Mathematical Modeling Mini-Courses (3MC) presents:

International Conference on Recent Developments in Mathematical Modeling in Biology

29-31 March 2023

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Mathematical Modeling Mini-Courses (3MC) presents:

International Conference on Recent Developments in Mathematical Modeling in Biology

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Venues for the lectures: G1-102 (plenary lectures, regular talks), G1-112 (regular talks)

Wifi: Eduroam is available on campus. Alternatives will be announced during the event.

Website: https://natural-sciences.nwu.ac.za/paa/3MC-Conference-BM

Program

Wednesday 29 March	
08:00-08:45	Registration
08:45-09:00	Opening
09:00-10:00	Michael Li
10:00-10:30	Tea break
10:30-11:00	Lagura/Chirove
11:00-11:30	Malinzi/Okpeku
11:30-12:30	Sophie Dabo-Niang
12:30-13:30	Lunch
13:30-14:30	Sibusiso Moyo
14:30-15:00	Tea break
15:00-15:30	Maragere/Nyabadza
15:30-16:00	Mukhtar/Koutou
16:00-17:00	Michael Chapwanya
18:00----	Conference dinner

Thursday 30 March	
08:00-09:00	Jomar Rabajante
09:00-10:00	Jacek Banasiak
10:00-10:30	Tea break
10:30-11:00	Tantawy/Mamboundou
11:00-11:30	Adenane/Bansilan
11:30-12:30	Kailash Patidar
12:30-13:30	Lunch
13:30-14:30	Winston Garira
14:30-15:00	Tea break
15:00-15:30	Ramantoanina/Chazuka
15:30-16:00	Mohammadi/Tiruneh
16:00-17:00	James Watmough

Friday 31 March	
08:00-09:00	Stephanie Portet
09:00-10:00	Rachid Ouifki
10:00-10:30	Tea break
10:30-11:00	Modise/Ogunfowote
11:00-11:30	Edogbanya
11:30-12:30	Julien Arino
12:30-12:40	Closing
12:40-13:30	Lunch and farewell

Plenary addresses

Prof Julien Arino

Title: Case introductions in the context of SARS-CoV-2 infections

Abstract: COVID-19, the disease caused by SARS-CoV-2, has spread far and wide in the slightly more than three years since its initial detection, with virtually no place on earth not having reported cases during that period. Most national-level jurisdictions have reported cases continuously since first importing the disease. However, looking into the pattern of spread in more detail, one realizes that at the local level, spread was and remains heterogeneous. The further one "zooms" in, the more likely one is to observe periods during which disease spread took place, separated by periods with no apparent transmission chains. SARS-CoV-2 infections were often asymptomatic, so it is possible that some of these apparent extinction events are linked to the existence of persistent silent transmission chains. However, it is also likely that some of these observed temporary extinctions are indeed what they seem to be. The local level resurgences that follow such periods are linked to introductions, highlighting the need for a better understanding of that process. I will present work about case introductions carried out since the start of the pandemic, involving a variety of models, using both ODE and continuous time Markov chains.

Prof Jacek Banasiak

Title: Multiple time scales and long-term dynamics in epidemiological modelling

Abstract: Mathematical models in epidemiology often combine processes acting on widely different time scales. For instance, in malaria, we have interacting populations, human hosts, and mosquitoes, which evolve at different rates. In age-structured populations, the recovery rate is often much higher than the demographic rates. This offers a way to simplify the models using the tools from the singular perturbation theory.

In this talk, we present a survey of recent work in this field, including uniform in-time estimates and the emergence of the so-called canard solutions, and show how they can be applied to achieve a meaningful reduction in the complexity of some epidemiological models.

Prof Michael Chapwanya

Title: Design of Mickens' schemes for models in mathematical biology. Application to Ebola Virus Disease

Abstract: In this talk we discuss the relationship between continuous dynamical systems and their numerical methods for computer simulations – viewed as discrete dynamical systems. Numerical examples, with application to Ebola Virus Disease, are provided to demonstrate that numerical schemes satisfying the notion of dynamic consistency can be constructed using the nonstandard finite difference method.

Prof Sophie Dabo-Niang

Title: Investigating spatial scan statistics for multivariate functional data

Abstract: In environmental surveillance, cluster detection of environmental black spots is of major interest due to the adverse health effects of pollutants, as well as their known synergistic effect. Thus, this paper introduces new spatial scan statistics for multivariate functional data, applicable for detecting clusters of abnormal air pollutants concentrations measured spatially at a very fine scale in northern France in October 2021 taking into account their correlations.

