Ollscoil na Gaillimhe
University of Galway

School of Mathematical and Statistical Sciences

Annual Research Day 2026

15 April 2026

Programme

	Talks take place in the Human Biology Building HBB-G019 Coffee, lunch, posters, and reception take place in the HBB Atrium
9:00–9:10	**Cathal Seoighe**, Head of School: Opening Remarks
9:10–9:20	**Prof. David J. Burn**, President of the University: Opening Remarks
9:20–9:40	**Rachel Quinlan** (University of Galway) *What we can do (in Mathematics)*
9:40–10:00	**Gregory Wheeler** (University of Galway) *On the Usability and Interpretability of Whole-Slide Image Data for Molecular Profiling in Paediatric Brain Cancers*
10:00–11:00	**Lightning talks** Thomas Hayes • Michael Joyce Maher • Parastoo Niloofar • Forough Pazhuheian
11:00–11:30	**Tea and coffee**
11:30–12:10	**Dana Mackey** (TUDublin) *A medley of optical patterning models*
12:10–12:30	**Autumn Johnson** (University of Galway) *Functional data analysis of sensor-derived pulmonary artery pressures to predict cardiac output*
12:30–13:00	**Ted Vaughan** (IHDI) *Institute for Health Discovery and Innovation - Scientific Direction and Future Opportunities*
13:00–14:00	**Lunch**
14:00–14:20	**Michael McGettrick** (University of Galway) *Quantum Music*
14:20–15:15	**Showcase networking talks:** • James McDermott (School of Computer Science) • Kate Reddington (School of Biological and Chemical Sciences) • Jamie Concannon (School of Engineering) • Nazre Batool (School of Computer Science) • Cynthia Coleman (REMEDI, School of Medicine) • Niamh Hynes (CÚRAM)
15:15–17:00	**Poster session, reception, and prizes**

Contents

1 Introduction

Ba mhaith liom fáilte mhór chroíúil a chuir romhaibh go dtí Lá Taighde Scoil na nEolaíochtaí Matamaitice agus Staitistice!

Welcome to the Research Day of the School of Mathematical and Statistical Sciences. The Research Day is an opportunity to celebrate the research we do and our research achievements and to learn about the research of colleagues. As usual, there has been more to celebrate in the past year than I have space to mention (for a more comprehensive list, please refer to the monthly research updates, kindly curated for us by Anton Baykalov), but I would like to give a flavour of some of these achievements. Although they have not been announced publicly yet, Research Ireland has made the decision to award seven Research Centres. These are major inter-institutional initiatives that are a flagship of the national research funding landscape. Remarkably, researchers from our School are involved in four of them, including as co-applicants and research theme leads. This is a testament to the breadth of the research in our School and the extent to which our research enables progress across research domains. The ARC Hub in Health Tech, on which Andrew Simpkin is a co-PI and leads on Algorithms & AI/ML models, was also successful, with funding of €34M awarded. COGENT, an EU-funded cohort-based PhD programme in Mathematics launched in December and this talented group of PhD researchers is already having a great impact in the School. For the first time, our School also received substantial external funding (through the Research Ireland Discover programme) to promote STEM through Irish (comhghairdeas le Fintan Hegarty as an éacht sin a bhaint amach). Work towards the Institutional Review of Research Progress (IRRP) is also in full swing at the moment and I would like to thank everyone who has been involved in that, especially our Director of Research, Angela Carnevale, research case study authors and the IRRP working group.

This research day takes place at a time of change and uncertainty, both in the wider world and within our own world of research. In my own area, elaborate claims are being made about various foundation models and researchers have been exploring the capacity of virtual computational biology labs to make new discoveries. You may also have seen people claiming to prove theorems using AI models or performing sophisticated analyses that would until recently have required a high level of expertise. While some of the fanfare may not yet be warranted and it is sometimes hard to disentangle the hype from the real progress, it is becoming difficult not to think that these ongoing developments willhave a profound impact on how we do research at some stage. That will be in the back of my mind at this year's Research Day and also next month at the first School of Maths Away Day, which will provide an opportunity to reflect on how we can adapt to these rapid advances, enabling us to continue make research contributions, and expand our research ambition, in this changing world.

While most of us will get an update on the work of our colleagues, the Research Day gives new members of staff the chance to gain an overview of the research in the School for the first time. I would like, therefore, to take this opportunity to give a particularly warm welcome to the event to those members of staff who are attending it for the first time, Jesse Lansdown, Ilia Pirashvili, Gregory Wheeler and Leonel Herrera-Alsina, as well as all of the postdoctoral and PhD researchers who have joined us over the past year. I hope you enjoy the day and that you will get a sense of how your research might connect with the research of some of your new colleagues.

Lastly, I would like to thank and congratulate the organizers of this event – Davood Roshan, Anton Baykalov (who produced this booklet), Mark Howard, Mary Kelly, Andrew Simpkin and Nastaran Sharifian – as well as our external speakers, Dana Mackey and Ted Vaughan and everyone from within the School who is contributing the talks and posters that are the basis of this event. My apologies if I have left anyone out.

I wish everyone a very enjoyable and stimulating Research Day and fair winds for your research over the year ahead.

Bain taitneamh as an Lá Taighde agus guím gach rath ar bhur gcuid taighde don bhliain amach romhainn!

Cathal Seoighe

Head of School

2 Abstracts of invited talks

Autumn Johnson (University of Galway)

Functional data analysis of sensor-derived pulmonary artery pressures to predict cardiac output

Heart failure affects approximately 64 million people worldwide [1]. With the condition resulting in compromised cardiac function, the quality of life and survival rates are poor, while the burden on the healthcare system is high [2]. Cardiac output (CO) is a crucial measure of heart function that refers to the volume of blood the heart pumps per minute. Continuous monitoring of CO could enable clinicians to assess the severity of the heart condition, tailor therapeutic interventions, and evaluate treatment response [3]. However, the current gold standard for measuring CO is unsuitable for continuous monitoring or long-term use [4].

New technology using internally implanted sensors has shown promise for remote patient management and reducing the number of patient hospitalisations [5, 6]. These devices measure pulmonary artery pressure and provide clinicians with continuous pulse waveforms for remote viewing. This work investigates the predictive capabilities of the high-frequency functional waveform data for cardiac output prediction.

Continuous pulmonary artery pressure (PAP) recordings from 179 patients undergoing thermodilution measurement were segmented into individual cardiac cycles through a customised automated detection pipeline. Each cycle was smoothed using P-splines and represented as a function over a normalised cardiac interval. This process produced a structured set of over 4000 functional observations nested within patients. To summarise variation across this data structure, multilevel functional principal components analysis (mFPCA) was applied, capturing between-patient differences in overall waveform morphology as well as within-patient, beat-level variation. The resulting mFPCA scores provided a low-dimensional representation of the high-resolution waveform for predictive modelling.

Predictive models, including linear regression, regularised models, and machine learning methods, were trained on 80% of the data using combinations of clinical covariates and mFPCA scores. On testing, across all predictor sets, the LASSO model achieved the lowest median absolute error (MAE) on the remain 20% of data, with best performance observed for the combination of clinical variables and mFPCA scores (14% error).

These findings demonstrate the potential of functional representations of PAP waveforms for non-invasive prediction of cardiac output and thus for improving the remote care of heart failure patients.

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Dana Mackey (TUDublin)

A medley of optical patterning models

Optical patterning refers to the creation of periodic refractive index structures, widely used in holographic and photonic devices. The models we work with consist of systems of nonlinear PDEs describing diffusion and polymerisation in photosensitive materials. This talk reviews three such problems in 1 and 2-dimensional domains, which have been proposed by the IEO (Industrial and Engineering Optics) Centre at TU Dublin.

Michael McGettrick (University of Galway)

Quantum Music

We present a method to generate sequences of musical chords from the triadic tonnetz using quantum walks. Considering the triadic tonnetz as a bipartite graph with 24 nodes, of degree 3, our walk moves between neighboring chords on the graph (that always differ in just one note). Given the degree 3 nature of the associated graph, it lends itself naturally to a quantum walk using a three state quantum system (or qutrit). Up to permutations, we match each of these 3 quantum states to the changes in the 3 notes of the triad (moving either from major to minor, or vice versa). This corresponds exactly to the Parallel, Relative and Leittonwechsel moves in Neo-Riemannian theory. We show that our quantum algorithm generates chord sequences that differ from those generated by classical random walks. Our choice of the Grover coin as unitary matrix gives us partial localization, which leads to the musically desirable feature of not straying too far away from our home key (starting point). The talk will include an audio demo of chords generated by our quantum algorithm. All our code is freely available on GitHub.
This is joint work with James McDermott, Maziar Kanani and Noah Shore (Galway) and Jerry Swan (York).

Rachel Quinlan (University of Galway)

What we can do (in Mathematics)

This talk will consider what it means to do research in mathematics, what constitutes progress in the subject, and why that is worthy of our attention and of the resources of a university. I will share a few excerpts from my work in algebra and (more recently) in mathematical origami.

Gregory Wheeler (University of Galway)

On the Usability and Interpretability of Whole-Slide Image Data for Molecular Profiling in Paediatric Brain Cancers

Molecular profiling of tumours via genome or exome sequencing has become increasingly common in cancer care and has shown substantial improvement of treatment outcomes for many cancers. Due to costs, turn-around times, and specialised staff requirements, adoption of these methods as a first-line standard-of-care has lagged, with pathologists primarily relying on H&E-stained whole-slide images (WSI) for tumour classification and grading. Recent AI tools have aimed to streamline the existing slide interpretation workflow by converting slides to vectors of numeric values which efficiently capture tumour morphological features, allowing for automated classification. This study instead aimed to augment rather than replace the existing pathology workflow by combining WSI with molecular information obtained from exome sequencing, methylation array, and RNA-based fusion detection. This approach, if successful, would allow greatly improved early insights into molecular features of tumours assessed via WSI-based pathology, with reduced cost and processing time compared to sequencing-based testing.

For this study the Molecular Characterization Initiative (MCI) paediatric CNS disease cohort, which contains both high-resolution WSI and detailed molecular information for all samples, was used. First, the transferrability of foundational models developed for adult cancers to paediatric specimens was assessed. Next, the accuracy of AI models trained on the MCI data to detect the presence of specific known molecular alterrations such as BRAF V600E variants and KIAA1549::BRAF fusions was tested. Finally, using clusters of image tiles correlated with molecular tumour classifications, the biological interpretability of the relationships identified was evaluated with the assistance of an expert pathologist. Briefly, it was found that foundation models developed using adult samples are highly transferrable to paediatric samples; while some molecular characteristics were reliably identified from WSI by models, some (including BRAF alterrations) were substantially below the level required for clinical unility; finally, slide tile clusters identified by the models matched the biological expectations, and in some cases may have revealed new morphological characteristics that fit with biological expectations but are not documented in existing literature. In summary, this approach presents a promising avenue to augmenting WSI-based tumour testing, with early findings largely matching with biological expectations; however, accuracy often does not reach the levels required for clinical standard-of-care, suggesting that methodological adjustments or additional data are required.

3 Abstracts of lightning talks

A Thermodynamic Framework for Active Force Generation, Strain Inhomogeneity, and Hypertrophy in Skeletal Muscle

Thomas Hayes
Supervisors: Giuseppe Zurlo, Eoin McEvoy

Skeletal muscle adapts to mechanical loading and disease through remodelling of its subcellular architecture [1]. Strain inhomogeneities have been observed within the force-generating structures of muscle cells, suggesting a non-convex energetic response at the microscale. We present a thermodynamic framework that couples micromechanics with subcellular geometry to describe hypertrophy and active force generation. We introduce a novel activity-associated strain-energy density directly informed by cross-bridge energetics [2] and sarcomere geometry, providing an energetically consistent link between molecular attachment kinetics, macroscopic active stress, and structural adaptation of the contractile machinery. We further account for inhomogeneous strains within the sarcomere, which redistribute deformation across force-generating structures and allow some regions to remain mechanically favourable for cross-bridge binding even when the overall muscle is stretched. This provides a mechanism by which active force can be sustained over a wider range of extensions than would be predicted under homogeneous deformation assumptions. We embed the formulation in a finite-growth setting in which growth acts as a density-preserving remodelling process that shields sarcomere structures from macroscopic overstretch. This opens a route to mechanistic interpretation of loading responses, the emergence of spatial heterogeneity, and muscle adaptation in conditions such as sarcopenia and ALS.

This research is conducted with the financial support of Taighde Éireann – Research Ireland under Grant number GOIPG/2024/4523.

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Odd diagram classes and their hidden structure

Michael Joyce Maher
Supervisor: Angela Carnevale

Odd analogues of Rothe diagrams for permutations in type A Coxeter groups, called odd diagrams, were introduced and studied in [1]. Permutations can be partitioned by their odd diagrams, resulting in what we call odd diagram classes. Odd diagram classes were studied in [2] and a particularly surprising result from that paper is that odd diagram classes are Bruhat intervals. It has also been shown in [3] that these odd diagram classes are rank symmetric. In that paper the authors conjectured that the Kazhdan-Lusztig polynomial associated to any odd diagram class is equal to 1.

In this talk, I take a combinatorial view of the hidden structure inside odd diagram classes. The starting point is the observation that these intervals appear to have a block structure, and that such a structure would explain why the Kazhdan-Lusztig polynomial is equal to 1. The aim of this talk is to explain why this hidden structure always exists. To do this, I introduce index sets, which record the positions a given value can occupy across an odd diagram class, and discuss the combinatorial properties of these sets that explain why this hidden structure must occur.

Supported by the College of Science and Engineering, University of Galway

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Comparative Analysis of Covariate-adjusted Mean Residual Life Estimation With Parametric and Semi-Parametric Approaches: A simulation Study

Parastoo Niloofar
Supervisors: John Newell, Shirin Moghaddam, Amir Jalali, Alberto ALvarez-Iglesias

Mean Residual Life (MRL) is a fundamental measure widely utilized in various fields, including reliability theory and survival analysis, to provide insights into the expected remaining lifetime of a subject, given survival up to a specific time point. However, estimating MRL poses significant challenges, particularly in the presence of censored observations. Administrative censoring substantially influences the tail behaviour of the survival curve, complicating its extrapolation. This difficulty arises due to the heavy reliance on extreme values, which are inherently rare and sparsely distributed in survival studies. Moreover, right censoring not only impacts the tail of the survival curve but also alters its overall shape, further complicating estimation procedures. Several methodologies have been proposed to estimate MRL in the presence of right and administrative censoring. One approach integrates parametric and non-parametric methods to approximate the tail of the survival distribution, leveraging limited information available before the study's termination. Another approach treats censored observations as missing data and employs parametric Bayesian techniques to estimate the censored observations. This study conducts a comparative analysis of these two methods, evaluating their performance across various simulation settings. Moreover, this study will explore the covariate-adjusted MRL in the presence of right and administrative censoring.

Multivariate Adaptive Reference Regions in Longitudinal data monitoring

Forough Pazhuheian
Supervisors: Davood Roshan, John Newell

In recent years, the introduction of adaptive reference ranges has played a crucial role in personalized monitoring, allowing for the detection of abnormal values while accounting for an individual's biomarker variability over time. Existing literature on adaptive reference ranges has focusing on one biomarker at a time. However, modern diagnostics increasingly use panels of multiple biomarkers that are biologically and clinically related. Interpreting each biomarker separately increases the risk of false positives and may hide important patterns that only appear when the biomarkers are considered together. A more suitable approach is the multivariate adaptive reference region, a joint region in biomarker space that controls false alarm probability for the profile as a whole rather than for each biomarker individually. Designing multivariate, adaptive reference regions has several methodological challenges. First, dependence among biomarkers must be modelled to control the joint error rate and to borrow strength across analytes. Second, covariate effects (like age, sex, or other demographic characters) should be incorporated to avoid widening regions or introducing bias. Third, the method must be longitudinal and adaptive, updating an individual's reference region as more

data accrue while remaining robust. Computational efficiency is equally important, as the approach should allow rapid evaluation and incorporation of new patient data without the need to complete re computation. This study develops and evaluates a multivariate adaptive reference region that extends our univariate adaptive framework to panels of biomarkers measured serially. The proposed method couples a multivariate mixed-effects framework with a sequential estimation procedure designed to update parameter estimates as new observations are incorporated. Through simulation and application to real world data, we compare the proposed multivariate adaptive reference region against univariate reference ranges metrics by computing false positive rate. [1].

References

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4 Abstracts of posters

RePlas-GT: A novel workflow combining bioinformatic approaches to horizontal gene transfer detection and pathogenicity in prokaryotes

Stephen Allen
Supervisor: Cathal Seoighe (School of Mathematical and Statistical Sciences, University of Galway), Georgios Miliotis (School of Medicine, University of Galway), Matthew Dorman (Department of Microbiology, Trinity College Dublin)

Background:

Horizontal gene transfer (HGT) allows bacteria to rapidly adapt to new environments by acquiring novel genes, contributing to the spread of antimicrobial resistance (AMR) and virulence genes. Interactions between human bacterial pathogens and AMR bacteria in the environment or animal microbiome can transfer resistance genes to these pathogens, affecting human health. Understanding HGT is therefore critical to develop effective mitigation against AMR.

Objectives:

To investigate whether AMR genes present in bacterial genomes are associated with HGT we are developing a workflow for detecting HGT in bacterial isolates, contextualized by their AMR and virulence profile. Our workflow combines established tools to process whole genome short-read sequences, isolate plasmid assemblies, identify resistances and detect HGT.

Methods:

Short-read Illumina sequences from Salmonella Typhi and S. Typhimurium L2 isolates with known plasmids were downloaded from GenBank, trimmed using fastp and asssembled with SPAdes. Downstream analysis was performed using our Snakemake workflow RePlas-GT. Using CheckM2 to assess assembly quality; genomes with <5% contamination were retained. AMR and virulence genes were identified with Abricate using Resfinder and VFDB databases. Plasmid assemblies were identified and extracted using GplasCC. Chromosomal HGT events were detected across samples using Gubbins. Associations between AMR and HGT were determined by overlaying the positions of AMR genes and HGT events.

Results:

RePlas-GT identified and reconstructed the IncFII/IncHI2 plasmid in 63% of positive control samples(n=39), and identified dfrA1,sul1,sul2 and blaTEM genes in the isolated plasmid assemblies, in agreement with the literature. Two misclassifications occurred in the negative control(n=83). No association was observed between chromosomal HGT events and chromosomal AMR genes in this dataset.

Conclusions:

RePlas-GT demonstrated a low false-positive rate for plasmid detection, though sensitivity could be improved. Future work will extend the pipeline to detect HGT within plasmids using SHIP, applying the workflow to investigate associations between HGT, AMR, virulence, and plasmids in Salmonella outbreaks in Ireland.

Modelling Composition Response Data with Application to Clot Composition Observed for Acute Ischemic Stroke (AIS) Patients

Malak Almutairi
Supervisors: Emma Holian, Karen Doyle

Modelling composition response data presents challenges due to the nature of multivariate proportions for multiple elements making up the whole composition of an individual sample. Specifically, the challenges of modelling composition response data include bounded responses, bounded on the continuous scale between 0 and 1, correlation between multivariate responses, and multivariate responses within the sample constrained to sum to 1 being proportions of the composition of the entire sample [2]. To address these challenges, this poster investigates the modelling of composition response data, focusing on thrombotic material extracted from Acute Ischemic Stroke (AIS) patients using mechanical thrombectomy, which

measures five components making up the clot composition. The aim is to model composition response considering the effects of factors that may influence changes in clot composition. When univariate response data are continuous and bounded between 0 and 1, using a statistical analysis assuming a normal error structure can lead to biased and incorrect estimates. Therefore, an appropriate model like beta regression should be used for reliable parameter estimates rather than normal linear regression. Expanding to the multivariate response setting Dirichlet regression is an appropriate modelling approach. We discuss cases when it is appropriate to use Beta or Dirichlet regression over Linear regression with normal error structure. We explore available R packages, **betareg, DirichletReg, MCMCglmm** [1] [3] [4], and discuss their performance in modelling composition response data.

