

# Staggered Adoption DID Analysis: COVID-19 Vaccine Mandates

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## Setting and Data

The concept of this analysis is based on that in [Rains and Richards \(2024\)](#). The authors seek to understand the effect of COVID-19 vaccine mandates for state employees, which were implemented in 20 U.S. states, beginning on different dates in August–October 2021 ([Ballotpedia](#)). The vaccination data used are from the [CDC’s COVID Vaccination Trends](#) data set. Note that the data might vary somewhat from that in the Rains and Richards (2024) [replication files](#).

The goal of the analysis is to test the hypothesis that the state mandates increased either the number of first vaccinations in the state or the proportion of the state’s adult population that was fully vaccinated. Although not used by Rains and Richards (2024), we use non-mandate states as controls.

The data are available in the `mandate.Rda` file. `Vax_weekly` contains the full data set, by state and summarized by MMWR week, for January 2021 through May 2023, for two variables: `SCP` has the proportion of the adult population that has a complete vaccination series and `D1P` has the proportion of the adult population with at least one dose. The weekly increments are in the `_diff` variables. Information on the mandate for each start are in the `Mandate_Start`, `ever_mandate`, and `mandate` variables, and lead/lag information by week is in `Wks_mandate` and `LeadLag`.

First, load the data into R.

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

## Libraries

Again, we will use `tidyverse` and `knitr` for general coding and `lme4` for clustered TWFE models. [Roth et al. \(2023\)](#) has a summary table with R packages that implement advanced DID methods. We will use three of them:

1. `bacondecomp` implements the decomposition from [Goodman-Bacon \(2021\)](#);
2. `did2s`, described in [Butts and Gardner \(2022\)](#), implements the two-stage DID approach of [Gardner \(2021\)](#), as well as many other proposed methods including the dynamic specification of [Borusyak et al. \(2024\)](#), the IW estimator of [Sun and Abraham \(2021\)](#), and the aggregated approach of [Callaway and Sant'Anna \(2021\)](#); and
3. `DIDmultiplegt` implements the first-difference approach of [de Chaisemartin and d'Haultfoeuille \(2020\)](#) (if you're on a Mac, you may need to install `Xcode` from the App Store or `XQuartz` first and re-start R). Versions of this approach that can handle a wider array of settings, laid out in [de Chaisemartin and d'Haultfoeuille \(2023\)](#) and [de Chaisemartin and d'Haultfoeuille \(2024\)](#), along with sped-up analytic standard errors are implemented in the `DIDmultiplegtDYN`, which requires Java for installation.

We now load the required libraries.

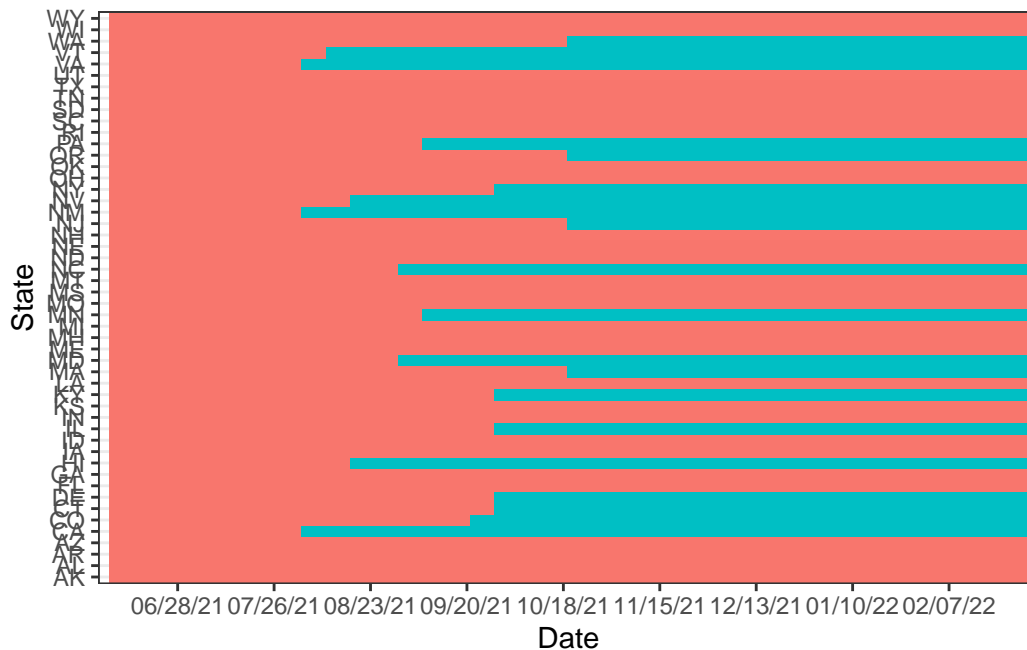
```
## If you have not installed these packages before,  
## run the following line:  
# install.packages(c("bacondecomp","did2s","DIDmultiplegt"))  
## Either way, load the libraries:  
library(tidyverse)  
library(knitr)  
library(lme4)  
library(bacondecomp)  
library(did2s)  
library(DIDmultiplegt)
```

## Graphical Exploration

We begin by plotting the time series for visual inspection. First, we plot a timeline of the mandate times.

```
## Plot time series of mandates themselves:  
#| fig-cap: "Plot of state employee vaccination mandate timings, U.S. states, June 2021-February 2022"  
#| fig-alt: "A bar plot with bars for each state over the time range specified, with twenty states in each group"  
ggplot(data=Vax_weekly,  
       mapping=aes(x=End_Date,y=State, fill=mandate)) +  
  geom_tile(width=8) +  
  scale_x_date(name="Date", date_breaks="4 weeks", expand=c(0,0),  
              limits=c(as.Date("2021-06-05"),as.Date("2022-03-05")),  
              date_labels="%m/%d/%y") +  
  theme_bw() + guides(fill="none")
```

Warning: Removed 4250 rows containing missing values or values outside the scale range (`geom\_tile()`).



We can then plot the time series of the outcomes by state, noting which states implement a mandate and when.

```
## Get lists of the states in the data and the states with a mandate at some point
states <- unique(Vax_weekly %>% pull(State))
mandate_states <- unique(Vax_weekly %>%
  dplyr::filter(mandate) %>% pull(State))
```

```
## Plot time series of first-dose proportion by state:
#| fig-cap: "Plot of the proportion of U.S. adults with at least one COVID-19 vaccine dose, 1
#| fig-alt: "A line plot with lines for each state for dates from June 2021 to February 2022
ggplot() +
  geom_line(data=Vax_weekly %>%
    dplyr::filter(!(State %in% mandate_states)),
    mapping=aes(x=End_Date, y=D1P, group=State),
    color="grey50", linetype="dashed") +
  geom_line(data=Vax_weekly %>%
    dplyr::filter(State %in% mandate_states),
    mapping=aes(x=End_Date, y=D1P, group=State,
      color=mandate),
```

