Sex Misclassification in the BRFSS and its Implications for Assessing Transgender and Gender Nonconforming Reproductive Health: A Quantitative Bias Analysis

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Abstract

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National surveys based on probability sampling methods, such as the Behavior Risk Factor and Surveillance Survey (BRFSS), are crucial tools for unbiased estimates of disparities in health and healthcare access among gender minorities. The BRFSS began offering an optional sexual orientation and gender identity module in 2014, capturing transgender and gender nonconforming (TGNC) identity among respondents. Although the BRFSS provides much needed data on the TGNC community, self-identified TGNC respondents are still vulnerable to misclassification of sex assigned at birth. This study applied quantitative bias analysis to explore the magnitude and direction of the systematic bias present in measures of reproductive health that result from this misclassification. Our findings suggest that TGNC individuals with misclassified sex assigned at birth are demographically distinct from those who are asked sex-specific questions, suggesting that there is significant selection bias present in the BRFSS measures of reproductive health. We use multivariate Poisson regression with robust standard errors to estimate the association between gender identity and four sex-specific outcomes: lifetime PSA testing, lifetime Pap testing, hysterectomy, and pregnancy. We then compare two analytic methods to explore the degree of bias in these estimates, including single and multiple imputation models and simple probabilistic bias adjustments. Our results demonstrate that estimated associations among gender nonconforming respondents are the most vulnerable to small degrees of bias, while estimates among transgender women and men are more robust to small and moderate degrees of bias. This study provides evidence that BRFSS data report non-representative samples of TGNC individuals who are asked questions about their reproductive health, and that these outcomes are subsequently vulnerable to bias. Therefore, researchers who use BRFSS data to examine reproductive health outcomes should not reported results as unbiased population-based estimates. This study further demonstrates that implementation of validated sex assigned at birth and gender identity question in national surveys is critical.

INTRODUCTION

Transgender and gender nonconforming (TGNC) individuals face structural and socioeconomic barriers to accessing both gender affirming and primary health care, resulting in well documented health disparities.[1,2] However, to date, there are considerable gaps in the published literature on transgender health, with few studies that address general health status or access to preventative healthcare.[1,3]

National surveys that are based on probability sampling methods, such as the Behavior Risk Factor and Surveillance Survey (BRFSS), are crucial tools in developing unbiased estimates that accurately measure health disparities.[4] Until recently, nationally representative survey data has not included gender identity questions.[5,6] Consequently, the majority of studies on transgender health have been based on community and clinical samples that are not representative of the TGNC population in the US.[3,4] Beginning in 2014, the BRFSS began offering an optional module of sexual orientation and gender identity (SOGI), and a growing number of studies have used nationally representative survey data to investigate TGNC characteristics and health disparities.[4,7–15]

Although the BRFSS provides much needed data on the TGNC community, it is still vulnerable to misclassification of sex assigned at birth among self-identified TGNC respondents.[16,17] To date, the BRFSS has not adopted the use of validated sex and gender identity survey questions, and previous studies suggest that the BRFSS misclassifies sex for up to 30% of TGNC respondents.[18] Additionally, the BRFSS makes binary cisnormative assumptions regarding reproductive anatomy, implemented in their protocol as skip patterns based on sex. As a result of sex misclassification and sex-based skip patterns, a large portion of TGNC respondents are precluded from answering questions related to their reproductive anatomy, such as questions about Papanicolau (Pap) testing, and prostate-specific antigen (PSA) testing. Therefore, it is likely that the BRFSS does not adequately capture rates of screening or the prevalence of reproductive health outcomes, such as pregnancy or hysterectomy, among transgender individuals due to conflicting and missing data. Despite these limitations, no studies examine the impact of these biases on assessing TGNC reproductive health.[14,15]

Quantitative bias analysis is a method of modeling systematic, or nonrandom error, that can bias the results of epidemiological research, including issues of misclassification, missing data, selection bias, and confounding.[19,20] When combined with conventional confidence intervals that model random error, quantitative bias analysis can inform more realistic estimates of the total uncertainty. This study applies multiple bias modeling methods to explore the magnitude and directionality of the bias resulting from sex misclassification in the BRFSS. Specifically, we quantify the bias in the estimated association between transgender identity and four sex-specific outcomes: lifetime PSA testing, lifetime Pap testing, pregnancy, and history of a hysterectomy. These results will inform potential response bias in current estimates of transgender health that rely on complete case analysis methods and use national survey data.

METHODS

DATA

Data for this study are from the 2014, 2015 and 2016 Behavior Risk Factor and Surveillance Survey (BRFSS). The BRFSS is a state-based system of telephone health surveys overseen by the Center for Disease Control and Prevention (CDC). Eligible participants are non-institutionalized adults aged 18 or over and currently living in the United States. The BRFSS uses complex probability sampling methods so that data are collected from a representative sample within each state. When combined, it is designed to be representative of the states and years included.[21] Not all states use the SOGI module, but there has been increasing uptake from year-to-year: 20 states participated in 2014, 21 in 2015, and most recently, 26 states in 2016. All analyses use pooled, weighted data from all states that participated in the SOGI module.

MEASURES

The BRFSS protocol designates a binary sex variable (*male, female,* or *refused*) at several possible steps in the interview: (1) during eligibility screening questions, (2) during household enumeration questions, or (3) during demographic questions. In all three locations, the language in the interview script does not distinguish between sex assigned at birth and gender identity, for example, by conflating individuals who identify as *men* with *male sex assigned at birth*. When not asked explicitly by the interviewer, sex is designated by the interviewer based on the sound of the participant's voice.[18] Therefore, this measure, which we will refer to as the *BRFSS designated sex,* is not a valid or reliable measure of sex assigned at birth among TGNC respondents.

Gender identity is ascertained through the SOGI module, in which respondents are asked "Do you consider yourself to be transgender?" Participants who responded yes were then asked if they identify as *transgender male-to-female, female-to-male*, or *gender nonconforming*. Participants can also respond *no, don't know/not sure*, and *refused*. In our analyses, individuals who respond *no* to this item are considered cisgender, such that individuals with female BRFSS designated sex

are assumed to be cisgender women, and individuals with male BRFSS designated sex are assumed to be cisgender men. Individuals who identify as *transgender, male-to-female* are further referred to as transgender women and we assume that their sex assigned at birth is male, regardless of how their sex was designated in the BRFSS data. Similarly, individuals who identify as *transgender, female-to-male* are further referred to as transgender men and we assume that their sex assigned at birth is female. We are unable to infer the sex assigned at birth of individuals who identify as gender non-conforming (GNC). Individuals who responded as don't know/not sure or refused are excluded from all analyses.

We consider four outcomes that are subject to sex-specific skip patterns in the BRFSS: lifetime PSA testing, lifetime Pap testing, history of hysterectomy, and currently pregnant. These measures are subject to skip patterns based on the BRFSS designated sex. The PSA testing item is further restricted to individuals 40 years old and older, and the pregnancy item is restricted to individuals 44 years old and younger who have not had a hysterectomy.

We also consider demographic characteristics and measures of healthcare access among TGNC respondents. Respondents reported their age in 5 year strata, and their race/ethnicity as White, Black, American Indian/Alaska Native, Asian, Native Hawaiian/Pacific Islander, Hispanic, multiracial, or other. Socioeconomic status, is captured through three different variables: unemployment status, annual income (< $15,000, $15,000–$24,999, $25,000–$34,999, $35,000–49,999, and >$50,000), and educational attainment (did not graduate from high school, graduated from high school, attended college or technical school, graduated from college or technical school). Partnership status is defined as married or living with a partner, separated/divorced/widowed, or never married. Sexual orientation is also assessed through the SOGI module (straight, lesbian or gay, bisexual, other, don't know/not sure). Urban or rural residence is a variable calculated by BRFSS based of metropolitan statistical area (MSA) regions (in city center of an MSA, within a county of an MSA, suburban county of an MSA, or rural). General health status is measured by self-reported fair or poor general health. Healthcare access is measured across three variables: self-reported lack of any kind of healthcare coverage, no personal doctor or primary healthcare provider, and inability to see a doctor due to cost within the last year.

ANALYSES

Our aim is to quantify the bias in the estimated association between transgender identity and four sex-specific outcomes: lifetime PSA testing, lifetime Pap testing, pregnancy, and history of a hysterectomy. Therefore, we first must evaluate the association between gender identity and four sex-specific outcomes as observed in the data, by using complete cases analysis. We use Poisson regression with robust standard errors to estimate the crude and adjusted prevalence ratios (PR) for each outcome.[22] The analytic model for never having had a PSA test compares transgender women and GNC individuals to cisgender men. The analytic models for currently being pregnant, having had a hysterectomy, and never having a Pap test compare transgender men and GNC individuals to cisgender women. Weights developed for and provided by the BRFSS and complex sampling methods were used to account for complex survey sampling methods. Age, socioeconomic status, race/ethnicity, general health status, partnership status, and healthcare coverage are identified *a priori* as confounders of the relationship between gender identity and reproductive health outcomes.

This naïve approach accounts for random error, in the form of estimated robust standard errors and confidence intervals; However, it fails to account for systematic bias. This is addressed through bias modeling, in which we assess the how the magnitude and direction of nonrandom bias impacts uncertainty in the associations found in the complete-case analysis.

We also provide counts and survey weighted proportions of responses to the four sex-specific questions by gender identity, as well as demographic characteristics of respondents by BRFSS designated sex.

BIAS MODELING

Table 1 summarizes how current BRFSS protocol and the reliance of sex-based skip patterns in the BRFSS results in misclassified sex assigned at birth and ultimately a non-representative sample of TGNC individuals .[18] This has two consequences: first, TGNC individuals are asked questions that are not relevant to their anatomy (Cell C in Table 1), resulting in an inflation of *no, I don't know,* and *refused* responses to sex-specific questions. Second, there are individuals who may retain anatomical structures (e.g. a uterus) relevant to sex-specific questions (e.g. history of a hysterectomy), who are precluded from the sample (Cell D in Table 1).

We compare two approaches to multiple bias modeling, with the aim to quantify the bias resulting from the misclassification of sex assigned at birth and the subsequent missing data. The two conceptual models and associated analytic approaches for modeling bias are presented in **Table 2.**

For the purposes of bias modeling, we use sex assigned at birth as an imperfect proxy for anatomical structures.[17] Specifically, we assume that individuals assigned male at birth (cisgender men, transgender women and GNC people) are unable to experience pregnancy or hysterectomy, and are not eligible for cervical Pap testing. We similarly assume that

individuals assigned female at birth (cisgender women, transgender men and GNC people) do not have a prostate and are not eligible for PSA testing. Further, we are unable to infer the sex assigned at birth of individuals who identify as GNC.

Approach One: Selection Bias Modeling

We first consider a simple selection bias model. The directed acyclic graph (DAG) in **Table 2** demonstrates how the prevalence of sex-specific outcomes is conditioned on BRFSS designated sex, and subsequent inclusion into the subsample of respondents asked sex-specific questions. We adjust for this selection bias in two discrete steps: first, we perform a record-level adjustment to exclude individuals who are incorrectly included in the sample. Second, we perform a summary-level adjustment to account for individuals who are incorrectly excluded from the sample.[20]

Record-level adjustment. The incorrect inclusion of TGNC individuals whose sex assigned at birth does not match the BRFSS designated sex inflates *no, I don't know,* and *refused* responses. Therefore, we exclude transgender men's responses for outcomes relevant to people assigned male at birth (e.g. PSA testing). We similarly exclude transgender women's responses for outcomes relevant to people assigned female at birth (e.g. currently being pregnant, having had a hysterectomy, and never having a Pap test). However, unlike for transgender men and women, we are unable to infer the sex-assigned a birth for GNC individuals. Therefore, we conduct a probabilistic record level adjustment using Monte Carlo sampling methods (1,000 randomly sampled scenarios) where for each scenario we exclude a random subset of GNC individuals who respond as *no, I don't know,* or *refused* under the assumption that they are individuals for whom the sex-specific questions are not anatomically relevant. For this adjustment, we assume a proportion of BRFSS designated sex misclassification that is similar to what isobserved among transgender men and women, that is, 30% as per Riley and colleagues.[18] Following each record-level adjustment, we estimate the prevalence ratio, $\widehat{\mathrm{PR}}$, using the same analytic multivariate Poisson model specified for the complete-cases analysis.

Summary-level adjustment. We then conduct a simple summary-level selection bias adjustment using Monte Carlo sampling methods to account for TGNC respondents incorrectly excluded from sex-specific questions. The prevalence ratio estimated after the record-level adjustment is multiplied by a bias adjustment factor, the selection bias odds ratio, OR_{select}, so that prevalence ratio adjusted for systematic bias is $\mathrm{PR}_{adj} = \widehat{\mathrm{PR}} \times \mathrm{OR}_{select}$.[20] When transgender individuals with the outcome are preferentially included, or over selected, this implies that $\mathrm{OR}_{select} < 1$, so our bias adjusted prevalence ratio decreases. Conversely, when transgender individuals with the outcome are preferentially excluded, or under selected, this implies that $\mathrm{OR}_{select} > 1$, so our bias adjusted prevalence ratio increases. Since there is no existing literature to inform the direction or degree of selection bias, we assign a uniform distribution to model a large range of possible selection bias scenarios, with OR_{select} ranging from 0.10 to 10.0. We randomly sample 100,000 selection bias scenarios and estimate bias-adjusted prevalence ratios that combine both systematic bias and random errors. Refer to **Appendix I** for mathematical details.

