Synthetic Control Analysis: COVID-19 Vaccine Lotteries

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Setting and Data

There are several published analyses of the effect of COVID-19 vaccine lotteries in the U.S. We use the data and analysis based on that by Lang et al. (2023). The replication files that are used are available through Harvard Dataverse.

Fuller et al. (2022) conducted a multiple-state analysis using the synthetic control, and have data available on Harvard Dataverse as well. Other analyses include Sehgal (2021) and Brehm et al. (2022).

Focusing on the Ohio Vax-A-Million lottery, we explore whether the lottery incentive, which was announced on May 12, 2021, had a noticeable impact on Ohio's vaccination rates. The outcome considered is the percentage of the adult population fully vaccinated for COVID-19; note that the lottery only required a first dose for entry.

The outcome data were obtained by Lang et al. from Our World In Data's database, which draws from CDC reports. The relevant data for our analyses are in `lottery_lang.Rda`. `lang_0624` contains weekly case, vaccination, and death numbers by state, along with indicators and week numbers for any states that implemented their own lottery. These data are complete through late June 2021 (used in the main analysis in the publication), while `lang_0912` extends the data through mid-September. `lang_ann_dates` has announcement dates and notes on lotteries in various states. Note that the data used by Fuller et al. are available in `lottery_fuller.Rda` for comparison.

First, load the data into R.

```
load(file="../data/lottery_lang.Rda")
```

Libraries

Again, we will use `tidyverse` and `knitr` for general coding. Several packages are available for synthetic control fitting, including: `Synth`, developed by the original authors of Abadie et al. (2010); `gsynth`, which implements the generalized SC method; and `microsynth`, which allows for disaggregated, micro-level data. We will use two others:

1. `tidysynth`, which has a more user-friendly, tidyverse-style implementation of SC; and
2. `augsynth`, which additionally allows for Augmented SC (to be discussed later) and staggered adoption SC. For the most recent version of `R`, this has to be installed from GitHub using the `devtools` package.

We now load the required libraries.

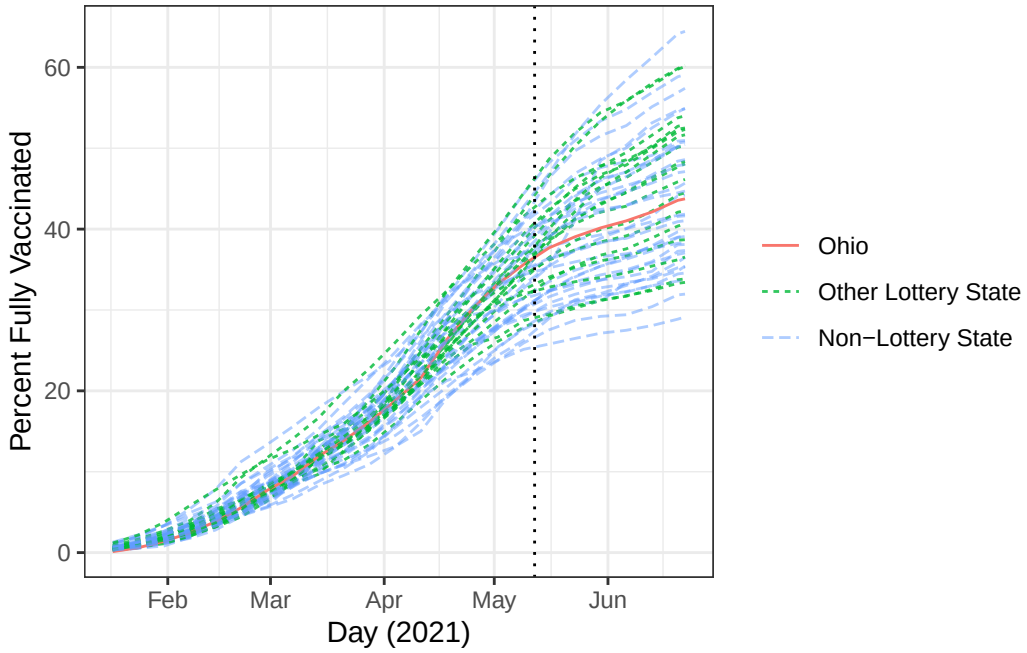
```
## If you have not installed these packages before,
##  run the following line:
# install.packages(c("tidysynth","devtools"))
## Either way, require the libraries:
require(tidyverse)
require(knitr)
require(tidysynth)
require(devtools)
## If augsynth has not yet been installed, run the following line:
# devtools::install_github("ebenmichael/augsynth")
require(augsynth)
```

Graphical Exploration

We begin by plotting the time series for visual inspection. First, we plot the percent fully vaccinated over time, up to late June 2021.

```
## We first save the annnouncement date for Ohio's lottery:
Ohio_ann <- lang_ann_dates %>% dplyr::filter(state=="OH") %>%
  pull(lott_date)
## Plot time series of mandates themselves:
#| fig-cap: "Plot of fully vaccinated percentages by state and lottery status, January-June 2
#| fig-alt: "A line plot with line for each state over the time range specified. Ohio is high
ggplot(data=lang_0624,
       mapping=aes(group=state,linetype=type,color=type,alpha=type,
                   x=last_day,y=people_fully_vaccinated_per_hundred)) +
  scale_alpha_manual(name=NULL, breaks=c("Ohio","Other Lottery State","Non-Lottery State"),
                     values=c(1,0.8,0.5)) +
```

```
  geom_line() + theme_bw() +
  geom_vline(xintercept=Ohio_ann, linetype="dotted") +
  labs(x="Day (2021)", y="Percent Fully Vaccinated",
       linetype=NULL,color=NULL)
```



We can do the same with the larger data set to see if there are later time patterns that should be explored.

```
ggplot(data=lang_0912,
       mapping=aes(group=state,linetype=type,color=type,alpha=type,
                   x=last_day,y=people_fully_vaccinated_per_hundred)) +
  scale_alpha_manual(name=NULL, breaks=c("Ohio","Other Lottery State","Non-Lottery State"),
                     values=c(1,0.8,0.5)) +
  geom_line() + theme_bw() +
  geom_vline(xintercept=Ohio_ann, linetype="dotted") +
  labs(x="Day (2021)", y="Percent Fully Vaccinated",
       linetype=NULL,color=NULL)
```

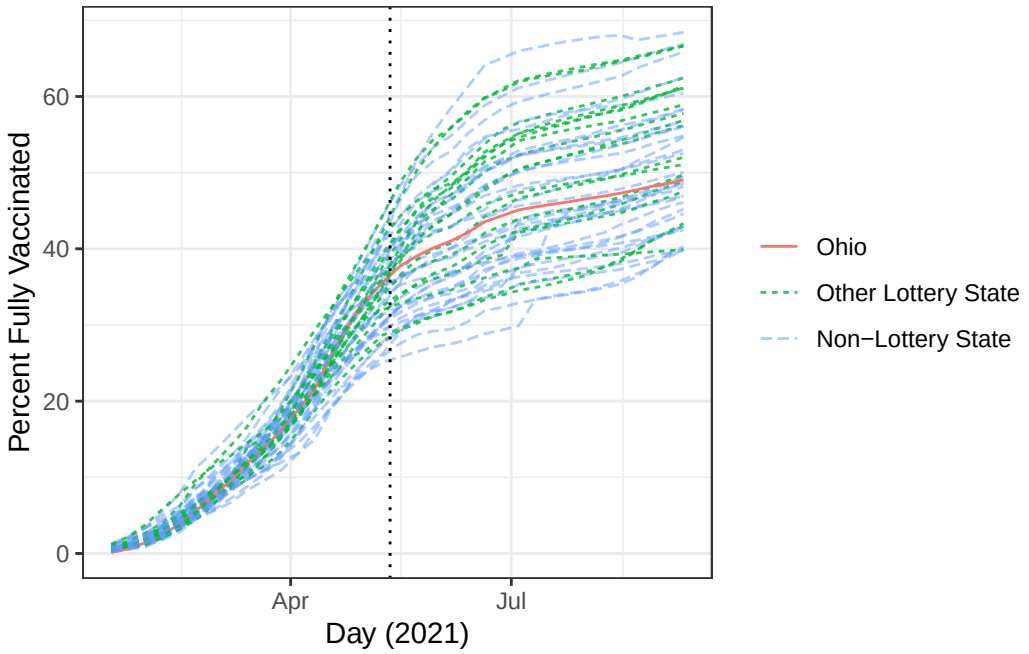


Figure 1: Plot of fully vaccinated percentages by state and lottery status, January–September 2021

We can also plot Ohio versus the average outcome of the other states, grouped by whether they had a lottery.

```
## Create data set that averages across states within each group:
lang_avg <- lang_0624 %>% group_by(type,week,last_day) %>%
  dplyr::summarize(full_vax_avg=mean(people_fully_vaccinated_per_hundred,
                                     na.rm=TRUE))
```

```
`summarise()` has grouped output by 'type', 'week'. You can override using the
`.groups` argument.
```

```
ggplot(data=lang_avg,
       mapping=aes(linetype=type,color=type,alpha=type,
                   x=last_day,y=full_vax_avg)) +
  geom_line(linewidth=1.3) + theme_bw() +
  scale_alpha_manual(name=NULL,
                     breaks=c("Ohio","Other Lottery State",
                              "Non-Lottery State"),
                     labels=c("Ohio","Other Lottery States (Mean)",
                              "Non-Lottery States (Mean)"),
```

```
                    values=c(1,0.8,0.5)) +
scale_linetype_manual(name=NULL,
                      breaks=c("Ohio","Other Lottery State",
                            "Non-Lottery State"),
                      labels=c("Ohio","Other Lottery States (Mean)",
                            "Non-Lottery States (Mean)"),
                      values=c("solid","dotted","dashed")) +
scale_color_manual(name=NULL,
                   breaks=c("Ohio","Other Lottery State",
                            "Non-Lottery State"),
                   labels=c("Ohio","Other Lottery States (Mean)",
                            "Non-Lottery States (Mean)"),
                   values=c("red","forestgreen","blue")) +
geom_vline(xintercept=Ohio_ann, linetype="dotted") +
labs(x="Day (2021)", y="Percent Fully Vaccinated")
```

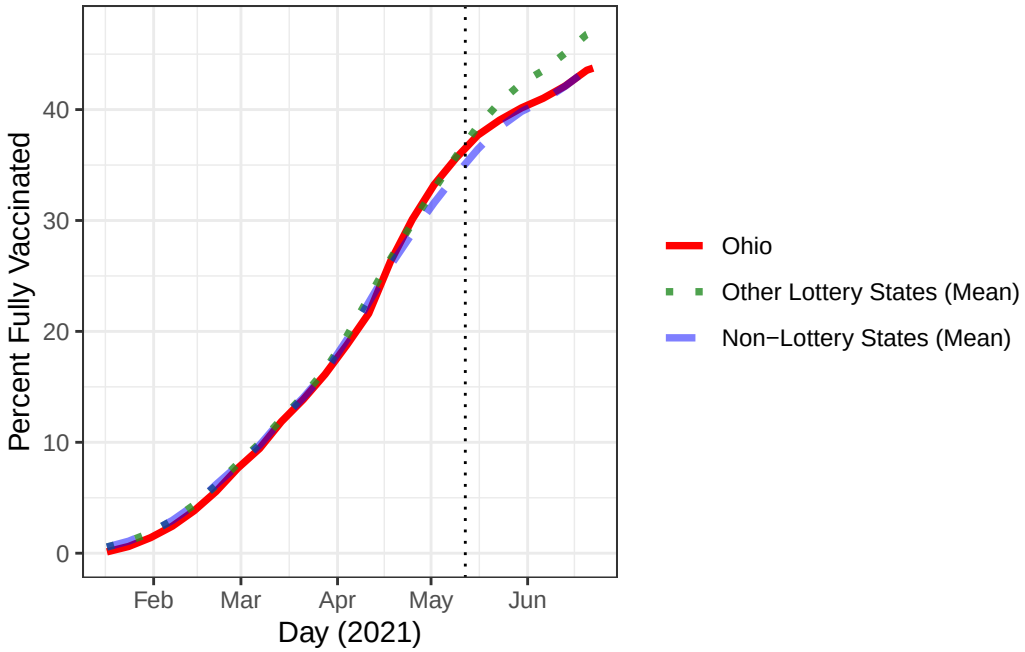


Figure 2: Plot of average fully vaccinated percentages by lottery status, January–June 2021. Note the mean is computed across states, not weighted by population.

