

# Propensity Score Weighting using machine learning

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## **Introduction**

## **Simulation and Evaluation**

## **Related Contents**

# Introduction

# Reviewed Paper

## Estimation

Reviewed and apply Lee et al. (2010): estimate propensity score using

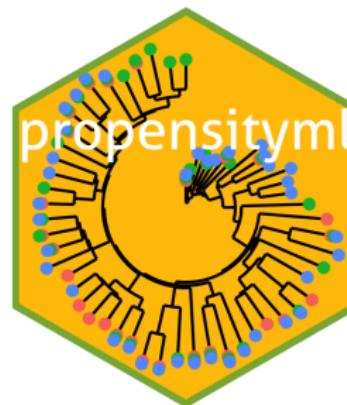
- ▶ Logistic regression: `glm()`
- ▶ Random forests: `randomForest::randomForest()`
- ▶ SVM (Pirracchio et al., 2014): `e1071::svm()`

## Evaluation

- ▶ Average standardized absolute mean distance
- ▶ Empirical distribution of IPTW
- ▶ IPW and SIPW

# My Own Package

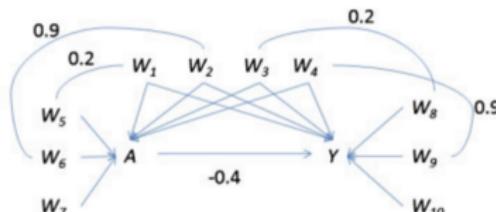
```
# remotes::install_github("ygeunkim/propensityml")
library(propensityml)
```



# Simulation Study

Simulation setting by Setoguchi et al. (2008):

- ▶ 10 covariates: confounders, exposure predictors, outcome predictors
- ▶ Treatment (exposure), true propensity score
- ▶ Continuous outcome



A: exposure

Y: outcome

$W_1-W_4$ : confounders

$W_5-W_7$ : exposure predictors

$W_8-W_{10}$ : outcome predictors

Binary variables: A,  $W_1$ ,  $W_3$ ,  $W_6$ ,  $W_8$ ,  $W_9$

Continuous variables: Y,  $W_2$ ,  $W_4$ ,  $W_7$ ,  $W_{10}$

**Figure 1:** Simulation Data - Each  $W$  and  $A$  can be as  $X$  and  $Z$  in the course, respectively

## Correlation Matrix

of covariates:

# Scenarios

## True propensity score

Define  $e(\mathbf{X}_i)$  for each scenario (A, B, F, G):

**A** Additivity and linearity:

$$P(Z = 1 | \mathbf{X}_i) = \frac{1}{1 + \exp(-(\beta_0 + \beta_1 X_1 + \dots + \beta_7 X_7))}$$

**B** Moderate non-linearity: 3 quadratic term

$$P(Z = 1 | \mathbf{X}_i) = \frac{1}{1 + \exp(-(\beta_0 + \beta_1 X_1 + \dots + \beta_7 X_7 + \beta_2 X_2^2))}$$

**F** Moderate non-linearity: 10 two-way interaction terms

**G** Moderate non-additivity and non-linearity: 10 two-way interaction terms and 3 quadratic terms

## True Parameters

$$(\beta_0, \beta_1, \dots, \beta_7)^T = (0, 0.8, -0.25, 0.6, -0.4, -0.8, -0.5, 0.7)^T$$

# Outcome

$$Y = \alpha_0 + \alpha_1 X_1 + \cdots + \alpha_4 X_4 + \alpha_5 X_8 + \cdots + \alpha_7 X_{10} + \gamma Z$$

where

- ▶  $(\alpha_0, \alpha_1, \dots, \alpha_7)^T = (-3.85, 0.3, -0.36, -73, -0.2, 0.71, -0.19, 0.26)^T$
- ▶  $\gamma = -0.4$ : True effect

