Report on Results for Study 1

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0.1 The Design

We made a research design where pairs of survey respondents were created so as to be nearly identical on ideology. These pairs were also created so that the overall research design compared favorably with a pair-randomized experiment and otherwise produced extremely homogeneous comparisons in terms of age, education, gender, race, partisanship, family income, and missingness on family income.

Because some of the same respondents were repeated between the November and December surveys, we kept only the first response for use in this file, which represents our primary analysis.

```
library(here)
```

```
## here() starts at /Users/jwbowers/Documents/PROJECTS/ThePolicyLab/COVID-VaccinesSocialNorms-private
```

```
source(here("src", "R", "000_constants_and_utils.R"))
source(here("src/R", "001_rmd_setup.R"))
```

```
## Loading required package: survival
```

```
## Loading required package: SparseM
```

```
##
## Attaching package: 'SparseM'
```

```
## The following object is masked from 'package:base':
##
##      backsolve
```

```
library(kableExtra)
library(tidyverse)
library(estimatr)
library(coin)
library(sensemakr)
library(sensitivitymult)

load(file = here(MATCHES_DIR, "dat_plus_matches_study1_first.rda"), verbose = TRUE)
```

```
Loading objects:
  dat3
  tab
  pair_diffs
  xbres_vars
  xbres
dat3_1 <- dat3
load(file = here(MATCHES_DIR, "outcome_analysis_study1_first.rda"), verbose = TRUE)
```

```
Loading objects:
  dat3
  xbres
  lm_mask_fam
  lm_test_fam
  lm_perc_fam
  lm_perc_neigh
  lm_perc_city
  lm_perc_state
  xb1
```

```
    mvtest1
    mvtest2
    mvtest3
    mvtest4
    test_city_vs_bigger
    test_neigh_vs_bigger
    test_fam_vs_bigger
    sursfit
    risk_res
    vaxrisk_res
    vaxrisk_inv_res
stopifnot(nrow(dat3) == nrow(dat3_1))
```

Our design consists of 824 respondents from surveys 5–8 placed into pairs that were required to be the same on partisanship and survey. Is this a good research design for our question? Our main goal is to break the relationship between perceptions and potential confounders within pair — that is, we aim to create pairs such that the person who, say, perceives more of their family wearing masks is no more or less likely to be the older member of the pair (or the democrat in the pair, or the more well-educated member of the pair, etc..). Within pair comparisons of perceptions in such a design then cannot be said to be confounded by the variables that we balanced.

We present a few pieces of information about our design here.

First, we show balance on average. The following table shows that the pairs have nearly the same mean values on the key covariates that we aim to balance.

```
kable(tab[order(tab[, "Diffs"]), ])
```

	Mean 1	Mean 2	Diffs
agegood	48.5971	49.0170	-0.4199
covid_know	0.7597	0.7765	-0.0168
relig_scale	0.3261	0.3390	-0.0129
faminc_new.NA	0.0704	0.0728	-0.0024
dem_rep_oth	2.0413	2.0413	0.0000
female	0.5680	0.5680	0.0000
race_new	1.2015	1.2015	0.0000
trust_in_science	3.9066	3.9066	0.0000
covid_subj_know	3.6000	3.6000	0.0000
educ	3.7379	3.6723	0.0655
ideo5	3.0801	2.9854	0.0947
faminc_new_Imp	6.4080	6.1994	0.2086

```
pd_means <- sapply(pair_diffs, mean, na.rm = TRUE)
pd_quants <- sapply(pair_diffs, function(x) {
  quantile(abs(x), probs = c(0, .1, .25, .5, .75, .9, 1), na.rm = TRUE)
})

pd_tab <- as.data.frame(rbind(pd_quants, pd_means))[, -1]
pd_tab$quantity <- c(row.names(pd_quants), "mean_diff")
pd_tab <- relocate(pd_tab, quantity)
```

