

Infectiousness of SARS-CoV-2 breakthrough infections and reinfections during the Omicron wave

Sophia Tan

8/29/2022

In this study, we use detailed, anonymized data from 35 California state prisons to estimate the relative infectiousness of Omicron SARS-CoV-2 breakthrough infections and reinfections. We use SARS-CoV-2 testing data, COVID-19 vaccination data, and nightly housing data among residents to identify index cases and their close contacts. We defined index cases as residents with a positive SARS-CoV-2 test and assumed they were infectious for 5 days. We defined close contacts as residents who shared a cell with an index case for at least one night while the index case was infectious.

Index cases were included in the statistical analysis if they met the following inclusion criteria:

- first positive test occurred during the Omicron wave (12/15/2021-5/20/2022)
- resident was incarcerated during the entire pandemic (4/1/2020-5/20/2022)
- resident stayed in a 180 cell, 270 cell, or solid door cell during their infectious period

Index cases were excluded if:

- resident had no housing data during the 5 day infectious period
- resident received a negative PCR test during the 5 day infectious period
- resident has a contact with a positive test within 2 days of exposure
- resident had no valid close contacts

Close contacts were included if all the following criteria were met:

- resident had a negative SARS-CoV-2 test within 2 days before or after first exposure to an index case
- resident had follow up testing data between 3 days after first exposure and 14 days after last exposure to an index case

Close contacts were excluded if:

- any room shared with the index case during the infectious period had more than 10 total residents

If an index case has more than one close contact, a single close contact is chosen at random.

