Dynamically Adjusting Case-Reporting Policy to Maximize Privacy and Utility in the Face of a Pandemic

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ABSTRACT

Managing a pandemic requires continuous dissemination of infectious disease surveillance data. Legislation permits sharing de-identified patient data; however, current de-identification approaches are time-consuming and do not flex with changes in infection rates or population demographics over time. In this paper, we introduce a framework to dynamically adapt de-identification for near-real time sharing of patient-level surveillance data. The framework leverages a simulation mechanism, capable of being applied to any geographic level, to forecast and manage disclosure risks. We use data from Johns Hopkins University and the Centers for Disease Control and Prevention to demonstrate the framework’s effectiveness in maintaining the privacy risk below a threshold based on public health standards for COVID-19 county-level case data from August 2020 to April 2021. Across all US counties, the framework’s approach meets the threshold for 95.2% of daily data releases, while a policy based on current de-identification techniques meets the threshold for only 24.6%.
INTRODUCTION

The novel coronavirus 2019 (COVID-19) pandemic has put a spotlight on infectious disease surveillance systems\textsuperscript{1} and the importance of making such information widely accessible\textsuperscript{2}. It is evident that sharing surveillance data in a timely manner can support a wide variety of public health endeavors (e.g., from modeling disease transmissibility and severity to simulation of interventions\textsuperscript{3–6}), as well as enable the general public to gain situational awareness of outbreaks\textsuperscript{4,7}. In recognition of such benefits, over the past year, various organizations have worked to broaden access to large epidemiological datasets. Recent instantiations of COVID-19 initiatives include the National COVID Cohort Collaborative (N3C) of the U.S. National Institutes of Health\textsuperscript{8}, the Datavant COVID-19 Research Database\textsuperscript{9}, the Centers for Disease Control and Prevention’s (CDC) COVID-19 Case Surveillance datasets\textsuperscript{10–12}, and the Global.health data science initiative\textsuperscript{13}, among others.

While advances in surveillance have spurred rapid growth in the volume and diversity of epidemiological resources, data sharing on a wide scale remains limited\textsuperscript{14}. This is due to numerous social and political factors, but it is evident that privacy is a core driving factor. In the United States, for instance, much of the infectious disease data is captured by organizations who are subject to the Health Insurance Portability and Accountability Act of 1996 (HIPAA) and related laws and policies. Under HIPAA, an organization is permitted to publicly share patient-level data only when it is de-identified, that is, when the data "does not identify an individual and … there is no reasonable basis to believe that the information can be used to identify an individual."\textsuperscript{15} Even when organizations
are not covered by HIPAA, they may be permitted to share data in a de-identified form as well. For example, the California Consumer Protection Act (CCPA) which recently went into effect at the end of 2020, as well as the Virginia Consumer Data Protection Act (VCDPA), which goes into effect in 2023, both provide exemptions to de-identified data sharing\textsuperscript{16,17}. However, transforming data into a de-identified form is a non-trivial endeavor. Numerous demonstration attacks have shown that, with the right background knowledge, a data recipient can leverage residual information in the records to re-identify the individuals to whom the data corresponds\textsuperscript{18–23}. Concerns over such intrusions to anonymity have discouraged organizations from sharing data\textsuperscript{24,25}, which raises the importance of the question of how organizations can best comply with regulatory requirements while facilitating infectious disease surveillance.

While state laws such as CCPA and VCDPA are vague on the technical implementation of de-identification, HIPAA enables this notion to be satisfied through two alternative mechanisms. The first is Safe Harbor, which requires the suppression of eighteen direct (e.g., patient name) and quasi-identifying features (e.g., geocodes with populations smaller than 20,000 residents). However, Safe Harbor requires the suppression or alteration of epidemiologically critical factors, such as reducing dates of events to the year of event, rendering such a policy useless for continuous monitoring of infectious disease. The alternative mechanism is Expert Determination, which allows “[a] person with appropriate knowledge of and experience with generally accepted statistical and scientific principles and methods” to determine that “the risk is very small that the information could be used to identify an individual who is a subject of the information.”\textsuperscript{26}
Various methods have been developed to assess re-identification risk and design de-identification policies under Expert Determination; however, these methods assume that data have already been collected and are ready for dissemination. In doing so, they also assume that the number of records in the dataset remains fixed\textsuperscript{27}. These assumptions differ from the requirements of case reporting in the face of a pandemic, motivating the need for methods that forecast surveillance data and account for the fact that re-identification risk will vary over time. Time is also a factor. Waiting to publish the data will hinder the ability to characterize the current state and evolution of an outbreak\textsuperscript{1,2,28,29}. Furthermore, several factors affect the privacy risk, including the demographics of the people infected\textsuperscript{18,20}, the geolocations to which the pandemic spreads\textsuperscript{30,31}, and the infection rate.

In this paper, we introduce a computational approach to adaptively generate policies that support the sharing of patient-level epidemiological data in a de-identified form. The underlying framework simulates disease cases to estimate the longitudinal privacy risk of sharing infected individuals’ quasi-identifier information at different levels of granularity (i.e., under different data release policies) in the absence of actual patient data. The privacy risk estimates (i.e., measurements of how likely an individual in the dataset can be re-identified) inform the data sharer in periodically selecting a data sharing policy, according to the expected number of new disease cases and the sharer’s information priorities. Prospective risk estimation and policy selection will enable near real-time data sharing to support disease monitoring. We specifically apply the framework to illustrate how policies could be developed to share patient health
information in the COVID-19 pandemic, and compare such policies to a more traditional de-identification approach that relies on a retrospective risk assessment. Acknowledging the potential for disparities in the privacy afforded to various subpopulations, we also briefly investigate the fairness of data sharing policies.

It should be recognized that the framework generalizes to any type of epidemiological disease spread, adjusts for the demographic diversity of individual US counties, and relies on public data sources. The framework’s approach can also be reused to address emerging data sharing needs, such as for vaccine registries. Dynamically adapting data sharing policies holds the potential to consistently share more data with the public in a timely and privacy-preserving manner, fueling our data-driven response to infectious disease.

RESULTS

Privacy risk estimation framework

Our proposed framework provides longitudinal privacy risk estimates for a data sharing policy within a specified geographic region. In this research, we apply this framework to simulate disease spread on a county level to match the format of the COVID-19 surveillance data made accessible by the CDC. We provide a summary of the framework’s features to contextualize the results, and reserve additional technical details for the Methods section.
Figure 1 provides a summary of our framework. The framework begins by selecting a data sharing policy, which defines the generalization of each quasi-identifying feature considered. In this paper, we consider the basic demographic features and the date of diagnosis as quasi-identifiers, since these are the typical features that organizations have been requested to share (Table 1). However, we note the framework is sufficiently flexible to evaluate any quasi-identifier. The second step in the framework generates the distribution of the county level population on the quasi-identifying features according to the selected data sharing policy. We use data from the U.S. Census Bureau to calculate the number of people in the county that fall into each demographic group, where each group is defined by a unique combination of values for the features in Table 1, excluding date of diagnosis. The more granular the quasi-identifying features, the greater the number of potential groups.

Figure 1. Privacy risk estimation framework. The curved rectangles represent processes, the cylinders represent data, and the hexagons represent user-defined parameters. The algorithm that performs the processes within the black box is in the core of the proposed framework, employs Monte Carlo random sampling, and is presented in greater detail in the Methods section. To obtain the privacy risk distributions, the simulation is repeated \( n \) times. The circled numbers denote the framework steps.

The third step applies a Monte Carlo simulation (represented by the black box in Figure 1) to obtain the privacy risk distributions using the county level population distribution.
computed in the previous step and the time series of new disease case counts. To simulate the COVID-19 pandemic, we input the time series of new disease cases from the Johns Hopkins COVID-19 tracking data\textsuperscript{35}. The framework’s algorithm initializes the full population in the county to be the uninfected population. For each time point, and given the disease case count, we randomly sample the same number of people without replacement from the uninfected population to form the newly reported patient dataset. The framework assumes individuals are not re-infected (for simplicity, considering a potentially negligible COVID-19 reinfection rate\textsuperscript{36}) and assumes equal weighting across all individuals when sampling (to model the general uncertainty of disease spread, particularly in pandemics\textsuperscript{37}).

