AMP24 Booklet of Abstracts

Plenary Talks

Title TBC
Tom Finnie, UK Health Security Agency

With no biology degree or wet lab experience, what does a mathematician reeeaally do in a bioinformatics team?
Michael Pearce, NeoChromosome

Michael Pearce is currently a Senior Machine Learning Researcher at NeoChromosome, a subsidiary of Opentrons with its headquarters in New York, in a new bioinformatics team. In 2019, he was awarded a PhD degree in Maths and Complexity Science from the University of Warwick, focusing on Bayesian statistics and optimization, with internships at Google Deepmind in London and Uber AI in San Francisco. After his PhD and prior to his current role, he worked as a machine learning researcher at several startups, including Anyvision (a unicorn face recognition startup in Northern Ireland and Israel) and Zenith AI (a startup aiming to make no-code graphical "drag and drop" ML platform for model creation and deployment). See more details on his website: https://bayesianblog.com/

Contributed Talks

Steering opinion dynamics through control of social networks
Andrew Nugent, University of Warwick

We propose a new control problem for opinion dynamics on evolving networks. The controls modify the strength of connections in the network, rather than influencing opinions directly, with the overall goal of steering the population towards a target opinion. This requires that the social network remains sufficiently connected, the population does not break into separate opinion clusters, and that the target opinion remains accessible. We present several results on the existence of controls and discuss methods for finding them.

Modelling and Predicting Online Vaccination Views using Bow-tie Decomposition
Yueting Han, University of Warwick

Social media has become increasingly important in shaping public vaccination views, especially since the COVID-19 outbreak. This paper uses bow-tie structure to analyse a

temporal dataset of directed online social networks that represent the information exchange among anti-vaccination, pro-vaccination and neutral Facebook pages. Bow-tie structure decomposes a network into seven components, with two components, strongly connected component (SCC) and out-periphery component (OUT), emphasized in this paper: SCC is the largest strongly connected component, acting as an 'information magnifier', and OUT contains all nodes with a directed path from a node in SCC, acting as an 'information creator'. We consistently observe statistically significant bow-tie structures with different dominant components for each vaccination group over time. In particular, the anti-vaccination group has a large OUT, and the pro-vaccination group has a large SCC. We further investigate changes in opinions over time, as measured by fan count variations, using agent-based simulations and machine learning models. Across both methods, accounting for bow-tie decomposition better reflects information flow differences among vaccination groups and improves our opinion dynamics prediction results. The modelling frameworks we consider can be applied to any multi-stance temporal network and could form a basis for exploring opinion dynamics using bow-tie structure in a wide range of applications.

Financial contagion on multiplex networks
Malvina Bozhidarova, University of Nottingham

We introduce an innovative approach for modelling the spread of financial crises in complex networks, combining financial data, Extreme Value Theory and an epidemiological transmission model. We address two critical aspects of contagion: one driven by direct financial connections (fundamentals-based contagion) and another triggered by broader global impacts (pure contagion). Using data from 398 companies' stock prices, geography, and economic sectors, we create a multiplex network model on which a Susceptible- Infected-Recovered transmission model is defined. By studying stock prices during the 2008 and 2020 crises, we test our model's ability to predict crisis spread. The results show its effectiveness in forecasting crisis propagation, emphasizing the importance of each layer in the network for predicting specific impacts during crises.

Fast and accurate computations of acoustic scattering by self-similar fractal inhomogeneities
Joshua Bannister, University College London

The heterogeneous Helmholtz equation (HHE) is a classical model for scattering of time-harmonic acoustic waves by a compactly supported penetrable inhomogeneity on which the wave number is modulated. In this talk, we present a novel, provably accurate finite element method (FEM) that allows us to solve this problem on a certain class of self-similar fractal inhomogeneities, such as the Koch snowflake, Gosper Island and Fudgeflake. Unlike previous studies, our approach does not approximate the fractal by a polygon, yielding a linearly convergent method that avoids "fractal stair-casing" errors, which give methods that converge at rates that depend on the Hausdorff dimension of the inhomogeneities boundary.

