Prognostic Propensity Scores: A Method Accounting for the Correlations of the Covariates with Both the Treatment and the Outcome Variables in Matching and Diagnostics

Authors and Affiliations:

Nianbo Dong
University of Missouri
14 Hill Hall, Columbia, MO 65211
Phone: (573) 882-1495
dong.nianbo@gmail.com

Metin Bulus
University of Missouri
14 Hill Hall, Columbia, MO 65211
mbnt9@mail.missouri.edu
Prognostic Propensity Scores: A Method Accounting for the Correlations of the Covariates with Both the Treatment and the Outcome Variables in Matching and Diagnostics

Background
Propensity scores (PS, Rosenbaum & Rubin, 1983) and prognostic scores (PGS, Hansen, 2006, 2008; Wyss et al., 2015) are two summary scores to address confounding for treatment effect estimation. PS focus on capturing the associations of the covariates and the treatment variable and PGS focus on capturing the associations of the covariates and the outcome variable. Because the associations of the covariates with both the treatment and the outcome variables may affect accuracy of treatment effect estimates, combining PS and PGS may have desirable properties. Hansen (2006) combined PS and PGS into a single index using Mahalanobis distance and used this index for full matching. He concluded that full matching on the combined index resulted in smaller bias and variance compared to matching on PS alone. Kelcey (2013) further compared full matching on the combined index proposed by Hansen (2006) to full matching on PS (0.1 caliper size), and full matching on PS within PGS strata (quintiles). Kelcey (2013) concluded that full matching on PS within PGS strata is superior to full matching on the combined index, and full matching on PS alone. A more comprehensive simulation study was conducted by Leacy and Stuart (2014) to compare full matching on the combined index with full matching on PGS within PS calipers (0.2 caliper size), subclassification based on a grid of 5 x 5 subcells obtained from quintiles of PS and PGS, full matching on PS or PGS alone, and subclassification (quintiles) on PS or PGS. Leacy and Stuart (2014) concluded that full matching on the combined index and full matching on PGS within PS calipers are superior to other methods. Albeit contradictory in their findings with regard to performance of the combined index, it is difficult to draw any definite conclusion since all three studies only have full matching on PS in common as a comparison method. Nevertheless, results are encouraging and warrant further exploration of combining PS and PGS.

Furthermore, the diagnostics for PS that commonly rely on covariate-based absolute standardized difference (ASD) or PS-based standardized difference (PSSD), may not apply to PGS or its joint use with PS. The PGS-based standardized difference (PGSSD) was suggested as a measure of balance for both PS and PGS (Stuart, Lee, & Leacy, 2013). However, diagnostics for the joint use of PS and PGS have not been investigated to date.

Purpose
The purpose is twofold: (1) We propose an alternative method to combine PS and PGS, and compare its performance to regression adjustment, optimal matching on PS, and optimal matching on PGS, and (2) We propose a correlation-based balance measure for diagnostics.

Research Design
Let a matrix of covariates be denoted as \( X \), and define PS as \( X\alpha \), where \( \alpha \) being a column vector of standardized regression weights to predict treatment status \( (T) \). For the same matrix of \( X \), let PGS be denoted as \( X\beta \), where \( \beta \) being a column vector of standardized regression weights to predict the outcome \( (Y) \). Then the **prognostic propensity score** (PGPS) is defined based on redefined weights as

\[
\text{PGPS} = X(diag[\alpha\beta^T]).
\]
This combined score (rather than combined index derived from Mahalanobis distance) is used for optimal matching (Ming & Rosenbaum, 2001).

We also propose a correlation based covariate balance measure, which can be used to diagnose PS, PGS, and PGPS. Let the correlation between the covariates and the treatment status \(T\) be denoted in vector form as \(\text{corr}(X, T)\), the correlation between the covariates and the outcome \(Y\) in vector form as \(\text{corr}(X, Y)\), and number of covariates as \(N\), then the proposed covariate balance measure is defined as:

\[
R_{XT}R_{XY} = \frac{[\text{corr}(X, T)^T \text{corr}(X, Y)]}{N}.
\]

We conducted Monte Carlo simulation to compare the root mean square error (RMSE) of the treatment effect estimates among several estimation methods: analysis of variance (ANOVA), regression (REG), prognostic score (PGS), propensity score (PS), and prognostic propensity score (PGPS), as well as the doubly robust methods by including covariates in the outcome models (doubly robust prognostic score (DR.PGS), doubly robust prognostic score (DR.PS), and doubly robust prognostic propensity score (DR.PGPS)). Balance measure, \(R_{XT}R_{XY}\), were compared with other balance measures regarding the correlations between the balance measures and bias. Simulation scenarios \((n = 576)\) are adapted from Ali et al. (2014) and Stuart, Lee, and Leacy (2013). See Appendix A for further details.

