

Supplementary Materials for “Causal inference with multiple concurrent medications: a comparison of methods and an application in multidrug-resistant tuberculosis”

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1. Brief Overview of the Data Generation Mechanisms along with their R code

This section gives a brief introduction to the Data Generation Scenarios as mentioned in **Section 3.1**.

Data Generation Scenario 1: We generate 12 independent baseline covariates represented by X_1, \dots, X_{12} which follow a standard uniform distribution. We then generate 4 medications represented by A^1, \dots, A^4 using the baseline covariates and sample them from a multinomial bernoulli distribution. We also have a positive pairwise correlation of 0.15 between A^1 and A^2 and a 0.25 correlation between A^3 and A^4 . None of the other treatments were correlated otherwise. This sampling was performed using the *rmobin* function in the package *bindata*. The outcome variable Y was generated using a logistic model using the baseline covariates and the medications, which includes first order interactions between (X_i, X_j) , (X_i, A^j) and (A^i, A^j) . The R code for the generation of this data is as follows:

```
library(bindata)
n <- 500
set.seed(2010)
#Covariate Generation
X_1 <- runif(n,0,1)
X_2 <- runif(n,0,1)
X_3 <- runif(n,0,1)
X_4 <- runif(n,0,1)
X_5 <- runif(n,0,1)
X_6 <- runif(n,0,1)
X_7 <- runif(n,0,1)
X_8 <- runif(n,0,1)
X_9 <- runif(n,0,1)
X_10 <- runif(n,0,1)
X_11 <- runif(n,0,1)
X_12 <- runif(n,0,1)

#Medication Generation
pA_1 <- plogis(0.7*X_1 - 0.87*X_3 + X_5 + X_7 + 0.8*X_2 - 1.6*X_4)
pA_2 <- plogis(0.9*X_1 - 0.66*X_3 + 0.8*X_5 + X_7 - 0.8*X_6)
pA_3 <- plogis(1.4*X_1 - 0.45*X_3 + 0.4*X_5 - X_7 - X_8)
pA_4 <- plogis(1.8*X_1 - 0.95*X_3 - 0.1*X_5 - X_7 - X_12)

m <- diag(4)
m[1,2] <- 0.15
m[2,1] <- 0.15
m[4,3] <- 0.25
m[3,4] <- 0.25
```

```

#Considering positive binary correlations between A_1, A_2 as 0.15 and A_3, A_4 as 0.25
A <- matrix(nrow=n,ncol=4)
for (i in 1:n){
  prob <- c(pA_1[i],pA_2[i],pA_3[i],pA_4[i])
  A[i,] <- rmvbin(1, margprob = prob, bincorr = m)
}

#Separating the array obtained above into separate medications
Gap <- as.data.frame(A)
A_1 <- Gap[,1]
A_2 <- Gap[,2]
A_3 <- Gap[,3]
A_4 <- Gap[,4]

#Generating the outcome model
pY <- plogis(-1.8 + 1.2*X_1*A_3 + 2.15*X_3*A_1 - 0.5*X_5*X_9 + 3.89*X_7*X_1
            + X_10*A_2 - 1.5*X_11*A_4 + 4.2*(1-A_1)*A_3 + 15*(1-A_2)*A_4)
Y <- rbinom(n, 1, prob=pY)

```

Data Generation Scenario II: We generate 14 independent baseline covariates represented by X_1, \dots, X_{14} which follow a standard uniform distribution or a standard normal distribution. We then generate 8 medications represented by A^1, \dots, A^8 using the baseline covariates and sample them from a multinomial bernoulli distribution. We also have a positive pairwise correlation of 0.15 between A^1 and A^2 , a 0.25 correlation between A^3 and A^4 , a 0.15 correlation between A^5 and A^6 and a 0.25 correlation between A^7 and A^8 . None of the other treatments were correlated otherwise. This sampling was again performed using the *rmvbin* function in the package *bindata*. The outcome variable Y was generated using a logistic model using the baseline covariates and the medications, which also includes first order interactions and second order interactions. The R code for the generation of this data is as follows:

```

set.seed(2100)
#Covariate Generation
n <- 500
X_1 <- runif(n,0,1)
X_2 <- runif(n,0,1)
X_3 <- runif(n,0,1)
X_4 <- runif(n,0,1)
X_5 <- runif(n,0,1)
X_6 <- runif(n,0,1)
X_7 <- runif(n,0,1)
X_8 <- runif(n,0,1)
X_9 <- rnorm(n,0,1)
X_10 <- runif(n,0,1)
X_11 <- runif(n,0,1)
X_12 <- rnorm(n,0,1)
X_13 <- runif(n,0,1)
X_14 <- runif(n,0,1)

#Medication Generation
pA_1 <- plogis(0.5*X_1 + 2.3*X_2 + 0.74*X_3 - 1.8*X_4)

