Real-time Zika risk assessment in the United States

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Abstract

Background: The southern United States (US) may be vulnerable to outbreaks of Zika Virus (ZIKV), given the broad distribution of ZIKV vector species and periodic ZIKV introductions by travelers returning from affected regions. If autochthonous (locally-acquired) cases appear within the US, policymakers will seek early and accurate indicators of self-sustaining transmission to inform intervention efforts. However, given ZIKV's low reporting rates and the geographic variability in both importations and transmission potential, a small cluster of reported cases may reflect diverse scenarios, ranging from multiple self-limiting but independent introductions to a self-sustaining local epidemic.

Methods and Findings: We developed a stochastic model that captures variation and uncertainty in ZIKV case reporting, importations, and transmission, and applied it to assess county-level risk throughout the state of Texas. For each of the 254 counties, we estimated the future epidemic risk as a function of reported autochthonous cases and evaluated a national recommendation to trigger interventions immediately following the first two reported cases of locally-transmitted ZIKV. Our analysis suggests that the regions of greatest risk for sustained ZIKV transmission include 21 Texas counties along the Texas-Mexico border, in the Houston Metro Area, and throughout the I-35 Corridor from San Antonio to Waco. Variation in vector habitat suitability drives epidemic risk variation, and can be exacerbated by uncertainty in reporting rate. Upon detection of a second locally transmitted case, the threat of epidemic expansion will depend critically on local vulnerability. For high risk Texas counties, we estimate this likelihood to be 64%, assuming an August 2016 risk projection and a 20% reporting rate.

Conclusions: With reliable estimates of key epidemiological parameters, including reporting rates and vector abundance, this framework can help optimize the timing and spatial allocation of public health resources to fight ZIKV in the US.

53 **Introduction**

54 In February 2016, Zika virus (ZIKV) was declared a Public Health Emergency of International
55 Concern [1]. As of 25 July of 2016, the World Health Organization (WHO) confirmed mosquito-
56 transmitted cases in 65 countries and territories, with over 500,000 suspected and confirmed cases in the
57 Americas alone [2,3]. In the US, the potential range of one of the primary vectors for ZIKV, *Aedes*
58 *aegypti*, is thought to include at least 30 states [4]. Texas ranks among the most vulnerable states for
59 ZIKV transmission, given its suitable climate, international airports, and geographical proximity to
60 affected countries [4–9]. Of the 1,306 imported ZIKV cases in the US, 73 have occurred in Texas. While
61 these importations have yet to spark autochthonous (local) transmission, Texas has historically sustained
62 several small, autochthonous outbreaks (ranging from 4 - 25 confirmed cases) of another arbovirus
63 vectored by *Ae. Aegypti*—dengue (DENV) [10,11].

64 As peak mosquito season approaches in the US and more cases are introduced via international
65 travelers from the Americas, public health decision makers will face considerable uncertainty in gauging
66 the severity of the threat and in effectively initiating interventions, given the large fraction of undetected
67 ZIKV cases (asymptomatic and symptomatic) as well as the shifting economic balance between
68 intervention expenditure and disease burden [12–15]. Depending on the ZIKV symptomatic fraction,
69 reliability and rapidity of diagnostics, importation rate, and transmission rate, the detection of five
70 autochthonous cases in a single Texas county, for example, may indicate a small chain of cases from a
71 single importation, a self-limiting outbreak, or even a large, hidden epidemic underway (Fig 1). These
72 diverging possibilities have historical precedents. In French Polynesia, a handful of suspected ZIKV cases
73 were reported by October 2013; two months later an estimated 14,000-29,000 individuals had been
74 infected [12,13]. By contrast, Dominica had 18 confirmed cases in early 2016 without a subsequent
75 epidemic [14]. To address the uncertainty, the CDC recently issued conservative guidelines for state and
76 local agencies; they recommend initiation of public health responses following local reporting of *two* non-
77 familial autochthonous ZIKV cases [16].