What about within-pair differences? The following table summarizes the differences within pairs. For example, it tells us that across the 412 pairs, half differ by less than 1 points on the 5 point ideology scale, less than 1 point on the 6 point education scale, less than 5 years of age. When the value for the median difference (the row labeled 50%) is 0, this means that more than half of the pairs were identical on that variable. All pairs were identical in terms of the survey (since the surveys were fielded at different times). The worse differences we see are 2 points difference in ideology (for 10% of pairs) and less than 10% of pairs differed by as much as 9 years of age. We judge that these are quite small differences in substantive terms, and again, suggest that we have created a research design that limits the confounding effects of covariates on our targeted relationship.

```
pd_tab
```

```
          quantity      ideo     educ      age female race_new dem_rep_oth  faminc faminc_NA trust_in_science covid_know covid_know_NA
0%              0% 0.000000 0.00000   0.0000      0        0           0 0.00000   0.00000                0   0.000000             0
10%            10% 0.000000 0.00000   1.0000      0        0           0 0.00000   0.00000                0   0.000000             0
25%            25% 0.000000 0.00000   2.0000      0        0           0 1.00000   0.00000                0   0.000000             0
50%            50% 1.000000 1.00000   5.0000      0        0           0 1.03829   0.00000                0   0.125000             0
75%            75% 1.000000 1.00000   7.0000      0        0           0 2.03829   0.00000                0   0.250000             0
90%            90% 2.000000 1.00000   9.0000      0        0           0 3.00000   0.00000                0   0.250000             0
100%          100% 2.000000 1.00000  10.0000      0        0           0 3.00000   1.00000                0   0.375000             0
pd_means mean_diff 0.007282 0.05583  -0.1772      0        0           0 0.03837  -0.01214                0   0.007282             0
          covid_subj_know covid_subj_know_NA relig_scale percdiff
```

```
0%                   0           0   0.000000    0.625
10%                  0           0   0.016861   81.863
25%                  0           0   0.057715  178.812
50%                  0           0   0.153495  410.812
75%                  0           0   0.275264  671.719
90%                  0           0   0.362864  968.688
100%                 0           0   0.450747 1569.625
pd_means             0           0   0.006189  471.199
## No need to show that pairs tend to differ on average perceptions --- that is what we want but doesn't have to do with evaluating the matches
kableExtra::kable(pd_tab %>% select(-percdiff), digits = 2)
```

	quantity	ideo	educ	age	female	race_new	dem_rep_oth	faminc	faminc_NA	trust_in_science	covid_know
0%	0%	0.00	0.00	0.00	0	0	0	0.00	0.00	0	0.00
10%	10%	0.00	0.00	1.00	0	0	0	0.00	0.00	0	0.00
25%	25%	0.00	0.00	2.00	0	0	0	1.00	0.00	0	0.00
50%	50%	1.00	1.00	5.00	0	0	0	1.04	0.00	0	0.12
75%	75%	1.00	1.00	7.00	0	0	0	2.04	0.00	0	0.25
90%	90%	2.00	1.00	9.00	0	0	0	3.00	0.00	0	0.25
100%	100%	2.00	1.00	10.00	0	0	0	3.00	1.00	0	0.38
pd_means	mean_diff	0.01	0.06	-0.18	0	0	0	0.04	-0.01	0	0.01

