A celebratory symposium
MathBioFest 2018
07-08 November 2018
Department of Mathematics
Imperial College London | South Kensington Campus

Speakers
Becca Asquith | Imperial College
Anne Babtie | Imperial College
Tom Bell | Imperial College
Mark Chaplain | St Andrews
Andrew King | Swansea
Philip Maini FRS | Oxford
Alfonso Martínez-Arias | Cambridge
Karen Page | UCL

Immunology
Cell biology
Microbial ecology
Cancer Biology
Animal behaviour
Mathematical Biology
Stem cells
Developmental biology

Organisers
Diego Oyarzún
José Carrillo
Mauricio Barahona

The Year of Mathematical Biology 2018
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Welcome note
MathBioFest 2018 - a celebratory symposium

Welcome to Imperial’s celebration of the Year of the Mathematical Biology. The workshop will offer a bird’s eye view of the achievements and challenges for mathematics in the life sciences. We aim to celebrate the achievements of mathematics at the interface with biology in its broadest sense. We have prepared an exciting programme with a mix of broad-audience talks and research presentations. These will showcase the pivotal role that mathematical reasoning plays in fields as diverse as molecular biology, animal behaviour, and epidemiology.

The symposium is part of the Year of Mathematical Biology 2018 initiative from the European Mathematical Society and the European Society for Mathematical and Theoretical Biology alongside a series of events happening all across Europe.

Organising Committee:
Diego Oyarzún
Jose Carrillo
Mauricio Barahona

*With thanks to the EPSRC Centre for Mathematics of Precision Healthcare and Imperial College London, Department of Mathematics (Platform Workshop Support Grant, Workshop Award DW012DO) for their support.*
Programme
Day 1
Date: 7\textsuperscript{th} November
Location: Huxley Building, Clore Lecture Hall

14:00 – 14:30  Arrival, registration and coffee
14:30 – 14:45  Introduction (Diego Oyarzún, Jose Carrillo, Mauricio Barahona)
14:45 – 15:45  Alfonso Martínez-Arias (University of Cambridge)
  \textit{The ideal and the possible: a matter of genes, cells and numbers}
15:45 – 16:00  Coffee break
16:00 – 17:00  Mark Chaplain (University of St Andrews)
  \textit{A mathematical framework for modelling the metastatic spread of cancer}
17:00 – 18:00  Reception
Day 2
Date: 8th November
Location: 170 Queen’s Gate, Council Room

09:45 – 10:15  Arrival and coffee
10:15 – 11:00  Becca Asquith (Imperial College London)
               *KIRs, Immune cell dynamics & Control of Chronic Viral Infection*
11:00 – 11:30  Coffee break
11:30 – 12:15  Andrew King (Swansea University)
               *Sociality, heterogeneity, organisation and leadership in animal societies.*
12:15 – 13:00  Ann Babtie (Imperial College London)
               *Inferring gene regulatory networks from single cell data*
13:00 – 14:15  Lunch
14:15 – 15:00  Tom Bell (Imperial College London)
               *Ecology and evolution of inter-specific interactions in bacterial communities*
15:00 – 15:45  Karen Page (University College London)
               *Mathematical modelling of the vertebrate neural tube*
15:45 – 16:15  Coffee break
16:15 – 17:15  Philip Maini (University of Oxford)
               *Does mathematics have anything to do with biology?*
17:15 – 17:30  Concluding remarks (Diego Oyarzún)
Useful information
Location: Imperial College London, South Kensington Campus.
Day 1: Huxley Building (number 13 on the map below), 180 Queen's Gate, SW7 2AZ. Lectures will take place in the Clore Lecture Hall.
Day 2: 170 Queen's Gate, 170 Queen’s Gate, SW7 5HF. Lectures will take place in the Council Room.

Directions to Imperial College London: A map of the Campus is overleaf. Google maps works really well to find the quickest route to the college campus by walking or public transport. An alternative is the TFL journey planner which is available online.

