OLLSCOIL NA GAILLIMHE
UNIVERSITY OF GALWAY

School of Mathematical and Statistical Sciences

14th Annual Research Day

16 April 2025

Programme

	Talks take place HBB-G019 Coffee, lunch, posters, and reception take place TBA
9:20–9:30	**Cathal Seoighe**, Head of School: Opening Remarks
9:30–10:00	**Joshua Maglione**, (University of Galway) *Zeta functions and hyperplane arrangements*
10:00–10:30	**Yueyun Zhu** (University of Galway) *Derivative multivariate functional principal component analysis and its application to coronary artery disease*
10:30–11:00	**Frances Fahy** (Ryan Institute) *Interrelations between mathematics and environmental research: the Role of the Ryan Institute*
11:00–11:30	**Tea and coffee**
11:30–12:00	**Griffen Small** (University of Galway) *Modelling the Non-Linear Viscoelastic Behaviour of Brain Tissue in Torsion*
12:00–13:00	**Lightning talks** John Andrew • Mehak Chopra • David Cormican • Anna Großbach Aisling Mac Aree • Vikrant Pratap • Noah Shore • Janhavi Tarale
13:00–14:10	**Lunch and Poster Session**
14:10–14:40	**Lars Jermiin** (University of Galway) *TBA*
14:45–15:30	**Eimear Byrne** (UCD) *Codes and Matroids*
15:30–17:00	**Poster session, reception, and prizes**

Contents

1 Introduction

...

Welcome to...

2 Abstracts of invited talks

Eimear Byrne (University College Dublin)

Codes and Matroids

Matroid theory goes back to the Whitney's work of the 1930s. It has evolved from ideas in graph theory, geometry, and lattice theory. There are also well-known connections to linear codes. When viewed as a rank function on a lattice, matroids have traditionally been studied in the Boolean lattice. More recently, the q-analogue of a matroid (a q-matroid) has been studied, wherein the Boolean lattice is replaced with the lattice of subspaces of a vector space over a finite field. Similar to matroids, q-matroids have strong connections to codes, namely to rank-metric codes. In this talk we will give an introduction to this topic and mention some recent results in the area.

Joshua Maglione (University of Galway)

Zeta functions and hyperplane arrangements

We define a class of multivariate rational functions associated with hyperplane arrangements called flag Hilbert–Poincaré series. We show how these rational functions are connected to local Igusa zeta functions and class counting zeta functions for certain graphical group schemes studied by Rossmann and Voll. We report on a general self-reciprocity result and a non-negativity result of the numerator polynomial under a coarsening, and we explore other connections within algebraic combinatorics. We report on joint works with Christopher Voll and with Galen Dorpalen-Barry and Christian Stump.

Griffen Small (University of Galway)

Modelling the Non-Linear Viscoelastic Behaviour of Brain Tissue in Torsion

Brain tissue accommodates non-linear deformations and exhibits time-dependent mechanical behaviour. The latter is one of the most pronounced features of brain tissue, manifesting itself primarily through so-called viscoelastic effects. One key effect is stress relaxation, where the stress decreases over time when brain tissue is deformed and then held in place. While the literature is replete with non-linear viscoelastic models, they are generally cumbersome and computationally expensive, making model fitting and the estimation of brain tissue's material parameters difficult. The modified quasi-linear viscoelastic (MQLV) model, recently reappraised by De Pascalis et al. [1] and Balbi et al. [2], offers a simpler alternative for modelling brain tissue's viscoelastic behaviour but remains underutilised and has yet to be validated with experiments.

Torsion is one of the most robust deformation modes for measuring brain tissue's mechanical properties. It can be readily implemented using a rotational rheometer, which measures both the torque and normal force required to twist a cylindrical sample [3]. However, previous studies on brain tissue's viscoelasticity have focused on measuring only on torque, overlooking the additional insights provided by normal force measurements [4].

In this presentation, we present a novel protocol for characterising the viscoelastic properties of brain tissue, based on the torsion deformation mode and the MQLV model. We performed ramp-and-hold relaxation tests on freshly slaughtered cylindrical ovine brain samples (25 mm diameter

and 10 mm height). The tests were conducted using a commercial rheometer at varying twist rates of $\{40, 240, 400\}$ rad m^{-1} s^{-1}, with a fixed twist of 88 rad m^{-1}. The viscoelastic material parameters were estimated by simultaneously fitting the measured torque and normal force to the MQLV model's analytical predictions [5]. The model's predictions were further validated through finite element simulations of the experiments using the open-source software FEniCS [6]. Our results demonstrate that the model accurately fits the experimental data, with the estimated elastic material parameters aligning well with those reported in previous studies on brain samples under torsion [3]. By allowing us to obtain two independent datasets (torque and normal force) from a single test, our proposed protocol provides us with a much more efficient and accessible alternative to traditional multi-mode protocols, which often rely on expensive, custom-made experimental rings or multiple testing devices; in contrast, our protocol can be easily implemented in any commercially available rheometer.

Beyond advancing brain tissue's mechanical characterisation and validating the efficacy of the MQLV model, our results have broader implications. When coupled with bespoke finite element models, the material parameters estimated in this study could enhance our understanding of the forces and deformations associated with traumatic brain injury, which could contribute to the design of improved headgear for sports such as boxing and motorsports. Additionally, our novel protocol offers new insights into the mechanical behaviour of soft tissues beyond the brain.

This work has emanated from research jointly funded by Taighde Éireann – Research Ireland under grant number GOIPG/2024/3552 (Griffen Small), and by the College of Science and Engineering at the University of Galway under the Millennium Fund scheme for the project "Modelling Brain Mechanics" (Valentina Balbi).

References

[1] R. De Pascalis, D. I. Abrahams, W. J. Parnell, *On nonlinear viscoelastic deformations: a reappraisal of Fung's quasi-linear viscoelastic model*, Proc. R. Soc. A: Math. Phys. Eng. Sci. 470 (2166) (2014) 20140058.

[2] V. Balbi, T. Shearer, W. J. Parnell, *Tensor decomposition for modified quasi-linear viscoelastic models: Towards a fully non-linear theory*, Math. Mech. Solids 0 (0) (2023) 1–25.

[3] V. Balbi, A. Trotta, M. Destrade, A. Ní Annaidh, *Poynting effect of brain matter in torsion*, Soft Matter 15 (25) (2019) 5147–5153.

[4] S. Chatelin, A. Constantinesco, R. Willinger, *Fifty years of brain tissue mechanical testing: from in vitro to in vivo investigations*, Biorheology 47 (5–6) (2010) 255–276.

[5] M. Righi, V. Balbi, *Foundations of viscoelasticity and application to soft tissue mechanics*, in: J. Málek, E. Süli (Eds.), Modeling Biomaterials, Springer, 2021, Ch. 3, pp. 71–103.

[6] M. Alnæs, J. Blechta, J. Hake, A. Johansson, B. Kehlet, A. Logg, C. Richardson, J. Ring, M. E. Rognes, G. N. Wells, *The FEniCS project version 1.5*, Archive of Numerical Software 3 (100) (2015) 9–23.

Yueyun Zhu (University of Galway)

Derivative multivariate functional principal component analysis and its application to coronary artery disease

With the development of wearable monitoring devices and sensors, increasingly large and complex datasets are being recorded. Such data often exhibit non-linear patterns and estimating the rate of change (i.e, derivatives) is particularly informative for understanding the underlying dynamics.

Functional principal component analysis (FPCA) is a powerful tool, which represents the infinite-dimensional functional data into the Karhunen-Loève expansion with a set of orthogonal functional principal components (FPCs) and functional principal component scores (FPC-scores). Multivariate FPCA (MFPCA) is an extension of FPCA to accommodate multiple correlated features. The multivariate FPCs (MFPCs) capture the joint variation between different features and the associated multivariate FPC-scores (MFPC-scores) summarize this variation as numerical values.

To estimate the derivatives of multivariate functional data, we proposed a new method, namely the derivative of multivariate functional principal component analysis (DMFPCA). Analogously to MFPCA, the derivative MFPCs (DMFPCs) capture the joint variation for the derivatives of different features and the derivative MFPC-scores (DMFPC-scores) summarize this joint variation as numerical values.

We applied MFPCA and DMFPCA to the quantitative flow ratio (QFR) and vessel diameter obtained from angiograms. MFPCA was employed to estimate MFPC-scores, which were used as predictors in a penalized logistic regression to classify physiological patterns of coronary artery disease. DMFPCA was employed to investigate the underlying dynamics between diameter and QFR, providing guidance for selecting the optimal stent location during percutaneous coronary intervention.

3 Abstracts of lightning talks

Fatigue prediction in outdoor running using Functional Data Analysis

John Andrew
Supervisor: Prof. Andrew J. Simpkin

Fatigue affects athletes' performance so, monitoring it is vital in elite sports. Assessing fatigue helps optimise athletes' performance and their readiness to train. Objective assessment of fatigue is usually done in specialised laboratories that are expensive (facilities, personnel, etc.). Low-cost lightweight sensors offer a compelling alternative, but the high-throughput data they collect are complex and functional in nature. In this study, we aim to predict fatigue onset during running using data from wearable sensors.

Data were available from 19 athletes running 400M under normal conditions (healthy) and again under fatigued conditions with a sensor mounted on their lumbar spine. The running involved three segments, running under healthy condition followed by fatiguing protocol, and later finished by running when fatigued. In all three segments, the sensor captured six signals 256 times per second: the accelerometer in three directions (X, Y, Z) and the gyroscope in three directions (X, Y, Z). We broke the long, time series signals into individual strides forming a series of functional strides arising longitudinally. We use multilevel functional principal component analysis (mFPCA) [1], a functional data analysis (FDA) approach for dimensional reduction and use the low dimension representation as the predictors to predict fatigue. FDA frameworks enable us to use all the collected data over the run and hence avoid wasting of information. We analysed acceleration signals in the X, Y and Z directions, and compared the fatigue prediction performance of each direction separately. The acceleration in the Y direction seems to be the best predictor when compared to acceleration in X, in Z. Our approach achieves an average accuracy of 94% (SD = 0.05) on external datasets when using acceleration in Y direction. These findings may serve as a foundation in creating a fatigue monitoring and assessment tool using wearable sensor technology.

References

[1] Cui, Erjia and Li, Ruonan and Crainiceanu, Ciprian M and Xiao, Luo. *Fast multilevel functional principal component analysis.* Journal of Computational and Graphical Statistics, 2023.

Impact of cell-type specific variations and age on aortic distensibility

Mehak Chopra
Supervisors: Niamh Hynes, Cathal Seoighe

Background

Aortic distensibility is the ability of arteries to expand with pulse pressure induced by the cardiac cycle, and it often diminishes with age [1][2]. Previous genome-wide association (GWA) studies have identified SNPs linked to distensibility. Despite the established genetic associations, the mechanisms driving changes in distensibility remain unclear. This study aims to illuminate factors influencing distensibility using existing gene expression data, focusing on age related changes in aortic cellular composition, alongside associated genetic variations and cell type-specific gene expression (CT-GE).

Methods:

We applied a deep-learning model to segment 62,497 CMRI images from UK Biobank and calculated aortic distensibility [3]. GWA was conducted on 56,765 participants using BOLT-LMM [4]. We utilized CIBERSORTx to perform gene expression deconvolution on 432 GTEx participants with aortic gene expression data, analyzing changes in cell composition and CT-GE associated with age and GWA hits [5].

Results:

Distensibility was calculated for 56,765 subjects. None of the 33 independent SNPs across 12 loci from the GWA showed an association

with inferred cellular proportions, following fdr correction. Cellular proportions of Pericytes and Fibroblast-I declined with age, whereas vascular smooth muscle cells-II (VSMC) tended to increase. Further, CT-GE analysis revealed associations of GWA SNPs with *SRR* gene expression in VSMC-I, VSMC-II, and Fibroblast-I cells and with expression of *CDH13* in VSMC-II.

Conclusions:

This study contributes to the understanding of variation in aortic distensibility associated with age and genotype. Examining variation in aortic distensibility through the lens of gene expression in the relevant tissue suggested that variation in the expression of *SRR* in VSMC-II and Fibroblast-I, and *CDH13* in VSMC-II could contribute to the observed genetic associations.

This research has emanated with the financial support of Science Foundation Ireland under Grant number [18/CRT/6214].

References

[1] Mikola H, Pahkala K, Rönnemaa, Viikari JS, Niinikoski H, Jokinen H, Salo P, Simell Olli, Juonala M,, Raitakari Olli T. *Distensibility of the aorta and carotid artery and left ventricular mass from childhood to early adulthood.* Hypertension, 2015 Jan;65(1):146-52.

[2] Nethononda RM, Lewandowski AJ, Stewart R, Kylinterias I, Whitworth P, Francis J, Leeson P, Watkins H, Neubauer S, Rider OJ. *Gender specific patterns of age-related decline in aortic stiffness: a cardiovascular magnetic resonance study including normal ranges.* J Cardiovasc Magn Reson. 2015 Feb 19;17(1):20.

