

LEEDS 2019: ECO-EVOLUTIONARY DYNAMICS (L19EEDs) WORKSHOP

“Fluctuations, tipping points and emergence in eco-evolutionary dynamics”

University of Leeds, School of Mathematics, 2-5 July 2019

Useful information, programme and booklet of abstracts

Organizing Committee

Dr Sandro Azaele, School of Mathematics, University of Leeds.

Dr Matteo Cavaliere, SCMDT, Manchester Metropolitan University.

Dr Mauro Mobilia, School of Mathematics, University of Leeds.

Special thanks to Helen Copeland (Leeds School of Maths' Reception)

Sponsored by



and

EPSRC Network Plus in Emergence and Physics Far From Equilibrium 2016-19



Useful information

General inquiries can be addressed to the **Maths Reception** (+44 (0)113 343 5130), on level 9. Welcome packs will be available at the registration desk that will be opposite to the Maths Reception.

All talks will be held in the **MALL** of the School of Mathematics which is located on level 8. The MALL can be accessed through a lift located at the main entrance at level 9 of the School of Mathematics. The Mathematics building is the number 84 on the [campus map](#)

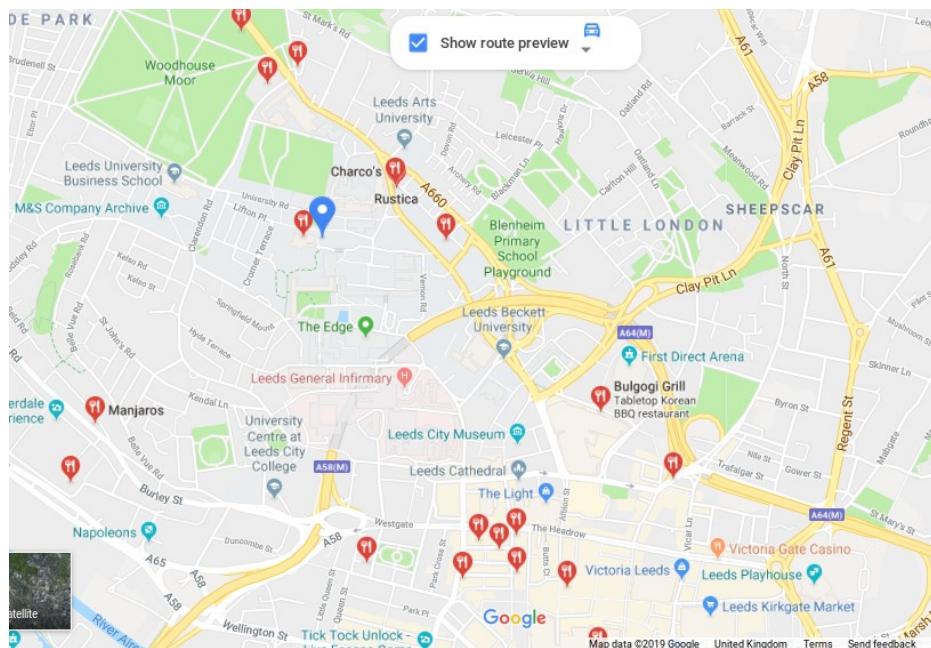
All **coffee breaks** and refreshments will be served in the School's Reading Room on Level 9.

On Tuesday 2nd and Wednesday 3rd July, **lunches** will be served on Level 8 (close to the MALL). On Thursday 4th and Friday 5th July, we will have lunch in the Reading Room on Level 9.

For each keynote speaker, a desk has been reserved in our **Research Visitors' Centre** (RVC) on level 10 of the School of Maths (ask the Maths Reception.)

WiFi: access to an eduroam network will be available on campus.

Dinner: There are many **restaurants**, pubs, and other eateries near the university...



Speakers and EPSRC Network Plus participants are asked to pay for their **travel and subsistence expenses**, and claim them back for **reimbursement**. This should be done using the **provided claim form** (from the University of Leeds or Manchester) to be returned at the indicated address along with all **original receipts**. We have arranged for the **hotel bills** to be directly covered by the Leeds School of Maths.

Invited speakers and participants supported by the EPSRC Network Plus will be accommodated at

