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## Estimating the unseen emergence of COVID-19 in the US

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## 22 **Abstract**

23           As SARS-CoV-2 emerged as a global threat in early 2020, China enacted rapid and strict  
24 lock-down orders to prevent introductions and suppress transmission. In contrast, the United  
25 States federal government did not enact national orders. State and local authorities were left to  
26 make rapid decisions based on limited case data and scientific information to protect their  
27 communities. To support local decision making in early 2020, we developed a model for  
28 estimating the probability of an *unseen* COVID-19 epidemic in each US county based on the  
29 number of confirmed cases. We found that counties with only a single reported case by April  
30 13th had a 50% chance that SARS-CoV-2 was already spreading widely. By that date, 85% of  
31 US counties covering 96% of the population had reported at least one case. Given the low rates  
32 of testing and reporting early in the pandemic, taking action upon the detection of just one or a  
33 few cases may be prudent.

34

## 35 **Author Summary**

36           By March 28, 2020, only 3 months after the first US case of COVID-19 was detected,  
37 COVID-19 emerged in all 50 US states. Officials were forced to weigh the economic and  
38 societal costs of strict social distancing measures against the future risks of COVID-19  
39 hospitalizations and mortality in their communities. To support local decision makers throughout  
40 the US, we developed a simple model to determine the chance that COVID-19 was spreading  
41 unseen based on scant reported case counts. In mid-April, 85% of US counties containing 96%  
42 of the population had reported at least one confirmed case. Our model predicted that each of  
43 those counties thus faced at least a 50% chance that the virus was already spreading widely.

44 Aggressive pandemic mitigation measures, even before a threat is fully apparent, are particularly  
45 critical when testing resources are limited.

46

## 47 **Introduction**

48 The pandemic caused by the 2019 novel coronavirus (COVID-19) has claimed over  
49 242,000 American lives as of early November 2020 and may kill tens of thousands more by the  
50 end of the year [1-3]. Early in the pandemic, when confirmed case counts were still relatively  
51 low across the US, the federal government left decision making largely to state and local public  
52 authorities. Amidst great uncertainty, they faced the unprecedented challenge of balancing the  
53 threat of a mostly unseen but deadly virus against the economic and societal costs of shelter-in-  
54 place and travel restrictions. At the time, most SARS-CoV-2 (the virus responsible for COVID-  
55 19) cases were not reported due to the high proportion of mild and asymptomatic infections,  
56 limited laboratory testing capacity and strict requirements for receiving tests (e.g. travel or  
57 contact with someone from Wuhan, China) [4,5]. The CDC estimated that only one in ten  
58 COVID-19 infections were reported during the early phase of the pandemic [6].

59 As the first cases of COVID-19 were reported, decision makers urgently needed to  
60 determine whether these cases reflected sporadic clusters stemming from recent introductions or  
61 sustained community transmission that might evolve into a large epidemic. In the southern US,  
62 the 2016 expansion of Zika Virus (ZIKV) across the Americas posed a similar challenge. Cryptic  
63 transmission meant that by the time a few cases were reported, a large epidemic could already be  
64 underway [7]. Here, we describe a stochastic susceptible-exposed-infected-recovered  
65 compartmental model framework for estimating the magnitude of an epidemic threat from scarce  
66 case data. The approach was originally developed to support situational awareness for ZIKV then

67 adapted for COVID-19. We apply it to estimating the risk of unseen COVID-19 waves in  
68 counties across the US during the emergence phase of the pandemic in 2020.

