SOC-GA 2332 Intro to Stats Lab 13

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11/26/2025

Part 0: Logistics

- **Problem set 4** due on Dec. 5th, 11:59pm
  - Treat `numsibling` as fixed within household even though it doesn't make a ton of sense
- **Replication Part II** due Dec. 15th, 5:00pm (no extensions)
  - Grades for Part I coming shortly

Replication project tips

- Knit consistently and frequently as you write code
  - If you do hit a knitting error:
    - Start commenting things out until you can get it to run and then work backwards
    - Delete everything from your environment (broom) and run your code from the beginning
- If you're hitting space issues on your computer, feel free to use a smaller sample (ex. 1%)
- Papers should be formatted as clean, final projects
  - Code chunks not showing
  - Text formatted correctly and consistently
  - Figures and tables numbered & labelled, with all text clearly readable
  - Utilize the template on GitHub or RMarkdown cheatsheets
- Read instructions completely and carefully
- Comment up your code (both for me and for your future self!)
- Get started early so you can take advantage of your resources (peers, office hours, class, etc.)

Part 1: Exploring data sample

- Today we are going to review a specific type of weighting, Inverse Probability of Treatment Weighting (IPTW). We will use the Early Childhood Longitudinal Study dataset.
- We will examine the effect of going to a Catholic school (`catholic = 1`), as opposed to a public school (`catholic = 0`), on students' standardized math score (`c5r2mtsc_std`). The pre-treatment covariates are:
  - `race_white`: Is the student white (1) or not (0)?
  - `p5hmage`: Mother's age
  - `w3income`: Family income
  - `p5numpla`: Number of places the student has lived for at least 4 months
  - `w3momed_hsb`: Is the mother's education level high-school or below (1) or some college or more (0)?

```r
## import data
ecls <- read.csv("data/ecls.csv")

## covariates variable name vector
ecls_cov <- c('race_white', 'p5hmage', 'w3income', 'p5numpla', 'w3momed_hsb')

## remove observations with NAs
ecls_nomiss <- ecls %>%
  select(c5r2mtsc_std, catholic, all_of(ecls_cov)) %>%
  na.omit()
```

Explore sample

- First let's see if there is any apparent difference in outcome by school type without controlling for any covariates

```r
## check difference in mean outcomes by school type
ecls %>%
  group_by(catholic) %>%
  summarise(n_students = n(),
            mean_math = mean(c5r2mtsc_std),
            std_error_math = sd(c5r2mtsc_std) / sqrt(n_students))
```

```
## # A tibble: 2 x 4
##   catholic n_students mean_math std_error_math
##      <int>      <int>     <dbl>          <dbl>
## 1        0       9568   -0.0306         0.0104
## 2        1       1510    0.194          0.0224
```

```r
## two Sample t-test: (H0: mean math scores do not differ by school types)
with(ecls, t.test(c5r2mtsc_std ~ catholic))
```

```
##
##  Welch Two Sample t-test
##
## data:  c5r2mtsc_std by catholic
## t = -9.1069, df = 2214.5, p-value < 0.00000000000000022
## alternative hypothesis: true difference in means between group 0 and group 1 is not equal to 0
## 95 percent confidence interval:
##  -0.2727988 -0.1761292
## sample estimates:
## mean in group 0 mean in group 1
##     -0.03059583      0.19386817
```

