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Inferring COVID-19 testing and vaccination behavior from New Jersey testing data

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Characterizing the relationship between disease testing behaviors and infectious disease dynamics is of great importance for public health. Tests for both current and past infection can influence disease-related behaviors at the individual level, while population-level knowledge of an epidemic's course may feed back to affect one's likelihood of taking a test. The COVID-19 pandemic has generated testing data on an unprecedented scale for tests detecting both current infection (PCR, antigen) and past infection (serology); this opens the way to characterizing the complex relationship between testing behavior and infection dynamics. Leveraging a rich database of individualized COVID-19 testing histories in New Jersey, we analyze the behavioral relationships between PCR and serology tests, infection, and vaccination. We quantify interactions between individuals' test-taking tendencies and their past testing and infection histories, finding that PCR tests were disproportionately taken by people currently infected, and serology tests were disproportionately taken by people with past infection or vaccination. The effects of previous positive test results on testing behavior are less consistent, as individuals with past PCR positives were more likely to take subsequent PCR and serology tests at some periods of the epidemic time course and less likely at others. Lastly, we fit a model to the titer values collected from serology tests to infer vaccination trends, finding a marked decrease in vaccination rates among individuals who had previously received a positive PCR test. These results exemplify the utility of individualized testing histories in uncovering hidden behavioral variables affecting testing and vaccination.

COVID-19 | disease testing behavior | serology

Significance

Characterization of infectious disease dynamics largely neglects behavioral factors that shape when one chooses to test for infectious disease status, the kinds of tests one uses, and the consequences of knowing one's infection status. Analyzing an individualized database of COVID-19 test results, we show that test-taking tendencies are affected by people's past infection and testing histories, in ways which vary over time and by the type of test being taken. Furthermore, we find that vaccination rates for COVID-19 were significantly reduced among people who had previously taken positive PCR tests. These results clarify how COVID-19 testing behaviors have shaped the pandemic's course in complex and often subtle ways.

Human behavior plays an integral yet arguably understudied role in the dynamics of infectious diseases. The COVID-19 pandemic made clear how behaviors such as heterogeneity in contact (1, 2), mask-wearing (3, 4), lockdown fatigue (5, 6), vaccine hesitancy (7, 8), and testing for current and past infection (9, 10) can affect epidemics at multiple scales. Thus, clarifying relationships between behaviors and infection has both applied and theoretical importance in understanding the complexities of infection dynamics.

It is especially crucial to understand the behaviors that govern infectious disease testing, as testing is one of the primary fronts by which the public and scientists alike gather information about an epidemic's course (11, 12). In order to properly account for the biases that exist in reported testing data and uncover an epidemic's true trajectory, it is necessary to be cognizant of the various ways disease surveillance is carried out at different scales (13, 14).

With COVID-19, many individuals reacted to the pandemic through weekly or even daily testing for current infection status, using PCR and antigen tests to help identify asymptomatic infections. As a result, COVID-19 was met with an unprecedented volume of tests and subsequent quarantines, significantly reducing the number of asymptomatic transmissions and overall cases (10, 15, 16). This pattern of mass testing also kept people continually informed of the pandemic's magnitude through PCR-reported case counts, prompting governments to institute nonpharmaceutical interventions such as social distancing and mask-wearing guidelines. Additionally, serology (antibody) tests, which test for an immune response indicative of past infection, have also been used throughout the COVID-19 pandemic and affected its course. Many serology tests have been provided in hospitals, in randomized serosurveys, or by individuals curious about their immune status, especially after initial surges of infection when diagnostic tests were not yet available (17, 18). This amount of information on past infection has aided greatly in determining the breadth of immunity across populations worldwide (19).

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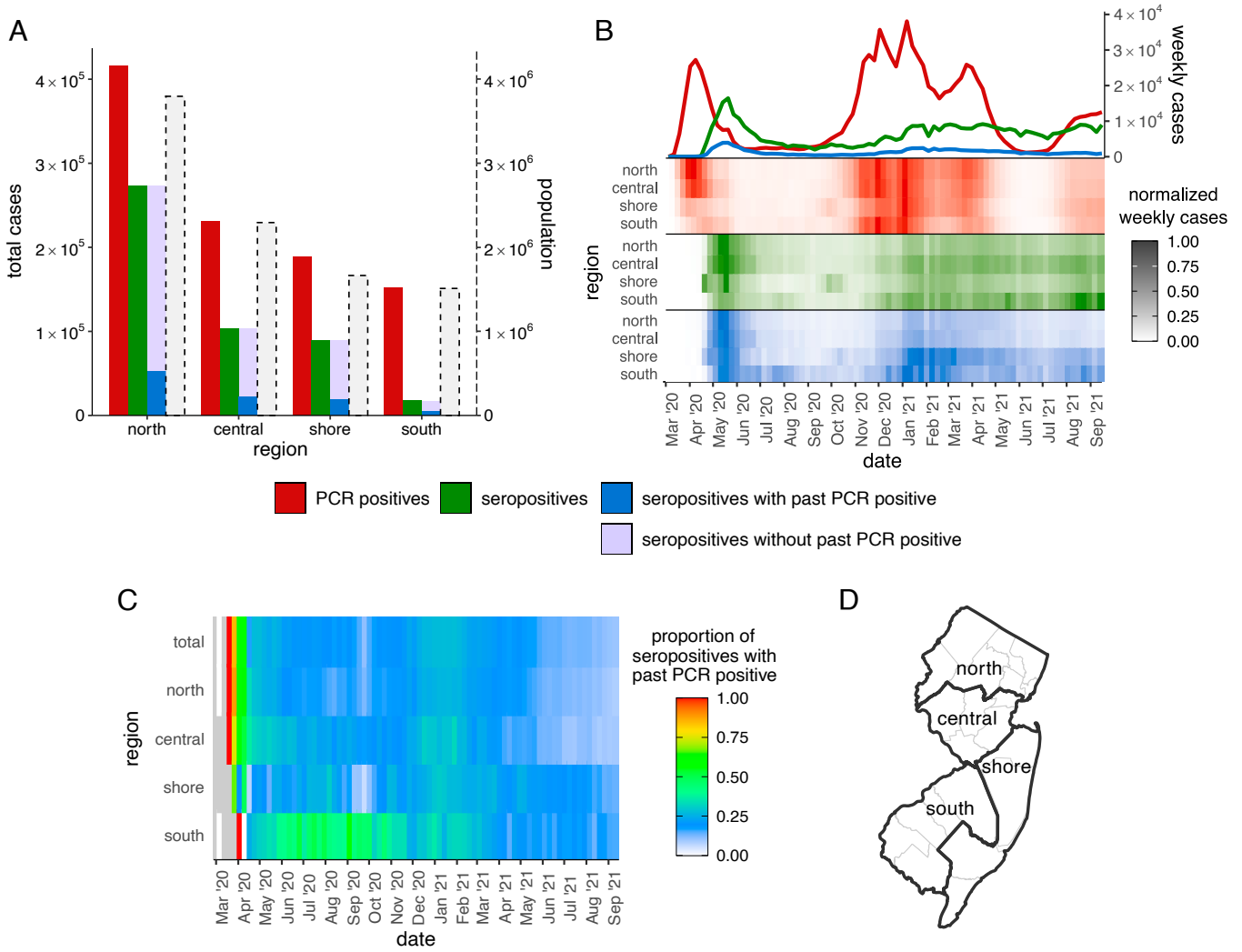