References

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A Review on Electrocardiogram Markers and Genetic Factors in Predicting Peripheral Arterial Disease Outcomes

George Aryee
Supervisor: Davood Roshan

Peripheral arterial disease (PAD) is a chronic circulatory condition characterized by the narrowing or blockage of arteries supplying blood to the extremities, most commonly the lower limbs. PAD affects over 230 million people worldwide and is expected to increase significantly by 2045 due to changes in risk factors such as diabetes and kidney failure, which influence disease prognosis. It is associated with increased risks of amputation, limb ischemia, stroke, heart attack, and cardiovascular death. Despite advances in diagnostic and therapeutic strategies, PAD remains underdiagnosed and undertreated, partly due to its heterogeneous clinical presentation and the lack of robust predictive tools for disease progression and associated outcomes, which vary significantly across populations.

Current studies primarily use clinical and lifestyle factors to predict PAD outcomes, including mortality, major adverse cardiovascular events (MACE), and major adverse limb events (MALE). However, electrocardiogram (ECG) and genetic data despite being informative in other cardiovascular conditions have received limited attention in predicting PAD outcomes. This highlights an important gap in current research.

Therefore, this poster presents a comprehensive literature review aimed at identifying commonly used predictive features, including ECG markers and genetic factors, as well as the statistical and machine learning models applied in predicting PAD outcomes.

Addressing this gap will not only advance methodological approaches to PAD outcome prediction but may also improve early identification of high-risk patients, enable timely interventions, reduce unnecessary procedures, and support more efficient allocation of healthcare resources.

Supported by (support source, if any); delete otherwise.

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Handling Missing Binary Outcomes in Cluster Randomised Trials: A Simulation Study Comparing Mean Score and Joint Latent Normal Modelling Methods

Nirdesh Bakshi
Supervisor: Neil O'Leary

Cluster randomised trials (CRTs) frequently involve correlated outcomes within clusters alongside incomplete outcome data. In practice, these challenges are often addressed separately, with analyses either accounting for clustering while ignoring missingness or handling missing data without respecting the hierarchical structure [1]. Such approaches can lead to biased or inefficient estimates of treatment effects, particularly for binary outcomes, which are commonly used as primary endpoints in CRTs. Robust and practically implementable methods are therefore required to jointly address clustering and missing data within a unified framework [2].

We consider two approaches for analysing incomplete binary outcomes in CRTs. The first is the mean score method, a pattern-mixture estimating equation approach that incorporates sensitivity parameters into a single imputation framework. It is computationally efficient, non-stochastic, and yields parameters that are directly interpretable on the marginal scale, though its performance in clustered settings remains underexplored [3]. The second approach is two-level joint latent normal multiple imputation, which specifies a multivariate normal model with cluster-level random effects to generate imputations under a coherent hierarchical framework [4]. This approach naturally accommodates clustering and propagates uncertainty through multiple imputation. Importantly, it does not prescribe a specific substantive analysis model post-imputation, offering flexibility to align the analysis with the target estimand [5]. However, it relies on latent scale assumptions and may be sensitive to model specification.

We conduct a simulation study to evaluate the finite-sample performance of these methods in two-arm CRTs with missing binary outcomes. Both approaches are benchmarked against complete case analysis. The estimand of interest is the population-averaged treatment effect, expressed as a marginal log-odds ratio. Data are generated under a marginal logistic model with cluster-level correlation induced via a latent structure, with the treatment effect specified directly on the marginal scale to ensure alignment between the data-generating mechanism and the estimand. We vary key design parameters, including the number of clusters per arm, cluster size, intra-cluster correlation, treatment effect, and proportion of missing data under a missing at random mechanism. Performance is assessed using bias, confidence interval coverage, precision, and Type I error.

Preliminary findings indicate that both methods exhibit degraded performance when the number of clusters is small, though with distinct operating characteristics. Bias was generally low across all scenarios, but greater instability was observed in small cluster settings. The mean score method demonstrated undercoverage in small-cluster settings and consistently inflated Type I error rates. In contrast, the joint latent normal multiple imputation approach achieved coverage closer to nominal levels and maintained better control of Type I error in comparison, albeit with higher variance and reduced precision. As the number of clusters increased, the performance of both methods improved. These findings highlight a trade-off between efficiency and inferential validity, with implications for method selection in small-sample CRT settings. The results also highlight the importance of adequate cluster sizes for reliable inference and motivate further investigation into method robustness in small-sample CRT settings. Future work should focus

on refining methods to improve inferential validity in small-cluster settings, where standard approaches may perform poorly.

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Wave Propagation in Layered Media using Physics Informed Neural Network

Yash Bhandakkar
Supervisor: Bharat B Tripathi, Karen Doyle

Background, Motivation & Objective: Stroke is the second leading cause of death globally, and understanding its mechanical properties is essential for improving outcomes of mechanical thrombectomy, a standard treatment for strokes. The mechanical properties of a clot govern the propagation of wave in it. However, most of the work has focused on homogeneous composition [1], although they are naturally heterogeneous. Shear waves in soft tissues are nonlinear in nature; for simplicity, we will start with the linear regime. Recently, PINNs [2] have been used to model the wave propagation, which incorporates the governing equation to model wave physics. Here, we aim to model the wave propagation in heterogeneous media using Multinet PINNs.

Statement of Contribution: We model wave propagation in heterogeneous media, particularly layered media with drastic changes in material properties, leading to material discontinuities at interfaces. Discontinuity at the interface leads to partial reflection and transmission at the material interface governed by the impedance mismatch. Multinet PINNs are introduced to model wave propagation, in which individual neural networks operate independently and are coupled via the interface continuity condition.

Results and Discussions: The results show that Multinet PINNs can model wave propagation with an interface. Wave reflection and transmission were captured only using the known physics and proper implementation of the interface condition. The relative L2 error for the impedance ratios of 1.68 and 13.34 were less than 1%, indicating the efficiency of Multinet PINNs in modeling wave behaviour in layered heterogeneous media.

Acknowledgement:
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Khemraj Shukla,and George Em Karniadakis Physics-Informed Neural Network(PINNs) for Wave Propagation and Full Waveform Inversions *Journal of Geophysical Research: Solid Earth* , 2022

Physics informed neural operators for modelling nonlinear waves

Ciarán Campbell
Supervisor: Bharat B. Tripathi

Motivation and Objective: Concussion due to traumatic head impact is a major health problem worldwide. The brain is a nonlinear viscoelastic soft solid that propagates shear shock waves during large deformation [1]. This requires real-time predictions for deployability in detecting concussion. Physics informed neural networks make instant predictions, but only for the specific Initial Value Boundary Problem (IVBP) that they are trained on. Physics informed neural operators provide a family of solutions to IBVPs in real-time because the initial condition, PDEs variable coefficients, etc., are taken taken as input to the network.

Statement of Contribution: We implement physics-informed neural operators with the DeepONet architecture [2] to model the solution operator of nonlinear wave PDEs without using data. This data-free approach means that the residual of the PDE, the initial condition, and boundary conditions are the only information provided for training. We consider two types of input parameters: 1) initial condition and 2) variable wave speed (a PDE coefficient). We use Gaussian Random Fields to sample random functions. If the input parameter is the initial condition then we modify this function space so that the solution satisfies the boundary conditions.

Results and Conclusion: We successfully develop physics informed neural operators to model the advection equation and the viscous Burger's equation with sufficient accuracy. The advection equation is a canonical linear wave transportation problem for which we learned mappings between either initial condition or variable wave speed to the solution operator. We progress to the viscous Burgers' equation as a fundamental nonlinear wave problem.

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Identifying cell type-specific differential gene-sets in thoracic aortic aneurysms

Mehak Chopra
Supervisors: Niamh Hynes, Cathal Seoighe

This study was conducted during PhD placement and further developed using data from the Aortic Institute at Yale University, with contributions and support from Alokkumar Jha (Center for Neurogenetics, Weill Cornell Medicine, USA), Jennifer M. Kwan (Section of Cardiovascular Medicine, Yale University, USA), Bulat Ziganshin, and John Elefteriades (Section of Cardiac Surgery, Yale University, USA)

Unlike other cardiovascular diseases (CVDs), which have seen consistent improvements in survival over the last two decades, there have been no improvements in survival in aortic disease over the last 4 decades. Aneurysm of the aorta is a bulge or ballooning of the aorta that can potentially rupture and cause life-threatening internal bleeding, leading to sudden death. Treatment of aortic aneurysms includes invasive methods such as open surgical repair and less invasive alternatives like endovascular aneurysm repair. Despite these advances, an entirely non-invasive protocol is still lacking that can help diagnose and repair aortic aneurysms. Researchers at the Aortic Institute,

Yale University have attempted to identify blood gene expression biomarkers that are predictive of aortic aneurysms. This study builds on their previous efforts by analysing the same dataset to investigate the cellular composition and cell type specific changes in gene expression in the blood of aneurysm cases, relative to controls, using gene expression deconvolution. Our findings have revealed significant differences in the proportions of Neutrophils, Monocytes, and CD4 activated T cells in cases and controls. We have also noted variations in the neutrophil-to-lymphocyte (NLR) ratio, which aligns with previous research suggesting that NLR ratio could be considered as an important inflammatory marker in aortic aneurysms. Intriguingly, using cell type-specific differential expression analysis, we found that gene sets that are normally expressed in the aorta were differentially expressed between aneurysm cases and controls in neutrophils, and CD4 activated T cells. Overall, this study aims to infer cellular proportions and cell type-specific gene expression in blood in order to shed light on the differences in immune cells between healthy individuals and those with aortic aneurysms. The altered proportions and gene expression patterns in Neutrophils, CD4 activated T cells, and NLR suggests that these cell types may be informative about the presence of aortic aneurysms.

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Ask$^{\mathbf{m}}$ Zeta Functions and Traceless Matrices

David Cormican
Supervisor: Tobias Rossmann

Let K be a quadratic algebraic number field and $\mathfrak{O}_K$ its ring of integers. For prime p inert in O_K and almost all p which split in O_K, we present recent work giving the ask zeta function of the change of scalars $\mathfrak{gu}_d(\mathfrak{O}_K/\mathbb{Z}) \otimes \mathbb{Z}_p$ and $\mathfrak{su}_d(\mathfrak{O}_K/\mathbb{Z}) \otimes \mathbb{Z}_p$ for the general and special unitary Lie algebras of dimension $d > 1$ over $\mathfrak{O}_K$. We note that these local ask zeta functions are identical, except in the case of the $d = 2$ where the prime p splits. We will also explain the links between this work and earlier investigations of ask squared zeta functions for $\mathfrak{gl}_d(\mathbb{Z}_p)$.

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T2DIAbetes (Type 2 Diabetes Integrated Atlas): A web-based tool to study Type 2 Diabetes using tissue-specific atlases

Nupur Dubey
Supervisors: Cynthia M. Coleman and Pilib Ó Broin

Diabetes is a chronic metabolic disorder affecting 589 million adults worldwide [1]. It presents as a persistent increase in blood glucose levels due to impaired insulin production, utilisation, or sensitivity [2]. Across the three broad categories of diabetes (type 1, type 2, and gestational diabetes), the most widespread is type 2 diabetes mellitus (T2DM), which is marked by beta cell dysfunction along with insulin resistance [3]. There is increased interest in bioinformatic analysis of data to identify potential genes and pathways involved in T2DM [4]. Integrated single-cell reference atlases help understand disease-specific cell states, investigate population heterogeneity, and can also be used to analyse new datasets [5].

In this project, we are developing a web application that hosts an atlas to drive research progress on T2DM. Here, we describe ongoing work to develop an atlas consisting of publicly available datasets that can be explored to study the effects of T2DM on different cell types by querying tissue-specific atlases generated by integrating existing single-cell RNA sequencing (scRNA-seq) T2DM datasets. The application will also provide a platform for researchers to explore and visualise pre-processed publicly available datasets from T2DM scRNA-seq studies and serve as a resource for the T2DM research community.

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Ask zeta functions associated with hypergraphs

Mario Falciatore
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In the study of the average size of kernels of generic matrices with support constraints, hypergraphs can be seen as parameters of a class of modules of matrices over compact discrete valuation rings. A strong uniformity result [1, Thm A] of the ask (Average Size of Kernel) zeta functions allows us to connect a unique rational function $W_H(X,T)$ to any hypergraph H that does not depend on the choice of the discrete valuation ring.

This correspondence raises several natural questions about the relationship between hypergraphs and rational functions. In particular, although an explicit formula for $W_H(X,T)$ in terms of the poset of flags of subsets of the vertex set provides candidate factors for the denominator and possible poles, it remains unclear how sharp this prediction is. We present preliminary results that begin to relate structural properties of H to analytic features of $W_H(X,T)$, offering initial evidence towards a more systematic understanding.

Moreover, we investigate how $W_H(X,T)$ behaves under natural operations on hypergraphs. This approach leads to new results on the Hadamard product of certain classes of rational functions arising in this context.

Our purpose is to find answers to some of the questions arising from the study of ask zeta functions of hypergraphs and on some properties of the underlying hypergraphs. As part of this program, we construct a database of hypergraphs up to isomorphism together with their ask zeta functions, and we use machine learning techniques to detect patterns linking combinatorial properties of hypergraphs with analytic properties of the corresponding rational functions.

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Ideal zeta functions of Lie rings arising from hyperplane arrangements

Deborah Gonçalves Fabri
Supervisor: Joshua Maglione

We study ideal zeta functions of class-2 Lie rings associated with 2-dimensional hyperplane arrangements with multiplicities. Starting from a multi-arrangement

$$Q_\Delta = y^{\gamma_\infty} \prod_{k \in \Delta} (x - ky)^{\gamma_k},$$

we construct a family of Lie rings L_Δ whose commutator structure reflects the combinatorics of the arrangement and which may be viewed as central amalgams of higher Heisenberg Lie rings. The local ideal zeta function $\zeta^{\triangleleft}_{L_\Delta,p}(s)$ counts finite-index $\mathbb{Z}_p$-lattices in $L_{\Delta,p} = L_\Delta \otimes_{\mathbb{Z}} \mathbb{Z}_p$ that are closed under the Lie bracket, weighted by their index. Using an upper-triangular parametrisation of lattices, we express this counting problem as a p-adic integral whose domain is determined by divisibility conditions arising from the bracket relations. The resulting singular geometry is resolved by a blow-up, and the resulting chart-wise counting problems are encoded in affine semigroups and semigroup modules whose Hilbert series are computed via finite free resolutions. For almost all primes, we obtain an explicit local formula for $\zeta^{\triangleleft}_{L_\Delta,p}(s)$, as well as results on the local and global abscissae of convergence, giving a uniform description for hyperplane arrangements with non-negative multiplicities such as Q_Δ.

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Exhaustive Optimisation of Automorphism Groups for Stabiliser Codes

Aisling Mac Aree
Supervisor: Mark Howard

An important measure of utility for a quantum code is the identification of *which* logical operations can be implemented fault-tolerantly on its codespace. We introduce a framework which leverages the automorphism groups of associated classical codes, the choice of logical basis and exploitation of code equivalence to construct all distinct implementable realisations of each valid logical operation for a given $[[n, k, d]]$ code. We establish conjugacy classes and group transversals (unrelated to transversality) as key explanatory concepts. We subsequently motivate and calculate two figures-of-merit that can be optimised with this framework and may be advantageous for both magic state cultivation and experimental purposes.

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A Bayesian Ranking of the Olympic Medal Table

Cormac MacDermott
Supervisors: John Ferguson, Carl Scarrott

Evaluating a country's sporting success can provide insight into its decision-making and the infrastructure used to develop athletic talent. The Olympic Games [2] serve as a global benchmark, yet conventional medal tables can be overly influenced by population size and can be highly variable, particularly for smaller nations where outcomes are more affected by stochastic fluctuations.

The standard lexicographic medal table ranks NOCs by medal counts, prioritising gold over silver and then bronze, inherently favouring

larger populations with deeper talent pools. A common alternative is the per-capita medal count which normalises totals by population size. However, it is highly sensitive to stochastic variation for smaller nations, in which a single medal can substantially change rankings between games. More advanced approaches include the U-index [1], which ranks nations by the probability of winning their observed medal count, or more, under a null binomial model, assuming equal per-capita medal-winning capability. However, a fundamental drawback of p-value-based methods is their sensitivity to sample size [8]; a larger population yields a smaller standard error and, therefore, a smaller p-value regardless of whether the performance warrants it. Consequently, small nations with limited population cannot accumulate sufficient evidence to rank highly, while large nations are pushed artificially outward, upward if above the global average rate of medal wins, downward if below.

We propose a hierarchical Bayesian model that estimates each country's true per-capita medal rate via shrinkage, ordering nations by their estimated "long-run" per-capita medal rate. Specifically, the number of athletes from country c winning exactly i medals is modelled as

$$M_{i,c} \sim \text{Poisson}(n_c \cdot p_{i,c}), \tag{1}$$

where n_c is population size and $p_{i,c}$ is the probability of winning i medals. Multi-medallists are modelled as independent Poisson random variables with a conditional probability structure that shares information across medal tiers, aiding MCMC convergence. Posterior inference is performed via Gibbs sampling using the `rjags` package [5, 6], incorporating population data from the UN Population Division [7] and official Olympic medal data [2]. Small nations with sparse medal counts are stabilised toward the global average, while large nations are driven by their own medal counts.

A key novelty of our approach is that the Bayesian framework yields full posterior distributions over both the inferred medals-per-capita performance and the induced ranks, providing a measure of uncertainty in each country's ranking position. These posterior rank distributions highlight cases where apparent differences between neighbouring countries are not credibly distinguishable. Posterior rank summaries give a more interpretable ordering of national sporting performance while making uncertainty in comparative performance explicit.

In this poster, we apply our algorithm to rank and compare country-level performance at Paris 2024. A simulation study confirms that large-population countries, such as the United States, can attain high rankings under our framework with realistic Olympic medal tallies. Full results across all Olympic Games since Athens 2004 are available in an interactive Shiny application [3], which supports sorting, filtering, and direct comparison for a user-selected country. All ranking methods and source code are provided in the accompanying GitHub repository [4]. Finally, we acknowledge that users of Olympic ranking schemes may have differing goals, and no single scheme is universally ideal. Therefore, we advocate presenting multiple ranking schemes alongside one another to enable fully informed comparison.

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Conditioning of linear systems coming from Singularly Perturbed Convection–Diffusion Problems

Jekaterina Mosalska
Supervisor: Niall Madden

Singularly perturbed convection-diffusion problems arise in many applications, such as fluid dynamics and transport processes. These problems often exhibit sharp boundary or interior layers, which makes them challenging to approximate numerically [3]. Standard discretization methods typically lead to large linear systems that are poorly conditioned and therefore difficult to solve efficiently [1].

In this work, we study finite difference discretizations with upwinding on layer-adapted Shishkin meshes for convection-diffusion equations in one and two dimensions. In the one-dimensional case, we analyse the structure of the resulting matrices and prove bounds on their condition numbers, showing how these depend on the mesh size and the perturbation parameter. Numerical experiments in Python confirm the theoretical results.

We extend the study to the two-dimensional case, where the matrices are more complex, and investigate the behaviour of the condition number numerically. The results agree well with the one-dimensional theory and provide a basis for efficient solution methods [2].

Future work will focus on extending the theoretical results to the two-dimensional case and developing effective LU-based preconditioners for these systems [4].