Hotel Ibis Leeds Centre

Marlborough Street 23

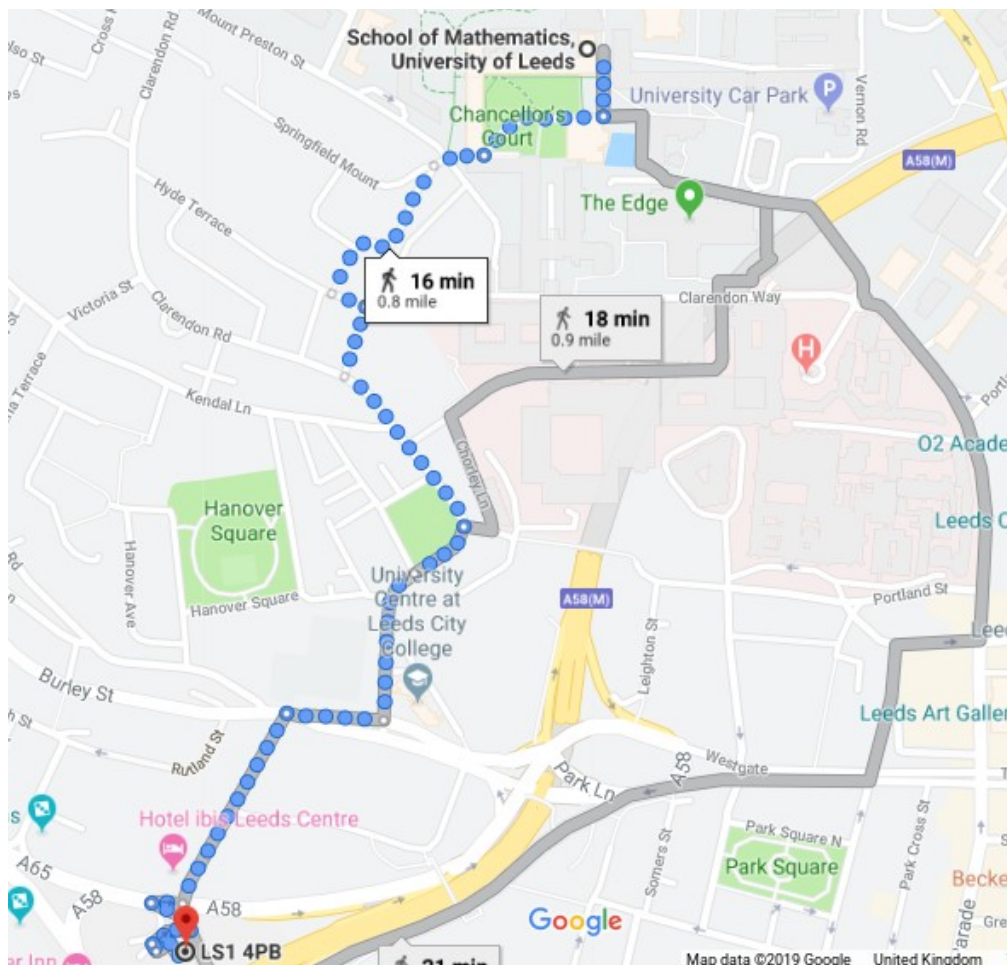
LS1 4PB LEEDS

Telephone: +441133969000 Email: H3652@accor.com

The Hotel Ibis is at about 12-minute walking distance from Leeds Train Station.

Alternatively, a taxi ride would last about 7-10 minutes and cost about £5.

The School of Maths is at about 16-minute walking distance from the Hotel Ibis.



List of participants (as of 1st July)

Steve SMYE	S.W.Smye@leeds.ac.uk
John LOVETT	J.Lovett@leeds.ac.uk
Piyush SRIVASTAVA	P.Srivastava@leeds.ac.uk
Yuwei LI	fs17yl@leeds.ac.uk
John HOLDEN	py13jh@leeds.ac.uk
Alexis MERCADAL RAMIREZ	Alexis.Mercadal-Ramirez@warwick.ac.uk
Bethany ALLEN	eebja@leeds.ac.uk
Xiang Li	mmxl@leeds.ac.uk
Graeme LLOYD	G.T.Lloyd@leeds.ac.uk
Aleksandra ARDASEVA	aleksandra.ardaseva@dtc.ox.ac.uk
Daniel INAFUKU	inafuku2@illinois.edu
Ivan SUDAKOV	isudakov1@udayton.edu
Jonathan WARD	amtjw@leeds.ac.uk
Joseph BARON	joseph.baron@postgrad.manchester.ac.uk
Steve SAIT	S.M.Sait@leeds.ac.uk
Robert WEST	mmrw@leeds.ac.uk
Leonardo MIELE	mmlm@leeds.ac.uk
Weini HUANG	weini.huang@qmul.ac.uk
Niccolo' ZAGLI	n.zagli18@imperial.ac.uk
Ernesto BERRIOS	ernesto.berrios@manchester.ac.uk
Giacomo BALDO	mmgb@leeds.ac.uk
Liam LACHS	liamlachs@gmail.com
Yvonne KRUMBECK	yk436@bath.ac.uk
Laura SIDHOM	laura.mm@hotmail.co.uk
Eduardo Henrique COLOMBO	ecolombo@ifisc.uib-csic.es
Nadav SHNERB	nadav.shnerb@gmail.com
Michael ASSAF	michael.assaf@mail.huji.ac.il
Christopher CLEMENTS	c.clements@bristol.ac.uk
Elaine CROOKS	e.c.m.crooks@swansea.ac.uk
Nigel GOLDENFELD	nigel@illinois.edu
Jose JIMENEZ	j.jimenez@surrey.ac.uk
Stefan KLUMPP	stefan.klumpp@phys.uni-goettingen.de
Sara MITRI	sara.mitri@unil.ch
David HALES	daphal2@gmail.com
Remus STANA	mmrls@leeds.ac.uk
Ramesh VAIDHISWARAN	vaidhiswaran.ramesh17@imperial.ac.uk
Stephen GRIFFITHS	S.D.Griffiths@leeds.ac.uk
Fabio Peruzzo	f.xuzzo@gmail.com
Sandro AZAELE	S.Azaele@leeds.ac.uk
Matteo CAVALIERE	M.Cavaliere@mmu.ac.uk
Mauro MOBILIA	M.Mobilia@leeds.ac.uk

