QUANTIFYING ADAPTIVE CAPACITY OF SOCIOECOLOGICAL SYSTEMS

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Socioecological systems (SESs), like agro-food systems, forestry systems, and fisheries, are coupled ecological and socioeconomic systems that explicitly involve human actors (agents). These systems are subject to an increasing demand for food, feed, fuel, and freshwater under a scenario of climate change. There is an increasing concern that these systems may not prove to be resilient against these pressures and will fail in their future delivery of services.

Resilience is an emergent property of complex, adaptive systems characterized by nonlinear feedback mechanisms between environmental and socioeconomic variables. Any assessment of SES resilience therefore requires a proper conceptualization and preferably quantification of resilience. The applicability of the commonly used *return time* [1] - the time it takes after a perturbation to return to a reference value - is limited for quantifying SES resilience because it does not take into account adaptive capacity, i.e., "the capacity of a [SES] to absorb disturbance and reorganize while undergoing change so as to still retain essentially the same function, structure, identity, and feedbacks" [2]. Adaptive capacity may result from mechanisms that for instance involve learning, technical development, or social behaviour in human actors, possibly resulting in new links between actors and components. In essence, because of adaptive capacity a SES may structurally change under pressure, in turn also changing how it will respond to future pressures.

To better address adaptive capacity we consider an alternative measure for SES resilience based on entropy [3]. It quantifies the effect of the loss or addition of 'routes' via which information, mass, energy, or some other quantity can transfer from one subject to another within a unit of time (e.g., money transferred from one person to another within a day, or carbon transferred from one species to another within a year). The capacity for system development in this is given as

$$C = A + \Phi \, . \quad (1)$$

This measure allows for a natural interpretation of adaptive capacity: the efficiency A strongly decreases if a flow breaks up into many small flows, but the effect of the loss of one of those flows, quantified by the 'reserve' Φ, is minimal; optimized flows on the other hand have maximum efficiency A but also are at maximum risk from disruption ($\Phi = 0$).

We apply the above 'entropy' measure to a case study involving an agent-based model (ABM) describing a simplified agro-food system with producers who produce different food sources, traders who want to optimize their sellings, and consumers who try to fulfil health objectives. The links between different actors can vary over time, thus generating capacity to cope with perturbations such as 'bad harvests', 'loss of stocks', or 'hype foods'. The utility of the measure is demonstrated through simulations in which different close-to-reality actor network structures are considered, like 'reverse pyramid' (many consumers, few producers) and 'hourglass' (many producers and consumers, few traders) structures.

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Parallel Session

Mathematical Methods in Biology V

USING SIMULATION MODELS TO ASSESS RESILIENCE

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Keywords: Resilience, Agent-based model, Ordinary differential equation.

Many social-ecological systems (SES) are under pressure from human activities and environmental changes. Thus, it is important to study their resilience against such pressures. Resilience may be generated by various mechanisms, such as stabilising feedbacks, spatial interactions, diversity of system components, and mechanisms for adaptation and learning. Simulation models are an important tool for assessment of resilience, because these models help us to test the effects of various assumptions on interactions and feedbacks within the system. But, not all types of simulation models may be equally suitable for this purpose. We compare two commonly used model types for describing SES, namely ordinary differential equation (ODE) models and agent-based models (ABMs), to evaluate their capability to cover different mechanisms that generate resilience. ODE models have the advantage that advanced methodologies for bifurcation analysis and sensitivity analysis are available to quantify resilience, whereas ABMs allow for the description of more types of mechanisms for resilience.

As test-case, we consider a system in which consumers compete for a renewable common-pool resource [1]. The system is modelled as an ABM, in which the consumers are agents with identical decision rules but individually varying characteristics. This ABM is spatially explicit and updated in discrete time-steps. During a time-step, each consumer may decide to either move to a neighbouring location, harvest from the present location, or remain inactive to conserve energy. This decision is based on the state of the agent and its local surroundings. In addition, over time agents are born, die, and procreate; newly born agents inherit their characteristics from their parents with minor modifications, allowing for evolution through natural selection [2].

We examine whether an ODE model can be fitted to replicate the behaviour of the ABM, i.e., to evaluate whether an ODE model can cover all relevant ABM output [3]. We investigate how both models respond to external shocks, and apply resilience measures such as return time to quantify resilience. The results show that the ODE model can reproduce the behaviour of the ABM, if some mechanisms relevant for resilience are excluded. Specifically, the ODE model does not capture effects of agent adaptation, or local differences in space.

