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Sample Selection Models without Exclusion Restrictions: Parameter Heterogeneity and Partial Identification*

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July, 2021

Abstract

This paper studies semiparametric versions of the classical sample selection model (Heckman (1976, 1979)) without exclusion restrictions. We extend the analysis in Honoré and Hu (2020) by allowing for parameter heterogeneity and derive implications of this model. We also consider models that allow for heteroskedasticity and briefly discuss other extensions. The key ideas are illustrated in a simple wage regression for females. We find that the derived implications of a semiparametric version of Heckman's classical sample selection model are consistent with the data for women with no college education, but strongly rejected for women with a college degree or more.

Key Word: Selection, Heterogeneity, Heteroskedasticity, Exclusion Restrictions, Identification

JEL Code: C01, C14, C21, C24

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1 Introduction

This paper revisits Heckman’s classical sample selection model (Heckman (1976, 1979))

$$y_i^* = x_i' \beta + \varepsilon_i, \tag{1}$$

where $y_i = y_i^*$ is observed if

$$d_i \equiv 1 \{w_i' \gamma + \nu_i > 0\} = 1. \tag{2}$$

The variables w_i and d_i are assumed to be observed for everybody, while it is only necessary to observe x_i when $d_i = 1$. The parameter vector, β , is the object of interest. The intercepts in (1) and (2) are implicitly captured in ε_i and ν_i , respectively.

In his seminal papers, Heckman (1976, 1979) considered estimation of this model under the assumption that (ε_i, ν_i) are distributed according to a bivariate normal distribution independently of (x_i, w_i) . Later research, such as Powell (1987), was able to relax the normality assumption provided that there are elements in w_i that are excluded from x_i . See Powell (1994) for a survey of this literature. Unfortunately, such exclusion restrictions can sometimes be difficult to find.¹ In Honoré and Hu (2020), we therefore investigated what one can learn about β in the model defined by equations (1) and (2) if there are no exclusion restrictions, so $w_i = x_i$, and the only distributional assumption on the pair of errors, (ε_i, ν_i) , is that it is independent of x_i . The parameter vector, β , is generally² not point identified in that case, but it turns out that provided that γ is identified up to scale, the identified region for β is a line segment in \mathbb{R}^k , where k is the dimensionality of β . The empirical example in Honoré and Hu (2020) suggests that this identified region can be small enough to be empirically useful.

In a series of papers, James Heckman has emphasized the importance of allowing for individual-specific heterogeneity in econometric models (see, for example, Heckman (2001)). In this paper, we consider generalizations of the classical sample selection model that allow for

¹For example, Krueger and Whitmore (2001) estimated a sample selection model assuming normality “as there is no exclusion restriction.”

²Chamberlain (1986) shows that one can identify β if x_i has unbounded support.

heterogeneity in the main parameter of interest, as well as for conditional heteroskedasticity. Since the standard sample selection model is generally not point identified without exclusion restrictions, the models considered here will also only be partially identified.

Our aim is to provide identified sets that can be empirically useful, although we do not claim that they are sharp. We illustrate the usefulness of the identified sets by constructing identified regions in a simple wage regression with sample selection. In our application, the coefficient on a dummy variable for being white will be the parameter of interest.

Lee (2009) also considered a sample selection model without exclusion restrictions. He focused on the effect of a binary explanatory variable, “treatment”, in a sample selection model. Lee’s setup is much less parametric than the Heckman sample selection model, and he was able to derive tight bounds for the mean effect of treatment for the subset of individuals who would have been selected into the sample whether or not they are treated. Lee (2009)’s bounds have been used in a number of different contexts, but some papers have pointed out that the Lee bounds can be too wide to be useful in practice. For example, Barrow and Rouse (2018) wrote “Unfortunately, Lee Bounds estimates (Lee, 2009) are quite wide and largely uninformative.” Since Lee’s bounds are the tightest possible under his assumptions, this suggests that in those cases, either one should give up on estimating sample selection models, or one should maintain more structure. In addition, the parameter that Lee considers is the mean effect of treatment for the subset of individuals who would have been selected into the sample whether or not they are treated. It is not entirely clear why one should be interested in this particular average effect if there is parameter heterogeneity.

The potential for parameter heterogeneity in the outcome equation of a sample selection model is the main motivation for this paper. We also briefly discuss a number of other extensions to the general framework displayed in equations (1) and (2). Specifically, we consider the implications of heteroskedasticity in (1), the potential for identification through nonlinearities in (2), and panel data versions of the basic model. Finally, we briefly consider a potential outcomes version of the sample selection model.

Our approach builds on the insights in Honoré and Hu (2020). We review the basic idea of that paper in Section 2. In Section 3, we consider a model in which the parameter of interest is allowed to be heterogeneous, and Section 4 provides an empirical illustration of

the ideas in Section 3. Section 5 allows for heteroskedasticity in (1). The ideas here are illustrated in the empirical Subsection 5.3. Section 6 investigates various generalizations and Section 7 writes the model in terms of potential outcomes. Section 8 concludes.

Throughout the paper, we focus on the parameter on a binary (0/1) explanatory variable (the “treatment”), but we allow for additional continuous “controls.” In most of the paper, we also maintain the assumption that the heterogeneous parameter is independent of the random errors in the model.

2 Identification Strategy in the Simplest Case

[Honoré and Hu \(2020\)](#) discuss identification without exclusion restrictions in the classical sample selection model

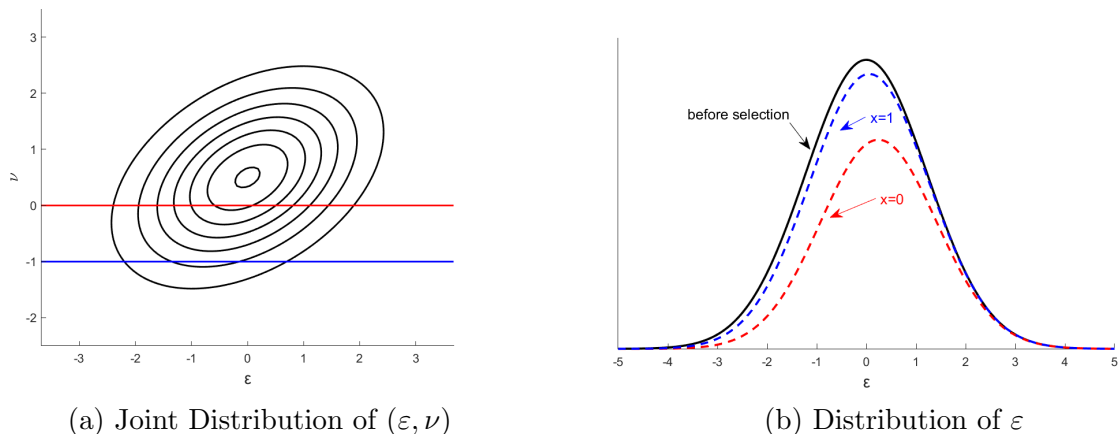
$$y_i^* = x_i' \beta + \varepsilon_i, \tag{3}$$

where $y_i = y_i^*$ is observed if $d_i \equiv 1 \{x_i' \gamma + \nu_i > 0\} = 1$, and (ε_i, ν_i) is independent of x_i . The main insight in that paper is based on the simpler model where there is a single explanatory variable, which is binary taking each of the values 0 and 1 with positive probability. In that case, there is no loss of generality in assuming that $\gamma = 1$.

The left hand panel of Figure 1 displays the joint distribution of (ε_i, ν_i) and the two horizontal lines depict the fact that one only observes y_i when $\nu_i > 0$ (when $x_i = 0$) or when $\nu_i > -1$ (when $x_i = 1$). The right hand panel of Figure 1 shows the marginal density of ε_i before selection, as well as the density times the probability of selection conditional on ε_i for $x_i = 0$ and $x_i = 1$. The interpretation of the latter two graphs is that the sample selection puts some probability mass at “ ε_i is unobserved”; the remaining mass is then distributed with density given by the two graphs (depending on $x_i = 0$ or $x_i = 1$). Below, we refer to those two graphs as “sub-densities” because they integrate to the probability of selection (as opposed to integrating to 1).

The key assumption in the selection model is that the selection is monotone in x_i , meaning that an individual with a particular draw of (ε_i, ν_i) who is selected into the sample when $x_i = 0$, would also be selected with $x_i = 1$. This implies that the sub-density of ε_i when x_i is

Figure 1: Distribution of ε Before and After Selection



1 in Figure 1 is above the sub-density when x_i is 0. This in turn implies that the sub-density of $y_i - \beta$ for $x_i = 1$ is above the sub-density of y_i for $x_i = 0$. [Honoré and Hu \(2020\)](#) show that this characterizes the sharp identified region for β . The paper then uses the same insight to construct a sharp identified set for β in the case x_i is multidimensional and not necessarily binary. Finally, [Honoré and Hu \(2020\)](#) propose estimation of a non-sharp identified region for β by considering interval probabilities rather than densities.

The sample selection equation (2) is essential for the approach in [Honoré and Hu \(2020\)](#). This equation implies that the sample selection is monotone in $w_i' \gamma$ for a given draw of the errors (ε_i, ν_i) , and it is this monotonicity that leads to comparisons like the one in the right hand side of Figure 1.

3 Parameter Heterogeneity

[Heckman \(2001\)](#) and others have emphasized the importance of heterogeneity. This is also implicit in the analysis in [Lee \(2009\)](#), who derived bounds for the average parameter value in a certain subset of the population.

One way to introduce heterogeneity in the sample selection model is by allowing a subset of the parameters to vary across individuals. For example, if x_{i1} is the variable of interest,

then one might specify the model

$$y_i^* = x_{1i}\beta_{1i} + x_{2i}'\beta_2 + \varepsilon_i,$$

where $y_i = y_i^*$ is observed if $d_i = 1$, where $d_i = 1 \{x_i'\gamma + \nu_i > 0\}$, and where $x_i = (x_{1i}, x_{2i})$. Without a scale normalization of ν_i , γ is at best identified up to scale, and the sign of each element of γ is identified. We assume the first element³ of γ is not 0, and we normalize γ so that $|\gamma_1| = 1$.

