Vaccine 36 (2018) 751–757

Contents lists available at ScienceDirect

Vaccine

journal homepage: www.elsevier.com/locate/vaccine

The impact of selection bias on vaccine effectiveness estimates from test-negative studies

Michael L. Jackson *, C. Hallie Phillips, Joyce Benoit, Erika Kiniry, Lawrence Madziwa, Jennifer C. Nelson, Lisa A. Jackson

Kaiser Permanente Washington Health Research Institute, 1730 Minor Ave, Suite 1600, Seattle, WA 98101-1448, United States

ARTICLE INFO

Article history:
Received 6 June 2017
Received in revised form 5 December 2017
Accepted 7 December 2017
Available online 15 December 2017

Keywords:
Influenza
Human
Methodology
Bias (Epidemiology)
Vaccine effectiveness

ABSTRACT

Introduction: Estimates of vaccine effectiveness (VE) from test-negative studies may be subject to selection bias. In the context of influenza VE, we used simulations to identify situations in which meaningful selection bias can occur. We also analyzed observational study data for evidence of selection bias.
Methods: For the simulation study, we defined a hypothetical population whose members are at risk for acute respiratory illness (ARI) due to influenza and other pathogens. An unmeasured "healthcare seeking proclivity" affects both probability of vaccination and probability of seeking care for an ARI. We varied the direction and magnitude of these effects and identified situations where meaningful bias occurred. For the observational study, we reanalyzed data from the United States Influenza VE Network, an ongoing test-negative study. We compared "bias-naïve" VE estimates to bias-adjusted estimates, which used data from the source populations to correct for sampling bias.
Results: In the simulation study, an unmeasured care-seeking proclivity could create selection bias if persons with influenza ARI were more (or less) likely to seek care than persons with non-influenza ARI. However, selection bias was only meaningful when rates of care seeking between influenza ARI and non-influenza ARI were very different. In the observational study, the bias-naïve VE estimate of 55% (95% CI, 47-–62%) was trivially different from the bias-adjusted VE estimate of 57% (95% CI, 49-–63%).
Conclusions: In combination, these studies suggest that while selection bias is possible in test-negative VE studies, this bias in unlikely to be meaningful under conditions likely to be encountered in practice. Researchers and public health officials can continue to rely on VE estimates from test-negative studies.

1. Introduction

Observational studies of vaccine effectiveness (VE) are increasingly using the test-negative design [1]. In this design, eligible subjects are any patients who seek care for a defined clinical syndrome; in the case of influenza vaccine, this would be acute respiratory illness (ARI) or influenza-like illness (ILI). All enrolled subjects are tested for the pathogen of interest, and VE is estimated as one minus the ratio of the odds of vaccination among those testing positive to the odds among those testing negative. Although the test-negative design was first introduced in 1980 for estimating pneumococcal vaccine effectiveness [2], it did not see meaningful use until it began to be applied to observational studies of influenza vaccination in 2005 [3]. Since then, this design has become the standard approach for estimating influenza VE [4–6], and has been applied to rotavirus and cholera vaccines as well [7,8].

With the growing popularity of this design, research has increasingly focused on understanding the properties and potential biases of test-negative studies [9]. Recent studies have tested the underlying assumptions of the design [10–12], validated the design against randomized controlled trials [13], and evaluated the impact of information biases such as imperfect test sensitivity [14]. However, the potential impact of selection bias in this context has received little attention. Selection bias occurs when the association between vaccine and disease in the study subjects is different from the association in the full population [15]. For example, selection bias can arise in cohort studies through differential loss to follow-up between exposed and unexposed subjects, or in case-control studies through inappropriate selection of controls. Test-negative studies of influenza vaccines restrict the study population to persons seeking care for an ARI. Seeking care for ARI depends both on having an ARI and on factors that affect

* Corresponding author.
E-mail address: jackson.ml@ghc.org (M.L. Jackson).

https://doi.org/10.1016/j.vaccine.2017.12.022
0264-410X/

healthcare seeking behavior, such as socioeconomic status and insurance coverage. As pointed out by Sullivan and colleagues, conditioning (by restriction) on whether one seeks care for an ARI can induce selection bias [16].

While selection bias is theoretically possible in test-negative studies, the magnitude of this bias in practice is unclear. In this paper, we use simulations to quantify the magnitude of selection bias under a wide range of assumptions about the underlying associations between care-seeking behavior, influenza risk, and vaccination. We then look for evidence of selection bias in observational data where the full source population at-risk (from which the test-negative sample is drawn) is available to (1) estimate the probability of selection into a test-negative study using measured covariates and (2) use this information to correct VE estimates for potential selection bias. Specifically, we re-analyze data from Kaiser Permanente Washington (KP WA), one of the five sites in the United States Influenza Vaccine Effectiveness (US Flu VE) Network [5,17,18]. We compared naïve VE estimates using a test-negative design with estimates that account for selection bias using inverse probability of selection weighting (IPSW).