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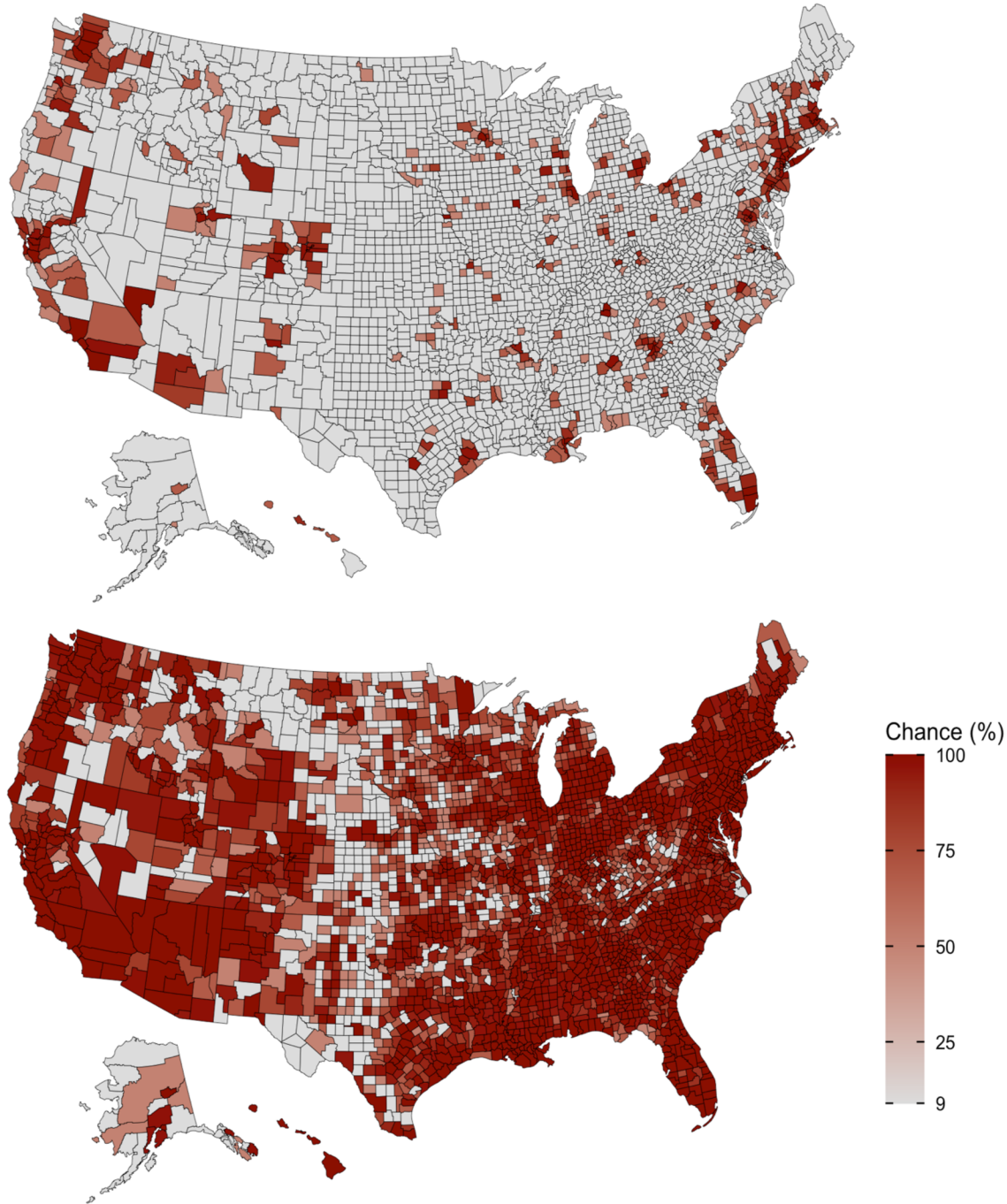
## 70 **Results**

71 We modeled the stochastic emergence of COVID-19 accounting for potential  
72 superspreading events, asymptomatic infections, and epidemiological characteristics. We  
73 assumed all US counties had roughly similar transmission rates. The chance that a county had  
74 emerging COVID-19 waves ranged from 9% for zero detected cases to 100% for 25 or more (Fig  
75 1). By March 16, 2020, counties cumulatively reported between 0 and 489 cases totaling 4,009  
76 nationally. Epidemic risk exceeded 50% in roughly 15% of the 3,142 counties covering 63% of  
77 the US population. By April 13, 2020, total reported cases in the US climbed to 467,158.  
78 Consequently, we estimated that over 85% of US counties comprising 96% of the national  
79 population had at least a 50% chance of having an epidemic already underway (Fig 1).