As a final check, we compare our design to an established standard: a pair-randomized experiment. If we were to randomize which member of a pair perceived more versus less mask wearing in their social network, we would expect no systematic relationships between perceptions and these covariates within pairs — across many covariates, we would see some relationships, but if we were really to randomize, we would know exactly the distribution that these differences would take. This kind of firm knowledge of a standard for an unconfounded design suggests that we compare our non-randomized design to the equivalent randomized design in the process of arguing in favor of the design. Moreover @hansenbowers2008 showed that a single test can summarize the relationship between many covariates and a randomized intervention — thus allowing us to avoid the multiple comparisons problem of looking at many different covariate tests. That result for this design provides us with p=0.65 for the test of the hypothesis that the covariate-to-perception relationship is what we would observe in an experiment: that is, we have no strong argument against that null in this case. The subsequent table summarizes the variable-by-variable results. Again, we see that the person who is ranked as perceiving more positive health behaviors is no more or less likely to be older, etc.. That is, those covariates cannot strongly confound any comparisons we make within these pairs.

```
xbres$overall
```

```
        chisquare df p.value
matched     5.056  7  0.6531
xbres_vars <- data.frame(xbres$results[, c("rankperc=0", "rankperc=1", "adj.diff", "std.diff", "p"), "matched"])
xbres_vars$padj <- p.adjust(xbres_vars$p, method = "holm")
kable(arrange(xbres_vars, p), digits = 3)
```

	rankperc.0	rankperc.1	adj.diff	std.diff	p	padj
educ	3.677	3.733	0.056	0.038	0.132	1
faminc_new.NATRUE	0.078	0.066	-0.012	-0.047	0.297	1
covid_know	0.763	0.771	0.007	0.052	0.388	1
agegood	48.896	48.718	-0.177	-0.010	0.534	1
relig_scale	0.329	0.336	0.006	0.033	0.557	1
faminc_new	6.282	6.320	0.039	0.012	0.672	1
ideo5	3.029	3.036	0.007	0.005	0.888	1
trust_in_science	3.907	3.907	0.000	0.000	1.000	1
covid_subj_know	3.976	3.976	0.000	0.000	1.000	1
covid_know.NATRUE	0.061	0.061	0.000	0.000	1.000	1
covid_subj_know.NATRUE	0.939	0.939	0.000	0.000	1.000	1

0.2   Outcome Analysis

Our analysis of outcomes is quite simple: we regress reports of respondents' own intentions to be vaccinated, test, and wear masks on reports of those respondents' perception of such intentions in their social networks, conditional on pair. This amounts to comparing the own-intentions of the higher-perceiver within pair to the own-intentions of the lower-perceiver within pair and taking the average. We report HC2 standard errors.

I am just printing out the results here in raw form. First the scales of the variables to make interpretation easier:

```
somevars <- unique(c(
  all.vars(formula(lm_perc_fam)),
```

```
  all.vars(formula(lm_perc_neigh)),
  all.vars(formula(lm_perc_city)),
  all.vars(formula(lm_perc_state)),
  all.vars(formula(lm_mask_fam)),
  all.vars(formula(lm_test_fam))
))
```

```
kableExtra::kable(summary(dat3[, somevars]))
```

	q1	q60_1a	q60_2a	q60_3a	q60_4a	q7	q100	q29	q25new
	Min. :1.00	Min. :0.00	Min. :0.00	Min. :0.00	Min. :0.00	Min. :1.00	Min. :2.0	Min. :1.00	Min. :1.00
	1st Qu.:3.00	1st Qu.:1.00	1st Qu.:2.00	1st Qu.:2.00	1st Qu.:3.00	1st Qu.:2.00	1st Qu.:4.0	1st Qu.:4.00	1st Qu.:2.00
	Median :4.00	Median :3.00	Median :3.00	Median :3.00	Median :3.00	Median :4.00	Median :4.0	Median :5.00	Median :2.00
	Mean :3.76	Mean :3.09	Mean :2.83	Mean :3.04	Mean :3.18	Mean :3.39	Mean :4.2	Mean :4.64	Mean :3.03
	3rd Qu.:5.00	3rd Qu.:5.00	3rd Qu.:4.00	3rd Qu.:4.00	3rd Qu.:4.00	3rd Qu.:5.00	3rd Qu.:5.0	3rd Qu.:6.00	3rd Qu.:4.00
	Max. :5.00	Max. :6.00	Max. :6.00	Max. :6.00	Max. :6.00	Max. :5.00	Max. :5.0	Max. :6.00	Max. :7.00
	NA	NA	NA	NA	NA	NA	NA's :774	NA	NA