2. Methods

2.1. Simulation study

We simulated a series of test-negative influenza VE studies, with relevant variables defined by a directed acyclic graph (Fig. 1). We simulated a population of individuals who are stratified according to three binary variables: receipt of influenza vaccine prior to the start of influenza season (V); presence of some confounder (C) that can alter the probability of vaccination and the risk of ARI due to influenza and due to other pathogens; and some inherent care-seeking proclivity (X). Care-seeking proclivity may increase the probability of vaccination and the probability of seeking care among individuals who develop an ARI. The log odds of vaccination are:

$$logit(V = 1) = logit(\alpha_V) + \beta C + \gamma X$$

where α_V is the log odds of vaccination when C = 0 and X = 0 (Table 1). We assume that C and X do not have any (multiplicative) interaction on V.

In this population, individuals may experience ARI due to influenza (D) or ARI due to other respiratory viruses (O) at rates λ_D and λ_O, respectively. Rates of ARI due to either cause may be affected by confounder C, and the rate of influenza ARI (but not non-influenza ARI) may be affected by vaccination V. The mean rate of influenza ARI is:

$$log(\lambda_D) = \log(\mu_D) + \delta C + \theta V$$

where μ_D is the mean rate of D when C = 0 and V = 0, δ is the log rate ratio associated with C = 1, and θ is the log rate ratio associated with vaccination (i.e., 1-VE). The corresponding rate of ARI due to other respiratory viruses is:

$$log(\lambda_O) = \log(\mu_O) + \delta C$$

Individuals who develop ARI due to either cause may seek care (S) and be sampled into the test-negative study population; only individuals who develop ARI seek care. Among those with influenza ARI, the log odds of seeking care are:

$$logit(S = 1) = logit(\sigma) + \rho X$$

and the log odds among those with ARI due to other respiratory viruses are:

$$logit(S = 1) = logit(\varphi) + \rho X$$

where ρ is the log odds of seeking care when X = 1, and σ and φ is the probabilities of seeking care when X = 0 for influenza ARI and non-influenza ARI, respectively. Individuals enrolled in the test-negative study are tested for influenza (T).

To focus these simulations on selection bias, we assume there is no information bias (e.g., we assume perfect ascertainment of exposure and outcome in all study subjects). Coupled with the assumption that vaccine does not affect influenza severity among those infected, seeking care for influenza ARI is synonymous with a positive laboratory test for influenza (T), and estimated VE against medically attended influenza is equivalent to VE against influenza disease (D) in our simulations. We also assume that X is not a cause of D or O, other than through V, i.e., that X is not a confounder. Whether this is realistic in practice is uncertain, but this assumption separates the potential for selection bias from confounding due to X.

This simulation involves 12 parameters (Table 1). We fixed values of seven parameters based on prior outpatient studies of influenza VE and prior simulation studies [5,14,18]. For the remaining parameters, we ran separate simulations across combinations of the listed values (Table 1) of: (a) the prevalence of care-seeking proclivity (α_X); (b) the association between care-seeking proclivity and actual care-seeking (ρ); (c) the association between care-seeking proclivity and vaccination (γ); and (d) the probabilities that a person with ARI would seek care (σ for influenza ARI, φ

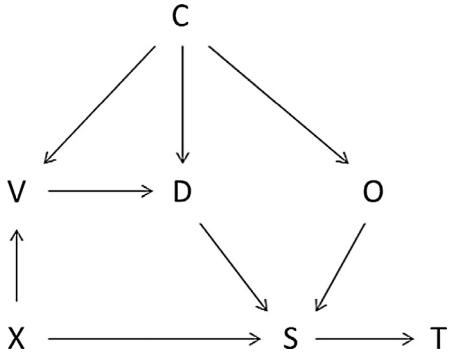

Fig. 1. Directed acyclic graph illustrating associations between variables in simulation models. *Footnote:* C, confounder; V, influenza vaccination; D, acute respiratory illness due to influenza; O, acute respiratory illness due to non-influenza pathogen; X, care-seeking proclivity; S, seeking care for acute respiratory illness; T, testing for influenza.

Table 1
Parameters used in simulation model.