Except where we explicitly state otherwise, we will assume that β_{1i} , (ε_i, ν_i) , and x_i are independent. For identification of the distribution of β_{1i} , this can be relaxed somewhat by conditioning on x_{2i} . We do not pursue this because it is unlikely to be useful in practice when x_{2i} is multidimensional and contains continuously distributed variables. The assumption that β_{1i} is independent of (ε_i, ν_i) is strong; however, it is clear that some assumption of this type is necessary in order to make statements about, say, the population mean of β_{1i} .⁴ The assumptions that ν_i is independent of x_i and that γ is constant again imply that the sample selection is monotone in $x_i'\gamma$.

3.1 Binary Regressor

We first consider the case with only one explanatory variable, x_i , which is binary. We assume that $\gamma_1 = 1$, so that the sample selection is more severe when x_i is 0 than when it is 1. We observe

$$y_i = x_i\beta_i + \varepsilon_i \quad \text{if} \quad x_i + \nu_i > 0.$$

The key observation again is that the selection is monotone in x_i . Individuals who are selected with $x_i = 0$ would also be selected with $x_i = 1$ and with the same (ε_i, ν_i) . For any

³If all elements of γ are 0, then this is known from the population distribution of the data, and in that case there is no sample selection bias.

⁴For example, while [Lee \(2009\)](#) does not make such an assumption, the bounds derived in that paper are for the average treatment effect for the individuals who would have been selected into the sample whether or not they were treated. Conditional expectations like that can only be turned into population-wide expectations by making additional assumptions.

set A , we therefore have

$$\begin{aligned} P(\varepsilon_i \in A, \nu_i > -1) &= P(\varepsilon_i \in A, \nu_i > 0) + P(\varepsilon_i \in A, 0 \geq \nu_i > -1) \\ &\geq P(\varepsilon_i \in A, \nu_i > 0). \end{aligned}$$

It therefore follows that

$$P(\varepsilon_i + b \in A, \nu_i > -1) \geq P(\varepsilon_i + b \in A, \nu_i > 0) \text{ for any } b. \quad (4)$$

In this special case, β_i only matters when $x_i = 1$. As a result, we do not need to assume that β_i and x_i are independent. Instead we assume that (ε_i, ν_i) is independent of x_i and that β_i is independent of (ε_i, ν_i) conditional on $x_i = 1$. The distribution of β_i conditional on $x_i = 1$, F_β , belongs to some class of distributions \mathcal{F}_β . The class of distributions could be a parametric family of distributions, or F_β could be left nonparametric. Typically, the class of distributions for β_i will include degenerate distributions, in which case the model with parameter homogeneity becomes a special case of the model considered here. With this, (4) implies

$$\int P(\varepsilon_i + b \in A, \nu_i > -1) dF_\beta(b) \geq \int P(\varepsilon_i + b \in A, \nu_i > 0) dF_\beta(b). \quad (5)$$

Recalling that $y_i = \beta_i + \varepsilon_i$ when $x_i = 1$ and $y_i = \varepsilon_i$ when $x_i = 0$, equation (5) becomes

$$P(y_i \in A, d_i = 1 | x_i = 1) \geq \int P(y_i + b \in A, d_i = 1 | x_i = 0) dF_\beta(b),$$

so one identified set for F_β is

$$\left\{ F \in \mathcal{F}_\beta : P(y_i \in A, d_i = 1 | x_i = 1) \geq \int P(y_i + b \in A, d_i = 1 | x_i = 0) dF(b) \right\}. \quad (6)$$

For example, if we restrict β to be discrete, taking on K values with probabilities π_k , then

the distribution of β must belong to

$$\left\{ \left(K, \{\beta_k, \pi_k\}_{k=1}^K \right) : P(y_i \in A, d_i = 1 | x_i = 1) \geq \sum_k \pi_k P(y_i + \beta_k \in A, d_i = 1 | x_i = 0) \text{ for all } A, \sum_k \pi_k = 1 \right\}.$$

This places restrictions on K and $\{\beta_k, \pi_k\}_{k=1}^K$. In the applications below, we specify K , but it could in principle be considered a parameter to be estimated or bounded.

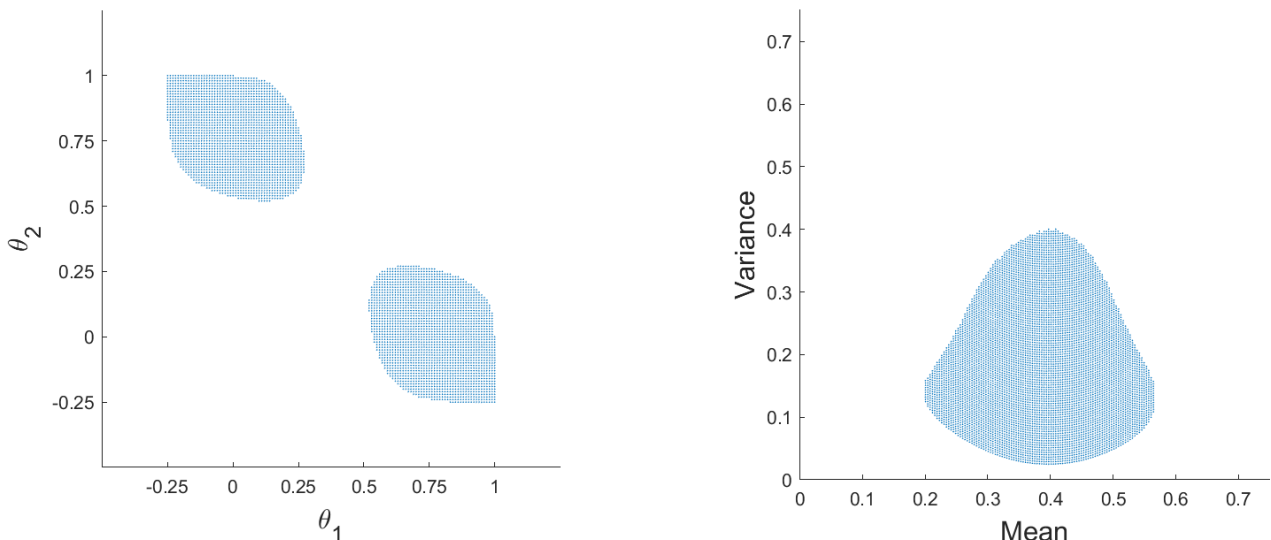
Since β_i is allowed to depend on x_i , the restriction that β_i takes a finite number of values, K , is similar in spirit to the group-specific heterogeneity studied in [Bonhomme and Manresa \(2015\)](#).

Example 1 *Let (ε_i, ν_i) be distributed according to a bivariate normal distribution with $E[\varepsilon_i] = 0$, $E[\nu_i] = 1$, $V[\varepsilon_i] = 1$, $V[\nu_i] = 1$ and $\text{cov}(\varepsilon_i, \nu_i) = 0.5$, and let $P(\beta_{1i} = 0) = P(\beta_{1i} = 1) = \frac{1}{2}$. If the researcher knows that β_{1i} has a discrete distribution with two equally likely points of support, θ_1 and θ_2 , but does not know the distribution of (ε_i, ν_i) , then the identified region for (θ_1, θ_2) is as depicted in the left hand panel of [Figure 2](#). The identified set is symmetric around the 45-degree line since the two points of support enter the model symmetrically.*

It is difficult to graphically present the identified set of a parameter of dimension higher than two. In those cases, it can be useful to present identified regions for summary statistics of the parameter. For example, when the object of interest is a distribution, one might present the joint identified set for the mean and the variance.

Example 2 (Continuation of Example 1) *Consider the same data generating process as in [Example 1](#). If the researcher knows that β_{1i} has a discrete distribution with two points of support, but does not know the associated probabilities, then the identified region for the mean and variance of β_{1i} is as depicted in the right hand panel of [Figure 2](#). Combined with [1](#), this example illustrates that the sample selection model with parameter heterogeneity is far from point-identified even when the distribution of the heterogeneity is tightly parameterized, but that one can still construct informative bounds on objects of interest such as the mean and the variance of the heterogeneous parameter.*

Figure 2: Examples 1 and 2



(a) Identified Region for points of support

(b) Identified region for $(E[\beta_{1i}], SD[\beta_{1i}])$

The same line of argument can be used to find the identified set for the distribution of β_{1i} when $\gamma = -1$, that is, the case where the selection is more severe when x_i is 1 than when it is 0. It is

$$\left\{ (\beta_k, \pi_k) : P(y_i \in A, d_i = 1 | x_i = 1) \leq \sum_k \pi_k P(y_i + \beta_k \in A, d_i = 1 | x_i = 0) \text{ for all } A, \sum_k \pi_k = 1 \right\}.$$

3.2 Generalization to Multiple x

We now turn to the more general case where x_{1i} is still a binary (0/1) “treatment”, but there are additional explanatory variables. For simplicity, we assume that these have homogeneous parameters and that γ_1 is positive (and normalized to 1). Specifically,

$$y_i^* = x_{1i}\beta_{1i} + x'_{2i}\beta_2 + \varepsilon_i,$$

where $y_i = y_i^*$ is observed when $d_i \equiv 1 \{x'_i\gamma + \nu_i > 0\}$ equals 1. We maintain the assumption that $\beta_{1i}, (\varepsilon_i, \nu_i,)$ and x_i are independent. We also assume that a set of sufficient conditions

for γ to be identified up to scale are satisfied⁵ (see for example [Klein and Spady \(1993\)](#)) and that conditional on $d_i = 1$, $(\varepsilon_i, x'_{2i}, x'_i\gamma)$ satisfy the conditions on (U_i, X_i, Z_i) in [Robinson \(1988\)](#). The distribution of the heterogeneous parameter, β_{1i} , can in principle be continuous or discrete, although we restrict it to be discrete in the application in the next section. We assume that $E[\beta_{1i}]$ is finite. The selection equation, $d_i \equiv 1 \{x'_i\gamma + \nu_i > 0\}$, is a monotonicity assumption which states that if y_i is observed for an individual with $x'_i\gamma = \xi_1$, then y_i would also be observed if $x'_i\gamma = \xi_2 > \xi_1$ and (ε_i, ν_i) is left unchanged.

