1135-34-3241 **Deborah Shutt*** (`shutt_d@hotmail.com`), Virginia Military Institute, **Sara Y Del Valle** (`shutt_d@hotmail.com`), Los Alamos National Laboratory, **Carrie A Manore** (`shutt_d@hotmail.com`), Los Alamos National Laboratory, **Stephen Pankavich** (`shutt_d@hotmail.com`), Colorado School of Mines, and **Aaron T Porter** (`shutt_d@hotmail.com`), Colorado School of Mines. *A Stochastic Model and Bayesian Estimation of Important Outbreak Characteristics for Zika in South and Central America*

As South and Central American countries prepare for increased birth defects from Zika virus outbreaks and plan for mitigation strategies to minimize ongoing and future outbreaks, understanding important characteristics of Zika outbreaks and how they vary across regions is important. We developed a mathematical model for the 2015/2016 Zika outbreak in South and Central America. We fit the model to publicly available data, using Approximate Bayesian Computation to estimate parameter distributions and provide uncertainty quantification. An important model input is the at-risk susceptible population, which can vary with a number of factors including climate, elevation, population density, and socio-economic status. We informed this initial condition using the highest historically reported dengue incidence. We then estimated the basic reproduction number, or the expected number of new human infections arising from a single infected human, to range between 4 and 6 in most South American regions. We estimated the reporting rates and the number of pregnant women that were infected with Zika. The uncertainty in parameter estimates highlights a need for research and data collection that will better constrain parameter ranges. (Received October 02, 2017)

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