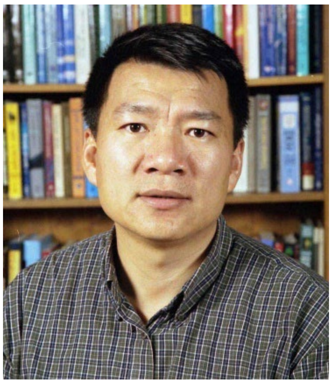
Mathematically, our methodology is derived from a functional multivariate analysis of variance (MANOVA), an adaptation of the Hotelling T2-test statistic, and a multivariate extension of the Wilcoxon test statistic. The approaches were evaluated in a simulation study and then applied to the air pollution dataset.

Prof Winston Garira

Title: Theoretical Foundations for Single Scale Mathematical Modelling of Disease Dynamics

Abstract: Most of the progress in the development of single scale mathematical and computational models for the study of infectious disease dynamics which span over a century now is built on a body of knowledge that has been developed to address single scale descriptions of infectious disease dynamics based on understanding disease transmission process. Although this single scale modelling of infectious disease dynamics is now founded on a body of knowledge with a long history, dating back to about three centuries now, that knowledge has not yet been formalized into a scientific theory. In this talk, I will discuss the formalization of this accumulated body of knowledge into a scientific theory called the transmission mechanism theory of disease dynamics which states that at every scale of organization of an infectious disease system, disease dynamics is determined by transmission as the main dynamic disease process. I will also discuss how the transmission mechanism theory of disease dynamics has recently been extended by our research group into new radical scientific theory for multiscale modelling of infectious disease dynamics called the replication-transmission relativity theory. Throughout this talk, my aim is to show that our description of natural phenomena using scientific theories is a dynamic process because these scientific theories often only adequately describe the phenomenon studied up to a certain time. As time progresses, new knowledge often emerges as we refine the domains of observation to improve the accuracy of measurement and description.

Prof Michael Li



Title: Why do mathematical models over-project COVID-19 epidemics?

Abstract: During the COVID-19 pandemic, mathematical modeling has been widely adopted as a research tool for public health, and modelling results have played an important role informing public health responses to COVID-19. Through two years of highly intensified modeling activities, it has also become apparent that mathematical models tend to over-project the size of an epidemic wave; often over 60% of the susceptible population would be infected during a single wave. While many reasons for the over-projection were considered, from a lack of data and information to the assumptions that no public health interventions were incorporated in the projections, counter arguments abound. This has not only impacted public's confidence in the modeling in general, but also caused much confusion and frustration among modelers, leading to claims that our standard epidemic models are great for studying underlying dynamics but simply have no predictive power.

Are there mathematical insights that can explain the observed over-projections? Indeed, I will show that the well-known final-size formula, which links the basic reproduction number R0 to the final size of an epidemic, predicts that over 60% of the population will be infected during an epidemic with R0 around 2. Then the question becomes how to improve standard epidemic models to produce accurate long-term predictions for real-world epidemics?

I will touch on several pitfalls in the modeling process that can impact the accuracy and reliability of model projections, including mismatching model outputs to data, mistaking model calibration with model validation, and unidentifiability issues in model parameter estimation. In the last part of the talk, I will demonstrate that incorporating human behavioural changes into epidemic models can improve model accuracy and reliability of model projections.

Prof Sibusiso Moyo

Title: Recent Developments in Symmetries of Differential Equations and their Role in Mathematical Modelling of Natural Phenomena

Abstract: Most natural phenomena can be modelled by nonlinear differential equations or systems of equations. Mathematical models that arise from modelling such phenomena have applications in disciplines like Biology, Physics, Cosmology, Chemistry, Engineering, Economics, Social Sciences etc. The concept of symmetry analysis is a group theoretic tool that is used to analyse models that are nonlinear or linear to better understand their properties and integrability conditions. In this plenary session, some applications and the role symmetry methods play coupled with other well-known methods is demonstrated. With the advent of the pandemic and the rise in public health issues nationally and globally due to the pandemic, examples in pandemic modelling and relations of how this work relates in addressing the sustainable development goals is presented. Additionally, as part of research and innovation management, the work being done at Stellenbosch University together with the Centers of Excellence and Research Focus Areas is also highlighted with a view of potential areas for future directions and inter-disciplinary, inter-institutional collaborations.

Prof Rachid Ouifki

Title: Oncolytic Virotherapy: Virus delivery and virus-immune interactions, a mathematical modelling approach

Abstract: Oncolytic viruses (i.e. viruses that selectively replicate and destroy cancer cells while keeping normal cells unharmed) have emerged as promising novel therapeutic strategy against most advanced types of cancers. However, their delivery to tumor sites, and the antiviral immune response remain two major obstacles for the success of such therapy. In this talk, we will explore possible ways to overcome these obstacles. We start by investigating the interplay between oncolytic potency and reduced virus tumor specificity. Then we explore the mechanisms of using mesenchymal stem cells (MSCs) loaded with oncolytic viruses for delivering virotherapeutic agents to the tumor site. Additionally, we assess the potential success of combining virotherapy with another promising therapy that uses the chimeric antigen receptor T (CAR-T) cells. Finally, we explore the impacts of delays in virus delivery on the outcomes of virotherapy.