To construct bounds for the distribution of β_{1i} , one can pick an arbitrary b_2 and apply (6) with y replaced by $y - x'_2b_2$. This gives a (possibly empty) identified set for the distribution of β_{1i} for each b_2 . One identified set for the distribution of β_{1i} is then the union (over b_2) of these. Unfortunately, this approach is difficult to implement, unless the dimensionality of x_{2i} is small. We therefore pursue an alternative approach.

Conditional on selection, and conditional on β_{1i} , we have

$$y_i = x_{1i}\beta_{1i} + x'_{2i}\beta_2 + g(x'_i\gamma) + u_i,$$

where $g(x'_i\gamma) = E[\varepsilon_i | x_i, x'_i\gamma + \nu_i > 0]$ and $E[u_i | x_i, \beta_{1i}] = 0$. This implies that

$$\begin{aligned} E[y_i | x'_i\gamma] &= E[x_{1i} | x'_i\gamma] E[\beta_{1i} | x'_i\gamma] + E[x_{2i} | x'_i\gamma] \beta_2 + g(x'_i\gamma) \\ &= E[x_{1i} | x'_i\gamma] \beta_{1i} - E[x_{1i} | x'_i\gamma] (\beta_{1i} - E[\beta_{1i} | x'_i\gamma]) + E[x_{2i} | x'_i\gamma] \beta_2 + g(x'_i\gamma) \end{aligned}$$

and therefore

$$y_i - E[y_i | x'_i\gamma] = (x_{1i} - E[x_{1i} | x'_i\gamma]) \beta_{1i} + (x_{2i} - E[x_{2i} | x'_i\gamma])' \beta_2 - E[x_{1i} | x'_i\gamma] (\beta_{1i} - E[\beta_{1i} | x'_i\gamma]) + u_i.$$

As in [Honoré and Hu \(2020\)](#), $(x_{1i} - E[x_{1i} | x'_i\gamma]) + (x_{2i} - E[x_{2i} | x'_i\gamma])' \gamma_2 = 0$. We therefore

⁵When γ is not point-identified up to scale, the approach below can be applied to each point in the identified set for γ .

have

$$\begin{aligned}
y_i - E[y_i | x_i' \gamma] &= -(x_{2i} - E[x_{2i} | x_i' \gamma])' \gamma_2 \beta_{1i} + (x_{2i} - E[x_{2i} | x_i' \gamma])' \beta_2 \\
&\quad - E[x_{1i} | x_i' \gamma] (\beta_{1i} - E[\beta_{1i} | x_i' \gamma]) + u_i \\
&= (x_{2i} - E[x_{2i} | x_i' \gamma])' (\beta_2 - \gamma_2 \beta_{1i}) - E[x_{1i} | x_i' \gamma] (\beta_{1i} - E[\beta_{1i} | x_i' \gamma]) + u_i \\
&= (x_{2i} - E[x_{2i} | x_i' \gamma])' (\beta_2 - \gamma_2 E[\beta_{1i} | x_i' \gamma]) - E[x_{1i} | x_i' \gamma] (\beta_{1i} - E[\beta_{1i} | x_i' \gamma]) + u_i \\
&\quad - (x_{2i} - E[x_{2i} | x_i' \gamma])' \gamma_2 (\beta_{1i} - E[\beta_{1i} | x_i' \gamma])
\end{aligned}$$

Since the last three terms have mean 0 conditional on x_i , and β_{1i} is assumed to be independent of x_i (so $E[\beta_{1i} | x_i' \gamma] = E[\beta_{1i}]$), this implies that

$$\alpha_2 \equiv (\beta_2 - \gamma_2 E[\beta_{1i}])$$

is identified provided that $(x_{2i} - E[x_{2i} | x_i' \gamma])$ has full rank.

Having identified α_2 , we write

$$\begin{aligned}
y_i^* - x_{2i}' \alpha_2 &= y_i^* - x_{2i}' (\beta_2 - \gamma_2 E[\beta_{1i}]) = x_{1i} \beta_{1i} + x_{2i}' \beta_2 + \varepsilon_i - x_{2i}' (\beta_2 - \gamma_2 E[\beta_{1i}]) \\
&= x_{1i} \beta_{1i} + (x_{2i}' \gamma_2) E[\beta_{1i}] + \varepsilon_i,
\end{aligned}$$

or

$$y_i^* - x_{2i}' \alpha_2 - (x_{2i}' \gamma_2) E[\beta_{1i}] = x_{1i} \beta_{1i} + \varepsilon_i.$$

In other words

$$y_i^* - x_{2i}' \alpha_2 - (x_{2i}' \gamma_2) E[\beta_{1i}] = \varepsilon_i \quad \text{when} \quad x_{1i} = 0 \quad (7)$$

and

$$y_i^* - x_{2i}' \alpha_2 - (x_{2i}' \gamma_2) E[\beta_{1i}] = \beta_{1i} + \varepsilon_i \quad \text{when} \quad x_{1i} = 1. \quad (8)$$

Thinking of the left hand side as a dependent variable, equations (7) and (8) have the same structure as the problem in Section 3.1. The main difference is that to arrive at (7) and (8) we assumed independence between β_{1i} and x_i . This was not necessary when there is a single, binary, explanatory variable. Moreover, the selection probability is now monotone in

the index $x'_i\gamma$.

Combining (7) and (8), we have

$$y_i^* - x'_{2i}\alpha_2 - (x'_{2i}\gamma_2) E[\beta_{1i}] + 1\{x_{1i} = 0\} \beta_{1i} = \beta_{1i} + \varepsilon_i.$$

Hence, for any interval A and for $\xi_1 < \xi_2$,

$$\begin{aligned} P((y_i^* - x'_{2i}\alpha_2 - (x'_{2i}\gamma_2) E[\beta_{1i}] + 1\{x_{1i} = 0\} \beta_{1i}) \in A, d_i = 1 | x'_i\gamma = \xi_2) &\geq \\ P((y_i^* - x'_{2i}\alpha_2 - (x'_{2i}\gamma_2) E[\beta_{1i}] + 1\{x_{1i} = 0\} \beta_{1i}) \in A, d_i = 1 | x'_i\gamma = \xi_1). \end{aligned} \quad (9)$$

Therefore we can construct an identified set for the distribution of β_{1i} , F , as

$$\left\{ F \in \mathcal{F}_\beta : \int P((y_i - x'_{2i}\alpha_2 - (x'_{2i}\gamma_2) E_F[\beta_{1i}] + b) \in A, d_i = 1 | x'_i\gamma = \xi_2) dF(b) \geq \int P((y_i - x'_{2i}\alpha_2 - (x'_{2i}\gamma_2) E_F[\beta_{1i}] + b) \in A, d_i = 1 | x'_i\gamma = \xi_1) dF(b) \right\}$$

for all $\xi_1 < \xi_2$. We use the notation $E_F[\beta_{1i}]$ as a reminder that the expectation of β_{1i} in (9) will depend on F .

For each F in the identified set for the distribution of β_{1i} , the average treatment effect is $E_F[\beta_{1i}]$. The remaining parameter vector, β_2 , is given by $\alpha_2 + \gamma_2 E_F[\beta_{1i}]$ where γ_2 is identified from the semiparametric discrete choice model $d_i \equiv 1\{x'_i\gamma + \nu_i > 0\}$ with $\gamma = (\gamma_1, \gamma_2)'$ and the normalization that $\gamma_1 = 1$.

4 Empirical Illustration

To illustrate the approach outlined above, we consider a simple sample selection model for wages for females. The question is how to make statements about the coefficient on being white, β_1 , without exclusion restrictions.

We first estimate the model under joint normality of the errors using the maximum likelihood estimator and Heckman's two-step estimator. The parameters of the model are not point-identified without a distributional assumption on the errors. We therefore next

apply the method in [Honoré and Hu \(2020\)](#) to construct a confidence region for β_1 under the assumption that this parameter is homogenous. After that, we use the approach discussed in [Section 3.2](#) to estimate a (two point) discrete distribution for β_1 .

Using the Current Population Survey from 1982 to 2018, we construct a data set of 1,060,351 females aged 25 to 65. Of them, 552,446 are working and have a recorded (real) wage. The explanatory variable of interest is a dummy for being white, and the additional explanatory variables are the unemployment rate, a time trend, age, age-squared, and two education indicators (one for some college, and one for college and beyond).

[Table 1](#) reports the maximum likelihood estimates that assume joint normality of (ε_i, ν_i) for the full sample and for the three subsamples defined by educational group. [Table 2](#) reports the corresponding 2-step estimates. Comparing the estimates in [Table 1](#) and [Table 2](#) makes it very clear that the normality assumption is violated. For example, under the null that the normality assumption is satisfied, the standard error of the difference in the estimates of the coefficient on being white for the full sample would be 0.0036. The difference in the point estimates is 0.0225, which leads to a t-statistic of more than 6. The values of the corresponding t-statistics for the three subsample are all above 2.3 in absolute value.