```

```

pA_2 <- plogis(0.4*X_1 + 2.5*X_2 + 0.87*X_3 - 1.5*X_5)
pA_3 <- plogis(0.8*X_1 - 0.4*X_2 + 0.34*X_3 + 0.8*X_6)
pA_4 <- plogis(0.7*X_1 - 0.65*X_2 + 0.55*X_3 + 1.1*X_7)
pA_5 <- plogis(1.9*X_1 - 0.33*X_2 + 1.67*X_3 - 0.6*X_8)
pA_6 <- plogis(1.5*X_1 - 0.53*X_2 + 1.88*X_3 - 0.3*X_9)
pA_7 <- plogis(-0.85*X_1 + 1.35*X_2 - 0.99*X_3 + 1.4*X_7)
pA_8 <- plogis(-0.65*X_1 + 1.03*X_2 - 0.875*X_3 + 1.1*X_6)

m <- diag(4)
m[1,2] <- 0.15
m[2,1] <- 0.15
m[4,3] <- 0.25
m[3,4] <- 0.25

#Considering positive binary correlations between A_1, A_2 as 0.15 and A_3, A_4 as 0.25
A <- matrix(nrow=n,ncol=4)
for (i in 1:n){
  prob <- c(pA_1[i],pA_2[i],pA_3[i],pA_4[i])
  A[i,] <- rmvbin(1, margprob = prob, bincorr = m)
}

#Considering positive binary correlations between A_5, A_6 as 0.15 and A_7, A_8 as 0.25
B <- matrix(nrow=n,ncol=4)
for (i in 1:n){
  prob <- c(pA_5[i],pA_6[i],pA_7[i],pA_8[i])
  B[i,] <- rmvbin(1, margprob = prob, bincorr = m)
}

#Separating the array obtained above into separate medications
Gap <- as.data.frame(A)
A_1 <- Gap[,1]
A_2 <- Gap[,2]
A_3 <- Gap[,3]
A_4 <- Gap[,4]

Gap <- as.data.frame(B)
A_5 <- Gap[,1]
A_6 <- Gap[,2]
A_7 <- Gap[,3]
A_8 <- Gap[,4]

#Generating the outcome model
pY <- plogis(-1.3 + 0.8*X_1 + 0.89*X_2*A_2 + 1.5*X_11*A_8 - 1.8*X_13
+ 0.9*X_14*A_1*A_8 + 0.4*A_1*A_2*A_5 + 7.2*(1-A_2)*X_9*X_12
- 15*(1-A_7)*A_6 - 12*X_9*(1-A_7) - X_10*(1-A_8)*(1-A_7)
+ 5*(1-A_8)*(1-A_1) + 5*(1-A_1)*X_12*X_14)
Y <- rbinom(n, 1, prob=pY)

```

2. Comparison of methods with a large number of possible regimens

We generated 1,000 datasets of sample size $n = 500$, using Data Generation Scenario 2. In our simulation data, out of the 256 possible regimens, roughly 150 different regimens occurred in each dataset. Some of these regimens were only followed by several subjects, making the corresponding GPSs difficult to estimate. In order to speed up the computation of the multi-class classification, one might consider removing the observations with the most sparsely observed regimens in order to fit the model. It is expected that this should not affect the prediction of the probabilities of the most prevalent regimens as they represent a very small part of the overall regimen probability space.

To investigate this, we considered three different approaches. The first approach took the entire dataset and classified for all of the regimens observed in the model. We then created a new dataset containing 80% of the original regimens in the data, by removing the subjects with the least occurring 20% of regimens. This new subsetted data became the basis for obtaining the model for SVMs and Softmax Regression. The fitted model was then used to compute the GPS for regimen 1 for all n individuals in the dataset. The final simulation was carried out by performing the modeling after removal of the 30% of the least occurring regimens in the original dataset and carrying out the same method as explained above.

Table 1 displays the simulation results for this case (using the same statistical methods described in Section 3.3 of the manuscript). Without subsetting, only TMLE was nearly unbiased when implemented with all GPS methods though PSA(I) had low bias when implemented with GBMs. The results obtained after removing the rarest 20% and 30% were consistent with the full sample results for all methods. The computational times taken by SVMs on a local laptop computer when removing 0%, 20% and 30% of the original regimens were 5, 3, and 2 seconds, respectively. Similarly, the runtimes taken by Softmax regression for the same three datasets were 412, 234, and 202 seconds, respectively. The GBMs implemented in the `twang` package estimate the probability of every regimen separately versus all others. Therefore, removing the observations with rare regimens would not help the estimation speed or accuracy. The runtime results suggest that this subsetting approach can greatly reduce computational time for SVMs and Softmax regression without affecting the statistical results.

