



**4th Annual One Health Symposium
Monday, 24 November 2025
Livingstone, Zambia**

Symposium Announcement:

In conjunction with the Southern Africa Mathematical Sciences Association (SAMSAS) Annual Conference and the Masamu Advanced Study Institute (MASI) and Workshops in Mathematical Sciences, an international research symposium will be held on Monday, November 24, 2025 in Livingstone, Zambia

Symposium Theme: “Mathematics Connecting to One Health”

The symposium will focus on the interconnection of human, animal, climate change, and environmental health. We will highlight the previous work done by the network and work on future collaborative research areas and knowledge transfer. By using mathematical and statistical tools and research teams from different disciplines and geographical areas, as well as utilizing policy makers and practitioners, we can inform policy and practices to improve the health of all.

Target Participants: Allied Health organizations, agencies, government, industry, nonprofits, and academia.

The symposium will provide an opportunity for researchers and practitioners to showcase their current research work through 15-minute presentations or poster presentations for participants to highlight their current research work and needs for future work.

Online applications/abstract submissions can be completed at <https://masamu.auburn.edu>. Please submit by September 27, 2025.

Themes for Presentations and Posters:

1. Malaria/HIV modeling
2. Stigma modeling
3. Climate Change
4. Rapid Epidemic Detection Systems
5. COVID-19 modeling
6. Common diseases shared by animals and humans
7. Transmission modeling of zoonotic and environmentally induced diseases
8. Reverse zoonotic disease transmission
9. Monkeypox

Tentative Agenda:

- 08:30 Welcome (UNAM official)
- 08:45 Logistics and introductions
- 09:00 Presentations
- 12:00 Lunch (Keynote Speaker)
- 13:30 Poster session
- 14:45 Breakout sessions
- 17:00 Reception/Networking
- 18:30 Adjourn



Virtual 2025 SAMSA One Health Symposium
Sunday, 23 November 2025
All times Central Africa Time (CAT) (GMT+2)



Agenda		
16:00	Opening Greetings	
Presentations I		
	Speaker	Title
16:10	Jessica Kingsley	Modeling Crimean Congo Hemorrhagic Fever
16:30	Zhisheng Shuai	A Tale of Two Incidence Functions in Epidemiological Models
16:50	Joseph Malinzi	Mathematical Modeling of the synergistic anti-cancer effects of combining two oncolytic viruses
17:10	Gakololang Rannyere	Stochastic Modelling of cholera transmission under environmental noise
17:30	Morelyn Sigauke	Analysis of mitigation strategies in three-age group clustered pneumonia transmission dynamics
17:50	Short Break	
Presentations II		
	Speaker	Title
18:00	Claris Shoko	Machine Learning Algorithms for the Prediction of the Spread of COVID-19 in Namibia
18:20	Felix Majeke	Predicting Infectious Disease Outbreaks Using AI and Statistical Models. A Case Study of COVID-19 in Zimbabwe.
18:40	Thatayaone Lucas Gasebonno	A Dynamic Model of Human and Environmental Pathways with Strategic Interventions for Investigating the Spread of Mpox
19:00	Bapati Babedi Matebesi	Mathematical modelling of within host dynamics of Respiratory Syncytial Virus
19:20	John Bosco Hatson Njagarah	Analysis of mitigation strategies for Respiratory Syncytial Virus in presence of super spreaders: A <i>modelling Perspective</i>
19:40	Discussion	
19:55	Final Comments and Closing	
20:00	Adjourn	

Jessica Kingsley
Department of Mathematics,
University of Tennessee, Knoxville,
USA

Title: Modeling Crimean Congo Hemorrhagic Fever

Abstract: Crimean Congo Hemorrhagic Fever (CCHF) is a tick-borne illness that affects animals and humans in countries across Africa, Asia, and now Europe. Ticks transmit this disease to susceptible hosts by feeding on them and can acquire the disease by feeding on an infected host. Ticks feed on different hosts at different stages in their life cycle: larvae and nymphs feed on small mammals, while adults feed on large mammals. Another aspect of the spread of CCHF is tick co-feeding. Co-feeding occurs when ticks feed on the same susceptible host within close proximity. If one tick is infected and the other is susceptible, the susceptible tick can become infected during co-feeding while the host remains susceptible. Very few mathematical models exist in literature that explore the epidemiological effects of tick co-feeding. In this talk, I will present an ODE compartment model of the spread of CCHF that accounts for the life cycle of ticks and co-feeding dynamics. Preliminary results to fit the model to data and observations in Uganda and Namibia will be presented as well. This work is supported by the MASAMU program with funding from a National Science Foundation (NSF) grant based at Auburn University.