The algorithm computes the re-identification risk on the patient set at each time point, according to a specified risk measure (see Methods for more details). There are various methods of measuring privacy risk\textsuperscript{27}. In this paper, we measure the relative uniqueness in a dataset as the proportion of individuals in the dataset that fall into a group of size $k$ or less, where each group is defined by a unique set of quasi-identifier values\textsuperscript{38,39}. We refer to this measure as the $PK$ risk and evaluate it given a set of $k$ values consistent with the standard thresholds used by public health authorities\textsuperscript{40–44}. The $PK$ risk measures the privacy risk under the assumption a data recipient knows 1) an individual belongs in the dataset, 2) the individual’s name and quasi-identifying information, and 3) the individual was diagnosed with the disease of interest within a window of time. The more unique the record’s representation, the more likely the data recipient can re-identify the individual based on the released quasi-identifying information\textsuperscript{18,20}. In
practice, obtaining such patient information is difficult\textsuperscript{21,45}. Thus, evaluating the PK risk models the worst-case scenario to provide an upper bound of re-identification risk for the dataset. To demonstrate the approach’s flexibility and to offer a different perspective on privacy risk, we further analyze the amortized re-identification risk\textsuperscript{46} in the Supplementary Information. The amortized re-identification risk differs from the PK risk in that it relaxes assumptions 1) and 3).

We would like to highlight that when applying the PK risk measure, we assume the attacker knows the diagnosis occurred within a lagging period of time (e.g., within one, three, or five days prior to the documented date). We allow this flexible assumption as it is unlikely a data recipient knows the targeted individual’s exact diagnosis date\textsuperscript{47}, especially when the time from a diagnostic test to case report extends beyond one day. The group corresponding to an individual contains all patients in the simulated patient set that match the individual on the demographic features, with a diagnosis date falling into the lagging period.
| Field                  | Generalization Strategy          | Generalization Example |
|------------------------|----------------------------------|------------------------|
| State of residence     | None*                            | NA                     |
| County of residence    | None*                            | NA                     |
| Date of diagnosis      | Combine into week ranges          | 01/05/21 → 01/03/21-01/09/21 |
|                        | (Sunday-Saturday†)               |                        |
| Year of birth          | Convert to age ranges            | 1980 → 40-45 years old |
| Sex                    | Nullify value                    | Female → null, Male → null |
| Race                   | Combine race groups              | AIAN → AIAN or PI, PI→ AIAN or PI |
| Ethnicity              | Nullify value                    | Hispanic-Latino → null, Non-Hispanic → null |

Table 1. The quasi-identifiers considered in this study. The middle column describes the generalization strategy for each quasi-identifier. The third column provides an example generalization for each quasi-identifier. In the case of sex and ethnicity, the information is either included or null. AIAN = American Indian/Alaskan Native, PI = Pacific Islander. *These values cannot be generalized since we simulate on a county level. †This definition of a week is consistent with the one used by the CDC’s COVID-19 case forecasts. The fourth and final step of the framework uses the privacy risk distributions to estimate when the policy meets a privacy risk threshold. Computing the longitudinal privacy risk estimates under various data sharing policies for the same county identifies which policies likely meet the threshold at each point in the time series. The data sharer can then choose which policy to apply according to information priorities (e.g., prioritizing age granularity over sex granularity).
Dynamic policy search

To dynamically adapt policies according to an expected infection rate, we identify policies that likely meet a specific PK risk threshold at varying quantities of new case records. For this policy search, we choose a $k$ value of 10 as a typical group size incorporated into guidance issued at the state\textsuperscript{41–44} and federal\textsuperscript{40} level. We henceforth refer to the PK risk calculated when $k=10$ as PK10. The PK10 threshold is set to 0.01; i.e., the percentage of records falling into a demographic group of size 10 or smaller should be less than or equal to 1%. Similar investigations for $k$ of 5 and 20 (which are other common group size thresholds used by state and federal public health authorities) are provided in the Supplementary Information (Supplementary Figures 1 and 2).

The search uses the privacy risk estimation framework to evaluate 96 alternative data sharing policies for each U.S. county (with available census tract information) across a range of case count values. The policies include six potential generalizations of age, four generalizations of race, two generalizations of sex, and two generalizations of ethnicity. The quasi-identifier generalization options follow a hierarchical structure, where moving up the hierarchy generalizes the information to increase privacy at the cost of utility\textsuperscript{49}. For each policy, county, and case number combination, the framework generates 1,000 PK10 estimates. The upper bound of the estimates’ 95% quantile range is then compared to the PK10 threshold. A policy meets the threshold when the upper bound is less than or equal to 0.01. We choose to evaluate a policy in this manner to increase the likelihood supported policies meet the privacy risk threshold in
application. Note, the data sharer can adjust the size of the quantile range to increase or decrease the confidence a policy will meet a specific privacy risk threshold.

We summarize the policy search results in Figure 2. To aid in readability, we represent the generalization of each quasi-identifier in a policy with a four-character alphanumeric code. The first character designates the age generalization, the second the race generalization, the third the sex generalization, and the fourth the ethnicity generalization. We further summarize the results by categorizing US counties by population size.

We find that once a policy meets the PK10 threshold for a given number of cases, it is unlikely records fall into a demographic group of size 10 or less. Further increasing the case volume increases the number of records in each group and decreases the PK10 value. As such, a policy is listed under the smallest case quantity at which the policy meets the PK10 threshold for every county in the category. It should also be noted there exists a parent-child relationship between policies. For example, policy 2*** is the parent of policy 3***, where the sole difference between the policies is that the former generalizes age to a lesser degree than the latter. When a parent policy meets the PK10 threshold, all its child policies also meet the threshold.

As Figure 2 displays, the number of acceptable policies increases with the number of new cases. In most cases, larger counties achieve more acceptable policies than smaller counties at a given case quantity. The maximum number of acceptable policies is 73. The most granular policies across all county categories are 1C*e, 2Bse, and
3Ase. Each of these policies prioritizes different types of information. Policy 1C*e, for instance, offers the most granular age information at the cost of race and sex information. Policy 3Ase, on the other hand, reduces age granularity to increase race and sex specificity.

| Number of new cases in time period |
|------------------------------------|
| 10  | 11  | 50  | 75  | 150 | 300 | 500 | 750 | 1k  | 1.25k | 1.5k | 2k  | 2.5k | 3k  | 4k  | 5.75k | 10k | 15k | 20k |
| (0, 1k) |
| Do not share | "s" | "s" | 4** | 4** | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| 1k, 50k | Do not share | "s" | "s" | 4** | 4** | 3** | 2** | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| 50k, 100k | Do not share | "s" | 4** | 4** | 4** | 4** | 4** | 4** | 4** | 4** | 4** | 4** | 4** | 4** | 4** | 4** | 4** | 4** | 4** |
| 100k, 1M | Do not share | "s" | 4** | 4** | 4** | 4** | 4** | 4** | 4** | 4** | 4** | 4** | 4** | 4** | 4** | 4** | 4** | 4** | 4** |
| 1M+ | Do not share | "s" | 4** | 4** | 4** | 4** | 4** | 4** | 4** | 4** | 4** | 4** | 4** | 4** | 4** | 4** | 4** | 4** | 4** |

Policy Code:
- Age: *: No age
- 1: 5-year age range, 90+ 4: 0-59, 60+
- 3: 0-29, 30-59, 60-89, 90+
- 2: 15-year age range, 90+ 0: Year of birth
- Race: *: No race
- A: Black/White, Not Black/White
- B: Black, White, Asian, Other
- C: Black, White, Asian
- American Indian/Alaskan Native, Native Hawaiian/Pacific Islander, Mixed, Other
- Ethnicity: *: No ethnicity
- e: Hispanic-Latino, Non-Hispanic
- Sex: *: No sex
- s: Male, Female

Figure 2. Policies with a PK10 upper bound (calculated as the upper bound of the 95% quantile range of 1,000 framework simulations) less than or equal to 0.01 at varying disease case volume thresholds. A four-character alphanumeric code indicates the policy’s generalization levels. All policies additionally include state and county of residence and some generalization of diagnosis date. A policy is eligible to be listed under the minimum number of new cases (table column) at which it meets the PK10 threshold for every county in the category (table row). A maximum of two policies are listed in each cell among the actual number of policies supported. The number in the bottom right-hand corner of each cell indicates how many of the 96 searched policies meet the risk threshold at the case volume.