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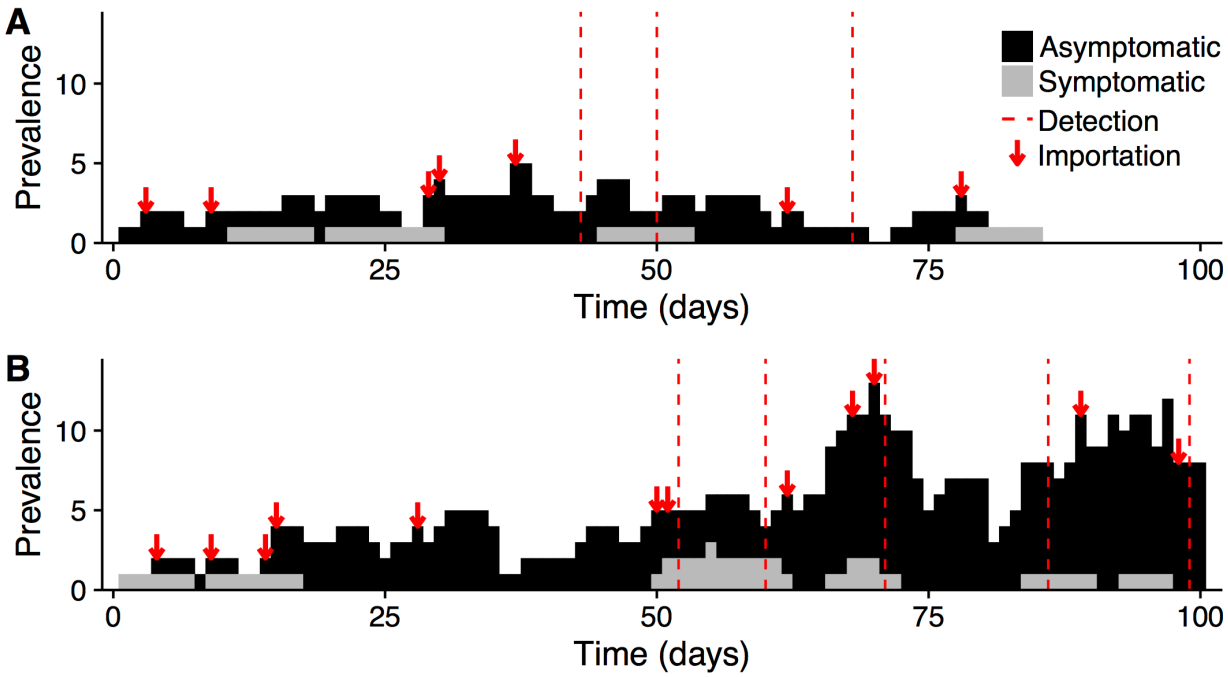

Fig 1. ZIKV emergence scenarios. A ZIKV infection could spark **(A)** a self-limiting outbreak or **(B)** a growing epidemic**.** Cases are partitioned into symptomatic (grey) and asymptomatic (black). Arrows indicate new ZIKV importations by infected travelers and vertical dashed lines indicate case reporting events. On the 75th day, these divergent scenarios are almost indistinguishable to public health surveillance, as exactly three cases have been detected in both. By the 100th day, the outbreak (A) has died out with 21 total infections while the epidemic (B) continues to grow with already 67 total infections. Each scenario is a single stochastic realization of the model with R_0=1.1, reporting rate of 10%, and introduction rate of 0.1 case/day.

Here, we develop a model to support real-time ZIKV risk assessment that accounts for uncertainty regarding ZIKV epidemiology, including importation rates, reporting rates, and local vector population density. This framework can be readily updated as our understanding of ZIKV evolves to provide situational awareness and actionable guidance for public health officials. By simulating ZIKV transmission using a stochastic branching process model [17] based on recent ZIKV data, we estimated ZIKV epidemic risk for each of the 254 counties in Texas, both initially and as a function of the cumulative number of reported autochthonous ZIKV cases. Further, we estimate county-level epidemic risks corresponding to the recommended two-case trigger and demonstrate the design of county-specific triggers indicative of imminent epidemic expansion. Our results suggest that counties along the Texas-

Mexico border, in the Houston Metro Area, and throughout the I-35 Corridor from San Antonio to Waco are at highest risk for sustained epidemics.

Methods

Risk-assessment methodological overview

In our study, we first estimated county-level ZIKV importation rates and sustained transmission risk (R_0) for Texas in August of 2016. For each county, we then used these estimates to simulate 10,000 stochastic ZIKV outbreaks. Finally, we analyzed the simulated outbreaks to determine spatiotemporal variation in ZIKV risk and estimate current and future epidemic risk from the number of reported autochthonous cases (Fig S1).

Estimating County Importation Rates

Our analysis assumes that any ZIKV outbreaks in Texas originate with infected travelers returning from regions with ZIKV activity. To estimate the ZIKV importation rate for specific counties, we (1) estimated the Texas statewide importation rate (expected number of imported cases per day), (2) estimated the probability that the next Texas import will arrive in each county, and (3) took the product of the state importation rate and each county importation probability.

1. During the first quarter of 2016, 27 travel-associated cases of ZIKV were reported in Texas, with 11 occurring in Houston's Harris County [18], yielding a baseline first quarter estimate of 0.3 imported cases per day throughout Texas. In 2014 and 2015, arbovirus introductions into Texas were threefold higher during the third quarter than the first quarter of each year, perhaps driven by seasonal increases in arbovirus activity in endemic regions and the approximately 40% increase from quarter 1 to quarter 3 in total number of international travelers to the US [19]. Taking this as a *baseline* (lower bound) scenario, we projected a corresponding increase in ZIKV importations to 0.9 cases per day (statewide) for the third quarter. We also considered an *elevated* importation scenario, in which the first quarter cases (27) in Texas represent only the

symptomatic (20%) imported cases, corresponding to a projected third quarter statewide importation rate of 4.5 cases per day.