Discussion Questions

1. Does the above plot indicate that parallel trends would be reasonable?

2. On visual inspection, does it appear that the lottery was effective?

Synthetic Control

Fit Model

We will fit the synthetic control for Ohio, using only non-lottery states as the potential control units. For now, we will use only the pre-intervention time periods as predictors, ignoring any other covariates, and optimize the fit over the full pre-intervention window. We use the `synthetic_control` function from the `tidysynth` package. Note that this may take a minute or two to run.

```
## Conduct SC analysis for Ohio, excluding other lottery states:
synth_ohio <- lang_0624 %>% dplyr::filter(type != "Other Lottery State") %>%
  ## initialize SC object by specifying outcome, unit variable, time variable,
  ### and when/where intervention turns on:
  synthetic_control(outcome=people_fully_vaccinated_per_hundred,
                    unit=state,
                    time=centered_week,
                    i_unit="OH",
                    i_time=0,
                    generate_placebos=T) %>%
  ## create predictors for SC model:
  generate_predictor(time_window=-17,lag17=people_fully_vaccinated_per_hundred) %>%
  generate_predictor(time_window=-16,lag16=people_fully_vaccinated_per_hundred) %>%
  generate_predictor(time_window=-15,lag15=people_fully_vaccinated_per_hundred) %>%
  generate_predictor(time_window=-14,lag14=people_fully_vaccinated_per_hundred) %>%
  generate_predictor(time_window=-13,lag13=people_fully_vaccinated_per_hundred) %>%
  generate_predictor(time_window=-12,lag12=people_fully_vaccinated_per_hundred) %>%
  generate_predictor(time_window=-11,lag11=people_fully_vaccinated_per_hundred) %>%
  generate_predictor(time_window=-10,lag10=people_fully_vaccinated_per_hundred) %>%
  generate_predictor(time_window=-9,lag09=people_fully_vaccinated_per_hundred) %>%
  generate_predictor(time_window=-8,lag08=people_fully_vaccinated_per_hundred) %>%
  generate_predictor(time_window=-7,lag07=people_fully_vaccinated_per_hundred) %>%
  generate_predictor(time_window=-6,lag06=people_fully_vaccinated_per_hundred) %>%
  generate_predictor(time_window=-5,lag05=people_fully_vaccinated_per_hundred) %>%
  generate_predictor(time_window=-4,lag04=people_fully_vaccinated_per_hundred) %>%
  generate_predictor(time_window=-3,lag03=people_fully_vaccinated_per_hundred) %>%
  generate_predictor(time_window=-2,lag02=people_fully_vaccinated_per_hundred) %>%
  generate_predictor(time_window=-1,lag01=people_fully_vaccinated_per_hundred) %>%
  ## generate SC weights:
  generate_weights(optimization_window=(-17):(-1),
```

```
                    margin_ipop = .02,sigf_ipop = 7,bound_ipop = 6) %>%
  ## run SC:
  generate_control()
```

The `synth_ohio` object contains all of the information about the fit. `tidysynth` provides many functions to pull the results for inspection.

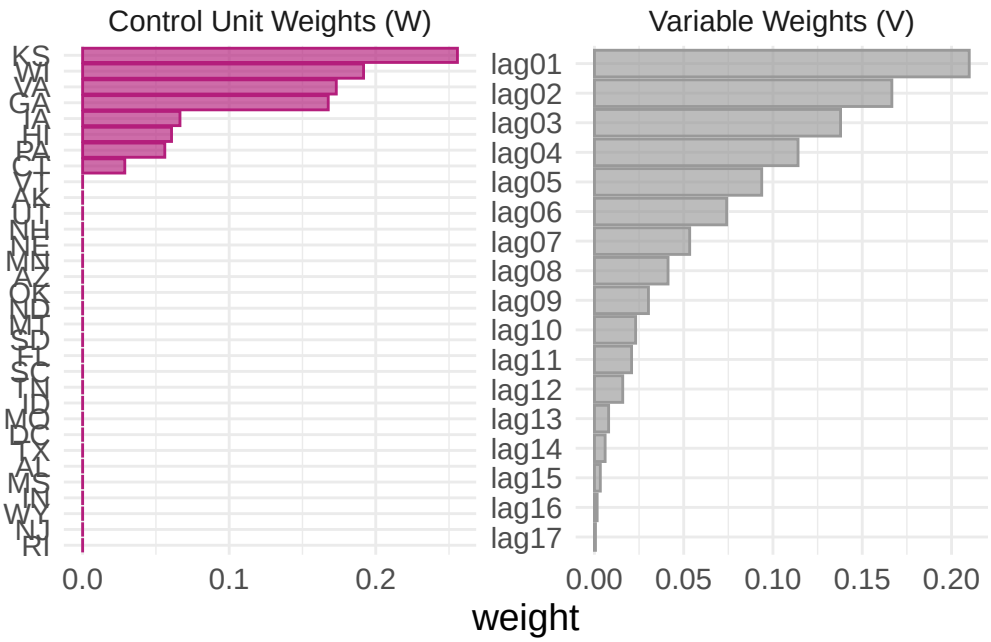
Inspect Fit

We can investigate the weights given to different control units and variables:

```
## Pull weights and print in descending order
synth_ohio %>% grab_unit_weights() %>%
  dplyr::filter(weight > 0.001) %>% dplyr::arrange(desc(weight))
```

```
# A tibble: 8 x 2
  unit  weight
  <chr>  <dbl>
1 KS    0.256
2 WI    0.192
3 VA    0.173
4 GA    0.168
5 IA    0.0664
6 HI    0.0607
7 PA    0.0561
8 CT    0.0288
```

```
## Plot the weights for control units and variables.
#| fig-cap: "Control unit and variable weights for synthetic control fit of Ohio's fully vac
#| fig-alt: "Left: bar plot of control unit weights. The positive weights are only for Kansas
## Plot weights on control units and variables:
synth_ohio %>% plot_weights()
```



The top four control states by weight are Kansas, Wisconsin, Viriginia, and Georgia. **Do these seem reasonable?** The variables are given weight in reverse chronological order: **does this make sense for minimizing pre-intervention MSPE?**

We can also examine the pre-intervention fit directly between true Ohio, synthetic Ohio, and the average of the donor pool.

```
## Examine fit:
synth_ohio %>% grab_balance_table()
```

```
# A tibble: 17 x 4
   variable    OH synthetic_OH donor_sample
   <chr>    <dbl>        <dbl>        <dbl>
 1 lag17     0.12        0.362        0.554
 2 lag16     0.61        0.775        1.09
 3 lag15     1.4         1.43         1.88
 4 lag14     2.44        2.41         2.96
 5 lag13     3.83        3.76         4.33
 6 lag12     5.56        5.71         6.19
 7 lag11     7.67        7.69         7.91
 8 lag10     9.44        9.50         9.75
 9 lag09    11.9        11.8         12.0
10 lag08    13.9        13.8         14.0
11 lag07    16.1        16.1         16.3
```

```
12 lag06    18.8        18.8        19.2
13 lag05    21.6        22.2        22.6
14 lag04    26.3        26.1        25.9
15 lag03    30.1        29.8        28.9
16 lag02    33.2        33.0        31.6
17 lag01    35.6        35.8        34.1
```

Plot Results

We can plot both the observed and synthetic time series themselves, and the gap between them.

```
synth_ohio %>% plot_trends() +
  labs(x="Weeks from Lottery Announcement",
       y="Percent Fully Vaccinated",
       title=NULL) +
  theme_bw()
```

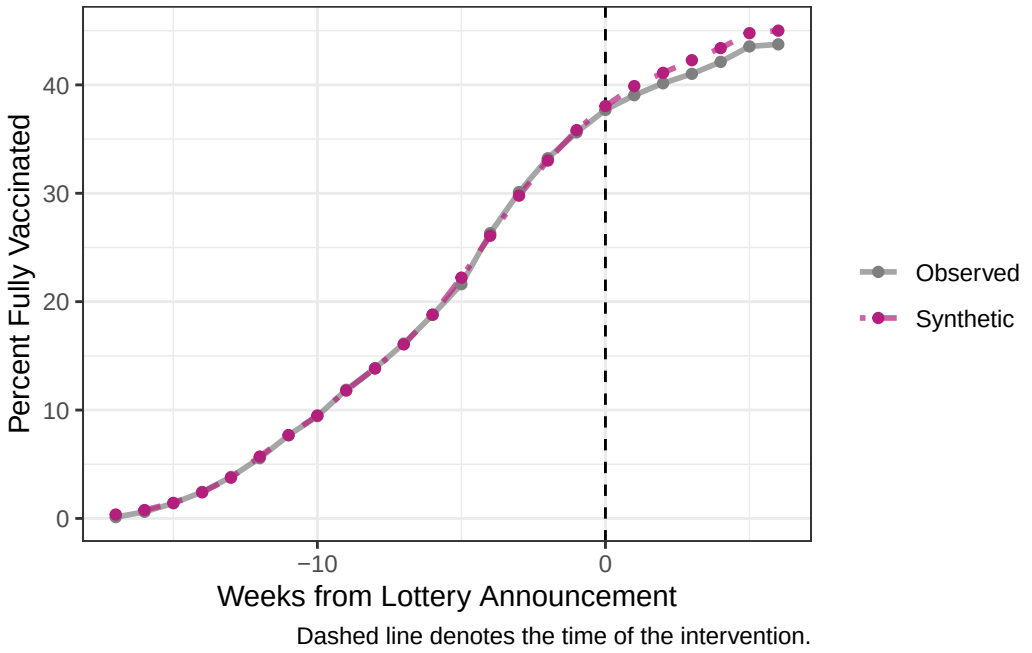


Figure 3: Time series of observed and synthetic Ohio's percent fully vaccinated rate by week (centered at lottery announcement date, May 12, 2021).

```
synth_ohio %>% plot_differences() +
  labs(x="Weeks from Lottery Announcement",
       y="Difference in Percent Fully Vaccinated, Observed-Synthetic",
       title=NULL) +
  theme_bw()
```

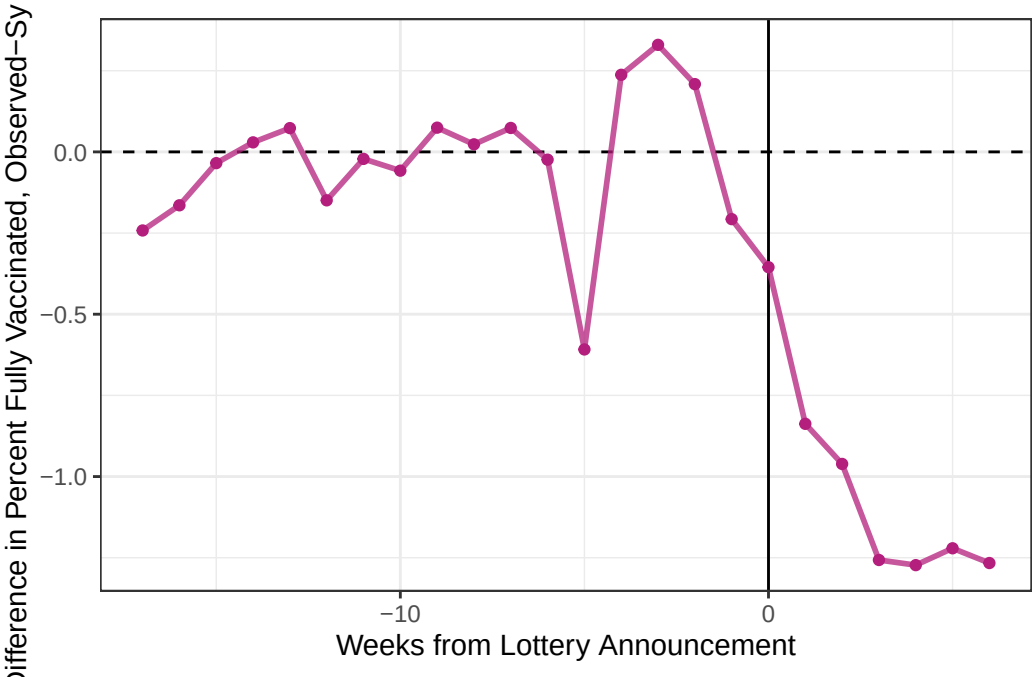


Figure 4: Time series of the difference, Observed – Synthetic Ohio, in percent fully vaccinated rate by week (centered at lottery announcement date, May 12, 2021).