[3] Nethononda RM, Lewandowski AJ, Stewart R, Kylinterias I, Whitworth P, Francis J, Leeson P, Watkins H, Neubauer S, Rider OJ. *Recurrent neural networks for aortic image sequence segmentation with sparse annotations.* Medical Image Computing and Computer Assisted Intervention–MICCAI 2018.

[4] Loh PR, Kichaev G, Gazal S, Schoech AP, Price AL. *Mixed-model association for biobank-scale datasets.* Nat genetics, 2018 Jul;50(7):906-908.

[5] Newman AM, Steen CB, Liu CL, Gentles AJ, Chaudhuri AA, Scherer F, Khodadoust MS, Esfahani MS, Luca BA, Steiner D, Diehn M, Alizadeh AA. *Determining cell type abundance and expression from bulk tissues with digital cytometry.* Nat Biotechnol., 2019 Jul;37(7):773-782.

ASK Zeta Functions of Unitary Lie Algebras over p-adic Integers

David Cormican
Supervisor: Tobias Rossmann

We consider a module M of $d \times e$ matrices over a commutative ring R, or equivalently a submodule of $\mathrm{Hom}(R^d, R^e)$ where R^k is the free module of rank k over R. Suppose R is a discrete valuation ring (DVR) with a unique maximal ideal $\mathfrak{p}$ of finite index. We define M_n to be the image of M under the reduction of matrix entries modulo $\mathfrak{p}^n$ and further define the average size of kernel (ASK) zeta function of M to be:

$$Z_M^{\mathrm{ask}} = \sum_{n \geq 0} a_n T^n$$

where $a_n = \frac{1}{|M_n|} \sum_{a \in M_n} |\mathrm{Ker}(a)|$ is the average size of kernel of entries in M_n

The p-adic integers, $\mathbb{Z}_p$ are a DVR in which the maximal ideal, $p\mathbb{Z}_p$ has index p. Earlier work [1] has found closed form expressions for the ASK zeta functions of the classical Lie algebras over $\mathbb{Z}_p$. Here we present new results for the general and special unitary Lie algebras, $\mathfrak{gu}_d(\mathcal{O}_K/\mathbb{Z}_p)$ and $\mathfrak{su}_d(\mathcal{O}_K/\mathbb{Z}_p)$, where K is a quadratic extension of $\mathbb{Q}_p$ with ring of integers $\mathcal{O}_K$. Specifically, we show for both of these cases that the ASK zeta function is equal to that of the special orthogonal Lie algebra in

dimension $2d$, giving the following formulae:

$$Z^{\mathrm{ask}}_{\mathfrak{gu}_d(\mathcal{O}_K/\mathbb{Z}_p)}(T) = Z^{\mathrm{ask}}_{\mathfrak{su}_d(\mathcal{O}_K/\mathbb{Z}_p)}(T) = Z^{\mathrm{ask}}_{\mathfrak{so}_{2d}(\mathbb{Z}_p)}(T) = \frac{1-p^{1-2d}T}{(1-T)(1-pT)}$$

Supported by the University of Galway through the Hardiman scholarship programme.

References

[1] Tobias Rossmann. *The average size of the kernel of a matrix and orbits of linear groups, II: duality.* Proc. Lond Math. Soc. (3) 117.3 (2018), pp. 574-616.

Genetic Determinants of DNA Methylation Across Early Development: Insights from a Longitudinal South African Cohort

Anna Großbach
Supervisor: **AJ Simpkin**
Co-authors: **AA Lussier, EC Dunn**

Epigenetic mechanisms, such as DNA methylation (DNAm), play a key role in genomic regulation and can shape various phenotypic outcomes. DNAm patterns are influenced by both genetic architecture and environmental exposures. Understanding the genetic contribution is essential for unraveling the complex interactions with environmental factors, particularly during early childhood - a period marked by rapid developmental changes and heightened susceptibility to environmental influences. Central to the genetic-epigenetic interplay are methylation quantitative trait loci (mQTLs) - genetic loci influencing DNAm states, either locally (*cis*-mQTL) or across larger genomic distances (*trans*-mQTL). While previous large cohort studies have mostly identified stable *cis*-mQTL effects across different life stages, the dynamic nature of mQTLs, especially *trans*-mQTLs, during early development remains underexplored due to limited longitudinal cohort data and the analytical challenges of large-scale association studies.

In this study, we investigated the dynamics of *cis*- and *trans*-mQTLs during early childhood using data from the Drakenstein Child Health Study (DCHS; n=1,143), a longitudinal South African birth cohort. DCHS provides genetic information from over 6 million loci and DNAm data from 900k CpG sites across whole blood samples collected at ages 1, 3, and 5. Using linear regression, we analysed the additive effects of each SNP on average DNAm at each CpG site, separately, for each time point. To validate our findings and explore ancestry-specific associations, we replicated our results across four large-scale mQTL databases, across different age-groups and ancestries. Additionally, we characterized the functional properties of mQTL groups using enrichment analyses.

Our results showed a substantial overlap of *cis*-mQTLs across all three time points, indicating mostly stable *cis*-mQTL effects. However, we also observed nearly 50% age-specific *trans*-mQTLs effects during early childhood, marking a novel discovery in the field. These age-specific mQTLs were enriched in regions associated with transcriptional control and gene regulation. Replication results showed a large overlap in *cis*-mQTLs across ancestries, while *trans*-mQTLs exhibited more ancestry-specific effects.

These results suggest that genetic influences on DNAm are dynamic, evolving across development to regulate age-sensitive processes. This highlights the complex interplay between genetics and epigenetics in developmental trajectories, which may have key implications for later disease susceptibility. Ultimately, our findings provide valuable insights for future studies aiming to identify genetic causal anchors for DNAm in childhood and observational research, particularly in historically underrepresented populations.

Supported by Research Ireland through the Research Ireland Centre for Research Training in Genomics Data Science under Grant number 18/CRT/6214 and the EU's Horizon 2020 research and innovation program un-

der the Marie Sklodowska-Curie grant H2020-MSCA-COFUND-2019-945385.

Constructing Fault-Tolerant Sets of Logical Operators for Quantum Stabilizer Codes

Aisling Mac Aree
Supervisor: Dr. Mark Howard

A quantum code protects k logical qubits by embedding them into a system of n physical qubits. When constructing a quantum code, it is advantageous to determine which logical operations can be performed *fault-tolerantly* on the codespace.

It is well known that a certain class of quantum error correcting codes, known as *stabilizer codes*, can be represented as classical codes over $GF(4)$ [1]. By exploiting this representation, we observe that the automorphism group of a classical $GF(4)$ code corresponds to a set of operations which preserve the codespace of the associated quantum code. Consequently, this automorphism group describes a set of fault-tolerant logical operators for the corresponding quantum stabilizer code.

This talk aims to explore how the group-theoretic structure of classical $GF(4)$ codes can be exploited for the purpose of constructing *desirable* sets of logical operators for quantum codes.

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

References

[1] A. R. Calderbank and E. M Rains and P. W. Shor and N. J. A. Sloane *quant-ph/9608006*.

Modelling Higher-Order Hyperelasticity in Soft Solids using Physics Informed Neural Networks without Labelled Data

Vikrant Pratap
Supervisor: Dr Bharat B Tripathi

Background, Motivation & Objective: Mild traumatic brain injury can result from shear shock wave formation in the brain due to impacts in contact sports, road accidents, and similar scenarios [1]. These highly nonlinear deformations are best represented by a fourth-order Landau hyperelastic model, rather than lower-order models like Neo-Hookean or Mooney-Rivlin. While conventional finite element solvers provide robust and accurate estimates, their high computational cost limits real-time applications. PINNs have emerged as a promising alternative for real-time brain deformation modelling by solving PDEs through a neural network that minimises system residuals while enforcing boundary conditions [2].

Statement of Contribution: This study presents the first attempt to model fourth-order deformations in soft solids using PINNs [3]. The proposed Causal-Marching Physics-Informed Neural Networks (CMPINNs) introduces multinet for multimaterial deformation with novel enforcement of incompressibility mitigating floating point errors. The automated optimal model selection is implemented across load steps using the lowest training loss. It introduces a hyperparameter optimization strategy for the CMPINNs framework, specifically designed for modelling hyperelasticity.

Results, Discussions & Conclusions: The accuracy of CMPINNs is evaluated for solving the Neo-Hookean hyperelastic model under soft and hard-constrained boundary conditions [4]. The CMPINNs model is developed for fourth-order hyperelastic models undergoing isotropic incompressible deformations, including uniaxial and biaxial tension/compression, simple shear, and pure shear. Additionally, three test cases involving spatially varying material properties and inhomogeneous deformations are conducted to evaluate the efficiency of multinet CMPINNs, with results benchmarked against numerical solutions. CMPINNs exhibit a significantly higher level of accuracy, outperforming vanilla PINNs in their ability to capture nonlinear deformations.

Supported by *College of Science and Engineering, University of Galway.*

References

[1] B. B. Tripathi et al. Journal of Computational Physics, 2019.

[2] M. Raissi et al. Journal of Computational Physics, 2019.

[3] V. Pratap et al. Brain Research Bulletin, 2025.

[4] V. Pratap et al. 9th ECCOMAS, 2024.

Dynamic Time-Frequency Decompositions as Unique Fingerprints for Time-Series Feature Extraction

Noah Shore
Supervisor: Michael Mc Gettrick

This presentation will highlight research done on the use of wavelet transforms serving as unique fingerprints for time series data. Opening with a discussion of the challenges in time-frequency decompositions derived from the uncertainty principle [2] and laying out the motivations for a dynamic mesh resolution in the *transform space*.

The motivation for a dynamic decomposition leads into a discussion of audio data as time series, wavelet transform computation [1], and an overview of wavelet coherence analysis [3], including examples from other domains. The wavelet transform coefficients will be used to show the spectrograms of both recorded Irish music and synthetically generated tunes.

The talk will include a live demonstration of the capabilities of the wavelet coherence model by recording a tune and matching the wavelet transform up against a database of sheet music to, without deep learning or the internet, correctly identify the tune.

References

[1] Arts, L.P.A., van den Broek, E.L. The fast continuous wavelet transformation (fCWT) for real-time, high-quality, noise-resistant time–frequency analysis. Nat Comput Sci 2, 47–58 (2022). https://doi.org/10.1038/s43588-021-00183-z

[2] Gabor, D. "Theory of communication." Journal of the Institution of Electrical Engineers - Part III: Radio and Communication Engineering, 93(26), 429-457 (1946).

[3] Chavez, M., Cazelles, B. Detecting dynamic spatial correlation patterns with generalized wavelet coherence and non-stationary surrogate data. Sci Rep 9, 7389 (2019).

Modulation of Elastic Instabilities by Strain-Induced Stiffening in Soft Particulate Composites

Janhavi Tarale
Supervisor: Stephan Rudykh

Soft particulate composites, widely used in engineering and biomedical applications, exhibit nonlinear mechanical behavior due to their ability to undergo large deformations. These materials often experience elastic instabilities, which were historically viewed as failure modes. However, recent research has shown that these instabilities can be leveraged to design materials with tunable properties, enabling applications in wave manipulation through tunable phononic bandgaps, auxetic materials, and adaptive metamaterials.

Recently, Li et al. [1] experimentally observed wavy pattern formation in soft particulate composites under large deformations, which was later numerically analyzed by Chen et al. [2] using Bloch-Floquet analysis. However, their study used neo-Hookean material model to undertake the material behavior, which fails to capture the limiting extensibility of polymer chains in soft materials. To address this limitation and investigate the influence of material stiffening caused by particle interactions, we employ the Gent material model [3]. This model effectively captures nonlinear stiffening effects in soft particulate composites through a single locking parameter, J_m.

Through this study, we find that material stiffening does not universally promote earlier instability in soft particulate composites; rather, its effect is geometry-dependent, sometimes enhancing stability. This leads to a non-monotonic relationship between critical strain and stiffening, mediated by particle interactions. Moreover, we observe a shift in buckling patterns, transitioning from microscopic to macroscopic modes, akin to those in fiber- and laminate-reinforced soft composites. These insights deepen our understanding of instability mechanics in soft composites and open new avenues for designing materials with programmable mechanical responses.

References

[1] Li, J., Slesarenko, V., and Rudykh, S., *Microscopic instabilities and elastic wave propagation in finitely deformed laminates with compressible hyperelastic phases*, Eur. J. Mech. A. Solids **73**, 126–136 (2019). doi: 10.1016/j.euromechsol.2018.07.004.

[2] Chen, D., Arora, N., Xiang, Y., Li, J., Slesarenko, V., and Rudykh, S., *Instability-induced patterns and their post-buckling development in soft particulate composites*, Mech. Mater. **175**, 104482 (2022). doi: 10.1016/j.mechmat.2022.104482.