Fig. 1. (*A*) Total number of positive tests over the study period for each New Jersey region and in three main categories of tests: PCR tests (red), serology tests (green), and serology tests associated with a past PCR positive (blue). Seropositives with no past PCR positive are also shown (lavender). Dashed light gray bars show the population of each New Jersey region. (*B*) Positive tests from the three main categories, but over time. The *Top* panel shows the total positive tests for each category across all regions, and each heatmap shows the positive tests of one type broken up by New Jersey regions and normalized to the maximum in that region over this time period (so heatmap values range from 0 to 1). (*C*) Proportion of positive serology tests per week whose test-takers had a past PCR positive, for all of New Jersey ("total") and broken up by region. Gray cells indicate no serology tests were taken in that region that week. (*D*) The map shows how the New Jersey counties are grouped into different regions for this analysis.

Despite the obvious and overwhelming benefits of infectious disease testing in general, the distribution of these tests has been found to be biased in many ways: toward certain demographic factors (gender, race, ethnicity, geographic location, and socioeconomic status) (20–22); toward symptomatic or asymptomatic infections (23, 24); and toward mass testing settings like schools, workplaces, and hospitals (25–27). And testing can unintentionally foster a false sense of security. Low PCR-reported case counts can promote riskier behaviors at the population-wide scale, a phenomenon which has led to many instances of populations relaxing their COVID-19 restrictions prematurely (28, 29). At the individual scale, negative PCR results can be perceived as permission slips for partaking in large gatherings and other risky situations (9). On the other hand, positive test results of any kind can cause the test-taker to be overly confident in the natural immunity they may have acquired, to the point of encouraging riskier behaviors or even eschewing vaccination (7)—despite the potential for reinfection, especially among the unvaccinated (30). In these ways, COVID-19 PCR, antigen, and serology tests have the ability to significantly influence transmission dynamics; however, the relative impacts of these different testing behaviors are not immediately clear.

In this paper, we examine how testing behavior may have influenced the dynamics of COVID-19 through a database from the New Jersey Department of Health (NJDOH), which recorded individualized testing histories for everyone who has taken a COVID-19 PCR or serology test in the state. The large-scale, continuous use of PCR and serology tests through the first 2 y of the pandemic allows us to investigate how test-taking behaviors for the two kinds of tests have interacted with each other, and how such interactions vary by geographical area (Fig. 1). One immediate benefit of such a database is the ability to crudely estimate the magnitude of true COVID-19 incidence: since only PCR tests are reported in official COVID-19 case counts, all serology positives from test-takers without an associated PCR positive (the lavender bars in Fig. 1*A*) are unreported cases (indicating an even larger mass of cases unreported by either kind of test).

Fig. 2. Log odds ratios over time, with the red lines at 0 indicating independence between exposure and outcome, positive values indicating a positive association between exposure and outcome, and the negative values indicating a negative association. Black curves show the mean log odds ratio, while the dashed blue curves on either side show the 95% CI. In (*A* and *B*), the exposure is whether the test-taker has a current COVID-19 infection or has had a past infection/vaccination, respectively, and the outcome is taking a PCR or serology test, respectively, in the present. In (*C* and *D*), the exposure is whether the test-taker has ever had a PCR positive in the past, and again the outcome is taking a PCR or serology test, respectively, in the present.

With the added feature of individualized testing histories, we can also calculate odds ratios characterizing how these testing behaviors have interacted with each other and the test-taker's past infection history to shape the dynamics of COVID-19 testing in New Jersey. For example, having a COVID-19 infection could make one either more or less likely to take a test, depending on testing availability and uncertainty in one's infection status. We discuss how knowledge of odds ratios relating infection to testing behaviors can be used to estimate incidence more effectively. We also focus on whether people had a past PCR positive result as an important behavioral exposure, since a PCR positive may also encourage or discourage future testing depending on one's confidence in their PCR diagnosis and curiosity about their resulting immunity (31). The odds ratios we derive clarify these interactions and shed light on the biases behind reported testing data.

Finally, building off observations that vaccination can increase one's serology titer values [which roughly quantify the strength of immunity from a serology test (32)], we develop a model leveraging serology titer values to infer behavioral parameters characterizing how COVID-19 testing history has affected people's likelihood and timing of getting vaccinated. We observe that titer values from positive serology tests after the onset of vaccination were lower on average for test-takers who had previously received a positive PCR result (Fig. 3*B*) and show that this trend is a result of people with past PCR-confirmed infections having lower vaccination rates during the first 8 mo of vaccination in New Jersey. We thus highlight the need in future epidemics for more data-recording practices that link tests (and ideally vaccination records) at the individual level, along with randomized surveys to uncover attitudes toward testing and vaccination after infection.