80 Based on COVID-19 case detection rates [6] for the week of April 13, 2020, we  
81 estimated that sustained community transmission was probable as soon as even one case was  
82 confirmed (Fig 2). At a moderate transmission rate (i.e.  $R_e=1.5$ ), the first case in a county signals  
83 a 50% chance that an epidemic was underway. For a high transmission rate (i.e.  $R_e=3.0$ ), as may  
84 be expected before COVID-19 lockdowns, the estimated risk increased to 83%. The projected  
85 risks are generally higher for both larger transmission rates and lowercase detection rates. For  
86 example, when  $R_e$  is 1.5, the expected epidemic risk associated with a single case is 50% and  
87 increases to 63% when the case detection rate drops from one in ten (10%) to one in twenty  
88 (5%). For outbreaks that eventually spread widely, the expected time between the first COVID-  
89 19 case report and the epidemic reaching 1,000 cumulative infections was 7.5 (95% CI 3.9-16.3)

90 weeks. The expected time between the tenth reported case and 1,000 cumulative infections  
91 shrank by 41% to 4.4 (95% CI 2.1-11.4) weeks (Fig 3).

92 As a retrospective validation of our model, we compared our estimates to reported case  
93 counts. We cannot know, with certainty, if and when epidemics began spreading in most US  
94 counties. As a proxy, we assess whether case counts increased by at least five in the week  
95 following our estimate on March 16 (Fig 4, middle line). We find that our estimates for the  
96 probability of an ongoing epidemic (*epidemic risk*) are highly consistent with the fraction of  
97 counties that exhibited jumps in reported cases. The cumulative number of reported cases in a  
98 county by March 16 was a significant predictor of whether the number of new reported cases in  
99 the following week (March 16-23) was at least one, five, or ten cases (logistic regression,  
100  $p < 0.001$ ). A one unit increase in cumulative reported cases increased the odds of a county  
101 detecting at least one, five, or ten new cases by March 23 by 7.92 (95% CI 5.98-10.80), 4.90  
102 (95% CI 4.14-5.99), and 3.16 (95% CI 2.80-3.63), respectively.