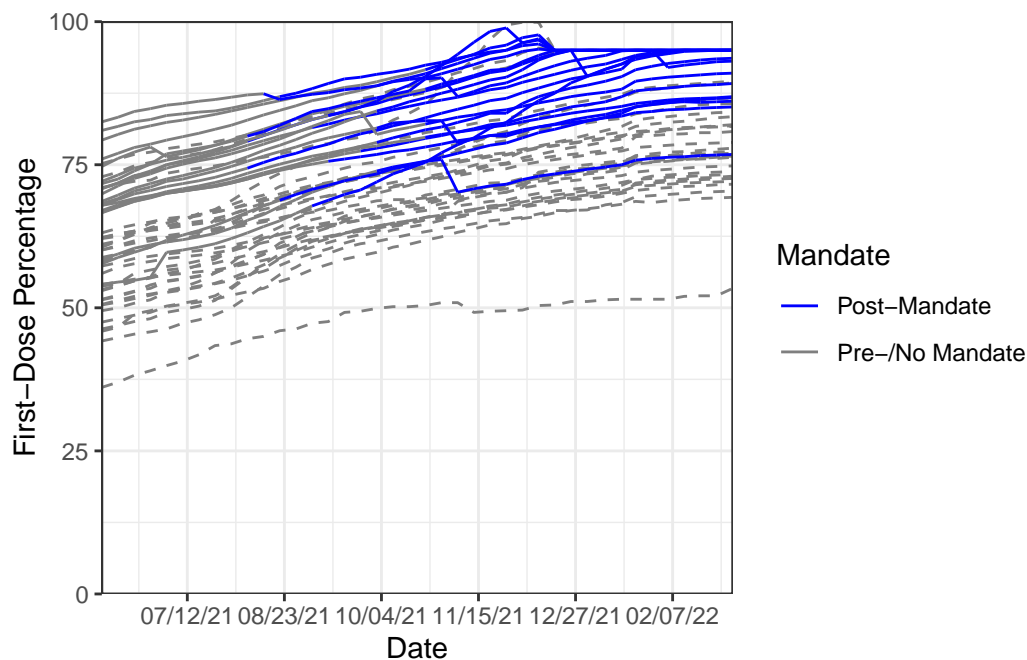
```

    linetype="solid") +
  scale_color_manual(name="Mandate",
    breaks=c(TRUE,FALSE),
    values=c("blue","grey50"),
    labels=c("Post-Mandate","Pre-/No Mandate")) +
  scale_y_continuous(name="First-Dose Percentage",
    limits=c(0,100), expand=c(0,0)) +
  scale_x_date(name="Date", date_breaks="6 weeks",
    expand=c(0,0),
    limits=c(as.Date("2021-06-05"),as.Date("2022-03-05")),
    date_labels="%m/%d/%y") +
  theme_bw()

```

Warning: Removed 2490 rows containing missing values or values outside the scale range (`geom\_line()`).

Warning: Removed 1660 rows containing missing values or values outside the scale range (`geom\_line()`).



Several states appear to have implausible declines or rates at 100. We can identify data errors that explain some of these peculiarities, e.g. [New Hampshire](#), [Pennsylvania](#), and [Washington](#). We will exclude these three states from the analysis, but a full analysis should examine the

other states as well. We will also limit the analysis weeks to 2021, MMWR weeks 25–42 to both be more focused on timing around the implementation of mandates and exclude some data errors found at other times.

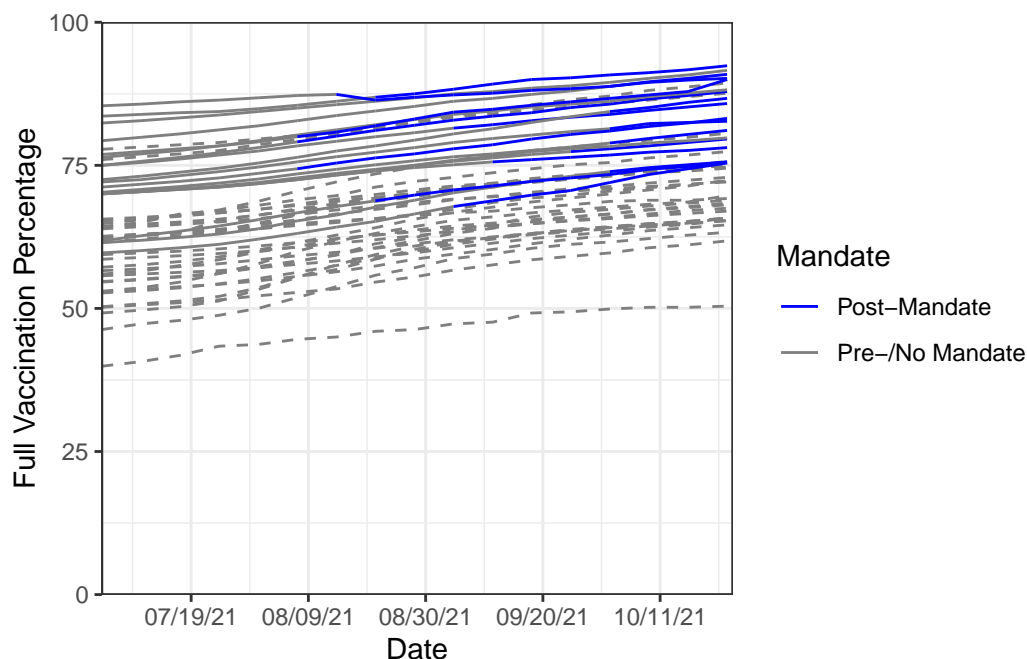
```
## Exclude New Hampshire, Pennsylvania, Washington:
Vax_adj <- Vax_weekly %>%
  dplyr::filter(!(State %in% c("NH","PA","WA")))
## Select weeks for analysis:
Yr_Wk_Sel <- paste0("2021_",(25:42))
```

We re-plot on this adjusted group of states and weeks.

```
## Plot time series of first-dose proportion by state in smaller time window:
#| fig-cap: "Plot of the proportion of U.S. adults with at least one COVID-19 vaccine dose, 1
#| fig-alt: "A line plot with lines for each state for dates from July 2021 to October 2021, 1
ggplot() +
  geom_line(data=Vax_adj %>%
    dplyr::filter(!(State %in% mandate_states),
      Yr_Wk %in% Yr_Wk_Sel),
    mapping=aes(x=End_Date, y=D1P, group=State),
    color="grey50", linetype="dashed") +
  geom_line(data=Vax_adj %>%
    dplyr::filter(State %in% mandate_states,
      Yr_Wk %in% Yr_Wk_Sel),
    mapping=aes(x=End_Date, y=D1P, group=State,
      color=mandate),
    linetype="solid") +
  scale_color_manual(name="Mandate",
    breaks=c(TRUE,FALSE),
    values=c("blue","grey50"),
    labels=c("Post-Mandate","Pre-/No Mandate")) +
  scale_y_continuous(name="Full Vaccination Percentage",
    limits=c(0,100), expand=c(0,0)) +
  scale_x_date(name="Date", date_breaks="3 weeks", expand=c(0,0),
    limits=c(as.Date("2021-07-03"),as.Date("2021-10-24")),
    date_labels="%m/%d/%y") +
  theme_bw()
```

Warning: Removed 29 rows containing missing values or values outside the scale range (`geom\_line()`).

Warning: Removed 18 rows containing missing values or values outside the scale range (`geom\_line()`).



Similar plotting and analyses could be done on the complete series percentage by replacing D1P in the above code by SCP.

## Discussion Questions

1. Is one outcome (first-dose vs. full vaccination percentage) better suited to answering the question of interest than the other? Which is more likely to have a noticeable effect?
2. Does parallel trends seem like a reasonable assumption here? What might cause non-parallel trends?
3. Is checking parallel pre-trends a good justification for parallel trends post-intervention here? What might change the relationship between trends over time?
4. What forms of effect heterogeneity may be present in this staggered adoption setting?