- *Question:* How would we interpret this t-test?
- Now let's explore the relationship between school type and other covariates.
- *Question:* What is endogenous sampling?
- To check if we might be endogenous sampling, we first examine the difference in means by treatment status for covariates.

```r
## check difference in means for pre-treatment covariates by school types
## summarise group means for covariates
ecls %>%
  group_by(catholic) %>%
```

```
  select(one_of(ecls_cov)) %>%
  summarise_all(funs(mean(., na.rm = T)))
```

```
## # A tibble: 2 x 6
##   catholic race_white p5hmage w3income p5numpla w3momed_hsb
##      <int>      <dbl>   <dbl>    <dbl>    <dbl>       <dbl>
## 1        0      0.556    37.6   54889.     1.13       0.464
## 2        1      0.725    39.6   82074.     1.09       0.227
```

```
## Two sample t-test for every covariate
## lapply: a build-in loop that apply the t-test function along the name vector
lapply(ecls_cov, function(v){
  t.test(ecls[, v] ~ ecls[, 'catholic'])
})
```

```
## [[1]]
##
##  Welch Two Sample t-test
##
## data:  ecls[, v] by ecls[, "catholic"]
## t = -13.453, df = 2143.3, p-value < 0.00000000000000022
## alternative hypothesis: true difference in means between group 0 and group 1 is not equal to 0
## 95 percent confidence interval:
##  -0.1936817 -0.1444003
## sample estimates:
## mean in group 0 mean in group 1
##       0.5561246       0.7251656
##
##
## [[2]]
##
##  Welch Two Sample t-test
##
## data:  ecls[, v] by ecls[, "catholic"]
## t = -12.665, df = 2186.9, p-value < 0.00000000000000022
## alternative hypothesis: true difference in means between group 0 and group 1 is not equal to 0
## 95 percent confidence interval:
##  -2.326071 -1.702317
## sample estimates:
## mean in group 0 mean in group 1
##        37.56097        39.57516
##
##
## [[3]]
##
##  Welch Two Sample t-test
##
## data:  ecls[, v] by ecls[, "catholic"]
## t = -20.25, df = 1825.1, p-value < 0.00000000000000022
## alternative hypothesis: true difference in means between group 0 and group 1 is not equal to 0
## 95 percent confidence interval:
##  -29818.10 -24552.18
## sample estimates:
## mean in group 0 mean in group 1
##        54889.16        82074.30
```

```
##
##
## [[4]]
##
##  Welch Two Sample t-test
##
## data:  ecls[, v] by ecls[, "catholic"]
## t = 4.2458, df = 2233.7, p-value = 0.00002267
## alternative hypothesis: true difference in means between group 0 and group 1 is not equal to 0
## 95 percent confidence interval:
##  0.02150833 0.05842896
## sample estimates:
## mean in group 0 mean in group 1
##        1.132669        1.092701
##
##
## [[5]]
##
##  Welch Two Sample t-test
##
## data:  ecls[, v] by ecls[, "catholic"]
## t = 18.855, df = 2107.3, p-value < 0.00000000000000022
## alternative hypothesis: true difference in means between group 0 and group 1 is not equal to 0
## 95 percent confidence interval:
##  0.2122471 0.2615226
## sample estimates:
## mean in group 0 mean in group 1
##       0.4640918       0.2272069
```

- As we can see, the difference in mean for covariates are statistically significant.

Part 2: Propensity Score

- *Question:* What is Inverse Probability of Treatment Weighting (IPTW)?
- *Question:* Why might we use IPTW?
- To conduct IPTW, we usually use propensity scores.
- Propensity scores are a one-number summary of all the different covariates' values for each individual. In this case, we'll use them to represent the probability of being treated given a set of pre-treatment covariates.
- In `R`, we can estimate propensity score given the covariates by fitting a logistic regression with the treatment status as the outcome and covariates as predictors. So basically we're trying to predict what each observation's probability of being treated is.
  - We still leverage the strong ignorability assumption and correct specification assumption to derive an unbiased estimate of the true propensity score.
    - *Question:* What are these two assumptions?
- Now let's try to fit propensity scores to our data. In reality this is usually a much longer and more iterative process, but for this demonstration I've simplified it into fitting a simple logistic regression. There are also ML algorithms that will find the best propensity score formula for you (ex. using SuperLearner throught the`WeightIt` package).