To estimate the semiparametric version of the sample selection model that acknowledges that the coefficients are only partially identified without exclusion restrictions, we turn the constraints in [\(9\)](#) into a finite number of moment inequalities by first dividing the range of $x'_i \widehat{\gamma}$ into five regions, C_ℓ , defined by quintiles. For a given candidate distribution of β_{1i} , we then divide the range of $y - x'_2 \widehat{\alpha}_2 - (x'_{2i} \widehat{\gamma}_2) E_F[\beta_{1i}]$ into ten regions, A_j , defined by the deciles of $y - x'_2 \widehat{\alpha}_2 - (x'_{2i} \widehat{\gamma}_2) E_F[\beta_{1i}]$. This gives moment conditions of the type

$$E [1 \{ (y_i^* - x'_{2i} \alpha_2 - (x'_{2i} \gamma_2) E_F[\beta_{1i}] + 1 \{x_{1i} = 0\} \beta_{1i}) \in A_j, d_i = 1 \} | x'_i \gamma \in C_\ell] \geq \quad (10)$$

$$E [1 \{ (y_i^* - x'_{2i} \alpha_2 - (x'_{2i} \gamma_2) E_F[\beta_{1i}] + 1 \{x_{1i} = 0\} \beta_{1i}) \in A_j, d_i = 1 \} | x'_i \gamma \in C_{\ell-1}].$$

Since the distribution of ν is left unspecified, we should in principle estimate γ semi-parametrically, for example by employing the maximum rank estimator of [Han \(1987\)](#) or the estimator proposed by [Klein and Spady \(1993\)](#). These can be difficult and computationally expensive to calculate. Below, we calculate confidence sets by subsampling, and we therefore

Table 1: Parametric Estimation under Normality (MLE)

	All	No College	Some College	College Plus
White	0.062 (0.002)	0.117 (0.003)	0.060 (0.003)	0.020 (0.003)
Unemployment Rate	0.012 (0.000)	0.011 (0.001)	0.006 (0.001)	0.006 (0.001)
Year	0.004 (0.000)	0.002 (0.000)	0.000 (0.000)	0.007 (0.000)
Age	0.241 (0.006)	0.272 (0.015)	0.528 (0.013)	0.502 (0.011)
Age-Squared	-0.021 (0.001)	-0.028 (0.002)	-0.057 (0.002)	-0.053 (0.001)
Some College	0.195 (0.002)			
College Plus	0.528 (0.002)			
Constant	1.112 (0.016)	0.923 (0.041)	0.527 (0.032)	1.083 (0.026)
Observations	1,060,351	519,750	264,233	276,368

Standard errors in parentheses

estimate γ by a logit maximum likelihood. Following [Robinson \(1988\)](#), we estimate α_2 by regressing $y_i - \widehat{E}[y_i | x_i' \widehat{\gamma}]$ on $(x_{2i} - \widehat{E}[x_{2i} | x_i' \widehat{\gamma}])$, where the \widehat{E} 's are constructed by kernel estimation. The estimator of the distribution of β_{1i} is then defined by minimizing the sum of the squares of the negative deviations between the sample analogs of the left and right hand sides of (10). Specifically, we define

$$\begin{aligned}
R_{j\ell}(F) &= E_F \left[\widehat{E} \left[1 \{ (y_i^* - x_{2i}' \widehat{\alpha}_2 - (x_{2i}' \widehat{\gamma}_2) E_F[\beta_{1i}] + 1 \{ x_{1i} = 0 \} \beta_{1i}) \in A_j, d_i = 1 \} | x_i' \widehat{\gamma} \in C_\ell \right] \right],
\end{aligned}$$

where \widehat{E} refers to sample averages as well as averaging β_{1i} over the distribution F , and

Table 2: Parametric Estimation under Normality (2-Step)

	All	No College	Some College	College Plus
White	0.040 (0.004)	0.081 (0.012)	0.073 (0.006)	0.095 (0.027)
Unemployment Rate	0.016 (0.001)	0.017 (0.002)	-0.001 (0.002)	-0.007 (0.006)
Year	0.005 (0.000)	0.003 (0.000)	-0.002 (0.001)	0.001 (0.002)
Age	0.037 (0.033)	0.012 (0.085)	0.976 (0.127)	1.684 (0.322)
Age-Squared	0.007 (0.004)	0.005 (0.011)	-0.117 (0.017)	-0.233 (0.049)
Some College	0.144 (0.008)			
College Plus	0.449 (0.012)			
Constant	1.715 (0.095)	1.641 (0.234)	-0.672 (0.339)	-2.344 (0.927)
Observations	1,060,351	519,750	264,233	276,368

Standard errors in parentheses

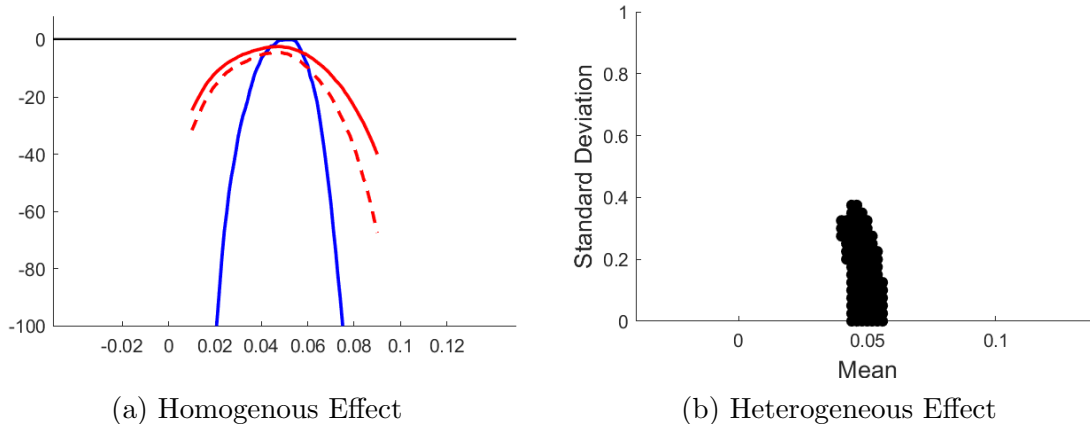
$E_F[\beta_{1i}]$ is the expectation of β_{1i} calculated using F . We then calculate the objective function

$$Q_n(F) = - \sum_{\ell,j} \max \{R_{j,\ell-1}(F) - R_{j,\ell}(F), 0\}^2 \quad (11)$$

for the distributions, F , under consideration.

We first calculate the identified region for the coefficient on the dummy for being white (β_1) in a model with homogeneous parameters. In other words, F is degenerate. In this case, the approach here is the same as that in [Honoré and Hu \(2020\)](#). The left hand panel of [Figure 3](#) displays the objective function, (11), as a function of the parameter, as well as the 20% (the solid red line) and 5% (the dashed red line) critical value functions calculated using sub-sampling (see [Canay and Shaikh \(2017\)](#)) for the full sample. We generate 1,000 sub-samples, each having sample size equal to 50,000. The left hand panel of [Figure 3](#) shows the 95% confidence interval for the coefficient on being white to be (0.042, 0.060). This overlaps

Figure 3: Estimated Effect. Full Sample.



with the confidence intervals suggested by the maximum likelihood estimator and by the 2-step estimator which assume normality. It is quite time-consuming to calculate the critical values by subsampling. For the remaining results, we therefore generate 250 subsamples and report 20% critical regions.

In the right panel of Figure 3, we report the 80% confidence region for the identified set in a model in which the coefficient on the dummy for being white is allowed to take on two values, θ_1 and θ_2 , with probabilities p and $1 - p$. We restrict θ_1 and θ_2 to be between -1 and 1 , and the grid for p is $0, 0.05, 0.10, \dots, 0.50$. The confidence set is calculated by sub-sampling as above.

The identified region in the right panel of Figure 3 contains points for which the standard deviation of the parameter of interest is 0. This is consistent with the fact that the left hand panel of Figure 3 gives a non-empty confidence region under the assumption of parameter homogeneity. On the other hand, the identified regions also contain points for which the standard deviation of β_1 is quite high relative to its mean. The identified set for the average effect, $E[\beta_{1i}]$, is fairly small, although it does include points that are lower than the 80% confidence region that would be obtained under the assumption that β_1 is homogenous.⁶

Figures 4, 5, and 6 show the estimated effects for the three subsamples defined by educa-

⁶As pointed out by a referee, it might not be interesting to estimate the effect of being White *conditional* on education. We performed the calculations leading to Figure 3 excluding education as an explanatory variable. This model is strongly rejected by the data, and we therefore do not pursue this further in this paper.

Figure 4: Estimated Effect. No College.

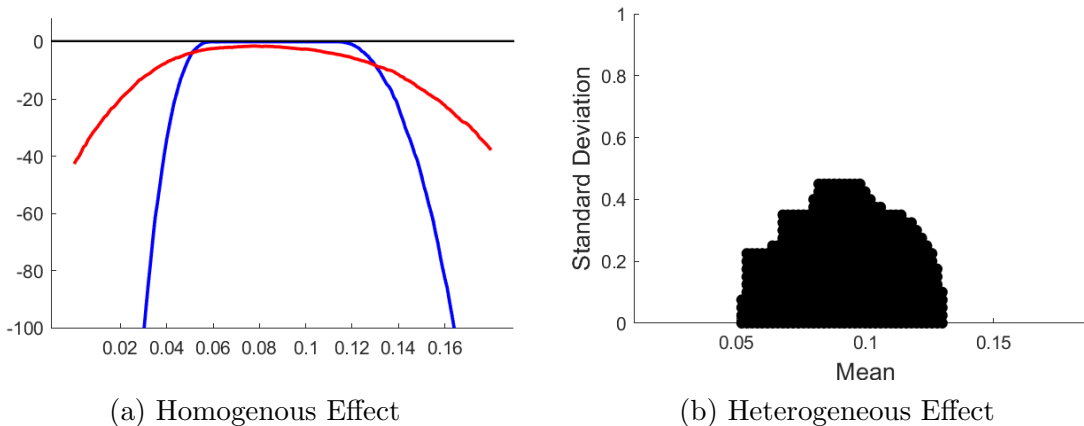
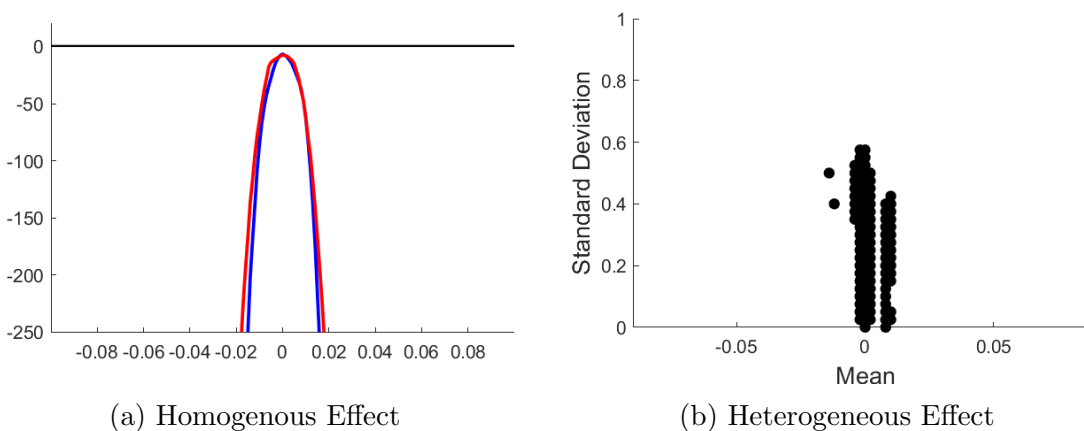


Figure 5: Estimated Effect. Some College.



tion group. Since the sample sizes for these subsets are smaller than for the full data set (see Table 1), we use sub-sample sizes of 30,000, 20,000, and 20,000 for the three subsamples.