This modeling approach benefits from its simplicity, but is limited in that it does not utilize the demographic and health information we know about the 30% of transgender individuals who were not asked sex-specific questions. Therefore, we consider a second modeling approach that relies on imputation methods.

Approach Two: Missing Data and Unknown Confounding

Alternatively, we model the systematic bias as a missing data problem, whereby TGNC individuals for whom their sex assigned at birth does not match the BRFSS designated sex are missing data for reproductive health questions. Prior studies suggest that misclassification is nonrandom and also associated with the sex-specific outcomes of interest; thus, there is an underlying missing data process that is non-ignorable.[18,23–25] Therefore, we also assume that there is an unknown confounding mechanism driving this missingness **(Table 2).** We adjust for missing data and confounding in two discrete steps: first, we use multiple imputation methods to impute missing outcome variables and perform a record level adjustment to exclude individuals who are incorrectly included in the sample (Cell C in Table 1). Second, we perform a summary-level adjustment for unknown confounding. Lastly, we consider single imputation models to bound our estimates.

Record-level adjustment. Multiple imputation by chain equations (MICE) is statistical technique for handling missing data, whereby the observed data are used to jointly estimate plausible values for missing observations.[23,25,26] We use MICE to impute the missing outcome variables due to the method's flexibility to accommodate categorical variables and skip patterns. The imputation model includes survey year, indicators for each state, and inability to seek medical care due to cost in the past year, in addition to all variables in the analytic model (gender identity, age, income, unemployment status, educational attainment, race and ethnicity, general health status, partnership status, and healthcare coverage). For each sex-specific outcome we create 30 imputed datasets, and assess trace plots for evidence of convergence and good fit.[27]

As in approach one, we exclude transgender men's responses to PSA testing, and exclude transgender women's responses to PSA testing, hysterectomy, and pregnancy questions. However, because we are unable to condition on the

inferred sex assigned at birth for GNC individuals, imputing sex-specific outcome for all GNC individuals inappropriately relies on information from individuals who do not have the relevant anatomy. Therefore, imputation is not reliable among GNC respondents and this method can only be applied to model bias with respect to transgender men and women. After implementing MICE and record-level adjustments, we estimate the prevalence ratio, $\widehat{\mathrm{PR}}$, using the same analytic multi-variate Poisson model specified for the complete-cases analysis on the imputed datasets.

In addition to developing a model that jointly estimates missing values, we consider two single-imputation models that explore the two extreme scenarios in which data can be missing. For all TGNC respondents who are missing data on a sex-specific outcome, we first assume that all excluded individuals had the outcome and impute a value of 1 for each relevant sex-specific outcome. Second, we assume that all excluded TGNC individuals did not have the outcome, and impute a value of 0 for each relevant sex-specific outcome. For each scenario, we estimate the prevalence ratio, $\widehat{\mathrm{PR}}$, using the same analytic multi-variate Poisson model specified for the complete-cases analysis. These results enable us to estimate the bounds of association that we could see in the observed data.

Summary-level adjustment. Multiple imputation relies on the assumption that data are missing at random (MAR).[23,25] However, we presume that sex misclassification and sex-based skip patterns in the BRFSS results in nonrandom missingness. That is, there is an unknown confounder associated with missingness and reproductive health outcomes among TGNC respondents. Due to this nonrandom mechanism, the prevalence ratios estimated from MICE subsequently need to be adjusted for unknown confounding. We define the risk ratio due to confounding as RR_{conf}, and the prevalence ratio adjusted for confounding as $\mathrm{PR}_{adj} = \frac{\widehat{\mathrm{PR}}}{\mathrm{RR}_{conf}}$.[20]

As in approach one, in the absence of literature to inform the direction or degree of confounding, we assign a uniform distribution to model a large range of possible confounding scenarios. We allow RR_{conf} to range between 0.10 and 10.0.[28] Using Monte Carlo methods, we randomly sample 100,000 confounding scenarios and estimate bias-adjusted prevalence ratios that combine both systematic bias and random errors. Refer to **Appendix II** for additional details.

Statistical analyses and multiple imputation were conducted in Stata version 15.1 and Monte Carlo simulations were performed in R version 3.4.2.

RESULTS

Combining BRFSS data from 2014, 2015 and 2016 survey years, a total of 518,982 participants responded to the gender identity question and were included in our sample. The data include 1,078 transgender women, 701 transgender men, and 450 gender nonconforming individuals.

Table 3 presents demographic characteristics and measures of healthcare access, comparing individuals who were asked and precluded from sex-specific questions. Congruent with past studies based only on 2014 data, sex assigned at birth is presumed to be misclassified among 29.6% (319/1,078) of transgender women and 30.2% (212/701) of transgender men. These results also suggest that individuals who were excluded from the sample as a result of sex misclassification are demographically distinct from those who were included. Transgender women who are excluded from PSA testing questions are younger, more likely to be a racial minority, have significantly lower incomes, and poorer self-reported health and access to healthcare compared to individuals who were included in the sample asked about PSA testing. Transgender men who are excluded from Pap testing, hysterectomy, and pregnancy questions are more likely to have White or Asian race, have higher incomes, are more likely to be employed, partnered and identify as straight, and have better self-reported health and access to healthcare compared to individuals who were included in the sample. We are unable to infer the sex assigned at birth of GNC respondents, and therefore are unable to determine the demographic profile of individuals who were and were not asked questions relevant to their anatomy. However, we see that the demographic profile of individuals also differs based on the BRFSS designated sex.

Table 4 presents the responses and survey weighted proportions to the four sex-specific questions of interest by gender identity. We observe that 51.6% of transgender women and 59.4% of GNC individuals age 40 or older have never had a PSA test, compared to 44% of cisgender men; 22.8% of transgender men and 45.6% of GNC individuals have never had a Pap test, compared to 9.9% of cisgender women. We also observe that 15.9% of transgender men and 21.5% of GNC individuals have had a hysterectomy, compared to 20.6% of cisgender women; and, 1.9% of transgender men and 2.6% of GNC individuals were pregnant at the time of phone interview, compared to 4.0% of cisgender women. These proportions, however, are subject to selection bias and may not be a representative sample of the TGNC population.

Table 5 reports the result of the crude and covariate adjusted results from a complete case analysis. Complete case regression analyses do not account for systematic biases, but suggest that after adjusting for demographic and socioeconomic factors, TGNC respondents have similar prevalence of PSA testing (transgender women PR 1.09, 95% CI:

0.81, 1.48; GNC PR 0.95, 95% CI: 0.70, 1.31) when compared to cisgender men; that transgender men more are likely to have had hysterectomy (PR 1.26, 95% CI: 0.99, 1.61) and less likely to pregnant (PR 0.38, 95% CI: 0.13, 1.15), while GNC respondents have similar prevalence of hysterectomy (PR 0.86, 95% CI: 0.68,1.08) and pregnancy (PR 0.76, 95% CI: 0.23, 2.58), when compared to cisgender women. Lastly, the complete cases analysis suggests that TGNC respondents are more likely to have never had a Pap test (transgender men PR 1.72, 95% CI: 0.98, 3.03; GNC PR 2.71, 95% CI: 2.07, 3.55) than cisgender women. For transgender men and women, we are unable to determine from complete case analysis alone whether these prevalence ratios represent an underestimate or overestimate of the true association. Additionally, for GNC respondents we are unable to determine the degree to which our estimates are biased by the inflation of *no, I don't know,* and *refused* responses.

Table 6 reports the results of the imputed regression analyses. We first compare the results of our regression analysis using the imputed datasets to the complete-case analysis **(Table 5)**. We observe that the MICE estimates are all similar to the complete-case analysis results, but move slightly towards to null in the imputed models. This suggest that, prior to modeling the impact of an unknown confounder, we predict that the association between gender identity and reproductive health outcomes is attenuated, based solely on difference in demographics, socioeconomic status and measures of healthcare access. That is, the BRFSS protocol and misclassification of sex assigned at birth results in a sample with lower rates of PSA and Pap testing, lower prevalence of pregnancy, and higher prevalence of hysterectomy.

The single imputation results, also presented in **Table 6** explore the upper and lower bounds of the association between gender identity and reproductive health outcomes. These results suggest that the true PR for sex-specific outcomes can range both above and below 1. However, the range of possible PRs for lifetime PSA testing and hysterectomy is modest compared to the possible range for lifetime Pap testing and pregnancy. For example, the PR for never lifetime PSA testing is at most 1.55 (95% CI: 1.37,1.75) and 1.72 (95% CI: 1.37, 2.17) for transgender women and GNC individuals, respectively. The lower bounds are similarly informative, suggesting that pregnancy is at the very least 1/10th as prevalent among TGNC individual (transgender men PR 0.27, 95% CI: 0.09, 0.78; GNC PR 0.33, 95% CI: 0.10, 1.07). Additionally, the lower bounds suggest that Pap testing is similar among TGNC individuals and cisgender women only under the extreme assumption that TGNC missing data have all had a Pap test in their lifetime (transgender men PR 0.98, 95% CI: 0.53, 1.80; GNC PR 1.04, 95% CI: 0.61, 1.78). The upper bounds suggest that Pap testing is, at most 4.32 (95% CI: 3.36,5.54) and 6.38 (95% CI: 5.15, 7,91) times less prevalent among transgender men and GNC individuals, respectively.

The results of both bias modeling approaches are reported in **Table 7** and **Figures 1-4.** As described above, we choose uniform distributions for the bias adjustment factors—the selection bias OR and the RR due to confounding—ranging between 0.10 and 10.0 to evaluate the PR resulting from a wide range of bias scenarios. Therefore, **Table 7** reports the minimum and maximum adjustment factors guaranteeing that the bias-adjusted PR is either above or below 1. **Figure 1** presents the range of selection bias scenarios that can result in PR either above or below 1, as well as the range of scenarios in which the PR is guaranteed to be above 1 or below 1. The larger the range in which the resulting PR can be either above or below 1, the more vulnerable an estimate is the selection bias. **Figure 2** presents similar ranges for the RR due to confounding. **Figures 3 and 4** display the range of PR for varying bias scenarios for approaches one and two, respectively. In these figure, the heavy black horizontal line represents a PR of 1, and the shaded regions represent the regression results reported in **Table 5** from the covariate-adjusted complete case analysis (**Figure 3**) and the regression results reported in **Table 6** from the MICE based analysis (**Figure 4**).

Both bias modeling approaches suggest that the PR estimates for hysterectomy among TGNC individuals, lifetime PSA testing among transgender women and Pap testing among transgender men are robust to small degrees of systematic bias. In contrast, the PR estimates for pregnancy among TGNC individuals, as well as lifetime PSA testing and Pap testing among GNC individuals are highly sensitive to systematic bias. When we examine the range of selection bias scenarios that would result in an association either above or below 1 we observe wide overlapping ranges for PSA testing (OR_{select}: 0.45, 9.89), Pap testing (OR_{select}: 0.23, 5.00), and pregnancy (OR_{select}: 0.18, 9.38) among GNC individuals. We similarly see that pregnancy among transgender men is highly sensitive to selection bias (OR_{select}: 0.53, 9.99). This is reinforced in the **Figure 3**, where the blue bars representing the range of PRs contain 1 for almost all values of the selection bias OR.

By way of example, consider PSA testing among transgender women: Approach one suggests that a PR greater than 1.0 is possible for a wide range of scenarios, but that a selection bias OR of 1.49 or higher guarantees that our bias adjusted association is greater than 1. This would imply that transgender women have a lower prevalence of lifetime PSA testing than cisgender men. Equivalently, if we suspect that transgender women who never had a PSA test were preferentially excluded from the sample at least 1.5 times as often as those who have had a PSA test, then the complete case results may be lower bound of the true association. We obtain similar results for Pap testing and hysterectomy among transgender men: a selection bias OR of 2.05 or higher guarantees that our bias adjusted association is such that

transgender men have a lower prevalence of lifetime Pap testing than cisgender women; and, a selection bias OR of 1.09 or higher guarantees that our bias adjusted association is such that transgender men have a higher prevalence of hysterectomy than cisgender women. However, the results in **Figure 3** demonstrate that these estimates are still very vulnerable to large degrees' selection bias.

Approach two mirrors these results. **Table 7** and **Figures 2 and 4** demonstrate that the imputed results are still highly sensitive to confounding, and reinforce our findings from approach one.

DISCUSSION

The BRFSS began offering an optional module on sexual orientation and gender identity (SOGI) in 2014. However, methodological issues result in systematic bias for questions related to reproductive health, whereby 29.6% (319/1,078) of transgender women and 30.2% (212/701) of transgender men are precluded from answering questions related to their reproductive anatomy. Therefore, the BRFSS provides a non-representative sample of TGNC individuals asked questions about PSA and Pap testing, hysterectomy, and pregnancy, as well as other reproductive health outcomes.[18]

We applied quantitative bias methods to explore the magnitude and direction of bias in estimated associations between gender identity and reproductive health outcomes. Our results demonstrate that while all associations are sensitive to large degrees of bias, estimates among GNC respondents are the most vulnerable to small degrees of bias, while estimates of lifetime PSA testing among transgender women, and lifetime Pap testing and hysterectomy among transgender men are most robust to small and moderate degrees of bias. Further, single-imputation models enabled us to estimate upper and lower bounds for each prevalence ratio. We found that the range of possible associations between gender identity, lifetime PSA testing and hysterectomy is modest compared to the possible range for lifetime Pap testing and pregnancy. Nonetheless, the upper and lower bounds placed on the estimated associations are informative given the current sparsity of literature on reproductive health outcomes in TGNC populations.

