

**2018 October Workshop on Trends in  
Modeling and Analysis in Life Sciences**

**Book of Abstracts**

**4 – 6 October 2018  
Amanzingwe Conference & Lodge  
Hartbeespoort  
South Africa**

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**Hosted by Department of  
Mathematics & Applied Mathematics  
Faculty of Natural and Agricultural  
Sciences  
University of Pretoria**



# Information

## Sponsors

- Department of Mathematics and Applied Mathematics, University of Pretoria,
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- DST-NRF SARChI Chair in Mathematical Models and Methods in Bioengineering and Biosciences (M<sup>3</sup>B<sup>2</sup>).

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# Welcome message

Over the years, the application of Mathematics in Biology and Life Sciences opened new and interesting mathematical research problems, in particular, in the areas of Mathematical epidemiology, cancer modeling, ecology, bioengineering, etc.

The main goal of this meeting is to bring together researchers (faculty, post-docs, postgraduate students, etc.) in Biomathematics to discuss current topics and share emerging research questions in the area. The workshop intends to provide a forum for interactions between mathematicians and researchers in biology and life sciences. We are pleased to announce that a total of 30 delegates will take part in this workshop and the following 13 institutions are represented: Arizona State University, CIRAD-France, Rhodes University, SACEMA, University of Cape Town, University of eSwatini, University of KwaZulu Natal, University of Limpopo, University of Lorraine, University of Pretoria, University of South Africa, University of Witwatersrand and University of Zululand.

This gathering coincides with the 10th anniversary celebration of Mathematical Biology as a focus area within the Department of Mathematics and Applied Mathematics at University of Pretoria. It builds on very successful research activities such as workshops and conferences in the area of Biomathematics organized by the Department.

The organisers acknowledge the support of the DST/NRF Center of Excellence in Mathematical and Statistical Sciences, the DST/NRF SARCHI Chair in Mathematical Models and Methods in Bioengineering and Biosciences and the University of Pretoria - the host of the event.

We wish all participants a productive time at the workshop!

For The Organising Committee  
Michael Chapwanya



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# Plenary Talks

## On the mathematics of pattern formation

Roumen Anguelov

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05 Oct  
8:15am  
Ama.3

We consider dynamical systems defined in a space of functions over one- or two-dimensional spatial domain. Often such dynamical systems are defined via systems of reaction-diffusion PDEs. Our interest is in the case when the system has no spatially uniform fixed points or if it has, they are unstable. This is the case when patterns emerge. We will consider stationary patterns, periodic patterns and travelling waves. We will discuss the Turing instability theorem, stationary and oscillating patterns produced via the interaction between reaction and diffusion, representing diffusion via integral operators, travelling waves in the setting of bi-stable systems.

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04 Oct  
3:00pm  
Ama.3

## On applications of mathematical modelling and mathematical epidemiology in crop protection

Dumont Yves

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Crop protection and, more generally food safety, has become a major concern in many countries around the world, and in particular in Southern countries.

In the past, many field experiments were conducted to develop and test new technics, new crop varieties, and, of course, new pest control methods. Now, this is almost impossible because these experiments are often long, expensive, difficult to conduct, and/or to reproduce.

Modelling, and in particular Mathematical Modelling (including Mathematical Analysis, and Numerical Simulations) are more than needed as a complementary approach to these experiments, in order to be able to select the most important traits or variables to study, as well as the relevant field experiments to conduct, in order to improve our knowledge and also to obtain valuable data/information to validate the model(s).

In this talk, I will present several applications of Mathematics in crop protection, including plant vector-borne diseases, plant bio-agressors.... In particular I would like to emphasize the importance of joined collaborations between modelers and field experts, leading not only to novel and original experiments but also to novel, original, and challenging mathematical problems with, even better, practical applications in the field.

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# Mathematics of Infectious Diseases: Past, Present and Future

Abba Gumel

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05 Oct  
7:30am  
Ama.3

Mathematics has, historically, played (and continues to play) a major role in providing insight into the transmission dynamics of emerging and re-emerging diseases, dating back the work of Daniel Bernoulli in the 1800s. I will discuss the history and contributions of mathematics in disease dynamics, with emphasis on current trends, advances and challenges.

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# Research, Innovation and Education towards Malaria Elimination: How does Mathematical Modeling fit in this picture?

