NUI Galway
OÉ Gaillimh

School of Mathematics, Statistics and Applied Mathematics Research Day
1 May 2013

Programme

9:30-9:45	Ray Ryan	Opening Remarks
9:45-10:00	Lokesh Joshi	Comments from NUIG VP for Research
10:00-10:30	Dane Flannery	Computing with infinite linear groups: achievements and challenges
10:30-11:00	Tea and Coffee	
11:00-11:30	Haixuan Yang	Constellation of human soluble protein complexes
11:30-12:00	Claas Röver	How difficult is Shunting?
12:00-12:30	Jeremiah Murphy	Mathematical modelling of ligaments, muscles and tendons.
12:30-2:00	Lunch and Poster Session in Concourse	
2:00-2:30	Patrick Farrell	Adjoints of finite element models
2:30-3:30	Blitz Session	
3:30-5:00	Poster Session in Concourse	
5:00	Reception and Presentation of Poster Prizes in Staff Club, Quadrangle	

1 Introduction

Welcome to the annual Research Day in the School of Mathematics, Statistics and Applied Mathematics. We have had another fruitful year of research activity.

A major highlight has been the outstanding achievement of Professor Donal O'Regan, who has just published his 1,000th peer-reviewed mathematical article. He is now one of the most prolific authors in the history of Mathematics in the world. Over the 2002-2006 period, Donal authored an average of 56 articles per year according to MathSciNet, the most extensive database of mathematical works. To put this number in perspective, during that same period the whole island of Ireland produced an average of 142 mathematical articles per year, according to the Forfás bibliometric report (Research Strengths in Ireland), putting his contribution at nearly 40% of the entire Irish output. Donal was honoured last year by being elected a Member of the Royal Irish Academy.

Professor John Hinde has been elected President of the International Biometric Society. The International Biometric Society is an international society promoting the development and application of statistical and mathematical theory and methods in the biosciences, including agriculture, biomedical science and public health, ecology, environmental sciences, forestry, and allied disciplines. John's elevation to this post is a great honour for the School and the University.

In spite of very difficult funding restrictions, the School has recruited six new PhD students and we have been very fortunate in making a new appointment: Dr Haixuan Yang has taken up the new post of Lecturer in Statistical Bioinformatics. This appointment adds to our growing strength in a vital new area. We also graduated our first two PhDs in Bioinformatics this year, Miguel Lacerda and Paul Geeleher. Another of our Bioinformatics PhD students, Paul Korir, represented the School in the first Galway Threesis competion, with his talk on the Impact of a Mutation on the Stapling Up of Genes. Using an analogy based on common office stationery, Paul explained his research on the impact of a mutation that affects a core component of the splicing machinery ('stapler'). This mutation is known to cause an eye disease called retinitis pigmentosa. His work, conducted under the supervision of Professor Cathal Seoighe, provides evidence that this mutation leads to 'stapling errors' that affect many genes. Paul made the final round of the competition and was placed second overall.

We hosted several conferences and workshops during the year, including

- The 6th de Brún Workshop: Linear Algebra and Matrix Theory - connections, applications and computations, organized by Professor Graham Ellis, Dr Niall Madden and Dr Rachel Quinlan, in December 2012. The proceedings of the Fifth de Brún Workshop on Probabilistic Group Theory, Combinatorics, and Computing, edited by Dr Dane Flannery and Dr Alla Detinko from the School, have now been published by Springer.

- The 1st Irish Meeting for Linear Algebra Research, organized by Dr Niall Madden and Dr Rachel Quinlan, was also held in December 2012.

- Two Summer Schools in Biostatistics were held in June 2012, organized by Dr John Newell.

- A Workshop on Statistical Analysis with Missing Data using Multiple Imputation was held in December 2012, organized by Dr John Newell.

- The annual Groups in Galway conference was held in May 2012, organized by Dr Javier Aramayona and Dr Claas Roever, with a wide range of eminent invited speakers from around the world.