Table 1: Monte Carlo means and standard errors for different causal estimators that utilize the generalized propensity score. Data with a sample size of $n = 500$ were drawn from Data Generation Scenario 2 and 1,000 replicates were used. The true value for regimen 1 is $\mathbb{E}(Y^1) = 0.55$. SVM: Support Vector Machine; GBM: Generalized Boosted Model; IPTW: Inverse Probability of Treatment Weighting; PSA: Propensity Score Adjustment; TMLE: Targeted Maximum Likelihood Estimation. Outcome regression models were fit by (I) regimen and (II) treatments as main terms covariates. $Q_n \text{ corr}$ indicates whether the outcome model includes the true treatment-treatment interactions.

Class Truncation %		0	20	30
Median n observations removed		0	30	45
	$Q_n \text{ corr}$	Reg 1	Reg 1	Reg 1
SVM				
IPTW	N/A	0.58(0.08)	0.58(0.08)	0.58(0.08)
PSA(I)	Y	0.57(0.08)	0.57(0.08)	0.57(0.08)
PSA(II)	N	0.45(0.05)	0.45(0.05)	0.45(0.05)
TMLE(I)	Y	0.55(0.11)	0.54(0.11)	0.55(0.11)
TMLE(II)	N	0.56(0.08)	0.55(0.09)	0.55(0.09)
Softmax Regression				
IPTW	N/A	0.55(0.13)	0.55(0.13)	0.56(0.13)
PSA(I)	Y	0.57(0.08)	0.57(0.08)	0.57(0.08)
PSA(II)	N	0.44(0.05)	0.44(0.05)	0.45(0.05)
TMLE(I)	Y	0.55(0.11)	0.55(0.11)	0.55(0.11)
TMLE(II)	N	0.55(0.12)	0.55(0.12)	0.55(0.12)
GBM				
IPTW	N/A	0.57(0.09)	—	—
PSA(I)	Y	0.56(0.12)	—	—
PSA(II)	N	0.42(0.05)	—	—
TMLE(I)	Y	0.54(0.11)	—	—
TMLE(II)	N	0.55(0.09)	—	—

3. Summary statistics for the support of the regimens in the simulation studies

This section presents the tables for summary statistics and the plots for the supports for regimens 1 and 2 for simulation study I and regimen 1 for simulation study II, where simulation study I refers to the simulation study presented in Section 3 of the paper and simulation study II refers to the simulation study presented in Section 2 of the supplementary material. We define the “support” of a regimen to be the number of patients exposed to that regimen in the dataset.

Table 2: Summary Statistics for support for regimen 1 and regimen 2 for simulation study I.

	$n = 500$		$n = 1000$	
	<i>Reg 1</i>	<i>Reg 2</i>	<i>Reg 1</i>	<i>Reg 2</i>
Minimum	68.00	29.00	147.00	74.00
1 st Quantile	87.00	46.00	177.00	94.00
Median	92.00	51.00	185.00	101.00
Mean	92.48	51.04	184.90	100.90
3 rd Quantile	98.00	56.00	193.00	107.00
Maximum	122.00	75.00	226.00	131.00

Table 3: Summary Statistics for support for regimen 1 for simulation study II with $n = 500$.

<i>Reg 1</i>	
Minimum	16.00
1 st Quantile	33.00
Median	37.00
Mean	36.75
3 rd Quantile	41.00
Maximum	55.00

Figure 1: Histogram for the support of the top 2 regimens for Simulation Study I for $n = 500$.

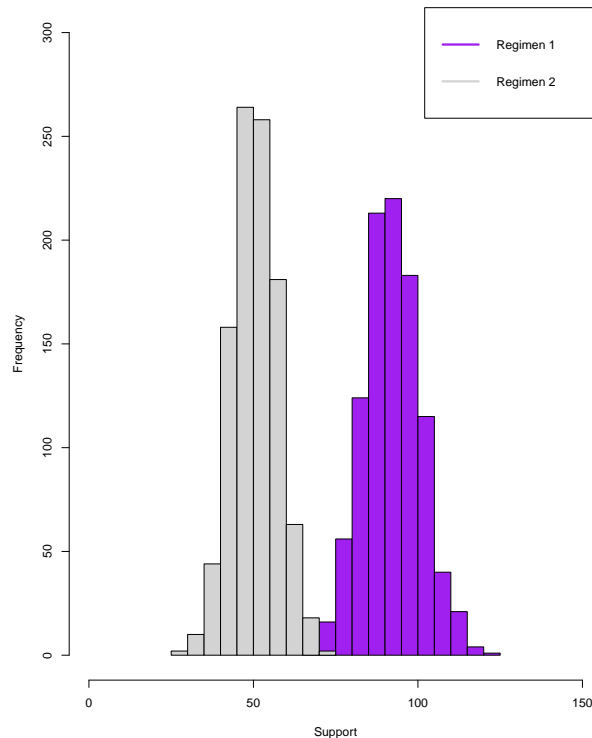


Figure 2: Histogram for the support of the top 2 regimens for Simulation Study I for $n = 1000$.

