**Scottish Complex Network Society (SCoNeS) Inaugural Meeting (9 May 2025)**

**Abstracts**

**Keynote address**

**Mathew Williams** (Scotland Chief Scientific Adviser for Environment, Natural Resources and Agriculture) - How can complex, dynamic data inform government decision making?

**Invited Talks**

**István Kiss** (Northeastern University) - Taming Complexity: From Spreading Processes and Network Reconstruction to Higher-Order Networks

In this presentation, I will illustrate the challenges and opportunities posed by high-dimensional models and complex data through a series of research problems I have worked on. Beginning with work conducted during the COVID-19 pandemic, I will discuss outbreak control strategies across single and metapopulation models, domiciliary care systems, and single-parent households — highlighting ethical challenges where improved population-level outcomes may come at a disproportionate cost to certain individuals or groups.

Next, I will explore network reconstructability directly from epidemic data alone, showing how reducing the state space by learning network structures through simulations enables their use as informative priors in inference settings. Additionally, I will introduce a new inference paradigm – dynamic survival analysis – that naturally links data and model.

The final part of my presentation will be two-fold: first, I will demonstrate how I leveraged higher-order network theory and dynamic mode decomposition to analyse individual and collective temporal patterns in the tanker shipping network. Finally, I will close with an outlook on recent work on contagion processes on group-based structures such as hypergraphs.

**Anna Murgatroyd** (Newcastle University) - Selecting indicators and optimizing decision rules for long-term planning of complex water supply networks

Having adopted a rule-based plan, decision makers can monitor critical variables to trigger timely adaptation actions when the variables pass their predetermined thresholds. However, establishing a strategy that is comprised of a set of decision rules raises methodological challenges: (i) to identify observable indicators that provide reliable information about current and future change, (ii) to choose suitable statistics to characterize nonstationary time series that are germane to system performance, and (iii) to optimize threshold levels that trigger interventions. We present a methodology that addresses these methodological challenges whilst explicitly balancing expected risks of water shortages with the costs of intervention in the water supply system. The four-step framework uses a multiobjective evolutionary algorithm to search for and to identify the combinations of indicator-informed decision rules that govern if, when, and what supply options should be included in the water resource system. The rule-based strategies are dynamically tested against an extensive ensemble of future climate and demand scenarios to examine the trade-offs between strategy cost and level of service. The framework is applied to the London water system (England) using regional climate simulations to identify strategic rules for a 60-year planning period. The results demonstrate the utility of the framework, identifying observable indicators and decision thresholds that are used in optimal rule-based planning strategies.

**Contributed Talks**

**Agathe Bouis** (University of Strathclyde) - Structure and Influence: differing insights from networks’ adjacency and Laplacian eigenspectra

(Authors: Agathe Bouis, Ruaridh Clark, Malcolm Macdonald)

Synchronisation is a pervasive phenomenon of emerging collective behaviour observed to develop spontaneously across both natural and engineered systems. The process and patterns of synchronisation are highly influenced by initial conditions and network topology, with synchronisation following a network’s hierarchal structure, such that it will first develop at a local level with conglomeration of local clusters often leading to synchronisation at a global scale. The structure and influence of global and local features play a key role in a network’s synchronisation. Structure considers the community clustering that emerges from variation in the relative density of connectivity between sets of nodes. Influence refers to a node’s ability to affect the dynamical state of other nodes due to its position within the network’s topology. Structure and influence measures can be uncovered through eigenspectra analyses performed on the network’s adjacency and Laplacian matrix respectively. Ring networks exhibit patterns of stable and unstable synchronisation, despite simple topological forms, and distinctive spectral fingerprints. Intersecting ring networks combine simple ring topologies with hubs of high connectivity at the intersections, to provide a clear case study for examining structure and influence through the lens of network eigenspectrum. This study extends into real-world intersecting rings, namely satellite constellation networks, where distributed time synchronisation is fundamental to securing resilient global navigation satellite systems; a fundamental capability that underpins critical national infrastructure. This study explores the differing insight from adjacency and Laplacian eigenspectrum. The adjacency eigenspectrum detects salient network structures, e.g. hubs of high connectivity. The Laplacian spectrum identifies the relative influence of nodes, due to their spanning trees of effective communication that correspond to the salient network structures. Understanding these differing insights has broad applicability in the study of networks systems, from identifying local road network hubs to identifying influence and disease propagation in resilient ant colonies.