Programme of Tuesday 2nd July

All talks in the MALL on level 8 of the School of Maths

9:00-10:00 Registration at Level 9 of the School of Mathematics

10:00-10:15 Open

10:15-11:15 **Christopher Clements** (University of Bristol, UK)

“Predicting the future of biological systems”

11:15-11:40 Coffee break in the Reading Room at Level 9

11:40-12:10 **Weini Huang** (Queen Mary University London, UK)

“Eco-evolutionary dynamics under changing trade-offs driven by predator-prey coevolution”

12:10-14:00 Lunch break at Level 8 of the School of Mathematics

14:00-15:00 **Elaine Crooks** (University of Swansea, UK)

“Invasion speeds in a competition-diffusion model with mutation”.

15:00-15:30 Coffee break in the Reading Room at Level 9

15:30-16:00 **Joseph Baron** (University of Manchester, UK)

“Synchronisation, amplification and coherence of noise-induced cycles in a model of the somite segmentation clock”

16:00-16:30 **Giacomo Baldo** (University of Leeds, UK)

“Memory granularity effects on evolutionary games”

16:30-17:30 Informal discussions and networking

Programme of Wednesday 3rd July

All talks in the MALL on level 8 of the School of Maths

10:00-10:05 Open

10:05-11:05 **José Jimenez** (University of Surrey, UK)

“Impact of molecular interventions on eco-evo dynamics of experimentally tractable microbial systems”

11:05-11:30 Coffee break in the Reading Room at Level 9

11:30-12:00 **John Lovett** (University of Leeds, UK)

“Assessing sustainability in North America’s ecosystems using criticality and information theory”

12:00-12:30 **Yvonne Krumbeck** (University of Bath, UK)

“Fitness differences suppress the number of mating types in evolving isogamous species”

12:30-14:00 Lunch break at Level 8 of the School of Mathematics

14:00-15:00 **Sara Mitri** (Université de Lausanne, CH):

“Eco-evolutionary dynamics in a synthetic bacterial community”

15:00-15:30 Coffee break in the Reading Room at Level 9

15:30-16:00 **Ernesto Berríos** (University of Manchester, UK)

“Hypermutators drive multi-drug resistance evolution during antibiotic therapy”

16:00-16:30 **Leonardo Miele** (University of Leeds, UK)

“Neutrality in selection-mutation dynamics”

16:30-17:30 Informal discussions and networking

Programme of Thursday 4rd July

All talks in the MALL on level 8 of the School of Maths

10:00-10:05 Open

10:05-11:05 **Michael Assaf** (The Hebrew University of Jerusalem, IL)

“Rare events in interacting populations: the role of environmental noise and spatial heterogeneity”

11:05-11:30 Coffee break in the Reading Room at Level 9

11:30-12:00 **Nadav Shnerb** (Bar-Ilan University, IL)

“Stochasticity induced stabilization and evolution in varying environment”

12:00-12:30 **Aleksandra Ardaseva** (Oxford University, UK)

“Analysis of cancer dynamics in fluctuating environments”

12:30-14:00 Lunch break in the Reading Room at Level 9

14:00-15:00 **Stefan Klumpp** (University of Göttingen, DE)

“Heterogeneous populations in temporally or spatially fluctuating environments”

15:00-15:30 **Ivan Sudakov** (University of Dayton, USA)

The feedback mechanisms in climate-ecosystem coupling leading to species extinction

15:30-16:00 Coffee break in the Reading Room at Level 9

16:00-16:30 **Robert West** (University of Leeds, UK)

“Fixation properties of rock-paper-scissors games in populations of fluctuating size”

16:30-17:00 **Fabio Peruzzo** (University of Leeds, UK)

“Analytical abundance distributions in a spatial stochastic model for ecosystems”

17:00 -18:00 Informal discussions and networking

18:30 Conference dinner (keynote speakers and organisers, details to follow)

Programme of Friday 5th July

All talks in the MALL on level 8 of the School of Maths

10:10-10:15 Open

10:15-11:15 **Nigel Goldenfeld** (University of Illinois at Urbana-Champaign, USA)