## TWFE Models

First, we fit TWFE models (using `lmer` to get clustered confidence intervals), the so-called “static” specification. We fit it once with just the fixed effects, and once adding `D1P_prior` as a covariate.

```
## Fit TWFE model with no covariates:
TWFE_D1P <- lmer(D1P~factor(MMWR_week)+State+mandate+(1|State),
  data=Vax_weekly %>%
  dplyr::filter(Yr_Wk %in% Yr_Wk_Sel))
## Get 95% CI:
TWFE_D1P_CI <- confint(TWFE_D1P, parm="mandateTRUE", level=0.95)
```

Computing profile confidence intervals ...

```
## Fit TWFE model with prior-week as covariate:
TWFE_D1P_ctrl <- lmer(D1P~D1P_prior+factor(MMWR_week)+State+
  mandate+(1|State),
  data=Vax_weekly %>%
  dplyr::filter(Yr_Wk %in% Yr_Wk_Sel))
TWFE_D1P_ctrl_CI <- confint(TWFE_D1P_ctrl,
  parm="mandateTRUE", level=0.95)
```

Computing profile confidence intervals ...

```
## Summarize results from the two models:
TWFE_results <- tibble(Model=c("Fixed Effects Only",
  "Fixed Effects + Prior Week Value"),
  Estimate=format(c(summary(TWFE_D1P)$coefficients["mandateTRUE"],"Estimate",
    summary(TWFE_D1P_ctrl)$coefficients["mandateTRUE"],"Estimate"),
  `95% CI`=c(paste(format(TWFE_D1P_CI["mandateTRUE"],), digits=3, nsmall=1),
    paste(format(TWFE_D1P_ctrl_CI["mandateTRUE"],), digits=3, nsmall=1))

## Print the formatted table:
knitr::kable(TWFE_results,
  caption="Table 1. Results from TWFE models on first-dose percentage.")
```

Table 1: Table 1. Results from TWFE models on first-dose percentage.

Model	Estimate	95% CI
Fixed Effects Only	-0.3803	-0.6869, -0.0738
Fixed Effects + Prior Week Value	0.0208	-0.0659, 0.1074

The two models give diverging results, with fairly large confidence intervals, leading to no clear conclusion. The estimates are hard to interpret as well given the changing circumstances of the states involved.

## Goodman-Bacon Decomposition

We can conduct the Goodman-Bacon decomposition of the TWFE model to identify the weights given to different comparisons.

```
## Conduct the decomposition and print summary:
bacon <- bacon(D1P~mandate,
              data=Vax_adj %>%
                dplyr::filter(Yr_Wk %in% Yr_Wk_Sel),
              id_var="State",
              time_var="MMWR_week")
```

	type	weight	avg_est
1	Earlier vs Later Treated	0.14186	0.03461
2	Later vs Earlier Treated	0.05819	0.01646
3	Treated vs Untreated	0.79995	-0.61141

```
## Full decomposition:
```

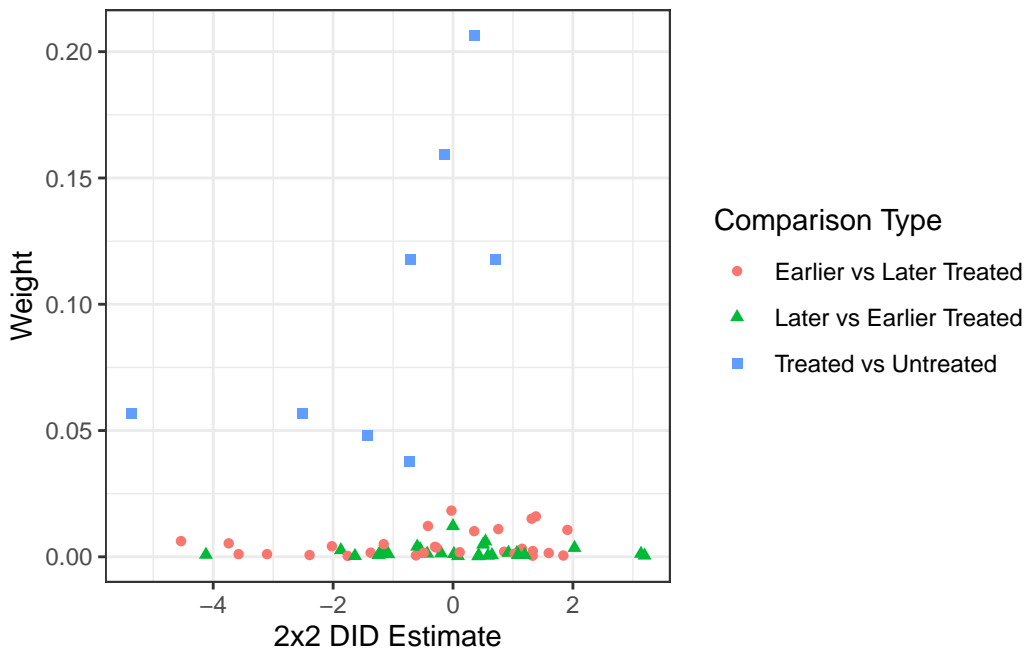
```
bacon
```

	treated	untreated		estimate	weight	type
2	31	99999	-0.1401340996	0.1591059182		Treated vs Untreated
3	38	99999	-1.4331034483	0.0478790958		Treated vs Untreated
4	39	99999	0.3643349754	0.2062484125		Treated vs Untreated
5	33	99999	-0.7011206897	0.1178562357		Treated vs Untreated
6	42	99999	-0.7325219743	0.0375666751		Treated vs Untreated
7	35	99999	0.7076293103	0.1178562357		Treated vs Untreated
8	36	99999	-2.5052843708	0.0567183134		Treated vs Untreated
9	32	99999	-5.3682937752	0.0567183134		Treated vs Untreated
12	38	31	-1.1695238095	0.0026670053		Later vs Earlier Treated
13	39	31	-0.0008333333	0.0121920244		Later vs Earlier Treated
14	33	31	-0.5483333333	0.0030480061		Later vs Earlier Treated
15	42	31	-1.1666666667	0.0025146050		Later vs Earlier Treated
16	35	31	0.5020833333	0.0048768098		Later vs Earlier Treated
17	36	31	-1.8704761905	0.0026670053		Later vs Earlier Treated
18	32	31	-4.1212121212	0.0008382017		Later vs Earlier Treated
20	31	38	1.1515873016	0.0032004064		Earlier vs Later Treated
22	39	38	0.4300000000	0.0005080010		Later vs Earlier Treated
23	33	38	0.8525000000	0.0020320041		Earlier vs Later Treated
24	42	38	0.0833333333	0.0003048006		Later vs Earlier Treated
25	35	38	1.5966666667	0.0015240030		Earlier vs Later Treated



