Student Conference in Complexity Science

Book of Abstracts
Biological Complexity

Brighton 19-22 August 2014

Biological Complexity

Wednesday, 20th August 2014

11:20 - 12:40   Ecology

THE SWARM AND THE MOSQUITO: EMERGENT GROUP PROPERTIES ARISING FROM LOCAL ACOUSTIC INTERACTIONS

Andy Aldersley, University of Bristol, UK (andy.aldersley@bristol.ac.uk)

Mosquitoes form swarms that serve important functions in mating behaviour. Males fly together producing a "coherent" unit, which attracts the attentions of nearby females, who approach individually in the search for a mate. The precise mechanisms that support swarm formation and cohesion are unknown, yet may well rely on acoustic interactions between the individual males and females. Paired mosquitoes are known to modulate their wing beat frequencies in response to the sounds produced by their partner, a phenomenon that plays an important role in the male-female courtship routine. Knowledge of swarm dynamics is central to our understanding of how these insects breed, but also allows us to address pertinent questions with regards to emergent behaviours in animal aggregations. Of primary interest is investigating how group-level properties can emerge and change with varying membership numbers, or, put another way, how many mosquitoes are required to form a swarm? Using a combination of experimental research and data-driven computational approaches, we are able to probe how local interactions in the acoustic field give rise to group-level characteristics of mosquito swarms. This talk will describe the methods we use to study these processes, will present recent findings, and discuss them in the context of the broader literature.

BIG FISH AND WIGGLY LINES: USING HIDDEN MARKOV MODELS TO DESCRIBE IMPERFECT TIME-SERIES

Joe Scutt Phillips, University of Southampton, UK (joe.scuttphillips@soton.ac.uk)

Open ocean predators inhabit a vast three-dimensional world, governed not by physical habitat but rather by complex and dynamic phenomena such as thermally-structured bodies of water and the location and abundance of prey. The temporal and spatial scales that these animals behave on prohibit the undertaking of controlled experiments, and so in describing and examining behaviour we are limited to imperfect data collected from bio-logging devices, alongside simulation experiments. Certain behaviours are exploited by fisherman in commercially important marine animals, although a full understanding of these behaviours and the driving mechanisms behind them are not well understood. Large scale bias and uncertainty in fishing data mean understanding the link between these individual-scale behaviours and exploitation is impossible. Similarly, bio-logging time-series do not allow us to explicitly observe behaviour, but rather give us distinct, but noisy, patterns in movements that are believed to emerge from underlying motivations. Here, we show how hidden Markov modelling for multivariate time-series can be used to overcome the problems of autocorrelation and paucity of information in bio-logging data analysis, and quantitively inform both mechanistic individual-based or phenomenological population dynamics models.

LANDSCAPE-SCALE CONSERVATION: THE ROLE OF SPACE AND TIME IN THE REALISATION OF BIODIVERSITY BENEFITS

Nick Synes, University of Southampton, UK (n.synes@soton.ac.uk)

Using RangeShifter, a novel modelling platform which combines population dynamics with individual-based dispersal behaviour, this study tests a number of landscape-scale conservation actions, and their impact on biodiversity. A number of artificial species have been parameterised within RangeShifter, broadly representing the real dispersal and life-history traits of UK woodland animal species. Species are parameterised with process-based dispersal, rather than a correlative dispersal kernel, meaning that their dispersal ability is dependent on the landscape matrix. Real landscapes are used, and

future landscapes have been created to represent land management actions such as habitat improvement, restoration, creation and landscape matrix modifications. Previous studies on landscape management have often simulated instantaneous impacts on biodiversity when management decisions are made. Here, landscape transitions through time are more realistically represented through the use of empirical data on the time-lag between the initial actions and the realisation of biodiversity impacts. Different spatial allocation routines are being tested to examine the effects of habitat creation both adjacent to and away from existing habitat patches. This study should provide guidance on the impacts that different land management strategies will have on animal populations. This will include tests of whether stepping stone habitats can provide genuine biodiversity benefits. It will also provide guidance on the relative biodiversity benefits of habitat creation versus improvement of existing habitat.

CITIZEN PARTICIPATION IN ECOLOGICAL MONITORING: THE STORY OF THE NEW FOREST CICADA

Davide Zilli, University of Southampton (dz2v07@ecs.soton.ac.uk)

The New Forest Cicada (Cicadetta montana s. str.) is the only cicada native to the UK. During May to July it sings with a very characteristic high-pitched song, which is particularly difficult for most adults to hear. Sightings of the cicada within the New Forest date back to 1812, but the last unconfirmed sighting was in 2000. However, it's quite possible that colonies remain undiscovered in less visited parts of the forest. The New Forest Cicada Project (www.newforestcicada.info) is exploring the use of smartphones to enhance human hearing and help them detect and recognise the song of the cicada. We developed an app that can automatically recognise the call of this insect and report a geo-located, time-stamped survey that can analysed further by professional entomologists. After a first year of deployment, the app has collected over 6000 reports from over 1000 users. In this talk, I will describe the importance of smartphone technologies to enable wide participation in scientific research and discuss how the many sensors with which these devices are equipped, together with their ubiquity in every-day life, can enable a new interaction with our surrounding environment.