**Dimitris Christopoulos** (Edinburgh Business School, Heriot-Watt University) - System Complexity in Technological Innovation

Data on hydrogen technologies, decarbonization research and more broadly green innovation are employed to address the link between invention and innovation revealed in the patent network analysis of technological frontiers (Dekker et al.). In particular we seek to address how collaboration patterns are affected by public funding (Smith et al.); and the impact of finance on green innovation (Christopoulos et al.).

We identify challenges to green innovation, empirically determine their scope and magnitude and recommend policy to corporate and public actors that will improve processes of public and private funding and optimise the efficiency of innovation systems.

**Javier Escudero** (University of Edinburgh) - Graph-Based Permutation Patterns for the Analysis of Task-Related fMRI Signals on DTI Networks in Mild Cognitive Impairment

Entropy metrics (for example, permutation entropy) are nonlinear measures of irregularity in time series (one-dimensional data). Some of these entropy metrics can be generalised to data on periodic structures such as a grid or lattice pattern (two-dimensional data) using its symmetry, thus enabling their application to images. Until very recently, these metrics had not been developed for signals sampled on irregular domains, defined by a graph. Here, we describe the first entropy metric to analyse signals measured over irregular graphs, which generalises permutation entropy, a well-established nonlinear metric based on the comparison of neighbouring values within patterns in a time series. Our algorithm is based on comparing signal values on neighbouring nodes, using the adjacency matrix. We show that this generalisation preserves the properties of classical permutation entropy for time series and the recent permutation entropy for images, and it can be applied to any graph structure with synthetic and real signals. Furthermore, we build on permutation entropy for graph signals to introduce a novel approach to evaluate graph signals at the vertex level: graph-based permutation patterns. Synthetic datasets show the efficacy of our method. We reveal that dynamics in graph signals can be discerned using our graph-based patterns. These are then validated in DTI and fMRI data acquired during a working memory task in mild cognitive impairment, where we explore functional brain signals on structural white matter networks. Our findings suggest that graph-based permutation patterns in individual brain regions change as the disease progresses, demonstrating potential as a method of analyzing graph-signals at a granular scale.

**Lindsey Garner-Knapp** (Centre for Inclusive Trade Policy, University of Sussex) - Social Network Analysis and Actor-Network Theory: Exploring the Role of Devolved Officials in Free Trade Agreement Negotiations

The everyday work that goes into the making of Free Trade Agreements (FTAs) from the subcentral government level is often invisible to the public, akin to being black boxed (Latour 1999). Who is included in the intra-actions that are embedded in these everyday encounters is equally opaque. This paper seeks to follow the everyday intra-actions to map the hub-and-spoke approach that the official above describes as key to how they engage in FTA negotiation processes.

Unlike other studies which seek to identify a causal relationship between the work of policymakers and the policy text or FTA – the perceived telos – this research aims to understand the policy-making process, in which interlocutors are involved and how the interlocutors come together, relate, collaborate, assemble, co-create throughout the negotiation process along these lines transcending the policy or FTA both materially (the text) and temporally (the processes). In doing so, this paper challenges the human-centric conceptualisation of the policy-making process that has dominated the realist, social science literature; instead, I present the active and agentive role of humans, nonhumans, and networks they co-create.

My ambition was to create a map of interlocutors that recognised both the policy network officials identified as informing their work on FTA negotiation processes and to leverage this data collection process to explore the tools officials employed to (re)create their network of interlocutors. To do this, I required the support of the senior leadership team of the trade policy division but also the buy-in from the officials whom I would be working with directly. As a result, this work is founded on SNA and ethnographic fieldwork conducted with a devolved government's trade policy team over three months from November 2022-January 2023.

