The Impact of Heteroskedasticity in Observational Studies of Causal Effects

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Abstract

There is a large and rapidly growing causal inference literature, yet little is known about the impact of heteroskedasticity in popular causal settings. In observational studies where the presence of heteroskedasticity can not be ruled out with certainty, its effects in both treatment assignment and response generation must be studied. Our approach is Bayesian and involves specific modeling whose practical adequacy is then addressed through model comparisons. We build upon and extend existing methods for several well-known settings such as sharp and fuzzy regression discontinuity designs, the potential outcomes framework, and propensity score matching. Key features of our approach in these settings include flexible modeling and context-specific computationally efficient estimation algorithms, the ability to recover various functions of the treatment parameters, and an improved efficiency of estimation relative to alternatives that employ only a subset of the data in the analysis. Simulation studies are used to gauge the adequacy of the proposed methods, while their practical applicability is studied in three applications – we examine the effect of academic probation on subsequent academic performance, the influence of Medigap on healthcare expenditures, and the impact of COVID-19 vaccination on mental well-being. These applications illustrate the consequences of misspecification and provide strong evidence that the presence of heteroskedasticity should not be ignored.

`Keywords:` Bayesian estimation; Markov chain Monte Carlo; Regression discontinuity; Potential outcomes; Propensity score; Academic performance; Healthcare expenditure; Mental health.

1 Introduction

The formulation of an identification framework through which the observed outcomes for the treated and untreated units can be compared plays a central role in observational studies of causal effects because of complications due to non-random treatment assignment, correlation due to unobserved confounders, or the fundamental missingess of counterfactual outcomes at the unit level. A variety of parametric, semi-parametric and nonparametric approaches have been proposed in the literature

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that have dealt with the effect of continuous, binary, and categorical treatments in non-experimental settings in both classical and Bayesian contexts. Instrumental variable, regression discontinuity, potential outcome, and matching estimators, among others, have been proposed and implemented in applications. Classical approaches have tended to center around estimators that are robust to potential misspecifications of the data-generating process (DGP), which is often not explicitly stated, and inference is asymptotic. Bayesian methods, which we adopt in this paper, have instead focused on the DGP directly and explicitly, leading to finite-sample inferences; possible misspecification is handled by employing flexible modeling and specification searches through formal model comparisons.

One strand of the Bayesian literature has focused on estimating treatment effects in continuous and discrete (binary, ordinal, and count) instrumental variable models (Koop and Tobias, 2004; Mintz et al., 2013; Li and Tobias, 2014; Vossmeyer, 2014a), settings with sequential outcomes Munkin (2011), as well as models with nonparametric endogeneity (Kline and Tobias, 2008; Chib et al., 2009). Instrumental variable models typically require the exclusion of the instruments from the main regression equation of interest, but this is often the source of much contention in applied research. In this context, Chan and Tobias (2015) propose methods for analyzing models with imperfect instruments which do not necessarily satisfy the exclusion restriction and could appear in both the endogenous variable and main response equation. Extensions to models of endogeneity that also involve sample selection have been presented in Chib et al. (2009), Vossmeyer (2014b), and Vossmeyer (2016) (see also van Hasselt, 2014).

Another branch in the Bayesian treatment effect research has extended the potential outcomes framework for causal analysis (Roy, 1951; Rubin, 1974, 1977, 1978, 2004, 2005) in cross-sectional settings with continuous or discrete outcome variables in the presence of binary or categorical treatments (see, e.g., Munkin and Trivedi, 1999; Chib and Hamilton, 2000; Munkin, 2003; Munkin and Trivedi, 2003; Deb et al., 2006; Li and Tobias, 2008, 2011). Extensions to longitudinal settings have been addressed in (Chib and Hamilton, 2002; Jacobi et al., 2016). Estimation has been approached both by explicitly simulating the counterfactuals from their joint distribution with the observed outcomes (Li et al., 2004) and by only involving the observed outcomes Chib (2007). Heckman et al. (2014) proposed a way to model the joint distribution of potential outcomes by incorporating a latent factor.

Following the seminal work of Rosenbaum and Rubin (1983), much interest has also been devoted to the specification and estimation of propensity score methods (Dehejia and Wahba, 1999; Imai and van Dyk, 2004; Brand and Halaby, 2006; Zhao, 2008; Caliendo and Kopeinig, 2008; An, 2010; Zhao et al., 2020; Chaudhuri and Howley, 2022; Duan et al., 2023). A recent review is offered in Rosenbaum and Rubin (2022). The framework is useful because it is simple and theoretically powerful; yet, in practice results from its application have often been mixed. The potential for misspecification of the propensity score can weaken the performance of matching estimators, which motivates our work in this area.

We also focus on causal analysis done within the regression discontinuity design (RDD) framework. The RDD approach, introduced in Thistlethwaite and Campbell (1960) aims to address causal inference in a quasi-experimental settings where treatment assignments are based on another variable with a known cutoff, and with the assumption that there is a discontinuous treatment assignment rule at the cutoff point. There are many different many applications and extensions in the literature (see Hahn et al., 2001; Calonico et al., 2014a,b; Cattaneo et al., 2015; Dong, 2015; Dong and Lewbel, 2015; Fletcher and Tokmouline, 2018; Dong, 2019; Wright, 2020; Dong et al., 2023, among others), yet Bayesian analysis has been relatively recent (Chib and Jacobi, 2016; Branson et al., 2019; Geneletti et al., 2019; Chib et al., 2023).

Although there is a large and rapidly growing body of causal methodology, little is known about the impact of heteroskedasticity in most popular causal models. One exception is Ferman and Pinto (2019) who show that even in linear specifications such as difference-in-differences, standard methods may perform poorly in the presence of heteroskedasticity, especially in small samples, and derive techniques to correct for it. In non-linear contexts, including those mentioned earlier, however, the adverse effects of heteroskedasticity in both treatment assignment and response generation are expected to be amplified by any non-linearity and therefore require a deeper understanding. We pursue this objective in the Bayesian paradigm through modeling whose practical adequacy is then addressed by model comparisons. The analysis of the treatment effect and all other parameters of interest is then based on the relevant posterior distribution that is obtained as a by-product of Markov chain Monte Carlo (MCMC) simulation.

The rest of the paper is organized as follows. In Section 2 we build upon and extend existing Bayesian methods for the sharp and fuzzy regression discontinuity designs in which we couple

nonparametric modeling of the running variable with a model for heteroskedasticity. In Section 3 we develop modeling and estimation techniques for the analysis of a heteroskedastic potential outcomes framework. In Section 4 we examine the effect of heteroskedasticity on the performance of propensity score matching. In each of the aforementioned causal contexts, we present MCMC estimation algorithms, study their performance and the impact of heteroskedasticity in simulation studies, and employ them in applications to gauge their practical relevance. We also provide ways for computing marginal likelihoods for formal Bayesian model comparisons. Our applications involve the effect of academic probation on subsequent academic performance, the influence of Medigap on healthcare expenditures, and the impact of COVID-19 vaccination on mental well-being.

2 Regression Discontinuity Design

In this section we address both the sharp and fuzzy versions of the RDD framework with several aims in mind. First, we incorporate heteroskedasticity into the analysis and provide the necessary estimation techniques. Second, in line with Branson et al. (2019) and Chib et al. (2023), we employ flexible function modeling to safeguard against misspecification while improving efficiency by utilizing all available data, in contrast to estimators that only focus on a subset of observations around the cutoff point. Finally, we address the adequacy of key specification assumptions through formal model comparisons.

2.1 Sharp Regression Discontinuity Design

In a sharp RD setting, the treatment $T_i \in \{0, 1\}$ for unit $i = 1, \ldots, n$ is determined by a running variable w_i and a known cutoff w^* such that $T_i = \mathbb{1}\{w_i \geq w^*\}$. The potential outcomes of unit i are denoted by y_{i0} and y_{i1} for $T_i = 0$ and $T_i = 1$, respectively, and we suppose that they are generated by the additive specification

$$y_{ij} = g_j(w_i) + x_i'\beta_j + \varepsilon_{ij}, \quad \varepsilon_{ij} \sim N\left(0, \sigma_{ij}^2\right), \quad \ln(\sigma_{ij}^2) = z_i'\gamma_j, \quad \text{for} \quad j \in \{0, 1\}, \tag{1}$$

and we observe $y_i = (1 - T_i)\, y_{i0} + T_i y_{i1}$. Heterogeneity in this setting is introduced by letting $\ln(\sigma_{ij}^2) = z_i'\gamma_j$ for some collection of variables z_i that are believed to affect the behavior of the variance parameter and could include, but are not necessarily limited to variables in $\{x_i, w_i\}$ or their interactions. As specified in equation (1), the model is one of structural change between the

treated and untreated samples. Thus, intuitively, estimation can simply be performed separately within each sub-sample. However, estimation has typically been performed under the assumption that $\beta_0 = \beta_1$, which puts the emphasis on the discontinuity in running variable and, if confirmed by the data – a testable assumption that should be examined in applications as done in Section 2.2 – makes inference more precise. In the literature, the RD average treatment effect (RD ATE) is defined as

$$\begin{aligned} \tau_{SRD} &\equiv \lim_{w \downarrow w^{*+}} E(Y_1|w, x_i) - \lim_{w \uparrow w^{*-}} E(Y_0|w, x_i) \\ &= \lim_{w \downarrow w^{*+}} E\left(g_1(w) + x_i'\beta_1\right) - \lim_{w \uparrow w^{*-}} E\left(g_0(w) + x_i'\beta_0\right) , \end{aligned} \tag{2}$$

which, in the special case when $\beta_1 = \beta_0$, leads to

$$\tau_{SRD} = \lim_{w \downarrow w^{*+}} g_1(w) - \lim_{w \uparrow w^{*-}} g_0(w) . \tag{3}$$

The function $g_j(\cdot)$ plays a crucial role here, and is modeled nonparametrically with only local penalties for smoothness in order to mitigate the potential for undue influence of values of w far from w^* on the estimated values of $g_j(\cdot)$ close to w^* (Gelman and Imbens, 2019). Flexible functional modeling can be implemented through a variety of approaches including B-splines, regression splines, natural splines, truncated power series, or wavelets, among others (for a review, see, e.g., Ruppert et al., 2003; Ahamada and Flachaire, 2010). Here we focus on flexible modeling through Gaussian random fields Poirier (1973); Shiller (1984); Williams (1998); Fahrmeir and Lang (2001); Koop and Poirier (2004); Koop et al. (2005); Rue and Held (2005); Chib and Jeliazkov (2006); Chan and Jeliazkov (2009a); Jeliazkov (2013); Branson et al. (2019) because it allows for smoothing at every observed value of the running variable (instead of a coarse set of knots), while retaining key desirable computational properties. Extensions of the model in (1) to an additive nonparametric mean structure for the covariates x_i can be implemented as in Koop et al. (2005), Jeliazkov (2013), or Panagiotelis and Smith (2008), whereas extensions beyond normality can be pursued by employing scale mixtures of normals (Andrews and Mallows, 1974) or Dirichlet process mixtures (Ferguson, 1973; Antoniak, 1974). Chib and Greenberg (2010) combine nonparametric mean and error distribution modeling.

To facilitate the modeling and derivations, for the observations $(T_i, y_i, w_i, x_i, x_i)$, $i = 1, \ldots, n$, we define the vectors $y_0 \equiv (y_1, \ldots, y_{n_0})'$, $w_0 \equiv (w_1, \ldots, w_{n_0})'$, $y_1 \equiv (y_{n_0+1}, \ldots, y_n)'$, and $w_1 \equiv (w_{n_0+1}, \ldots, w_n)'$. To define the functions $g_j(\cdot)$, we denote the *unique ordered values* of w_j as ν_j,

i.e., $\nu_0 = (w_{0,\min}, \ldots, w^*)' = (v_{01}, \ldots, \nu_{0m_0})'$ $\nu_1 = (w^*, \ldots, w_{1,\max})' \equiv (\nu_{11}, \ldots, \nu_{1m_1})'$, with m_j being the number of elements in ν_j. Note that the cutoff w^* is un both ν_0 and ν_1 so as to enable computation of quantity of $g_0(w^*)$ and $g_1(w^*)$ in each MCMC iteration.

With these definitions, for $j \in \{0, 1\}$, $g_j = (g(\nu_{j1}), \ldots, g(\nu_{jm_j}))' \equiv (g_{j1}, \ldots, g_{jm_j})'$, we let the function evaluations follow a second order Markov process

$$g_{jl} = \left(1 + \frac{h_{jl}}{h_{jl-1}}\right) g_{jl-1} - \frac{h_{jl}}{h_{jl-1}} g_{jl-2} + \mu_{jl},$$

where $h_{jl} \equiv \nu_{jl} - \nu_{jl-1}$, $\mu_{jl} \sim N(0, \tau_j^2 h_{jl})$ and the process is initialized at

$$\begin{pmatrix} g_{j1} \\ g_{j2} \end{pmatrix} | \tau_j^2 \sim N\left(\begin{pmatrix} g_{j10} \\ g_{j20} \end{pmatrix}, \tau_j^2 G_{j0} \right),$$

where G_{j0} is a 2×2 symmetric positive definite matrix and τ^2 is a smoothness parameter whose magnitude determines the penalty to deviations from a locally linear relationship. Letting

$$H_j = \begin{pmatrix} 1 & & & & \\ & 1 & & & \\ \frac{h_{j3}}{h_{j2}} & -(1 + \frac{h_{j3}}{h_{j2}}) & 1 & & \\ & \ddots & \ddots & \ddots & \\ & & \frac{h_{jm}}{h_{jm-1}} & -(1 + \frac{h_{jm}}{h_{jm-1}}) & 1 \end{pmatrix}, \quad \Sigma_j = \begin{pmatrix} G_{j0} & & & \\ & h_{j3} & & \\ & & \ddots & \\ & & & h_{jm} \end{pmatrix},$$

we obtain the joint distribution $g_j | \tau_j^2 \sim N(g_{j0}, \tau_j^2 K_j^{-1})$, where $g_{j0} = H_j^{-1}(g_{j10}, g_{j20}, 0, \ldots, 0)'$ and $K_j = H_j' \Sigma_j^{-1} H_j$. Of key importance is the fact that K is a banded and operations involving it are of order $\mathcal{O}(n)$ (Chib and Jeliazkov, 2006). With this definition of g_j, $j \in \{0, 1\}$, stacking the model in (1), we can write

$$y_j = Q_j g_j + X_j \beta_j + \varepsilon_j, \quad \varepsilon_j \sim N(0, \Omega_j), \quad \Omega_j = \text{diag}\left(\{\sigma_{ij}^2\}_{i=1}^{n_j}\right), \quad \ln(\sigma_{ij}^2) = z_i' \gamma_j,$$

where Q_j is a $n \times m$ incidence matrices with entries $Q_j(i, k) = 1$ if $w_{ji} = \nu_{jk}$, and 0 otherwise. Consequently, the model is completed by the prior distributions

$$g_j | \tau_j^2 \sim N(g_{j0}, \tau_j^2 K_j^{-1}), \quad \tau_j^2 \sim IG(t_{\nu 0}/2, t_{d0}/2), \quad \beta_j \sim N(b_{j0}, B_{j0}), \quad \gamma_j \sim N(\gamma_{j0}, \Gamma_{j0}), \tag{4}$$

which, combined with the data density

$$f\left(y | g_0, g_1, \tau_0^2, \tau_1^2, \beta_0, \beta_1, \gamma_0, \gamma_1\right) = f_N\left(y_0 | Q_0 g_0 + X_0 \beta_0, \Omega_0\right) f_N\left(y_1 | Q_1 g_1 + X_1 \beta_1, \Omega_1\right)$$

leads to a joint posterior distribution that can be sampled by MCMC methods as discussed in Algorithm 1. We use computationally efficient precision-based sampling methods in the sampling

of g_j, and follow Chan et al. (2006), Gu et al. (2009), Gamerman (1997) and Nott and Leonte (2004) to form a Metropolis-Hastings proposal density based on iteratively reweighted least squares to sample the parameter γ_j. This is a more computationally efficient sampling method relative to conventional tailoring by optimization at every MCMC step. The homoskedastic model can be estimated as a special case by simply setting $z_i = 1$. The quantities in equations (2) and (3) are then computed as simple averages using the output of the MCMC sampler.

Algorithm 1 (Semi-parametric Sharp RDD)

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(1) Sample $[g_j|y_j, \beta_j, \tau_j^2, \gamma_j] \sim N(\hat{g}_j, \hat{G}_j)$, where $\hat{G}_j = (\frac{K_j}{\tau_j^2} + Q_j'\Omega_j^{-1}Q_j)^{-1}$ and $\hat{g}_j = \hat{G}_j(\frac{1}{\tau_j^2}K_j g_{j0} + Q_j'\Omega_j^{-1}(y_j - X_j\beta_j))$.

