Mathematical Modeling Mini-Courses (3MC) presents:

International Conference on Mathematical Modeling in Biology and Life Sciences

28 February-1 March 2024

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International Conference on Mathematical Modeling in Biology and Life Sciences
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Venues for the lectures: Building E7, rooms 312 (plenary talks (Px), regular talks (Rx and Rxa)) and 311 (regular talks (Rxb)).

Wifi: Eduroam is available on campus. Alternatively, you can use NWU Guest wifi. We will announce the password at the beginning of the conference.

Website: https://natural-sciences.nwu.ac.za/paa/3MC-Conference-2024

Program

Wednesday 28 February	
09:00-09:15	Registration
09:15-09:30	Opening
09:30-10:30	P1: Etienne-Manneville & Portet
10:30-11:00	R1a: Kabiwa Kadje (312)
10:30-11:00	R1b: Netshikweta (311)
11:00-11:30	Coffee and tea break
11:30-12:00	R2a: Maphiri (312)
11:30-12:00	R2b: Magagula (311)
12:00-13:00	P2: Banasiak
13:00-14:00	Lunch
14:00-15:00	P3: Agusto
15:00-15:30	Coffee and tea break
15:30-16:00	R3: Chirove (312)
16:00-16:30	R4a: Helikumi (312)
16:00-16:30	R4b: Foko (311)

Thursday 29 February	
09:00-10:00	Plenary 4: Sfakianakis
10:00-10:30	R5a: Qwabe (312)
10:00-10:30	R5b: Malinzi (311)
10:30-11:00	Coffee and tea break
11:00-12:00	P5: Lubuma
12:00-12:30	R6a: Ouemba Tasse (312)
12:00-12:30	R6b: Mupedza (311)
12:30-13:00	R7a: Maina (312)
12:30-13:00	R7b: Mnisi (311)
13:00-14:00	Lunch
14:00-15:00	P6: Ouifki
15:00-15:30	Coffee and tea break
15:30-16:30	P7: Watmough
18:00----	Conference dinner (H4)

Friday 1 March	
09:00-10:00	P8: Fabris-Rotelli
10:00-10:30	R8a: Ramanantoanina (312)
10:00-10:30	R8b: Roberts (311)
10:30-11:00	Coffee and tea break
11:00-12:00	P9: Arino
12:00-12:30	Prizes and closing
12:30-13:30	Lunch

Plenary addresses

Professor Folashade Agusto

Title: Prescribed fire: Exploring the effect of fire on tick-borne diseases

Abstract: In recent times tick ranges have been expanding due in part to rising temperatures as a consequence of climate change, thereby increasing the risks and prevalence of tick-borne illnesses across the country. Thus, it is vital to find practical ways of managing tick populations. Prescribed fires are a common form of land management practices; it is time and cost-efficient when applied across large amounts of land. In this seminar, I investigate the effects of prescribed fire intensity and the duration between burns on the prevalence of tick-borne illnesses as temperature rises. Using stage-structured tick-host models with impulsive differential equations our results indicate that prescribed fire intensity has a larger impact in reducing disease prevalence than frequency between burns. Exploring the use of prescribed burns in preventing the establishment of ticks into new areas shows that fewer burns are ineffective at preventing their establishment because ticks can recover relatively quickly following a burn, but frequent, long-term prescribed burns can slow and possibly prevent their establishment.

Professor Julien Arino

Title: Modelling a multiple pathogen / multiple species system

Abstract: In the context of the ongoing climate change crisis, the range of aquatic species is changing much faster than it used to. This has implications in terms of pathogen propagation, since species that used to interact infrequently now come into contact more frequently. This has the potential of introducing pathogens into ecosystems from which they were absent to that point. The work presented here is motivated by the situation in the Western Canadian Arctic and the Mackenzie River system, where some resident species are increasingly collocated with vagrant salmon species who spend much of their time in distant ecosystems. A simple ODE model is formulated for the transmission of multiple pathogens between multiple species. The corresponding continuous time Markov chain and its multitype branching process approximation are then studied in order to characterise the probability that a pathogen becomes establishes in a species from which it was absent. Computational analysis of some simple cases are also presented.

Professor Jacek Banasiak

Title: Direct Lyapunov method - known and less known

Abstract: Lyapunov functions are workhorses of the stability theory of dynamical systems. However, mainly, only a small number of possibilities offered by the theory is used. In this, mostly survey, talk, we will describe its less-known aspects, such as nondifferentiable Lyapunov functions or inverse Lyapunov theorems, and their applications in mathematical biology.