Descriptive results suggest that TGNC individuals excluded from answering sex-specific questions are demographically distinct from those who were included in the sample. This supports our hypothesis that there is significant selection bias present in the BRFSS measures of reproductive health among TGNC respondents. The results of survey weighted responses and the complete-case regression do not account for systematic bias, but suggest that: lifetime Pap testing is less prevalent among TGNC individuals when compared to cisgender women, while lifetime PSA testing is similar among TGNC individuals and cisgender men; and, the prevalence of hysterectomy was also similar among TGNC individuals and cisgender women. It also suggests that 1.9% of transgender men and 2.6% of GNC individuals were pregnant at the time of interview, compared to 4.0% of cisgender women. Regression analysis confers these results that the prevalence of pregnancy among TGNC respondents is lower than, but not statistically different from, cisgender women.

There is limited literature in which to contextualize these estimates. A systematic review suggests that the proportion of transgender men who are up to date on their Pap testing is between 5.0% and 9.2% lower than cisgender women, based on clinical and community samples.[29] Estimates of the prevalence of hysterectomy among transgender men range from 5.5% to 14%.[2,30–32] Despite documented cases of prostate cancer among transgender women, there are no studies that examine rates of PSA testing.[33,34] And overall, there are few studies that characterize the general or reproductive health of GNC populations, with the majority of TGNC literature focusing on binary gender identities.[3,14] Lastly, several studies have documented transgender men's experience with pregnancy, but their sampling methods preclude an estimate of the prevalence of pregnancy.[35–37] Therefore, despite the presence of bias, our results suggesting that the prevalence of pregnancy among transgender men and GNC individuals may be similar to cisgender women is novel. This has important implications about the availability of trans-competent and inclusive family planning, antenatal care, and birthing services for TGNC individuals experiencing pregnancy.

A strength of this study is that we compared two approaches of modeling the systematic bias that results from the misclassification of sex assigned at birth and the subsequent missing data. The first approach considered a selection bias model, while the second approach modeled bias as a missing data problem. The first bias modeling approach is limited in that it does not use the available information on demographics, socioeconomic status, and healthcare access of individuals who are missing data on sex-specific outcomes. In contrast, while the second approach employs this information through multiple imputation methods, we are unable to apply this methodology among GNC respondents due to our inability to specify a multiple imputation model conditional on an assumed sex assigned at birth.[25] The fact that the results of these two approaches reinforce each other lends credence to our findings.

Due to the lack of external data to inform the degree of selection bias or confounding, we instead considered a wide range of bias scenarios. Future validation studies that allow us to estimate the true selection probabilities among TGNC respondents would allow more accurate estimates of the selection bias odds ratio.[19] Similarly, additional data could inform bounds on the risk ratio due confounding, per Flanders and Khoury.[28]

Another limitation of our analysis is the reliance of sex assigned at birth as an imperfect proxy for anatomy. By excluding transgender women from an analysis of Pap testing, pregnancy and hysterectomy, we also infer that all transgender men possess a cervix and uterus. Similarly, by excluding transgender men from our analyses of PSA testing, we infer that all transgender women possess a prostate. However, these assumptions do not account for intersex individuals or individuals who pursue other gender affirming procedures. Therefore, our denominator of who is at risk may be inflated.

Further, we are unable to apply bias modeling methods to all sex-specific outcomes, specifically questions related to mammograms and breast exams. According the American Cancer Society, all individuals with breast tissue who over the age of 40 should have the option of beginning annual screening.[38] However, the presence or absence of breast tissue depends on a wide range of individual gender affirming choices a TGNC person chooses to pursue and subsequently has access to, including hormone replacement therapy and "top" surgery.[2]

As with all health surveys, the BRFSS relies on self-report. Therefore, the measure of transgender identity is not a true measure of gender identity, but also a measure of willingness to report TGNC identities. We hypothesize that willingness to report is strongly associated with both regional and personal factors, including the sociopolitical context where a person lives, geography, race, and age. Therefore, we expect some measurement error in reported gender identity as well as residual confounding due to limited variables available in the BRFSS to capture factors that influence willingness to report. Additionally, the BRFSS only samples non-incarcerated, non-institutionalized individuals. This explicitly excludes group homes, shelters and all other institutions. Due to disproportionate rates of incarceration among transgender women of color, and extremely high rates of homelessness among TGNC individuals, the BRFSS is not able to capture these particularly vulnerable populations.[2]

The BRFSS and other national surveys that are based on probability sampling methods, are crucial tools in aiding our understanding of health disparities among gender minorities. This study provides evidence that BRFSS data report non-representative samples of TGNC individuals who are asked questions about their reproductive health, and that these outcomes are subsequently vulnerable to bias. Therefore, additional attention to survey methodologies and implementation of validated sex and gender identity question are critical. Specifically, surveys should explicitly ask all participants about their sex assigned at birth, and should avoid cisnormative assumptions about sex and anatomy, including reliance on sex-based skip patterns.[17] Additionally, researchers who use BRFSS data to examine reproductive health outcomes should not reported their results as unbiased population-based estimates. Ideally, such estimates should be accompanied by quantitative bias analysis that acknowledge the impact of the systematic misclassification of sex and missing data that are induced by the BRFSS methodologies.

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Table 1: Misclassification of Sex Assigned at Birth by BRFSS Protocol and the Subsequent Transgender and Gender Nonconforming Respondents who were Asked and Precluded from Sex-Specific Questions

	Asked Sex-Specific Questions	**Not Asked Sex-Specific Questions**
Sex Assigned at Birth **Does** Match BRFSS Designated Sex	(A) TGNC respondents are **correctly included** in the sample	(B) TGNC respondents are **correctly excluded** from the sample
Sex Assigned at Birth **Does Not** Match BRFSS Designated Sex	(C) TGNC respondents are **incorrectly included** in the sample.	(D) TGNC respondents are **incorrectly excluded** from the sample.

Table 2: Overview of Multiple-Bias Modeling Approaches

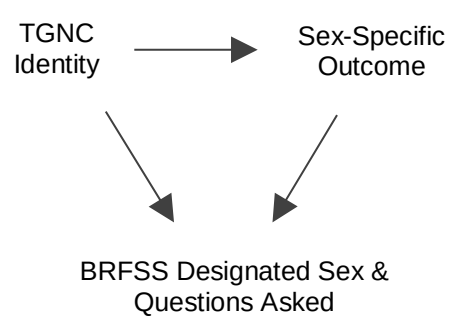
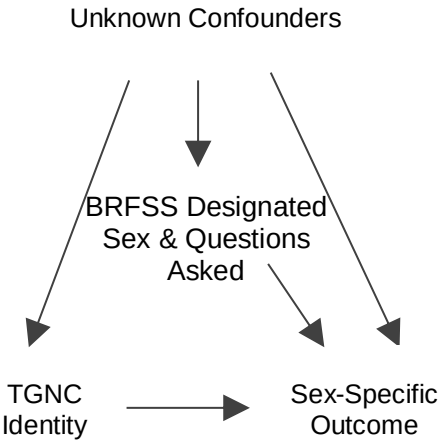
	Approach One: Selection Bias	**Approach Two: Missing Data & Unknown Confounding**
Directional Acyclic Graph (DAG):		
Analytic Step 1: Record-Level Adjustments	Remove TGNC individuals incorrectly included in the sample (cell C in Table 1): • For transgender men and women, exclude individuals based on their inferred sex assigned at birth. • For GNC individuals, use Monte Carlo sampling methods to remove 30% of the inflated *no, I don't know,* and *refused* responses.	First, use single-imputation to model extreme scenarios in which TGNC individuals missing data either all had the outcome, or all did not have the outcome. Second, use multiple imputation by chained equations (MICE) to impute missing outcomes for TGNC individuals who were incorrectly excluded from the sample (cell D in Table 1). Remove TGNC individuals incorrectly included in the sample using similar methods as approach one.
Analytic Step 2: Summary-Level Adjustments	Conduct a probabilistic adjustment for selection bias that results from individuals being incorrectly excluded from the sample (cell D in Table 1). Using Monte Carlo sampling methods, multiply the estimated prevalence ratio, $\widehat{\mathrm{PR}}$, by the selection bias odds ratio, OR_{select}, to obtain a measure of association that accounts for systematic bias: $\mathrm{PR}_{adj} = \widehat{\mathrm{PR}} \times \mathrm{OR}_{select}$	Conduct a probabilistic adjustment to MICE based estimates to further account for the unknown confounding that underlies the missingness (i.e. because sex-specific outcomes have non-ignorable missingness). Using Monte Carlo sampling methods, divide the estimated prevalence ratio, $\widehat{\mathrm{PR}}$, by the risk ratio due to confounding, RR_{conf}, to obtain a measure of association that accounts for systematic bias $\mathrm{PR}_{adj} = \frac{\widehat{\mathrm{PR}}}{\mathrm{RR}_{conf}}$

Table 3. Demographic and Health Related Characteristics of Transgender and Gender Nonconforming Respondents Asked and Precluded from Sex-Specific Questions

	No. (%)					
	Transgender Women		**Transgender Men**		**Gender Nonconforming[3]**	
Demographic Characteristics	Asked Relevant Sex-Specific Questions[1] (n = 759)	Not Asked Relevant Sex-Specific Questions[2] (n = 319)	Asked Relevant Sex-Specific Questions[2] (n = 489)	Not Asked Relevant Sex-Specific Questions[1] (n = 212)	Only asked about Pap testing, Hysterectomy, Pregnancy[2] (n = 319)	Only asked about PSA testing[1] (n = 759)
Age (years)						
18 - 24	61 (17.9%)	24 (22.7%)	36 (20.4%)	29 (24.3%)	30 (22.7%)	26 (17.9%)
25 - 34	70 (14.2%)	30 (12.9%)	44 (21.3%)	17 (13.7%)	41 (12.9%)	42 (14.2%)
35 - 44	89 (13.9%)	30 (18.9%)	57 (19.4%)	26 (28.4%)	27 (18.9%)	21 (13.9%)
45 - 54	134 (16.5%)	52 (16.7%)	77 (11.5%)	41 (9.6%)	33 (16.7%)	28 (16.5%)
55 - 64	185 (22.8%)	88 (14.6%)	109 (14%)	38 (7.5%)	34 (14.6%)	45 (22.8%)
> 65	215 (14.7%)	89 (14.2%)	160 (13.5%)	60 (16.7%)	61 (14.2%)	60 (14.7%)
Race/ethnicity						
White	537 (58%)	220 (55.3%)	328 (45.2%)	151 (58%)	158 (55.3%)	143 (58%)
Black/African American	66 (12.5%)	30 (14.6%)	50 (17.1%)	18 (12.2%)	21 (14.6%)	14 (12.5%)
American Indian/ Alaska Native	15 (0.9%)	6 (3.8%)	8 (0.7%)	0 (0%)	4 (3.8%)	3 (0.9%)
Asian	31 (9%)	8 (1.5%)	12 (0.9%)	12 (9.8%)	6 (1.5%)	11 (9%)
Native Hawaiian/ Pacific Islander	9 (0.1%)	5 (0.5%)	9 (1.2%)	2 (1%)	4 (0.5%)	1 (0.1%)
Other	6 (1%)	3 (0.4%)	4 (0.8%)	1 (0%)	2 (0.4%)	3 (1%)
Multiracial	19 (0.7%)	12 (4.8%)	14 (1.6%)	10 (2.1%)	12 (4.8%)	16 (0.7%)
Hispanic/Latino	61 (17.8%)	30 (19%)	56 (32.7%)	13 (17%)	15 (19%)	27 (17.8%)
Highest Education						
Did not graduate from high school	116 (29.7%)	42 (18.2%)	86 (29.8%)	23 (22.9%)	14 (18.2%)	31 (29.7%)
Graduated high school	314 (33.8%)	105 (34.2%)	183 (32%)	85 (46.2%)	65 (34.2%)	84 (33.8%)
Attended college or technical school	191 (24.2%)	98 (33.1%)	128 (29.7%)	53 (17.9%)	85 (33.1%)	51 (24.2%)
Graduated from college or technical school	134 (12.3%)	72 (14.6%)	91 (8.5%)	49 (13%)	64 (14.6%)	56 (12.3%)
Annual Income						
< $15,000	99 (16.3%)	65 (32.6%)	94 (30%)	28 (12.8%)	41 (32.6%)	33 (16.3%)
$15,000 - $24,999	156 (21.9%)	64 (21.2%)	100 (25.9%)	30 (20.1%)	49 (21.2%)	45 (21.9%)
$25,000 - $34,999	79 (17.6%)	27 (9%)	58 (13.7%)	25 (19%)	21 (9%)	20 (17.6%)
$35,000 - $49,999	98 (9.1%)	34 (11.8%)	54 (9%)	38 (12.5%)	24 (11.8%)	30 (9.1%)
> $50,000	244 (35.2%)	75 (25.5%)	108 (21.3%)	66 (35.5%)	52 (25.5%)	71 (35.2%)
Employment status						
Employed or self-employed	389 (62.4%)	116 (43.8%)	174 (54.3%)	112 (63.9%)	94 (43.8%)	106 (62.4%)
Unemployed	46 (8.9%)	29 (11.5%)	35 (6.9%)	8 (7.6%)	14 (11.5%)	20 (8.9%)
Homemaker	7 (0.7%)	27 (11.4%)	52 (13.3%)	0 (0%)	16 (11.4%)	3 (0.7%)
Student	23 (4.1%)	8 (8.7%)	14 (5.6%)	10 (3.8%)	17 (8.7%)	9 (4.1%)
Retired	215 (15%)	82 (10.8%)	131 (10.1%)	48 (16.7%)	52 (10.8%)	61 (15%)
Unable to work	75 (8.9%)	53 (13.8%)	79 (9.8%)	30 (8%)	32 (13.8%)	22 (8.9%)