Our method is based on reformulating the HHE into the Lippmann-Schwinger integral equation (LSE) on the fractal inhomogeneity and then exploiting their self-similarity to mesh them by scaled and rotated copies of themselves, producing novel self-similar meshes that fully capture their geometry. We then define piecewise constant approximations to this mesh, allowing us to derive their convergence, accuracy and stability from the classical FEM literature.

Then, using recent fractal quadrature results, we exploit the self-similarity of the mesh and properties of the LSE to compute the entries of the resulting Galerkin matrix with quadratic accuracy. Finally, we exploit the geometry of the mesh to accelerate iterative solutions of the resulting dense linear system via an FFT-based compression method, resulting in O(N) storage of the linear system and O(N logN) operations per iteration, where N denotes the number of self-similar elements in the mesh.

ESFEM schemes for the Cahn-Hilliard equation on an evolving surface
Tom Sales, University of Warwick

In recent years there has been interest on partial differential equations (PDEs) posed on domains which evolve in time, and in particular evolving surfaces. Applications for these systems can be found, for example, in the study of lipid biomembranes. In this talk we consider the Cahn–Hilliard equation on an evolving surface and discuss the numerical analysis of some fully discrete numerical schemes. We will briefly discuss a framework for PDEs on evolving domains, and techniques for the discretisation of PDEs on evolving surfaces via the evolving surface finite element method (ESFEM). Assuming a smooth potential function, we outline the difficulties in the numerical analysis and discuss error bounds for an isoparametric ESFEM in space, backward Euler (and implicit-explicit) in time discretisation.

Riemann problems in the retinal circulation
Ifeanyi Onah, University of Glasgow

We have considered the flow in a vessel with discontinuous stiffness, examining a Riemann problem around the point of discontinuity. As expected, the discontinuous initial wave profile breaks up into four standard cases, each with a contact discontinuity at the jump in material properties. However, we find that for some parameter combinations the rarefaction can interact with the stationary wave leading to resonant wave profiles with an extra propagating shock.

Spatio-Temporal Patterns forming in FitzHugh-Nagumo Model
Hardik Poptani, University of Liverpool

In 1952, Hodgkin and Huxley created a groundbreaking model describing the initiation and propagation of action potentials in neurons using nonlinear differential equations. Taking inspiration, FitzHugh (1961) has simplified the Hodgkin-Huxley model into two variables describing the mathematical properties of excitation and propagation of sodium and potassium ions in neurons with Nagumo (1962) creating an electrical circuit for the experiment. The simplification of the Hodgkin-Huxley model has caused a huge impact and created interest in modelling excitability, multistability and oscillations in nonlinear systems due to the fact that the FitzHugh-Nagumo model is the simplest model which can be used to describe all these phenomena. Indeed, FitzHugh-Nagumo equations have been popularised as a prototype reaction-diffusion system which can also reproduce such phenomena as travelling waves in nerve fibre or formation of Turing Patterns. For this presentation, we will be talking about the spatio-temporal patterns observed in FitzHugh-Nagumo model along with using Fourier analysis to compute the amplitude of the Turing Patterns observed in one of the regimes, and link one of the observed patterns to an application of modelling pattern formation E-coli due to chemotaxis.

When brain meets information: mathematical modelling of entropy change to external stimulation

Zonglun Li, University College London

Brain can be seen as a giant reservoir composed of neurons and other cell types. It is widely believed that numerous learning mechanisms are taking place simultaneously through neuronal interactions in order to modulate synaptic weights which can potentially regulate information processing. However, it is still largely unclear how external stimuli may affect synaptic connections and therefore, information storage and transmission. Spike Timing Dependent Plasticity (STDP) is a form of biologically plausible rules enabled by the temporal difference between spike arrival times of pre- and postsynaptic neurons. It is reckoned to facilitate learning and information storage in the brain, as well as the formation of neuronal circuits during brain development. In addition, the Shannon entropy is a pivotal measure in information theory to quantify the amount of disorder, or uncertainty of complex systems. Hence, in this work, we employed a mathematical model to study the tendency of entropy change in the reservoir when subject to external stimulation through STDP rules. We will show that our model manages to shed more light on some existing experimental observations regarding the entropy change in human brain under deep stimulation from a modelling perspective. Besides, we will also exhibit some other intriguing patterns that are not observed in vivo yet.