06 Oct  
8:15am  
Ama.3

Taneshka Kruger

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Malaria, a vector borne disease, is unlike other infectious diseases in that it is not caused by a single biological entity. Rather, the disease is the result of a highly complex interplay between three biological systems each with its own complex life-cycle, environment, habits and pathogenesis profiles. Furthermore, the transmission of malaria is compounded by the current global environment with travellers' malaria repeatedly reintroducing the disease and global climatic changes forecasting a significant increase in malaria cases. The Sustainable Development Goals (SDGs) propose that malaria cases and mortality will be reduced by at least 90% and that malaria will be eliminated in 35 countries by the year 2030. However, no single strategy will be adequate for controlling and eliminating malaria, and innovative research approaches are essential for achieving malaria elimination in southern Africa. The University of Pretoria Institute for Sustainable Malaria Control (UP ISMC) contributes towards the malaria elimination agenda through high quality, trans-disciplinary research, and novel innovation. The Institute endeavours to coordinate and promote collaborative malaria research within the UP and to foster collaboration between other top institutions and entities (regional, nationally and internationally) to generate new knowledge and support new activities pertaining to safer and sustainable malaria control and management strategies in Africa, with the ultimate goal of malaria elimination in mind. The diverse group of researchers within the UP ISMC encompass all aspects of malaria. Research groups (clusters) focus on human health, parasite control and vector control, with research occurring within and across clusters. Research is also being done on how best to manage these methods at a trans-disciplinary level. Community involvement and education are addressed as part of health promotion and a commitment exists to changing community behaviour towards malaria. Mathematical Modeling may contribute towards the ongoing battle to eliminate the dreaded malaria disease. Models could help with research challenges pertaining to malaria control; assist in predicting potential malaria outbreaks; or simply to determine what contributes towards a mosquito's selective biting behaviour. The scope for modeling in malaria control is thus essentially limitless. By combining effort and using all the tools in the malaria control toolbox, only then can malaria be defeated.

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# Reaction-Diffusion PDE modelling and simulation of picornaviruses' infection cycles

Justin Munganga

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04 Oct  
4:15pm  
Ama.3

Emerging and re-emerging diseases and drug resistant pathogens have made the problem more serious for humans. Viruses encode relatively few genes and these viruses have always been constantly infecting and affecting microbial hosts like human beings and others which encode more than 20000 genes. A good approach to combat this integrated approach of systems biology is to understand the complexity inherent in virus-host interactions and translating it into preventive medicine to fight viral infections [2, 3]. In this talk, we present a model based on Systems Biology [1,4-6], using Reaction- Diffusion PDE model for virus-host interaction. We assume that all the interacting species diffuse and also the terms are supposed to follow Fick's Law with constant diffusion coefficients.

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# Assessing designs for vaccine efficacy trials during epidemics of severe disease

06 Oct  
7:30am  
Ama.3

Juliet Pulliam

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The Ebola epidemic in West Africa ignited impassioned debate regarding the ethics of vaccine efficacy trials during the widespread epidemic of a highly fatal pathogen. One side argued that vaccines should be made available to those at high risk as soon as possible after the successful conclusion of Phase II safety trials, because this approach had the potential to save the most lives, while others argued that Phase III clinical trials to evaluate vaccine efficacy were necessary, because deployment of an untested (and therefore potentially ineffective) vaccine would risk wasting a vast amount of resources. Using the Ebola epidemic in West Africa as a case study, I'll describe how simulation can be used to compare potential study designs for vaccine efficacy trials and how quantitative approaches can be used to better understand the trade-offs between the scientific utility of a vaccine trial and the risk to trial participants.

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# Contributed Posters

## Bi-stable dynamics of a host-pathogen model

Anguelov Roumen, Bekker Rebecca, and Dumont Yves

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05 Oct  
10:30am  
Ama.3

Rising demand and the impact of plant pathogens are two of the many reasons the global food supply is currently experiencing tremendous pressure. Fortunately research into plant pathogens can lead to a better understanding of the underlying processes, and can suggest possible control strategies to mitigate the impact on the global crop yield. We present a host-pathogen model, considering a pathogen that is completely dependent on the host for nutrients, with the ability to travel short distances in search of new hosts. The basic reproduction number is found to be less than unity for all parameter values. However, under certain conditions, the temporal model admits two endemic equilibria in addition to the pathogen free equilibrium (PFE). The PFE is always locally asymptotically stable and two sets of sufficient conditions for the global asymptotic stability are derived using two methods: (i) LaSalle's Invariance Principle, and (ii) the construction of a monotone system that approximates the model from above. Additionally, conditions for the persistence of the infection are derived. The model is extended to include spatial diffusion of a subpopulation of the pathogen, and numerical investigations are carried out. Indeed, in the setting of bistability travelling wave solutions exist which connect the PFE and an endemic equilibrium.