Prof Kailash Patidar

Title: Slow-fast dynamical systems in mathematical biology

Abstract: In this talk, we will discuss a few prototype models describing slow-fast dynamical systems arising in mathematical biology. Many of these models are singularly perturbed in nature and hence special treatment is required to understand the dynamics that they govern. We will discuss the challenges encountered with their qualitative analyses followed by a quick overview of robust numerical methods that one may use to obtain reliable solutions of such models.

Prof Stephanie Portet

Title: Modelling cytoskeleton: case study of intermediate filaments

Abstract: Intermediate filaments (IFs) are one of the components of the cytoskeleton, which is a network of structural proteins in cells. IFs are involved in cell mechanics, signaling and migration. The organization of intermediate filaments in networks is the major determinant of their functions in cells. Their spatial and temporal organization results from the interplay between assembly/disassembly processes and different types of transport. An overview of mathematical models used to investigate important mechanisms such as the filament elongation or intracellular transport of filaments will be presented.

Prof. Jomar F. Rabajante

Title: Soft skills for mathematical modelers of biological systems

Abstract: A mathematical modeler is expected to possess good quantitative and critical thinking skills. In addition to these skills, soft skills are also crucial to succeed in the mathematical modeling practice. In this talk, I will present the significance of developing creativity (especially in designing the mathematical model and in presenting outputs), proficiency in communicating with various audiences (including news agencies), diplomacy and negotiation abilities (especially when dealing with the government and other organizations), teamwork (including working with people from other disciplines), and capability to do foresight (especially as input to anticipatory planning). In each soft skill, I will provide simple stories based on our experience in the Philippines, including our experience in fighting COVID-19. To end the talk, I will discuss ethical standards in mathematical modeling.

Prof James Watmough

Title: Stage-structured dispersal in marine species with a pelagic larval stage

Abstract: Aquatic species often have radically different dispersal mechanisms at different life history stages. For example, a rapidly dispersing pelagic larval stage dispersing in a current and a sessile or slow dispersing adult stage. We use a structured integro-difference equation model of the spread of the green crab up the northwest coast of the Atlantic as a case study to examine the dependence of invasion dynamics on both adult and larval dispersal. Adding an additional dispersive stage increases invasion spread rates. However, it is unclear how the sensitivity of spread rate to underlying parameters might change with additional dispersive stages. Knowledge on the sensitivity of spread rate to demographic and dispersal parameters helps inform management strategies.

Regular presentations

Rim Adenane, Ibn Tofail University, Kenitra, Morocco

Title: On the *R* Formula and explicit mathematical epidemiology results on age renewal kernels: some examples

Abstract: A very large class of ODE epidemic models which will be presented in this work enjoys the property of admitting also an integral renewal formulation, with respect to an "age of infection kernel" a(t) which has a matrix exponential form.
Some crucial results studied in [Avram et al., 2023] will be presented, and some examples of the (A,B)-Arino models of one class of susceptibles will be addressed.

Keywords: (A,B) Arino-Brauer epidemic models;epidemic models; varying population models; stability; next-generation matrix approach; basic replacement number; vaccination; waning immunity; endemic equilibria.

References

[Avram et al., 2023] Avram, F., Adenane, R., Basnarkov, L., Bianchin, G., Goreac, D., and Halanay, A. (2023). An age of infection kernel, an R formula, and further results for Arin-Brauer (A,B) matrix epidemic models with varying populations, waning immunity, and disease and vaccination fatalities. Mathematics, 11(6).

Norvin P. Bansilan, University of the Philippines Los Baños, Philippines

Title: Mathematical Investigation of Individual Strategies to Eliminate Schistosomiasis Japonica

Abstract: Schistosomiasis (SCH) japonica is an acute and chronic parasitic disease caused by the blood flukes Schistosoma japonicum. Among the three dominant species of schistosome, S. japonicum is a highly zoonotic species that affect both humans and animals. This makes the transmission dynamics of the infection more complex and not easy to control. Despite the efforts to control the disease, it remains a public health concern in many regions, particularly the Philippines. In this paper, our main goal is to illustrate and compare the effectiveness of individual strategies to eliminate SCH japonica using mathematical modeling. Such interventions include human and animal chemotherapy; water, sanitation, and hygiene (WaSH); pasture prohibition; and snail control by vegetation clearing and/or molluscicides. In our model, we incorporate human-definitive, animal-reservoir, snail-intermediate, miracidia, and cercariae populations. Based on our model results, preventing human and animal exposure to contaminated water is more successful than chemotherapy alone. Behavioral modification, health education, animal removal, use of tractors, and support from the Local Government Units are some strategies to consider in implementing WaSH and pasture prohibition.
Joint work with Allen Jethro I. Alonte, Martha Elizabeth Betson, Vachel Gay V. Paller, Joaquin M. Prada, Jomar F. Rabajante.