In-silico image-based modelling of morphogen diffusion

Yi Ting Loo, University of Warwick

Morphogens are intercellular signalling molecules providing spatial information to cells in developing tissues to coordinate cell fate decisions. The spatial information is encoded within long-ranged concentration gradients of the morphogen. Experimental

measurements of morphogen diffusivity vary significantly depending on experimental approach. Such differences have been used to argue against diffusion as a viable mechanism of morphogen gradient formation. Using particle modelling on realistic zebrafish brain images, we demonstrate that accounting for the local tissue architecture in concert with including receptor binding is sufficient to explain a range of biological observations. This demonstrates that (hindered) diffusion-driven transport is a viable mechanism of gradient formation of morphogens.

First order strong convergence of the projected Euler-Maruyama method for scalar SDEs defined in the positive domain
Yiyi Tang, University of Strathclyde

In 2014, Neuenkirch and Szpruch established the drift-implicit Euler-Maruyama method for a series of scalar stochastic differential equations which take values in a domain. Their numerical methods are valid for several important SDE models, e.g., the A¨ıt-Sahalia model, the constant elasticity of volatility model, the Heston-3/2 volatility model and so on. They proved that the drift-implicit Euler-Maruyama method converges to the exact solution with order one. However, expensive computational cost is required for implementation of this implicit numerical method. In this paper, we will introduce the projected EulerMaruyama method for a series of scalar stochastic differential equations which take values in the positive domain. The projected Euler-Maruyama method is an explicit numerical method and we will show that it is also p-strongly convergent with order one.

Some algorithms for the Rao decomposition of a quasimartingale
Timothy Kang, Imperial College London

Quasimartingales are a class of stochastic processes which can be considered as ‘stochastic counterparts’ to functions of finite variation. A crucial property of a quasimartingale is that it can be expressed as the difference of two non-negative supermartingales. Moreover, there is a unique choice of non-negative supermartingales - its Rao decomposition.
Ascoli introduced an algorithm in 1934 that expresses a given function of finite variation (defined on a compact real interval) as the difference of two increasing functions. At the turn of the century, Zalgaller introduced an algorithm which expresses certain continuous functions (again defined on a compact real interval) as the difference of two continuous convex functions.
Taking inspiration from these two algorithms, we present some algorithms that return the Rao decomposition of a given quasimartingale. After introducing them, we outline a proof of their validity.
We then discuss some properties of each algorithm and compare the algorithms. We finish by presenting potential areas to which any of these algorithms can be applied.

Tracking a Target Moving Randomly on a Line
Hengjian Zhang, London School of Economics

This paper aim to minimise a performance index consist with expectation of discounted square distance between the controlled process and target plus a proportional cost. we used HJB equation to derive the optimal strategy.

Optimal curing rate in SIS epidemics
Ryan McFadden, Heriot-Watt University

We consider a susceptible-infected-susceptible (SIS) epidemic model on a graph, with a homogeneous infection rate and heterogeneous curing rates. We set an overall network curing rate, Δ, and study optimal allocation of curing rates to nodes, in terms of the expected time to the extinction of the epidemic. As other parameters are fixed, we study these allocations as the infection rate tends to 0 and ∞. Our findings suggest that homogeneous curing rates are optimal in both limits for certain regular graphs, not all, but are not optimal otherwise. We illustrate our findings via a numerical study for star graphs.