Matching

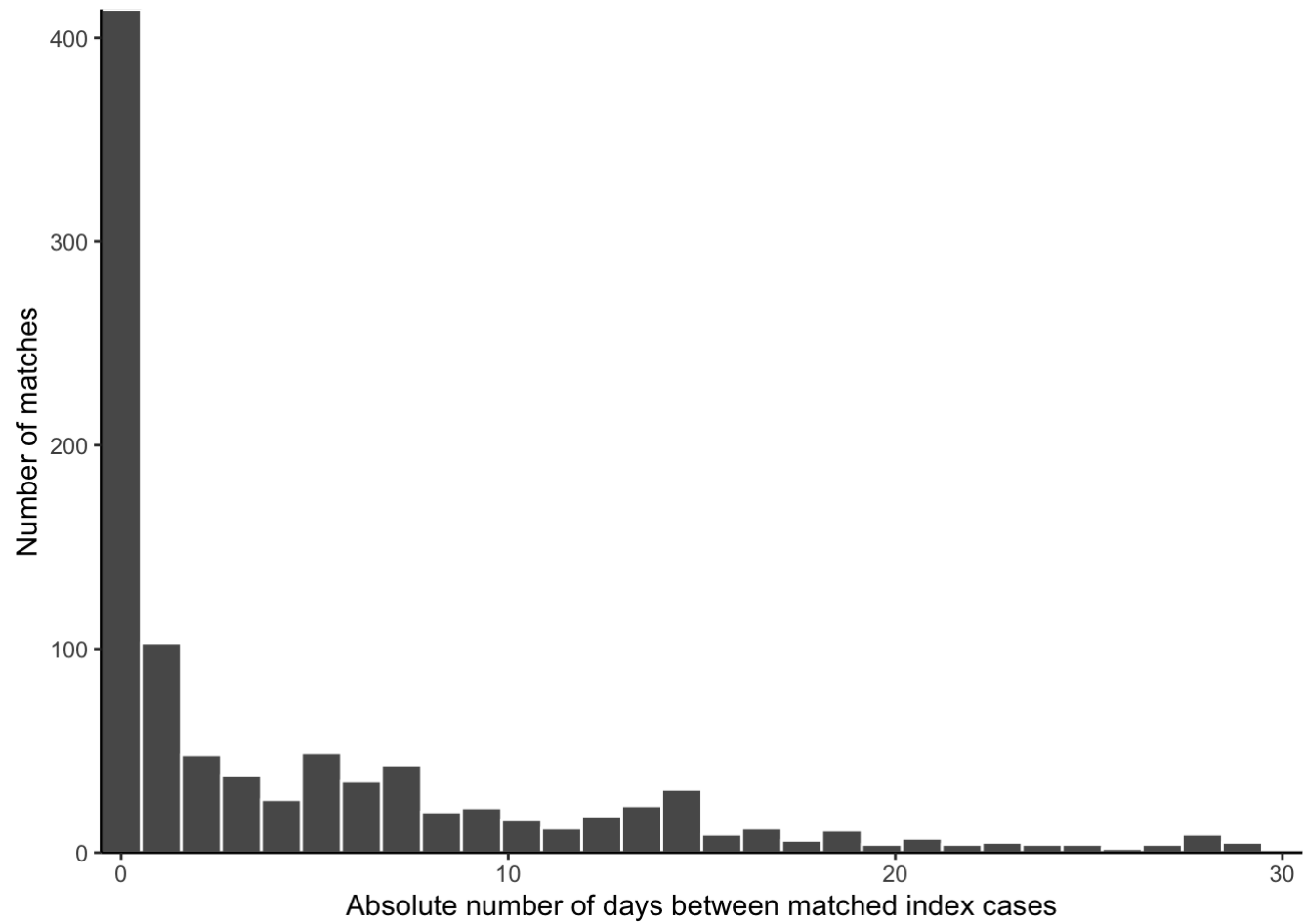
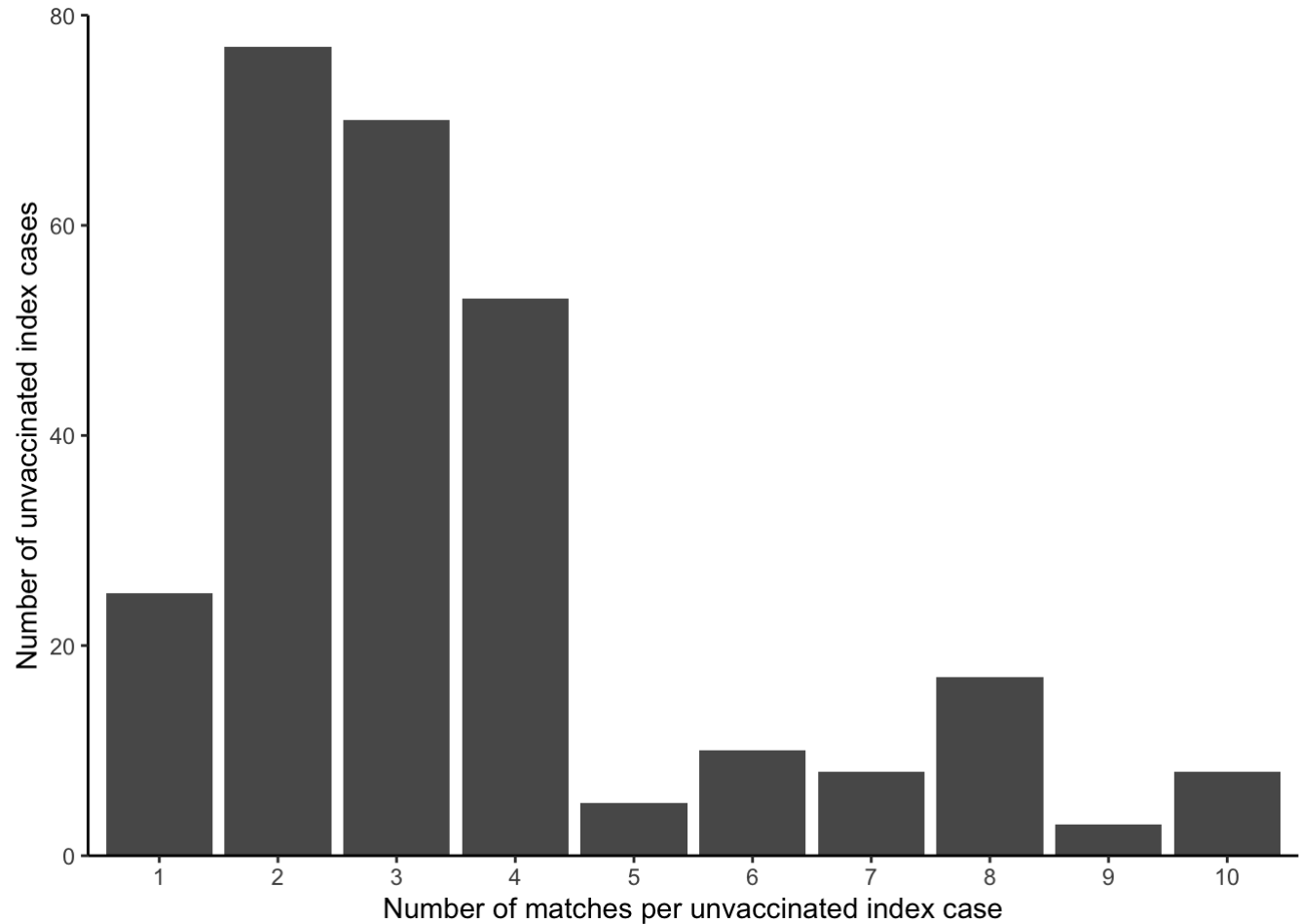
We first matched unvaccinated and vaccinated index cases in a 1:10 ratio by institution (exactly) and time (within 30 days).

```
# create distance matrix for matching
# calculate pair-wise difference (in days) in the date of first positive test for index cases
distance_matrix <- dist(as.matrix(d%>%select(Day)%>%mutate(Day=as.numeric(Day))), diag = T, upper = T) %>% as.matrix()

# match using the matchit package
m <- matchit(treatment ~ Day + Institution, data = d,
             method = "nearest", exact = "Institution", caliper = 30, std.caliper = F,
             distance = distance_matrix, ratio=10, replace = F)
summary(m)
```

```
##
## Call:
## matchit(formula = treatment ~ Day + Institution, data = d, method = "nearest",
##         distance = distance_matrix, exact = "Institution", replace = F,
##         caliper = 30, std.caliper = F, ratio = 10)
##
## Summary of Balance for All Data:
##           Means Treated Means Control Std. Mean Diff. Var. Ratio eCDF Mean
## Day           19021.4382      19024.4146      -0.1075      1.1996      0.0404
## Institution      22.4099       20.1799       0.2343      1.1301      0.0680
##           eCDF Max
## Day              0.1087
## Institution      0.1674
##
##
## Summary of Balance for Matched Data:
##           Means Treated Means Control Std. Mean Diff. Var. Ratio eCDF Mean
## Day           19020.8841      19023.8031      -0.1055      1.0013      0.0289
## Institution      22.2428       22.2428       0.0000      1.0022      0.0000
##           eCDF Max Std. Pair Dist.
## Day              0.0874          0.1712
## Institution      0.0000          0.0000
##
## Sample Sizes:
##           Control Treated
## All           1112.      283
## Matched (ESS)  710.92    276
## Matched        985.      276
## Unmatched      127.       7
## Discarded       0.       0
```

```
#final matched dataset
final <- match.data(m)
```