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Long-Read Single-Cell Sequencing of Acute Myeloid Leukaemia Samples Allows for the Characterisation of Leukaemic Cells Revealing Altered Metabolism and Isoform Usage during Disease Progression

Micheál Ó Dálaigh
Supervisors: Eva Szegezdi, Pilib Ó Broin

Background: Acute myeloid leukaemia (AML) results in poorly-differentiated white blood cells accumulating in the bone marrow, interfering with normal blood cell function. Normal and malignant haematopoiesis occur simultaneously in AML; methods to identify leukaemic cells in bone marrow samples are therefore necessary.

Single cell transcriptomics (scRNA-seq) has been used to infer the presence of cancer-relevant genomic alterations to classify cells as malignant or normal. This approach is complicated by the sparse data provided by Illumina short-read sequencing (SRS), which biases coverage towards the mRNA capture site. PacBio Kinnex scRNA-seq utilises long-read sequencing (LRS) to cover the whole transcript and is compatible with existing 10x cDNA libraries.

Here, we use PacBio Kinnex to identify and characterise the malignant cells in patient-derived AML samples, previously sequenced with Illumina SRS.

Methods: 28 patient samples harbouring a range of AML-relevant genomic alterations were resequenced with PacBio Kinnex scRNA-seq. pbfusion, VarTrix, Seurat FindMarkers, and clusterProfiler were used for fusion gene identification, single-cell genotyping, differential gene expression analysis, and gene ontology enrichment analysis respectively.

Results: LRS identified more cells with malignant characteristics than SRS; e.g. in the same *NPM1*-mutated sample, the LRS data identified $\sim$ 3x more (1000 vs 280) mutant *NPM1* cells than the SRS data. LRS identified *KMT2A*::*MLLT3* and *DEK*::*NUP214* fusions in relevant samples which were not detectable in cognate SRS data. LRS data also enables isoform-level resolution of gene expression data and we identified a case of differential *MCL1* isoform usage in one patient sample; the longer anti-apoptoptic transcript was favoured at diagnosis and remission and predominantly expressed by *NPM1*-mutated leukaemic cells, whereas at remission, the primary isoform was the shorter pro-apoptotic transcript.

Gene ontology enrichment analysis of the differentially-expressed genes between diagnosis and relapse revealed altered metabolism of the leukaemic cells across multiple patients, with biological processes related to oxidative phosphorylation upregulated at relapse.

Conclusions: LRS identifies more malignant cells than SRS by improving coverage of AML mutation sites. LRS data also allow for the characterisation of leukaemic cells through the analysis of both gene and isoform expression data. These results highlight the benefits of using long-read scRNA-seq sequencing to characterise cancer samples.

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The degree of the class-counting polynomial of a graph

Lucrezia Prosperi
Supervisors: Angela Carnevale, Tobias Rossmann

Each graph Γ, together with a commutative ring, gives rise to an associated graphical group whose conjugacy classes are enumerated by a polynomial $f_\Gamma(X)$, called the *class-counting polynomial* of Γ [2]. The degree of this polynomial is intrinsically linked to a new graph invariant, denoted by η [1]. This invariant is determined by two factors: the number of connected components of the induced subgraphs of Γ, and the cardinality of the boundary. The invariant η is the focus of this work, with the aim of analyzing both its combinatorial nature and its computational complexity. We investigate its behavior under basic graph operations, such as adding and deleting edges, and establish structural properties that allow recursive approaches in specific classes of graphs. In particular, we show that for trees, the invariant η coincides with the *path partition number*. A fast polynomial-time algorithm is known for computing the path partition number [3]. This yields an efficient method for computing $\eta(T)$ when T is a tree. Beyond trees, however, this correspondence breaks down. We provide examples showing that the gap between the two invariants can be arbitrarily large. Nevertheless, meaningful bounds can be derived by considering spanning trees, leading to new classes of graphs for which η can be explicitly computed. From a computational perspective, when the focus shifts to general graphs, we proved that determining $\eta(\Gamma)$ is NP-hard.

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Spectra of cactus graphs and their gain graphs

Yannan Qian
Supervisor: Angela Carnevale, Matteo Cavaleri

The spectrum of a graph is the set of the eigenvalues of some matrix representation (usually its adjacency matrix) of the graph itself. A graph is said to be determined by its spectrum if there are no non-isomorphic graphs that have the same spectrum. Gain graphs are like labeled graphs with directions but the label of each edge are elements of some group G, and the label is the inverse element for the inverse direction. The spectra of graphs can be extended to gain graph as G-spectra by the representations of group elements. There are two main questions: which graphs are determined by their spectra, and which graphs are determined by their G-spectra. Both questions are investigated here for cactus graphs. I found a new family of graphs that are determined by their spectra, and showed the limitation for a powerful method on searching for cospectral graphs. For gain graphs, if the underlying graph is a cactus graph and determined by its spectrum, the gain graph is determined by its G-spectrum when the group G is ambivalent.

Modelling Complex Evolutionary Processes During Phylogenetic Analysis of Genomic Sequence Data

Mohit Rana
Supervisors: John Ferguson, Lars Jermiin

Phylogenetic inference plays a pivotal role in generating our understanding of the origin and evolution of species (e.g., pests and pathogens). This is because each inferred phylogenetic tree provides a framework for visualising the evolutionary relationship among these species (*NAR Genom. Bioinform.* 2, lqaa041). Inferring phylogenetic trees requires accurate modelling of the evolutionary processes that led to the observed differences among genomes. Current molecular phylogenetic methods assume that all parts of the genomes have evolved under the same clocklike conditions. However, a growing body of evidence suggests that the evolutionary process is more complex (*Syst. Biol.* 53, 638–643), implying that it often violates the phylogenetic assumption of evolution under stationary, reversible, and time-homogeneous (SRH) Markovian conditions (*Bioinformatics* 22, 1225–1231). Most model-based phylogenetic methods assumes evolution under SRH conditions, and many of these methods are able to accomodate some violation of this assumption. However, whether a phylogenetic method is able to infer the correct phylogeny depends not only on how dissimilar evolutionary processes are along different edges in the true, but unknown, tree but also on the length of internal edges in this tree. We must be able to account for this complexity when inferring phylogenetic estimates.

Directional mutation pressure (DMP) is a term used to describe non-random patterns of mutation in DNA. In theoretical terms, DMP occurs when $\mu_D \neq 0.5$, where $\mu_D = u/(u+v)$, u is the rate of change from nucleotides A or T to nucleotides C or G, and v is the rate of change in the opposite direction. Here, we use estimates of DMP to reveal that 41 mitochondrial genomes from animals and fungi must have evolved under different conditions, predominantly under AT pressure. This has had a

detectable impact on proteins encoded by these mitochondrial genomes. The results show that the 41 genomes must have evolved under non-stationary conditions, with substantial heterogeneity in DMP along different lineages. These findings demonstrate a key limitation of standard phylogenetic methods.

To address this challenge, we will develop phylogenetic methods that accurately capture the observed complexity of molecular evolution. Specifically, we will extend the HAL-HAS method (*Syst. Biol.* 63, 726–742) that models rate heterogeneity across lineages and across sites in DNA. The extension will be a substantial improvement that addresses current software limitations in molecular phylogenetics.

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nf-hlamajority: An Automated Nextflow Pipeline for Consensus HLA Genotyping in Neoantigen Prediction Workflows

Kevin Ryan
Supervisors: Pilib Ó Broin (School of Mathematical & Statistical Sciences, Institute for Health Discovery and Innovation), Laura Barkley (Lambe Institute for Translational Research)

Motivation

Neoantigens are non-self peptides that can induce an immune response. They arise from protein-altering genomic and transcriptomic variants and are of particular interest for cancer vaccine development. Neoantigen prediction pipelines use bulk DNA and RNA sequencing data to identify these variants, translate them *in silico* into peptides, and predict peptide immunogenicity. Human Leukocyte Antigen (HLA) genotyping is a critical step in these pipelines, and Claeys et al.[1] found that a majority voting approach improved HLA typing accuracy over any single tool alone. Currently, no end-to-end pipeline exists to apply this approach, and it has not been integrated into broader neoantigen prediction workflows.

Results and discussion

We developed *nf-hlamajority*, a Nextflow pipeline that performs HLA class I genotyping on DNA sequencing data using Optitype, Polysolver, HLA*LA, and Kourami[2, 3, 4, 5]. For each HLA gene, the pipeline assigns the HLA genotype called by the majority of tools. Using PCR-derived genotypes as a gold standard, we benchmarked nf-hlamajority using whole-exome sequencing data from the 1000 Genomes Project. nf-hlamajority achieved an accuracy of 98.9%, 99.0% and 99.1% on the HLA-A, B and C genes, respectively, confirming the benefit of the majority-voting approach. To improve an existing end-to-end neoantigen prediction pipeline, we integrated nf-hlamajority with Landscape of Effective Neoantigens Software (LENS)[6], implementing this combined pipeline in the cloud using AWS Batch. This integration results in a more accurate, accessible and scalable end-to-end pipeline for neoantigen prediction.

Availability and implementation

nf-hlamajority is published under an open source MIT license and is available at: `https://github.com/kevinpryan/nf-hlamajority`

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Modelling Survival Extremes for Health Economic Decisions

Sivagami Nedumaran
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In health economic evaluation, Quality-Adjusted Life Years (QALYs) form the basis for the calculation of the Incremental Cost-Effectiveness Ratio (ICER), a key statistic used by policymakers to assess the cost-effectiveness of new treatments and to inform reimbursement decisions [1]. QALYs are derived by combining quality-of-life weights with life years gained, which in turn requires estimates of mean survival time. Accurate estimation of mean survival is therefore important in healthcare decision-making.

A fundamental challenge is that survival data are frequently incomplete due to different forms of censoring [2]. At the end of a study, a proportion of patients, often referred to as long-term survivors, may not yet have experienced the event of interest, leading to administrative censoring, while others may be lost to follow-up, resulting in random censoring. Administrative censoring implies incomplete follow-up, meaning the upper tail of the survival distribution is missing. Since the mean survival time corresponds to the area under the survival curve, missing tail information can lead to systematic underestimation of life years gained, QALYs, and ultimately the ICER. Although parametric models are commonly used to extrapolate the survival curves beyond observed follow-up, competing models that fit equally well in the bulk of the data may differ substantially in their tail behaviour, producing markedly different mean survival estimates. The magnitude and structure of this bias, particularly under substantial administrative censoring, remain insufficiently understood.

In this poster, a hybrid approach to survival extrapolation that combines the nonparametric Kaplan–Meier estimator [4] with an extreme value tail model based on the Generalised Pareto Distribution (GPD) [5, 3] is investigated. A peaks-over-threshold framework is used to model exceedances beyond a data-driven threshold while retaining the empirical Kaplan-Meier survival estimate below it. Extensive simulation studies under varying levels of random and administrative censoring will be presented to evaluate the hybrid estimator's performance in recovering mean survival time, high quantiles, and overall tail behaviour.

The results show that when censoring is limited to random dropout, or when overall censoring remains light (including both random and administrative components), the hybrid estimator performs well and yields stable estimates of extreme quantiles. However, as the degree of administrative censoring increases, the tail sample shrinks leading to loss of tail information and subsequently systematic underestimation of extreme quantiles. These results provide clarity on when tail-based extrapolation is reliable and highlight the need for caution when the proportion of administrative censoring is high.

Building on these findings, the next phase of the project will extend to automated threshold selection procedures [6], including settings where thresholds and tail parameters depend on covariates such as treatment group or patient characteristics. By developing user-friendly software and applying the methods to publicly available datasets, this research aims to improve transparency and robustness in survival extrapolation, thereby strengthening cost-effectiveness evidence used in healthcare policy.

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Numerical Computation of Haemodynamic Parameters using Firedrake

Sean Tobin
Supervisors: Niall Madden, Niamh Hynes

Abdominal aortic aneurysms (AAAs) comprise the most common type of aneurysm, and have a high mortality rate of approximately 80% [1]. The current clinical practice for determining whether an aneurysm is sufficient enraged as to demand a intervention is based, mainly, on the diameter of the vessel. However, there are far more factors, contributing to the rupture of an aneurysm, including blood pressure, vessel compliance, patient-specific geometry, and wall shear stress. In fact, the calculation based on vessel diameter is using this a proxy for shear stress [2]. Therefore, it is desirable to estimate wall shear stress directly through mathematical and numerical modelling of the fluid flow.

In this study, we develop an algorithm that solves for blood pressure and flow velocity, and subsequently computes both wall shear stress and time-averaged wall shear stress. We use the Python-based Firedrake [3] to implement the FEM. We present results a simplified two-dimensional aortic domain. Our next steps will be to extend this to three dimensions, using data sets from the literature (e.g., [4]).

Following that we aim to apply the methods to data in a synthetic data set, results from which will server as training data for a surrogate model. That in turn would greatly expedite the computational process, and allowing for faster diagnosis of the risk of aneurysm rupture.

Supported by *Taighde Éireann – Research Ireland, under Grant number 13/RC/2073_P2.*

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Transcriptomic Dysregulation of Bone Marrow Mesenchymal Stromal Cells in Type 2 Diabetes Mellitus

Jingyan Wang
Supervisors: Katarzyna Goljanek-Whysall, Pilib Ó Broin, Cynthia M Colman

Type 2 diabetes mellitus (T2DM) is a chronic disease, characterized by elevated blood sugar levels, leading to complications like osteopathy[1]. Bone marrow mesenchymal stromal cells (BM-MSCs) play a crucial role in bone regeneration and were widely studied for their therapeutic potential in regenerative medicine[2, 3]. T2DM-induced osteopathy is associated with impaired bone quality, with reduced BM-MSC numbers and diminished BM-MSC differentiation capacity[4]. However, the transcriptomic mechanisms driving BM-MSCs impairments of T2DM remain unclear.

BM-MSCs from 27 donors (13 individuals with T2DM: 7 females, 6 males; 14 without T2DM: 8 females, 6 male) were expanded for 1 passage for bulk RNA sequencing. Gene expression profiles were analysed across all donors, and within sex-specific subgroups. Differentially expressed genes (DEGs) were identified using DESeq2, common DEGs were identified by UpsetR, qRT-PCR was performed for validation. Both primary BM-MSCs and immortalized MSCs (iMSC#3) were subjected to osteogenic differentiation to assess DEG expression dynamics[5].

Transcriptomic analysis identified 82 DEGs across all donors with T2DM. Sex-specific comparisons revealed 195 DEGs in female donors with T2DM and 115 DEGs in male donors with T2DM ($\log_2|FC| \geq 2$, $p < 0.05$, by DESeq2), with 3 DEGs shared among all groups. Discrepancies were observed between RNA-seq and RT-PCR validation in donor sample. Notably, as DEG2 is inversely regulated during osteogenesis according to a previous study, it was consistently downregulated during early osteogenic differentiation in both BM-MSCs and iMSC#3, paralleling established timing of osteogenic mar kers expression and its role as negative regulator.

These findings revealed T2DM-associated transcriptomic dysregulation in BM-MSCs. The discrepancies between sequencing data and wet-lab validation could be attributed to the limited number of donor sample available for qRT-PCR. The downregulation of DEG2 during a 21-day differentiation process on cells parallels the established timing of osteogenic marker expression, supporting the role of DEG2 as a negative regulator of osteogenesis. Meanwhile, iMSC#3 recapitulate the gene expression patterns of primary BM-MSCs during osteogenesis, suggesting that iMSC#3 can serve as a robust cellular model for studying T2DM-induced osteopathy, thereby addressing the limited availability of primary samples.

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Wave Propagation in Layered Media using Physics Informed Neural Network

Yash Bhandakkar
Supervisor: Bharat B Tripathi and Karen Doyle

Background, Motivation & Objective: Stroke is the second leading cause of death globally, and understanding its mechanical properties is essential for improving outcomes of mechanical thrombectomy, a standard treatment for strokes. The mechanical properties of a clot govern the propagation of wave in it. However, most of the work has focused on homogeneous composition [1], although they are naturally heterogeneous. Shear waves in soft tissues are nonlinear in nature; for simplicity, we will start with the linear regime. Recently, PINNs [2] have been used to model the wave propagation, which incorporates the governing equation to model wave physics. Here, we aim to model the wave propagation in heterogeneous media using Multinet PINNs.

Statement of Contribution: We model wave propagation in heterogeneous media, particularly layered media with drastic changes in material properties, leading to material discontinuities at interfaces. Discontinuity at the interface leads to partial reflection and transmission at the material interface governed by the impedance mismatch. Multinet PINNs are introduced to model wave propagation, in which individual neural networks operate independently and are coupled via the interface continuity condition.

Results and Discussions: The results show that Multinet PINNs can model wave propagation with an interface. Wave reflection and transmission were captured only using the known physics and proper implementation of the interface condition. The relative L2 error for the impedance ratios of 1.68 and 13.34 were less than 1%, indicating the efficiency of Multinet PINNs in modeling wave behaviour in layered heterogeneous media.

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5 Abstracts of PhD and Masters theses

5.1 PhD theses

Development, implementation and evaluation of computational methods to quantify intratumoral heterogeneity and microsatellite instability

Harrison Anthony
Supervisor: Prof. Cathal Seoighe

Tumors are populations of aberrant cells that have genetic, epigenetic, and phenotypic differences to normal cells. When these differences are exhibited between cancer cells, it is referred to as intratumoral heterogeneity (ITH), and ITH is associated with several major issues in cancer like treatment resistance, relapse, and metastasis. One enabling characteristic of cancer that drives these differences is genome instability — the increased rate of genetic changes in the genome of a cell. When instability manifests in the short tandem repeats in the genome, it is known as microsatellite instability (MSI), and MSI is used to guide immune checkpoint inhibitor treatment.

Given the clinical relevance of both ITH and MSI, researchers have created methods and tools to detect them in sequencing data with varying levels of success. Several tools that detect MSI are reported to have near-perfect performance but do not sufficiently disclose what types of data they can be used with. ITH on the other hand is poorly defined and few methods exist that capture the overall genetic aspect of it. Furthermore, there has yet to be an in-depth investigation into whether MSI itself is a heterogeneous phenomenon.

The central aim of this thesis is to investigate novel ways to quantify the genetic aspects of ITH and determine whether MSI is a subclonal phenomenon. This central aim is achieved through three goals in which we (1) quantify somatic and germline variation using population genetics and determine its relationship to relapse and MSI, (2) benchmark the leading tools used to identify MSI to clarify their scope and performance, and (3) quantify ITH in MSI at the single-cell level.

Chapter 2 addressed the first goal by exploring the use of population genetics statistics in large pan-cancer data. We first investigated whether these statistics when used to measure the somatic variation of a cancer sample could be used to predict whether an individual will relapse. Although we identified several cancer-type specific results related to relapse, we were not able to replicate all these findings after accounting for tumor purity and ploidy. We also investigated if another statistic that measured individual germline heterozygosity had any relationship to MSI score. Similarly, we did not find a relationship between germline variation and MSI score, but we did discover relationships between MSI score and the confounding factors of tumor purity and self-reported population group. The impact of these potential confounding factors should be taken into account when MSI score is used as a clinical biomarker.

Next, in Chapter 3 we assessed the performance of the leading tools used to detect MSI in sequencing data. This was done by examining how each MSI tool performed on several sequencing datasets. Making use of this curated data, we validated most of the published performance metrics of these tools but identified several previously unreported shortcomings. The most significant of these findings was that there was a large drop in performance when applying tools originally evaluated on whole exome sequencing data to whole genome sequencing data. We also discovered that an as yet unpublished tool was able to outperform nearly all others on most data types.

Lastly, we used the knowledge gained through the previous two chapters to investigate whether MSI tumors consisted of a mixture of cells with and without MSI. To do this, we collected all publicly available single-cell sequencing data that had paired clinical MSI status. Then we created a novel computational pipeline built around two machine-learning based methods to classify cancer cells as having MSI based on gene expression. This led to several findings,

with the most important being that approximately one-third of all individuals in the analysis had evidence of cells with and without MSI in their samples. This directly challenges the current binary classification approaches used in research and clinical settings.