The case number values are window-size agnostic, such that the policy search results hold regardless of the length of the time period considered. For example, assume a county with fewer than 1,000 residents, updates its disease surveillance dataset daily. Further, assume the county adjusts for data recipients’ uncertainty around the exact
diagnosis date by evaluating the PK10 on a 3-day lagging period. When the expected number of new cases from the current day and the previous two days sum to 50, the current day’s records should be generalized according to either policy **** or **s*. The same policies are supported if, instead, the dataset is updated weekly (and diagnosis date is generalized to week of diagnosis) and 50 new cases are expected for the current week.

**Dynamic policy evaluation**

We use the summarized policy search results listed in Figure 2 and forecasted COVID-19 disease case counts to evaluate dynamic policy selection in the context of the COVID-19 pandemic. In this experiment, we measure the proportion of data releases in which the PK10 likely remains below the policy search threshold, i.e., 0.01. Dynamic policies are evaluated for two distinct alternative data sharing scenarios: 1) a daily release schedule with 1-day lagging period assumption and 2) a weekly release schedule. The daily release schedule shares the actual date of diagnosis. The weekly release schedule generalizes the date to the week of diagnosis.

The dynamic policy for each county is selected according to the CDC’s COVID-19 forecasts and the policy search results. The CDC’s ensemble model forecasts the one-week increase in COVID-19 cases for each U.S. county. We rely on the ensemble model because it demonstrates superior accuracy over other models available through the CDC. For the evaluation, we collected all model predictions dating back to August 2020. We use daily increase predictions by uniformly distributing the weekly
increase point estimate across each day of the week. In selecting policies for the daily release schedule, we use the minimum number of predicted new cases in the week. This applies the most generalized, and therefore most privacy preserving, policy to all new cases reported in the week. For the weekly release schedule, we use the forecasted one-week increase.

After selecting the sequence of policies for each county, we estimate the privacy risk of sharing the actual reported number of records via the privacy risk estimation framework. We define the actual number of disease cases per day or week by the Johns Hopkins COVID-19 tracking data. The PK10 risk value for each time point in each county is calculated as the upper bound of the 95% quantile range of 1,000 simulations. The evaluation measures the proportion of releases the upper bound remains below 0.01. We summarize the results, categorizing counties in the same manner as the policy search, in Table 2.

We additionally evaluate the application of a static policy designed with current, retrospective de-identification methods, akin to that applied to the CDC’s COVID-19 Public Use Data with Geography\textsuperscript{10}. The policy, hereafter referred to as the $k$-anonymous policy, shares age intervals in the form (0-17, 18-49, 50-64, and 65+); fully specified race, ethnicity, sex, and state and county of residence; and date or week of diagnosis. We note the CDC’s policy, from which the $k$-anonymous policy derives, was developed to meet regulatory requirements and public health standards under a different release schedule (once every two weeks) and in a retrospective manner (the
actual patient records are collected, de-identified and released in a batch). The CDC’s policy is designed to achieve $11$-anonymity (i.e., $PK_{11} = 0$) by generalizing the date of diagnosis to month and by nulling out quasi-identifier information for small groups\textsuperscript{10,12,52}. Thus, the $k$-anonymous policy resembles a policy developed with traditional de-identification methods such as the one used by CDC, but notably differs in its treatment of dates of events and in its assumption of no suppression. We further note this last feature is unique to sharing surveillance data in near-real time, as our approach aims to support. Specifically, \textit{suppression cannot be applied with confidence} because it is almost impossible to forecast exactly which records will fall into small demographic groups.
| County Population Size | k-anonymous Policy Average | Dynamic Policy Average | k-anonymous Policy Average | Dynamic Policy Average |
|------------------------|----------------------------|------------------------|----------------------------|------------------------|
| < 1,000 (n = 35)       | 0.887 [0.791, 0.997]      | 1 [1, 1]               | 0.551 [0.251, 0.978]      | 0.999 [0.974, 1]       |
| 1,000 - 50,000 (n = 2,129) | 0.308 [0.038, 0.797]     | 0.962 [0.872, 1]       | 0.049 [0, 0.368]         | 0.958 [0.868, 1]       |
| 50,000 - 100,000 (n = 398) | 0.106 [0.004, 0.545]     | 0.905 [0.812, 0.989]   | 0.002 [0, 0.026]         | 0.984 [0.921, 1]       |
| 100,000 - 1,000,000 (n = 538) | 0.079 [0, 0.410]         | 0.944 [0.850, 1]       | 0.006 [0, 0]             | 0.986 [0.947, 1]       |
| > 1,000,000 (n = 39) | 0.052 [0.004, 0.226]     | 0.957 [0.880, 1]       | 0.072 [0, 0.379]         | 0.966 [0.868, 1]       |

Table 2. Average proportion of time periods where the upper bound of the 95% quantile range of the PK10 risk is less than or equal to 0.01 in the COVID-19 pandemic (August 2, 2020 to April 24, 2021). The average and 95% quantile range in each cell are taken across all counties in the corresponding population size category. The k-anonymous policy shares age intervals (0-17, 18-49, 50-64, and 65+), race (Black or African American, White, Asian, American Indian or Alaskan Native, Native Hawaiian or Pacific Islander, Mixed, and Other), ethnicity (Hispanic-Latino and Non-Hispanic), sex (Female and Male), and state and county of residency. The k-anonymous policy is statically applied to each release. The daily release PK10 estimates apply a 1-day lagging period, while the weekly release estimates assume the actual date of diagnosis is generalized to week of diagnosis.

There are several major findings. First, dynamically adapting the policy meets the PK10 threshold more frequently than statically applying the k-anonymous policy. On average, the dynamic policy meets the threshold for at least 90.5% of the 266 daily releases and 95.8% of the 38 weekly releases. The k-anonymous policy meets the threshold as few as 5.2% of the daily releases and 0.2% of the weekly releases. Second, we find that
new cases do not occur every day or every week in the smaller counties. As such, there are fewer days the PK10 upper bound can potentially exceed the threshold, inflating proportions in smaller counties.

**Case Study: Davidson County, TN**

To provide a specific illustration of the dynamic policy approach to daily releasing updated, record-level disease surveillance data, we consider Davidson County, Tennessee, a metro region with a population of approximately 630,000 residents. In this case study, we again select a policy on a weekly basis according to the CDC ensemble model’s point estimates and the policy search results. To demonstrate how the framework incorporates the data recipient’s potential knowledge of diagnosis date, and accounting for the general turnaround time of COVID-19 diagnostic tests results\(^{53-55}\), we set a 3-day lagging period. Under these constraints, weekly dynamic policy selection first calculates a 3-day rolling sum of new disease case numbers through the coming week. The minimum value of the rolling sum is used to select the policy. To evaluate the dynamic policy under optimal case load forecasting, we repeat the process by replacing the forecasted case counts with the actual case numbers in policy selection.

Figure 3 shows how the forecasted case volumes do not match the weekly seasonality of the actual reported cases in Davidson County. Consequently, the CDC ensemble model tends to overestimate case loads, leading to the selection of more granular policies. Despite the rippling effects of the overestimation, the 95% quantile range of the forecast-driven PK10 remains below 0.01 throughout most of the time frame. Only three
days exceed the threshold, across which the mean PK10 value exceeds the threshold only one time. Notably, the PK10 never exceeds the threshold when selecting policies according to the actual case counts. Adapting the policy according to perfect forecasts produces optimal performance.

**Figure 3.** Dynamic policy selection applied to Davidson County, TN in the COVID-19 pandemic (August 2, 2020 to April 24, 2021). (Top) The 3-day rolling sum of the forecasted and actual case counts reported in Davidson County. The forecasted counts are from the CDC’s COVID-19 ensemble model and the actual counts are from the Johns Hopkins surveillance data. The blue triangles and red squares denote the minimum value within each week (defined as Sunday-
Saturday per the CDC model’s definition). The minimum values are used to select a policy from policy search results. (Middle) The selected policy at the beginning of each week in the pandemic. Each policy is represented by a 4-character alphanumeric code following the key in Figure 2. The policies are ordered by increasing case count thresholds from bottom to top. Green circles indicate agreement between the policies selected from the forecasted and actual case counts. (Bottom) The PK10 from sharing the actual number of records under the two sequences of policies detailed in the middle graph. The expectation and 95% quantile range are calculated from 1,000 independent framework simulations, while applying a 3-day lagging period assumption. The horizontal dashed line marks the PK10 threshold of 0.01.