The outcomes of this work are multiple. First, using SNA, I mapped the human and nonhuman interlocutors identified by the trade policy team officials. This was a broad set of interlocutors across multiple jurisdictions, and geographic areas, and included multiple documents, organizations, groups, and people. Including nonhumans broadens the use of SNA and affords other insights to come forward, like recognising the agency of documents like FTAs and policies and organisations like the WTO in policy-making. Likewise, scholarship on policy assemblages like Ureta (2014) or Fox and Alldred (2021) and policy networks like Knoke (2014) or Riles (2010) might find value in using a network-mapping tool such as SNAs especially if paired with ethnographic interviews – a pairing that others have suggested (Vicsek, Király, and Kónya 2016).

Second, I show how officials (re)create relationships with a multiplicity of interlocutors who both inform their work and whom they regularly also inform. These connections are maintained through regular and ongoing interactions. Arguably, it is no surprise that the interlocutors with the greatest measure of centrality were those who had significant and sustained exchanges with the trade policy officials.

These relationships, imagined within a hub-and-spoke structure, also include a multiplicity of brokers who maintaining relationships. It is important to re-emphasise that the role of these brokers, relationships, and network only exist when they are being (re)made (Latour 2005) as they are not fixed entities. Rather, officials describe the doings and sayings that create these temporary and emergent networks. Brokerage, therefore, is a productive relational verb actively associating actants, visualised in SNA as adjacent ties (Freeman 1978). Using brokerage in this way can make visible what is often black boxed.

And, finally, different methods reveal different knowledge. Building on my previous interviews with this devolved government, I was able to explore the policy-making processes through the everyday doings and sayings of these officials. The ambition of conducting an ethnography was to better understand the day-to-day interactions, activities, and policy networks that inform the work of FTA negotiations from a devolved government perspective. The observations that I was able to tend to while participating within this team “demonstrates what an ‘ethnographic sensibility’ and that ineffable quality of ‘being there’ brings to a research project that interviewing alone does not and cannot” (Yanow n.d., 310). Being there afforded not just observations and access but an opportunity to reciprocate (Baker 2016).

**Poster Presentations**

**Dominic Arthur** (The Roslin Institute, University of Edinburgh) - Threshold-Free Genomic Clustering Reveals Superspreading Events in SARS-CoV-2 Outbreaks

A superspreading event (SSE) is an occurrence within a specific context - such as a gathering, workplace, or hospital - where transmission from a single primary source results in an unusually large number of secondary infections, thereby disproportionately amplifying the spread of an infectious disease outbreak.

SSEs have profoundly influenced the transmission dynamics of several outbreaks, including during the COVID-19 pandemic. However, their sporadic nature makes prediction challenging, as SSEs are influenced by a complex interplay of biological, behavioural, and environmental factors. The extensive genomic data collected during the pandemic presents an opportunity for retrospective analyses to identify the factors driving these transmission patterns.

Building on previous investigations, we developed a probability-based model that integrates pairwise genetic and temporal distances to infer transmission clusters likely associated with SSEs. The model was applied to both empirical and synthetic SARS-CoV-2 datasets and compared to a recently published regression-based approach for clustering. The results demonstrate the potential of the proposed threshold-free method to provide insights into the epidemiological and evolutionary dynamics of SSEs and inform public health responses.

Challenges such as low sampling density, high stochastic variability, and biased data can undermine model performance and hinder the accurate identification of SSEs. Using data obtained from Public Health Scotland, future efforts will focus on characterising the spatiotemporal dynamics of SSEs and their impacts during the COVID-19 pandemic in Scotland.

**Sergio Azevedo** (Federal Universidy of Campina Grande) - Network Analysis of Cattle Movement and Characterization of Epidemiological Factors and Patterns of Bovine Brucellosis in the State of Paraíba, Northeastern Brazil