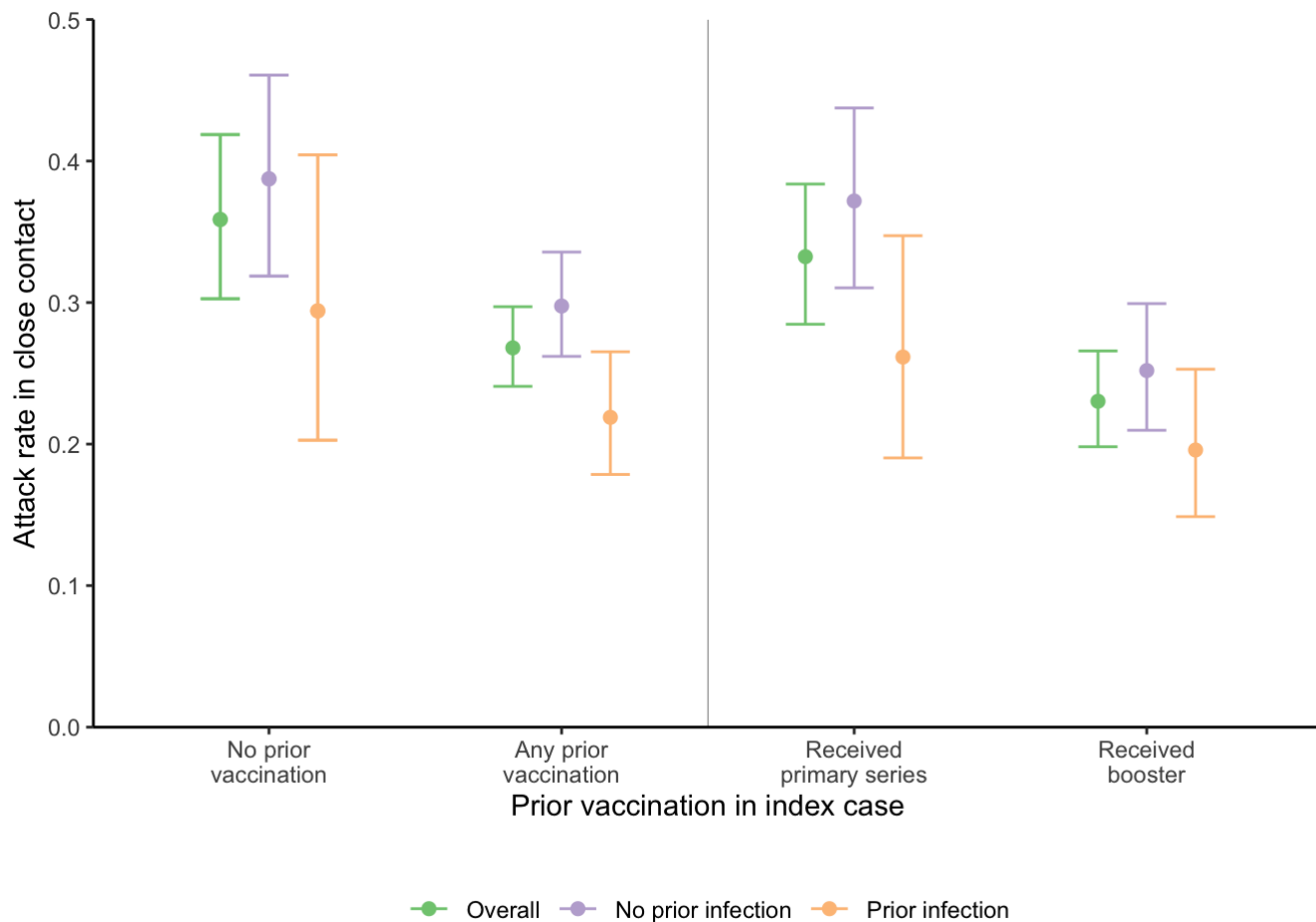


Unadjusted attack risks

We calculated crude attack rates of Omicron SARS-CoV-2 infection. We estimated 95% binomial confidence intervals.

```
## [1] "The overall attack rate in the study population is 29% (95% CI: 26–31)"
```

Attack rate (%) (95% CI)	No prior vaccination	Prior vaccination
No prior infection	38.7 (31.9, 46.1)	29.8 (26.2, 33.6)
Prior infection	29.4 (20.3, 40.4)	21.9 (17.9, 26.5)



Relative attack risks

We used cluster-robust Poisson regression models to estimate the relative risk of transmission in vaccinated and/or previously infected index cases.

Main model and results

```
# pre-specified main model
model <- glm(contact_status ~ index_prior_vacc + index_prior_inf +
             num_vacc_doses+has_prior_inf+incidence_log+Institution, data=final, weights=weights, family="poisson")

# find SE of linear combination of covariates (prior vaccination and prior infection) by hand
error <- c(sqrt(t(c(0,1,1,rep(0,28))) %*% vcovCR(model, cluster = final$subclass, type="CR2") %*% c(0,1,1,rep(0,28))))

# robust standard errors
model <- coef_test(model, vcov = "CR2", cluster = final$subclass) %>% data.frame(row.names = NULL)
```

Relative % change in attack rate of infection in close contact (95% CI)

Index case	Prior vaccination only	-24.3 (-37.1, -8.8)
	Prior infection only	-21.7 (-36.4, -3.6)
Close contact	Number of vaccine doses 1 dose	1.2 (-8.1, 11.4)
	2 doses	2.3 (-15.6, 24.1)
	≥3 doses	3.5 (-22.5, 38.2)
	Prior infection only	-16.9 (-33, 3.1)
Institution	SARS-CoV-2 incidence in the 7 days preceding the positive test in the index case (natural log scale)	10.6 (-3.4, 26.6)

Additional analyses

We tested different vaccine definitions, the relationship between infection and vaccination, and impact of time since vaccination on infectiousness.

