Proposal for Yuganthi Liyanage's Ph.D. Preliminary Exam

1. The prelim exam will be held on April 22, 2025.

2. The proposed prelim exam will focus on identifiability analysis of nonlinear ordinary differential equation (ODE) models, with applications to infectious disease modeling. The core of the student's thesis involves investigating both structural and practical identifiability of parameters in ODE-based transmission models.

   The student is expected to give a presentation introducing the concept of identifiability and its importance in parameter estimation. The talk will cover the differential algebra approach for structural identifiability and briefly compare it to other available methods. The student will demonstrate the use of software tools for identifiability analysis on a simple example model. In addition, the presentation will include an overview of practical identifiability, highlighting methods such as Monte Carlo Simulation (MCS) and the profile likelihood approach.

   In the question and answer session, the student will demonstrate familiarity with identifiability analysis methods, challenges in parameter estimation for nonlinear ODE models, and how identifiability affects the accuracy of model predictions in infectious disease research.

   To prepare for the exam, the student will use the following references:

   - Miao, H., Xia, X., Perelson, A. S., & Wu, H. (2011). On identifiability of nonlinear ODE models and applications in viral dynamics. *SIAM Review*, 53(1), 3–39.
   - Bellu, G., Saccomani, M. P., Audoly, S., & D'Angiò, L. (2007). DAISY: A new software tool to test global identifiability of biological and physiological systems. *Computer Methods and Programs in Biomedicine*, 88(1), 52–61.
   - Dong, R., Goodbrake, C., Harrington, H., & Pogudin, G. (2023). Differential Elimination for Dynamical Models via Projections with Applications to Structural Identifiability. *SIAM Journal on Applied Algebra and Geometry*, 7, 194–235.
   - Liyanage, Y. R., Heitzman-Breen, N., Tuncer, N., & Ciupe, S. M. (2024). Identifiability investigation of within-host models of acute virus infection. *Mathematical Biosciences and Engineering*, 21(10), 7394–7420.