Title: A Tale of Two Incidence Functions in Epidemiological Models

Speaker: Zhisheng Shuai, University of Central Florida, Orlando, USA

Abstract: The selection of incidence functions in epidemiological models plays a critical role in shaping the disease dynamics, particularly in populations of varying sizes. In this presentation, we examine a model that incorporates post-infection mortality and partial immunity, comparing the effects of mass-action and standard incidence functions. With the mass-action incidence, the model exhibits periodic solutions under certain parameter conditions. In contrast, applying the standard incidence reduces the likelihood of periodic solutions, potentially eliminating them entirely.

Mathematical Modeling of the synergistic anti-cancer effects of combining two oncolytic viruses

Joseph Malinzi

Department of Mathematics, Faculty of Science and Engineering, University of Eswatini, Private Bag 4, Kwaluseni, Eswatini

This research investigates the synergistic anti-cancer effects of combining Vaccinia (VV) and Vesicular stomatitis (VSV) oncolytic viruses for cancer treatment. A mathematical model, based on an experiment where a combination of VV and VSV demonstrated synergistic oncolytic activity in vitro and in vivo, is constructed. The model is subsequently fitted to the experimental data and parameters are estimated. The model's solutions long-term behavior have been analyzed, allowing us to determine thresholds that are critical for cancer eradication, a global sensitivity analysis has been conducted to determine the parameters that most significantly influence the treatment outcome and several numerical simulations have been carried out to test certain hypotheses regarding the effects of the combination. Optimal time delays (τ_1 and τ_2 representing optimal virus initial delivery of VV and VSV), to minimize tumor cell count during treatment, will be determined.

****This is joint work with Raluca Eftimie, Anotida Madzvamuse, Rachid Ouifki, Amina Eladdadi and Helen Byrne.**

Stochastic Modelling of cholera transmission under environmental noise

Gakololang Rannyere^{1*}, John Boscoh Hatson Njagarah¹,
Barbara Szomolay², Edward Lungu¹

¹Department of Mathematics and Statistical Sciences, Botswana International University of Science and Technology, Plot 10071, Boseja Ward, Private Bag 16, Palapye, Botswana.

²Cardiff University School of Medicine, Division of Infection and Immunity, CF14 4XN, Cardiff, United Kingdom.

*Corresponding author(s). E-mail(s): rg14100306@biust.ac.bw;
Contributing authors: njagarahh@biust.ac.bw; szomolayb@cardiff.ac.uk;
edwardlungu1950@gmail.com;

Abstract

Cholera transmission is influenced by environmental variability. Deterministic model though very useful fail to capture the variability in a system. In this study, we develop and analyse stochastic cholera models to investigate how environmental noise affects key epidemiological processes.

We consider a baseline deterministic cholera model and formulate two separate stochastic extensions. In the first model, environmental noise is introduced into the death-related parameters, representing fluctuations in natural mortality and bacterial decay influenced by environmental conditions. In the second model, stochastic perturbations are applied to the transmission parameters, capturing variability in exposure risk arising from changes in water contamination, sanitation practices, and ecological factors. Using Itô stochastic calculus, we examine positivity, boundedness, and long-term behaviour of each model.