Professors Sandrine Etienne-Manneville and Stephanie Portet

Title: Intracellular dynamics and transport of cytoplasmic intermediate filaments

Abstract: Intermediate filaments are one of the components of the cytoskeleton. These long elastic homo- or hetero-polymers spread throughout the cytoplasm to form a scaffolding network, which plays a key role in the control of cell mechanics, cell morphology and cell and tissue integrity. The organization of the intermediate filament networks is the major determinant of their functions in cells and tightly regulated by a combination of intracellular processes. The dynamic spatio-temporal regulation of the network results from the interplay between assembly/disassembly of filaments, filament bundling and different types of intracellular transport. An overview of biological processes involved in the intermediate filament organization and dynamic rearrangements will be presented as well as experimental techniques, mathematical models and their combination used to investigate important mechanisms related to this problem.

Professor Inger Fabris-Rotelli

Title: Advances in Spatial Linear Networks

Abstract: This talk will cover the use of linear networks in Spatial Statistics. A variety of methods will be discussed involving analysis in a linear network space. Applications in informal roads, criminology and disease mapping will be presented.

Professor Jean Lubuma

Title: Nonstandard finite difference models of the Ebola virus disease and related optimal control problems

Abstract: Ebola Virus Disease (EVD) outbreaks in Sub Saharan Africa often come with unprecedented challenges. For instance, for the 2014-2016 West Africa EVD, the largest and severest outbreak with a total of 28,616 cases and 11,310 deaths, one of the serious challenges was that the outbreak simultaneously arose in three different countries (viz. Guinea, Liberia and Sierra Leone) to and from which migrations and travel of people by road and air were considerable, despite the implementation the exit screening measure at the borders, as recommended by the World Health Organization. In this talk, we construct a metapopulation model to study the transmission dynamics as well as the control and management of the disease. In each patch, we consider an extended Susceptible-Exposed-Infective-Recovered (SEIR) type-model enriched by three more compartments that account for disease induced deceased, isolated and quarantined individuals. Our focus is three-fold. Firstly, we investigate the stability of the disease-free equilibrium and boundary equilibria in terms of various threshold parameters such as the control reproduction number. Secondly, we design nonstandard finite difference (NSFD) schemes that replicate the feature of the continuous model. Thirdly, we take the work at another level. That is to consider two optimal control problems. The first problem is defined through the exit-entry screening of travellers, while the second one combines the exit screening with the vaccination intervention. The well-posedness of both problems is proved by Pontryagin's maximum principle. For each optimal control problem, we construct a new Forward-Backward-Sweep-Method (FBSM) in which the state variable system is approximated by a NSFD scheme, which is dynamically consistent with respect to the continuous model. Numerical simulations, based on real data from the three most affected countries mentioned above, are provided to support the theory. They confirm the superiority of the NSFD schemes over the standard ones. In particular, a new fact is observed: the classical Euler-based scheme annihilates the impact of the optimal control on infection numbers, while the nonstandard Euler-based scheme faithfully replicates it.

Professor Rachid Ouifki

Title: From the estrogen paradox to the guardian of the genome. Insights from mathematical modelling into breast cancer treatment

Abstract: Estrogen plays a dual role in breast cancer, stimulating its growth while also being effective in its treatment. This is referred to as "the estrogen paradox". Therapies centered around estrogen have shown efficacy in reducing the risk of cancer recurrence. Moreover, the p53 protein, termed "the guardian of the genome", plays a pivotal role in preventing breast cancer by regulating genes involved in DNA repair, cell cycle arrest, and inducing apoptosis when DNA damage is too severe. However, when administered as standalone interventions, both therapies exhibit limited success in treating breast cancer. Therefore, it is imperative to explore their potential when combined.

Given the complex interplay between estrogen and the protein p53, we will present an overview of these two treatment modalities, considering their individual limitations and strengths. We will also use mathematical modelling to explore the interaction dynamics between these two factors, and their link to the estrogen papadox. Additionally, we will use optimal control theory to investigate potential avenues for optimizing breast cancer treatment combination strategies.

Professor Nikolaos Sfakianakis

Title: The filament based lamellipodium model: where the mathematical cell motility begins

Abstract: The lamellipodium is a thin, sheet-like structure that is found in the propagating front of fast moving cells like fibroblasts, keratocytes, cancer cells, and more. It is a dense network of linear biopolymers of the protein actin, termed actin-filaments. These actin-filaments are highly dynamic structures that participate in a plethora of processes such as polymerization, nucleation, capping, fragmentation, and more.