# Function to reproduce Setoguchi et al. (2008)

```
sim_outcome(n = 1000, covmat = build_covariate()) %>%
  glimpse(width = 50)
#> Rows: 1,000
#> Columns: 13
#> $ w1           <fct> 0, 1, 1, 1, 0, 1, 1, 1, ...
#> $ w2           <dbl> -0.2801, 0.3065, 0.6329...
#> $ w3           <fct> 0, 0, 0, 1, 1, 1, 1, ...
#> $ w4           <dbl> 1.6575, -1.4404, -1.939...
#> $ w5           <fct> 1, 1, 1, 0, 0, 1, 0, 0, ...
#> $ w6           <fct> 0, 1, 1, 0, 0, 1, 1, 0, ...
#> $ w7           <dbl> 0.4874, -0.0162, -0.155...
#> $ w8           <fct> 1, 1, 0, 0, 1, 0, 1, 1, ...
#> $ w9           <fct> 1, 0, 0, 1, 1, 0, 1, 0, ...
#> $ w10          <dbl> -0.3054, 0.5939, 0.4179...
#> $ exposure     <fct> 1, 1, 1, 1, 1, 0, 1, 1, ...
#> $ y            <dbl> -120.253, 0.942, -51.95...
#> $ exposure_prob <dbl> 0.5000, 0.9072, 0.3465, ...
```

## Simulation and Evaluation

# Monte Carlo simulation

- ▶ For simulation, 1000 replicates
- ▶ Sample size: 1000

```
doMC::registerDoMC(cores = 4)
mc_list <- mc_setoguchi(
  N = 1000, n_dat = 1000, scenario = scen,
  parallel = TRUE
)
```

Columns that indicate MC and Scenario: mcname, scenario

```
mc_list[, .N, .(mcname, scenario)]
#>      mcname scenario     N
#> 1:      1          A 1000
#> 2:      2          A 1000
#> 3:      3          A 1000
#> 4:      4          A 1000
#> 5:      5          A 1000
#> ---
#> 3996:   996          G 1000
#> 3997:   997          G 1000
#> 3998:   998          G 1000
#> 3999:   999          G 1000
#> 4000:  1000          G 1000
```

# Average standardized absolute mean distance (ASAM)

- ▶ Covariate balancing: standardized mean difference, which is standardized by pooled sd
- ▶ Average the abs(covariate balancing) across all the covariates
- ▶ Lower: treatment and control groups are more similar w.r.t. the given covariates.

```
doMC::registerDoMC(cores = 8)
logit_asam <-
  mc_list %>%
  compute_asam(
    treatment = "exposure", outcome = "y", exclude = "exposure_prob",
    formula = exposure ~ . - y - exposure_prob, method = "logit",
    mc_col = "mcname", sc_col = "scenario", parallel = TRUE
  )
```

## ASAM for each model

Scenarios	Model			
	Logistic	RandomForests	SVM (Linear)	SVM (Radial)
A	0.011	0.011	0.009	0.010
B	0.033	0.030	0.041	0.042
F	0.035	0.033	0.041	0.041
G	0.076	0.075	0.080	0.080

- ▶ Under 0.2 is acceptable (Lee et al., 2010)
- ▶ All are OK.

# Effect estimator

## Estimation of Treatment Effect

- ▶ Inverse probability of treatment weighing (IPTW):

$$IPTW_i = \frac{Z_i}{\hat{e}_i} + \frac{1 - Z_i}{1 - \hat{e}_i}$$

- ▶ Weight 1 vs  $\frac{\hat{e}_i}{1 - \hat{e}_i}$ :

$$Z_i - \frac{\hat{e}_i(1 - Z_i)}{1 - \hat{e}_i}$$

- ▶ Inverse probability weighting (IPW):  $\hat{\Delta}_{IPW}$
- ▶ Stabilized inverse probability weighting (SIPW):  $\hat{\Delta}_{SIPW}$