(2) Sample $[\beta_j|y_j, g_j, \gamma_j] \sim N(\hat{\beta}_j, \hat{B}_j)$, where $\hat{B}_j = (B_{j0}^{-1} + X_j'\Omega_j^{-1}X_j)^{-1}$, and $\hat{\beta}_j = \hat{B}_j\left(B_{j0}^{-1}b_{j0} + X_j'\Omega_j^{-1}(y_j - Q_j g_j)\right)$.

(3) Sample $[\tau_j^2|g_j] \sim IG\left(\frac{t_{\nu_{j0}}+m_j}{2}, \frac{t_{d_{j0}}+(g_j-g_{j0})'K(g_j-g_{j0})}{2}\right)$.

(4) Sample $[\gamma_j|y_j, g_j, \beta_j]$ using the Metropolis-Hasting algorithm.

(a) Define

$$e_{ij}^c = \left(y_{ij} - g_j^c(w_i) - x_i'\beta_j^c\right)^2$$
$$\eta_{ij}^c = z_i'\gamma_j^c + \frac{e_{ij}^c - \sigma_{ij}^{2c}}{\sigma_{ij}^{2c}}, \quad \eta_j^c = \left(\eta_{1j}^c, \ldots, \eta_{n_j}^c\right)',$$

where σ_{ij}^{2c}, g_j^c and β_j^c are the current values of σ_{ij}^2, g_j and β_j.

(b) Using the iteratively reweighted least squares algorithm, we obtain a proposal value γ_j^p from the proposal density, which is $T_\nu(\gamma_j^p|\hat{\gamma}_j^p, V_j^p)$, where $V_j^p = (\Gamma_{0j}^{-1} + \frac{1}{2}Z_j'Z_j)^{-1}$ and $\hat{\gamma}_j^p = V_j^p(\Gamma_{j0}^{-1}\gamma_{j0} + \frac{1}{2}Z_j'\eta_j^c)$. We obtain $q(\gamma_j^c|\hat{\gamma}_j^c, V_j^c)$ in the reverse direction moving from the proposed value to the current value.

(c) The acceptance rate α is defined as

$$\alpha = \frac{f\left(y_j|g_j^c, \beta_j^c, \gamma_j^p\right)\pi\left(\gamma_j^p|\gamma_{j0}, \Gamma_{j0}\right)}{f\left(y_j|g_j^c, \beta_j^c, \gamma_j^c\right)\pi\left(\gamma_j^c|\gamma_{j0}, \Gamma_{j0}\right)} \times \frac{q\left(\gamma_j^c|\hat{\gamma}_j^c, V_j^c\right)}{q\left(\gamma_j^p|\hat{\gamma}_j^p, V_j^p\right)}.$$

If the proposed value is not accepted, γ_j^c is repeated in the next iteration.

To adapt our estimation approach to binary outcomes $y_i \in \{0,1\}$, we use data augmentation as in Albert and Chib (1993) and introduce the latent variables y_i^* such that $y_i = \mathbb{1}\{y^* \geq 0\}$, s.t.,

$$y_{ij}^* = g_j(w_i) + x_i'\beta_j + \varepsilon_{ij}, \quad \varepsilon_{ij} \sim N\left(0, \sigma_{ij}^2\right), \quad \ln(\sigma_{ij}^2) = z_i'\gamma_j, \quad \text{for} \quad j \in \{0,1\}. \tag{5}$$

For identification purposes, the vector z_i, which plays a role in determining the variance, does not include a constant term (Gu et al., 2009). The variance in the homoskedastic version of the model is fixed at 1 and is not estimated.

The complete data likelihood can be expressed as

$$\begin{aligned}
&f\left(y, y^* | g_0, g_1, \beta_0, \beta_1, \gamma_0, \gamma_1, \tau_0^2, \tau_1^2\right) \\
&= \prod_{i:T_i=0} \left(\left(f_N\left(y_i^* | g_0(w_i) + x_i'\beta_0, \sigma_{i0}^2\right) \mathbb{1}\{y_i^* \geq 0\}\right)^{y_i} \left(f_N\left(y_i^* | g_0(w_i) + x_i'\beta_0, \sigma_{i0}^2\right) \mathbb{1}\{y_i^* < 0\}\right)^{1-y_i} \right) \\
&\times \prod_{i:T_i=1} \left(\left(f_N\left(y_i^* | g_1(w_i) + x_i'\beta_1, \sigma_{i1}^2\right) \mathbb{1}\{y_i^* \geq 0\}\right)^{y_i} \left(f_N\left(y_i^* | g_1(w_i) + x_i'\beta_1, \sigma_{i1}^2\right) \mathbb{1}\{y_i^* < 0\}\right)^{1-y_i} \right),
\end{aligned}$$

which, combined with the priors in (4) produces the joint posterior that is sampled as in Algorithm 2. The RD ATE in the case of a binary outcome is defined as

$$\begin{aligned}
\tau_{SRD} &= \lim_{w \downarrow w^{*+}} E(Y_1 | w, x_i, z_i) - \lim_{w \uparrow w^{*-}} E(Y_0 | w, x_i, z_i) \\
&= \lim_{w \downarrow w^{*+}} \Phi\left(\frac{g_1 + x_i'\beta_1}{\sqrt{\exp(z_i'\gamma_1)}}\right) - \lim_{w \uparrow w^{*-}} \Phi\left(\frac{g_0 + x_i'\beta_0}{\sqrt{\exp(z_i'\gamma_0)}}\right),
\end{aligned}$$

which can be estimated directly using the MCMC output.

2.1.1 Bayesian Model Comparison and Marginal Likelihood Estimation

We represent the posterior model probability of model $\mathcal{M}_s$ given the data y as

$$P(\mathcal{M}_s | y) \propto P(\mathcal{M}_s) m(y | \mathcal{M}_s),$$

where $P(\mathcal{M}_s)$ denotes prior probability and $m(y|\mathcal{M}_s)$ denotes marginal likelihood of model $\mathcal{M}_s$, defined $m(y|\mathcal{M}_s) = \int f(y|\mathcal{M}_s, \Theta_s)\pi(\Theta_s|\mathcal{M}_s)\, d\Theta_s$. The marginal likelihood can be shown (Chib, 1995) as

$$m(y|\mathcal{M}_s) = \frac{f(y|\mathcal{M}_s, \Theta_s)\, \pi(\Theta_s|\mathcal{M}_s)}{\pi(\Theta_s|y, \mathcal{M}_s)}, \tag{6}$$

which holds for any Θ_s in the parameter space. The terms in the numerator, $f(y|\mathcal{M}_s, \Theta_s)$ and $\pi(\Theta_s|\mathcal{M}_s)$, are normally straightforward to compute. Consequently, the primary challenge in estimation lies in obtaining the estimates of the posterior ordinate.

Algorithm 2 (Semi-parametric Sharp RDD with Binary Outcome Variable)

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(1) Sample $[g_j|y_j^*, \beta_j, \tau_j^2, \gamma_j] \sim N\left(\hat{g}_j, \hat{G}_j\right)$, where $\hat{G}_j = \left(\frac{K_j}{\tau_j^2} + Q_j'\Omega_j^{-1}Q_j\right)^{-1}$ and $\hat{g}_j = \hat{G}_j\left(\frac{1}{\tau_j^2}K_j g_{j0} + Q_j'\Omega_j^{-1}\left(y_j^* - X_j\beta_j\right)\right)$.

(2) Sample $[\beta_j|y_j^*, g_j, \gamma_j] \sim N\left(\hat{\beta}_j, \hat{B}_j\right)$, where $\hat{B}_j = \left(B_{j0}^{-1} + X_j'\Omega_j^{-1}X_j\right)^{-1}$, and $\hat{\beta}_j = \hat{B}_j\left(B_{j0}^{-1}b_{j0} + X_j'\Omega_j^{-1}\left(y_j^* - Q_j g_j\right)\right)$.

(3) Sample $[\tau_j^2|g_j] \sim IG\left(\frac{t_{\nu_{j0}}+m_j}{2}, \frac{t_{d_{j0}}+(g_j-g_{j0})'K(g_j-g_{j0})}{2}\right)$.

(4) Sample $[\gamma_j|y_j^*, g_j, \beta_j]$ using the Metropolis-Hasting algorithm.

(a) Define

$$e_{ij}^c = \left(y_{ij}^* - g_j^c(w_i) - x_i'\beta_j^c\right)^2$$
$$\eta_{ij}^c = z_i'\gamma_j^c + \frac{e_{ij}^c - \sigma_{ij}^{2c}}{\sigma_{ij}^{2c}}, \quad \eta_j^c = \left(\eta_{1j}^c, \ldots, \eta_{n_j}^c\right)',$$

where σ_{ij}^{2c}, g_j^c and β_j^c are the current values of σ_{ij}^2, g_j and β_j.

(b) Using the iteratively reweighted least squares algorithm, we obtain a proposal value γ_j^p from the proposal density, which is $T_\nu(\gamma_j^p|\hat{\gamma}_j^p, V_j^p)$, where $V_j^p = (\Gamma_{0j}^{-1} + \frac{1}{2}Z_j'Z_j)^{-1}$ and $\hat{\gamma}_j^p = V_j^p(\Gamma_{j0}^{-1}\gamma_{j0} + \frac{1}{2}Z_j'\eta_j^c)$. We obtain $q(\gamma_j^c|\hat{\gamma}_j^c, V_j^c)$ in the reverse direction moving from the proposed value to the current value.

(c) The acceptance rate α is defined as

$$\alpha = \frac{f\left(y_j^*|g_j^c, \beta_j^c, \gamma_j^p\right)\pi\left(\gamma_j^p|\gamma_{j0}, \Gamma_{j0}\right)}{f\left(y_j^*|g_j^c, \beta_j^c, \gamma_j^c\right)\pi\left(\gamma_j^c|\gamma_{j0}, \Gamma_{j0}\right)} \times \frac{q\left(\gamma_j^c|\hat{\gamma}_j^c, V_j^c\right)}{q\left(\gamma_j^p|\hat{\gamma}_j^p, V_j^p\right)}.$$

If the proposed value is not accepted, γ_j^c is repeated in the next iteration.

(5) Sample $[y_{ij}^*|y_{ij}, g_j, \beta_j, \gamma_j] \sim TN\left(g_j(\omega_i) + x_i'\beta_j, \exp\left(z_i'\gamma_j\right)\right)$, where $y_{ij}^* \in (-\infty, 0)$ if $y_i = 0$, and $y_{ij}^* \in [0, \infty)$ if $y_i = 1$.

The Bayesian model comparison, replying on marginal likelihoods and their ratios, commonly known as Bayes factors (Kass and Raftery, 1995), has some preferred properties. These include yielding finite-sample model probabilities, competing models can be either nested or non-nested,

exhibiting favorable asymptotic behavior that aligns with the information criterion proposed by Schwarz (1978), and offer a measure of sequential out-of-sample predictive fit, as illustrated by

$$\begin{aligned} m(y|\mathcal{M}_s) &= \prod_{i=1}^{n} m(y_i|\{y_j\}_{j<i}, \mathcal{M}_s) \\ &= \prod_{i=1}^{n} \int f(y_i|\{y_j\}_{j<i}, \Theta_s, \mathcal{M}_s)\pi(\Theta_s|\{y_j\}_{j<i}, \mathcal{M}_s)\, d\Theta_s. \end{aligned}$$

Hence, the model adequacy, as reflected in the marginal likelihood, aligns with the cumulative out-of-sample predictive performance. This evaluation involves assessing the fit of y_i with respect to the posterior density, employing the data $y_{j\,j<i}$ up to the ith data point. This differs from the in-sample measures of fit that are condition on the entire dataset y, and split-sample comparison, where the outcome could be sensitive to the selection of estimation and comparison samples. The marginal likelihood remains unaffected by permutations in the order of data.

In the remainder of our discussion, we suppress the model indicator $\mathcal{M}_f$ to simplify the notation. Relative to the methods of Chib (1995) and Chib and Jeliazkov (2001) which employ different MCMC runs to estimate the joint posterior in the denominator of equation (6), we introduce a method that does not require additional MCMC runs. In particular, let $\theta_j = (\beta_j, g_j, \tau_j^2)$, and note that the marginal likelihood can be written as

$$\hat{m}\left(y_j\right) = \frac{f\left(y_j|\theta_j^*, \gamma_j^*\right)\pi\left(\theta_j^*, \gamma_j^*\right)}{\pi\left(\theta_j^*|y_j\right)\pi\left(\gamma_j^*|y_j, \theta_j^*\right)},$$

but instead of estimating $\pi(\theta_j^*|y_j)$ in separate runs, we employ the CRT method as discussed in Jeliazkov and Lee (2010) to estimate $\pi(\theta^*|y_j)$ as

$$\hat{\pi}\left(\theta_j^*|y\right) = G^{-1}\sum_{g=1}^{G} K\left(\theta_j^{(g)}, \theta_j^*|y_j\right), \tag{7}$$

where

$$K\left(\theta, \theta^*|y\right) = \prod_{g=1}^{G} \pi\left(\theta_r^*|y, \{\theta_s^*\}_{(s<r)}, \{\theta_s^{(g)}\}_{(s>r)}\right),$$

and $\{\theta^{(g)}\}_{g=1}^{G}$ are draws from the posterior distribution using the MCMC output. This method avoids the computation of the ordinates for (β_j, g_j, τ_j^2) individually, which reduces the computational intensity. In the discrete outcome case where $y_i \in \{0, 1\}$, we average the transition kernels over the latent variable y_{ij}^*.

The ordinate $\hat{\pi}\left(\gamma_j^*|y_j,\theta_j^*\right)$ is obtained as

$$\hat{\pi}\left(\gamma_j^*|y_j,\theta_j^*\right)=\frac{E\left\{\alpha\left(\gamma_j^{(s)},\gamma_j^*|y,\theta_j^*\right)q\left(\gamma^{(s)},\gamma^*|y,\theta_j^*\right)\right\}}{E\left\{\alpha\left(\gamma^*,\gamma^{(l)}|y,\theta_j^*\right)\right\}}, \tag{8}$$

where the expectation in the numerator is obtained with draws from $\pi(\gamma_j|y_j,\theta_j^*)$, and the denominator is with respect to $q(\gamma_j^*,\gamma_j|y,\theta_j^*)$. The computation in the binary case is done analogously, but integration is also done over the latent y_{ij}^*.

2.1.2 Simulation Results

In this simulation study, we test the performance of the MCMC algorithm, assess the influence of ignored heteroskedasticity, and examine the effectiveness of the model comparison technique. We simulate the data as

$$g_0(w)=1-\sin(w+1)+(w+1)^2,\quad g_1(w)=-1-\sin(w)+w^2,\quad w\sim U[-1,1],$$
$$\gamma_j\sim N(0,I),\quad \beta_j\sim N(0,I),\quad X\sim N(0,I),\quad Z=(1,w,X_1),$$

where X_1 is the first column of the generated covariates X. We report means, standard deviations, and 95% credible intervals of the posterior distribution for the treatment effect in each model. Additionally, we present marginal likelihood estimates to facilitate model comparisons. We also report the RD ATE estimates, standard errors and 95% confidence intervals provided by RDRobust (Calonico et al., 2017).

The marginal likelihood and the estimated treatment effect is presented in Table 1. The heteroskedastic model is recommended in all scenarios. As the sample size increases, both homoskedastic and heteroskedastic models yield point estimates that approach the true treatment effect. With larger sample sizes, we gain stronger evidence in favor of the heteroskedastic model based on the marginal likelihood estimates. Both Bayesian homoskedastic and heteroskedastic models provide more precise estimates compared to RDRobust. This is primarily because RDRobust relies on data points around the cutoff, while our model utilizes all available data points. We confirmed through sensitivity checks that the reduction in variability is not simply driven by the priors. The results are presented in Appendix A Table 15.

We conducted a simulation studies with the restriction that $\beta_0=\beta_1$, with all the other parameters sampled the same way as stated before. The simulation results are presented in Table 2. It's

evident from the results that the Bayesian heteroskedastic model yields more efficient estimates compared to the others.

Table 1: RD ATE with Continuous Outcome Variable ($\beta_1 \neq \beta_0$)

	Model	True ATE	RD ATE	SD	95% CI	Marg. Like.	Obs.
n = 500	Homoskedastic	-2.2357	-2.3638	0.2514	(-2.8657, -1.8774)	-765.22	500
	Heteroskedastic	-2.2357	-2.2616	0.1774	(-2.6127, -1.9173)	-617.77	500
	RDRobust	-2.2357	-2.6305	0.6780	(-4.1775, -1.0734)		(49, 68)
n = 5000	Homoskedastic	-2.2195	-2.0420	0.1289	(-2.2936, -1.7872)	-8711.93	5000
	Heteroskedastic	-2.2195	-2.0996	0.1062	(-2.3055, -1.8885)	-7929.93	5000
	RDRobust	-2.2195	-2.1892	0.2142	(-2.7119, -1.7242)		(955, 994)
n = 50000	Homoskedastic	-2.2092	-2.1987	0.0409	(-2.2793, -2.1191)	-68715.40	50000
	Heteroskedastic	-2.2092	-2.1993	0.0283	(-2.2550,-2.1439)	-59044.64	50000
	RDRobust	-2.2092	-2.0633	0.0690	(-2.2046, -1.8831)		(7983, 8124)

SD: Standard deviation for the Bayesian methods; Standard Error for RDRobust.
CI: Credible Interval for the Bayesian methods; Confidence Interval fro RDRobust.
Obs: Number of observations used in the analysis.