**Case Study: Perry County, TN**

We next consider Perry County, Tennessee as a second case study, to illustrate how policies shift when moving from a larger metropolitan region to a smaller rural area. Perry County is smaller than Davidson County, with around 8,000 residents. We apply the same procedure as the previous case study, including the 3-day lagging period assumption.

Figure 4 displays the results. When the case counts remain relatively small from August through October 2020 and after January 2021, the selected policies from each data source indicate that record-level data should not be shared on a daily basis. Between those intervals the 3-day rolling sums begin oscillating above and below 10 cases, where the forecasted values again overestimate the weekly minimum case loads. As such, the policies frequently disagree on whether to share record-level data under the **** policy or to not share. Though the policies differ by only one case count threshold level, the difference results in multiple large spikes in the PK10. When sharing fewer than 10 new case records in a 3-day window under the forecast-driven dynamic policy, the complete 95% quantile range hits a PK10 of 1.0. This is because sharing less than 10 records under any policy will place all the new records into a demographic group
smaller than size 10. Despite the privacy leaks in forecast-driven dynamic policy, the dynamic policy guided by the actual disease case counts again maintains the PK10 values below the threshold throughout the time frame.

Figure 4. Dynamic policy selection applied to Perry County, TN in the COVID-19 pandemic (August 2, 2020 to April 24, 2021). (Top) The 3-day rolling sum of the forecasted and actual case counts reported in Davidson County. The forecasted counts are from the CDC’s COVID-19 ensemble model and the actual counts are from the Johns Hopkins surveillance data. The blue triangles and red squares denote the minimum value within each week (defined as Sunday-Saturday per the CDC model’s definition). The minimum values are used to select a policy from policy search results. (Middle) The selected policy at the beginning of each week in the
pandemic. Each policy is represented by a 4-character alphanumeric code following the key in Figure 2. The policies are ordered by increasing case count thresholds from bottom to top. Green circles indicate agreement between the policies selected from the forecasted and actual case counts. (Bottom) The PK10 from sharing the actual number of records under the two sequences of policies detailed in the middle graph. The expectation and 95% quantile range are calculated from 1,000 independent framework simulations, while applying a 3-day lagging period assumption. The quantile ranges are too narrow to be seen outside the mean. The horizontal dashed line marks the PK10 threshold of 0.01.

**Policy fairness**

Fairness is an important emerging concept in the artificial intelligence and privacy communities\(^{56}\). Since our framework does not account for how the data will be applied, there is no direct approach to assess how different data sharing policies affect algorithmic fairness. Rather, we apply the framework to investigate how a data sharing policy is likely to distribute the privacy risk across demographic groups. Specifically, we measure how the PK risk stratifies across racial groups at \(k=5\), \(k=10\), and \(k=20\). We calculate the expected proportion of the overall PK risk to which each race corresponds when applying a single policy (1Bse, according to the key in Figure 2) for the duration of the COVID-19 pandemic. The case counts input into the framework are the actual counts from the Johns Hopkins data.

According to the census data, 61.4% of Davidson County residents are White, 27.7% are Black, 7.8% fall into the new Other group, and 3.0% are Asian. Figure 5 clearly illustrates the proportion of the privacy risk each group bears is not equal and varies over time. Within Davidson County, Black individuals most frequently bear the greatest risk at all three \(k\) values. Additionally, the proportion stratification widens as \(k\) increases. The policy’s race generalization partly balances the stratification. Since the policy generalizes the initial racial groups American Indian/Alaskan Native, Native
Hawaiian/Pacific Islander, Mixed, and Other into a new Other group, these initial groups share the same proportion of the privacy risk.

**Figure 5.** The proportion of the overall expected PK5 (Top), PK10 (Middle), and PK20 (Bottom) each racial group bears throughout the COVID-19 pandemic, when applying a 1Bse policy to Davidson County, TN. Proportion of risk is reported as the average of 1,000 independent framework simulations with a 5-day lagging period assumption. The racial groups are based on the U.S. Census: 1) Asian, 2) Black, 3) White, and 4) Other, which is composed of Alaskan Native/American Indian, Pacific Islander/Native Hawaiian, Two or More Races, and Some Other Race.
DISCUSSION

This paper introduces a framework to dynamically adjust data sharing policies for surveillance efforts. The framework forecasts privacy risk according to the expected volume of new cases, enabling data sharers to fix policies before seeing case loads. This framework empowers a more flexible and reliable approach to de-identifying surveillance data than current static policy techniques. We demonstrate how dynamically changing the policy according to the case count thresholds, per the framework’s recommendations, maintains the privacy risk below the specified privacy risk threshold more frequently than statically applying a policy developed through retrospective de-identification methods. The dynamic policy balances utility by permitting the policy to fluctuate with the infection rate and by allowing the data sharer to select from a set of acceptable policies according to information priorities. Further, the framework’s ability to forecast privacy risk bypasses the time delay of accumulating large numbers of patient records before performing a risk assessment. This is crucial as effective disease monitoring requires timely data sharing. Forecasting also enables greater consistency in quasi-identifier representation, as the policy can be selected and maintained throughout the forecasted interval of time. Moreover, predicting which policies provide sufficient privacy protection could potentially automate patient de-identification.

Despite the merits of this work, we wish to highlight several limitations to guide future extensions and transition into application. First, dynamically adapting the policy according to the CDC ensemble model’s forecasts did not always meet the privacy risk
threshold. However, the framework's policy search results remain relatively robust. Policies chosen from forecasted counts are typically similar or close to those chosen from actual case counts. And when overestimating the number of cases, the privacy risk does not always dramatically exceed the threshold. Furthermore, we selected policies according to a 95% empirical confidence interval, but the policy search can readily incorporate larger confidence intervals as organizations deem desirable. Expanding the intervals further increases the likelihood the dynamic policy will meet the threshold in application. Moreover, when adjusting policies according to the actual case counts, the privacy risk never exceeds the threshold. Thus, the dynamic policy approach can be improved through more accurate forecasts and a model that accounts for potential case load overestimation.

Second, our approach does not incorporate suppression to protect the most unique patient records in the dataset. This is because it is nearly impossible to accurately forecast the exact records which will fall into small demographic groups. It is possible, however, during the enforcement of a selected policy (using our privacy risk estimation framework) to suppress actual patient records that need to be published and fall into population demographic bins corresponding to very few individuals, such as patient records that are population uniques, or patient records that correspond to population groups with fewer than $k$ individuals (for PK risk). Such records with certainty would not meet the $k$-anonymity requirement. Additional risk analysis can be performed to estimate the risk of actual records in not meeting the $k$-anonymity requirement in a data release, and suppress fields in records that are associated with a high estimated risk.
Still, the framework’s policy search and the policy selection approach depend on many adjustable parameters (e.g., the number of performed simulations, the expected number of new disease cases, the specific bins randomly selected to simulate new cases, the size of the quantile range used for the confidence a policy will meet a given risk threshold), which can be adjusted to mitigate the need for suppression.

Third, as we aim to generally support public data sharing, we focus on privacy risk without measuring the utility of a data sharing policy. Though we provide the data sharer with policy options, from which they can choose how to prioritize sharing quasi-identifier information, we do not address the more complex problem of policy planning. For instance, maximizing the granularity of one quasi-identifier early in the time series could hinder policy flexibility in the future. In the scenario where another quasi-identifier becomes important to public health research later, the data sharer may want to change the generalization of previously released data to complement the new priority. However, if the earlier policy has already consumed the available privacy risk, the policy may not be altered without potentially exposing patients’ identities. Previously released data may be shared again with more detail, but not less. Future work should quantitatively measure data utility to inform data sharers when to maintain a more general policy, to preserve the ability to choose a path toward a specific information priority later.

Fourth, the privacy risk estimation framework depends on random sampling methods that may not realistically simulate the pandemic spread of disease. We assign an equal likelihood of infection to all uninfected county residents at any given time in the
simulations, and do not allow reinfections. In reality, the actual likelihood varies according to contact patterns of infectious individuals (i.e., through households or at work)\textsuperscript{57,58}, and reinfections are possible, though not likely in the case of COVID-19\textsuperscript{36}. Still, we believe that Monte Carlo simulations, constrained to run within the relatively contained geographic region of a county, provide a reasonable range and estimate of infection outcomes, as they have shown to be adept at simulating complex, high-dimensional patterns\textsuperscript{59}. Further framework refinement should address the possibility of reinfection for diseases for which reinfection is more likely.