Upcoming events include Groups in Galway 2013, a Topology conference in July this year, organized by Dr Aisling McCluskey and a Workshop on Visualisation of Data in Social Sciences. This is a joint venture between

CORE, the Complex Systems research centre jointly organized by Dr Petri Piiroinen, and the newly established Whitaker Institute, with which the School is already forming promising research collaborations. Active participation in the annual Galway Science and Technology Festival, Science Experience Workshops, the Mathematics Enrichment Programme, and the School TYFridays programme, to mention just a few, are all contributing to spreading the message of the School's wide ranging activities in the mathematical sciences. I would like to express my appreciation to the staff and the research students in the School for their generosity and enthusiasm in making these possible.

Ray Ryan
Head of School

2 Presentations

Computing with infinite linear groups: achievements and challenges

Dane Flannery

School of Mathematics, Statistics and Applied Mathematics

We survey progress over the past few years in computing with finitely generated linear groups over an infinite domain. We indicate some important open questions and suggest avenues for continuing research.

Constellation of human soluble protein complexes

Haixuan Yang

School of Mathematics, Statistics and Applied Mathematics

Cellular processes often depend on stable physical associations between proteins. Despite recent progress, knowledge of the composition of human protein complexes remains limited. To close this gap, we applied an integrative global proteomic profiling approach, based on chromatographic separation of cultured human cell extracts into more than one thousand biochemical fractions that were subsequently analyzed by quantitative tandem mass spectrometry, to systematically identify a network of 13,993 high-confidence physical interactions among 3,006 stably associated soluble human proteins. This results in 622 putative protein complexes, depicted as constellation within a cell – proteins as stars and a cell as a universe. Most of these complexes are linked to core biological processes and encompass both candidate disease genes and unannotated proteins to inform on mechanism.

How difficult is Shunting?

Claas Röver

School of Mathematics, Statistics and Applied Mathematics

One of the easiest ways to bring structure into a countable set is to introduce some order. I'll talk about the 'pure' mathematics of a fixed number of shunting tracks that meet at a single point such that precisely two are connected there at any one time.

Mathematical modelling of ligaments, muscles and tendons.

Jerry Murphy

School of Mathematics, Statistics and Applied Mathematics, NUIG and Department of Mechanical Engineering, DCU

Ligaments, muscles and tendons share the same physical characteristics: they are incompressible, non-linearly elastic, transversely isotropic materials. There is a well-developed mathematical model for materials with these characteristics. The difficulties encountered when matching experimental data with this theory are described.

Adjoints of finite element models

Patrick E. Farrell

Imperial College London

The derivatives of PDE models are key ingredients in many important algorithms of computational mathematics. They find applications in diverse areas such as sensitivity analysis, PDE-constrained optimisation, continuation and bifurcation analysis, error estimation, and generalised stability theory.

These derivatives, computed using the so-called tangent linear and adjoint models, have made an enormous impact in certain scientific fields (such as aeronautics, meteorology, and oceanography). However, their use in other areas has been hampered by the great practical difficulty of the derivation and implementation of tangent linear and adjoint models. In his recent book, Naumann (2011) describes the problem of the robust automated derivation of parallel tangent linear and adjoint models as "one of the great open problems in the field of high-performance scientific computing".

In this talk, we present an elegant solution to this problem for the common case where the forward model may be written in variational form, and discuss some of its applications.

---

3 Blitz Session

- John Hinde, *Finite mixture model clustering of SNP data*

- Alexander Rahm, *On a question of Serre*

- Luigi Vergori, *On the finite element implementation of anisotropic elasticity*

- Graham Ellis, *The fundamental group of protein complements*

- Cathal Seoighe, *Gene expression deconvolution: new tools and applications*

- Rachel Quinlan, *How to cover a finite vector space with hyperplanes*

---

4 Poster Session

Genome wide DNA methylation patterns of colonic epithelial cells of Ulcerative Colitis patients

Alan Barnicle

Supervisors: Laurence Egan, Cathal Seoighe

Ulcerative colitis associated cancer (UCAC) is the subtype of colorectal cancer (CRC) that is associated with inflammatory bowel disease (IBD). Within 30 years of disease onset, more than 20% of IBD patients develop UCAC, and more than 50% of these patients will die from UCAC. The strong connection between inflammation and cancer progression has been well documented; however, an increasing body of evidence suggests that epigenetic changes, specifically DNA methylation, may play an important role in the pathogenesis of UCAC. Here we investigate genome wide methylation levels of ulcerative colitis (UC) patients to develop an integrative model for DNA methylation induced UCAC.