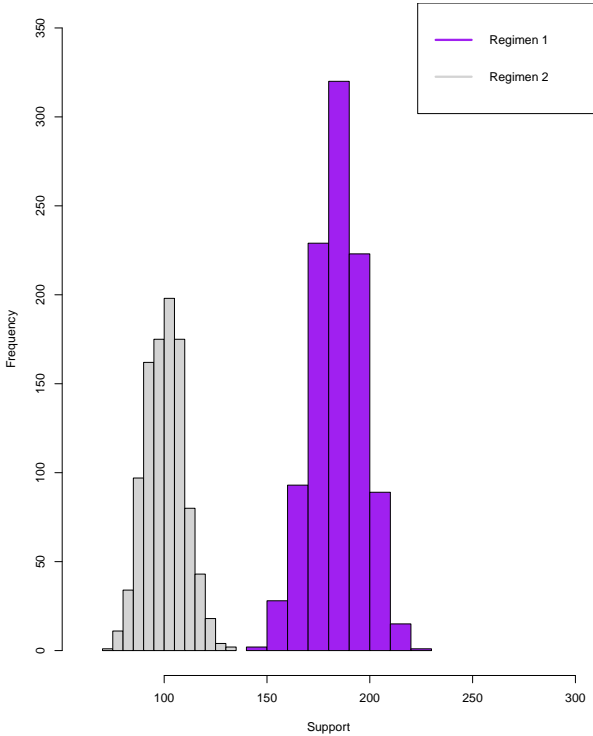
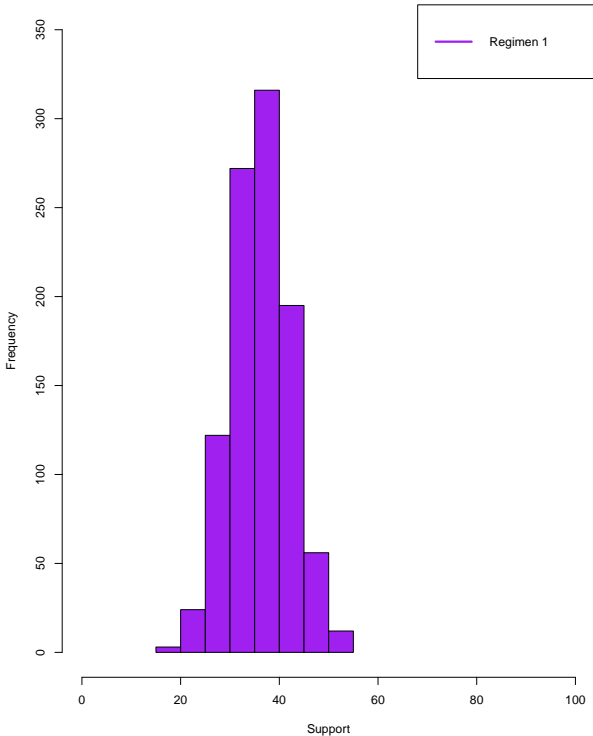


Figure 3: Histogram for the support of Regimen 1 for Simulation Study II for $n = 500$.



4. Summary Statistics for the weights obtained by the different estimating methods

This section contains the summary statistics of the weights obtained by SVM, Softmax Regression and GBM over 50 datasets for the regimens in simulation study I.

Table 4: Summary Statistics for the weights obtained by the different estimating methods for regimen 1 for simulation study I over 50 datasets with $n = 1000$.

	SVM	Softmax Regression	GBM
Minimum	2.66	1.39	1.12
1 st Quantile	4.44	4.04	4.35
Median	5.37	6.19	6.23
Mean	6.11	8.38	7.20
3 rd Quantile	6.97	10.08	8.88
Maximum	39.30	229.67	106.49

Table 5: Summary Statistics for the weights obtained by the different estimating methods for regimen 2 for simulation study I over 50 datasets with $n = 1000$.