26	36	38	-0.6181818182	0.0005588011	Earlier vs Later	Treated
27	32	38	-3.1023809524	0.0010668021	Earlier vs Later	Treated
29	31	39	-0.0263888889	0.0182880366	Earlier vs Later	Treated
30	38	39	-1.3738461538	0.0016510033	Earlier vs Later	Treated
32	33	39	-0.4183333333	0.0121920244	Earlier vs Later	Treated
33	42	39	0.0155555556	0.0011430023	Later vs Earlier	Treated
34	35	39	0.3530000000	0.0101600203	Earlier vs Later	Treated
35	36	39	-2.0200000000	0.0041910084	Earlier vs Later	Treated
36	32	39	-4.5371428571	0.0062230124	Earlier vs Later	Treated
38	31	33	0.1111111111	0.0018288037	Earlier vs Later	Treated
39	38	33	-0.4300000000	0.0012700025	Later vs Earlier	Treated
40	39	33	0.5416666667	0.0060960122	Later vs Earlier	Treated
42	42	33	-0.1981481481	0.0013716027	Later vs Earlier	Treated
43	35	33	0.9250000000	0.0016256033	Later vs Earlier	Treated
44	36	33	-1.2214285714	0.0010668021	Later vs Earlier	Treated
45	32	33	-1.7571428571	0.0003556007	Earlier vs Later	Treated
47	31	42	1.3111111111	0.0150876302	Earlier vs Later	Treated
48	38	42	-0.3012820513	0.0039624079	Earlier vs Later	Treated
49	39	42	1.3822222222	0.0160020320	Earlier vs Later	Treated
50	33	42	0.7560185185	0.0109728219	Earlier vs Later	Treated
52	35	42	1.9080952381	0.0106680213	Earlier vs Later	Treated
53	36	42	-1.1560606061	0.0050292101	Earlier vs Later	Treated
54	32	42	-3.7414285714	0.0053340107	Earlier vs Later	Treated
56	31	35	-0.2763888889	0.0036576073	Earlier vs Later	Treated
57	38	35	-1.2433333333	0.0007620015	Later vs Earlier	Treated
58	39	35	-0.5975000000	0.0040640081	Later vs Earlier	Treated
59	33	35	-0.4875000000	0.0016256033	Earlier vs Later	Treated
60	42	35	-1.0785714286	0.0010668021	Later vs Earlier	Treated
62	36	35	-1.6357142857	0.0003556007	Later vs Earlier	Treated
63	32	35	-3.5761904762	0.0010668021	Earlier vs Later	Treated
65	31	36	1.3311111111	0.0022860046	Earlier vs Later	Treated
66	38	36	0.4200000000	0.0002540005	Later vs Earlier	Treated
67	39	36	1.0650000000	0.0015240030	Later vs Earlier	Treated
68	33	36	1.0250000000	0.0012192024	Earlier vs Later	Treated
69	42	36	0.5833333333	0.0004572009	Later vs Earlier	Treated
70	35	36	1.8400000000	0.0005080010	Earlier vs Later	Treated
72	32	36	-2.3928571429	0.0007112014	Earlier vs Later	Treated
74	31	32	1.3277777778	0.0004572009	Earlier vs Later	Treated
75	38	32	1.0833333333	0.0007620015	Later vs Earlier	Treated
76	39	32	2.0264285714	0.0035560071	Later vs Earlier	Treated
77	33	32	3.1950000000	0.0005080010	Later vs Earlier	Treated
78	42	32	1.1966666667	0.0007620015	Later vs Earlier	Treated
79	35	32	3.1354166667	0.0012192024	Later vs Earlier	Treated

```
## Plot decomposition results:
#| fig-cap: "Goodman-Bacon decomposition plot for TWFE model with no covariates"
#| fig-alt: "Scatter plot of 2x2 DID weight vs estimate with three types of points: Earlier
ggplot(data=bacon,
       mapping=aes(x=estimate,y=weight,
                   shape=type,color=type)) +
geom_point() + theme_bw() +
labs(x="2x2 DID Estimate", y="Weight",
     shape="Comparison Type",
     color="Comparison Type")
```



The decomposition indicates that the vast majority of the weight is on Treated vs Untreated comparisons (because of the large number of untreated units). One particular observation has a large negative estimate driving the overall estimate.

We can also get the overall weights associated with each timing group, by taking their total weight when used as a treated group minus their total weight when used as a control group.

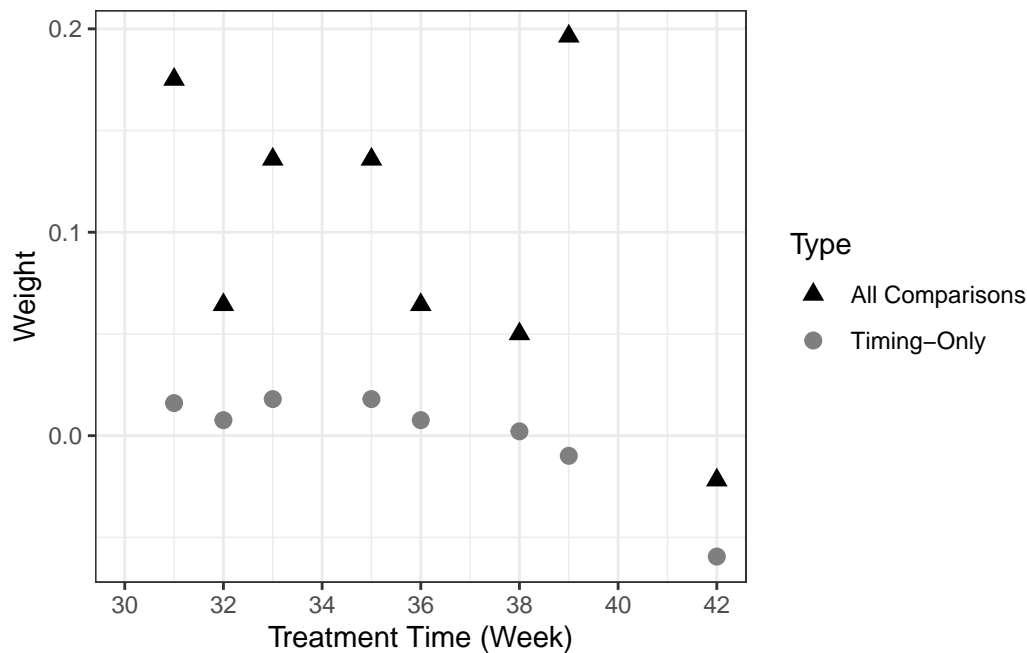
```
## Get total weight as a treated group for all comparisons:
Ov_Wt <- bacon %>%
  group_by(treated) %>%
  dplyr::summarize(PosWeight=sum(weight)) %>%
```

```

rename(`Treatment Time (Week)`==treated) %>%
ungroup() %>%
## Add a column with total weight as treated group for only
# timing comparisons
left_join(bacon %>% dplyr::filter(untreated != 99999) %>%
  group_by(treated) %>%
  dplyr::summarize(PosWeightTiming=sum(weight)),
  by=join_by(`Treatment Time (Week)`==treated)) %>%
## Add a column with total weight as control group:
left_join(bacon %>% group_by(untreated) %>%
  dplyr::summarize(NegWeight=sum(weight)),
  by=join_by(`Treatment Time (Week)`==untreated)) %>%
## Subtract to get overall weight
mutate(Weight=PosWeight-NegWeight,
  WeightTiming=PosWeightTiming-NegWeight) %>%
## Pivot longer for plotting:
pivot_longer(cols=starts_with("Weight"),
  names_to="Type", values_to="Weight")

## Plot decomposition results:
#| fig-cap: "Goodman-Bacon decomposition plot of overall weights on each timing group for TW
#| fig-alt: "Scatter plot of weight vs. treatment time for each timing group. The black tria
ggplot(data=Ov_Wt,
  mapping=aes(x=`Treatment Time (Week)`,y=Weight,
    shape=Type, color=Type)) +
geom_point(size=2.5) +
scale_x_continuous(limits=c(30,42),breaks=seq(30,42,by=2)) +
scale_shape_manual(breaks=c("Weight","WeightTiming"),
  labels=c("All Comparisons","Timing-Only"),
  values=c("triangle","circle")) +
scale_color_manual(breaks=c("Weight","WeightTiming"),
  labels=c("All Comparisons","Timing-Only"),
  values=c("black","grey50")) +
theme_bw()

```



The final switching group receives a negative overall weight, as it is used as a control group for the earlier-switching groups. Because there are so many control states compared to treated states, however, other timing groups do not get negative total weights. This does not mean that none of their (potentially heterogeneous) effects are given a negative weight in the estimand however.