2. We defined county-specific import risk as the probability that the next imported case in Texas will occur in that county. To build a predictive model for import risk, we fit a probabilistic model (maximum entropy) [20] of importation risk to 183 DENV, 38 CHIKV, and 31 ZIKV Texas importations reported at the county level from 2002 to 2016 and informative socioeconomic, environmental, and travel variables (Supplement §1.1). Given the geographic and biological overlap between ZIKV, DENV and Chikungunya (CHIKV), we used historical DENV and CHIKV importation data to supplement ZIKV importations in the importation risk model, while recognizing that future ZIKV importations may be fueled by large epidemic waves in neighboring regions and summer travel, and thus far exceed recent DENV and CHIKV importations [21]. Currently, DENV, CHIKV, and ZIKV importation patterns differ most noticeably along the Texas-Mexico border. Endemic DENV transmission and sporadic CHIKV outbreaks in Mexico historically have spilled over into neighboring Texas counties. In contrast, ZIKV is not yet as widespread in Mexico as it is in Central and South America, with only one reported ZIKV importation along the border to date (Val Verde County). We included DENV and CHIKV importation data in the model fitting so as to consider potential future importations pressure from Mexico, as ZIKV continues its northward expansion. To find informative predictors for ZIKV importation risk, we analyzed 72 socio-economic, environmental, and travel variables, and removed near duplicate variables and those that contributed least to model performance, based on out-of-sample cross validation [22,23], reducing the original set of 72 variables to 10 (Tables S3-S4).

Estimating County Transmission Risk

The risk of ZIKV emergence following an imported case will depend on the likelihood of mosquito-borne local transmission. For each Texas county, we used the Ross-Macdonald formulation to

148 estimate the ZIKV reproduction number (R_0), which is the average number of secondary infections caused
149 by the introduction of a single infectious individual into a fully susceptible population (Supplement §1.2)
150 [24]. To parameterize the model (Table S5), we used mosquito life history estimates from a combination
151 of DENV and ZIKV studies and estimated *Ae. aegypti* abundance for each county [5]. For parameters that
152 are sensitive to temperature (i.e., mosquito mortality and the extrinsic incubation period), we adjusted the
153 mosquito parameters using average reported Texas county temperatures for the month of August [25].
154
155 ZIKV Outbreak Simulation Model
156 To transmit ZIKV, a mosquito must bite an infected human, the mosquito must get infected with
157 the virus, and then the infected mosquito must bite a susceptible human. We assumed that mosquito-borne
158 transmission would be the main driver of epidemic dynamics, so we did not include sexual transmission
159 in our model. Rather than explicitly model the full transmission cycle, we aggregated the two-part cycle
160 of ZIKV transmission (mosquito-to-human and human-to-mosquito) into a single exposure period, and do
161 not explicitly model mosquitos. For the purposes of this study, we need only ensure that the model
162 produces a realistic human-to-human generation time of ZIKV transmission.
163 The resultant model thus follows a Susceptible-Exposed-Infectious-Recovered (SEIR)
164 transmission process stemming from a single ZIKV infection using a Markov branching process model
165 (Fig S2). The temporal evolution of the compartments is governed by daily probabilities of infected
166 individuals transitioning between S, E, I, and R states, and new ZIKV cases arising from importations or
167 autochthonous transmission (Table S6). We treat days as discrete generations, and the next disease state
168 progression depends solely on the current state and the transition probabilities. We assume that infectious
169 cases cause a Poisson distributed number of secondary cases per day (via human to mosquito to human
170 transmission), and infectious individuals are introduced daily according to a Poisson distributed number
171 of cases around the importation. Furthermore, *Infectious* cases are categorized into reported and
172 unreported cases according to a reporting rate. We assume that reporting rates approximately correspond
173 to the percentage (~20%) of symptomatic ZIKV infections [14] and occur at the same rate for imported

174 and locally acquired cases. Additionally we make the simplifying assumption that reported cases transmit
175 ZIKV at the same rate as unreported cases. We track imported and autochthonous cases separately, and
176 conduct risk analyses based on reported autochthonous cases only, under the assumption that public
177 health officials will have immediate and reliable travel histories for all reported cases [16].

178 To accurately model the timing of ZIKV outbreaks, we fit the ZIKV generation time to recent
179 estimates (Supplement §2.4) [26]. The generation time measures the average duration from initial
180 symptom onset to the subsequent exposure of a secondary case, and is estimated to range from 10 to 23
181 days for ZIKV [26]. In our model, the generation time corresponds to the exposure period followed by
182 half of the infectious period. First, we fit the infectious period in our model to human ZIKV estimates for
183 duration of viral shedding, which we assumed to be the length of the infectious period but may be an
184 underestimate of the total length. Specifically, we solved for transition rates of a Boxcar Model [27] that
185 produce an infectious period with mean duration of 9.88 days (Table S6) [28]. Then, we fit the exposure
186 period to achieve the empirical ZIKV generation time distribution [26], yielding a mean exposure period
187 of 10.4 days (95% CI 6-17) and a mean generation time of 15.3 days (95% CI 9.5-23.5). Given that the
188 exposure period includes human and mosquito incubation periods and mosquito biting rates, this range is
189 consistent with the estimated 5.9 day human ZIKV incubation period [28]. While there is much
190 uncertainty regarding ZIKV transmission, our model framework is flexible to extensions and updates as
191 we learn more about ZIKV epidemiology including reporting rates, transmission probabilities, clinical
192 features, and outside importation pressures.

193

194 Simulations

195 For each county risk scenario, defined by a specified importation rate, transmission rate, and
196 reporting rate, we ran 10,000 stochastic simulations. Each simulation began with a single imported
197 infectious case and terminated either when there were no individuals left in either the *Exposed* or
198 *Infectious* classes or the cumulative number of autochthonous infections reached 2,000. We classified
199 simulations as either epidemics or self-limiting outbreaks; epidemics are all simulations that fulfill two

criteria: reach 2,000 cumulative autochthonous infections and have a maximum daily prevalence exceeding 50 autochthonous cases (Figs S3).