Perceptions of vaccination intentions of others strongly predicts own intentions — recall that we are very strongly holding constant ideology here.

```
lm_perc_fam
```

```
       Estimate Std. Error t value Pr(>|t|) CI Lower CI Upper  DF
q60_1a   0.3451    0.03021   11.42 1.96e-26   0.2857   0.4045 411
```
```
lm_perc_neigh
```

```
       Estimate Std. Error t value  Pr(>|t|) CI Lower CI Upper  DF
q60_2a   0.2975    0.03636   8.183 3.511e-15    0.226    0.369 411
```
```
lm_perc_city
```

```
       Estimate Std. Error t value  Pr(>|t|) CI Lower CI Upper  DF
q60_3a   0.2812    0.04161   6.758 4.793e-11   0.1994    0.363 411
```
```
lm_perc_state
```

```
       Estimate Std. Error t value    Pr(>|t|) CI Lower CI Upper  DF
q60_4a      0.24    0.04854   4.945 0.000001113   0.1446   0.3354 411
```

Notice the pattern: family predicts more strongly than neighborhood, and in turn neighborhood than city, and city than state. Could we see this by chance? We used a seemingly unrelated regression framework to test hypotheses of equality among the coefficients shown above:

```
test_fam_vs_bigger
```

```
Linear hypothesis test (Chi^2 statistic of a Wald test)

Hypothesis:
fam_q60_1a_c - neigh_q60_2a_c = 0
fam_q60_1a_c - city_q60_3a_c = 0
fam_q60_1a_c - state_q60_4a_c = 0

Model 1: restricted model
Model 2: sursfit

  Res.Df Df Chisq Pr(>Chisq)
1   3291
2   3288  3  8.04      0.045 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
```
test_neigh_vs_bigger
```

```
Linear hypothesis test (Chi^2 statistic of a Wald test)

Hypothesis:
neigh_q60_2a_c - city_q60_3a_c = 0
neigh_q60_2a_c - state_q60_4a_c = 0

Model 1: restricted model
Model 2: sursfit

  Res.Df Df Chisq Pr(>Chisq)
1   3290
2   3288  2  1.89       0.39
```
```
test_city_vs_bigger
```

```
Linear hypothesis test (Chi^2 statistic of a Wald test)
```

4

```
Hypothesis:
city_q60_3a_c - state_q60_4a_c = 0

Model 1: restricted model
Model 2: sursfit

  Res.Df Df Chisq Pr(>Chisq)
1   3289
2   3288  1  0.89       0.35
```

The effects of social perceptions of mask wearing and testing on those intentions.

```
summary(lm_mask_fam)
```

```
Call:
lm_robust(formula = q7 ~ q100, data = dat3, fixed_effects = ~bm)

Standard error type:  HC2

Coefficients:
     Estimate Std. Error t value Pr(>|t|) CI Lower CI Upper DF
q100    0.927     0.0475    19.5 3.15e-16    0.829     1.02 24

Multiple R-squared:  0.875 ,    Adjusted R-squared:  0.745
Multiple R-squared (proj. model):  0.783 ,  Adjusted R-squared (proj. model):  0.556
F-statistic (proj. model):  381 on 1 and 24 DF,  p-value: 3.15e-16
```

```
summary(lm_test_fam)
```

```
Call:
lm_robust(formula = q29 ~ q25new, data = dat3, fixed_effects = ~bm)

Standard error type:  HC2

Coefficients:
       Estimate Std. Error t value Pr(>|t|) CI Lower CI Upper  DF
q25new    0.288     0.0525    5.48 7.46e-08    0.184    0.391 411

