Propensity Score Weighting using machine learning

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Propensity Score Weighting

Introduction

Simulation and Evaluation

Related Contents

Introduction

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
- Emprical 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

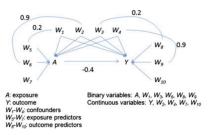


Figure 1: Simulation Data - Each W and A can be as X and Z in the course, respectively

Correlation Matrix

of covariates:

$$\begin{bmatrix} 1 & 0 & 0 & 0 & 0.2 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0.9 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0.9 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0.2 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0.9 & 0 \\ 0.2 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0.9 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0.2 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0.2 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0.9 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0.9 & 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \end{bmatrix}$$

Scenarios

True propensity score

Define $e(X_i)$ for each scenario (A, B, F, G):

A Additivity and linearity:

$$P(Z = 1 \mid X_i) = \frac{1}{1 + \exp(-(\beta_0 + \beta_1 X_1 + \dots + \beta_7 X_7))}$$

B Moderate non-linearity: 3 quadratic term

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

- 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

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

where

- $(\alpha_0, \alpha_1, \dots, \alpha_7)^T = (-3.85, 0.3, -0.36, -73, -0.2, 0.71, -0.19, 0.26)^T$
- $ightharpoonup \gamma = -0.4$: 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, 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,...
#> $ u
           <dbl> -120.253, 0.942, -51.95...
#> $ exposure_prob <dbl> 0.5000, 0.9072, 0.3465,...
```

Simulation and Evaluation

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
)</pre>
```

Columns that indicate MC and Scenario: mcname, scenario

```
mc_list[, .N, .(mcname, scenario)]
       mename scenario
                  A 1000
  2: 2 A 1000
  3: 3 A 1000
    4:
       4 A 1000
                  A 1000
    5:
          996 G 1000
#> 3996:
          997
                 G 1000
#> 3997.
#> 3998:
         998
                  G 1000
#> 3999:
          999
                   G 1000
#\\ /000 · 1000
                  C 1000
```

Average standardized absolute mean distance (ASAM)

- Covariate balancing: standardized mean differece, 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

 Table 1: ASAM performance

Scenarios	Logistic regression	Random forests	SVM
A	0.012	0.012	0.010
В	0.031	0.028	0.041
F	0.036	0.034	0.043
G	0.077	0.074	0.081

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

Effect estimator

Estimation of ATE

Inverse probability of treatment weighing (IPTW):

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

- Inverse probability weighting (IPW): weighted regression of outcome on treatment $\hat{\Delta}_{IPW}$
- ▶ Stabilized inverse probability weighting (SIPW): $\hat{\Delta}_{SIPW}$

Evaluation

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

Inverse Probability of Treatment Weighing

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

Empirical Distribution of IPTW

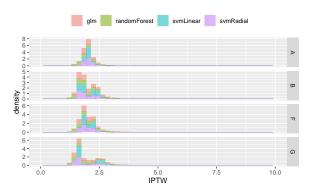


Figure 2: Empirical Distribution of IPTW

IPW and SIPW

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

- weight of treatment: 1
- weight of control: $\frac{p_i}{1-p_i}$
- ▶ If ê is proper
 - then two weights are similar
 - ► ATE estimate: difference of weighted means

Empirical Distribution of IPW

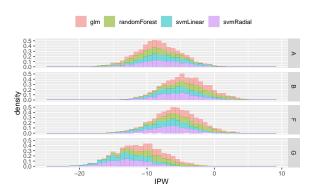


Figure 3: Empirical Distribution of IPW

Empirical Distribution of SIPW

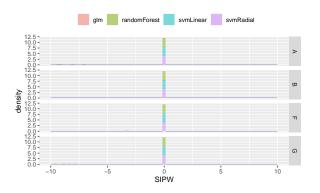


Figure 4: Empirical Distribution of SIPW

Performance Metric of IPW

		Model			
Metric	Scenarios	Logistic regression	Random forests	SVM (Linear)	SVM (Radial)
bias	Α	8.88	9.57	8.24	8.42
	В	4.21	4.27	5.95	5.99
	F	5.25	5.37	7.31	7.16
	G	9.78	9.62	13.11	13.34
estimate	Α	-8.47	-9.16	-7.83	-8.00
	В	-3.33	-3.15	-5.37	-5.38
	F	-4.69	-4.73	-6.88	-6.71
	G	-9.38	-9.21	-12.71	-12.94
mse	Α	74.18	88.14	66.38	69.79
	В	18.29	19.72	35.49	35.89
	F	27.58	30.11	52.09	50.13
	G	89.72	89.86	161.94	166.77
sd	A	3.00	3.38	3.35	3.47
	В	3.11	3.48	3.28	3.33
	F	3.02	3.38	3.18	3.22
	G	3.02	3.50	3.24	3.08

Performance Metric of SIPW

		Model			
Metric	Scenarios	Logistic regression	Random forests	SVM (Linear)	SVM (Radial)
bias	A	0.402	0.402	0.402	0.402
	В	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
	В	-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
	В	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
	В	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

Related Contents

About this project

Project repository

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

Project package

https://github.com/ygeunkim/propensityml

About the Machine

```
sessionInfo()
#> R version 4.0.3 (2020-10-10)
#> Platform: x86_64-apple-darwin17.0 (64-bit)
#> Running under: macOS Catalina 10.15.7
#>
#> Matrix products: default
#> BLAS: /Library/Frameworks/R. framework/Versions/4.0/Resources/lib/libRblas.dylib
#> LAPACK: /Library/Frameworks/R. framework/Versions/4.0/Resources/lib/libRlapack.dylib
#>
#> locale:
#> [1] en US.UTF-8/en US.UTF-8/en US.UTF-8/C/en US.UTF-8/en US.UTF-8
#>
#> attached base packages:
#> [1] parallel stats graphics grDevices utils
                                                        datasets methods
#> [8] base
#>
#> other attached packages:
#> [1] propensityml 0.0.0.9000 kableExtra 1.3.1
                                                        knitr 1.30
#> [4] rmdtool 0.1.0
                               foreach 1.5.1
                                                        data.table 1.13.2
#> [7] forcats 0.5.0
                               stringr_1.4.0
                                                        dplyr_1.0.2
#> [10] purrr 0.3.4
                               readr 1.4.0
                                                        tidyr 1.1.2
#> [13] tibble 3.0.4
                               applot2 3.3.2
                                                        tidyverse 1.3.0
#>
#> loaded via a namespace (and not attached):
#> [1] Rcpp 1.0.5
                           mutnorm 1.1-1
                                               lubridate 1.7.9.2
#> [4] lattice_0.20-41
                           class 7.3-17
                                               utf8_1.1.4
#> [7] assertthat_0.2.1
                            digest_0.6.27
                                               R6 2.5.0
#> [10] cellranger 1.1.0
                            backports 1.2.0
                                               reprex 0.3.0
#> [13] evaluate_0.14
                            e1071_1.7-4
                                               httr_1.4.2
#> [16] pillar_1.4.7
                            rlang_0.4.9
                                               readxl_1.3.1
#> [19] rstudioapi 0.13
                            rpart 4.1-15
                                               Matrix 1.2-18
```

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.