Quantifying SARS-CoV-2 infection risk within the Apple/Google exposure notification framework to inform quarantine recommendations

Amanda M. Wilson¹, Nathan Aviles², Paloma I. Beamer¹, Zsombor Szabo³, Kacey C. Ernst¹, Joanna Masel⁴,*

¹ Mel & Enid Zuckerman College of Public Health, University of Arizona
² Graduate Interdisciplinary Program in Statistics, University of Arizona
³ Engineering, Covid-Watch
⁴ Ecology & Evolutionary Biology, University of Arizona
* corresponding author masel@email.arizona.edu

ORCIDs: AMW 0000-0003-3259-8169, NA 0000-0001-9998-4406, PB 0000-0001-5287-2183, ZS 0000-0002-3653-1378, KE 0000-0002-3346-7788 JM 0000-0002-7398-2127

Abstract

Background: Bluetooth-based exposure notification apps can supplement manual contact tracing to reduce SARS-CoV-2 transmission. Their speed, scalability, and privacy preservation are generally acknowledged, but less exploited are smartphones’ accurate measurement of duration, and ability to automatically calculate risk from multiple inputs.

Methods: We model uncertainty in the shape of an exhaled virus-containing plume, inhalation parameters, and distance as a function of Bluetooth attenuation. We assume relative rates of viral shedding depend on the timing of exposure relative to symptom onset. We calibrate an exponential dose-response curve on the basis of the infection probabilities of household contacts. The conditional probability of current or future infectiousness, conditioned on how long post-exposure an exposed individual has been free of symptoms, decreases during quarantine, with shape determined by the distribution of incubation periods, proportion of asymptomatic cases, and distribution of asymptomatic shedding durations. It can be adjusted for negative test results using Bayes Theorem.

Findings: As an example of our calculations, fifteen minutes of close contact with a high-shedding individual, given a 15% asymptomatic infection rate and no testing, would require 5- and 14-day quarantine for their risk of current or future infectiousness to fall below 0.84% and 0.14% risk, respectively.

Interpretation: The Covid-Watch app is currently programmed either to use a threshold on initial infection risk to determine 14-day quarantine onset, or on the conditional probability of current and future infectiousness conditions to determine both quarantine and duration. Either threshold can be set by public health authorities.

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NOTE: This preprint reports new research that has not been certified by peer review and should not be used to guide clinical practice.
1.0 Preface

This preprint is a description of ongoing work, uploaded for the purposes of rapid sharing. A later update to this preprint will include a description of alpha and possibly also beta testing data, and its use in calibrating the risk scoring system described here, according to the methods described here. We acknowledge the following team members who we expect to be co-authors upon addition of this content: Tina White, James Petrie, Sudha Ram, Yuanxia Li, Michelle Xie, Noriko Tamari, Sameer Halai, and Janet Mcillece.

2.0 Background

Manual contact tracing followed by quarantine of known contacts is a critical method for containing or mitigating the spread of communicable diseases during outbreaks or pandemics. It is, however, extremely resource and time-intensive. New technologies can supplement this approach. Manual contact tracing can be effective for COVID-19, however, a significant challenge is the extremely short window of time between an index case presenting for testing and their infected contacts beginning to shed infectious virus. Automatic exposure notification approaches based on Bluetooth proximity have the potential to achieve many of the benefits of contact tracing, while also providing more rapid notification, in addition to greater privacy, more objective recall of contacts including those whose identity is unknown to the index case, and greater scalability. The two approaches of contact tracing and exposure notifications are not mutually exclusive and may interact e.g. when those receiving digital exposure notifications are referred to human contact tracers for the information and support needed for quarantine adherence and further investigation.

The core of both approaches is to determine who should be quarantined, and for how long. For the purpose of containment, the World Health Organization (WHO) defined a close contact to include those face-to-face with a COVID-19 case within 1 meter and for >15 minutes, or those in direct physical contact with the COVID-19 case for any duration of time. The Centers for Disease Control (CDC)’s definition is more sensitive, encompassing any proximity within 6 feet for at least 15 minutes, while noting that data to inform this definition are limited (available at https://www.cdc.gov/coronavirus/2019-ncov/php/public-health-recommendations.html, accessed on 7/1/2020). European guidance focuses on either face-to-face contact within 2 meters or at greater distance without face to face contact if within a closed environment, in both cases for at least 15 minutes, while acknowledging that “Longer duration of contact is assumed to increase the risk of transmission; the 15-minute limit is arbitrarily selected for practical purpose” (available at https://www.ecdc.europa.eu/en/covid-19-contact-tracing-public-health-management, accessed on 7/1/2020). In practice, many manual contact tracing programs in the United States are still not fully operational and suffer from extremely high caseloads (15,000 cases in one day in Florida), acutely limiting the ability to conduct thorough contact tracing on all cases.

Digital exposure sensing has some advantages and some disadvantages compared to manual contact tracing. We expect digital systems to be more reliable than human recall with respect to the duration of exposure, and not subject to bias towards known vs. unknown contacts, but to be less reliable with respect to distance, whether the interaction was face to face, intimacy of the contact (household member vs. casual contact) and environmental factors such as mask use and whether the interaction took place indoors or outdoors. Apps supply an opportunity to
assess risk quantitatively according to a formula that combines all available data on exposure(s). More precise measures of duration can be combined with the (considerable) uncertainties in Bluetooth assessments of distance and in the modeled level of infectious shedding of the index case, to determine the probability of infection from that exposure. Determining the threshold for entering quarantine based on probability of infection should yield better results than from combining three binary thresholds for duration, distance, and the infectious period of the index case. Determining the threshold for exiting quarantine based on the conditional probability of current or future infectiousness can optimize the reduction in disease transmission per day of quarantine recommended.

The aim of contact tracing and subsequent quarantine is to reduce transmission at an individual and population level. The effective reproductive number \( R(t) \) must fall below 1, which can occur through a combination of measures rather than contact tracing alone, before the number of cases will decline. However, decreasing \( R(t) \) still has many benefits even if not brought below one. It flattens the curve to spread out the burden on healthcare over time, it buys society more time to build healthcare capacity, and it improves the odds that herd immunity can be delayed until a vaccine becomes available. Even if herd immunity is eventually reached, it reduces the degree to which herd immunity is overshot.\(^\text{10}\)

Conservative criteria and durations for quarantine, to which all quarantined individuals adhere, provide the best chance for containment. WHO recommendations for quarantine were explicitly designed for containment\(^\text{7}\), and have since been made even more conservative in their CDC and European iterations. However, these conservative approaches assign equal risk and corresponding response to all contacts that meet their respective definitions, despite significant variation in the actual risk of infection. Overly broad recommendations for quarantine could lead to low quarantine adherence\(^\text{11}\) particularly in low-resource communities, defeating efforts to contain and slow disease spread. It may be more effective to estimate risk as accurately and consistently as possible in order to balance feasibility of adherence to the measures and risk of subsequent ongoing transmission from the exposure.