Inference

Placebo in-space tests are conducted by default in `synthetic_control` and can be plotted. The default plot prunes those with pre-intervention square root of the MSPE values above twice the value for the actual analysis, but this can be turned off with `prune=FALSE`.

```
synth_ohio %>% plot_placebos() +
  labs(x="Weeks from Lottery Announcement",
       y="Difference in Percent Fully Vaccinated, Observed-Synthetic",
       title=NULL) +
  theme_bw()
```

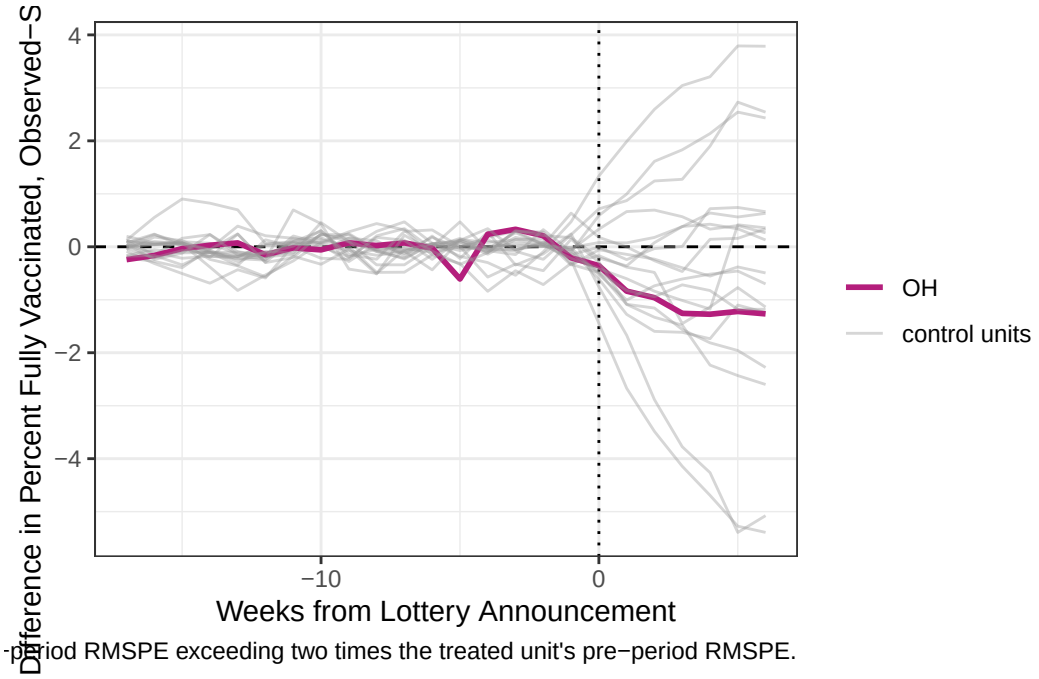


Figure 5: Actual and placebo synthetic control gaps in percent fully vaccinated rate by week (centered at lottery announcement date, May 12, 2021), excluding placebos with high pre-intervention MSPE values.

```
synth_ohio %>% plot_placebos(prune=FALSE) +
  labs(x="Weeks from Lottery Announcement",
       y="Difference in Percent Fully Vaccinated, Observed-Synthetic",
       title=NULL) +
  theme_bw()
```

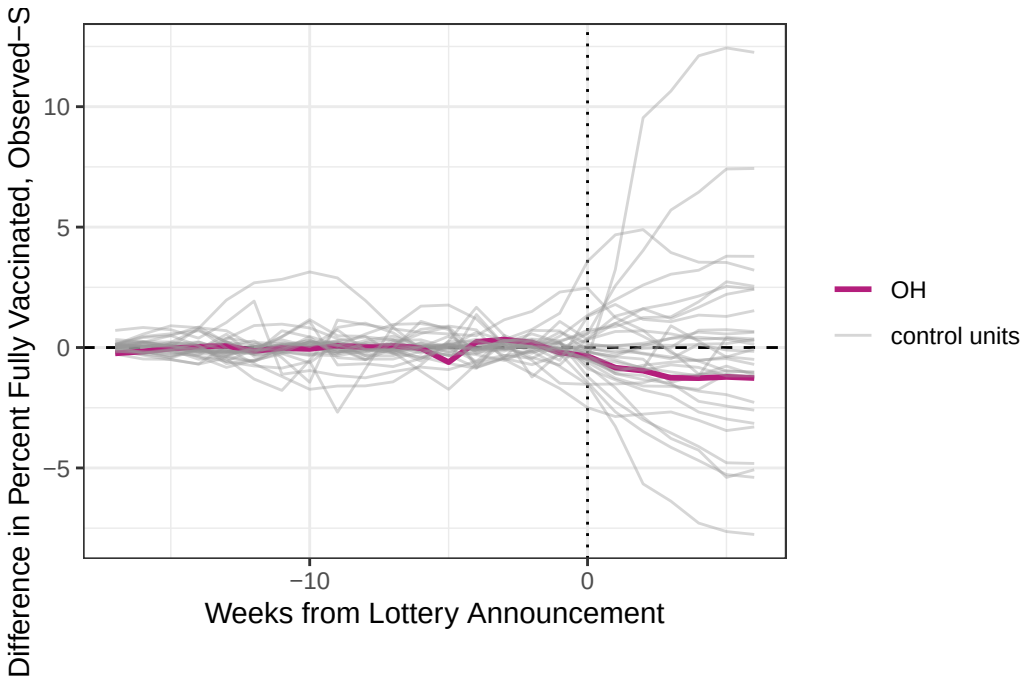


Figure 6: Actual and placebo synthetic control gaps in percent fully vaccinated rate by week (centered at lottery announcement date, May 12, 2021), all placebos.

One measure of the reliability of the results is to compare the post-intervention MSPE to the pre-intervention MSPE. The result for the actual analysis can be compared to the distribution of the placebo analyses.

```
synth_ohio %>% plot_mspe_ratio() +
  labs(title=NULL) +
  theme_bw()
```

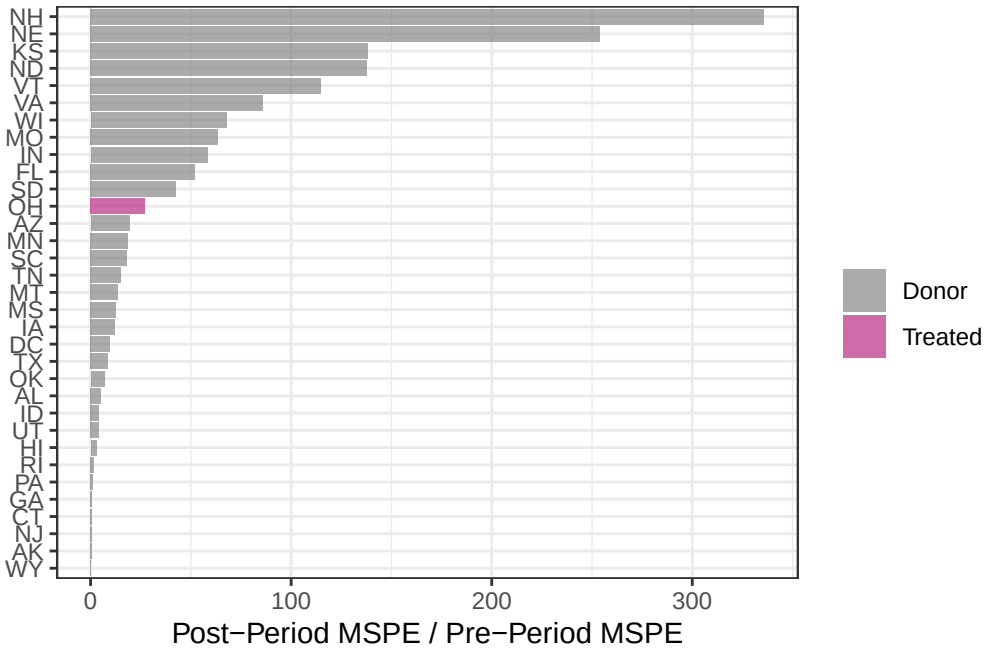


Figure 7: Ratio of the pre- and post-intervention MSPE, actual and placebo synthetic control analysis

An exact p-value can be computed from this distribution, by observing how many control units have as or more extreme ratios. This is done in the fit function and can be accessed using `grab_significance`.

```
## Get all pre- and post-intervention MSPEs, ratios, and ranks:
synth_ohio %>% grab_significance()
```

```
# A tibble: 33 x 8
   unit_name type  pre_mspe post_mspe mspe_ratio  rank fishers_exact_pvalue
   <chr>     <chr>    <dbl>     <dbl>      <dbl> <int>                <dbl>
 1 NH        Donor   0.331     111.        336.      1               0.0303
 2 NE        Donor   0.0645     16.4       254.      2               0.0606
 3 KS        Donor   0.139      19.2       138.      3               0.0909
 4 ND        Donor   0.309      42.5       138.      4               0.121
 5 VT        Donor   0.301      34.5       115.      5               0.152
 6 VA        Donor   0.0463      3.98       85.9     6               0.182
 7 WI        Donor   0.0560      3.80       67.8     7               0.212
 8 MO        Donor   0.0329      2.09       63.5     8               0.242
 9 IN        Donor   0.168       9.83       58.3     9               0.273
10 FL        Donor   0.0689      3.58       51.9    10               0.303
```

```
# i 23 more rows
# i 1 more variable: z_score <dbl>
```

```
## Get pre- and post-intervention MSPEs, ratio, and p-value
### for actual treated unit(s) only:
synth_ohio %>% grab_significance() %>%
  dplyr::filter(type=="Treated")
```

```
# A tibble: 1 x 8
  unit_name type    pre_mspe post_mspe mspe_ratio  rank fishers_exact_pvalue
  <chr>     <chr>      <dbl>     <dbl>      <dbl> <int>                <dbl>
1 OH        Treated   0.0488      1.32       27.0    12                0.364
# i 1 more variable: z_score <dbl>
```

A similar exact p-value can be computed using any other estimator. We can get this by pulling the results at each time point using `grab_synthetic_control()`. We then compare the actual estimate to the placebo estimates.

```
## Pull the synthetic control results for each time point:
SC_res <- synth_ohio %>% grab_synthetic_control(placebo=TRUE) %>%
  mutate(diff=real_y-synth_y)
SC_res
```

```
# A tibble: 792 x 6
   .id   .placebo time_unit real_y synth_y    diff
   <chr>    <dbl>     <dbl>  <dbl>   <dbl>   <dbl>
 1 OH           0       -17   0.12   0.362 -0.242
 2 OH           0       -16   0.61   0.775 -0.165
 3 OH           0       -15   1.4    1.43  -0.0346
 4 OH           0       -14   2.44   2.41   0.0294
 5 OH           0       -13   3.83   3.76   0.0732
 6 OH           0       -12   5.56   5.71  -0.149
 7 OH           0       -11   7.67   7.69  -0.0216
 8 OH           0       -10   9.44   9.50  -0.0578
 9 OH           0        -9  11.9   11.8    0.0746
10 OH           0        -8  13.9   13.8    0.0233
# i 782 more rows
```

```r
## For each time period, compute a permutation p-value
time_an <- function(time) {
  SC_res_time <- SC_res %>% dplyr::filter(time_unit==time)
  Est <- SC_res_time %>% dplyr::filter(.placebo==0) %>% pull(diff)
  P.Val <- mean(abs(SC_res_time %>% pull(diff)) >= abs(Est))
  return(c(time_unit=time,estimate=Est,p.value=P.Val))
}
by_time_res <- as_tibble(t(sapply(X=unique(SC_res %>% pull(time_unit)),
                                  FUN=time_an)))
by_time_res
```

```
# A tibble: 24 x 3
   time_unit estimate p.value
       <dbl>    <dbl>   <dbl>
 1       -17  -0.242    0.121
 2       -16  -0.165    0.576
 3       -15  -0.0346   0.939
 4       -14   0.0294   0.970
 5       -13   0.0732   0.970
 6       -12  -0.149    0.667
 7       -11  -0.0216   0.939
 8       -10  -0.0578   0.848
 9        -9   0.0746   0.848
10        -8   0.0233   1
# i 14 more rows
```

We can plot these placebo test p-values as well:

```r
ggplot(data=by_time_res) +
  geom_point(mapping=aes(x=time_unit, y=p.value), size=1.5) +
  theme_bw() +
  geom_hline(yintercept=0.05, color="red",
             linetype="dotted", size=1.3) +
  geom_vline(xintercept=0, linetype="dotted",
             linewidth=1.3) +
  scale_y_continuous(limits=c(0,1), expand=expansion(),
                     breaks=seq(0,1,by=0.2)) +
  labs(title=NULL,
       x="Weeks from Lottery Announcement",
       y="Placebo Test P-Values")
```

```
Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
i Please use `linewidth` instead.
```