Multiple R-squared:  0.59 , Adjusted R-squared:  0.178
Multiple R-squared (proj. model):  0.0785 , Adjusted R-squared (proj. model):  -0.845
F-statistic (proj. model):   30 on 1 and 411 DF,  p-value: 7.46e-08
```

1 Sensitivity Analysis

This study was not randomized, but we are making statistical inferences as if it were — as if perceptions were randomly assigned within these pairs. We know that we have some biases here, but are limited in regards our data. Although we have adjusted for some of the largest drivers of perceptions, we have not managed to control them all. How large of an unobserved effect on perceptions have to be in order to over turn our results? We present two modes of sensitivity analysis here.

1.1 Hazlett and Cinelli

Our first approach builds on the approach in Cinelli and Hazlett in which they posit a linear regression model and imagine unobserved confounders. They propose a "Robustness Value" or a value of the influence of an unobserved confounder on **both** the outcome and treatment above which our substantive interpretation of our result would change. For example, we print out the results for the effect of perceptions of family below. The key piece for us is the `Robustness Value, q=1,alpha=.05`: this is the value above which we could no longer claim to detect effects (the other values are more liberal — values that would be required to make our relationships exactly zero in magnitude).

```
sens_perc_fam <- sensemakr(
  estimate = lm_perc_fam$coef["q60_1a"],
  se = lm_perc_fam$std.error["q60_1a"], dof = lm_perc_fam$df
)
summary(sens_perc_fam)
```

```
Sensitivity Analysis to Unobserved Confounding

Model Formula: "Data provided manually"

Null hypothesis: q = 1 and reduce = TRUE
-- This means we are considering biases that reduce the absolute value of the current estimate.
```

```
-- The null hypothesis deemed problematic is H0:tau = 0

Unadjusted Estimates of 'D':
  Coef. estimate: 0.345
  Standard Error: 0.03
  t-value (H0:tau = 0): 11.42

Sensitivity Statistics:
  Partial R2 of treatment with outcome: 0.241
  Robustness Value, q = 1: 0.427
  Robustness Value, q = 1, alpha = 0.05: 0.37

Verbal interpretation of sensitivity statistics:

-- Partial R2 of the treatment with the outcome: an extreme confounder (orthogonal to the covariates) that explains 100% of the residual variance

-- Robustness Value, q = 1: unobserved confounders (orthogonal to the covariates) that explain more than 42.7% of the residual variance of both th

-- Robustness Value, q = 1, alpha = 0.05: unobserved confounders (orthogonal to the covariates) that explain more than 37% of the residual varianc
sens_perc_fam

Sensitivity Analysis to Unobserved Confounding

Model Formula: "Data provided manually"

Null hypothesis: q = 1 and reduce = TRUE

Unadjusted Estimates of ' D ':
  Coef. estimate: 0.345
  Standard Error: 0.03
  t-value: 11.42

Sensitivity Statistics:
  Partial R2 of treatment with outcome: 0.241
  Robustness Value, q = 1 : 0.427
  Robustness Value, q = 1 alpha = 0.05 : 0.37

For more information, check summary.
```

So, we would need some covariates that are unrelated the variables included in the pairing that would explain more than 37% of the variation in **both** the outcome **and** perceptions in order for our statistical tests to not-reject the null of no effects.

The other Robustness Values are displayed below.

All of the values are pretty large: what can we imagine that could predict perceptions and vaccination intention independently of all of the variables in the pairing as strongly as would be required below?

```
get_rv_qa_value <- function(model) {
  res <- sensemakr(
    estimate = model$coef[1],
    se = lm_perc_fam$std.error[1], dof = lm_perc_fam$df
  )
  return(res$sensitivity_stats$rv_qa)
}

robustness_values <- sapply(ls(patt = "^lm_mask|^lm_perc|^lm_test"), function(lmname) {
  get_rv_qa_value(get(lmname))
})

sort(robustness_values, decreasing = TRUE)

  lm_mask_fam   lm_perc_fam lm_perc_neigh   lm_test_fam  lm_perc_city lm_perc_state
       0.7325        0.3701        0.3204        0.3096        0.3024        0.2545
```

1.2   Rosenbaum Style

Paul Rosenbaum developed an approach to sensitivity analysis that Hazlett and Cinelli build on. It involves positing an unobserved factor that, within pair, changes the probability of "selection into treatment" away from uniform. Our "treatment" variable here has 7 categories, so we change the analysis a bit here: the question becomes whether the person who perceives more within a pair (rank of perceptions = 1) also tends to be the person with more positive vaccination intentions. In this formulation, if two people do not differ in perceptions, then this pair adds nothing to the analysis and they are dropped. The table below shows the estimates and p-values from a regression of outcomes on within-pair rank in perception.

