



Modeling Zika

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Zika is an infectious disease transmitted by *Ae. aegypti* and *Ae. Albopictus* mosquitoes species, which are found also in the US. Zika is endemic in Puerto Rico and has exhibited local transmission in Florida and Texas. Other routes of transmission of Zika are through sexual contact or from a mother to the fetus. In general Zika infection is mild but it can lead Guillain-Barré Syndrome in adults and to severe birth defects in newborns to mothers with Zika infection. We model Zika infection within the vector and the host. We consider six population-level models of Zika, which use various combinations of disease transmission (vector and direct) and infectious classes (asymptomatic and pregnant). Using cumulative incidences and cumulative pregnant incidences from the 2016 Zika outbreak in Florida, we test the models for structural and practical identifiability. We find that the models are structurally identifiable but that direct transmission rates are not practically identifiable from these data. Further, fixing the recovery rates improves overall identifiability. Elasticity analysis of the Reproduction number suggests that the mosquito-to-human ratio, mosquito life span and biting rate have the greatest potential of reducing the reproduction number of Zika. These observations imply that control measures reducing mosquito numbers, life span or biting rate would have the highest impact.

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