Table 2: ATE with Continuous Outcome Variable ($\beta_1 = \beta_0$)

	Model	True ATE	RD ATE	SD	95% CI	Marg. Like.	Obs.
n = 500	Homoskedastic	-2.1585	-2.3144	0.2276	(-2.7632, -1.8710)	-784.62	500
	Heteroskedastic	-2.1585	-2.3964	0.1764	(-2.7449, -2.0534)	-680.02	500
	RDRobust	-2.1585	-2.3896	0.2250	(-2.8610, -1.8196)		(72, 80)
n = 5000	Homoskedastic	-2.1585	-2.0998	0.1131	(-2.3201, -1.8770)	-7811.57	5000
	Heteroskedastic	-2.1585	-2.1142	0.1097	(-2.3281, -1.8978)	-7621.34	5000
	RDRobust	-2.1585	-1.9219	0.1603	(-2.2203, -1.5017)		(2424, 2576)
n = 50000	Homoskedastic	-2.1585	-2.148	0.0393	(-2.2242, -2.0698)	-54592.15	50000
	Heteroskedastic	-2.1585	-2.1579	0.0292	(-2.2149, -2.1002)	-48880.91	50000
	RDRobust	-2.1585	-2.1474	0.0323	(-2.2132, -2.0644)		(7429, 7479)

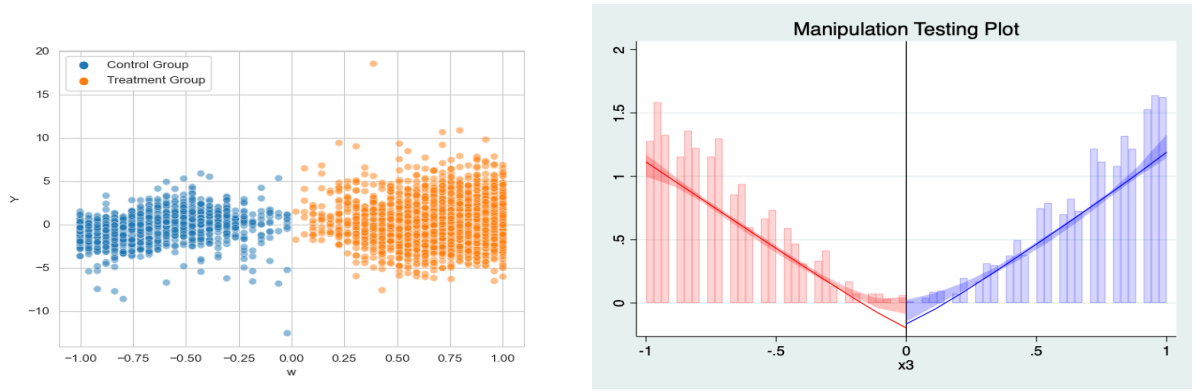
We explore a more extreme scenario with fewer data points around the cutoff and a more pronounced presence of heteroskedasticity. We collect a sample of data with a sample size of 5000 from the following DGP,

$$g_0(w) = \sin(w) + \exp\left(-20(w+0.5)^2\right), \quad g_1(w) = 1.2 - \sin(w) - \exp\left(-20(w-0.5)^2\right),$$
$$\gamma_0 = (-2,2,1)', \quad \gamma_1 = (-2,2,-1)', \quad \beta_j \sim N(0,I), \quad X \sim N(0,I), \quad Z = (1, ||w| - 1.5|, X1).$$

We also study the performance of our method relative to alternatives in cases where the cutoff point is in a low density region of w. The sampled data and density is presented in Figure 1. The generated data passed the frequentist density test (McCrary, 2008) with p-value 0.4655. The estimated RD ATE is provided in Table 3. The estimated parameter $\hat{g}_0$ and $\hat{g}_1$ can be found in

Figure 2. Based on the figure, the homoskedastic model estimates were significantly affected by the outliers near the cutoff point, which ultimately resulted in biased estimates for the RD ATE. The heteroskedastic model, on the other hand, can estimate the true function well. This is due to the fact that the data points are weighted correctly in the heteroskedastic model but not in the homoskedastic model. Thus, ignoring the heteroskedasticity can be problematic in this case. In this example, RDRobust yielded a notably wide 95% confidence interval, primarily due to the dramatically smaller number of data points near the cutoff.

Figure 1: Data and Running Variable Density



(a) Data

(b) Running Variable Density

Table 3: RD ATE Results

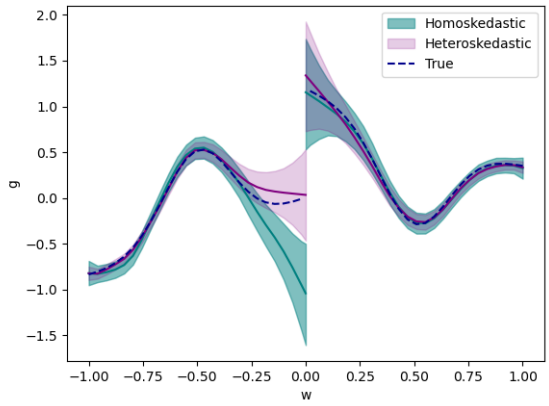
Model	True ATE	RD ATE	SD	95% CI	Marg. Like.	Obs.
Homoskedastic	1.2005	2.2085	0.4174	(1.3831, 3.0230)	-7642.76	5000
Heteroskedastic	1.2005	1.3185	0.3986	(0.5307, 2.0935)	-6066.56	5000
RDRobust	1.2005	2.0958	0.8682	(-0.1510, 4.1174)		(202, 190)

We simulated the data for models with binary outcomes from

$$g_0(w) = 1 - \sin(w+1) + (w+1)^2, \quad g_1(w) = -1 - \sin(w) + w^2, \quad w \sim U[-1,1],$$
$$\gamma_0 = \gamma_1 = 2, \quad \beta_j \sim N(0,I), \quad X \sim N(0,I), \quad Z = (||w| - 1.5|).$$

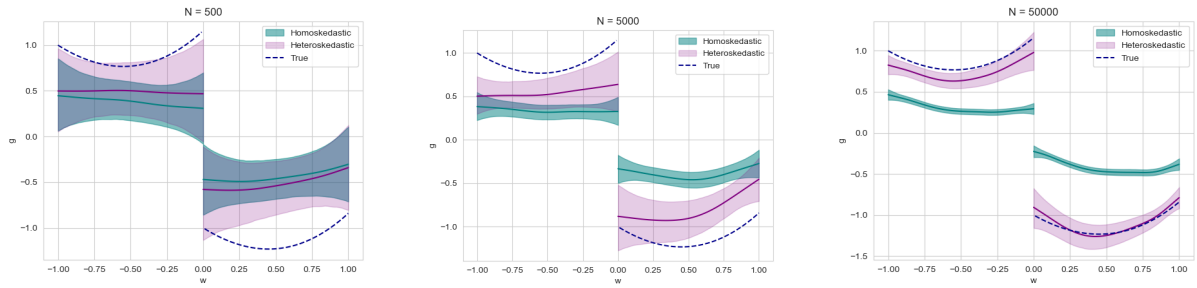
The estimated nonparametric parameter $\hat{g}_0$ and $\hat{g}_1$ are depicted in Figure 3. Table 4 presents the RD ATE and marginal likelihood statistics. Heteroskedastic model provides consistent estimates when the sample size increases, whereas both the homoskedastic model and RDRobust exhibit inconsistencies in this context. The impact of ignoring heteroskedasticity is amplified by more

Figure 2: Estimated Parameters $\hat{g}$



prominent non-linear features of the model. With a larger sample size, strong evidence emerges in support of the heteroskedastic model.

Figure 3: Estimated g with Binary Outcome Variable



(a) N= 500 (b) N = 5000 (c) N = 50000

2.2 Application: The Effects of Academic Probation on Academic Performance

Academic probation is commonly used as a catalyst to motivate students and improve their effort level. Fletcher and Tokmouline (2018) and Wright (2020) employed regression discontinuity design to evaluate the impact of academic probation on academic performance. We use the data from Texas Higher Education Opportunity Project (THEOP) to study the impact of academic probation on students' academic performance. The treated group consists of students who received academic probation at the end of their first semester. The outcome variables are the students' GPA of two subsequent semesters as well as their graduation rate. We use the longitudinal administrative data

Table 4: RD ATE with Binary Outcome Variable

	Model	True ATE	RD ATE	SD	95% CI	Marg. Like.	Obs.
n = 500	Homoskedastic	-0.2303	-0.2114	0.0845	(-0.3741, -0.0432)	-308.03	500
	Heteroskedastic	-0.2303	-0.2284	0.0842	(-0.3906, -0.0607)	-305.56	500
	RDRobust	-0.2303	-0.2262	0.1318	(-0.5405, 0.0801)		(109, 91)
n = 5000	Homoskedastic	-0.2579	-0.2202	0.0364	(-0.2916, -0.1488)	-2812.35	5000
	Heteroskedastic	-0.2579	-0.2700	0.0372	(-0.3422, -0.1963)	-2775.49	5000
	RDRobust	-0.2579	-0.2218	0.0480	(-0.3411, -0.1167)		(941, 932)
n = 50000	Homoskedastic	-0.2566	-0.1689	0.0159	(-0.2002, -0.1377)	-27844.71	50000
	Heteroskedastic	-0.2566	-0.2427	0.0177	(-0.2775, -0.2079)	-27470.32	50000
	RDRobust	-0.2566	-0.1756	0.0174	(-0.2194, -0.1386)		(6949, 7155)

from University of Texas, Austin (UT Austin) with students admitted from 1991 through 2000. At UT Austin, students receive the treatment if their cumulative GPA is under 2.0. The students must raise their GPA above the threshold, otherwise they can be dismissed from the university. We include the covariates, including the student's gender, citizenship, race, standardized SAT score, high school decile, private high school indicator, and if they have a major in first semester. The summary of statistics for the data are presented in Table 5, 6 and 7.

One key underlying assumption for the sharp RD design is that the students near the threshold can not manipulate their GPA. Following McCrary (2008), we run a density test of the running variable. The t-test statistic is -1.0027 with a p-value of 0.3160. Thus, there is no evidence showing that student manipulate their GPA to avoid the treatment. Additionally, since the GPA data is rounded to the nearest tenth, it is possible that some students with a GPA of 1.95-1.99, who received the treatment, but are categorized as the control group. To address this issue, we eliminate the students who have a first semester cumulative GPA of exact 2.0. We only use the covariates X and Z where students who have a first semester GPA of exact 2.0 for treatment effect estimation.

In our analysis, we specifically focus on the effect of heteroskedasticity and sidestep potential complications that may arise due to sample selection or endogeneity related to the decision to stay in school (see, e.g., Dong, 2019). We performed analysis employing both homoskedastic and heteroskedastic models, using model comparison techniques to assess the practical significance of heteroskedasticity.

The estimated function $\hat{g}_0$ and $\hat{g}_1$ are represented in Figure 4, and the RD ATE estimates and the marginal likelihoods are provided in Table 8. Notably, academic probation are practically relevant to the subsequent semester GPAs in all the Bayesian models, while the impact is

Table 5: Summary of Statistics: Second Semester GPA

Variable	Control (37980) Mean	Control (37980) SD	Treatment (5789) Mean	Treatment (5789) SD
Female	0.516	0.500	0.386	0.487
Non US Citizen	0.003	0.052	0.002	0.039
Minority	0.032	0.175	0.068	0.252
SAT (Standardized)	0.081	0.997	-0.398	0.911
Second Decile (High School)	0.264	0.441	0.309	0.462
Third Decile (High School)	0.119	0.324	0.209	0.406
Fourth Decile or Below (High School)	0.082	0.275	0.224	0.417
Private High School	0.051	0.220	0.047	0.212
Has Major	0.754	0.431	0.696	0.460
Second semester term GPA	3.003	0.762	2.026	0.892
First semester term GPA	3.205	0.546	1.335	0.495

Table 6: Summary of Statistics: Third Semester GPA

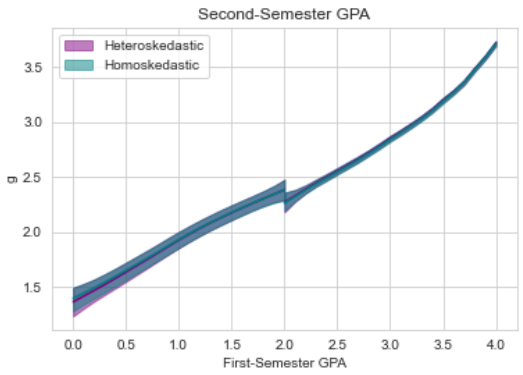
Variable	Control (36738) Mean	Control (36738) SD	Treatment (4366) Mean	Treatment (4366) SD
Female	0.515	0.500	0.390	0.488
Non US Citizen	0.003	0.053	0.002	0.043
Minority	0.032	0.176	0.066	0.248
SAT (Standardized)	0.068	0.997	-0.401	0.917
Second Decile (High School)	0.263	0.440	0.311	0.463
Third Decile (High School)	0.119	0.323	0.207	0.405
Fourth Decile or Below (High School)	0.082	0.274	0.227	0.419
Private High School	0.051	0.221	0.049	0.217
Has Major	0.755	0.430	0.694	0.461
Third semester term GPA	2.949	0.805	2.168	0.892
First semester term GPA	3.213	0.544	1.414	0.445

not statistically significant at 5% level based on the RDRobust result. The impacts of academic probation on graduation rates are not obvious according to the results of all models. Additionally, the marginal likelihoods suggest that the heteroskedastic model, with the constraint that $\beta_0 = \beta_1$, is the preferred choice in all scenarios except for the final analysis focusing on graduation rates, where the homoskedastic model with $\beta_0 = \beta_1$ is preferred.

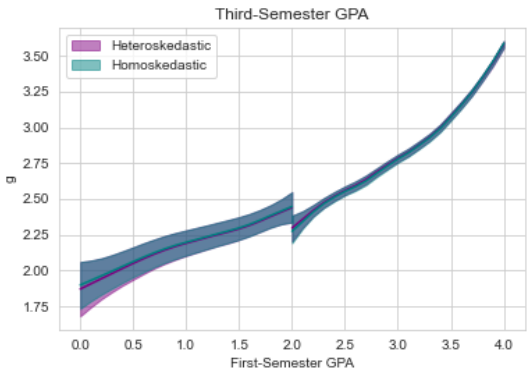
Table 7: Summary of Statistics: Graduation

Variable	Control (38525) Mean	SD	Treatment (6494) Mean	SD
Female	0.517	0.500	0.387	0.487
Non US Citizen	0.003	0.052	0.001	0.037
Minority	0.032	0.175	0.066	0.248
SAT (Standardized)	0.084	0.997	-0.378	0.917
Second Decile (High School)	0.264	0.441	0.305	0.461
Third Decile (High School)	0.119	0.324	0.213	0.409
Fourth Decile or Below (High School)	0.082	0.275	0.225	0.418
Private High School	0.051	0.220	0.048	0.214
Has Major	0.753	0.431	0.693	0.461
4-Year Graduation	0.527	0.499	0.126	0.332
Graduation	0.802	0.399	0.329	0.470

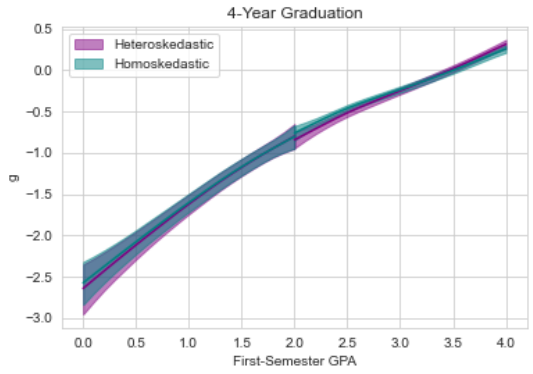
Figure 4: Estimated Nonparametric Parameters