To illustrate this problem, we note that the average number of close contacts per infected individual has been estimated to be 59\(^\text{12}\) with well-resourced manual contact tracing able to trace 27-31.\(^\text{13,14}\) High community prevalence of infection, e.g. currently estimated as \(~3.9\%\) in Arizona\(^\text{15}\) at the time of writing (July 15) (including estimated undiagnosed infections, but also including individuals already isolated), combined with digital methods that are likely to pick up many contacts not meeting current public health definitions of a contact and high app uptake could result in as high a proportion of people recommended to be in quarantine as a general order to stay home regardless of exposure status. EU guidance suggests that during app rollout, quarantine could be recommended only to those at highest risk as a way to avoid quarantining large numbers of people unnecessarily, which may result in low acceptability and uptake of the app.\(^\text{16}\)

Because of this, we advocate for exposure notification strategies that target quarantine recommendations to those who are most likely to be infected (and thus infectious). If an app were nearly universally adopted by all smartphone users (e.g., if Google/Apple pushed it via the operating system), and within a week it recommended that half the population enter quarantine, people may cease to pay attention to the notifications or adhere to the recommendations,
negating any benefit potentially offered by the app. Setting higher thresholds for quarantine could help avoid this scenario. Public health authorities can also use quantitative risk assessments to prioritize limited resources such as testing, assistance with the delivery of food and other essentials, and quarantine facilities such as hotels, targeting them toward those most likely to be infected and hence infectious.

Here we lay out a framework for such quantitative risk assessment, based on the capabilities of Bluetooth proximity sensing under the decentralized protocol of the Google/Apple Exposure Notification (GAEN) API. The risk of infection depends on dose, which in turn depends on the shedding rate of the infected individual (affecting the amount of the pathogen in the air), and on the duration and distance of the interaction. As days go by without onset of symptoms, the probability of future infectiousness decreases, because the probability is conditioned on lack of symptoms for an increasing stretch of time.

To be consistent, quarantine would end when the risk of infection falls below the same risk threshold used to decide who should enter quarantine. This procedure would assign shorter quarantines following lower risk interactions, with the steepest slope around the median incubation period. Note that this assumes that variation is in probability of infection, rather than in dose conditional on infection (given that higher dose is likely to lead to shorter incubation time) – we return to this point in the Discussion. Clear messaging is still possible, with the app either giving only the date on which quarantine ends, or summarizing quantitative information through a daily risk score that falls each day in the absence of symptoms or positive test results. The app can also recommend an optimal date for testing.

When a user reports positive infection status, the GAEN framework (Figure 1) allows apps to assign a “Transmission Risk Level” to each day that they might have been shedding, and to communicate this level to the receiver’s phone via a Temporary Exposure Key (TEK). These Transmission Risk Levels can be assigned on the basis of date of symptom onset or test date. On the receiver’s device, the GAEN framework can record the Bluetooth attenuation as a rough estimate of distance, and the duration of exposure.
Figure 1. Overview of risk assessment approach for a single exposure. We report on preliminary calibration to inform infection risk calculated on the receiver’s phone.

Here we propose a risk scoring system for use in a GAEN or similar framework. We parameterize it based on currently available data about COVID-19 infection risk factors, while proposing a system flexible enough to be continually improved as more is learned about viral dynamics. We demonstrate how this risk scoring system could be applied either to an approach aimed at slowing transmission in a community outbreak far from containment, or with a more stringent threshold in a community where outbreaks have been contained within a country’s borders but there is still need for active monitoring and surveillance because borders are not closed. Our group plans to pilot and evaluate the Covid-Watch app using portions of this scheme on the campus of the University of Arizona.

3.0 Methods

3.1 Overview of Approach

Our microbial exposure model estimates the airborne spread of viral particles from an emitter’s mouth following a Gaussian plume formation, and their subsequent inhalation by contacts. We
use a Monte Carlo approach to average across a variety of sources of variability and uncertainty that affect the estimated inhaled dose.

The GAEN v1.1 framework records durations only up to 30 minutes, in order to protect anonymity of COVID-positive patients by limiting the risk that users will be able guess the source of their exposure, while still meeting contact definitions that invoke minimum exposure duration of 15 minutes. We note that when a high risk threshold is chosen by a community attempting to limit the proportion of the population under quarantine, this 30-minute cap will prevent the app from achieving resolution among high risk exposures, and thus prevent it from targeting quarantine recommendations and material resources to those at highest risk of being infected and subsequently infecting others. The GAEN allows for durations to be recorded separately within three bins of attenuation, thus allowing a total exposure duration of 90 minutes if the attenuation varies in the necessary manner over the exposure. We calculate a weighted sum of the three durations, using the weights to capture the differences in expected dose (number of inhaled particles over an exposure time). Note that GAEN v1.5 (not yet released) will lift this cap, but will impose limits to our ability to differentiate among Transmission Risk Levels (discussed below). We focus here on GAEN v1.1, but our scheme can be adapted for later versions.

To inform our choice of weights, we first sample distance as a function of which bin attenuation falls within, and then we capture uncertainty in angle relative to the plume through random sampling. The average interpersonal distance during close contact in a graduate student office in China was found to be 0.81 m,\(^{18}\) making 1 m a good threshold for distances likely to reflect face to face interactions, where the plume is directed at the exposed individual. At greater distances, many individuals will not be directly facing one another but rather side-by-side or in another geometric formation regarding the emission plume and the inhalation zone of the one being exposed. We also sample from variance in inhalation and exhalation rates. We set the weights to represent relative mean doses as a function of attenuation.

While it has been demonstrated that wind velocity and relative humidity are important factors for determining droplet and fine aerosol dispersion and deposition,\(^{19,20}\) as is mask usage, these are uncertain factors that are not recorded by the app, especially considering that interactions may occur indoors or outdoors. Therefore, our approach to the risk per exposure focuses on the distance, duration of the interaction, infection status, and relative shedding rates of individuals in the interaction. By not accounting for deposition, and by assuming that masks are either not worn or not worn effectively, we will tend to overestimate dose at greater distances, and in the presence of masks. This will implicitly lower the app-imposed risk tolerance of individuals who comply with public health guidelines that recommend masks and physical distancing, and who might therefore also be more inclined to comply with quarantine recommendations. The 2-meter rule was based on the assumption that transmission is via large droplets for which deposition occurs over this distance – this no longer appears to be the case,\(^{21,22}\) supporting our assignment of some risk to greater distances.

From this dose calculated as the weighted sum of exposure durations, we use an exponential dose-response curve to calculate the probability of infection. This curve has a single composite parameter representing the product of the conversion from arbitrary units to viral particles and the probability with which each viral particle might independently initiate infection. We calibrate the value of this composite parameter so that probabilities of infection given long exposures match those observed for household contacts.
The overall approach is summarized in Figure 1, describing how each of the following modeling pieces are used to inform an infection risk. Parameter values and their descriptions and sources can be seen in Table 1 for calculations performed by the app and in Table 2 for parameters we used during calibration.