[3] Gent, A. N., *A new constitutive relation for rubber*, Rubber Chemistry and Technology **69**(1), 59–61 (1996). doi: 10.5254/1.3538357.

4 Abstracts of posters

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

Malak Almutairi
Supervisors: Dr. Emma Holian & Prof. 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 modeling 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. 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 the composition response considering the effects of factors that may influence changes in clot composition. Given these constraints, using a traditional statistical analysis that assumes a normal error structure, for continuous univariate response data bounded between 0 and 1, can lead to biased and incorrect estimates. Therefore, an appropriate model such as beta regression should be used for reliable parameter estimates rather than normal linear regression. For the multivariate case, Dirichlet regression is an appropriate modeling approach. Through systematic comparison of different modelling approaches across a range of varied dataset features, we assess their performance in scenarios where data show asymmetry or where mass points lie close to the boundaries of the proportion scale in the observed response distributions. These methods are then applied to our cohort of AIS patients to group and model clot composition with candidate predictors, such as the type of extraction device, hospital of procedure, etiology categorization and the use of tPA drug treatment.

References

[1] E. A. Geissinger, C. L. L. Khoo, I. C. Richmond, S. J. M. Faulkner, & D. C. Schneider. A Case for Beta Regression in the Natural Sciences. Ecosphere, 13(2), e3940, 2022.

[2] J. D. Hadfield. MCMC Methods for Multi-response Generalized Linear Mixed Models: The MCMCglmm R Package. *Journal of Statistical Software*, **33**:1–22, 2010.

[3] M. Maier. *DirichletReg: Dirichlet Regression for Compositional Data in R*. Research Report Series / Department of Statistics and Mathematics, No. 125, 2014.

[4] V. Saini, L. Guada, & D. R. Yavagal. Global Epidemiology of Stroke and Access to Acute Ischemic Stroke Interventions. *Neurology*, **97**:S6–S16, 2021.

[5] M. Tsagris & C. Stewart. Compositional regression: A Review and Future Directions. *Journal of Applied Statistics*, **48**(2):218–235, 2021.

Intratumoral heterogeneity in microsatellite instability status at single-cell resolution

Harrison Anthony
Supervisor: Prof. Cathal Seoighe

Diversity within a tumor is a critical piece of information for cancer treatment and research. The cumulative diversity is known as intratumoral heterogeneity (ITH), and is important to study because high ITH has been linked to poor patient outcomes [1] and complicates the interpretation of biomarkers[2]. One such biomarker, microsatellite instability, is characterized by large changes in the repeating regions of DNA and is used to help guide immune checkpoint inhibitor treatment. While cancers with high microsatellite instability (MSI-H) are susceptible to this therapy, the response rate can be low [3] and intrinsic treatment resistance is common [4]. It has been hypothesized that these issues could be attributed to ITH, but one area still not addressed is whether MSI itself is a heterogeneous phenomenon. To investigate this, we collected all publicly available single-cell RNA sequencing data that had paired, clinical MSI status and developed a novel computational pipeline to identify MSI-H cells and assess ITH in MSI. In total, we curated a collection of 56 publicly available, single-cell RNA sequencing samples from 32 individuals. All samples were processed with a computational pipeline, which in brief filters and scales the data, identifies clusters of cells, distinguishes cancer cells from normal, and classifies cancer cells as MSI-H or as microsatellite stable (MSS). Heterogeneity is summarized using the analysis of variance F test statistic based on the MSI scores obtained from each cluster of cancer cells. This is complemented by differential gene expression analysis between cancer clusters. Five of the 32 individuals showed evidence of divergence in MSI status between distinct clusters of cancer cells ($F > 30$). The individual with the highest level of heterogeneity ($F = 75.2$) had seven distinct cancer cell clusters comprising a total of 779 cells. In contrast, the F statistic of the individual with the lowest level of heterogeneity was 5.1 (based on 6 cancer cell clusters comprising 470 cells). Tukey HSD analysis showed 17 significantly different cluster pairs for the individual with high heterogeneity whereas only five were found for the individual with low heterogeneity. These results are reinforced by differential gene expression between MSI-H and MSS cells. The individual with high heterogeneity had nine differentially expressed genes, whereas the individual with low heterogeneity only had two. These

results suggest that heterogeneity in MSI is more common than previously reported and imply that multiple, multi-regional tests could be required to improve MSI as a biomarker by accounting for ITH. Further studies are warranted to determine the frequency of heterogeneity in this biomarker at the population level, and whether the presence of both MSI-H and MSS subclones can have clinical impacts, including the potential to result in more rapid evolution of resistance to treatments for which MSI-H is a biomarker.

Supported by Research Ireland through the Research Ireland Centre for Research Training in Genomics Data Science under grant number 18/CRT/6214.

References

[1] Marusyk A, Janiszewska M, Polyak K. Intratumor Heterogeneity: The Rosetta Stone of Therapy Resistance. *Cancer Cell*. 2020 Apr 13;37(4):471-484.

[2] Gilson P, Merlin JL, Harlé A. Deciphering Tumour Heterogeneity: From Tissue to Liquid Biopsy *Cancers (Basel)*. 2022 Mar 8;14(6):1384.

[3] Battaglin F, Naseem M, Lenz HJ, Salem ME. Microsatellite instability in colorectal cancer: overview of its clinical significance and novel perspectives. *Clin Adv Hematol Oncol*. 2018 Nov;16(11):735-745.

[4] Wang R, Lian J, Wang X, Pang X, Xu B, Tang S, Shao J, Lu H. Intrinsic resistance and efficacy of immunotherapy in microsatellite instability-high colorectal cancer: A systematic review and meta-analysis. *Biomol Biomed*. 2023 Mar 16;23(2):198-208.

Algebraic and Geometric Structures of Tensors

Deborah Gonçalves Fabri
Supervisor: Dr. Joshua Maglione

The Baer correspondence associates p-groups of class 2 with alternating bilinear maps (tensors), which can be represented as matrices of linear forms. From these tensors, we construct and analyse algebraic structures like centroids and adjoint algebras that are used to decide tensor isomorphism - closely related to the group isomorphism problem. We have recently begun looking at tensors arising from hyperplane arrangements over finite fields, considering both their geometric and combinatorial properties. An important tool is the geometric analysis of the determinantal (or Pfaffian) hypersurfaces.

References

[1] J. Maglione and M. Stanojkovski *Smooth Cuboids in Group Theory*. arXiv:2212.03941v4 [math.GR], 2025.

Regional Structure-Function Coupling in Bipolar Disorder

Shir Dahan
Supervisors: Pilib Ó Broin, Dara M Cannon

MRI studies suggest structural and functional differences in bipolar disorder (BD) compared to healthy controls. Recent studies look at the coupling of structural and functional connectivity (SC-FC coupling) to provides insight on the structural contributions of neural activation coordination. SC-FC coupling was found to vary between regions, whereby unimodal regions such as visual cortex show strong coupling, whereas transmodal regions, such as in the limbic network, show weaker coupling [1]. Disrupted SC-FC coupling has been reported in euthymic BD using a single-subject atlas (AAL90) [2]. We aim, using an expanded sample and atlas, to identify regional alterations in SC-FC coupling involving emotion processing circuitry in euthymic BD.

The study included a BD diagnosis (ICD-10) group and a control group from the UK Biobank. We used the release of structural connectomes from diffusion MRI, using SIFT2 weighted matrices, and regional functional time-series [3]. Parcellation for SC and FC was based on the cortical 200/500 region Schaefer 7-network and the subcortical 16/54 region Melbourne atlases, resulting in 216 and 554 nodes. Functional matrices were constructed using Pearson's correlation and partial correlation for comparisons, for each pair of regions. We quantified SC-FC coupling using a multilinear regression with the predicted variable as the vector of functional edges from one region to all others, and the predictors as vectors of structural edges from the same region to all others using sift2 weights, path length, Euclidean distance and communicability. We then calculated the R^2 between predicted and observed functional vectors to estimate the regional SC-FC coupling [1], resulting in 216 R^2 values per participant. A gamma GLM (log link) was constructed for each node to identify SC-FC coupling differences between BD and controls. Covariates included age, sex, imaging centre, and diagnosis. The dependent variable was Z-transformed regional SC-FC coupling values. Results were Bonferroni corrected for the number of brain regions.

BD (n=163) and controls (n=326) were age (62±7) and sex (52% female) matched. Average network SC-FC coupling was high in the visual (R^2=0.21), dorsal attention (R^2=0.12) and somatomotor (mean R^2=0.12) networks, lower in the limbic network (mean R^2=0.07) and lowest across the subcortex (mean R^2=0.06). A significant effect of diagnosis was identified with altered coupling in the left temporal pole (b=0.28, p=0.010, Z=4.07), left supramarginal gyrus (b=-0.26, p=0.001, Z=-4.47), left precentral gyrus (b=-0.24, p=0.006, Z=-4.04), right frontal pole (b=-0.20, p=0.038, Z=-3.47).

SC-FC coupling was highest in the visual network and lowest in limbic cortical and subcortical regions, aligning with previous findings supporting the theory that SC-FC coupling reflects an anatomical organization of hierarchies from unimodal to transmodal regions [1]. The

subcortex showed the lowest coupling, unlike previous findings on the Human Connectome Project data, where coupling, estimated using Spearman's correlation, was high in subcortical regions as well as visual regions [4]. Higher SC-FC coupling in BD compared to controls in the temporal pole of the limbic network extends previous demonstrations of altered connectivity within the limbic network as a trait feature of BD persisting into euthymia [5]. Taken with altered coupling of the frontoparietal network (lower coupling in the frontal pole), these findings extend our understanding of integrated structure-function underpinnings of cognitive and emotion processing disruption in euthymic BD.

This research was funded by Research Ireland through the Research Ireland Centre for Research Training in Genomics Data Science under Grant number 18/CRT/6214 .

References

[1] B. Vázquez-Rodríguez et al., "Gradients of structure–function tethering across neocortex," Proc Natl Acad Sci U S A, vol. 116, no. 42, pp. 21219–21227, Oct. 2019, doi: 10.1073/pnas.1903403116.

[2] R. Zhang et al., "Aberrant brain structural-functional connectivity coupling in euthymic bipolar disorder," Hum Brain Mapp, vol. 4, no. 12, pp. 3452–3463, 2019, doi: 10.1002/hbm.24608.

[3] S. Mansour L., M. A. Di Biase, R. E. Smith, A. Zalesky, and C. Seguin, "Connectomes for 40,000 UK Biobank participants: A multi-modal, multi-scale brain network resource," Neuroimage, vol. 283, Dec. 2023, doi: 10.1016/j.neuroimage.2023.120407.

[4] Z. Gu, K. W. Jamison, M. R. Sabuncu, and A. Kuceyeski, "Heritability and interindividual variability of regional structure-function coupling," Nat Commun, vol. 12, no. 1, Dec. 2021, doi: 10.1038/s41467-021-25184-4.

[5] L. Nabulsi et al., "Bipolar Disorder and Gender Are Associated with Frontolimbic and Basal Ganglia Dysconnectivity: A Study of Topological Variance Using Network Analysis," Brain Connect, vol. 9, no. 10, pp. 745–759, Dec. 2019, doi: 10.1089/brain.2019.0667.

Single-cell transcriptomic profiling of human bone marrow-derived mesenchymal stem cells in type 2 diabetes

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

Diabetes is a chronic disorder affecting 540 million people worldwide [1]. It presents a persistent increase in blood glucose levels as a result of ineffective production or utilisation of insulin. Among the three types of diabetes, the most widespread, type 2 diabetes mellitus (T2DM), is marked by beta cell dysfunction along with insulin resistance [2]. Diabetic osteopathy, or bone disease, is a significant comorbidity of diabetes and is characterised by changes in bone microarchitecture that lead to increased fracture risk through impaired bone formation and increased bone resorption [3, 4]. Current studies that consider osteopathy as a complication of diabetes, focus on lifestyle changes and pharmacological therapy to control hyperglycemia [5]. Most of the available therapies are reactive, hence the need for therapies with preventative and/or rejuvenating potential.

This study aims to identify miRNA-based therapies for T2DM-induced osteopathy. To do this, single-cell transcriptomic profiling of human bone marrow-derived mesenchymal stem cells (hBM-MSCs) will be performed. The analysis of this data will help identify miRNAs that regulate T2DM-induced differentially expressed genes (DEGs). Subsequently, we propose to develop an interactive web-based application that provides a platform for users to upload and visualise single-cell RNA sequencing datasets for miRNA target prediction and study their effects under different disease conditions.

References

[1] International Diabetes Federation. *Diabetes basics*. Available at: `https://idf.org/about-diabetes/what-is-diabetes/` (Accessed: 28 March 2025), 2024.