Rank distributions of graphs over the field of two elements

Badriah Safarji
Supervisors: Rachel Quinlan and Cian O'Brien

A square matrix M represents a graph Γ if its nonzero off-diagonal entries encode the adjacencies of Γ according to a fixed vertex ordering. Over the field of two elements, we study the distribution of ranks within the affine space of all matrices representing a particular graph. The motivating question is which graphs of order n are represented by more matrices of rank $n-1$ than of rank n. This reflects the fact that the most frequently occurring rank is not n but $n-1$ in the space of all $n \times n$ matrices over $\mathbb{F}_2$, a property which is exceptional to $\mathbb{F}_2$. This thesis focuses on connected graphs that have a path or cycle as a subgraph induced on all but one vertex.

The Mechanics of Biological Growth: A Study Through the Vertex Model

Mohsen Daman
Supervisors: Giuseppe Zurlo (Galway, primary supervisor), Roberto Paroni (Pisa, IT)

This doctoral thesis investigates the mechanics of growth and remodeling in biological tissues through a discrete framework known as the vertex model. While this model has been extensively used for numerical simulations in biological contexts, the present work focuses on a fundamental aspect: the generation of elastic stresses in vertex-based systems. This study introduces the concept of incompatibility in such tissues, a well-established source of residual stresses in continuous mechanics in the absence of external loads.

A key contribution of this thesis is the identification and characterization of two distinct types of incompatibility in the vertex model. The first, termed internal incompatibility, arises when the target area and perimeter of individual cells violate the isometric inequality. Internal incompatibility is recognized as a regulator of the critical transition between fluid-like and solid-like cell behavior, which plays a crucial role in processes such as cancer cell migration. The second, termed external incompatibility, pertains to the manner in which cells are interconnected to form specific tissue morphologies. Both types of incompatibility act as sources of residual stresses in tissues described through the vertex model.

The second part of this work explores the consequences of elastic stress accumulation on the possibility of inelastic tissue evolution. Specifically, the study examines phase transitions, including T1, T2, and T3 transitions, as well as cell division, analyzing how such non-elastic processes enable the system to evolve toward a minimal energy configuration. This evolution represents a potential pathway for growth in biological tissues.

The analysis, implemented using a MATLAB code, further investigates the influence of parameters such as area stiffness, perimeter stiffness, and line tension on growth progression, to single out the conditions leading to the instabilization of initially flat or regular surfaces. Preliminary results suggest that incompatibilities and stiffness parameters significantly contribute to the onset of corrugations at the interface between domains with differing control parameters. These findings open the door to explore connections with tumor growth, particularly in the context of metastasis spreading into healthy tissues.

Generating Functions for the Casimir Invariants of Simple Lie Algebras

Michael Flattery
Supervisor: Michael Tuite

In this thesis we consider the theory of finite-dimensional, complex, simple Lie algebras, their irreducible representations and Casimir operators. We review the classification of these simple Lie algebras and an overview of constructions of characters of their representations, including Klymik's formula for decomposing tensor products of irreducible representations. We describe a new efficient method for evaluating the characters of irreducible representations using Freudenthal's formula and present the characters of each fundamental representation of the simple Lie algebras. We review Okubo's formula for calculating the eigenvalues of general degree Casimir Operators on irreducible representations. Using Klymik's formula and Okubo's formula, we obtain a new formula for efficiently calculating these eigenvalues. We apply our result to derive closed expressions for the generating functions of these eigenvalues for the first fundamental representations of the non-exceptional Lie algebras.

Dynamics of Epigenetics in Early Life: Uncovering Genetic and Environmental Determinants from Infancy to Adolescence

Anna Großbach
Supervisor: Andrew Simpkin

DNA methylation (DNAm) is an epigenetic modification involving the addition of a methyl group to DNA without altering the genetic sequence. DNAm can regulate gene expression and thereby influence phenotypes, including disease susceptibility. Genome-wide DNAm patterns are dynamic, changing throughout life in response to both endogenous factors (such as developmental processes and genetics) and exogenous factors (such as environmental exposures and disease). Early-life epigenetic changes may shape developmental trajectories and contribute to later disease risk. However, most epigenetic research to date has focused on adult cohorts and cross-sectional data, leaving major gaps in our understanding of how DNAm patterns develop in childhood and evolve over time. Here, we investigate the dynamics of DNAm across childhood and adolescence, focusing on two epigenetic biomarkers: (1) epigenetic age and (2) methylation quantitative trait loci (mQTLs).

Epigenetic age (EA) estimates an individual's biological age based on age-associated DNAm patterns. While EA has been widely studied in adults and shown to predict health and lifespan, its applicability in paediatric populations remains unclear. The increasing availability of longitudinal cohorts offers new opportunities to study EA trajectories, yet a lack of methodological consensus limits reproducibility.

In this thesis, we first conducted simulation studies to identify appropriate approaches for modelling longitudinal EA. We then applied these methods to examine bidirectional associations between internalising symptoms (IS) and EA from early childhood to early adulthood in two large, socioeconomically and ethnically distinct cohorts. Our results indicate that persistently high or increasing IS during childhood are associated with accelerated EA across childhood and adolescence. No evidence was found for the reverse effect - that is, accelerated EA did not predict later IS. These findings suggest that early mental health problems may shape biological ageing trajectories across development.

Methylation quantitative trait loci (mQTL) are genetic variants that influence DNAm at specific sites. To date, no longitudinal studies have examined mQTL effects in early childhood, particularly in non-European populations. We analysed mQTL dynamics in a paediatric South African cohort, revealing diverse trajectories ranging from stable to increasing or attenuating effects across early childhood. Replication in independent cohorts supported the robustness of these findings and highlighted both age-related and ancestry-

specific effects. These results indicate that early childhood represents a critical window during which genetic influences may disproportionately shape DNAm and, consequently, phenotypic development.

Together, these studies provide novel insights into the dynamics of DNAm across childhood and adolescence and underscore the importance of longitudinal and diverse cohort designs to accurately capture epigenetic changes over time.

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Computational approaches for therapeutic target discovery to ameliorate muscle wasting during ageing

Karen Guerrero-Vázquez
Supervisors: Dr. Katarzyna Goljanek-Whysall & Dr. Pilib Ó Broin

Ageing is a fundamental biological process characterised by a progressive decline in physiological function, significantly impacting muscle mass and function, a condition known as sarcopenia. Age-related muscle decline is a public health priority given the ageing population and an unmet medical need. MicroRNAs (miRNAs) have emerged as key regulators of cellular processes implicated in regulating muscle homeostasis and sarcopenia, yet their complex regulatory networks pose challenges for therapeutic target identification. Concurrently, the concept of 'biological age' has gained interest, potentially offering a more accurate representation of an individual's physiological status than chronological age. Machine learning (ML) approaches have shown promise in predicting biological age from genomic data.

In this work I integrated machine learning (ML) approaches, through the development of advanced analytical tools and databases, to characterise the complex miRNA regulatory networks in muscle ageing and identify potential therapeutic targets for sarcopenia. Furthermore, I demonstrated that ML approaches can predict chronological age based on muscle gene expression, providing personalised insights into ageing trajectories. I created a novel software suite, miRKat, to analyse miRNA regulatory networks, integrating multiple data types into a customisable scoring system to prioritise relevant miRNAs.

Applied to muscle data, miRKat identified 13 miRNAs of interest, likely mechanistically involved in muscle ageing, for further investigation, including known regulators like miR-9 and miR-181, alongside novel candidates such as miR-449. The application of ML, particularly CatBoost, accurately predicted skeletal muscle chronological age from gene expression changes, with an R2 of 0.96 and an RMSE of 6.90 years, and identified a set of 21 consistently influential genes in muscle ageing signatures. Four of these genes were functionally validated in C. elegans. This approach identified shared and personalised muscle ageing gene signatures and highlighted key pathways involved in muscle.

In summary, this research led to the develop-

ment of miRKat, a computational suite that facilitates the analysis of miRNA regulatory networks, offering a novel perspective on muscle ageing and sarcopenia. The ML approach identified a signature of muscle ageing based on changes in gene expression, highlighting key genes associated with muscle ageing, and network analyses revealed microRNAs targeting these genes. This work extends the current understanding of the mechanisms underlying sarcopenia, identifying candidate biomarkers of muscle ageing and potential therapeutic targets, and providing tools for microRNA research.

Modelling Motion Tracking Data in Elite Soccer to Classify and Quantify Collision Intensity

Pearce Harney-Nolan
Supervisor: Prof. John Newell

This thesis addresses a gap in sports analytics by developing a Collision Severity Index (CSI) for soccer using in-game motion tracking data from the English Premier League, without relying on accelerometers (which are unavailable in most soccer contexts). The work involved manually labelling collision-related events across 20 EPL matches to create a Soccer Match Collision Dataset, which underpinned a series of studies covering feature extraction, event detection, and the classification of tackle and collision types using machine learning models. The core contribution is the CSI itself, developed using Principal Component Analysis (PCA) on variables captured around the point of contact in collisions. Both a general CSI and collision-specific variants were produced, and these were shown to discriminate well across severity levels (heavy, medium, light, and barely contact). The resulting collision severity scores were aggregated into player loading scores, with a practical R Shiny dashboard — featuring a collision-hurt map — built to support analysts, medical staff, and coaches in post-match rehabilitation planning, injury risk identification, and decisions around player rest and substitution.

Insights into Cancer-Related Phenotypes from Gene-Trait Coevolution and Gene Copy Number Variation Within and Between Species

Sophie Matthews
Supervisor: Prof. Cathal Seoighe

Copy number variants (CNVs) are a significant source of genomic variation, often encompassing whole genes and thereby, potentially, altering gene dosage between individuals. These changes can influence disease susceptibility, with some variants conferring risk while others may have protective effects. Over evolutionary timescales, variation in gene copy number has long been studied as a source of phenotypic novelty and has also been proposed to contribute to inter-specific variation in disease risk. In mammals, for example, an increased copy number of tumour suppressor genes is hypothesised to mitigate cancer risk for large and long-lived species. In this thesis, we investigated the impact of changes in gene copy number at both scales: within human populations, to assess direct functional associations with disease, and across the mammalian phylogeny, to explore association with cancer-related phenotypes. Building on this work, we further investigated how molecular evolutionary rates coevolve with lifespan and body size, offering a complementary perspective on the genomic basis of cancer susceptibility and trait evolution. In Chapter 2, we examined the relationship between gene copy number variation and disease risk in humans. Motivated by the two-hit model of cancer causation, we hypothesised that copy number variants that increase the number of intact copies of tumour suppressor genes could reduce cancer susceptibility. We found suggestive evidence that supports this hypothesis, demonstrating that the presence of at least one duplication of a tumour suppressor gene harbouring a driver mutation is associated with reduced cancer incidence. We also identified association between gene deletions and cancer incidence. Additional genome-

wide analyses revealed further associations between gene copy number and other disease phenotypes, highlighting the impact of gene copy number on human disease.

In Chapter 3, we expanded this investigation across species, taking a comparative approach to assess the relationships between gene copy number and cancer risk, lifespan, or body size across mammals. While we did not find examples of genes for which the copy number was associated with lifespan or body size, we identified several genes for which copy number was associated with cancer prevalence across species. We also found several gene sets where aggregate copy number was linked to malignancy rate, with the strongest association identified for gene sets related to transforming growth factor-beta (TGF-β), a key regulator of cancer progression. These findings suggest that variation in gene copy number may help explain interspecies differences in cancer prevalence among mammals.

In Chapter 4, we shifted our focus from gene copy number to sequence evolution, investigating how molecular evolutionary rates coevolve with life-history traits such as lifespan and body size. We examined the methodological challenges involved in detecting gene–trait coevolution, comparing standard linear regression with phylogenetic approaches including RERconverge and Coevol. In addition, we developed a novel coevolutionary modelling approach which effectively controlled false positives in simulated datasets, but failed to do so in real sequence data, potentially due to incomplete correction for heterotachy. As an alternative, we developed and applied a phylogenetic generalized least squares (PGLS) approach to identify genes for which the non-synonymous substitution rate was accelerated or decelerated relative to the genomic background in a way that is correlated with life-history traits. Together, this thesis integrates different facets of gene evolution to advance our understanding of how genomic changes may influence cancer susceptibility and life-history traits across recent and evolutionary timescales.

A Multi-Scale Computational Analysis of the Tumor Microenvironment in Blood Cancers: From Single-Cell to Spatial Determinants of Therapy Response

Jacopo Umberto Verga
Supervisors: Dr. Eva Szegezdi, Dr. Pilib Ó Broin, Prof. Michael O'Dwyer

The tumor microenvironment (TME) in hematological malignancies like Multiple Myeloma (MM) is a major driver of immune evasion and therapeutic resistance, limiting the efficacy of even advanced immunotherapies. A key mechanism of this immune failure is the functional exhaustion of effector cells, such as Natural Killer (NK) cells, but the dynamic molecular and spatial programs governing this process remain poorly understood. This thesis addresses this gap by developing and applying a multi-scale computational framework, integrating single-cell RNA sequencing(scRNA-seq), novel network-based algorithms and spatially-resolved proteomics to deconstruct the TME.

First, the construction of a comprehensive single-cell atlas of the MM disease continuum, spanning from asymptomatic precursor conditions to relapsed/refractory disease, revealed that NK cell exhaustion is an early and progressively accumulating event in myelomagenesis. This analysis identified the key transcriptional signatures and intrinsic regulatory hubs, including the glucocorticoid receptor (NR3C1), that define the exhausted NK cell state.

To move from observation to intervention, a novel computational framework was developed, combining maximum-flow network theory and a multi-objective genetic algorithm to rationally prioritize therapeutic targets within the exhaustion signaling network. This framework was encapsulated into a reproducible 'Target-Rank' pipeline and applied in a comparative analysis, which demonstrated that the mechanisms of exhaustion are highly context-dependent, revealing divergent, disease-specific vulnerabilities in the chronic inflammatory TME of MM versus the acute metabolic TME of Acute Myeloid Leukemia (AML).

Finally, shifting from dissociated cells to intact

tissue, high-plex Imaging Mass Cytometry of patient bone marrow biopsies revealed that the pre-treatment spatial architecture is a powerful predictor of clinical outcomes. The enrichment of specific immunosuppressive or immune-inflamed "cellular neighborhoods" was significantly associated with Progression-Free Survival and the incidence of severe toxicities following Chimeric Antigen Receptor (CAR) T-cell therapy.

Collectively, this body of work demonstrates that the cellular composition, intracellular signaling networks and spatial organization of the TME are deterministic features of blood cancers that can be computationally modeled to identify novel therapeutic targets and predictive biomarkers. This provides a robust, multi-layered rationale for developing tailored, microenvironment-directed immunotherapies to improve patient outcomes.

Adverse Drug Reaction Profile Prediction: Denoising, Signal Enhancement and Missing Row Imputation

Yezhao Zhong
Supervisor: Haixuan Yang, Cathal Seoighe

Adverse Drug Reactions (ADRs) cause significant risks to human health, making it essential to identify potential ADRs in the early-stage of drug development. However, this process is costly and time-consuming. Therefore, developing advanced computational methods to predict ADR profiles is important. We developed a series of approaches to enhance ADR profile prediction across three main strategies. First, to address noise in imbalanced ADR data, we proposed a novel hybrid method, Kernel Regression (KR) on V (VKR), which combines Nonnegative Matrix Factorization (NMF) with KR on the drug-component matrix V derived from NMF. Second, we introduced Smoothed KR (SKR) to enhance signal detection for rare ADRs. Finally, we developed a missing row imputation strategy to enrich drug databases by imputing missing rows of features for non-overlapping drugs, increasing the dataset's breadth and predictive capability. Our three strategies yielded significant improvements. VKR demonstrated superior performance over existing methods on both single features and integrated features. SKR significantly improved prediction performance for rare ADRs, outperforming other methods in this challenging category, while improvements for common ADRs were more modest. The extended size of dataset further enhanced model performance with both the single features and the integrated features, indicating the benefit of the missing row imputation strategy. Together, these methods provide a robust framework for ADR prediction, addressing ADR data noise, rare ADR detection, and limitations of ADR data usage. VKR effectively reduces noise introduced by imbalanced data and the binary representation of drug-ADR data, while SKR addresses the gap in rare ADR prediction, which is crucial for real-world applications. Current models often overlook rare ADRs due to the dominance of common ADR signals. However, capturing these rare ADRs, which often lead to severe cases, is crucial for comprehensive drug safety assessment. The limited overlap of drugs across feature databases significantly reduces usable training data, making the missing row imputation strategy a valuable addition for preserving critical drug information and improving predictive outcomes.

5.2 Research Masters theses

Wavelet-Based Time-Frequency Fingerprinting for Feature Extraction of Traditional Irish Music

Noah Shore
Supervisor: Michael Mc Gettrick

This work presents a wavelet-based approach to time-frequency fingerprinting for time series feature extraction, with a focus on audio identification from live recordings of traditional Irish tunes. The challenges of identifying features in time-series data are addressed by employing a continuous wavelet transform to extract

spectral features and wavelet coherence analysis is used to compare recorded audio spectrograms to synthetically generated tunes. The synthetic tunes are derived from ABC notation, which is a common symbolic representation for Irish music. Experimental results demonstrate that the wavelet-based method can accurately and efficiently identify recorded tunes. This research study also details the performance of the wavelet coherence model, highlighting its strengths over other methods of time-frequency decomposition. Additionally, we discuss and deploy the model on several applications beyond music, including in EEG signal analysis and financial time series forecasting.

6 Staff profiles

Balbi,V.

Current research interests

My main research interests lie in the mechanics of soft materials, with a particular focus on the constitutive modelling of soft biological tissues. I develop nonlinear elastic and viscoelastic models that capture large deformations, time-dependent behaviour, and the influence of underlying microstructure (e.g. fibre reinforcement and heterogeneity). I am also interested in developing robust experimental protocols suitable for soft tissues to reliably characterise their complex mechanical response. An additional strand of my research focusses on auxetic behaviour in engineered materials and its potential applications. I am particularly interested in the onset and evolution of instabilities in soft materials (conventional and auxetic), such as pattern formation and wrinkling.

Recent publications

[1] G. Small, F. Ballatore, C. Giverso, V. Balbi. Modelling the non-linear viscoelastic behaviour of brain tissue in torsion. *Soft Matter*, 21 (26), 5268-5283, 2025.

[2] SP. Venkata, Y. Fu, H. Danesh, M. Destrade, V. Balbi. Wrinkling instability of 3D auxetic bilayers in tension. *J Mech Phys Solids*, 106301, 2024.

[3] V. Balbi, T. Shearer, W.J. Parnell. Tensor decomposition for modified quasi-linear viscoelastic models: Towards a fully nonlinear theory. *Math Mech Solids*, 29 (6), 1064-1088, 2024.

[4] G. Small, H. Berjamin, V. Balbi. Poynting effect in fluid-saturated poroelastic soft materials in torsion. *Int J NonLin Mech*, 159, 104601, 2024.

Research activities

- Invited Talk: Workshop on Mathematics and Mechanics of Biological Tissues, Padova - June 2025.
- Invited Talk: Euromech Colloqium on Stability and Bifurcation problems in nonlinear solid mechanics, Glasgow - April 2025.
- Supervision: Griffen Small successfully defended his thesis on "Modelling the Non-Linear Viscoelastic Behaviour of Brain Tissue in Torsion" in September 2025.
- I am a member of the International Society for Interaction of Mechan- ics and Mathematics.