```r
dat3 <- dat3 %>%
  group_by(bm) %>%
  mutate(
    q60_1a_rank = rank(q60_1a) - 1,
    q60_2a_rank = rank(q60_2a) - 1,
    q60_3a_rank = rank(q60_3a) - 1,
    q60_4a_rank = rank(q60_4a) - 1,
    q100_rank = rank(q100) - 1,
    q25_new_rank = rank(q25new) - 1
  ) %>%
  ungroup()

## Notice that sometimes the higher perceiver has a 1 and sometimes a 6 (mostly higher numbers of course).
with(dat3, table(q60_1a_rank, q60_1a, exclude = c()))
```

```
           q60_1a
q60_1a_rank   0   1   2   3   4   5   6
        0    41 119  48  75  43  13   0
        0.5  10  36   2  30  16  50   2
        1     0  19  22  67  58 121  52
```

```r
lm_perc_fam_rank <- lm_robust(q1 ~ q60_1a_rank, fixed_effects = ~bm, data = dat3)
lm_perc_neigh_rank <- lm_robust(q1 ~ q60_2a_rank, fixed_effects = ~bm, data = dat3)
lm_perc_city_rank <- lm_robust(q1 ~ q60_3a_rank, fixed_effects = ~bm, data = dat3)
lm_perc_state_rank <- lm_robust(q1 ~ q60_4a_rank, fixed_effects = ~bm, data = dat3)
lm_mask_fam_rank <- lm_robust(q7 ~ q100_rank, fixed_effects = ~bm, data = dat3)
lm_test_fam_rank <- lm_robust(q29 ~ q25_new_rank, fixed_effects = ~bm, data = dat3)

## These are just to help us understand the results below:
## the pattern of estimates and statistical tests should be the same as when we use the full scale
lm_rank_res_lst <- lapply(ls(patt = "_rank$"), function(lmnm) {
  res <- tidy(get(lmnm))
  res$model <- lmnm
  return(res)
})
lm_rank_res <- bind_rows(lm_rank_res_lst) %>%
  select(term, estimate, p.value, conf.low, conf.high, model, outcome) %>%
  mutate(across(where(is.numeric), round, 3))
lm_rank_res
```

```
          term estimate p.value conf.low conf.high              model outcome
1    q100_rank   -0.157   0.087   -0.336     0.023   lm_mask_fam_rank      q7
2  q60_3a_rank    0.497   0.000    0.324     0.670   lm_perc_city_rank     q1
3  q60_1a_rank    0.776   0.000    0.619     0.933   lm_perc_fam_rank     q1
4  q60_2a_rank    0.598   0.000    0.440     0.755 lm_perc_neigh_rank     q1
5  q60_4a_rank    0.399   0.000    0.215     0.582 lm_perc_state_rank     q1
6 q25_new_rank    0.719   0.000    0.481     0.956   lm_test_fam_rank    q29
```

```r
## here is the p-value with no bias
find_gamma_lim(g = 1, y = "q1", dat = dat3, z = "q60_1a_rank", return = "all")$pval
```

```
[1] 0
```

```r
lm_perc_fam_rank ## notice basically same
```

```
            Estimate Std. Error t value  Pr(>|t|) CI Lower CI Upper  DF
q60_1a_rank   0.7758    0.07976   9.727 2.918e-20    0.619   0.9326 411
## Now find the Gamma (or size of the selection effect) required to drive p>=.05
sens_perc_fam_G <- uniroot(f = find_gamma_lim, y = "q1", z = "q60_1a_rank", dat = dat3, lower = 1, upper = 20)
## Here is the Gamma value: the covariate has to cause the person to be 4 times more likely to be the higher perceiver within the same pair
sens_perc_fam_G$root
```