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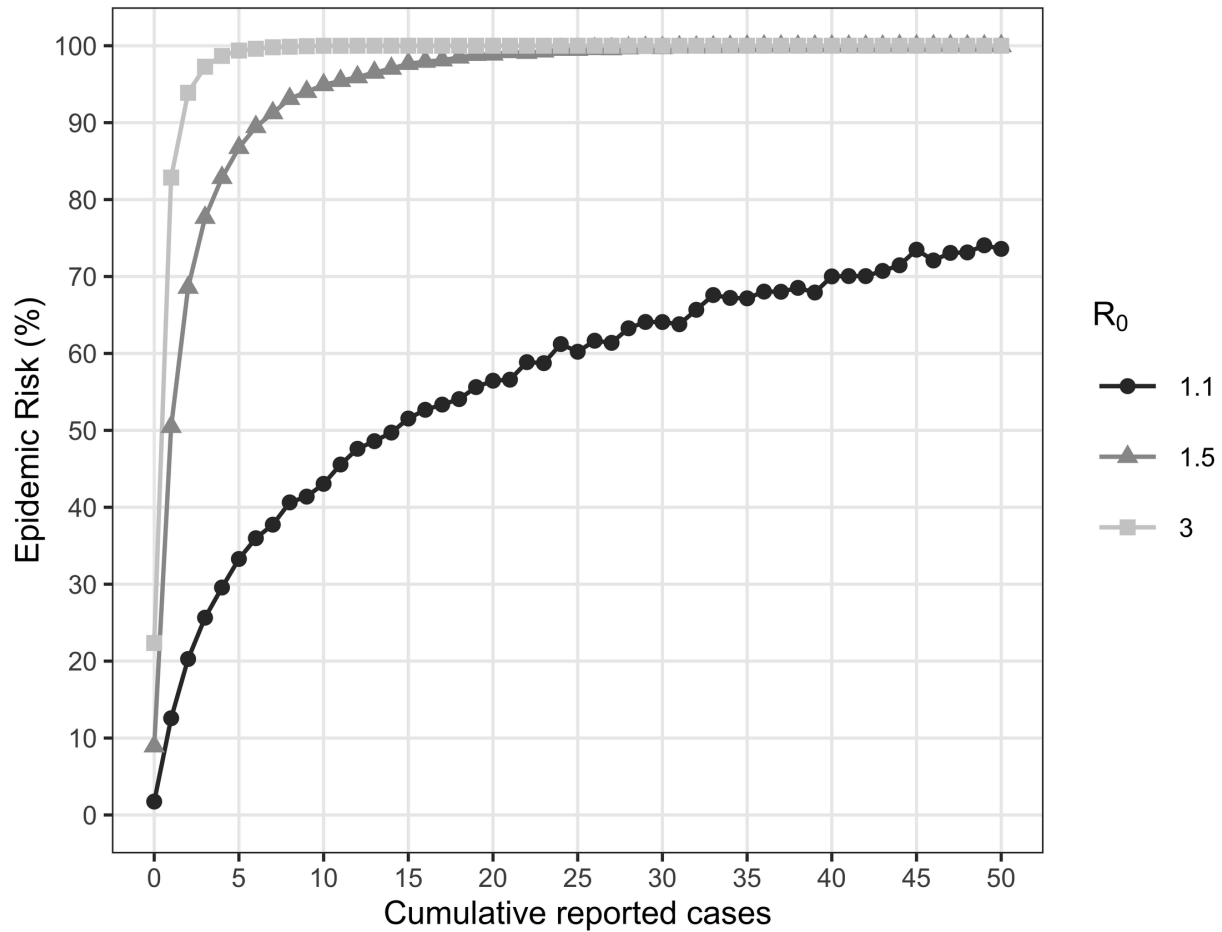
104 **Fig 1. Risk of ongoing COVID-19 epidemics in the 3,142 US counties as of March 16 (top)**

105 **and April 13, 2020 (bottom).** The chance of an unseen epidemic (*epidemic risk*) in a county

106 reporting only a single reported case is 50%; for a county reporting zero cases, the chance is 9%.

