Programme for LMS Conference (Pevensey 1, 1A6)

Time	(Tuesday) 10th September	(Wednesday) 11th September	(Thursday) 12th September
10am – 10.30am		Mathematical modelling for public health 10am: James Van Yperen 10.50am: Jasmina Panovksa-Griffiths 11.40am: Chris Hadjichrysanthou	From microbial dynamics to cell-drug interactions: unravelling the complexity of human diseases with mathematical insights 10am: Carina Dunlop 10.50am: Eduard Campillo-Funollet 11.40am: Marianna Cerasuolo
10.30am – 11am			
11am – 11.30am			
11.30am – 12pm			
12pm – 12.30pm	Registration & Welcome		
12.30pm – 1pm	Lunch & Coffee	Lunch & Coffee	Lunch & Farewells
1pm – 1.30pm			
1.30pm – 2pm			
2pm – 2.30pm	Shape optimisation at Sussex 2pm: Estefania Loayza Romero 2.50pm: Philip Herbert 3.40pm: Alberto Paganini	Mathematical modelling for public health 2pm: Kat Rock 2.50pm: Chris Overton 3.40pm: Francesco Di Lauro	
2.30pm – 3pm			
3pm – 3.30pm			
3.30pm – 4pm			
4pm – 4.30pm			
4.30pm – 5pm			
5pm – 5.30pm			
5.30pm – 6pm			
6pm – 7pm			
7pm –	Conference Dinner 1	Conference Dinner 2	

Speaker information

Shape optimisation at Sussex

Estefania Loayza Romero
Title: Discrete Geodesic Calculus for Complete Riemannian Metrics

Abstract: Geodesic calculus on Riemannian manifolds refers to the exponential and logarithmic mappings, the parallel transport, and the Riemannian connection, whose evaluation involves solving complex systems of second-order ordinary differential equations. Closed expressions for solving such problems can be obtained only in exceptional cases. This fact is important while dealing with optimisation problems on manifolds since we require the evaluation of such mappings multiple times per iteration.

In this talk, we will develop a discrete geodesic calculus based on the definition of an inexpensive dissimilarity measure which approximates the Riemannian distance. We will focus on complete Riemannian metrics as the ones described in [Gordon, 1973], for which a simple dissimilarity measure can be identified by exploiting their specific structure. We will present numerical experiments in three different manifolds showing the advantage of working within this framework.

Philip Herbert
Title: The convergence of a steepest descent method in PDE constrained optimisation problems using the Lipschitz topology

Abstract: In this talk, we discuss a novel method in PDE constrained shape optimisation. We begin by introducing the concept of PDE constrained shape optimisation. While it is known that many shape optimisation problems have a solution, their approximation in a meaningful way is non-trivial. To find a minimiser, it is typical to use first order methods. The novel method we propose is to deform the shape with fields which are a direction of steepest descent in the topology of $W^{1,\infty}$.

We present an analysis of this in a discrete setting along with the existence of directions of steepest descent. Several numerical experiments will be considered which compare a classical Hilbertian approach to this novel approach. Time permitting, we will also discuss the optimisation of the topology.

Alberto Paganini
Title: Automated numerical shape optimization with finite elements

Abstract: In this talk I will describe how the finite element method enables a natural implementation of the moving-mesh shape optimization method that generalized straightforwardly to higher-order discretization. I will also explain how finite element software can automated the evaluation of shape derivative along finite element directions. Finally, I will present how these aspects have been realized in the automated PDE-constrained shape optimization toolbox fireshape.

Mathematical modelling for public health

James Van Yperen
Title: Queue&A&E: what mathematical modelling can tell you about your waiting times

Abstract: TBC

Jasmina Panovska-Griffiths
Title: Modelling for timely and responsive COVID-19 epidemic tracking in the UK: the process and lessons learned for future outbreak preparedness

Abstract: This talk will give an overview of the modelling for policy that my group did over the COVID-19 epidemic, highlighting the generation of the epidemic metrics from an ensemble of models and the responsive modelling using a stochastic agent-based modelling called Covasim. I will discuss lessons learned from modelling the pandemic, and pick on one aspect we have developed recently to improve calibration of stochastic models. In particular, I will show how machine learning can be applied to infectious disease modelling to make calibration more efficient and discuss why this is crucial part of the development of the next generation infectious disease models.

Chris Hadjichrysanthou
Title: Preparing for the next pandemic: development of mathematical and computational tools for the assessment of novel treatments for respiratory virus infections

Abstract:
Some first modelling efforts towards the assessment of a new approach to combat pathogenic respiratory viruses using novel broadly neutralising antibodies will be presented.