Zviiteyi Chazuka, University of South Africa, South Africa

Title: Modeling and analysis of an HIV model with control strategies and cost-effectiveness

Abstract: Despite the global commitment to reducing new HIV infections and the provision of access to antiretroviral treatment, HIV still remains a serious public health concern. Preexposure prophylaxis (PrEP) has contributed immensely to the reduction of new infections yet like other HIV prevention methods, the lack of proper adherence has reduced its overall effectiveness. We propose an optimal control model for the dynamics of HIV in the presence of control measures such as pre-exposure prophylaxis (PrEP), condom use and treatment. The model considers a triple control where ($u{*}1(t)$,

represents condom use, $u*2$ (t) represents PrEP and $u*3(t)$), represents antiretroviral therapy. Existence of the optimal control is proved and Pontryagin's maximum principle is applied to establish the optimal control conditions. The control reproduction number, R_c, was computed and analysis shows that when $R_c < 1$, HIV infection can be eradicated. Numerical simulations were performed using demographic and epidemiological parameters for South Africa and presented in both 2D and 3D plots. Results from the numerical simulations indicate that a combination of proper condom use and adherence to PrEP reduces new HIV infections within the community. On the other hand a combination of all the three controls effectively ensures the eradication of HIV infection within the population. In addition to the presented analysis we will also consider cost-effectiveness analysis to establish the costs associated with the use of a combination of controls. We envisage that the results from the analysis should advise policy makers.
Joint work with Chinwendu E. Madubueze, Edinah Mudimu, Dephney Mathebula.

Keywords: Pre-exposure prophylaxis, Adherence, Optimal Control, Pontryagin's maximum principle, Cost-effectiveness

Faraimunache Chirove, University of Johannesburg, South Africa

Title: On the impact of hierarchy-of-resort-resort treatment-seeking behavior on malaria infection

Abstract: Malaria is still a huge public health problem and many lives would be saved if access to good quality, affordable and efficacious medicines were readily available. There is a widespread integration of indigenous and allopathic medicine in Africa and many developing countries with a huge proportion of populations relying on traditional medicine and local medicinal plants for primary health care, as a choice or when there is no access to other medicine. Some of the major anti-malarial drugs such as the quinine and artemisinin trace their origin to complementary, alternative and traditional medicine. Antimalarial drugs form part of a wider set of products where quality is not directly observable at the time of purchase, and only partially observable when used. So fake antimalarial drugs widespread use is also associated to hierarchy of resort treatment seeking behavior becoming a threat towards malaria treatment efforts with a long run possibility of adverse effects and development of drug resistance. We focus our attention on quantifying the impact of hierarchy of resort treatment seeking behavior on malaria disease on the prevalence of malaria infection as well as the prevalence of drug resistance to malaria infection. Important thresholds are computed that determine the conditions for disease.

Helen Olaronke Edogbanya, Federal University Lokoja, Nigeria

Title: Mathematical analysis of zika virus with optimal control

Abstract: Zika virus transmission model was formulated and analyzed with three nonlinear forces of infection from infected mosquito, asymptomatic and symptomatic humans. The sensitivity indices of the associated parameters of the model with respect to the basic reproduction number are calculated to identify intervention strategies for prevention and control of Zika virus. Multiple time-dependent optimal controls are considered. The analysis based on the use of optimal control theory made popular by Pontryagin's maximum principle is carried out, and the resulting optimality system is quantitatively simulated to investigate the impact of the controls on the dynamics of Zika virus. In addition, the effects of non-linearity of the forces of infection and other key parameters on the disease transmission are illustrated.

Keywords: Zika virus, Basic reproduction number, Non-autonomous model, Optimal control

Ousmane Koutou, University Joseph KI-ZERBO, Burkina Faso

Title: Mathematical analysis of the impact of the media coverage in mitigating the outbreak of Covid-19

Abstract: In this talk, I will present a mathematical model with a standard incidence rate to assess the role of media such as Facebook, television, radio and Tweeter in the mitigation of the outbreak of COVID19. The basic reproduction number R0 which is the threshold dynamics parameter between the disappearance and the persistence of the disease has been calculated. It is obvious to see that it varies directly to the number of hospitalized people, asymptomatic, symptomatic carriers and the impact of media coverage. The local and the global stabilities of the model have also been investigated by using the Routh-Hurwitz criterion and the Lyapunov's functional technique, respectively. Furthermore, we have performed a local sensitivity analysis to assess the impact of any variation in each one of the model parameters on the threshold R0 and the course of the disease accordingly. We have also computed the approximate rate at which herd immunity will occur when any control measure is implemented. To finish, we have presented some numerical simulation result by using some available data from the literature to corroborate our theoretical findings.