Keywords: cholera, environmental noise, stochastic differential equation

Abstract

Name: Morelyn Sigauke

Title: Analysis of mitigation strategies in three-age group clustered pneumonia transmission dynamics



Supervisors:

1. Dr. J. H.B. Njagarah (Department of Mathematics & Statistical Sciences, Faculty of Sciences, BIUST, E-mail: njagarahh@biust.ac.bw)
2. Dr. B. Szomolay (School of Medicine, Cardiff University, E-mail: SzomolayB@cardiff.ac.uk)
3. Prof. S. M. Kassa (Department of Mathematics & Statistical Sciences, Faculty of Sciences, BIUST, E-mail: kassas@biust.ac.bw)

Pneumonia is a debilitating illness mostly prevalent among children under five, the elderly over 64, and individuals with pre-existing health conditions or weakened immune systems. Owing to the distinct transmission rates in different age groups, a 3 age-band clustered model is developed to influence of capture the inter-and intra age-group pneumonia transmission dynamics. The study established essential properties of the model including positivity and boundedness of solutions, and the existence of steady states and the conditions under which the disease may be contained. Through global sensitivity analysis it was observed that the processes described by parameters related to transmission and recovery rates were the most influential in changes on infection levels across all age groups. In addition, numerical results showed that interventions targeting the middle age group are more effective in containing pneumonia infection in the population in the long-term. Additionally, the results showed that while the middle age group is linked to high transmission of pneumonia, the children and elderly age-groups experience a higher prevalence of the infection. However, by introducing interventions such as protective measures for the middle and elderly age-groups, vaccination for children, and treatment across all three age groups, particularly focusing on treating a smaller number of middle-aged individuals, infection levels can be lowered, the time to peak infection values can be delayed, and the likelihood of eventual eradication can be enhanced.

Keywords: Age-band clustered model, Intra-age group contact, Inter-age group contact, Pneumonia mitigation measures, Global Sensitivity Analysis, Numerical simulations

Machine Learning Algorithms for the Prediction of the Spread of COVID-19 in Namibia

Claris Shoko¹  and Eriyoti Chikodza² 
shokoc@ub.ac.bw¹, chikodzae@ub.ac.bw²

^{1,2}University of Botswana, plot 4775 Notwane Rd Gaborone Botswana

November 11, 2025

Abstract

Improving the accuracy and stability of daily COVID-19 forecasts is crucial for effectively managing and controlling the pandemic. This chapter compares the performance of different machine-learning algorithms in predicting and forecasting the spread of COVID-19 in Namibia. Machine learning approaches that include the support vector machine (SVM), the TBATS, the generalized additive model (GAM), and the Stochastic Gradient Boosting Machine (SGBM) approach are compared. Selection of the best-performing model is done using plots of forecasts from fitted models on the test dataset since plots are visually appealing. A further selection of the best model is done using key performance indicators (KPIs), that is, root mean square error (RMSE), mean absolute percentage error (MAPE), and the coefficient of determination R². Results show that the positive rate, reproductive rate, and stringency index contribute significantly (p-values < 0.05) to the spread of COVID-19 in Namibia. From the fitted models GAM and the SVM linear kernel function are the best performers in forecasting daily COVID-19, although based on KPIs GAM outperforms the SVM linear kernel function. This study recommends the use of both models to help solve the forecasting problem and the identification of significant regressors. Accurate prediction and forecasting help in giving the health sector early warning signs and preparedness to help manage and control epidemics. This will go a long way in helping achievement of the Sustainable Development Goal number 3 of health and wellness.

Keywords: COVID-19; Machine learning algorithms; SVM kernel functions; Generalised additive model; Stochastic gradient boosting machine; Namibia.

*¹ Corresponding author: Tel.: +267 78 129 442. Email address: shokoc@ub.ac.bw (C. Shoko)

Predicting Infectious Disease Outbreaks Using AI and Statistical Models. A Case Study of COVID-19 in Zimbabwe.

Loveness Matare and Felix Majeke

Mathematics and Computer Science, Great Zimbabwe University, Off Great Zimbabwe Rd, Masvingo, Zimbabwe;