3.2 Transmission Risk Levels

Transmission risk level in the GAEN API is a proxy for the magnitude of viral shedding and can be set by the app on the basis of a simple questionnaire administered to users reporting a positive diagnosis. We use this to inform expected shedding $S$.

The first question we ask to inform transmission risk levels is "What day did your symptoms start"? A curve fit to known transmission events suggests peak transmission the day before symptom onset, and essentially no transmission more than three days before symptom onset. However, this might be confounded with behavioral changes with symptom onset, with ascertainment bias in terms of which transmission events are easiest to document, with possible errors in the direction of transmission given the variability of incubation periods, and with assumptions regarding the shape of the curve. Worse, the analysis appears to have significant technical flaws.

A second source of information is quantitative PCR. However, this may reflect non-infectious viral remnants, especially late in the course of disease, where the proportion of culture-positive PCR results tends to decrease. However, this decline is also expected from a simple dose-response curve, where the probability of culture-positivity decreases as the amount of shedding decreases late in infection, i.e. the decline in infectivity might be quantitative rather than qualitative.
| Parameter | Description | Distribution or Point Value | References |
|-----------|-------------|----------------------------|------------|
| $S$       | Viral shedding rate in arbitrary units that are proportional to viral copies/m³ | $10^1$ 5-6 days pre- or 8-11 days post-symptom onset | 10-fold range informed by TCID50 measures<sup>25</sup>, timing informed by<sup>24,26–28</sup> |
| $S$       | Viral shedding rate in arbitrary units that are proportional to viral copies/m³ | $10^{1.2}$ 4 days pre- or 6-7 days post-symptom onset, or asymptomatic within 2-4 days of test | |
| $S$       | Viral shedding rate in arbitrary units that are proportional to viral copies/m³ | $10^{1.4}$ 3 days pre- or 5 days post-symptom onset, or asymptomatic within 1 day of test | |
| $S$       | Viral shedding rate in arbitrary units that are proportional to viral copies/m³ | $10^{1.6}$ 4 days post-symptom onset | |
| $S$       | Viral shedding rate in arbitrary units that are proportional to viral copies/m³ | $10^{1.8}$ 2 days pre- or 3 days post-symptom onset | |
| $S$       | Viral shedding rate in arbitrary units that are proportional to viral copies/m³ | $10^2$ 1 day pre- to 2 days post-symptom onset | |
| $T_{\text{low}}, T_{\text{med}}, T_{\text{high}}$ | Duration of exposure | Low, medium and high Bluetooth attenuation durations are multiplied by weights available on request, together with attenuation thresholds | This study’s methods applied to unpublished data |
| $\lambda$ | Probability that one viral particle establishes infection × conversion from arbitrary units | $3.78 \times 10^{-6}$ | Calibrated from secondary attack rate of household contacts = 30%.<sup>29</sup> |
| Fraction of asymptomatic infections | Higher values lead to longer quarantine | 15% for a population, but depends on age |<sup>30,31</sup> |
| Incubation period | Days until symptom onset | Probabilities for {0,1,2,...} days = {0.4E-05,0.011842,0.008541,0.181965,0.207344,0.174979,0.123761,0.081488,0.051057,0.031469,0.018734,0.011235,0.006786,0.00422,0.002518,0.001626,0.000978,0.000592,0.000364,0.000231,0.00014,0.000093,0.00062,0.00004,0.000025,0.000017,0.000011,0.000008} |<sup>32</sup> |
| Asymptomatic shedding duration | We assume that asymptomatic shedding begins 3 days before what would have been the day of symptom onset if symptomatic, or else immediately upon infection, whichever occurs later | Cumulative probabilities for days {5,6,7,...}={0.05405405,0.09459459,0.12162162,0.14864864,0.18198198,0.21621621,0.25675675,0.31081081,0.37837838,0.43243243,0.48648648,0.54054054,0.55405405,0.62162162,0.66216162,0.70270270,0.75675676,0.78738738,0.82432432,0.85135135,0.86846846,0.86846846,0.89189189,0.90540540,0.94594594,0.959459,0.959459,0.97927927,0.986486,0.986486,0.986486,0.986486,0.986486,0.986486,0.986486} |<sup>33</sup> |
| Tolerated threshold for probability of current or future infectiousness | Set by public health agency, cognizant of limitations in current calibration of $\lambda$ | Benchmark of 0.14% | This study |
Table 2. Parameter values used by us to calibrate parameter values in Table 1

| Parameter | Description | Distribution or Point Value | References |
|-----------|-------------|-----------------------------|------------|
| $X$       | Exhalation rate | Normal(16.3, 4.15), left-truncated at zero | 34         |
| $A$       | Cross-sectional area of the mouth. Used to calculate the breath velocity, $U$ from $X$ | Uniform(23, 59) (cm$^2$) | 35         |
| $I_y$     | “Lateral intensity” of plume deviation | Uniform(0.08, 0.25) | 36         |
| $I_z$     | “Vertical intensity” of plume deviation | Uniform(0.03, 0.07) |           |
| $I$       | Inhalation rate | Normal(16.3, 4.15), left-truncated at zero | 34         |
| $\rho$    | Distance      | Sampled from attenuation-distance dataset to inform weights. Uniform(.5, 1) when calibrating $\lambda$ | Unpublished preliminary dataset – more data needed |
| $\varphi$ | Angle between the z-axis and the xy-plane | Used while informing weights. If $\rho \leq 1$ m, $\varphi = \pi/2$, if $\rho > 1$ m, $\varphi$ randomly sampled from Triangular(min= $\pi/4$, mode= $\pi/2$, max= $3\pi/4$) | 1 m. cutoff for face-to-face interaction informed by 37 |
| $\theta$  | Angle between x and y axes | Used while informing weights. If $\rho \leq 1$ m, $\theta = 0$, if $\rho > 1$ m, $\theta$ randomly sampled from Uniform(0, $2\pi$) | 1 m. cutoff for face-to-face interaction informed by 37 |

While informed by the two sources of data above, we focus the most on data in which virus was successfully cultured from patient samples, as a clear indication of infectivity. Arons et al. 26 took prospective samples throughout a nursing home, and were able to culture virus from six days before symptom onset until nine days after symptom onset, with little quantitative trend in shedding rate conditional on a positive test. In hospitalized patients, Wölfel et al. 28 were unable to isolate live virus from cultures more than 8 days post symptom onset, despite PCR evidence of high shedding. In one case report, live virus has been isolated 18 days after symptom onset, but this seems to be an outlier.38 Bullard et al. 25 quantified both TCID50 and PCR for 7 days post symptom onset, and saw an approximately 10-fold decline in infectious dose. We note that culture methods may not be sensitive enough to capture low concentrations.26 We nevertheless use this TCID50 data as motivation in assuming a 10-fold dynamic range in shedding rates as a function of day relative to symptom onset. More studies measuring infectivity in a quantitative manner are needed. Encouragingly, agreement of culture data to epidemiological modeling improved after corrections to the latter were made.24

A final source of information comes from detailed Taiwanese contact tracing14, who found a 1.0% symptomatic attack rate (95% CI 0.6-1.6%) for those exposed within five days of symptom onset, and 0% (95% CI 0–0.4%) for those exposed after. Risk from exclusively pre-symptomatic exposure was 0.7% (95% CI 0.2%-2.4%).