**Findings and Discussion**

This is an ongoing study. We report partial simulation results from 500 replications for each scenario below. Table 1 and Figure 1 present the results of root mean square error (RMSE) of various estimation methods in 576 simulation scenarios. Overall, there is no superiority of PGPS in terms of RMSE. The doubly robust methods (DR.PGS; DR.PS; DR.PGPS) perform similarly better than the methods (PGS; PS; PGPS) without including covariates in the outcome model, and better than regression.

Simulation results may guide researchers as to when PGS may be a better option compared to regression adjustment and PS. There are already some studies focusing on these comparisons (Argobast & Ray, 2011; Argobast et al, 2012; Pfeiffer & Riedl, 2015; Schmidt et al, 2016; Wyss et al., 2015; Xu et al., 2016). These studies concluded that PS and PGS have different characteristics that may reduce bias under different circumstances, in particular when treatment-to-control ratio is small. We will identify specific scenarios where some methods are better than the others in the final paper.

Finally, this study shows that \(R_{XT}R_{XY}\) balance measure have higher correlation with bias and relatively more robust to estimation methods (PS, PGS, and PGPS) (Table 2 and Figure 2). The second best measure, PGSSSD is superior to ASD or PSD, confirming Stuart, Lee, and Leacy (2013) findings. Nonetheless, this holds when the outcome model is correctly specified, or when there is no omitted variables in the outcome model. In all other cases, we recommend using \(R_{XT}R_{XY}\) balance measure regardless of method because it has the highest correlation when models are miss-specified, and it is more robust to estimation methods.
References


### Table 1

*Root Mean Squared Error of Various Estimation Methods in 576 Simulation Scenarios*

<table>
<thead>
<tr>
<th>Sample</th>
<th>Estimation Method</th>
<th>Mean</th>
<th>LCL Mean</th>
<th>UCL Mean</th>
<th>SD</th>
<th>Median</th>
<th>Min</th>
<th>Max</th>
</tr>
</thead>
<tbody>
<tr>
<td>Full Sample</td>
<td>ANOVA</td>
<td>0.642</td>
<td>0.626</td>
<td>0.659</td>
<td>0.207</td>
<td>0.564</td>
<td>0.427</td>
<td>1.048</td>
</tr>
<tr>
<td></td>
<td>REG</td>
<td>0.202</td>
<td>0.192</td>
<td>0.212</td>
<td>0.121</td>
<td>0.185</td>
<td>0.013</td>
<td>0.513</td>
</tr>
<tr>
<td>Common Support Sample</td>
<td>DR.PGPS</td>
<td>0.164</td>
<td>0.153</td>
<td>0.175</td>
<td>0.134</td>
<td>0.118</td>
<td>0.015</td>
<td>0.533</td>
</tr>
<tr>
<td></td>
<td>DR.PGS</td>
<td>0.172</td>
<td>0.161</td>
<td>0.182</td>
<td>0.131</td>
<td>0.123</td>
<td>0.015</td>
<td>0.531</td>
</tr>
<tr>
<td></td>
<td>DR.PS</td>
<td>0.174</td>
<td>0.164</td>
<td>0.185</td>
<td>0.131</td>
<td>0.128</td>
<td>0.015</td>
<td>0.527</td>
</tr>
<tr>
<td></td>
<td>PGPS</td>
<td>0.277</td>
<td>0.267</td>
<td>0.286</td>
<td>0.114</td>
<td>0.232</td>
<td>0.117</td>
<td>0.613</td>
</tr>
<tr>
<td></td>
<td>PGS</td>
<td>0.259</td>
<td>0.250</td>
<td>0.267</td>
<td>0.105</td>
<td>0.240</td>
<td>0.060</td>
<td>0.594</td>
</tr>
<tr>
<td></td>
<td>PS</td>
<td>0.269</td>
<td>0.261</td>
<td>0.277</td>
<td>0.098</td>
<td>0.242</td>
<td>0.134</td>
<td>0.598</td>
</tr>
</tbody>
</table>