Baykalov, Anton

Current research interests

In general, my research is in the field of Algebra, more specifically Group Theory. This includes questions about groups, their representations, and related combinatorial structures. Currently, I am working with Angela Carnevale and Tobias Rossmann on a project involving explicit computations of zeta functions of groups, algebras, and other algebraic structures. In particular, I am interested in using machine learning to assist with these computations.

Recent publications

[1] A.A. Baykalov, A. Devillers, C.E. Praeger, *Proper partial linear spaces affording imprimitive rank 3 automorphism groups.* J. Algebra 688 (2026), 454-526. DOI 10.1016/j.jalgebra.2025.09.020

[2] A.A. Baykalov, *Base sizes for finite unitary and symplectic groups with solvable stabilisers.* Internat. J. Algebra Comput. 35 (2025), no. 6, 823-908. DOI 10.1142/S0218196725500237

[3] A.A. Baykalov, *Base sizes for finite linear groups with solvable stabilisers.* J. Group Theory 28 (2025), no. 5, pp. 1003-1077. DOI 10.1515/jgth-2023-0125

Research activities

- In November 2025 I visited at SUSTech, Shenzhen, China for two weeks to work on a research project with Mikko Korhonen.
- I am currently organising *Machine Learning for Mathematics* reading group. Here we study ways in which machine learning can be used to solve (or inspire solutions to) problems in mathematics.
- I am co-organising (with A. Carnevale, J. Maglione and T. Rossmann) the graduate school *MathLearn* (3–5 June 2026), University of Galway.

Carnevale, Angela

Current research interests

My research is mainly in the field of algebraic and enumerative combinatorics. Two projects I am currently working on are: the study of a Bruhat order on Latin squares (with C. O'Brien); the study of a graph invariant arising from the enumeration of conjugacy classes of certain groups (with L. Prosperi and T. Rossmann). I am also part of the *MathLearn* research group based at the University of Galway, working on developing tools to apply machine learning to research in pure mathematics.

Recent publications

[1] A. Carnevale, V. D. Moustakas, and T. Rossmann, *Coloured shuffle compatibility, Hadamard products, and ask zeta functions.* Bull. London Math. Soc., 57 (2025), 2132–2154.

Research activities

- I was a CRM-Simons Scholar in Residence at LACIM and UQÀM (Montréal, Canada) during June–July 2025. I was awarded funding for my stay, and invited to give the Québec Mathematical Sciences Colloquium.
- Other invited talks: CMS Summer meeting 2025, Combinatorics section, Laval (Canada) ♦ INTRICATO 2026, Rome (Italy)
- I co-organised two instalments of *Symbolic Enumeration in Algebra* (with P. Lins, J. Maglione, T. Rossmann and C. Voll; 05/2025 and 12/2025)
- I am co-organising (with A. Baykalov, J. Maglione and T. Rossmann) the graduate school *MathLearn* (3–5 June 2026), University of Galway.
- I am co-organising (with R. Osburn, T. Rossmann, W. Veys and C. Voll) the *Sixth International Workshop on Zeta Functions in Algebra and Geometry*, 8–12 June 2026, University of Galway.
- I am a co-chair of the Organising Committee of FPSAC 2027 at the University of Galway.
- I currently supervise four PhD students: M. J. Maher (since 2022), Yannan Qian (co-supervised by M. Cavaleri, since 2024), M. Falciatore (co-supervised by T. Rossmann, since 2024), L. Prosperi (co-supervised by T. Rossmann, since 2024).

Chen, Fei (Jerry)

Current research interests

Mathematical modeling and its efficient solution methods, especially interested in multi-organ digital twin modeling that aims to enhance the utilization of novel approach methodologies to replace animal testing.

Recent publications

[1] H. Baza, F. Chen, T. Turiv, S. Sergij, O. Lavrentovich. Bend instabilities and topological turbulence in shear-aligned living liquid crystal. *Soft Matter*, 2026.

[2] A. Buccini, F. Chen, M. Pasha, L. Reichel. Krylov subspace based FISTA-type methods for linear discrete ill-posed problems. *Numerical Linear Algebra with Applications*, 32(1):e2610, 2025.

[3] A. Buccini, F. Chen, O. De la Cruz Cabrera, L. Reichel. Fast alternating fitting methods for trigonometric curves for large data sets. *Applied Numerical Mathematics*, 208:104–134, 2025.

Research activities

- A member of the STEP4NAM (Step up the use for new approach methodologies) research project, which aims to enhance the utilization of novel approach methodologies to replace animal testing.
- Convergence behavior of GMRES on Toeplitz systems.

Cruickshank, James

Current research interests

I am interested in combinatorics, algebra, topology, discrete geometry, commutative algebra, topological graph theory and homological algebra

Recent publications

[1] James Cruickshank, Sean Dewar, and Derek Kitson. Algebraic connectivity in normed spaces. *Linear Algebra and its Applications*, 739:10–42, 2026.

[2] James Cruickshank, Bill Jackson, Tibor Jordán, and Shin-ichi Tanigawa. Rigidity of graphs and frameworks: A matroid theoretic approach, 2025. available at https://arxiv.org/abs/2508.11636 To appear in: *Surveys in Combinatorics*

[3] James Cruickshank, Bill Jackson, and Shin-ichi Tanigawa. Volume rigidity of simplicial manifolds, 2025. available at https://arxiv.org/abs/2503.01647. To appear in: *Combinatorica*

[4] James Cruickshank, Bill Jackson, and Shin-ichi Tanigawa. Rigidity of symmetric simplicial complexes and the lower bound theorem. *Forum Math. Sigma*, 13:Paper No. e4, 22, 2025.

Research activities

- Co-organiser of "Rigid structures in algebraic combinatorics and algebraic statistics" May 18-22, 2026 at ICMS, Edinburgh.
- University of Galway co-PI for the COGENT MSCA Doctoral Network (€3.6M).
- Co-supervising (with Graham Ellis) 2 PhD students: Giulia Orrù and Frederik Wunden.
- Gave a talk at the DCUCD Discrete Maths Seminar, November 2025.
- External examiner for PhD exam at Lancaster University, June 2025.
- Invited speaker at Algebraic Combinatorics in Ancona, June 2025.
- Refereed 4 journal papers.
- 2 journal submissions currently under review.

Destrade, Michel

Current research interests

I work on the modelling of dielectric and magneto-elastic elastomers, on elastic waves travelling in soft tissues and in stressed solids, on the imaging of soft solids, and on the wrinkling of auxetic materials.

Recent publications

[1] M. Destrade, G. Zurlo, Nonlinear Elasticity. A Consise Masterclass for Undergraduates. Springer (2025).

[2] A. Nielsen, A. Barkley, N. Bazgan, A. Jaeger, M. Destrade. Mapping Frontier Research on the New European Bauhaus. European Research Council Executive Agency, Publications Office of the European Union, 2025.

[3] H. Berjamin, M. Destrade, G. Saccomandi. The KP equation of plane elastodynamics. SIAM Journal on Applied Mathematics. 25 (2025) 1458-1474.

[4] S. Pamulaparthi Venkata, Y.-X. Fu, Y.-B. Fu, H. Danesh, M. Destrade, V. Balbi. Wrinkling instability of 3D auxetic bilayers in tension. Journal of the Mechanics and Physics of Solids. 204 (2025) 106301.

[5] B. Wu, L. Kong, W. Chen, D. Riccobelli, M. Destrade. Electro-mechanical wrinkling of soft dielectric films bonded to hyperelastic substrates. Journal of the Mechanics and Physics of Solids. 209 (2026) 106490.

Research activities

- *Conferences/Seminars*: Brussels, Hangzhou, Limerick, Sichuan, Zhuji.
- *Graduate Course*: Zhejiang University, Hangzhou, China.
- *Appointments*: Seconded National Expert at the European Research Council in Brussels; Editorial Board Member: Proceedings of the Royal Society A, Mechanics of Soft Solids; Adjunct Professor at University College Dublin and Zhejiang University; Directeur de Recherche at Institut d'Alembert, CNRS, Paris, France (on leave); Member of the International Brain Mechanics and Trauma Lab (Oxford).

Ferguson, John.

Current research interests

Bayesian statistical modelling, causal inference, statistical approaches in genetics and bioinformatics and medical statistics. Recently, I have spent time thinking about estimating attributable fractions with survey data, correcting for selection bias in case only analyses of disease severity and influence function-based approaches in medical statistics.

Recent publications

[1] A. Forde, G. Hemani, and J. Ferguson. Simulated sample splitting approach to address biases due to instrument selection and participant overlap in two-sample Mendelian Randomization studies. *bioRxiv*, pages 2025–11, 2025.

[2] C. MacDermott, C. J. Scarrott, and J. Ferguson. Bayes-ically fair: A Bayesian Ranking of the Olympic Medal Table. *arXiv preprint arXiv:2510.14723*, 2025.

[3] J. Ferguson. Calculation of lifetime relative risks from summary cohort data and application to calculation of attributable fractions. *Ann. Epidemiol.*, 102:102–113, 2025.

[4] C. Reddin, G. J. Hankey, J. Ferguson, et al. Influence of age on the association of vascular risk factors with acute stroke (INTERSTROKE): a case–control study. *Lancet Healthy Longev.*, 6(6), 2025.

[5] P. Gillespie, R. Mahon, C. Newman, A. Alvarez-Iglesias, J. Ferguson, et al. Cost effectiveness of early metformin in addition to usual care in the reduction of gestational diabetes mellitus effects (EMERGE)—A randomised placebo-controlled clinical trial. *Diabetic Medicine*, 42(6):e70036, 2025.

Research activities

- Associate Editor for JRSS Series C
- PhD external examiner at the University of Bristol, December 2025
- Invited talks at the Karolinska Institutet (Simulated Sample Splitting: MR-SIMSS) and the Public Health Agency of Sweden (Advice for estimating PAF with survey data).

- Member of the International Society of Clinical Biostatistics National Groups Subcommittee
- Currently supervising 2 PhD students (one as primary supervisor)

Hegarty, Fintan

Current research interests

Is í an phríomhsprioc atá agam ná an Ghaeilge a chur chun cinn i réimsí STEM, agus suim agam sna bealaí ar fad é sin a chur i gcrích, ach tá spéis ar leith agam sna réimsí taighde seo a leanas:

- Oideachas sna teangacha mionlaithe; go háirithe an Ghaelollscolaíocht.
- Úsáid na teicneolaíochta ó thaobh teagaisc agus measúnú de, agus na féidearthachtaí atá ann le haghaidh cúrsaí idirdhisciplíneacha.
- Cúrsaí inbhuanaitheachta agus an mhatamaitic a bhaineann leo.

Research activities

- Maoiniú Discover €268,000 faighte ó Thaighde Éireann chun clár náisiúnta tograí chun STEM as Gaeilge a chur chun cinn a bhainistiú.
- Lá na Matamaitice as Gaeilge reáchtáilte mar chuid de MathsWeek.
- Sraith seimeanár "Léachtaí le linn Lóin" reáchtáilte.
- I gcomhar le C. Seoighe, cruinniú ar an nGaelollscolaíocht le Coiste na Gaeilge, na Gaeltachta, agus Phobal Labhartha na Gaeilge sa Dáil.
- Aoichainteanna: le haghaidh EngineersIreland mar chuid d'imeacht Innealtóireacht agus Inbhuanaitheacht, agus cás-staidéar le haghaidh an HEA Educational for Sustainable Development Spotlight Series.
- Cás-staidéar foilsithe le A. Carnevale mar chuid den HEA ESD Spotlight Series 2025 Case Studies Compendium.
- Tuairisc ar "Gender Balance among Staff in Irish Mathematical Sciences Departments" le R. Hill, N. Madden, agus P. Phelan curtha faoi bhráid an IMS Bulletin.

Herrera-Alsina, Leonel

Current research interests

I am mostly interested in exploring the processes driving the changes in accumulation and spatial distribution of species over time. In particular I look at how phylogenetic trees inform us about those processes. To answer some of my research questions, I develop the necessary computing tools. These approaches are based either on likelihood calculations or forward simulations. All realms of life are fascinating to me: my research interests includes birds, bats, palm trees, archeobacteria, butterflies, damselflies, amphipods, cichlids, and water beetles. I have a growing interest in building and programming electronics to collect data or tackle problems in our communities.

Research outputs

Below, three Papers published with my new University of Galway affiliation.

Recent publications

[1] Silva C., Cavender-Bares J., Simon M., Herrera-Alsina L., Silva V., Gagnon E., Oliveira R., and Pinto-Ledezma J. Evolutionary and environmental drivers of deciduousness in a legume genus. *New Phytologist*, In press, 2026.

[2] Osborne O., Wood D., Dobreva M., Dunning L. T., Tucker R., Coates S. Pellicer J., Holmber J,Algar A. C., Bocedi G., Gubry-Rangin C., Herrera Alsina L., Juliandi B., Lancaster L., Touzet P.,

Travis J., and Papadopulos A. High-quality genome assembly and linkage map for a rapidly evolving plant species: Silene uniflora. *G3: Genes, Genomes, Genetics*, 16(3), 2026.

[3] Xie H., Wang Y., Zhang L., Li Y., Cheng R., Liang X., Shrestha N., Herrera-Alsina L., Chang H., Wong K.M., Keming Y., Chen X., Trad R. J., Neves D., Dimitrov D., Zhao P., Xu X., and Liu J. Why Are Magnoliaceae So Diverse in the Tropics? Disentangling the Roles of Diversification and Time-for-Speciation Effects. *Journal of Systematics and Evolution*, https://doi.org/10.1111/jse.70039, 2026.

Research activities

- Very excited to join the School and University.

Holian, Emma

Current research interests

Modelling Composition Response data, influencing factors in blood clot composition via Dirichlet Regression. Prognostic models in Breast Cancer, modelling treatment outcome on longitudinal biomarkers, variable selection in survival models. Statistical methods in Genomics Data Science, change point status multi-response modelling in Copy Number Alterations. Classification and cluster analysis of longitudinal data profiles via mixture modelling, Regression Cluster Model (RCM). Statistical challenges in environmental impact studies and climate data, challenges of left-censored distributions in groundwater data. Pedagogy in Mathematical and Statistical learning and public engagement.

Recent publications

[1] M. Davey, *et al.* Evaluating the Role of Circulating MicroRNAs in Predicting Long-Term Survival Outcomes in Breast Cancer: A Prospective, Multicenter Clinical Trial. *Journal of the American College of Surgeons*, 2023. 236(2), 317-327.

[2] L. King, A. Flaus, E. Holian, A.Golden. Survival Outcomes are Associated with Genomic Instability in Luminal Breast Cancers. *Plos One*, 2021.

[3] E. McGrory, E. Holian, L. Morrison. Assessment of groundwater processes using censored data analysis incorporating non-detect chemical, physical, and biological data. *Journal Of Contaminant Hydrology*, 2020.

Research activities

- *Modeling composition response data with application to clot composition observed for Acute Ischemic Stroke (AIS) patients*, a collaboration: Prof Karen Doyle, Department of Physiology, School of Medicine and Centre for Research in Medical Devices (CÚRAM). Post-doc researcher: Dr Amanda Forde, Ph.D Student: Malak Almutairi.

- A Contextualised Review of the Role that Sense of Belonging and Identity plays in Academic Success and Persistence within Science programmes at University of Galway, *Academic Practice thesis 2026*.

- *Figuring out Y (FOY)*, outreach and research initiative:. Collaborators: Dr Mairead Greene, CELT; Dr Mária Slavíčková, Comenius University in Bratislava, Slovakia. ENLIGHT PLUS Award €5,000 November 2024.

Howard, Mark

Current research interests

I'm primarily interested in quantum information theory, specifically:

- Stabilizer formalism (generalization to d-level systems, quantum error-correcting codes, Gottesman-Knill theorem)

- Clifford group and classical simulability of restricted quantum circuits
- Discrete Wigner functions (negative quasiprobabilities, relationship with GK theorem)
- Magic state distillation and quantum fault tolerance more generally
- Nonlocality & Contextuality, Mutually unbiased bases, SIC-POVMs, foundations of quantum theory

Recent publications

[1] Aisling Mac Aree and Mark Howard. Exhaustive Optimisation of Automorphism Groups for Stabiliser Codes. https://arxiv.org/abs/2604.01282, 2026.

Research activities

- Invited Keynote "Overview of Stabilizers and Magic", Mathematical Foundations of Quantum Advantage SFU Vancouver.
- Ph.D. Examiner for Université Bourgogne Europe and Sorbonne Université - LIP6, Paris
- Supervising 2 PhD students since Sept 2022: Aisling MacAree (Royal Society and COSE funded) and Mark Ryder (IRC funded) working on Quantum Error Correction & Fault Tolerance.

Jermiin, Lars S.

Current Research Interests

My research falls under the fields of molecular phylogenetics and evolution, bioinformatics, and comparative genomics. It includes method development as well as analyses of real data. Currently, the focus is on:

- **Directional Mutation Pressure** — DMP is a term describing non-random patterns of mutation in DNA. Software to obtain estimates of different types of DMP from real data has been developed and is now being used to study animal mitochondrial genomes (with Mohit Rana, John Ferguson & Dennis Lavrov), coronavirus genomes (with Clodagh Gormley & Matthew Dorman), and bacterial genomes (with Matthew Dorman).

- **Accuracy of Multiple Sequence Alignments** — Accurate estimates of MSAs are needed in molecular phylogenetics and comparative genomics. Currently, the accuracy of MSA methods is measured using distances between inferred MSAs and assumed-to-be-correct MSAs. However, the distances used may not be suitable, and the assumed-to-be-correct MSAs may not be so either. In this research, the suitability of different distances for comparing MSAs is assessed (with Tanya Golubchik & James Cruickshank), and the best distances are applied to data sets that: (1) mimic alternatively-spliced mRNAs, or (2) evolved over a tree (with Moya Caulfield, Rachel Keane, Divyansh Gupta, Angela McGaughran & Tanya Golubchik).

- **A Minimum Reporting Standard for multi-gene MSAs** — A MRS for MSAs improves transparency, reproducibility, and accountability of research when MSAs are used. An MRS for multi-gene MSAs has been accepted for publication [1].

- **Model selection** — Model-based phylogenetics plays a key role in the analysis of genomic data [2]. Typically, an optimal model of sequence evolution is needed during such analysis. Usually, this model is inferred from the data under stationary, reversible, and homogeneous (SRH) evolutionary conditions [3]. In this research, we develop new statistical procedures to test the hypothesis of evolution under SRH conditions (with John Robinson & Vivek Jayaswal).

- **Phylogenetic estimation** — Popular model-based molecular phylogenetic methods may return biased estimates if the data evolved under non-SRH conditions. To counter this problem, I am developed new phylogenetic methods [4, 5]. However, for various reasons neither of these methods are widely used. Current research aims to make one method [4] more flexible and faster (with Mohit Rana, Thomas Wong, John Robinson, Vivek Jayaswal & John Ferguson). More general phylogenetic methods may also be implemented.

- **Origin and evolution of honeybees in Ireland** — Honeybees are pollinators and producers of wax and honey. The Irish honeybee is important because it is well adapted to the Irish climate and ecosystems. Sadly, it is at risk of extinction due to honeybees from the south of Europe. Apart from some morphological differences, it is not known what distinguishes the Irish honeybee from other honeybees. To solve this issue, work is under way to find suitable diagnostic genetic markers. Large amounts DNA are emerging, and bioinformatics tools are being re-purposed to identify such genetic markers (with Marissa Fernandez, Stephen Smith & Grace McCormack).

- **Evolution of plants** — Plants have played a key role on our planet for at least 600 million years. The evolution of plants is of scientific and general interest, and chloroplast genomic data play a central role in this research. Early work of these data has shown that they are unlikely to have evolved under SRH conditions, so a phylogenetic study of 99 chloroplast genomes — ranging from plants to algae — was begun, using HAL-HAS [4]. The work is almost done (with Thomas Wong).

