School of Mathematical and Statistical Sciences
Arizona State University

M E M O R A N D U M

DATE: June 23, 2022

TO: Faculty and Students

FROM: Professor(s) John Fricks
Chair/Co-Chairs of Wilmer Osvaldo Martinez Rivera
Defense for the PhD in Statistics
Committee Members Dan Cheng
Mark Reiser
Shiwei Lan
Shuang Zhou

DEFENSE ANNOUNCEMENT

Candidate: Wilmer Osvaldo Martinez Rivera

Defense Date: 07/08/2022

Defense Time: 1:00 PM

Virtual Meeting Link: https://asu.zoom.us/j/84054332384

Title: Estimation for Disease Models Across Scales

Please share this information with colleagues and other students, especially those studying in similar fields. Faculty and students are encouraged to attend. The defending candidate will give a 40 minute talk, after which the committee members will ask questions. There may be time for questions from those in attendance. But, guests are primarily invited to attend as observers and will be excused when the committee begins its deliberations or if the committee wishes to question the candidate privately.

ABSTRACT
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Abstract

Tracking disease cases is an essential task in public health; however, tracking the number of cases of a disease may be difficult not every infection can be recorded by public health authorities. Notably, this may happen with whole country measles case reports, even such countries with robust registration systems. Eilertson et al. (2019) propose using a state-space model combined with maximum likelihood methods for estimating measles transmission. A Bayesian approach that uses particle MCMC (pMCMC) is proposed to estimate the parameters of the non-linear state-space model developed in Eilertson et al. (2019) and similar previous studies. We illustrate the performance of this approach by calculating posterior estimates of the model parameters and predictions of the unobserved states in simulations and case studies. Also, iteration filtering (IF2) is used as a support method to verify the Bayesian estimation and to inform the selection of prior distributions.

In the second half of the thesis, a birth-death process is proposed to model the unobserved population size of a disease vector. This model studies the effect of a disease vector population size on a second affected population. The second population follows a non-homogenous Poisson process when condition on the vector process with a transition rate given by a scaled version of the vector population. The observation model also measures a potential threshold event when the host species population size surpasses a certain level yielding a higher transmission rate. A maximum likelihood procedure is developed for this model, which combines particle filtering with the MM algorithm and extends the work of Crawford et al. (2014).