ONE HEALTH SYMPOSIUM

November 20, 2023
Plenary Room (Conference Room 1)
Protea Hotel Fire and Ice! Pretoria Menlyn

9:00-9:15	Welcome, Prof Vinesh Maharaj, Deputy Dean of Research, Faculty of Natural and Agricultural Sciences (NAS), University of Pretoria (Professor Samuel Manda Presiding)
9:15-9:20	Objectives and expected outcomes (Overtoun Jenda)
9:30-9:50	speaker Farai Nyabadza
9:55-10:15	speaker Folashade Agusto
10:30-10:45	Break
10:50-11:10	speaker Samuel Manda
11:15-noon	Discussion Groups: Making policy and its effects. Breakout Room 1: Meeting Room 1 Breakout Room 2: Plenary Room Breakout Room 3: Conference Room 3
Noon-1:25	Lunch
1:30-1:50	speaker Tesfalem A. Tegegn, Meeting Room 1; Jacek Banasiak, Plenary Room
1:55-2:15	speaker Ding-Geng Chen, Meeting Room 1; Joseph Malinzi, Plenary Room
2:20-2:40	speakers Delport, R.; Hugo, J.; Mandel-Mntla, E., Meeting Room 1; Stéphane Yanick Tchoumi, Plenary Room
2:40-2:50	Break
2:55-3:05	speaker Suzanne Lenhart
3:10-3:55	Discussion Groups, possible topics, Vaccination Planning and Effects, Hospital Acquired Infections Breakout Room 1: Meeting Room 1 Breakout Room 2: Plenary Room Breakout Room 3: Conference Room 3
4:00-4:30	Group Reports
4:30	Closing (Professor Suzanne Lenhart)

ABSTRACTS

Presenter: Farai Nyabadza (University of Johannesburg, South Africa)

Title: Incorporating policy changes in disease models
Abstract: The management of infectious diseases has evolved in the past few decades. It is now clear that policies can evolve as a disease progresses in a population, with a good example being the COVID-19 pandemic, where policies were dynamic and, at times erratic. In this talk, we consider a number of mathematical models in which policy changes were imperative. We track the changes in policies using piece-wise systems of differential equations. The focus will be on how such models are formulated, analyzed, and interpreted. Thresholds that define disease persistence will be established and discussed. The implications of the policy changes are discussed, and the implications of these changes to epidemics are articulated. The results presented have a crucial impact on how policy changes affect and continue to influence the trajectory of infectious diseases.

Presenter: Folashade Agusto (University of Kansas, USA)

Title: COVID-19: Assessing the impact of mitigation policies on mental health using network analysis

Abstract: To manage the spread of the COVID-19 virus several federal and state-level health-related mandates were put in place in the United States, including lockdowns. These policies could have adverse effects on the mental health state of the populace. In this study, we assess the impact of COVID-19 policy actions on mental health in the United States using mental health-related indicators such as feeling anxious, feeling depressed, and worried about finances. We analyzed survey data from the Delphi Group at Carnegie Mellon University using clustering algorithms and dynamic connectome obtained by carrying out sliding window analysis. We found that between March 3rd, 2021, and January 10th, 2022, states in the south geographic region showed similar trends for reported values of feeling anxious and worried about finances. There were no identifiable communities clustering for feeling depressed. We observed a high degree of correlation among southern and republican states for feeling anxious and feeling depressed which seemingly overlapped with an increase in COVID-19-related cases, deaths, hospitalizations, and rapid spread of the COVID-19 Delta variant.

Presenter: Samuel Manda (University of Pretoria, South Africa)

Title: Towards Health Survey Data Integration for Public Health Policy in Sub-Saharan Africa

Abstract: Several key health indicators are routinely collected in health surveys but not in censuses. However, health surveys are often powered to provide enough samples of the population at the regional or country levels. Thus health estimates at lower levels could be imprecise and unstable due to the small numbers accrued at these levels. Also, most health sample surveys are run as stand-alone surveys and may not collect all the required health variables. To lessen the costs associated with designing and implementing representative surveys at the desired geographic levels or surveys with complete data, we could leverage available survey data to provide health estimates of health indicators by complementing with auxiliary data from census and administrative records or other surveys. Combining information from different sources to obtain an improved official health estimate could be desired by health policymakers to reduce public health costs. This talk will review some current survey data integration methods, with typical examples.