Table 3 continued

	No. (%)					
	Transgender Women		**Transgender Men**		**Gender Nonconforming[3]**	
	Asked Relevant Sex-Specific Questions[1] (n = 759)	Not Asked Relevant Sex-Specific Questions[2] (n = 319)	Asked Relevant Sex-Specific Questions[2] (n = 489)	Not Asked Relevant Sex-Specific Questions[1] (n = 212)	Only asked about Pap testing, Hysterectomy, Pregnancy[2] (n = 319)	Only asked about PSA testing[1] (n = 759)
Marital status						
Married, or living with partner	395 (51.3%)	134 (52.3%)	206 (34.4%)	111 (50.3%)	92 (52.3%)	115 (51.3%)
Separated, divorced or widowed	174 (15.9%)	115 (24.8%)	175 (25.4%)	45 (17.7%)	68 (24.8%)	49 (15.9%)
Never Married	187 (32.8%)	69 (23%)	103 (40.2%)	55 (32%)	67 (23%)	56 (32.8%)
Sexual Orientation						
Straight	610 (75.2%)	250 (74.5%)	393 (64.3%)	172 (71.1%)	134 (74.5%)	134 (75.2%)
Lesbian or Gay	35 (3.6%)	16 (6%)	28 (21.8%)	11 (8%)	19 (6%)	15 (3.6%)
Bisexual	64 (12.2%)	27 (13.7%)	37 (8.5%)	18 (15.9%)	40 (13.7%)	51 (12.2%)
Other	22 (6.2%)	14 (4.9%)	10 (1.3%)	3 (3.7%)	24 (4.9%)	12 (6.2%)
Don't Know/Not Sure	18 (2.7%)	3 (0.9%)	12 (4%)	4 (1.3%)	5 (0.9%)	3 (2.7%)
Urban/Rural Residence						
In city center of MSA	136 (35.1%)	76 (42.4%)	114 (40.8%)	42 (40%)	49 (42.4%)	45 (35.1%)
Outside city center, within county of MSA	62 (30%)	30 (23.5%)	40 (23.2%)	9 (10.5%)	22 (23.5%)	20 (30%)
Suburban county of MSA	51 (12.4%)	26 (16.6%)	45 (16.6%)	15 (29.8%)	14 (16.6%)	12 (12.4%)
Rural	150 (22.6%)	51 (17.5%)	91 (19.4%)	26 (19.8%)	36 (17.5%)	33 (22.6%)
Health Related Measures						
Poor/Fair General Health	176 (15.9%)	86 (22.9%)	151 (24.7%)	41 (13.6%)	69 (22.9%)	64 (15.9%)
No health care coverage	85 (16.2%)	27 (21%)	54 (20.9%)	26 (20.8%)	25 (21%)	31 (16.2%)
No personal doctor/ health care provider	135 (26.8%)	51 (23.3%)	73 (34.6%)	40 (35.3%)	39 (23.3%)	51 (26.8%)
Could not see doctor due to cost in past year	97 (16.5%)	53 (29.8%)	72 (29.5%)	23 (21.5%)	37 (29.8%)	33 (16.5%)

Unweighted counts and survey weighted percentages from the 2014, 2015, and 2016 BRFSS states participating in the SOGI module.
[1] BRFSS designated sex is male; respondents are subsequently asked question about PSA testing, and precluded from questions related to Pap testing, hysterectomy, and pregnancy.
[2] BRFSS designated sex is female; respondents are subsequently asked question related to Pap testing, hysterectomy, and pregnancy, and precluded from questions about PSA testing.
[3] We are unable to infer the sex assigned at birth of gender nonconforming respondents. Therefore, we are unable to determine which respondents are asked sex-specific questions relevant to their anatomy, and those who are not.

Table 4. Responses to Sex-Specific Questions by Gender Identity

Reproductive Health Outcomes	No. (%) Transgender Women (n = 1,078)	Transgender Men (n = 701)	Gender Nonconforming (n = 450)	Cisgender Women (n = 298,391)	Cisgender Men (n = 218,362)
Lifetime PSA Test[1]					
Yes	201 (44.2%)		48 (35.1%)		68,677 (48.6%)
No	178 (51.6%)		41 (59.4%)		45,506 (44%)
Don't Know	14 (1.0%)		2 (0.9%)		5,058 (3.8%)
Refused	2 (3.2%)		1 (4.6%)		573 (3.6%)
Missing	193		51		51,306
Not Asked[2]	248		146		0
Lifetime Pap Test[3]					
Yes		290 (75.9%)	125 (53%)	195,295 (86.5%)	
No		45 (22.8%)	31 (45.6%)	12,289 (9.9%)	
Don't Know		2 (0.7%)	1 (0.8%)	846 (0.4%)	
Refused		2 (0.6%)	2 (0.6%)	786 (3.3%)	
Missing		150	69	89,175	
Not Asked[4]		212	222	0	
Hysterectomy[5]					
Yes		91 (15.9%)	40 (21.5%)	54,947 (20.6%)	
No		226 (83.9%)	95 (77.8%)	132,527 (75.6%)	
Don't Know		1 (0.1%)	0 (0.0%)	232 (0.2%)	
Refused		1 (0.1%)	2 (0.6%)	809 (3.6%)	
Missing		170	91	109,874	
Not Asked[4]		212	222	0	
Currently Pregnant[6]					
Yes		5 (1.9%)	5 (2.6%)	2,638 (4.0%)	
No		131 (98%)	92 (97.1%)	66,639 (93%)	
Don't Know		0 (0.0%)	1 (0.3%)	202 (0.3%)	
Refused		1 (0.1%)	0 (0.0%)	309 (2.7%)	
Missing		0	0	1	
Not Asked[4]		72	89	0	

Unweighted counts and survey weighted percentages from the 2014, 2015, and 2016 BRFSS states participating in the SOGI module. We do not report responses of transgender men whose BRFSS designated sex is male, nor do we report the responses of transgender women whose BRFSS designated sex is female.

[1] These data are restricted to respondents 40 years or older and whose BRFSS designated sex is male.

[2] Respondent's sex assigned at birth was designated female in the BRFSS.

[3] These data are restricted to respondents whose BRFSS designated sex is female.

[4] Respondent's sex assigned at birth was designated male in the BRFSS.

[5] These data are restricted to non-pregnant respondents whose BRFSS designated sex is female.

[6] These data are restricted to respondents 44 years or younger and whose BRFSS designated sex is female.

Table 5. Complete-Case Analysis Regression Results

Outcome/Gender Identity	Complete-Case Analysis	
	Crude PR	Adjusted PR[1]
	PR (95% CI)	*PR (95% CI)*
Never Lifetime PSA Test		
Transgender women	1.17 (0.89, 1.55)	1.09 (0.81, 1.48)
Gender nonconforming	1.35 (0.87, 2.10)	0.95 (0.70, 1.31)
Never Lifetime Pap Test		
Transgender men	2.31 (1.31, 4.08)	1.72 (0.98, 3.03)
Gender nonconforming	4.63 (3.17, 6.76)	2.71 (2.07, 3.55)
Has had Hysterectomy		
Transgender men	0.97 (0.76, 1.23)	1.26 (0.99, 1.61)
Gender nonconforming	0.63 (0.43, 0.91)	0.86 (0.68, 1.08)
Currently Pregnant		
Transgender men	0.47 (0.14, 1.53)	0.38 (0.13, 1.15)
Gender nonconforming	0.65 (0.21, 1.94)	0.76 (0.23, 2.58)

Referent group for PSA testing is cisgender men; referent group for Pap testing, hysterectomy and pregnancy is cisgender women.
[1]Adjusted for race, age, unemployment, income, education, partnership status, poor health, and no insurance coverage.

Table 6. Single Imputation and Multiple Imputation Regression Results

Outcome/Gender Identity	Single Imputation Models		MICE Model
	Lower Bound PR[1]	Upper Bound PR[2]	PR
	PR (95% CI)	*PR (95% CI)*	*PR (95% CI)*
Never Lifetime PSA Test			
Transgender women	0.57 (0.38, 0.84)	1.55 (1.37, 1.75)	1.03 (0.82, 1.31)
Gender nonconforming	0.49 (0.28, 0.86)	1.72 (1.37, 2.17)	—
Never Lifetime Pap Test			
Transgender men	0.98 (0.53, 1.80)	4.32 (3.36, 5.54)	1.26 (0.77, 2.06)
Gender nonconforming	1.04 (0.61, 1.78)	6.38 (5.15, 7.91)	—
Has had Hysterectomy			
Transgender men	0.66 (0.49, 0.89)	1.50 (1.33, 1.70)	1.15 (0.95, 1.41)
Gender nonconforming	0.25 (0.17, 0.38)	1.50 (1.34, 1.68)	—
Currently Pregnant			
Transgender men	0.27 (0.09, 0.78)	9.76 (5.98, 15.93)	0.59 (0.17, 1.99)
Gender nonconforming	0.33 (0.10, 1.07)	15.17 (10.55, 21.82)	—

Referent group for PSA testing is cisgender men; referent group for Pap testing, hysterectomy and pregnancy is cisgender women. All estimates adjusted for race, age, unemployment, income, education, partnership status, poor health, and no insurance coverage.
[1] Single-imputation model assuming all TGNC respondents missing outcome data did not have the outcome; that is, individuals missing data have had a PSA or Pap test once in their lifetime, have not had a hysterectomy, or was not pregnant at the time of interview.
[2] Single-imputation model assuming all TGNC respondents missing outcome data did have the outcome; that is, individuals missing data have never had a PSA or Pap test, have had a hysterectomy, or were pregnant at the time of interview.

Table 7. Magnitude of Bias Adjustment Factors Required to Change the Direction of Association of the Systematic Bias and Random Error Adjusted Prevalence Ratios

Outcome/Gender Identity	Approach One: Selection Bias		Approach Two: Missing Data and Confounding	
	Maximum Selection Bias OR Guaranteeing PR < 1	*Minimum Selection Bias OR Guaranteeing PR > 1*	*Minimum RR due to Confounding Guaranteeing PR < 1*	*Maximum RR due to Confounding Guaranteeing PR > 1*
Never Lifetime PSA Test				
Transgender women	0.54	1.49	1.55	0.73
Gender nonconforming	0.45	9.89		
Never Lifetime Pap Test				
Transgender men	0.27	2.05	3.56	0.59
Gender nonconforming	0.23	5.00		
Has had Hysterectomy				
Transgender men	0.53	1.09	1.57	0.92
Gender nonconforming	0.73	1.38		
Currently Pregnant				
Transgender men	0.53	9.99	5.90	0.12
Gender nonconforming	0.18	9.38		

This analysis explores the impacts of bias adjustment factors, the selection bias OR and the RR due to confounding, ranging from 0.10 to 10.0 on the systematic bias and random error adjusted prevalence ratios (PR).

