

When “Representative” Surveys Fail:  
Can a Non-ignorable Missingness Mechanism Explain Bias  
in Estimates of COVID-19 Vaccine Uptake?

Rebecca Andridge

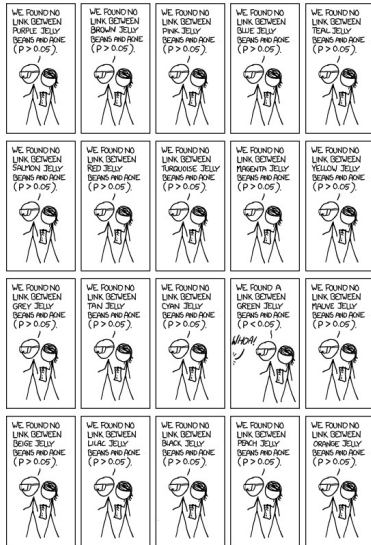
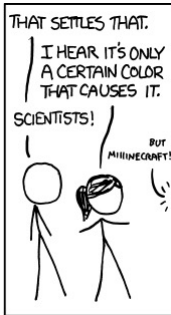
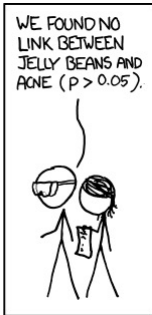
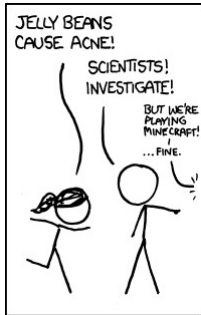
The Ohio State University College of Public Health

March 13, 2024

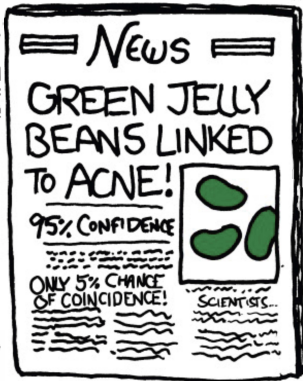
# Outline

- 1 The Problem
- 2 The Large COVID-19 Surveys
- 3 Proxy Pattern-Mixture Model (PPMM) for Binary Outcomes
- 4 Results from Applying PPMM to COVID-19 Surveys
- 5 Summary and Related/Future Work

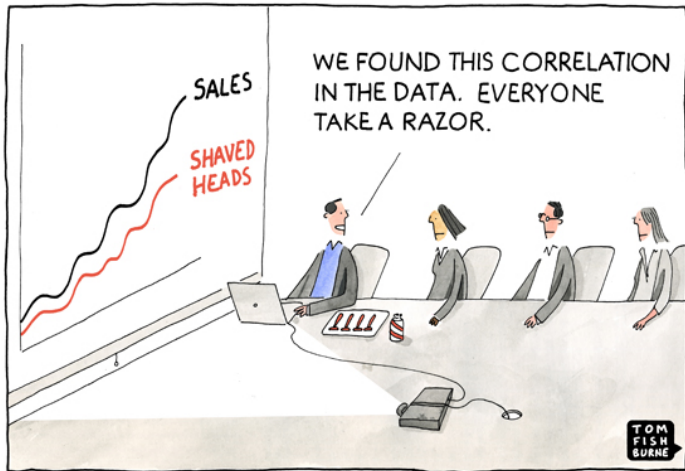
# "Big Data": Friend or Foe?



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# "Big Data": Friend or Foe?

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by Tom Fishburne



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# “Big Data”: Friend or Foe?

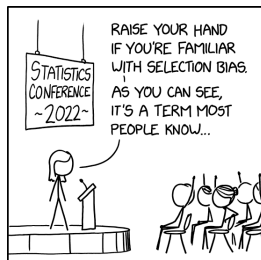
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- Multiple testing
- “Spurious correlations”

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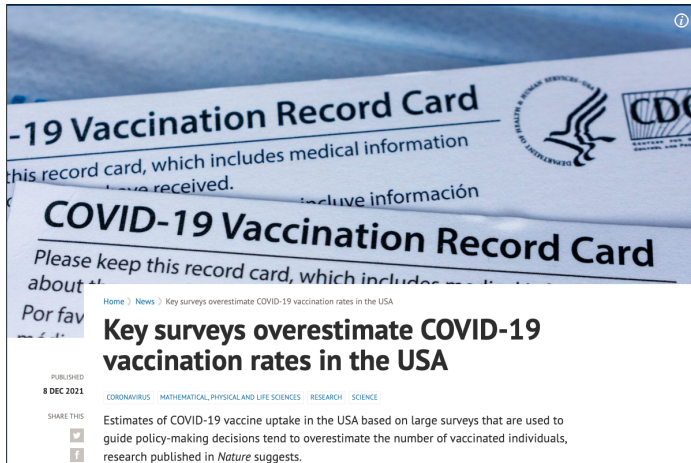
Another major issue: **Selection bias**