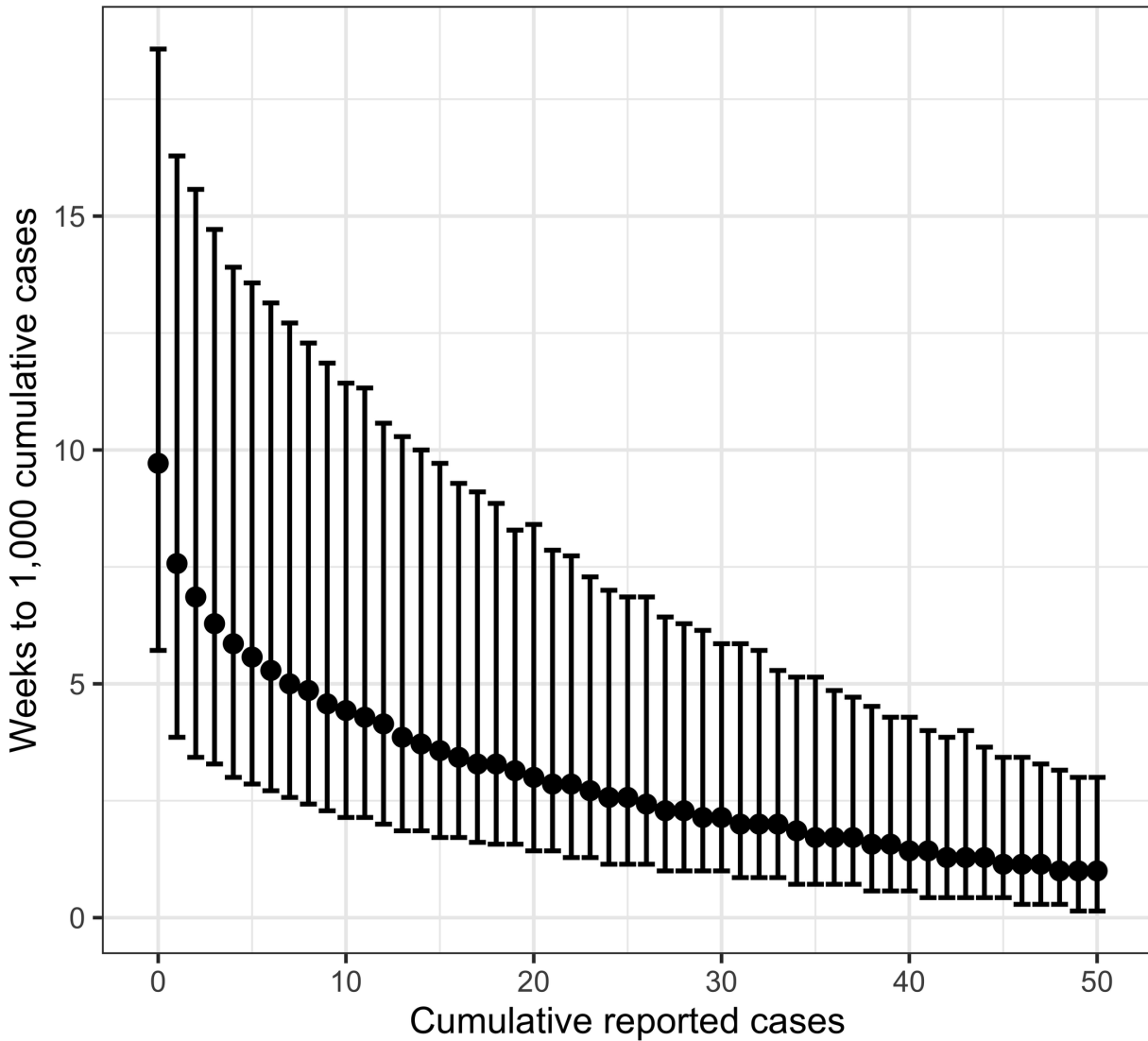
107 The model used in both maps assumes  $R_e=1.5$ , a 10% case detection rate, and a generation time

108 of six days.