## Dynamic Specification and Alternative Estimators

The `event_study` function in the `did2s` package implements many proposed DID/staggered adoption methods. These can be chosen using the `estimator` option, or all can be fit by setting `estimator="all"`.

```
## Run event_study function with estimator="all":
ES <- event_study(data=Vax_adj %>% dplyr::filter(Yr_Wk %in% Yr_Wk_Sel) %>%
  left_join(Vax_weekly %>% dplyr::filter(LeadLag==0) %>%
    dplyr::select(State,MMWR_week) %>%
    rename(First_Week=MMWR_week),
  by=join_by(State)) %>%
  left_join(tibble(State=unique(Vax_weekly %>% pull(State))) %>%
    arrange(State) %>%
    mutate(StateID=1:length(unique(Vax_weekly %>% pull(State))))
  by=join_by(State)),
  yname="SCP",
```

```
idname="StateID",  
gname="First_Week",  
tname="MMWR_week",  
estimator="all")
```

Note these estimators rely on different underlying assumptions. See Table 2 of <https://arxiv.org/abs/2006.04650>

Estimating TWFE Model

Estimating using Gardner (2021)

Estimating using Callaway and Sant'Anna (2020)

Warning in pre\_process\_did(yname = yname, tname = tname, idname = idname, : Be aware that the  
Check groups: 30,31,32,34,35,37,41.

Warning in did::att\_gt(yname = yname, tname = tname, idname = idname, gname =  
gname, : Not returning pre-test Wald statistic due to singular covariance  
matrix

Estimating using Sun and Abraham (2020)

Estimating using Borusyak, Jaravel, Spiess (2021)

Estimating using Roth and Sant'Anna (2021)

Warning in staggered::staggered(data\_staggered, i = idname, t = tname, g =  
gname, : The treatment cohorts g = 37, 35, 31 have a single cross-sectional  
unit only. We drop these cohorts.

Warning in compute\_se\_Thetahat\_beta(beta = beta, Ybar\_g\_list, A\_theta\_list, :  
var\_conservative is less than adjustmentFactor  
Warning in compute\_se\_Thetahat\_beta(beta = beta, Ybar\_g\_list, A\_theta\_list, :  
var\_conservative is less than adjustmentFactor  
Warning in compute\_se\_Thetahat\_beta(beta = beta, Ybar\_g\_list, A\_theta\_list, :  
var\_conservative is less than adjustmentFactor  
Warning in compute\_se\_Thetahat\_beta(beta = beta, Ybar\_g\_list, A\_theta\_list, :  
var\_conservative is less than adjustmentFactor  
Warning in compute\_se\_Thetahat\_beta(beta = beta, Ybar\_g\_list, A\_theta\_list, :

```
var_conservative is less than adjustmentFactor
Warning in compute_se_Thetahat_beta(beta = beta, Ybar_g_list, A_theta_list, :
var_conservative is less than adjustmentFactor
Warning in compute_se_Thetahat_beta(beta = beta, Ybar_g_list, A_theta_list, :
var_conservative is less than adjustmentFactor
```

```
## List all results:
```

```
ES
```

	estimator	term	estimate	std.error
	<char>	<num>	<num>	<num>
1:	TWFE	-16	1.3746881	0.7170926
2:	TWFE	-15	0.9791773	0.8620365
3:	TWFE	-14	0.9784814	0.7868187
4:	TWFE	-13	0.4526908	0.5695002
5:	TWFE	-12	0.5844473	0.5250245
---				
164: Borusyak, Jaravel, Spiess (2021)		8	-0.7063972	0.4807238
165: Borusyak, Jaravel, Spiess (2021)		9	-1.0444807	0.5019715
166: Borusyak, Jaravel, Spiess (2021)		10	-1.0671403	0.5265563
167: Borusyak, Jaravel, Spiess (2021)		11	-1.2019869	0.4521723
168: Borusyak, Jaravel, Spiess (2021)		12	0.6096405	0.4369625

```
## Pick out a specific method:
```

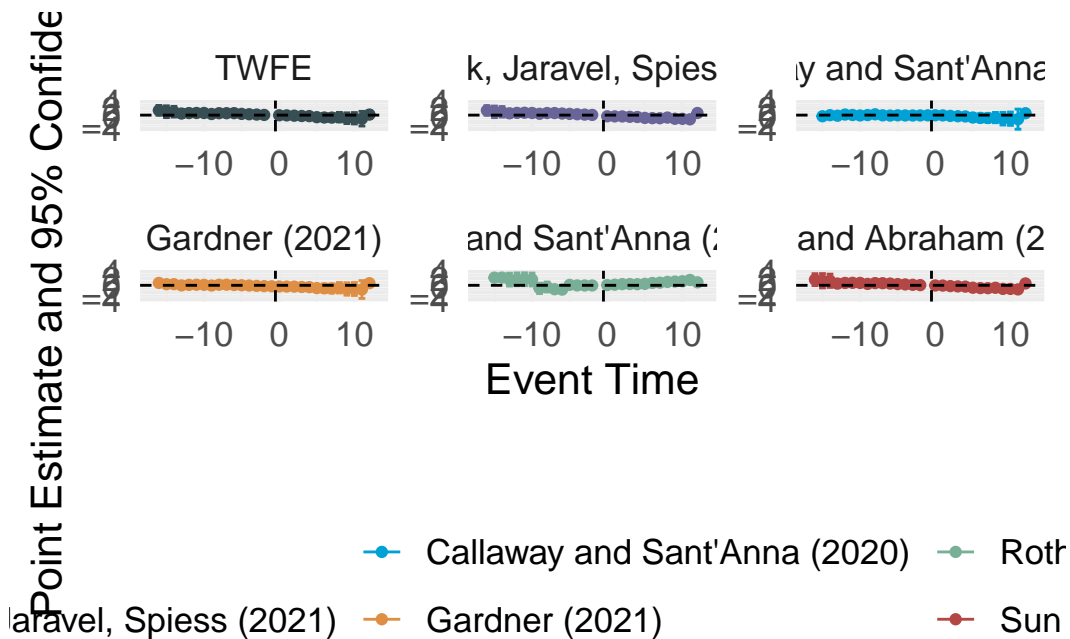
```
ES %>% dplyr::filter(estimator=="Borusyak, Jaravel, Spiess (2021)")
```

	estimator	term	estimate	std.error
	<char>	<num>	<num>	<num>
1: Borusyak, Jaravel, Spiess (2021)		-16	1.34598013	0.70908568
2: Borusyak, Jaravel, Spiess (2021)		-15	0.94532769	0.85061961
3: Borusyak, Jaravel, Spiess (2021)		-14	0.94846115	0.77636228
4: Borusyak, Jaravel, Spiess (2021)		-13	0.52003764	0.56208885
5: Borusyak, Jaravel, Spiess (2021)		-12	0.63385061	0.51713071
6: Borusyak, Jaravel, Spiess (2021)		-11	0.67239117	0.47076990
7: Borusyak, Jaravel, Spiess (2021)		-10	0.61391508	0.40097055
8: Borusyak, Jaravel, Spiess (2021)		-9	0.37487793	0.40346127
9: Borusyak, Jaravel, Spiess (2021)		-8	0.59443575	0.32235189
10: Borusyak, Jaravel, Spiess (2021)		-7	0.59071367	0.28004896
11: Borusyak, Jaravel, Spiess (2021)		-6	0.45524881	0.22419105
12: Borusyak, Jaravel, Spiess (2021)		-5	0.35311548	0.18409354
13: Borusyak, Jaravel, Spiess (2021)		-4	0.25422824	0.14313427