Existence and Stability of Solution for Time-Delayed Nonlinear Fractional Differential Equations
Shiferaw Geremew Kebede, Arba Minch University

The objective of this study is to analyze the existence and stability of solutions for a mathematical model of nonlinear systems of time-delayed fractional differential equations involving Atangana-Baleanu-Caputo (ABC) fractional derivatives with vaccination. The epidemiological states of the total population are classified as susceptible individuals S(t), infected individuals I(t),
quarantined individuals Q(t), recovered individuals R(t), vaccinated individuals V(t) and insusceptible/protected persons P(t) . By considering coordinate transformation, we linearize our system and obtain a matrix coefficient for the proposed time-delayed fractional differential equation. We establish sufficient requirements and inequalities using the generalized Gronwall inequality and Krasnoselskii's fixed-point theorem to prove the existence of solution for
our problem. Additionally, we construct sufficient requirements for stability analysis by employing the Laplace transform and matrix measure theory. We also investigate criteria for the local stability of the epidemic and disease-free equilibrium points. Finally, we provide a numerical illustration to validate the effectiveness of our results.

Separating compartmental behaviour for non-selfish individuals in an epidemic
Mark Lynch, University of Warwick

How can I care about others in an epidemic? Population behaviour in an epidemic can be viewed as a “differential game”: Rational, well informed individuals seek to maximise their own utility function by modifying their behaviour. This behaviour affects the course of the epidemic in an SIR compartmental model. Typically, this analysis involves a single behavioural class, or multiple behavioural classes depending on fixed attributes such as occupation or age. Less studied are models in which individuals change their behaviour depending on which compartment they are in. Given a utility, one can solve the related game theoretic problem to derive Nash equilibrium system dynamics. When the costs in the utility only pertain to the individual, infected individuals never socially distance because modifying their behaviour cannot improve their situation. We study the case where individuals care about other members of the population. Their behaviour will then change in order to protect others from incurring the cost of being infected and/or of having to socially distance. We quantify the degree to which individuals must care about the population in order to rationally target disease eradication through social distancing.

Weyl-Dirac Operators: Theory and Applications
Nikolaos Alexandrakis, Lancaster University

The study of Dirac operators was very popular during several periods in the previous century. This was particularly true for two reasons: First, Dirac-type equations help us understand certain properties of elementary particles (like the spin of electrons) and second, they motivated the development of then-new Mathematics, for example, Spin Geometry. In recent years, interest has risen again, because understanding a particular class of such equations, the magnetic Weyl-Dirac equations can shed light on the development of electric devices based on graphene. In this talk, we'll briefly present some early and recent advances in this peculiar area of Mathematics.

Automating generation of scalings for dimensional analysis
Hollis Williams, King Abdullah University of Science and Technology

Traditional techniques for identifying the dimensionless quantities which are relevant for a physical system involve a large amount of algebraic manipulation. Another approach is dimensional analysis, which is often applied either via Rayleigh's method or the Buckingham Pi theorem. This theorem has the advantage of not requiring any physical assumptions apart from the principle of dimensional homogeneity. In this presentation, we describe a web application we have developed which automates the entire process of dimensional analysis, including conversion of relevant quantities to SI base units, generation of all possible sets of dimensionless groups, and plotting of all possible candidate scalings.

Coupling proper generalised decomposition and overlapping domain decomposition to efficiently solve linear parametric PDEs

Ben Evans, Loughborough University

In practical applications such as design, optimisation and control, it is often necessary to solve the system of interest for many states. Parametric PDEs enable the creation of a mathematical model that accounts for all possible states of the system. However, solving these parametric PDEs can be computationally infeasible using standard approaches, e.g. finite elements, due to the high-dimensionality of the problem and the cost of computing each instance of interest.

We can efficiently obtain solutions of parametric PDEs dependent upon the parameters, called surrogate models, using model order reduction strategies. For this talk, we will apply the proper generalised decomposition (PGD) approach to obtain the surrogate models. However, when working with complex large-scale geometries and varying physics, as is often the case in practical applications, constructing these surrogate models can become computationally expensive because of the number of globally coupled unknowns.