Correspondence: fmajeke@gzu.ac.zw

Abstract: This study explores the integration of artificial intelligence (AI), statistical, and spatial statistical models to improve the prediction of infectious disease outbreaks, focusing on COVID-19 in Zimbabwe. By combining machine learning techniques such as Long Short-Term Memory (LSTM) networks with classical time series approaches (ARIMA) and spatial analysis methods (Moran's I), a hybrid forecasting framework was developed. This framework leverages multi-source epidemiological, spatial, and contextual data to capture complex temporal and spatial dependencies inherent in epidemic dynamics. Evaluations using real-world COVID-19 data demonstrate that the hybrid AISpatial-Statistical-Time Series (AISTS) model significantly outperforms traditional models in forecast, precision, particularly in identifying outbreak hotspots and predicting case surges. The study highlights the critical role of spatial autocorrelation and non-linear temporal patterns, which are often overlooked in conventional models. Despite challenges such as data quality issues and computational complexity, the integrated approach provides robust and interpretable forecasts that can inform public health preparedness and resource allocation. The findings offer valuable information for early warning system epidemics and support data-driven decision-making in resource-limited settings. This research contributes novel methodologies for epidemic modeling, emphasizing the synergy between AI and spatial statistics to improve health outcomes in Zimbabwe and similar environments.

Keywords: Artificial Intelligence, Spatial Statistics, COVID-19 forecasting, Hybrid Model, Epidemic Modeling

A Dynamic Model of Human and Environmental Pathways with Strategic Interventions for Investigating the Spread of Mpox

Thatayaone Lucas Gasebonno^a, John Njagarah^b, Saheed Akindeinde^c & Edward Lungu^d

^a Botswana International University of Science and Technology

GT12001197@biust.ac.bw

^b Botswana International University of Science and Technology

njagarahh@biust.ac.bw

^c Botswana International University of Science and Technology

akindeindes@biust.ac.bw

^d Botswana International University of Science and Technology

lungue@biust.ac.bw

Abstract

Monkeypox is an infectious disease caused by the monkeypox virus (MPXV). It is endemic in Central and West Africa, with a high incidence in the Democratic Republic of the Congo (DRC). However, the dynamics of the disease in the DRC are not well understood. We propose a mathematical model for monkeypox transmission that includes environmental variables to analyse its dynamics among human populations. The endemic equilibrium of the model was formulated in two cases; where it is assumed that the microbes in the environment have no impact on the spread of Mpox, and it was shown that the endemic equilibrium is unique and exists when \mathcal{R}_0 is greater than unity. The case where the changes in pathogen concentration in the environment was considered. It is shown that the model exhibits backward bifurcation at \mathcal{R}_0 equal to unity indicates that lowering \mathcal{R}_0 below 1 may not eliminate Mpox when the disease is already endemic, due to the stable endemic equilibrium. Numerical simulations, based on outbreak data from the DRC, indicate that accelerating recovery, improving isolation, and reducing environmental contamination substantially reduce transmission rates. Our findings highlight the essential requirement for comprehensive interventions addressing both behavioural and environmental factors, especially in environments with limited resources.

Keywords: Monkeypox, Democratic Republic of the Congo (DRC), environmental transmission, microbes, interventions.

Category: Mathematical Biology

References

- [1] Gessain, A., Nakoune, E., Yazdanpanah, Y. (2022): Monkeypox. *New England Journal of Medicine*, vol 387, doi:10.1056/NEJMra2208860
- [2] Collins, O. C., Duffy, K. J. (2024): Dynamics and control of mpox disease using two modelling approaches. *Modelling Earth Systems and Environment*, vol 10.