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Bovine brucellosis, caused by *Brucella abortus*, remains an important zoonosis that impacts public health, livestock productivity, and the rural economy. In the state of Paraíba, the dynamics of cattle movement and epidemiological factors associated with the disease were investigated to better understand dissemination patterns and to support more effective control strategies. Through complex network analysis using data from Animal Transit Guides (GTA) from 2012 to 2022, it was observed that properties positive for brucellosis exhibit greater connectivity in movement networks, being identified as critical points in the disease’s dissemination. These properties showed higher in-degree and out-degree connections, as well as greater participation in contact chains, acting as "super-spreaders" and contributing to the persistence of the disease. Factors such as the absence of adequate biosafety practices, commercialization of animals without strict sanitary control, and underreporting of cases were key elements in maintaining brucellosis in the state. Additionally, the multivariate characterization of risk factors in rural properties revealed that inadequate management practices - such as the lack of systematic vaccination, purchase of animals without secure provenance, cohabitation of multiple animal species, and the use of calving areas without effective sanitary control - significantly increase the probability of infection. Statistical analysis using Principal Component Analysis (PCA) and Self-Organizing Maps (SOM) allowed the identification of distinct risk profiles among properties, demonstrating that inadequate practices tend to occur in clusters, thus increasing the risk of dissemination. These findings highlight the importance of integrating advanced epidemiological tools, such as network analysis and multivariate methods, into the planning of brucellosis control programs.

Keywords: *Brucella abortus*, risk factors, complex networks, epidemiology, bovine brucellosis.

**Aidan Brown** (University of Edinburgh) - The origin of sustained oscillations in simple infection models

We study the SIRS (Susceptible, Infected, Removed, Susceptible) epidemic model, both analytically and on a square lattice. The analytic, mean-field model has just two stable solutions: a disease free state post outbreak/epidemic, and an endemic state with a constant infected fraction of the population. When the model is implemented with noise, or on a lattice, a third state is possible, featuring regular oscillations. This is understood as a cycle of boom and bust, where an epidemic sweeps through, and dies out leaving a small number of isolated infected individuals. As immunity wanes, herd immunity is lost throughout the population and the epidemic repeats. These oscillations are an intrinsic feature of the system itself, not driven by external factors such as seasonality, behavioural changes or evolution of the infective agent.

In this presentation I will explore the necessary conditions for these intrinsic sustained oscillations. They do not require explicit spatial or network properties. However, they do require us to go beyond the mean-field, e.g., by tracking the fraction of contacts between infected and susceptible individuals. As far as we can tell, oscillations are also only obtained within non-deterministic models.

**Charlotte Bunnenberg** (University of Aberdeen) - Combing graph theory and eco-evolutionary simulations to analyse functional connectivity through time and space

Genetic diversity loss, a key yet often overlooked component of biodiversity, affects population fitness, adaptive potential, and species extinction risk. A crucial strategy for mitigating this loss and enabling species to adapt to changing climates and landscapes is to enhance landscape connectivity. Connected landscapes facilitate species range shifts, promote gene flow among fragmented populations, and support biodiversity conservation.  
Assessing connectivity in dynamic ecosystems requires effective methods, yet most existing frameworks assume static landscapes. In reality, landscapes evolve due to natural processes and human-driven changes. This static assumption can lead to underestimations of available habitat and overestimations of isolation and extinction rates. Research suggests that historical connectivity often better explains present-day biodiversity patterns than current connectivity, underscoring the need for temporal dynamics in connectivity assessments. Despite technological advancements, a comprehensive methodological framework integrating temporal dynamics remains lacking, prompting calls for approaches that incorporate both spatial and temporal connectivity to improve conservation decision-making.

Graph theory has been used to quantify spatio-temporal connectivity, yet existing frameworks addressing temporal dynamics are limited. Expanding the spatio-temporal framework presents a promising opportunity for more accurate assessments of connectivity.

To fill this gap, I am developing a mathematical framework to represent spatio-temporal landscape connectivity using graph theory. By using multi-layer networks, the framework will be able to capture the functional connectivity of species across space and time, providing a more comprehensive understanding of landscape dynamics. The framework will allow users to represent and evaluate connectivity using a variety of network metrics and will be implemented as an R package. A key strength of the framework will be its seamless integration with the R package of the eco-evolutionary modelling platform RangeShifter (https://rangeshifter.github.io/). This integration will allow users to perform in-depth connectivity analyses following their process-based simulations. By linking eco-evolutionary dynamics with spatio-temporal connectivity analysis, the package will enhance the ability of researchers and conservation practitioners to make informed decisions about habitat management and biodiversity conservation. It will provide a powerful methodological framework to advance connectivity research in an era of environmental change by overcoming the limitations of static models and incorporating temporal complexity.