Also a problem for “Big Surveys” with **low response rates**

- “Big Data” = Non-probability samples → **Selection bias**
- “Big Surveys” = Probability samples → **Nonresponse bias**

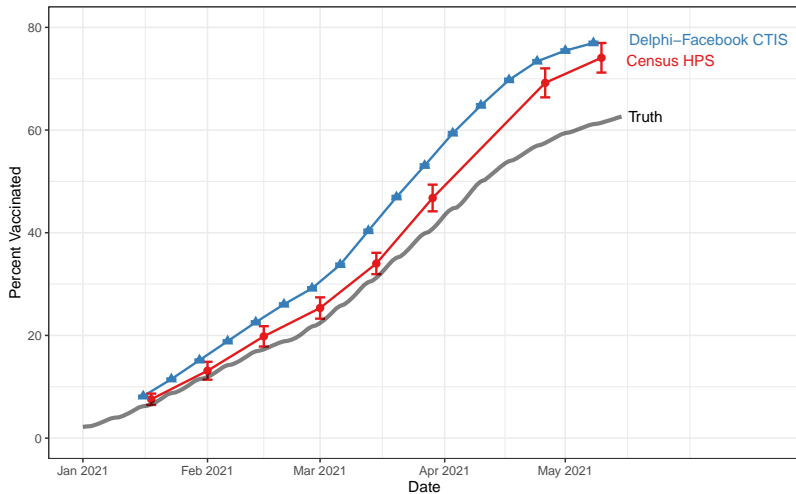


# “Big (COVID) Surveys” = “Big Miss” . . .



Published study: Bradley et al. 2021, Nature

# (Over-)Estimation of COVID-19 Vaccine Uptake



*“Big Data Paradox: The bigger the data, the surer we fool ourselves”* (Meng 2018, p.702)

# Problem Statement

**Goal:** Estimate population proportion from probability samples with very low response rates (effectively non-probability samples)

→ *Proportion having at least one dose of COVID-19 vaccine*

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**Approach:** Use the **Proxy Pattern-Mixture Model (PPMM)** to assess potential nonresponse/selection bias in proportion estimates (Andridge and Little 2020; Andridge et al. 2019)

→ *Sensitivity analysis allowing survey participation to depend on vaccine status*

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# Census Household Pulse Survey (HPS)\*

- Launched April 23, 2020; still ongoing
- Collaboration between 8+ agencies
- Online survey (Qualtrics)
- Repeated cross-sectional probability samples
- Sampling frame: Census Bureau Master Address File  
*where at least one email address or cell phone known*
- 1- and then 2-week waves
- n=68,000-80,000 respondents per wave [Jan-May 2021]



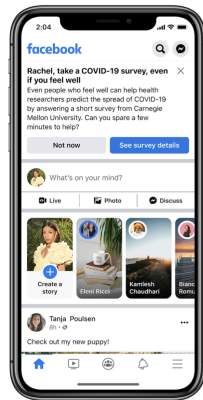
Q: *Have you received a COVID-19 vaccine?* {Yes, No}

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\* <https://www.census.gov/data/experimental-data-products/household-pulse-survey.html>

# Delphi-Facebook COVID-19 Trends and Impacts Survey (CTIS)\*

- Launched April 6, 2020; Ended June 25, 2022
- Both U.S. and Global samples
- Online survey (Qualtrics)
- Repeated cross-sectional probability samples
- Sampling frame: Facebook users 18+ who were active on the platform in the last month
- Daily samples (pooled into weekly waves)
- n=160,000-290,000 respondents per wave [Jan-May 2021]



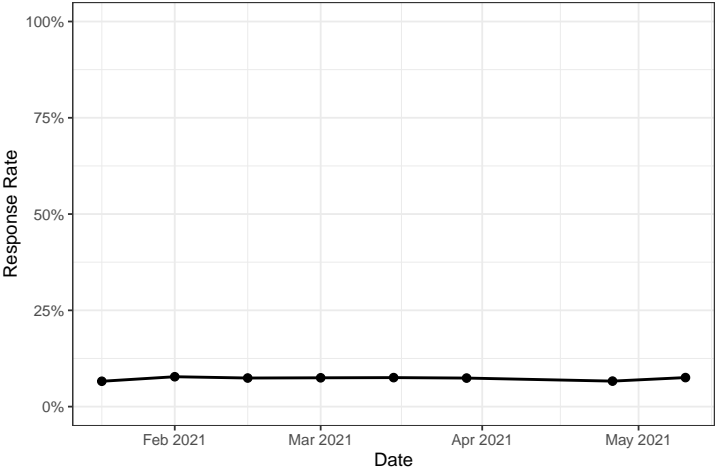
Q: *Have you had a COVID-19 vaccination?* {Yes, No, I don't know}