Table 2
Correlations of Covariate Balance Measure with Bias in 576 Simulation Scenarios

<table>
<thead>
<tr>
<th>Estimation Method</th>
<th>Covariate Balance Measure</th>
<th>Mean</th>
<th>LCL Mean</th>
<th>UCL Mean</th>
<th>SD</th>
<th>Min</th>
<th>Max</th>
</tr>
</thead>
<tbody>
<tr>
<td>ASD</td>
<td>ASD</td>
<td>0.257</td>
<td>0.242</td>
<td>0.273</td>
<td>0.190</td>
<td>-0.189</td>
<td>0.646</td>
</tr>
<tr>
<td></td>
<td>PGPSSD</td>
<td>0.376</td>
<td>0.361</td>
<td>0.391</td>
<td>0.182</td>
<td>-0.024</td>
<td>0.815</td>
</tr>
<tr>
<td>PGPS</td>
<td>PGSSD</td>
<td>0.573</td>
<td>0.556</td>
<td>0.591</td>
<td>0.212</td>
<td>-0.097</td>
<td>0.949</td>
</tr>
<tr>
<td></td>
<td>PSSD</td>
<td>0.338</td>
<td>0.316</td>
<td>0.360</td>
<td>0.268</td>
<td>-0.311</td>
<td>0.811</td>
</tr>
<tr>
<td></td>
<td>RxtRxy</td>
<td>0.731</td>
<td>0.720</td>
<td>0.743</td>
<td>0.137</td>
<td>0.184</td>
<td>0.888</td>
</tr>
<tr>
<td>PGS</td>
<td>ASD</td>
<td>0.204</td>
<td>0.194</td>
<td>0.215</td>
<td>0.124</td>
<td>-0.155</td>
<td>0.603</td>
</tr>
<tr>
<td></td>
<td>PGPSSD</td>
<td>0.309</td>
<td>0.295</td>
<td>0.323</td>
<td>0.174</td>
<td>-0.109</td>
<td>0.769</td>
</tr>
<tr>
<td></td>
<td>PGSSD</td>
<td>0.384</td>
<td>0.361</td>
<td>0.406</td>
<td>0.276</td>
<td>-0.250</td>
<td>0.902</td>
</tr>
<tr>
<td></td>
<td>PSSD</td>
<td>0.248</td>
<td>0.229</td>
<td>0.266</td>
<td>0.226</td>
<td>-0.415</td>
<td>0.775</td>
</tr>
<tr>
<td></td>
<td>RxtRxy</td>
<td>0.609</td>
<td>0.599</td>
<td>0.620</td>
<td>0.131</td>
<td>0.164</td>
<td>0.805</td>
</tr>
<tr>
<td>PS</td>
<td>ASD</td>
<td>0.438</td>
<td>0.420</td>
<td>0.457</td>
<td>0.226</td>
<td>-0.135</td>
<td>0.841</td>
</tr>
<tr>
<td></td>
<td>PGPSSD</td>
<td>0.496</td>
<td>0.477</td>
<td>0.516</td>
<td>0.238</td>
<td>-0.144</td>
<td>0.904</td>
</tr>
<tr>
<td></td>
<td>PGSSD</td>
<td>0.547</td>
<td>0.526</td>
<td>0.569</td>
<td>0.263</td>
<td>-0.140</td>
<td>0.947</td>
</tr>
<tr>
<td></td>
<td>PSSD</td>
<td>0.495</td>
<td>0.474</td>
<td>0.517</td>
<td>0.265</td>
<td>-0.099</td>
<td>0.895</td>
</tr>
<tr>
<td></td>
<td>RxtRxy</td>
<td>0.617</td>
<td>0.601</td>
<td>0.633</td>
<td>0.197</td>
<td>0.030</td>
<td>0.906</td>
</tr>
</tbody>
</table>

Figure 1. Optimal Matching within Common Support Sample

Note. DR.PGPS: Doubly Robust Prognostic Propensity Score. DR.PGS: Doubly Robust Prognostic Score. DR.PS: Doubly Robust Prognostic Score. PGPS: Prognostic Propensity Score. PGS: Prognostic Score. PS: Propensity Score.
REG: Regression.