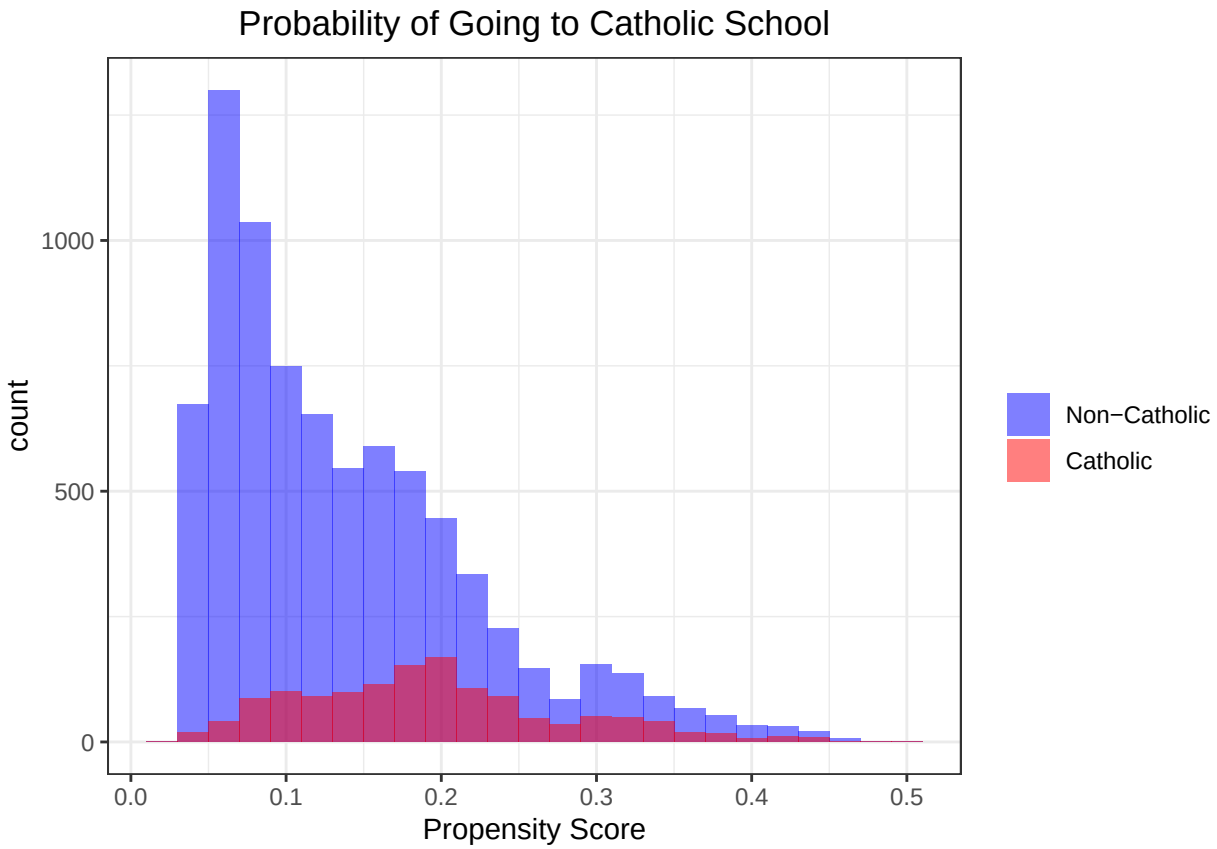
```r
## rescale income
ecls <- ecls %>% mutate(w3income_1k = w3income/1000)

## fit a logistic regress to generate propensity score using covariates
m_ps <- glm(catholic ~ race_white + w3income_1k + p5hmage + p5numpla + w3momed_hsb,
            family = binomial(), data = ecls)
summary(m_ps)
```

```
##
## Call:
## glm(formula = catholic ~ race_white + w3income_1k + p5hmage +
##     p5numpla + w3momed_hsb, family = binomial(), data = ecls)
##
## Coefficients:
##               Estimate Std. Error z value             Pr(>|z|)
## (Intercept) -3.2125519  0.2379826 -13.499 < 0.0000000000000002 ***
## race_white   0.3145014  0.0700895   4.487        0.00000721848 ***
## w3income_1k  0.0073038  0.0006495  11.245 < 0.0000000000000002 ***
## p5hmage      0.0292168  0.0050771   5.755        0.00000000869 ***
## p5numpla    -0.1439392  0.0912255  -1.578                0.115
## w3momed_hsb -0.6935868  0.0743207  -9.332 < 0.0000000000000002 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 7701.3  on 9266  degrees of freedom
## Residual deviance: 7168.8  on 9261  degrees of freedom
##   (1811 observations deleted due to missingness)
## AIC: 7180.8
##
## Number of Fisher Scoring iterations: 5
```

```r
## use above model to generate propensity
## (the probability of being treated given a set of pre-treatment covariates)
prs_df <- data.frame(pr_score = predict(m_ps, type = "response"),
                     catholic = m_ps$model$catholic)

## check the region of common support
## in every unit in the treatment, is there a control unit
prs_df %>%
  ggplot(aes(x = pr_score, fill = as.factor(catholic))) +
  geom_histogram(binwidth = 0.02, alpha = 0.5, position="identity") +
  ggtitle("Probability of Going to Catholic School") +
  xlab("Propensity Score") +
  theme_bw() +
  theme(plot.title = element_text(hjust = 0.5)) +
  scale_fill_manual(name=" ",
                    values = c("blue", "red"),
                    labels = c("Non-Catholic", "Catholic"))
```