\* <https://delphi.cmu.edu/covid19/ctis/>



# Big Surveys, Small Response Rates

Census HPS Response Rates\*



\* Percent who responded out of all sampled persons

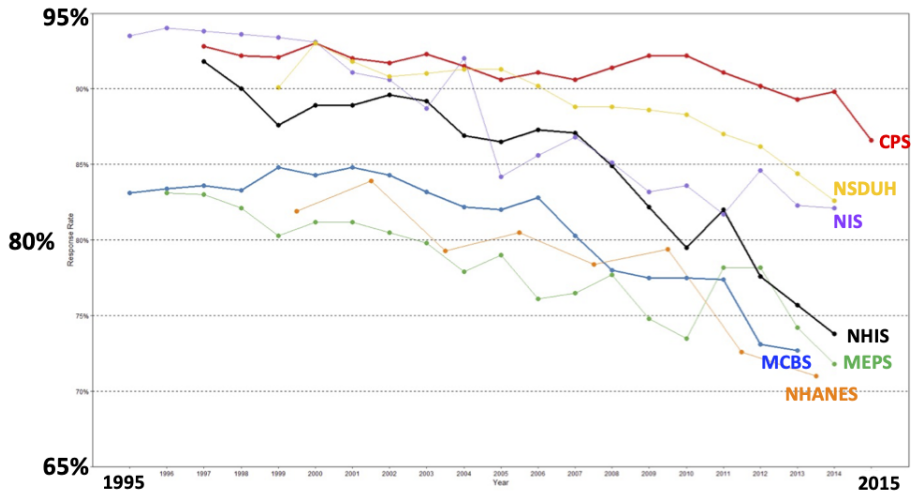
# Big Surveys, Small Response Rates

## Delphi-Facebook Cooperation Rates\*



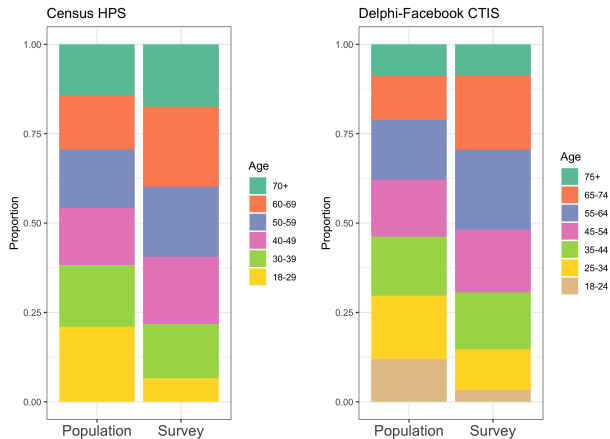
\* Percent who responded out of all who saw survey invite (logged into FB)

# Compare to Traditional "Big Survey" Response Rates



# COVID Surveys: Respondents don't resemble Population

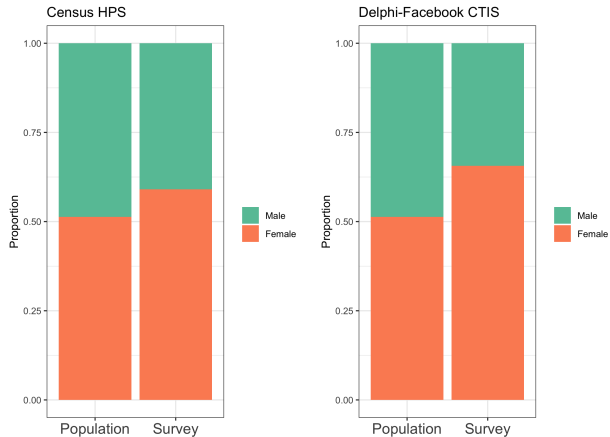
Age\*



\* Demographics shown for last wave analyzed of each survey

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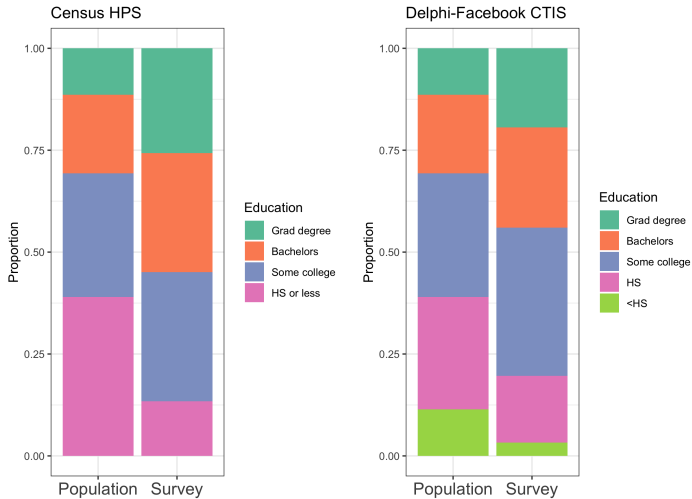
## Gender\*