Parameter	Symbol	Value (s)
Prevalence of confounder C	α_C	0.3
Prevalence of care-seeking proclivity X	α_X	0.1, 0.25, 0.333, 0.5, 0.75, 0.9
Prevalence of vaccination V, when C = 0 and X = 0	α_V	0.4
Odds ratio for V from C	exp(β)	2
Odds ratio for V from X	exp(γ)	0.1, 0.25, 0.5, 1, 2, 4, 10
Rate influenza ARI (D), when C = 0 and V = 0	μ_D	0.1522/year (approximate risk, 0.05 per influenza season)
Rate of non-influenza ARI (O), when C = 0 and V = 0	μ_O	0.4566 (approximate risk, 0.15 per influenza season)
Rate ratio for D and O from C	exp(δ)	2
Rate ratio for D from V	exp(θ)	0.5 (i.e., 50% VE)
Probability of sampling S, when O = 1 and X = 0	φ	0.25, 0.3
Probability of sampling S, when D = 1 and X = 0	σ	0.3, 0.33, 0.6
Odds ratio for S from X	exp(ρ)	0.1, 0.25, 0.5, 1, 2, 4, 10

for other ARI), which were informed by household studies of respiratory illnesses [19,20]. In each simulation, we sampled all individuals who sought care for an ARI and estimated the odds ratio for influenza for vaccinated vs. unvaccinated subjects among these individuals using a test-negative design. We assumed that the confounder C was observable, and adjusted for it in our analyses. In contrast, we assumed care-seeking proclivity X was not observable, and did not adjust for it when estimating VE. In each simulation we calculated the relative percent bias as the percent difference in the estimated odds ratio from the true simulated odds ratio of 0.5 (corresponding to an assumed VE of 50%). Odds ratios were estimated using logistic regression models. All simulations were conducted using R version 3.3.2 (The R Foundation for Statistical Computing, Vienna, Austria).

2.2. Observational data example

KP WA is an integrated healthcare organization in the Puget Sound region of western Washington State. KP WA has participated in the US Flu VE Network since the 2011/12 influenza season, with the goal of providing annual estimates of influenza VE [5,17,18]. KP WA US Flu VE Network enrollees are all members of KP WA, and so are drawn from a fully enumerated population on whom extensive administrative and healthcare data are available electronically. Data from the full KP WA population can be used to estimate the probability that a particular KP WA member is sampled into a test-negative study conducted within the US Flu VE Network.

For this, we first defined annual cohorts of KP WA members ≥6 months of age whose primary medical clinic was one at which US Flu VE surveillance occurred. The 6 month age cut-off was used because influenza vaccines are not recommended for children <6 months of age. We defined cohorts as of September 1st for the 2011/12, 2012/13, 2013/14, and 2015/16 influenza seasons; 2014/15 was excluded, as VE was low that year due to mismatch between vaccine virus strains and circulating influenza viruses [5]. We used KP WA administrative and medical databases to identify characteristics that might be predictive of care-seeking for ARI in these cohort members. These included age, sex, race/ethnicity, type and frequency of medical encounters over the previous 12 months, and (among adults) use of preventative services such as screening tests for breast, cervical, prostate, or colon cancer. For additional measures of socioeconomic status we used geocoded patient addresses to define measures of race/ethnicity, education, and income in participants' census tracts of residence.

During each influenza season, we identified KP WA members who sought care at a KP WA medical center for an ARI, defined as respiratory illness with cough (2011/12 season, fever or cough) of less than eight days duration [21]. Eligible and consenting patients were enrolled into the US Flu VE Network study. For the present analyses, we restricted our population to US Flu VE enrollees whose home medical clinic was one of the KP WA clinics at which ARI surveillance was being conducted. At the time of enrollment all study subjects answered questions on the course of illness, demographics, and influenza risk factors such as high-risk health conditions, self-rated health status, and exposure to cigarette smoke. All study subjects were tested for influenza infection via real-time reverse transcriptase polymerase chain reaction (rRT-PCR) as previously described [21]. Subjects testing positive for influenza were considered to be cases, with subjects testing negative composing the comparison group. We excluded subjects testing negative who were enrolled prior to the first influenza-positive subject or after the last influenza-positive subject each year.

The exposure of interest is receipt of at least one dose of seasonal influenza vaccine, defined based on KP WA's immunization registry. Subjects were considered to be vaccinated 14 days after receiving a first dose of any seasonal influenza vaccine. Because our primary interest is on assessing selection bias rather than estimating VE, we did not stratify vaccinations by type (e.g. inactivated vs. live attenuated) or manufacturer.

Using these test-negative data, we first estimated bias-naïve VE estimates of influenza VE that ignore possible selection bias, which is the standard approach in test-negative studies of influenza VE. For this, we estimated odds ratios (ORs), adjusting for variables that have generally been included as potential confounders in past US Flu VE Network models: age (using linear tail-restricted cubic spline functions), sex, race/ethnicity, presence of high-risk health conditions, self-rated health status, and calendar time. ORs were estimated overall and stratified by study year and by age group. Influenza VE was estimated as $100\% * (1 - \mathrm{OR})$.