Outbreak Analysis

Policymakers must often make decisions in the face of uncertainty, such as when and where to initiate ZIKV interventions. Our stochastic framework allows us to provide real-time county-level risk assessments as reported cases accumulate. For each county, we found the probability that an outbreak will progress into an epidemic (reach 2,000 cases with a maximum daily prevalence over 50), as a function of the number of reported cases. We call this *epidemic risk*. To solve for epidemic risk in a county following the xth reported autochthonous case, we first find all simulations (of 10,000 total) that experience at least x reported autochthonous cases, and then calculate the proportion of those that are ultimately classified as epidemics. For example, consider a county in which 1,000 of 10,000 simulated outbreaks reach at least two reported autochthonous cases; the remaining 9,000 simulations dissipate with only one or zero case reports. If only 50 of the 1,000 simulations ultimately fulfill the two epidemic criteria, then the estimated epidemic risk following two reported cases in that county would be 5%. This simple classification scheme performs quite well, only rarely misclassifying a string of small outbreaks as an epidemic, with the probability of such an error increasing with the importation rate. For example, epidemics should not occur when R_0=0.9. If the importation rate is high, however, overlapping series of moderate outbreaks may occasionally meet the two epidemic criteria. Even under the highest importation rate we considered (0.3 cases/day), only 1% of outbreaks were misclassified.

This method can be applied to evaluate universal triggers (like the recently recommended two-case trigger) or derive robust triggers based on local importation and transmission risks as well as the risk tolerance of public health agencies. For example, if a policymaker would like to initiate interventions as soon as the risk of an epidemic reaches 30%, we would simulate local ZIKV transmission and solve for the number of reported cases at which the probability of an epidemic first exceeds 30%. Generally, the recommended triggers decrease as the policymaker threshold for action decreases (for example,

226 policymakers would act sooner (fewer reported cases) for a 10% versus 30% threshold) and as the local
227 transmission potential increases (*e.g.* R_0 = 1.5 versus R_0 = 1.2). A policymaker wishing to trigger
228 interventions early, upon even a low probability of epidemic spread, has a low tolerance for failing to
229 intervene but may waste resources on unnecessary interventions; a policymaker willing to wait longer,
230 has a higher risk tolerance, but may implement interventions too late in the course of the outbreak.
231
232 *County Uncertainty Analysis*
233 We took two approaches to addressing uncertainty in the model parameters. First, we conducted a
234 sensitivity analysis to address the considerable uncertainty regarding several inputs into our estimation of
235 R_0, including mosquito biology, ZIKV epidemiology, and human-mosquito interactions (Supplement §4).
236 For most factors, the county estimates of R_0 simply scale linearly with changes in the factor. However,
237 county-specific human-mosquito contact rates can change relative county risks based on assumptions
238 regarding the socioeconomic effect on human-mosquito interactions (Fig S5-6), and county risk moves
239 southward as the summer heat subsides (Fig S7). Second, given the considerable uncertainty regarding
240 ZIKV epidemiology, we examined a scenario where the absolute values of both R_0 and importation rate
241 are unknown, but lie within plausible ranges for Texas. To do so, we randomly sampled 10,000
242 simulations from the high risk Texas county outbreaks (counties with R_0>1), creating an amalgamous
243 high risk county, and completed the outbreak analysis as we do with individual counties.
244
245 **Results**
246 To develop a ZIKV risk assessment framework for Texas counties, we first estimate county-level
247 ZIKV importation and transmission rates for August 2016. ZIKV importation risk within Texas is
248 predicted by variables reflecting urbanization, mobility patterns, and socioeconomic status (Table S3),
249 and is concentrated in metropolitan counties of Texas (Fig 2A). The two highest risk counties--Harris,
250 which includes Houston and has an estimated 27% chance of receiving the next imported Texas case, and
251 Travis, which includes Austin and has a 10% chance of the next importation--contain international

airports. Other high risk regions include Brazos County, the Dallas and San Antonio metropolitan areas, and several counties along the Texas-Mexico border.