Part 3: Inverse probability weighting

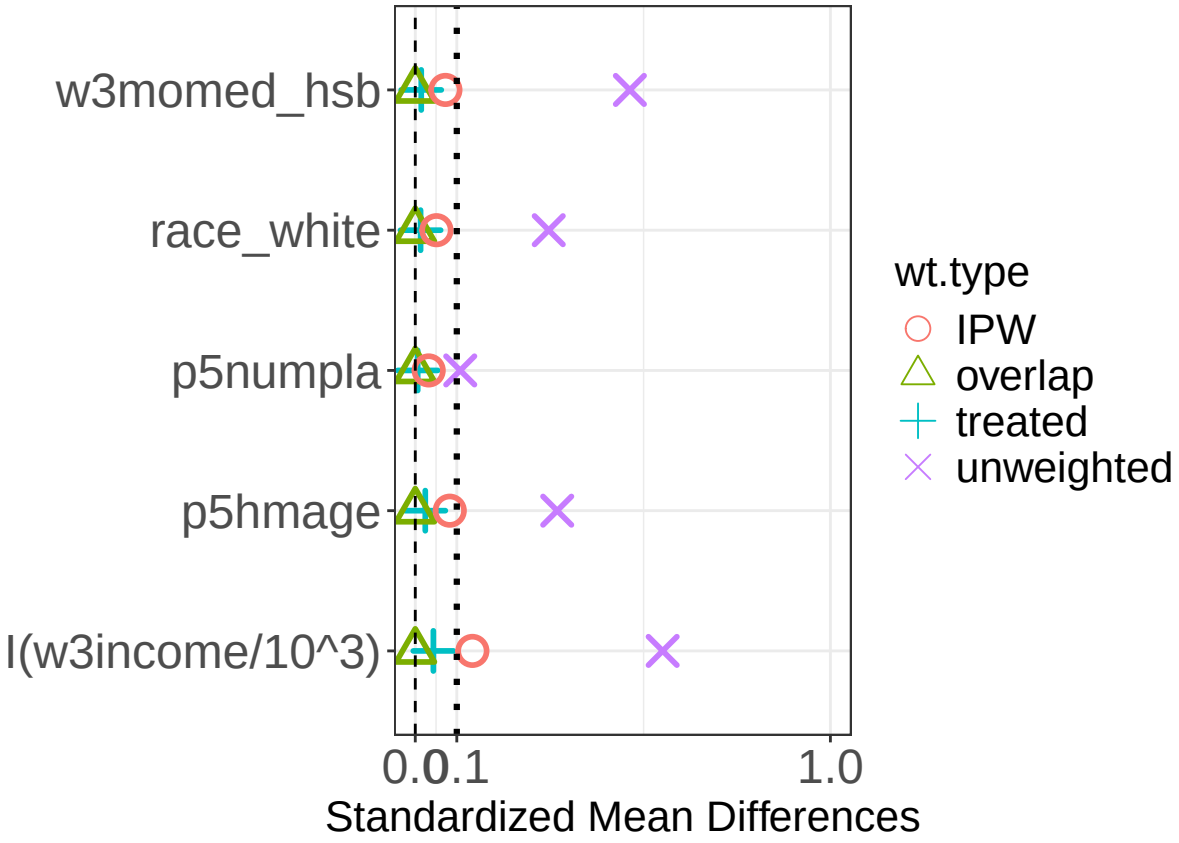
- Use propensity scores to weight units based on their probabilities of being treated.
  - e(x) is the propensity score
  - w_1 is weights if the unit is treated
  - w_0 is weights if the unit is untreated
- There are several options that measure different quantities of interest
  - `IPW` measures ATE. $weight(w_1, w_0) = (\frac{1}{e(x)}, \frac{1}{1-e(x)})$
    - The core of `IPW` is to create a weighted treatment group and a weighted control group whose covariates' distribution resembles the distribution of the whole sample
  - `treated` measures ATT. $weight(w_1, w_0) = (1, \frac{e(x)}{1-e(x)})$
    - The core of `treated` is to create only a weighted control group whose covariates' distribution resembles the distribution of the unweighted treatment group
  - `overlap` measures ATO (Average Treatment on Overlap). $weight(w_1, w_0) = (1 - e(x), e(x))$
    - The core of `overlap` is to give more weights to the observations near the center of the propensity, or the units under "equipoise"
- You may check this site for more detailed explanations

```
## matching algorithm
ps.formula <- catholic ~ race_white + p5hmage +
                  I(w3income / 10^3) + p5numpla + w3momed_hsb

bal.ipw <- SumStat(ps.formula = ps.formula, zname ="catholic",
weight = c("treated", "overlap", "IPW"), data = ecls_nomiss)

# check balance by weight type
```

```
plot(bal.ipw)
```