We conclude that the most suitable modelling approach depends on what mechanisms cause resilience in the studied system. If resilience results from system-level feedbacks, then ODE models may be suitable for assessing this resilience. If, in contrast, agent adaptation or localised agent interactions contribute to resilience, then ABMs seem more suitable.

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Parallel Session

Mathematical Methods in Biology V

POSITION PREDICTION OF NEIGHBOURS CAN GENERATE MILLING FLOCKS

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Keywords: Collectiv behaviour, Flocking, Anticipation, Pattern formation.

Humans and many other species make intuitive forecast-models in order to aim for an optimal future position in a group or flock. We have in [1] investigated a minimal version of the implications for collective behaviour of such intuitive predictions by setting up a model of interacting particles according to a pairwise potential, as a proxy for an advantageous position in the group, and where the forecast ability of each particle consists of linear extrapolations of their neighbours future positions after a given constant anticipation time τ. Analysing this set we find for example typically transient times for the flock to start milling, depending on τ, the potential and the initial positions and we can show that the kinetic energy of our system dissipate as $1/t$. In order to make the system as simple as possible, the particles are not self-propelled, in contrast to most other flocking models. We will also discuss brand new results, by the second co-author, regarding the interplay between anticipation and self-propelling by comparing and fusing the models in [1] and [2].

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Parallel Session

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STUDYING PSYCHOPHYSICAL LAWS IN THE SUPERORGANISM THROUGH A NOVEL AUTOMATED ANALYSIS TOOL

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Keywords: Swarm cognition, Psychophysical laws, Weber's law, Honeybee nest-hunting, Collective decision-making.

Reasoning about collective behaviour is inherently difficult, as the non-linear interactions between individuals give rise to complex emergent dynamics. Mathematical tools have been developed to systematically analyse collective behaviour in such systems, yet these frequently require extensive formal training and technical ability to apply. These difficulties raise a barrier-to-entry for practitioners wishing to analyse models of collective behaviour. However, rigorous modelling of collective behaviour is required to make progress in understanding and applying it. Here we present *MuMoT*, an accessible tool which aims to automate the process of modelling and analysing collective behaviour, as far as possible. We focus our attention on the general class of systems described by reaction kinetics, involving interactions between components that change state as a result, as these are easily understood and extracted from data by life scientists, and correspond to algorithms for component-level controllers in engineering applications. By providing simple automated access to advanced mathematical techniques from statistical physics, nonlinear dynamical systems analysis, and computational simulation, we hope to advance standards in modelling collective behaviour.

During this presentation, we showcase the functioning of *MuMoT* to perform a theoretical analysis that shows how a superorganism may react to stimulus variations according to psychophysical laws observed in humans and other animals. We investigate an empirically-motivated honeybee house-hunting model, which describes a value-sensitive decision process over potential nest-sites, at the level of the colony. In this study, we show how colony decision time increases with the number of available nests, in agreement with the Hick-Hyman law of psychophysics, and decreases with mean nest quality, in agreement with Piéron's law. We also show that colony error rate depends on mean nest quality, and difference in quality, in agreement with Weber's law. Psychophysical laws, particularly Weber's law, have been found in diverse species, including unicellular organisms. Our theoretical results predict that superorganisms may also exhibit such behaviour, suggesting that these laws arise from fundamental mechanisms of information processing and decision-making. Finally, we propose a combined psychophysical law which unifies Hick-Hyman's law and Piéron's law, traditionally studied independently; this unified law makes predictions that can be empirically tested.

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Parallel Session

Mathematical Methods in Biology V

CROSS-DIFFUSION PREDATOR-PREY MODELS ARISING BY TIME-SCALE ARGUMENTS

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Keywords: Predator-prey, Cross-diffusion, Turing instability.

Starting from *microscopic models* incorporating the dynamics of handling and searching predators, or active and hidden prey, we obtain reaction cross-diffusion systems of predator-prey type involving classical functional responses, by the exploitation of different time-scales. We also provide a study of the Turing instability domain of the obtained equations and (in the case of the Beddington-DeAngelis functional response) compare it to the same instability domain when the cross diffusion is replaced by a standard diffusion.

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