## Evaluation

- ▶ Empirical distribution
  - ▶ Histogram or boxplot
  - ▶ Bias: difference between true effect ( $\gamma = -0.4$ )
  - ▶ Standard deviation

# Inverse Probability of Treatment Weighing

```
doMC::registerDoMC(cores = 8)
wt_logit <-
  mc_list %>%
  add_weighting(
    treatment = "exposure",
    formula = exposure ~ . - y - exposure_prob, method = "I"
    mc_col = "mcname", sc_col = "scenario", parallel = TRUE
  )
```

# Empirical Distribution of Propensity Scores

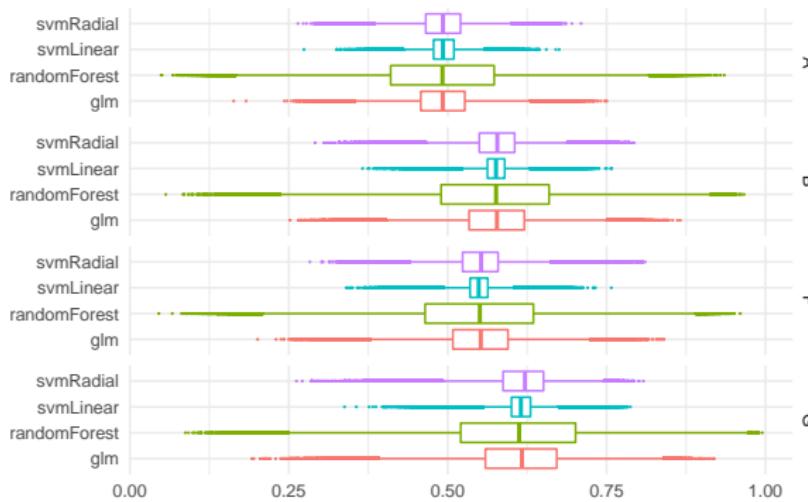


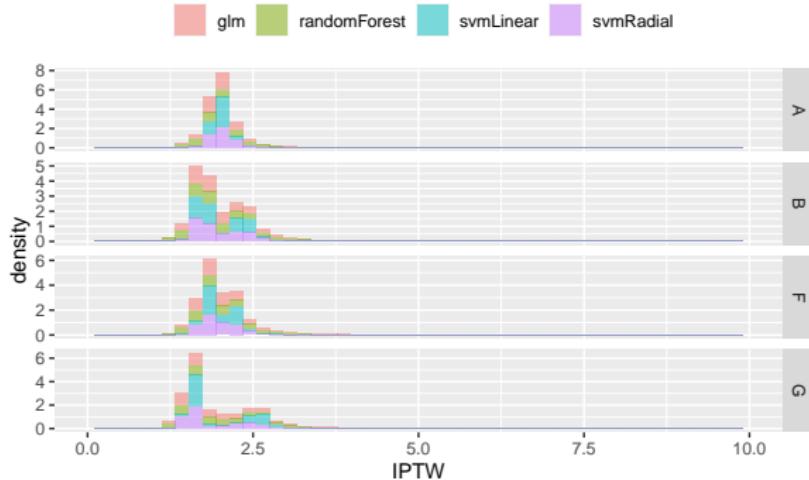
Figure 2: Propensity Scores

## Comments about Propensity Scores

What method leads to more extreme PS, i.e. close to 0 or 1?