Presenter: Tesfalem A. Tegegn (University of Pretoria, South Africa)

Title: On Contribution of Vaccines in the Transmission and Control of COVID-19 in South Africa: from mathematical modeling point of view

Abstract: The COVID-19 pandemic had profoundly changed the way we lived and perceived our lives. The successful delivery of vaccines together with relentless effort from all stakeholders helped us to “reclaim our normal way life”. In this article, we propose a mathematical model that incorporates most features of COVID-19 transmission dynamics to investigate the contribution of vaccines to control the pandemic. The basic reproduction number of the model, denoted by R_0 is calculated. During imperfect vaccination and recovery does not lead into permanent immunity, we have shown that the model could exhibit a backward bifurcation when $R_0 < 1$. With perfect vaccination and recovery guarantees permanent immunity, the disease-free equilibrium is globally asymptotically stable for $R_0 < 1$ and unstable for $R_0 > 1$. Numerical experiments are also conducted to support the theoretical analysis. The model is fitted into a real data from open sources and the sensitivity analysis of the basic reproduction number with respect to involved parameters is done to identify the most sensitive parameters for control intervention. Finally, we conclude from the numerical experiments that vaccines have significantly improved the recovery rate from COVID-19 infection but do not offer complete protection.

Presenter: Prof Jacek Banasiak (University of Pretoria) - Primary Author
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Title: Impact of Demography on the Dynamics of Malaria

Abstract: Epidemiological models should account for the vital dynamics when the disease duration is comparable with the lifespan of affected individuals, the disease is lethal or recurring, or when we study the disease's long-term impact on the population. The authors often use ad hoc or generic population equations to describe the vital dynamics. In the talk, using a malaria model as an example, we shall show that the used population model can dramatically affect the dynamics of the disease. Therefore, the selection of the latter requires extreme care.

Presenter: Ding-Geng Chen (University of Pretoria, South Africa / Arizona State University, USA)

Title: Estimate COVID-19 Vaccine Efficacy When the Time-to-Infection for Unvaccinated Group is Unknown.

Abstract: The COVID-19 pandemic has caused significant morbidity and mortality, as well as social and economic disruption worldwide. In order to reduce these effects, a global effort to develop effective vaccines against the COVID-19 virus has produced various options with the effectiveness assessed on the rate of infection between vaccinated and unvaccinated groups, which has been used for important policy decision-making on vaccination effectiveness ever since. However, the rate of infection is an over-simplified index in assessing the vaccination effectiveness overall, which should be strengthened to address the duration of protection with time-to-infection effect. The fundamental challenge in

estimating the vaccination effect over time is that the time-to-infection for unvaccinated group is unknown due to nonexistent vaccination time. This presentation is to discuss the biostatistical methodological development to fill this knowledge gap to propose a Weibull regression model. This model treats the nonexistent vaccination time for the unvaccinated group as nuisance parameters and estimate the vaccination effectiveness along with these nuisance parameters. The performance of the proposed approach and its properties is empirically investigated through a simulation study, and its applicability is illustrated using a real-data example from the Arizona State University COVID-19 serological prevalence data.

This presentation is based on our recent publication: Ding-Geng Chen, Yunro Chung, Kassu Mehari Beyene (2023). Estimate Time-To-Infection (TTI) Vaccination Effect When TTI for Unvaccinated Group is Unknown. Statistics in Biosciences. Accepted.

Presenter: Dr J. Malinzi (University of Eswatini)

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Title: On COVID-19 transmission dynamics and the impact of vaccination: mathematical modeling and numerical simulations

Abstract: This study aims to forecast the potential COVID-19 trends and determine how long a wave could be, taking into consideration the current vaccination rates. The model is calibrated using South African reported data for the first four waves of COVID-19, and the data for the fifth wave are used to test the validity of the model forecast. The model is qualitatively analyzed by determining equilibria and their stability, calculating the basic reproduction number R0 and investigating the local and global sensitivity analysis with respect to R0. The impact of vaccination and control interventions are investigated via a series of numerical simulations. Based on the fitted data and simulations, we observed that massive vaccination would only be beneficial (deaths averting) if a highly effective vaccine is used, particularly in combination with nonpharmaceutical interventions. Furthermore, our forecasts demonstrate that increased vaccination coverage in SSA increases population immunity leading to low daily infection numbers in potential future waves. Our findings could be helpful in guiding policy makers and governments in designing vaccination strategies and the implementation of other COVID-19 mitigation strategies.