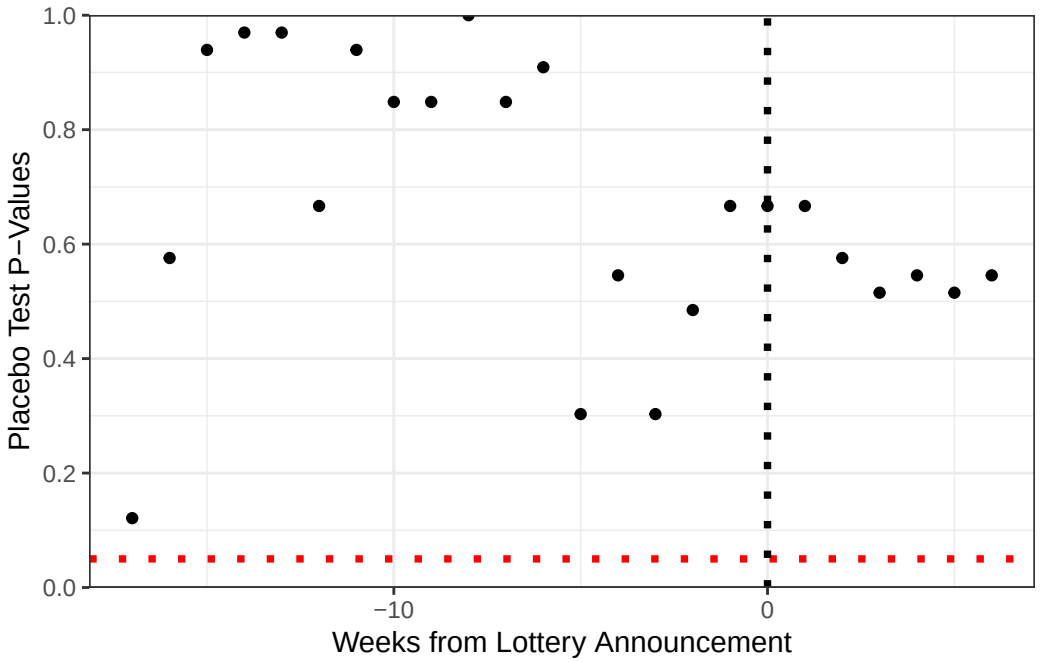


Figure 8: Placebo test p-value for estimate at each week

Discussion Questions

1. How would you interpret these results?
2. Would other specifications (outcomes, scales, etc.) be more convincing or conducive to answering the question?
3. Do the key assumptions for SC seem reasonable here? Why or why not?

Additional Analysis: Incorporating Covariates

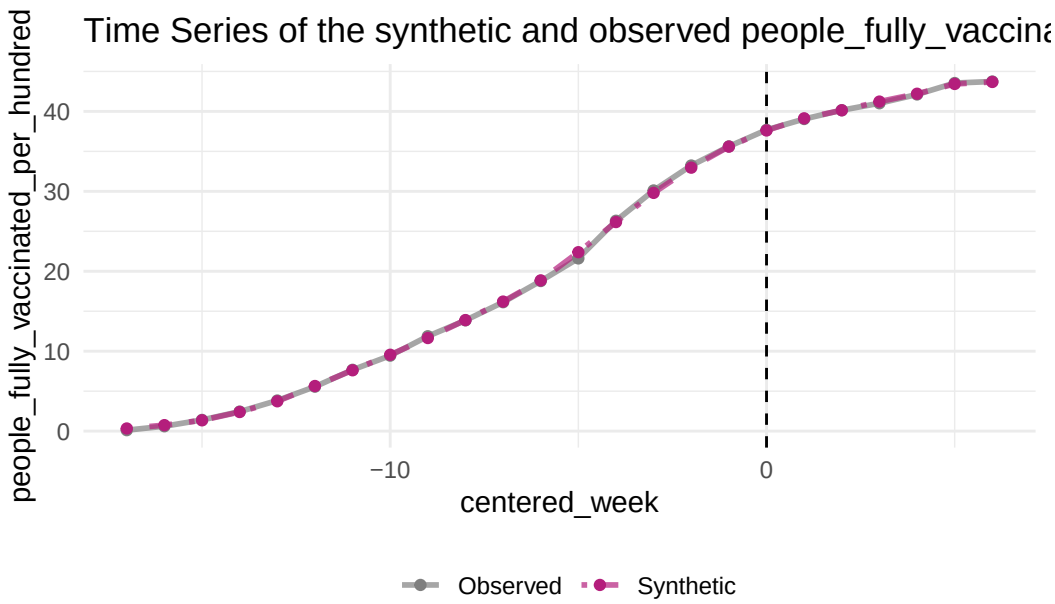
We can try another specification that incorporates some covariates other than the pre-intervention outcome itself. We will incorporate total COVID-19 cases and deaths and average daily vaccinations (per million population) in the week prior to the announcement, as well as the average weekly case and death rates in the prior month. To avoid overfitting, we will average together every four weeks of pre-intervention outcome data as covariates, but optimize covariate weights on the full pre-treatment trajectory.

```r
## Create synthetic control fit with covariates:
synth_oh_cov <- lang_0624 %>% dplyr::filter(type != "Other Lottery State") %>%
  ## initialize SC object by specifying outcome, unit variable, time variable,
  ### and when/where intervention turns on:
  synthetic_control(outcome=people_fully_vaccinated_per_hundred,
                    unit=state,
                    time=centered_week,
                    i_unit="OH",
                    i_time=0,
                    generate_placebos=T) %>%
  ## create predictors for SC model:
  ### four-week groups for outcome:
  generate_predictor(time_window=-17:-14,lag17_14=mean(people_fully_vaccinated_per_hundred,
                                                       na.rm=TRUE)) %>%
  generate_predictor(time_window=-13:-10,lag13_10=mean(people_fully_vaccinated_per_hundred,
                                                       na.rm=TRUE)) %>%
  generate_predictor(time_window=-9:-6,lag9_6=mean(people_fully_vaccinated_per_hundred,
                                                   na.rm=TRUE)) %>%
  generate_predictor(time_window=-5:-2,lag5_2=mean(people_fully_vaccinated_per_hundred,
                                                   na.rm=TRUE)) %>%
  ### outcome, case rate, death rate, and vaccination rate in week prior:
  generate_predictor(time_window=-1,
                     lag01=people_fully_vaccinated_per_hundred,
                     total_cases=tot_cases_per_million,
                     total_deaths=tot_death_per_million,
                     vax_rate=daily_vaccinations_per_million) %>%
  ### four previous week average for cases and deaths:
  generate_predictor(time_window=-5:-2,
                     recent_cases=mean(new_case_per_million,
                                       na.rm=TRUE),
                     recent_deaths=mean(new_death_per_million,
                                        na.rm=TRUE)) %>%
  ## generate SC weights on same optimization window:
  generate_weights(optimization_window=-17:-1,
                   margin_ipop = .02,sigf_ipop = 7,bound_ipop = 6) %>%
  ## run SC:
  generate_control()

### Examine fit and results:
synth_oh_cov %>% plot_weights()
```


```
synth_oh_cov %>% grab_balance_table()
```

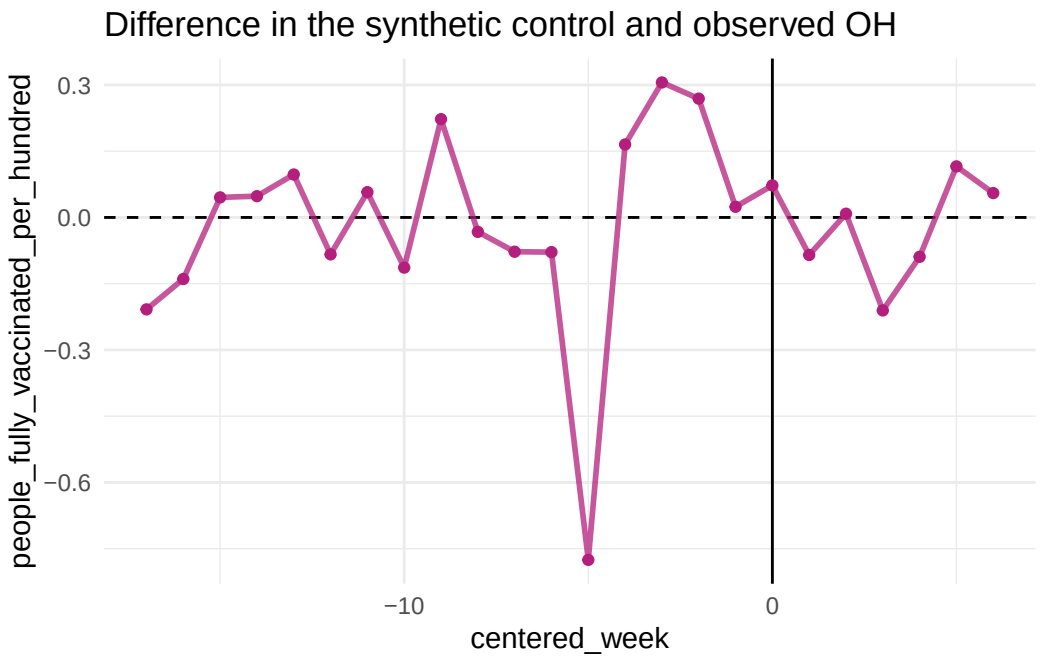
```
# A tibble: 10 x 4
   variable            OH synthetic_OH donor_sample
   <chr>            <dbl>        <dbl>        <dbl>
 1 lag17_14          1.14         1.21         1.62
 2 lag13_10          6.62         6.64         7.05
 3 lag9_6           15.2         15.2         15.4
 4 lag5_2           27.8         27.8         27.2
 5 lag01            35.6         35.6         34.1
 6 total_cases   92694.       110433.      102717.
 7 total_deaths   1662.        1665.        1637.
 8 vax_rate      36997        38907.       39114.
 9 recent_cases   1091.         902.        1159.
10 recent_deaths    13.6         12.0         10.6
```

```
synth_oh_cov %>% plot_trends()
```

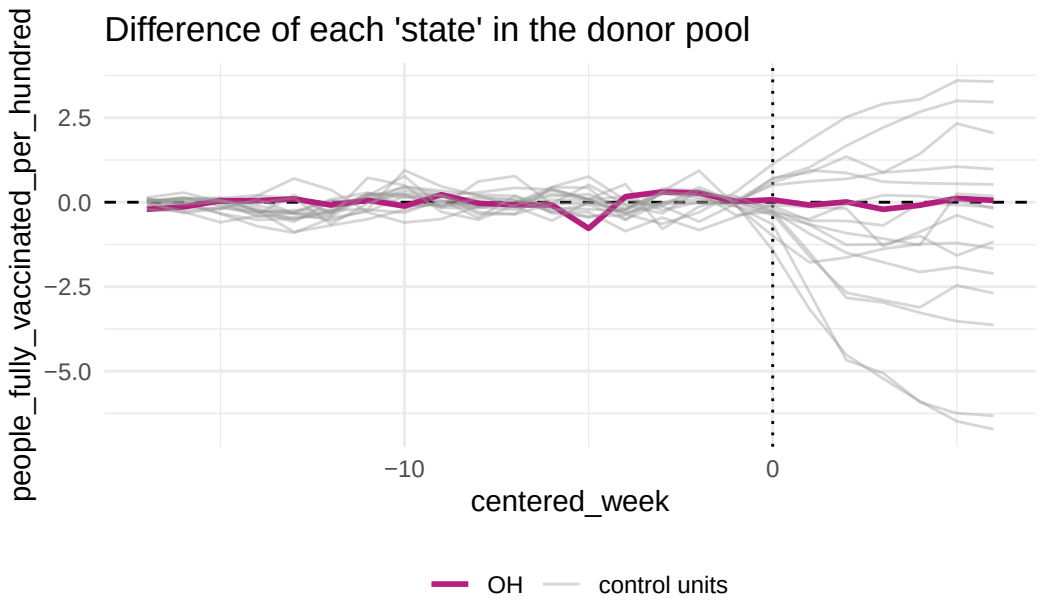


Dashed line denotes the time of the intervention.

```
synth_oh_cov %>% plot_differences()
```



```
synth_oh_cov %>% plot_placebos()
```



acebo cases with a pre−period RMSPE exceeding two times the treated unit's pre−period RMSPE.

```
synth_oh_cov %>% grab_significance() %>%
  dplyr::filter(type=="Treated")
```

```
# A tibble: 1 x 8
  unit_name type    pre_mspe post_mspe mspe_ratio  rank fishers_exact_pvalue
  <chr>     <chr>      <dbl>     <dbl>      <dbl> <int>                <dbl>
1 OH        Treated   0.0535    0.0127      0.237    33                    1
# i 1 more variable: z_score <dbl>
```

This specification has a slightly higher pre-intervention MSPE (0.053 compared to 0.049 in the initial specification), but gives an estimated effect nearly indistinguishable from 0. The control unit weights are somewhat changed, but the variable weights still place the vast majority of weight on pre-intervention outcomes.