Utilising domain decomposition (DD) methods alongside PGD allows us to overcome this computational bottleneck by introducing problems with fewer degrees of freedom. In this talk, we will see an overview of how overlapping DD methods can be coupled with PGD, followed by numerical results demonstrating the accuracy and efficiency of the proposed strategy. We will solve linear parametric elliptic PDEs and discuss the accuracy of the obtained solutions. Particular attention will be given to the region where the subdomains overlap when analysing the accuracy of the solutions. We will also comment on the computational cost of the method in comparison to a standard DD-FEM approach.

Bayesian Optimisation for Non-Convex Two-Stage Stochastic Optimisation Problems

Jack Buckingham, University of Warwick

Bayesian optimisation is a sample-efficient method for solving expensive, black-box optimisation problems. Stochastic programming concerns optimisation under uncertainty where, typically, average performance is the quantity of interest. In the first stage of a two-stage problem, here-and-now decisions must be made in the face of this uncertainty, while in the second stage, wait-and-see decisions are made after the uncertainty has been resolved. Typically, methods in stochastic programming assume that the objective is cheap to evaluate, and that it is linear or convex. This work applies Bayesian optimisation to solve non-convex, two-stage stochastic programs which are expensive to evaluate.

In this talk, I will present a knowledge-gradient based acquisition function to solve such problems, with a guarantee of asymptotic consistency. Experiments demonstrate empirically that these outperform the naive approach of optimising the two types of

variables sequentially, both on synthetic and real-world examples, in a variety of dimensions, length scales and levels of observation noise.

From Less to More in 3D Reconstruction by Variational Models with Applications
Yiyao Zhang, University of Liverpool & National Tsing Hua University

In many imaging applications, the obtained images are often in low resolution or even have missing data due to practical and hardware limitations, which can impact subsequent 3D reconstruction. For instance, X-ray imaging carries radiation risks, limiting data collection time. Terahertz (THz) imaging, while safe, is slow and affected by diffraction and noise. Magnetic Resonance Imaging (MRI) struggles with the small region of interest in a high-resolution image. To address these challenges, a new framework using the Euler-Elastica regulariser is presented to reconstruct high-resolution surfaces from a few low-resolution 2D slices, combining mathematical models with local edge features and global smoothness. Two algorithms are developed (a projected gradient descent method and the alternating direction method of multipliers), and quantitative comparisons based on discrete curvatures show superiority over other regularisers. Practical examples in X-ray, MRI, and THz imaging validate its effectiveness, offering potential applications in medical imaging and computer vision. Joint work with Prof Ke Chen (Strathclyde and Liverpool), and Prof Shang-Hua Yang (NTHU, Taiwan).

Direct Molecular Simulation of 1D Normal Shock Waves with a Neural Network Collision Model
Nicholas Daultry Ball, University of Oxford

Direct Molecular Simulation (DMS) is a method of simulating gas dynamics which replaces the phenomenological collision models of Direct Simulation Monte Carlo with direct simulation of the collision dynamics. While parameters in models such as the commonly used variable hard spheres must be estimated from experimental viscosity measurements, DMS requires only a model of the microscopic interactions between particles [1]. This method can reproduce results from
full Molecular Dynamics (MD) simulations, at a significantly lower computational cost since the positions and velocities of all particles need not be tracked. However, the requirement to simulate large numbers of molecular trajectories on the fly means that the method is still significantly slower than traditional DSMC methods. In order to save this computational cost it is desirable to precompute trajectories and use this data to infer dynamics for the molecular collisions. This work
aims to use machine learning to achieve improved computational efficiency over DMS while retaining its accuracy. We obtain a dataset of Argon collisions via classical trajectory calculation with the Lennard-Jones potential, and train a multi-layer fully-connected network to predict the deflection angle of a collision from the relative velocity and impact parameter. We incorporate this model into the DMS algorithm,

replacing the integration of the collision trajectory with evaluation of the neural network, and apply it to the formation of normal shock waves. Results for the Argon shockwave show that the neural network model is able to reproduce shock profiles obtained from DMS, while substantially reducing the computational time required. We present results evaluating the accuracy of the DSMC with neural network against data from experiments, DMS and MD simulations at Mach numbers 1 ≤ M ≤ 9 and Knudsen numbers ranging from continuum Kn ≃ 10−5 to transitional Kn ≃ 0.1