We then estimated bias-adjusted influenza VE that attempted to account for possible selection bias using IPSW [22,23]. In IPSW, data from the full source population are used to estimate the probability that each member of the source population would be enrolled in the study. More specifically, let S indicate selection into the study (by seeking care for an ARI, being approached for study enrollment, and consenting to participate) and **Z** be some vector of covariates. We use the source population to estimate $P(S = 1|\mathbf{Z} = z)$. In this case, the goal is that the covariates in **Z** capture the relevant aspects of care-seeking proclivity that may create selection bias (Fig. 1). After using data on the source population to estimate $P(S = 1|\mathbf{Z} = z)$, we then assign each subject in the study sample (i.e., all the US Flu VE Network enrollees) a sampling weight based on the inverse of the sampling probabilities. Here, we use the stabilized weights, as $P(S = 1)/P(S = 1|\mathbf{Z} = z)$. Because predictors of care-seeking may differ between adults and children, we fit separate models for children aged <18 years and adults aged ≥18 years.

After estimating the stabilized weights for our enrollees, we repeated the estimation of adjusted VE using the sampling weights. To assess the possible impact of selection bias on test-negative VE estimates, we compared the bias-naïve VE estimates with the bias-adjusted VE estimates, in each study year and overall. If the estimates were qualitatively different (i.e., sufficiently different to alter our interpretation of VE), we took this as evidence for meaningful selection bias. All analyses were conducted using SAS Version 9.3 (SAS Institute, Cary NC). Note that, unlike our simulations, estimated VE against medically-attended disease from the observational data example may not be equivalent to VE against influenza infection/disease, if vaccine does in fact affect disease severity.

3. Results

3.1. Simulation study

As expected based on the DAG (Fig. 1), test-negative VE estimates were only biased when all of the following were true:

- Care-seeking proclivity (X) affects the odds of sampling (i.e., $e^{\rho} \neq 1$);
- Care-seeking proclivity affects the odds of vaccination (i.e., $e^{\gamma} \neq 1$);
- Persons with influenza ARI and non-influenza ARI were not equally likely to seek care (i.e., $\sigma \neq \varphi$).

When these conditions were met, the magnitude of bias depended on the magnitude of these associations. When care-seeking was 10% more likely for influenza ARI as for ARI due to other pathogens, the observed bias was trivial over most tested scenarios (Fig. 2A). The maximum relative bias was −3.7% (corresponding to an estimated VE of 48.2%), and this was only observed