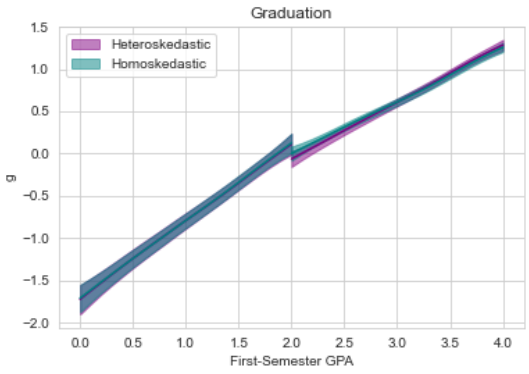
(a) Second-Semester GPA



(b) Third-Semester GPA



(c) 4-Year Graduation Rate



(d) Graduation Rate

Table 8: RD ATE Results

Outcomes	Models	RD ATE	SD	95% CI	Marg. Like.	Obs.
Second-Semester GPA	Homoskedastic	0.1709	0.0489	(0.0745, 0.2664)	-42714.08	43769
	Homoskedastic ($\beta_0 = \beta_1$)	0.1705	0.0501	(0.0715, 0.2684)	-42677.36	43769
	Heteroskedastic	0.1731	0.0556	(0.0641, 0.2825)	-41248.43	43769
	Heteroskedastic($\beta_0 = \beta_1$)	0.1709	0.0564	(0.0603, 0.2820)	-41211.59	43769
	RDRobust	-0.1434	0.1022	(-0.4538, 0.2644)		(1937, 3030)
Third-Semester GPA	Homoskedastic	0.1567	0.0570	(0.0461, 0.2700)	-44410.90	41104
	Homoskedastic ($\beta_0 = \beta_1$)	0.1410	0.0580	(0.0282, 0.2561)	-44383.80	41104
	Heteroskedastic	0.1391	0.0597	(0.0239, 0.2581)	-43617.56	41104
	Heteroskedastic($\beta_0 = \beta_1$)	0.1232	0.0399	(0.0063, 0.2436)	-43592.42	41104
	RDRobust	-0.1357	0.1070	(-0.4276, 0.3372)		(1671, 2824)
4-Year Graduation	Homoskedastic	-0.0198	0.0224	(-0.0633, 0.0246)	-27662.02	45019
	Homoskedastic ($\beta_0 = \beta_1$)	-0.0249	0.0223	(-0.0678, 0.0195)	-27633.59	45019
	Heteroskedastic	-0.0270	0.0218	(-0.0691, 0.0165)	-27650.87	45019
	Heteroskedastic($\beta_0 = \beta_1$)	-0.0295	0.0214	(-0.0711, 0.0132)	-27626.26	45019
	RDRobust	-0.0343	0.0535	(-0.3026, 0.0796)		(2022, 3138)
Graduation	Homoskedastic	0.0213	0.0238	(-0.0254, 0.0679)	-21776.01	45019
	Homoskedastic ($\beta_0 = \beta_1$)	0.0129	0.0239	(-0.0338, 0.0601)	-21755.11	45019
	Heteroskedastic	0.0076	0.0233	(-0.0380, 0.0532)	-21762.14	45019
	Heteroskedastic($\beta_0 = \beta_1$)	0.0116	0.0237	(-0.0349, 0.0580)	-21756.64	45019
	RDRobust	-0.0074	0.0627	(-0.3038, 0.1396)		(2022, 3138)

2.3 Fuzzy Regression Discontinuity Design

In this section, we present a Bayesian fuzzy RD model and outline the corresponding estimation algorithm. To help illustrate this model, we employ simulations. Following Chib et al. (2023), we posit the existence of an unobserved discrete confounding variable s which categorizes individuals into one of these three types: compliers (denoted as c), never-takers (denoted as n) who never take the treatment, and always-takers (denoted as a) who always take the treatment. The treatment status for compliers is $T = \mathbb{1}\{w \geq w^* | s = c\}$. The sample data in the fuzzy RD case is summarized by Table 9.

Table 9: Fuzzy RD Data

	$w < w*$	$w \geq w*$
T = 0	c, n	n
T = 1	a	c, a

The model can be specified as

$$
\begin{aligned}
&s = c : T = \mathbb{1}\{w \geq w^*\}, \quad y_{ij} = g_j\left(w_i\right) + x_i'\beta_j + \varepsilon_{ij}, \quad \varepsilon_{ij} \sim N\left(0, \sigma_{ij}^2\right), \quad \ln\left(\sigma_{ij}^2\right) = Z_{ij}'\gamma_j \\
&s = a : T = 1, \quad y_i = g_a\left(w_i\right) + x_i'\beta_a + \varepsilon_{ia}, \quad \varepsilon_{ia} \sim N\left(0, \sigma_{ia}^2\right), \quad \ln\left(\sigma_{ia}^2\right) = Z_{ia}'\gamma_a \\
&s = n : T = 0, \quad y_i = g_n\left(w_i\right) + x_i'\beta_n + \varepsilon_{in}, \quad \varepsilon_{in} \sim N\left(0, \sigma_{in}^2\right), \quad \ln\left(\sigma_{in}^2\right) = Z_{in}'\gamma_n \\
&P(s = k) = q_k > 0, \quad \forall k \in \{c, a, n\}, \quad q_c + q_n + q_a = 1.
\end{aligned}
$$

The RD ATE is defined as

$$
\begin{aligned}
\tau_{FRD} &\equiv \lim_{z \downarrow \tau^+} E\left(Y_1 | w, x_i, s = c\right) - \lim_{z \uparrow \tau^-} E\left(Y_0 | w, x_i, s = c\right) \\
&= \lim_{w \downarrow w^{*+}} E\left(g_1(w) + x_i'\beta_1\right) - \lim_{w \uparrow w^{*-}} E\left(g_0(w) + x_i'\beta_0\right).
\end{aligned}
$$

The likelihood function is expressed as

$$
\begin{aligned}
L = &\prod_{i \in I_{00}} \left(q_c f_N\left(y_i | g_0(w_i) + x_i'\beta_0, \sigma_{i0}^2\right) + q_n f_N\left(y_i | g_n(w_i) + x_i'\beta_n, \sigma_{in}^2\right)\right) \\
&\prod_{i \in I_{10}} q_n f_N\left(y_i | g_n(w_i) + x_i'\beta_n, \sigma_{in}^2\right) \prod_{i \in I_{01}} q_a f_N\left(y_i | g_a(w_i) + x_i'\beta_a, \sigma_{ia}^2\right) \\
&\prod_{i \in I_{11}} \left(q_c \phi\left(y_i | g_1(w_i) + x_i'\beta_1, \sigma_{i1}^2\right) + q_a f_N\left(y_i | g_a(w_i) + x_i'\beta_a, \sigma_{ia}^2\right)\right)
\end{aligned}
$$

where I_{iT} is the group of observations where $i = \mathbb{1}\{w \geq w^*\}$, T is the treatment variable, and ϕ is the probability density function (PDF) of the normal distribution.

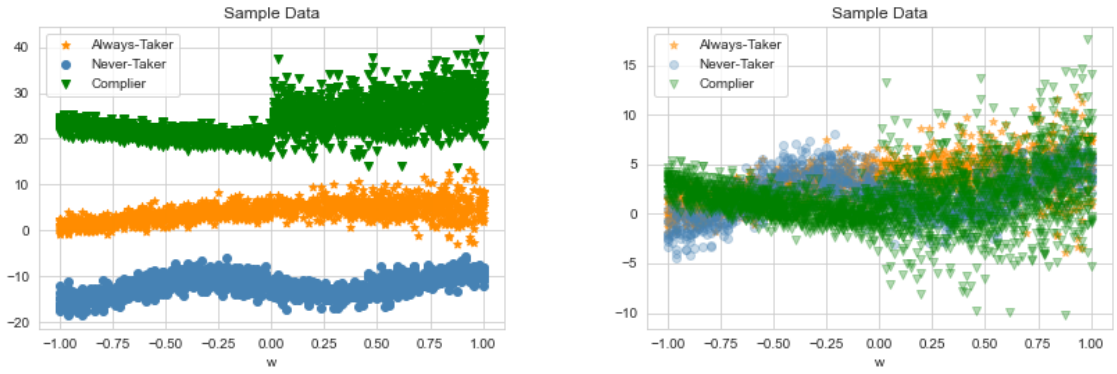
We specify the prior distribution of $q = (q_a, q_n, q_c)$ as $q \sim Dir(n_{a0}, n_{n0}, n_{c0})$. All the other parameters follows the same prior distribution as discussed in section 2.1. The vectors g_a and g_n are of dimension $m = m_0 + m_1$,where m_0 is the dimension of vector ν_0, and m_1 is the dimension of vector ν_1. The unique ordered values of the running variable w_0 and w_1, denoted by ν_0 and ν_1. The function evaluations g_0 and g_1 are vectors of dimension m_0 and m_1, respectively. In the estimation process, the nonparametric functions in each group are updated using both the prior information and observations that were categorized into this specific group in each iteration. The posterior distribution for the type variable s is specified as

$$
\begin{aligned}
&Pr\left(s_i = c | y_i, g_j, \beta_j, \tau_j^2, \gamma_j\right) \propto q_c f_N\left(y_i | g_i(w_i) + x_i'\beta_j, \sigma_{ij}^2\right), \\
&Pr\left(s_i = n | y_i, g_n, \beta_n, \tau_n^2, \gamma_n\right) \propto q_n f_N\left(y_i | g_n(w_i) + x_i'\beta_n, \sigma_{in}^2\right), \\
&Pr\left(s_i = a | y_i, g_a, \beta_a, \tau_a^2, \gamma_a\right) \propto q_a f_N\left(y_i | g_a(w_i) + x_i'\beta_a, \sigma_{ia}^2\right).
\end{aligned} \tag{9}
$$

The joint posterior distribution can be sampled as in Algorithm 3. We conducted a simulation study to assess the algorithm's performance and evaluate the influence of heteroskedasticity within

the framework of the fuzzy RD model. The simulated data are visualized in Figure 5. In the first sample, the data for each group are well-separated, while in the second sample, the data for each group are mixed together. The nonparametric functions estimated for each group are presented in Figure 6 and Figure 7. In this context, it is important to highlight the possibility of misclassification and label switching, which can occur when the clusters are not well-separated (Celeux, 1998), so we advise practitioners to examine their results prior to drawing definitive conclusions in applications where clusters are not well-separated, as there is no current consensus solution to this problem.

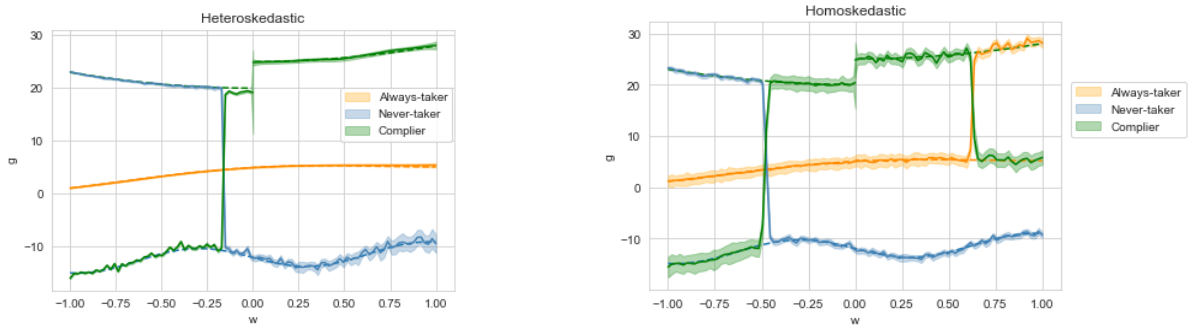
Figure 5: Simulated Data



(a) Well-separated Sample

(b) Poorly-separated Sample

Figure 6: Well-separated Data



(a) Heteroskedastic

(b) Homoskedastic

Algorithm 3 (Semi-parametric Fuzzy RDD)

---

(1) Sample the type variable s, where the posterior distribution of s is summarized by Equation (9).

(2) Sample $q = (q_a, q_n, q_c) \sim Dir\left(n_{a0} + n_a, n_{n0} + n_n, n_{c0} + n_c\right)$, where n_a, n_n and n_c are the sample size of the observations that are categorized into always-takers, never-takers and compliers correspondingly in the previous step.

(3) For all possible values of ν, we update g_j using the samples that were categorized as compliers in the previous step. We sample $[g_j|y_j, \beta_j, \tau_j^2, \gamma_j] \sim N\left(\hat{g}_j, \hat{G}_j\right)$, where $\hat{G}_j = \left(\frac{K_j}{\tau_j^2} + Q_j'\Omega_j^{-1}Q_j\right)^{-1}$ and $\hat{g}_j = \hat{G}_j\left(\frac{1}{\tau_j^2}K_j g_{j0} + Q_j'\Omega_j^{-1}\left(y_j - X_j\beta_j\right)\right)$. We repeat this step for all the compliers and never-takers.

(4) Sample $[\beta_j|y_j, g_j, \gamma_j] \sim N\left(\hat{\beta}_j, \hat{B}_j\right)$, where $\hat{B}_j = \left(B_{j0}^{-1} + X_j'\Omega_j^{-1}X_j\right)^{-1}$, and $\hat{\beta}_j = \hat{B}_j\left(B_{j0}^{-1}b_{j0} + X_j'\Omega_j^{-1}(y_j - Q_j g_j\right)$. Sample $[\beta_a|y_a, g_a, \gamma_a]$, and $[\beta_n|y_n, g_n, \gamma_n]$ in a similar way.

(5) Sample $[\tau_j^2|g_j] \sim IG\left(\frac{t_{\nu_{j0}} + m_j}{2}, \frac{t_{d_{j0}} + (g_j - g_{j0})'K_j(g_j - g_{j0})}{2}\right)$. Repeat this step to sample $[\tau_a^2|g_a]$ and $[\tau_n^2|g_n]$.

(6) Sample $[\gamma_j|y_j^*, g_j, \beta_j]$ using the Metropolis-Hasting algorithm.

   (a) Define

$$e_{ij}^c = \left(y_{ij}^* - g_j^c(w_i) - x_i'\beta_j^c\right)^2$$
$$\eta_{ij}^c = z_i'\gamma_j^c + \frac{e_{ij}^c - \sigma_{ij}^{2c}}{\sigma_{ij}^{2c}}, \quad \eta_j^c = \left(\eta_{1j}^c, \ldots, \eta_{n_j}^c\right)',$$

   where σ_{ij}^{2c}, g_j^c and β_j^c are the current values of σ_{ij}^2, g_j and β_j.

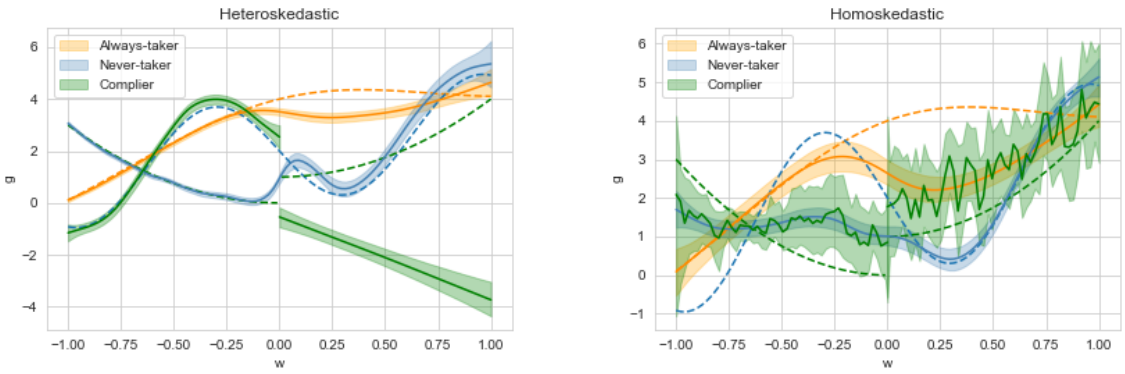
   (b) Using the iteratively reweighed least squares algorithm, we obtain a proposal value γ_j^p from the proposal density, which is $T_\nu(\gamma_j^p|\hat{\gamma}_j^p, V_j^p)$, where $V_j^p = (\Gamma_{0j}^{-1} + \frac{1}{2}Z_j'Z_j)^{-1}$ and $\hat{\gamma}_j^p = V_j^p(\Gamma_{j0}^{-1}\gamma_{j0} + \frac{1}{2}Z_j'\eta_j^c)$. We obtain $q(\gamma_j^c|\hat{\gamma}_j^c, V_j^c)$ in the reverse direction moving from the proposed value to the current value.

   (c) The acceptance rate α is defined as

$$\alpha = \frac{f\left(y_j^*|g_j^c, \beta_j^c, \gamma_j^p\right)\pi\left(\gamma_j^p|\gamma_{j0}, \Gamma_{j0}\right)}{f\left(y_j^*|g_j^c, \beta_j^c, \gamma_j^c\right)\pi\left(\gamma_j^c|\gamma_{j0}, \Gamma_{j0}\right)} \times \frac{q\left(\gamma_j^c|\hat{\gamma}_j^c, V_j^c\right)}{q\left(\gamma_j^p|\hat{\gamma}_j^p, V_j^p\right)}.$$

   If the proposed value is not accepted, γ_j^c is repeated in the next iteration. We repeat this step for always-takers and never-takers to sample $[\gamma_a|y_a^*, g_j, \beta_a]$ and $[\gamma_n|y_n^*, g_n, \beta_n]$.