Augmented Synthetic Control

Using `augsynth` Function

We can re-fit the Ohio SC analysis using the `augsynth` function from the `augsynth` package. By default this package uses all pre-treatment outcome variables as the predictors.

```r
### First, create a dataset with a treatment indicator:
OH_data <- lang_0624 %>%
  dplyr::filter(type2 %in% c("Ohio","Non-Lottery State")) %>%
  mutate(treated=if_else(state=="OH" & rel_week >= 0,1,0))
### Then, run the augsynth function:
OH_as <- augsynth(form=people_fully_vaccinated_per_hundred~treated, # outcome~treatment
                  unit=stateF, # units, as a factor variable
                  time=week, # time period variable
                  data=OH_data, # data set
                  progfunc="None", # fits without any outcome model
                  scm=TRUE, # fits with SC weighting
                  fixedeff=FALSE) # fits without de-meaning/intercepts
```

```
One outcome and one treatment time found. Running single_augsynth.
```

```r
## Prints average ATT estimate in post-intervention periods:
OH_as
```

```
Call:
single_augsynth(form = form, unit = !!enquo(unit), time = !!enquo(time),
    t_int = t_int, data = data, progfunc = "None", scm = TRUE,
    fixedeff = FALSE)

Average ATT Estimate: -1.024
```

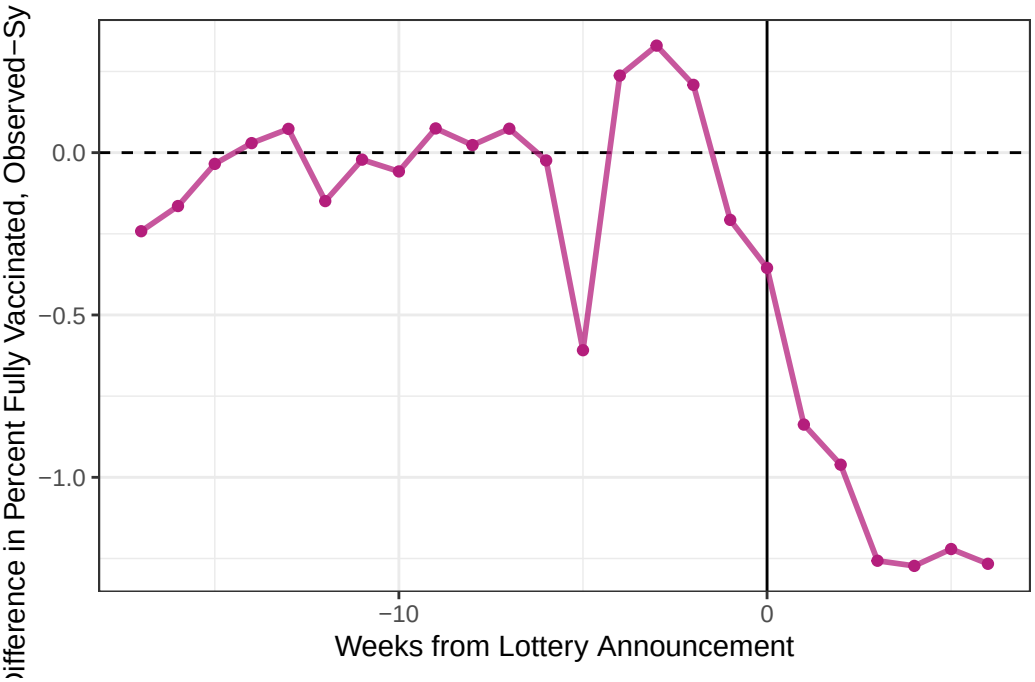
```r
## Prints estimate for each time period with conformal inference CI:
summary(OH_as)
```

```
Call:
single_augsynth(form = form, unit = !!enquo(unit), time = !!enquo(time),
    t_int = t_int, data = data, progfunc = "None", scm = TRUE,
    fixedeff = FALSE)

Average ATT Estimate (p Value for Joint Null):  -1.02   ( 0.71 )
L2 Imbalance: 0.868
Percent improvement from uniform weights: 72%

Avg Estimated Bias: NA
```

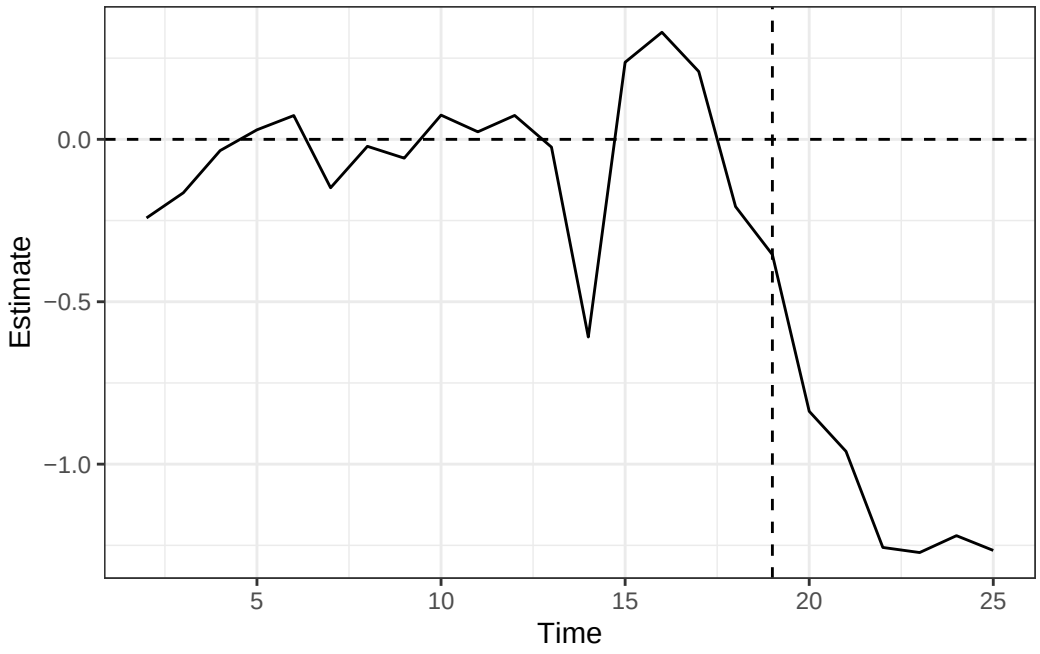
```
Inference type: Conformal inference

 Time Estimate 95% CI Lower Bound 95% CI Upper Bound p Value
   19   -0.355             -2.498              1.788   0.554
   20   -0.837             -2.980              1.306   0.505
   21   -0.961             -3.104              1.182   0.506
   22   -1.257             -3.400              0.887   0.496
   23   -1.272             -3.415              0.871   0.696
   24   -1.220             -3.363              0.923   0.740
   25   -1.266             -3.409              0.878   0.760
```

We can then compare the original SC fit from the `tidysynth` package to the `augsynth` fit with SC on but outcome model and fixed effects off. Note that the `augsynth` plot calls can take a minute to run.

```
## The original SC fit from the tidysynth package:
#| fig-cap: "Time series of the difference, Observed - Synthetic Ohio, in percent fully vacci
#| fig-alt: "Line plot that fluctuates near 0 from Week -17 to -6, is at -0.6 at Week -5, bet
synth_ohio %>% plot_differences() +
  labs(x="Weeks from Lottery Announcement",
       y="Difference in Percent Fully Vaccinated, Observed-Synthetic",
       title=NULL) +
  theme_bw()
```




```
## The new SC fit from the augsynth package:
#| fig-cap: "Time series of the difference, Observed - Synthetic Ohio, in percent fully vacci
#| fig-alt: "Line plot that is the same as the previous plot, except the x-axis goes from 0 t
plot(OH_as,
     inf=FALSE) # Suppresses plotting of conformal inference CIs
```



These plots give the same results!

In both cases, the pre-treatment fit is fairly good but not exact. We can alter the options to see different results.

We can try a ridge outcome model first:

```
### Run the augsynth fit with a ridge outcome model and SC
OH_as_r <- augsynth(form=people_fully_vaccinated_per_hundred~treated, # outcome~treatment
                    unit=stateF, # units, as a factor variable
                    time=week, # time period variable
                    data=OH_data, # data set
                    progfunc="Ridge", # fits with ridge outcome model
                    scm=TRUE, # fits with SC weighting
                    fixedeff=FALSE) # fits without de-meaning/intercepts
```

```
One outcome and one treatment time found. Running single_augsynth.
```

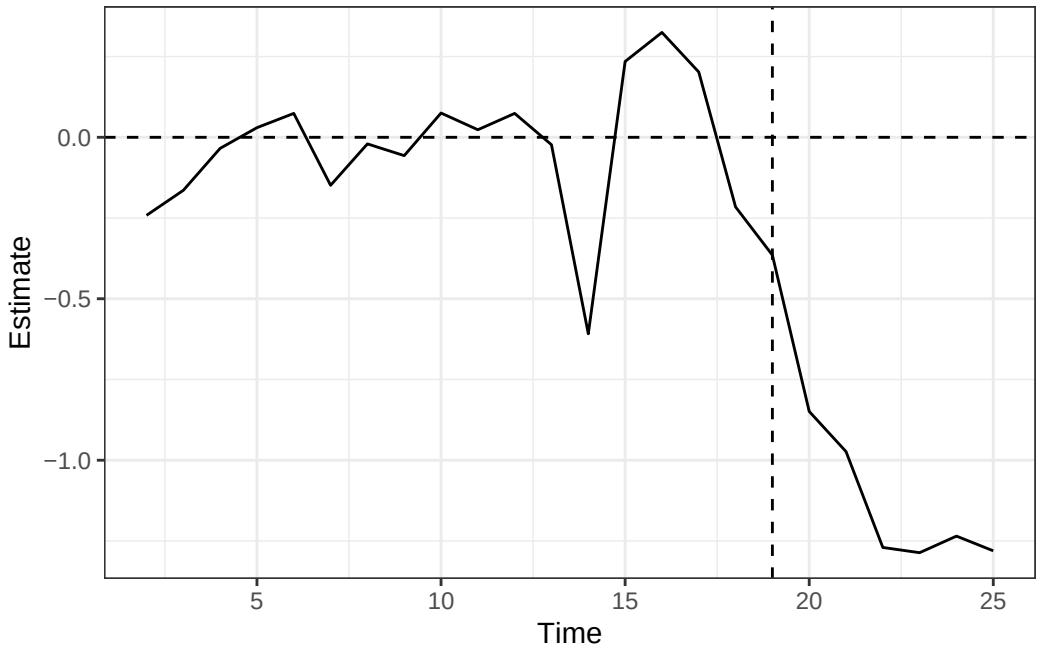
```
## Prints average ATT estimate in post-intervention periods:
OH_as_r
```

```
Call:
single_augsynth(form = form, unit = !!enquo(unit), time = !!enquo(time),
```

```
    t_int = t_int, data = data, progfunc = "Ridge", scm = TRUE,
    fixedeff = FALSE)
```

```
Average ATT Estimate: -1.037
```

```
## The ridge-adjusted SC fit from the augsynth package:
#| fig-cap: "Time series of the difference, Observed - Ridge-adjusted Synthetic Ohio, in per
#| fig-alt: "Line plot that is very similar to the previous plot."
plot(OH_as_r,
     inf=FALSE) # Suppresses plotting of conformal inference CIs
```



This is very similar to the previous fit. We can try adding unit fixed effects (de-mean or intercept-shifted SC) instead:

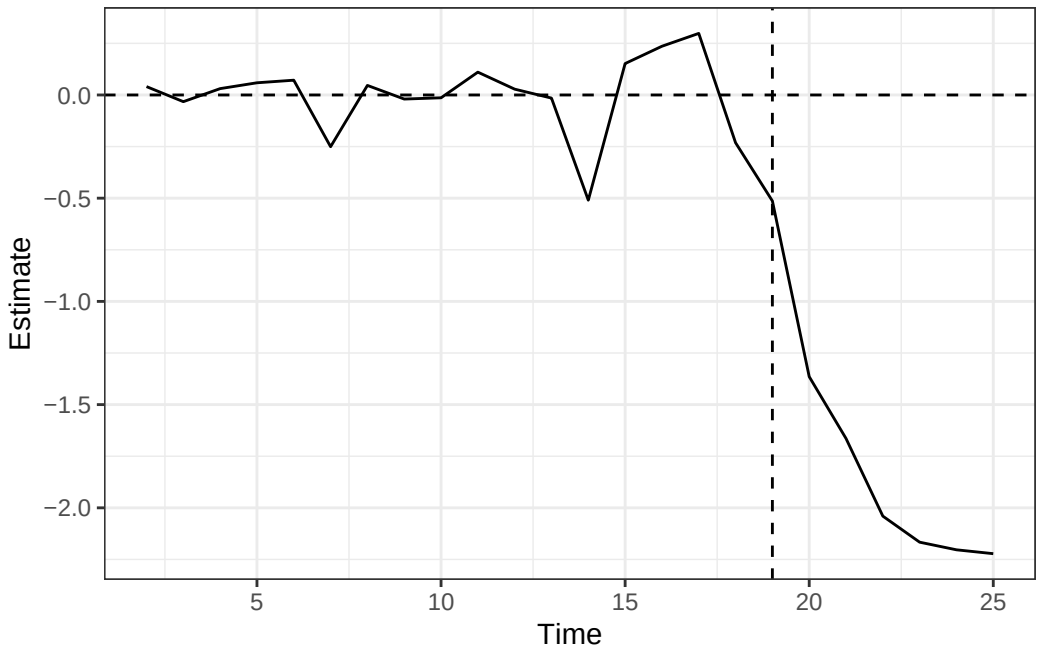
```
### Run the augsynth fit with fixed effects and no outcome model
OH_as_fe <- augsynth(form=people_fully_vaccinated_per_hundred~treated, # outcome~treatment
                     unit=stateF, # units, as a factor variable
                     time=week, # time period variable
                     data=OH_data, # data set
                     progfunc="None", # fits without outcome model
                     scm=TRUE, # fits with SC weighting
                     fixedeff=TRUE) # fits with de-meaning/intercepts
```

```
One outcome and one treatment time found. Running single_augsynth.
```

```
## Prints average ATT estimate in post-intervention periods:
OH_as_fe
```

```
Call:
single_augsynth(form = form, unit = !!enquo(unit), time = !!enquo(time),
    t_int = t_int, data = data, progfunc = "None", scm = TRUE,
    fixedeff = TRUE)

Average ATT Estimate: -1.739
```

```
## The de-meaned SC fit from the augsynth package:
#| fig-cap: "Time series of the difference, Observed - de-meaned Synthetic Ohio, in percent i
#| fig-alt: "Line plot that fluctuates near 0, never exceeding 0.5 in either direction, from
plot(OH_as_fe,
     inf=FALSE) # Suppresses plotting of conformal inference CIs
```



Some of the fluctuations are smoothed out here, as the SC fit is just matching the time trend without needing to match the level of the pre-intervention outcome. This produces a smoother and larger estimate of the intervention effect. However, this requires a different assumption: that matching de-meaned outcomes pre-intervention leads to stable weights.

Analysis of Other States

As we saw, both New Mexico and Maine implemented lotteries, but may be outside of the "convex hull" condition required for SC.

```
ggplot(data=lang_0624,
       mapping=aes(group=state, linetype=type2, color=type2,
                   alpha=type2, linewidth=type2,
                   x=last_day,y=people_fully_vaccinated_per_hundred)) +
  scale_alpha_manual(name=NULL, breaks=c("Ohio","New Mexico","Maine",
                                         "Other Lottery State",
                                         "Non-Lottery State"),
                     values=c(1,1,1,0.5,0.8)) +
  scale_linewidth_manual(name=NULL, breaks=c("Ohio","New Mexico","Maine",
                                         "Other Lottery State",
                                         "Non-Lottery State"),
                         values=c(1.3,1.3,1.3,1,1)) +
  geom_line() + theme_bw() +
  geom_vline(data=lang_0624 %>%
               dplyr::filter(type2 %in% c("Ohio","New Mexico","Maine"),
                                          rel_week==0),
             mapping=aes(xintercept=lott_date, group=type2, color=type2),
             linetype="dotted") +
  labs(x="Day (2021)", y="Percent Fully Vaccinated",
       linetype=NULL,color=NULL)
```

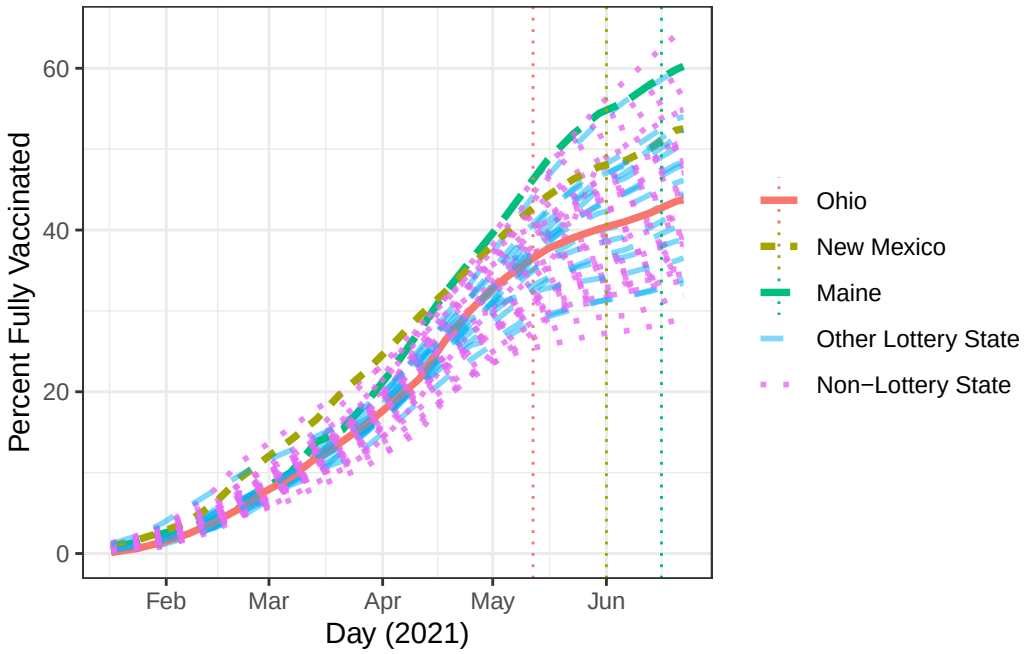


Figure 9: Plot of percent fully vaccinated rates by U.S. state, Jan.-Sept. 2021

We can create data sets for both New Mexico and Maine, and then fit various SC models.

```
## Create data set for New Mexico as treated unit:
NM_data <- lang_0624 %>%
  dplyr::filter(type2 %in% c("New Mexico","Non-Lottery State")) %>%
  mutate(treated=if_else(state=="NM" & rel_week >= 0,1,0))
## Create data set for Maine as treated unit:
ME_data <- lang_0624 %>%
  dplyr::filter(type2 %in% c("Maine","Non-Lottery State")) %>%
  mutate(treated=if_else(state=="ME" & rel_week >= 0,1,0))

## Fit standard SCs using augsynth:
NM_as <- augsynth(form=people_fully_vaccinated_per_hundred~treated,
                  unit=stateF,
                  time=week,
                  data=NM_data,
                  progfunc="None", scm=TRUE, fixedeff=FALSE)
```

```
One outcome and one treatment time found. Running single_augsynth.
```

```
ME_as <- augsynth(form=people_fully_vaccinated_per_hundred~treated,
                  unit=stateF,
                  time=week,
                  data=ME_data,
                  progfunc="None", scm=TRUE, fixedeff=FALSE)
```

```
One outcome and one treatment time found. Running single_augsynth.
```

Starting with New Mexico, we can plot the standard SC and see the weights it gives:

```
plot(NM_as,
     inf=FALSE)
```

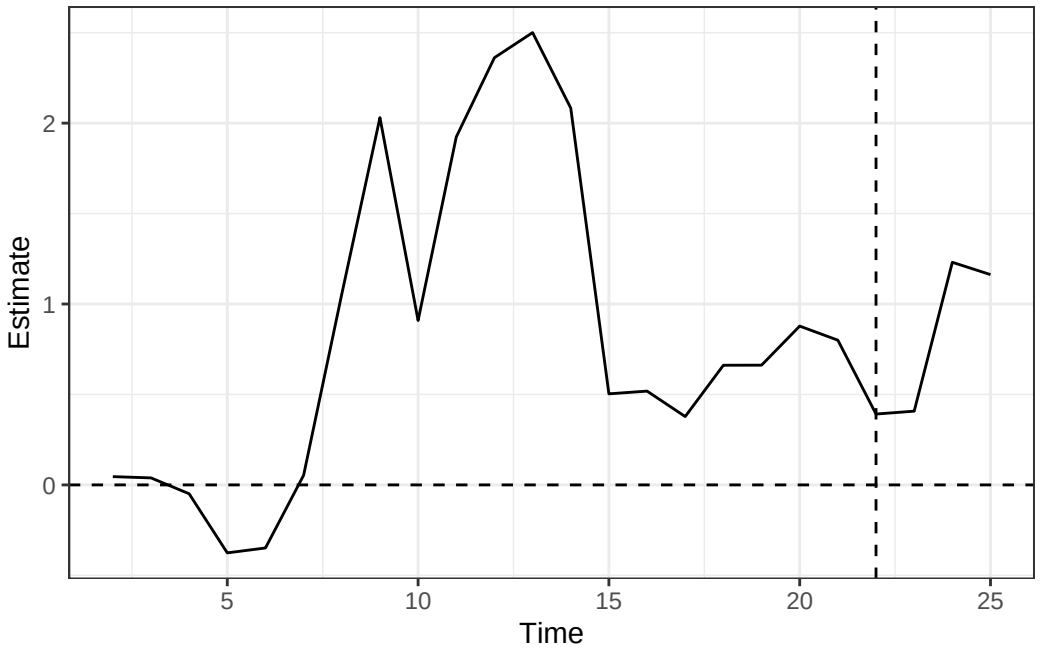


Figure 10: Time series of the difference, Observed – Synthetic New Mexico, in percent fully vaccinated rate by week, starting from the week ending 1/17/21.

```
## Create a data set with the weights and sort largest to smallest in absolute value.
NM_as_w <- tibble(State=rownames(NM_as$weights),
                  Weight=NM_as$weights[,1]) %>%
  arrange(desc(abs(Weight)))
## Print results:
NM_as_w
```

```
# A tibble: 32 x 2
   State   Weight
   <chr>    <dbl>
 1 CT     5.49e-1
 2 AK     4.48e-1
 3 SD     2.86e-3
 4 KS    -1.24e-8
 5 FL    -6.50e-9
 6 DC    -5.81e-9
 7 TX    -4.84e-9
 8 UT    -4.73e-9
 9 AZ    -4.56e-9
10 GA    -4.53e-9
# i 22 more rows
```

Clearly, the pre-treatment fit is poor here, and the synthetic control is underestimating the true outcome value because New Mexico had very high vaccination rates even before the intervention. Note that some weights appear negative but essentially round to 0.

Adding a fixed effects term will be able to center the pre-treatment fit closer to zero.

```
## Fit de-meaned SC using augsynth:
NM_as_fe <- augsynth(form=people_fully_vaccinated_per_hundred~treated,
                     unit=stateF,
                     time=week,
                     data=NM_data,
                     progfunc="None", scm=TRUE, fixedeff=TRUE)
```

```
One outcome and one treatment time found. Running single_augsynth.
```

```
plot(NM_as_fe,
     inf=FALSE)
```

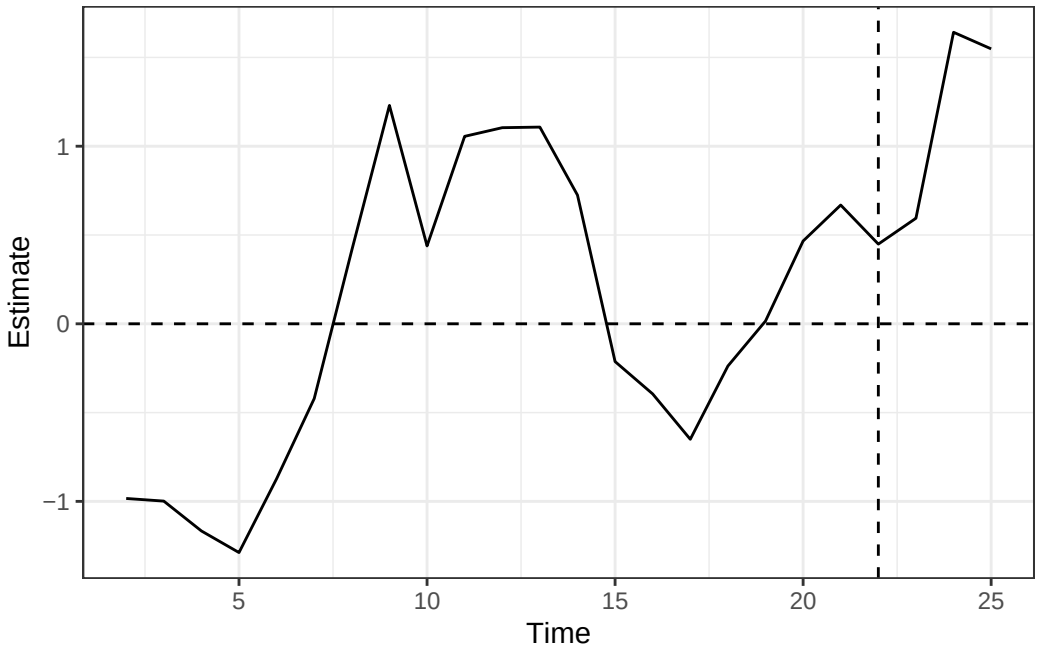


Figure 11: Time series of the difference, Observed – De-meaned Synthetic New Mexico, in percent fully vaccinated rate by week, starting from the week ending 1/17/21.