Figure 2. Covariate Balance Measure Correlation with Bias
Appendix A. Simulation Framework

The following figure demonstrates the relationship of covariates and confounders with the treatment and the outcome variables. Unlike Ali et al (2014), X9 is not in this framework (related to neither treatment nor outcome). We also modified coefficients due to having a continuous outcome instead of a binary outcome. We adapted model specifications from Stuart, Lee and Leacy (2013), and modified them by considering both prognostic score and propensity scores models.

Figure A1. Association of Covariates and Confounders with Treatment and Outcome

True Models:
\[
\logit(p_t) = \alpha_0 + \alpha_1 x_1 + \alpha_2 x_2 + \alpha_3 x_4 + \alpha_4 x_5 + \alpha_5 x_7 + \alpha_6 x_8 + \alpha_7 x_4 + \alpha_8 x_5 + \alpha_9 x_8 + \alpha_{10} x_4 x_5 + \alpha_{11} x_4 x_6 + \alpha_{12} x_5^2 + \alpha_{12} x_5^2
\]
\[
y = \beta_0 + \gamma t + \beta_1 x_1 + \beta_2 x_2 + \beta_3 x_4 + \beta_4 x_5 + \beta_5 x_6 + \beta_6 x_4 + \beta_7 x_4 + \beta_8 x_5 + \beta_9 x_6 + \beta_{10} x_4 x_5 + \beta_{11} x_4 x_6 + \beta_{12} x_5^2
\]

Color and Font Codes:
- X7, X8: only treatment
- X1, X2, X4, X5: both treatment and outcome
- X3, X6: only outcome
- X1, X2, X3, X7: binary \{Bernoulli (p), where p= (.30, .40, .50, .70)}
- X4, X5, X6, X8: continuous \{all \sim \text{Normal (0, 1)}\}

In this study, for the true treatment model the intercept value is assigned such that treatment-to-control ratio is approximately .30. We further used acceptance-rejection technique and discarded samples having less than .20 and more than .40 treatment-to-control ratio.
Table A1. *Four Scenarios for True Model Coefficients*

