Preliminary Report

NIMBioS Short-Term Visitors Olivia Brozek and Matthew Glomski A Structured Population Model for Marburg Hemorrhagic Fever

Public Information:

Marburg hemorrhagic fever (MHF) is a rare and highly fatal disease caused by a virus from the same family as Ebola. MHF has been studied using the well-known compartmental susceptible-exposed-infectious-removed (SEIR) model. During our short-term visit at NIMBioS, we considered extensions to this model, incorporating time-dependent transmission parameters and additional population compartments to better capture the dynamics of the disease. With NIMBioS postdoctoral fellow Dr. Calistus Ngonghala, we examined the models first in a dynamical systems context, via stability analysis at equilibria. We then took a numerical approach to the model, working to computationally identify best-fit parameter values. Our future plans include to: (a) formalize equilibria analysis; (b) extend MATLAB code written by Dr. Ngonghala to arrive at final best-fit parameter values; and (c) prepare a paper summarizing our findings.

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