The most striking finding in Figures 4, 5, and 6 is that the confidence set is empty for the subset of observations with at least a college degree. This suggests that the simple sample selection model is inconsistent with the data. We also find it interesting that the location of the maximum of the objective function for this group is slightly negative. This is consistent with the pseudo-maximum-likelihood estimate of the coefficient of being white in Table 1 being low (0.0195, with a robust standard error of 0.0033) for this sample.

The left hand panel of Figure 5 is difficult to read because we have kept the scale of the x-axis the same across Figures 3 to 6. Figure 7 shows the same objective function using

Figure 6: Estimated Effect. College Plus.

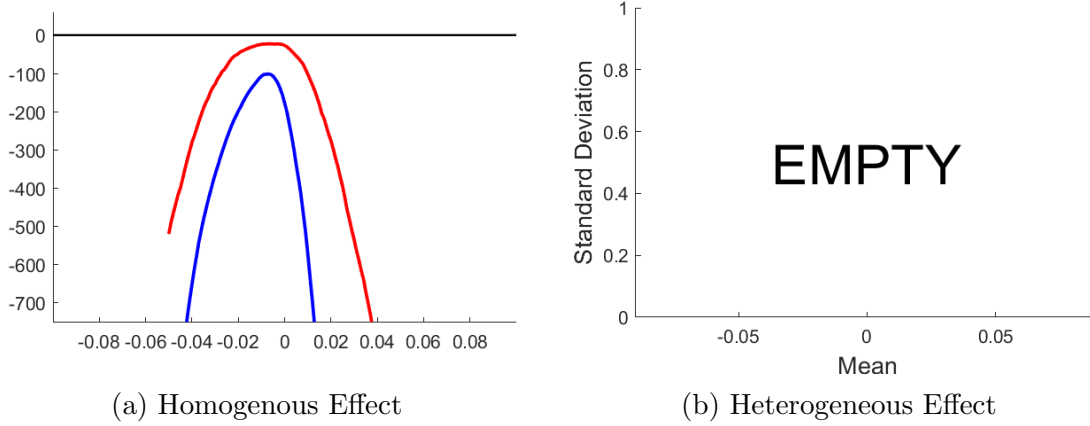
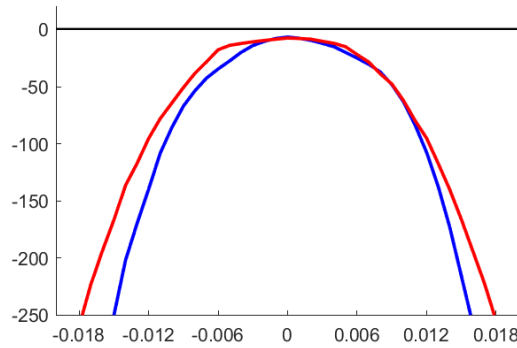


Figure 7: Estimated Effect. Some College.



a different scale. Formally speaking, it suggests a very small 80% confidence interval for a homogeneous β_1 . However, it also suggests that this apparent precision is due to the fact that the model is only marginally not rejected by the data.

We also note that the scale of the objective functions in the left hand panels of Figures 3 and 4 are quite different from those in Figures 5 and 6. Informally, this hints at the samples of women with some college and at least a college degree being more at odds with the simple sample selection model than the other samples.

Figure 4 suggests that the derived implications of the classical sample selection model are consistent with the data. As noted above, the parametric maximum likelihood and two-step estimation results obtained by estimating the model under the assumption of normality lead to parameter estimates that are statistically significantly different from each other,

Figure 8: Estimated Effect Using More Bins. Full Sample.

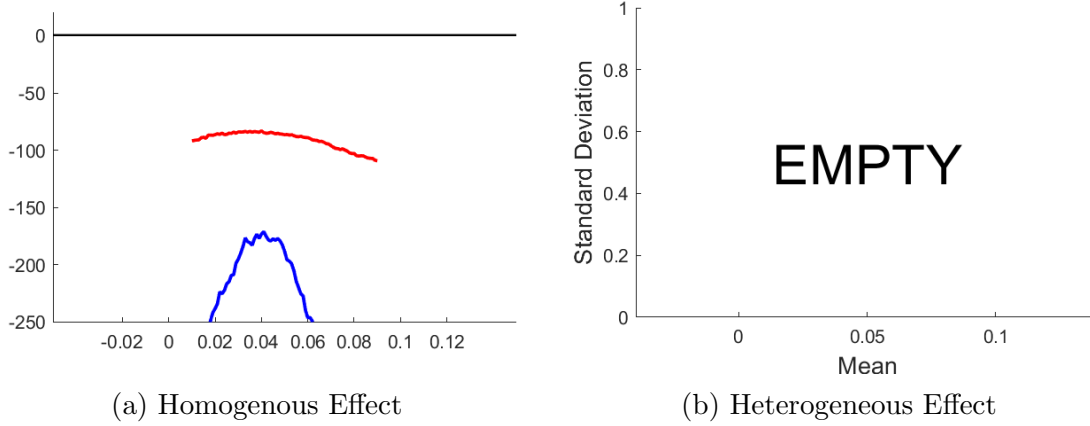
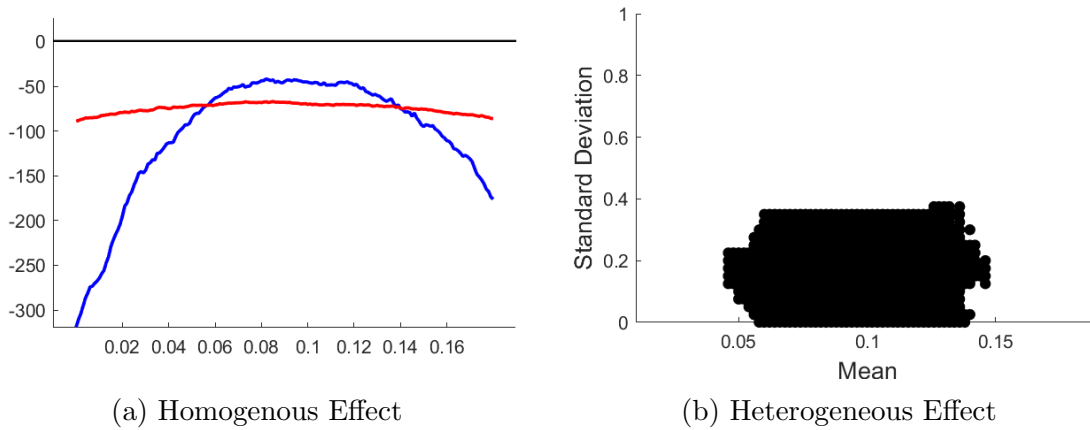


Figure 9: Estimated Effect Using More Bins. No College.



suggesting that the normality assumption is violated. For example, the absolute value of the t-tests for testing equality of each coefficient ranges between 2.1 and 3.1.

The equation (10) aggregates the constraints in equation (9) into 50 moment inequalities. One might worry that will lead to important loss of information. In Figures 8, 9, 10, and 11, we present the confidence sets that are obtained by dividing both the distribution of $x'_i \hat{\gamma}$ and of $y - x'_2 \hat{\alpha}_2 - (x'_{2i} \hat{\gamma}_2) E_F [\beta_{1i}]$ into 15 intervals, each based on their percentiles. As anticipated, this leads to smaller confidence regions, and the model is now rejected on the full sample.

Figure 10: Estimated Effect Using More Bins. Some College.

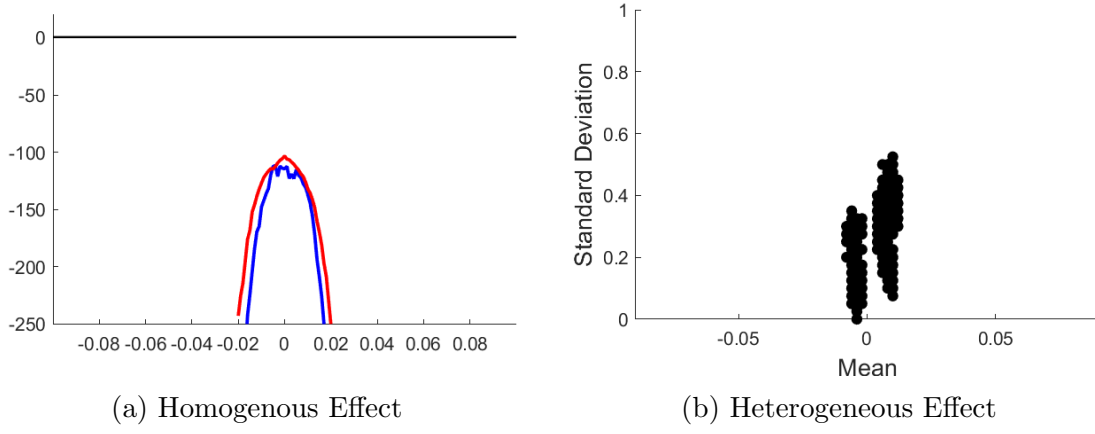
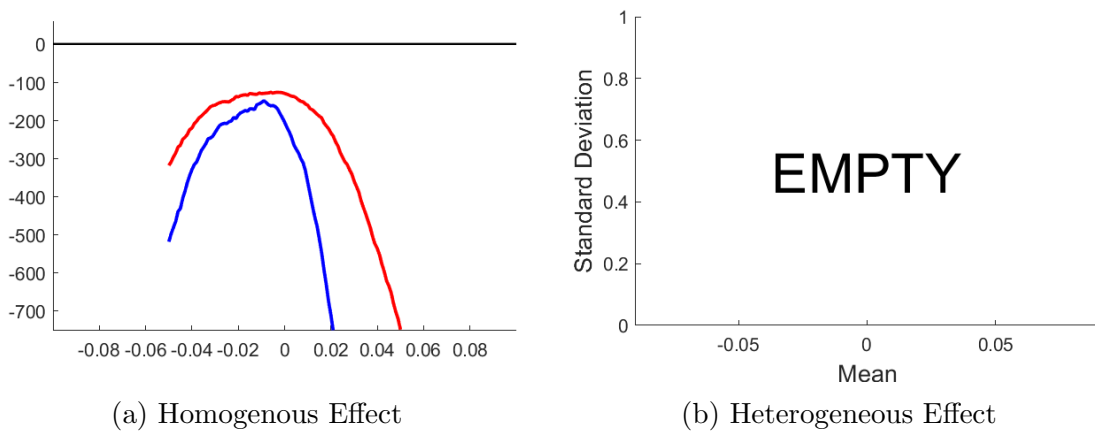


Figure 11: Estimated Effect Using More Bins. College Plus.