Results

Fig. 1 summarizes the frequencies of positive PCR and serology tests from the New Jersey COVID-19 testing database, also capturing some of the interaction between the two kinds of tests by separating seropositive tests into those with an associated past PCR positive and those without. The total counts of these positive tests over the first 20 mo of the pandemic are shown in Fig. 1*A*. Separating New Jersey into four regions (given by the map in Fig. 1*D*), the total counts of PCR positives were roughly proportional to the population size of each region,

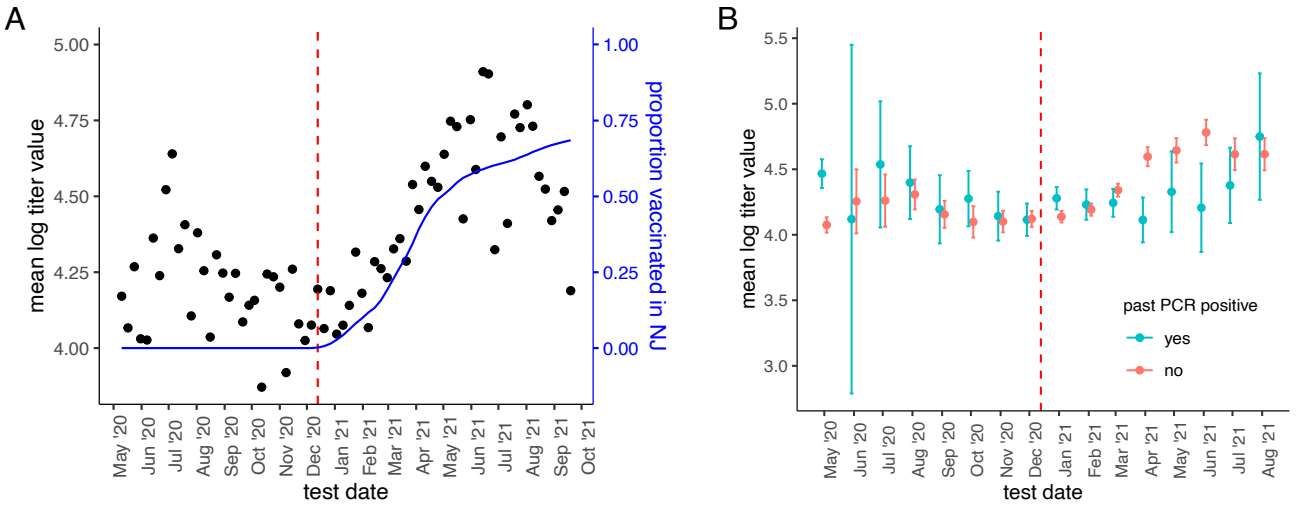

Fig. 3. (*A*) The mean log titer value by week, restricted to only positive serology tests used for the serology model. The blue curve shows the uptake of COVID-19 vaccinations in New Jersey. (*B*) Mean log titer value by month restricted to positive serology tests and broken up by whether their test-taker had a past PCR positive. Points show the mean and error bars show 95% CI. The red dashed line in both plots indicates the onset of vaccination in New Jersey.

with about 10% of individuals in each region receiving a PCR positive over this time period. Serology positive counts were more uneven, with about 7% of inhabitants in the northern counties receiving a seropositive as compared to only 1% of inhabitants in the southern counties. Peaks of seropositives, including for those with past PCR positive, reliably followed the two major peaks of PCR positives (Fig. 1*B*). The timing of these peaks was fairly consistent across the four geographical regions, though the southern and shore counties had more pronounced second peaks of PCR positives and of seropositives with past PCR positives.

The southern counties have a much greater proportion of seropositives previously reported by PCR, as compared to the other regions throughout 2020 (Fig. 1*C*). The other three regions were consistent in having the proportion of seropositives with past PCR positive peak at the beginning of the pandemic and then taper off until a minor second peak around the same time as the second PCR positive peak. Aside from the two peaks, these three regions stay relatively constant with about 20 to 30% of their seropositives at any time previously reported by PCR. In contrast, the proportion of all serology tests (including seronegatives) that were taken by people with a past PCR positive steadily increases over time in all regions, to a maximum of around 10 to 15% depending on the region (*SI Appendix*, Fig. S14).

While not the focus of this work, we estimated weekly COVID-19 incidence to aid in our other analyses. The incidence curves we estimate and the resulting underreporting multipliers are shown in *SI Appendix*, Figs. S7 and S8, respectively. We estimate underreporting multipliers steadily declining from 6.8 to 18.3 (95% CI) in mid-March 2020 to 1.5 to 3.9 in August 2020, after which the underreporting multiplier fluctuates roughly in tandem with the fluctuations in PCR-reported cases, with peaks at 3.8 to 10.1 in mid-December and at 4.8 to 12.7 in June 2021.

Odds Ratios. The odds ratios we derive reveal the time-varying interactions between different testing behaviors and COVID-19 infections. PCR tests were always taken disproportionately by currently infected individuals, as the log odds ratio of taking a PCR test conditional on current infection ($\theta_{I,P}(w)$) is always significantly greater than zero (Fig. 2*A*). Fluctuations in this log odds ratios appear to be negatively correlated with the fluctuations in estimated COVID-19 incidence, with troughs in the odds ratio occurring approximately at or soon after peaks in the case counts (*SI Appendix*, Figs. S10–S12). Near the beginning of the pandemic, we also see that serology tests were taken disproportionately by people who had been infected in the past, as shown by the highly positive initial values of the log odds ratio of taking a serology test conditional on past infection ($\theta_{I,S}(w)$; Fig. 2*B*). However, serology tests taken later in the study period were much less likely to be associated with a past infection or vaccination as this log odds ratio declines closer to 0. Even so, both PCR and serology tests were almost always taken more often by individuals who were currently infected (for PCR tests) or previously infected (for serology tests).