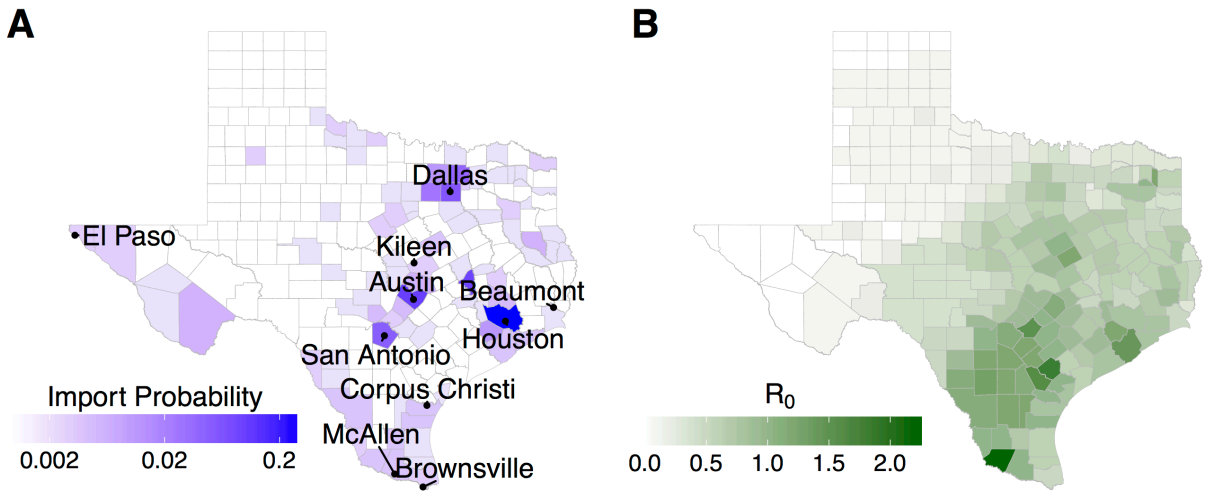

Fig 2. ZIKV importation and transmission risk estimates across Texas. (A) Color indicates the probability that the next ZIKV import will occur in a given county for each of the 254 Texas counties. Probability is colored on a log scale. The 10 most populous cities in Texas are labeled. Houston's Harris County has 2.7 times greater chance than Austin's Travis County of receiving the next imported case. **(B)** Estimated county-level R_0 for ZIKV (See Fig S5-11 for sensitivity analysis).

Our county-level estimates of autochthonous ZIKV transmission risk (Fig 2B) suggest that the majority of Texas counties (87%) have an estimated R_0 below one, and thus are unlikely to sustain epidemics. The Southeast region of Texas has the highest estimated transmission risk, driven primarily by high mosquito habitat suitability. These estimates are sensitive to uncertainty in several parameters (Fig S5-11), and can be updated as we learn more about ZIKV. While the average transmission risk may be higher or lower than our baseline assumption, and will certainly vary seasonally, the relative risks of regions and counties are robust (Fig S6-S10), and allow us to conduct plausible case studies and identify at risk areas for enhanced surveillance and preparedness efforts. Given the uncertainty underlying the

county R_0 estimates, we also aggregate the 21 highest estimates into a plausible distribution for a high risk Texas county, ranging from $R_0 = 1.0$ to $R_0 = 2.2$ with a median of 1.1.

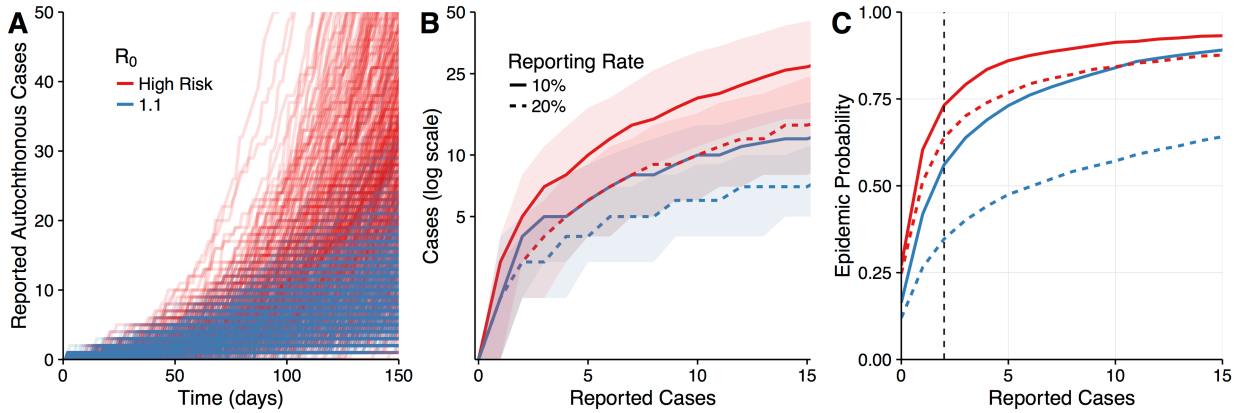

Fig 3. Real-time risk-assessment for ZIKV situational awareness and forecasting. (A) Simulated outbreaks, assuming an importation rate of 0.01 case per day, for a known (moderate risk) R_0 (blue) or an unknown high risk R_0 (red). Two thousand randomly sampled simulations are shown for each scenario. (B) Total number of (current) autochthonous cases as a function of the cumulative reported autochthonous cases, assuming an importation rate of 0.01 case per day, for a known R_0 (blue) or an unknown high-risk R_0 (red), and a relatively high (dashed) or low (solid) reporting rate. Ribbons indicate 50% quantiles. (C) The increasing probability of imminent epidemic expansion as reported autochthonous cases accumulate, compared across the high risk (red) and known moderate risk (blue) for a low (solid) and high (dashed) reporting rate. Suppose cases arise in a high risk county and a policymaker wishes to trigger a response as soon as two cases are reported (vertical line). With a 20% reporting rate there is a 64% probability of an ensuing epidemic.