Figure 1. Range of Selection Bias Scenarios for Systematic Bias and Random Error Adjusted Prevalence Ratios Greater than and Less than One by Sex-Specific Outcome and Gender Identity

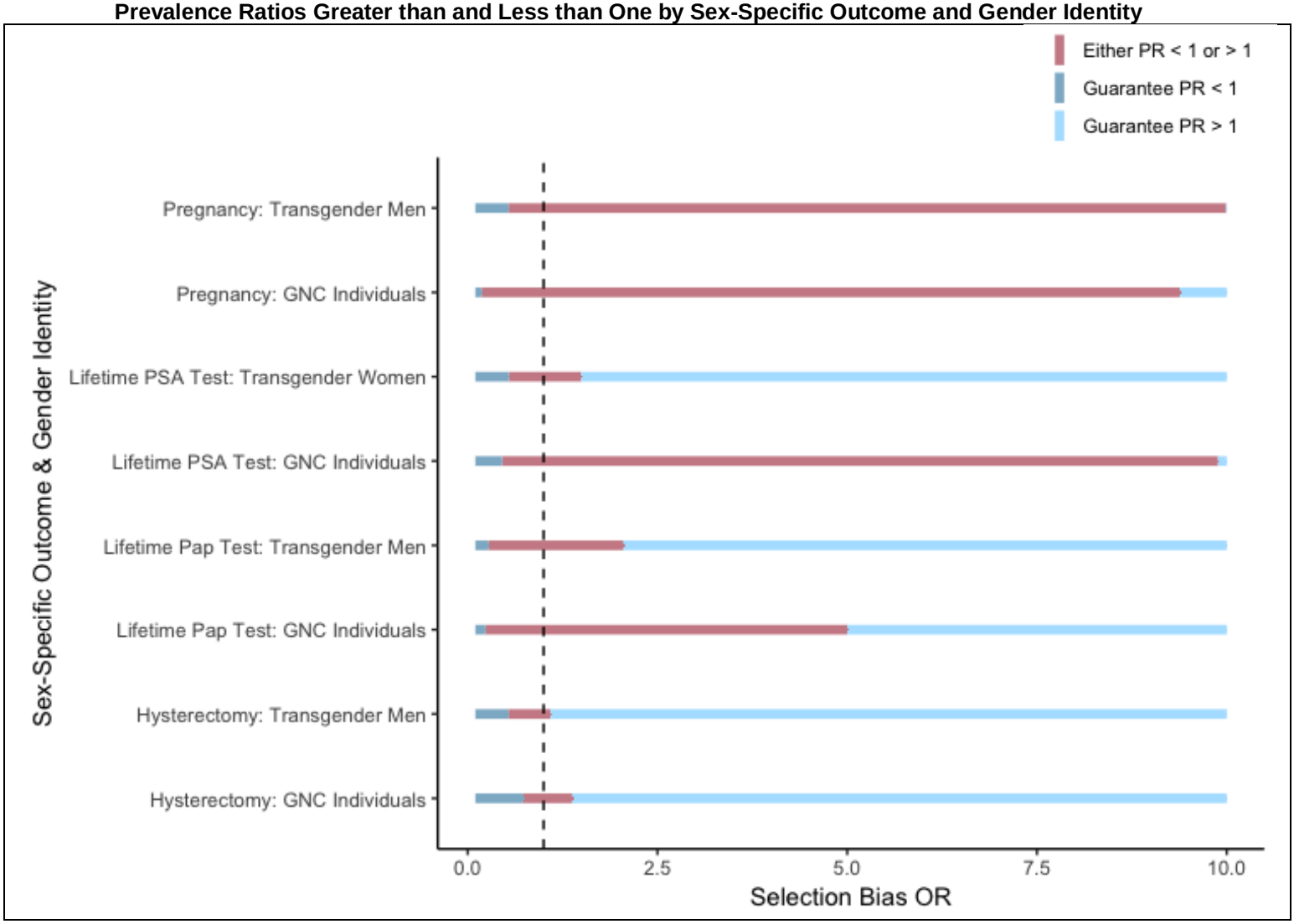


Figure 2. Range of Confounding Scenarios for Systematic Bias and Random Error Adjusted Prevalence Ratios Greater than and Less than One by Sex-Specific Outcome and Gender Identity

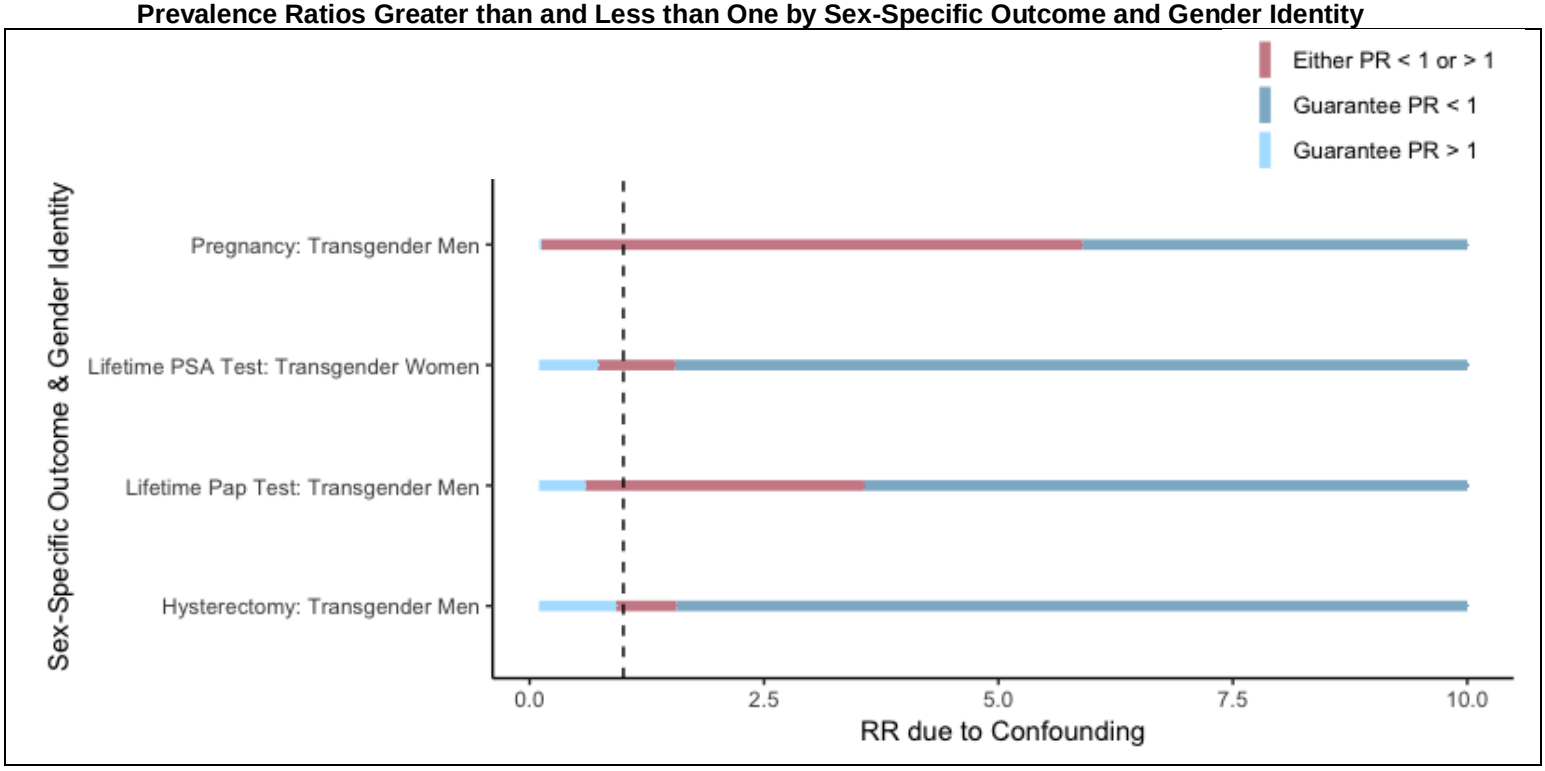
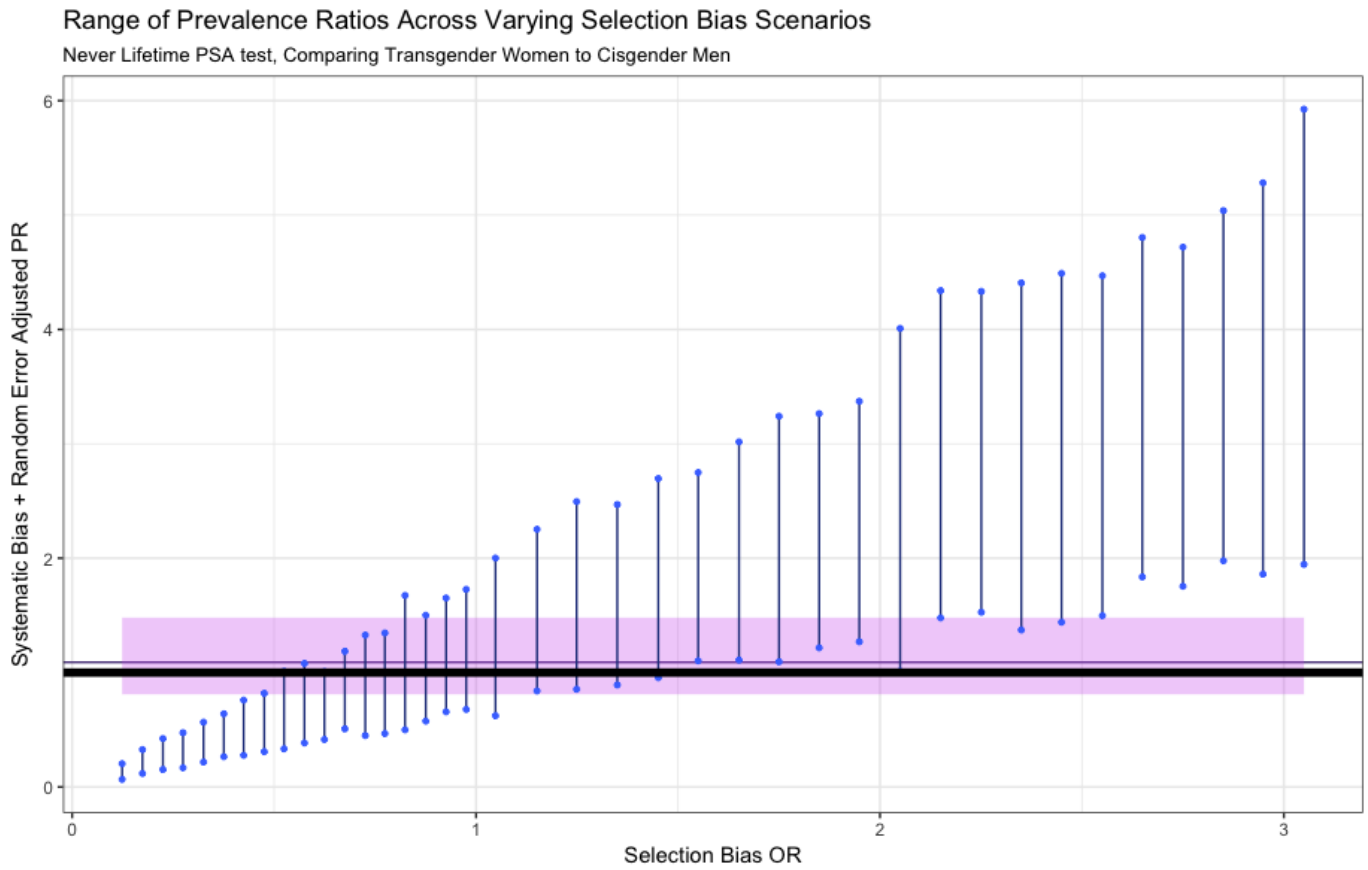
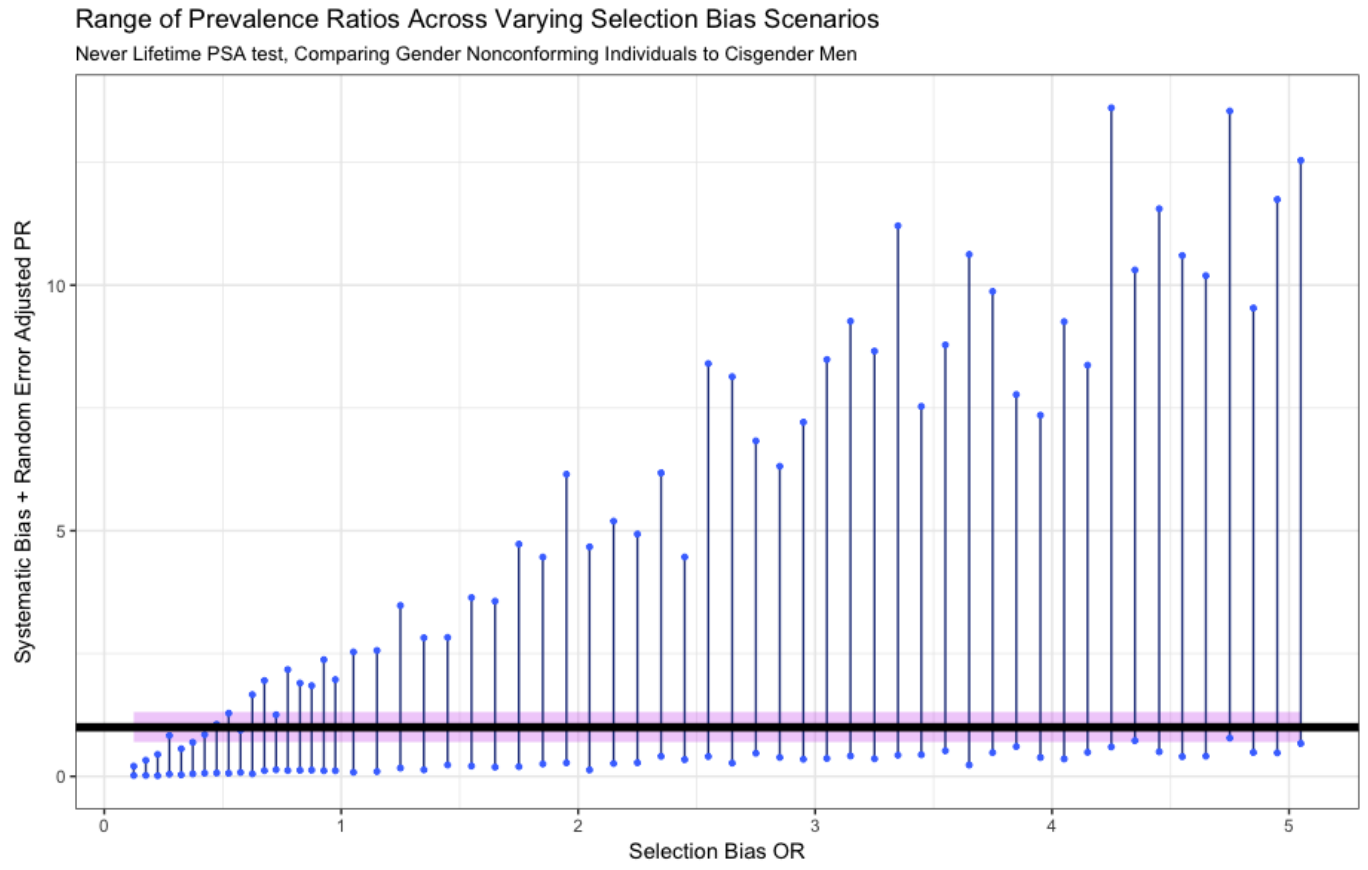
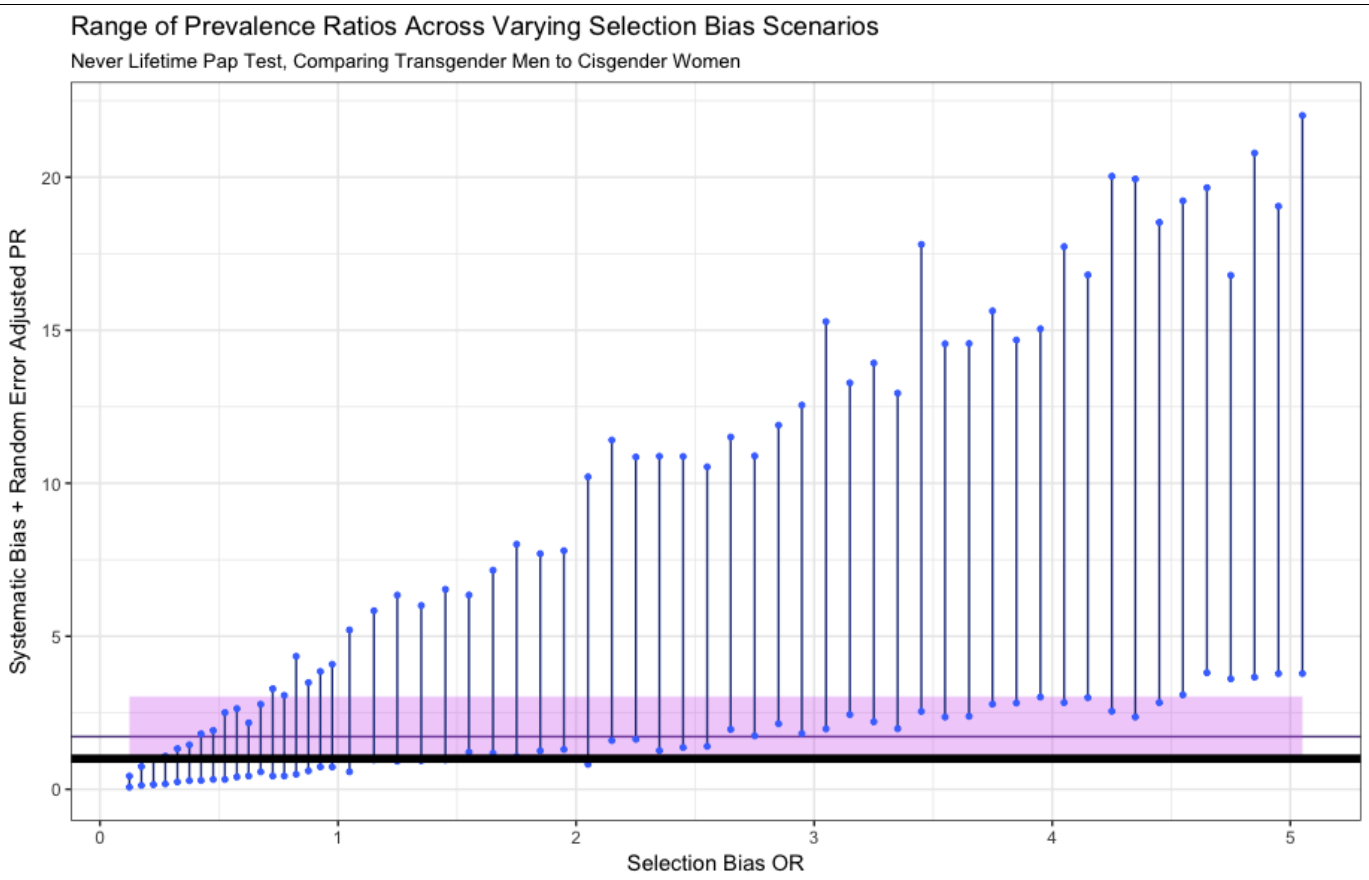
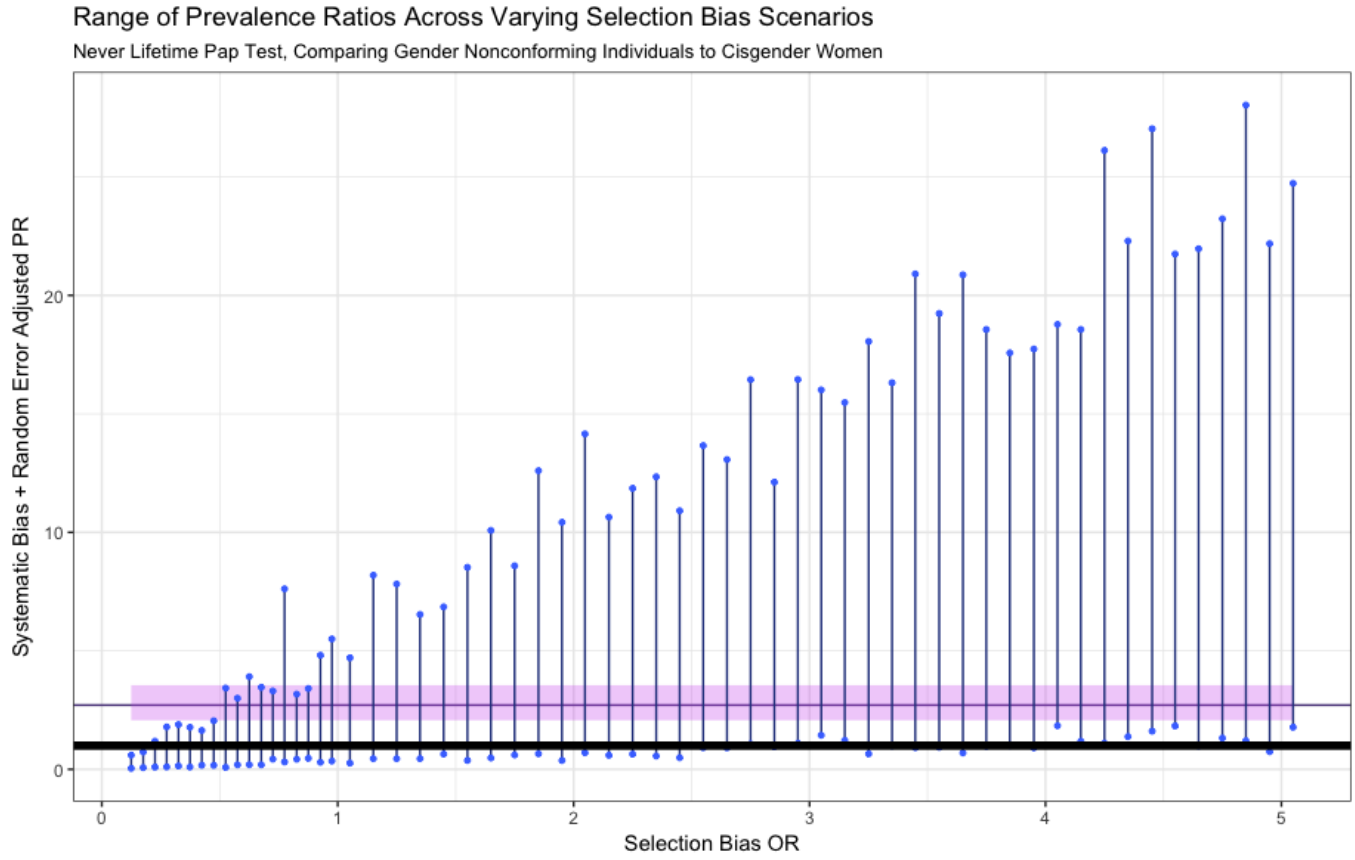