The odds ratios also imply that past testing history, specifically previous PCR positive results, can impact one's decisions to take a PCR or serology test. At the beginning of the pandemic, PCR tests were proportionally more likely to be taken by those who had already received a PCR positive ($\theta_{P_p,P}(w) > 0$), but over time the corresponding odds ratio steadily declines to the opposite extreme where those *without* a past PCR were more likely to take a PCR test ($\theta_{P_p,P}(w) < 0$; Fig. 2*C*). The effect of having a past PCR positive on taking a serology test, however, fluctuated between a positive association ($\theta_{P_p,S}(w) > 0$) and a negative association ($\theta_{P_p,S}(w) < 0$; Fig. 2*D*). The negative associations, when those with past PCR positive were less likely to take a serology test, happened largely when weekly COVID-19 incidence was peaking, while the odds ratio tended to be positive during periods of lower case counts (*SI Appendix*, Figs. S10–S12).

The effect of having a past PCR positive on taking a serology test which gives a positive result, however, behaves more regularly. The additional odds ratio in supplement (*SI Appendix*, Fig. S13) shows that positive serology results are always positively associated with past PCR positives, though the strength of this association steadily declines over time toward independence between positive serology tests and past PCR positives.

Serology Model. More can be gleaned about testing behavior by considering the serology tests' titer values through the serology model. The ability to use titers to infer behavioral trends

regarding testing and vaccination is justified by three observations on the power of passively collected testing data. First, average titers over time increase greatly following the onset of vaccination in New Jersey, even when restricting to positive serology tests to control for changes in test positivity (Fig. 3*A*). This increase mimics the rise of vaccine intake in New Jersey, demonstrating that the IgG spike-protein serology tests we analyze can indeed detect vaccine-caused immune boosting.

Second, this vaccine-induced increase in titers among positive serology tests is much greater initially for those without past PCR positive (Fig. 3*B*), suggesting that having a past PCR positive result is associated with a decreased likelihood of getting a vaccine during the early stages of vaccination. Even when considering all serology tests—including negative serology tests which disproportionately reduce the average titers for people without past PCR positive—the titers for those without past PCR positive overtake the titers of those with past PCR positive once vaccination starts (solid lines in Fig. 5).

Third, when restricting to serology tests associated with past PCR positives, we can plot titer values against the delay from the PCR positive test date to the serology test date to recover known within-host serological trajectories from the literature (Fig. 4). This suggests that the PCR positive date can approximate the infection onset date, allowing us to infer the time of infection for the tests in the New Jersey database. We make use of this assumption and the serology tests' titer values to fit a model, which first determines parameters related to within-host serological trajectories using a submodel restricted to just tests which have associated past PCR positives, and then uses these serological trajectory parameters to glean additional behavioral parameters from the whole serology dataset.

The serology submodel restricted to tests with past PCR positive predicts titer values reasonably well for smaller delays from PCR positive to serology test, qualitatively matching fits from controlled clinical studies but with a slightly later peak time (33) (Fig. 4). For longer delays from past PCR positive, mean log titer values skew higher than the predictions, as this submodel does not properly account for vaccinations, which are more common for serology tests with longer delays.

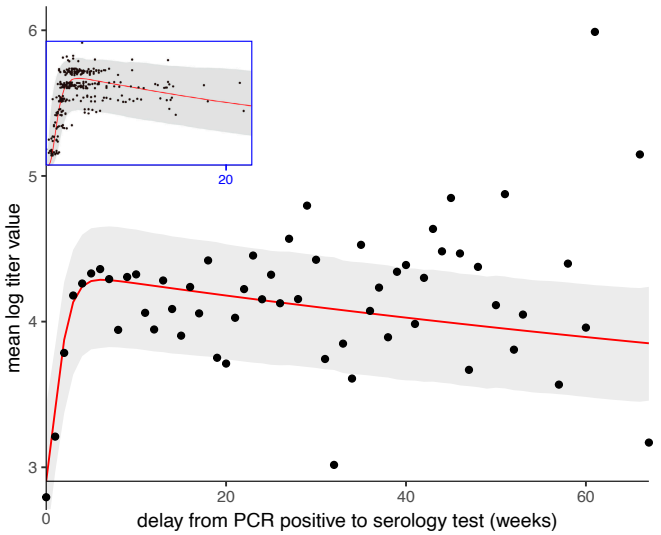

Fig. 4. Restricted to serology tests whose test-takers had past PCR positive, the mean log titer value plotted against the delay from positive PCR test to serology test. The red curve shows the fit from our serology submodel restricted to tests with past PCR positive, with the gray area showing the union of the 95% CI from five age classes. The blue-bordered *Inset* shows an analogous plot from a controlled clinical study (33), with the *x*-axis of the *Inset* lining up with the *x*-axis of the larger plot.

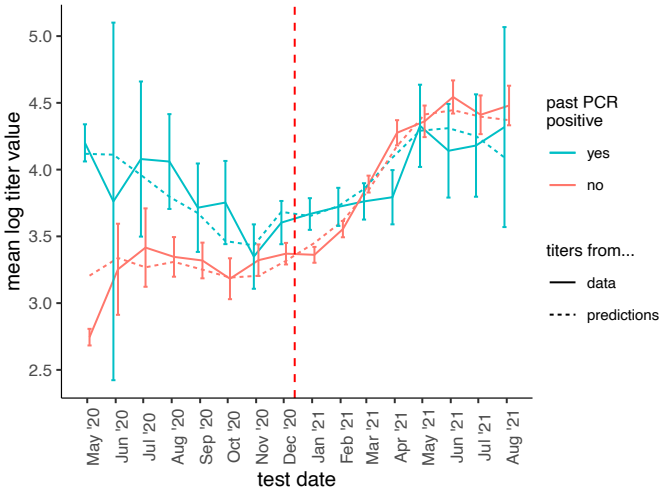

Fig. 5. An example fit from the full serology model. Solid curves and error bars show the mean log titer value and 95% CI from the database's serology titers, broken up by whether the test-taker had a past PCR positive. Dashed curves show the predictions from the serology model, also broken up by past PCR positive. The red dashed vertical line shows the onset of vaccination in New Jersey.