“Stochastic Turing Patterns in the Biosphere: From Brains To Biofilms”

11:15-11:45 Coffee break in the Reading Room at Level 9

11:45-12:30 **Eduardo Henrique Colombo** (University of the Balearic Islands, ES)

“Spatial eco-evolutionary feedbacks mediate coexistence in prey-predator systems”

12:30-14:00 Lunch break in the Reading Room at Level 9

14:00-14:45 **Nadav Shnerb** (Bar-Ilan University, IL)

“Vegetation dynamics and the possibility of a catastrophic desertification transition”

14:45-15:15 **Laura Sidhom** (University of Manchester, UK)

“Stability and diversity in random Lotka-Volterra systems with non-linear functional response”

15:15-15:45 **Daniel Inafuku** (University of Illinois at Urbana-Champaign, USA)

“Towards a New Theory of Biological Information”

15:45-16:15 **Remus Stana** (University of Leeds, UK)

“Modeling molecular diffusion in cellular environment”

16:15-16:30 Close

16:30-17:30 Informal discussions over reception in the Reading Room at Level 9

Booklet of Abstracts

Keynote and Contributed Talks

Michael Assaf

The Hebrew University of Jerusalem, IL

Rare events in interacting populations: the role of environmental noise and spatial heterogeneity

Systems containing a discrete population of interacting agents dwell most of the time in the vicinity of some attractor, undergoing small random excursions around it, while large deviations from the typical behavior are extremely rare. Yet, it is precisely these extreme, rare events, giving rise e.g. to population extinction, switching between cellular phenotypic states, or fixation and loss of biodiversity, which may be of key practical importance. In most cases, dynamics of such systems are studied within the so-called well-mixed framework, while accounting for demographic noise only. In other words, in the usual setting, spatial degrees of freedom as well as environmental (or extrinsic) noise, are often omitted. In this talk I will review two extensions of this scenario. In the first, the effect of adding extrinsic noise on the frequency of rare events will be studied, as function of the external noise parameters (magnitude, correlation time and statistics). In the second extension, I will consider a population residing on a heterogeneous network, and show how rare events are influenced by the complex spatial topology of individuals. To this end, I will present analytical and numerical techniques that enable the accurate and efficient analysis of large deviations in such complex, many-body problems.

Christopher Clements

University of Bristol, UK

Predicting the future of biological systems

Predicting the future states of biological systems is critical if we are to efficiently and effectively preserve biodiversity in the face of ongoing environmental change. However, doing so is challenging, as ecological systems are inherently high dimensional, non-linear, and stochastic, and the data available to make such predictions are often spatially and temporally data limited. These challenges mean that process-to-pattern methods, such as mechanistic models, are often impossible to parameterise for populations or species of conservation interest. Alternatively, the collapse of a population may be inferred from signals detected in available data, a so-called pattern-to-process approach. Recent work has shown that shifts in the distribution of fitness related phenotypic traits such as body size may be particularly useful signals of the collapse of populations, as they indicate the loss of resilience in the system and loss of structure in a population. I will discuss recent research in this area, and the potential for such trait-based approaches to help inform conservation decision making.

Elaine Crooks

University of Swansea, UK

Invasion speeds in a competition-diffusion model with mutation

We consider a reaction-diffusion system modelling the growth, dispersal and mutation of two phenotypes. This model was proposed in by Elliott and Cornell (2012), who presented evidence that for a class of dispersal and growth coefficients and a small mutation rate, the two phenotypes spread into the unstable extinction state at a single speed that is faster than either phenotype would spread in the absence of mutation. After first showing that, under reasonable conditions on the mutation and competition parameters, the spreading speed of the two phenotypes is indeed determined by the linearisation about the extinction state, we prove that the spreading speed is a non-increasing function of the mutation rate (implying that greater mixing between phenotypes leads to slower propagation), determine the ratio at which the phenotypes occur in the leading edge in the limit of vanishing mutation, and discuss the effect of trade-offs between dispersal and growth on the spreading speed of the phenotypes. This talk is based on joint work with Luca Börger and Aled Morris (Swansea).

[Nigel Goldenfeld](#)

University of Illinois at Urbana-Champaign, USA

Stochastic Turing Patterns in the Biosphere: From Brains To Biofilms

Why are the patterns of plankton in the ocean so patchy? Why do frequently described geometrical hallucinations tend to fall into one of four different classes of pattern? Why don't we see hallucinations all the time? And why do populations in ecosystems tend to have noisy cycles in abundance? This talk explains how these phenomena all arise from the discreteness of the underlying entities, be they the on-off states of neurons or the numbers of bacteria in a fluid volume of ocean, or the number of signaling molecules in a biofilm. I explain how tools from statistical mechanics can yield insights into these phenomena, and report on a range of studies that include the evolution of the primate visual cortex, the behavior of signalling molecules in a forward-engineered synthetic biofilm, and the fluctuating patterns and populations of marine ecosystems.