Figure 7: Poorly-separated Data



(a) Heteroskedastic

(b) Homoskedastic

3 Potential Outcome Framework

In this section, we introduce a potential outcome framework (Roy, 1951; Rubin, 1974, 1977, 1978, 2004, 2005) with self-selection for estimating the treatment effect, following the approach outlined in Chib (2007). We assume that there are two potential outcome variables y_0 and y_1 for the treated and untreated states. The binary treatment status T is determined by a latent variable T^* and $T = \mathbb{1}\{T^* \geq 0\}$. We also assume that there is heteroskedasticity in both the treatment assignment and the outcome.

The model can be represented as

$$y_i = X_i\beta + \epsilon_i, \epsilon_i \sim N(0, \Omega_i)$$

where

$$y_i = \begin{pmatrix} T_i^* \\ y_{0i} \\ y_{1i} \end{pmatrix}, \quad X_i = \begin{pmatrix} x'_{Ti} & 0 & 0 \\ 0 & x'_{0i} & 0 \\ 0 & 0 & x'_{1i} \end{pmatrix}, \quad \beta = \begin{pmatrix} \beta'_T \\ \beta'_0 \\ \beta'_1 \end{pmatrix} \quad \text{, and } \varepsilon = \begin{pmatrix} \varepsilon_{Ti} \\ \varepsilon_{0i} \\ \varepsilon_{1i} \end{pmatrix}.$$

Let N_j denote the sample $\{i : T_i = j\}$ and n_j to denote the cardinality of N_j, where $j \in \{0, 1\}$. The covariance matrix Ω_i is defined as

$$\Omega_i = \begin{pmatrix} \omega_{TTi} & \omega_{T0i} & \omega_{T1i} \\ \omega_{0di} & \omega_{00i} & \omega_{01i} \\ \omega_{1di} & \omega_{10i} & \omega_{11i} \end{pmatrix}.$$

Due to the missing counterfactuals, ω_{01i} is not identified. To simplify the notation in the subsequent

discussion, we introduce the following matrices

$$\Omega_{0i} = \begin{pmatrix} \omega_{TTi} & \omega_{T0i} \\ \omega_{0Ti} & \omega_{00i} \end{pmatrix}, \quad \Omega_1 = \begin{pmatrix} \omega_{TTi} & \omega_{T1i} \\ \omega_{1Ti} & \omega_{11i} \end{pmatrix}, \quad J_0 = \begin{pmatrix} I & 0 & 0 \\ 0 & 0 & I \end{pmatrix}, \quad J_1 = \begin{pmatrix} 0 & I & 0 \\ 0 & 0 & I \end{pmatrix},$$
$$\tilde{X}_{i0} = \begin{pmatrix} x'_{Ti} & 0 \\ 0 & x'_{0i} \end{pmatrix}, \quad \tilde{X}_{i1} = \begin{pmatrix} x'_{Ti} & 0 \\ 0 & x'_{1i} \end{pmatrix}, \quad \tilde{y}_{i0} = \begin{pmatrix} T_i^* \\ y_{0i} \end{pmatrix}, \quad \tilde{y}_{i1} = \begin{pmatrix} T_i^* \\ y_{1i} \end{pmatrix}.$$

Thus we have $J_0\beta = (\beta'_T, \beta'_0)$ and $J_1\beta = (\beta'_T, \beta'_1)$. The complete data density function is specified as

$$f(y_0, y_1, T^*|\beta_0, \beta_1, \Omega_0, \Omega_1) = \left[\prod_{i\in N_0} f\left(\tilde{y}_{i0}|\beta_0, \Omega_{i0}\right) \mathbb{1}\{T_i^* < 0\}\right] \left[\prod_{i\in N_1} f\left(\tilde{y}_{i1}|\beta_1, \Omega_{i1}\right) \mathbb{1}\{T_i^* \geq 0\}\right].$$

In the homoskedastic model, we impose a restriction where $\omega_{TTi} = 1$ for the purpose of identification. We define the covariance matrices and several variables as

$$\Omega_0 = \begin{pmatrix} 1 & \omega_{T0} \\ \omega_{0T} & \omega_{00} \end{pmatrix}, \qquad \Omega_1 = \begin{pmatrix} 1 & \omega_{T1} \\ \omega_{1T} & \omega_{11} \end{pmatrix},$$
$$\Omega_{22\cdot 1} = \omega_{11} - \omega_{1T}\omega_{T1}, \quad \Omega_{22\cdot 0} = \omega_{00} - \omega_{0T}\omega_{T0}.$$

We assume that $\Omega_{22\cdot j} \sim IG\left(\frac{r_j}{2}, \frac{R_j}{2}\right)$ for $j \in \{0, 1\}$.[1] Under this assumption, the conditional distribution of $\omega_{jT}|\Omega_{jj\cdot 2} \sim N\left(q_j, \Omega_{22\cdot j}\right)$. Furthermore, we specify the prior distribution of β as β is $\beta \sim N\left(b_0, B_0\right)$. The estimation algorithm is summarized in Algorithm 4.

To expand the model to the case of multivariate heteroskedasticity, we decompose the covariance matrices (Chan and Jeliazkov, 2009b) as

$$\Omega_{0i} = L_0 G_{0i} L'_0, \quad \Omega_{1i} = L_1 G_{1i} L'_1,$$

where for $j \in \{0, 1\}$,

$$L_j \equiv \begin{pmatrix} 1 & 0 \\ a_{jT} & 1 \end{pmatrix}, G_{ji} \equiv \begin{pmatrix} \lambda_{Ti} & 0 \\ 0 & \lambda_{ji} \end{pmatrix}.$$

The model can be rewritten as

$$\begin{pmatrix} T_i^* \\ y_{ji} \end{pmatrix} = \begin{pmatrix} x'_{Ti} & \mathbf{0} \\ \mathbf{0} & x'_{ji} \end{pmatrix} \begin{pmatrix} \beta_T \\ \beta_j \end{pmatrix} + L_j \begin{pmatrix} \psi_{Ti} \\ \psi_{ji} \end{pmatrix}, \text{where } \begin{pmatrix} \psi_{Ti} \\ \psi_{ji} \end{pmatrix} \sim N\left(\mathbf{0}, G_{ji}\right),$$

or

$$T_i^* = x'_{Ti}\beta_T + \psi_{Ti}, \quad y_{ji} = x'_{ji}\beta_j + a_{jT}\psi_{Ti} + \psi_{ji}, \quad \psi_{ji} \sim N(0, \lambda_{ji}), \quad \psi_{Ti} \sim N(0, \lambda_{Ti}),$$
$$\lambda_{ji} = \exp(Z'_{ji}\gamma_j), \quad \lambda_{Tj} = \exp(Z'_{Ti}\gamma_T).$$

[1] If $\Omega_{22\cdot j}$ were a matrix, the generalization would be $\Omega_{22\cdot j} \sim IW\left(r_j, R_j\right)$.

Algorithm 4 (Bayesian Potential Outcome Framework with Homoskedasticity)

---

(1) Sample $\beta \sim N\left(\hat{b}, \hat{B}\right)$, where $\hat{b} = \hat{B}\left(B_0^{-1}b_0 + \sum_{i\in N_0} J_0'\tilde{X}_{i0}'\Omega_0^{-1}\tilde{y}_{i0} + \sum_{i\in N_1} J_1'\tilde{X}_{i1}'\Omega_1^{-1}\tilde{y}_{i1}\right)$, and $\hat{B} = \left(B_0^{-1} + \sum_{i\in N_0} J_0'\tilde{X}_{i0}'\Omega_0^{-1}\tilde{X}_{i0}J_0 + \sum_{i\in N_1} J_1'\tilde{X}_{i1}'\Omega_1^{-1}\tilde{X}_{i1}J_1\right)^{-1}$.

(2) Sample $T_i^* \sim TN\left(\mu_{Tij}, \hat{\omega}_{TT}\right)$, where $T_i^* \in (-\infty, 0)$ if $i \in N_0$, $T_i^* \in [0, \infty)$ if $i \in N_1$, $\mu_{2ij} = x_{Ti}'\beta_T + \omega_{jT}\omega_{jj}^{-1}\left(y_{ji} - x_{ji}'\beta_j\right)$, and $\hat{\omega}_{22} = 1 - \omega_{jT}\omega_{jj}^{-1}\omega_{jT}$.

(3) For $i \in N_j$,

$$\pi\left(\omega_{j2}|\Omega_{22\cdot j}, \beta, y_i, z_i\right) = \pi\left(\omega_{jT}|\Omega_{22\cdot j}\right)\pi\left(y_j|z\right) = f_N\left(\omega_{jT}|q_t, \Omega_{22\cdot j}\right)\prod_{i\in N_j} f_N\left(y_{ji}|\mu_{ji|2}, \Omega_{22\cdot j}\right).$$

where $\mu_{ji|2} = x_{ji}'\beta_j + \omega_{jT}\left(T_i^* - x_{iT}'\beta_T\right)$. Thus the posterior distribution for ω_{jT} is $\omega_{jT} \sim N\left(\hat{q}_j, \hat{\omega}_{22\cdot j}\right)$, where $\hat{\omega}_{22\cdot j} = \left(\Omega_{22\cdot j}^{-1} + \left(\sum_{i=1}^{n_j}\left(\varepsilon_{Ti}^2\Omega_{22\cdot j}^{-1}\right)\right)^{-1}\right)^{-1}$, and $\hat{q}_j = \hat{\omega}_{22\cdot j}\left(\Omega_{22\cdot j}^{-1}q_t + \Omega_{22\cdot j}^{-1}\sum_{i=1}^{n_j}\varepsilon_{Ti}\varepsilon_{ji}\right)$, where $\varepsilon_{ji} \equiv y_{ji} - x_{ji}'\beta_j$ and $\varepsilon_{Ti} \equiv T_i^* - x_{Ti}'\beta_T$.

(4) For $i \in N_j$,

$$\pi\left(\Omega_{22\cdot j}|\omega_{jT}, \beta, y_i, T^*\right) = \pi\left(\Omega_{22\cdot j}\right) f_N\left(\omega_{jT}|q_t, \Omega_{22\cdot j}\right)\prod_{i\in N_j} f_N\left(y_{ji}|\mu_{ji|2}, \Omega_{22\cdot j}\right).$$

The posterior distribution is as follows: $\Omega_{22\cdot j} \sim IG\left(\frac{\hat{\nu}}{2}, \frac{\hat{O}_j}{2}\right)$, where $\hat{\nu} = \nu + 1 + n_j$, and $\hat{O}_j = O_j + \left(\omega_{jT} - q_t\right)^2 + \sum_{i\in N_j}\left(\epsilon_{ji} - \omega_{jT}\epsilon_{Ti}\right)^2$.

The prior distributions are specified as

$$\beta \sim N(b_0, B_0), \quad \gamma_j \sim N(\gamma_{0j}, \Gamma_{0j}), \quad \gamma_T \sim N(\gamma_{0T}, \Gamma_{0T}), \quad a_{jd} \sim N(a_{0j}, A_{0j}),$$

and the estimation algorithm is detailed in Algorithm 5. In our model, the average treatment effect (ATE) and the average treatment effect on the treated (ATT) are defined as

$$ATE = E(Y_1 - Y_0) = E(x_i'\beta_1 - x_i'\beta_0), \quad ATT = E(Y_1 - Y_0|D = 1) = E(x_{1i}'\beta_1 - x_{1i}'\beta_0),$$

and they can be estimated using the MCMC output.

Algorithm 5 (Bayesian Potential Outcome Framework with Heteroskedasticity)

(1) Sample $\beta \sim N\left(\hat{b}, \hat{B}\right)$, where $\hat{b} = \hat{B}\left(B_0^{-1}b_0 + \sum_{i\in N_0} J_0'\tilde{X}_{i0}'\Omega_0^{-1}\tilde{y}_{i0} + \sum_{i\in N_1} J_1'\tilde{X}_{i1}'\Omega_1^{-1}\tilde{y}_{i1}\right)$, and $\hat{B} = \left(B_0^{-1} + \sum_{i\in N_0} J_0'\tilde{X}_{i0}'\Omega_0^{-1}\tilde{X}_{i0}J_0 + \sum_{i\in N_1} J_1'\tilde{X}_{i1}'\Omega_1^{-1}\tilde{X}_{i1}J_1\right)^{-1}$.

(2) Sample $T_i^* \sim TN\left(\mu_{2ij}, \hat{\omega}_{22i}\right)$, where $T_i^* \in (-\infty, 0)$ if $i \in N_0$, $T_i^* \in [0, \infty)$ if $i \in N_1$, $\mu_{2ij} = x_{Ti}'\beta_T + \omega_{jTi}\omega_{jji}^{-1}\left(y_{ji} - x_{ji}'\beta_j\right)$, and $\hat{\omega}_{TTi} = \omega_{TTi} - \omega_{jTi}\omega_{jji}^{-1}\omega_{jTi}$.

(3) Sample $a_{jT} \sim N\left(\hat{a}_j, \hat{A}_j\right)$ where $\hat{A}_j = \left(A_{0j}^{-1} + \sum_{i=1}^{n_j}\psi_{Ti}'\lambda_{ji}^{-1}\psi_{Ti}\right)^{-1}$ and $\hat{a}_j = \hat{A}_j\left(A_{0j}^{-1}a_{0j} + \sum_{i=1}^{n_j}\psi_{Ti}'\lambda_{ji}^{-1}u_{ij}\right)$, where $u_{ji} \equiv y_{ji} - x_{ji}'\beta_j$.

(4) Sample $[\gamma_T | a_{0T}, a_{1T}, \beta_T, T^*]$ using the Metropolis-Hasting algorithm.

(a) Define

$$e_{Ti}^c = \left(T_i^* - X_{Ti}'\beta_T^c\right)^2$$
$$\eta_{Ti}^c = Z_{Ti}'\gamma_T^c + \frac{e_{Ti}^c - \omega_{TTi}^c}{\omega_{TTi}^c}, \quad \eta_T^c = \left(\eta_{1j}^c, ..., \eta_n^c\right)'.$$

where ω_{TTi}^c and β_T^c are the current values of ω_{TTi} and β_T.

(b) Using the iteratively reweighted least squares algorithm, we obtain a proposal value γ_T^p from the proposal density, which is $T_\nu(\gamma_T^p | \hat{\gamma}_T^p, V_T^p)$, where $V_T^p = (\Gamma_{0T}^{-1} + \frac{1}{2}Z_T'Z_T)^{-1}$ and $\hat{\gamma}_T^p = V_T^p(\Gamma_{T0}^{-1}\gamma_{T0} + \frac{1}{2}Z_T'\eta_T^c)$. We obtain $q(\gamma_T^c | \hat{\gamma}_T^c, V_T^c)$ in the reverse direction moving from the proposed value to the current value.

(c) The acceptance rate α is defined as

$$\alpha = \frac{f\left(T_i^* | a_{0T}, a_{1T}, \beta_T^c, \gamma_T^p\right)\pi\left(\gamma_T^p | \gamma_{T0}, \Gamma_{T0}\right)}{f(T_i^* | a_{0T}, a_{1T}, \beta_T^c, \gamma_T^c)\pi\left(\gamma_T^c | \gamma_{T0}, \Gamma_{T0}\right)} \times \frac{q\left(\gamma_T^c | \hat{\gamma}_T^c, V_T^c\right)}{q\left(\gamma_T^p | \hat{\gamma}_T^p, V_T^p\right)}.$$

If the proposed value is not accepted, γ_T^c is repeated in the next iteration.

(5) We define e_{ji}^c and η_{ji}^c as

$$e_{ji}^c = \left(y_{ji} - X_{ji}'\beta_j^c - a_{jT}^c\psi_{Ti}\right)^2,$$
$$\eta_{ji}^c = Z_{ji}'\gamma_j^c + \frac{e_{ji}^c - \omega_{jji}^c}{\omega_{jji}^c}, \quad \eta_j^c = \left(\eta_{j1}^c, \ldots, \eta_{jn_j}^c\right)'.$$

$[\gamma_j | a_{jT}, \beta_j]$ can be sampled in a similar manner as described in Step (4).

In the homoskedastic case, the posterior ordinate can be estimated similarly to Section 2.1.1 using the CRT method. To estimate the marginal likelihood in the heteroskedastic model, let θ denote the parameters (β, a_{1T}, a_{0T}). The posterior ordinate of $\hat{\pi}(\theta^*|y, T^*)$ can also be estimated using the CRT method as discussed in Section 2.1.1. The posterior ordinate of $\hat{\pi}\left(\gamma_T^*|y, \theta^*, T^*\right), \hat{\pi}\left(\gamma_1^*|y, \theta^*, T^*\right),$ and $\hat{\pi}\left(\gamma_0^*|y, \theta^*, T^*\right)$ can be sampled similarly to Section 2.1.1.