Fifth, the framework does not compute the re-identification risk of sharing a specific record. Rather, it estimates the range and expectation of privacy risk for a population. Future work should evaluate how well different privacy risk measures, applied within the framework, forecast the re-identification risk of sharing actual disease surveillance data.

Finally, we show the privacy risk of a policy may unequally stratify across racial groups within a county and the policy search did not include fairness in the search criteria. Equitable privacy in data sharing is currently underexplored and remains an important topic to be addressed\textsuperscript{56}. Future work should develop methods to assess privacy fairness, from which the policy search can be refined.

METHODS

Framework algorithm inputs
The Monte Carlo privacy risk estimation framework’s core algorithm (denoted by the black box in Figure 1) calculates the privacy risk estimates from four inputs: 1) the county’s demographic distribution, transformed according to the data sharing policy; 2) the time series of the number of new cases reported in the county, adjusted to match the generalization of date of diagnosis in the policy; 3) the size of the lagging period; and 4) the privacy risk measure.

The first input is the demographic distribution. The distribution defines the number of county residents that fall into each demographic group, where each group is defined by a unique set of quasi-identifier values (excluding the date of diagnosis). For example, assume a policy designates sharing state and county of residence, date of diagnosis, and 30-year age ranges. The input distribution is the number of people living in the county that fall into each 30-year age interval. We obtain the county distributions for the quasi-identifiers listed in Table 1 from the U.S. Census PCT12 tables.

Each PCT12 table contains joint statistics on age, sex, and county for a given Census-defined race. An additional table (PCT12H) provides joint statistics for Hispanic-Latino residents without race, while another (PCT12I) provides the joint statistics of non-Hispanic white residents. We calculate joint statistics for age, race, sex, ethnicity, and county of residence by first subtracting the PCT12I table from the white race table (PCT12A). The remainder is the number of white, Hispanic-Latino residents per race, sex, and county combination. We then subtract these statistics from the PCT12H table. The new remainder is the number of non-white, Hispanic-Latino residents. We distribute
the non-white, Hispanic-Latino individuals among the remaining races proportional to
the size of each racial group per age, sex, and county combination. For example,
assume 15 people in Davidson County are non-white, 35 years old, and female.
Further, assume 5 of the 15 residents are Asian and the other 10 are black or African
American. Now, if there are 9 non-white, Hispanic, 35-year-old female residents in
Davidson, we assign 3 of the 5 Asian residents and 6 of the 10 black or African
American residents as Hispanic-Latino. Though this method may not accurately capture
the true joint statistics of age, race, sex, and ethnicity per U.S. county, it provides a
reasonable estimate for the framework. Distributing the Hispanic-Latino residents
across all races spreads the county’s demographic distribution more equally among
demographic groups. Randomly sampling from a more uniform distribution models the
worst-case scenario, where individuals are more likely to be uniquely represented in the
simulated dataset\textsuperscript{60}. The final joint statistics for age, race, sex, ethnicity, and county are
used to define the demographic distributions for each county, where the counts are
aggregated according to the data sharing policy’s generalization specifications.

The second input is the time series, which defines the number of new disease cases
reported, or the number of new records added to the dataset, per time period. The
algorithm calculates the privacy risk at each time point in the time series. A time series
with a daily periodicity simulates a data sharing policy that does not generalize date of
diagnosis. A time series with a weekly periodicity simulates a policy that generalizes the
actual date to week of diagnosis. The week definition (e.g., a new week starts every
Sunday) defines when the updated dataset is shared in the simulation. We use the
Johns Hopkins COVID-19 tracking data for COVID-19 disease case times series. The Johns Hopkins data provides the reported number of COVID-19 cases diagnosed in each U.S. county on each day. We convert the time series from the Johns Hopkins data to weekly case count series by summing cases within each week.

The third input is the length of the lagging period. This value is a positive number that adjusts the privacy risk calculation according to the assumed knowledge of a data recipient regarding the date of diagnosis. For example, if new disease cases are not reported until three to five days after obtaining the test sample, it is unlikely that the data recipient can know the exact date of diagnosis of an individual in the dataset. It would be more reasonable in such a case to set a 3-day lagging period, which suggests the data recipient knows at best the 3-day range in which the patient was diagnosed. A 1-day lagging period (equivalent to no lag) in this scenario would overestimate the data recipient’s capabilities, inflate the privacy risk estimate, and potentially lead to unnecessary generalization of the data.

The final input is the privacy risk measure. Different measures consider different types of re-identification attacks. Here, we show the PK risk, which is evaluated on a window of disease case records throughout the time series. We also show the marketer risk measure in the Supplementary Information, which is evaluated on the cumulative dataset at each time point.

*Framework algorithm – PK risk*
The algorithm follows the process described in Figure 6 to evaluate the privacy risk. The algorithm first creates the uninfected population from the input demographic distribution, where each county resident is uniquely represented by their demographic group (step 1). It then sums each value in *Cases* to obtain the total number of disease cases that will occur in the time series (2). The algorithm then applies Monte Carlo sampling to choose who gets “infected” from *UninfectedPop* and returns the list of individuals in random order (3). The sampling selects individuals without replacement, assuming equal weights across the entire uninfected population. Sampling one time without replacement prevents individual reinfection in the simulation. After initializing two lists (4 and 5), the algorithm enters a loop, which iterates for each value in the input time series (6). The first step within the loop removes the first $c$ individuals from *InfectedPop*, counts how many of the individuals fall into each demographic group, and returns a vector of the results (7). The *NewCases* vector is added to a list of vectors from previous iterations, whose maximum size is the user-defined *lag* (8-11). To evaluate the PK risk under the lagging period assumption, the algorithm calculates the cell-wise sum of the vectors in *RecentCases* (12). The resulting vector, *CasesInPeriod*, represents the number of records for each unique combination of quasi-identifier values in the dataset, whose date of diagnosis falls within the lagging period. The PK risk is then calculated on this final vector (13) and appended to the results (14) before proceeding to the next loop iteration.
The PK risk calculation is based on a formulation posed by Skinner and Elliott\textsuperscript{39}. In the equation, let \( J \) denote the number of unique demographic groups allowed by the data sharing policy. Let \( F_j \) denote the number of records in demographic group \( j \), for \( j = 1, \ldots, J \). Let \( I(\cdot) \) denote the indicator function, where \( I(A) = 1 \) when \( A \) is true and \( I(A) = 0 \) otherwise. The PK risk is therefore

\[
\frac{1}{N} \sum_{k=1}^{K} \sum_{j=1}^{J} I(F_j = k) \cdot k
\]  

(1)
where $N$ is the total number of records shared in the lagging period and $K$ is the user-defined $k$ value. The result is the proportion of the records shared in the lagging period that fall into a demographic group of size $K$ or less.

Repeating the algorithm produces a distribution of risk outcomes at each point in the time series. The distribution can be analyzed for the expectation, the range, and confidence intervals of the privacy risk measure.

**PK risk algorithm complexity**

We walk through the algorithm’s worst-case time complexity. When each county citizen falls into its own demographic group, step 1 makes $n$ executions, where $n$ is the size of the county’s population. Similarly, if every citizen is infected at some point in the time series, there are $n$ Monte Carlo random sampling executions. Within the loop, when all the cases occur on the same time point, step 7 makes $n$ executions. The remaining steps execute in constant time until the PK risk calculation in step 13. The PK risk calculation executes $l$ times, where $l$ equals $K$ in Eqn. 1, for each non-empty demographic group. The value of $l$ typically remains between 1 and 20. When the number of groups equals the number of citizens, there are $ln$ executions made. The complexity for the loop, and subsequently the algorithm, is therefore $O(ln)$. Repeating the algorithm for $m$ simulations increases the complexity to $O(mln)$. The number of simulations, $m$, is typically on the order of 1,000. Since most US counties possess more than 1,000 residents (and may exceed 1,000,000), $n$ dominates the time complexity.
**Policy search**

The policy search, summarized in Figure 2, applies the framework to calculate the PK10 estimates for combinations of data sharing policy, case count number, and county in a brute force manner. The feature generalization options for the policies follow the generalization hierarchy presented in Figure 7. The PK10 risk is calculated on 1,000 simulations, for each policy, case count, and county combination. We then compare the upper bound of the 95% quantile range of the simulations to the PK10 threshold. We choose to represent the PK10 distribution by the empirical confidence interval’s upper bound to increase the likelihood the outcome remains below the threshold in practice. If the upper bound is less than or equal to 0.01 for every county in the size category, the policy is marked as an acceptable policy. When a policy does not meet the threshold, the policy is removed from the list of potential policies for the remainder of counties in the county size category, at the case count value. The policy’s parent policies are also removed. We acknowledge that previously developed policy search strategies\(^{61,62}\) could be applied to the framework’s output, but this type of policy search is not a focus of this paper nor necessary to search the limited number of policies presented here.
Figure 7. The generalization hierarchies for age, race, sex, and ethnicity used in this paper, adapted from those of Wan et al. Each horizontal level is a potential generalization state for the data sharing policy. For example, the policy could specify generalizing age to 5-year age intervals to 15-year age intervals, or broader ranges. We represent year of birth as 1-year age at the bottom of the Age hierarchy. Moving up the hierarchies, the data becomes more generalized to increase privacy. An asterisk indicates the feature is generalized to a null value for all individuals, which is equivalent to suppression or non-release of the corresponding field.