We use 6 of the 8 Transmission Risk Levels in the GAEN API to capture this range, evenly spaced on a log scale between 10 and 100 in arbitrary units, reserving the use of levels 7 and 8 for individuals for testing purposes and any future functionality. These levels could also be
manipulated for testing purposes, e.g. to help learn, if individuals voluntarily enter exposure
details into a manual contact tracing database, how transmission risk varies in the real world,
rather than just in TCID50 studies, as a function of a symptomatic status and time. We note that
Transmission Risk Levels have been deprecated in the announced GAEN v1.5, and replaced
with only two possible levels of infectiousness. While the functionality of v1.1 should be
preserved, we note that usage of Transmission Risk Levels would need to be standardized
across different apps in order to ensure interoperability. In the description below, we outline not
just our use of v1.1, but also the use we would make of six levels of infectiousness if they were
to again be made available in a future API version. The assignments we use in this framework
can of course be improved as more data become available. Our call for more than two levels of
infectiousness comes from the fact that a systematic 10-fold difference in TCID50 has been
observed, and that such a large difference seems to warrant more levels.

Based on a holistic reading of the four sources of evidence described above, we assign the
maximum level of 6 from one day pre-symptom onset to two days post-symptom onset. Five or
six days before symptom onset we assign level 1, four days before we assign level 2, three
days before level 3, and two days before level 5. Three days after symptom onset we assign
level 5, four days after level 4, five days after level 3, 6-7 days after level 2, and 8-11 days after
level 1.

For users who report a positive test but no symptoms, there is likely a reason they were tested,
and so we ask for the most likely day of exposure, if known. If provided, we assume that
shedding did not begin until two days after exposure, at the earliest. We also ask for the date of
sampling for the positive test (which can be reported by the healthcare provider rather than the
app user) and assume peak shedding at around this time. Subject to the constraint from day of
exposure, we assign transmission risk level 3 to dates within with one day of the test, and level
2 to dates between 2 and 4 days of the test, although as discussed below, one study reports
substantially longer shedding than these 9 days.33 There is some evidence that viral shedding is
lower in asymptomatic vs. symptomatic cases,30,39 while another study indicates the shedding
magnitudes may be similar.40 Note that we assume that those with no symptoms at the time
they receive a positive test result are asymptomatic rather than pre-symptomatic – should test
turnaround times be sufficiently fast, it would be useful for users to be able to report symptom
onset after the fact and trigger a change to previously reported Transmission Risk Levels, and
we recommend that this functionality be added, together with restoring a greater number of
Transmission Risk Levels, in future versions of the GAEN framework.

3.3 Estimation of Exposure Concentrations

We model a Gaussian plume41 originating from the emitter’s face at (0,0,0). The x axis
represents the direction that the transmitter is facing and breathing toward with breath velocity \( U \)
(m/s). Diffusion causes spread away from y=0 or z=0. The viral concentration is then

\[
C(x, y, z) = \frac{Q}{U} \frac{1}{2\pi \sigma_y \sigma_z} e^{-\frac{y^2}{2\sigma_y^2}} e^{-\frac{z^2}{2\sigma_z^2}}
\]

\( Q = SX \)
where \( Q \) is virus emitted per second and is equal to the product of shedding rate, \( S \), (in arbitrary units proportional to copies/m\(^3\)) and an exhalation rate, \( X \), (taken from measured inhalation rates in m\(^3\)/s), yielding arbitrary units proportional to copies per second being generated (eq 1.1). We sample our exhalation rates from a normal distribution of inhalation rates where mean and standard deviation, 16.3 and 4.15 m\(^3\)/day, respectively, were informed by the 16-21 year old range from Table 6-1 in the Exposure Factors Handbook (2011). To avoid negative exhalation rates, this distribution was left-truncated at zero. The velocity of breath (m/s) was determined by dividing the exhalation rate (m\(^3\)/s) by the cross-sectional area of an open mouth (m\(^2\)), which is the area over which air is assumed to be exhaled at the plume source. The cross-sectional area was informed by a Uniform distribution with minimum and maximum cross-sectional areas measured for an open mouth with a “large bite” configuration, ranging from 23 to 59 cm\(^2\).35

To capture the shape of the plume, we use:

\[
\sigma_y = I_y x \\
\sigma_z = I_z x
\]  

Assuming moderately stable conditions, \( I_y \) and \( I_z \) were randomly sampled from uniform distributions with minimums and maximums of 0.08-0.25 and 0.03-0.07, respectively.36

We note that inhalation and exhalation rates are both likely important to risk. For example, one infected dance instructor spread COVID-19 to 7/26 other instructors at a four hour workshop, representing a similar risk as for household contacts, despite the presumption that most were at >2 m. distance for most of this time. Limited air circulation or increased respiratory rates are important factors that cannot be captured in the GAEN approach, but the four-hour duration of the workshop could be, combined with considerable uncertainty in the relationship between Bluetooth attenuation and distance, in order to correctly capture the high risk of such a scenario.

3.4 Inhalation Dose per Interaction

An inhaled dose of viral particles due to person-to-person interactions was estimated based on the duration of the interaction (minutes) \( (T) \), the concentration of virus in the air at this x-y-z coordinate during the interaction (arbitrary units of viral particles/m\(^3\)) \( C(x, y, z) \), and inhalation rates (m\(^3\)/minute) \( (I) \),

\[
D = T \cdot I \cdot C(x, y, z)
\]

Inhalation rates were randomly sampled from the same distribution as exhalation rates but allowing for a different value per iteration. As with exhalation rates, we left-truncated the distribution to avoid negative inhalation rates and therefore negative doses.

3.5 Attenuation bins and their relative risks

Using the model described above, we sample a distance compatible with the attenuation bin in question, and then sample angle, inhalation and exhalation rate, and cross-section of an open
mouth to obtain a mean dose/time for that attenuation bin. Our code holds shedding rate and exposure duration constant at 50 arbitrary units/m² and 30 minutes, in order to isolate the effect of distance on differences in dose between attenuation buckets.

Preliminary alpha testing data on GAEN v.1.1 (unpublished dataset) provided us with a set of distances between phones, combined with measured attenuations, across a range of phone models, and possible interference from nearby objects. Note that improvements made in the forthcoming GAEN v1.5 are expected to improve our ability to estimate distance as a function of attenuation. While useful, we note that new experimental data would be required for recalibration. Note that our method is not based on mapping thresholds in distance to thresholds in Bluetooth attenuation, but instead on resampling from the probability distribution of distance as a function of attenuation.