[2] E. Dale Abel, Anna L. Gloyn, Carmella Evans-Molina, Joshua J. Joseph, Shivani Misra, Utpal B. Pajvani, Judith Simcox, Katalin Susztak, and Daniel J. Drucker. *Diabetes mellitus – Progress and opportunities in the evolving epidemic*. Cell, 187(15):3789–3820, 2024. `https://doi.org/10.1016/j.cell.2024.06.029`.

[3] A. Shu, M. T. Yin, E. Stein, S. Cremers, E. Dworakowski, R. Ives, and M. R. Rubin. *Bone structure and turnover in type 2 diabetes mellitus*. Osteoporosis International, 23(2):635–641, 2012. `https://doi.org/10.1007/s00198-011-1595-0`.

[4] P. Sharma, R. K. Sharma, and K. Gaur. *Understanding the impact of diabetes on bone health: A clinical review*. Metabolism Open, 24:100330, 2024. `https://doi.org/10.1016/j.metop.2024.100330`.

[5] B. Wu, Z. Fu, X. Wang, P. Zhou, Q. Yang, Y. Jiang, and D. Zhu. *A narrative review of diabetic bone disease: Characteristics, pathogenesis, and treatment*. Frontiers in Endocrinology, 13, 2022. Frontiers Media S.A. `https://doi.org/10.3389/fendo.2022.1052592`.

Ask zeta functions associated with hypergraphs

Mario Falciatore
Supervisors: Angela Carnevale, Tobias Rossmann

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. At this point, several questions arise about the relationship between hypergraphs and rational functions. In particular, although we have an explicit formula for $W_H(X,T)$ based on the poset of flags of subsets of the set of vertices of H, this provides candidate factors for the denominator and for the poles of $W_H(X,T)$, but it remains unknown how good this prediction is and how we could connect the property of $W_H(X,T)$ with some invariants of H. Moreover, less is known about hypergraphs than it is for graphs, which leads us to study properties of hypergraphs, such as the number of hypergraphs with a fixed number of vertices and hyperedges, and the asymptotic behaviour of this number.
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. An important step in this direction is to create a database of hypergraphs, up to isomorphism, with their ask zeta functions and to derive some properties of them. In this way, using techniques from machine learning, we aim to find patterns that can connect hypergraphs and their ask zeta functions, which are currently hidden from our eyes.
Supported by Research Ireland, grant 22/FFP-P/11449

References

[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 vi+ 120 pp.

5-Methylcytosine in the Cnidarian *Hydractinia symbiolongicarpus*

Paula Hillenbrand
Supervisor: Uri Frank, Lars Jermiin

5-Methylcytosine (5mC) is a key DNA modification that regulates gene expression and is most commonly found in the CpG dinucleotide context in eukaryotes. Recent advances in methylation sequencing have revealed diverse 5mC patterns across the eukaryotic tree of life, challenging previous assumptions of hypermethylated genomes being exclusive to vertebrates. For example, species from the Porifera phylum show up to 80% global methylation, while other invertebrates, such as *Caenorhabditis elegans*, lack 5mC completely [1]. The role of 5mC also varies with genomic context: methylation at gene regulatory elements and transposable elements typically represses transcription, while methylation in gene bodies correlates with active gene expression.

In mammals, 5mC is crucial for tissue homeostasis and development, regulating the expression of key developmental genes. Similar roles for 5mC in invertebrates are emerging [2]. To better understand the gene regulatory functions of 5mC, cell type-specific 5mC maps are required. The cnidarian *Hydractinia symbiolongicarpus* offers a valuable model due to its ability to generate transgenic reporter animals, allowing for cell type-specific methylation analysis. Furthermore, *Hydractinia* maintains a population of pluripotent adult stem cells [3], which can be isolated for methylation sequencing, providing insights into 5mC variation during differentiation.

This poster presents preliminary 5mC data from *Hydractinia*, using bulk nanopore sequencing data and phylogenetic analyses. Initial findings suggest reproducible mosaic DNA methylation patterns and identify the 5mC toolkit in this species. These results provide a foundation for future studies on the functional roles of 5mC in a variety of *Hydractinia* cell types, offerning the unique opportunity to study roles of 5mC in stem cell differentiation.

Supported by Research Ireland Centre for Research Training in Genomics Data Science.

References

[1] Alex de Mendoza, Ryan Lister, and Ozren Bogdanovic. *Evolution of DNA Methylome Diversity in Eukaryotes.* Journal of Molecular Biology, 432(6):1687–1705, 2020.

[2] Ksenia Skvortsova, Stephanie Bertrand, Danila Voronov, Paul E. Duckett, Samuel E. Ross, Marta Silvia Magri, Ignacio Maeso, Robert J. Weatheritt, Jose Luis Gómez Skarmeta, and Ozren Bogdanovic. *Active DNA demethylation of developmental cis-regulatory regions predates vertebrate origins.* Science Advances, 8, 2022.

[3] Áine Varley, Helen R. Horkan, Emma T. McMahon, Gabriel Krasovec, and Uri Frank. *Pluripotent, germ cell competent adult stem cells underlie cnidarian regenerative ability and clonal growth.* Current Biology, 33(9):1712–1722, 2023.

Odd inversion sets and their associated Turán graphs

Michael Joyce Maher
Supervisor: Dr. Angela Carnevale

Odd analogs of inversion sets for permutations in type A Coxeter groups, called odd inversion sets, were introduced and studied in [1]. These are a close relative of the combinatorial object knows as odd diagrams, which were first defined and studied in the same paper. Odd diagrams haves some surprising properties, namely, permutations in a group 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, I have proven this conjecture as part of my PhD project.

Inspired by the nice combinatorial properties of odd diagrams, I carried out a further analysis of the structure of odd inversion classes. In this poster we will show that odd inversion classes have some surprising properties of their own.

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

References

[1] F. Brenti and A. Carnevale *Odd length: odd diagrams and descent classes,*. Discrete Math., 344 (2021), no. 5, Paper No. 112308, 17pp.

[2] F. Brenti, A. Carnevale, and B. E. Tenner *Odd diagrams, Bruhat order, and pattern avoidance*. Comb. Theory 2 (2022), No. 1, Paper 13, 19 pages.

[3] Neil J.Y. Fan and Peter L. Guo *Poincaré Polynomials of Odd Diagram Classes.* SIAM J. Discrete Math. 36 (2022), No. 3, 2225–2237.

A Bayesian Ranking of the Olympic Medal Table

Cormac MacDermott
Supervisors: John Ferguson, Carl Scarrott

The Olympic Games serve as a benchmark to assess sporting success, with 206 National Olympic Committees (NOCs) competing in Paris 2024 across 329 events in 32 sports and 48 disciplines [2] for the prestige of an Olympic medal. The standard lexicographic medal table ranks NOCs by medal counts, prioritising gold over silver and then bronze. Such rankings inherently favour larger populations, as they have a larger talent pool competing across multiple events.

A common alternative ranking is the per-capita medal count, which normalises medal totals by population size to empirically estimate the probability of any individual winning a medal. While this approach attempts to account for population differences, it is highly sensitive to stochastic variation, particularly for smaller nations where even a single medal can substantially inflate rankings. Not to diminish the outstanding achievement of such athletes, these per-capita rankings often overemphasise medal-winning performances from countries with small populations which would be highly volatile between games.

Advanced methods have been proposed to rank countries, including [1] which ranks nations based on a value equivalent to a transformed p-value from comparing actual medal counts to an equal-capability reference null model. However, a substantial drawback with p-value-based methods is their sensitivity to sample size [6]. In this context, due to the smaller samples of medal attempts for small NOCs, their p-values cannot attain the level of significance that larger NOCs can attain, and as a result, the ranking will favour larger countries.

We propose a Bayesian ranking algorithm that orders by the "long-run" per-capita medal rate for each NOC, rather than by the observed medal counts. The ranking algorithm utilises hierarchical Bayesian modeling to produce more stable rankings by borrowing information across nations. Its key advantage is to effectively shrink estimates for smaller countries, mitigating the undue influence of stochasticity in their rankings and providing better estimates of long-run performance estimates, while accounting for population size for larger NOCs with well-established sporting infrastructures.

Our Bayesian model assumes that the number of unique medal-winning athletes follows a Poisson distribution, with the probability of winning multiple medals having a hierarchical structure to share information across NOCs. We implement this framework using Gibbs sampling in JAGS [4, 5], incorporating population data from UN Population Statistics [3] and official Olympic medal data [2].

In this poster, we apply our algorithm to rank country-level performance over the last 6 Olympic cycles. In particular, we will focus on Ireland's trajectory compared to the best-performing countries, and contrast our results with per-capita rankings.

References

[1] Robert C Duncan and Andrew Parece. Population-adjusted national rankings in the Olympics. *Journal of Sports Analytics*, 10(1):87–104, 2024.

[2] International Olympic Committee. Official Olympic Games Data, 2025. Available from www.olympics.com/ioc.

[3] United Nations. Un department of economics, population division - data downloads, 2025.

[4] Martyn Plummer. JAGS version 4.3.0 user manual, 2017.

[5] Martyn Plummer. *rjags: Bayesian Graphical Models using MCMC*, 2024. R package version 4-16.

[6] Ronald L Wasserstein and Nicole A Lazar. The ASA statement on *p*-values: Context, process, and purpose. *The American Statistician*, 70(2):129–133, 2016.

Co-evolutionary models: exploring gene-phenotype associations across mammals

Sophie Matthews
Supervisor: Cathal Seoighe

Understanding the coevolution between genes and phenotypic traits is essential for unraveling the underlying evolutionary dynamics across species. Traditional correlation methods fail to capture these associations as they do not account for phylogenetic relatedness, and trait reconstruction can lead to error accumulation as the reconstruction propagates along the tree. While some studies still rely on these basic correlation tests, others have developed coevolutionary models that account for the complexities of phylogenetic data. Coevol (Lartillot and Poujol, 2011) is a probabilistic framework that jointly models molecular substitution rates (dN/dS) and continuous phenotypic traits using a multivariate Brownian diffusion process. It employs Markov Chain Monte Carlo (MCMC) methods to estimate the covariance between substitution rates and phenotypic traits, providing a robust framework for assessing coevolution. In this study, we apply Coevol to all protein coding genes across over 100 mammalian species, to identify genes whose evolutionary rates are associated with life-history traits lifespan and body size. Additionally, we are developing a new coevolution model that examines whether gene evolution is influenced by phenotypic changes. This study contributes to the growing body of knowledge on gene-phenotype coevolution and the methodologies used to explore these relationships across evolutionary time.

Predicting acute myeloid leukaemia survival time using deep learning on cross-platform gene expression

Tyler Medina
Supervisor: Cathal Seoighe

Acute myeloid leukaemia (AML) is an aggressive bone marrow cancer characterized by a high rate of therapy resistance and variable patient outcomes, necessitating accurate prognosis to guide treatment. Machine learning models such as LASSO have been used on AML gene expression data to evaluate prognostic factors including cancer stemness and treatment resistance. However, these models use aggressive feature selection, including *a priori* selection of drug metabolism genes, and do not perform well on some patient cohorts, possibly due in part to mixed use of normalized microarray and RNA-seq training data.[1]

In this study, we propose a custom neural network architecture that accommodates both microarray and RNA-seq gene expression data as input. This architecture features a sparse hidden layer in which each node represents the expression of a gene, each of which is connected to a pair of nodes in the input layer, one for each assay of that gene. Patients are expected to have data from one gene expression assay or the other, but not both. This model avoids normalization or conversion of data between technologies, and instead assumes that each method captures its own representation of the same gene expression. The network can then learn the relationship between these technologies, as well as between gene expression and patient outcomes including survival. In this way, the learned weights of the network essentially supplement patient data in a flexible combined model that is potentially more accurate than using either technology alone.

This cross-platform model is useful in clinical settings where RNA-seq is cost-prohibitive despite its advantages. By training on both RNA-seq and microarrays, we aim to extend the insights of RNA-seq research to resource-limited environments where microarrays remain prevalent. Additionally, this approach can be scaled to include technologies like small targeted gene expression panels as sequencing efforts advance.

This research was funded by Research Ireland through the Research Ireland Centre for Research Training in Genomics Data Science under grant number 18/CRT/6214, and by H2020 Marie Skłodowska-Curie Actions grant H2020-MSCACOFUND-2019-945385.

References

[1] Abdelrahman H. Elsayed et al. *Integrated drug resistance and leukemic stemness gene-expression scores predict outcomes in large cohort of over 3500 AML patients from 10 trials.* NPJ Precision Oncology, 8, 168, 2024

A Max-Plus Approach to Preconditioning Singularly Perturbed Problem

Jekaterina Mosalska
Supervisor: Niall Madden

Singularly perturbed problems appear in many areas, such as fluid dynamics, control theory, and engineering. These problems often involve sharp changes (called layers or gradients), which make them difficult to solve using standard numerical methods [4]. When we discretize these problems, we end up with large and ill-conditioned linear systems that are hard to solve efficiently [2]. To deal with this, we need good preconditioners to help iterative solvers work faster [3].