5 Heteroskedasticity

Most of the classical literature on the estimation of semiparametric sample selection models assumes that the error in the outcome equation is independent of the explanatory variables. [Donald \(1995\)](#) is a notable early exception. That paper assumes joint normality of the errors, but allows their variance matrix to depend arbitrarily on the explanatory variables. In other words, [Donald \(1995\)](#) introduces heteroskedasticity by multiplying the errors by an unknown function of x . In the spirit of this, [Chen and Khan \(2003\)](#) allow for multiplicative heteroskedasticity in both the selection equation and the outcome equation. That paper maintains an exclusion restriction.⁷

In this subsection, we first investigate identification when the error in the outcome equation is allowed to have multiplicative heteroskedasticity and then proceed to the more general case. We maintain the assumption that the error in the selection equation is independent of the explanatory variable. The reason is that heteroskedasticity in the selection equation can actually aid in the identification of β . See, for example, [Ahn and Powell \(1993\)](#), [Chen and Khan \(2003\)](#), [Escanciano, Jacho-Chávez, and Lewbel \(2016\)](#) and the discussion in [Section 6.2](#).

5.1 Univariate x

We start by introducing multiplicative heteroskedasticity in the outcome equation of the simple model [\(3\)](#), where the only explanatory variable is binary. In this subsection, we assume that the parameter is homogeneous, so the only complication is the heteroskedasticity. In order to simplify the exposition, we focus on the case where the sample selection is more severe when $x_i = 0$ than when $x_i = 1$ (i.e. γ in the sample selection equation is positive and normalized to 1).

Multiplicative heteroskedasticity only makes sense after one has controlled for the level (for example, the mean or the median) of the errors. We therefore write

⁷[Klein and Vella \(2009\)](#) consider a related model with a dummy endogenous variable. That paper allows for heteroskedasticity in both equations, and the heteroskedasticity in the selection equation is assumed to be multiplicative; see also [Klein and Vella \(2010\)](#).

$$y_i = \beta_0 + x_i\beta + \sigma(x_i)\varepsilon_i \quad \text{is observed if} \quad x_i + \nu_i > 0. \quad (12)$$

When $\sigma(x)$ is constant, β_0 becomes part of ε_i . Otherwise, β_0 is the level around which the multiplicative heteroskedasticity operates. Below, we use σ to denote $\sigma(1)$. Since the distribution of ε_i is unspecified, there is no loss of generality in assuming that $\sigma(0) = 1$.

As before, the monotonicity of the selection equation implies that

$$P(\varepsilon_i \in A, \nu_i > 0) \leq P(\varepsilon_i \in A, \nu_i > -1)$$

for any A . Since ε_i is independent of x_i , and with $d_i = 1\{x_i + \nu_i > 0\}$, this can be written as

$$P(\varepsilon_i \in A, d_i = 1 | x_i = 0) \leq P(\varepsilon_i \in A, d_i = 1 | x_i = 1).$$

As $y_i = \varepsilon_i + \beta_0$ when $x_i = 0$, and $y_i = \beta_0 + \beta + \sigma\varepsilon_i$ when $x_i = 1$, the true $(\beta_0 + \beta, \sigma)$ must therefore satisfy

$$P(y_i - \beta_0 \in A, d_i = 1 | x_i = 0) \leq P((y_i - \beta - \beta_0)/\sigma \in A, d_i = 1 | x_i = 1).$$

This gives the following identified set for (β_0, β, σ) :

$$\{(b_0, b, s) : P(y_i - b_0 \in A, d_i = 1 | x_i = 0) \leq P((y_i - b_0 - b)/s \in A, d_i = 1 | x_i = 1) \text{ for all } A\}.$$

This can be extended to a model with non-multiplicative heteroskedasticity. Suppose that when $x_i = 0$ we observe

$$y_i = \varepsilon_i^0 \quad \text{if} \quad \nu_i > 0,$$

and when $x_i = 1$ we observe

$$y_i = \beta + \varepsilon_i^1 \quad \text{if} \quad \nu_i > -1.$$

As before, x_i is independent of the errors $(\varepsilon_i^0, \varepsilon_i^1, \nu_i)$, and β_0 is now implicit in ε_i^0 and ε_i^1 . Of course, without restrictions on the distributions of ε_i^0 and ε_i^1 , β will be unidentified since

one can incorporate it in ε_i^1 . We therefore have in mind that their distributions, F_0 and F_1 , belong to some class of distributions, \mathcal{F} . For example, F_0 and F_1 could be restricted to having mean or median equal to 0.

For simplicity, assume that \mathcal{F} restricts both ε_i^0 and ε_i^1 to have continuous, strictly increasing cumulative distribution functions, F_0 and F_1 , respectively. Then ε_i^0 is distributed like $F_0^{-1}(F_1(\varepsilon_i^1))$.

As before, we have the inequality

$$P(\varepsilon_i^0 \in A, d_i = 1 | x_i = 0) \leq P(\varepsilon_i^0 \in A, d_i = 1 | x_i = 1),$$

or

$$P(\varepsilon_i^0 \in A, d_i = 1 | x_i = 0) \leq P(F_0^{-1}(F_1(\varepsilon_i^1)) \in A, d_i = 1 | x_i = 1).$$

Let $g(\cdot) = F_0^{-1}(F_1(\cdot))$. Using the fact that $\varepsilon_i^0 = y_i$ when $x_i = 0$ and that $\varepsilon_i^1 = y_i - \beta$ when $x_i = 1$, we then have

$$P(y_i \in A, d_i = 1 | x_i = 0) \leq P(g(y_i - \beta) \in A, d_i = 1 | x_i = 1).$$

So one identified set for β is

$\{b : \text{There exists an increasing function, } g(\cdot) = F_0^{-1}(F_1(\cdot)) \text{ with } F_0, F_1 \in \mathcal{F}, \text{ such that}$

$$P(y_i \in A, d_i = 1 | x_i = 0) \leq P(g(y_i - b) \in A, d_i = 1 | x_i = 1) \text{ for all } A\}.$$

Restrictions on the form of heteroskedasticity will appear as restrictions on the function g in the expression above. For example, with the multiplicative heteroskedasticity above, $\varepsilon_i^0 = \beta_0 + \varepsilon_i$ and $\varepsilon_i^1 = \beta_0 + \beta_1 + \sigma\varepsilon_i$. Therefore $F_1(a) = F_0(\beta_0 + (a - \beta_0 - \beta_1)/\sigma)$ and $g(y_i) = F_0^{-1}(F_1(y_i)) = \beta_0 + (a - \beta_0 - \beta_1)/\sigma$.

5.2 Multiple x and Heteroskedasticity

Allowing for heteroskedasticity is more complicated when the model includes additional explanatory variables.

Consider the model

$$y_i^* = \beta_0 + x_i' \beta + \sigma(x_i) \varepsilon_i,$$

where σ belongs to a class of heteroskedasticity functions. When $\sigma(x_i)$ is constant, β_0 can be incorporated into ε_i . When $\sigma(x_i)$ is not constant, β_0 is implicitly defined as the central tendency parameter around which the multiplicative heteroskedasticity operates.

For the true heteroskedasticity parameter, σ ,

$$y_i^* / \sigma(x_i) = \beta_0 / \sigma(x_i) + x_i / \sigma(x_i)' \beta + \varepsilon_i. \quad (13)$$

Suppose that the function σ is known and is not a constant. The explanatory variables in (13) are then not the same as in the sample selection equation, and the key assumption for identification is that conditional on $x_i' \gamma$, $[1 / \sigma(x_i), x_i / \sigma(x_i)]$ has “full rank” (i.e., is not contained in a linear subspace of \mathbb{R}^{k+1} (with probability 1)). This will typically be satisfied unless $\sigma(x_i)$ is constant.

One possible approach for bounding β (in the population) would then be to apply the following procedure to each candidate function, $\sigma(x_i)$. If $[1 / \sigma(x_i), x_i / \sigma(x_i)]$ has full rank conditional on $x_i' \gamma$, then this identifies $\beta(\sigma)$. It must then be the case that

$$\begin{aligned} P((y_i - x_i' \beta(\sigma)) / \sigma(x_i) \in A, d_i = 1 | x_i' \gamma = \xi_1) \\ \leq P((y_i - x_i' \beta(\sigma)) / \sigma(x_i) \in A, d_i = 1 | x_i' \gamma = \xi_2) \end{aligned} \quad (14)$$

for all A and $\xi_1 < \xi_2$. If that is not the case, then that $\sigma(x_i)$ can be eliminated from the identified set. If $[1 / \sigma(x_i), x_i / \sigma(x_i)]$ does not have full rank conditional on $x_i' \gamma$, then [Honoré and Hu \(2020\)](#) delivers the identified set for β for that σ . If that identified set is empty, then σ can be eliminated from the identified set.