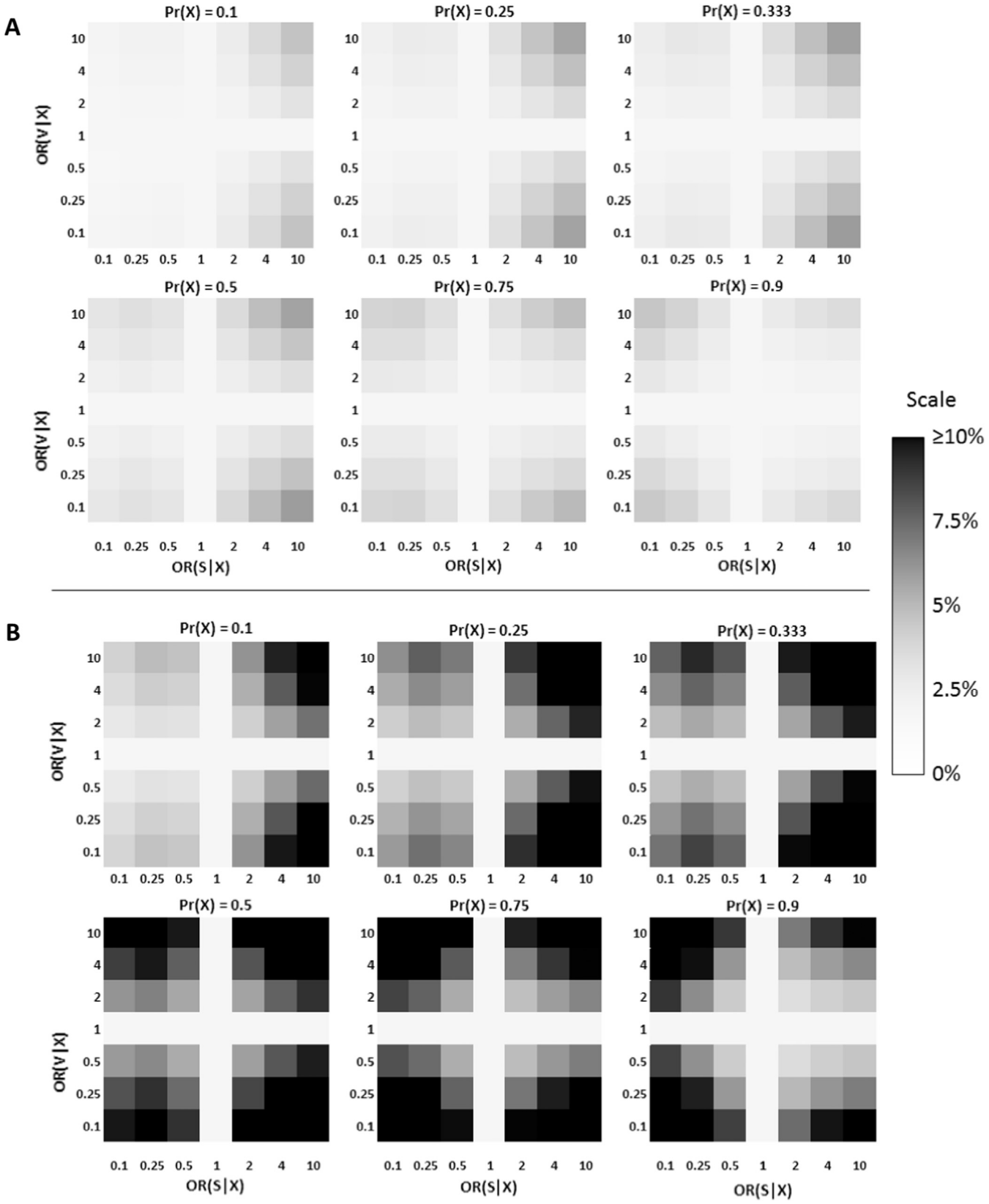

Fig. 2. Absolute percent bias in vaccine effectiveness estimates from simulated test-negative studies, varying prevalence of care-seeking proclivity (X), odds ratio for care seeking (S) based on X, and odds ratio for vaccination (V) based on X. (A) Simulations assuming care-seeking is 10% more likely for influenza than for non-influenza ARI; (B) Simulations assuming care-seeking twice as likely for influenza than for non-influenza ARI.

when X was common and very strongly associated with both vaccination and care-seeking (i.e., e^{γ} and e^{ρ} both $\leq$0.25 or $\geq$4).

When care-seeking was twice as likely for influenza ARI as for ARI due to other pathogens (i.e., when $\sigma = 0.6$ and $\varphi = 0.3$), simulated selection bias could be much greater, with maximum relative bias of −32.5% (Fig. 2B). For a true VE of 50%, this corresponds to an estimated VE of 33.8%. This magnitude of bias was only observed under extreme associations between X and both vaccination and care-seeking. Under less extreme scenarios, bias was considerably lower. Regardless of the prevalence of X, bias of greater than 5% (e.g. estimated VE of <47.5% or >52.5%) was only observed when X at least doubled (or halved) the risk of both vaccination and care-seeking (i.e., e^{γ} and e^{ρ} both $\leq$0.5 or $\geq$2).

3.2. Observational data example

The source cohorts varied from 81,568 KP WA members in 2012/13 to 125,171 members in 2015/16. Of these cohorts, the number enrolled as US Flu VE Network subjects ranged from 914 (2012/13) to 1518 (2015/16). Compared to the members of the source cohorts, US Flu VE Network subjects were more likely to be children aged <18 years, of White race, and to be female. US Flu VE Network subjects were also more likely to have been hospitalized and had more outpatient visits than members of the source cohorts. Models to predict sampling into the US Flu VE Network were moderately predictive both in children aged <18 years (c-statistic, 0.69) and in adults aged $\geq$18 years (c-statistic, 0.64).

Among the US Flu VE Network subjects, those testing positive were more likely to be aged 9–64 years, to be male, to present within 4 days of illness onset, and to self-report "excellent" health status, compared to those testing negative (Table 2). Those testing positive were less likely to be of White race or to have a high-risk health condition. In children, the sampling weights were estimated using age, season, race, history of well visits and ambulatory care visits, recent hospitalizations, and census-level education, income, and racial distribution. In adults, the sampling weights were estimated using the same variables, with the exception of census-level racial distribution, and additionally including sex and use of screening tests for blood lipids or cancer. Weighting the US Flu VE Network subjects based on sampling probabilities altered the age distribution, with the weighted population more likely to include adults $\geq$18 years of age. Weighting also increased the proportion who were male and decreased the proportion who were White and non-Hispanic.

The overall bias-naïve VE estimate was 55% (95% CI, 47–62%) across all four years. After weighting the population based on sampling probabilities, the bias-adjusted VE estimate was nearly identical (57%, 95% CI, 49–63%). When stratifying by year and by age group, bias-naïve estimates were never significantly different from the bias-adjusted estimates (Fig. 3). In most cases the point estimates were trivially different. The exceptions were estimated VE for the 2012/13 season and estimated VE in adults aged 65 years and older. For 2012/13, the bias-adjusted estimate (48%, 95% CI 26–63%) was 17 percent larger than the bias-naïve estimate (41%, 95% CI 15–59%). For adults aged 65 years and older, the bias-adjusted estimate (63%, 95% CI 44–76%) was 21 percent larger than the bias-naïve estimate (52%, 95% CI 24–69%).

4. Discussion

Our simulations found VE estimates from test-negative studies can indeed be impacted by selection bias, as suggested by Sullivan

Table 2
Characteristics of US Flu VE Network enrollees by influenza test results, in both the original population and after inverse probability of sampling weighting.