Recent publications

[1] L.S. Jermiin, D., T.K.F. Wong, S. Kalyaanamoorthy, K. Meuseman, D.K. Yeates. Improving the transparency, reproducibility, and accountability of multiple sequence alignment. *Meth. Mol. Biol*, ??:???–???, 2026 (**invited**).

[2] L.S. Jermiin, D., R.A. Catullo, B.R. Holland. A new phylogenetic protocol: Dealing with model misspecification and confirmation bias in molecular phylogenetics. *NAR Genom. Bioinform* 2, lqaa041, 2020.

[3] S. Kalyaanamoorthy, B.Q. Minh, T.K.F. Wong, A. von Haeseler, L.S. Jermiin. ModelFinder: Fast model selection for accurate phylogenetic estimates. *Nature Meth.*, 14, 587–589, 2017.

[4] V. Jayaswal, T.K.F. Wong, J. Robinson, L. Poladian, L.S. Jermiin. Mixture models of nucleotide sequence evolution that account for heterogeneity in the substitution process across sites and across lineages. *Syst. Biol.*, 63, 726–742, 2014.

[5] V. Vera-Ruiz, J. Robinson, L.S. Jermiin. A likelihood-ratio test for lumpability of phylogenetic data: Is the Markovian property of an evolutionary process retained in recoded DNA? *Syst. Biol.*, 71, 660–672, 2022.

Lansdown, Jesse

Current research interests

My research is mainly in algebraic combinatorics, in particular the theory of association schemes. My interests also include permutation groups, finite geometry, graph theory, designs and codes, and combinatorial computing.

Recent publications

[1] Bamberg, J., Lansdown, J. The synchronisation hierarchy via coherent configurations. *Linear Algebra and its Applications*, 735, 203-221, 2026.

[2] Heering, P., Lansdown, J., Metsch, K. Maximum Erdős-Ko-Rado sets of chambers and their antidesigns in vector-spaces of even dimension. *Journal of Combinatorial Theory, Series A*, 217, 2026.

[3] Lansdown, J., Martin, W. J. Rational Delsarte designs and Galois fusions of association schemes. *Canadian Mathematical Bulletin*, 1–20, 2025.

Research activities

- Invited seminar talk at Queen's University Belfast, February 2026
- Invited seminar talk at the "Algebraic Graph Theory Seminar", University of Waterloo (online), February 2026
- Invited conference talk at "Algebraic Combinatorics Mini-Workshop: Honoring the Mathematical Journey of Professor Akihiro Munemasa", Sendai, Japan, March 2026
- Research visit Tohoku University, March/April 2026

Madden, Niall

Current research interests

My research is in numerical analysis, mainly finite element methods for partial differential equations, and numerical linear algebra. I work on their mathematical properties of these methods, their implementation (especially on HPC) and their applications to problems in engineering and medicine.

Research outputs

Please list up to five of your recent (most significant) publications or provide such details in the bibliography below.

[1] Scott P. MacLachlan, Niall Madden, Thái Anh Nhan. A Boundary-Layer Preconditioner for Singularly Perturbed Convection Diffusion. SIAM J. Matrix Anal. Appl. 43 (2022), no. 2, 561–583. .

[2] R. Hill and **N. Madden**. Layer-adapted meshes for singularly perturbed problems via mesh partial differential equations and a posteriori information. arXiv:2311.01274. 2023.

[3] G. Saha, N. Poddar, K.K. Mondal and **N. Madden** Hydrodynamic dispersion of volatile contaminant in an open channel flow using a fitted operator approach. *Proc ICNDA 2024*. Springer Proceedings in Physics. 2024.

[4] F. Hegarty, R. Hill, N. Madden and P. Phelan. Gender Balance among Staff in Irish Mathematical Sciences Departments, 2020–2025. *Under Review* (2026).

Research activities

- I hosted the 21st Workshop on Numerical Methods for Problems with Layer Phenomena here at University of Galway, 24-25 April 2025.
- I presented at the Computational Mathematics and Applications Seminar, Mathematical Institute, University of Oxford, 4 Dec 2025.
- I gave conference and workshop presentations at the Layer Phenomena Workshop (Galway) in April 2025; the 4th Irish Linear Algebra & Matrix Theory Meeting, MIC, April 2025; the Irish SIAM Student Chapter Conference, Limerick, May 2025; 2nd European Fluid Dynamics Conference, UCD, August 2025; 1st Irish Fluid Dynamics Meeting, University College Dublin, January 2026.
- Team members this year include: Fei Jerry Chen (Interreg funded PDR) who is working on developing digital twins of ICU patients; Nanda Poddar (RI funded PDR), who left for a permanent posted in Chennai in December; Alexander Shchepetkin (Marine Institute funded PDR, with Indiana Olbert as lead PI) with whom I worked on widely-reported project on storm surges; Fintan Hegarty

(HEA funded PDR), who worked with me for two months on a gender equality project, Sean Tobin (RI funded PGR) who is working on FEMs in aortic domains; and Jekaterina Mosalska (PGR) who is working on linear solvers for convection-diffusion problems.

Maglione, Joshua

Current research interests

My research interests are in computational algebra, asymptotic group theory, and algebraic combinatorics. I develop efficient algorithms to aid in various isomorphism problems. The Group Isomorphism Problem is closely related to the Tensor Isomorphism Problem, so I am also interested in tensors, their structure, and their applications to algebra. I also apply combinatorial tools to understand and compute certain p-adic integrals com- ing from zeta functions of groups and rings and Igusa's zeta function. These can be used to better understand enumerative aspects of groups, rings, and algebras such as the number of finite-index subgroups of a group.

Recent publications

[1] Claudia Alfes, Joshua Maglione, Christopher Voll, Symplectic Hecke eigenbases from Ehrhart polynomials, preprint, `arXiv:2507.11728`.

[2] Peter A. Brooksbank, Heiko Dietrich, Joshua Maglione, Eamonn A. O'Brien, James B. Wilson, Categorification of characteristic structures, *Forum Math. Sigma* **14** (2026), Paper No. e13, 46 pp.

[3] Joshua Maglione and Mima Stanojkovski, Smooth cuboids in group theory, *Algebra Number Theory* **19** (2025), no. 5, 967–1006.

[4] Joshua Maglione and Christopher Voll, Hall-Littlewood polynomials, affine Schubert series, and lattice enumeration, *Sém. Lothar. Combin.* **93B** (2025), Art. 22, 12 pp.

Research activities

- Invited talks: MFO Workshop *Computational Group Theory*, MFO Workshop *Cohomological methods in automorphic forms and enumerative algebra*, *SPP Combinatorial Synergies: Annual conference* at Leibniz University Hannover, *17th International Symposium of Natural Sciences* at Incheon National University, *Boole Colloquium in Mathematics* at UCC.
- Presented a poster at FPSAC 2026 at Hokkaido University in Japan.
- Conferences organized: *Groups in Galway* (May 2025), *Symbolic Enumeration in Algebra* (May & December 2025)

McCluskey, Aisling

Current research interests

My current research interests revolve around generalising the classic notion of betweenness in Euclidean geometry to the realm of metric spaces. Betweenness relations arising in connection with metric spaces include the usual metric betweenness of Karl Menger, as well as versions of betweenness (for example, ultrametric spaces) that make sense in light of generalized triangle (in)equalities. An interesting and emerging concept is that of 'straightenable' metrics, which demands that intervals (in the context of betweenness) have a characteristic reflective of geometric straightness.
I am also interested in the scholarship of teaching and learning (SoTL) in the context of university mathematics education. A current focus is on assessment strategy that provokes and promotes deep and engaged learning. A further interest is in 'educating the educators' in the context of initial teacher education at post-primary level.

Recent publications

[1] A. McCluskey, J. Grant McLoughlin, K. O'Sullivan. The Junior Mathematics Enrichment programme at Galway, Ireland

International Perspectives on Mathematics Outreach, Research in Mathematics Education series, UK: Emerald publishing, March 2026

Research activities

- Galway Topology Colloquium at University of Birmingham July 20 - 22, 2025
- Set Theory and Topology in Messina conference at University of Messina Sept 3 - 6, 2025

Mc Gettrick, Michael

Current research interests

Quantum algorithms, quantum games, quantum walks; applications of quantum algorithms to (music) composition; information content in and structure of music.

Recent publications

[1] M. McGettrick and P. McGettrick The Kolmogorov Complexity of Traditional Irish Dance Music. *Computer Music Journal*, 48 (4): 65–72 2024.

Research activities

- Galway partner in the ENLIGHT+ Quantum for Biomedicine initiative (Q-Bio), 2026.
- Member of the Irish Mathematical Society, the Association for Computing Machinery (USA) and the Peer Review College of the Engineering and Physical Sciences Research Council (UK).
- Reviewer for GECCO 2026 (The Genetic and Evolutionary Computation Conference).
- "Quantum walks on graphs", invited talk at the Université du Littoral Côte d'Opale (Calais, France), June 2025.
- One PhD student (Ian Craig) and one research masters student (Noah Shore).

Newell, John

Current research interests

My current research interests are in the development and application of statistical methods in clinical research, health data science, sports science and Translational Statistics.

Recent publications

[1] Roshan D, Das K, Daniels D, Pedlar CR, Catterson P, Newell J. Adaptive reference ranges: From A to Z. *PLoS One,* , 20(5), (2025).

[2] A Alsahafi, J Newell, M Newell, T Kropmans. A Comparative Analysis of Objective Structured Clinical Examination (OSCE) Observed Scores and Global Rating Scores using a Novel Approac. *European Journal of Education and Pedagogy*, (2025).

[3] Daniels, D., Roshan, D., Lewis, N. A., Newell, J., Bruinvels, G., Catterson, P., Pedlar, C. R. Early warning system for player recovery? A series of case studies illustrating the application of individualised adaptive reference ranges in the longitudinal blood monitoring of English Premier League soccer players. *Biomarkers*, 30(3), 232–245, (2025).

Research activities

- Grants:

  CURAM (funded PI with one 1 Postdoctoral Researcher), Insight (funded PI with one 1 Postdoctoral Researcher), HRB Primary Care Clinical Trials Network Ireland (Biostatistician).

- Postgraduates:

  Current Postgraduates: 1 PhD student, 3 co-supervised PhD students in the University of Limerick.

- Software:

R package 'DynNom' for generating Dynamic Nomograms, 93,000+ downloads to date.

- Invited Talks:

  'A Conversation around Data Equity in Professional Sports'. NBA Performance Summit, Malaga, July 2025

  'Are we meeting the challenge? [in memory of Dr. Kathleen O'Sullivan]'. Conference on Applied Statistics in Ireland, Galway, May 2025.

Fitz-Simon, Nicola.

Current research interests

I am an applied statistician with my primary research interest being statistical causal inference, especially as applied to observational studies on human health. I also have research interests in the intersection between infectious disease modelling and causal inference. I have developed a recent research interest in small area estimation using sparse data from complex survey designs, and interactive visualisations to communicate results to stakeholders.

Research activities

- Ghana and Uganda D-Card Project: Small area estimation of key indicators of diabetes and hypertension. Funded by the World Diabetes Foundation, in collaboration with the World Health Organization.
- Reports submitted to WHO: Technical Reports on methodology and full and summary results for each country and Shiny App currently in use by local stakeholders in Ghana and to be rolled out in Uganda.
- Fitz-Simon N, Malekpour M, Tapela N, Agboyigbor K, Farzadfar F. Small area estimation of risk factors for diabetes in Ghana and Uganda. Paper under review by WHO collaborators for submission to Lancet Public Health.
- Invited speaker, Women in the Mathematical Sciences Day, 12th May 2025, Galway: *Using statistical models for small area estimation*
- Conference presentation, Nordic-Baltic Biometric Conference, June 9-12 2025, Oslo. *A hierarchical bivariate logistic model for estimation of small-area prevalences*
- Fellow of the Royal Statistical Society (past secretary of the RSS Medical Section), Member of the Irish Statistical Association, Member of the International Society for Clinical Biostatistics.

Ó Broin, Pilib

Current research interests

My research interests lie primarily in clinical/translational bioinformatics with a particular focus on the development and application of machine learning methods for genomic data in the cancer, immunology, and neuroscience domains.

Research outputs

[1] 'An ELIXIR scoping review on domain-specific evaluation metrics for synthetic data in life sciences'. Styliani-Christina Fragkouli, Somya Iqbal, Lisa Crossman, Barbara Gravel, Nagat Masued, Mark Onders, Devesh Haseja, Alex Stikkelman, Alfonso Valencia, Tom Lenaerts, Fotis Psomopoulos, Pilib Ó Broin, Núria Queralt-Rosinach, Davide Cirillo. *NAR Genomics and Bioinformatics* 8 (1), (2026)

[2] 'Deriving Mendelian randomization-based causal networks of brain imaging phenotypes and bipolar disorder'. Shane O'Connell, Brielin C Brown, Dara M Cannon, Pilib Ó Broin, Nadine Parker, Dag Alnæs, Lars T Westlye, Saikat Banerjee, Leila Nabulsi, Emma Corley, Ole A Andreassen, David A

Knowles, Niamh Mullins. *Biological Psychiatry: Cognitive Neuroscience and Neuroimaging* 11 (1), (2026)

[3] 'Aurantio-obtusin modulates Wilms Tumour 1 within the breast tumour microenvironment reducing immunosuppression and tumour growth'. Rui Li, Dómhnall J O'Connor, Barry Digby, Pilib Ó Broin, Xiao Hu, Ning Ge, Paul G Loftus, Vatsal Kumar, Eoin McEvoy, Stephen J Elliman, Michael J Kerin, Laura R Barkley. *Cell Communication and Signaling* 23 (1), (2025)

[4] 'Deep feature batch correction using ComBat for machine learning applications in computational pathology'. P Murchan, P Ó Broin, AM Baird, O Sheils, SP Finn. *Journal of Pathology Informatics* 15 (3), (2024)

Research activities

- My research group this year included: 3 postdoctoral researchers, 7 PhD students, and 1 research assistant. 2 PhD students (Jacopo Umberto Verga and Karen Guerrero-Vázquez) defended their theses.
- Active Research funding: CRT in Genomics Data Science, SFI ADAPT Centre, SFI Frontiers for the Future, Disruptive Technologies Innovation Fund, HEA North-South Research Programme.
- External activities: Executive board member, Translational Medicine Alliance Ireland (TMAI); External advisory board, SEARCH (IHI) project; Management committee member, COST action CA22103; Senior Council, Irish Association for Cancer Research; Organizing committee, IACR 2026, Galway; Deputy Head-of-Node, ELIXIR Ireland.
- Memberships: Irish & European Association for Cancer Research (IACR & EACR); International Society for Computational Biology (ISCB); Irish & European Society for Human Genetics (ISHG & ESHG); Marie Curie Alumni Association (MCAA).

O'Leary, Neil

Current research interests

A wide range of methodological interests; in particular the design and analysis of clinical trials, multilevel modelling of clustered and longitudinal data, along with other applied research interests in causal inference in observational studies, survey techniques and missing data.

Recent publications

[1] E. Woelders, Y. Onuma, K. Ninomiya, N. O'Leary, *et al.* Parsimonious versus extensive bleeding score: can we simplify risk stratification after percutaneous coronary intervention and reduce bleeding events by de-escalation of the antiplatelet strategy? *Open Heart*, 12:e003083, 2025.

[2] S. Kageyama, N. O'Leary, P. Revaiah, K. Ninomiya, S. Masuda, *et al.* Quantitative flow ratio for the prediction of coronary events after percutaneous coronary intervention. *EuroIntervention*, 20(1):104, 2024.

[3] H. Hara, N. O'Leary, M. Ono, Y. Onuma, P.W. Serruys. A comparison of risk prediction models for patients with acute coronary syndromes. *EuroIntervention*, 17(16):1362, 2022.

[4] K. Ninomiya, S. Kageyama, H. Shiomi, N. Kotoku, S. Masuda, P.C. Revaiah, *et al.* Can machine learning aid the selection of percutaneous vs surgical revascularization? *Journal of the American College of Cardiology*, 82(22):2113, 2023.

[5] H. Hara, N. O'Leary, M. Ono, Y. Onuma, P.W. Serruys. A comparison of risk prediction models for patients with acute coronary syndromes. *EuroIntervention*, 17(16):1362, 2022.

Research activities

- PhD supervision: Nirdesh Bakshi, *Statistical Methods for Missing Data in Randomised Controlled Trials.*
- Collaboration with the CORRIB Research Center for Advanced Imaging and Core laboratory, the Health Research Board Trials Methodology Research Network and the Irish National Survey of Sexual Health research team.
- Co-Investigator on Horizon Europe 'Health' 2026 grant application on chronic pain management in young people.
- Reviewer for *NIHR Journals Library Health Technology Assessments*, for *BMJ Open* and for *Dutch Heart Foundation Fellowship Awards.*

Pfeiffer, Götz

Current research interests

Reflection groups, hyperplane arrangements, Orlik-Solomon algebras, Hecke algebras, Chow rings of matroids, equivariant log concavity, formal concept analysis.

Recent publications

[1] J. Matthew Douglass, Götz Pfeiffer and Gerhard Röhrle. Parabolic Normalizers in Finite Coxeter Groups as Subdirect Products. 25 pages, to appear in *J. Group Theory.*

[2] J. Matthew Douglass, Götz Pfeiffer and Gerhard Röhrle. Invariants and semi-invariants in the cohomology of the complement of a reflection arrangement. *Math. Ann.* **392** (2025), 2803–2851.

[3] Koushik Paul and Götz Pfeiffer. Computing Young's Natural Representations for Generalized Symmetric Groups. *J. Algebra*, 25 pages.

[4] Eirini Chavli and Götz Pfeiffer. The BMM Symmetrising Trace Conjecture for Families of Complex Reflection Groups of Rank Two. arXiv:2503.05259

Research activities

- April 23–24, 2025: Research Visit Ruhr University Bochum, Germany.
- June 30 – July 4, 2025: Lecture Course at Summer School "Algebra: classic topics and current trends", National Technical University of Athens, Greece.
- July 14–18, 2025: Applications of Computer Algebra, Heraklion, Greece.
- August 28–29: Invited Talk at IMS September Meeting, Maynooth University.
- September 19, 2025: Rapporteur for PhD Defense at Université de Tours, France.
- December 8–12, 2025: Research Visit Ruhr University Bochum, Germany.
- Papers referreed: 8.
- MathSciNet Reviews: 6.
- Editorial Board Member: Journal of Symbolic Computation; Mathematical Proceedings of the Royal Irish Academy.
- Member: Irish Mathematical Society; American Mathematical Society.

Quinlan, Rachel

Current research interests

My primary research interest is in combinatorial and algebraic aspects of matrix theory, especially in rank properties for matrix subspaces, the combinatorics of alternating sign matrices, and connections between matrices and graphs.

Another area of activity is in the relationship between mathematics and the visual arts, especially tessellation origami. I am interested in the effectiveness of art as a means of mathematical expression and communication, and also mathematical discovery.

Research outputs

[1] Cian O'Brien and Rachel Quinlan, *Groups of singular alternating sign matrices*, Electronic Journal of Linear Algebra, Vol. 41, 288–303, 2025.

[2] Rachel Quinlan, *A tale of three p4g origami models and local frieze symmetry*, Proceedings of the 2025 Bridges Conference, 2025.

[3] Dana Saleh and Rachel Quinlan, *2-uniform covering groups of elementary abelian 2-groups*, Communications in Algebra, Vol. 52, no. 2. 630-656, 2024.

[4] Cian O'Brien and Rachel Quinlan. *Alternating sign matrices of finite multiplicative order*, Linear Algebra and its Applications, Vol. 631, 332-358, 2022.