- Estimate ATT, ATO, and ATE:

```
## average treatment effect among the treated population
att <- PSweight(ps.formula = ps.formula, yname = "c5r2mtsc_std", data = ecls_nomiss, family = "gaussian"
weight = "treated")

## average treatment effect among the overlap population
ato <- PSweight(ps.formula = ps.formula, yname = "c5r2mtsc_std", data = ecls_nomiss, family = "gaussian"
weight = "overlap")

## average treatment effect using IPW
ate <- PSweight(ps.formula = ps.formula, yname = "c5r2mtsc_std", data = ecls_nomiss, family = "gaussian"
weight = "IPW")

## check results
summary(att)
```

```
##
## Closed-form inference:
##
## Original group value:  0, 1
## Treatment group value:  1
##
## Contrast:
##             0 1
## Contrast 1 -1 1
```

```
##
##            Estimate Std.Error      lwr       upr    Pr(>|z|)
## Contrast 1 -0.12161   0.02595 -0.17247 -0.070751 0.000002781 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(ate)
```

```
##
## Closed-form inference:
##
## Original group value:  0, 1
##
## Contrast:
##             0 1
## Contrast 1 -1 1
##
##              Estimate  Std.Error        lwr      upr Pr(>|z|)
## Contrast 1 -0.0087096  0.0290430 -0.0656329 0.048214   0.7643
```

- *Question:* Why is ATE and ATT different?

Exercise

Instead of removing observations with NAs, use one of the missing data strategies we covered in previous labs (see Lab 7). Then, run a regression to see whether school type affects math score. Do you get the same results as when you use IPTW? Why or why not?