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05 Oct  
10:30am  
Ama.3

## A model of biofilm growth

Chapwanya Michael

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We provide and analyse a model for the growth of bacterial biofilms based on the concept of an extracellular polymeric substance as a polymer solution, whose viscoelastic rheology is described by the classical Flory-Huggins theory. We show that one-dimensional solutions exist, which take the form at large times of travelling waves, and we characterize their form and speed in terms of the describing parameters of the problem. Numerical solutions of the time-dependent problem converge to the travelling wave solutions.

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# Optimal control model for yellow fever

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05 Oct  
10:30am  
Ama.3

We present a yellow fever model with vertical transmission in vectors. The model takes into account disease prevention in humans using bed nets and vaccination (which is in short supply), as well as mosquito control via the application of larvicides (to clear aquatic mosquitoes) and adulticides (to clear adult mosquitoes). The basic offspring and associated reproduction numbers of the model are computed. Stability analysis of the equilibrium points of the model are presented.

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# Application of center manifold theory to discretised epidemiological models and nonstandard finite difference schemes

05 Oct  
10:30am  
Ama.3

Roumen, Anguelov, Kenneth N. Dukuza, Jean M-S. Lubuma

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**Abstract.** In this study we propose a discrete theorem for  $n$ -dimensional maps with a simple eigenvalue 1. This theorem is a discrete analogue of the theorem on the paper by authors in [3] for  $n$ -dimensional nonlinear dynamical system of ODEs with a simple zero eigenvalue. We discretise continuous epidemiological models using the Nonstandard Finite Difference Method (NSFDM), see [1], and then apply the theorem to investigate the existence of backward bifurcation phenomenon at  $\mathcal{R}_0 = 1$  in the discrete system. Results show that the proposed theorem and the theorem in [3] lead to the same conditions for the occurrence of a backward bifurcation.

## References

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# **A rabies epidemic model among Wild African dogs**

Chapwanya Michael, Dumani Phindile, and Ouifki Rachid

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05 Oct  
10:30am  
Ama.3

Wildlife conservation is crucial in preventing endangered species from becoming extinct and disease outbreaks is one of the biggest threats. Rabies is one of the devastating viruses that can almost be impossible to control once an outbreak occurs. There is no effective treatment or cure of rabies once symptoms show. In this poster presentation, we propose a deterministic rabies model that takes into account the contaminated environment and incubation period of the virus to better understand the transmission and progression dynamics of the disease, as well as to seek to predict the effectiveness of control strategies. Qualitative and numerical analysis are provided.

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05 Oct  
10:30am  
Ama.3

## Effects of incidence functions and treatment on the dynamics of consistent cholera model with time delay

Adam. S. Hassan

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Cholera is a severe diarrhoeal bacterium disease that can result in death within hours if left unattended. It becomes a substantial global public health problem, especially in poor - resource countries, internally displaced camps e.t.c., lacking sufficient access to clean water and sanitation facilities. According to [1], in 2015, 23 countries reported a total of 172,454 cholera-related deaths. After the first outbreak in the Bay of Bengal, of recent, cholera epidemics re-emerged in Zimbabwe (2008) and Haiti (2010) causing a total of about 12,942 deaths [2]. Many mathematical cholera models were developed for example see [3]. However, not much has been explored on the effects of time delay and incidence functions due to human and/or pathogens mixing behaviours and treatment strategies of the infectives. A new realistic delay differential equation-cholera model using different incidence functions and treatments using two sources of infections is formulated and fully analyzed. The effects of delay and different incidence functions and the treatment strategies are shown and compared with the existing literature. A dynamically consistent discrete model is constructed to validate basic properties of the continuous models using nonstandard finite difference methods [4].