Maria Czarina T. Lagura, Ateneo de Manila University, Philippines

Title: Mathematical modelling for the COVID-19 dynamics with vaccination and reinfection

Abstract: In this paper, we develop a compartmental model for the transmission dynamics of COVID-19 incorporating the vaccination program and the possibility of reinfection among recoveries. Using the next generation matrix method, we derive the basic reproduction number R_0. Moreover, we use R_0 along with other conditions to determine equilibrium solutions. When $R_0 < 1$, we establish conditions for the global asymptotic stability of the disease-free equilibrium solution. On the other hand, when $R_0 > 1$, then there exists a unique endemic equilibrium solution and we establish conditions for its global asymptotic stability. Finally, we use numerical solutions to verify the results of our stability analysis.
Joint work with Roden Jason A. David and Elvira P. de Lara-Tuprio.

Joseph Malinzi, University of Eswatini, Eswatini

Title: On some aspects of COVID-19 transmission dynamics, number of waves and impact of vaccination: from mathematical modeling, sensitivity analysis and numerical simulations

Abstract: In this paper, an SEIRV model framework is presented for analysing the transmission dynamics of COVID-19 with the aim of investigating the effect of COVID-19 vaccination on possible duration of wave occurrences and to determine the effect of vaccination rate and efficacy. A thorough qualitative analysis is carried out. This includes determining model equilibria and their stability, determining R_0, investigating the existence of backward bifurcation, determining the existence of an endemic equilibrium and carrying out sensitivity analysis. The model is calibrated using South African reported data for COVID-19 from the start of the epidemic until February 2022. The model is fit to data for all the waves implying that parameter values that represent all the four waves are obtained. A local and global sensitivity analysis is carried out in order to determine the factors, in the form of parameters, that most influence the dynamics of the disease progression. The results depict that the combination of NPIs with vaccination would certainly beat COVID-19 even in the absence of a cure for the disease. It was further observed that massive vaccination would only be beneficial if a highly effective vaccine is used. The mathematical model, analytical and numerical results in this study can be adopted to study the dynamics of COVID-19 in any country or region and make future forecasts.
Joint work with Victor Ogesa Juma, Chinwendu Emilian Madubueze, John Mwaonanji, Godwin Nwachukwu Nkem, Elias Mwakilama, Tinashe Victor Mupedza, Vincent Nandwa Chiteri, Shaibu Osman, Tawanda Matthew Mazikana, Emmanuel Afolabi Bakare, Isabel Linda-Zulu Moyo, Pretty Cynthia Nyalala, Eduard Campillo-Funollet, Farai Nyabadza and Anotida Madzvamuse.

Hermane Mambili Mamboundou, University of KwaZulu-Natal, South Africa

Title: Studying the effect of parasite switching in optimal control analysis of sleeping sickness

Abstract: We construct and analyse an immunological mathematical model to explore the within-host dynamics of a neglected tropical vector disease called Human African Trypanosomiasis (HAT). The parasite that causes the disease evades the immune system by switching to different parasite types. The disease is modelled with six ordinary differential equations representing the type 1 and type 2 parasites, naïve macrophages, classical macrophages, alternative activated macrophages, and cytokines. The model is first analysed without any control measures, and the analysis reveals the existence of one disease-free equilibrium state and two endemic equilibrium states, one of which is where both type 1 and type 2 parasite co-exist and the other only has one parasite type. Furthermore, the effect of control measures on the persistence and extinction of the parasite is investigated. Two optimal control models looking at the effect of two drugs are presented; the first drug focuses on the invasion of the parasite and the other targeting the growth rate of the parasite. Results show that the first drug steers the system from the co-existing endemic state to the parasite type 2 endemic state, but the growth inhibitor drug clears the host of the parasite.

Bothwell Maregere, University of Venda, South Africa

Title: Multiscale Model of Malaria Disease Dynamics that Incorporate the Effects of Temperature Changes

Abstract: This study is based on direct transmitted vector-borne disease mechanism which has the entire pathogen life cycle which is strictly internal (i.e., inside-host environment) of two hosts (i.e., human and mosquito). The main objective of this study is to develop a coupled multiscale model of the malaria disease system to evaluate the impact of temperature changes on malaria replication-transmission multiscale dynamics. In this study, we presented a coupled multiscale model for the malaria disease system based on a combination of two categories of multiscale models of infectious disease systems: (a) an embedded multiscale model for mosquitoes that integrates within-mosquito host scale and between-mosquito host scale, and (b) nested multiscale model for humans that integrates within-human host scale and between-human host scale. The multiscale model of malaria disease system dynamics was solved both analytically and numerically. The disease-free equilibrium state was established to be locally and globally asymptotically stable. Using the fixed-point theorem, the stability of the endemic equilibrium was observed to be stable. The results from the graphs indicated that as the temperature increases the population of infected humans, the population of infected mosquitoes, community gametocytes load, and community sporozoites load increases and reaches the optimum when the temperature is between 280C and 320C and decreases thereafter as the temperature continues to increase. From our analytical results, we confirmed that the variation of temperature plays an important role in the replication-transmission of malaria disease dynamics. In conclusion, the results presented in this study are useful in advising the policymakers and those who are responsible to implement effective malaria health interventions in endemic regions with malaria disease and to adopt better strategies for improving the control of malaria diseases.