3.1 Simulation

In this section, we performed a simulation study to gauge MCMC efficiency, evaluate the consequences of neglected heteroskedasticity, and validate the model comparison technique. We report mean, standard deviations, and 95% credible intervals of the posterior distribution for the treatment effects in each model.

We run 3 simulation sets with sample size $n = \{500, 5000, 50000\}$. The data are generated from

$$X_0 \sim (1, N(0,1)), \quad X_1 = X_0, \quad X_d = (X_0, N(0,1)), \quad \beta \sim N(0, I), \quad \gamma_0 \sim N(0, I),$$
$$\gamma_1 \sim N(0, I), \quad \gamma_d \sim N(0, I), \quad a_{0T} = -0.2, \quad a_{1T} = 0.2.$$

The estimated ATE and ATT are summarized in Table 10. In all cases, the heteroskedastic model emerges as the recommended choice based on the marginal likelihood results. These findings highlight that ignoring heteroskedasticity when it is present, leads to inconsistent and biased estimates for both ATE and ATT.

Table 10: Treatment Effects Estimation (Simulation)

	Model		TRUE	Estimated	SD	95% CI	Marg. Like.
n = 500	Heteroskedastic	**ATE**	-2.3573	-2.3030	0.1910	(-2.6775, -1.9268)	-798.15
		ATT	-1.4987	-1.4693	0.2512	(-1.9608, -0.9737)	
	Homoskedastic	**ATE**	-2.3573	-1.5441	0.2865	(-2.1134, -0.9846)	-853.74
		ATT	-1.4987	-0.8222	-0.3577	(-1.5287, -0.1122)	
n = 5000	Heteroskedastic	**ATE**	-0.4869	-0.4704	0.1476	(-0.7504, -0.1610)	-7073.77
		ATT	-0.5669	-0.5367	0.1546	(-0.8296, -0.2127)	
	Homoskedastic	**ATE**	-0.4869	-1.4841	0.3421	(-2.1683, -0.8130)	-8108.51
		ATT	-0.5669	-1.5631	0.3610	(-2.2862, -0.8552)	
n = 50000	Heteroskedastic	**ATE**	-1.7010	-1.6709	0.0328	(-1.7359, -1.6069)	-77644.71
		ATT	-2.6833	-2.6595	0.0330	(-2.7244, -2.5950)	
	Homoskedastic	**ATE**	-1.7010	-3.1775	0.0403	(-3.2569, -3.0985)	-90039.30
		ATT	-2.6833	-3.3340	0.0308	(-3.3937, -3.2732)	

3.2 Application: The Effects of Medigap on Healthcare Expenditure

In this application, we consider the influence of private health insurance on healthcare expenditures of the elderly using the Medical Expenditure Panel Survey (MEPS). For individuals aged 65 and above, Medicare provides coverage, but some seniors opt to purchase private insurance known as Medigap to supplement their Medicare benefits. Medigap policies typically offer enhanced coverage compared to the basic Medicare policy, and individuals often choose them in the belief that they can reduce out-of-pocket healthcare costs.

We partition the data into two distinct subsets. One sample spans the years 2018 to 2019 prior to the COVID-19 pandemic, and the other comprises survey data from 2020. This division accounts for the potential impact of the pandemic on individuals' behavior. In our study, we assess the impact of acquiring Medigap policies on out-of-pocket healthcare expenditures, employing both heteroskedastic and homoskedastic models.

We incorporate self-perceived health status variables, the number of chronic conditions, location, and various demographic variables as covariates that influence healthcare expenditures. We assume that family income only affect the purchase of the private insurance, and it would not affect the health care utilization directly. Variable definitions and summary statistics are presented in Table 11. In the regression, age is standardized, and due to excessive right skew, expenditure (in thousands of dollars) is stabilized using the square root transformation (Amaratunga and Cabrera, 2001). Additionally, we assume that the variance of the treatment assignment depends on family income, and the variance of the expenditure depends on age and the number of chronic conditions. In this application, our primary focus remains on the effects of heteroskedasticity, while sidestepping issues with choice of specific Medigap plans based on their anticipated healthcare expenditures and potential endogeneity of the Medicaid variable.

The estimated ATE and ATT are presented in Table 12. The heteroskedastic model suggests a negative impact of Medigap on health care expenditure, while the homoskedastic model indicates a positive impact. The marginal likelihood results recommend the heteroskedastic model for both samples. Parameter estimates are reported in Appendix B.

Table 11: Variable Definition and Summary Statistics

Variables	Description	2020 5019		2018, 2019 10226	
		Mean	SD	Mean	SD
AGE	AGE	73.52	6.24	73.65	6.42
FAMINC	Family income (as percentage of poverty line)	4.11	3.88	4.19	3.90
NUM_VISIT	# Office-based provider visits	10.11	14.53	12.19	16.63
NUM_CHRON	# Chronic conditions	3.93	2.26	3.82	2.25
EXCHLTH	=1 if self-perceived health is excellent	0.16	0.37	0.17	0.38
POORHLTH	=1 if self-perceived health is poor	0.04	0.19	0.05	0.22
EXCMHLTH	=1 of self-perceived mental health is excellent	0.28	0.45	0.30	0.46
POORMHLTH	=1 of self-perceived mental health is poor	0.02	0.14	0.02	0.15
EMPLOYEED	=1 if the person is employed	0.20	0.40	0.19	0.39
PRIVATE	=1 if the person has private insurance	0.43	0.50	0.46	0.50
NORTHEAST	=1 if lives in northeastern U.S.	0.18	0.38	0.17	0.38
MIDWEST	=1 if lives in midwestern U.S.	0.21	0.41	0.21	0.41
WEST	=1 if lives in western U.S.	0.24	0.43	0.24	0.43
MALE	=1 if MALE	0.44	0.50	0.45	0.50
BLACK	=1 if the person is African American	0.12	0.33	0.13	0.33
MARRIED	=1 if the person is married	0.50	0.50	0.53	0.50
COLLEGE	=1 if the person has a college degree	0.33	0.47	0.30	0.46
MEDICAID	=1 if the person is covered by Medicaid	0.14	0.35	0.14	0.34
ANYLIM	=1 if the person has a condition which limits activities of daily living	0.48	0.50	0.47	0.50
Expenditure	Total Amount paid by self or family	1434	6413	1496	4391

Table 12: Treatment Effects Estimation

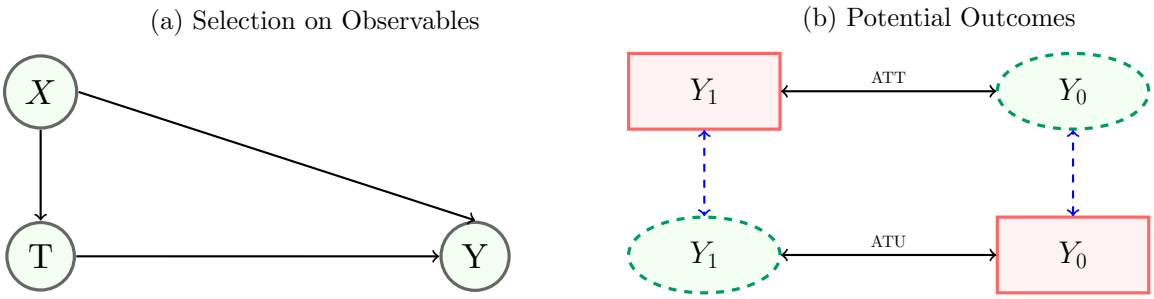
Year	**Model**		**Estimate**	**SD**	**95% CI**	**Marginal Likelihood**
2018, 2019	Homoskedastic	ATE	0.0162	0.0014	(0.0133, 0.0188)	22243.61
		ATT	0.0170	0.0013	(0.0144, 0.0195)	
	Heteroskedastic	ATE	-0.0058	0.0009	(-0.0076, -0.0040)	25365.03
		ATT	-0.0016	0.0009	(-0.0034, 0.0001)	
2020	Homoskedastic	ATE	0.0075	0.0029	(0.0023, 0.0139)	10602.64
		ATT	0.0066	0.0031	(0.0015, 0.0136)	
	Heteroskedastic	ATE	-0.0057	0.0011	(-0.0080, -0.0035)	12181.05
		ATT	-0.0014	0.0011	(-0.0036, 0.0008)	

4 Propensity Score Matching

Let $p(x) \equiv \Pr(T = 1|x)$ denote the propensity score, which represents the conditional probability of assignment to treatment given the covariates x. Propensity score matching (Rosenbaum and Rubin, 1983) is a popular method for estimating causal treatment effects. The approach is instrumental in mitigating selection bias by leveraging the propensity score as a balancing score that effectively enables the creation of comparable control and treatment groups. The key ideas behind propensity score matching are captured in Figure 8. Specifically, Figure 8a depicts the key assumption of selection on observables, whereas Figure 8b demonstrates that the fundamental

problem of estimating treatment effects is caused by the missing counterfactuals. In practice, we have the observed treated and untreated outcomes denoted by the rectangles in Figure 8b, whereas the dashed ovals are the unobserved counterfactuals. The idea behind matching observations on the basis of the propensity score is to generate subsamples from the observed treated and untreated groups that are comparable to one another as a means of uncovering the unobserved counterfactuals and estimating the desired treatment effect. Specifically, a subsample of untreated units whose characteristics closely match those of treated units can inform us about the ATT, while the average treatment effect on the untreated (ATU) can be evaluated by matching in the opposite direction. The ATE can then be calculated as a weighted average of ATT and the ATU.

Figure 8: Illustration



The approach is valid when $x \perp\!\!\!\perp T|p(x)$. To see this, note that by the definition of the propensity score, we have that $f\left(T|p\left(x\right),x\right) = f\left(T|p\left(x\right)\right)$, whereby $f\left(x|p\left(x\right),T\right) = \frac{f(T|p(x),x)f(x|p(x))}{f(T|p(x))} = f\left(x|p\left(x\right)\right)$. In this sense, conditioning on the propensity score generates "balanced" samples of treated and untreated units with similar characteristics x. Crucially, however, proper specification of the propensity score is required for the theory to hold, so that the search for a $p(x)$ that is supported by the data serves as the motivation for our study, especially as it relates to possibly omitted heteroskedasticity.

To study this issue, we employ a heteroskedastic model for the propensity score. Owing to the nonlinearity of the setting, Jensen's inequality implies that erroneously omitting heteroskedasticity will impact the bias and consistency properties of estimators and can not be dealt with by simply adjusting the standard errors. For $i = 1, \ldots, n$, the heteroskedastic probit model is specified as

$$T_i = \mathbb{1}\{T_i^* \geq 0\} = \mathbb{1}\{x_i'\beta + \nu_i \geq 0\}, \qquad \nu_i \sim N(0, \sigma_i^2).$$

In the homoskedastic case, for identification purposes we impose the constraint that the variance of

ν_i equals 1. In the heteroskedastic model, we assume that $var(\nu_i) = \exp(z_i'\gamma)$ and for identification z_i does not include a constant term. We specify the prior distributions $\beta \sim N(b_0, B_0)$ and $\gamma \sim N(\gamma_0, \Gamma_0)$. Algorithms 6 and 7 provide details on the propensity score estimation.

Algorithm 6 (Bayesian Propensity Score Estimation with Homoskedasticity)

---

(1) Sample $\beta \sim N\left(\hat{b}, \hat{B}\right)$, where $\hat{b} = \hat{B}\left(B_0^{-1}b_0 + \sum_{i \in N} x_i T_i^*\right)$, and $\hat{B} = \left(B_0^{-1} + \sum_{i \in N} x_i x_i^{'}\right)^{-1}$.

(2) Sample $T_i^* \sim TN(\mu_i, 1)$, where $T_i^* \in (-\infty, 0)$ if $T_i = 0$, and $T_i^* \in [0, \infty)$ if $T_i = 1$, where $\mu_i = x_i'\beta$, and the variance is 1.

An estimate of the marginal likelihood for the homoskedastic model and heteroskedastic models is easily obtained as a simplification as the approach in Section 2.1.1.

4.1 Simulation

Empirical researchers normally incorporate the higher-order and interaction terms to improve the balance of the matched samples if it failed in the beginning (Dehejia and Wahba, 1999; Caliendo and Kopeinig, 2008). In this section, we illustrate that neglected heteroskedasticity can lead to the emergence of imbalanced samples. The specification of a model with heteroskedasticity is one approach for address misspecification in addition to other possible step that can be taken, such as considering misspecification of the mean function.

The simulation study is based on the data in Dehejia and Wahba (1999), which comes from the National Supported Work Demonstration (NSW) and the panel study of income dynamics (PSID). The treatment T is the NSW participation. We believe that the variables age, education (educ), if the subject is Black or Hispanic, if the subject is married (married), real earnings in 1975 (RE75) and real earnings in 1974 (RE94) will affect the outcome variable of interest. There are 185 observations in the treatment group, and 2490 observations in the control group. We assume that DGP for the treatment assignment is

$$T_i = \{-2 - 0.17age_i - 0.001educ_i + 0.3744nodegree_i - 0.9630married_i + 1.2285black_i +$$
$$1.219hispanic_i - 0.000005RE74_i - 0.0001RE74_i + \nu_i \geq 0\}, \quad \nu_i \sim N(0, age_i).$$

Algorithm 7 (Bayesian Propensity Score Estimation with Heteroskedasticity)

---

(1) Sample $\beta \sim N\left(\hat{b}, \hat{B}\right)$, where $\hat{b} = \hat{B}\left(B_0^{-1}b_0 + \sum_i x_i \exp(z_i'\gamma)^{-1}T_i^*\right)$, and $\hat{B} = \left(B_0^{-1} + \sum_i x_i \exp(z_i'\gamma)^{-1}x_i'\right)^{-1}$.

(2) Sample $T_i^* \sim TN\left(\mu_i, \exp(z_i'\gamma)\right)$, where $T_i^* \in (-\infty, 0)$ if $T_i = 0$, $T_i^* \in [0, \infty)$ if $T_i = 1$, $\mu_i = x_i'\beta$.

(3) Sample $[\gamma|\beta, T^*]$ using the Metropolis-Hasting algorithm.

(a) Define

$$e_i^c = \left(T_i^* - x_i'\beta^c\right)^2$$
$$\eta_i^c = Z_i'\gamma^c + \frac{e_{Ti}^c - \exp\left(z_i'\gamma^c\right)}{\exp\left(z_i'\gamma^c\right)}, \quad \eta^c = \left(\eta_i^c, \ldots, \eta_n^c\right)',$$

where γ^c and β^c are the current values of γ and β.

(b) Using the iteratively reweighted least squares algorithm, we obtain a proposal value γ^p from the proposal density, which is $T_\nu(\gamma^p|\hat{\gamma}^p, V^p)$, where $V^p = (\Gamma_0^{-1} + \frac{1}{2}Z'Z)^{-1}$ and $\hat{\gamma}^p = V^p(\Gamma_0^{-1}\gamma_0 + \frac{1}{2}Z'\eta^c)$. We obtain $q(\gamma^c|\hat{\gamma}^c, V^c)$ in the reverse direction moving from the proposed value to the current value. Z is defined as $Z \equiv (z_0', z_1, ..., z_n)'$, which contains covariates that determines the variance.

(c) The acceptance rate α is defined as

$$\alpha = \frac{f\left(T_i^*|\beta^c, \gamma^p\right)\pi\left(\gamma^p|\gamma_0, \Gamma_0\right)}{f\left(T_i^*|\beta^c, \gamma^c\right)\pi\left(\gamma^c|\gamma_0, \Gamma_0\right)} \times \frac{q\left(\gamma^c|\hat{\gamma}^c, V^c\right)}{q\left(\gamma^p|\hat{\gamma}^p, V^p\right)}.$$

If the proposed value is not accepted, γ^c is repeated in the next iteration.