	Original		Weighted	
Variable	Influenza-negative	Influenza-positive	Influenza-negative	Influenza-positive
Season				
2011/12	841 (21%)	170 (21%)	799 (21%)	183 (21%)
2012/13	733 (19%)	181 (22%)	755 (20%)	210 (24%)
2013/14	1093 (28%)	203 (25%)	1043 (27%)	207 (24%)
2015/16	1266 (32%)	252 (31%)	1268 (33%)	274 (31%)
Age group				
6m to 8y	691 (18%)	97 (12%)	481 (12%)	88 (10%)
9–17y	296 (8%)	78 (10%)	466 (12%)	120 (14%)
18–49y	1345 (34%)	319 (40%)	1352 (35%)	342 (39%)
50–64y	846 (22%)	194 (24%)	789 (20%)	192 (22%)
65+y	755 (19%)	118 (15%)	777 (20%)	132 (15%)
Male	1567 (40%)	345 (43%)	1760 (46%)	435 (50%)
Hispanic ethnicity	291 (7%)	52 (6%)	235 (6%)	48 (5%)
Race				
White	3195 (81%)	637 (79%)	3024 (78%)	660 (76%)
Black	173 (4%)	48 (6%)	187 (5%)	58 (7%)
Asian	355 (9%)	74 (9%)	440 (11%)	103 (12%)
Native hawaiian/pacific islander	48 (1%)	8 (1%)	56 (1%)	9 (1%)
American indian/Alaska native	69 (2%)	13 (2%)	57 (1%)	16 (2%)
Other	202 (5%)	43 (5%)	209 (5%)	50 (6%)
Interval from onset to enrollment				
<3 days	752 (19%)	224 (28%)	727 (19%)	234 (27%)
3–4 days	1484 (38%)	322 (40%)	1436 (37%)	363 (41%)
5–7 days	1697 (43%)	260 (32%)	1703 (44%)	277 (32%)
Any high risk condition	1755 (45%)	337 (42%)	1620 (42%)	331 (38%)
Self-rated health				
Excellent	1152 (29%)	275 (34%)	1162 (30%)	302 (35%)
Very Good	1490 (38%)	302 (37%)	1494 (39%)	345 (39%)
Good	992 (25%)	164 (20%)	958 (25%)	165 (19%)
Fair	262 (7%)	54 (7%)	221 (6%)	49 (6%)
Poor	33 (1%)	11 (1%)	27 (1%)	13 (2%)
Refused	4 (0%)	(0%)	3 (0%)	(0%)