Keamogecoe Modise, University of Johannesburg, South Africa

Title: An obesity and covid-19 co-infection model

Abstract: Despite its rapid growth and having now reached endemic levels, obesity continues to grow at an alarming rate globally. Obesity is known to be an epidemic currently and we wish to model the evolution of obesity prior to, and now especially during the current Covid-19 times. The advent of Covid-19 resulted in increased deaths for the obese globally. We assess a dual-infection SEIR model with hospitalization and no cross-immunity. The results presented are key to understanding how the emergence of Covid-19 impacted already existing epidemics. The potential of such findings in quantifying the impact of future pandemics on existing epidemics is immense.

Seyyed Abbas Mohammadi, University of the Witwatersrand, South Africa

Title: Optimizing the total population of a single species in a diffusive logistic model

Abstract: In this talk, we investigate the maximization of the total population of a single species which is governed by a stationary diffusive logistic equation with a fixed amount of resources. The qualitative characteristics of the maximizers, such as symmetry, will be discussed for large diffusivity. Our findings are consistent with other research that claims concentrated resources are advantageous for maximizing the total population for large diffusion. Then, an optimality condition for the maximizer is derived based upon rearrangement theory. We develop an efficient numerical algorithm applicable to domains with different geometries in order to compute the maximizer. With an eye on biological interpretations, our numerical simulations give a real insight into the qualitative properties of the maximizer.

Abdulaziz Mukhtar, University of the Western Cape, South Africa

Title: Investigating the influence of climate variability on malaria transmission using a mosquito-human malaria model

Abstract: The Republic of South Sudan is among the countries still severely confronted by malaria. Little is known about the effect of local environmental conditions that may contribute to the severity of the disease in different altitude areas. Mathematics models can bring insight to improve our perception of host-parasite interactions, especially regarding conjectures that attribute this gravity to climatic factors. We develop and analyze a mosquito-host disease-based model that includes temperature and rainfall. Using a maximum-likelihood approach, the model has been parameterized and validated using time series data of trends in malaria cases for different climatic regions. We studied the model's key properties, not limited to equilibria, stability, and the basic reproduction number R_0 with its sensitivity index. In addition, the effect of rainfall and temperature on mosquito abundance was examined. The results obtained in this study show that the disease behavior changes with the change in the local climate. Therefore, this study substantiated our claim that the disease was more severe in the tropics than in a hot semi-arid region due to climatic conditions and should be treated as such whenever an intervention against malaria is applicable.

Farai Nyabadza, University of Johannesburg, South Africa

Title: Incorporating policy changes in epidemic models

Abstract: The role of policy changes in shaping the trajectory of an epidemic has been documented. The explicit modelling of policy changes is not well documented. In this talk, we look at how policies are incorporated into epidemic models. We illustrate how dynamic policies are modelled by considering the HIV/AIDS epidemic in Botswana. We track the changes in Botswana's HIV/AIDS response and treatment policies using a piece-wise system of differential equations. The policy changes are easily tracked in three epochs. Models for each era are formulated from a grand model that can be linked to all the epochs. The grand model's steady states are determined and analysed in terms of the model reproduction number, R_0: The model exhibits a backward bifurcation, where a stable disease-free equilibrium coexists with a stable endemic equilibrium when $R_0 < 1$: The stability of the models for the other epochs can be derived from that of the grand model by setting some parameters to zero. The models are fitted to HIV/AIDS prevalence data from Botswana for the past three decades. The changes in the populations in each compartment are tracked as the response to the disease and treatment policy changed over time. Finally, projections are made to determine the possible trajectory of HIV/AIDS in Botswana. The implications of the policy changes are easily seen, and a discussion on how these changes impacted the epidemic is articulated. The results presented have a crucial impact on how policy changes affected and continue to influence the trajectory of the epidemic in Botswana.