14: Borusyak, Jaravel, Spiess (2021)	-3	0.15245679	0.09494747
15: Borusyak, Jaravel, Spiess (2021)	-2	0.05922846	0.04783152
16: Borusyak, Jaravel, Spiess (2021)	0	-0.33738616	0.20149141
17: Borusyak, Jaravel, Spiess (2021)	1	-0.35826346	0.23090451
18: Borusyak, Jaravel, Spiess (2021)	2	-0.37457823	0.26070118
19: Borusyak, Jaravel, Spiess (2021)	3	-0.47842488	0.30785285
20: Borusyak, Jaravel, Spiess (2021)	4	-0.53291082	0.34662250
21: Borusyak, Jaravel, Spiess (2021)	5	-0.80408403	0.34269134
22: Borusyak, Jaravel, Spiess (2021)	6	-0.87106514	0.40041263
23: Borusyak, Jaravel, Spiess (2021)	7	-0.89918359	0.41749779
24: Borusyak, Jaravel, Spiess (2021)	8	-0.70639721	0.48072376
25: Borusyak, Jaravel, Spiess (2021)	9	-1.04448070	0.50197151
26: Borusyak, Jaravel, Spiess (2021)	10	-1.06714031	0.52655626
27: Borusyak, Jaravel, Spiess (2021)	11	-1.20198694	0.45217230
28: Borusyak, Jaravel, Spiess (2021)	12	0.60964054	0.43696246

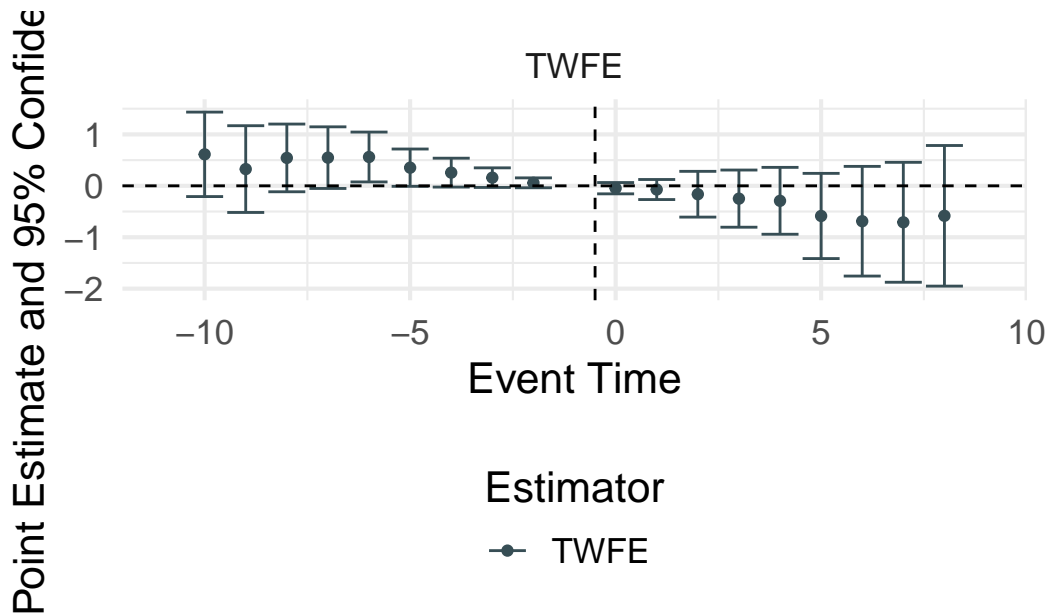
estimator    term    estimate    std.error

```
## Plot the results of the various estimators:
#| fig-cap: "Event-study results from various staggered adoption methods on the effect of st
#| fig-alt: "Six event-study plots showing effect estimates and 95% confidence intervals at c
plot_event_study(ES)
```



For easier inspection, particular estimators can be plotted alone, and the lead/lag times to show can be specified.

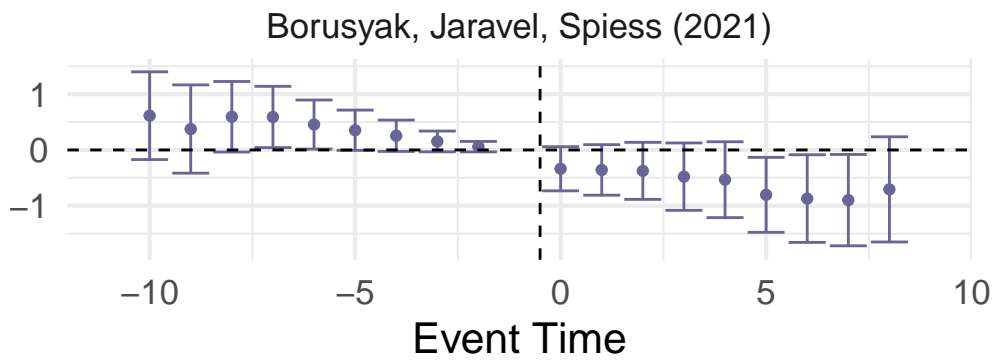
```
## Plot the results for just the dynamic estimator:
#| fig-cap: "Event-study results using the dynamic specification of the TWFE model on the ef
#| fig-alt: "A single event-study plot showing effect estimates and 95% confidence intervals
plot_event_study(ES %>%
  dplyr::filter(estimator=="TWFE"),
  horizon=c(-10,8))
```



```
## Plot the results for just the dynamic estimator:
#| fig-cap: "Event-study results using the dynamic specification described in Borusyak et al
#| fig-alt: "A single event-study plot showing effect estimates and 95% confidence intervals
plot_event_study(ES %>%
  dplyr::filter(estimator=="Borusyak, Jaravel, Spiess (2021)"),
  horizon=c(-10,8))
```