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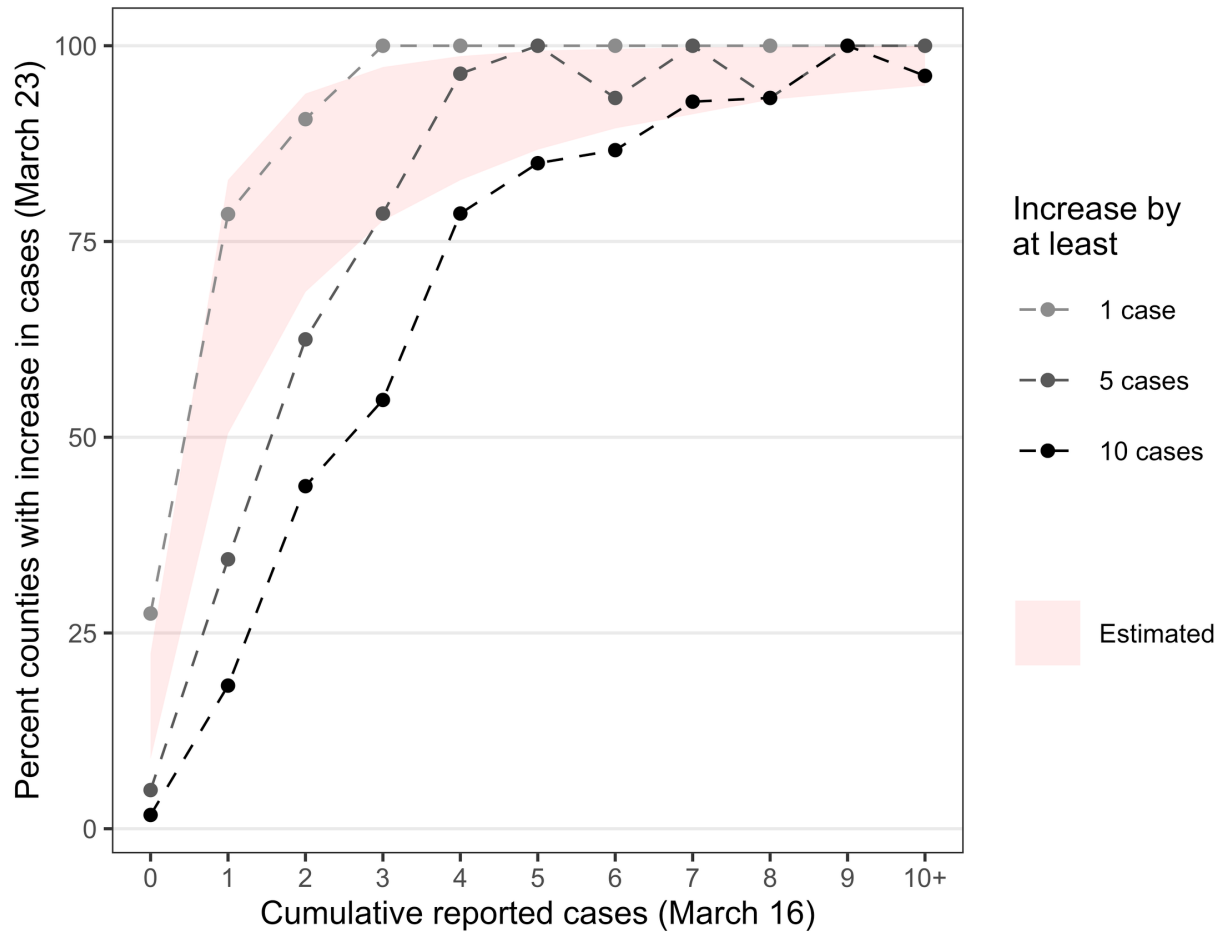
110 **Fig 2. Sensitivity analysis with respect to the effective reproduction number ( $R_e$ ).** For a  
111 given number of reported cases, the estimated risk of an epidemic increased with  $R_e$ . By the time  
112 a single case is reported, there is a 13%, 50% or 83% chance of an ongoing epidemic for  $R_e$  of  
113 1.1, 1.5 or 3.0, respectively.



114

115 **Fig 3. Expected time until the local epidemic exceeds 1,000 cumulative cases.** For a given  
116 number of cumulative *reported* cases (x-axis), we assume an epidemic is underway then estimate  
117 the median and 95% CI (error bars) number of weeks until the cumulative *total* cases exceed  
118 1,000. When the first case is reported, we would expect cumulative cases to surpass 1,000 in 7.5  
119 (95% CI 3.9-16.3) weeks; when the 10th case is reported, the expected lead time shrinks to 4.4  
120 (95% CI 2.1-11.4) weeks. The estimates are based on 100,000 stochastic simulations assuming  
121  $R_e=1.5$ , a 10% case detection rate, and generation time of six days.





122

123 **Fig 4. Proportion of all US counties in which COVID-19 case counts increased from March**

124 **16 to 23.** The light, medium and dark gray lines correspond to increases of at least one, five, or

125 ten new cases within one week, respectively. The red ribbon indicates the model estimates for

126 the probability that an epidemic is underway, given the cumulative reported cases indicated on

127 the x-axis. The bottom and top of the ribbon correspond to scenarios in which  $R_e=1.5$  and  $R_e=3.0$ ,

128 respectively. These estimates are calculated based on 100,000 simulations for each reproduction

129 number, assuming a 10% case detection rate and a generation time of six days. The odds of a

130 county detecting at least five new cases increased by 4.90 (95% CI 4.14-5.99) for every one unit

131 increase in cases on March 16. For example, a county with one case on March 16 was roughly

132 five times more likely to have at least six cases a week later than a county with no reported cases.