Under a single set of epidemiological conditions, wide ranges of outbreaks are possible (Fig 3A). The relationship between what policymakers can observe (cumulative reported cases) and what they wish to know (current prevalence) can be obscured by such uncertainty, and will depend critically on both the transmission and reporting rates (Fig 3B). If key drivers, such as R_0, can be estimated with confidence, then the breadth of possibilities narrows, enabling more precise surveillance. For example, under a known moderate R_0 scenario and with a 20% reporting rate, ten cumulative reported cases corresponds to an expected prevalence of 6 cases with a 95% CI of 1-16; under an unknown but high R_0 scenario, the same

289 number of cases corresponds to an expected prevalence of 10 cases with a much wider 95% CI of 2-32
290 (Fig 3B).

291 We apply our model to characterize time-varying epidemic risk as cases accumulate in a given
292 county. Under both a known moderate risk and unknown high risk scenario, we track the probability of
293 epidemic expansion following each additional reported case (Fig 3C). Across the full range of reported
294 cases, the probability of epidemic spread is always higher in the high risk scenario, with the moderate risk
295 scenario showing more sensitivity to the reporting rate. These curves can support both real-time risk
296 assessment as cases accumulate and the identification of surveillance triggers indicating when risk
297 exceeds a specified threshold. For example, suppose a policymaker wanted to initiate an intervention
298 upon two reported cases and thought the reporting rate was 20%, this would correspond with a 64%
299 probability of an epidemic in the high risk county but only 35% in the known moderate risk county.
300 Alternatively suppose a policy maker wishes to initiate an intervention when the chance of an epidemic
301 exceeds 50%. In the high risk scenario, they should act immediately following the 1st reported case; in
302 the moderate risk scenario, the corresponding trigger ranges from two to seven reported cases, depending
303 on the reporting rate. As the policymaker's threshold (risk tolerance) increases, the recommended
304 surveillance triggers can be adjusted accordingly.

305 To evaluate a universal intervention trigger of two reported autochthonous cases, we estimate
306 both the probability of a trigger event (two such cases) in each county and the level of epidemic risk at the
307 moment a trigger event occurs (second case reported) in each county. Assuming a baseline importation
308 rate extrapolated from recent importations to August 2016 and a 20% reporting rate, only a minority of
309 counties are likely to experience a trigger event (Fig 4A). While 231 of the 254 counties (91%) have non-
310 zero probabilities of experiencing two reported autochthonous cases, only 63 counties have at least a 10%
311 chance of such an event, with the remaining 168 counties having a median probability of 0.017 (range
312 0.0004 to 0.089). Next, assuming that a second autochthonous case has indeed been reported, we find that
313 the underlying epidemic risk varies widely, with most counties having near zero epidemic probabilities
314 and a few counties far exceeding a 50% chance of epidemic expansion. For example, two reported

autochthonous cases in Starr County, along the Texas-Mexico border, correspond to a 99% chance of ongoing transmission. The greater San Antonio metropolitan region appears to be the highest risk metropolitan region with four of its eight counties having a higher than 25% probability of experiencing two reported autochthonous cases; in those four counties, the epidemic risk upon detection of a second case ranges from 19-90%. Houston metropolitan region is also a high risk region with its second (Fort Bend) and fourth (Brazoria) largest counties having a 39% and 45% chance of sustaining two reported autochthonous cases, respectively, with corresponding epidemic risks of 67% and 86% thereafter.

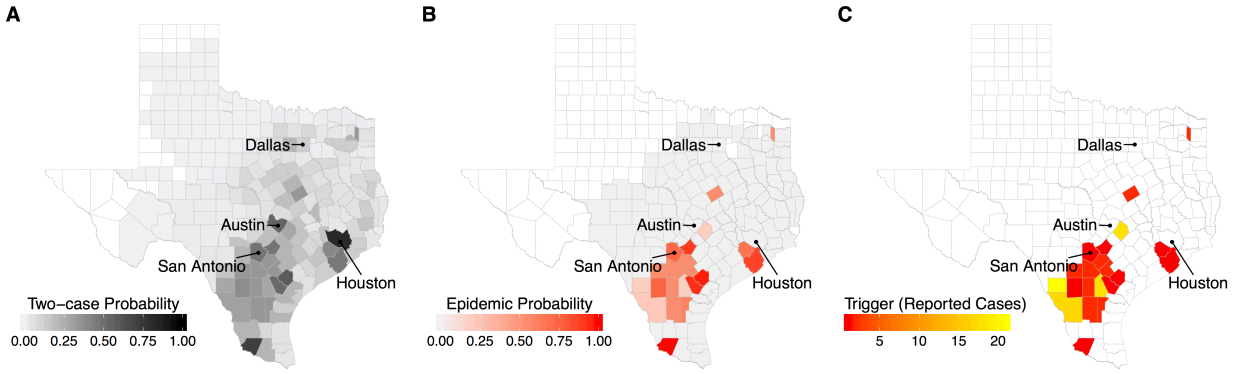

Fig 4. Texas county ZIKV risk assessment. (A) Probability of an outbreak with at least two reported autochthonous ZIKV cases. **(B)** The probability of epidemic expansion at the moment the second autochthonous ZIKV case is reported in a county. White counties never reach two reported cases across all 10,000 simulated outbreaks; light gray counties reach two cases, but never experience epidemics. **(C)** Recommended county-level surveillance triggers (number of reported autochthonous cases) indicating that the probability of epidemic expansion has exceeded 50%. White counties indicate that fewer than 1% of the 10,000 simulated outbreaks reached two reported cases. All three maps assume a 20% reporting rate and a baseline importation scenario for August 2016 (81 cases statewide per 90 days) projected from historical arbovirus data. (Figure S4 provides corresponding estimates under a worse case elevated importation scenario).