These processes are important for the structure and functionality of the lamellipodium and the motility of the cell. They are, to a large extent, affected by the extracellular environment; for example, the chemical landscape in which the cell of resides and the local composition and architecture of the Extracellular Matrix (ECM), lead to biased motility responses of the cell. When in proximity to each other, they develop cell-cell adhesion via specialized transmembrane proteins of the cadherin family. Collectively, they coagulate to clusters of cells that eventually merge to form cell monolayers.

We model these phenomena using the Filament Based Lamellipodium Model (FBLM); an anisotropic, two-phase, two-dimensional, continuum model that describes the dynamics the lamellipodium at the level of actin-filaments and their interactions. The model distinguishes between two families (phases) of filaments and includes the interactions between them, as well as between the network of the filaments and the extracellular environment. The FBLM was first proposed in [1] and later extended in [2,4,5]. The FBLM is endowed with a problem specific Finite Element Method (FEM) that we have previously developed in [3].

In this talk we present the basic components of the FBLM and the FEM and focus on a series of simulations reproducing fundamental components of the motility of the cells, such us chemotaxis, haptotaxis, interaction with the environment [3,4]. We also present our new findings with respect to cell-cell collision and adhesion, as well as the formation of clusters of cells and cell monolayers [5]. To confront the increased computational needs of the monolayer, we have developed a parallel version of our numerical method which we also address in this talk.

References

[1] D. Oelz, C. Schmeiser. How do cells move? in Cell mechanics: from single scale-based models to multiscale modeling, (2010)

[2] A. Manhart, D. Oelz, C. Schmeiser, N. Sfakianakis, An extended Filament Based Lamellipodium: Model produces various moving cell shapes in the presence of chemotactic signals, (2015)

[3] A. Manhart, D. Oelz, C. Schmeiser, N. Sfakianakis. Numerical treatment of the filament based lamellipodium model (FBLM) (2016)

[4] N. Sfakianakis, A. Brunk, Stability, convergence, and sensitivity analysis of the FBLM and the corresponding FEM, (2018)

[5] N. Sfakianakis, D. Peurichard, C. Schmeiser, and A. Brunk, The FBLM-FEM: from cell-cell adhesion to cluster formation, (2018)

Professor James Watmough

Title: Infections, invasions, immunity, and multiple stable states

Abstract: Many theoretical problems in ecology, epidemiology and immunology can be cast as characterizing and quantifying the response of an ecosystem to a disturbance. Depending on the size and nature of the disturbance, the system may return quickly to equilibrium, or transition between multiple equilibria, or embark on wild and exciting transient dynamics.
As a consequence, the objective of an intervention and control measures is not necessarily to eradicate the pathogen, but to determine the time and duration of intervention required to shift the dynamics into the basin of attraction of the desired state. In this seminar we'll explore some of the consequences of multiple steady states and interesting transient solutions in simple epidemiological, ecological and immunological systems.

Regular presentations

On the impact of migration on the dynamics of a tick-borne disease

Faraimunashe Chirove, University of Johannesburg, South Africa

Abstract: Spatial heterogeneity and migration of hosts and ticks have an impact on the spread, extinction and persistence of tick-borne diseases. In this paper, we investigate the impact of between-patch migration of white-tailed deer and lone star ticks on the dynamics of a tick-borne disease using a system of Ito stochastic differential equations. Results are illustrated for a two-patch deterministic and stochastic models. The results suggest that the probability of probability of disease extinction can be increased if deer and tick movement are controlled or prohibited especially when there is an outbreak in one or both patches. Screening of infectives in protected areas such as deer farms, private game parks or reserves, etc. before they migrate to other areas can be one of the intervention strategies for controlling and preventing disease spread in a multipatch environment.

Reference
1) Milliward Maliyoni, Holly D Gaff, Keshlan S Govinder, Faraimunashe Chirove, (2023), Multipatch stochastic epidemic model for the dynamics of a tick bone disease, *Frontiers in Applied Mathematics and Statistics*, 9, 1122410.