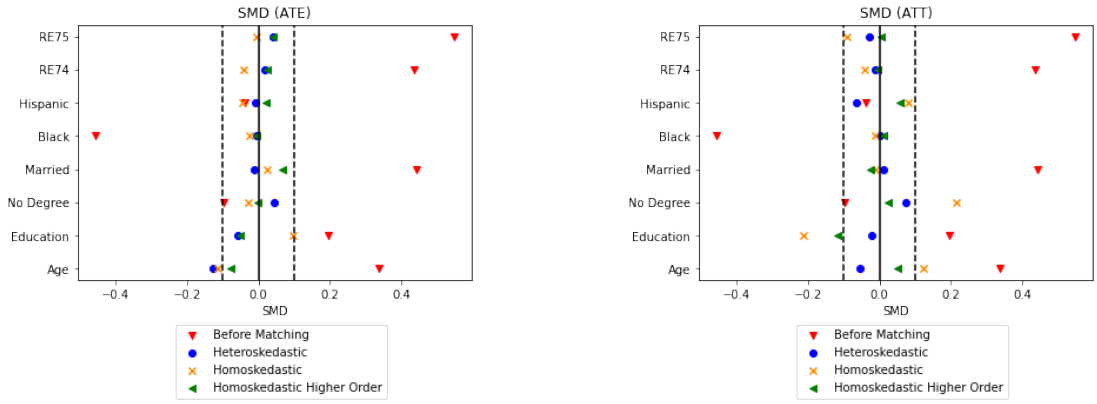
We use the standardized mean difference (SMD) as a balance measure. (Rosenbaum and Rubin (1985) and Thoemmes (2012)). A SMD exceeding 0.1 can be considered as a sign of imbalance. (Zhang et al. (2019)). SMD is calculated as

$$SMD = \frac{\bar{X}_T - \bar{X}_C}{\sqrt{\frac{S_T^2 + S_C^2}{2}}},$$

where $\bar{X}_T$ and $\bar{X}_C$ are the sample averages, and S_T^2 and S_C^2 are the standard deviations for the treatment and control groups, respectively. We employ nearest neighbor matching with replacement with a radius of 0.2 times the standard deviation of the estimated propensity score (Austin, 2011; Chaudhuri and Howley, 2022).

Three models are estimated: the correctly specified heteroskedastic model, the homoskedastic model with all covariates, and the extended homoskedastic model incorporating all covariates, age squared (age^2), and interactions between age and other covariates. Figure 9 shows the SMD before and after matching. Before matching, the covariates are imbalanced. The heteroskedastic model effectively enhances balance within both the ATE and ATT samples. In this example, the homoskedastic model falls short of achieving balance in the ATT estimation sample. However, by including higher order and interaction terms, the balance is improved.

Figure 9: SMD



(a) SMD (ATE)

(b) SMD (ATT)

4.2 Application: The Effects of COVID-19 Vaccination on Mental Well-being

Chaudhuri and Howley (2022) evaluate the impact of COVID-19 vaccination on mental health. The treatment variable is if the subject received any dose of COVID-19 vaccine. This is a sample of wave 7 and 8 of COVID-19 surveys by the UK Household Longitudinal Study (University of Essex, Institute for Social and Economic Research, 2021). This survey recorded the vaccination, demographic and mental health information. The outcome variable in this study is assessed using the GHQ-12 questionnaire, which is designed to evaluate an individual's mental health condition through a series of 12 questions. Each question in the GHQ-12 is rated on a four-point scale. The resulting GHQ scores can range from 0 to 36. In the context of this particular sample, it is important to note that the GHQ scores have been reversed, such that a score of 36 indicates the highest level of mental health, while a score of 0 signifies a markedly diminished level of mental well-being in the evaluated individuals. The summary of statistics of the key variables are presented

in Table 13.

Table 13: Summary of Statistics

Variables	Control Group (12423) Mean	SD	Treatment Group (9562) Mean	SD
GHQ-12	23.1388	6.1476	24.0396	5.6400
AGE	49.1924	15.6416	61.6679	13.8353
Burn in UK	0.8653	0.3414	0.9012	0.2984
Clinical Vulnerable	0.3417	0.4743	0.5646	0.4958
Male	0.4204	0.4936	0.4147	0.4927
Key Worker	0.2491	0.4325	0.2509	0.4335
Couple	0.6871	0.4637	0.7287	0.4446
Willingness to take vaccine	0.9059	0.2920	0.9507	0.2164

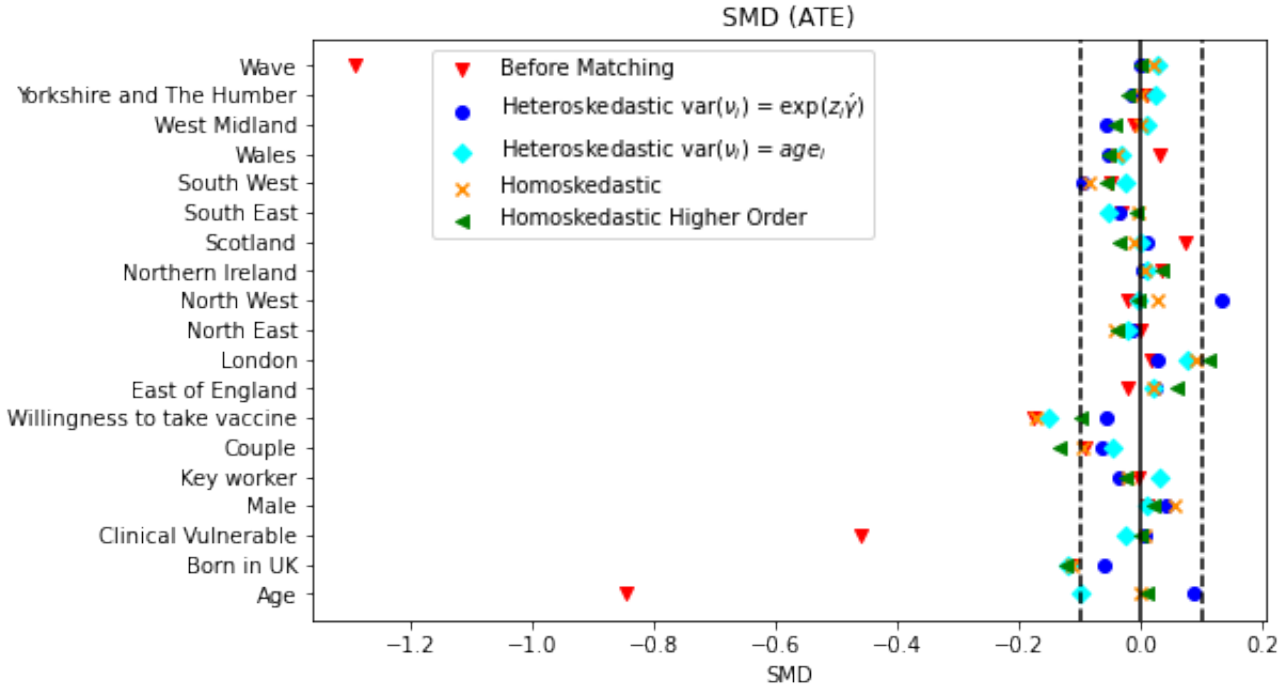
We estimated the treatment effects using four models. The first one is the heteroskedastic model with variance $var(\nu_i) = \exp(z_i'\gamma)$, while the second model is more parsimonious with variance $var(\nu_i) = age_i$. The third model is a homoskedastic model with all the covariates, and the fourth model incorporates age^2 and all the interaction terms between age and other covariates.

The estimated impact of COVID-19 vaccination on mental well-being is presented in Table 14. The marginal likelihood results suggest that the heteroskedastic model with $var(\nu_i) = \exp(z_i'\gamma)$ fits the data better. The results suggest that COVID-19 Vaccination is expected to improve mental health. Figure 10 shows the SMD before and after matching. The figure shows that for the ATE samples, all the models can improve the balance. For the ATT samples, the heteroskedastic model with $var(\nu_i) = \exp(z_i'\gamma)$ performs better than the alternatives.

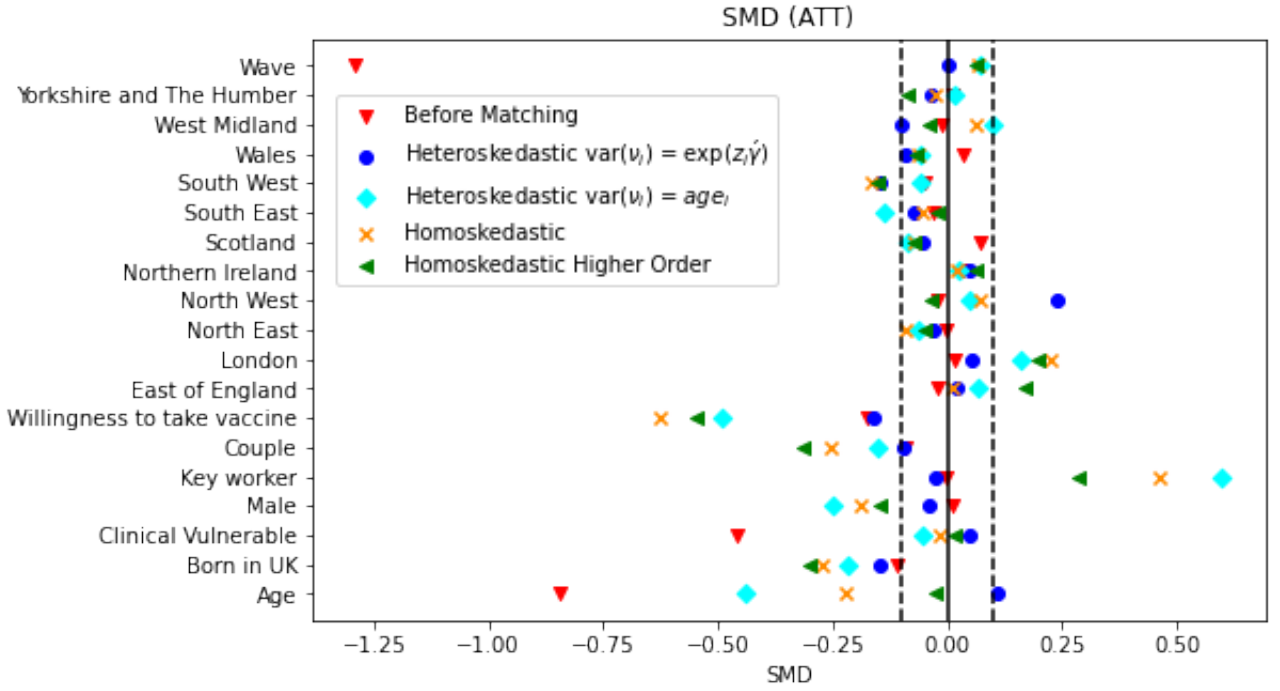
Table 14: Impact of COVID-19 Vaccination on Mental Health

Model	ATE Mean	SD	95% CI	ATT Mean	SD	95% CI	Marginal Likelihood
Heteroskedastic ($var(\nu_i) = \exp(z_i'\gamma)$)	1.2018	0.2206	(0.7585, 1.6391)	2.5916	0.4681	(1.6778, 3.5173)	-7687.86
Heteroskedastic ($var(\nu_i) = age_i^2$)	0.5227	0.1232	(0.2993, 0.7653)	1.3593	0.2237	(0.9183, 1.7994)	-9337.68
Homoskedastic	0.3851	0.1179	(0.1525, 0.6109)	1.1477	0.2229	(0.7168, 1.6037)	-8753.30
Homoskedastic (Higher-order)	0.3628	0.1251	(0.1306, 0.6353)	0.9407	0.2316	(0.5139, 1.4600)	-8030.50

Figure 10: SMD (COVID-19)



(a) SMD (ATE Sample)



(b) SMD (ATT Sample)

5 Conclusion

This paper has studied the impact of heteroskedasticity in regression discontinuity designs, potential outcome models, and propensity score matching. Because of the nonlinearities in these contexts, the question of whether heteroskedasticity is present has to be addressed directly, as it can lead to bias and inconsistency with consequences can not be handled by correcting the standard errors. In our Bayesian context, we treat the presence of heteroskedasticity as a question of model uncertainty. On the computational side, we develop new computationally efficient simulation-based estimation algorithms tailored to each setting and discuss their implementation in computing marginal likelihoods to enable formal model comparison. Moreover, we propose an approach for reducing the number of reduced MCMC runs required for marginal likelihood estimation in settings with multiple parameter blocks.

Simulation studies have been provided in order to evaluate the empirical consequences of omitted heteroskedasticity, assess the performance of the proposed estimation algorithms, and validate the proposed model comparison techniques. Our investigation has revealed that when non-linearity is pronounced, ignoring heteroskedasticity can result in biased estimates of treatment effects. We also find that the proposed MCMC methods perform well and can recover the true parameters and models used in generating the data.

To assess the practical applicability and relevance of our methods, the paper has devoted considerable attention to several applications. In particular, we have explored the impact of academic probation on students' academic performance, the effects of Medigap policies on out-of-pocket healthcare expenditures, and the influence of COVID-19 vaccination on mental well-being. RDD results suggest that academic probation improves subsequent semester GPA, while exhibiting no discernible impact on graduation rates. Using a potential outcome modeling framework in our second application, we find that that Medigap policies are expected to reduce out-of-pocket healthcare expenditures. Finally, results from propensity score matching indicate that COVID-19 vaccination improved the mental well-being of vaccine recipients in the UK. Based on model comparisons in each application, we found that heteroskedastic models were favored in most settings, although there were instances in which the simpler homoskedastic specifications were adequate. The results emphasize the importance of allowing for heteroskedasticity in observational observational studies of causal effects and demonstrate that the presence of heteroskedasticity can be uncovered through

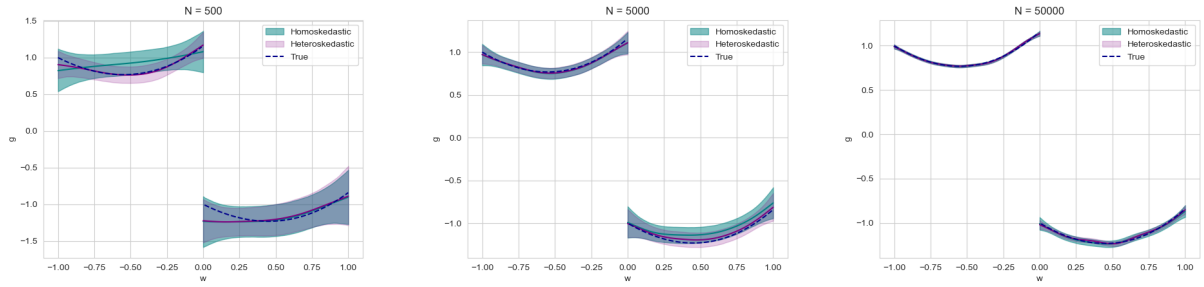
model comparisons. While our analysis has primarily centered on the effects of heteroskedasticity, we believe that other concerns such as sample selection or endogeneity may also be present in many settings. We intend to study their impact, as well as their interactions with heteroskedasticity, on treatment effect estimation in future work.

A Sharp Regression Discontinuity Design: Other Simulation Results

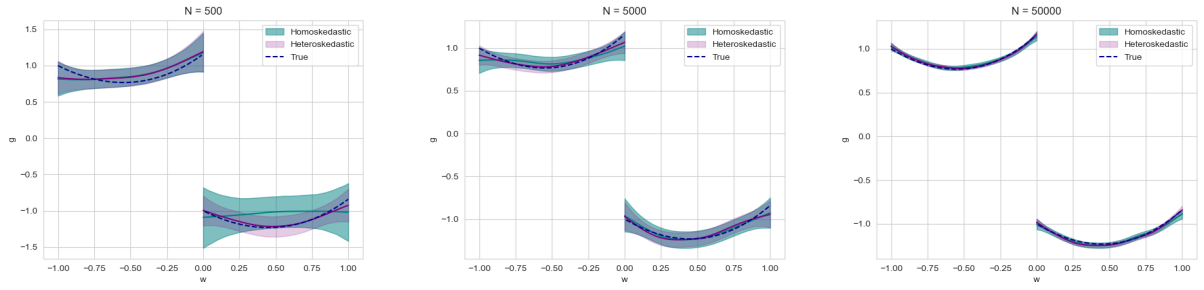
Table 15: ATE with Continuous Outcome Variable (Robustness Check)

	Model	True ATE	RD ATE	SD	95% CI
n = 500	Homoskedastic	-2.2357	-2.3684	0.2494	(-2.8652, -1.8849)
	Heteroskedastic	-2.2357	-2.4144	0.2309	(-2.8728, 1.9686)
	RDRobust	-2.2357	-2.6305	0.6780	(-4.1775, -1.0734)
n = 5000	Homoskedastic	-2.2195	-2.0407	0.1271	(-2.2888, -1.7895)
	Heteroskedastic	-2.2195	-2.0941	0.1061	(-2.2996, -1.8834)
	RDRobust	-2.2195	-2.1892	0.2142	(-2.7119, -1.7242)
n = 50000	Homoskedastic	-2.2092	-2.1986	0.0409	(-2.2793, -2.1191)
	Heteroskedastic	-2.2092	-2.1991	0.0288	(-2.2557, -2.1427)
	RDRobust	-2.2092	-2.0633	0.0690	(-2.2046, -1.8831)

Figure 11: $\hat{g}$ with Continuous Outcome Variable



(a) $\beta_1 = \beta_0$, N = 500 (b) $\beta_1 = \beta_0$, N = 5000 (c) $\beta_1 = \beta_0$, N = 50000



(d) $\beta_1 \neq \beta_0$, N = 500 (e) $\beta_1 \neq \beta_0$, N = 5000 (f) $\beta_1 \neq \beta_0$, N = 50000

B MEPS: Coefficients

Table 16: Heteroskedastic Model (2020)