Varying vaccine definition

```
# run with index case number of vaccine doses
model <- glm(contact_status ~ index_prior_vacc_doses + index_prior_inf +
             num_vacc_doses+has_prior_inf+incidence_log+Institution, data=final, weights=weights, family="poisson")
model <- coef_test(model, vcov = "CR2", cluster = final$subclass) %>% data.frame(row.names=NULL)
```

```
# index case has either any vaccination or prior infection
model <- glm(contact_status ~ index_has_vacc_or_inf +
              num_vacc_doses+has_prior_inf+incidence_log+Institution, data=final, weights=weights, family="poisson")
model <- coef_test(model, vcov = "CR2", cluster = final$subclass) %>% data.frame(row.names = NULL)
```

```
# contact has any vaccination
final <- final %>% mutate(contact_has_vacc=ifelse(num_vacc_doses>0, 1, 0))
model <- glm(contact_status ~ index_prior_vacc + index_prior_inf +
              contact_has_vacc+has_prior_inf+incidence_log+Institution, data=final, weights=weights, family="poisson")
model <- coef_test(model, vcov = "CR2", cluster = final$subclass) %>% data.frame(row.names=NULL)
```

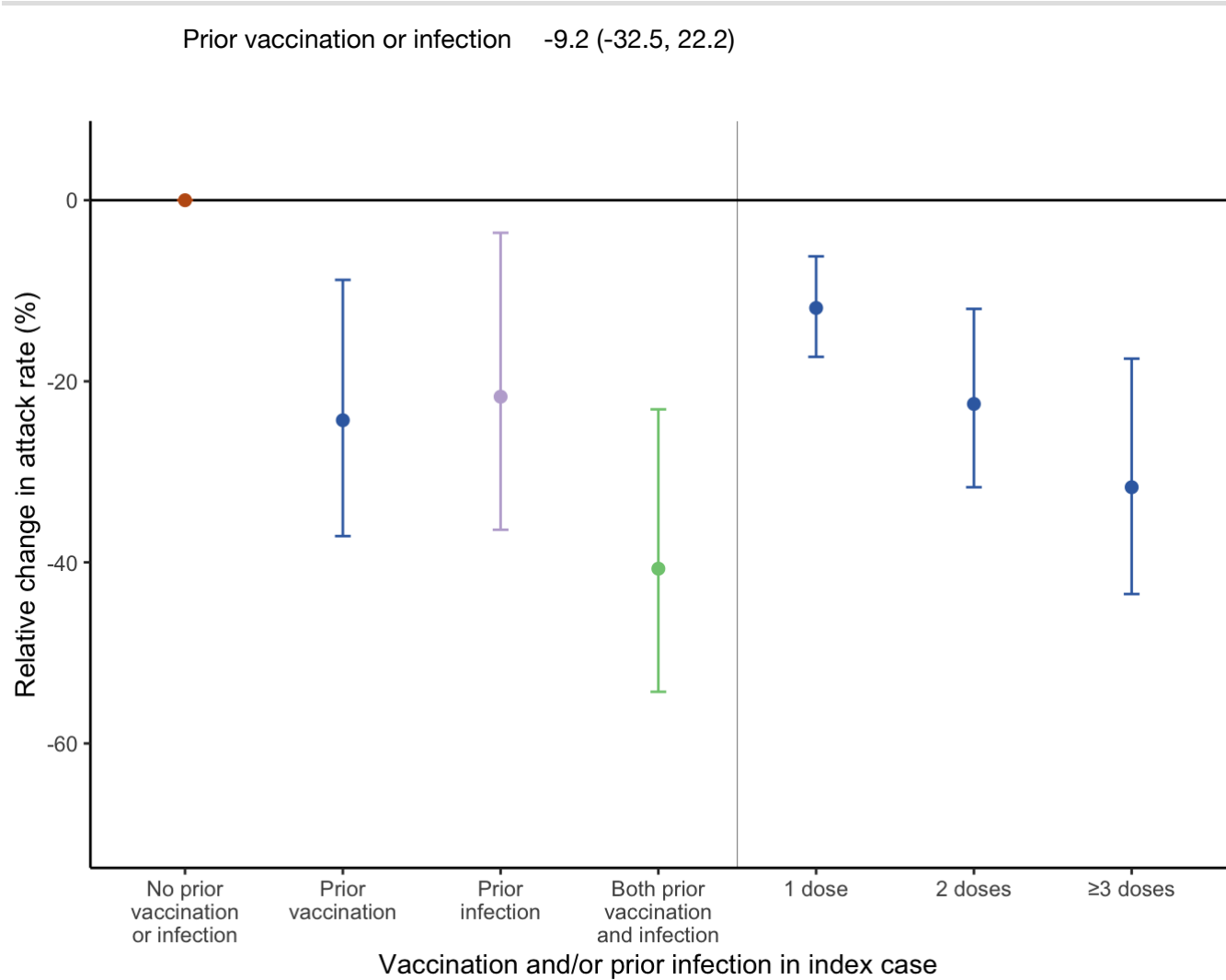
```
# contact has either any vaccination or infection
final <- final %>% mutate(contact_has_vacc_or_inf = ifelse(contact_has_vacc|has_prior_inf, 1, 0))
model <- glm(contact_status ~ index_prior_vacc + index_prior_inf +
              contact_has_vacc_or_inf+incidence_log+Institution, data=final, weights=weights, family="poisson")

model <- coef_test(model, vcov = "CR2", cluster = final$subclass) %>% data.frame(row.names=NULL)
```