Analysis and numerical approximation of stationary second-order Mean Field Game partial differential inclusions
Yohance Osborne, University College London

Mean Field Games (MFG) are models for Nash equilibria of large population stochastic differential games of optimal control. Under simplifying assumptions, these equilibria are described by non-linear systems in which a Hamilton—Jacobi—Bellman (HJB) equation and a Kolmogorov—Fokker—Planck (KFP) equation are coupled. In the classical formulation of the MFG system, the advective term of the KFP equation involves a partial derivative of the Hamiltonian that is assumed to be continuous. However, in many cases of practical interest, the underlying optimal control problem of the MFG may give rise to bang-bang controls, which typically lead to non-differentiable Hamiltonians.
In this talk we present results on the analysis and numerical approximation of stationary second-order MFG systems for the general case of convex, Lipschitz, but possibly non-differentiable Hamiltonians. In particular, we propose a generalization of the MFG system as a Partial Differential Inclusion (PDI) based on interpreting the partial derivative of the Hamiltonian in terms of subdifferentials of convex functions. We prove the existence of unique weak solutions to MFG PDIs under a monotonicity condition similar to one that has been considered previously by Lasry \& Lions. Moreover, we introduce a monotone finite element discretization of the weak formulation of MFG PDIs and present theorems on the strong convergence of the approximations to the value function in the H^1-norm and the strong convergence of the approximations to the density function in L^q-norms. We conclude the talk with discussion of some numerical experiments involving non-smooth solutions.

Modelling seawater intrusion beneath marine ice sheets
Gabriel Cairns, University of Oxford

The dynamics of marine-terminating glaciers in West Antarctica are dominated by the presence of water between the ice and the bedrock. In particular, sedimentary basins beneath these glaciers act as important sources or sinks of water at this ice-bed interface. These sedimentary basins contain both freshwater supplied from the ice-bed interface and saltwater introduced from the ocean at previous points in glacial history. By developing a mathematical model for the dynamics of fresh and saline groundwater in subglacial sedimentary basins, we show that even a physically simple model displays complex and subtle behaviours, associated with sedimentary basin geometry

and with ice sheet growth and retreat in response to climate changes on geological timescales. We show that seawater intrusion has significant effects on the exchange of freshwater with the ice-bed interface, and consider the ways in which present-day observations of groundwater salinity can reveal insights into ice-sheet history, and thus into the future stability of the West Antarctic ice sheet to climate change.

Applying Stochastic Dynamical System Methods to Ship Capsize Problem
Jiayao Shao, University of Warwick

Ship stability is a crucial subject in naval architecture. In this project, we employ a nonlinear ship dynamics model with heave-roll coupling in beam seas and investigate its stability from the perspective of Large Deviation Theory. To simulate wave excitation, we introduce degenerate filtered noise into the ship motion equations. We analyse the model using a method called the 'Hamiltonian Optimal Control Method'. Furthermore, due to the special property of the ship dynamics, we divide the process of ship capsize into three parts, to allow this event to happen under infinite time scale.

Poster Session

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A Numerical Study of Point Forces in a Multi-Dimensional Elastic Model for Tumors
Sabia Asghar, Hasselt University

Spatio-Temporal Patterns forming in FitzHugh-Nagumo Model
Hardik Poptani, University of Liverpool

Exploration of the Best Option with the Presence of Global change
Phurinut Srisawad, University of Warwick

Dynamic Mechanism Design for Repeated Games with Asymmetric Information: A Recursive Approach
Samridh Aggarwal, London School of Economics

Ocean wave-induced microplastic transport in the presence of the Basset-Boussinesq history force
Mary Eby, Heriot-Watt University