[5] Rachel Quinlan, Moumita Shau and Fernando Szechtman. *Linear diophantine equations in several variables*, Linear Algebra and its Applications, Vol. 630, 67–90, 2022.

Research activities

- My PhD student Badriah Safarji (co-supervised with Cian O'Brien) successfully finished in January 2026. Currently supervising the PhD research of Colin McDonagh.
- Presentations in 2025: 26th Conference of the International Linear Algebra Society (Kaohsiung, two talks), Bridges 2025 (Eindhoven), 4th Irish Linear Algebra and Matrix Theory Meeting (Limerick).
- Local chairperson of the Bridges Conference on Mathematics and the Arts, which will be hosted by the University of Galway in August 2026.
- Current president of the Irish Mathematical Society.

Roshan, Davood

Current research interests

My primary research interest is in the longitudinal analysis of clinical biomarkers and outcomes. In particular, I focus on developing statistical models and algorithms to generate adaptive reference regions from high-dimensional streaming data generated by medical devices. The development of real-time early warning systems is a key enabler for enhanced patient monitoring and improved clinical care. More recently, my research has expanded to include image and signal processing, with a focus on the analysis of multimodal biomedical data for prediction, diagnosis, and clinical decision support across a range of application areas. I also have a particular interest in translational statistics, data visualisation, and data science, with a focus on developing predictive tools for real-world clinical applications.

Research outputs

- Lal B, Abolghasemi V, Gravina R, O'Keeffe D, Roshan D. Compressed learning for real-time ECG signals classification. IEEE Sensors Journal. 2026 Feb 6. https://doi.org/10.1109/JSEN.2026.3660078
- Ivory JD, Sezgin D, Coutts PM, Roshan D, Hobbs CM, Soriano JV, O'gara JP, Gallagher D, Gethin G. Clinical Signs and Symptoms of Biofilm in Chronic Wounds. What Do Practitioners Think? Consensus Through an Electronic Delphi Survey. International Wound Journal. 2025 Nov;22(11):e70771. https://doi.org/10.1111/iwj.70771
- Pazhuheian P, Newell J, and Roshan D. Covariate-adjusted adaptive reference ranges in longitudinal monitoring of clinical biomarkers. The 39th International Workshop on Statistical Modelling, 2025.
- Shah, M. H., Roshan, D., Pugh, J., Murray, J., Fuller, C., Kung, S., Reville, A., O'Connor, S. (2025). Personalised Cognitive Monitoring in Jockeys

Through Adaptive Reference Ranges. International Conference on Health, Safety and Welfare of Jockeys (ICHSWJ), Hong Kong.

- Shah, M. H., Roshan, D., Pugh, J., Murray, J., Fuller, C., Kung, S., Reville, A.,O'Connor, S. (2025). Improving Concussion Safety in Jockeys Through Regression-Based Norms for Pen-and-Paper Assessments. International Conference on Health, Safety and Welfare of Jockeys (ICHSWJ), Hong Kong.

- Shah, M. H., Roshan, D., Pugh, J., Murray, J., Fuller, C., Kung, S., Reville, A., O'Connor, S. (2025). Jockey-Specific IMPACT Norms: Strengthening Concussion Protocols for Safer Racing. International Conference on Health, Safety and Welfare of Jockeys (ICHSWJ), Hong Kong.

Research activities

- Grants (successful):
  - Hardiman Scholarship (€124,000), (PI): to supervise a PhD student in Biostatistics, University of Galway, Ireland.
  - Funded Investigator at CÚRAM.
- Grants (pending):
  - HRB Secondary Data Analysis Projects, *Transforming Longitudinal Care (TLC): Enhancing Blood Pressure Monitoring in Healthcare Settings* (€346,855.00, PI).
  - Research Ireland Investigator Programme, *Statistical Tools for Reference Estimation and Adaptive Monitoring (STREAM)* (€625,000.00, PI).
- Delivered a public talk titled *"Challenge Your Limits!"* at the Pint of Science, Ireland.
- Delivered an invited talk titled *"Beyond the Confidence!"* at the Department of Mathematics, Statistics, and Computer Science seminar series, University of Tehran.
- Half-day workshop for primary school children as part of the HRB-TMN START 2025 Competition at University of Galway to increase their awareness about study designs, observational studies, data collection, and data analysis.
- Chief organiser of the 45th Conference on Applied Statistics, Ireland, Galway, Ireland.
- Organising committee of 39th International Workshop on Statistical Modelling, Limerick, Ireland.
- 3 PhD students, 2 Postdoctoral Researchers.
- Memberships: Young-ISA, Irish Statistical Association (Website Manager), International Society for Clinical Biostatistics, International Biometric Society, Statistical Modelling Society.

Rossmann, Tobias

Current research interests

I'm interested in algebra, combinatorics, and number theory. My main research focus is on zeta functions arising from algebraic counting problems.

Recent publications

[1] T. Rossmann and C. Voll, *Groups, graphs, and hypergraphs: average sizes of kernels of generic matrices with support constraints.* Mem. Amer. Math. Soc. 294 (2024), no. 1465, v+120 pp.

[2] T. Rossmann, *On the enumeration of orbits of unipotent groups over finite fields.* Proc. Amer. Math. Soc. 153 (2025), no. 2, 479–495.

[3] A. Carnevale, V. D. Moustakas, and T. Rossmann, *Coloured shuffle compatibility, Hadamard products, and ask zeta functions.* Bull. Lond. Math. Soc. 57 (2025), no. 7, 2132–2154.

[4] T. Rossmann and C. Voll, *Ask zeta functions of joins of graphs.* Preprint, arXiv:2505.10263, 60 pages.

Research activities

- I am co-PI (jointly with A. Carnevale) on a Research Ireland Frontiers for the Future Project on *Machine learning and explicit computations of zeta functions in algebra* (2024–2028, grant no. 22/FFP-P/11449).
- Together with A. Carnevale, P. Lins, J. Maglione, and C. Voll, I co-organise the SEA (Symbolic Enumeration in Algebra) seminar series.
- (Upcoming:) I co-organise two workshops that will take place this year: (1) *Sixth International Workshop on Zeta Functions in Algebra and Geometry* (with A. Carnevale, R. Osburn, W. Veys, and C. Voll). (2) MathLearn: Machine Learning ∩ Pure Mathematics (with A. Baykalov, A. Carnevale, and J. Maglione).
- Talks at: CSMQ (Montreal), workshop on "Computational Group Theory" (Oberwolfach), follow-up workshop on "Logic and Algorithms in Group Theory" (HIM), and workshop on "Cohomology Theories for Automorphic Forms and Enumerative Algebra" (Oberwolfach).
- I am a member of the Editorial Board of Experimental Mathematics.
- I currently supervise three PhD students: D. Cormican (since 2023), M. Falciatore (co-supervised by A. Carnevale, since 2024), L. Prosperi (co-supervised by A. Carnevale, since 2024). I am also mentoring a postdoctoral researcher, A. Baykalov (since 2025).

Ryan, Ray

Current research interests

Functional Analysis: polynomial and holomorphic functions on complex Banach spaces and Banach lattices; tensor products of Banach lattices.

Recent publications

[1] C. Boyd, R. Ryan, N. Snigireva, Holomorphic functions on complex Banach lattices. *Trans.Amer.Math.Soc. 378 (2025), no.8, 5899–5925.*

Scarrott, Carl

Current research interests

My key three research platforms are in (1) methodological and computational developments for extreme value modelling, with applications in environment, health and finance, (2) biostatistical modelling in health research and (3) applied statistics in environmental science, engineering and exercise science.

Research outputs

Please list up to five of your recent (most significant) publications or provide such details in the bibliography below.

- Pedlar, C.R., Myrissa, K., Barry, M., Khwaja, I.G., Simpkin, A.J., Newell, J., Scarrott, C.J., Whyte, G.P., Kipps, C., and Baggish, A.L. Medical encounters at community-based physical activity events (parkrun) in the UK. *British Journal of Sports Medicine*, 55, 1420-1426, 2021.
- MacDermott, C., Scarrott, C.J. and Ferguson, J. (2024). Are Olympic medals a true indicator of a nation's sporting prowess? RTÉ Brainstorm https://www.rte.ie/brainstorm.
- MacDermott, C., Scarrott, C.J. and Ferguson, J. (2025). Bayes-ically fair: A Bayesian ranking of the Olympic medal table. arXiv preprint arXiv:2510.14723.

Research activities

- PhD students: Cormac MacDermott and Sivagami Nedumaran
- Seminars: University of Canterbury, New Zealand and Victoria University of Wellington, New Zealand
- Sabbatical: 1 January 2025 - 31 December 2025

Seoighe, Cathal

Current research interests

Research interests are mainly in genomics (especially cancer genomics) and molecular evolution; in particular, development and application of models and computational methods to analyze molecular sequence evolution and gene expression data and the analysis of genomic data in order to generate insights into the links between genomic and phenotypic variation.

Research outputs

Recent publications

[1] H. Anthony and C. Seoighe. Intratumoral heterogeneity in microsatellite instability status at single cell resolution. *iScience*, 2026.

[2] S. Matthews, V. Nikoonejad Fard, M. Tollis, and C. Seoighe. Variable gene copy number in cancer-related pathways is associated with cancer prevalence across mammals. *Molecular Biology and Evolution*, 42(3):msaf056, 2025.

[3] T. D. Medina, D. Bennett, and C. Seoighe. Consistent asymmetry in dna damage artefacts across target regions in exome sequencing data. *NAR Genomics and Bioinformatics*, 7(3):lqaf120, 2025.

[4] C. Seoighe, S. Connaire, and M. Chopra. Probing the limits of cis-acting gene regulation using a model of allelic imbalance quantitative trait loci. *PLoS Genetics*, 21(4):e1011446, 2025.

Research activities

- Scientific Director of the SFI Centre for Research Training in Genomics Data Science
- Research group consists of one postdoctoral researcher, 2 PhD students (principal supervisor) and two co-supervised PhD student
- Co-applicant on the Irish Medicines – Personalised Advanced Cellular Therapies (IMPACT) Research Centre proposal submitted March 2025

Sharifian, Nastaran

Current research interests

My primary research interests include longitudinal and survival analysis, functional data analysis, high-dimensional data modelling, and advanced statistical and machine learning methods, particularly in clinical and health-related applications. My Research focuses on developing novel statistical methods starting from data-motivated problems, where either the existing methods are not adequate, or there is no methodology for data analysis. Recently, I have developed a strong interest in the role of Public and Patient Involvement (PPI) within statistical methodologies and data science researches.

Recent publications

[1] K. Burke, J. Ward, O. McGrath, M. Singh, G. Okoh, **N. Sharifian**, P. MacCarron, S. Murphy, A. Fowler, M. Vynnycky, W. Lee, D. Mewada, T. Cardoso, E. Grua, C. Agnew, E. Maekawa, M. Akhi , M. McGuigan, S. Kuthe, and B. Glaser, " Unlocking the objective of energy efficient steel-making by robust scrap melting with the help of advanced algorithms *Mathematics in Industry Reports (MIIR)*, **1**, 1-34. 2026

[2] **Sharifian, N**., Simpkin, A., and et al., Gender Differences in Providers' Perceptions of Key Care Priorities for Very Old

ICU Patients: Secondary Analysis of ESICM Recommendations *Journal of Intensive Medicine*, (Under review). 2026

Research activities

- August 2024 - to present: Editorial board member and reviewer, *American Journal of Theoretical and Applied Statistics*.
- August 2024 - to present: Co-organizer of School seminars, School of Mathematical and Statistical Sciences, University of Galway.
- April 2025: Main organizer for the Online *Youn-ISA Webinar Joint with the BIR Committee on Statistical Ecology* in Ireland.
- July 2025: A conference paper "Multivariate functional principal component analysis to predict exercise type in compression therapy". Presented in *the 39th International Workshop on Statistical Modelling (IWSM 2025)*, University of Limerick, Limerick, Ireland. And also presented in *the Health Discovery and Innovation Seminar Series* and *the 45th Conference on Applied Statistics* in Ireland, The School of Mathematical and Statistical Sciences, University of Galway.
- September 2025 - to present: Research Committee member, School of Mathematical and Statistical Sciences, University of Galway.
- September 2025: Awarded €1000 funding from **PPI Ignite Network** to deliver and organize the workshop "From Numbers to Narratives: Understanding Health Research Through Data" as part of **National PPI Festival 2025**.
- October 2025: Main organizer of awarded Hybrid PPI workshop as part of National PPI Festival 2025.
- September 2025 - June 2025: Supervised a MSc project, Phoebe Hui Lei Wong and Anushka Muley and Phoebe Hui Lei Wong, Master of Health Data Science at the University of Galway, "Joint Models of Longitudinal Outcomes and Time-to-Event Data".
- December 2025 - 2026: Visiting Researcher at *the BT Ireland Innovation Centre (BTIIC)*, Ulster University, contributing to a large-scale, industry-focused research programme addressing applied modelling challenges in collaboration with academic and industry partners.
- January 2026: "Optimising Compression Therapy Using Functional Data Analysis and Biometric Monitoring". Accepted as an oral presentation at *the 33rd International Biometric Conference (IBC2026)*, Seoul, South Korea.

Simpkin, Andrew

Current research interests

Multilevel multivariate functional data; derivative estimation; longitudinal GWAS

Recent publications

[1] S. Golovkine, E. Gunning, E., A.J. Simpkin, N. Bargary. On the use of the Gram matrix for multivariate functional principal components analysis. *Journal of Multivariate Analysis*, 2025

[2] S. Geremia, T. Gaillat, N. Ballier, A.J. Simpkin. Exploring the cross-lingual influence of linguistic complexity in second language writing assessment. *Assessing Writing*, 2025

[3] Y. Zhu, A.J. Simpkin. Prediction of time to insulin initiation in gestational diabetes mellitus: a secondary analysis of the EMERGE trial *Diabetes Research and Clinical Practice*, 2025.

Research activities

- Current research grants:
  - Simpkin AJ (co-PI). ARC Hub for HealthTech. July 2025 to December 2029 €34,000,000
  - Simpkin AJ (PI). HealAsyst: A multifactorial wound treatment monitoring system for intelligent healing of chronic wounds. April 2023 to September 2026; €1,214,000
  - Simpkin AJ, Healy C (co-PIs). VOCAL: Voice of the Child in Family Law Mediation: Overcoming barriers to ensure Participation as a right, not a privilege. August 2024 to August 2026; €218,212
- Graduate students: John Andrew *Longitudinal functional data*; Solomon Beer *Lifecourse modelling with time varying covariates*; Emmanuelle Orsini *Concurrent modelling of cognition and metabolomics*; Erwan Louveau *Joint modelling of functional and survival data*; Zoe Hart *Early Molecular Markers for Cognitive Health in Psychosis*
- Postdoctoral researchers: Autumn O'Donnell *Longitudinal functional data analysis for pulmonary pressure waveforms*; Nastaran Sharifian *Modelling multivariate sensor data*; Kishor Shirsat *Designing studies for sensor data*; Yueyun Zhu *Developments and applications in multivariate and multilevel FDA*

Snigireva, Nina

Current research interests

I am interested in the existence and properties of attractors and invariant measures for Iterated Function Systems and Chaos Game Algorithm. I am also investigating polynomials and holomorphic functions on Banach Lattices.

Recent publications

[1] C. Boyd, R. Ryan, N. Snigireva, Holomorphic Functions on Complex Banach Lattices *Transactions of the American Mathematical Society*, **378**, no. 8 (2025)

[2] K. Leśniak, N. Snigireva, F. Strobin, A. Vince, Highly Non-contractive Iterated Function Systems on Euclidean Space Can Have an Attractor, *Journal of Dynamics and Differential Equations*, **37**, no. 3 (2025)

Research activities

- An invited talk *Weakly Contractive and Noncontractive Iterated Function Systems* at the One Day Function Theory Meeting which took place on the 1st of September 2025 at De Morgan House in London.
- Research visit to my collaborator Krzysztof Leśniak at Nicolaus Copernicus University, Toruń, Poland from 26th July to 3rd August 2025.
- Visited the Functional Analysis research group at Universidad Torcuato Di Tella, Buenos Aires, Argentina from the 17th of June to the 8th of July 2025 and gave a talk *Power Series with Regular Terms on Complex Banach Lattices* at the Di Tella Workshop on Analysis and Beyond which took place on the 18th and 19th of June 2025.
- Reviewing and refereeing.

Wheeler, Gregory L.

Current research interests

My research interests are primarily focused on evolutionary processes in cancer, both in terms of how understanding these processes can improve disease treatment outcomes and in how observations in cancer can offer insights into the natural world. Before my faculty appointment at University of Galway, I worked as a scientist at Nationwide Children's Hospital (Ohio,

United States), with my most notable projects involving clonal evolution in metastatic breast cancer, slide image analysis in paediatric brain cancer, and methods development to improve interpretation of copy-number variants (CNVs) and structural variants (SVs) in cancer and genetic diseases. I have continued these projects and plan to expand into related areas of research. My earlier work involved understanding evolutionary convergence and the origin of novel traits in carnivorous plants, research which I would welcome the opportunity to continue.

Recent publications

[1] Miller, A., Shah, T., Strawser, C., Rivaldi, A., Wilson, S., Zhong, H., Lucyshyn, J., Garfinkle, E., ..., Wheeler, G., et al. (2025) MRD4U: A path to development for personalized liquid biopsy for children with central nervous system tumors. *BMC Cancer*. **25**, 1365.

[2] Mathew, M., Potter, S., Schieffer, K., O'Donovan, J., Garfinkle, E., Paxton, S., Setty, B., Lazow, M., ..., Wheeler, G., et al. (2025) Comprehensive Genomic Characterization of Congenital and Infantile Cancers Reveals High Yield of Medically Meaningful Findings. *JCO Precision Oncology*. **9** pp. e2400910.

[3] Sezgin, Y., Snyder, G., Saljoughian, N., Maguire, C., Gokalp, E., Jaganathan, D., D'Ambrosio, E., Ozes, B., Wheeler, G., Kelly, B. , et al. (2025) REpair of heterozygous Mutations independent of Exogenous Donor template with high efficiency (REMEDY) using allele specific CRISPR targeting and HDR enhancers. *BioRxiv*. pp. 2025-05.

[4] Macke, E., Miller, A., Colwell, C., Gonzalez, M., Hunter, J., Venkata, L., Walker, L., Wheeler, G., Wilson, R., Mardis, E. , et al. (2025) Optical Genome Mapping (OGM) Identifies Multiple Structural Variants in a Case With Atypical Phelan-McDermid Syndrome. *American Journal Of Medical Genetics Part A*. **197**, e63929.

Research activities

- Pending application to HRB Secondary Data Analysis Projects (SDAP), *A Toolkit for Automated Molecular Insights from Slide Pathology*, (co-PI, €346,542).
- Invited presentation at All-Ireland Cancer Liquid Biopsies (CLuB) Consortium: *Personalised liquid biopsy for early recurrence detection in paediatric brain tumours.*
- Invited research proposal reviewer CLuB Bright Sparks (x2).
- Presentation to US National Cancer Institute (NCI) webinar series: *Predicting genetic alterations in pediatric gliomas from routine histopathology using deep learning.*
- Poster presentation at VIBE 2025: *Clonal Heterogeneity in Metastatic Breast Cancer: Insights from Aurora US.*
- Membership in the Institute for Health Discovery and Innovation (IHDI) and associate membership in the Institute for Clinical Trials (ICT).
- Supervision of two Bioinformatics MSc student projects, to be completed at the end of the summer semester.

Yaar, Asfand

Current research interests

My research focuses on integrating histopathology and genomic data to improve disease diagnosis and improve our understanding of complex medical conditions, with a particular focus on ovarian cancer. I am especially interested in developing data-driven approaches to address real-world challenges in healthcare, where existing methods are limited or insufficient.