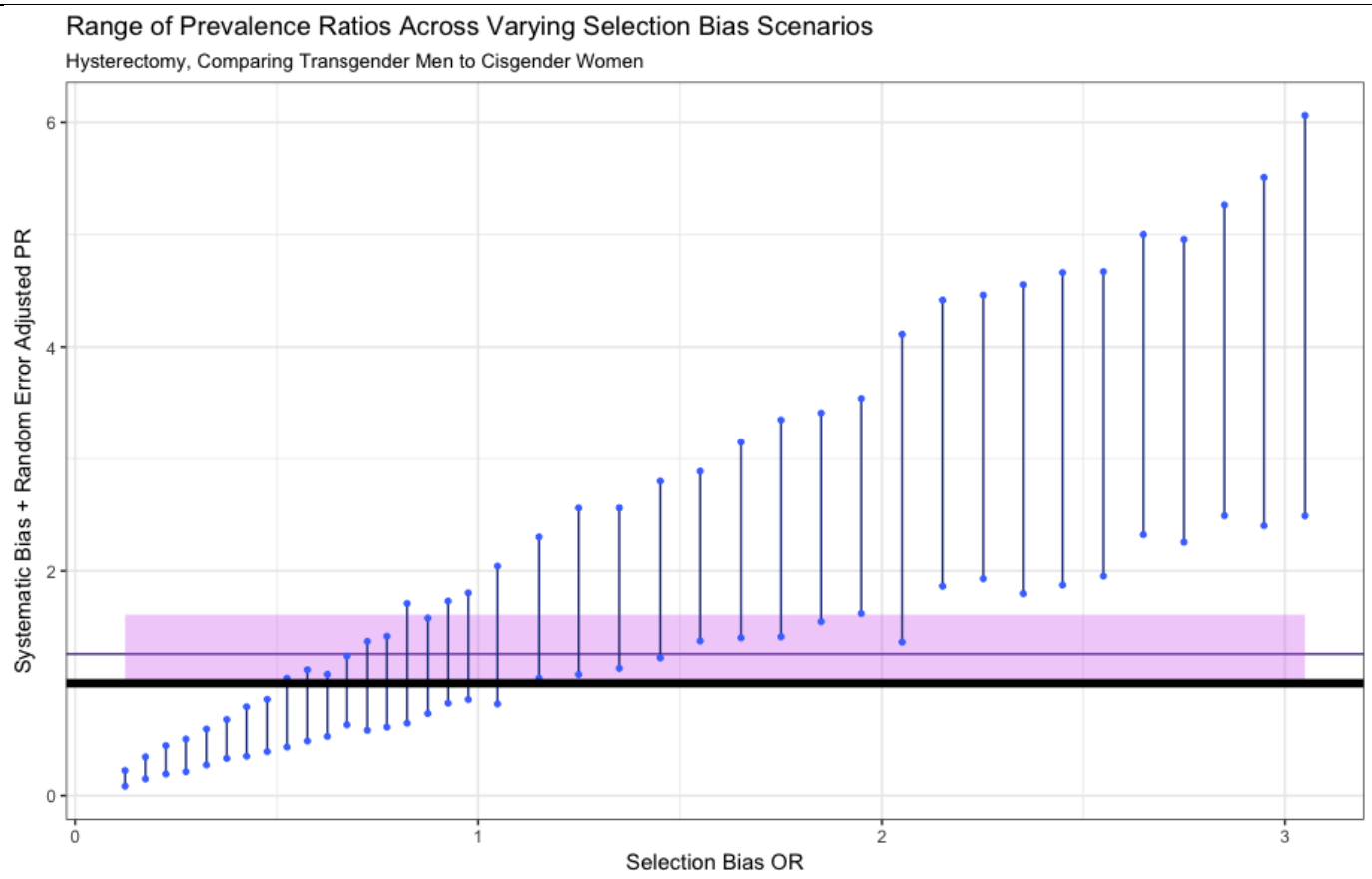
Figure 3. Range of Prevalence Ratios for Varying Selection Bias Scenarios (Approach One), by Sex-Specific Outcome and Gender Identity