The full serology model fit to all tests better accounts for vaccinations, predicting mean log titers well throughout the time period studied and for serology tests both with and without past PCR positive (Fig. 5). Importantly, the model fits the time-varying parameter $r_{VP}(w)$—which describes the relative vaccination rate for people with past PCR positive compared to those without past PCR positive—to be substantially less than 1, from around 0.15 at first and increasing to 0.6 to 0.7 (Fig. 6). This signifies that people with past PCR positive were about 15% as likely to get vaccinated at the onset of vaccination as people without past PCR positive, though this difference eventually becomes less pronounced as vaccine uptake for those with past PCR positive later catches up (Fig. 6). Thus, the observed trend that vaccination has a lesser impact on average titers for those with past PCR positive (Fig. 3*B*) can be explained by a reduced vaccination rate for this group, dispelling the null hypothesis that this trend could be explained solely by differences in vaccine uptake between different age classes. The rejection of this null hypothesis makes sense with the fact that older individuals in New Jersey got vaccinated earlier but were also more likely to have past PCR positives (*SI Appendix*, Fig. S17).

Model fits for other parameters and sensitivity analyses can be found in *SI Appendix*.

Discussion

The intersection between testing behavior and disease is likely to be a critical driver of feedbacks that shape infection dynamics. Our analysis of a database with uniquely detailed individualized COVID-19 testing histories provides a lens onto factors that underlie the decision to test for an infection; namely, past testing and infection history shape the decisions to get tested (by PCR or serology) or vaccinated for COVID-19. These dependencies change over time, and differ between geographic regions within the state of New Jersey. Our results can be interpreted as describing the testing-related behavior of an average New Jersey

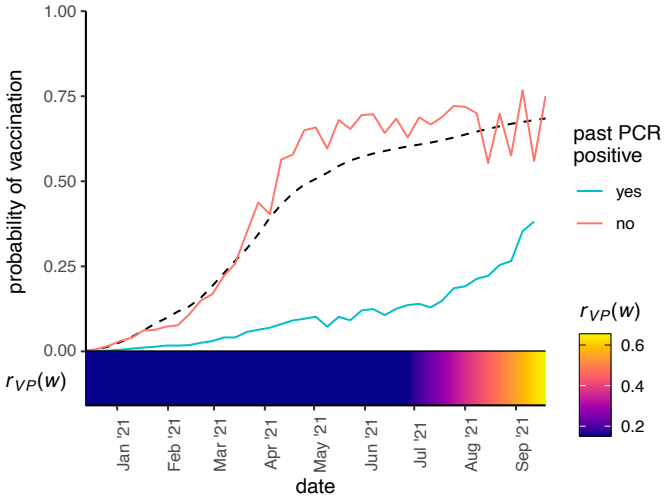

Fig. 6. Curves show the predicted vaccination rates from the serology model fit shown in Fig. 5, broken up by past PCR positive. The dashed curve shows the actual increase in vaccination coverage over time across everyone in New Jersey. The vaccine uptake curves are nonmonotonic due to the model averaging over several age classes. The heatmap below shows the fitted value of the parameter $r_{VP}(w)$, which varies with week w and controls the ratio of vaccination rates between those with past PCR positive to those without past PCR positive. The model fits r_{VP} to have a value less than 1 over this time period, indicating reduced vaccination among those with past PCR positive.

resident during the COVID-19 pandemic, although it should be noted that such behaviors may differ vastly between individuals as well and in often polarizing ways (9, 34, 35). Though this study is not able to fully tackle heterogeneities in testing behavior (except between people with past PCR positives and those without) due to limitations with data and anonymity, future work can hopefully expand these analyses to see how results differ over demographic groups, testing settings, symptomatic statuses, and a wider range of past testing histories. Doing so can help expose the various biases that exist in testing availability by gender, race, ethnicity, geographic location, and socioeconomic status.

Odds Ratios. The average New Jersey resident was found to be much more likely to take a PCR test for current infection when they were actually infected (Fig. 2*A*), and only slightly more likely to take a serology test for past infection when they had a past infection (Fig. 2*B*). These behavioral trends make sense in light of the monetary and time costs of taking a COVID-19 test (9), which can deter people from taking tests unless they strongly suspect they may be infected. However, these costs could also elicit the opposite reaction from people who deem testing unnecessary when they are already fairly certain they are infected. While the average New Jersey resident generally acted according to the first of these two lines of reasoning, fluctuations in the odds ratio relating current infection status to taking a PCR test (Fig. 2*A*) reveal that both of these behavioral factors were likely at play at different times.

These fluctuations may be better understood by their inverse correlation with the peaks and valleys of COVID-19 incidence (*SI Appendix*, Figs. S10–S12). Specifically, the average individual was generally less inclined to get a suspected COVID-19 infection tested by PCR during times of higher population-level incidence. Such a phenomenon could have several potential explanations: during outbreak peaks, there is a relative scarcity of COVID-19 tests (36); a higher prior probability of a suspected infection actually being COVID-19 and thus less uncertainty to be resolved by taking a test; and a heightened caution which could result in self-quarantining even without a formal COVID-19 diagnosis. A notable exception to this pattern is the very high initial values of this odds ratio and the odds ratio relating serology testing to past infection during the pandemic's first peak, signifying that PCR and serology tests were originally reserved mostly for those with suspected infections.