Presenters: Delport, R.; Hugo, J.; Mandel-Mntla, E. (University of Pretoria, South Africa)

Title: Establishing a linkage between the South African Population Research Infrastructure Network (SAPRIN) and OneHealth research initiative and interventions

Abstract: SAPRIN surveillance data is captured in low-income communities using a longitudinal study design to monitor demographic parameters that reflect health and socio-economic changes within different urban forms in the absence/presence of environmental stressors. The survey captures household data, including spatial data of all structures, individual attributes of household members and demographic events; household socio-economic status comprising data on access to utilities/services, dwelling construction, household assets, financial situation, food security, access to government social welfare support and experience of crime, as well as individual health data.
The Gauteng Research Triangle (GTR), constituted by The University of Pretoria, -Witwatersrand and -Johannesburg afforded the possibility of establishing the first urban node for surveillance. The Gauteng Research Triangle INitiative for the Study of Population, Infrastructure and Regional Economic Development (GRT-I), opened up opportunities for significant community-based trans-disciplinary research in Hillbrow, Atteridgdeville and in Melusi, which is an informal settlement.

The expected outcomes and impacts of the SAPRIN are to:

- provide a versatile inter-disciplinary **research platform**
- produce ongoing research **data** for policy development and evaluation
- produce routinely-updated **thematic reports** on population health and socio-economic wellbeing
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- establish clear links with the **national statistical system**
- effectively engage **community structures**
- provide a resource for **post-graduate** research training and ongoing career development

Conducting studies in the SAPRIN surveillance population affords the opportunity to link study participants to their SAPRIN surveillance data for distal outcome observations.

The following future actions were outlined during the first meeting between OneHealth research groups from the UP and other institutions and GRT-I:

- To map existing One Health-related projects in and around the GRT-I node and identify overlaps and gaps
- To identify existing ongoing work where collaboration is possible in terms of sharing of samples, data collection and data sharing.
- To document existing service delivery activities related to Human Health Care, Veterinary Care and Environment Care in the GRT-I node, identify needs and gaps and plan interventions and collaborations.
- To adapt the existing GRT-I Urban Module to optimize data collection for One Health work.

We trust that structured collaboration between One-Health and SAPRIN will contribute to successful interventions that are based on a comprehensive knowledge base.

Presenter: Stéphane Yanick Tchoumi (University of Pretoria, South Africa)
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Title: A Mathematical Model for Malaria Transmission Dynamics with Differential Susceptibility and Partial Immunity

Abstract:
Introduction: Malaria is a deadly vector-borne infectious disease with high prevalence in the world's endemic tropical and subtropical regions. Differences in individuals' disease susceptibility may lead to their differentiation of susceptibility to infection. We formulate a mathematical model for malaria

transmission dynamics that accounts for the host's differential susceptibility, where partial immunity is acquired after infection.

Objective: To formulate a mathematical model of malaria with differential susceptibility, in order to assess its impact on malaria transmission dynamics.

Methods: We first carried out a mathematical analysis of our model, including determining the DFE, calculating the basic reproduction rate and studying the existence of an endemic equilibrium for the special case n=2. We then carried out numerical simulations.

Results: We have shown that the DFE is locally asymptotically stable and that for n=2, we can have 0, 1 or 2 endemic equilibria. Graphical representations show that the transient transmission dynamics of the infected components are indistinguishable when there is no inflow into the susceptible classes. When there is an inflow into the various susceptible classes, the graphs of the infected component of the model are fundamentally different, showing that individuals who have been infected multiple times tend to be less infected over time. Knowledge of the inflow rate and the infection reduction rate due to prior infection in each class could be key drivers to mitigate the burden of malaria in a community.

Conclusion: To better understand how differential susceptibility acquired through partial immunity affects the transmission dynamics of malaria, we formulated a compartmental model, based on a system of non-linear differential equations, where the human population is sub-divided into groups according to their disease status and their susceptibility levels, with disease progression stages and partial immunity. Numerical simulations are then carried out to assess the potential impact of differential susceptibility of malaria transmission dynamics. From the graphical representations, the total number of infections drops when increasing the number of infected classes with inflow to all of them, with the higher classes having decreased susceptibility.

Presenter: Suzanne Lenhart (University of Tennessee, USA)

Title: Metapopulation model to evaluate C.difficile potential vaccine interventions

Abstract: Clostridioides difficile (C Diff) is one of the underlying causes of healthcare-associated infections. It colonizes the large intestine, can cause colitis and diarrhea, and can be fatal in some cases. This disease has a comparatively higher prevalence rate in the hospital and nursing facility populations than in the community. A vaccine is a potential preventative measure. However, the vaccine is available only in clinical trials. We present the potential effect of vaccination on the prevalence of the disease in a heterogeneous population. For that, we developed a deterministic model of differential equations of the disease flow in a metapopulation of community, hospital, and skilled nursing facilities. We assume that the vaccine is available only in hospitals and nursing facilities. We applied the vaccine efficacy on susceptibility, colonization, infectiousness, and clinical disease with the group of vaccinated individuals.