<table>
<thead>
<tr>
<th>True Models (TM)</th>
<th>True Model Coefficients</th>
</tr>
</thead>
</table>
| **TM1: Propensity score model and outcome model coefficients are both in increasing order** | Main effects in propensity score model (PSM)  
$\alpha_3, \alpha_4, \alpha_6: \log(1.5), \log(2), \log(3)$ for cont  
$\alpha_1, \alpha_2, \alpha_5: \log(1.2), \log(1.5), \log(2)$ for binary  
Interactions and quadratic terms in PSM  
$\alpha_7, \alpha_8, \alpha_9, \alpha_{10}, \alpha_{11}, \alpha_{12}: \log(1.1), \log(1.2), \log(1.3), \log(1.4), \log(1.5), \log(1.6)$  
Main effects in outcome model (OM)  
$\gamma: 0$ or $0.5$ or $1$  
$\beta_4, \beta_5, \beta_6: 0.40, 0.70, 1$ for cont  
$\beta_1, \beta_2, \beta_3: 0.20, 0.40, 0.70$ for binary  
Interactions and quadratic terms in OM  
$\beta_7, \beta_8, \beta_9, \beta_{10}, \beta_{11}, \beta_{12}: 0.1, 0.2, 0.3, 0.4, 0.5, 0.6$ |
| **TM2: Propensity score model coefficients are in increasing order when outcome model coefficients are in decreasing order** | Main effects in propensity score model (PSM)  
$\alpha_3, \alpha_4, \alpha_6: \log(1.5), \log(2), \log(3)$ for cont  
$\alpha_1, \alpha_2, \alpha_5: \log(1.2), \log(1.5), \log(2)$ for binary  
Interactions and quadratic terms in PSM  
$\alpha_7, \alpha_8, \alpha_9, \alpha_{10}, \alpha_{11}, \alpha_{12}: \log(1.1), \log(1.2), \log(1.3), \log(1.4), \log(1.5), \log(1.6)$  
Main effects in outcome model (OM)  
$\gamma: 0$ or $0.5$ or $1$  
$\beta_4, \beta_5, \beta_6: 1, 0.70, 0.40$ for cont  
$\beta_1, \beta_2, \beta_3: 0.70, 0.40, 0.20$ for binary  
Interactions and quadratic terms in OM  
$\beta_7, \beta_8, \beta_9, \beta_{10}, \beta_{11}, \beta_{12}: 0.6, 0.5, 0.4, 0.3, 0.2, 0.1$ |
| **TM3: Propensity score model coefficients are in decreasing order when outcome model coefficients are in increasing order** | Main effects in propensity score model (PSM)  
$\alpha_3, \alpha_4, \alpha_6: \log(3), \log(2), \log(1.5)$ for cont  
$\alpha_1, \alpha_2, \alpha_5: \log(2), \log(1.5), \log(1.2)$ for binary  
Interactions and quadratic terms in PSM  
$\alpha_7, \alpha_8, \alpha_9, \alpha_{10}, \alpha_{11}, \alpha_{12}: \log(1.6), \log(1.5), \log(1.4), \log(1.3), \log(1.2), \log(1.1)$  
Main effects in outcome model (OM)  
$\gamma: 0$ or $0.5$ or $1$  
$\beta_4, \beta_5, \beta_6: 0.40, 0.70, 1$ for cont  
$\beta_1, \beta_2, \beta_3: 0.20, 0.40, 0.70$ for binary  
Interactions and quadratic terms in OM  
$\beta_7, \beta_8, \beta_9, \beta_{10}, \beta_{11}, \beta_{12}: 0.1, 0.2, 0.3, 0.4, 0.5, 0.6$ |
| **TM4: Propensity score model and outcome model coefficients are both in decreasing order** | Main effects in propensity score model (PSM)  
$\alpha_3, \alpha_4, \alpha_6: \log(3), \log(2), \log(1.5)$ for cont  
$\alpha_1, \alpha_2, \alpha_5: \log(2), \log(1.5), \log(1.2)$ for binary  
Interactions and quadratic terms in PSM  
$\alpha_7, \alpha_8, \alpha_9, \alpha_{10}, \alpha_{11}, \alpha_{12}: \log(1.6), \log(1.5), \log(1.4), \log(1.3), \log(1.2), \log(1.1)$  
Main effects in outcome model (OM)  
$\gamma: 0$ or $0.5$ or $1$  
$\beta_4, \beta_5, \beta_6: 1, 0.70, 0.40$ for cont  
$\beta_1, \beta_2, \beta_3: 0.70, 0.40, 0.20$ for binary  
Interactions and quadratic terms in OM  
$\beta_7, \beta_8, \beta_9, \beta_{10}, \beta_{11}, \beta_{12}: 0.6, 0.5, 0.4, 0.3, 0.2, 0.1$ |
Model Specifications (MS)
Propensity Score Model (PSM)
Prognostic Score Model (PGSM)
Outcome Model (OM)

MS1: True treatment model
PSM1:
\[
\logit(p_t) = \alpha_0 + \alpha_1 \tilde{x}_1 + \alpha_2 \tilde{x}_2 + \alpha_3 \tilde{x}_3 + \alpha_4 \tilde{x}_4 + \alpha_5 \tilde{x}_5 + \alpha_6 \tilde{x}_6 + \alpha_7 \tilde{x}_7 + \alpha_8 \tilde{x}_8 + \alpha_9 \tilde{x}_9 + \alpha_{10} \tilde{x}_{10} + \alpha_{11} \tilde{x}_{11} + \alpha_{12} \tilde{x}_{12}
\]

PGSM1:
\[
y' = \xi_0 + \xi_1 \tilde{x}_1 + \xi_2 \tilde{x}_2 + \xi_3 \tilde{x}_3 + \xi_4 \tilde{x}_4 + \xi_5 \tilde{x}_5 + \xi_6 \tilde{x}_6 + \xi_7 \tilde{x}_7 + \xi_8 \tilde{x}_8 + \xi_9 \tilde{x}_9 + \xi_{10} \tilde{x}_{10} + \xi_{11} \tilde{x}_{11} + \xi_{12} \tilde{x}_{12}
\]

OM1:
\[
y = \beta_0 + \gamma \tilde{t} + \beta_1 \tilde{t} + \beta_2 \tilde{t} + \beta_3 \tilde{t} + \beta_4 \tilde{t} + \beta_5 \tilde{t} + \beta_6 \tilde{t} + \beta_7 \tilde{t} + \beta_8 \tilde{t} + \beta_9 \tilde{t} + \beta_{10} \tilde{t} + \beta_{11} \tilde{t} + \beta_{12} \tilde{t}
\]

