_E(e)u_1(e, 0)u_1(e, 1)}{\{u_1(e, 0) + u_1(e, 1)\alpha\}^2} d\mu(e)\right] \\ &= E\left[\frac{\{u_1(e, 0)u_2(e, 1) - u_1(e, 1)u_2(e, 0)\}}{\{u_1(e, 0) + u_1(e, 1)\alpha\}^2}\right] / E\left[\frac{u_1(e, 0)u_1(e, 1)}{\{u_1(e, 0) + u_1(e, 1)\alpha\}^2}\right], \end{aligned}$$

thus, we have $E(\partial S_{\text{eff}}/\partial \alpha) = 0$.

The fact that $E(\partial S_{\text{eff}}/\partial \alpha) = 0$, in combination with $\hat{\alpha} - \alpha = o_p(1)$, yields

$$\left\{E\left(\frac{\partial S_{\text{eff}}}{\partial \beta^T}\right) + o_p(1)\right\} n^{1/2}(\hat{\beta} - \beta_0) = -n^{-1/2} \sum_{i=1}^n S_{\text{eff}}(x_i) + o_p(1).$$

Thus, we indeed have $n^{1/2}(\hat{\beta} - \beta_0) \sim N(0, V)$ asymptotically.

In fact, the classical $N^{1/2}(\hat{\beta} - \beta_0) \sim N(0, V)$ also holds. This is because

$$N^{1/2}(\hat{\beta} - \beta_0) - n^{1/2}(\hat{\beta} - \beta_0) = \frac{m}{N^{1/2} + n^{1/2}}(\hat{\beta} - \beta_0) \rightarrow \frac{N^{0.9}}{N} n^{1/2}(\hat{\beta} - \beta_0) \rightarrow 0$$

when $N \rightarrow \infty$. Thus, our estimator is semiparametric efficient. Because of the equivalence result developed in Section 2, the estimator is also semiparametric efficient for case-control data. We split the data set into two groups with sizes m and n for simplicity of the asymptotic analysis. In reality, one can certainly use the whole data set in each stage of the estimation.

Acknowledgments

This work was supported by NSF Grant DMS-0906341.

References

- Allen, A.S., Satten, G.A. and Tsiatis, A.A. (2005). Locally-efficient robust estimation of haplotype-disease association in family-based studies. *Biometrika* **92** 559–571. [MR2202646](#)
- Bickel, P.J., Klaassen, C.A.J., Ritov, Y. and Wellner, J.A. (1993). *Efficient and Adaptive Estimation for Semiparametric Models*. Baltimore: The Johns Hopkins Univ. Press. [MR1245941](#)
- Breslow, N.E., Robins, J.M. and Wellner, J.A. (2000). On the semi-parametric efficiency of logistic regression under case-control sampling. *Bernoulli* **6** 447–455. [MR1762555](#)
- Chatterjee, N. and Carroll, R.J. (2005). Semiparametric maximum likelihood estimation exploring gene-environment independence in case-control studies. *Biometrika* **92** 399–418. [MR2201367](#)
- Ma, Y., Genton, M.G. and Tsiatis, A.A. (2005). Locally efficient semiparametric estimators for generalized skew-elliptical distributions. *J. Amer. Statist. Assoc.* **100** 980–989. [MR2201024](#)
- Ma, Y. and Tsiatis, A.A. (2006). On closed form semiparametric estimators for measurement error models. *Statist. Sinica* **16** 183–193. [MR2256086](#)
- McNeney, W.B. (1998). Asymptotic efficiency in semiparametric models with non-i.i.d. data. Ph.D. thesis, Univ. of Washington.
- Prentice, R.L. and Pyke, R. (1979). Logistic disease incidence models and case-control studies. *Biometrika* **66** 403–411. [MR0556730](#)
- Rabinowitz, D. (2000). Computing the efficient score in semi-parametric problems. *Statist. Sinica* **10** 265–280. [MR1742112](#)
- Spinka, C., Carroll, R.J. and Chatterjee, N. (2005). Analysis of case-control studies of genetic and environmental factors with missing genetic information and hyplotype-phase ambiguity. *Genetic Epidemiology* **29** 108–127.
- Tsiatis, A.A. and Ma, Y. (2004). Locally efficient semiparametric estimators for functional measurement error models. *Biometrika* **91** 835–848. [MR2126036](#)

Received April 2008 and revised April 2009