Recent publications

[1] A. Yaar, A. Asif, S. E. A. Raza, N. Rajpoot, and F. Minhas, Cross-domain knowledge transfer for prediction of chemosensitivity in ovarian cancer patients, In *Proceedings of the IEEE/CVF Conference on Computer Vision and Pattern Recognition Workshops*, pp. 928–929, 2020.

[2] A. Yaar, M. Rosano, A. Furnari, A. Härmä, and G. M. Farinella, ViLaBot: Connecting Vision and Language for Robots That Assist Humans at Home, In *2024 IEEE International Conference on Metrology for eXtended Reality, Artificial Intelligence and Neural Engineering (MetroXRAINE)*, pp. 1206–1211, IEEE, 2024.

[3] A. Yaar, H. F. Ates, and B. K. Gunturk, Deep learning-based blind image super-resolution using iterative networks, In *2021 International Conference on Visual Communications and Image Processing (VCIP)*, pp. 01–05, IEEE, 2021.

[4] A. Yaar, I. Rodin, G. M. Farinella, and A. Furnari, A benchmark of egocentric scene graph prediction methods for understanding human-object interactions, In *International Conference on Image Analysis and Processing*, pp. 445–456, Springer, 2025.

Yang, Haixuan

Current research interests

My focus is in Bioinformatics & Statistical Modelling, especially of network data such as protein-protein interactions, co-expression, and functional similarity. A bio-molecular network can be viewed as a collection of nodes, representing the bio-molecules, connected by links, representing relations between the bio-molecules. I am working on inferring valuable information from bio-molecular networks.

Research outputs

Please list up to five of your recent (most significant) publications or provide such details in the bibliography below.

Recent publications

[1] S. de Siqueira Santos, H. Yang, A. Galeano, A. Paccanaro. Host centric drug repurposing for viral diseases. *PLoS Computational Biology*, 21(4): e1012876. https://doi.org/10.1371/journal.pcbi.1012876, 2025.

[2] Y. Zhong, C. Seoighe, H. Yang. Non-Negative matrix factorization combined with kernel regression for the prediction of adverse drug reaction profiles. *Bioinformatics Advances*, 4(1):vbae009, 2024.

[3] M. Timilsina, V. Nováček, M. d'Aquin, H. Yang. Boundary heat diffusion classifier for a semi-supervised learning in a multilayer network embedding. *Neural Networks*, 156:205-217, 2022.

[4] M. Torres, H. Yang, A.E. Romero, A. Paccanaro. Protein function prediction for newly sequenced organisms. *Nature Machine Intelligence*, 3(12):1050-1060, 2021.

[5]

Zhu, Yueyun

Current research interests

My research focuses on functional data analysis. I developed a new method to estimate the covariance of derivatives of functional data, which plays an important role in derivative-based functional principal component analysis (FPCA). In addition, I am working on developing multistate models to study the weaning process for patients receiving invasive mechanical ventilation.

Recent publications

[1] Y. Zhu, A.J. Simpkin, Prediction of time to insulin initiation in gestational diabetes mellitus: a secondary analysis of the EMERGE trial. *Diabetes Research and Clinical Practice*, 113070, 2025.

[2] S. Fezzi, Y. Zhu, A.J. Simpkin, Predicting functional results of percutaneous coronary intervention using machine learning modelling. *International Journal of Cardiology*, 134183, 2026.

Research activities

- Poster presentation in 39th International Workshop on Statistical Modelling (IWSM), July 2025. “A Cox model with functional principal component scores to predict insulin initiation in women with gestational diabetes."
- Poster presentation in 45th Conference on Applied Statistics in Ireland (CASI), May 2025. “A Cox model with functional principal component scores to predict insulin initiation in women with gestational diabetes."

Zurlo, Giuseppe

Current research interests

I work in the broad field of Continuum Mechanics. Lately I am interested at the modeling of growing bodies, at the behavior of soft tissues at large stretches and the instabilities they develop, and more generally at the interactions of elasticity with other fields, like chemistry, electricity and magnetism.

Research outputs

Recent publications

[1] Zurlo G, Destrade M., Straight-to-helicoid transition of twisted cords. Proceedings of the Royal Society A 482: 20251044 (2026).

[2] Truskinovsky L., Zurlo G., Active chemomechanical solitons, Physical Review E 113, 034215 (2026).

[3] Destrade M. , Zurlo G., Nonlinear Elasticity. A Concise Masterclass for Undergraduates. Springer (2025).

[4] Erlich A., Zurlo G., The geometric nature of homeostatic stress in biological growth, Journal of the Mechanics and Physics of Solids 201, 106155 (2025).

Research activities

- *Conferences/Seminars*: Politecnico di Bari, Italy (2025); Tianjin University, China (2025); University of Wien, Austria (2025).
- *Sabbaticals*: Sabbatical Leave for Research, January - June 2025, Politecnico di Bari, Italy.
- *Graduate Course*: Summer School of Mathematical Physics of Ravello, Italy (2025); PhD course in Nonlinear Elasticity, Politecnico di Bari, Italy (2025).
- *Current research grants*: Collaborator on ANR (Agence Nationale de la Recherche), AAPG2024 “Grow-size”, PI Alexander Erlich, total funds 400k€sector CES45 “Interfaces: mathematiques, sciences du numerique, biologie, sante”.
- *Appointments*: Editorial Board Member: Mathematics and Mechanics of Solids (2025).
- *Graduate students:* Mohsen Daman, Double PhD between University of Galway and Università di Pisa (Italy), completed in 2025; Thomas Hayes, University of Galway; Abhirami Anil Gayathry, external co-supervision at the University of Exeter, UK.

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7 Visitors

Hohlweg, Christophe (Université du Québec à Montréal)
Visiting: Angela Carnevale

Dates of visit: 8 October 2025 – 24 October 2025
Research activity

We worked on a conjecture revolving around involutions in Coxeter groups and so-called ancestors. We made progress in type A and also related the conjecture to weak and Bruhat orders. Christophe gave a talk at the School Seminar.

D'Adderio, Michele (Pisa University)
Visiting: Angela Carnevale

Dates of visit: 2 February 2026 – 6 February 2026
Research activity

We worked on permutation statistics identities arising from work on chromatic quasysimmetric functions. We also worked on the organisation of FPSAC 2027, and Michele gave a talk at the School Seminar.

Karim Adiprasito, Ryoshun Oba (IMJ - Paris Rive Gauche)
Visiting: James Cruickshank

Dates of visit: 29 September 2025 – 3 October 2025
Research activity

Both visitors gave talks in the School seminar series and collaborated on a research project on Rigidity Theory and Lefschets Properties of Stanley-Reisner rings.

McCluskey, Connell. (Wilfrid Laurier University)
Visiting: N. Madden, R. Quinlan, J. Cruickshank

Dates of visit: 9 May – 18 July 2025
Research activity

I visited Rachel Quinlan, Niall Madden and James Cruickshank. I studied the asymptotic smoothness of hybrid dynamical systems, for which I found the resources of the James Hardiman Library particularly useful. During my visit, I attended the "Women in the Mathematical Sciences Day" conference on May 12.

Farrell, Patrick. (University of Oxford)
Visiting: N. Madden

Dates of visit: 14–20 April, and 10 July – 29 August, 2025.
Research activity

Patrick worked on a framework for deriving kinetic equations for fluids with molecules with internal microstructure (e.g. rodlike molecules with orientation). More details at `https://arxiv.org/abs/2508.10744`.

Xenophontos, Christos. (University of Cyprus)
Visiting: N. Madden

Dates of visit: 25 – 28 November, 2025.
Research activity

Christos and Niall worked on the implementation of FEMs for certain 4th-order singularly perturbed differential equations.

Voll, Christopher (Bielefeld University)
Visiting: Joshua Maglione

Dates of visit: 13 May 2025 – 27 May 2025, 13 February 2026 – 27 February 2026
Research activity

Christopher attended Groups in Galway 2025 and helped organise Symbolic Enumeration in Algebra. In May, we also discussed work related to finishing our recent preprint Symplectic Hecke eigenbases from Ehrhart polynomials as well as working with Florian Schreier-Aigner. In February, we discussed work related to lattice enumeration and submodule zeta functions.

Allen, Kevin (University College Cork)
Visiting: Joshua Maglione

Dates of visit: 25 March 2026 – 27 March 2026

Research activity

Kevin gave a talk at the School seminar on 26 March. We discussed q-series and combinatorial aspects of modular forms.

Schreier-Aigner, Florian (University of Vienna)
Visiting: Joshua Maglione

Dates of visit: 13 May 2025 – 20 May 2025
Research activity

Florian spoke at the School Seminar on 14 May. We, together with Christopher Voll, discussed combinatorial aspects related to lattice enumeration and symmetric functions.

Breen, Jane. (Ontario Tech University, Canada)
Visiting: Rachel Quinlan

Dates of visit: December 8 – 10 2025 and March 23 – 26 2026
Research activity

Collaboration on a project that investigates properties of the affine spaces of symmetric matrices with a prescribed off-diagonal zero-nonzero pattern determined by a graph. During her December visit, Jane was the external examiner for the PhD of Badriah Sadarji, and presented a seminar on *Kemeny's constant for Markov chains and random walks on graphs.*

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8 Events, Conferences, meetings, and workshops

21st Workshop on Numerical Methods for Problems with Layer Phenomena
Dates: 24–25 April, 2025
Speakers: Sebastian Franz (TU Dresden), Alan F. Hegarty (University of Limerick), Seán Kelly (University of Limerick), Natalia Kopteva (University of Limerick), Katherine MacKenzie (University of Strathclyde), Niall Madden (University of Galway), Jekaterina Mosalska (University of Galway), Neofytos Neofytou (University of Cyprus), Christos Pervolianakis (Friedrich-Schiller-Universität Jena), Nanda Poddar (University of Galway), Jenny Power (University of Bath), Martin Stynes (Beijing CSRC), Sean Tobin (University of Galway). Alex Trenam (Heriot-Watt University), Christos Xenophontos (University of Cyprus) Marwa Zainelabdeen (WIAS, Berlin).
Organisers: Niall Madden, Jekaterina Mosalska, Nanda Poddar, Sean Tobin.
Funders: Irish Mathematical Society, University of Galway
Web page: `niallmadden.ie/LayerPhenomena2025`

The 45th Conference on Applied Statistics in Ireland
Dates: 12–14 May 2025
Invited Speakers: Anthony Davison (École polytechnique fédérale de Lausanne), Adrian Raftery (University of Washington), Daniela De Angelis (University of Cambridge), Patrick Lucey (Stats Perform)
Organisers: Galway stats group
Funders: Irish Statistical Association
Web page: `https://casi.ie/2025/`

Groups in Galway 2025
Dates: 15–16 May 2025
Speakers: Anton Baykalov (University of Galway), Iker de las Heras (University of the Basque Country), Brita Nucinkis (Royal Holloway, University of London), Götz Pfeiffer (University of Galway), Margherita Piccolo (University of Hagen), Anitha Thillaisundaram (Lund University), Gareth Tracey (University of Warwick).
Organisers: Joshua Maglione, Rachel Quinlan
Funders: Irish Mathematical Society, Research Ireland
Web page: `https://groupsingalway.github.io`

SEA (Symbolic Enumeration in Algebra) Seminar
Dates: 19 May 2025
Speaker: Robert Osburn (University College Dublin) **Organisers:** Angela Carnevale, Paula Lins (Lincoln), Joshua Maglione, Tobias Rossmann, Christopher Voll (Bielefeld)
Funders: Research Ireland, German Research Foundation
Web page: `https://sea-series.github.io/2025/01/01/Osburn.html`

Lá na Matamaitice as Gaeilge
Dates: 12 Deireadh Fómhair 2025
Speakers: Aonghus Ó hAlmhain (Airtel ATN), Donncha Ó hEallaithe (Ollscoil Teicneolaíochta an Atlantaigh), Tríona Nic Fhinn (An Chomhairle um Oideachas Gaeltachta agus Gaelscolaíochta), Kevin Scannell (Saint Louis University), Lily Ní Leathlobhair (), David Stifter (Ollscoil Mhá Nuad), Leo Creedon (Ollscoil Teicneolaíochta an Atlantaigh), Fintan Hegarty (Ollscoil na Gaillimhe), Ciara Egan (Ollscoil na Gaillimhe), Cathal Seoighe (Ollscoil na Gaillimhe), Rachel Quinan (Ollscoil na Gaillimhe)
Organisers: Aonghus Ó hAlmhain, Fintan Hegarty, Leo Creedon
Funders: MathsWeekIreland, Ollscoil na Gaillimhe
Web page: `https://etim.ie/la-na-matamaitice-as-gaeilge`

An tOll. Cathal Seoighe ag bronnadh Duais Christofides ar Roseanna Bailey.

COGENT Winter School
Dates: 1–12 December 2025
Speakers: Bettina Eick (TU Braunschweig), Graham Ellis (University of Galway), Thomas Breuer (RWTH Aachen University), Max Horn (RPTU Kaiserslautern-Landau), Bill Allombert (Institut de Mathématiques de Bordeaux), Aurel Page (Institut de Mathématiques de Bordeaux), Herbert Gangl (Durhan University), Philippe Elbaz-Vincent (Université Grenoble Alpes), Haluk Sengun (University of Sheffield), Sander Dahmen (Vrije Universiteit Amsterdam), Alain Chavarri Villarello (Vrije Universiteit Amsterdam), Mehdi Mhalla (CNRS), Jean Fasel (Université Grenoble Alpes), Rachel Quinlan (University of Galway)
Organisers: Graham Ellis, James Cruickshank
Funders: Horizon Europe
Web page: `https://www.cogent-network.eu/en/COGENT-WinterSchool`

9 School seminar

[1] Colm Mulcahy, Spelman College, Georgia and South East Technological University, Waterford. *From One, Two, Many, to ABC (or ten reasons why mathematics isn't as easy as 1,2,3)*, 17/04/2025. (Contact: Rachel Quinlan)

[2] Florian Schreier-Aigner, University of Vienna. *Growth diagram proofs for the Littlewood identities*, 14/05/2025. (Contact: Joshua Maglione)

[3] Andrea Fontanella, TCD. *Stepping into the Quantum Universe: Black Holes and Holography*, 29/05/2025. (Contact: Michael McGettrick)

[4] Joshuah Heath, Nordita Sweden. *Entanglement spectrum of matchgate circuits with universal and non-universal resources*, 05/06/2025. (Contact: Mark Howard)

[5] Elise Lockwood, Oregon State University. *"Counting Is Hard" but It's Rewarding and Fun: Insights from a Research Program in Combinatorics Education*, 05/09/2025. (Contact: Kirsten Pfeiffer)

[6] Paul Levy, Lancaster University. *Lusztig's Special Pieces Conjecture*, 17/09/2025. (Contact: Michael Tuite)

[7] Myrto Manolaki, UCD. *Universal composition operators and complex dynamics*, 29/09/2025. (Contact: Nina Snigireva)

[8] Ryoshun Oba, IMJ-Paris Rive Gauche. *From (face) rings to stresses*, 30/09/2025. (Contact: James Cruickshank)

[9] Karim Adiprasito, IMJ-Paris Rive Gauche. *The Hard Lefschetz property*, 02/10/2025. (Contact: James Cruickshank)

[10] Christophe Hohlweg, Université du Québec à Montréal. *Reflections on Coxeter systems*, 09/10/2025. (Contact: Angela Carnevale)

[11] Jesse Lansdown, University of Galway. *Applications of association schemes via Delsarte theory*, 16/10/2025. (Contact: Haixuan Yang)

[12] Brendan Guilfoyle, Munster Technological University, Tralee. *Null hypersurfaces: from CT scans to the Critical Catenoid Conjecture*, 23/10/2025. (Contact: James Cruickshank)

[13] Erin Evelyn Gabriel, The University of Copenhagen. *Improved small-sample inference for functions of parameters in the k-sample multinomial problem*, 30/10/2025. (Contact: Nicola Fitz-Simon)

[14] Andrew Smith, UCD. *Fractals and Continuous-Time Gambling*, 06/11/2025. (Contact: Nina Snigireva)

[15] Michael Zurel, Simon Fraser University. *Efficient classical simulation of some quantum computations*, 13/11/2025. (Contact: Mark Howard)

[16] Giuseppe Zurlo, University of Galway. *Why am I stuck at five foot eight?*, 20/11/2025. (Contact: Haixuan Yang)

[17] Paul Yousefi, University of Bristol. *Machine learning strategies for biomarker development in peripheral tissues*, 21/11/2025. (Contact: Andrew Simpkin)

[18] Ruben von Boxtel, Princess Máxima Center for Pediatric Oncology in Utrecht. *Tracing cancer origins using single-cell genomes*, 25/11/2025. (Contact: Cathal Seoighe)

[19] Jane Breen, Ontario Technological University. *Kemeny's constant for Markov chains and random walks on graphs*, 10/12/2025. (Contact: Rachel Quinlan)

[20] Lasse Bjørn Kristensen, University of Copenhagen. *All I want for Christmas is ground states*, 11/12/2025. (Contact: Michael McGettrick)

[21] Fei Chen, University of Galway. *Fast Alternating Fitting Methods for Trigonometric Curves for Large Data*, 29/01/2026. (Contact: Niall Madden)

[22] Michele D'Adderio, University of Pisa. *q,t-combinatorics and sand-piles*, 05/02/2026. (Contact: Angela Carnevale)

[23] Michel Destrade, University of Galway. *An introduction to the European Research Council grants*, 26/02/2026. (Contact: Haixuan Yang)

[24] Ilia Pirashvili, University of Galway. *The Geometry of Monoids*, 12/03/2026. (Contact: Haixuan Yang)

[25] Kevin Allen, UCC. *Partitions, Overpartitions and Rank Deviations*, 26/03/2026. (Contact: Joshua Maglione)

10 Léachtaí le linn Lóin

[1] Timirí STEM as Gaeilge, Ollscoil na Gaillimhe. *Tae agus Plé leis na Timirí*, 20/10/2025.

[2] Fintan Hegarty, Ollscoil na Gaillimhe. *Matamaitic Apacailipsis na Zombaithe*, 28/10/2025.

[3] Rachel-Áine Ní Mharascáil, Ollscoil na Gaillimhe. *Draíocht na Ríomheolaíochta*, 03/11/2025.

[4] Rachel Quinlan, Ollscoil na Gaillimhe. *Oragámaí geoiméadrach - Ealaín sa Mhata*, 10/11/2025.

[5] Aisling McCluskey, Ollscoil na Gaillimhe. *1,2,3,... Éigríoch!*, 17/11/2025.

[6] Kevin Jennings, Ollscoil na Gaillimhe. *Mata agus Ceol*, 24/11/2025.

[7] Timirí STEM as Gaeilge, Ollscoil na Gaillimhe. *Tae agus Plé leis na Timirí*, 09/02/2026.

[8] Neil Ó Laoghaire, Ollscoil na Gaillimhe. *Sonraí spásúla; an teorann dheiridh!*, 16/02/2026.

[9] Caoimhe Ní Bhradáin agus Aifric Nic Niallais, Ollscoil na Gaillimhe agus Coláiste na Tríonóide. *Léargas ar Thaighde agus Theicneolaíocht Thogra ABAIR.IE*, 09/03/2026.

[10] Deirdre Ní Chonghaile agus Oksana Dereza, Ollscoil Chathair Bhaile Átha Cliath agus Ollscoil na Gaillimhe. *An Gaodhal*, 24/03/2026.

[11] Clodagh Gormley agus Leah Kyne, Ollscoil na Gaillimhe. *Teiripe Ocsaigin Hipearbarrach*, 30/03/2026.

(Contact: Fintan Hegarty)