Analysis of a delayed spatiotemporal model of HBV infection with logistic growth

Séverin Foko, University of The Witwatersrand, South Africa

Abstract: In this paper, following previous works of ours, we deal with a mathematical model of hepatitis B virus (HBV) infection. We assume spatial diffusion of free HBV particles, logistic growth for both healthy and infected hepatocytes, and use the standard incidence function for viral infection. Moreover, one time delay is introduced to account for actual virus production. Another time delay is used to account for virus maturation. The existence, uniqueness, positivity and boundedness of solutions are established. Analyzing the model qualitatively and using a Lyapunov functional, we establish the existence of a threshold T0 such that, if the basic reproduction number R0 verifies R0 ≤ T0 < 1, the infection-free equilibrium is globally asymptotically stable. When R0 is greater than one, we discuss the local asymptotic stability of the unique endemic equilibrium and the occurrence of a Hopf bifurcation. Also, when R0 is greater than one, the system is uniformly persistent, which means that the HBV infection is endemic. Finally, we carry out some relevant numerical simulations to clarify and interpret the theoretical results.
This talk is based on joint work with C. Tadmon.

Dog screening as a novel complementary guinea worm disease control tool to mitigate persistence in Chad: a modeling study

Mlyashimbi Helikumi, Mbeya University of Science and Technology, Tanzania

Abstract: A free-roaming dog population remains one of the major public health problems in many developing countries. In this study, we investigated the potential impact of owned roaming and stray dogs on the persistence and possible eradication of Guinea worm disease (GWD) in Chad. We developed and analysed a multi-host of Guinea worm; and considered dogs as the definitive hosts, and fish as the intermediate hosts. Currently, GWD cases in the human population are low; hence, we ignored the human population in this study. We derived the reproduction number and explored how it depends on different model parameters that define it. We calibrated the proposed model with data from literature and validated it with recently reported GWD monthly data for dog infection in Chad from 2019 to 2022. Results show that detection and tethering of infectious owned free-roaming dogs combined with culling of stray dogs are effective disease management strategies. Hence, attainment of certain threshold levels for these interventions could lead to disease eradication. Overall, the study revealed how different factors could be applied to effectively manage GWD transmission in the dog population. Findings from this study could be used to support decision-making in GWD control strategies.

Exploring the role of water stress and soil on banana-plantain production: a mathematical modelling approach

Camelle Kabiwa Kadje, University of Douala/Aims-Cameroon, Cameroon

Abstract: The aim of this talk is to investigate the role of water stress and soil on banana-plantain plants production. We propose a mathematical model for the dynamics growth of banana-plantain plants that takes into account the concentration of available water in the soil, water stress, banana-plantain plant production, plants compensation and delay. We present the theoretical analysis of the model with and without water stress. More precisely, we show that the full model is well-posed. For each model, we compute the trivial equilibria and derive two thresholds parameters that determine the outcome of water stress within a plantation. Further, we perform numerical simulations to illustrate the theory. The role of the water stress on the plant production is numerically investigated. We found that the water stress can cause about 63.27% of loss of banana-plantain production within a plantation with 1600 rejects initially planted. This suggests that climate change plays a detrimental role on banana-plantains production. We also numerically proved that Fine Sandy Loamy soil is more resistant to water than Silty Clay soil and Loamy soil.

Mathematical Modeling of Malaria Dynamics: Integrating Indoor Residual Spray (IRS), Long Lasting Insecticide Treated Nets (LLINs), and Attractive Toxic Sugar Baits (ATSBs) for Sustainable Control Strategies in Sub-Saharan Africa

Vusi Mpendulo Magagula, University of Eswatini, Eswatini

Abstract: Malaria remains a significant public health challenge, particularly in Sub-Saharan Africa, where it exerts a heavy burden on health systems and economies. In the pursuit of sustainable control strategies, this study presents a mathematical modeling approach to assess the integration of various interventions, namely Indoor Residual Spray (IRS), Long Lasting Insecticide Treated Nets (LLINs), and Attractive Toxic Sugar Baits (ATSBs). By leveraging mathematical modeling techniques, we aim to understand the complex dynamics of malaria transmission and the potential impact of combining these interventions on disease prevalence and transmission rates. The model incorporates key factors influencing malaria dynamics, including vector population dynamics, human-mosquito interactions, and the efficacy of each intervention. Through mathematical simulations, we explore the synergistic effects of integrating IRS, LLINs, and ATSBs, considering different coverage levels and deployment strategies. Moreover, we investigate the long-term sustainability of these integrated approaches, accounting for factors such as insecticide resistance and behavioral adaptations in mosquito populations.