From this preliminary dataset, we sample the distance \( \rho \) in meters from the emitter by sampling from the observed probability of distance given a certain Bluetooth attenuation. For distances \( \leq 1 \) meter, we assume face to face interactions, consistent with distances measured for “interpersonal” interactions \(^{37}\). Therefore, for interactions in this close range (\( \leq 1 \)m), we assumed two people interacting are directly in front of each other along the x-axis \((\varphi = \pi /2, \theta=0)\). For interactions beyond the close range (>1m), we sample \( \theta \) from a uniform 360 degrees \((\text{min}=0, \text{max}=2\pi)\), and the angle between the z axis and the xy-plane, \( \varphi \), was randomly sampled from a triangular distribution \((\text{min}=\pi/4, \text{mode}=\pi/2, \text{max}=3\pi/4)\). We then convert from spherical units to \((x,y,z)\) to apply Eq. 1. We assumed that scenarios where the person exposed was behind the emitter \((x<0)\) resulted in a zero dose.

To select the threshold values \((a, b)\) demarcating 3 attenuation bins, we optimized the differences in mean dose between two randomly sampled attenuation measurements. Specifically, we maximized the value of

\[
d(a, b) = \sqrt{2p_Ap_B(A-B)^2 + 2p_Bp_C(B-C)^2 + 2p_Ap_C(C-A)^2}
\]

where \(A, B\) and \(C\) are the average doses \(D\) from Eq. 4, averaged across Monte Carlo sampling described in the section above, corresponding to bins \((0, a)\), \((a, b)\), and \((b, +)\), and \(p_A, p_B, \) and \(p_C\) are the probabilities that an attenuation will fall within that bin.

We used preliminary experimental data, for the distribution of pairs of distance and attenuation, we found an optimal partition pair of attenuation thresholds, with \(~10\)-fold difference in weights. Note that this is of the same order as the \(10\)-fold difference in Transmission Risk Values.

Variation in duration among real exposures is larger, and will be able to be recorded in GAEN v1.5.

This procedure for setting weights will need to be repeated as more data is collected and/or any changes are made in how the GAEN API calculates Bluetooth attenuation. Future data could include both controlled settings to measure the distance-attenuation relationship and hence values of \(A, B, \) and \(C\), combined with more natural settings to inform the \(p_A, p_B, \) and \(p_C\) values likely to be seen in real use.

3.6 Dose-response curve

We use an exponential dose response curve, which is derived from the assumption that each host is susceptible and that each virus has an independent probability of survival and
subsequent initialization of infection, so that “organisms among replicated doses” follow a Poisson distribution.\textsuperscript{17} In our case, this probability $k$, multiplied by a constant $C$ to convert from arbitrary units to number of viruses, sets the parameter $\lambda = kC$ in the equation

\[ P(\text{infection}) = 1 - \exp(-\lambda D), \] (5)

where dose $D$ comes from a shedding rate multiplied by a weighted sum of time spent within 3 attenuation ranges. An exponential dose-response curve is superior to the approximate beta-Poisson for some viruses, according to evaluations by the Center for Advancing Microbial Risk Assessment (CAMRA) through their QMRA wiki: http://qmrawiki.org/content/recommended-best-fit-parameters. These viruses include adenovirus, enterovirus, poliovirus, and SARS-CoV-1.

Our weighted sum of durations and our $S$ estimates are both in arbitrary units. We therefore fit $\lambda$ to obtain infection probabilities that are compatible with household spread, where infection risk is relatively well documented, albeit still quite uncertain. Asymptomatic infection and low test sensitivity can both deflate estimated infection risks, while indirect chains of infection via a third household member can inflate them. A meta-analysis by Curmei et al.\textsuperscript{29} attempted to correct for these complications, and estimated a secondary attack rate of household contacts of 30%. We assume exposure is equivalent to 8 hours with the maximum shedding rate in the lowest attenuation. We found that $\lambda = 3.78 \times 10^{-6}$ yields infection probability of 0.30 for this scenario.

Note that the best way to calibrate $\lambda$ would be after the app is piloted or rolled out, with manual contact tracers compiling exposure characteristics and relating them to the rate of subsequent infection. Our calibration is necessarily highly approximate but should not affect the rank order of risks.

3.7 Adjusted probability of infectiousness as a function of time and tests since exposure

So far, we have estimated the probability of infection from an exposure. To calculate the probability of infection on a subsequent day, conditional on no symptoms until that day, we apply a discount factor based both on time elapsed without symptoms and also any negative test results. We multiply the probability of infection from an exposure with this discount factor to determine the remaining risk of infectiousness from a given exposure.

Traditional quarantine guidelines are binary (either 14 days from date of last exposure, or no quarantine required). However, the risk of onward transmission declines as a function of time elapsed since exposure, because the probability of infection is a conditional probability, and each day without symptoms provides more information to make current or future infectiousness less likely. A consistent approach to risk, combined with a desire to impose quarantine days in the most efficient manner possible to combat disease spread, suggests that individuals should quarantine for longer following a higher-risk exposure (Figure 2A vs 2B).
Figure 2. Applying a consistent risk tolerance causes quarantine duration to be a function both of initial risk and of the tolerated degree of risk. Initial risk in A) is from 15 minutes of close contact with an individual around the time of symptom onset, that in B) is with someone at the margins of the infectious period who is shedding at a 10-fold lower rate. The lowest risk threshold shown with grey shading is that implied by a 14 day quarantine duration. We assume 15% of infections are asymptomatic and that no testing is performed. Day 0 is included in the total quarantine times, i.e. a 14 day quarantine means that the individual is released on Day 14.

To calculate residual risk of infection as a function of initial risk plus time since exposure, we use the probability distribution of incubation periods from Lauer et al.32, available at https://iddynamics.jhsph.edu/apps/shiny/activemonitr/. Note that it is possible that incubation periods are even more dispersed than reported here43; this could be coded to lengthen quarantine recommendations. To calculate risk of current or future infectiousness, we assume a fraction of symptomatic vs. asymptomatic cases and take an average of the discount factors applying in each case. Across a population, 15% of infections are estimated to be asymptomatic.30,31 Younger users are more likely to be asymptomatic44, so the fraction of asymptomatic cases could be personalized on the basis of user age if that information is collected on a voluntary basis. For the symptomatic cases, we discount according to the probability of subsequently developing symptoms, given that symptoms have not appeared yet.

For the asymptomatic cases, we combine the incubation periods from Lauer et al.32 with the distribution of shedding durations from Long et al.33, including both symptomatic and asymptomatic cases in the latter. While Long et al. report slightly longer durations for asymptomatic shedding, three other studies45–47, for which we were unable to obtain the data, report the opposite. We assume that shedding begins 3 days before what would have been the day of symptom onset if symptomatic, or else immediately upon infection, whichever occurs later. Using this assumption, we calculate the probability distribution of the day that shedding ends, given both the distribution of incubation periods and the distribution of shedding durations. Long shedding periods ensure less discounting for the asymptomatic fraction (Figure 3A) that
can be mitigated by testing (Figure 3B, described in Section below). Note that strictly speaking, our “quarantine” recommendations are, through their treatment of the possibility of undiagnosed asymptomatic infection, a combination of quarantine and isolation.

