Vita

Candidate's name: Ravindu Gimantha Upasena

Universities Attended:

Monash University (2019)
Bachelors of Engineering
Honours

University of New Brunswick (2025)
Masters of Science

Dynamics of multi-strain epidemic models and the impact of masking and vaccination

UNIVERSITY OF NEW BRUNSWICK

THESIS DEFENCE AND EXAMINATION

in Partial Fulfillment

of the Requirement for the Degree of
Master of Science

by

Ravindu G. Upasena

in the Department of Mathematics & Statistics

U.N.B., Fredericton, N.B.

Tuesday, April 29th, 2025
1:30 p.m.

Tilley Hall, Room 302

Examining Committee

Dr. Lin Wang	Supervisor
Dr. James Watmough	Internal Examiner
Dr. Zhen Lei	External Examiner
Dr. Viqar Husain	Chair of Oral Examination

Abstract

Mathematical modeling of infectious diseases is essential for designing public health policies and evaluating disease control strategies. While existing studies have explored the dynamics of multiple strains in both homogeneous and non-homogeneous populations, they often fail to adequately represent asymptomatic infections and waning immunity. This thesis addresses these gaps by developing and analyzing two mathematical models.

The first model, an SIARS model, examines disease dynamics in a homogeneous population exposed to multiple strains without health interventions. The strain-specific basic reproduction numbers are identified, which determine the overall basic reproduction number. Additionally, conditions for the existence and stability of strain-dominant equilibria are established. Numerical simulations validate these theoretical findings and further explore strain competition outcomes.

The second model, an SVIARS model, extends the SIARS framework by incorporating mask usage and vaccination in a non-homogeneous population. Although deriving a closed-form basic reproduction number in high-dimensional epidemic models is challenging, this study successfully identifies the strain-specific reproduction numbers, enabling an explicit expression for the overall basic reproduction number. Numerical analyses further examine how the basic reproduction number varies with different levels of intervention-related parameters and identify key efficacy thresholds essential for effective disease control.

The findings obtained in this thesis offer valuable insights for public health decision-making, providing practical recommendations for mitigating multi-strain infectious disease outbreaks.