[Jose Jimenez](#)

University of Surrey, UK

Impact of molecular interventions on eco-evo dynamics of experimentally tractable microbial systems

As a result of natural selection, microorganisms tend to maximise their fitness in any given environmental condition. This leads to a multilevel process of optimisation that produces the microbial strains (and communities) best adapted to the ecological constraints of a particular niche. The predictable manipulation of microbial communities is desirable for a number of applications such as those related to the prevention of pathogenic processes. Our capabilities to modify these communities on demand towards achieving a goal are, however, hindered by the complexity of interactions between the organisms present in these communities as well as by their interactions with their environment. In this talk I will present our recent work on population dynamics of bacterial communities under lab controlled conditions. I will focus on two case scenarios: the influence of factors such as population structure in the transmission of antibiotic resistance genes, and on the engineering of strains of *Pseudomonas aeruginosa* for the invasion of microbial populations exploiting the social biology linked to the siderophore pyoverdine.

Stefan Klumpp

University of Göttingen, DE

Heterogeneous populations in temporally or spatially fluctuating environments

The fitness of microbes is given by the rate of their proliferation in growth-promoting conditions and the success of their strategies for survival under stress conditions. Cells living in fluctuating environments need to evolve strategies to combine proliferation and stress tolerance. One common such strategy is phenotypic heterogeneity with phenotypic switching rates adapted to characteristic times of the fluctuating environment. I will discuss several aspects of such heterogeneous populations from a theoretical point of view, specifically the question whether heterogeneity is always beneficial, and how heterogeneity can be beneficial for populations spreading in space if the growth and survival conditions are variable in space. As an outlook I may also touch upon the interplay of population dynamics and mechanics in the case of bacterial colonies and biofilms.

[Sara Mitri](#)

Université de Lausanne, CH

Eco-evolutionary dynamics in a synthetic bacterial community

Eco-evolutionary dynamics are little understood within large microbial communities. Disentangling how microbial species interact with one another and how these interactions co-evolve over time needs to first be carried out on simpler ecosystems. We have focused on a synthetic bacterial community consisting of just four species involved in bioremediation. Using a well-defined medium, the four species grow in a closed system, in which we can closely follow bacterial abundances, the interactions between the four species and their genetic changes, during short- and long-term evolutionary experiment. We first show that the species have positive growth effects on one another and that this depends on growth medium composition. We then ask: what will happen to these positive interactions over time? Over approximately 500 generations, we find that species abundances fluctuate following patterns that differ depending on community composition. Out of five replicate communities containing all four species, three resulted in stable co-existence. We find that positive interactions are maintained in this four-species community, but are lost when species grow alone.

Aleksandra Ardaseva

University of Oxford, UK

Analysis of cancer dynamics in fluctuating environments

Malignant tumours typically have highly irregular vascular architecture with chaotic blood flow leading to spatio-temporal heterogeneity in concentrations of nutrients, metabolites, and drugs. Such variability requires cells to adapt to potentially lethal variations in environmental conditions. Risk spreading through spontaneous phenotypic variations is an evolutionary strategy that allows species to survive in temporally varying environments. It allows individuals within a species to diversify their phenotypes ensuring that at least some of them can survive in the face of sudden environmental change. We aim to investigate whether cancer cells may adopt this strategy when dealing with rapidly changing levels of nutrient due to temporally-varying blood flow. Here, we consider a system of nonlocal partial differential equations modelling the evolutionary dynamics of two competing phenotype-structured cell populations in periodically-fluctuating environments. The phenotypic state of each cell is represented by a continuous variable, and the phenotypic landscape of the populations evolves in time due to variations in the nutrient. In order to assess the evolutionary role played by risk spreading, we consider the case where the two cell populations undergo spontaneous phenotypic variations with different probabilities. The results obtained suggest that under relatively large and fast periodic oscillations, which bring about alternating cycles of starvation and nutrient abundance, higher rates of spontaneous phenotypic variations represent a competitive advantage. We discuss the implications of our results in the context of cancer metabolism.

Giacomo Baldo

University of Leeds, UK

Memory granularity effects on evolutionary games

Within a population, individual memory greatly influences individual and collective behaviour. Here, we consider a game-theoretical model of a large well-mixed population of individuals faced by a general problem, which is a choice between two available strategies. Previous research has highlighted the emergence of fluctuations and limit cycles at the collective level around the mixed equilibrium of the underlying game due to the effect of memory. We develop a two-faceted description of memory, which includes length and granularity. We show that the precision of the individual's perception of the outside social environment is an important element determining the transition between synchronous and asynchronous collective states, and between periodic oscillations and random fluctuations of the group behaviour. Our results indicate that finely grained memories do not necessarily yield evolutionary advantages.