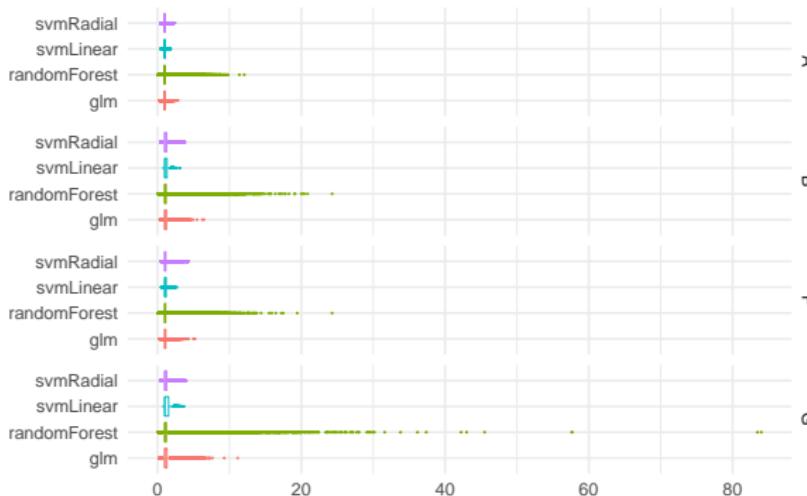
1. Random forest
2. Logistic regression
3. SVM (radial kernel)
4. SVM (linear kernel)

# Empirical Distribution of IPTW



**Figure 3:** Empirical Distribution of IPTW

# Empirical Distribution of Weights for the Control Group



**Figure 4:** Weights for the Control Group

## Comments about Weights

- ▶ Recall that extreme PS
  - 1. Random forest
  - 2. Logistic regression
  - 3. SVM (radial kernel)
  - 4. SVM (linear kernel)
- ▶ This result is same in the weight.

# SIPW

```
doMC::registerDoMC(cores = 8)
sipw_logit <-
  mc_list %>%
  compute_sipw(
    treatment = "exposure", outcome = "y",
    formula = exposure ~ . - y - exposure_prob, method = "logit",
    mc_col = "mcname", sc_col = "scenario", parallel = TRUE
  )
```

# Performance Metric of SIPW

Metric	Scenarios	Model			
		Logistic regression	Random forests	SVM (Linear)	SVM (Radial)
bias	A	0.402	0.402	0.402	0.402
	B	0.401	0.401	0.401	0.401
	F	0.401	0.401	0.402	0.402
	G	0.402	0.402	0.403	0.403
estimate	A	-0.002	-0.002	-0.002	-0.002
	B	-0.001	-0.001	-0.001	-0.001
	F	-0.001	-0.001	-0.002	-0.002
	G	-0.002	-0.002	-0.003	-0.003
mse	A	0.158	0.158	0.158	0.158
	B	0.159	0.159	0.159	0.159
	F	0.159	0.159	0.159	0.159
	G	0.158	0.158	0.157	0.157
sd	A	0.001	0.001	0.001	0.001
	B	0.001	0.001	0.001	0.001
	F	0.001	0.001	0.001	0.001
	G	0.001	0.001	0.001	0.001

## Related Contents

# About this project

## Project repository

<https://github.com/ygeunkim/psweighting-ml>

## Project package

<https://github.com/ygeunkim/propensityml>

# About the Machine

```
sessioninfo::session_info()[[1]]  
#>   setting  value  
#>   version  R version 4.0.3 (2020-10-10)  
#>   os        macOS Catalina 10.15.7  
#>   system    x86_64, darwin17.0  
#>   ui        X11  
#>   language (EN)  
#>   collate   en_US.UTF-8  
#>   ctype     en_US.UTF-8  
#>   tz        Asia/Seoul  
#>   date      2020-12-06
```

## References I

- Lee, B. K., Lessler, J., and Stuart, E. A. (2010). Improving propensity score weighting using machine learning. *Statistics in Medicine*, 29(3):337–346.
- Pirracchio, R., Petersen, M. L., and van der Laan, M. (2014). Improving propensity score estimators' robustness to model misspecification using super learner. *American Journal of Epidemiology*, 181(2):108–119.
- Setoguchi, S., Schneeweiss, S., Brookhart, M. A., Glynn, R. J., and Cook, E. F. (2008). Evaluating uses of data mining techniques in propensity score estimation: a simulation study. *Pharmacoepidemiology and Drug Safety*, 17(6):546–555.