Our findings highlight the potential of integrated control strategies in significantly reducing malaria transmission and burden in Sub-Saharan Africa. We identify optimal combinations of interventions and deployment strategies that maximize effectiveness while considering resource constraints and operational feasibility. Furthermore, we discuss the implications of our results for policy-makers and public health practitioners, emphasizing the importance of tailored, evidence-based approaches for sustainable malaria control in endemic regions. Overall, this study contributes to the growing body of research on malaria control by providing insights into the dynamics of integrated intervention strategies. By combining mathematical modeling with empirical data and field observations, we offer valuable guidance for designing and implementing effective, sustainable malaria control programs in Sub-Saharan Africa and beyond.

An Age-structured Mathematical Model for HIV and TB Co-infection using Optimal Control

Robert Maina, Strathmore University, Kenya

Abstract: HIV has been identified as significant risk factor estimated to contribute to TB burden in Kenya. Models formulated for the co-infection have treated the whole population homogeneously while its evident that susceptibility and effects of treatment vary for different age groups. In this talk, an age structured mathematical model for HIV and TB co-infection with optimal control is proposed. HIV testing & treatment, tuberculosis prevention & treatment, and viral load suppression will be considered for optimization. Minimization techniques and Markov Chain Monte Carlo (MCMC) will be used to determine model parameters. Runge Kutta method of order 5 will be used to solve the system for its high accuracy and flexibility. Disease free equilibrium, endemic equilibrium and the reproduction number of the model will be computed. This research can be used in the Ministry of Health (MOH) for emphasis on most effective interventions as well as a basis study tool that can be recreated for other co-infections.

Mathematical Modeling of the Synergistic Effects of Combining Two Oncolytic Viruses in Cancer Treatment

Joseph Malinzi, University of Eswatini, Eswatini

Abstract: This research investigates the synergistic effects of combining two oncolytic viruses, that is, vaccinia and vesicular stomatitis, for cancer treatment. Oncolytic virotherapy employs genetically engineered viruses to infect and destroy tumor cells, resulting in fewer side effects compared to traditional treatments like chemotherapy. The main objective of this study is to develop and analyse mathematical models that describe the combined effects of these two viruses. A combined analytical-numerical approach is utilized to characterize the transient and qualitative dynamics of the models.

Multiscale Modelling of Norovirus Transmission Dynamics in Human Population

Azwindini Maphiri, University of Venda, South Africa

Abstract: Noroviruses are the main cause of both sporadic and epidemic gastroenteritis, and they are very contagious. They are the most frequent cause of food poisoning, community-acquired diarrhoea, and gastroenteritis in people of all ages. Traditional approaches for modelling foodborne infections rely on the principles and concepts of the transmission mechanism theory that considers transmission to be the primary cause of infectious disease spread at the between-host scale. Due to high risk of foodborne diseases and large number of deaths associated with foodborne diseases caused by noroviruses, it is important to establish a multiscale model based on replication-transmission relativity theory, that can assist in identifying significant factors that contribute to the spread of infection. The replication-transmission relativity theory is a new theory designed for the purpose of multiscale modelling of infectious disease systems, accounting for variations in time and space by incorporating pathogen replication that leads to transmission. This work aims to develop a nested multiscale model that integrates the between-host submodel which considers the transmission dynamics of norovirus disease and within-host submodel which considers the replication dynamics of norovirus at the infection site within-host an infected human to assess the influence of within-host disease dynamics on between-host diseases dynamics. We construct a non-standard finite difference scheme to prove the positivity and stability of the multiscale model. Numerical simulations show that the influence of within-host dynamics on between-host dynamics has a great effect on the disease progression. The results show that targeting within-host parameters will be more helpful in reducing the burden on infections caused by norovirus.

Optimal Control Analysis Of The Antiretroviral Therapy Of The Human T-cell Lymphotropic Virus Type 1 (HTLV-1) Infection

Siyamthanda Gift Mnisi, University of KwaZulu-Natal, South Africa

Abstract: Human T-cell Lymphotropic Virus Type 1 (HTLV-1) has been a threatening pandemic for the past 40 years in certain parts of the world. HTLV-1 infects the CD4+ T-cells in the human body. In this study we modelled the interaction between the CD4+ T-cells and the HTLV-1 virus, taking into account that the actively infected cell does not undergo mitotic division. We started by discussing the

background of the HTLV-1 virus, associated diseases and the modes of transmission. A deterministic mathematical model was developed to capture the interaction between CD4+ T-cells and the HTLV-1 virus, and the model exhibits two equilibrium points namely, the disease-free equilibrium and the endemic equilibrium.