Joseph Baron

University of Manchester, UK

Synchronisation, amplification and coherence of noise-induced cycles in a model of the somite segmentation clock

Somite segmentation is a process in the development of vertebrates where clumps of mesodermal cells (the somites) assemble along what will become the spine. The somites form in a very regular manner, “budding off” rhythmically as the embryo grows. The prevailing theoretical framework for this process is the clock-wavefront model, put forward by Cooke and Zeeman in 1976. This model supposes that each cell in the presomitic mesoderm (PSM) possess an internal “clock” which is synchronised with its neighbours. It is thought that the cyclic expression of proteins (such as Hes or Her) constitute this putative clock and that the cycles in neighbouring cells are kept synchronised via Delta-Notch signalling. Previously, most theoretical treatments of the somite segmentation clock have used deterministic equations to model the cycles of gene expression in the PSM. Such an approach, while useful, can ignore noise-induced cycles which come about due to the intrinsic noise that arises from the stochastic nature of the transcription and translation processes. In this talk, I will discuss how the combination of delayed effects in the transcription/translation process combined with intrinsic noise can give rise to sustained cycles of gene expression in the PSM. I will go on to discuss how Delta-notch signalling can not only act to synchronise oscillation in neighbouring cells but also amplify these oscillations and make them more coherent.

Ernesto Berríos

University of Manchester, UK

Hypermutators drive multi-drug resistance evolution during antibiotic therapy

There is an urgent need for novel approaches capable of halting the evolution of antibiotic resistance. Combination therapies, treatments involving two or more antibiotics, have been used to prevent resistance evolution in a number of contexts, particularly against HIV and cancer. Motivated by this success, the use of antibiotic combinations is a proposed strategy for countering the global rise in antibiotic resistant bacterial infections. In this talk, a study of the potential for bacterial populations to overcome combination therapy is presented. Here, I will explore the evolution of multi-drug resistance during single-drug and combination treatment by using experiments and stochastic simulations. The experiments involved bacterial strain *Escherichia coli* str. K-12 substr. BW25113 exposed to rifampicin, nalidixic acid, or a combination of both; the simulations are based on binomial distributions, which reproduce the diauxic growth of bacteria. The success of combination therapy is predicated on simultaneous acquisition of more than one resistance being rare (due to low mutation rates) and sequential acquisition being prevented by the presence of multiple drugs. However, I will discuss that introducing “hypermutators” (subpopulations with an elevated mutation rate) could allow multi-drug resistance to evolve sequentially. Given that mutators are often found in bacterial infections, our results suggest caution in assuming combination therapies will be a panacea for the antibiotic resistance crisis.

Eduardo Henrique Colombo

University of the Balearic Islands, ES

Spatial eco-evolutionary feedbacks mediate coexistence in prey-predator systems

Eco-evolutionary frameworks can explain certain features of communities in which ecological and evolutionary processes occur over comparable timescales. In the particular case of prey-predator systems, a combination of empirical and theoretical studies have explored this possibility, showing that the evolution of prey traits, predator traits or the coevolution of both can contribute to the stability of the community, as well as to the emergence of various types of population cycles. However, these studies overlook that interactions are spatially constrained, a crucial ingredient known to foster species coexistence per se. Here, we investigate whether evolutionary dynamics interacts with the spatial structure of a prey-predator community in which both species show limited mobility and predators perceptual ranges are subject to natural selection. In these conditions, our results unveil an eco-evolutionary feedback between species spatial mixing and predators perceptual range: different levels of species mixing select for different perceptual ranges, which in turn reshape the spatial distribution of preys and their interaction with predators. This emergent pattern of interspecific interactions feeds back to the efficiency of the various perceptual ranges, thus selecting for new ones. Finally, since prey-predator mixing is the key factor that regulates the intensity of predation, we explore the community-level implications of such feedback and show that it controls both coexistence times and species extinction probabilities.

Weini Huang

Queen Mary University of London, UK

Eco-evolutionary dynamics under changing trade-offs driven by predator-prey coevolution

The shape of trade-offs between traits of organisms can determine diversity in populations. We hypothesised that the shape of trade-offs can change because of species coevolution. We validated the existence of such dynamical trade-offs in a predator-prey (ciliate-bacteria) coevolving experiment and observed prey defence becomes more costly over time. We built a stochastic model with random mutations to study the impact of dynamical trade-offs on predator-prey cycles and intra-specific diversity. With coevolution, prey diversity is higher if the defence is cheaper, and the predator diversity increases first but decreases later when defence is extremely cheap. Starting from a naïve prey and predator type (i.e. lowest defence for prey and lowest predation ability for predator), coevolution leads to a lower prey diversity compared to the evolution of only prey species. This is because the trade-offs become in general more costly under coevolution. We further measured the change of diversity over time in our experimental systems to compare with our theoretical results.