This research explores the use of Max-Plus Algebra to design preconditioners for such systems. Max-Plus methods, based on tropical algebra and graph theory, offer a new way to estimate the size of matrix entries [1]. Using this approach, we develop preconditioners suited for finite element and finite difference methods applied to reaction-diffusion and convection-diffusion equations.

Early results show that Max-Plus-based preconditioners improve the convergence and stability of iterative

solvers, and often perform better than traditional techniques. This work contributes to more efficient numerical methods for solving multi-scale problems and has potential applications in fields like computational fluid dynamics and large-scale scientific computing.

References

[1] J. Hook and F. Tisseur. Incomplete LU preconditioner based on max-plus approximation. *SIAM J. Matrix Anal. Appl.*, 38(4):1160–1189, 2017.

[2] S. MacLachlan and N. Madden. Robust solution of singularly perturbed problems using multigrid methods. *SIAM J. Sci. Comput.*, 35(5):A2225–A2254, 2013.

[3] T.A. Nhan, S. MacLachlan, and N. Madden. Boundary layer preconditioners for finite-element discretizations of singularly perturbed reaction-diffusion problems. *Numerical Algorithms*, 79:281–310, 2018.

[4] Stynes, M. and Stynes, D. (2018). *Convection-diffusion problems*, volume 196 of *Graduate Studies in Mathematics*. American Mathematical Society, Providence, RI.

A Series of Mathematical Induction Activities to Promote De-ritualization Processes: A Teaching Experiment

Latifah Mustofa Lestyanto
Supervisor: Dr. Kirsten Pfeiffer

The aim of this poster is to introduce de-ritualization in commognition theory and suggest a series of teaching and learning activities which we developed to advance de-ritualization processes.

Commognition is a theoretical framework that views mathematics as a form of discourse [1]. In this theory, ritualization and de-ritualization are interconnected parts of the same learning process, and both of them are important. Rituals are necessary stepping stones for new discourses, an inevitable presence in the learning, and can later transform into explorations [2]. In ritualization, learners imitate expert performances before they can fully understand the usefulness and success of their own actions. When learners start to actively participate in discourse, making persistent efforts to figure out the purpose and applicability of the discourse, their rituals gradually transform into exploration, which is defined as de-ritualization [2].

Proof by induction is often introduced as a ritualized set of steps followed by tasks for students to copy these steps, and students learn to apply it as a procedure without awareness about its meaning [3]. This tendency indicates an overemphasis on ritualization. We developed a series of teaching and learning activities to provide opportunities for de-ritualization as well as ritualization. In this poster we describe some of the activities and explain how they have the potential to encourage de-ritualization processes.

A teaching experiment will be utilized as the main methodology for this study. The methodology of the teaching experiment is a research approach designed to understand the mathematical learning and reasoning of students through direct interaction and teaching [4]. Last semester, we tested our teaching and learning activities with a group of first-year mathematics undergraduate students at Universitas Negeri Malang, Indonesia, and gathered data in the form of classroom video recordings, students' written works, and students' interview audio recordings. We are in the process of analyzing these data to identify de-ritualization processes appearing during students' learning.

Supported by Indonesia Endowment Fund for Education (LPDP).

References

[1] Sfard, A. (2008). *Thinking as Communicating: Human Development, the Growth of Discourses, and Mathematizing*. Cambridge University Press.

[2] Lavie, I., Steiner, A., and Sfard, A. (2019). Routines we live by: from ritual to exploration. *Educational Studies in Mathematics*, 101(2). https://doi.org/10.1007/s10649-018-9817-4.

[3] Telloni, A. I., and Malara, N. A. (2021). Constructive and metacognitive teaching path at university level on the Principle of Mathematical Induction. *Teaching Mathematics and Computer Sciences*, 19(1). https://doi.org/10.5485/tmcs.2021.0525.

[4] Steffe, L. P., and Thompson, P. W. (2000). Teaching experiment methodology: Underlying principles and essential elements. In R.Lesh and A.E. Kelly (Eds.). *Research design in mathematics and science education* (pp. 267- 307). Hillsdale, NJ: Erlbaum.

Space Weather and Exoplanet Habitability: Proxima Centauri

Deirdre Ní Chonchubhair
Supervisor: Dr. Aaron Golden

Proxima Centauri, the nearest stellar neighbour to Earth beyond the Sun, at a distance of 1.3pc, is an active M5.5 dwarf star with one confirmed and two candidate exoplanets. Flaring, an outburst of electromagnetic radiation, is common in magnetically active stars including the Sun and can be observed across the electromagnetic spectrum. Flares that produce coronal mass ejections from the Sun can interact with the Earths' magnetic field, causing aurorae around the poles, but can also cause disruption to power lines and satellites. Stellar flares can reach much greater energies than solar flares, which may have a significant impact on exoplanet

habitability. Here we present results from high time resolution U-band observations of Proxima Centauri using the Sutherland High Speed Optical Camera (SHOC) on the 1.9m telescope at the South African Astronomical Observatory. These data were taken over seven contiguous nights in April 2019 and coincide with TESS (Transiting Exoplanet Survey Satellite) space telescope observations of Proxima Centauri at this epoch. Using SHOC's superior cadence, varying from 0.1 to 3 seconds, and comparing to the 120 second TESS cadence we explore flare incidence and frequency rates compared to that determined from TESS.

Sensitivity analyses for partially missing binary outcome data in randomised controlled trials.

Name Nirdesh Bakshi
Supervisor: Dr. Neil O'Leary

Assumptions about missing outcome data in clinical trials—especially when data may be Missing Not at Random (MNAR)—are inherently untestable. This makes sensitivity analysis essential for assessing the robustness of trial conclusions. However, standard approaches to sensitivity analysis are under-utilized, partly due to a lack of intuitive and systematic methods for exploring alternative missingness assumptions. Enhanced Tipping Point (ETP) displays, originally developed by [1] [2] based on the work of [3], offer a powerful visual framework for this task. These displays map the potential impact of different combinations of missing outcomes across treatment arms on key trial estimates, offering clear insight into the stability of conclusions under varying missingness scenarios.

In this work, we implement two types of ETP displays using the SPHERE study (secondary prevention of heart disease in general practice: randomised controlled trial) dataset, where the binary outcome indicates whether a participant was hospitalized (1) or not (0) during 12 months of follow-up. Our focus is on estimating the average treatment effect—defined as the difference in hospitalization proportions between treatment and control arms. In this trial the outcome variable was not recorded or missing for 5.48 per cent patients.

The first ETP display replicates the classical tipping-point heatmap, showing how the treatment effect estimate varies across all possible combinations of the binary outcome proportions in the treatment and control groups. The second ETP display contrasts two model-based average treatment effect estimates: one derived from imputing missing outcomes under a Missing at Random (MAR) assumption conditional only on treatment allocation, and another derived using auxiliary covariates in addition to treatment. Auxiliary covariates are fully observed and prognostic for the outcome. The second display reveals how incorporating auxiliary information yields more realistic distribution of imputed values, in contrast to the more optimistic MAR- treatment allocation only imputation. This highlights the importance of model specification in sensitivity analysis and the risks of underestimating uncertainty under naive assumptions .

Finally, our ongoing work is to extend these graphical tools to incorporate δ-adjustment techniques—commonly used for sensitivity analysis in continuous outcomes—to binary outcomes via a log-odds scale approach. In contrast to continuous outcomes where δ-adjustments can be directly made to imputed values, adjustment of binary outcomes is not straightforward due to their bounded, discrete support. Standard imputation implementations (such as mice in R) do not permit post hoc modification of posterior distributions used for imputation. Our approach addresses this gap by modifying the posterior parameter draws on the log-odds scale before imputing missing values, effectively shifting the underlying imputation model rather than its outputs. This shall enable interpretable and controlled sensitivity analyses for binary data, aligning imputation strategies more closely with the underlying assumptions about missingness. Such δ-adjustments also lend themselves to graphical displays in the manner of ETP displays, but with conditional log-odds, rather than counts of events as the sensitivity parameter to be varied. By doing so, our work will extend the δ-adjustment framework into a domain where current methods are limited, offering a structured and accessible tool for missingness analysis in trials with binary outcomes.

References

[1] V. Liublinska and D. B. Rubin, "Enhanced Tipping Point Displays," *Journal on Survey Methods*, 2012.

[2] V. Liublinska and D. B. Rubin, "Sensitivity analysis for a partially missing binary outcome in a two-arm randomized clinical trial," *Wiley Online Library*, 2014.

[3] X. Yan, S. Lee, and N. Li, "Missing data handling methods in medical device clinical trials," *Journal of Biopharmaceutical Statistics*, vol. 19, no. 6, pp. 1085–1098, 2009.

Long-Read Resequencing of Acute Myeloid Leukaemia Single-Cell RNA Sequencing Samples Improves Detection of Malignant Genomic Alterations

Micheál Ó Dálaigh
Supervisors: Eva Szegezdi, Pilib Ó Broin

Background: Acute myeloid leukaemia (AML) is an aggressive cancer, resulting in the accumulation of poorly differentiated white blood cells in the bone marrow. Due to normal and malignant haematopoiesis occurring simultaneously, methods are required to separate these cell populations in bone marrow aspirate samples.

Single cell transcriptomics (scRNA-seq) data have been used in recent years to infer the presence of genomic alterations (single-nucleotide variants, insertions/deletions, fusion genes) which allow cells with cancer-relevant alterations to be identified. One of the most popular scRNA-seq platforms, 10x Genomics, is limited by its use of Illumina short-read sequencing, which biases coverage towards one end of the transcript. PacBio Kinnex scRNA-seq utilises long-read sequencing to cover entire transcripts and is compatible with existing 10x cDNA libraries. Here, we investigate the ability of Kinnex to identify the malignant cell population in primary, patient-derived AML samples previously sequenced with the 10x 3' workflow by identifying genomic alterations linked to malignant transformation.

Methods: 4 patient samples harbouring a range of different genomic alterations relevant to AML (e.g. TET2/DNMT3A point mutations, an NPM1 insertion, and a DEK::NUP214 fusion) were resequenced with the Kinnex scRNA-seq kit and processed with the single-cell Iso-Seq analysis pipeline. CTAT-Mutations and pbfusion were used for variant calling and fusion gene identification respectively. VarTrix was used to assign identified CTAT-Mutations variants to individual cells.

Results: Kinnex recovered 29% fewer cells than 10x across the 4 samples. For cells which were sequenced with both technologies, CTAT-Mutations identified approximately 63% more single-nucleotide cancer-relevant variants in the Kinnex data than the 10x. On average, the Kinnex data covered AML mutation hotspot sites in NRAS, TET2, FLT3, DNMT3A, and NPM1 in 1.84x more cells; e.g. in an NPM1 mutated sample, Kinnex data revealed approximately 3x more (1000 vs. 280) mutant NPM1 cells than 10x. The Kinnex data also identified the DEK::NUP214 fusion which was not detectable in the corresponding 10x data.

Conclusions: Despite the lower number of cells recovered, the Kinnex data identified more malignant cells with a higher confidence by improving coverage of AML mutation hotspots located distal to the 3' of relevant transcripts. Kinnex scRNA-seq data display a superior ability to detect multiple genomic alterations, highlighting the benefits of using long-read sequencing to characterise cancer samples in single-cell studies.

Supported by Research Ireland under grant number 18/CRT/6214

On the degree of the class-counting polynomial of a graph

Lucrezia Prosperi
Supervisors: Angela Carnevale, Tobias Rossmann

Each graph Γ, along with a choice of commutative ring, defines an associated graphical group. The function that enumerates the conjugacy classes of this graphical group is a polynomial, known as the *class-counting polynomial* of Γ, denoted by $f_\Gamma(X)$. A central goal of this research is to investigate the degree of this polynomial, which is intrinsically linked to a new graph invariant, denoted by η. This invariant, η, is determined by two factors: the number of connected components of the induced subgraphs of Γ, and the cardinality of the boundary. To further explore this, we define the *class-size polynomial* of Γ, $F_\Gamma(X,Y)$, a polynomial in two variables with integer coefficients. This polynomial is directly related to the enumeration of conjugacy classes, and a corollary of the main result in [1] establishes that $f_\Gamma(X) = F_\Gamma(X,1)$. The degree of the class-counting polynomial is determined directly by the invariant η. In terms of computation, there are two known ways to calculate η. One method involves the dominating sets of the graph, while the other one is defined by running over all the subsets of the vertex set. Both are exponential-time algorithms. We address the challenge of proving that η is an NP-hard problem, or finding a polynomial algorithm to compute it. Furthermore, it remains an open question whether η is related to other graph invariants. Gaining insight into this relationship could provide a deeper understanding of the first problem. To address both challenges, we employ machine learning techniques, which are particularly effective in identifying patterns and relationships that may not be immediately apparent.