Relative % change in attack rate of infection in close contact (95% CI)

Index case	Prior vaccination only	-24.3 (-37.1, -8.8)
	Number of vaccine doses 1 dose	-11.9 (-17.3, -6.2)
	2 doses	-22.5 (-31.7, -12)
	≥3 doses	-31.7 (-43.5, -17.5)
	Prior vaccination or infection	-30.2 (-43, -14.6)
Close contact	Prior vaccination only	3.2 (-20.5, 34)
	Number of vaccine doses 1 dose	1.2 (-8.1, 11.4)
	2 doses	2.3 (-15.6, 24.1)
	≥3 doses	3.5 (-22.5, 38.2)

Relative % change in attack rate of infection in close contact
(95% CI)



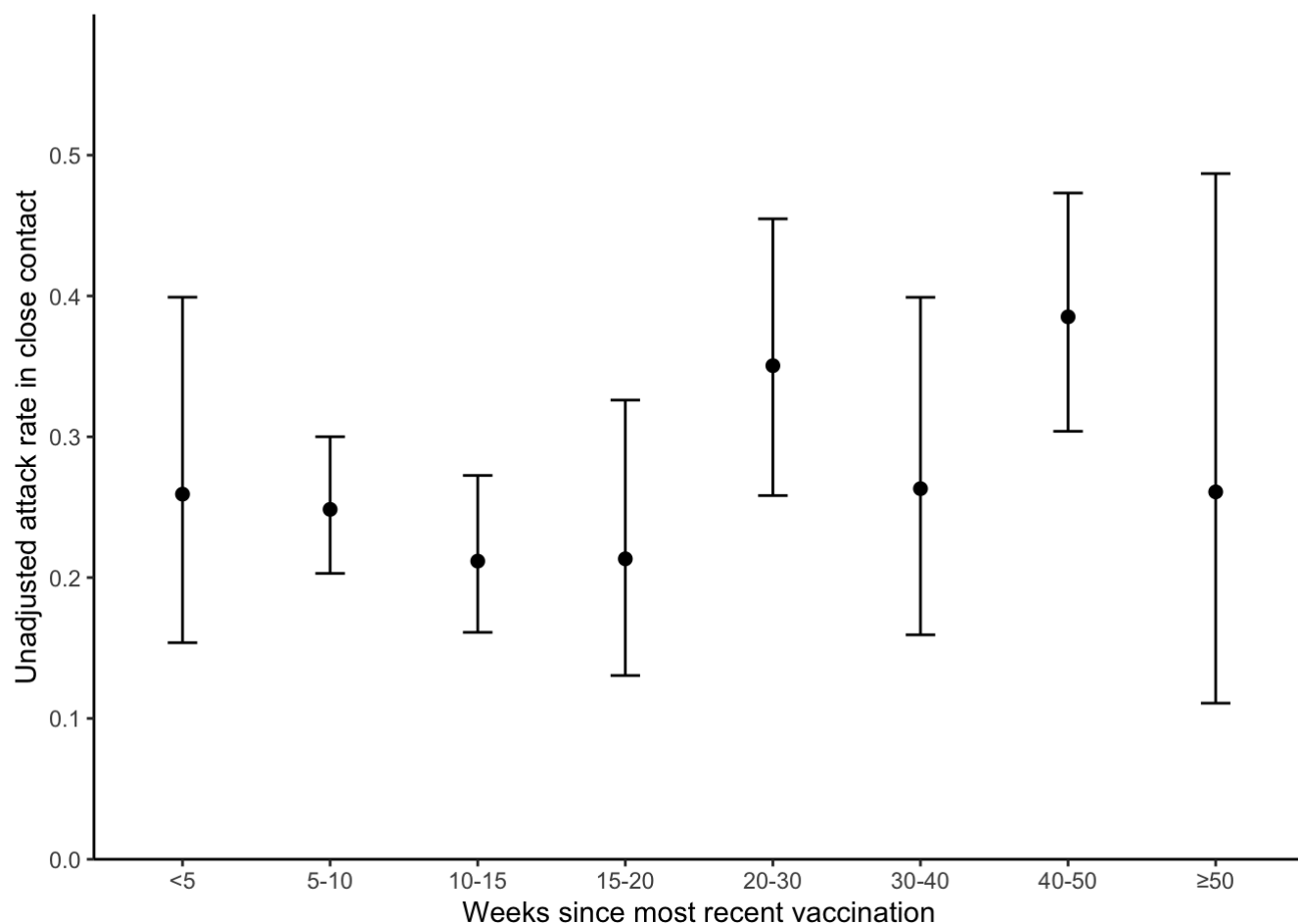
Interaction between prior infection and prior vaccination

```
## testing interaction between prior vaccination and infection in the index case
model <- glm(contact_status ~ index_prior_vacc + index_prior_inf + index_prior_vacc*index_prior_inf +
              num_vacc_doses+has_prior_inf+incidence_log+Institution, data=final, weights=weights, family="poisson")
model <- coef_test(model, vcov = "CR2", cluster = final$subclass) %>% as.data.frame()
```

Relative % change in attack rate of infection in close contact
(95% CI)

Prior vaccination	-25.9 (-40.7, -7.4)
Prior infection	-26.2 (-49.5, 7.9)
Interaction between vaccination and prior infection	8.3 (-31.6, 71.6)

Time since most vaccination or infection



```
# relationship between time since most recent vaccination and infection in close contact
model <- glm(contact_status ~ index_prior_inf + index_weeks_since_vacc +