**Tube**

South Kensington and Gloucester Road (District, Circle and Piccadilly Lines) are the closest Underground stations to the college. Walking to the college takes approximately 10 minutes from both stations.

**Bus**

9 Aldwych - Hammersmith Broadway, alight at the Royal Albert Hall
10 Kings Cross Station - Hammersmith Broadway, alight at the Royal Albert Hall
52 Victoria Bus Station - Willesden Bus Garage, alight at the Royal Albert Hall
360 Elephant and Castle Station - Prince Consort Rd, alight at Prince Consort Rd
14 Tottenham Court Road - Putney Heath, alight at South Kensington Station
49 Battersea Rise - Shepherd's Bush, alight at South Kensington Station
70 Acton - South Kensington Station, alight at South Kensington Station
74 Baker Street Station - Putney, alight at South Kensington Station
345 Peckham Bus Station - South Kensington Station, alight at South Kensington Station
414 Maida Vale - Putney Bridge, alight at South Kensington Station
430 South Kensington Station - Minstead Gardens SW15

For London Transport ticket information, check the TFL website (http://www.tfl.gov.uk/) or download the Visitor Guide to London.

Train
London Victoria and London Paddington are the nearest National Rail train stations.

Car/Taxi
Uber app – the easiest and cheapest way to request a car. Black cabs can also be hailed anywhere.

Cycling
There are a number of public bicycle racks located towards the South side of the building. Bicycles are left on these racks at your own risk and Imperial College cannot take responsibility for any loss or damage. There are also several Santander Cycle Hire docking stations within walking distance of the College. The closest one is on Prince Consort Road just outside the RSM building. For further information visit the Santander Cycle Hire website. You can find the best cycling route by using the Transport for London cycling pages.
Abstracts

Alfonso Martínez-Arias
University of Cambridge, Department of Genetics
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The ideal and the possible: a matter of genes, cells and numbers

Mathematics plays a central role in modern biology despite the fundamental differences in aims and methods of the two disciplines. In the talk I shall discuss the manner in which biological systems resist a mathematical treatment and yet need mathematics to understand their structure and function.
A mathematical framework for modelling the metastatic spread of cancer

Cancer is a complex disease that starts with mutations of key genes in one cell or a small group of cells at a primary site in the body. If these cancer cells continue to grow successfully and at some later stage invade the surrounding tissue and acquire a vascular network (tumour-induced angiogenesis), they can then spread to distant secondary sites in the body. This process, known as metastatic spread, is responsible for around 90% of deaths from cancer and is one of the so-called hallmarks of cancer. Although many models exist of various aspects of cancer growth (avascular growth, tumour-induced angiogenesis, the immune response to cancer, invasion), only a very few models of metastatic spread exist and none are of an explicitly spatial nature. In this talk we present a mathematical modelling framework that captures the interconnected processes of invasion and metastatic spread of individual cancer cells in a spatially explicit manner - a multi-grid, hybrid, individual-based approach. This framework accounts for the spatio-temporal evolution of mesenchymal- and epithelial-like cancer cells, as well as MT1-MMP, MMP-2 dynamics and interactions with the extracellular matrix.
Chronic viral infections such as human immunodeficiency virus (HIV-1), hepatitis C virus (HCV) and human T cell leukemia virus (HTLV-1) are marked by huge between-individual variation in outcome. Some people infected with HIV-1 will develop AIDS in less than 5 years others will remain healthy for 10 years or more. In HCV infection, some individuals spontaneously clear the virus others develop persistent infection and subsequent risk of liver failure. Similarly in HTLV-1 infection, some individuals remain lifelong healthy carriers of the virus whilst others will develop an aggressive, rapidly fatal leukemia.