Daniel Inafuku

University of Illinois at Urbana-Champaign, USA

Towards a New Theory of Biological Information

Many attempts have been made to understand biomolecular machines, such as the ribosome, from a computational and information-theoretic perspective. However, it is well-understood that current information theory is limited to symbolic (i.e., syntactic) manipulations only and is not equipped to deal with objects that possess functions beyond such manipulations. In this study, we present a quantitative analysis of the information-processing abilities of several biomolecular machines that demonstrates their capacities for biological information. Furthermore, we argue that such machines possess functions that lie beyond the scope of traditional Shannon information theory and require a new description to completely characterize them. Finally, we propose new ways to extend current models by rigorously abstracting the structure and dynamics of these machines.

Jon Lovett

University of Leeds, UK

Assessing sustainability in North America's ecosystems using criticality and information theory

Sustainability is a key concept in economic and policy debates. Nevertheless, it is usually treated only in a qualitative way and has eluded quantitative analysis. Here, we propose a sustainability index based on the premise that sustainable systems do not lose or gain Fisher Information over time. We test this approach using time series data from the AmeriFlux network that measures ecosystem respiration, water and energy fluxes in order to elucidate two key sustainability features: ecosystem health and stability. A novel definition of ecosystem health is developed based on the concept of criticality, which implies that if a system's fluctuations are scale invariant then the system is in a balance between robustness and adaptability

Yvonne Krumbeck

University of Bath

Fitness differences suppress the number of mating types in evolving isogamous species.

Sexual reproduction is not always synonymous with the existence of two morphologically different sexes; isogamous species produce sex cells of equal size, typically falling into multiple distinct self-incompatible classes, termed mating types. A longstanding open question in evolutionary biology is: what governs the number of mating types? Simple theoretical arguments imply an advantage to rare types, suggesting the number of types should grow consistently, however, empirical observations are very different. While some isogamous species exhibit thousands of mating types, most have fewer than five.

In this talk, I present a mathematical model to quantify the role of fitness variation -- characterised by different mortality rates -- in determining the number of mating types emerging in simple evolutionary models. Our approach is based on a separation of time scales between short-term population dynamics and long-term evolutionary changes. We predict that the number of mating types decreases as the variance of mortality increases. Our analytical results are consistent with existing empirical data and thus provide a potential resolution to this longstanding question.

Leonardo Miele

University of Leeds, UK

Neutrality in selection-mutation dynamics

Since the introduction of Kimura's neutral theory and of Wright's notion of fitness landscape, neutrality and selection have been largely but usually independently studied by the theorists' community. Their use has generally been relegated to the molecular and phenotypic level, and eventually lead to the formation of two proper school of thoughts. However, recent experimental evidence has revealed that genomic networks are usually pervaded by neutral genotypes. The redundancy of neutral genotypes seems to be a key feature of the genotype space at various scales (e.g. metabolic, proteic, gene regulatory), and suggests that a realistic description of the evolutionary dynamics should reconcile neutrality and selection, with random mutations providing the innovative force. To our knowledge, a rigorous study of the role of neutrality in selection-mutation models is still missing in the theoretical literature. In this talk I will present a simple mathematical model describing the evolution of a population with continuous traits undergoing mutations and natural selection. Particularly, I will show how the interplay between neutrality and selection can generate non-trivial behaviours, where optimal individuals are not the fittest ones.

Fabio Peruzzo

University of Leeds, UK

Analytical abundance distributions in a spatial stochastic model for ecosystems

In this talk I will discuss the mathematical properties of a minimal model framework for the dynamics of ecological systems where individuals undergo local birth-death, immigration and local jumps on a regular lattice. Even if the model violates detailed balance, within a physically interesting regime, dominated by fluctuations, it is possible to calculate analytically the probability distribution of the number of individuals living in a given volume in any dimension. In the resulting distribution spatial effects are encoded in appropriate functions of space, which are calculated explicitly, and the validity of such formulae is confirmed by simulations. I will also show how these results can be used to infer the spatial empirical distributions of tree species in two lowland tropical forest inventories. In fact, the model allows to link observations of some of the most important ecological descriptors in a unified framework, and the predictions are shown to match data well.

Nadav Shnerb

Bar-Ilan University, IL

Stochasticity induced stabilization and evolution in varying environment

Noise and fluctuations are ubiquitous features of living systems. In particular the reproductive success of individuals is affected by many random factors. Some of these factors, like the local availability of nutrients or accidental encounters with predators, act on the level of a single individual (demographic stochasticity). Others, like fluctuations in temperature and precipitation rates, affect entire populations (environmental stochasticity). Environmental stochasticity is known to be the dominant mechanism when the population is large, but demographic noise becomes important close to extinction/fixation points. Accordingly, one must take account of both in order to calculate the chance of fixation, the time to extinction/fixation, speed of evolution and other parameters that affect the evolutionary process.