Given that a universal trigger may signal highly disparate levels of ZIKV risk, policymakers might seek to adapt their triggers to local conditions. Suppose a policymaker wishes to design trigger that indicate a 50% chance of an emerging epidemic (Fig 4C). Under the baseline importation and reporting rates, only 21 of the 254 counties in Texas are expected to reach a 50% epidemic probability, with

336 triggers ranging from one (Starr County) to 21 (Dimmit County) reported autochthonous cases, with a
337 median of two cases. The remaining counties have less than a 1% chance of experiencing sustained ZIKV
338 transmission. Under an elevated importation scenario, assuming that only one fifth of ZIKV importations
339 (the symptomatic proportion) have been observed, we find that the recommended triggers decrease by a
340 mean of 1.5 reported cases (Fig S4) and the size of Texas' population at risk for sustained ZIKV
341 transmission is expected to increase from ~14% to ~30%, largely driven by increased risk in the Houston
342 metropolitan area.
343
344 **Discussion**
345 US public health authorities are responding to ZIKV importations and preparing for the
346 possibility of ZIKV outbreaks in vulnerable regions this season and in future seasons. A key challenge is
347 knowing when and where to initiate interventions based on potentially sparse and biased ZIKV case
348 reports. Our simple model is designed to address this challenge by providing county-specific epidemic
349 risk estimates as a function of reported cases. We demonstrate its application across the 254 ecologically
350 and demographically diverse counties of Texas, a high risk state [6,7,9]. Based on county-level estimates
351 for ZIKV importation and transmission rates (Fig 2), we expect that most Texas counties are not at risk
352 for a sustained ZIKV epidemic (Fig 4). However, 30% of Texas' population may reside in vulnerable
353 regions, including the cities of Austin, San Antonio, and Waco along the I-35 corridor, Houston, and the
354 Rio Grande Valley. The higher the ZIKV importation rate in these locations, the higher the chance of an
355 epidemic (Fig S4). However, even in the most high risk regions of Texas, we expect far more limited
356 ZIKV transmission than observed in Central America, South America, and Puerto Rico, where R_0 has
357 been estimated to be as high as 11 [24,29,30]. Our analysis is consistent with recent introductions of
358 DENV and CHIKV into Texas that have failed to spark large epidemics.
359 Surveillance triggers--guidelines specifying situations that warrant intervention--are a key
360 component of many public health response plans. Given the urgency and uncertainty surrounding ZIKV,
361 *universal* recommendations can be both pragmatic and judicious. In choosing an appropriate trigger for an

362 environmentally and socioeconomically diverse region, policymakers must weigh the risks of acting
363 unnecessarily with those of responding too late. A risk averse policymaker will likely select a low trigger
364 (a small number of reported cases), ensuring early detection in the riskiest sites at the cost of false alarms
365 in low risk locations (Fig 4C). In that vein, the CDC recently issued conservative guidelines to state and
366 local public health agencies that suggest a two-case trigger for initiating interventions [16].

367 To assist Texas policymakers in interpreting this recommendation, we assessed the likelihood and
368 implication of a two-case trigger for each of Texas' 254 counties, under a scenario projected from recent
369 ZIKV data to August 2016. Across counties, there is enormous variation in both the chance of a trigger
370 and the magnitude of the public health threat if and when two cases are reported. If and when two
371 autochthonous ZIKV cases are reported, only 18 of Texas' 254 counties have over a 20% chance of
372 experiencing sustained transmission (under our baseline scenario); in most of the remaining 236 counties,
373 the threat is much lower.

374 Rather than implement a universal *trigger,* which may indicate different threats in different
375 locations, one could design local surveillance triggers that correspond to a universal *risk threshold*. Our
376 modeling framework can readily identify triggers (numbers of reported cases) for indicating any specified
377 epidemic event (e.g., prevalence reaching a threshold or imminent epidemic expansion) with any
378 specified risk tolerance (e.g., 10% or 50% chance of that the event has occurred), given local
379 epidemiological conditions. As a case study, we identify *epidemic expansion* triggers in each of Texas'
380 254 counties, each designed to indicate when the probability of an epidemic exceeds 50%. Across the 21
381 counties with non-negligible probabilities of an epidemic, the recommended triggers range from one to 21
382 reported autochthonous cases, highlighting Texas' spatial risk heterogeneity. These findings apply only to
383 the early, pre-epidemic phase of ZIKV in Texas, when travel from affected regions outside the contiguous
384 US is the primary importation source. If self-sustaining outbreaks emerge within Texas, there may be
385 county-to-county importations, particularly in high risk regions, that are not yet included in the model.

386 This simple framework offers a flexible means for bringing current data and expert knowledge to
387 assist critical public health decision making. The design of a trigger--both the event to be detected and the

388 probability threshold upon which to take action--requires extensive public health expertise and
389 deliberation. Our case studies were motivated by formal recommendations and informal discussions with
390 state and national public health agencies. They demonstrate our data-driven approach for relating
391 observed disease activity to underlying risk in the face of great uncertainty, and address the pros, cons and
392 complexity of developing universal versus regional action plans. However, they are not meant to critique
393 or validate any specific policies, and highlight the prudence of recent ZIKV planning efforts.