	SVM	Softmax Regression	GBM
Minimum	3.09	1.44	1.05
1 st Quantile	7.80	6.87	8.25
Median	11.08	12.99	13.73
Mean	13.11	23.98	17.06
3 rd Quantile	16.27	26.93	21.33
Maximum	96.00	1163.50	544.76

5. Summary for the Generalized Propensity Scores for the MDR-TB Data

This section contains the summary of the truncated and the untruncated GPS obtained for the MDR-TB data using the different machine learning methods explained in **Section 2.2**. The GPS of the regimens are given by pi1 to pi10, where pi1 denotes GPS for Regimen 1 in our study and pi10 denotes the GPS for Regimen 10 in the study as mentioned in **Section 4**. The summary contains the following values:

- **Min.:** Minimum value of the GPS for the regimen in the sample study
- **1st Qu.:** Value of the first quantile of the GPS for the regimen in the sample study
- **Median:** Median value of the GPS for the regimen in the sample study
- **Mean:** Mean value of the GPS for the regimen in the sample study
- **3rd Qu.:** Value of the third quantile of the GPS for the regimen in the sample study
- **Max.:** Maximum value of the GPS for the regimen in the sample study

`summary(Algorithm_Untruncated)` denotes the summary of the untruncated GPS obtained using Algorithm whereas `summary(Algorithm_Truncated)` denotes the summary of the truncated GPS (20% truncation) obtained using Algorithm as mentioned in **Section 4**.

```
summary(SVM_Untruncated)
```

```
##          pi1          pi2          pi3
## Min.    :0.0000844  Min.    :0.0001795  Min.    :0.0000585
## 1st Qu.:0.0003483  1st Qu.:0.0008688  1st Qu.:0.0007783
## Median :0.0007693  Median :0.0016455  Median :0.0031000
## Mean   :0.1568600  Mean   :0.0376882  Mean   :0.0280186
## 3rd Qu.:0.0084027  3rd Qu.:0.0056493  3rd Qu.:0.0157749
## Max.   :0.6704224  Max.   :0.1603302  Max.   :0.1602677
##          pi4          pi5          pi6
## Min.    :0.0000540  Min.    :0.0000441  Min.    :0.0004766
## 1st Qu.:0.0005957  1st Qu.:0.0006334  1st Qu.:0.0020562
## Median :0.0029060  Median :0.0014290  Median :0.0053386
## Mean   :0.0283911  Mean   :0.0207455  Mean   :0.0294543
## 3rd Qu.:0.0282561  3rd Qu.:0.0025562  3rd Qu.:0.0256537
## Max.   :0.3174220  Max.   :0.1382175  Max.   :0.2802544
##          pi7          pi8          pi9
## Min.    :0.0001285  Min.    :0.0002740  Min.    :0.0000968
## 1st Qu.:0.0005905  1st Qu.:0.0005881  1st Qu.:0.0009952
## Median :0.0012020  Median :0.0011180  Median :0.0026187
## Mean   :0.0180373  Mean   :0.0159779  Mean   :0.0156337
## 3rd Qu.:0.0049643  3rd Qu.:0.0019540  3rd Qu.:0.0054387
## Max.   :0.0815344  Max.   :0.1821654  Max.   :0.1104928
##          pi10
## Min.    :0.0002061
## 1st Qu.:0.0006178
## Median :0.0008883
## Mean   :0.0133153
## 3rd Qu.:0.0323348
## Max.   :0.0620212
```

```
summary(Softmax_Untruncated)
```

```
##          pi1          pi2          pi3
## Min.    :0.001606  Min.    :0.001009  Min.    :0.0009516
## 1st Qu.:0.017372  1st Qu.:0.007144  1st Qu.:0.0085008
```


## Median	:0.067361	Median	:0.021264	Median	:0.0225757
## Mean	:0.143315	Mean	:0.039558	Mean	:0.0366144
## 3rd Qu.	:0.192485	3rd Qu.	:0.055097	3rd Qu.	:0.0490858
## Max.	:0.673014	Max.	:0.177946	Max.	:0.1515242
##	pi4		pi5		pi6
## Min.	:0.001242	Min.	:0.0006062	Min.	:0.003809
## 1st Qu.	:0.005267	1st Qu.	:0.0053993	1st Qu.	:0.011288
## Median	:0.013764	Median	:0.0150462	Median	:0.018037
## Mean	:0.032116	Mean	:0.0272295	Mean	:0.025229
## 3rd Qu.	:0.029981	3rd Qu.	:0.0373691	3rd Qu.	:0.031908
## Max.	:0.298142	Max.	:0.1224405	Max.	:0.146441
##	pi7		pi8		pi9
## Min.	:0.0008831	Min.	:0.0006065	Min.	:0.0006481
## 1st Qu.	:0.0041477	1st Qu.	:0.0061504	1st Qu.	:0.0046522
## Median	:0.0123683	Median	:0.0129524	Median	:0.0124783
## Mean	:0.0193383	Mean	:0.0212144	Mean	:0.0219139
## 3rd Qu.	:0.0276799	3rd Qu.	:0.0239001	3rd Qu.	:0.0314892
## Max.	:0.0876790	Max.	:0.1267092	Max.	:0.0955858
##	pi10				
## Min.	:0.0004913				
## 1st Qu.	:0.0048800				
## Median	:0.0114627				
## Mean	:0.0162796				
## 3rd Qu.	:0.0284771				
## Max.	:0.0625170				

summary(GBM_Untruncated)