Oladele T Ogunfowote, University of Venda, South Africa

Title: A Nested Multiscale Model of Hepatitis B Virus Infection

Abstract: Hepatic viral infection remains a global health concern owing to its deadly nature. Most of the Mathematical Models employed to study viral infectious diseases are single scale and are unable to describe the complex nature of viral infections in detail, hence a new and improved approach will be required to study viral infection dynamics. In this study, we described the Replication – Transmission Relativity Theory of disease dynamics on the multiscale modelling of Hepatitis B viral infection. We adopt the Nested multiscale models at the cell level of biological organisation in which a new set of metrics to measure both at individual level and community level infectiousness are introduced. The model allows the study of the dynamics of virus inside infected cells as well as the release of virus from infected cells and the dynamics of subsequent new cell infections. Numerical simulations will be carried out to quantitatively investigate the influence of the within-cell on the between-cell transmission dynamics and will be used to evaluate the effectiveness of the treatment and preventive interventions.

Moses Okpeku, University of KwaZulu-Natal, South Africa

Title: Analytical forecast using the ARIMA model in modelling role of imported malaria in malaria endemic Limpopo province

Abstract: Investments and Efforts in malaria control and elimination in South Africa has yielded much gain over the years. Despite these efforts, imported malaria has been implicated in persistence of malaria endemism in some part of the country, and threatens elimination gains achieved. The persistence of malaria in Limpopo province has largely been attributed to imported cases in the province and has contributed to the slow pace of achieving the malaria-free target by 2025. An understanding of the contribution of imported cases, based on available surveillance data and modelling forecasts, will expedite planning and intervention towards elimination.

The study was conducted using eleven years data from the Limpopo Malaria Surveillance Database System which captured both passive and active malaria cases. Data analysis was done following the classification into either local or imported cases. An Auto Regressive Integrated Moving Average (ARIMA) model was developed to forecast malaria incidence based on temporal autocorrelation present in the incidence data.

The study found that out of 57,288 (X^2 = 896.363, P<0.001) people that were tested, 51,819 (X^2 = 896.363, P<0.001) cases were local while 5,469 (X^2 = 896.363, P<0.001) cases were imported. Mozambique 44.9% (2370), Zimbabwe 1,882 (35.7%) and Ethiopia 446 (8.5%) were the highest contributors of imported cases. The month of January recorded the highest incidence of cases while the least number of cases was in August. Analysis of the yearly figures shows an increasing trend and seasonal variation of recorded malaria cases. ARIMA (3,1,1) model used in predicting expected malaria case incidences for three consecutive years showed a decline in malaria incidences.

The retrospective analysis of this eleven year data has suggests that imported malaria accounted for 9.5% of all recorded malaria cases in Limpopo province. Although there are malaria control measures in place, there is need to strongly consider strengthening of health education campaigns on malaria prevention methods at the grass-root level as well as strengthening of indoor residual spray programs. Bodies that are collaborating towards malaria elimination in the Southern Africa region need to ensure a practical delivery on the objectives of the alliance in order to reduce the high incidences of imported malaria.

Keywords: Imported malaria, Limpopo province, Surveillance, Travel history, Forecast

Mihaja Ramanantoanina, University of Pretoria, South Africa

Title: Mathematical models of mutualistic populations in continuous and discrete time

Abstract: Mutualism is one of the central interspecies interactions in ecology, along with competitive and predator-prey interactions. Mutualistic interactions have been studied using mathematical models, but nowhere near as extensive as competitive and antagonistic interactions, despite their ubiquity. In this talk, we present well known continuous models of mutualistic interactions. Then we will consider existing approaches to formulate the corresponding discrete time models. Finally, we discuss the qualitative features of the continuous models and their discrete analogues.

Mohamed Tantawy, October 6 University, Egypt

Title: Modeling of DNA with Inharmonic Potential and Under Periodic Force Effects lead to damage