394 Importantly, our analyses rest on the recent and limited scientific investigations of ZIKV's
395 biology and epidemiology, and should be continually updated as our understanding matures. Specifically,
396 our county-level estimates of R_0 are sensitive to many underlying assumptions, particularly regarding
397 temperature-dependent and socioeconomic factors (Supplement §4). Although the risk of ZIKV
398 transmission may be much higher or lower than assumed in our baseline scenario, the relative
399 vulnerabilities of counties are fairly robust to our assumptions. Thus, counties with the highest estimated
400 risks should likely be prioritized for surveillance and interventions resources. Given the minimal
401 incursions of DENV and CHIKV into Texas, we suspect that, if anything, we may be underestimating the
402 socioeconomic and behavioral impediments to ZIKV transmission in the contiguous US, and thus
403 overestimating the transmission risk across Texas. While it is beyond the scope of the current paper,
404 these estimates may be further refined as more detailed arbovirus importation and outbreak data become
405 available.

406 The reporting rate dictates the relationship between observed cases and the underlying outbreak,
407 and its magnitude impacts the timeliness and precision of detection. If only a small fraction of cases are
408 reported, the first few reported cases may correspond to a wide range of underlying epidemiological
409 conditions, from isolated introductions to a growing epidemic. In contrast, if most cases are reported,
410 policymakers can wait longer (in terms of the number of reported cases) to trigger interventions and have
411 more confidence in their epidemiological assessments. ZIKV reporting rates are expected to remain quite
412 low, because an estimated 80% of infections are asymptomatic, and DENV reporting rates have
413 historically matched its asymptomatic proportion [14,31]. Obtaining a realistic estimate of the ZIKV

414 reporting rate is arguably as important as increasing the rate itself, with respect to reliable situational
415 awareness and forecasting. An estimated 8-22% of ZIKV infections were reported during the 2013-2014
416 outbreak in French Polynesia [30]; similarly, an estimated 10% have been reported during the ongoing
417 epidemic in Columbia [29]. While these provide a baseline estimate for the US, there are many factors
418 that could increase (or decrease) the reporting rate, such as ZIKV awareness among both the public and
419 health-care practitioners. Thus, rapid estimation of the reporting rate should be a high priority. While
420 some methods require extensive epidemiological data not typically available early in an outbreak [32], a
421 new method exploiting early outbreak viral sequence data was introduced during the recent West African
422 Ebola epidemic [33]. However, as of July 2016, there are no US ZIKV sequences available on GenBank
423 and few available from other regions.

424 Unlike other estimation methods, this framework is designed to support risk assessments both
425 prior to ZIKV outbreaks and, in real-time, upon the early detection of cases through the lens of potentially
426 sparse and biased surveillance data [34,35]. It can facilitate situational awareness, allowing analysts to
427 translate case counts into estimates of overall prevalence and the potential for future spread, albeit with
428 large error bars. It can also support the development of response plans, by forcing policymakers to be
429 explicit about risk tolerance, that is, the certainty needed before sounding an alarm, and quantifying the
430 consequences of premature or delayed interventions. For example, should ZIKV-related pregnancy
431 advisories be issued when there is only 5% chance of an impending epidemic? 10% chance? 80%? A
432 policymaker has to weigh the costs of false positives--resulting in unnecessary fear and/or intervention--
433 and false negatives--resulting in suboptimal disease control and prevention--complicated by the difficulty
434 inherent in distinguishing a false positive from a successful intervention. The more risk averse the
435 policymaker (with respect to false negatives), the earlier the trigger should be, which can be exacerbated
436 by low reporting rates, high importation rate, and inherent ZIKV transmission potential. In ZIKV prone
437 regions with low reporting rates, even risk tolerant policymakers should act quickly upon seeing initial
438 cases; in lower risk regions, longer waiting periods may be prudent.

This approach can be readily applied to other at risk states in the US. Given that Florida has experienced a higher importation of ZIKV cases than Texas (more than 270 as of the end of July 2016) and more locally acquired DENV cases since 2009 [36–38], the probability of sustained ZIKV transmission and public health threat following a second reported autochthonous cases may be higher in Florida than estimated for Texas.

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Code Availability

The R package, rtZIKVrisk, has been created to accompany the manuscript and can be found here: https://github.com/sjfox/rtZIKVrisk. The package provides functionality to simulate and analyze ZIKV outbreaks according to our framework, and recreate the figures presented in the manuscript.

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S1 Supporting Information. Supporting information for "Real-time Zika risk assessment in the United States."

S2 Supporting Data. Raw Texas county arbovirus importation data used for estimating county ZIKV importation risk. Data provided by Texas DSHS.

S3 Supporting Data. Raw county socioeconomic data used for estimating county ZIKV importation risk. Data accessed from: https://www.census.gov/programs-surveys/acs/data.html

S4 Supporting Data. Texas county ZIKV risk estimates used as inputs for the ZIKV simulation model. Outputs of the importation and transmission risk analysis.