##	pi1		pi2		pi3
## Min.	:0.002027	Min.	:0.0007163	Min.	:0.007166
## 1st Qu.	:0.003807	1st Qu.	:0.0009530	1st Qu.	:0.007206
## Median	:0.006176	Median	:0.0019908	Median	:0.008290
## Mean	:0.168206	Mean	:0.0404401	Mean	:0.029222
## 3rd Qu.	:0.010221	3rd Qu.	:0.0041522	3rd Qu.	:0.010328
## Max.	:0.764830	Max.	:0.3301783	Max.	:0.179817
##	pi4		pi5		pi6
## Min.	:0.0000014	Min.	:0.0000003	Min.	:0.007889
## 1st Qu.	:0.0000777	1st Qu.	:0.0000354	1st Qu.	:0.012612
## Median	:0.0004492	Median	:0.0003447	Median	:0.013787
## Mean	:0.0263304	Mean	:0.0232197	Mean	:0.022999
## 3rd Qu.	:0.0167375	3rd Qu.	:0.0005962	3rd Qu.	:0.016079
## Max.	:0.9999966	Max.	:0.3551773	Max.	:0.307409
##	pi7		pi8		pi9
## Min.	:0.0009184	Min.	:0.008467	Min.	:0.0000007
## 1st Qu.	:0.0011354	1st Qu.	:0.009411	1st Qu.	:0.0000590
## Median	:0.0020279	Median	:0.009560	Median	:0.0004007
## Mean	:0.0197763	Mean	:0.017003	Mean	:0.0167759
## 3rd Qu.	:0.0038864	3rd Qu.	:0.011996	3rd Qu.	:0.0027138
## Max.	:0.1147831	Max.	:0.053754	Max.	:0.9586112
##	pi10				
## Min.	:0.0000003				
## 1st Qu.	:0.0000269				
## Median	:0.0000887				
## Mean	:0.0152205				
## 3rd Qu.	:0.0221909				

```
## Max. :0.3435316
```

```
summary(SVM_Truncated)
```

```
##      pi1          pi2          pi3
## Min. :0.0002831 Min. :0.0007573 Min. :0.0002799
## 1st Qu.:0.0003483 1st Qu.:0.0008688 1st Qu.:0.0007783
## Median :0.0007693 Median :0.0016455 Median :0.0031000
## Mean   :0.1568845 Mean   :0.0377691 Mean   :0.0280471
## 3rd Qu.:0.0084027 3rd Qu.:0.0056493 3rd Qu.:0.0157749
## Max.   :0.6704224 Max.   :0.1603302 Max.   :0.1602677
##      pi4          pi5          pi6
## Min. :0.0003056 Min. :0.0001582 Min. :0.001543
## 1st Qu.:0.0005957 1st Qu.:0.0006334 1st Qu.:0.002056
## Median :0.0029060 Median :0.0014290 Median :0.005339
## Mean   :0.0284244 Mean   :0.0207595 Mean   :0.029564
## 3rd Qu.:0.0282561 3rd Qu.:0.0025562 3rd Qu.:0.025654
## Max.   :0.3174220 Max.   :0.1382175 Max.   :0.280254
##      pi7          pi8          pi9
## Min. :0.0004759 Min. :0.0005308 Min. :0.0003049
## 1st Qu.:0.0005905 1st Qu.:0.0005881 1st Qu.:0.0009952
## Median :0.0012020 Median :0.0011180 Median :0.0026187
## Mean   :0.0180826 Mean   :0.0159963 Mean   :0.0156600
## 3rd Qu.:0.0049643 3rd Qu.:0.0019540 3rd Qu.:0.0054387
## Max.   :0.0815344 Max.   :0.1821654 Max.   :0.1104928
##      pi10
## Min. :0.0005180
## 1st Qu.:0.0006178
## Median :0.0008883
## Mean   :0.0133594
## 3rd Qu.:0.0323348
## Max.   :0.0620212
```

```
summary(Softmax_Truncated)
```

```
##      pi1          pi2          pi3
## Min. :0.01423 Min. :0.005934 Min. :0.006702
## 1st Qu.:0.01737 1st Qu.:0.007144 1st Qu.:0.008501
## Median :0.06736 Median :0.021264 Median :0.022576
## Mean   :0.14408 Mean   :0.039938 Mean   :0.037119
## 3rd Qu.:0.19248 3rd Qu.:0.055097 3rd Qu.:0.049086
## Max.   :0.67301 Max.   :0.177946 Max.   :0.151524
##      pi4          pi5          pi6
## Min. :0.004416 Min. :0.004763 Min. :0.01005
## 1st Qu.:0.005267 1st Qu.:0.005399 1st Qu.:0.01129
## Median :0.013764 Median :0.015046 Median :0.01804
## Mean   :0.032373 Mean   :0.027548 Mean   :0.02563
## 3rd Qu.:0.029981 3rd Qu.:0.037369 3rd Qu.:0.03191
## Max.   :0.298142 Max.   :0.122440 Max.   :0.14644
##      pi7          pi8          pi9
## Min. :0.003598 Min. :0.005216 Min. :0.004309
## 1st Qu.:0.004148 1st Qu.:0.006150 1st Qu.:0.004652
## Median :0.012368 Median :0.012952 Median :0.012478
## Mean   :0.019558 Mean   :0.021613 Mean   :0.022207
## 3rd Qu.:0.027680 3rd Qu.:0.023900 3rd Qu.:0.031489
```

```

## Max. :0.087679 Max. :0.126709 Max. :0.095586
## pi0
## Min. :0.003998
## 1st Qu.:0.004880
## Median :0.011463
## Mean :0.016521
## 3rd Qu.:0.028477
## Max. :0.062517