Supported by Supported by Research Ireland, grant 22/FFP-P/11449

References

[1] Rossmann, T. *Enumerating conjugacy classes of graphical groups over finite fields.* Bull. Lond. Math. Soc. 54 (2022), no. 5, 1923–1943.

Cospectrality of Unicyclic Gain Graphs

Yannan Qian
Supervisor: Dr Angela Carnevale

Spectral graph theory is an important theory for studying the nature of graphs via analysing the eigenvalues of the matrix representation (usually adjacency matrix) of the graphs. Gain graphs are graphs whose edges are labelled by elements of a fixed group, with some tame conditions. Given a gain graph, the graph with the same vertices and edges and no weights is called the underlying graph. Spectral methods have been extended to gain graphs by using the representation theory of the corresponding gain groups. G-cospectrality means two G-gain graphs are cospectral with any unitary irreducible representation [2]. It can happen for some pairs of gain graphs that they have cospectral underlying graphs. Cyclic graphs C_n are determined by G-spectrum as their underlying graphs are determined by

thier spectrum (switching isomorphism if G-cospectral) [2]. We extended this result showing that the same is true for any unicyclic gain graphs with the same underlying graph. We find for unicyclic gain graphs with the same underling graph, they are switching isomorphic if they are G-cospectral. Lollipop graphs (a path with one end connected to a cycle) are also determined by their spectrum [1], so lollipop gain graphs are determined by G-spectrum. For many other unicyclic graphs, they are not determined by spectrum. Godsil-McKay switching is a common way to construct cospectral graphs [3]. We proved nonisomorphic cospectral unicyclic graphs cannot be constructed by Godsil-McKay switching. We also tried another method to make cospectral signed graphs by changing the signs of all edges of several nodes by sequence. We proved that this always produces switching isomorphic graphs. This can be extended to some specific groups (e.g. cyclic groups with even order) by generalizing the sign-change operation.

Supported by the China Scholarship Council.

References

[1] Romain Boulet, Bertrand Jouve. *The lollipop graph is determined by its spectrum.* The Electronic Journal of Combinatorics. 15.1 2008 R74.

[2] Matteo Cavaleri, Alfredo Donno. *On cospectrality of gain graphs.* Special Matrices. 10. 343-365. 10.1515/spma-2022-0169, 2022.

[3] Edwin R. van Dam, Willem H. Haemers. *Which graphs are determined by their spectrum?* Linear Algebra and its Applications, Volume 373, Pages 241–272, 2002.

***nf-hlamajority*: a Nextflow pipeline for consensus MHC class I genotyping and its application to neoantigen identification in breast and lung cancer stromal cells**

Kevin Ryan
Supervisors: Dr Pilib Ó Broin, Dr Laura Barkley
(Lambe Institute for Translational Research)

Introduction

Cancer-associated fibroblasts (CAFs) are a heterogeneous cell type found in the tumour microenvironment. CAFs can support tumour growth and metastasis and contribute to therapeutic resistance, making them a potential therapeutic target. Here, we aim to identify neoantigens resulting from somatic mutations in CAFs. HLA genotyping, a critical step for neoantigen prediction, can be performed using DNA sequencing data with various tools available. Claeys et al. [1] found that a majority voting approach improved HLA typing performance. No end-to-end pipeline exists to apply this approach, making it difficult for non-informaticians to implement. The objectives of this study were to: 1) develop a Nextflow pipeline implementing majority voting for MHC class I typing from DNA sequencing, and 2) use HLA calls from this pipeline to identify neoantigens in CAFs.

Methods

CAFs and corresponding tumour-associated normal fibroblasts (TANs) were cultured from the tissue of 11 patients with breast cancer (10 Luminal A, one triple-negative) and 10 patients with lung cancer (six adenocarcinoma, two squamous cell carcinoma, two of unknown subtype). Whole-exome sequencing (WES) and bulk RNA sequencing were carried out on all samples. Using our pipeline, *nf-hlamajority*, we carried out HLA typing on our patient WES data and WES data from 12 NCI-60 Human Tumor Cell lines using Optitype, Polysolver, HLA-LA, and Kourami. For each HLA gene, the pipeline assigned the HLA genotype called by the highest number of tools. These HLA genotypes were used as input to Landscape of Effective Neoantigens Software (LENS)[2], along with the WES and RNA-sequencing data, to identify CAF-specific neoantigens.

Results and discussion

Results from the NCI-60 dataset showed 97% accuracy, with 68 out of 70 HLA calls matching PCR-based genotyping. LENS identified potential neoantigens resulting from missense mutations, with more high-confidence expressed mutations observed in lung cancer CAFs compared to breast cancer CAFs (Welch's Two Sample t-test, $p = 0.017$). All missense mutations were private, although two lung cancer CAF samples had a mutation in the *COASY* gene. Interestingly, this gene and other genes harbouring mutations are implicated in lipid metabolic pathways. CAFs contribute to lipid metabolism within the TME, thus impacting cancer progression and tumour immunogenicity.

Conclusions

In this study, we have developed an automated pipeline for consensus HLA genotyping which we envisage will be useful to the research community. *nf-hlamajority* has helped us identify candidate neoantigens in breast and lung cancer CAFs. Future work will focus on validation using T-cell immunogenicity assays and investigating the CAF subpopulation distribution of our candidate neoantigens using single-cell RNA sequencing. This will improve our understanding of the potential of targeting CAF neoantigens to enhance the efficacy of anti-cancer therapies.

This publication has emanted from research supported in part by a research grant from Research Ireland under Grant number 18/CRT/6214

References

[1] A. Claeys et al. Benchmark of tools for in silico prediction of MHC class I and class II genotypes from NGS data. *BMC Genomics*, 24:247, May 2023

[2] S. P. Vensko Ii et al. LENS: Landscape of Effective Neoantigens Software. *Bioinformatics*, 39:6, June 2023

Magic State Distillation using Controlled-Clifford Gates

Mark Ryder
Supervisor: Dr. Mark Howard

Magic state distillation is an essential component required to enable fault-tolerant quantum computation. The Eastin-Knill theorem[1] shows that it is impossible to have a universal set of 'transversal' quantum operations, also known as quantum gates, within a quantum error correcting code. Some non-transversal gates are required, which are very resource-intensive, limiting the advantage quantum computers have over classical computers, and increasing the risk of an error corrupting the quantum algorithm.

Magic states are a quantum resource used to circumvent the Eastin-Knill theorem. Combining this premade quantum state with a group of quantum operations known as the Clifford group, we can create what's known as the T-gate. The Clifford group plus the T-gate creates a universal gate set for quantum computers, which allows us to perform any quantum algorithm with just that subset of gates.[2]

We create these magic states using magic state distillation, which works by taking several error-prone magic states, and 'distilling' them into fewer, but more error-resistant magic states. Error-resistant magic states are required to implement the non-transversal T-gate without introducing an error to the computation. However, the magic state distillation process currently demands a large fraction of the processing power of a quantum computer. Therefore, finding an efficient magic state distillation routine is a key component in enabling quantum algorithms to outperform their classical counterparts while remaining protected against errors.

In this poster, we will explore how a controlled-Clifford operation can be used to distil magic states, and compare its performance to other popular magic state distillation protocols.

Supported by the Research Ireland Postgraduate Scholarship.

References

[1] Bryan Eastin and Emanuel Knill. *Restrictions on Transversal Encoded Quantum Gate Sets.* Phys. Rev. Lett. 102, 110502, 2009.

[2] Sergey Bravyi and Alexei Kitaev. *Universal quantum computation with ideal Clifford gates and noisy ancillas.* Phys. Rev. A 71, 022316, 2005.

Rank distributions of matrix representations of graphs over $\mathbb{F}_2$

Badriah Safarji
Supervisors: Rachel Quinlan and Cian O'Brien

Over a finite field $\mathbb{F}$, the number of $n \times n$ matrices of rank r typically increases as r increases, $0 \leq r \leq n$. However, over the field of two elements $\mathbb{F}_2$, the most frequently occurring rank in $M_n(\mathbb{F}_2)$ is not n but $n-1$. The numbers of symmetric $\mathbb{F}_2$-matrices of rank n and $n-1$ coincide if n is odd and differ marginally if n is even [1]. This opens the door to a more thorough investigation of the distribution of the matrix ranks over the field of two elements.

Let Γ be a simple undirected graph. A symmetric matrix M with entries in a field $\mathbb{F}$ represents Γ if the off-diagonal entries of M correspond to edges of Γ in the sense that $M_{ij} \neq 0_{\mathbb{F}}$ if and only if x_i and x_j are adjacent in Γ. The diagonal entries of M are not subject to any constraints, and therefore there are many matrices representing Γ over $\mathbb{F}$. This project aims to identify and characterize simple graphs of order n with more $\mathbb{F}_2$-matrix representations of rank $n-1$ than rank n, a property rare over other finite fields.

We restrict our attention to connected graphs of order $n \geq 3$ that contain an induced subgraph isomorphic to P_{n-1}. This poster will present results on the rank distributions of matrix representations of such graphs over $\mathbb{F}_2$.

References

[1] MacWilliams, Jessie. *Orthogonal matrices over finite fields..* The American Mathematical Monthly 76.2 (1969): 152-164.

Modelling the Non-Linear Viscoelastic Behaviour of Brain Tissue in Torsion

Griffen Small
Supervisor: Valentina Balbi

Brain tissue accommodates non-linear deformations and exhibits time-dependent mechanical behaviour. The latter is one of the most pronounced features of brain tissue, manifesting itself primarily through so-called viscoelastic effects. One key effect is stress relaxation, where the stress decreases over time when brain tissue is deformed and then held in place. While the literature is replete with non-linear viscoelastic models, they are generally cumbersome and computationally expensive, making model fitting and the estimation of brain tissue's material parameters difficult. The modified quasi-linear viscoelastic (MQLV) model, recently reappraised by De Pascalis et al. [1] and Balbi et al. [2], offers a simpler alternative for modelling brain tissue's viscoelastic behaviour but remains underutilised and has yet to be validated with experiments.

Torsion is one of the most robust deformation modes for measuring brain tissue's mechanical properties. It can be readily implemented using a rotational rheometer, which measures both the torque and normal force required to twist a cylindrical sample [3]. However, previous studies on brain tissue's viscoelasticity have focused on measuring only on torque, overlooking the additional insights provided by normal force measurements [4].

In this presentation, we present a novel protocol for characterising the viscoelastic properties of brain tissue, based on the torsion deformation mode and the MQLV model. We performed ramp-and-hold relaxation tests on freshly slaughtered cylindrical ovine brain samples (25 mm diameter and 10 mm height). The tests were conducted using a commercial rheometer at varying twist rates of $\{40, 240, 400\}$ rad m^{-1} s^{-1}, with a fixed twist of 88 rad m^{-1}. The viscoelastic material parameters were estimated by simultaneously fitting the measured torque and normal force to the MQLV model's analytical predictions [5]. The model's predictions were further validated through finite element simulations of the experiments using the open-source software FEniCS [6]. Our results demonstrate that the model accurately fits the experimental data, with the estimated elastic material parameters aligning well with those reported in previous studies on brain samples under torsion [3]. By allowing us to obtain two independent datasets (torque and normal force) from a single test, our proposed protocol provides us with a much more efficient and accessible alternative to traditional multi-mode protocols, which often rely on expensive, custom-made experimental rings or multiple testing devices; in contrast, our protocol can be easily implemented in any commercially available rheometer.

Beyond advancing brain tissue's mechanical characterisation and validating the efficacy of the MQLV model, our results have broader implications. When coupled with bespoke finite element models, the material parameters estimated in this study could enhance our understanding of the forces and deformations associated with traumatic brain injury, which could contribute to the design of improved headgear for sports such as boxing and motorsports. Additionally, our novel protocol offers new insights into the mechanical behaviour of soft tissues beyond the brain.

This work has emanated from research jointly funded by Taighde Éireann – Research Ireland under grant number GOIPG/2024/3552 (Griffen Small), and by the College of Science and Engineering at the University of Galway under the Millennium Fund scheme for the project "Modelling Brain Mechanics" (Valentina Balbi).

References

[1] R. De Pascalis, D. I. Abrahams, W. J. Parnell, *On nonlinear viscoelastic deformations: a reappraisal of Fung's quasi-linear viscoelastic model*, Proc. R. Soc. A: Math. Phys. Eng. Sci. 470 (2166) (2014) 20140058.

[2] V. Balbi, T. Shearer, W. J. Parnell, *Tensor decomposition for modified quasi-linear viscoelastic models: Towards a fully non-linear theory*, Math. Mech. Solids 0 (0) (2023) 1–25.

[3] V. Balbi, A. Trotta, M. Destrade, A. Ní Annaidh, *Poynting effect of brain matter in torsion*, Soft Matter 15 (25) (2019) 5147–5153.

