

1125-92-573

**Deborah Shutt\***, 1500 Illinois, Golden, CO 80232, and **Carrie Manore, Sara Y. Del Valle, Aaron Porter** and **Stephen Pankavich**. *Determining important Zika outbreak characteristics via Approximate Bayesian Computation for epidemics in South and Central America*. Preliminary report.

Mosquito-borne diseases contribute significantly to the overall morbidity and mortality caused by infectious diseases in Central and South America. Newly emergent pathogens such as Zika virus in 2015 highlight the need for data and models to help understand the public health impact and develop mitigation strategies. Since Zika virus is newly emerging in the Americas, its impact on the naive population is unknown. We developed a mathematical model for Zika dynamics in Colombia, El Salvador, and Suriname. The number of people to contract the disease depends on factors such as climate, elevation, population density, sanitation and other socioeconomic and environmental factors. Therefore, the size of the susceptible at-risk demographic of a country may not be the entire population. Since dengue and Zika overlap geographically and share a common vector, *Aedes aegypti*, we used a calculated at-risk population size based on historically reported incidence rates for dengue from Colombia, El Salvador, and Suriname. We then used the Approximate Bayesian Computation method to estimate parameter distributions and calculate the reproductive number based on the Pan-American Health Organization's publicly available data. (Received September 06, 2016)