MS2: True outcome model
PSM2:
\[
\logit(p_t) = \alpha_0 + \alpha_1 \tilde{x}_1 + \alpha_2 \tilde{x}_2 + \alpha_3 \tilde{x}_3 + \alpha_4 \tilde{x}_4 + \alpha_5 \tilde{x}_5 + \alpha_6 \tilde{x}_6 + \alpha_7 \tilde{x}_7 + \alpha_8 \tilde{x}_8 + \alpha_9 \tilde{x}_9 + \alpha_{10} \tilde{x}_{10} + \alpha_{11} \tilde{x}_{11} + \alpha_{12} \tilde{x}_{12}
\]

PGSM2:
\[
y' = \xi_0 + \xi_1 \tilde{x}_1 + \xi_2 \tilde{x}_2 + \xi_3 \tilde{x}_3 + \xi_4 \tilde{x}_4 + \xi_5 \tilde{x}_5 + \xi_6 \tilde{x}_6 + \xi_7 \tilde{x}_7 + \xi_8 \tilde{x}_8 + \xi_9 \tilde{x}_9 + \xi_{10} \tilde{x}_{10} + \xi_{11} \tilde{x}_{11} + \xi_{12} \tilde{x}_{12}
\]

OM2:
\[
y = \beta_0 + \gamma \tilde{t} + \beta_1 \tilde{t} + \beta_2 \tilde{t} + \beta_3 \tilde{t} + \beta_4 \tilde{t} + \beta_5 \tilde{t} + \beta_6 \tilde{t} + \beta_7 \tilde{t} + \beta_8 \tilde{t} + \beta_9 \tilde{t} + \beta_{10} \tilde{t} + \beta_{11} \tilde{t} + \beta_{12} \tilde{t}
\]

MS3: Main effects for all covariates
PSM3:
\[
\logit(p_t) = \alpha_0 + \alpha_1 \tilde{x}_1 + \alpha_2 \tilde{x}_2 + \alpha_3 \tilde{x}_3 + \alpha_4 \tilde{x}_4 + \alpha_5 \tilde{x}_5 + \alpha_6 \tilde{x}_6 + \alpha_7 \tilde{x}_7 + \alpha_8 \tilde{x}_8
\]

PGSM3:
\[
y' = \xi_0 + \xi_1 \tilde{x}_1 + \xi_2 \tilde{x}_2 + \xi_3 \tilde{x}_3 + \xi_4 \tilde{x}_4 + \xi_5 \tilde{x}_5 + \xi_6 \tilde{x}_6 + \xi_7 \tilde{x}_7 + \xi_8 \tilde{x}_8
\]

OM3:
\[
y = \beta_0 + \gamma \tilde{t} + \beta_1 \tilde{t} + \beta_2 \tilde{t} + \beta_3 \tilde{t} + \beta_4 \tilde{t} + \beta_5 \tilde{t} + \beta_6 \tilde{t} + \beta_7 \tilde{t} + \beta_8 \tilde{t} + \beta_{10} \tilde{t}
\]

MS4: Main effects for six covariates related to treatment
PSM4:
\[
\logit(p_t) = \alpha_0 + \alpha_1 \tilde{x}_1 + \alpha_2 \tilde{x}_2 + \alpha_3 \tilde{x}_3 + \alpha_4 \tilde{x}_4 + \alpha_5 \tilde{x}_5 + \alpha_6 \tilde{x}_6
\]

PGSM4:
\[
y' = \xi_0 + \xi_1 \tilde{x}_1 + \xi_2 \tilde{x}_2 + \xi_3 \tilde{x}_3 + \xi_4 \tilde{x}_4 + \xi_5 \tilde{x}_5 + \xi_6 \tilde{x}_6
\]

OM4:
\[
y = \beta_0 + \gamma \tilde{t} + \beta_1 \tilde{t} + \beta_2 \tilde{t} + \beta_3 \tilde{t} + \beta_4 \tilde{t} + \beta_5 \tilde{t} + \beta_6 \tilde{t}
\]

MS5: Main effects for six covariates related to outcome
PSM5:
\[
\logit(p_t) = \alpha_0 + \alpha_1 \tilde{x}_1 + \alpha_2 \tilde{x}_2 + \alpha_3 \tilde{x}_3 + \alpha_4 \tilde{x}_4 + \alpha_5 \tilde{x}_5 + \alpha_6 \tilde{x}_6
\]