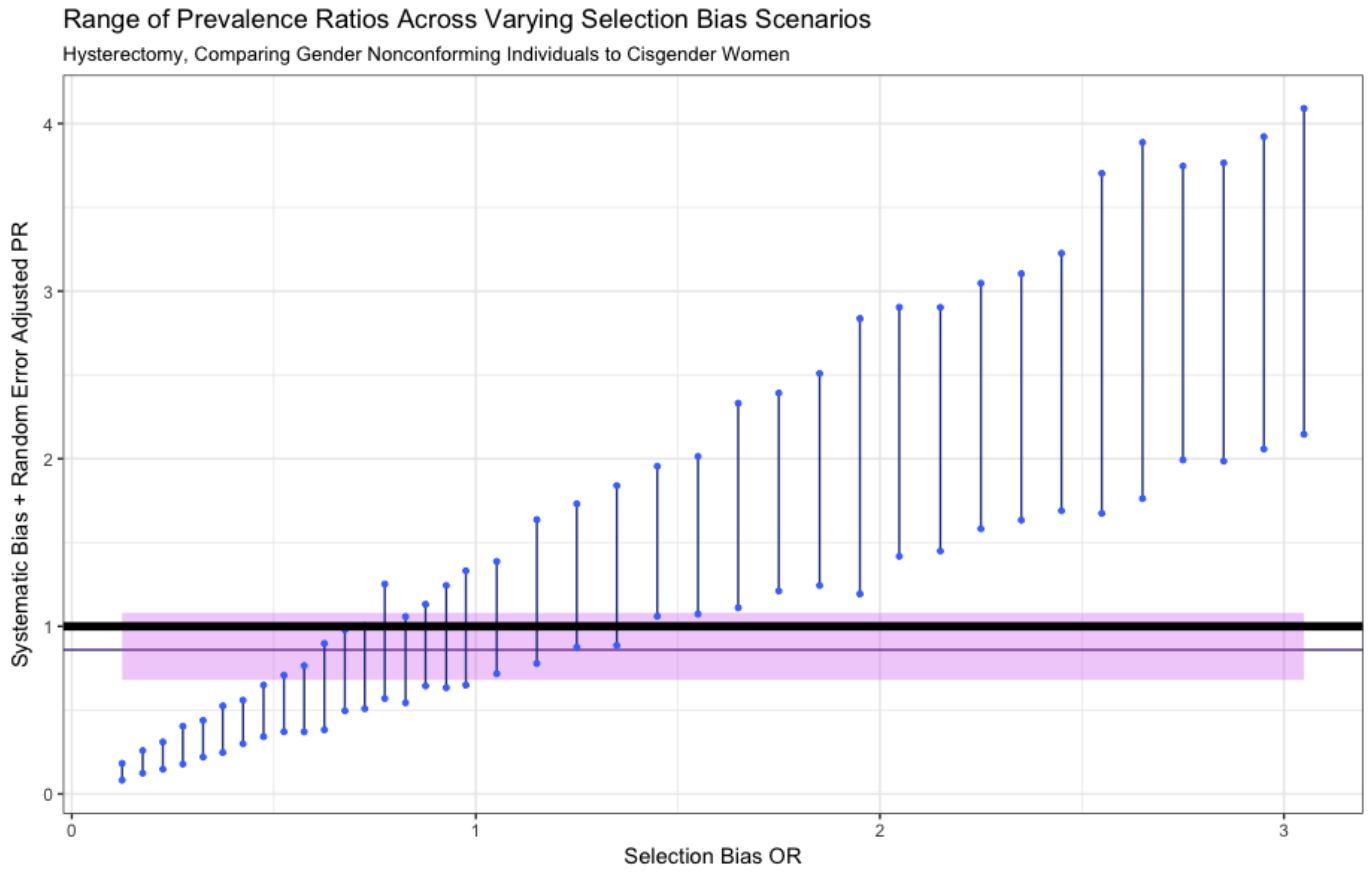


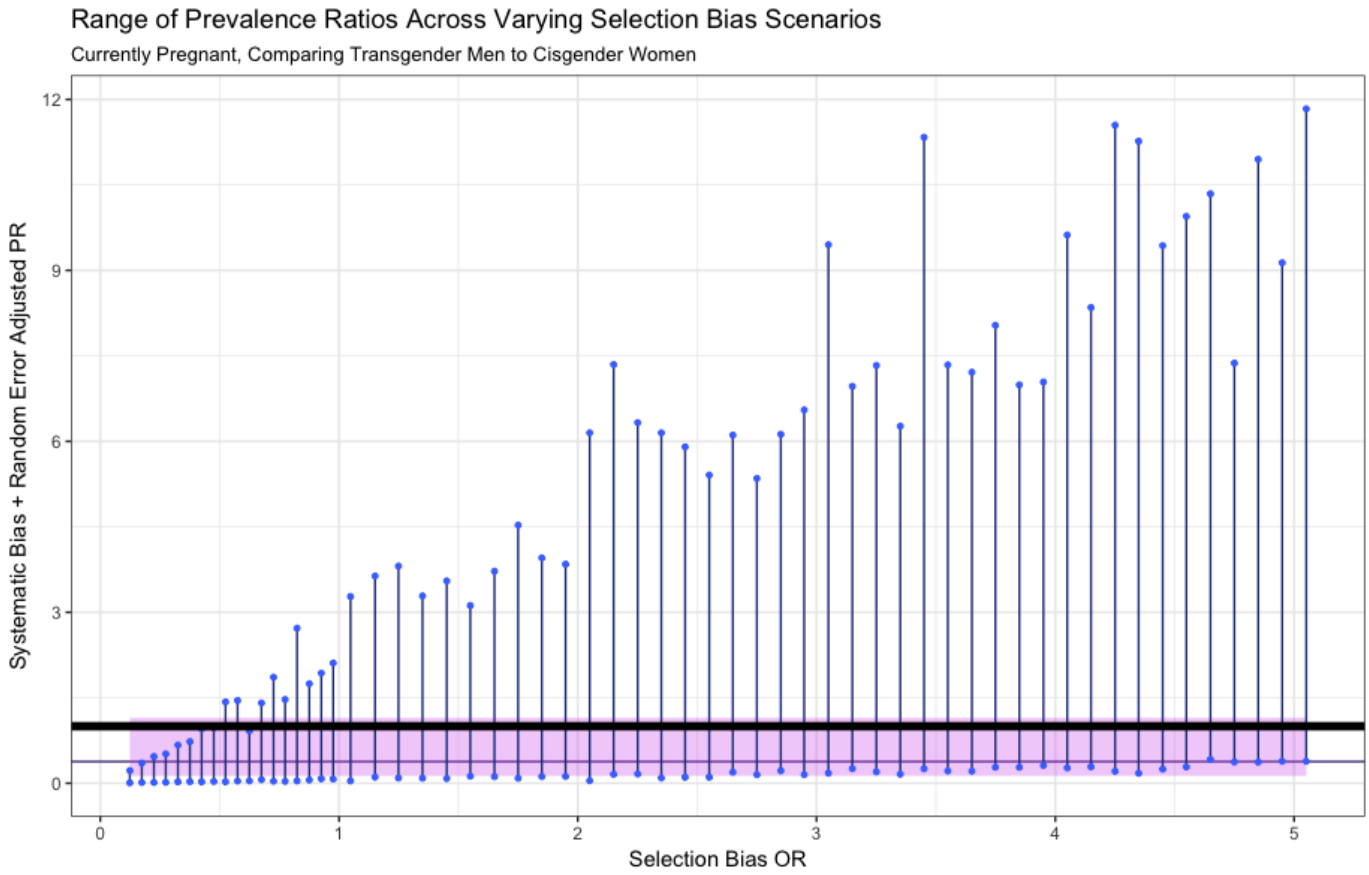


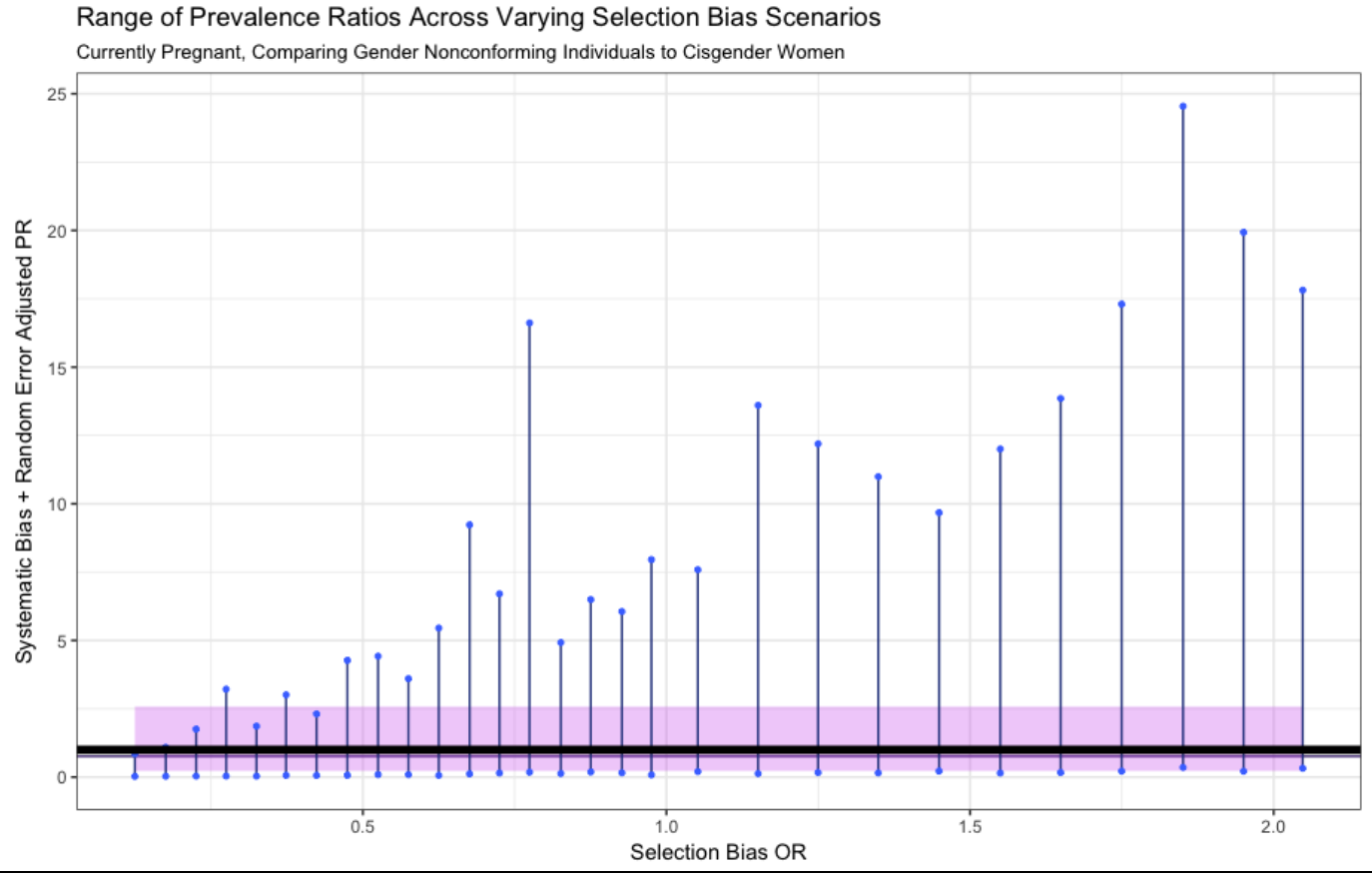

Range of Prevalence Ratios Across Varying Selection Bias Scenarios
Never Lifetime Pap Test, Comparing Transgender Men to Cisgender Women
Systematic Bias + Random Error Adjusted PR
0
5
10
15
20
0
1
2
3
4
5
Selection Bias OR


Range of Prevalence Ratios Across Varying Selection Bias Scenarios
Never Lifetime Pap Test, Comparing Gender Nonconforming Individuals to Cisgender Women
Systematic Bias + Random Error Adjusted PR
0
10
20
0
1
2
3
4
5
Selection Bias OR


Range of Prevalence Ratios Across Varying Selection Bias Scenarios
Hysterectomy, Comparing Transgender Men to Cisgender Women
Systematic Bias + Random Error Adjusted PR
Selection Bias OR
0
2
4
6
0
1
2
3

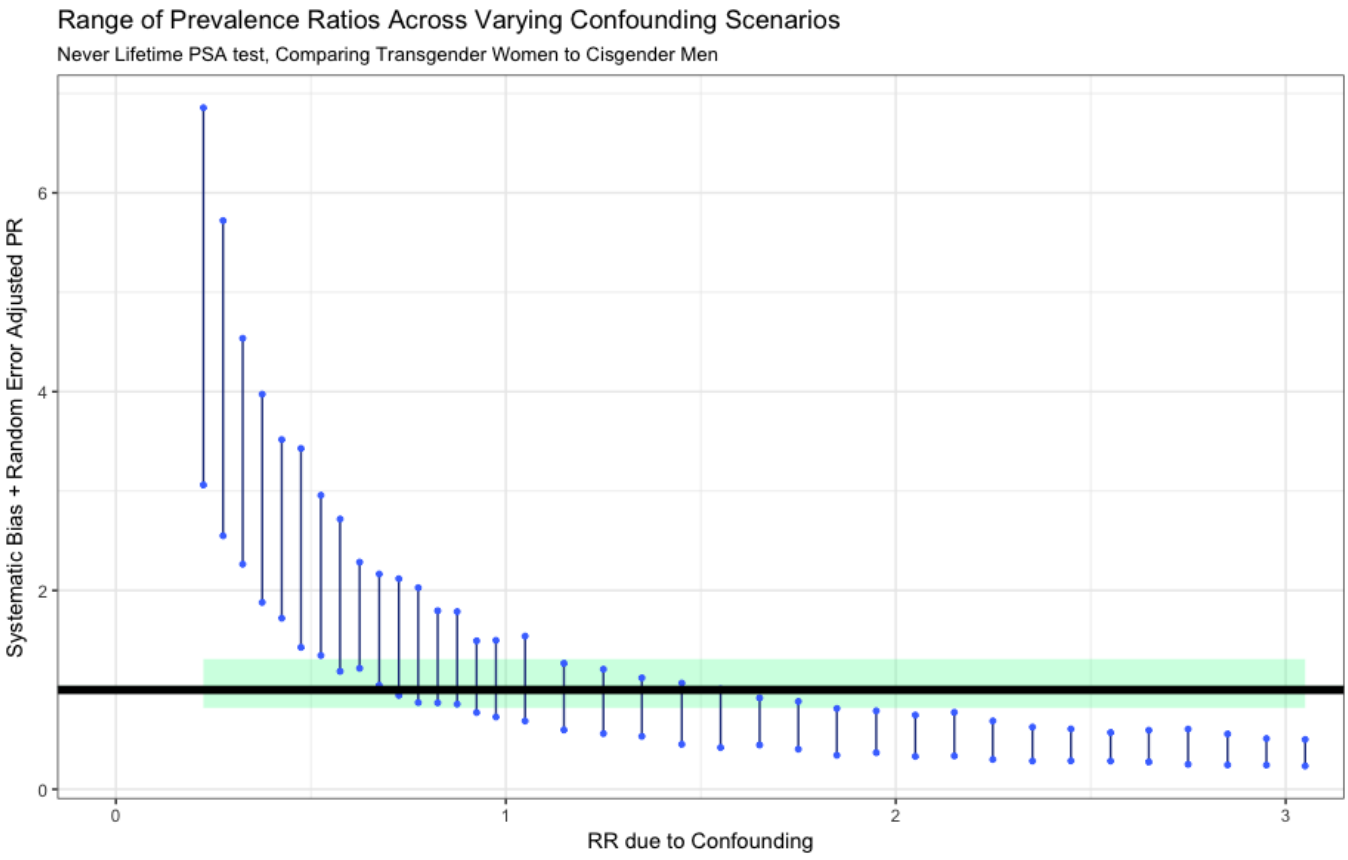

Range of Prevalence Ratios Across Varying Selection Bias Scenarios
Hysterectomy, Comparing Gender Nonconforming Individuals to Cisgender Women
Systematic Bias + Random Error Adjusted PR
Selection Bias OR
0
1
2
3
4
0
1
2
3