- 1 World Health Organization, Cholera 2015, *Weekly epidemiological record*, **91** (38) 433–440 (2016).
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# Mathematical models for the transmission dynamics of Bovine schistosomiasis with contaminated environment

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05 Oct  
10:30am  
Ama.3

Livestock production is one of the major ways of improving livelihood standards in the tropical and sub-tropical regions of the world. However, diseases such as bovine schistosomiasis compromise the productivity. It is for this reason that bovine schistosomiasis being one of the endemic diseases deserves attention since it causes significant economic losses within the affected regions. Though much work has been done on human schistosomiasis, mathematical models that have so far considered disease dynamics in bovines, particularly cattle, with respect to the economic value they have in the regions in question, are very rare. It is from this perspective that this study intends to devise mathematical models that can be used to understand schistosomiasis dynamics in bovines with regard to the role that the contaminated environment plays.

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# Are some prey sources more equal than others? Dealing with diet-tissue discrimination factors in stable isotope mixing models

05 Oct  
10:30am  
Ama.3

Kadye Wilbert

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Stable isotope mixing models are increasingly becoming a utility in trophic ecology and food web studies where they are used to quantitatively estimate and infer the proportional composition of different prey sources in consumer diets. Recently, Bayesian framework-based isotope mixing models have been developed in order to address challenges associated with estimating food sources in complex food webs, such as the occurrence of multiple prey sources, uncertainty associated with measurement, source and mixture process errors, and to incorporate concentration dependence and prior information for both sources and mixtures. Despite significant progress in refining isotope mixing models, the use of appropriate diet-tissue discrimination factors (DTDF), which have a direct influence on the correct interpretation of mixing models outputs, remain as one of the unresolved challenge. In order to address this challenge, an empirical laboratory feeding experiment was conducted using the Mozambique tilapia *Oreochromis mossambicus* to evaluate two objectives. First, the study explored how the isotope incorporation patterns into body tissues of *O. mossambicus*, and the associated DTDF varied among diets with different carbon and nitrogen stable isotope values. Second, this study compared the use of conventional literature-based DTDF with experimentally-derived diet-specific DTDF in isotope mixing models. Results from this study provided evidence of differential isotope incorporation patterns and variable DTDF for different diets. The implications of these variations, particularly when using isotope mixing models in aquatic food webs are further discussed.

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# What about the International Institute for Theoretical Ecology?

Laurie Henri

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05 Oct  
10:30am  
Ama.3

Is theoretical ecology a disparate set of theoretical ideas and tools, united only by the unity of ecology itself?

Does our response to the currently unfolding environmental catastrophe demand contributions from theoretical ecology?

Does theoretical ecology have the sort of reflective and guiding role that theory should have?

Axel Rosberg (Queen Mary University) answers:

- no (in principle, if not in practice)
- yes, very much so
- no, and that is a scandal.

Axel has proposed the formation of an International Institute for Theoretical Ecology. With the support of several people including myself, he has started making it happen.

In this poster, I present some aspects of the motivation for and the proposed structure and activities of the IITE.

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05 Oct  
10:30am  
Ama.3

## Dynamical systems for the declines of honeybee colonies

Mataeli B. Lerata<sup>1</sup>, Abdullahi A. Yusuf<sup>2</sup>, Jean M-S. Lubuma<sup>1</sup>

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Honeybees are not only extremely important for humans, but also for the entire ecosystem to function well. Beekeeping is fast declining globally regardless of the effort to sustain it. This decline in honeybee population constitutes a serious threat to ecosystem as well as foods security as honeybees are major pollinators of food crops. In this work, we extend the mathematical model that was formulated by Khoury et al. 2011. (KMB model) to a Social Parasitic (SP) model, that describes how honeybee colonies decline in South Africa. We also construct the discrete mathematical models that replicate that dynamics of the continuous KMB (in that there exists a critical value of foragers' death rate above which the colony declines to zero) and SP models (describing that the declines of the colony is inevitable in SP setting). Numerical simulations are provided to illustrate the fact that the decline of the honeybee colonies in SP setting is faster than in the KMB setting.

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# Optimal control analysis of a model for tumour growth under chemovirotherapy

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05 Oct  
10:30am  
Ama.3

Current research on cancer treatments suggests that combination treatments are the cutting edge for cancer therapy. Nonetheless, the design of an optimal protocol remains an open question. In this paper, we address the question on: “*what is the optimal chemotherapeutic drug and virus dosage combination for the elimination of tumour cells in body tissue?*” To this end, We construct a mathematical model, in the form of differential equations, describing the interactions between tumour cells, the immune response, and a treatment combination with chemotherapy and oncolytic viruses.