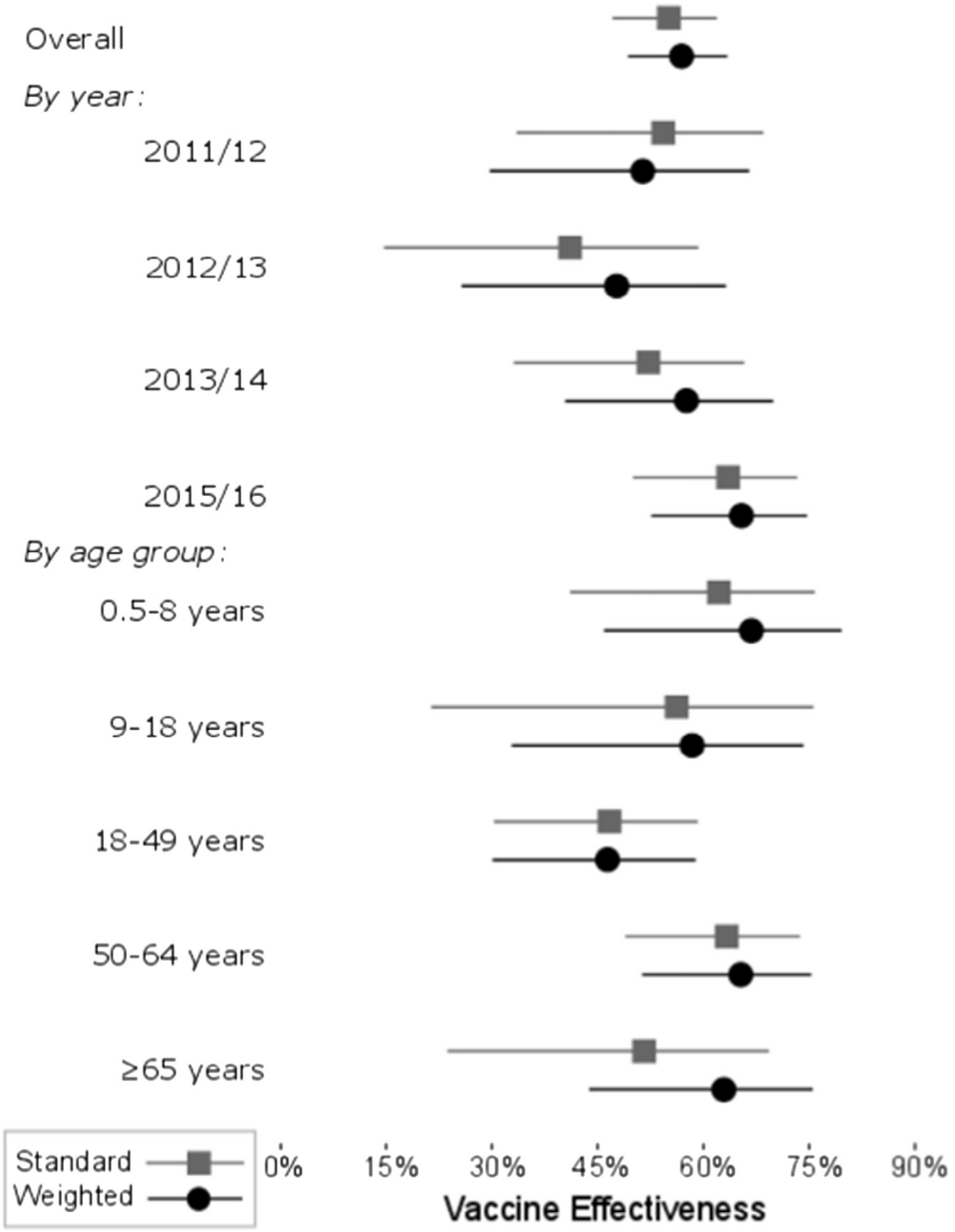

Fig. 3. Estimated influenza vaccine effectiveness, overall and stratified by year and age group, without account for selection bias (standard) and after accounting for selection bias (weighted).

and colleagues [16]. Fortunately for the use of the test-negative design, meaningful bias only occurred under relatively extreme simulated conditions. In particular, meaningful bias was only observed when the probability of seeking care for an ARI was twice as likely if the ARI was caused by influenza vs. another respiratory pathogen. In practice, care-seeking seems to be slightly more common for ARI due to influenza than for ARI due to other pathogens, but not nearly as extreme as required for meaningful bias in our simulations. In a recent household study, 23% of persons with non-influenza ARI symptoms sought medical care, compared to 27% of persons with influenza ARI symptoms [19]. At this level of differential care-seeking, the maximum bias in our simulations was −6.9% (Fig. 2), and that was only observed under extreme associations between care-seeking proclivity and both vaccination and selection into the study. These simulations suggest that, while present, selection bias is not likely to meaningfully impact test-negative VE estimates in most situations.

The findings of our observational study also support this conclusion. Our bias-naïve VE estimate was nearly unchanged after accounting for potential selection bias via IPSW (55% vs. 57%). This finding held true for most of our stratum-specific VE estimates across study years and age groups. We did observe clinically meaningful differences in point estimates between the bias-naïve and bias-adjusted estimates for 2012/13 and for adults ≥65 years of age. However, these were the strata with the fewest US Flu VE enrollees, and so were most susceptible to chance differences between the bias-naïve and bias-adjusted estimates, which is reflected in the wide and overlapping confidence intervals between

the estimates. Even assuming that these differences are the result of bias, the test-negative studies still correctly identified statistically significant VE in both of these relatively small subgroups.

This study had several important limitations to consider. Our simulations are necessarily a simplification of reality, and may have excluded important variables or relationships, such as potential interactions between care-seeking proclivity and confounding factor C. In our observational study, we used measurable data on care-seeking patterns, demographics, and proxies of socioeconomic status to define care-seeking proclivity. Other unmeasured factors may be associated with care-seeking and selection into the US Flu VE study, leaving the possibility of residual selection bias in our observational study. In addition, our observational study focused on VE estimated from outpatient settings, and our findings may not apply to test-negative studies from inpatient settings.

5. Conclusion

The test-negative design has become the global standard for observational studies of influenza VE, and results from test-negative studies are impacting vaccination recommendations. This study suggests that, under conditions likely to be encountered in practice, selection bias is not a major problem for VE estimates from test-negative studies.

Funding

This project was supported by the Centers for Disease Control and Prevention (CDC) through a cooperative agreement with Kaiser Permanente Washington Health Research Institute (U01 IP000466).

Conflict of interest

None.