Figure 3. The fraction of infected individuals who are asymptomatic and the availability of testing both strongly affect quarantine lengths. A.) Quarantine following 15 minutes of close contact with an index case at time of peak shedding must be longer to mitigate the risk of asymptomatic infection in the exposed individual. B) A negative test result, shown here as taking place on Day 4, can greatly shorten the long quarantine that would otherwise be required for a young individual for whom infection has a 50% chance of being asymptomatic. We apply Bayes theorem with 70% sensitivity and 100% specificity. Day 0 is included in the total quarantine times.

We currently consider the harm from the release of any infectious individual to be equivalent to that from the release of any other. Extensions of our approach could take into account greater harm from someone never quarantined and hence shedding for the full duration relative to someone released prematurely partway through asymptomatic or pre-symptomatic shedding, for whom a portion of the harm has already been mitigated. This would lead to steeper discounting.

3.8 Multiple Exposures and Total Risk

GAEN v1.1 will not record either a single long exposure or multiple exposures from a single individual beyond the 30 minutes cap for each of three attenuation bins, although this will change in v1.5. However, it will record exposures happening on different days (considered to change at midnight UTC) as independent exposures. To calculate total risk, we combine the probabilities $p_i$ of each exposure $i$, each discounted as described in the section above, as $1 - \prod_i (1 - p_i)$. We communicate total risk, and determine the appropriateness of quarantine, based on this combined probability.
Incorporation of negative test results can help exclude asymptomatic infection and hence allow for earlier release. From Bayes Theorem, and taking the false positive rate as negligible, a negative test result changes the probability of infection from $p$ to $Ep/(1-(1-E)p)$, where $E$ is the false negative rate. This could be taken as 0.3 \cite{48,49} or made dependent on the timing of the test relative to exposure, \cite{50} which would require distinct application between multiple exposures in its application.

Figures 2 and 3 illustrate scenarios of a single exposure. When there are multiple exposures, quarantine durations are determined with respect to total risk. The risk threshold for initiation and completion of quarantine are the same. In other words, risk is treated in an internally consistent fashion to achieve the maximum possible benefit from a given number of recommended quarantine days across a population.

The degree to which a public health authority chooses to be conservative vs. to minimize quarantine can be set through the selection of the risk threshold, as illustrated in Figure 2. When the threshold is set well below the probability that a randomly chosen member of the population is currently infected, it should be recognized that individuals agreeing to download and comply with the recommendations of the app are implicitly agreeing to adhere to higher standards than those implied by the current absence of a general stay-at-home order. At the time of writing (July 15), this rate is ~3.9% in Arizona.\cite{15} Such a high risk threshold is not currently practical in GAEN v1.1 due to the restriction on recording long duration exposures, which prevents discrimination among high risks, but will become possible in v1.5. We note that our formula for calibrating absolute risk is imperfectly calibrated, but better calibration is not likely to change this fact.

3.9 Recommending a day for testing

Kucirka et al.\cite{50} report a false negative rate as a function of the timing of a PCR test relative to symptom onset. They assume a fixed incubation period of 5 days, and use this both as a filter on their data, and to express their results in terms of time since exposure. We reran their code for different incubation periods, and calculated false negative rates in terms of time since exposure as a weighted average across different incubation periods as estimated by Lauer et al.\cite{32} and reported in Table 1. Before use as $E$ in Bayes Theorem above, they should be adjusted in a form of survivorship analysis; if testing is conditional on no symptoms to date, then the ratio of pre-symptomatic : asymptomatic individuals in the reference group will depend on time since exposure.

Approximating all as asymptomatic, we can use these false negative rates to recommend an optimal day for testing. For example, we could choose the days on which the probability of obtaining positive test results is highest. We calculate this probability as the sensitivity on that day × the conditional probability of infection on that day given no symptoms to date. Given exposures on multiple days, the sum of this product can be computed to choose a date for testing. Alternative criteria for optimization could also be devised, e.g. explicitly prioritizing highly exposed individuals whose calculated quarantine in the absence of a test would exceed 14 days.

4.0 Results

4.1 Range of scenarios that app can capture
To set the risk threshold used by our scheme to recommend quarantine, we consider the current advice for 14-day quarantine following 15 minutes of exposure in contact close enough to be logged as low attenuation. The risk of such an exposure depends on the degree of shedding, which is a function of the timing of exposure, e.g. relative to the onset of symptoms of the index case if symptomatic. An index case shedding at the peak rate has a 1.11% infection risk, which falls to a 0.14% probability of current or future infectiousness after 14 days of quarantine during which no symptoms appear. Note that this initial infection risk is broadly compatible with the attack rate reported in Taiwan (1.0%, 95% CI: 0.6-1.6%) for those interacting with index cases in the first 5 days of symptom onset, which is similar to the 0.88% (51/5,785) attack rate reported in South Korea.51

Based on this scenario, we use 0.14% as a benchmark threshold for the risk of current or future infectiousness, or as a default setting for public health authorities who seek to approximate the risk tolerance implied by current recommendations. Note that current advice treats the larger risk of longer exposure the same, making a 0.14% threshold more conservative because it is calculated to generate a 14-day quarantine for a minimal duration of exposure. However, this is at least partly offset by our assuming maximal shedding in calculating this benchmark example. In other words, while this threshold approximates the risk tolerance of current advice, the details of who is recommended for quarantine and for how long will be different in our quantification of total risk than it would be if we were to combine independent binary thresholds for infectious period of index case, duration of exposure, and distance to produce a quarantine duration of uniform length. This leads to more consistent treatment of risk to yield the greatest benefit in terms of transmission prevented per day of quarantine recommended.

Another benefit to using the quantitative risk framework described here is that the threshold can easily be adjusted by public health authorities to respond to local conditions. This could mean raising the threshold to in order to prevent excessive quarantine recommendations that might discourage both app uptake and quarantine compliance, or it could mean lowering it in populations that have achieved local containment and wish to be highly conservative against the threat of reintroduction.

A single exposure currently saturates at a maximum set by GAEN v1.1 of 30 minutes in each of the three attenuation bins, likely representing a high-risk interaction of significantly longer than 90 minutes. The formulae described above assign an infection probability of 3.59% given maximum Transmission Risk Level, results in an estimated 26-day quarantine/isolation in the absence of testing for the risk of current or future infectiousness to fall below 0.14%. A similarly maximal interaction, i.e. with 30 minutes in each attenuation bin, but with an index case at the minimum Transmission Risk level, corresponding to exposure timing that is not risk-free but falls just outside the window currently used by manual contact tracers, yields an infection probability of 0.36%, requiring 7 days of quarantine. Variation in quarantine length is to be expected – if total risk is scored consistently, some quarantines will be longer and others shorter, in order for residual infection probability, conditional on time elapsed without symptoms, to fall below a threshold set by the public health authority as acceptable.