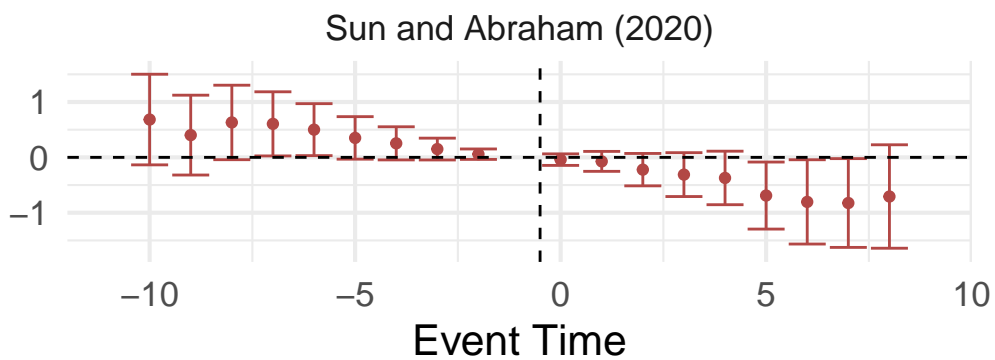


Point Estimate and 95% Confide

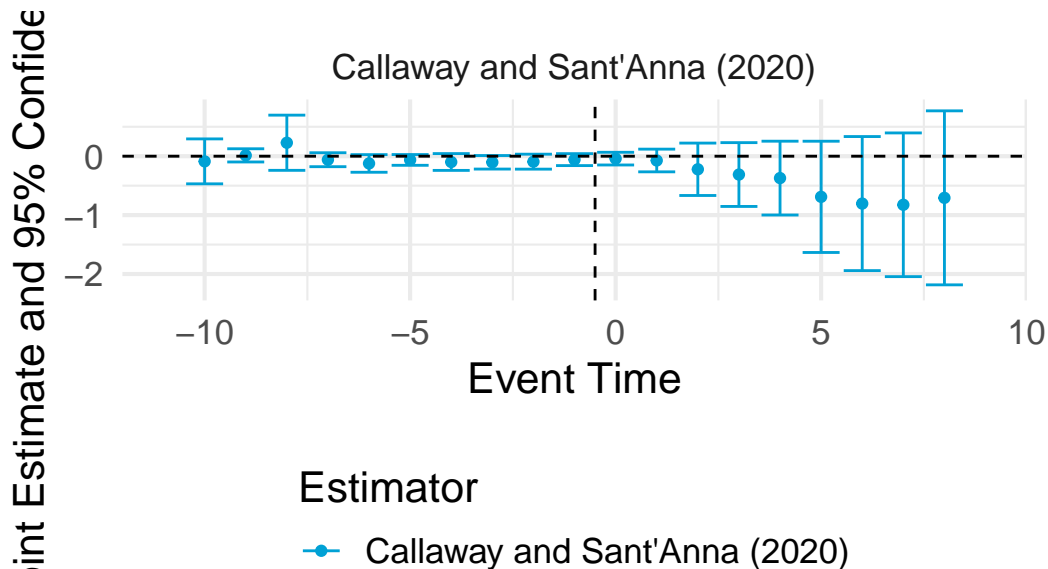


```
## Plot the results for just the Sun and Abraham estimator:  
#| fig-cap: "Event-study results using the estimator from Sun and Abraham (2020) on the effe  
#| fig-alt: "A single event-study plot showing effect estimates and 95% confidence intervals  
plot_event_study(ES %>%  
  dplyr::filter(estimator=="Sun and Abraham (2020)"),  
  horizon=c(-10,8))
```

Point Estimate and 95% Confide



```
## Plot the results for just the Callaway abnd Sant'Anna estimator:
#| fig-cap: "Event-study results using the estimator from Callaway and Sant'Anna (2020) on t
#| fig-alt: "A single event-study plot showing effect estimates and 95% confidence intervals
plot_event_study(ES %>%
  dplyr::filter(estimator=="Callaway and Sant'Anna (2020)",
    horizon=c(-10,8))
```



## First-Difference Switching Effect

Using the `did_multiplegt` function from the `DIDmultiplegt` package, we can fit the de Chaise-martin and d'Haultfoeuille (2020) method to estimate the average treatment effect of the first period after adoption. Standard errors can be derived using the `brep` and `cluster` options, but we set it to 0 here to speed up the analysis.

```
## First, we prepare a data set with a variable with the First_Week of
## mandate for each mandate state and a unique state ID number.
Vax_firstWeek <- Vax_adj %>%
  dplyr::filter(Yr_Wk %in% Yr_Wk_Sel) %>%
  left_join(Vax_adj %>%
    dplyr::filter(LeadLag==0) %>%
    dplyr::select(State,MMWR_week) %>%
    rename(First_Week=MMWR_week),
    by=join_by(State)) %>%
```

```

left_join(tibble(State=unique(Vax_adj %>% pull(State))) %>%
  arrange(State) %>%
  mutate(StateID=1:length(unique(Vax_adj %>% pull(State)))),
  by=join_by(State))
## Run analysis method:
dCdH <- did_multiplegt(mode="old",
  df=Vax_firstWeek,
  Y="D1P",
  G="StateID",
  T="MMWR_week",
  D="mandate",
  placebo=10,
  dynamic=7,
  brep=0,
  cluster="StateID")
## See full results:
dCdH

```

```

$effect
  treatment
-0.009937251

```

```

$N_effect
[1] 321

```

```

$N_switchers_effect
[1] 18

```

```

$dynamic_1
[1] -0.1409227

```

```

$N_dynamic_1
[1] 280

```

```

$N_switchers_effect_1
[1] 15

```

```

$dynamic_2
[1] -0.1573204

```

```

$N_dynamic_2
[1] 275

```

\$N\_switchers\_effect\_2  
[1] 15

\$dynamic\_3  
[1] -0.1712528

\$N\_dynamic\_3  
[1] 263

\$N\_switchers\_effect\_3  
[1] 15

\$dynamic\_4  
[1] -0.4340216

\$N\_dynamic\_4  
[1] 218

\$N\_switchers\_effect\_4  
[1] 10

\$dynamic\_5  
[1] -0.4988121

\$N\_dynamic\_5  
[1] 186

\$N\_switchers\_effect\_5  
[1] 9

\$dynamic\_6  
[1] -0.4722865

\$N\_dynamic\_6  
[1] 177

\$N\_switchers\_effect\_6  
[1] 9

\$dynamic\_7  
[1] -0.2888539

\$N\_dynamic\_7

[1] 138

\$N\_switchers\_effect\_7

[1] 8

\$placebo\_1

[1] -0.01750961

\$N\_placebo\_1

[1] 321

\$placebo\_2

[1] -0.06238722

\$N\_placebo\_2

[1] 321

\$placebo\_3

[1] -0.0511033

\$N\_placebo\_3

[1] 321

\$placebo\_4

[1] -0.04764996

\$N\_placebo\_4

[1] 321

\$placebo\_5

[1] -0.01803485

\$N\_placebo\_5

[1] 321

\$placebo\_6

[1] -0.08787976

\$N\_placebo\_6

[1] 274

\$placebo\_7

```
[1] -0.05460744
```

```
$N_placebo_7
```

```
[1] 230
```

```
$placebo_8
```

```
[1] -0.08344529
```

```
$N_placebo_8
```

```
[1] 187
```

```
$placebo_9
```

```
[1] 0.2252317
```

```
$N_placebo_9
```

```
[1] 187
```

```
$placebo_10
```

```
[1] -0.1133561
```

```
$N_placebo_10
```

```
[1] 146
```

The treatment effect estimate is -0.00994. We can also pull the dynamic and placebo effect estimates from the output.

```
## Creating data set of placebo (in-time) effects. Note the time is negated to match usual e
placebo <- as_tibble(dCdH) %>% dplyr::select(starts_with("placebo")) %>%
  pivot_longer(cols=everything(),
               names_to="Lead",
               names_prefix="placebo_",
               values_to="Estimate") %>%
  mutate(`Event Time`=-1*as.numeric(Lead))
## Creating data set of single first-switch estimate.
estimate <- tibble(`Event Time`=1,
                  Estimate=dCdH$effect["treatment"])
## Creating data set of dynamic effects. Note the time is incremented by 1 to match usual ev
dynamic <- as_tibble(dCdH) %>% dplyr::select(starts_with("dynamic")) %>%
  pivot_longer(cols=everything(),
               names_to="Lag",
               names_prefix="dynamic_",
               values_to="Estimate") %>%
```

```

  mutate(`Event Time`=as.numeric(Lag)+1)
## Combined event time data set from this method:
dCdH_comb <- bind_rows(placebo %>% dplyr::select(-Lead),
                        estimate,
                        dynamic %>% dplyr::select(-Lag))
dCdH_comb %>% arrange(`Event Time`)