The basic reproductive number gives the average number of newly infected individuals that result from one case of infection. It was calculated using the next-generation matrix approach. It was found that if the basic reproductive number $R0 < 1$, the disease-free equilibrium is always locally asymptotically stable and if $R0 > 1$, the endemic equilibrium exists and is locally asymptotically stable.

MATLAB ode45 is used to solve and compute the equations for the long-term behaviour of the system at the DFE and endemic state. We investigated the sensitivity of the model parameters with respect to the basic reproductive number and conducted numerical simulations of both the disease-free equilibrium and the endemic equilibrium point. The treatment of the infection was introduced by the optimal control and the treatment method was the protease inhibitor which targets the virus. The treatment method was found to be not effective and not enough for treating the infection, as when it is stopped after 28 days, the virus resurfaces, persisting the infection.

Optimizing Strategies for Anopheles Mosquito Control and Malaria Transmission Reduction in Zimbabwe

Tinashe Victor Mupedza, University of Zimbabwe, Zimbabwe

Abstract: Malaria remains one of the most significant public health challenges globally, with its transmission intricately linked to the anopheles mosquito. Understanding the population dynamics of these mosquitoes is vital for developing effective malaria control strategies. Our study focuses on exploring and identifying the best methods for controlling anopheles mosquito populations and reducing malaria transmission in Zimbabwe. In this presentation, we introduce a basic approach using a stochastic compartmental model. This model is specially designed to evaluate the impact of temperature variations on the lifecycle and population size of Anopheles mosquitoes. Considering the crucial influence of environmental factors, particularly temperature, on both the aquatic and adult stages of these vectors, our model provides detailed insights into their population trends under varying climatic conditions. The primary aim of our research is to assess various adult mosquito control strategies, with a special focus on the utilization of adulticides. By tailoring our model to the specific environmental and climatic conditions of Zimbabwe, we provide a contextual analysis that is directly applicable to the region. Our findings are intended to guide the implementation of the most effective mosquito control methods, offering a strategic approach to reduce malaria incidence. This study not only contributes to the body of knowledge in vector control but also proposes practical, region-specific solutions that can be adapted to similar environments in the fight against malaria.

This talk is based on joint work with A. Mhlanga.

Mathematical Modelling for Guiding Control and Elimination of Environmentally Transmitted Infectious Diseases: Implication from Multiscale Models

Rendani Netshikweta, University of Venda, South Africa

Abstract: Environmentally transmitted infectious diseases refer to diseases in which the environment (be water, food, soil, air, and contact surfaces) serves as a key driver for the transmission of pathogens from one host to another. The spread of these diseases is strongly influenced by factors such as sanitation practices, water quality, food safety, and overall environmental cleanliness. Effectively understanding and managing these environmental pathways are essential for preventing outbreaks and safeguarding public health. Mathematical modelling has played and continues to play a pivotal role in the study of environmentally transmitted infectious diseases, offering a quantitative framework for comprehending and predicting disease dynamics. Additionally, mathematical models assist in assessing the efficacy of various public health interventions in combating infectious epidemics. However, in the community of mathematical biology we are beginning to witness the growing appreciation that infectious diseases are complex systems due to several interrelated factors across different levels and scales of an organization of an infectious disease system that contribute to diseases intricate nature. In this regard, multiscale models in the study of infectious disease dynamics involve integrating information and processes across different spatial and temporal scales. These models aim to capture the complexity of interactions occurring at various levels, from the cellular and tissue level to the community and microecosystem level of organization of an infectious disease system. Thus, using multiscale modelling, we investigate the influence of initial infective inoculum dose and superinfection on the multiscale dynamics of environmentally transmitted infectious diseases using Paratuberculosis in ruminants as paradigm. The findings through simulation of the multiscale model for Paratuberculosis in ruminants demonstrate that once the minimum infectious dose is consumed, then the infection at the within-host scale is sustained more by pathogen replication than by super-infection. Our results can be generalized to imply that for any environmentally transmitted infectious disease systems with pathogen replication at the microscale, the super-infection might have an insignificant effect on the disease dynamics.