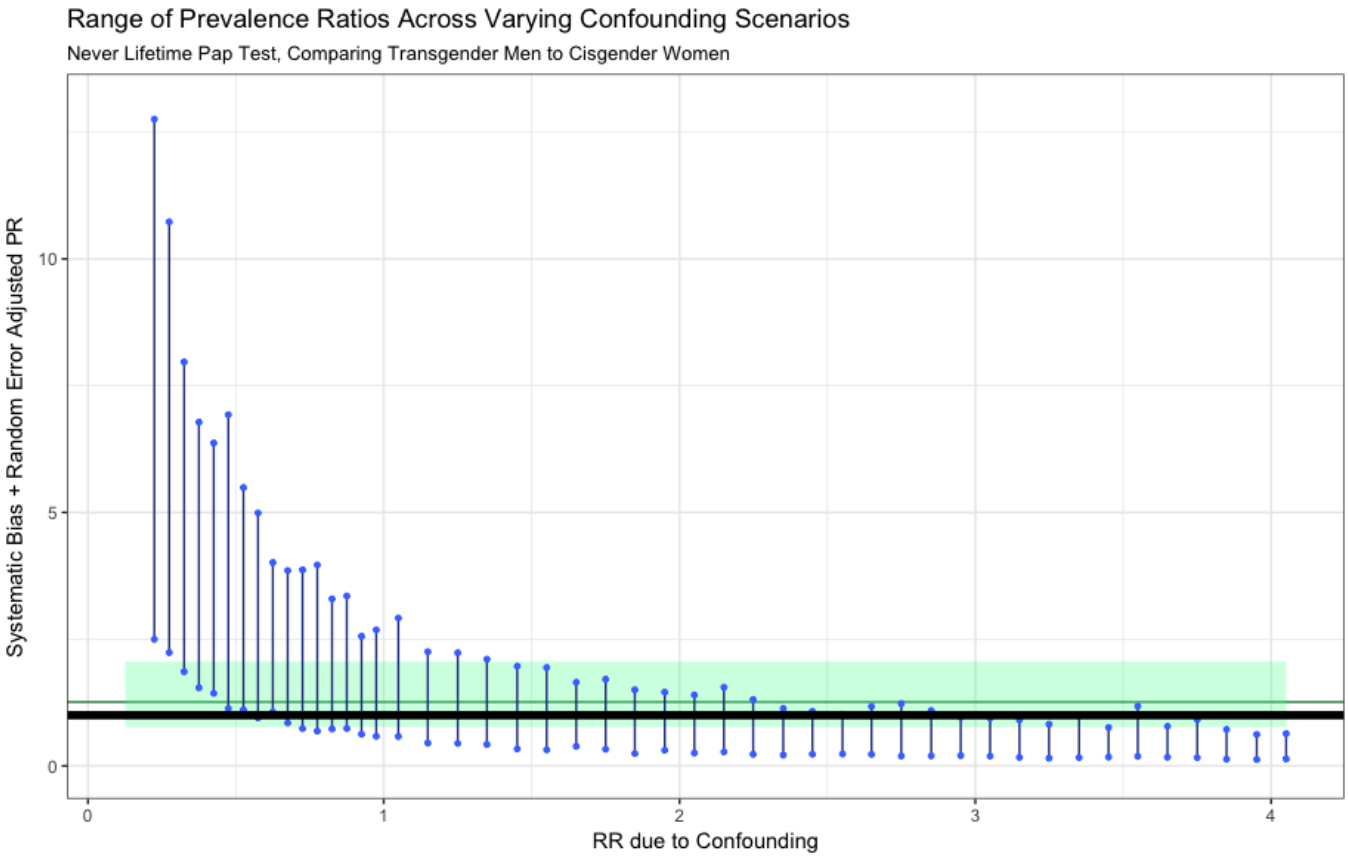


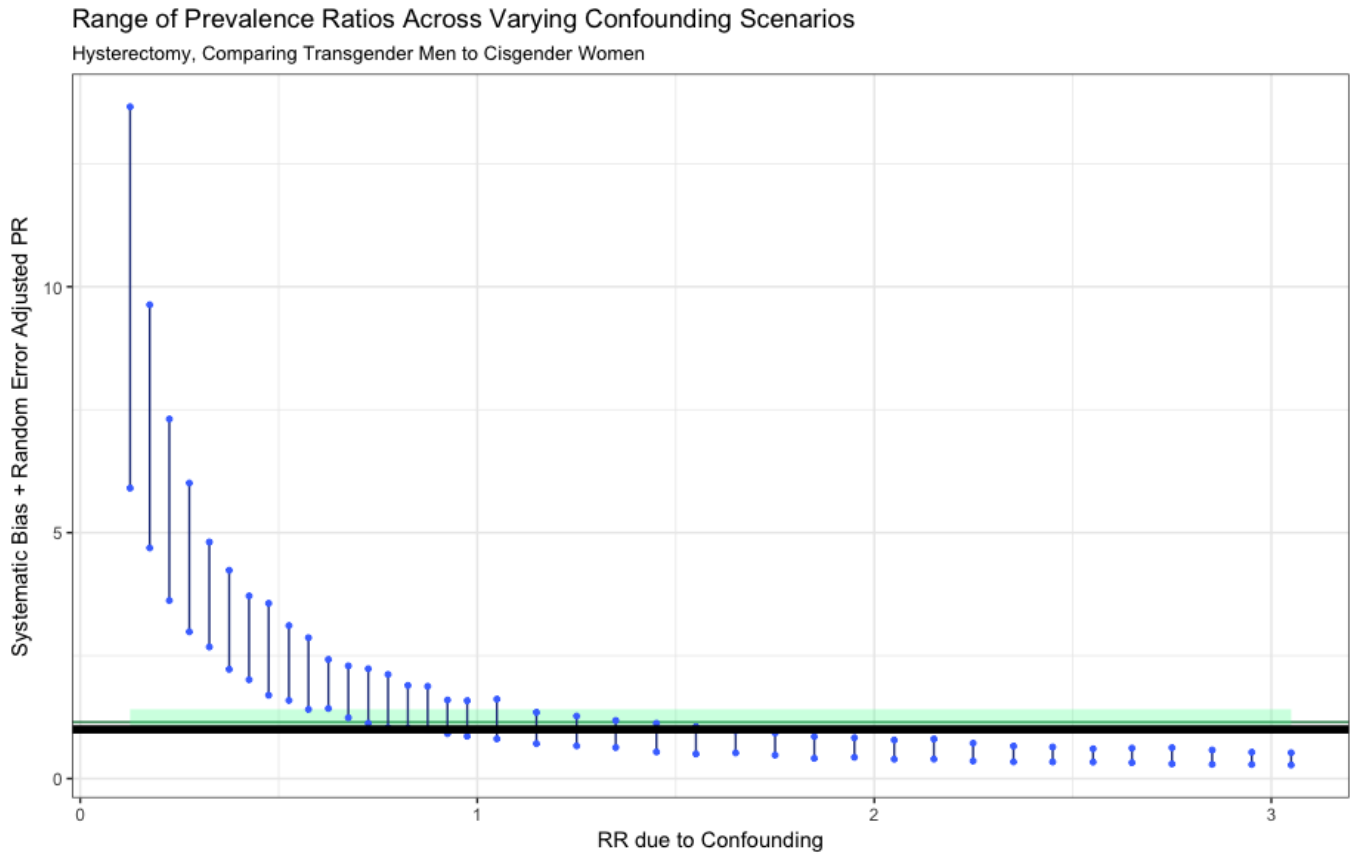


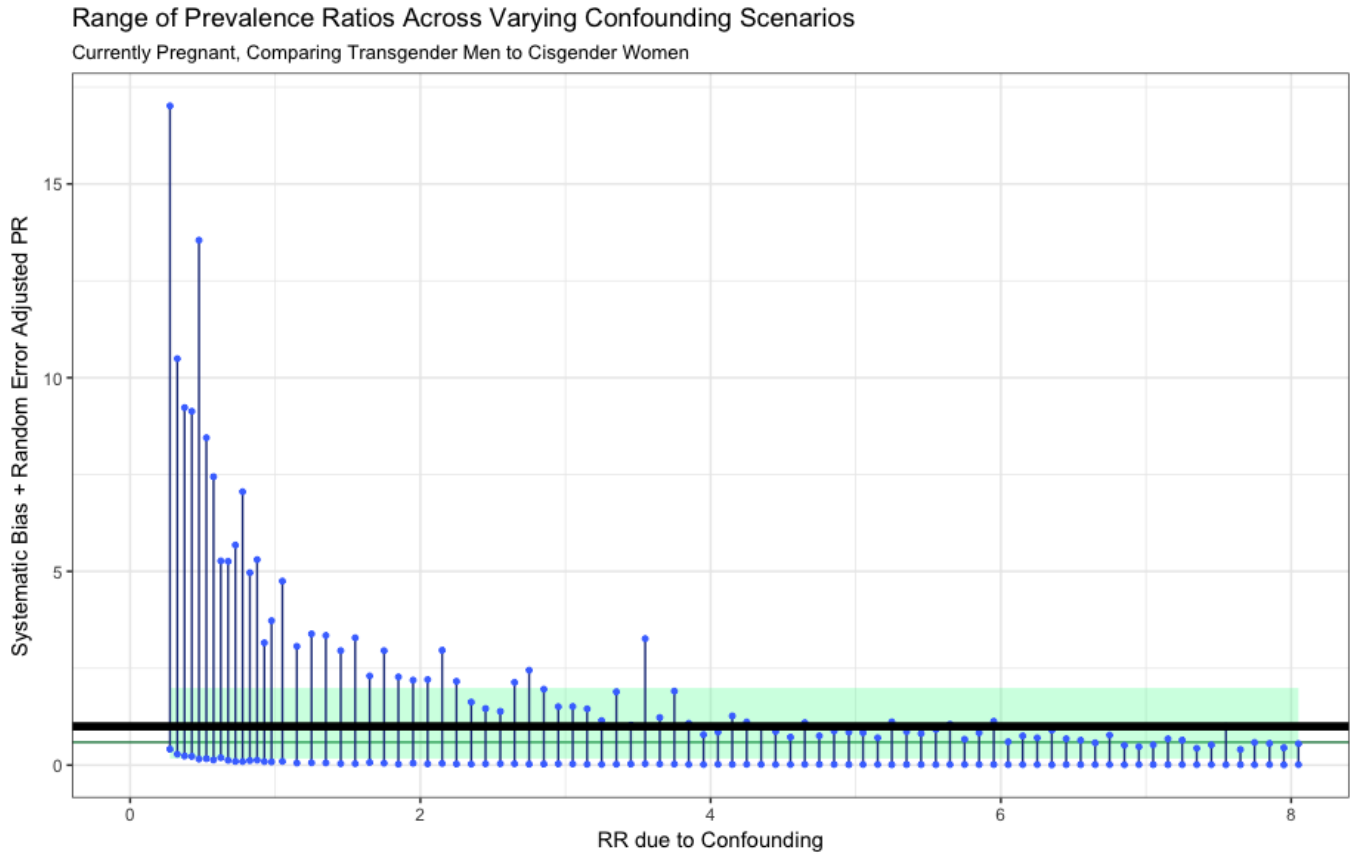
The vertical blue bars display the range of systematic bias and random error adjusted prevalence ratios across a range of selection bias scenarios. The black line indicates a PR of 1.0. The pink shaded region and dark pink line represent the point estimate and 95% confidence interval estimates from the adjusted complete case analysis (Table 5).

Figure 4. Range of Prevalence Ratios for Varying Confounding Scenarios (Approach Two), by Sex-Specific Outcome and Gender Identity









The vertical blue bars display the range of systematic bias and random error adjusted prevalence ratios across a range of selection bias scenarios. The black line indicates a PR of 1.0. The green shaded region and dark green line represent the point estimate and 95% confidence interval estimates from the multiple imputation analysis (Table 6).