```

```

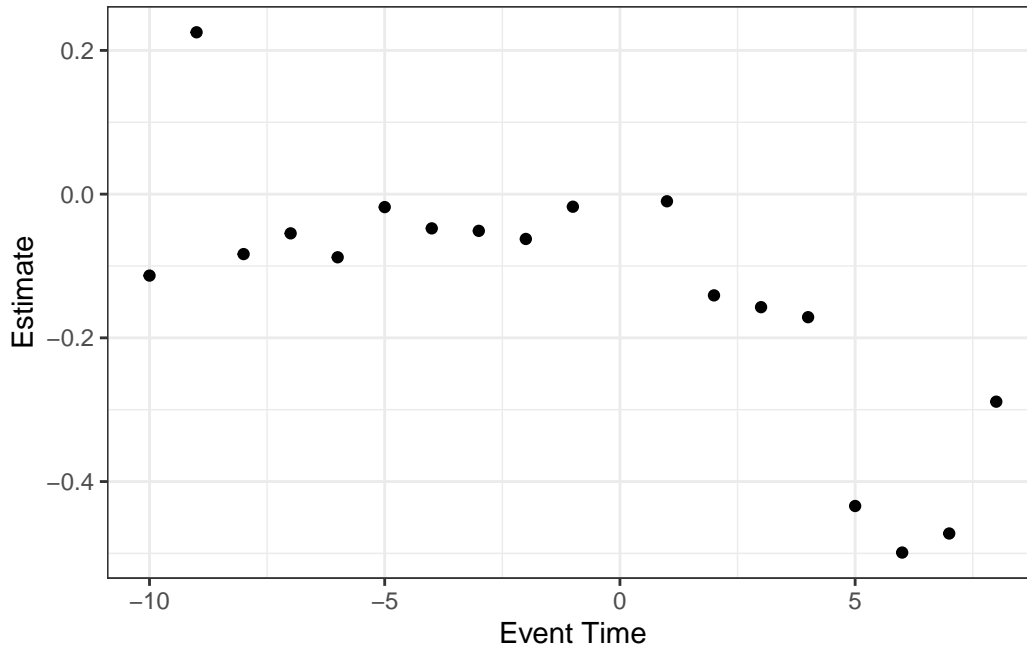
# A tibble: 18 x 2
  Estimate `Event Time`
    <dbl>      <dbl>
1 -0.113      -10
2  0.225       -9
3 -0.0834     -8
4 -0.0546     -7
5 -0.0879     -6
6 -0.0180     -5
7 -0.0476     -4
8 -0.0511     -3
9 -0.0624     -2
10 -0.0175    -1
11 -0.00994     1
12 -0.141      2
13 -0.157      3
14 -0.171      4
15 -0.434      5
16 -0.499      6
17 -0.472      7
18 -0.289      8

```

```

## Plot the results of first-switching analysis:
#| fig-cap: "Event-study results using the First-Switching Estimator from de Chaisemartin and
#| fig-alt: "A single event-study plot showing effect estimates at each lead/lag time from -10
ggplot(dCdH_comb) + geom_point(mapping=aes(x=`Event Time`, y=Estimate)) +
  theme_bw()

```



If you install the `DIDmultiplegtDYN` package, a faster implementation of standard errors and more standard interface is available through the `did_multiplegtDYN` function. Note that this package requires Java and at least R 4.3.3, and may cause errors in other settings. It also limits the pre-treatment periods that can be considered and changes exactly how they are fit, leading to differences from the above implementation.

```
## Run the following code only if you are able to install the
### DIDmultiplegtDYN package. Otherwise, delete or turn eval to false
### to avoid errors.
#| eval: true

## Run the above analysis with the DIDmultiplegtDYN package instead:
# install.packages("DIDmultiplegtDYN")
require(DIDmultiplegtDYN)
```

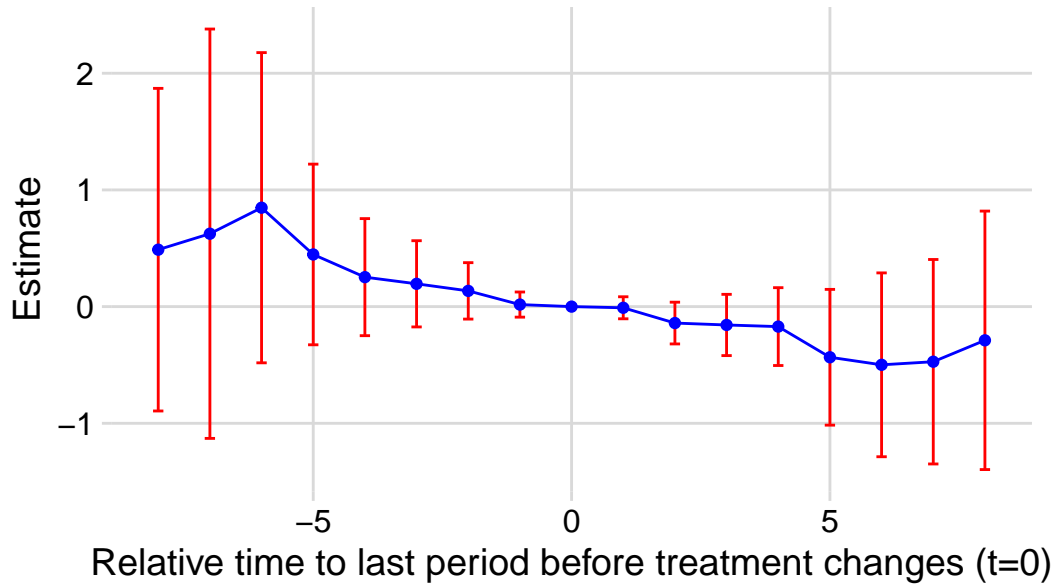
Loading required package: `DIDmultiplegtDYN`

```
dCdH_dyn <- did_multiplegt_dyn(df=Vax_firstWeek,
                               outcome="D1P",
                               group="StateID",
                               time="MMWR_week",
                               treatment="mandate",
                               effects=8,
```



```
placebo=8,
cluster="StateID",
graph_off=FALSE)
```

## DID, from last period before treatment changes



dCdH\_dyn

### Estimation of treatment effects: Event-study effects

	Estimate	SE	LB CI	UB CI	N	Switchers
Effect_1	-0.00994	0.04814	-0.10429	0.08441	321	18
Effect_2	-0.14092	0.09131	-0.31988	0.03804	280	15
Effect_3	-0.15732	0.13387	-0.41971	0.10507	275	15
Effect_4	-0.17125	0.17020	-0.50485	0.16234	263	15
Effect_5	-0.43402	0.29681	-1.01576	0.14772	218	10
Effect_6	-0.49881	0.40189	-1.28650	0.28887	186	9
Effect_7	-0.47229	0.44699	-1.34838	0.40381	177	9
Effect_8	-0.28885	0.56507	-1.39638	0.81867	138	8

Test of joint nullity of the effects : p-value = 0.0000

Average cumulative (total) effect per treatment unit

```

-----
Estimate      SE      LB CI      UB CI      N Switchers
-0.22841    0.21237  -0.64464    0.18783      545      99
Average number of time periods over which a treatment effect is accumulated: 3.8788

```

```

-----
Testing the parallel trends and no anticipation assumptions
-----

```

	Estimate	SE	LB CI	UB CI	N	Switchers
Placebo_1	0.01751	0.05495	-0.09019	0.12521	321	18
Placebo_2	0.13483	0.12339	-0.10701	0.37668	280	15
Placebo_3	0.19539	0.18846	-0.17399	0.56477	275	15
Placebo_4	0.25257	0.25594	-0.24907	0.75421	263	15
Placebo_5	0.44685	0.39496	-0.32725	1.22096	218	10
Placebo_6	0.84753	0.67821	-0.48173	2.17679	145	6
Placebo_7	0.62478	0.89497	-1.12932	2.37889	98	5
Placebo_8	0.48793	0.70533	-0.89448	1.87035	31	2

Test of joint nullity of the placebos : p-value = 0.0000

The development of this package was funded by the European Union.  
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## Additional Options

Other methods and specifications are possible, along with incorporating covariates into some of these methods. The review papers listed in the slides are a good place to start to investigate these.

## Discussion Question

Is this question and its associated data set a good fit for a DID/staggered adoption analysis? Why or why not?