Influence of the co-dynamics Ebola–COVID–19 in a population
Arsene Jaures Ouemba Tasse, University of Witwatersrand, South Africa

Abstract: In this talk, we investigate the influence of COVID-19 on the dynamics of Ebola Virus Disease. Although no co-infection by the two diseases has been reported, it is well known that the Ebola outbreaks which occurred during COVID-19 pandemic produced fewer cases than in the past, while all the efforts were devoted to fight against COVID-19 and the other diseases, including Ebola were neglected. In order to understand this unexpected fact, we propose a coupled Ebola–COVID–19 model. The Ebola-only and the COVID-19 only models are analysed. We prove for each of them that the basic reproduction number is a sharp threshold which ensures the elimination or the persistence of the disease.

The basic reproduction of the coupled model R0 is equal to max(R0E,R0C), with R0E and R0C , the basic reproduction numbers of Ebola and COVID-19, respectively. In the case of cross immunity, we prove that the Ebola-COVID-19 free equilibrium is locally asymptotically stable when R0 < 1. When either R0E > 1 or R0C > 1, one of the diseases persists while the other dies out (the disease with a basic reproduction number less than one), while when both R0E and R0C are greater than one, the two

diseases will persist. We fit this particular model to the reported data for the Kivu-EVD outbreak in 2018–2020. Since this outbreak overlapped before and during COVID-19, we split the data in two phases. Our results show that, the occurrence of COVID-19 lead (a) to a reduction by more than 52% of contacts between individuals; (b) to the reduction by half of the immigration; and (c) to the quickly burying of the Ebola-deceased individuals. These factors have tamped the level of EVD and sped up its elimination. Hence the occurrence of COVID-19 was favourable to the control of EVD. For the full coupled-model, we prove the existence of a unique interior equilibrium in some instances and the global stability of the DFE when R0 < 1.

This talk is based on joint work with Jean Lubuma and Berge Tsanou.

A Mathematical Perspective into p53 Signalling in Impacting on the Expression of the Transcription Factor E2F in CycD/Cdk4(6) Subsystem in Cancerous Cell

Nkululeko Qwabe, North-West University, South Africa

Abstract: Inhibitors play an important role in monitoring cell pathways. In this investigation we are assessing the effect of the production of the p53 protein in the CycD/Cdk4(6) subsystem. This gene plays an important role in regulating cell processes. These processes include DNA repair, cell quiescence and apoptosis. This process takes place at the G1 phase where a cell is in its growth stages. The expression of the p53 protein is not well understood but it is known that it is pulsatile and its production is in response to damaged DNA. This means that the more severe the cell DNA is damaged, the larger the expression of p53 gene is introduced into the cell system. By using MATLAB simulation we have been able produce different results on different expressions on p53. From our mathematical model we have been able to apply deterministic methods using dynamical system to assess existence of steady state limit–cycles in our solutions. This was done to assess the effect of the expression of the p53 gene on the cancerous cells. Oscillations has appeared to be of great significance in driving the oversight mechanisms in order to control the transcription factor, E2F. All these aspects are being assessed in attempting to put together a mathematical model that simulates the operations of a cell. This aspect of our investigation has been achieved.

Populations with spatially heterogeneous growth and dispersal rates in a shifting habitats

Mihaja Ramanantoanina, University of Pretoria, South Africa

Abstract: Many species are experiencing significant range shifts due to climate change. We present and analyse an integro-difference model that incorporates growth and dispersal in a shifting habitat. We extend existing models to include heterogeneity of the suitable habitat. We assume that the spatial heterogeneity of the suitable habitat affects both the growth and dispersal phases. The dispersal phase comprises two components: a habitat-dependent dispersal rate and a dispersal kernel, which reflects the dispersal distance. The model is used to study the impact of climate change on population dynamics and to investigate the effect of different dispersal rates. We focus on both the profile of the populations and their persistence in the shifting habitat. The results are consistent with existing literature for single-species models, which suggest that only species with intermediate dispersal ability can persist in a shifting habitat. Further investigation reveals different causes for the extinction of the species.