I will present results for a few generic models of two competing populations and high diversity assemblages, where stochasticity is superimposed on time-independent selective forces. A particular attention will be given to the possibility of stochasticity-induced stabilization (storage effect), where random environmental fluctuations enhanced biodiversity/polymorphism.

Nadav Shnerb

Bar-Ilan University, IL

Vegetation dynamics and the possibility of a catastrophic desertification transition.

The process of desertification in the semi-arid climatic zone is considered by many as a catastrophic regime shift, since the positive feedback of vegetation density on growth rates yields a system that admits alternative steady states. Some support to this idea comes from the analysis of static patterns, where peaks of the vegetation density histogram were associated with these alternative states.

We have developed a theoretical approach aimed at characterizing the transition by tracking the dynamics of spatial clusters. This technique reveals both the nature of the transition (continuous or catastrophic) and the distance from the transition point.

To test this tool, we carried out a large-scale empirical study of vegetation dynamics. We have analyzed vegetation density across 5.5 million squared kilometers of the African Sahel and the desert of Australia, with spatial resolution of 10 X 10 meters, using a few consecutive snapshots.

The results were disappointing. The local vegetation density (measured at a single pixel) moves towards the average of the corresponding rainfall line, indicating a purely negative feedback. Static patterns, like the double peak in the histogram of vegetation density, were shown to vary between censuses, with no apparent correlation with the actual dynamical features.

Laura Sidhom

University of Manchester, UK

Stability and diversity in random Lotka-Volterra systems with non-linear functional response

Ecosystem stability is important for maintaining a healthy microbiome, so understanding the factors that contribute to stability is of great relevance. We model an ecosystem of many interacting species, that evolve according to Lotka-Volterra dynamics, with interaction coefficients defined by a random payoff matrix. We investigate the effects of Holling type-2 inspired functional response on the stability of the ecosystem, and on its diversity. Our analysis is based on a path-integral approach, and verified with simulations. We find that non-linear functional response causes species growth to be bounded, increasing ecosystem stability. In the talk I will illustrate the model parameters, using examples of interactions found in nature. I will briefly discuss the generating-functional approach and the linear stability analysis, and discuss these results in terms of the human microbiome and explain how attributes of the host can influence its stability.

Ivan Sudakov

University of Dayton, USA

The feedback mechanisms in climate-ecosystem coupling leading to species extinction

We propose a model of multispecies populations surviving on distributed resources. System dynamics are investigated under changes in abiotic factors such as the climate, as parameterized through environmental temperature. In particular, we introduce a feedback between species abundances and resources via abiotic factors. This model is apparently the first of its kind to include a feedback mechanism coupling climate and ecosystem dynamics. The model explains the coexistence of many species, yet also displays the possibility of catastrophic bifurcations, where all species become extinct under the influence of abiotic factors. Also, we consider the dynamic model with random parameters for the climate-biosphere coupling to explain why the climate may stay stable over long-time intervals even if mass extinction in large ecosystems frequently occurs. The model shows that climate stability can be explained by mutual annihilation of many independent factors. One of the important consequences is that if biodiversity decreases then the random evolution of the biosphere can lead to global climate changes.

Robert West

University of Leeds, UK

Fixation properties of rock-paper-scissors games in populations of fluctuating size

We study the influence of external noise on a non-spatial three species logistic birth-death model with fitnesses that depend cyclically on the population composition according to the rock-paper-scissors game. External noise is modelled by letting the carrying capacity of the system follow a symmetric dichotomous Markov process, switching between a high value (indicating abundant resources) and a low value (scarce resources). We examine how different switching rates affect the fixation probabilities of each species, focusing on the differences with a fixed carrying capacity.

Remus Stana

University of Leeds, UK

Modeling molecular diffusion in cellular environment

Many cells of the immune system have receptors which are produced in the nucleus and these move under the influence of diffusion until they reach the outer membrane of the cell. Depending on the type of receptor, they might also diffuse on the surface of the cell until either a certain period of time has passed or the receptor encounters a peptide. After either of these events the receptors re-enter the cytoplasm and diffuse until they are absorbed by the nucleus. We are interested in the first passage properties of the receptors. Particularly, two quantities of great importance are the mean time T from synthesis of a receptor to its absorption back into the nucleus and the distribution of eventual hitting points on both the nucleus and the cytoplasm. We show how these quantities can be determined explicitly for two types of geometry, namely when the nucleus and membrane are concentric and eccentric, both in 2D and 3D. For this purpose, we derive an analytic expression for the Green's function of the Laplace equation for a domain bounded by non-concentric surfaces in two dimensions and three dimensions subject to absorbing outer surface and reflecting inner surface and vice versa. Utilizing the Green's function we derive an expression for T and compare with previous results in the literature. Furthermore, using the Green's function we calculate exact formula for hitting distribution and compare it with numerical results.