```

summary(GBM_Truncated)

```

## pi1 pi2 pi3
## Min. :0.003807 Min. :0.0009182 Min. :0.007206
## 1st Qu.:0.003807 1st Qu.:0.0009530 1st Qu.:0.007206
## Median :0.006176 Median :0.0019908 Median :0.008290
## Mean :0.168406 Mean :0.0404581 Mean :0.029225
## 3rd Qu.:0.010221 3rd Qu.:0.0041522 3rd Qu.:0.010328
## Max. :0.764830 Max. :0.3301783 Max. :0.179817
## pi4 pi5 pi6
## Min. :0.0000389 Min. :0.0000300 Min. :0.01138
## 1st Qu.:0.0000777 1st Qu.:0.0000354 1st Qu.:0.01261
## Median :0.0004492 Median :0.0003447 Median :0.01379
## Mean :0.0263347 Mean :0.0232217 Mean :0.02349
## 3rd Qu.:0.0167375 3rd Qu.:0.0005962 3rd Qu.:0.01608
## Max. :0.9999966 Max. :0.3551773 Max. :0.30741
## pi7 pi8 pi9
## Min. :0.001127 Min. :0.009411 Min. :0.0000432
## 1st Qu.:0.001135 1st Qu.:0.009411 1st Qu.:0.0000590
## Median :0.002028 Median :0.009560 Median :0.0004007
## Mean :0.019807 Mean :0.017013 Mean :0.0167803
## 3rd Qu.:0.003886 3rd Qu.:0.011996 3rd Qu.:0.0027138
## Max. :0.114783 Max. :0.053754 Max. :0.9586112
## pi10
## Min. :0.0000189
## 1st Qu.:0.0000269
## Median :0.0000887
## Mean :0.0152223
## 3rd Qu.:0.0221909
## Max. :0.3435316

```

6. Tables for the Probability estimates of treatment success of the truncated GPS(20% truncation) as mentioned in Section 4 for MDR-TB data

In a sensitivity analysis, 20% truncation was used to remove the smallest values of the Generalized Propensity Score for the top 10 available regimens. The point estimates of $E(Y^r)$ and the confidence intervals for the top 10 regimens are presented in Table 6 and 7. The GPS truncation resulted in at most small changes in the point estimates as opposed to the results obtained without the truncation of GPS and had similar conclusions to it.

Table 6: Estimates of the probability of treatment success along with the confidence intervals under regimens 1-5 for the MDR-TB application in Section 4 after 20% truncation of the GPS. SVM: Support Vector Machine; GBM: Generalized Boosted Model; IPTW: Inverse Probability of Treatment Weighting; PSA: Propensity Score Adjustment; TMLE: Targeted Maximum Likelihood Estimation. Outcome regression models were fit by (I) regimen and (II) treatments as main terms covariates.