Unveiling Systemic Biases in RNA-Sequencing Data: A PCA Approach for Enhanced Understanding of Gene-Gene Relationships in Cancer Research

Mienie Roberts, Texas A&M University-Central Texas, USA

Abstract: We investigate the crucial role of Principal Component Analysis (PCA) in dissecting inherent biases within cancer transcriptomic data, utilizing datasets from The Cancer Genome Atlas (TCGA) and Stand Up 2 Cancer (SU2C), with a specific focus on bladder and prostate cancers. By employing PCA, we unveil expression-level dependent biases, shedding light on critical nuances that impact downstream analyses. This exploration underscores the transformative power of PCA in uncovering hidden patterns and enhancing the accuracy of gene expression interpretations. Our findings refine our understanding of cancer biology, offering insights for more informed clinical decisions and targeted therapeutic interventions.
This paper is based on joint work with C. Thron, H.F. Bergom, J. Hwang, E. Boytim, and F. Jafari

Campus map

H4 Dampad Hall. Conference Dinner is here.
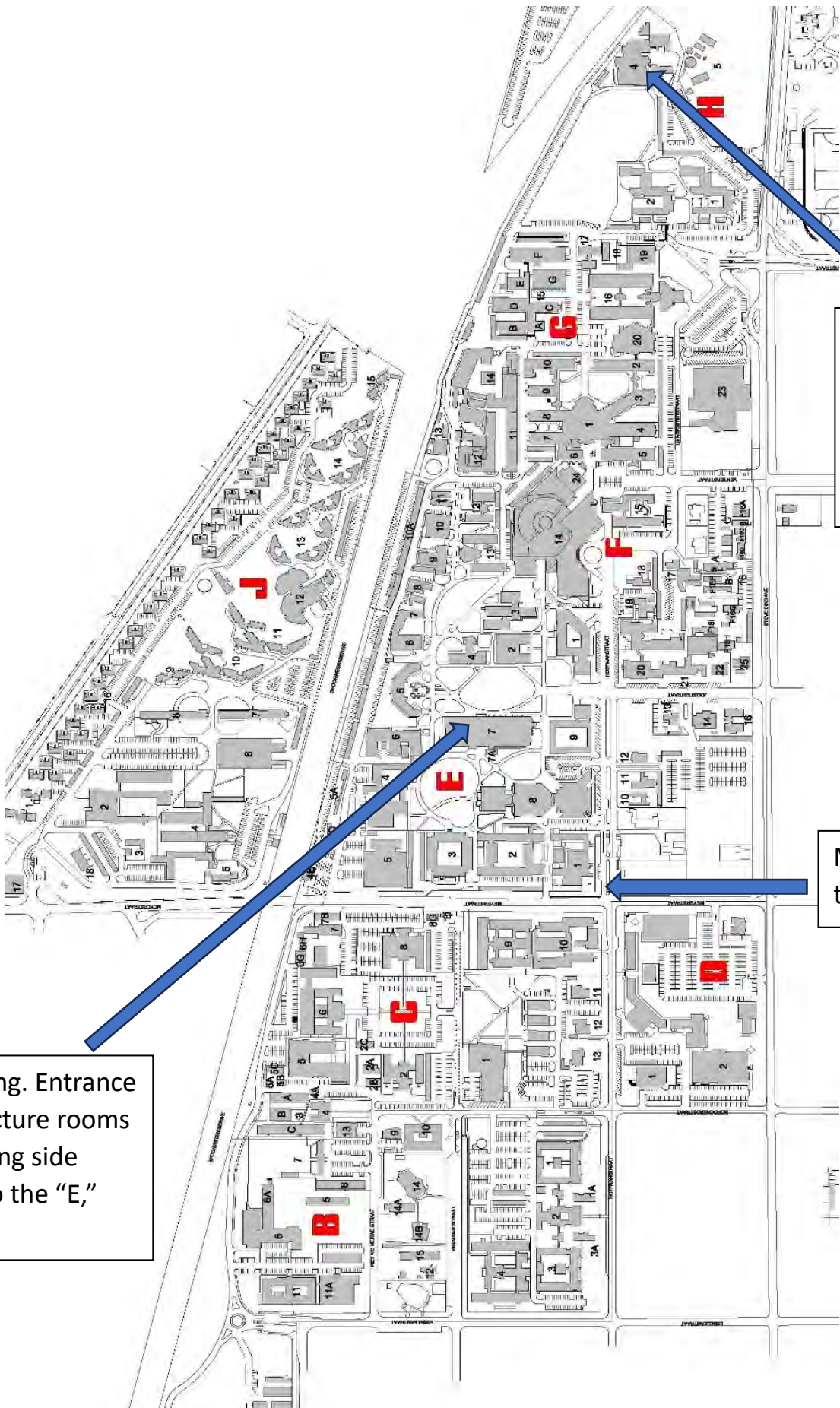
Main gate to campus

E7 building. Entrance to the lecture rooms on the long side closest to the "E," near 7A.