Stability analysis of the model with constant chemotherapy treatment rates shows that without any form of treatment, a tumour would grow to its maximum size. It also demonstrates that chemotherapy alone is capable of clearing tumour cells provided that the drug efficacy is greater than the intrinsic tumour growth rate. Furthermore, virotherapy alone may not be able to clear tumour cells from body tissue but would rather enhance chemotherapy if viruses with high viral potency are used. To evaluate the combined effect of virotherapy and chemotherapy we use the forward sensitivity index to perform a sensitivity analysis, with respect to chemotherapy key parameters, of the virus basic reproductive number and the tumour endemic equilibrium. The results from this sensitivity analysis indicate the existence of a *critical* dose of chemotherapy above which no further significant reduction in the tumour population can be observed. Numerical simulations suggest that a successful combinational therapy of the chemotherapeutic drugs and viruses depends mostly on the virus burst size, infection rate, and the amount of drugs supplied. Optimal control analysis was performed, by means of the Pontryagin’s maximum principle, to further refine predictions of the model with constant treatment rates by accounting for the treatment costs and sides effects. Results from this analysis suggest that the optimal drug and virus combination correspond to half their maximum tolerated doses. This is in agreement with the results from stability and sensitivity analyses.

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05 Oct  
10:30am  
Ama.3

## **A theoretical model of chronic Hepatitis B and Cirrhosis with sub-optimal adherence and drug resistance**

Manda Edna

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We formulate and analyze within-host hepatitis B viral theoretical mathematical model for hepatitis B virus infection in the chronic and cirrhotic phases of liver cancer with sub-optimal adherence and drug resistance. The model incorporates hepatocytes, hepatitis B virus, immune cells and cytokine dynamics using a system of ordinary differential equations. Treatment was captured using efficacy functions replicating the pharmacokinetics properties of two drugs, one of which is administered intravenously and the other orally. Our results suggest that natural drug resistance increases the hepatitis B virus burden more than sub-optimal adherence to drugs from both mono-therapies and combined therapies.

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# Indoor residual spraying as an intervention in malaria control: A mathematical approach

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05 Oct  
10:30am  
Ama.3

Indoor residual spraying (IRS) is used for malaria control. Recent studies have pointed out various health risks to those with prolonged exposure to IRS. These include cancer, male infertility, miscarriage, developmental delay, nervous system and liver damage. We aim to assess the long-term effects of IRS on malaria spread and health risks posed by exposure to IRS concurrently. To do so we propose an SEIR type model for the transmission dynamics of malaria. The model consists of a system of ordinary differential equations which factor in the intervention; IRS. We analyze this model to show its quantitative and qualitative behaviour. We derive the equilibria, their stability and the basic reproduction number,  $R_0$ , for this system. We observe the existence of backward bifurcation. Numerical simulations demonstrate the effect of Indoor Residual Spraying on malaria cases in Limpopo. The optimal level of intervention required to keep exposure to IRS at a minimum while reducing risk to malaria is demonstrated.

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# Oscillation Conditions for Difference Equations with a Monotone or Non-monotone Argument

05 Oct  
10:30am  
Ama.3

Moremedi Marcia

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Consider the first-order delay difference equation with a constant argument  $\Delta x(n) + p(n)x(n-k) = 0$   $n = 0, 1, 2, \dots$  and the delay difference equation with a variable argument  $\Delta x(n) + p(n)x(\tau(n)) = 0$   $n = 0, 1, 2, \dots$ , where  $p(n)$  is a sequence of nonnegative real numbers,  $k$  is a positive integer,  $\Delta x(n) = x(n+1) - x(n)$ , and  $\tau(n)$  is a sequence of integers such that  $\tau(n) \leq n-1$  for all  $n \geq 0$  and  $\lim_{n \rightarrow \infty} \tau(n) = \infty$ . A survey on the oscillation of all solutions to these equations is presented. Examples illustrating the results are given.