The calculations above assume that 15% of infections are asymptomatic. If we assume that 50% infections are asymptomatic, e.g. in a young age group, even a 15-minute contact registered as low attenuation and with peak shedding in the index case would require a 26 day quarantine/isolation to meet a 0.14% threshold (Figure 3). Note that the degree to which the risk of asymptomatic infection lengthens quarantine/isolation depends on our assumption about the distribution of shedding durations. We used those from Long et al. because it was the only
paper for which the raw data was available. More data on this point is needed, including the need to make available data from studies that have already been done45–47. More data is also needed to confirm whether late shedding is of non-viable virus, or if late shedding is merely at low rates that fall below the sensitivity of cell culture assays to detect viable virus. We currently assume the latter.

If exactly the same prolonged, high-risk interaction were all recorded in the low attenuation bin, only 30 minutes would be recorded. In this case the app would calculate infection risks of 2.21% and 0.22%, and quarantine durations of 21 days and 5 days for the maximum and minimum Transmission Risk Levels, respectively. This illustrates how the 30-minute cap on exposure durations can lead to inconsistent quarantine recommendations by amplifying chance variation in how Bluetooth attenuations are recorded. We acknowledge that extended durations are less privacy-preserving, because they increase the ability of exposed individuals to guess the source of their exposure. However, we feel that other solutions to this problem might exist, such as concealing all exposure details such as date and exposure duration within an app, and revealing only the total risk. At some point, the privacy considerations need to be weighed against the interests of better controlling disease spread with the most efficient requests for quarantine.

Note that the 15-minute close contact exposure with an index case at time of peak shedding, discussed above as our reference case, yields infection probabilities of 1.11% only if it is all successfully recorded in the low attenuation range. If the contact were logged in the medium attenuation bin instead, e.g. because the phone was in a bag, it would instead yield an infection probability of 0.61%, resulting in 9 days instead of 14 days quarantine to fall below a 0.14% risk threshold. For high attenuation, risk is 0.11%, resulting in no quarantine. These differences reflect the degree to which Bluetooth can distinguish distance under the current GAEN API. Improvements to GAEN and/or more data on the relationships between risk, distance, and attenuation might change our assessment of this degree.

The default calibration with a 0.14% risk threshold sets the threshold for some amount of quarantine at around 15 minutes of contact, sometimes more and sometimes less depending on the assessed level of viral shedding and on stochastic variation in how Bluetooth attenuation is recorded. The noisy relationship between attenuation and distance means that quarantine recommendations will include exposures at significantly greater than 2 m distance. However, these exposures are not risk-free either, in particular if taking place in an indoor environment, especially in cases with heavy breathing, such as exercise environments42 or choir rehearsals,52 where aerosols may mix throughout the room and also deposit on surfaces.

When the risk threshold is set high, e.g. to modestly below the current prevalence of infection in Arizona, it becomes difficult to get significant quarantine following single exposures, whose maximum risk is 3.59%. Relaxing the 30-minute cap on durations is necessary in order to get resolution among higher risks. Unless the cap on duration is removed, few single exposures will approach, let alone exceed, the overall probability of current infection in Arizona.

Note that when the infection risk of the average person in the population is high, we believe that stay home orders or population-level shutdowns are essential to reduce transmission, meaning that individual quarantines from the app would be replaced by a blanket quarantine order for all but essential workers. Under these circumstances, a GAEN app might still have utility for
essential workers. However, a GAEN app could be an inferior but still useful option should the political will for population-level shutdowns not exist.

4.2 Messaging on quarantine durations

The need for consistent guidance to the public is an important consideration for implementing tailored risk scoring and modified quarantine recommendations. If for the sake of a consistency, a public health authority is not willing to authorize variable quarantine recommendations, as is currently the case in Arizona, but only 0 or 14 day quarantines from time of the last individually significant exposure, then the threshold for going into quarantine at all would need to become more strict in order to maintain the same overall risk among the population under quarantine. In other words, retaining the same average probability of current or future infectiousness among the quarantined population would require some exposed individuals to no longer go into quarantine at all, in addition to others lengthening their quarantine out to 14 days. With a binary 0 or 14 day quarantine, the amount by which disease transmission is prevented per day of quarantine will be lower.

To avoid mixed messaging regarding quarantine durations, one option is to suppress all details about individual exposures from the user’s view, including their date. This has the additional advantage of decreasing the risk that users will be able to guess who exposed them, further preserving privacy. The app could then communicate only total risk, either as a binary recommendation for which days to quarantine, or also as a quantitative score in order to “gameify” the process of quarantine and give users positive feedback for each day they succeed in remaining at home until it falls to a lower level. Further research is needed to assess the most effective messaging strategies.

Conflicting messages can still arise if manual contact tracers trace an individual who also received an exposure notification. In this case, it is likely that the two recommend different end dates for quarantine. This is to be expected from our procedure for recommending variable quarantine durations, but we note that even if the app were to issue 14 day quarantine recommendations only, it could still arise because the individual has been exposed more than once, on different days, and the manual contact tracer is following up an index case who may not have used the app. Until there is reliable data on app performance, we recommend that the manual contact tracer’s protocol should override whatever the app says. Should the app turn out to perform well, an alternative procedure might eventually be to go with whichever protocol recommends the longer quarantine. An intermediate possibility is for the manual contact tracer to ask for exposure notification details, to determine whether it may be a different exposure to the one being manually traced.

5.0 Discussion

Here we quantify relative risk using Monte Carlo simulations and roughly calibrate it to absolute risk based on limited information from the infection probability of household contacts. Errors in calibration are likely but will generally not affect the rank order of risks. For example, adjusting the risk threshold of 0.14% for quarantine will have similar effects to adjusting the value of $\lambda$. Knowledge of absolute vs. relative risk does have some effect once some saturation in risk begins to occur, little of which will occur unless much longer durations are recorded.
The ability to adjust the risk threshold provides communities with flexibility in deciding how readily quarantine should be recommended and for how long. Communities that have achieved containment might choose to set a stricter threshold, mitigating the harms of longer quarantine through testing individuals once or twice, lowering their risk following each negative test. Communities with high prevalence might raise the threshold if it seems likely that the number of quarantine recommendations being issued by the app will cause it to fall out of use, reasoning that a harm reduction strategy for app use is better than using quarantine guidelines that the population is unwilling or unable to comply with. The Covid-Watch app is currently programmed either to use a threshold on infection risk to determine 14-day quarantine onset, or on risk of current and future infectiousness to determine both quarantine and duration. Either threshold can be set by public health authorities flexibly in the light of external factors such as level of community transmission, jurisdictional comfort with uncertainty related to exposure notification applications, and current public health science and recommendations.