PGSM5:
\[
y' = \xi_0 + \xi_1 \tilde{x}_1 + \xi_2 \tilde{x}_2 + \xi_3 \tilde{x}_3 + \xi_4 \tilde{x}_4 + \xi_5 \tilde{x}_5 + \xi_6 \tilde{x}_6
\]

OM5:
\[
y = \beta_0 + \gamma \tilde{t} + \beta_1 \tilde{t} + \beta_2 \tilde{t} + \beta_3 \tilde{t} + \beta_4 \tilde{t} + \beta_5 \tilde{t} + \beta_6 \tilde{t}
\]
MS6: Main effects for five covariates related to treatment, omit confounder strongly related to outcome
PSM6:
\[ \text{logit}(p_t) = \alpha_0 + \alpha_1 x_1 + \alpha_2 x_2 + \alpha_3 x_3 + \alpha_4 x_4 + \alpha_5 x_5 + \alpha_6 x_6 \]
PGSM6:
\[ y' = \xi_0 + \xi_1 x_2 + \xi_2 x_3 + \xi_3 x_4 + \xi_5 x_5 + \xi_6 x_6 \]
OM6:
\[ y = \beta_0 + \gamma t + \beta_1 x_2 + \beta_2 x_3 + \beta_3 x_4 + \beta_5 x_5 + \beta_6 x_6 \]

MS7: Main effects for five covariates related to outcome, add one covariate strongly related to treatment
PSM7:
\[ \text{logit}(p_t) = \alpha_0 + \alpha_1 x_1 + \alpha_2 x_2 + \alpha_3 x_3 + \alpha_4 x_4 + \alpha_5 x_5 + \alpha_6 x_6 \]
PGSM7:
\[ y' = \xi_0 + \xi_1 x_2 + \xi_2 x_3 + \xi_3 x_4 + \xi_4 x_5 + \xi_6 x_6 \]
OM7:
\[ y = \beta_0 + \gamma t + \beta_1 x_2 + \beta_2 x_3 + \beta_3 x_4 + \beta_4 x_5 + \beta_5 x_6 \]

MS8: Main effects for five covariates related to treatment, omit confounder weakly related to outcome
PSM8:
\[ \text{logit}(p_t) = \alpha_0 + \alpha_1 x_1 + \alpha_2 x_2 + \alpha_3 x_3 + \alpha_4 x_4 + \alpha_5 x_5 + \alpha_6 x_6 \]
PGSM8:
\[ y' = \xi_0 + \xi_1 x_2 + \xi_2 x_3 + \xi_3 x_4 + \xi_5 x_5 + \xi_6 x_6 \]
OM8:
\[ y = \beta_0 + \gamma t + \beta_1 x_2 + \beta_2 x_3 + \beta_3 x_4 + \beta_5 x_5 + \beta_6 x_6 \]

MS9: Main effects for five covariates related to outcome, omit confounder weakly related to treatment
PSM9:
\[ \text{logit}(p_t) = \alpha_0 + \alpha_1 x_1 + \alpha_2 x_2 + \alpha_3 x_3 + \alpha_4 x_4 + \alpha_5 x_5 + \alpha_6 x_6 \]
PGSM9:
\[ y' = \xi_0 + \xi_1 x_2 + \xi_2 x_3 + \xi_3 x_4 + \xi_5 x_5 + \xi_6 x_6 \]
OM9:
\[ y = \beta_0 + \gamma t + \beta_1 x_2 + \beta_2 x_3 + \beta_3 x_4 + \beta_4 x_5 + \beta_5 x_6 + \beta_6 x_6 \]

MS10: Main effects for six covariates related to treatment, add one covariate strongly related to outcome only
PSM10:
\[ \text{logit}(p_t) = \alpha_0 + \alpha_1 x_1 + \alpha_2 x_2 + \alpha_3 x_3 + \alpha_4 x_4 + \alpha_5 x_5 + \alpha_6 x_6 + \alpha_7 x_7 \]
PGSM10:
\[ y' = \xi_0 + \xi_1 x_2 + \xi_2 x_3 + \xi_3 x_4 + \xi_4 x_5 + \xi_5 x_5 + \xi_6 x_6 + \xi_7 x_7 \]
OM10:
\[ y = \beta_0 + \gamma t + \beta_1 x_2 + \beta_2 x_3 + \beta_3 x_4 + \beta_4 x_5 + \beta_5 x_5 + \beta_6 x_6 + \beta_7 x_7 \]