Thursday, 21th August 2014

11:20 - 12:40   Modelling Human Diseases

HOW TO ELIMINATE SOLUTES FROM THE BRAIN: THE ROLE OF ARTERIAL PULSATIONS

Alexandra Diem, University of Southampton, UK (A.K.Diem@soton.ac.uk)

Alzheimer's disease (AD) is the most common form of dementia and although it has been researched for over 100 years to date there is no cure. Its onset and progression is closely related to the accumulation of the neuronal metabolite amyloid beta (Aβ), which raises the question of how metabolites and waste products are eliminated from the brain normally. The brain does not have a true lymphatic system consisting of dedicated lymphatic vessels, which are found in other parts of the body and therefore has to eliminate metabolites differently. In recent years a connection between the pathology of AD and cerebrovascular diseases has been suggested and confirmed in various mice studies, which has lead to the assumption that interstitial fluid in the basement membranes in the walls of cerebral arteries provide the pathways for the perivascular drainage of Aβ with arterial pulsations as the pumping mechanism. However, perivascular drainage occurs in the reverse direction of blood flow, which could not be explained solely by arterial pulsations. In this study we develop a coupled mathematical and computational fluid-structure interaction model to explain the reverse drainage of Aβ in the young. The results of this model will have implications for the development of preventive medication and aims a guiding experimental research in order to eliminate the disease.

A CELLULAR AUTOMATON MODEL OF ATRIAL FIBRILLATION

Kishan Manani, Imperial College London, UK (kishan.manani08@imperial.ac.uk)

A single beat of the human heart is the result of complex electrical interactions within a network of heart cells which form heart muscle tissue (myocardium). Processes at all scales from molecular to organ level are important in determining proper heart function. Atrial fibrillation (AF), a heart rhythm disturbance, is alarmingly on the increase and occurs due to abnormal electrical wave propagation due to changes in the underlying medium at various scales. We present a cellular automata model of atrial fibrillation in which the essential features of the myocardium are taken into account, namely cellular branching, coupling and conduction. We find that as the underlying medium is altered that the mode of propagation undergoes a spontaneous transition from planar wavefronts to spiral waves and eventually small meandering wavelets. The transition mimics the natural progression of AF in patients from temporary bursts of abnormal wavefronts to a phase of persistent complex wave propagation. The simple model offers potential clinical insight into how the properties of myocardium initiate and maintain AF.

MODELING HIV VIRULENCE EVOLUTION IN THE CONTEXT OF IMMUNE ESCAPE

Christiaan H. van Dorp, Rob J. de Boer, Michiel van Boven, Universiteit Utrecht and National Institute for Public Health and the Environment, The Netherlands (c.h.vandorp@uu.nl)

A pathogen like HIV evolves rapidly under multiple levels of selection, and has to cope with a heterogeneous host population. Although these aspects have been studied before, the true nature of host-heterogeneity has not been addressed to our satisfaction. During (untreated) infection, HIV evades cellular immune responses and because of the massive polymorphism of the Human Leukocyte Antigen, the targets of these responses (epitopes) differ strongly between hosts. Supported by data, it has been suggested that HIV has evolved virulence levels that are optimal for transmission. Some models indeed predict this, but others caution that this mode of adaptation is not self-evident, mostly due to the short-sightedness of evolution during the infection of an individual host. Several theories have been proposed to better explain the evolution of virulence, and we aim to contribute to these attempts. We are developing a model of HIV's evolutionary dynamics that is highly detailed and realistic, and captures the interesting features of host-heterogeneity, immune escape and compensatory mutations, and selection on multiple levels. We hypothesize that these properties might be sufficient to explain HIV's observed virulence distribution.

VARIATIONAL BAYESIAN ANALYSIS OF BLOOD GLUCOSE TIME SERIES

Yan Zhang, University of Warwick, UK (zjwufei@gmail.com)

Diabetes is a lifelong condition in which the body cannot control blood glucose. Patients living with diabetes must learn to control blood glucose levels to avoid life-threatening situations. Researchers have been working on establishing an effective dynamic model to describe and predict blood glucose concentration levels for more than half a century. Many models have been developed to reflect the complex neuro-hormonal control system, but one of the major challenges remains is how to determine large amounts of parameters in these models while only the glucose concentration time series is provided. To simplify the model structure without losing the applicability, we used a top-down data driven approach to establish a stochastic nonlinear model with minimal order and minimal number of parameters tailored for each patient to describe and predict the response of blood glucose concentration to food intake. Various degrees of nonlinearities are considered for three groups of people (the control group, Type I diabetes and Type II diabetes group). Variational Bayesian method is applied to select the best model and infer the needed parameters. The parameters describe the dynamics and characteristics of the underlying physiological processes. Since the mechanisms of the glucose absorption are different for Type I, Type II diabetes and non-diabetic people, different distributions of parameters and noises for these groups are expected. The results from fifteen profiles with 72 hour continuous glucose time series shows that the glucose concentration change during 2 hours after food intake can be modelled by second order linear or nonlinear system for all three groups. The value of the parameters and intensities of the noises vary from peak to peak for a single profile. The analysis of variance for parameters and noise intensities shows significant differences between the control group and both diabetes group.