\* Limitation: gender used as a binary variable

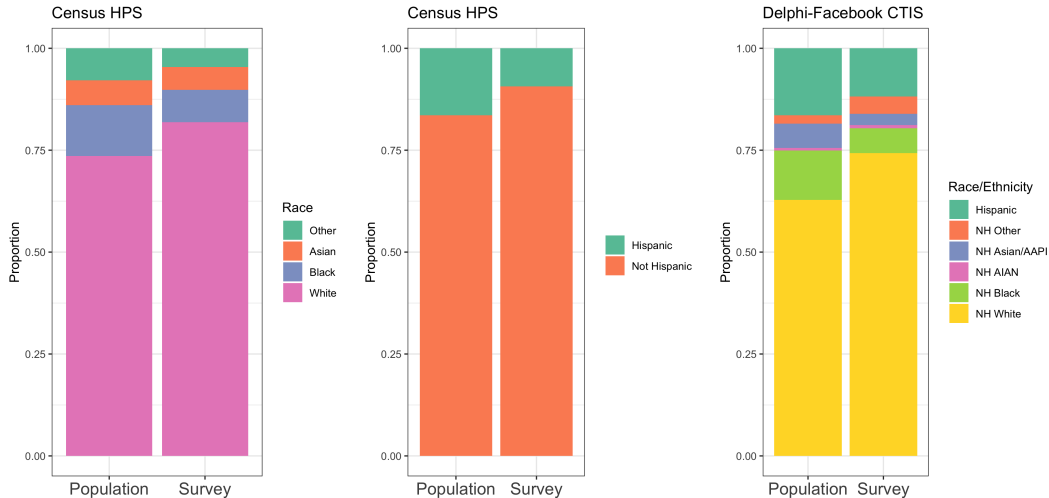
# COVID Surveys: Respondents don't resemble Population

## Education



# COVID Surveys: Respondents don't resemble Population

## Race and Ethnicity



## Solution: Nonresponse Weighting Adjustments

- Adjust sample weights to make respondents “look like” population
  - ▶ Upweight male, younger, lower education, non-white



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- Both surveys did this, but with limited demographic information:
  - ▶ Census HPS: age, gender<sup>1</sup>, race/ethnicity, education, state
  - ▶ Delphi-Facebook: age, gender<sup>2</sup>
  - ▶ Population data sources: American Community Survey, Current Population Survey

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<sup>1</sup>Limitation: gender collected as a binary variable

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- Weighting makes respondents look like the population **with respect to the weighting variables**
- Assumes that two people of the same (age, gender, race/ethnicity, education) or (age, gender) are **interchangeable**, one who participated and one who did not

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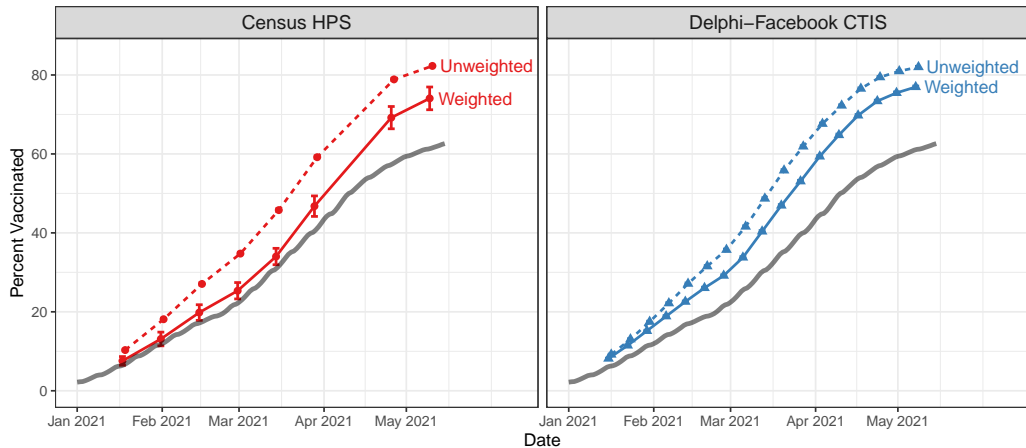
**Do we believe this assumption? In the context of COVID?**

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# Weighting Helped Somewhat... But Not Enough!



Weighted estimates closer to truth, but still biased  
Let's see if the PPMM can do better!