**Anna Gamza** (The Roslin Institute, University of Edinburgh) - Spatial aggregation areas for infectious contact network inferred from pathogen sequence data

As contact tracing is costly and usually provides subjective and fragmented data, study of infectious contact networks is difficult, especially for systems with complex transmission patterns. The genetic distance between pathogen sequence data, is correlated to the proximity of contacts on a transmission tree and is a direct insight into the contact patterns driving the spread of infection in a community or ecosystem. As such genetic distance can be used to determine the size of aggregation areas in spatial network by finding the best scales for aggregations of variables.

The transmission dynamics of Highly Pathogenic Avian Influenza (HPAI) is complex as it spans multiple bird species and production systems. To quantify the scales of potentially infectious interactions we use the genetic distances between HPAI H5N1 sequences in the 2020-2022 from Great Britain with the set of other variables (i.e. number of cases, wild bird abundance and poultry farms count) calculated over various geographical scales1. We demonstrate that spatial scales of aggregation depend both on the variable and the time of analysis. Variables that are directly describing HPAI outbreaks (number of wild and domestic bird cases) have different scales of aggregation for the variable type and period of analysis, while indirectly correlated, constant in time variables (wild bird abundance and farm density) generally have the same scale for both analysed periods.

Our study shows that the interactions driving complex transmission systems are variable, and separate spatial networks may need to be considered to represent a range of epidemiological interactions. The network with time dynamic spatial aggregation may be necessary for variables directly describing temporal changes of outbreaks.

**Abigail Hellman** (University of Edinburgh) - A comparative study of three network-based correlation analysis methods with [11C]glyburide whole-body PET

Positron emission tomography (PET) is a nuclear medicine approach to imaging and quantifying metabolic and physiological processes inside the body. Traditional PET only scans one section of the body at a time, but whole-body images can be made by changing the bed position many times during a scan. This increasingly common method, known as whole-body PET, produces large datasets including multiple organs, which provides the opportunity to apply new analysis methods to PET to understand if and how the data from different regions and subjects are related. Network analysis is employed here with whole-body PET as a quantification method for comparing data from different tissues and subjects, before and after a drug is administered. We trial three different methods of generating networks that each require differing levels of prior knowledge and can be used to answer different research questions, as a proof-of-principle test for deploying network analysis in whole-body PET.

Network analysis was performed on 22 PET scans, n=13 controls (48+/-17 years, 8 male), and n=9 drug subjects (40+/-19 years, 5 male, 7 control-matched). The analysis was performed on both dynamic and static data, where dynamic data displays tracer uptake over the course of time and static data is a single, averaged value from the last 15 minutes of scan time. All three analysis methods involve calculating the Pearson correlation coefficient (PCC), a measure of linear correlation. The first two methods were data-informed: one using dynamic data and looking at a single region at a time, while the other used static data but considered a profile of all regions. The final method was data-driven and used static data from all regions.

The single-region, dynamic, data-informed method successfully differentiated between the control and drug trial groups while utilizing data over the entire length of the scan; however, it still showed some correlation between the two groups. The static, data-informed method completely separated the trial groups with no correlations between but heavily relied on data-informed decisions. The final method compared between regions rather than treatment groups but successfully identify the regions characterized by significant differences between the two groups without relying on prior knowledge of the data. All networks are significant at p<0.05, determined for each method individually.

We have discussed here a few different methods of network analysis with Pearson correlation that can be employed with whole-body PET. Each method can be helpful for different scenarios – whether the focus is comparing between treatment groups, between regions, or within a single region, and whether an informed or data-driven method is preferred. Network analysis with the methods proposed here could be further applied to whole-body PET to elucidate complex relationships between organs and organ systems in healthy patients, and how the relationships change in drug or disease conditions.

**Ethan Hunter** (University of Glasgow)

The Firefighter problem models a spreading process (originally a fire, alternatively a contagious disease. rumour. etc.) on a graph. We play as a defender saving a single vertex per turn and, after each defence, fire spreads to the unburned and undefended neighbours of all burning vertices. This is computationally hard.

Inspired by research into spreadable rabies vaccines for bats. We study a variant of the Firefighter problem in which defence also spreads. Some approximation results are already known for this problem: we present some preliminary tractability and containment results to develop intuition for this problem, and encourage some pen-and-paper participation in epidemiology!