The odds ratios in Fig. 2 *C* and *D* show that test-taking is additionally affected by past test-taking behaviors, namely having a past PCR positive. Unlike the consistently positive effects of current or past infections on test-taking tendencies we observe in Fig. 2 *A* and *B*, the effects of past PCR positives are more ambiguous. The odds ratio relating PCR test-taking to having a past PCR positive (Fig. 2*C*) steadily declines over time, from a positive association at first to a negative association, perhaps indicative of a shift in the testing demographic away from people predisposed to repeat testing (e.g., people in higher risk scenarios or enrolled in regular testing programs). And the odds ratio relating serology test-taking to having a past PCR positive (Fig. 2*D*) fluctuates between positive and negative associations several times (these fluctuations also have negative correlations with the COVID-19 incidence curve; *SI Appendix*, Figs. S10–S12), with a highly positive initial value indicating that the restricted serology test availability at the beginning of the pandemic was prioritized for people with confirmed past infections [perhaps as part of longitudinal serological studies (33, 37)]. Thus, having a past PCR positive—which can be thought of as a proxy for knowing with certainty that one has been already infected with COVID-19—increased the likelihood of taking subsequent tests at some points in the pandemic and decreased the likelihood at other points, with PCR test-taking and serology test-taking behaviors switching between these two regimes at different times.

Interestingly, the effect of past PCR positives on future serology test-taking is vastly different if we consider only positive serology results. The supplemental log odds ratio which relates positive serology tests to having a past PCR positive (*SI Appendix*, Fig. S13) shows a consistently positive but steadily declining association between positive serology tests and past PCR positives. Thus, positive serology tests later in the pandemic are more likely to represent unreported infections (also supported by Fig. 1*C*), implying that serology tests may become more useful in revealing unreported infections as epidemics progress. The increasing use of at-home antigen tests throughout 2021 (38, 39) likely contributed to this trend, though this cannot be determined with the present data.

The results from these odds ratios highlight the complex relationships between test-taking behaviors in the past and present, which are highly dependent even on the types of tests in question. Differences in these results between PCR and serology tests occur because they are testing for fundamentally different phenomena, but may also be a result of differences in how biased the availability of each test type is: indeed, PCR testing volume was roughly proportional to population size across different regions of New Jersey, while serology testing volume was much more skewed (*SI Appendix*, Fig. S14*A*). Furthermore, the two behavioral exposures we examine—having a past infection and having a past PCR positive—may seem like similar phenomena, but the odds ratios show that they influenced future test-taking habits in completely different ways. Understanding the intricacies of these behavioral relationships can be useful in making sense

of reported case counts and how they might be biased in ever-changing ways throughout an epidemic.

Insights into Underreporting. While not the primary concern of this work, our simple method of estimating incidence in order to calculate odds ratios does provide underreporting multipliers that are in line with established estimates from the literature. The CDC estimates that the national underreporting multiplier from February 2020 to September 2021 is 4.0 (40), compared to our mean estimate of 4.2 for New Jersey's underreporting multiplier over a similar time period. Seroprevalence surveys have also given similar results: national underreporting multipliers derived by Angulo et al. (41) fall well within our confidence intervals for each of the time intervals they study. Our odds ratio calculations could be improved in future work by incorporating any of the numerous, more sophisticated incidence estimation procedures that exist in the literature, which use other data sources like seroprevalence surveys or wastewater surveillance to correct incidence estimates (41–45).

In the scope of this paper, our estimates of weekly incidence are only a means of calculating odds ratios relating infection to testing behavior. However, it is our hope that the results from our odds ratios could shed light on patterns common to similar types of odds ratios across broader socioepidemiological contexts. For example, if it is found in other infectious disease systems that the log odds ratio between being infected and testing for current infection is similar in magnitude to our $\theta_{I,P}(w)$ (which satisfies that description in our system), then we can potentially reverse these methods and use prior knowledge of odds ratios between infection and testing to better estimate incidence in the first place. Alternatively, a general pattern in odds ratios across systems might take the form of a relationship between odds ratio and incidence, as with the inverse correlation we observe between $\theta_{I,P}(w)$ and COVID-19 incidence (*SI Appendix*, Figs. S10–S12), thus describing common ways that underreporting varies between different stages of an epidemic. Using odds ratios as a marker to correct incidence in this way could be more valuable than using raw case counts, for example, as odds ratios are normalized to remove the influence of testing volume.

Serology Model. With the additional consideration of the serology tests' titer values, we have shown that passively collected data from PCR and serology tests at the individual level can be very powerful. Titers from the New Jersey testing database can recover the general shape of vaccine uptake and identify behavioral factors by which past testing history can influence vaccination (Fig. 3). The titers can even recreate serological trajectories from rigorously controlled longitudinal clinical trials (33) (Fig. 4), which can aid in the estimation of crucial parameters characterizing antibody dynamics.

Our serology model builds on these observations to estimate behavioral parameters relating past testing history to one's likelihood and timing of vaccination. Most importantly, the serology model robustly demonstrates that people with past PCR positive were less likely at the onset of vaccination to get vaccinated and took longer to do so. This confirms that the trend observed in Fig. 3*B* does have a behavioral origin related to past testing history.

But why might the average New Jersey resident be deterred by a past positive PCR result in future vaccination decisions? A likely significant driver of this common reaction was the CDC guideline to "consider delaying your vaccine by 3 months from … when you received a positive test" (46). It does appear that vaccine uptake from those with past PCR positive begins to catch up to uptake from those without past PCR positive toward the end of the study period (Fig. 6); however, the model predicts that it takes significantly longer than 3 mo for this gap in vaccine uptake to be bridged. Similarly, several studies promoted the idea that previously infected individuals should have the lowest COVID-19 vaccination priority (47–49), though no such policies were implemented in the United States.