```
[1] 3.498
```

```r
## Showing the the p value is .0501 in this case
find_gamma_lim(g = sens_perc_fam_G$root, y = "q1", z = "q60_1a_rank", dat = dat3, return = "all")$pval
```

```
[1] 0.05099
```

```r
## Now for the other variables
gamma_vals <- sapply(1:nrow(lm_rank_res), function(i) {
  message(lm_rank_res[i, "outcome"], " ", lm_rank_res[i, "term"])
  res_G <- try(uniroot(f = find_gamma_lim, y = lm_rank_res[i, "outcome"], z = lm_rank_res[i, "term"], dat = dat3, lower = 1, upper = 20))
  if (inherits(x = res_G, "try-error")) {
    res_G$root <- NA
  }
  return(res_G$root)
})
names(gamma_vals) <- lm_rank_res$term[1:nrow(lm_rank_res)]
sort(gamma_vals, decreasing = TRUE, na.last = TRUE)
```

```
 q60_1a_rank  q60_2a_rank q25_new_rank  q60_3a_rank  q60_4a_rank     q100_rank
```

```
      3.498         2.381         1.879         1.857         1.451         1.013
```

Notice that the stronger the relationship, the larger the bias required to drive the p-value above .05. Strongest effect is family, for example.

This next is the Rosenbaum and Silber approach to interpreting sensitivity parameters. Notice that the basic gamma values assume a gigantic relationship with the outcome.

```r
amps <- lapply(gamma_vals, function(theg) {
  if (is.na(theg)) {
    return(NA)
  }
  message(theg)
  my_amplify(theg, lambda = seq(theg + .001, 10))
})
names(amps) <- names(gamma_vals)

amps
```

```
$q100_rank
       delta lambda
 [1,] 27.310  1.014
 [2,]  1.039  2.014
 [3,]  1.026  3.014
 [4,]  1.022  4.014
 [5,]  1.020  5.014
 [6,]  1.018  6.014
 [7,]  1.017  7.014
 [8,]  1.017  8.014
 [9,]  1.016  9.014

$q60_3a_rank
         delta lambda
 [1,] 2449.421  1.858
 [2,]    4.302  2.858
 [3,]    3.080  3.858
 [4,]    2.672  4.858
 [5,]    2.468  5.858
 [6,]    2.346  6.858
 [7,]    2.265  7.858
 [8,]    2.206  8.858
 [9,]    2.163  9.858

$q60_1a_rank
          delta lambda
[1,] 11239.785  3.499
[2,]    14.723  4.499
[3,]     9.113  5.499
[4,]     7.242  6.499
[5,]     6.306  7.499
[6,]     5.745  8.499
[7,]     5.370  9.499

$q60_2a_rank
         delta lambda
[1,] 4673.846  2.382
[2,]    7.048  3.382
[3,]    4.716  4.382
[4,]    3.938  5.382
[5,]    3.549  6.382
[6,]    3.316  7.382
[7,]    3.160  8.382
[8,]    3.049  9.382

$q60_4a_rank
         delta lambda
 [1,] 1106.020  1.452
 [2,]    2.554  2.452
 [3,]    2.003  3.452
 [4,]    1.819  4.452
 [5,]    1.727  5.452
 [6,]    1.672  6.452
 [7,]    1.635  7.452
 [8,]    1.608  8.452
 [9,]    1.589  9.452

$q25_new_rank
        delta lambda
[1,] 2533.117   1.88
[2,]    4.408   2.88
```

```
[3,]    3.144   3.88
[4,]    2.723   4.88
[5,]    2.512   5.88
[6,]    2.385   6.88
[7,]    2.301   7.88
[8,]    2.241   8.88
[9,]    2.196   9.88
```