	Parameter	Mean	SD	95% CI			Parameter	Mean	SD	95% CI	
	const	-0.7584	0.0986	-0.9532	-0.5719	γ_T	FAMINC	0.1743	0.0076	0.1594	0.1893
	AGE	-0.0270	0.0321	-0.0893	0.0370		const	-8.6130	0.1125	-8.8395	-8.3974
	FAMINC	0.1734	0.0150	0.1444	0.2032	γ_0	AGE	0.4661	0.0513	0.3662	0.5676
	NUM_VISIT	0.0016	0.0019	-0.0022	0.0054		NUM_CHRON	0.0512	0.0263	-0.0052	0.1001
	NUM_CHRON	0.0123	0.0144	-0.0157	0.0406		const	-9.1443	0.1706	-9.4832	-8.8163
	EXCHLTH	0.0111	0.0991	-0.1841	0.2049	γ_1	AGE	0.4260	0.0743	0.2788	0.5715
	POORHLTH	0.0431	0.1605	-0.2715	0.3550		NUM_CHRON	0.0673	0.0327	0.0019	0.1296
	EXCMHLTH	-0.0145	0.0780	-0.1669	0.1387						
β_T	POORMHLTH	-0.4186	0.2427	-0.9074	0.0434						
	EMPLOYEED	0.1753	0.0899	0.0007	0.3535						
	NORTHEAST	-0.0914	0.0894	-0.2693	0.0821						
	MIDWEST	0.1390	0.0818	-0.0176	0.3036						
	WEST	-0.1954	0.0853	-0.3637	-0.0300						
	MALE	-0.0746	0.0627	-0.1975	0.0494						
	BLACK	-0.0576	0.0942	-0.2406	0.1301						
	MARRIED	0.0515	0.0659	-0.0781	0.1825						
	COLLEGE	0.0568	0.0711	-0.0841	0.1933						
	MEDICAID	-0.9967	0.1169	-1.2317	-0.7726						
	ANYLIM	0.0425	0.0659	-0.0875	0.1697						
	const	0.0036	0.0013	0.0011	0.0062						
	AGE	0.0009	0.0005	0.0000	0.0018						
	NUM_VISIT	0.0004	0.0000	0.0004	0.0005						
	NUM_CHRON	0.0012	0.0002	0.0008	0.0016						
	EXCHLTH	-0.0025	0.0013	-0.0050	0.0000						
	POORHLTH	0.0002	0.0020	-0.0037	0.0041						
	EXCMHLTH	-0.0002	0.0010	-0.0022	0.0019						
	POORMHLTH	0.0009	0.0027	-0.0044	0.0061						
b_0	EMPLOYEED	-0.0048	0.0012	-0.0071	-0.0025						
	NORTHEAST	0.0025	0.0012	0.0002	0.0047						
	MIDWEST	0.0000	0.0011	-0.0022	0.0022						
	WEST	0.0017	0.0011	-0.0005	0.0038						
	MALE	-0.0003	0.0008	-0.0019	0.0013						
	BLACK	-0.0021	0.0012	-0.0044	0.0002						
	MARRIED	-0.0034	0.0009	-0.0050	-0.0017						
	COLLEGE	-0.0013	0.0010	-0.0032	0.0007						
	MEDICAID	-0.0038	0.0011	-0.0059	-0.0017						
	ANYLIM	0.0047	0.0009	0.0030	0.0065						
	const	-0.0042	0.0017	-0.0075	-0.0008						
	AGE	0.0008	0.0005	-0.0002	0.0019						
	NUM_VISIT	0.0004	0.0000	0.0003	0.0004						
	NUM_CHRON	0.0014	0.0002	0.0009	0.0018						
	EXCHLTH	-0.0002	0.0014	-0.0029	0.0024						
	POORHLTH	0.0002	0.0029	-0.0056	0.0059						
	EXCMHLTH	0.0004	0.0011	-0.0018	0.0025						
	POORMHLTH	-0.0054	0.0048	-0.0149	0.0037						
b_1	EMPLOYEED	0.0046	0.0011	0.0025	0.0067						
	NORTHEAST	0.0019	0.0014	-0.0008	0.0046						
	MIDWEST	0.0046	0.0012	0.0022	0.0069						
	WEST	-0.0012	0.0012	-0.0036	0.0012						
	MALE	-0.0038	0.0009	-0.0056	-0.0020						
	BLACK	-0.0043	0.0015	-0.0073	-0.0013						
	MARRIED	0.0014	0.0010	-0.0005	0.0033						
	COLLEGE	0.0043	0.0010	0.0024	0.0061						
	MEDICAID	-0.0250	0.0026	-0.0302	-0.0201						
	ANYLIM	0.0051	0.0010	0.0031	0.0070						
	a_{0T}	-0.0147	0.0007	-0.0160	-0.0134						
	a_{1T}	0.0175	0.0007	0.0163	0.0188						

Table 17: Heteroskedastic Model (2018, 2019)

	Parameter	Mean	SD	95% CI			Parameter	Mean	SD	95% CI	
	const	-0.7571	0.0636	-0.8834	-0.6312	γ_T	FAMINC	0.1347	0.0055	0.1240	0.1457
	AGE	-0.0052	0.0207	-0.0456	0.0349		const	-8.4420	0.0786	-8.5970	-8.2916
	FAMINC	0.1512	0.0091	0.1334	0.1691	γ_0	AGE	0.3319	0.0311	0.2727	0.3930
	NUM_VISIT	0.0020	0.0011	-0.0001	0.0041		NUM_CHRON	0.0452	0.0138	0.0181	0.0719
	NUM_CHRON	0.0191	0.0093	0.0012	0.0376		const	-8.9472	0.1254	-9.2025	-8.7126
	EXCHLTH	-0.0787	0.0610	-0.1980	0.0405	γ_1	AGE	0.5289	0.0501	0.4290	0.6243
	POORHLTH	-0.0513	0.0915	-0.2332	0.1261		NUM_CHRON	0.0300	0.0226	-0.0136	0.0744
	EXCMHLTH	0.0584	0.0493	-0.0380	0.1543						
β_T	POORMHLTH	0.0874	0.1273	-0.1648	0.3352						
	EMPLOYEED	0.1563	0.0596	0.0391	0.2740						
	NORTHEAST	-0.0607	0.0584	-0.1747	0.0540						
	MIDWEST	0.1376	0.0528	0.0324	0.2404						
	WEST	-0.0801	0.0531	-0.1852	0.0232						
	MALE	-0.0064	0.0407	-0.0860	0.0725						
	BLACK	-0.0328	0.0602	-0.1503	0.0863						
	MARRIED	0.1239	0.0417	0.0406	0.2057						
	COLLEGE	0.1140	0.0491	0.0176	0.2073						
	MEDICAID	-1.0296	0.0750	-1.1787	-0.8822						
	ANYLIM	-0.0015	0.0435	-0.0879	0.0846						
	const	0.0103	0.0010	0.0084	0.0122						
	AGE	0.0016	0.0003	0.0010	0.0022						
	NUM_VISIT	0.0003	0.0000	0.0003	0.0003						
	NUM_CHRON	0.0009	0.0001	0.0006	0.0011						
	EXCHLTH	-0.0022	0.0009	-0.0040	-0.0005						
	POORHLTH	0.0014	0.0013	-0.0011	0.0039						
	EXCMHLTH	0.0001	0.0007	-0.0014	0.0015						
	POORMHLTH	-0.0007	0.0019	-0.0044	0.0029						
β_0	EMPLOYEED	-0.0055	0.0009	-0.0072	-0.0038						
	NORTHEAST	0.0023	0.0008	0.0007	0.0040						
	MIDWEST	-0.0003	0.0008	-0.0018	0.0013						
	WEST	0.0011	0.0008	-0.0005	0.0026						
	MALE	-0.0034	0.0006	-0.0045	-0.0022						
	BLACK	-0.0022	0.0008	-0.0038	-0.0005						
	MARRIED	-0.0032	0.0006	-0.0044	-0.0020						
	COLLEGE	0.0008	0.0008	-0.0007	0.0022						
	MEDICAID	-0.0078	0.0008	-0.0094	-0.0061						
	ANYLIM	0.0046	0.0006	0.0033	0.0058						
	const	-0.0041	0.0012	-0.0064	-0.0018						
	AGE	0.0012	0.0004	0.0005	0.0020						
	NUM_VISIT	0.0004	0.0000	0.0003	0.0004						
	NUM_CHRON	0.0017	0.0002	0.0014	0.0020						
	EXCHLTH	-0.0013	0.0009	-0.0031	0.0004						
	POORHLTH	0.0025	0.0017	-0.0009	0.0059						
	EXCMHLTH	0.0015	0.0007	0.0001	0.0030						
	POORMHLTH	0.0030	0.0025	-0.0020	0.0079						
β_1	EMPLOYEED	0.0054	0.0008	0.0039	0.0068						
	NORTHEAST	0.0031	0.0009	0.0013	0.0048						
	MIDWEST	0.0044	0.0008	0.0029	0.0060						
	WEST	0.0000	0.0008	-0.0016	0.0017						
	MALE	-0.0034	0.0006	-0.0046	-0.0022						
	BLACK	-0.0060	0.0010	-0.0079	-0.0040						
	MARRIED	0.0032	0.0007	0.0019	0.0046						
	COLLEGE	0.0065	0.0007	0.0052	0.0079						
	MEDICAID	-0.0264	0.0018	-0.0298	-0.0229						
	ANYLIM	0.0022	0.0007	0.0008	0.0035						
	a_{0T}	-0.0140	0.0006	-0.0151	-0.0128						
	a_{1T}	0.0190	0.0006	0.0179	0.0201						

Table 18: Homoskedastic Model

		2020				2018, 2019			
	Parameter	Mean	SD	95% CI		Mean	SD	95% CI	
β_T	const	-0.5358	0.0632	-0.6607	-0.4121	-0.4230	0.0431	-0.5069	-0.3388
	AGE	-0.0383	0.0202	-0.0773	0.0020	-0.0285	0.0141	-0.0557	-0.0004
	FAMINC	0.0652	0.0061	0.0534	0.0771	0.0483	0.0036	0.0412	0.0554
	NUM_VISIT	0.0023	0.0014	-0.0004	0.0050	0.0012	0.0008	-0.0003	0.0028
	NUM_CHRON	0.0149	0.0093	-0.0032	0.0328	0.0143	0.0063	0.0020	0.0267
	EXCHLTH	0.0139	0.0578	-0.0991	0.1266	-0.0540	0.0386	-0.1310	0.0208
	POORHLTH	-0.0268	0.1084	-0.2380	0.1874	-0.0843	0.0655	-0.2127	0.0430
	EXCMHLTH	0.0189	0.0461	-0.0702	0.1084	0.0484	0.0312	-0.0112	0.1096
	POORMHLTH	-0.3962	0.1640	-0.7170	-0.0755	0.0069	0.0919	-0.1762	0.1891
	EMPLOYEED	0.2225	0.0504	0.1244	0.3218	0.2120	0.0358	0.1424	0.2816
	NORTHEAST	0.0283	0.0555	-0.0801	0.1371	-0.0053	0.0381	-0.0785	0.0703
	MIDWEST	0.1533	0.0508	0.0526	0.2521	0.1160	0.0357	0.0468	0.1862
	WEST	-0.1175	0.0511	-0.2160	-0.0182	-0.0710	0.0348	-0.1399	-0.0032
	MALE	-0.0560	0.0389	-0.1324	0.0199	-0.0066	0.0264	-0.0582	0.0449
	BLACK	-0.0461	0.0625	-0.1686	0.0775	-0.0333	0.0421	-0.1147	0.0497
	MARRIED	0.1168	0.0409	0.0356	0.1948	0.1613	0.0279	0.1081	0.2159
	COLLEGE	0.1204	0.0435	0.0366	0.2053	0.1667	0.0301	0.1080	0.2256
	MEDICAID	-1.0880	0.0747	-1.2330	-0.9413	-1.0081	0.0518	-1.1115	-0.9081
	ANYLIM	0.0093	0.0424	-0.0742	0.0931	-0.0292	0.0289	-0.0854	0.0277
β_0	const	0.0113	0.0024	0.0059	0.0156	0.0091	0.0012	0.0067	0.0114
	AGE	0.0007	0.0005	-0.0004	0.0017	0.0016	0.0004	0.0009	0.0023
	NUM_VISIT	0.0005	0.0000	0.0005	0.0006	0.0004	0.0000	0.0003	0.0004
	NUM_CHRON	0.0010	0.0002	0.0005	0.0014	0.0007	0.0002	0.0004	0.0011
	EXCHLTH	-0.0024	0.0016	-0.0055	0.0008	-0.0014	0.0011	-0.0035	0.0006
	POORHLTH	-0.0023	0.0024	-0.0071	0.0024	0.0014	0.0015	-0.0017	0.0044
	EXCMHLTH	0.0003	0.0013	-0.0021	0.0028	0.0006	0.0009	-0.0011	0.0022
	POORMHLTH	0.0001	0.0032	-0.0060	0.0064	-0.0005	0.0022	-0.0048	0.0037
	EMPLOYEED	-0.0004	0.0016	-0.0035	0.0027	-0.0039	0.0010	-0.0059	-0.0019
	NORTHEAST	0.0032	0.0014	0.0004	0.0060	0.0030	0.0010	0.0010	0.0049
	MIDWEST	0.0019	0.0015	-0.0010	0.0048	0.0006	0.0010	-0.0013	0.0025
	WEST	0.0022	0.0013	-0.0004	0.0048	0.0025	0.0009	0.0007	0.0043
	MALE	-0.0004	0.0010	-0.0024	0.0016	-0.0033	0.0007	-0.0047	-0.0019
	BLACK	-0.0037	0.0015	-0.0066	-0.0008	-0.0030	0.0010	-0.0050	-0.0010
	MARRIED	0.0001	0.0011	-0.0022	0.0022	-0.0021	0.0007	-0.0036	-0.0006
	COLLEGE	0.0050	0.0013	0.0024	0.0075	0.0042	0.0009	0.0025	0.0059
	MEDICAID	-0.0119	0.0020	-0.0154	-0.0075	-0.0087	0.0010	-0.0107	-0.0066
	ANYLIM	0.0058	0.0011	0.0036	0.0079	0.0051	0.0008	0.0036	0.0066
β_1	const	0.0213	0.0028	0.0157	0.0266	0.0204	0.0017	0.0170	0.0238
	AGE	0.0015	0.0007	0.0001	0.0028	0.0011	0.0004	0.0002	0.0019
	NUM_VISIT	0.0004	0.0000	0.0003	0.0005	0.0004	0.0000	0.0003	0.0004
	NUM_CHRON	0.0010	0.0003	0.0003	0.0016	0.0012	0.0002	0.0008	0.0016
	EXCHLTH	-0.0008	0.0018	-0.0044	0.0028	0.0001	0.0011	-0.0020	0.0022
	POORHLTH	-0.0001	0.0041	-0.0080	0.0080	0.0043	0.0021	0.0001	0.0083
	EXCMHLTH	0.0005	0.0015	-0.0024	0.0034	0.0006	0.0009	-0.0011	0.0023
	POORMHLTH	0.0063	0.0069	-0.0075	0.0196	0.0035	0.0029	-0.0022	0.0092
	EMPLOYEED	0.0015	0.0016	-0.0015	0.0046	0.0025	0.0010	0.0007	0.0044
	NORTHEAST	0.0025	0.0018	-0.0011	0.0061	0.0035	0.0011	0.0013	0.0057
	MIDWEST	0.0013	0.0017	-0.0020	0.0046	0.0034	0.0010	0.0014	0.0053
	WEST	0.0004	0.0017	-0.0029	0.0039	0.0017	0.0010	-0.0003	0.0037
	MALE	-0.0026	0.0013	-0.0052	-0.0002	-0.0030	0.0008	-0.0045	-0.0015
	BLACK	-0.0054	0.0022	-0.0098	-0.0011	-0.0062	0.0013	-0.0088	-0.0037
	MARRIED	-0.0010	0.0014	-0.0036	0.0017	0.0008	0.0008	-0.0008	0.0025
	COLLEGE	0.0035	0.0013	0.0009	0.0062	0.0035	0.0008	0.0019	0.0051
	MEDICAID	-0.0065	0.0042	-0.0147	0.0014	-0.0091	0.0025	-0.0141	-0.0042
	ANYLIM	0.0063	0.0014	0.0035	0.0091	0.0038	0.0008	0.0021	0.0054
	ω_{00}	0.0007	0.0000	0.0007	0.0008	0.0007	0.0000	0.0007	0.0008
	ω_{11}	0.0008	0.0000	0.0008	0.0009	0.0006	0.0000	0.0006	0.0007
	ω_{02}	-0.0041	0.0033	-0.0123	0.0005	-0.0172	0.0009	-0.0189	-0.0152
	ω_{12}	-0.0026	0.0017	-0.0056	0.0009	-0.0021	0.0012	-0.0043	0.0006

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