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## PPMM for Binary Outcomes

- $Y$  = binary variable of interest, only available for respondents
  - ▶ Individual has received 1+ dose of vaccine
- $Z$  = auxiliary variables, available for respondents and **in aggregate** for population ( $\bar{Z}$ )
  - ▶ Age, gender, race/ethnicity, education (HPS)
- $S$  = indicator for unit selected **and** responded

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  - ▶  $Y = 1$  when  $U > 0$

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  - ▶  $Y = 1$  when  $U > 0$
- $X$  = “proxy” for  $Y$ , based on  $Z$ 
  - ▶ Constructed from probit regression:  $P(Y = 1|Z, S = 1) = \Phi(\alpha_0 + \alpha Z)$
  - ▶ Available at individual-level for selected/respondents:  $X = \hat{\alpha}_0 + \hat{\alpha}Z$
  - ▶ Available in aggregate for rest of population:  $\bar{X} = \hat{\alpha}_0 + \hat{\alpha}\bar{Z}$
  - ▶ Proxy strength = Biserial  $\text{Corr}(Y, X|S = 1) = \text{Corr}(U, X|S = 1)$



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General approach:

- Use pattern-mixture models to specify  $f(Y, X, S) = f(Y, X|S)f(S)$
- Only  $f(Y, X|S = 1)$  identifiable (and  $f(X|S = 0)$ )
- Make explicit, untestable assumption(s) about  $S$  to identify  $f(Y, X|S = 0)$
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Trick for convenience:

- Use latent  $U$  instead of binary  $Y$

## PPMM: Theory

- Assume a proxy pattern-mixture model\* for  $U$  and  $X$  given  $S$ :

$$(U, X | S = j) \sim N_2 \left( \begin{bmatrix} \mu_u^{(j)} \\ \mu_x^{(j)} \end{bmatrix}, \begin{bmatrix} \sigma_{uu}^{(j)} & \rho_{ux}^{(j)} \sqrt{\sigma_{uu}^{(j)} \sigma_{xx}^{(j)}} \\ \rho_{ux}^{(j)} \sqrt{\sigma_{uu}^{(j)} \sigma_{xx}^{(j)}} & \sigma_{xx}^{(j)} \end{bmatrix} \right)$$
$$S \sim \text{Bernoulli}(\pi)$$

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$$\mu_y = \Pr(Y = 1) = \Pr(U > 0) = \underbrace{\pi \Phi \left( \mu_u^{(1)} \right)}_{\text{respondents}} + (1 - \pi) \underbrace{\Phi \left( \mu_u^{(0)} / \sqrt{\sigma_{uu}^{(0)}} \right)}_{\text{rest of pop.}}$$

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- Problem: **unidentified parameters** =  $\{ \mu_u^{(0)}, \sigma_{uu}^{(0)}, \rho_{ux}^{(0)} \}$

\* Andridge and Little 2011, 2020

## PPMM: Theory

- Non-identifiable parameters  $\{\mu_u^{(0)}, \sigma_{uu}^{(0)}, \rho_{ux}^{(0)}\}$  are just identified by assumption about selection/response mechanism:

$$\Pr(S = 1|U, X, V) = f((1 - \phi)X^* + \phi U, V)$$

- ▶  $X^* = \frac{X}{\sqrt{\sigma_{xx}^{(1)}}} =$  rescaled proxy  $X$
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    - ▶  $0 < \phi < 1 \rightarrow \Pr(S = 1|U, X, V) = f((1 - \phi)X^* + \phi U, V)$       **Non-ignorable selection**

## PPMM: Theory

For a specified  $\phi$  we can estimate  $\mu_y$ :

$$\hat{\mu}_y = \underbrace{\hat{\pi} \Phi \left( \hat{\mu}_u^{(1)} \right)}_{\text{respondents}} + (1 - \hat{\pi}) \underbrace{\Phi \left( \hat{\mu}_u^{(0)} / \sqrt{\hat{\sigma}_{uu}^{(0)}} \right)}_{\text{rest of pop.}}$$

where

$$\hat{\mu}_u^{(0)} = \hat{\mu}_u^{(1)} + \left( \frac{\phi + (1 - \phi)\hat{\rho}_{ux}^{(1)}}{\phi\hat{\rho}_{ux}^{(1)} + (1 - \phi)} \right) \left( \frac{\hat{\mu}_x^{(0)} - \hat{\mu}_x^{(1)}}{\sqrt{\hat{\sigma}_{xx}^{(1)}}} \right)$$

$$\hat{\sigma}_{uu}^{(0)} = 1 + \left( \frac{\phi + (1 - \phi)\hat{\rho}_{ux}^{(1)}}{\phi\hat{\rho}_{ux}^{(1)} + (1 - \phi)} \right)^2 \left( \frac{\hat{\sigma}_{xx}^{(0)} - \hat{\sigma}_{xx}^{(1)}}{\hat{\sigma}_{xx}^{(1)}} \right)$$

$\hat{\pi}$  = estimated selection fraction

Biserial correlation *in selected sample* ( $\hat{\rho}_{ux}^{(1)}$ ) a very important component

# Estimation

“Modified” Maximum Likelihood (MML) estimation:

- $\hat{\pi}$  = selection fraction
- $\left\{ \hat{\mu}_x^{(1)}, \hat{\sigma}_{xx}^{(1)}, \hat{\mu}_x^{(0)}, \hat{\sigma}_{xx}^{(0)} \right\}$  = standard ML estimates (e.g.,  $\hat{\mu}_x^{(1)} = \bar{x}_{resp}$ )
- $\hat{\rho}_{ux}^{(1)}$  = biserial correlation estimated via two-step method (Olsson et al. 1982)
- $\hat{\mu}_u^{(1)} = \Phi^{-1}(\hat{\mu}_y^{(1)}) = \Phi^{-1}(\bar{y}_{resp})$  = from two-step method
- Suggested sensitivity analysis:  $\phi = \{0, 0.5, 1\}$

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Bayesian approach:

- Non-informative priors for identified parameters
- Incorporates uncertainty in the probit regression model for  $Y|Z, S = 1$  that creates  $X$
- No info in data about  $\phi$ , so take  $\phi \sim \text{Uniform}(0, 1)$   
(other priors are possible)

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# Available Data: COVID Surveys

## Microdata for survey respondents ( $S = 1$ ):

- $Y$  = vaccination status (received at least one dose)
  - ▶ Missing data treatment follows what the surveys did for reporting:
    - ★ Census HPS: If missing, assume “no”
    - ★ Delphi-Facebook CTIS: If missing, drop ( $\approx 6-7\%$ )
- $Z$  = auxiliary variables
  - ▶ Census HPS: age, gender, race, ethnicity, education
  - ▶ Delphi-Facebook CTIS: age, gender, race/ethnicity, education
  - ▶ Missing data treatment:
    - ★ Census HPS: No missing data (singly imputed by Census)
    - ★ Delphi-Facebook CTIS: If missing any, drop ( $\approx 15\%$  additional)
- Sample sizes:
  - ▶ Census HPS:  $n \approx 68,000-80,000$  per wave
  - ▶ Delphi-Facebook CTIS:  $n \approx 160,000-290,000$  per week



## Available Data: Population

Aggregate data ( $\bar{Z}$ ) for rest of population ( $S = 0$ ):

- Source: 2019 American Community Survey
  - ▶ Weighted estimates from ACS treated as “known”
  - ▶ Same as using ACS totals for weight adjustments
- Technically, 2019 ACS gives  $\bar{Z}$  for the full population, not just nonresponding – but selection fraction is tiny  
( $N \approx 250$  million, largest  $n \approx 250$  thousand)

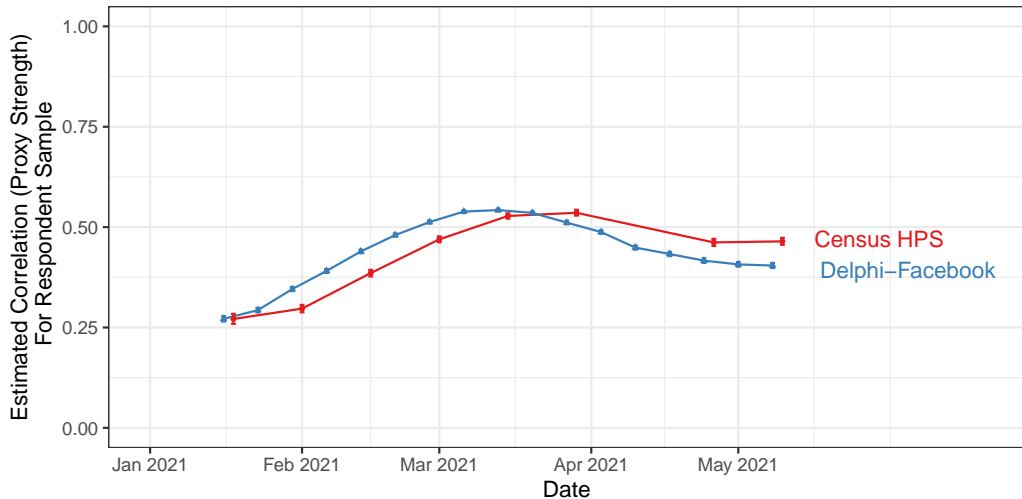
Population Truth:

- CDC benchmark numbers for vaccine uptake (retroactively corrected)