Suppose, for example,

$$y_i^* = \beta_0 + x_{1i} \beta_1 + x_{2i}' \beta_2 + \sigma(x_i) \varepsilon_i,$$

where x_{1i} is binary and one specifies the heteroskedasticity function to be a function of x_{1i}

alone:

$$\sigma(x_i) = \begin{cases} 1 & \text{if } x_{1i} = 0 \\ \sigma & \text{if } x_{1i} = 1. \end{cases}$$

In this case $x_i/\sigma(x_i)$ will not have full rank conditional on $x'_i\gamma$ if x is composed of all interactions between x_{1i} and a vector of variables w_i (in other words, $x_{2i} = ((1 - x_i) \cdot w_i, x_i \cdot w_i)$).

5.3 Empirical Illustration

The discussion in Section 4 suggests that our simple specification of the classical sample selection model is strongly rejected for the sample of women with a college degree or more. In this section, we explore whether the data are consistent with the derived implications of a version of the sample selection model in which the errors are heteroskedastic as a function of being white. Except for allowing for heteroskedasticity, the specification is the same as in Section 4.

For a set of values of σ (bounded away from 1), we consider the model

$$\begin{aligned} y_i^*/\sigma &= \beta_0/\sigma + \beta_1/\sigma + (x_{2i}/\sigma)' \beta_2 + \varepsilon_i & \text{when } x_{1i} = 1 & \text{ and} \\ y_i^* &= \beta_0 + x'_{2i}\beta_2 + \varepsilon_i & \text{when } x_{1i} = 0, \end{aligned}$$

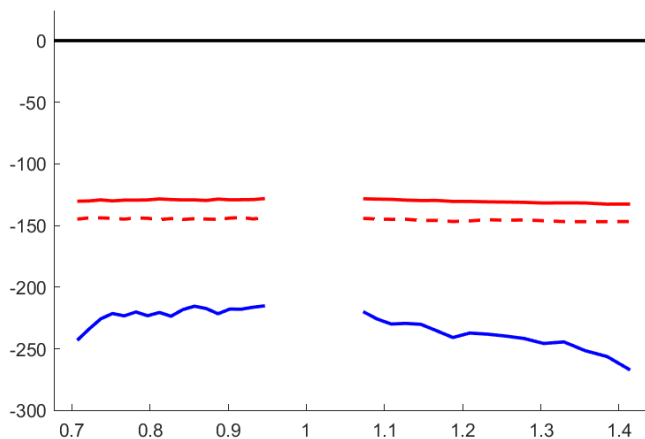
and $y_i = y_i^*$ is observed whenever $x_{1i} + x'_{2i}\gamma_2 + \nu_i > 0$. Here, x_{1i} is an indicator for being white. For each value of σ , we estimate this model using the estimator of the semiparametric sample selection model proposed by Powell (1987).⁸ We bound σ away from 1, because when σ is 1, the key identifying exclusion restriction for Powell's estimator is not satisfied, and we expect the inference to be arbitrarily poor when σ is arbitrarily close to 1.

Consider a collection of sets, A_j and C_ℓ , where the C_ℓ 's are increasing in the sense that the every element in $C_{\ell-1}$ is below each element in C_ℓ . We define

$$R_{j,\ell}(\sigma) = \widehat{E} \left[1 \left\{ \left(y_i^*/\sigma(x_i) - \widehat{\beta}_0/\sigma(x_i) - x'_i\widehat{\beta}/\sigma(x_i) \right) \in A_j, d_i = 1 \right\} \middle| x'_i\widehat{\gamma} \in C_\ell \right].$$

⁸We estimate the selection equation using a logit model, and we use a normal kernel and a bandwidth of 0.05 for the outcome equation.

Figure 12: Allowing for Heteroskedasticity



The functions $R_{j,\ell}(\sigma)$ estimate the terms on each side of the inequality in (14) aggregated over a set of values of ξ . In the population, and at the true parameter values, $R_{j,\ell}(\sigma) \leq R_{j,k}(\sigma)$ for $\ell < k$. We therefore define the objective function

$$Q_n(\sigma) = - \sum_{\ell,j} \max \{ R_{j,\ell-1}(F) - R_{j,\ell}(F), 0 \}^2.$$

If the model is correct and the sample is large, $Q_n(\sigma)$ should be close to 0 at the true σ .

As in Section 4, we calculate the 20% (the solid red line) and 5% (the dashed red line) critical value functions by subsampling using 1,000 subsamples with 20,000 observations in each. The resulting graphs are shown in Figure 12.

It is clear from Figure 12 that for the sample of women with a college degree or more, our simple specification of the classical sample selection model is still strongly rejected after allowing for heteroskedasticity.

6 Generalizations

In this section, we discuss identification in several extensions of the sample selection model above. Throughout, we assume that γ_1 is positive and normalized to 1. In other words, we

assume that everything else equal, the sample selection is less severe when x_{1i} is one than when it is zero.

6.1 β depends on ε

In the discussion in Section 3, we assumed that β_i is independent of (ε_i, ν_i) . This is a strong assumption. Here, we illustrate one way to proceed under the alternative (strong) assumption that β_i is a deterministic function of ε_i . To simplify the exposition, we focus on the case where there is only one binary explanatory variable:

$$y_i = \beta(\varepsilon_i)x_i + \varepsilon_i \quad \text{if} \quad x_i + \nu_i > 0.$$

For any interval, A , we have $P(\varepsilon_i \in A, d_i = 1 | x_i = 0) \leq P(\varepsilon_i \in A, d_i = 1 | x_i = 1)$ and hence

$$P(\beta(\varepsilon_i) + \varepsilon_i \in A, d_i = 1 | x_i = 0) \leq P(\beta(\varepsilon_i) + \varepsilon_i \in A, d_i = 1 | x_i = 1),$$

or

$$P(\beta(y_i) + y_i \in A, d_i = 1 | x_i = 0) \leq P(y_i \in A, d_i = 1 | x_i = 1).$$

This provides a set of restrictions which can be used to bound the function $\beta(\cdot)$.

6.2 Identification Through Possible Nonlinearity

The heteroskedasticity in Section 5.2 transformed the explanatory variable in the outcome equation from x_i to $x_i/\sigma(x_i)$, making the explanatory variables in the outcome equation a nonlinear function of the explanatory variable in the selection equation. This gives an exclusion restriction which can be used to achieve identification of β for a known function, σ . In the spirit of [Escanciano, Jacho-Chávez, and Lewbel \(2016\)](#), we can also consider identification through nonlinearities in the *selection* equation. The basic idea in that paper is that the nonlinearity in the selection equation can act as an excluded variable in the outcome equation (see also the discussion in [Ahn and Powell \(1993\)](#)).

To explore this avenue for identification in a model with parameter heterogeneity, we again start with the equation

$$y_i^* = x_{1i}\beta_{1i} + x'_{2i}\beta_2 + \varepsilon_i, \quad (15)$$

where β_{1i} is assumed to be independent of $(x_i, \nu_i, \varepsilon_i)$.

Without (much) loss of generality, assume that $d_i = 1 \{p(x_i) > \nu_i\}$ where ν_i is uniform (so $P(d_i = 1 | x_i) = p(x_i)$). Then

$$y_i = x_{1i}\beta_{1i} + x'_{2i}\beta_2 + h(p(x_i)) + u_i,$$

where $h(p(x_i)) = E[\varepsilon_i | p(x_i) > \nu_i]$, $u_i = \varepsilon_i - E[\varepsilon_i | p(x_i) > \nu_i]$, and $E[u_i | x_i, d_i = 1] = 0$.

Hence,

$$\begin{aligned} y_i - E[y_i | p(x_i), d_i = 1, \beta_{1i}] &= (x_{1i} - E[x_{1i} | p(x_i), d_i = 1, \beta_{1i}]) \beta_{1i} \\ &\quad + (x'_{2i} - E[x'_{2i} | p(x_i), d_i = 1, \beta_{1i}]) \beta_2 + \tilde{u}_i, \end{aligned}$$

where $\tilde{u}_i = u_i - E[u_i | p(x_i), d_i = 1, \beta_{1i}]$ has conditional mean 0. Since β_{1i} is assumed to be independent of $(x_i, \nu_i, \varepsilon_i)$, this becomes

$$\begin{aligned} y_i - E[y_i | p(x_i), d_i = 1] &= (x_{1i} - E[x_{1i} | p(x_i), d_i = 1]) E[\beta_{1i}] \\ &\quad + (x'_{2i} - E[x'_{2i} | p(x_i), d_i = 1]) \beta_2 + \tilde{\tilde{u}}_i, \end{aligned}$$

where $\tilde{\tilde{u}}_i = \tilde{u}_i + (x_{1i} - E[x_{1i} | p(x_i), d_i = 1, \beta_{1i}]) (\beta_{1i} - E[\beta_{1i}])$ has conditional mean 0. This identifies $(E[\beta_{1i}], \beta_2)$ subject to a rank condition on $((x_{1i} - E[x_{1i} | p(x_i), d_i = 1]), (x'_{2i} - E[x'_{2i} | p(x_i), d_i = 1]))$.

6.3 Panel Data

We finally note that the general approach outlined in this paper also applies to panel data versions of the sample selection model like the one studied in [Kyriazidou \(1997\)](#):

$$y_{it}^* = x'_{it}\beta + \alpha_i + \varepsilon_{it}$$

where y_{it}^* is observed whenever $x'_{it}\gamma + \delta_i + \nu_{it} > 0$. Here α_i and δ_i play the roles of fixed effects in the outcome and selection equations, respectively. It is well known that γ is identified up to scale subject to regularity conditions (see Manski (1987)), so from an identification point of view, we can consider it known.

