

Projections of Zika spread in the Continental US

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Abstract

Introduction

We provide projections for the autochthonous (i.e., local) transmission of Zika virus (ZIKV) in the continental United States. Projections are based on the global model developed in Ref. [1] and are informed by data on autochthonous transmission in the continental USA. The model generates stochastic simulations of epidemic spread in the Americas. As such, the model is fully stochastic and generates an ensemble of possible epidemic evolution for data that are observable, such as newly generated cases, time of arrival of the infection, and number of traveling carriers if Zika. For each state in the continental USA, numerical simulations allow the estimation the probability of observing local transmission and the expected number of Zika infections. We find that the state of Florida has the highest risk for Zika transmission. The analysis provided in this note should be considered as preliminary and motivated by rapid assessment of the possible trajectories of the Zika epidemic in the continental US. The model contains unavoidable

assumptions and approximations based on the current lack of precise data on Zika. A thorough sensitivity analysis concerning the model calibration is ongoing.

1 Methods

The model technical details are available in Ref. [1]. Briefly, We use a data-driven global stochastic epidemic model to project past and future spread of the Zika virus (ZIKV) in the Americas. The model has high spatial and temporal resolution, and integrates real-world demographic, human mobility, socioeconomic, temperature, and vector density data. The model has been calibrated using data by the Pan-American Health Organization (PAHO) [2], and sampling of a large number of dates and initial introduction in Brazil, as detailed in Ref. [1]. The calibrated model provides stochastic realizations used to estimate the spatiotemporal pattern of ZIKV spread in the Americas through December 2016. The stochastic simulations monitor the epidemic profiles across the Americas at spatial resolutions ranging from individual countries to specific urban areas. Here, we considered the results concerning individual states in the continental US. For each state in the continental US, we have selected profiles by constraining the statistical analysis to epidemic trajectories with no more than 100 ZIKV infections by Aug. 1st, 2016 within the states. The analysis, thus, assumes that no local outbreaks have been overlooked in the past months or generated a large number of undetected cases. The model considers both *Ae. aegypti* and *Ae. albopictus* mosquitoes as possible transmitters of the Zika virus. In the continental US, the number of cases locally generated is extremely small and each realization is prone to large fluctuations. For this reason, we report only aggregate state level data. The analysis of specific urban areas or counties would require an order of magnitude more generation of stochastic realizations. Thus, we must consider a trade-off between computational costs and the timely generation of the numerical results. We are currently investigating possible technical solutions to overcome the computational limits imposed by the large scale of the simulations.

2 Results

Figure 1 shows the epidemic trajectories (green shaded area is the 95% CI) in the various states that are susceptible to locally generated ZIKV transmission. The distributions are skewed toward the low numbers as visible from the median profiles, and this indicates that most of the outbreak size distributions have large accumulation at zero cases. Florida is the only exception that shows a median profile definitely above zero until November/December 2016. In Table 1, we report

the projected median number of cases, and the 95% CI, by September 15th, 2016. We observe, that in general, with the exception of Florida all states have a median number of cases close to zero. The confidence interval in each state is relatively wide and is due to the stochastic nature of the small and self-limiting outbreaks. Epidemic trajectories are, thus, dominated by noise and stochastic events. In Figure 2, we report the expected number of births from pregnancies infected with ZIKV during the first trimester due to local transmission by October 2017.

3 Discussion

From the numerical results, it appears that the number of Zika cases projected in the US is low. We observe that the number of ZIKV infected pregnancies generated by local transmission is very small, especially if compared with the travel associated 529 pregnant women in the United States with any laboratory evidence of possible Zika virus infection, as of August 20th, 2016. The presented projections do not consider interventions, including integrated vector control, and should be considered as worst case scenarios. As well, we are assuming that no undetected outbreaks in the continental US occurred before Aug. 1st. The presence of undetected autochthonous transmission may provide difference in the epidemic trajectories. For this reason projections should be updated every 2-3 weeks with data about the cases in the USA to reduce noise and constrain the magnitude of the epidemic trajectories. The projections, thus, may change with the addition of future data, conditioned on the observed spread of ZIKV in the US. It is important to note that these projections have been obtained by using a global model that monitors all countries in the Americas. The model has a number of assumptions and limitations discussed in Ref. [1]. For instance, the model does not consider sexual transmission. In areas with limited local transmission and small number of cases such as in the continental US, however, sexual transmission may account for a larger percentage of infections than in countries with intense vector transmission. Furthermore, the detailed analysis of specific geographical regions at a finer geographical resolution deserves a more specific sensitivity analysis and investigation of possible sources of noise. For instance, in the continental US, if only *Ae. aegypti* mosquitoes as competent vectors and not *Ae. Albopictus*, fewer states would experience outbreaks. Finally, future recalibration of the global model with new data from other countries and refined information on ZIKV transmission may provide corrections to the preliminary results provided here.

Acknowledgments

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References

- [1] Qian Zhang, Kaiyuan Sun, Matteo Chinazzi, Ana Pastore-Piontti, Natalie E Dean, Diana P Rojas, Stefano Merler, Dina Mistry, Piero Poletti, Luca Rossi, et al. Projected spread of zika virus in the americas. *bioRxiv*, page 066456, 2016.
- [2] Pan-American Health Organization. Zika virus infection, June 2016.