Sampling without replacement requires the case number to be less than the total county population. Therefore, policy search combinations are restricted to the set of counties whose total population exceeded the case count number. For example, the results for the (0, 1k) county size category at 300 cases were generated from the US counties with a total population in the interval [300, 1000).
We choose to summarize the policy results into tables to aid in readability and facilitate downstream applications. Summarization first groups results by population size to broadly incorporate its effect on the underlying entropy in each county’s demographic distribution, which influences the privacy risk\textsuperscript{63}. Summarization also involves limiting the policies listed in each cell to two or less. The first policies listed in each cell are those in the search results that 1) avoid suppressing quasi-identifier fields, 2) prioritize age granularity, and 3) are not child policies of any that meet the threshold.

*Estimating the risk of the dynamic policy*

The data sharing policy can be chosen according to the expected number of new cases based on the results of the policy search. We use the CDC ensemble prediction model’s one week estimates for policy selection in the evaluation (Table 2) and case studies (Figures 4 and 5). We specifically used the model’s point estimates, calculated as the median of the point estimates of the various prediction models. The ensemble model also has 0.025 quantile estimates from August through January, but we did not use these estimates because they could severely underestimate the case increases and subsequently overprioritize privacy at the cost of data utility.

We calculate each county’s PK10 estimates under the dynamic policy selection in the following manner. For a given county, we simulate the first policy listed in each cell of the summarized policy search results (Figure 2) for the corresponding county size. For example, if the county had less than 1,000 residents per the U.S. Census, we run 1,000 simulations for each ****, **s*, 4***, and 4*s*.
Each simulation uses the Johns Hopkins surveillance data to define the disease case time series from January 23, 2020 through April 24, 2021. This simulates sharing the actual number of disease records throughout the COVID-19 pandemic. Data preprocessing includes setting all negative daily case count values to zero. For simulating the daily release schedule (under any lagging period assumption), the input time series maintains a daily periodicity. To simulate the weekly release schedule, the preprocessed data is resampled into weekly periods, where the week is defined as Sunday to Saturday.

After calculating the county’s privacy risk estimates under each policy, we use the forecasted counts to select which of the policies to apply at the beginning of each week. For the daily release schedule, we select the policy according to the minimum forecasted rolling sum within the upcoming week. For the weekly release schedule, we use the forecasted weekly increase. We then concatenate the PK10 estimates from each policy's simulations by weekly increments, following the sequence of selected policies. The concatenated list of privacy risk estimates represents the county’s PK10 risk of sharing the actual number of disease records per day (for the daily release schedule) or per week (for the weekly release schedule) when dynamically selecting the data sharing policy.

This process for estimating the privacy risk of the dynamically adapting policy is applied to all counties in the evaluation in Table 2, under two release schedules. It is also
applied in the case studies. The case studies additionally included a variation, where each week’s policy is selected from the actual case numbers (from the Johns Hopkins data) instead of the forecasted case quantities. We add this variation to evaluate how well the dynamic policy meets the PK10 threshold when perfectly predicting future case loads.

**Fairness analysis**

The fairness analysis measures the proportion of the privacy risk each racial group carries when sharing the data under a single policy throughout the COVID-19 pandemic. The analysis applies the 1Bse policy, when sharing the updated dataset on a daily basis (the date of diagnosis was not generalized) with a 5-day lagging period assumption. The PK5, PK10, and PK20 are measured for four racial groups: 1) Asian, 2) Black, 3) White, and 4) Other. This new Other is composed of American Indian/Alaskan Native, Native Hawaiian/Pacific Islander, Two or More Races, and Some Other Race Alone values. The Johns Hopkins tracking data is input as the time series in the framework.

The fairness analysis algorithm builds upon the standard PK risk algorithm in Figure 6, substituting Eq. 1 in step 13 with Eq. 2.

\[
\frac{\sum_{k=1}^{K} \sum_{j \in J^r} I(F_j = k) \cdot k}{\sum_{k=1}^{K} \sum_{j=1}^{J} I(F_j = k) \cdot k}
\]

In Eq. 2, \(J^r\) represents the set of demographic groups allowed by the data sharing policy containing race value \(r\), where the set of distinct \(r\) values, \(R\), is determined by the
policy’s race generalization. $J^r$ is a subset of the complete set of unique demographic groups, such that $\sum_{r=1}^R |J^r| = J$. $F_{j^r}$ represents the number of records in demographic group $j^r$, for $j^r \in J^r$.

Eq. 2 thus corresponds to the proportion of all records in a group of size $K$ or less with a race value of $r$. The expected proportion is calculated as the mean of 1,000 simulations, for each racial group at each time point.

**Code**

All experiments are performed using Python (version 3.8). The code can be found at (GitHub link\(^1\)).

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**AUTHOR CONTRIBUTIONS**

J.T.B designed the framework and privacy model, wrote the computer code, performed the experiments, analyzed the results, and prepared the manuscript. C.Y., W.X, Z.Y., and Z.W. contributed to the conceptual design of the framework and privacy model,

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\(^1\) We will replace this text with the GitHub url once the manuscript is accepted for publication.
analyzed the results, and revised the manuscript. A.G.-D., M.K., and M.A.B supervised each component of the project.
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Supplementary Information

Additional PK risk policy guidance

We repeat our policy search for two additional \( k \) values: \( k = 5 \) and \( k = 20 \), while maintaining a threshold of 0.01 in both cases. We summarize the results in the same manner as Figure 2.

**Supplementary Figure 1.** Policies with a PK5 upper bound (calculated as the upper bound of the 95% quantile range of 1,000 framework simulations) less than or equal to 0.01 at varying disease case volume thresholds. A four-character alphanumeric code indicates the policy’s generalization levels. All policies additionally include state and county of residence and some generalization of diagnosis date. A policy is eligible to be listed under the minimum number of new cases (table column) at which it meets the PK5 threshold for every county in the category (table row). A maximum of two policies are listed in each cell among the actual number of policies supported. The number in the bottom right-hand corner of each cell indicates how many of the 96 searched policies meet the risk threshold at the case volume.
Supplementary Figure 2. Policies with a PK20 upper bound (calculated as the upper bound of the 95% quantile range of 1,000 framework simulations) less than or equal to 0.01 at varying disease case volume thresholds. A four-character alphanumeric code indicates the policy’s generalization levels. All policies additionally include state and county of residence and some generalization of diagnosis date. A policy is eligible to be listed under the minimum number of new cases (table column) at which it meets the PK20 threshold for every county in the category (table row). A maximum of two policies are listed in each cell among the actual number of policies supported. The number in the bottom right-hand corner of each cell indicates how many of the 96 searched policies meet the risk threshold at the case volume.

Marketer risk

A variety of privacy risk measures have been developed to account for different portions of the privacy risk distribution and different types of re-identification scenarios\cite{27}. In the main body of the manuscript, we apply the Monte Carlo framework to estimate the PK risk, an upper bound of the re-identification risk. Here, we use the framework to estimate the amortized re-identification risk, also known as the marketer risk\cite{46}. These two measures are not necessarily mutually exclusive. The PK risk considers the most unique records in the dataset, while the marketer risk measures the average
uniqueness of each record in the context of the surrounding population. We do not suggest which measure dictates the best privacy protection; rather, we provide an illustration of how to apply the framework under another privacy perspective. We leave the decision of how to use the measures to the data sharer.