## 133 **Discussion**

134           The timing and rate of COVID-19 emergence varied widely across the US. The earliest  
135 of the 3,142 US counties to report a case was Snohomish, Washington on January 21, 2020. By  
136 the first of March, April and May, 1%, 70% and 90% of all counties had reported at least one  
137 case, respectively. We estimate that, by the time a county reported its first case, it had at least a  
138 50% chance of harboring an unseen but growing epidemic. As of April 13, 2020, the risk  
139 exceeded 90% in 54% of counties containing 91% of the US population. The New York Times  
140 published real-time projections of our model in a national risk map on April 3, 2020, which  
141 spread awareness of the growing COVID-19 threat to the nation [8].

142           Proactive responses to COVID-19 have been estimated to shorten the duration of costly  
143 measures [9,10], whereas delays have likely cost lives [11]. If the goal of COVID-19  
144 interventions is to fully contain an emerging outbreak as quickly as possible, our study suggests  
145 that the first reported case should trigger action. The risk of an ongoing epidemic may already  
146 exceed 50% and delaying until ten cases have been reported, for example, may substantially  
147 reduce the window for corrective action and amassing adequate healthcare and other mitigation  
148 resources.

149           Our analyses make several key assumptions. Case detection rates may vary  
150 geographically and change through time depending on testing availability and regulations. Our  
151 assumption of 10% is based on a CDC seroprevalence study, which reported rates ranging from  
152 4% to 16% across ten sites [6]. We modeled superspreading events based on estimates for  
153 SARS-CoV in Singapore in 2003 [12], which are consistent with more recent reports for SARS-  
154 CoV-2 [13–15]. Our estimates do not account for repeated importations given the stay at home  
155 orders and travel restrictions at the time. Multiple introductions would reduce our estimated

156 levels of epidemic risk since detected cases could reflect independent clusters rather than  
157 continuous chains of transmission. Finally, our estimates depend on the effective reproduction  
158 number of the pandemic which can vary spatiotemporally depending on local policies, testing  
159 efforts, behavior, and population density [16,17]. Our estimates for mid-April, when much of the  
160 US was under shelter-in-place orders, assume a relatively low  $R_e$  of 1.5. Our retrospective  
161 validation using data from mid-March, when intervention efforts varied geographically,  
162 considers reproduction numbers ranging from 1.5 to 3.0.

163 This analysis, while simple, provided useful insight during a highly uncertain period of  
164 the COVID-19 pandemic and can be easily adapted to provide early situational awareness for  
165 future emerging infectious outbreaks. Our results suggest that proactive control measures may be  
166 prudent, even before the threat becomes apparent [18].

167

## 168 **Methods**

169 We obtained county-level estimates for confirmed and suspected COVID-19 cases from a  
170 data repository curated by the New York Times [19] and 2019 estimates of each county's  
171 population from the US Census Bureau [20]. We adapted the framework of another silent  
172 spreader—Zika Virus (ZIKV)—which threatened to emerge in southern US states in 2016 [7] to  
173 model COVID-19 in US counties. The discrete-time SEIR model assumes a branching process  
174 for early transmission in which the number of secondary infections per infected case is  
175 distributed according to a negative binomial distribution to capture occasional superspreading  
176 events, as estimated for SARS-CoV outbreaks in 2003 [12]. The exposure and infectious periods  
177 consist of “boxcars” to enforce the minimum number of days simulated individuals spent in each  
178 compartment. We account for imperfect detection and COVID-19 specific epidemiological

179 characteristics (details in Table 1). Our baseline scenario assumes the  $R_e$  of COVID-19 is 1.5,  
 180 accounting for ongoing social distancing measures across the US by mid-April, 2020 [21], and  
 181 10% detection of all cases. We do not explicitly model asymptomatic or pre-symptomatic  
 182 transmission and thus maintain a low detection probability for all infectious cases. To assess the  
 183 impact of these assumptions on our estimates, we conducted a sensitivity analysis that varied  $R_e$   
 184 (1.1 and 3.0) and detection rates (5%-40%).