Kat Rock
Title: Making impact on sleeping sickness policy: experiences of a mathematical modeller

Abstract: In this presentation, I will discuss my experience of challenges and successes in working as a mathematical modeller to support ministries of health with their sleeping sickness (human African trypanosomiasis; HAT) programmes. In particular, I will focus

on my work on the HAT modelling and economic predictions for policy (HAT MEPP) project which has been running since 2017 which aims to provide decision-making support for HAT elimination programmes in five endemic countries. I'll cover relationship building, translation of modelling outputs into policy-ready results, experiences of turning failures into learning opportunities and, of course, some success stories. By the end I hope to give the audience a taste of the modelling and technical work my team do, but more importantly a perspective of the large amount of non-modelling work required to integrate with health programmes.

Chris Overton

Title: Using mathematical modelling to estimate COVID-19 incidence and prevalence from the 2023/2024 Winter COVID Infection Study: A community cohort study

Abstract: The Winter COVID Infection Study ran from 14th November 2023 to 7th March 2024. This was a community cohort study, asking individuals to take lateral flow device tests, regardless of symptomatic status. A repeat testing design was used to estimate key epidemiological parameters, including test sensitivity and duration of positivity, which facilitated estimating the temporal varying incidence, prevalence, and infection hospitalisation risk from the raw LFD test positivity data. To model incidence and prevalence, bespoke hierarchical random walk models were constructed and used within a multi-level regression with poststratification framework to generate robust national estimates. These random walks were then modelled to the hospital admissions data to estimate the infection hospitalisation risk. In this talk, I will describe the models developed, the results obtained, and the challenges encountered during real-time modelling.

Francesco Di-Lauro

Title: Missing clusters in 20K HIV genomes from four African countries and the future of HIV prevention

Abstract: New HIV infections have been steadily declining across sub-Saharan Africa, leading UNAIDS to declare that, with current progress maintained, AIDS could cease to be a public health threat by 2030. In the Global North, HIV prevention is increasingly centred around rapid genetic analysis of transmission chains and outbreak control. To explore whether similar approaches could be used in high-prevalence epidemics in Africa, we compared the viral genetic structure of such epidemics to those in Europe, and to three mathematical models of generalised epidemics. In 19,968 genomes from four African countries, we found no large clusters of closely genetically linked viruses, suggesting that more generalised public health approaches are needed. Successful treatment and prevention programmes must take into account the underlying local structure of epidemics.

From microbial dynamics to cell-drug interactions: unravelling the complexity of human diseases with mathematical insights

Carina Dunlop

Title: Integrating mechanistic cancer models into pre-clinical drug trials: benefits and challenges of moving beyond growth laws to spatial modelling.

Abstract: TBC

Eduard Campillo-Funollet

Title: Modelling and analysis of genome replication data

Abstract:
Genome replication is a crucial process in biology. It is a stochastic process, and yet it must occur in an accurate manner in order to guarantee genome stability. We present a mean-field model for the polymerase usage in genome replication, together with a statistical model for the measurement error, and we fit the parameters of the model—efficiency of the origins of replication and replication speed—to experimental data from S. Pombe.

Marianna Cerasuolo

Title: A computational multi-scale approach to the therapeutic resistance of prostate cancer

Abstract: Over the past few years, numerous mathematical models have been proposed to describe the dynamics of prostate cancer during treatment. One of the predominant challenges has been accurately representing experiments conducted under in vivo conditions, as this is crucial for the models' suitability in clinical applications. This talk will present an interdisciplinary study on drug resistance in prostate cancer. By integrating experimental data, statistical analysis, and computational methods, we could devise potential therapeutic strategies to address drug resistance. The proposed models explore neuroendocrine transdifferentiation in prostate cancer in vivo under multiple drug therapies and account for the heterogeneity of the tumour microenvironment. As the behaviours of the prostate cancer cells and the various chemicals occur on different time scales, we considered a multi-scale hybrid approach, in which partial differential equations govern the behaviour of the drugs and other chemicals present in the tumour microenvironment (over the 'fast' timescale). A cellular automaton provides the rules for the dynamics of the tumour cells (over the

'slow' timescale). We will see how, through the computational analysis of the model solutions, it was possible to examine the spatial dynamics of tumour cells, assess the efficacy of various drug therapies in inhibiting prostate cancer growth, and find optimal drug combination strategies and treatment schedules to eradicate cancer cells and prevent metastases formation.