We can print the weights that come from the de-meaned SC fit. Notice there are meaningful differences from the standard SC fit weights.

```
## Create a data set with the weights and sort largest to smallest in absolute value.
NM_as_fe_w <- tibble(State=rownames(NM_as_fe$weights),
                     Weight=NM_as_fe$weights[,1]) %>%
  arrange(desc(abs(Weight)))
## Print results:
NM_as_fe_w
```

```
# A tibble: 32 x 2
   State   Weight
   <chr>    <dbl>
 1 CT     3.83e-1
 2 SD     3.51e-1
 3 AK     2.33e-1
 4 RI     3.27e-2
 5 KS    -6.58e-9
 6 FL    -5.88e-9
 7 TX    -4.94e-9
```

```
 8 UT    -4.52e-9
 9 GA    -4.02e-9
10 MO    -3.95e-9
# i 22 more rows
```

There remain large fluctuations in the pre-treatment fit. A ridge outcome model may be able to de-bias these fluctuations.

```
## Fit ridge-adjusted SC using augsynth:
NM_as_r <- augsynth(form=people_fully_vaccinated_per_hundred~treated,
                    unit=stateF,
                    time=week,
                    data=NM_data,
                    progfunc="Ridge", scm=TRUE, fixedeff=FALSE)
```

```
One outcome and one treatment time found. Running single_augsynth.
```

```
plot(NM_as_r,
     inf=FALSE)
```

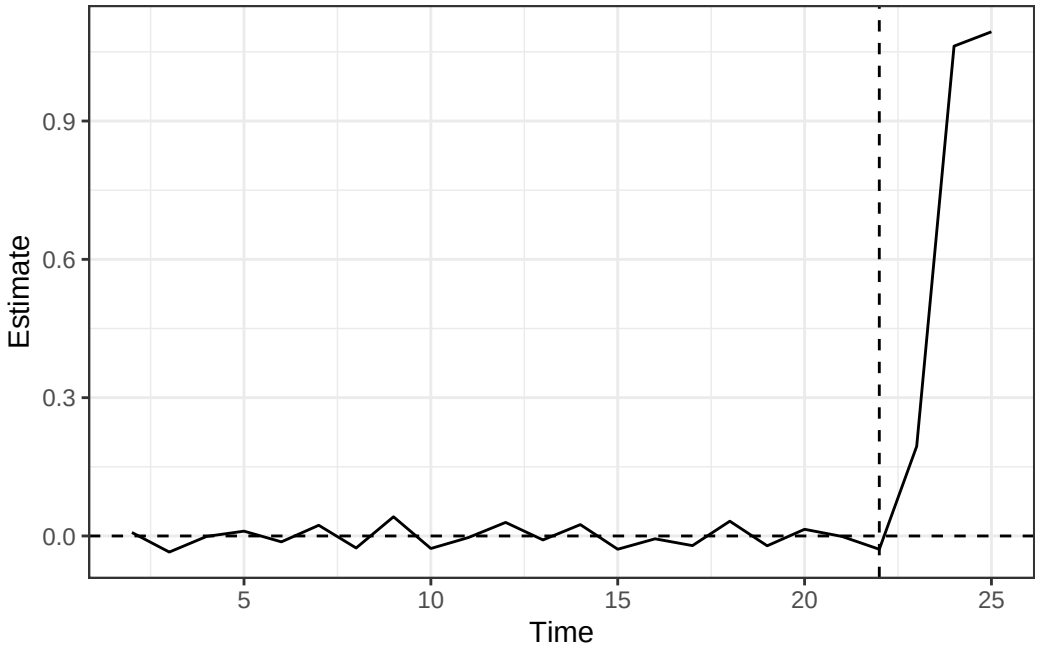


Figure 12: Time series of the difference, Observed – Ridge-adjusted Synthetic New Mexico, in percent fully vaccinated rate by week, starting from the week ending 1/17/21.

We can print the weights that come from the ridge-augmented SC fit. Notice there are meaningful differences from the previous weights and now there are states that get non-negligible negative weights.

```
## Create a data set with the weights and sort largest to smallest in absolute value.
NM_as_r_w <- tibble(State=rownames(NM_as_r$weights),
                    Weight=NM_as_r$weights[,1]) %>%
  arrange(desc(abs(Weight)))
## Print results:
NM_as_r_w
```

```
# A tibble: 32 x 2
   State Weight
   <chr>  <dbl>
 1 UT    -0.328
 2 RI     0.318
 3 HI     0.305
 4 SD     0.296
 5 IN     0.285
 6 KS    -0.266
 7 AK     0.235
 8 PA    -0.226
 9 CT     0.151
10 FL     0.150
# i 22 more rows
```

Turning now to Maine, we can plot the standard SC:

```
plot(ME_as,
     inf=FALSE)
```

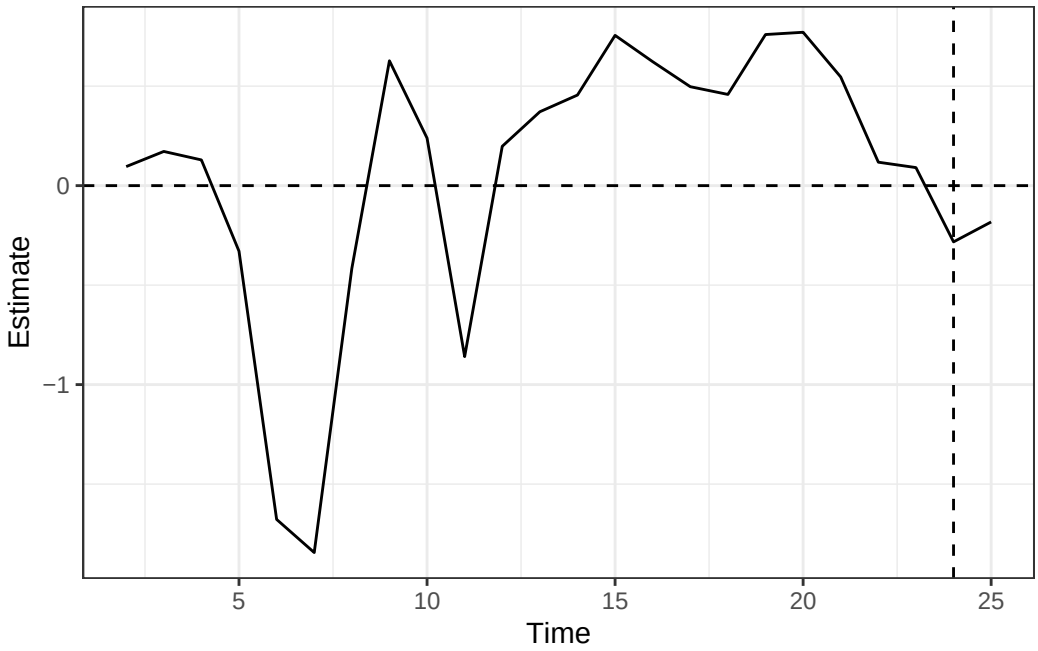


Figure 13: Time series of the difference, Observed – Synthetic Maine, in percent fully vaccinated rate by week, starting from the week ending 1/17/21.

Clearly, again, the pre-treatment fit is poor, with overestimation early on and underestimation closer to the start of treatment.

Since the pre-treatment gaps are roughly centered around 0, adding a fixed effects term will not have much effect.

```
## Fit de-meaned SC using augsynth:
ME_as_fe <- augsynth(form=people_fully_vaccinated_per_hundred~treated,
                     unit=stateF,
                     time=week,
                     data=ME_data,
                     progfunc="None", scm=TRUE, fixedeff=TRUE)
```

```
One outcome and one treatment time found. Running single_augsynth.
```

```
plot(ME_as_fe,
     inf=FALSE)
```

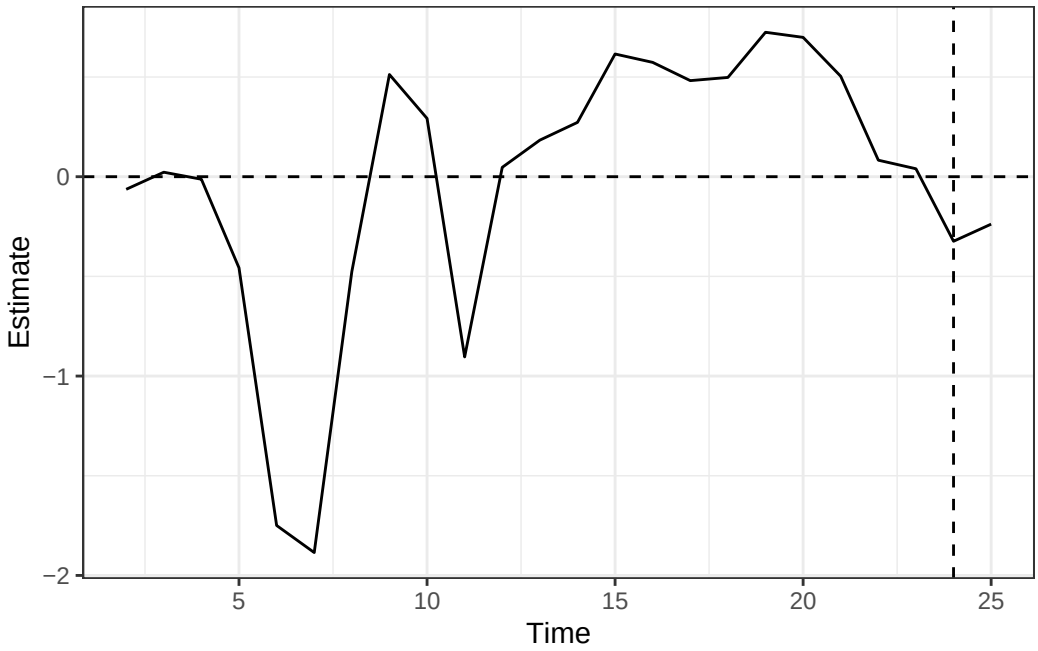


Figure 14: Time series of the difference, Observed – De-meaned Synthetic Maine, in percent fully vaccinated rate by week, starting from the week ending 1/17/21.

A ridge outcome model may be more useful here to de-bias the fluctuations.

```
## Fit ridge-adjusted SC using augsynth:
ME_as_r <- augsynth(form=people_fully_vaccinated_per_hundred~treated,
                    unit=stateF,
                    time=week,
                    data=ME_data,
                    progfunc="Ridge", scm=TRUE, fixedeff=FALSE)
```

```
One outcome and one treatment time found. Running single_augsynth.
```

```
plot(ME_as_r,
     inf=FALSE)
```

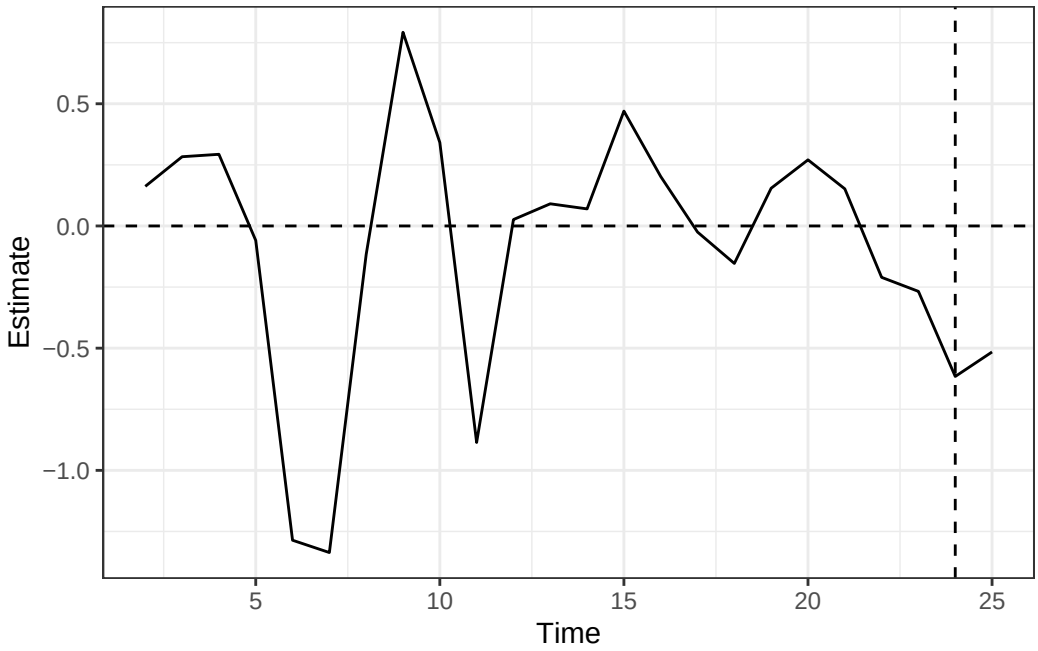


Figure 15: Time series of the difference, Observed – Ridge-adjusted Synthetic Maine, in percent fully vaccinated rate by week, starting from the week ending 1/17/21.