185

186 **Table 1. Model parameters used for simulating COVID-19 outbreaks.**

Parameter	Description	Estimate	Source
$R_e$	Effective reproduction number: Average number of new cases from one infected individual in a susceptible and non-susceptible population	1.5 1.1, 3.0	[22] [17]
$T_G$	Generation time (days): Average length of time between consecutive exposures $T_G = \frac{e}{\nu} + \left(\frac{1}{2}\right)\frac{n}{\delta} = T_E + \left(\frac{1}{2}\right)T_I$	6	[23,24]
$T_E$	Latent period (days)	1.25	Fit to $T_G$
$T_I$	Infectious period (days)	9.5	[23]
$e$	Number of exposed compartments in boxcar implementation (min days of exposure)	1	Fit to $T_G$

$n$	Number of infectious compartments in boxcar implementation (min days of infectiousness)	7	[23]
$\nu$	Incubation rate: Daily probability of progressing from one exposed compartment to the next	0.80	Fit to $T_G$
$\delta$	Recovery rate: Daily probability of progressing from one infectious compartment to the next	0.73	Fit to $T_I$
$\eta$	Daily detecting rate: The daily probability of an infectious individual being detected, $\frac{0.1}{T_I}$	0.01	[25]
$k$	Total dispersion parameter of negative binomial distribution	0.16	[12]
	R code for number of new infectious individuals drawn daily:  $rbinom(n = 1, prob = \frac{k}{R_0 + k}, size = \frac{k}{T_I})$		

188           We ran 100,000 stochastic outbreak simulations per scenario beginning with a single  
189 undetected case and ending when cumulative infections reached 2,000 or the outbreak died out  
190 (whichever came first). Because we model transmission as a branching process, the susceptible  
191 population does not deplete as in other compartmental SEIR models. Following the methodology  
192 of [7], simulated outbreaks that reached 2,000 cumulative cases and had a minimum prevalence  
193 of 50 cases per day were classified as epidemics. We calculated the probability of an epidemic  
194 for a given number of detected cases,  $x$ , by looking at all outbreaks that had  $x$  reported cases and  
195 calculating the proportion of those outbreaks that progressed to epidemics. We then matched  
196 county case numbers with the detected case number to obtain epidemic probabilities for each US  
197 county based on their reported cumulative number of cases. We use our baseline scenario to  
198 compare US maps of epidemic risk from March 16 and April 13, although  $R_e$  closer to 3.0 may  
199 be appropriate for mid-March. For simulations that became epidemics, we also calculated the  
200 distribution of lags (in weeks) between the day the  $x$ th case was reported and the day the  
201 epidemic surpassed 1,000 cumulative cases. Confidence intervals were calculated with the  
202 *quantile* function in R version 3.6.1 [26].

203           To validate epidemic risk, we fit three logistic regressions to if US counties reported at  
204 least one, five, or ten new cases over the week of March 16 to 23, 2020 (y-axis) and how many  
205 cumulative cases there were on March 16 (x-axis). First, counties were grouped by the number of  
206 reported cases on March 16. Counties with ten or more cases were put into one group due to the  
207 low number of counties with more than ten cases on March 16. Second, March 23rd case counts  
208 were subtracted from those on March 16 and the difference was classified as an increase of at  
209 least one, five, or ten cases (three separate binary classifications). Finally, a logistic regression  
210 was fit to each classification to determine if the number of cases on March 16 was a significant

211 predictor of new cases one week later. This week in mid-March was before lockdowns took  
212 place in the US and saw only a moderate increase in daily tests nationally (from 20,000 to  
213 60,000) [27]. We compare case counts from Monday to Monday to avoid weekend reporting  
214 bias. To readily compare with epidemic risk estimates, we plot the percent of counties with an  
215 increase in new cases with our epidemic risk estimates from  $R_e=1.5$  to  $R_e=3.0$ .

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