Mathematical modelling of within host dynamics of Respiratory Syncytial Virus

Bapati Babedi Matebesi^a, John Njagarah^b, Barbara Szomolay^c

^a Botswana International University of Science and Technology

MB19001439@biust.ac.bw

^b Botswana International University of Science and Technology

njagarahh@biust.ac.bw

^cCardiff University

SzomolayB@cardiff.ac.uk

Abstract

Respiratory Syncytial Virus (RSV) is a major cause of acute lower respiratory tract infections, particularly affecting infants, young children, the elderly, and individuals with weakened immune systems. It continues to pose a significant global health burden due to its high morbidity and mortality rates. Despite its clinical significance, effective treatment and prevention options remain limited, highlighting the need for a deeper understanding of the virus's behavior within the host and the host's immune response mechanisms. This thesis presents a detailed mathematical modeling study of the within-host dynamics of RSV infection. The model explicitly incorporates key biological processes, including viral replication, innate and adaptive immune responses, and cytokines regulation. A compartmental model framework is developed to represent the complex interactions among susceptible epithelial cells, infected cells, free virus particles, immune effectors, and cytokines. A thorough mathematical analysis is carried out to prove the positivity and boundedness of solutions, determine the disease-free equilibrium, investigate its local stability and calculate the basic reproduction number (\mathcal{R}_0) using the next-generation matrix method. A model fit to data and parameter estimation is conducted using available experimental and clinical data to ensure that the model accurately reflects observed infection dynamics. Sensitivity analysis is then performed using the Latin Hypercube Sampling (LHS) technique and Partial Rank Correlation Coefficients (PRCCs) to identify the most influential parameters on (\mathcal{R}_0). Numerical simulations are conducted to investigate various infection scenarios and intervention strategies, such as antiviral treatments and vaccination, assessing their effects on viral load and infected cell dynamics. The results emphasize the importance of immune response strength and timing in determining infection progression and viral control.

Keywords: Respiratory Syncytial Virus (RSV), innate and adaptive immune responses, reproduction number (\mathcal{R}_0), interventions.

Category: Mathematical Biology

References

- [1] Collins, P.L. and Graham, B.S., (2008). Viral and host factors in human respiratory syncytial virus pathogenesis. *Journal of virology*, 82(5), pp.2040-2055.
- [2] Griffiths, C., Drews, S.J. and Marchant, D.J., (2017). Respiratory syncytial virus: infection, detection, and new options for prevention and treatment. *Clinical microbiology reviews*, 30(1), pp.277-319.

Analysis of mitigation strategies for Respiratory Syncytial Virus in presence of super spreaders: *A modelling Perspective*

Lone Raphaladi Gasebonno^a, John Boscoh H. Njagarah^a, & Zhivko Nedev^b

^a Department of Mathematics and Statistical Sciences, Botswana International University of Science and Technology (BIUST), Private Bag 016, Palapye, Botswana

Lone Raphaladi: RL20000192@BIUST.AC.BW

John Boscoh H. Njagarah: njagarahh@biust.ac.bw

^b Department of Computing and Informatics, Botswana International University of Science and Technology, Plot 10071, Beseja, Ward, Palapye

nedevz@biust.ac.bw

Abstract

Respiratory Syncytial Virus (RSV) continues to pose a serious threat to global health, especially for young children, older adults, and people with weakened immune systems. Despite its impact, no vaccine has been licensed to prevent the disease, and there are many unanswered questions about the most effective ways to contain its spread, particularly when it comes to non-pharmaceutical measures. In this study, we developed a detailed mathematical model that captures the RSV transmission dynamics, including the often-overlooked roles of asymptomatic (super spreader) and post-symptomatic individuals. The model was comprehensively analysed to confirm its well-posedness and analytical solutions, and the basic reproduction number (R_0) was calculated, used to determine whether the disease will fade out or persist in a population. We also ran a sensitivity analysis using Latin Hypercube Sampling scheme to determine which factors most strongly influence the disease severity. Our findings show that reducing close contact between people, through measures like physical distancing or improved hygiene, has the greatest impact on containing the disease spread. On the other hand, efforts like widespread screening and isolating asymptomatic individuals only make a noticeable difference if contact rates remain stable, and even then, their effect is limited. Simulations further revealed that early action is key: introducing preventive measures at the start of an outbreak can delay and lower the peak, easing pressure on healthcare systems. These insights suggest that public health policies should prioritize early, broad-based interventions and long-term solutions like vaccination over labour-intensive isolation strategies.

Keywords: Respiratory syncytial virus, Global Stability analysis, Sensitivity analysis, Non-pharmaceutical interventions, Screen and Isolation, Contact suppression measures

Category: Mathematical Biology

References

- [1] Coultas, J., Smyth, R., Openshaw, P. ((2019)): Respiratory syncytial virus (RSV): a scourge from infancy to old age, *Thorax* 74: 986–993
- [2] P. Munywoki, D. Koech, C. Agoti, A. Bett, P. Cane, G. Medley, D. Nokes (2015): Respiratory Syncytial Virus Infections During an Epidemic in a Rural Kenyan Household Cohort *J Infect Dis.* 212: 1711–1718