Regimen	1	2	3	4	5
	OFX-KM- Z-EMB- ETH	OFX-KM- Z- ETH-CS	OFX-KM- PTO- CS-PAS	Z-EMB- RBT	OFX-SM- PTO- CS-PAS
SVM					
IPTW	0.47 (0.44,0.49)	0.71 (0.62,0.80)	0.59 (0.47,0.70)	0.27 (0.10,0.44)	0.31 (0.17,0.46)
PSA(I)	0.44	0.68	0.64	0.32	0.55
PSA(II)	0.66	0.69	0.64	0.42	0.68
TMLE(I)	0.61 (0.60,0.61)	0.78 (0.76,0.80)	0.64 (0.63,0.65)	0.54 (0.52,0.56)	0.31 (0.28,0.34)
TMLE(II)	0.49 (0.48,0.50)	0.69 (0.67,0.71)	0.60 (0.58,0.63)	0.34 (0.29,0.38)	0.37 (0.33,0.41)
Softmax Regression					
IPTW	0.46 (0.43,0.49)	0.65 (0.59,0.70)	0.56 (0.49,0.64)	0.27 (0.18,0.36)	0.37 (0.29,0.44)
PSA(I)	0.38	0.64	0.55	0.22	0.45
PSA(II)	0.56	0.65	0.59	0.36	0.62
TMLE(I)	0.61 (0.60,0.63)	0.69 (0.67,0.71)	0.61 (0.58,0.63)	0.56 (0.53,0.59)	0.37 (0.35,0.39)
TMLE(II)	0.48 (0.47,0.50)	0.64 (0.62,0.67)	0.59 (0.57,0.62)	0.26 (0.22,0.30)	0.45 (0.42,0.48)
GBM					
IPTW	0.55 (0.39,0.72)	0.80 (0.65,0.96)	0.59 (0.47,0.70)	0.25 (0.11,0.40)	0.27 (0.02,0.52)
PSA(I)	0.43	0.68	0.63	0.35	0.55
PSA(II)	0.65	0.68	0.64	0.37	0.66
TMLE(I)	0.63 (0.58,0.68)	0.84 (0.79,0.87)	0.60 (0.54,0.67)	0.54 (0.52,0.56)	0.27 (0.23,0.31)
TMLE(II)	0.55 (0.50,0.60)	0.77 (0.72,0.81)	0.57 (0.50,0.64)	0.34 (0.29,0.38)	0.30 (0.24,0.36)

Table 7: Estimates of the probability of treatment success along with the confidence intervals under regimens 6-10 for the MDR-TB application in Section 4 after 20% truncation of the GPS. SVM: Support Vector Machine; GBM: Generalized Boosted Model; IPTW: Inverse Probability of Treatment Weighting; PSA: Propensity Score Adjustment; TMLE: Targeted Maximum Likelihood Estimation. Outcome regression models were fit by (I) regimen and (II) treatments as main terms covariates.

Regimen	6 None	7 OFX-KM- Z- ETH	8 OFX-CM- Z- ETH-CS-PAS	9 OFX- PTO- CS-PAS	10 OFX-KM- Z-EMB- ETH-CS
SVM					
IPTW	0.19 (0.08,0.31)	0.56 (0.49,0.64)	0.67 (0.55,0.80)	0.57 (0.37,0.76)	0.56 (0.48,0.65)
PSA(I)	0.29	0.59	0.61	0.56	0.57
PSA(II)	0.38	0.63	0.61	0.58	0.67
TMLE(I)	0.21 (0.18,0.23)	0.58 (0.56,0.60)	0.66 (0.65,0.67)	0.62 (0.58,0.66)	0.60 (0.58,0.62)
TMLE(II)	0.24 (0.21,0.27)	0.58 (0.56,0.60)	0.60 (0.58,0.62)	0.58 (0.53,0.62)	0.57 (0.54,0.60)
Softmax Regression					
IPTW	0.31 (0.24,0.38)	0.56 (0.48,0.64)	0.69 (0.61,0.78)	0.45 (0.35,0.54)	0.56 (0.48,0.65)
PSA(I)	0.37	0.55	0.57	0.46	0.54
PSA(II)	0.38	0.56	0.59	0.50	0.65
TMLE(I)	0.25 (0.22,0.28)	0.56 (0.53,0.60)	0.69 (0.67,0.71)	0.56 (0.53,0.58)	0.59 (0.56,0.63)
TMLE(II)	0.36 (0.30,0.41)	0.56 (0.53,0.60)	0.62 (0.60,0.64)	0.49 (0.47,0.52)	0.56 (0.52,0.61)
GBM					
IPTW	0.24 (0.17,0.32)	0.68 (0.42,0.94)	0.75 (0.66,0.83)	0.56 (0.25,0.86)	0.55 (0.45,0.65)
PSA(I)	0.38	0.60	0.60	0.54	0.57
PSA(II)	0.40	0.63	0.60	0.52	0.65
TMLE(I)	0.25 (0.22,0.28)	0.67 (0.62,0.73)	0.73 (0.70,0.77)	0.62 (0.56,0.67)	0.59 (0.57,0.61)
TMLE(II)	0.26 (0.22,0.31)	0.65 (0.60,0.70)	0.67 (0.63,0.71)	0.58 (0.52,0.64)	0.55 (0.52,0.58)