MS11: Main effects for six covariates related to outcome, add one covariate strongly related to treatment only
PSM11:
\[ \text{logit}(p_t) = \alpha_0 + \alpha_1 x_1 + \alpha_2 x_2 + \alpha_3 x_3 + \alpha_4 x_4 + \alpha_5 x_5 + \alpha_6 x_6 + \alpha_7 x_7 \]
PGSM11:
\[ y' = \xi_0 + \xi_1 x_1 + \xi_2 x_2 + \xi_3 x_3 + \xi_4 x_4 + \xi_5 x_5 + \xi_6 x_6 + \xi_7 x_8 \]

OM11:
\[ y = \beta_0 + \gamma t + \beta_1 x_1 + \beta_2 x_2 + \beta_3 x_3 + \beta_4 x_4 + \beta_5 x_5 + \beta_6 x_6 + \beta_7 x_8 \]

MS12: Main effects for four covariates related to both treatment and outcome

PSM12:
\[ \text{logit}(p_t) = \alpha_0 + \alpha_1 x_1 + \alpha_2 x_2 + \alpha_3 x_3 + \alpha_4 x_4 \]

PGSM12:
\[ y' = \xi_0 + \xi_1 x_1 + \xi_2 x_2 + \xi_3 x_3 + \xi_4 x_4 \]

OM12:
\[ y = \beta_0 + \gamma t + \beta_1 x_1 + \beta_2 x_2 + \beta_3 x_3 + \beta_4 x_4 \]
<table>
<thead>
<tr>
<th>True Model (TM)</th>
<th>Treatment Effect (γ)</th>
<th>Sample Size</th>
<th>Estimation Method</th>
<th>Model Specification (MS)</th>
<th>Balance Measures</th>
</tr>
</thead>
<tbody>
<tr>
<td>(1) TM1</td>
<td>(1) 0</td>
<td>(1) 200</td>
<td>Regression</td>
<td>(1) MS1</td>
<td>(1) ASD</td>
</tr>
<tr>
<td>(2) TM2</td>
<td>(2) 0.5</td>
<td>(2) 400</td>
<td>PS</td>
<td>(2) MS2</td>
<td>(2) PSSD</td>
</tr>
<tr>
<td>(3) TM3</td>
<td>(3) 1</td>
<td>(3) 800</td>
<td>PGS</td>
<td>(3) MS3</td>
<td>(3) PGSSD</td>
</tr>
<tr>
<td>(4) TM4</td>
<td></td>
<td>(4) 1600</td>
<td>PGPS</td>
<td>(4) MS4</td>
<td>(4) PGPSSD</td>
</tr>
<tr>
<td>(1)</td>
<td></td>
<td></td>
<td>Doubly-robust PS</td>
<td>(5) MS5</td>
<td>(5) RXTRXY</td>
</tr>
<tr>
<td>(2)</td>
<td></td>
<td></td>
<td>Doubly-robust PGS</td>
<td>(6) MS6</td>
<td></td>
</tr>
<tr>
<td>(3)</td>
<td></td>
<td></td>
<td>Doubly-robust PGPS</td>
<td>(7) MS7</td>
<td></td>
</tr>
<tr>
<td>(4)</td>
<td></td>
<td></td>
<td>PS within CS</td>
<td>(8) MS8</td>
<td></td>
</tr>
<tr>
<td>(5)</td>
<td></td>
<td></td>
<td>PGS within CS</td>
<td>(9) MS9</td>
<td></td>
</tr>
<tr>
<td>(6)</td>
<td></td>
<td></td>
<td>PGPS within CS</td>
<td>(10) MS10</td>
<td></td>
</tr>
<tr>
<td>(7)</td>
<td></td>
<td></td>
<td>Doubly-robust PS within CS</td>
<td>(11) MS11</td>
<td></td>
</tr>
<tr>
<td>(8)</td>
<td></td>
<td></td>
<td>Doubly-robust PGS within CS</td>
<td>(12) MS12</td>
<td></td>
</tr>
</tbody>
</table>