**Thanakorn Jaemthaworn** (CRM, University of Edinburgh) - From Gene Expression to Network Topology: A New Framework for Cell State Representation

Cell differentiation, which refers to the transformation of stem cells into specific cell types, is a key challenge in developmental biology. The advent of single-cell RNA sequencing (scRNA-seq) has significantly advanced our ability to quantify gene expression within individual cells and to perform trajectory analysis of various cell states. Nevertheless, conventional techniques of trajectories inference, such as RNA velocity and minimum spanning trees (e.g., Monocle), frequently overlook the collective behaviour of genes, which may lead to a simplified interpretation of the cell transition from stem cells to differentiated cells. To address these limitations, we introduce a novel framework that redefines the representation of the cell state through cell-specific gene co-expression networks (CS-GCNs). We hypothesise that the topology of CS-GCNs encodes critical information about transitional dynamics. Our computational approach uses a new gene selection method that prioritises genes based on the high variance in correlation coefficients between gene pairs, diverging from the conventional focus on high-variance gene expression. By inferring gene dependencies for each cell, we construct CS-GCNs and reconstruct cell state graphs directly from topological features, bypassing the need for dimensionality reduction. This approach enhances our understanding of cell state dynamics and offers deeper insights into the mechanisms governing cell differentiation, potentially accelerating discoveries in developmental biology and regenerative medicine.

**Yiqing Liu** (University of Edinburgh) - Exploring Adaptive Temporal Dynamics for Diffusion in Complex Networks

Understanding the dynamics of diffusion processes, such as information spread in social networks or disease transmission, is a fundamental challenge in network science. While existing models often rely on fixed time scales or domain-specific parameters, real-world diffusion is inherently heterogeneous, nonlinear, and influenced by various user behaviors and external perturbations. This study aims to investigate the feasibility of capturing the self-consistent time windows predicting the diffusion phenomenon for the adaptive temporal frameworks across diverse contexts. The project will explore how network topology, interaction delays, and behavioral heterogeneity shape diffusion dynamics, with a focus on unifying principles that exceed domain-specific constraints.

**Chris Pooley** (BioSS) - BICI - General purpose software for inference and simulation using compartmental models

Compartmental models have long been used as a means of understanding the collective dynamics of interacting agents, with notable applications in epidemiology, chemistry and ecology. BICI is a new software tool we've been devloping which allows for arbitrary compartmental model specification and performs simulation, inference and posterior simulation.

Models can contain multiple interacting species, which can each be treated at a population or individual level. BICI can be run entirely using a point-and-click interface. Alternatively, a scripted language, referred to as “BICI-script”, can be used to construct, store, and export complex models and allow for them to be run on HPC (high performance computing)

For inference BICI takes in a variety of individual and/or population-level data, and priors can be specified from a large range of possibilities. Posterior parameter outputs include trace plots, distributions, correlations, and summary statistics (means and 95% credible intervals) as well as various diagnostic information (e.g., measuring MCMC convergence and helping to identify potential model misspecification). State outputs include various visualisations for populations, transitions and individuals.

**Gail Robertson** (Biomathematics and Statistics Scotland) - Graphical models as decision making tools in complex systems

Graphical models are probabilistic models in which a graph represents the dependence structure between variables representing components or events in a study system, and an associated statistical model allows these dependencies to be evaluated. There are several types of graphical models including Bayesian networks (BNs), probability trees, and chain event graphs (CEGs) and these can be used to address diverse real-world challenges. Bayesian networks are used in various applications to describe complex dependencies between different variables. However, they are less useful when representing asymmetric problems and are not explicitly designed for representing temporal events. By combining aspects of BNs and probability trees, CEGs can be used to compare competing storylines, which is particularly useful in applications in which different timelines of events or interpretations of a system are proposed. Although CEGs have only been developed recently, they have been applied to forensic science problems and have potential for use in various fields including epidemiology, land use management, and environmental sciences. In this presentation, I describe my experiences using graphical models in evaluating evidence from activity-level propositions in forensic science, using examples from topical murder and drug trafficking cases, and discuss developing a framework for these models to be applied to new areas.