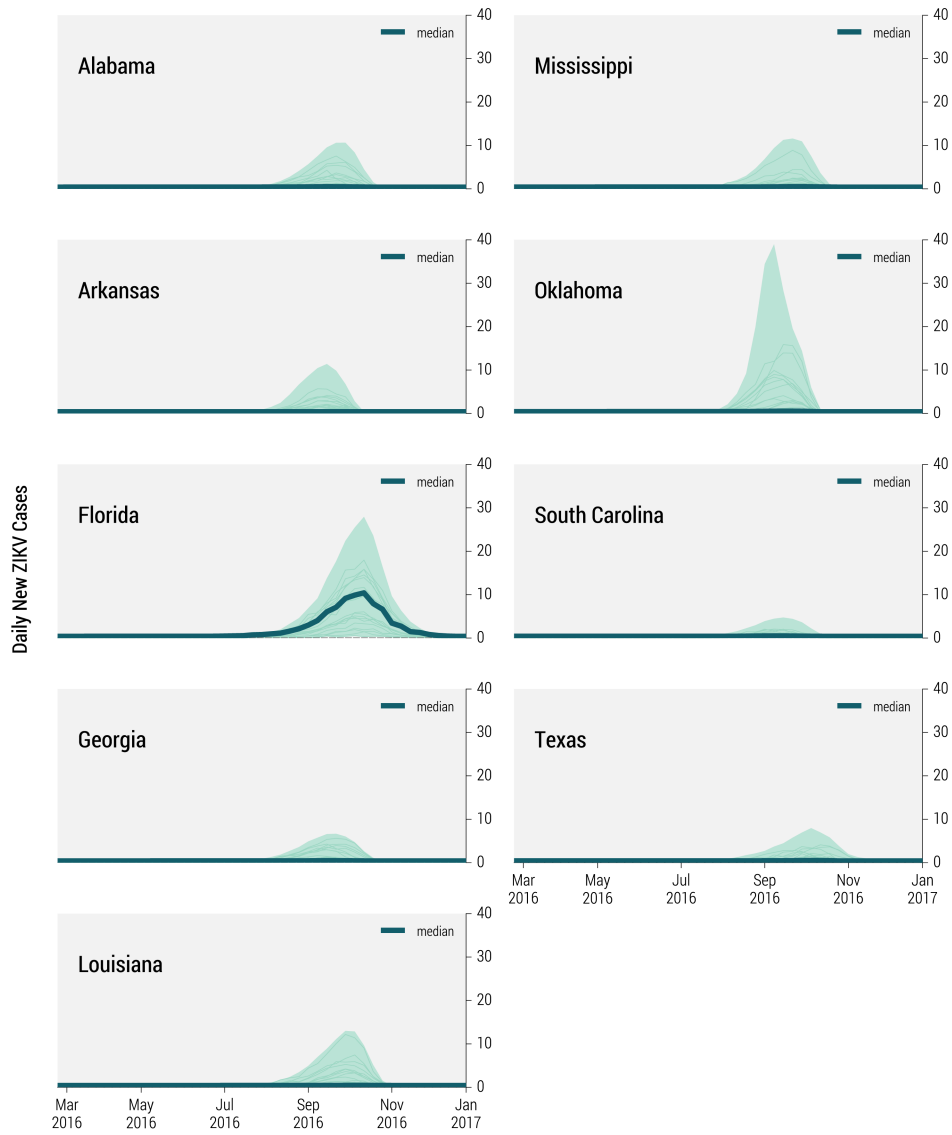


Figure 1: Epidemic profiles in case of outbreaks (green shaded area is the 95% CI) in the various states susceptible of locally generated ZIKV transmission.

State	By September 15, 2016	
	No. of infections	No. of cases (symptomatic)
	median 95%CI	median 95%CI
Alabama	11[0-911]	2[0-182]
Arkansas	3[0-1284]	1[0-257]
Florida	395[16-1029]	79[3-206]
Georgia	6[0-731]	1[0-146]
Louisiana	4[0-816]	1[0-163]
Mississippi	10[0-1043]	2[0-209]
Oklahoma	12[0-4081]	2[0-816]
South Carolina	16[0-631]	3[0-126]
Texas	5[0-478]	1[0-96]

Table 1: Median number of local transmitted infections and symptomatic cases and their 95% CI by state.

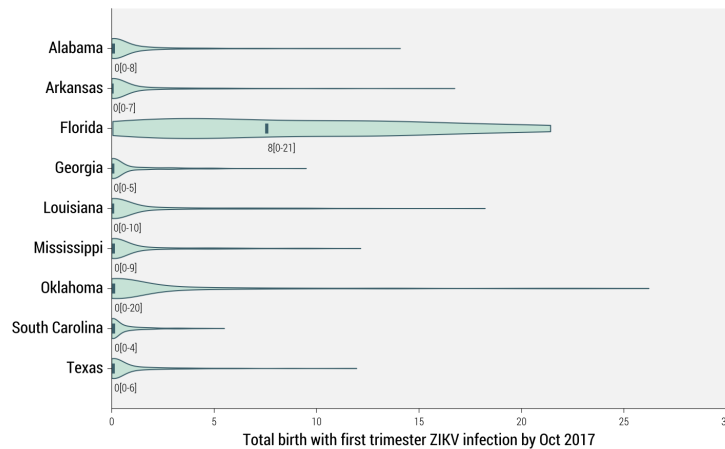


Figure 2: Median number and the 95% CI of births from ZIKV infected pregnancies (first trimester infections). The Kernel density plots reproducing the distribution of infected births shows a clear accumulation toward the low values.