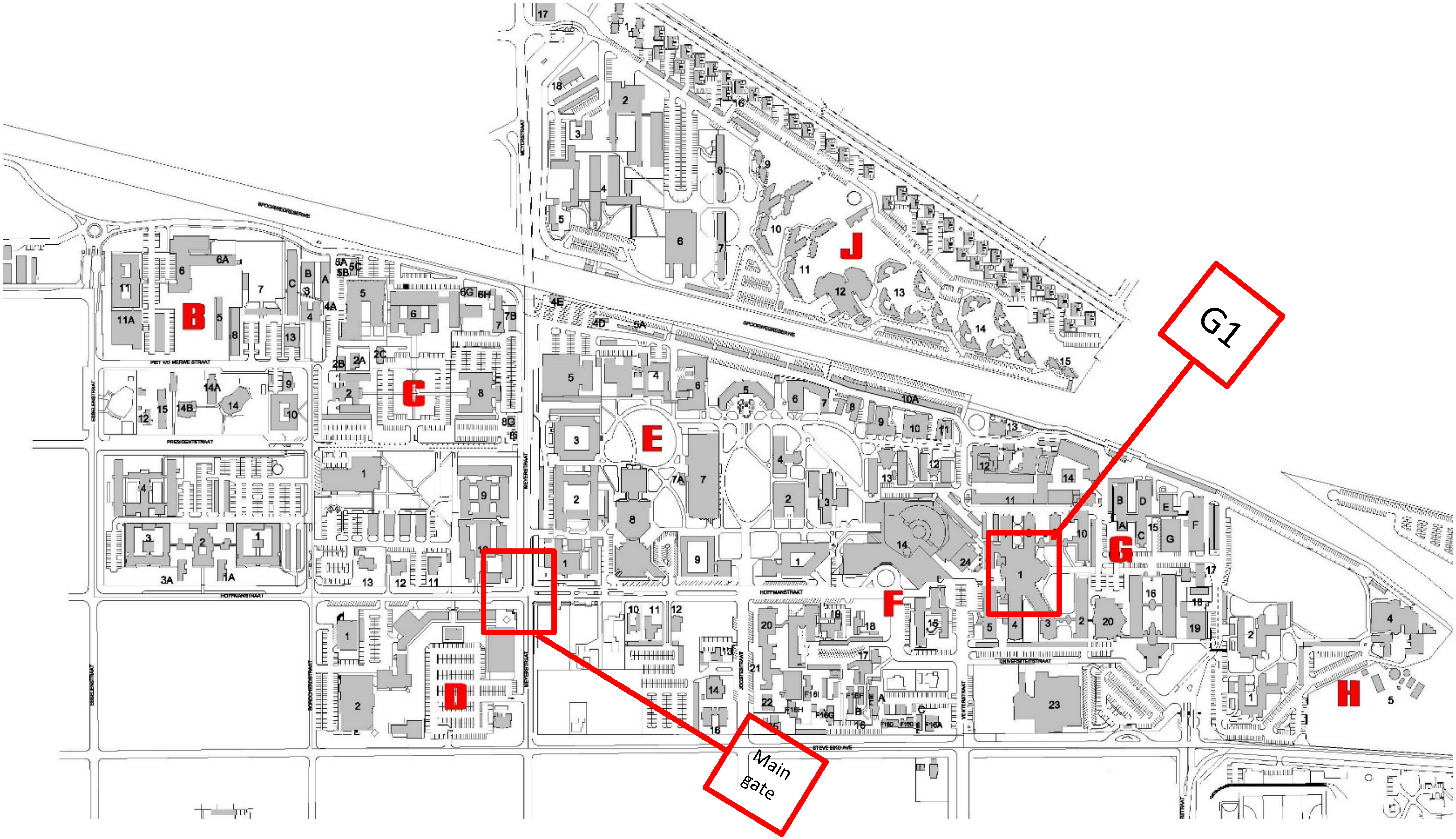
Abstract: The study of the motion of DNA molecules requires novel dynamical models. We propose a discrete and continuum model to describe the nonlinear dynamics DNA molecule with inharmonic potential and under periodic force effects. We consider two physical situations, the ideal or homogeneous state, the inhomogeneous or damage state and rotational model under magnitude of the external influence force. Our objective is to distinguish between the dynamics of DNA in the normal and damaged states. The unified and extended unified methods are used to find the exact solutions of the models in these cases, on the localization of bases in the opening motion of DNA, respectively. Here, it is found that, in the ideal case, the motion of DNA molecules is periodic. The inhomogeneous case under the high values of the inverse width of the backbone rigidity due to damage. Also, oscillator of motion show under chain curvature value, the strength of H-bonds between complementary DNA molecules and the effects of dissipation of interaction with the liquid surrounding the DNA molecule. It is found at high values of damping rate the distance of two chain increase and lead to damage.

Wubetea Tiruneh Adigo, Arba Minch University, Ethiopia

Title: Mathematical model for Covid-19 in the post-lockdown era

Abstract: Lockdown is one of the drastic measures implemented by governments to curtail the spread of the Covid-19 pandemic and save lives. However, it has caused unprecedented damages to the economy. This paper provides a quantitative approach to assess the impact of a gradual, post-lockdown context concerning the spread of the disease. We propose to create a special class of individuals called "protected" who are risk-free to be infected. We developed a mathematical epidemic model for Covid-19 which describes the interactions between susceptible and infected individuals. As a case study on South Africa, the sensitivity analysis shows that investing on the special class "protected" is a better approach to reducing new secondary infections as opposed to reducing the contact rate between susceptible and infected individuals, or having more recovered patients. The simulations reveal that the peak could be reached in September 2020. The number of infected and deaths could drastically increase as the proportion of individuals joining the special class decreases.

Campus map


G1
Main gate
B
C
D
E
F
G
H
J
SPOORWEGRESERWE
MEYERSTRAAT
PIET VD MERWE STRAAT
PRESIDENTSTRAAT
HOFFMANSTRAAT
UNIVERSITEITSTRAAT
STEVE BIKO AVE
ESSELENSTRAAT
BORCHERDSTRAAT
JOOSTESTRAAT
VERTERSTRAAT