[4] S. Chatelin, A. Constantinesco, R. Willinger, *Fifty years of brain tissue mechanical testing: from in vitro to in vivo investigations*, Biorheology 47 (5–6) (2010) 255–276.

[5] M. Righi, V. Balbi, *Foundations of viscoelasticity and application to soft tissue mechanics*, in: J. Málek, E. Süli (Eds.), Modeling Biomaterials, Springer, 2021, Ch. 3, pp. 71–103.

[6] M. Alnæs, J. Blechta, J. Hake, A. Johansson, B. Kehlet, A. Logg, C. Richardson, J. Ring, M. E. Rognes, G. N. Wells, *The FEniCS project version 1.5*, Archive of Numerical Software 3 (100) (2015) 9–23.

Numerical Modelling of Cardiovascular Haemodynamics

Sean Tobin
Supervisors: Niall Madden, Niamh Hynes

Abdominal Aortic Aneurysm, which involves the swelling of the aorta in the abdominal region of your body, puts the aorta at a serious risk of rupture. While there is no guarantee of this, if a rupture does occur, it is fatal in the vast majority of cases, with 172,427 recorded deaths attributed to it in 2019 alone [1]. The issue is in diagnosing the severity of the aneurysm, and deciding whether or not it is urgent to take action. Currently, the primary risk-of-rupture factor is taken to be the vessel radius, but in reality, it is far more complicated, with

factors such as blood pressure, vessel geometry, compliance, and shear stress playing significant roles in rupture causality.

Standard computational tools are often too resource intensive to run in a clinical setting, where results are needed in rear-real time. This motivates our project: to design an algorithm that can receive patient-specific data (especially geometry), and solve a system of PDEs to find a variety of physical quantities of interest. Upon validation with real-world data, the produced results could then be used as inputs to a surrogate model, which would greatly expedite the computation process.

In this presentation, we outline recent progress in developing a Finite Element Method (FEM)-based solver, using Firedrake, to find solutions of a nonlinear system of time-dependent PDEs that govern blood flow [2]. With an assumption that pressure can be expressed in terms of cross-sectional area, $A(t)$, given a cylindrical vessel which is homogeneous in its reference configuration, we solve for $A(t)$, and the blood flow rate, $Q(z,t)$.

Supported by CÚRAM.

References

[1] Merjulah Roby et al. *Automatic Segmentation of Abdominal Aortic Aneurysm from Computed Tomography Angiography Using a Patch-based Dilated UNet Model.* IEEE Access, 2025

[2] Formaggia, Luca, Daniele Lamponi, and Alfio Quarteroni. *One-dimensional models for blood flow in arteries.* Journal of engineering mathematics 47 (2003)

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 such as osteopathy[1]. Notably, the risk of osteopathy in individuals with T2DM is significantly influenced by sex[2]. Bone marrow mesenchymal stromal cells (BM-MSCs) play a crucial role in bone regeneration and have been widely studied for their therapeutic potential in tissue engineering and regenerative medicine[3, 4]. Recent studies have reported that T2DM-induced osteopathy is associated with impaired bone quality, primarily due to a reduction in BM-MSC numbers and their diminished differentiation capacity[5]. However, the underlying transcriptomic mechanisms driving these impairments remain unclear.

In this study, BM-MSCs were collected from 27 donors, including 13 individuals with T2DM (7 females, 6 males) and 14 without T2DM (8 females, 6 males), for bulk RNA sequencing. Gene expression profiles were analyzed across all donors, as well as within sex-specific subgroups. Differentially expressed genes (DEGs) were identified using DESeq2, followed by gene set enrichment analysis (GSEA) on the $\log_2$ fold-change values of all genes to explore differentially regulated pathways.

No distinct separation was observed between BM-MSCs from T2DM and non-T2DM donors on a PCA plot, however, 82 DEGs were identified in the overall T2DM donor group compared to controls, with 195 DEGs identified in female T2DM donors and 115 DEGs identified in male T2DM donors during sex-specific comparisons (log_2 FC $\geq 2, p < 0.05$). Differentially regulated pathways related to cell proliferation, immune response, and osteogenesis/adipogenesis were identified, but these pathways were not uniformly dysregulated in male and female T2DM donors. Interestingly, male and female T2DM donors exhibited distinct gene expression patterns within the osteoclast differentiation pathway.

In conclusion, this study provides novel insights into the transcriptomic dysregulation of BM-MSCs in T2DM, highlighting potential mechanisms contributing to BM-MSC dysfunction. Furthermore, our findings underscore the impact of sex-specific differences on BM-MSC transcriptome regulation, which may have implications for developing targeted therapeutic strategies.

Supported by China Scholarship Council and the Research Ireland (22/FFP-A/10736).

References

[1] M. Janghorbani, R. M. Van Dam, W. C. Willett, and F. B. Hu, "Systematic review of type 1 and type 2 diabetes mellitus and risk of fracture," vol. 166, no. 5, pp. 495–505.

[2] X. Wang, L. Jiang, and X. Shao, "Association Analysis of Insulin Resistance and Osteoporosis Risk in Chinese Patients with T2DM," vol. 17, pp. 909–916.

[3] J. S. Heo, Y. Choi, H.-S. Kim, and H. O. Kim, "Comparison of molecular profiles of human mesenchymal stem cells derived from bone marrow, umbilical cord blood, placenta and adipose tissue," vol. 37, no. 1, pp. 115–125.

[4] A. I. Caplan, "Mesenchymal stem cells," vol. 9, no. 5, pp. 641–650.

[5] F. C. Cassidy, C. Shortiss, C. G. Murphy, S. R. Kearns, W. Curtin, C. De Buitléir, T. O'Brien, and C. M. Coleman, "Impact of Type 2 Diabetes Mellitus on Human Bone Marrow Stromal Cell Number and Phenotypic Characteristics," vol. 21, no. 7, p. 2476.

5 Abstracts of PhD theses

6 Staff profiles

Balbi, V.

Current research interests

My research is in soft tissues mechanics, I am interested in both experimental and theoretical aspects. Due to their complexity, soft tissues are difficult to characterise mechanically. From the experimental viewpoint, I am interested in developing robust and reliable testing protocols suitable for different tissues. Theoretically, I develop new mathematical models to capture the non-linear mechanical behaviour of soft tissues. I am also interested in modelling wrinkling instabilities is soft meta-materials and biological tissues. Continuum mechanics, non-linear elasticity and visco-elasticity are my everyday tools.

Research outputs

In *Modelling the non-linear viscoelastic behaviour of brain tissue in torsion*, Griffen and I collaborated with researchers at the Politecnico di Torino. We developed a new testing protocol for brain tissue in torsion and we used a recently proposed modified quasi-linear viscoelastic model to fit the experimental data and determine the time-dependent parameters. We also validated our model with FE simulations in FeNiCs. This is the first study where two independent data (torque and axial force) are obtained from one test only and are simultaneously fitted to a QLV model.

In *Wrinkling instability of 3D auxetic bilayers in tension*, Sairam, Michel and I collaborated with researchers in Tianjin University and Keele University to investigate the wrinkling patterns that can occur when a rectangular auxetic bilayer is stretched. Opposite to conventional materials. auxetic materials expand in the direction perpendicular to stretching. We showed that in order for wrinkles to appear, the substrate of the bilayer must be more compressible than the film. We also implemented FE simulations of bilayers where the film auxeticity is introduced via a specific microstructural pattern. By varying the microstructural pattern (and thus the compressibility of the film), we showed that the critical stretch for instability matches our model prediction. This is the first study to investigate instabilities in tension of auxetic materials.

Research activities

- Post-Grads Supervision: Griffen Small(4^{th} year) and Sairam Venkata (graduated).
- Invited Talk: 2 Euromech Colloquiums (UK), Workshop on Mathematics and Mechanics of Biological Tissues (Italy). I am also organising a Doctoral School at the CISM in Udine this year.

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 data from complex survey designs, and visualisations to communicate results to stakeholders.

Research outputs

In preparation: Fitz-Simon N, Malekpour M, Tapelo N, Agboyigbor K, Farzadfar F. Small Area Estimation of indicators of diabetes and hypertension in Ghana and Uganda.

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. Technical Report, Paper and Shiny App forthcoming (under review by WHO collaborators).
- 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.

Flannery, Dane

Current research interests

Linear groups and computation, algebraic design theory.

Recent publications

[1] Generalized partially bent functions, generalized perfect arrays, and cocyclic Butson matrices (with R. Egan and J. A. Armario), Cryptography and Communications 16 (2024), no. 2, 323–337.

Research activities

- Invited lecturer, Computational Aspects of Thin Groups (3 June 2024–14 June 2024), Institute for Mathematical Sciences, National University of Singapore.
- Plenary speaker, 8th Workshop on Design Theory, Hadamard Matrices and Applications (26 May–30 May 2025), University of Seville.
- Research-in-Pairs (28 July 2025– 8 August 2025), Centre International de Rencontres Mathématiques Luminy, France.
- Associate Editor, Journal of Computational Algebra.

- Member of the Engineering and Physical Sciences Research Council UK Associate Peer Review College.
- Referee for Journal of Algebra, Journal of Algebraic Combinatorics, and the Mathematical Association of America.
- Reviewer for zbMATH and Mathematical Reviews.

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] Pierre-Emmanuel Emeriau, Mark Howard and Shane Mansfield, Quantum advantage in information retrieval. PRX Quantum, 3, 2, 020307, 2022.

Research activities

- Invited Keynote Speaker at First Workshop on Many-body quantum magic, Abu Dhabi, United Arab Emirates.
- Invited Participant and Speaker at BIRS Workshop on Quantum Circuit Design Automation, UBC Okanagan, Canada.
- Programme Committee member for QCNC 2024 Conference
- Ph.D. External Examiner at 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.
- Member of National Advisory Forum for Quantum Technologies

Madden, Niall

Current research interests

My research interests are in the fields of numerical analysis and scientific computing. I am particularly interested in numerical solution of partial differential equations, by finite element methods, and the efficient solution of applied problems through the application of modern computing techniques.

Research outputs

[1] 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. Feb 2024.

[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. Nov 2023.

[3] L. Loftus, **N. Madden**, P.A. Scott, A. Cooke, and N. McNicholas. The Gender Pay Gap and Irish Higher Education: University of Galway, a Case Study. *Adm. Sci.*, 13(11), 239, 2023. DOI: 10.3390/admsci13110239

Research activities

I gave invited seminars in University College Cork (April 2024), and Trinity College Dublin (September 2024), and presented at the International Conference on Boundary and Interior Layers (BAIL) in A Coruña (June 2024).

I successfully mentored Nanda Poddar's application for a Government of Ireland Postdoctoral Fellowship. Other team members this year have included Róisín Hill (PDR; funded by HEA GEEF), Alexander Shchepetkin (PDR, funding by Marine Institute, with Indiana Olbert as lead PI), Sean Tobin (PhD student, funded by CU-RAM, with Niamh Hynes as lead PI), and Jekaterina Mosalska (PhD student).

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.

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] D. Anderson, P. Bankston, A. McCluskey. Betweenness-induced convexity in hyperspaces of normed vector spaces *Journal of Convex Analysis,* 32 (1): 25–60, 2025

[2] A. McCluskey, J. Grant McLoughlin, K. O'Sullivan. Book chapter to appear in *International Perspectives on Mathematics Outreach*, Research in Mathematics Education series, UK: Emerald publishing, 2025

Research activities

- Co-host (with Nina Snigireva) of 22nd Galway Topology Colloquium https://maths.nuigalway.ie/galwaytopology/ on June 4-5, 2024
- PhD external examiner at UCC, November 2024

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.

Research outputs

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

Recent publications

[1] Daniels D, Roshan D, Lewis N, Newell J, et al. 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,* , 1-14, (2025).

[2] de Paula Oliveira T, Newell J. A hierarchical approach for evaluating athlete performance with an application in elite basketball. *Scientific Reports*, 14, 1717 (2024).

[3] Morrissey E.C., O'Grady L, Murphy PJ, Newell J, et al. Supporting GPs and people with hypertension to maximise medication use to control blood pressure: a pilot cluster RCT of the MIAMI intervention. *BMC Primary Care*, 25, 394 (2024).

[4] Casey D, Doyle P, Gallagher N, Newell J, et al. The Comprehensive Resilience-building psychosocial Intervention (CREST) for people with dementia in the community: a feasibility and acceptability study. *Pilot Feasibility Study*, 10, 136 (2024).

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: 2 PhD students, 2 co-supervised PhD students in the University of Limerick.
- Software:

  R package 'DynNom' for generating Dynamic Nomograms, 81,000+ downloads to date.

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 on a number of applied projects.
- Collaboration with the Health Research Board Trials Methodology Research Network on iHealth Facts health literacy project.
- Reviewer for *NIHR Journals Library Health Technology Assessments* and reviewer for *BMJ Open*.

