1073-37-213 Abhishek Pandey* (abhishe@g.clemson.edu), Mathematical Sciences, Clemson University, M-304 Martin Hall, Clemson, SC 29634-0975. Parameter Estimation and Model Selection for Dengue Transmission. Preliminary report.

The study of dengue dynamics at the population scale have significantly contributed to the understanding of dengue transmission. Most studies have used point estimates of parameter values derived from clinical and laboratory experiments: in particular, data on population-level parameters such as transmission or susceptibility are extremely limited due to inability to feasibly conduct experiments of infection in people and instead must be estimated from indirect population-level data. We suggest a Bayesian approach which uses Monte Carlo Markov Chain (MCMC) simulation to find estimates for the unknown parameters of a generic dengue mathematical model we formulated based on previous dengue models. Prior knowledge is combined with data on hospital visits to perform the statistical inference on the unknown parameters. Our model allows for the inclusion of different hypotheses about dengue epidemiology and we explore the consistency of clinical data with the epidemiological hypothesis by determining goodness of fit of the model to the data for each combination of hypothesis. We use Akaike Information Criterion and Bayes Information Criterion on the results from the Bayesian MCMC on our dengue model and select a model that most parsimoniously agrees with the data. (Received August 01, 2011)