The marketer risk considers a different attack scenario, where the data recipient attempts to re-identify as many individuals in the shared dataset as possible by matching the quasi-identifier values in the shared dataset to those in a separate, identified dataset. A common example of the latter is a voter registration list\textsuperscript{20,21}. Not every county resident registers to vote, but for simplicity, we assume in our analysis the data recipient possesses an identified dataset containing every county resident. This assumption models the worst-case scenario to provide an upper bound on the marketer risk. We further assume the dataset contains all demographic information listed in Table 1, except for the date of diagnosis. Excluding the date of diagnosis better approximates the information provided by a voter registration list.

Estimating the marketer risk requires a few adjustments to the PK risk estimation algorithm. First, the marketer risk is evaluated on the cumulative dataset at each time point as date of diagnosis is no longer considered a quasi-identifier, and therefore no longer separates records into quasi-identifying windows of time. Without the date of diagnosis, the user does not specify a lagging period size. Neither does the user specify a $k$ value, as the marketer risk measure incorporates all $k$ values. Supplementary Figure 5 describes the complete marketer risk estimation algorithm.
The first three steps of the marketer risk estimation algorithm are identical to the first three steps step in the PK risk estimation algorithm. The algorithm first creates uninfected population from the input demographic distribution (step 1), obtains the total number of disease cases in the time series (2), and applies Monte Carlo random sampling to select who gets “infected” and returns the list of individuals in random order (3). The sampling is performed without replacement assuming equal weights across the entire uninfected population. Individual reinfection is again prevented. The algorithm maintains the total number of disease cases, or records, per demographic group in AllCases. The vector is initialized to all zeros (4). After initializing the marketer risk
results list (5), the algorithm enters a loop, which iterates for each value in the input time series (6). The first step in the loop removes the first $c$ individuals from $\text{InfectedPop}$ and returns a vector of the new cases’ distribution across the demographic groups (7). The order of the $\text{NewCases}$ vector matches the order of $\text{AllCases}$. To evaluate the marketer risk on the cumulative dataset up to the time point corresponding to $c$, the algorithm adds the new cases to vector of previously reported cases (8). The resulting vector represents the number of records for each unique combination of quasi-identifier values in the cumulative dataset. The algorithm calculates the marketer risk on the updated $\text{AllCases}$ vector (9).

The marketer risk is calculated following the formulation from Dankar and El Emam\textsuperscript{46}. In Eq. 3, $J$ represents the number of unique demographic groups allowed by the data sharing policy. $f_j$ represents the number of records in demographic group $j$ in the shared dataset, for $j = 1, \ldots, J$. $F_j$ represents the number of records in demographic group $j$ in the identified dataset, for $j = 1, \ldots, J$. It follows that $f_j / F_j$ represents the expected proportion of correct matches between records in the shared and the identified datasets for demographic group $j$. $N$ represents the total number of records in the shared dataset

$$\frac{\sum_{j=1}^{J} f_j}{N}$$

(3)

The result is the expected proportion of the records in the shared dataset correctly matched to records in the identified dataset. The marketer risk value is appended to the list of marketer risk values at the end of each loop (13).
The marketer risk algorithm’s worst case time complexity follows that of the PK risk algorithm until the marketer risk calculation in step 9. The calculation executes one time for each non-empty demographic group. When the number of groups equals the number of citizens, there are \( n \) executions made. Therefore, the complexity for \( m \) simulations of the algorithm is to \( O(mn) \), where \( n \) is the size of the county’s population.

**Marketer risk-based policy search**

We apply the framework to search the same policy space as before (described in Figure 7) and identify data sharing policies that likely meet a marketer risk threshold at various dataset sizes. The search follows the same approach as the PK risk scenario. For each combination of U.S. county, case number, and policy we calculate the marketer risk on 1,000 independent simulations. From the 1,000 simulations, we calculate the upper bound of the 95% quantile range and compare the upper bound to a threshold of 0.01. The results indicate the minimum cumulative number of disease case records in the dataset at which a data sharing policy is supported for all counties in the population size category. We summarize the results in Supplementary Figure 3.

Selecting a policy according to the cumulative number of records notably affects dynamic policy application. First, selecting a policy now means applying the same set of quasi-identifier generalizations to the entire dataset, including previously released records. Second, changing the generalization scheme of previously released records creates a dependency between successively applied data sharing policies. The new policy must be a parent of the current policy. If it is not, the combined information across
dataset releases could expose patient identities. These differences prompt the data sharer to choose a path according to information priorities. To demonstrate, in Supplementary Figure 3, we select a single path for each county population category and generate a corresponding results table.

**Supplementary Figure 3.** (Top) Policies with a marketer risk upper bound (calculated as the upper bound of the 95% quantile range of 1,000 framework simulations) less than or equal to 0.01 at varying disease case volume thresholds. A four-character alphanumeric code indicates the policy’s generalization levels. All policies additionally include state and county of residence and some generalization of diagnosis date. A policy is eligible to be listed under the minimum number of new cases (table column) at which it meets the marketer risk threshold for every county in the category (table row). A maximum of two policies are listed in each cell among the
actual number of policies supported. The number in the bottom right-hand corner of each cell indicates how many of the 96 searched policies meet the risk threshold at the case volume. The purple circles indicate the starting policy for each county population category, from which the generalization paths are generated in the table below. (Bottom) The child-parent generalization path for each category. Moving from left to right in a row, each new policy listed is a parent of those previously listed.

Supplementary Figure 3 shows the number of acceptable policies increases with the cumulative number of records. For counties with more than one million residents, all 96 policies are supported when the dataset includes at least 100 records. The smallest counties achieve the fewest number of acceptable policies, with 19 equally feasible policies. There larger counties’ results display a pattern where the number of supported policies at 1,000 case records remains relatively constant as the size of the dataset increases. This pattern arises from an underlying difference between the marketer risk and the PK. For a given county and policy, the PK risk fluctuates with the number of case records shared in a time window. Conversely, the marketer risk for a given county and policy converges toward a specific value as more records are accumulated. The table also displays a different pattern for the two smallest categories, because the search removes counties with a total population less than the case number threshold of interest.

To further illustrate the relationship between the marketer risk and the size of the dataset, we apply the framework to a single data sharing policy throughout the COVID-19 pandemic in Davidson County, TN. The 1Ase policy (see the key in Supplementary Figure 3) is applied to a daily release schedule and allows for 532 potential demographic groups. Supplementary Figure 4 shows that as the size of the disease surveillance dataset increases, the expected (mean) marketer risk remains relatively
constant, and the range of risk converges toward the expectation. We note that the expected marketer risk represents the expected proportion of records correctly matched to the identified dataset. Though the proportion remains constant, the number of individuals at risk increases with the size of the dataset.

Supplementary Figure 4. Marketer risk estimation of 1Ase policy applied to daily releases of COVID-19 disease case surveillance data in Davidson County, TN. The expectation and quantile ranges were calculated from 1,000 independent simulations. The marketer risk is evaluated each day (Top) on the cumulative number of cases (Bottom). The orange dotted line represents the marketer risk when the size of the shared dataset is equal to the size of the population. The height of the dotted line was calculated according to Eq. 5.
The relatively constant value for the marketer risk expectation is intuitive. Since the date of diagnosis is not considered a quasi-identifier in the attack scenario, the demographic groups increase in size as more records are added to the dataset. As the number of records in group \( j \) in the shared dataset approaches the number of records in group \( j \) in the identified dataset, the marketer risk (Eq. 2) moves toward its limit, as shown in Eq.4:

\[
\frac{\sum_{j=1}^{J} 1}{n} = \frac{J}{n}
\]

where \( n \) is the size of the identified dataset/total population. Eq. 4 approximates the expected marketer risk estimated by the framework’s algorithm. The orange dotted line in Supplementary Figure 4 was calculated using Eq. 5:

\[
\frac{\sum_{j=1}^{\tilde{J}} 1}{n} = \frac{\tilde{J}}{n}
\]

where \( \tilde{J} \) is the number of demographic groups defined by the policy for which at least one person in the population corresponds. The value of \( \tilde{J} \) is obtained from the U.S. Census data. Thus, the expected marketer risk can be mathematically approximated from the framework inputs without the complete Monte Carlo simulation.

**Dynamic policy evaluation – marketer risk**

We repeat the evaluation from the main text of the paper, this time for the marketer risk-based policy search results. The succession of policies applied follows the generalization paths displayed in the bottom table in Supplementary Figure 3. Again, we consider a daily and a weekly release schedule in the context of the COVID-19 pandemic. Since date of diagnosis is not a quasi-identifier in this scenario, no date generalization is specified. We again compare the results of the framework-informed
dynamic policy selection to statically applying the $k$-anonymous policy described in the main text.