We are coupling analysis of genetic data from large patient cohorts with mechanistic mathematical modelling and in vitro and in vivo T cell dynamics experiments to gain insight into what determines the clinical outcome of viral infection.
Andrew King
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Sociality, heterogeneity, organisation and leadership in animal societies
Andrew J King(1), the SHOALgroup(1) & SHOALgroup collaborators(2)
(1) Department of Biosciences, College of Science, Swansea University, Swansea, SA2 8PP, UK;
(2) Various Institutions, Worldwide.

I will give an overview of the research my team conducts on the social behaviour of animals, highlighting how multiple disciplinary approaches resolve our understanding. I will explain how technological and methodological advances are providing us with the opportunity to quantify and model the heterogeneity that exists within the groups we study, and within the environments in which these groups live. In doing so, I will allow the audience to choose which research they would like to learn about in real-time, with options ranging from studies of fish, birds, ungulates, and primates (including people).
Inferring gene regulatory networks from single cell data

Single cell transcriptomic data are increasingly used to study the dynamics of gene expression during cell development. These data allow us to explore the genes and regulatory interactions involved in cell differentiation processes. We have developed an algorithm, PIDC, which uses multivariate information measures to identify regulatory relationships between genes. Information measures allow us to discern non-linear statistical relationships among random variables that are typically missed by conventional correlation measures. We compare our method to existing information theoretic-based inference algorithms, and illustrate its application to various experimental datasets including embryonic stem cells undergoing neuronal differentiation.
Ecology and evolution of inter-specific interactions in bacterial communities

Bacterial communities are enormously complex, with hundreds of interacting species in every drop of pond water. These communities are also ecologically and economically important: for example, they cycle nutrients to higher organisms and detoxify soil. Understanding how these complex communities impact these "ecosystem functions" is an important goal in microbial ecology research, but the research is constrained by the complexity of the communities. We will describe experiments using simplified communities to understand how interactions among bacteria change over ecological and evolutionary timescales and will explain how we will extend the experiments to more complex communities.
Mathematical modelling of the vertebrate neural tube

Cell adhesion, movement, division and differentiation contribute to pattern formation in developing tissues. This is true in the neural tube, where neurons differentiate in a characteristic pattern from a proliferating epithelium. We describe a vertex model of the pseudostratified epithelium and explain how changing the differentiation rate of cells can change the shape of clones, as is seen experimentally. We also show how the volume of cells follows a characteristic distribution, which may arise because the tissue is close to a jamming transition.
Philip Maini
University of Oxford, Wolfson Centre for Mathematical Biology Mathematical Institute
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Does mathematics have anything to do with biology?

In this talk, I will review a number of interdisciplinary collaborations in which I have been involved over the years that have coupled mathematical modelling with experimental studies to try to advance our understanding of processes in biology and medicine. Examples will include pattern formation in slime mold, somatic evolution in tumours, collective cell movement in neural crest. These are examples where verbal reasoning models are misleading and insufficient, while mathematical models can enhance our intuition.
Precision healthcare aims to tune interventions to the variability of individuals in factors like genes, lifestyle and environment. However, diseases, individuals and their social contexts are diverse; different treatments work differently for different individuals, groups and socio-environmental contexts.

Advances in ‘omics technologies, imaging, and molecular medicine mean that individuals can be characterised with rich, high-dimensional data. In addition, there is increasing access to data about groups and their socio-environmental contexts, as reflected in social network, demographic and epidemiological data. Integrating strata of data from the individual to the population, in an interpretable form can provide the basis for improved detection and intervention tools in medical science and clinical practice enriching decision-making in healthcare and minimising the inefficiencies of inadequate stratification.

The EPSRC Centre for Mathematics of Precision Healthcare aims to provide a venue for new mathematics, new data analysis pipelines, and a genuinely interdisciplinary approach by bringing together Imperial’s mathematicians, engineers and computer scientists with medical scientists and clinicians to address such issues across different areas in healthcare, from patient journeys to population-level analyses.

http://www.imperial.ac.uk/mathematics-precision-healthcare/

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