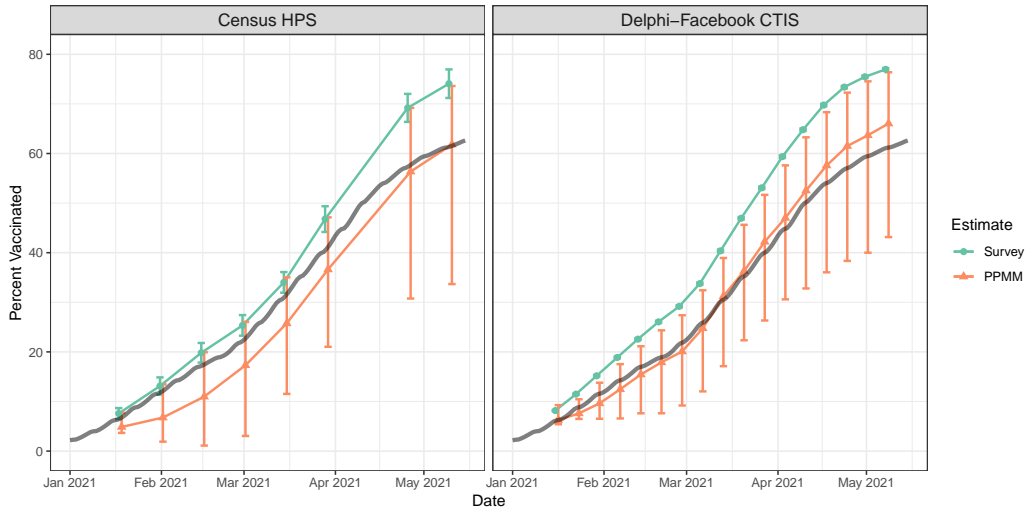
Estimation Details:

- Ignore sampling weights and treat as **non-probability samples**
- Bayesian approach with  $\phi \sim \text{Uniform}(0, 1)$

# Percent Vaccinated: Proxy Strength



# Percent Vaccinated: PPMM Estimates



## Percent Vaccinated: Summary

- PPMM correctly detected direction of selection bias for both surveys in all waves/weeks
- PPMM with  $\phi = 0.5$  remarkably close to truth for most CTIS weeks
- PPMM credible intervals cover the truth for both surveys in all waves/weeks
  - ▶ Direct survey estimates only covered truth twice (first two waves of Census HPS)
- PPMM credible intervals much wider than survey intervals despite large sample sizes
  - ▶ Reflects strength (weakness) of proxy model
  - ▶ Arguably a good feature: no “Big Data Paradox”!

# Percent Vaccine Hesitant

## Census HPS:

*Once a vaccine to prevent COVID-19 is available to you, would you . . .*

- 1 Definitely get a vaccine
- 2 Probably get a vaccine
- 3 Be unsure about getting a vaccine\* [hesitant]
- 4 Probably NOT get a vaccine [hesitant]
- 5 Definitely NOT get a vaccine [hesitant]

## Delphi-Facebook CTIS:

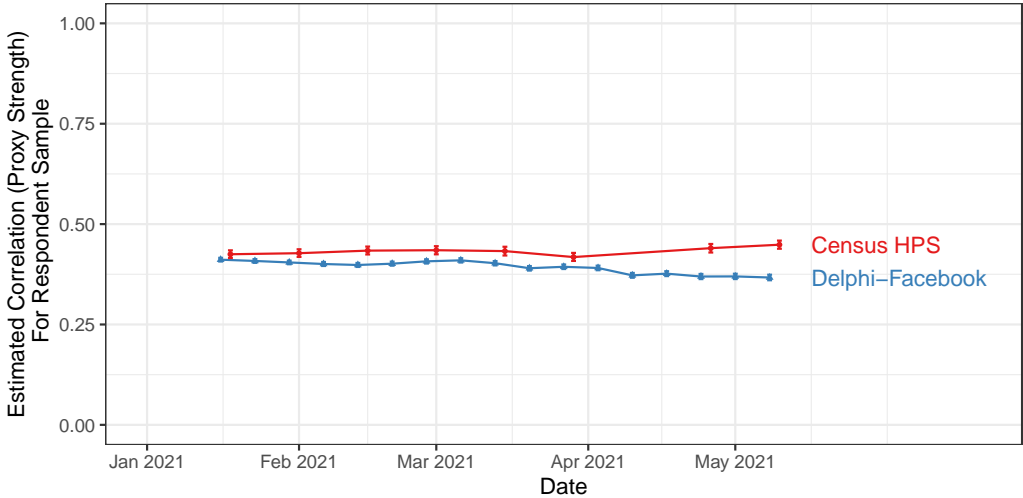
*If a vaccine to prevent COVID-19 were offered to you today, would you choose to get vaccinated?*

- 1 Yes, definitely
- 2 Yes, probably
- 3 No, probably not [hesitant]
- 4 No, definitely not [hesitant]