In the marketer risk scenario, we do not use the CDC’s COVID-19 ensemble prediction model to inform dynamic policy selection. Since the size of the dataset monotonically increases, the minimum number of case records will always occur on the first day of the week, regardless of the predicted weekly increase in case numbers. Therefore, at the beginning of each week (Sunday, to be consistent with the prior week definition) we use the current total number of disease case records in the dataset to select the policy for the upcoming week. This applies the most private policy to the week’s new cases while allowing the policy to potentially change on a weekly basis. The policy for the weekly release schedule is chosen according to the size of the cumulative dataset at the end of each week (Saturday). The privacy risk of sharing the actual number of case records is again estimated by inputting the Johns Hopkins COVID-19 tracking data into the framework. We restrict the results to the same time period as before for consistency. Supplementary Table 1 presents the results.

Dynamic policy selection, guided by the framework’s results, never exceeds the marketer risk threshold of 0.01. For the smallest county size category, the total case number never reaches 100 and no data is shared. Data is shared for all other county size categories. For county’s with at least 50,000 residents, the $k$-anonymous policy meets the marketer risk threshold as frequently as the dynamic policy, but with lesser data utility in terms of available demographic groups. The $k$-anonymous policy allows for
112 unique combinations of age, race, sex, and ethnicity. Under the dynamic policy selection and the case loads beginning in August 2020, counties with a population between 50,000 and 100,000 residents tend to share data with at least the 2Bse policy, which also designate 112 unique demographic groups. Counties with a population between 100,000 and 1,000,000 tend to share data with at least the 2Ase policy, which allows 196 groups. And the counties with at least 1 million residents apply the 0Ase policy that allows for 2,884 groups. The dynamic policy selection tailors the data sharing policy to both case load and county population to balance privacy and utility better than the $k$-anonymous policy at the marketer risk threshold of 0.01.
### Supplementary Table 1

Average proportion of time periods where the upper bound of the 95% quantile range of the marketer risk is less than or equal to 0.01 in the COVID-19 pandemic (August 2, 2020 to April 24, 2021). The average and 95% quantile range in each cell are taken across all counties in the corresponding population size category. The \( k \)-anonymous policy shares age intervals (0-17, 18-49, 50-64, and 65+), race (Black or African American, White, Asian, American Indian or Alaskan Native, Native Hawaiian or Pacific Islander, Mixed, and Other), ethnicity (Hispanic-Latino and Non-Hispanic), sex (Female and Male), and state and county of residency. The \( k \)-anonymous policy is statically applied to each release. The daily release PK10 estimates apply a 1-day lagging period, while the weekly release estimates assume the actual date of diagnosis is generalized to week of diagnosis.

| County Population | \( k \)-anonymous Policy | Dynamic Policy | \( k \)-anonymous Policy | Dynamic Policy |
|-------------------|--------------------------|----------------|--------------------------|----------------|
| < 1,000 (n = 35)  | 0.105 [0, 0.479]          | 1 [1, 1]       | 0.102 [0, 0.463]          | 1 [1, 1]       |
| 1,000 - 50,000 (n = 2,129) | 0.555 [0, 1]          | 1 [1, 1]       | 0.558 [0, 1]          | 1 [1, 1]       |
| 50,000 - 100,000 (n = 398) | 1 [1, 1]          | 1 [1, 1]       | 1 [1, 1]          | 1 [1, 1]       |
| 100,000 - 1,000,000 (n = 538) | 1 [1, 1]          | 1 [1, 1]       | 1 [1, 1]          | 1 [1, 1]       |
| > 1,000,000 (n = 39) | 1 [1, 1]          | 1 [1, 1]       | 1 [1, 1]          | 1 [1, 1]       |

**Marketer risk case studies**

In this section, we demonstrate how to apply the marketer risk-based guidance, revisiting Davidson and Perry counties. The case studies select the data sharing policy on a weekly basis for a daily release schedule, in the same manner as the evaluation above. The actual marketer risk is estimated from the Monte Carlo framework, using the
Johns Hopkins tracking data as input. We restrict the results to the same time interval as the case studies in the main paper. The results for Davidson County are presented in Supplementary Figure 5, and the results for Perry County are presented in Supplementary Figure 6.

As the generalization path in Supplementary Figure 3 instructs, the 1Ase policy is applied to each data release, as the size of the dataset remains above 250 throughout the time interval. The mean and 95% quantile range of the marketer risk remain below the threshold of 0.01 at each time point. The 95% quantile range, in this case, is too narrow to be seen outside the expectation.

The data sharing policy in Perry County, TN changes from 4*s* to 4Cs* the week after the number of disease case records in the dataset surpasses 500. The expectation and 95% quantile range of the marketer risk stay below the 0.01 marketer risk threshold throughout the time interval.
Supplementary Figure 5. Dynamic policy selection applied to Davidson County, TN in the COVID-19 pandemic (August 2, 2020 to April 24, 2021). (Top) The cumulative sum of the case counts reported in Davidson County, according to the Johns Hopkins COVID-19 tracking data. The red squares represent the case record number value and the end of the previous week (through Saturday) used in selecting the next week’s policy from Supplementary Figure 3. (Middle) The selected policy at the beginning of each week in the pandemic. Each policy is represented by a 4-character alphanumeric code following the key in Supplementary Figure 3. (Bottom) The marketer risk from sharing the actual number of records under the sequence of policies detailed in the middle graph. The expectation and 95% quantile range are calculated from 1,000 independent simulations. The horizontal dashed line marks the marketer risk threshold of 0.01.
Supplementary Figure 6. Dynamic policy selection applied to Perry County, TN in the COVID-19 pandemic (August 2, 2020 to April 24, 2021). (Top) The cumulative sum of the case counts reported in Davidson County, according to the Johns Hopkins COVID-19 tracking data. The red squares represent the case record number value and the end of the previous week (through Saturday) used in selecting the next week’s policy from Supplementary Figure 3. (Middle) The selected policy at the beginning of each week in the pandemic. Each policy is represented by a 4-character alphanumeric code following the key in Supplementary Figure 3. (Bottom) The marketer risk from sharing the actual number of records under the sequence of policies detailed in the middle graph. The expectation and 95% quantile range are calculated from 1,000 independent simulations. The horizontal dashed line marks the marketer risk threshold of 0.01.
Fairness Analysis – marketer risk

We repeat the fairness analysis of an individual policy, 1Bse, according to the marketer risk. The expected proportion of the marketer risk is calculated as the average of 1,000 simulations. Each simulation follows the algorithm in Supplementary Figure 5, replacing Eq. 3 in step (9) with Eq. 6, below:

\[
\frac{\sum_{j} f_{jr}}{\sum_{j=1}^{J} F_{j}}
\]

Similar to Eq. 2, \( J^r \) represents the set of demographic groups allowed by the data sharing policy containing race value \( r \), where the set of distinct \( r \) values, \( R \), is determined by the policy’s race generalization. \( f_{jr} \) and \( F_{jr} \) represent the number of records demographic group \( j^r \) in, for \( j^r \in J^r \), in the shared and identified datasets, respectively. The result is the proportion of the marketer risk corresponds to individuals with race value \( r \).
Supplementary Figure 7. Distribution of marketer privacy risk by racial group during the COVID-19 pandemic in Davidson County. The racial groups we consider are those provided in the U.S. Census: Black, White, Asian, Alaskan Native/American Indian, Pacific Islander/Native Hawaiian, Mixed race, and Other. The proportion of the overall Marketer risk each racial group bears throughout the COVID-19 pandemic, when applying a 1Bse policy (see key in Figure 2) in Davidson County, TN. The expected proportion is calculated as the mean of 1,000 independent simulations.

Supplementary Figure 7 shows that the expected proportion of the marketer risk each racial group bears fluctuates briefly at the beginning of the pandemic before ultimately converging to a relatively consistent value. The larger racial groups in the county, Black and White, have similar proportions, as do the smaller racial groups, Asian and Other.

The values to which the expectations converge can again be estimated by the number of non-empty groups for each racial group, calculated from the policy and the census data, using Eq. 7. Here, $|\bar{J}_r|$ represents the number non-empty demographic groups with race value $r$, for $r \in R$.

$$\frac{|\bar{J}_r|}{\sum_r |\bar{J}_r|}$$