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# Interrogating mathematical modelling: Current challenges and future directions

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05 Oct  
10:30am  
Ama.3

The rise and popularity of mathematical modelling in sub-Saharan Africa has been tremendous. In the last century, to date, models have been found to be useful tools to elucidate complicated biological relationships, to build a comprehensive description of biological processes and give insights on the future observed patterns. With the rise in the popularity are inherent challenges that need to be interrogated, from the mathematics, understanding of biological systems, the modelling itself, linking models to data and the interpretation of results. This talk is not only motivational but also highlights the current gaps, pitfalls and the future challenges as the growth and applications of mathematical modelling broadens. In particular we focus on the common mathematical modelling techniques and how they sometimes end up being mathematical with little applications. A discussion on good modelling practices and conclusions will be drawn from the talk.

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05 Oct  
10:30am  
Ama.3

## **The effect of conspecific support on the qualified competition equilibrium**

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The effect of conspecific support on the qualified competition equilibrium. The long term properties, like coexistence and extinction, are usually determined by the demographics of competing species or other competitive advantages. Here, we consider the effect of conspecific support on the coexistence of species. We show that, even if the competing species have the same demographics and interaction, their coexistence can be destabilized by sufficient level of conspecific support.

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# Cost-effectiveness analysis strategies for breast cancer treatment

Oke Segun Isaac  
University of Zululand

05 Oct  
10:30am  
Ama.3

We propose and analyse breast cancer model with combined anticancer drugs and ketogenic diet. In the first place, the stable Tumor-Free Equilibrium (TFE) of the model coexists with a stable endemic equilibrium when the invasion reproduction number,  $R_i$  is less than unity. However, Lyapunov function was constructed to prove that TFE is globally asymptotically stable and sensitivity index was calculated. Hence, we apply optimal control theory to investigate how the combination of anticancer drugs and ketogenic-diet should be implemented, for a certain period, in order to inhibit the tumor growth and eliminate cancer cells. Furthermore, we establish the existence of the optimality system and use Pontryagin's Maximum Principle (PMP) to characterize the optimal levels of the two treatment measures. However, the infection averted ratio (IAR), the decrement of tumor cells and incremental cost-effectiveness ratio (ICER) were calculated to investigate the cost-effectiveness of all possible combinations of the control strategies, while minimizing the implementation cost of the treatment strategy. In addition, the simulation results show that the combination of anticancer drugs and ketogenic diet is the most cost-effective strategy for treating breast cancer.

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# A mathematical model for melioidosis transmission dynamics

05 Oct  
10:30am  
Ama.3

Yibeltal A Terefe

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A deterministic model for the transmission dynamics of melioidosis disease in a population is designed and analysed. The model is shown to exhibit the phenomenon of backward bifurcation, where a stable disease-free equilibrium coexists with a stable endemic equilibrium when the basic reproduction number  $\mathcal{R}_0$  is less than one. It is further shown that the backward bifurcation dynamics is caused by the reinfection and relapse of individuals who recovered from the disease. In the absence of backward bifurcation, the global asymptotic stability of the disease-free equilibrium is shown whenever  $\mathcal{R}_0 < 1$ . Sensitivity analysis of the model, using the parameters relevant to the transmission dynamics of the melioidosis disease, is given. Numerical experiments are given to support the theoretical analysis of the model.

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# Some recent works on (fire-prone) savanna dynamics modelling

Yatat Valaire

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05 Oct  
10:30am  
Ama.3

The savanna biome encompasses variations of vegetation physiognomies that produce complex dynamical responses of plants to the rainfall gradients leading from tropical forests to hot deserts. Such responses are shaped by interactions between woody and grassy plants that can be either direct, disturbance-mediated (e.g. fire) or both. There has been increasing evidence that several (highly contrasted) vegetation physiognomies may durably coexist in humid savannas, which are fire-prone, suggesting multi-stability (i.e. mosaic of vegetation). Therefore, a major question consists on understanding/characterizing how fires may impact vegetation mosaic dynamics. This question has triggered several modelling efforts relying either on space-implicit or on space-explicit mathematical models ([1], [2], [3]). I will present some recent models designed to study fire-prone savanna dynamics and advocate the design of minimalistic models, capturing essential processes while retaining sufficient mathematical tractability and restricting themselves to a minimal set of parameters assessable from the overall literature [4]. Notably, based on fire frequency and mean annual rainfall parameter, several vegetation mosaic dynamics are presented. As prospects, collaborations with Dr. Y. Dumont and Prof. J. Banasiak will focus on the long term impact of herbivory disturbance on savanna dynamics.

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