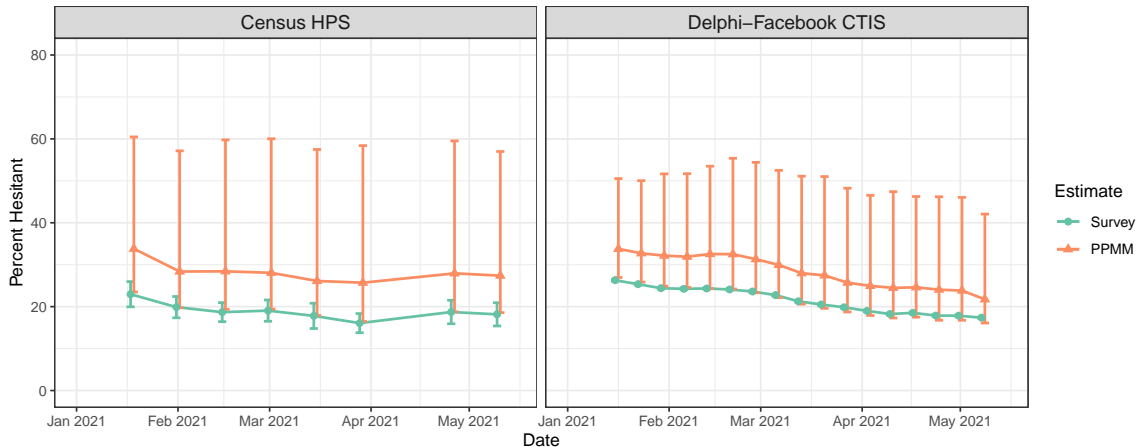
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\* option available starting in mid-April 2021

# Percent Vaccine Hesitant: Proxy Strength



# Percent Vaccine Hesitant: PPMM Estimates



$\phi = 0.5 \rightarrow$  hesitancy underestimated by  $\approx 9\%$  for HPS,  $\approx 7\%$  for CTIS

# Outline

- 1 The Problem
- 2 The Large COVID-19 Surveys
- 3 Proxy Pattern-Mixture Model (PPMM) for Binary Outcomes
- 4 Results from Applying PPMM to COVID-19 Surveys
- 5 Summary and Related/Future Work**



## Summary and Related Work

- PPMM provides a sensitivity analysis to assess the potential for non-ignorable nonresponse/selection bias
  - ▶  $\phi = 0$  – ignorable – could be “adjusted away”
  - ▶  $\phi = 1$  – extreme non-ignorable: selection depends only on  $Y$  (via  $U$ )
  - ▶  $\phi = 0.5$  – could be used as a compromise “estimate” of the bias

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  - ▶  $\phi = 0.5$  – could be used as a compromise “estimate” of the bias
- Only requires summary statistics for covariates  $Z$  for non-selected
  - ▶ Same information as often used for weighting
  - ▶ Could be used during data collection to compare potential for bias across a range of  $Y$
  - ▶ Easiest when population is well-defined and stable
    - ★ Example when it's *not* easy: Pre-election polling!\*
  - ▶ Key point: Need **strong predictors of  $Y$**  that are available at population-level

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\*West and Andridge 2023

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    - ★ Example when it's *not* easy: Pre-election polling!\*
  - ▶ Key point: Need **strong predictors of  $Y$**  that are available at population-level
- PPMMs also available for estimating means (including deviations from normality) and linear and probit regression coefficients<sup>†</sup>

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\* West and Andridge 2023

† Andridge and Little 2011, Little et al. 2020, Andridge and Thompson 2015, Yang and Little 2021, West et al. 2021

## Future Work / Extensions

### Methods development:

- Using the PPMM to generate non-ignorable selection weights
- Extend PPMM for nominal responses
- Extend PPMM to multivariate outcomes
- Adapt PPMM for generalizability of randomized trials in the presence of unmeasured effect modifiers (current R03)

### Additional applications:

- Apply PPMM to estimate *changes* in vaccine uptake (less biased?)
- Apply PPMM to variety of indicators to compare probability-based and opt-in online samples (AAPOR 2024 presentation)

Thank you!  
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Full paper online ahead of print:

Andridge, R.R. (2024). Using proxy pattern-mixture models to explain bias in estimates of COVID-19 vaccine uptake from two large surveys. *Journal of the Royal Statistical Society – Series A*,  
<https://doi.org/10.1093/jrssa/qnae005>.

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## BONUS SLIDE: How the PPMM Identification Works

Assumed model for  $U$  and  $X$  given  $S$ :  $(U, X|S = j) \sim$  Bivariate Normal

Assumed response mechanism:

$$\Pr(S = 1|U, X, V) = f((1 - \phi)X^* + \phi U, V)$$

If  $\phi = 0 \rightarrow$  response only depends on  $X$  (not  $U$ )

- Implies  $[U|X, S = 0] = [U|X, S = 1]$
- Regression parameters for  $[U|X, S = 0]$  are the same as for  $S = 1$
- Standard regression estimator (e.g., under MAR assumption)

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If  $0 < \phi < 1$ , let  $W = (1 - \phi)X^* + \phi U$  and  $[X|W, S = 0] = [X|W, S = 1]$