```r
amps_min <- sapply(amps[!is.na(amps)], function(mat) {
  mat[2, ]
})
## We are not looking at Independents because they are to heterogeneous
## So only consider q60_1 to 6 (not 7).
## The 4a result arises from using ranks (p=.08). So excluding that one too.
amps_min[, c("q60_1a_rank", "q60_2a_rank", "q60_3a_rank", "q60_4a_rank")]
```

```
        q60_1a_rank q60_2a_rank q60_3a_rank q60_4a_rank
delta        14.723       7.048       4.302       2.554
lambda        4.499       3.382       2.858       2.452
```

The p-value that we see for a given Γ (like 1.0131) can be produced from an unobserved covariate that increases the treatment odds (within all pairs) by lambda and increases the odds of a positive pair difference in outcomes by delta.

1.3   Auxiliary analyses

What if, in every pair, the person who reports that she perceives more vaccination support among her family and friends, neighbors, and people in her city and state does so because she *hopes* that they will be vaccinated — that is, she herself believes vaccination is good, so she hopes that those close to her will be vaccinated. This kind of wishful thinking or imagining a consensus almost certainly does not occur in *every* pair, but yet, we wonder in how many pairs we might see this phenomenon. Notice that saying "no one will vaccinate" for all levels and saying "everyone will vaccinate" at all levels both indicates a kind of wishful thinking (either believing that vaccination is bad and no one should do it, and believing that it is good that everyone should do it.) How many people exhibit this kind of response pattern? Do people with these response patterns tend to also report either a strongly negative or positive own intention? If few do, and this pattern does not strongly predict own intention, then we have less concern about wishful thinking driving our results.

Furthermore, we should note that this kind of false consensus or reverse causality would not necessarily imply the pattern of results that we see: someone who is not actually reporting perceptions but hopes or rationalizations is likely to project those to all groups, and not first to family and friends (or most strongly to them) and then less strongly as the group becomes more distant and diffuse.

We see here that very few people show this response pattern, too few to overturn our results (considering the sensitivity analysis above). Also, notice that those having this pattern are not perfectly homogeneous in their own intentions — those reporting that all will definitely be vaccinated at all levels are very likely to say that they will be vaccinated, and the converse is also true, but this is not a perfect relationship.

```r
table(dat3$q60_1a, exclude = c())
```

```
  0   1   2   3   4   5   6
 51 174  72 172 117 184  54
```

```r
table(dat3$q60_2a, exclude = c())
```

```
  0   1   2   3   4   5   6
 36 152 133 238 145  98  22
```

```r
table(dat3$q60_3a, exclude = c())
```

```
  0   1   2   3   4   5   6
 16 106 131 285 169  99  18
```

```r
table(dat3$q60_4a, exclude = c())
```

```
  0   1   2   3   4   5   6
 14  58 113 332 205  91  11
```

```r
dat3 <- dat3 %>% mutate(
  perc_all_vax = as.numeric(q60_1a == 6 & q60_2a == 6 & q60_3a == 6 & q60_4a == 6),
  perc_none_vax = as.numeric(q60_1a == 0 & q60_2a == 0 & q60_3a == 0 & q60_4a == 0)
)
```

```
## Very few people have this response pattern:
with(dat3, table(perc_all_vax, exclude = c()))
```

```
perc_all_vax
  0   1
818   6
```

```
with(dat3, table(perc_none_vax, exclude = c()))
```

```
perc_none_vax
  0   1
814  10
```

```
with(dat3, table(perc_all_vax, q1, exclude = c()))
```

```
            q1
perc_all_vax   1   2   3   4   5
           0  87  47 166 197 321
           1   0   1   0   0   5
```

```
with(dat3, table(perc_none_vax, q1, exclude = c()))
```

```
             q1
perc_none_vax   1   2   3   4   5
            0  83  48 163 194 326
            1   4   0   3   3   0
```

2 References