              num_vacc_doses + has_prior_inf + incidence_log + Institution, data=d, weights=w
              eights, family="poisson")
model <- coef_test(model, vcov = "CR2", cluster = d$subclass) %>% data.frame(row.names =
NULL)
```

```
# relationship between time since most recent infection and infection in close contact
model <- glm(contact_status ~ index_prior_vacc + index_weeks_since_inf +
              num_vacc_doses + has_prior_inf + incidence_log + Institution, data=d, weights=w
              eights, family="poisson")
model <- coef_test(model, vcov = "CR2", cluster = d$subclass) %>% data.frame(row.names =
NULL)
```

```
# relationship between time since most recent vaccination or infection and infection in
close contact
model <- glm(contact_status ~ index_weeks_since_inf_vacc +
              num_vacc_doses + has_prior_inf + incidence_log + Institution, data=d, weights=w
              eights, family="poisson")
model <- coef_test(model, vcov = "CR2", cluster = d$subclass) %>% data.frame(row.names =
NULL)
```


Relative % change in attack rate of infection in close contact (95% CI)

Time since last COVID-19 vaccine dose (per 5 weeks)	6 (2, 10.2)
Time since most recent SARS-CoV-2 infection (per 5 weeks)	5 (-2.7, 13.4)
Time since most recent vaccine or infection (per 5 weeks)	4.5 (1.7, 7.4)