References

[1] Jackson ML, Nelson JC. The test-negative design for estimating influenza vaccine effectiveness. Vaccine 2013;31:2165–8.
[2] Broome CV, Facklam RR, Fraser DW. Pneumococcal disease after pneumococcal vaccination: an alternative method to estimate the efficacy of pneumococcal vaccine. N Engl J Med 1980;303:549–52.
[3] Skowronski DM, Gilbert M, Tweed SA, Petric M, Li Y, Mak A, et al. Effectiveness of vaccine against medical consultation due to laboratory-confirmed influenza: results from a sentinel physician pilot project in British Columbia, 2004–2005. Can Commun Dis Rep 2005;31:181–91.
[4] Kissling E, Valenciano M, Buchholz U, Larrauri A, Cohen JM, Nunes B, et al. Influenza vaccine effectiveness estimates in Europe in a season with three influenza type/subtypes circulating: the I-MOVE multicentre case-control study, influenza season 2012/13. Euro Surveill 2014;19.
[5] Zimmerman RK, Nowalk MP, Chung J, Jackson ML, Jackson LA, Petrie JG, et al. 2014–2015 influenza vaccine effectiveness in the United States by vaccine type. Clin Infect Dis 2016.
[6] Sullivan SG, Chilver MB, Higgins G, Cheng AC, Stocks NP. Influenza vaccine effectiveness in Australia: results from the Australian Sentinel Practices Research Network. Med J Aust 2014;201:109–11.
[7] Ali M, You YA, Sur D, Kanungo S, Kim DR, Deen J, et al. Validity of the estimates of oral cholera vaccine effectiveness derived from the test-negative design. Vaccine 2016;34:479–85.
[8] Castilla J, Beristain X, Martinez-Artola V, Navascues A, Garcia Cenoz M, Alvarez N, et al. Effectiveness of rotavirus vaccines in preventing cases and hospitalizations due to rotavirus gastroenteritis in Navarre, Spain. Vaccine 2012;30:539–43.
[9] Sullivan SG, Feng S, Cowling BJ. Potential of the test-negative design for measuring influenza vaccine effectiveness: a systematic review. Expert Rev. Vaccines 2014;13:1571–91.
[10] Cowling BJ, Nishiura H. Virus interference and estimates of influenza vaccine effectiveness from test-negative studies. Epidemiology 2012;23:930–1.
[11] Foppa IM, Haber M, Ferdinands JM, Shay DK. The case test-negative design for studies of the effectiveness of influenza vaccine. Vaccine 2013;31:3104–9.
[12] Suzuki M, Camacho A, Ariyoshi K. Potential effect of virus interference on influenza vaccine effectiveness estimates in test-negative designs. Epidemiol Infect 2014;142:2642–6.
[13] De Serres G, Skowronski DM, Wu XW, Ambrose CS. The test-negative design: validity, accuracy and precision of vaccine efficacy estimates compared to the gold standard of randomised placebo-controlled clinical trials. Euro surveillance: bulletin Europeen sur les maladies transmissibles = Eur Commun Dis Bullet 2013;18.
[14] Jackson ML, Rothman KJ. Effects of imperfect test sensitivity and specificity on observational studies of influenza vaccine effectiveness. Vaccine 2015;33:1313–6.
[15] Hernan MA, Hernandez-Diaz S, Robins JM. A structural approach to selection bias. Epidemiology 2004;15:615–25.
[16] Sullivan SG, Tchetgen Tchetgen EJ, Cowling BJ. Theoretical basis of the test-negative study design for assessment of influenza vaccine effectiveness. Am J Epidemiol 2016;184:345–53.
[17] Gaglani M, Pruszynski J, Murthy K, Clipper L, Robertson A, Reis M, et al. Influenza vaccine effectiveness against 2009 pandemic influenza A(H1N1) virus differed by vaccine type during 2013–2014 in the United States. J Infect Dis 2016;213:1546–56.
[18] McLean HQ, Thompson MG, Sundaram ME, Kieke BA, Gaglani M, Murthy K, et al. Influenza vaccine effectiveness in the United States during 2012–2013: variable protection by age and virus type. J Infect Dis 2015;211:1529–40.
[19] Stockwell MS, Reed C, Vargas CY, Camargo S, Garretson AF, Alba LR, et al. MoSAIC: mobile surveillance for acute respiratory infections and influenza-like illness in the community. Am J Epidemiol 2014;180:1196–201.
[20] Ohmit SE, Petrie JG, Malosh RE, Cowling BJ, Thompson MG, Shay DK, et al. Influenza vaccine effectiveness in the community and the household. Clin Infect Dis 2013;56:1363–9.
[21] Ohmit SE, Thompson MG, Petrie JG, Thaker SN, Jackson ML, Belongia EA, et al. Influenza vaccine effectiveness in the 2011–2012 season: protection against each circulating virus and the effect of prior vaccination on estimates. Clin Infect Dis 2013;58:319–27.
[22] Haapea M, Veijola J, Tanskanen P, Jaaskelainen E, Isohanni M, Miettunen J. Use of inverse probability weighting to adjust for non-participation in estimating brain volumes in schizophrenia patients. Psychiatry Res 2011;194:326–32.
[23] Thompson CA, Arah OA. Selection bias modeling using observed data augmented with imputed record-level probabilities. Ann Epidemiol 2014;24:747–53.