Overall, we capture a 10-fold difference in risk due to the dependence of shedding rates on the timing of exposure. Variation in Bluetooth attenuation also provides about a 10-fold ability to distinguish risk, based on our simulations and limited preliminary distance-attenuation data. Apps can measure duration far more accurately than distance, but the GAEN v1.1 duration cap of 30 minutes, combined with the use of 5 minute windows, mean that only ~6-fold differences in risk are captured in this way, or up to ~18-fold when longer exposures absorb the stochastic variation in attenuation, or much longer in GAEN v1.5 where there is no cap on duration. With 15% cases being asymptomatic and no testing, the risk of current or future infectiousness falls ~9-fold over the first 14 days of quarantine. Under GAEN v1.5, risk will sometimes differ more between two individuals entering quarantine than when comparing the same individual before vs. after a 14-day quarantine. For this reason, our scheme could recommend quarantines significantly longer than 14 days. To avoid the hardship this would inflict, such individuals could be given priority access to testing, with negative test results acting to shorten (but not eliminate) their quarantine. Public health authorities could also opt to truncate quarantine at the current 14 days, i.e. to set a risk threshold only with respect to initial infection risk, and not with respect to the conditional probability of current or future infectiousness. This is the approach currently scheduled for pilot in Arizona.

We caution that our derived relationship between Bluetooth attenuation and infection risk is extremely approximate and model-dependent, as are our settings of Transmission Risk Levels. Both need to be calibrated with real world data on app users who report their app-recorded exposures to manual contact tracing efforts, who then track which users go on to test positive, and who are therefore able to mine the data to quantify the quantitative relationship between exposure details (duration, attenuation, Transmission Risk Level) and probability of infection. Transfer of this data to manual contact tracers’ contact management databases is critical to improve the targeting of quarantine recommendations to those at highest risk of being infected, which will make most efficient use of each day of quarantine recommended in order to reduce transmission.

Short of this, more quantitative data on infectivity would be extremely valuable. Our determination of shedding duration relies heavily on the prospective sampling of all individuals in a skilled nursing facility, where many patients subsequently got sick. Daily samples during similar outbreaks could be used to quantify how shedding varies both among individuals and as a function of time relative to symptom onset. TCID50 data would be ideal, but even Ct values
can be valuable for this purpose. However, the fact that the settings we originally chose based on infectivity data turned out to agree with the subsequently published correction to an influential epidemiological approach \(^\text{24}\) is encouraging.

The complete approach described here no longer recommends quarantine until the probability of current or future infectiousness falls a fixed amount relative to initial probability (estimated here as \(-9\) fold less than initial) and independently of what that initial probability is, but instead quarantine until the absolute probability falls below a threshold. A potential benefit of shorter quarantines is that they might significantly reduce the harms imposed by quarantine,\(^\text{11}\) and increase compliance\(^\text{53}\) (although see McVernon et al\(^\text{54}\)). Quarantining for 14 days post-exposure may be exceptionally challenging for essential workers, individuals without sick leave, or those who would endure significant financial hardship due to lost wages.

However, in populations with low risk tolerance but without testing access, quarantines calculated by our scheme might be long, especially if age is taken into account, with younger individuals issued longer quarantine periods to account for their greater risk of asymptomatic infection. If using the discounting portion of our approach, risk values can be used to prioritize such individuals for testing to avoid quarantines of over 14 days.

As the conditional probability of current or future infectiousness (conditioned on the exposed individual being asymptomatic) fluctuates throughout their quarantine period, messaging can also change. E.g., during the initial high risk days, users might be offered concrete resources such as grocery delivery, or the option to quarantine in a specialized facility in order to protect other household members, before transitioning to self-quarantine once risks falls. Even with self-quarantine, an app might distinguish between the days on which staying home is the highest priority vs. merely desirable.

As programmed in Covid-Watch on the basis of the unpublished dataset mentioned above, each day without symptoms lowers the residual risk of current and future infectiousness. To communicate this to users, one option is for the app to display both current and projected risk of infectiousness on a simple scale of 1 to 10, so users can see how that risk will fall with each day of quarantine. This visualization might change perceptions. E.g., an individual who wants to comply with a 14 day quarantine, but does not feel able to, might rush out to get groceries before starting their quarantine in earnest, while shedding virus pre-symptomatically. Visualizing projected risk into the future would then give the message that if the exposed individual can only make do for one more day before leaving the home for essentials, that will help, because if they do not develop symptoms, their risk will be lower even after a single day longer. Risk communication in an app could focus on day to day coaxing of this form.

Note that with symptom onset sometimes as early as two days after exposure, and given the possibility of pre-symptomatic shedding, we currently ignore the possibility that shedding might not yet have begun. Current testing turnaround times are mostly long, making this reasonable. However, if same-day tests become more widely available, our approach could be extended to directly communicate the risk of current infectiousness, rather than as is currently the case, the risk of current or future infectiousness. A significantly lower risk of infectiousness will be present on the day of exposure and perhaps also the day after. Delays in going into public to prepare for a long quarantine could inadvertently lead to pushing individuals past the latent period before
they go into public; displaying a full projected timeline of the projected risk of infectiousness could avert this, at the risk of significantly more complex messaging than “stay home until Friday”.

Note that low dose exposures, e.g. to asymptomatic individuals, may result in longer incubation periods, suggesting that low initial risk scores should have longer rather than shorter quarantines. We ignore this by assuming that risk scores primarily capture uncertainty in the likelihood of infection with a minimal dose, and not variation in the infecting dose once above the minimal. To see how this assumption arises from our model, note that the exponential dose-response curve we use assumes that each virus has an independent probability of initiating infection. The number of viruses responsible for the initial infection follows a Poisson distribution. When the absolute probability of infection per contact is low, as is the case for Covid-19, most infections will be initiated by only a single virus. Even for the 30% infection rate of household contacts, the probability under a Poisson distribution that infection is initiated with two or more viruses is only 3.7%. Without significant variation in the number of initiating viruses per infected patient, we no longer expect incubation time to depend on dose. However, our dose-response curve is calculated for the mean dose, rather than integrated across the probability distribution of possible doses. If real-world calibration data were collected, we would have a better basis to estimate, in natural settings, the variation in dose given similar assessed risk, e.g. due to high variance in shedding among transmitting individuals. If variance is high enough, then initiation with multiple viruses might be common enough to matter for high infection probabilities. Our simplifying assumption might therefore require overly long quarantines following very high risk exposures, but unless the variance is extreme, it might not significantly distort estimated probabilities among the range of lower risk exposures. We also note that the long quarantines we recommend for high risk exposures are driven more by the right tail of the distribution of asymptomatic shedding durations than by the right tail of the distribution of incubation periods. This further reduces the scope for the incubation time effect to distort the quarantine recommendations.

Our framework can be used not only to guide recommendations for who should quarantine and for how long, but also to allocate associated resources including quarantine facilities, grocery delivery and other social support, and priority for access to scarce tests. Both manual contact tracing and digital exposure notification require rapid testing to be effective. Given limited tests, targeting those at highest risk of infection will do the most good in finding new positive cases who are early enough in the course of infection for these approaches to stem transmission the most.

**Code Availability:** Code and necessary data are accessible under a Creative Commons license at [https://github.com/awilson12/risk_scoring](https://github.com/awilson12/risk_scoring)

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