If $x'_{i2}\gamma > x'_{i1}\gamma$, then $P(\varepsilon_{i2} \in A, d_{i2} = 1) \geq P(\varepsilon_{i1} \in A, d_{i1} = 1)$ as above. This implies that $P(\varepsilon_{i2} + \alpha_i \in A, d_{i2} = 1) \geq P(\varepsilon_{i1} + \alpha_i \in A, d_{i1} = 1)$. Writing this in terms of the observed y_{it} , we therefore have $P(y_{i2} - x'_{i2}\beta \in A, d_{i2} = 1) \geq P(y_{i1} - x'_{i1}\beta \in A, d_{i1} = 1)$. This suggests an identified set for β of the type

$$\begin{aligned} \{\beta : P(y_{i2} - x'_{i2}\beta \in A, d_{i2} = 1 | x'_{i2}\gamma > x'_{i1}\gamma) \\ \geq P(y_{i1} - x'_{i1}\beta \in A, d_{i1} = 1 | x'_{i2}\gamma > x'_{i1}\gamma) \text{ for all } A\}. \end{aligned}$$

7 Potential Outcomes

The key to the relative simplicity of the identified region discussed so far is that the heterogeneous parameter has been multiplied by a binary x_{1i} . This implies that when $x_{1i} = 0$, the distribution of y_i differs from the distribution of ε_i only because of the selection and the additional controls, x_{2i} . The heterogeneity of β_{1i} plays no role when $x_{1i} = 0$. In some cases, this might seem somewhat artificial. For example, in the empirical illustration in Section 4, the model would be different if we redefine x_{1i} to be 0 for whites and 1 for non-whites. One way to overcome this is to use the potential outcomes setup frequently used in the program evaluation literature. Within the structure of the selection model discussed here, one would specify the potential outcomes as⁹

$$y_i^* = \begin{cases} \beta_{0i} + x'_{2i}\beta_2 + \varepsilon_i & \text{when } x_{1i} = 0 \\ \beta_{1i} + x'_{2i}\beta_2 + \varepsilon_i & \text{when } x_{1i} = 1, \end{cases}$$

where y_i is observed if $x'_i\gamma + \nu_i > 0$. We assume that (β_{0i}, β_{1i}) is independent of $(\varepsilon_i, \nu_i, x_i)$, but β_{0i} and β_{1i} need not be independent of each other.

⁹Here β_2 is the same whether x_{1i} is 0 or 1. This is easily relaxed by interacting x_{2i} with x_{1i} .

To fix ideas, we first consider the case where there are no additional controls (x_{2i}) and where the selection is more severe when $x_{1i} = 0$ than when $x_{1i} = 1$ (i.e., $\gamma_1 = 1$). In this case,

$$P(\varepsilon_i \in A, d_i = 1 | x_{1i} = 0) \leq P(\varepsilon_i \in A, d_i = 1 | x_{1i} = 1)$$

for any set A . This implies that

$$P\left(\left(\varepsilon_i + \tilde{\beta}_{0i} + \tilde{\beta}_{1i}\right) \in A, d_i = 1 \mid x_{1i} = 0\right) \leq P\left(\left(\varepsilon_i + \tilde{\beta}_{0i} + \tilde{\beta}_{1i}\right) \in A, d_i = 1 \mid x_{1i} = 1\right), \quad (16)$$

where $\tilde{\beta}_{0i}$ and $\tilde{\beta}_{1i}$ are independent of each other, with $\tilde{\beta}_{0i}$ drawn from the marginal distribution of β_{0i} and $\tilde{\beta}_{1i}$ drawn from the marginal distribution of β_{1i} .

In terms of the observable data, y_i is distributed like $\varepsilon_i + \tilde{\beta}_{0i}$ when $x_{1i} = 0$ and like $\varepsilon_i + \tilde{\beta}_{1i}$ when $x_{1i} = 1$. Equation (16) can therefore be written as

$$P\left(\left(y_i + \tilde{\beta}_{1i}\right) \in A, d_i = 1 \mid x_{1i} = 0\right) \leq P\left(\left(y_i + \tilde{\beta}_{0i}\right) \in A, d_i = 1 \mid x_{1i} = 1\right),$$

where $\tilde{\beta}_{0i}$ and $\tilde{\beta}_{1i}$ are independent of the data and distributed as the marginal distributions of β_{0i} and β_{1i} , respectively. This yields constraints on the marginal distributions of β_{0i} and β_{1i} .

Additional controls, x_{2i} , can be dealt with as in Section 3. Conditional on selection, and conditional on (β_{0i}, β_{1i}) , we have

$$y_i = (1 - x_{1i})\beta_{0i} + x_{1i}\beta_{1i} + x'_{2i}\beta_2 + g(x'_i\gamma) + u_i,$$

where $g(x'_i\gamma) = E[\varepsilon_i | x_i, x'_i\gamma + \nu_i > 0]$ and $E[u_i | x_i, \beta_{1i}] = 0$.

Using that $(x_{1i} - E[x_{1i}|x'_i\gamma]) = -(x_{2i} - E[x_{2i}|x'_i\gamma])' \gamma_2$, we therefore have

$$\begin{aligned}
y_i - E[y_i|x'_i\gamma] &= (1 - x_{1i})\beta_{0i} + x_{1i}\beta_{1i} + (x_{2i} - E[x_{2i}|x'_i\gamma])' \beta_2 + u_i \\
&\quad - (1 - E[x_{1i}|x'_i\gamma]) E[\beta_{0i}] - E[x_{1i}|x'_i\gamma] E[\beta_{1i}] \\
&= (1 - x_{1i})(E[\beta_{0i}] + \beta_{0i} - E[\beta_{0i}]) + x_{1i}(E[\beta_{1i}] + \beta_{1i} - E[\beta_{1i}]) \\
&\quad + (x_{2i} - E[x_{2i}|x'_i\gamma])' \beta_2 + u_i - (1 - E[x_{1i}|x'_i\gamma]) E[\beta_{0i}] - E[x_{1i}|x'_i\gamma] E[\beta_{1i}] \\
&= (1 - x_{1i}) E[\beta_{0i}] + (1 - x_{1i})(\beta_{0i} - E[\beta_{0i}]) + x_{1i} E[\beta_{1i}] + x_{1i}(\beta_{1i} - E[\beta_{1i}]) \\
&\quad + (x_{2i} - E[x_{2i}|x'_i\gamma])' \beta_2 + u_i - (1 - E[x_{1i}|x'_i\gamma]) E[\beta_{0i}] - E[x_{1i}|x'_i\gamma] E[\beta_{1i}] \\
&= (x_{1i} - E[x_{1i}|x'_i\gamma]) E[\beta_{1i} - \beta_{0i}] + \\
&\quad (1 - x_{1i})(\beta_{0i} - E[\beta_{0i}]) + x_{1i}(\beta_{1i} - E[\beta_{1i}]) + (x_{2i} - E[x_{2i}|x'_i\gamma])' \beta_2 + u_i \\
&= (x_{2i} - E[x_{2i}|x'_i\gamma])' (\beta_2 - \gamma_2 E[\beta_{1i} - \beta_{0i}]) \\
&\quad + (1 - x_{1i})(\beta_{0i} - E[\beta_{0i}]) + x_{1i}(\beta_{1i} - E[\beta_{1i}]) + u_i
\end{aligned}$$

The term $(1 - x_{1i})(\beta_{0i} - E[\beta_{0i}]) + x_{1i}(\beta_{1i} - E[\beta_{1i}]) + u_i$ has mean 0 conditional on x_i , and we can therefore identify $\alpha_2 \equiv (\beta_2 - \gamma_2 E[\beta_{1i} - \beta_{0i}])$ by regressing $(y_i - E[y_i|x'_i\gamma])$ on $(x_{2i} - E[x_{2i}|x'_i\gamma])$.

With this, we have

$$\begin{aligned}
y_i^* - x'_{2i}\alpha_2 &= y_i^* - x'_{2i}(\beta_2 - \gamma_2 E[\beta_{1i} - \beta_{0i}]) \\
&= (1 - x_{1i})\beta_{0i} + x_{1i}\beta_{1i} + x'_{2i}\beta_2 + \varepsilon_i - x'_{2i}(\beta_2 - \gamma_2 E[\beta_{1i} - \beta_{0i}]) \\
&= (1 - x_{1i})\beta_{0i} + x_{1i}\beta_{1i} + x'_{2i}\gamma_2 E[\beta_{1i} - \beta_{0i}] + \varepsilon_i
\end{aligned}$$

or

$$y_i^* - x'_{2i}\alpha_2 + (1 - x_{1i})\beta_{1i} + x_{1i}\beta_{0i} - x'_{2i}\gamma_2 E[\beta_{1i} - \beta_{0i}] = \beta_{0i} + \beta_{1i} + \varepsilon_i.$$

The marginal distributions of β_{0i} and β_{1i} must therefore satisfy

$$\begin{aligned}
&P((y_i^* - x'_{2i}\alpha_2 + (1 - x_{1i})\beta_{1i} + x_{1i}\beta_{0i} - x'_{2i}\gamma_2 E[\beta_{1i} - \beta_{0i}]) \in A, d_i = 1 | x'_i\gamma = \xi_2) \\
&\geq P((y_i^* - x'_{2i}\alpha_2 + (1 - x_{1i})\beta_{1i} + x_{1i}\beta_{0i} - x'_{2i}\gamma_2 E[\beta_{1i} - \beta_{0i}]) \in A, d_i = 1 | x'_i\gamma = \xi_1)
\end{aligned}$$

for all intervals A and $\xi_2 > \xi_1$.

8 Conclusion

Semiparametric sample selection models are generally not point-identified without exclusion restrictions. In earlier work, [Honoré and Hu \(2020\)](#) derived the sharp identified region of the parameters in such a model. In this paper, we extend that analysis to allow for parameter heterogeneity and heteroskedasticity while maintaining the basic linearity, independence and monotonicity assumptions of the classical sample selection model. We also discuss a potential outcomes version of the sample selection model, identification through nonlinearities, and panel data versions of the model.

We illustrate the key insights in a simple wage regression for females, where the parameter of interest is the coefficient on a dummy variable for being white. We find that for the full sample, neither the introduction of parameter heterogeneity nor heteroskedasticity is sufficient for the data to be consistent with the model. The classical sample selection model is especially at odds with the data for the subsample of women with a college degree or more.

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