The ridge adjustment may be more useful if it is not capturing the fixed effects as well, so we can use both unit fixed effects and a ridge outcome model.

```
## Fit de-meaned and ridge-adjusted SC using augsynth:
ME_as_r_fe <- augsynth(form=people_fully_vaccinated_per_hundred~treated,
                   unit=stateF,
                   time=week,
                   data=ME_data,
                   progfunc="Ridge", scm=TRUE, fixedeff=TRUE)
```

```
One outcome and one treatment time found. Running single_augsynth.
```

```
plot(ME_as_r_fe,
     inf=FALSE)
```

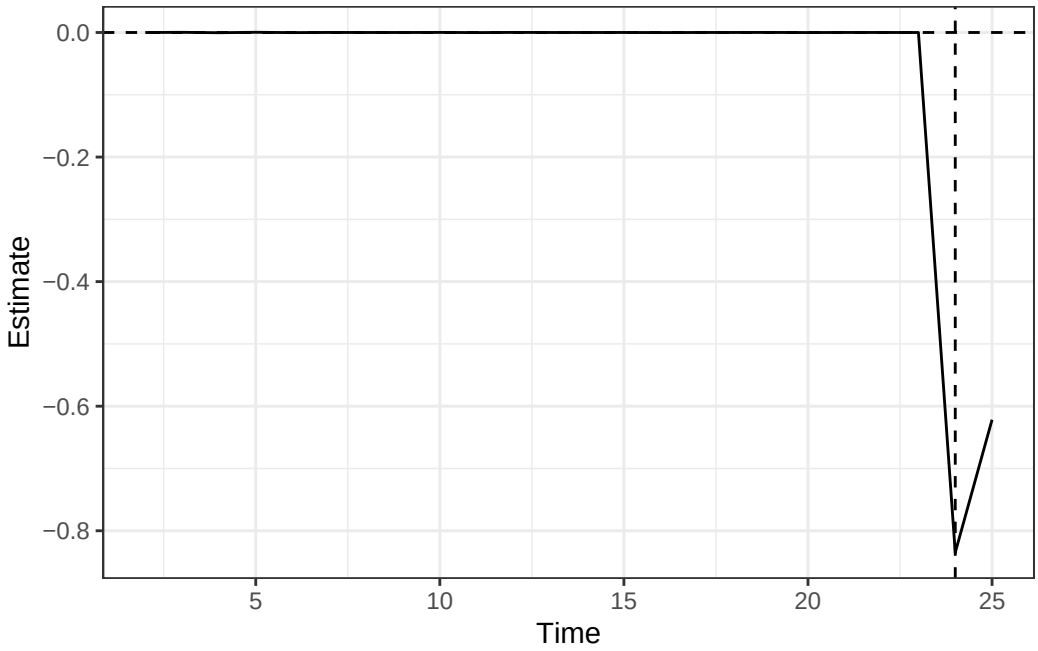


Figure 16: Time series of the difference, Observed – De-meaned and Ridge-adjusted Synthetic Maine, in percent fully vaccinated rate by week, starting from the week ending 1/17/21.

Clearly, this achieves an excellent pre-treatment fit, but it may in fact be over-fitting the data. The assumptions should be carefully considered in this model.

Another option is to fit the generalized SCM using the `gsynth` package. We first need to install and load the package.

```
# install.packages("gsynth") # Run once if not yet installed
library(gsynth)
```

```
## Syntax has been updated since v.1.2.0.
```

```
## Comments and suggestions -> yiqingxu@stanford.edu.
```

```
## Then we can fit the model using the GSYN option for progfunc:
ME_gsynth <- augsynth(form=people_fully_vaccinated_per_hundred~treated,
                  unit=stateF,
                  time=week,
                  data=ME_data,
                  progfunc="GSYN")
```

```
One outcome and one treatment time found. Running single_augsynth.


Cross-validating ...
 r = 0; sigma2 = 11.66101; IC = 2.93204; PC = 10.82591; MSPE = 31.94484
 r = 1; sigma2 = 1.40596; IC = 1.27501; PC = 2.46655; MSPE = 0.41149
 r = 2; sigma2 = 0.45730; IC = 0.59305; PC = 1.18116; MSPE = 0.21866
 r = 3; sigma2 = 0.25203; IC = 0.42115; PC = 0.86045; MSPE = 0.14212*
 r = 4; sigma2 = 0.15892; IC = 0.36661; PC = 0.67508; MSPE = 0.31365
 r = 5; sigma2 = 0.11782; IC = 0.45662; PC = 0.59902; MSPE = 0.73545

 r* = 3
```

```
plot(ME_gsynth,
     inf=FALSE)
```

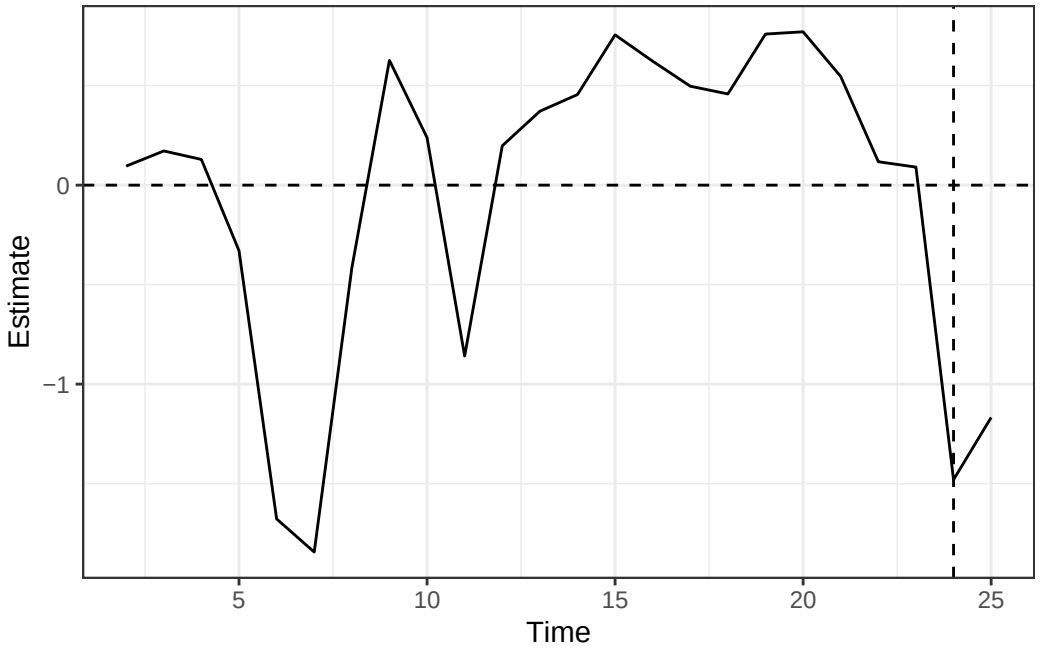


Figure 17: Time series of the difference, Observed – Generalized Synthetic Maine, in percent fully vaccinated rate by week, starting from the week ending 1/17/21.

Again, different assumptions are being made here, and should be carefully considered. This appears more similar to the initial SC fit, however it has a larger effect estimate.

Discussion Questions

1. Are the trade-offs of ASCM worthwhile for these other states?

Staggered Adoption

Finally, we can consider the multi-period, multi-unit staggered adoption case with the augmented synthetic control. We first set up the full data set by adding a treatment indicator variable, and then fit it using `augsynth`. Note that this defaults to including two-way fixed effects, balancing all pre-intervention periods, and partially pools the average and individual SC fits using the heuristic given by Ben-Michael et al. (2022).

```
## Create data set with indicator for treatment
Mult_data <- lang_0624 %>%
  mutate(treated=if_else(!lottery,0,if_else(rel_week>=0,1,0)))
## Fit augmented SC on full data set:
Mult_as <- augsynth(form=people_fully_vaccinated_per_hundred~treated,
                    unit=stateF,
                    time=week,
                    data=Mult_data)
```

```
More than one treatment time found. Running multisynth.
```

```
## Print results and summary:
Mult_as
```

```

Call:
multisynth(form = form, unit = !!enquo(unit), time = !!enquo(time),
    data = data)

Average ATT Estimate: -0.170
```

```
summary(Mult_as)
```

```

Call:
multisynth(form = form, unit = !!enquo(unit), time = !!enquo(time),
    data = data)
```

```
Average ATT Estimate (Std. Error): -0.170  (2.462)

Global L2 Imbalance: 0.034
Scaled Global L2 Imbalance: 0.042
Percent improvement from uniform global weights: 95.8

Individual L2 Imbalance: 0.386
Scaled Individual L2 Imbalance: 0.112
Percent improvement from uniform individual weights: 88.8

 Time Since Treatment   Level   Estimate Std.Error lower_bound upper_bound
                    0 Average -0.1157730  2.378888   -4.309502    4.812574
                    1 Average -0.2238981  2.549177   -4.761370    5.070716
```

The average effect is estimated to be -0.170, increasing from -0.115 in the first treated period to -0.224 in the second, although there are large standard errors throughout. We can plot the fit, which defaults to plotting all individual fits and the average:

```
plot(Mult_as)
```

```
Joining with `by = join_by(Level)`

Warning: The `<scale>` argument of `guides()` cannot be `FALSE`. Use "none" instead as
of ggplot2 3.3.4.
i The deprecated feature was likely used in the augsynth package.
  Please report the issue to the authors.

Warning: Removed 57 rows containing missing values or values outside the scale range
(`geom_line()`).

Warning: Removed 57 rows containing missing values or values outside the scale range
(`geom_point()`).

Warning: ggrepel: 15 unlabeled data points (too many overlaps). Consider
increasing max.overlaps
```

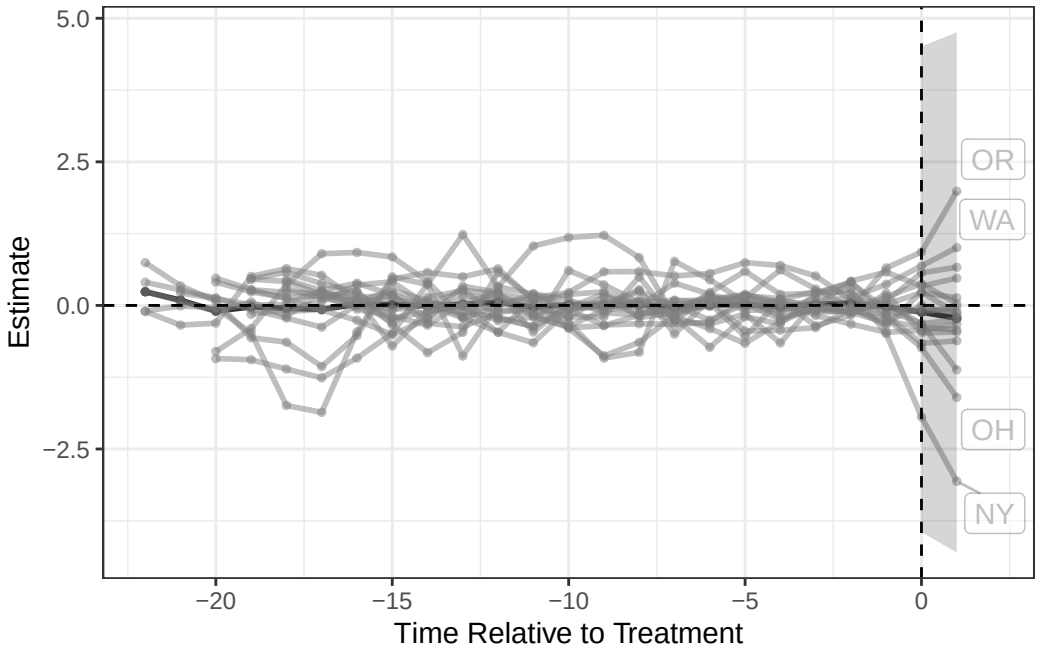


Figure 18: Time series of the difference in fully vaccinated percentage using staggered adoption synthetic control estimates for treated states, by time relative to intervention.