Another potential factor discouraging vaccination for those with a past PCR-confirmed infection is the idea that naturally acquired immunity renders vaccination obsolete. This notion has been fueled by misinformation surrounding the superiority of natural immunity (30, 50) and the outdated concept of "immunity passports," which would have allowed full resumption of normal activities following recovery from a COVID-19 infection (17, 51, 52). Surveys have found that a belief in preexisting immunity is a major contributor to COVID-19 vaccine hesitancy (7), while CDC guidelines against eschewing vaccination post-infection signify that this line of thinking has been a real issue (46). If misinformation discouraging people with past positive test results from getting vaccinated is in fact a significant driver of reduced vaccination rates, then campaigns to target such misinformation could prevent many infections and deaths in future epidemics.

The statistical link we find between past PCR positives and reduced vaccination could also be confounded by underlying variables, such as general risk-taking attitudes which could simultaneously make one more likely to get infected and less likely to get vaccinated; or the very act of taking a serology test, as our serology model cannot make predictions about the behaviors of those who have never taken a serology test. In order to tease apart these different possibilities, state-led efforts to collect personalized testing history data for future epidemics should also seek to incorporate vaccination status into these personalized histories so that vaccination history need not be inferred from serological titers. Randomized surveys explicitly asking about the impetuses behind certain testing and vaccination behaviors could also be useful in uncovering people's attitudes toward natural immunity and the subsequent necessity of vaccination.

Materials and Methods

New Jersey COVID-19 Testing Database. Throughout the COVID-19 pandemic, the NJDOH has kept track of all PCR and serology test results from hospitals and labs in New Jersey (as well as some antigen tests, though we did not analyze those, as far fewer are recorded by the state). Uniquely, all tests in this database identify their test-taker, allowing for all tests taken by a single individual to be grouped together while retaining the test-taker's anonymity. In this study, we focus on the first 20 mo of the pandemic, from March 2020 to September 2021, over which time the NJDOH recorded 16.1 million PCR tests and 1.8 million serology tests. There were 1.3 million distinct individuals who had taken at least one serology test (some taking multiple); 8.5% of serology tests were taken by someone who had a previous PCR positive result; and 6.9% have an associated numeric titer value quantifying the strength of the COVID-19 immune response measured by the serology test. Each test in the database has the testing date recorded, allowing us to examine the delays between taking different tests by the same individual, as well as demographic and geographic information on the test-taker.

Odds Ratios. Odds ratios calculate the strength of association between an exposure and an outcome [formally defined as the odds of experiencing the outcome given the exposure divided by the odds of experiencing the outcome given no exposure (53)]. For our analysis, the exposure is either having a current COVID-19 infection, having a past infection or vaccination, or having received a PCR positive result in the past; and the outcome is taking either a PCR or serology test in the "present" week (here the present week is a relative term that can mean any week w). From these three possible exposures and two possible outcomes, we calculate four distinct odds ratios, each across a time span ranging from $w = 1$ for the week of March 1, 2020, to $w = 82$ for the week of September 19, 2021.

Specifically, we define the following log odds ratios (the logarithms of the odds ratios):

- $\theta_{I,P}(w)$ measures how taking a PCR test in week w is associated with whether one has a current COVID-19 infection detectable by PCR.
- $\theta_{I,S}(w)$ measures how taking a serology test in week w is associated with whether one has had a past COVID-19 infection or vaccination detectable by serology.
- $\theta_{P_p,P}(w)$ measures how taking a PCR test is associated with whether one has received a positive PCR result in the past.
- $\theta_{P_p,S}(w)$ measures how taking a serology test is associated with whether one has received a positive PCR result in the past.

$$\theta_{I,P}(w) = \log\left(\frac{\text{odds(taking PCR test in week } w \mid \text{current infection})}{\text{odds(taking PCR test in week } w \mid \text{no current infection})}\right), \quad [1]$$

$$\theta_{I,S}(w) = \log\left(\frac{\text{odds(taking serology test in week } w \mid \text{past infection or vaccination})}{\text{odds(taking serology test in week } w \mid \text{no past infection or vaccination})}\right), \quad [2]$$

$$\theta_{P_p,P}(w) = \log\left(\frac{\text{odds(taking PCR test in week } w \mid \text{past PCR positive})}{\text{odds(taking PCR test in week } w \mid \text{no past PCR positive})}\right), \quad [3]$$

$$\theta_{P_p,S}(w) = \log\left(\frac{\text{odds(taking serology test in week } w \mid \text{past PCR positive})}{\text{odds(taking serology test in week } w \mid \text{no past PCR positive})}\right). \quad [4]$$

The exposure of whether one has received a positive PCR result in the past essentially indicates whether one knows with certainty that one has been infected before. Formally, the odds ratios can be expressed by Eqs. **1**–**4**, with the odds function defined as $\text{odds}(X \mid Y) = \mathbb{P}(X \mid Y) \,/\, \mathbb{P}(\text{not } X \mid Y)$ for any events X and Y.

Log odds ratios are calculated using the Fisher exact test on 2×2 contingency tables (54, 55), which record the number of people either matching the exposure or not (on the rows) while also either matching the outcome or not (on the columns). A log odds of 0 indicates that the outcome is completely independent of the exposure on average, while a positive log odds indicates a positive association between exposure and outcome such that the outcome is seen disproportionately more in people who have had the exposure (and the opposite for a negative log odds). For example, a value of $\theta_{I,P}(w) > 0$ indicates that, in week w, having a current COVID-19 infection tended to make people more likely to get a PCR test in that week; conversely, $\theta_{I,P}(w) < 0$ means a COVID-19 infection in week w made people less likely to get PCR tested that week; and $\theta_{I,P}(w) \approx 0$ shows that being infected on average had little effect on people's decisions to get PCR tested in week w.