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, and the combinatorics of alternating sign matrices.

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.

I am also interested in the teaching and learning of mathematics in higher education.

Research outputs

[1] Rachel Quinlan, *Frieze decompositions of wallpaper patterns: origami models for the cmm class*, Proceedings of the 2024 Bridges Conference, `bridgesmathart.org`, 2024.

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

[3] Rachel Quinlan, *Interchangeable Origami Wallpaper Patterns*, Proceedings of the 2023 Bridges Conference, `bridgesmathart.org`, 2023.

[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

- Supervising PhD students: Badriah Safarji (with Cian O'Brien), and Colin McDonagh.
- Presentations in 2024: ICEDIM Women in Mathematics Day (Limerick), and at the Bridges Conference (Richmond, Virginia), Ian Dangerfield public lecture (Hamilton Institute, Maynooth University).
- Guest editor for Linear Algebra and its Applications, and PRIMUS.
- Managing editor of *IMAGE*, a biannual publication of ILAS.
- Current president of the Irish Mathematical Society.

Roshan, Davood

Current research interests

My primary research interest is in the longitudinal analysis of clinical biomarkers. In particular, I am interested in developing statistical models and algorithms to generate adaptive reference regions from high dimensional streaming data from medical devices. The development of early-warning systems in real-time will be a key enabler for enhanced patient monitoring and care. I also have special interest in Translational Statistics, Data Visualisations and Data Science with a focus on developing predictive tools.

Research outputs

- Davood Roshan, Kishor Das, Diarmuid Daniels, Paul Catterson, Charles R Pedlar, and John Newell. Adaptive Reference Ranges: From A to Z. Plos One. doi: 10.1371/journal.pone.0323133
- Diarmuid Daniels, Davood Roshan, Nathan A. Lewis, John Newell, Georgie Bruinvels, Paul Catterson, Jamie Harley, Micheal Newell, Andrew Barr, and Charles R. Pedlar and. 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, 0(0):1–14, 2025. PMID: 40013720.
- Timothy McAleese, Neil Welch, Enda King, Davood Roshan, Niamh Keane, Kieran A Moran, Mark Jackson, Daniel Withers, Ray Moran, and Brian M Devitt. Primary anterior cruciate ligament reconstruction in level 1 athletes: Factors associated with return to play, reinjury, and knee function at 5 years of follow-up. The American Journal of Sports Medicine. 2025;53(4):777-790. doi:10.1177/03635465241313386

Research activities

- Grants (successful):
  - HRB Secondary Data Analysis Projects, *Riding Towards Safety: Advancing Concussion Identification, Prevention and Care in Irish Horse-Racing* (€173,125.00, co-PI).

  - Hardiman Scholarship (€110,000), (PI): to supervise a PhD student in Biostatistics, University of Galway, Ireland.
  - MedTrain+ Marie Skłodowksa- Curie Fellowship Programme at CÚRAM, *An Efficient Deep Learning Framework for Predicting Gene Expression from Histopathology Images in Ovarian Cancer Patients* (€135,000.00, PI) (PI)
- Grants (pending):
  - Science Foundation Ireland Frontiers for the Future Programme, *Detecting and Mitigating Against New and Emerging Cyber Threats in Irish Internet Traffic using Longitudinal Machine Learning* (€935,532.00, Collaborator).
  - 1 Hardiman PhD application (PI)
- Delivered keynote talk titled *"rAdIology: A statistical perspective"* at the RCSI Faculty of Radiologists and Radiation Oncologists Management in Imaging Meeting (April 2025).
- Delivered invited talk titled *"Challenge Your Limits!"* at the Department of Mathematics seminar series, University of Limerick (February 2025).
- Funded Investigator at CÚRAM.
- 2 PhD student, 2 Postdoctoral Researcher.
- Memberships: Young-ISA, Irish Statistical Association, International Society for Clinical Biostatistics, International Biometric Society, Statistical Modelling Society.

Rossmann, Tobias

Current research interests

My research is in algebra and neighbouring fields. My main research focus is on zeta functions arising from algebraic counting problems. Key themes include explicit computations and a ubiquitous dichotomy between tame and (geometrically) wild behaviour.

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] A. Carnevale, V. D. Moustakas, and T. Rossmann, *From coloured permutations to Hadamard products and zeta functions.* Sém. Lothar. Combin. 91B (2024), Art. 56, 12 pp.

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

[4] A. Carnevale, V. D. Moustakas, and T. Rossmann, *Coloured shuffle compatibility, Hadamard products, and ask zeta functions.* To appear in Bull. Lond. Math. Soc., arXiv:2407.01387, 21 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). This grant currently funds PhD students M. Falciatore and L. Prosperi and postdoctoral researcher A. Baykalov (see below).
- I gave an invited research-level course on *Enumerating orbits of groups* at the Research Programme *Combinatorial Methods in Enumerative Algebra*, ICTS Bangalore, India (December 2024).
- I co-organised *Groups in Galway 2024* (with A. Carnevale and J. Maglione; May 2024) and *Symbolic Enumeration in Algebra* (with A. Carnevale, P. Lins, J. Maglione, and C. Voll; July 2024 and May 2025).
- 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).

Simpkin, Andrew

Current research interests

Multilevel functional data; derivative estimation; longitudinal GWAS

Recent publications

[1] A. J. Simpkin, et al.. Effect of early and later prone positioning on outcomes in invasively ventilated COVID-19 patients with acute respiratory distress syndrome: analysis of the prospective COVID-19 critical care consortium cohort study. *Annals of Intensive Care*, 15(1):22, 2025.

[2] S. Golovkine, E. Gunning, A. J. Simpkin, N. Bargary. On the estimation of the number of components in multivariate functional principal component analysis. *Communications in Statistics*, 2025.

[3] A. Großbach, ..., A. J. Simpkin. Maximizing insights from longitudinal epigenetic age data: simulations, applications, and practical guidance. *Clinical Epigenetics*, 16(1):187, 2024.

Research activities

- Current research grants:
  - Simpkin AJ (PI). Insight-Endotronix Targeted Project. December 2024 to April 2026 €220,000
  - Simpkin AJ, Hynes N (co-PIs). HealAsyst: A multifactorial wound treatment monitoring system for intelligent healing of chronic wounds. April 2023 to March 2026; €1,214,000;
  - Simpkin AJ (PI), Bargary N. Modelling sensor data in recreational runners. Insight Platform Research Budget. February 2022 to January 2026; €112,000;
  - Simpkin AJ, Bargary N (co-PIs). Functional data Analysis for Sensor Technology. SFI Frontiers for the Future project. December 2020 to November 2024; €467,569;

- Graduate students: Anna Großbach *Longitudinal epigenetics*; John Andrew *Longitudinal functional data*; Solomon Beer *Lifecourse modelling with time varying covariates*
- 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*

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

I work in functional data analysis. Currently, my research focuses on derivative estimation for functional data. I am interested in developing new methodologies to estimate derivatives of multivariate and/or multilevel functional data within the framework of functional principal component analysis.

Recent publications

[1] Zhu, Y., Fezzi, S., Bargary, N., Ding, D., Scarsini, R., Lunardi, M., ...& Simpkin, A. J. (2025). Validation of Machine-Learning Angiography-Derived Physiological Pattern of Coronary Artery Disease. *European Heart Journal-Digital Health*, accepted.

[2] Zhu, Y., Golovkine, S., Bargary, N., Simpkin, A. J. (2025). Derivative Estimation of Multivariate Functional Data. *Computational Statistics & Data Analysis*, under review.

Research activities

- Conference talk: Estimation and application of derivative multivariate functional principal component analysis. 32nd International Biometric Conference (IBC), Dec 2024, Atlanta, USA.

7 Visitors

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

Dates of visit: July and August, 2024

Watson, Stephen. (York University, Toronto)
Visiting: Aisling McCluskey

Dates of visit: 4 Dec 2024 – 6 Dec 2024

Research activity

Initialisation of new research collaboration; presenting School seminar

---

8 Conferences, meetings, and workshops

9 School seminar

School Seminar

[1] Mehakpreet Singh, University of Limerick. *Efficient Mass-Preserving Finite Volume Approach for the Rennet-Induced Coagulation Equation*, 28/03/2024. (Contact: Niall Madden)

[2] Hannah Conroy Broderick, University College Dublin. *A simple formula for determining in vivo stress difference in human skin*, 18/04/2024. (Contact: Michel Destrade)

[3] Marcelo Dias, University of Edinburgh. *Some Investigations on Stress Localization in Thin Elastic Sheets*, 25/04/2024. (Contact: School of Engineering)

[4] Doireann O'Kiely, University of Limerick. *Moving out of plane: wrinkling and buckling*, 25/04/2024. (Contact: Michel Destrade)

[5] Murray Aitkin, University of Melbourne. *The Bayesian Bootstrap: the Universal Multinomial Model and non-informative Dirichlet Prior for statistical analysis*, 09/05/2024. (Contact: John Hinde, Carl Scarrott)

[6] Christopher Voll, Bielefeld University. *Ehrhart theory, Hecke series, and vertex enumeration in affine buildings*, 15/05/2024. (Contact: Joshua Maglione)

[7] Svetlana Petrenko, University College London. *Mathematical models of diatom frustule patterning*, 23/05/2024. (Contact: Stephan Rudykh)

[8] Artur Gower, University of Sheffield. *Designing sensors for wind turbines and other big rotating things*, 28/05/2024. (Contact: Valentina Balbi)

[9] Tom Shearer, University of Manchester. *Mathematical Modelling of Biological Soft Tissues*, 29/05/2024. (Contact: Valentina Balbi)

[10] Sairam Pamulaparthi Venkata, University of Galway. *(PhD Viva) Designing instabilities in inhomogeneous soft auxetic structures*, 18/06/2024.

[11] Marston Conder, University of Auckland. *Recent discoveries about finite quotients of triangle groups*, 04/09/2024. (Contact: Angela Carnevale)

[12] Mark Dukes, University College Dublin. *Ascent sequences, weak ascent sequences, and related combinatorial structures*, 05/09/2024. (Contact: Angela Carnevale)

[13] Doug Speed, Arhus University. *New tools for analyzing genome-wide association study data*, 12/09/2024. (Contact: Cathal Seoighe)

[14] Leonard Henckel, University College Dublin. *Graphical tools for selecting conditional instrumental sets*, 13/09/2024. (Contact: Nicola Fitz-Simon)

[15] James Cruickshank, University of Galway. *Combinatorial geometric constraint systems*, 03/10/2024.

[16] Oleksandra Gasanova, University of Duisburg-Essen. *Periodic lozenge tilings of the plane*, 10/10/2024. (Contact: Emil Skoldberg)

[17] Richard Aron, Kent State University. *Norm attainment and isometries*, 15/10/2024. (Contact: Nina Snigireva)

[18] Alberto Paccanaro, Royal Holloway University of London & FGV. *Machine learning algorithms for predicting disease genes, drug side effects and novel enzymes*, 17/10/2024. (Contact: Haixuan Yang)

[19] David Malone, Maynooth University. *Why is it Thursday, October 31st 2024, 15:00:00 UTC?*, 31/10/2024. (Contact: Rachel Quinlan)

[20] Niall Madden, University of Galway. *An enriched finite element space for boundary layer problems*, 14/11/2024.

[21] Colin Semple, University of Edinburgh. *Genomic instability and mitochondrial dysfunction drive high grade serous ovarian cancer*, 29/11/2024. (Contact: Cathal Seoighe)

[22] Stephen Watson, York University. *How to Describe all Semiorders*, 05/12/2024. (Contact: Aisling McCluskey)

[23] Seungjai Lee, Incheon National University. *Zeta functions of Lie algebras over finite fields*, 30/01/2025. (Contact: Joshua Maglione)

[24] Bartosz Wcislo, University of Gdansk. *Truth values and semantic paradoxes*, 06/02/2025. (Contact: Michael McGettrick)

[25] Christopher Voll, Bielefeld University. *Combinatorial aspects of lattice enumeration*, 13/02/2025. (Contact: Joshua Maglione)

[26] Andrew Simpkin, University of Galway. *Functional data analysis, genomics and learning English*, 20/02/2025.

[27] Helena Smigoc, University College Dublin. *Spectral arbitrariness for trees fails spectacularly*, 27/02/2025. (Contact: Rachel Quinlan)

[28] Mohsen Daman, University of Galway. *(PhD Viva) The Mechanics of Biological Growth: A Study Through The Vertex Model*, 12/03/2025.

[29] Peter Phelan, University of Galway. *(PhD Viva) DGA Structures on Minimal Free Resolutions of Binomial Edge Ideals*, 14/03/2025.

[30] Michael Mackey, University College Dublin. *Fixed points of spin factor automorphisms*, 03/04/2025. (Contact: Nina Snigireva)