The odds ratios require knowledge of COVID-19 incidence in New Jersey over time, in order to measure the number of people matching the exposures of past and present infection. We estimate the true incidence in a week from COVID-19 deaths in the following weeks, extrapolating backward from the deaths to infer the number of infections that occurred to produce that many deaths. Our approach roughly follows those of Jombart et al. (56) and McCulloh et al. (57), though instead of using a fixed infection fatality ratio, we utilize a time-varying fatality ratio proportional to published case fatality ratios in order to better capture changing trends in COVID-19-based mortality. We calculate our time-varying fatality ratio as $\text{IFR} \cdot \text{CFR}(w)/\overline{\text{CFR}}$ (*SI Appendix*, Fig. S9), where IFR is a constant infection fatality ratio drawn from a distribution from the literature (58), $\text{CFR}(w)$ is the time-varying case fatality ratio (59), and $\overline{\text{CFR}}$ is the mean of $\text{CFR}(w)$ over the study period.

Full descriptions of the contingency tables, other assumptions for the odds ratios, and incidence estimation can be found in *SI Appendix*, along with an analysis of a fifth odds ratio describing how having a past PCR positive can influence one's likelihood of taking a positive serology test (*SI Appendix*, Fig. S13).

Serology Model. We also built a model to take into account each serology test's titer value, which is a numeric indicator of the relative strength of one's immune response (60, 61). We use this value and information on the test-taker's past testing history to infer the probabilities that they have ever been infected and vaccinated prior to taking the serology test. For consistent comparison between titer values, we restrict our analysis to a specific group of IgG serology tests with reported numeric titer values all from the same provider (DiaSorin 2020), resulting in a total of 12,341 tests from May 2, 2020 to September 20, 2021. These tests all bind to the spike protein of SARS-CoV-2, allowing the tests to pick up natural infection as well as vaccination (62). To facilitate the modeling, we convert the tests' numeric titer values to a natural-log scale (33), on which they range from about 1.3 to 6.0 with the threshold for positivity at about 2.7.

This subsetted and transformed data reveals an interesting trend: average titer values predictably increase as vaccines are introduced to the state and the serology tests respond to vaccinations (Fig. 3*A*), but this increase is significantly slower and reduced for people with past PCR positives as compared to those without any past PCR positive (Fig. 3*B*). We therefore develop a more detailed serology model to rigorously evaluate whether this observed trend is a direct result of different vaccination rates between these two groups. The opposing null hypothesis would be that this trend is only a product of the different vaccination rates between age classes: since older age classes had earlier access to the vaccine, the patterns we see could be potentially caused by older individuals being less likely to have any past PCR positives. The New Jersey COVID-19 testing database records the age of each test-taker, allowing us to tease apart these two hypotheses.

The serology model first focuses on serology tests taken by people with a past PCR positive, which approximates when they were initially infected. With i indexing over the serology tests, we fit known within-host serological trajectories (33) (Fig. 4) to the titer values y_i based on the test-taker's age class a_i and delay τ_i from infection to serology test:

$$\mathbb{E}[y_i] = s_{a_i} + h_{a_i} F(\tau_i; \alpha_{a_i}, \beta_{a_i}) e^{-\lambda_{a_i}\tau_i}, \quad [5]$$

where $F(\tau; \alpha, \beta)$ represents the gamma cumulative distribution function with shape α and rate β, and age class a has baseline titer value s_a, maximum increase due to infection h_a, and exponential decline at rate λ_a.

With the serological parameters fit from the submodel of tests with past PCR positive, we then fit additional behavioral parameters for the full model taking in all of the serology tests. Most important of the behavioral parameters is $r_{VP}(w)$, which measures in week w how likely someone with past PCR positive is to get vaccinated as compared to someone without past PCR positive:

$$r_{VP}(w) = \frac{\mathbb{P}(\text{getting vaccinated in week } w \mid \text{past PCR positive})}{\mathbb{P}(\text{getting vaccinated in week } w \mid \text{no past PCR positive})}. \quad [6]$$

If r_{VP} is fit to be close to 1 the entire time, then the null hypothesis is true that the different vaccination rates between age classes are responsible for the observed trend shown in Fig. 3*B*. Conversely, a fitted value of $r_{VP} < 1$ would confirm the hypothesis that having a past PCR positive was a significant driver of the lower initial vaccination rates.

$$\mathbb{E}[y_i \mid X_i] = s_{a_i} + \mathbb{P}(i\text{'s test-taker has been infected} \mid X_i)\left[h_{a_i}F(\tau_i; \alpha_{a_i}, \beta_{a_i})e^{-\lambda_{a_i}\tau_i}\right] + \mathbb{P}(i\text{'s test-taker has been vaccinated} \mid X_i)\psi. \quad [7]$$

For each set of behavioral parameters and each serology test i, we calculate the probabilities of past infection and past vaccination–$\mathbb{P}(i$'s test-taker has been infected $\mid X_i)$ and $\mathbb{P}(i$'s test-taker has been vaccinated $\mid X_i)$–where X_i refers to one of three possible testing histories: serology test i has an associated past PCR positive; serology test i has no past PCR positive and has a positive result; or serology test i has no past PCR positive and has a negative result. Then the expectation of the titer value y_i for serology test i is modeled by Eq. **7**, where X_i is one of the same three testing history options, and ψ is an additional fitted parameter describing the average increase in titers due to vaccination. The expected titer value given by the right side of Eq. **7** is not completely independent of the actual titer value y_i, as y_i determines the positive/negative result of the test (by comparing y_i to the serology test's threshold value); and y_i helps simulate the delay τ_i from infection to testing date for tests without a past PCR positive from which to infer time of infection.

Both these steps utilize an MCMC fitting procedure implemented in RStan (*63*). Calculating the probabilities in Eq. **7** requires weekly age-dependent incidence estimates, which we derive using the same overall weekly incidence estimated for the odds ratios, divided into age groups in proportions derived from CDC seroprevalence data (*64*). See *SI Appendix* for a full description of the model and how the probabilities are calculated.

This study was deemed exempt by the Princeton University IRB office.

Data, Materials, and Software Availability. All code to reproduce the analyses and figures in this paper can be found at https://github.com/freedmanari/NJ-sero (*65*).

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