Pinch biopsies were acquired from recruited UC patients in University Hospital Galway. Highly purified epithelial populations were isolated from these biopsies and assessed by means of flow cytometry and phase contrast microscopy. Genomic DNA was then extracted from these cells for selective enrichment of methylated DNA through a restriction enzyme based assay called HELP (HpaII tiny fragment Enrichment by Ligation-mediated PCR). The HELP assay isolates sequences neighboring sites digested by the methylation-sensitive HpaII restriction enzyme for massive parallel sequencing. It can be used to quantifying methylation at more than 1.8 million loci in the human genome and allows for recognition of both CG dense and CG diminished genomic regions (Suzuki et al 2010).

The epigenetic landscape generated from this study should provide new molecular mechanisms and markers for ulcerative colitis associated colon cancer and potentially reveal new strategies for the design of inflammatory bowel disease treatments.

Algorithm for computing cohomology of $SL(2, \mathbb{Z}[\frac{1}{m}])$

Bui Anh Tuan

Supervisors: Graham Ellis

An algorithm for computing a free $\mathbb{Z}G$-resolution for any crystallographic group G has been implemented in HAP. This algorithm applies a perturbation technique of CTC Wall to the short exact sequence $1 \to T \to G \to P \to 1$ involving the finite point group P and the free abelian translation subgroup T. More efficient algorithms could be designed for specific classes of crystallographic groups. For instance, Mark Röder has designed and implemented an algorithm for arbitrary Bieberbach groups (*i.e.* crystallographic groups that act fixed-point freely on Euclidean space). Röder's algorithm uses convex hull computations to construct a fundamental domain for a Bieberbach group.

Motivated by the work of Röder, we focus attention in this paper on those n-dimensional crystallographic groups G that preserve some n-dimensional lattice $L \subset \mathbb{R}^n$ with the cubical fundamental domain. We design and implement an algortihm for producing a free $\mathbb{Z}G$-resolution of $\mathbb{Z}$ for such a group.

[1] Graham Ellis, James Harris, and Emil Sköldberg. Polytopal resolutions for finite groups. J. Reine Angew. Math. 598 (2006), 131-137.

[2] Marc Röder. HAPcryst package. 2007.

[3] Karel Dekimpe and Nansen Petrosyan. Homology of Hantzsche-Wendt Groups. Contemporary Mathematics, Volume 501, 2009.

---

author: Artur L. Gower, the work was co-authored with: M. Destrade and R.W.Ogden (School of Mathematics and Statistics, University of Glasgow, Scotland)

Title:Counter-intuitive results in acousto-elasticity

Abstract: The determination of the direction of greatest tension in a deformed solid is one of the main goals of acoustic non-destructive evaluation because, for isotropic solids, this direction coincides with the direction of greatest stress. Finding the direction of greatest stress is important in geophysics, oil prospecting, structural health monitoring, and for the non-destructive evaluation of the nonlinear elastic constants of materials (see e.g. [R.A. Guyer and P.A. Johnson, Nonlinear Mesoscopic Elasticity, Wiley, 2009]) .

In this poster we present results of the propagation of small-amplitude elastic waves in the body and on the surface of a deformed solid. We uncover examples of solids where the wave speed does not have its greatest value along the direction of greatest stretch, and/or can be extremal along directions which are oblique to the directions of greatest stretch. This goes against what was commonly accepted. This phenomena occurs because the coupling of acoustics and elasticity is a non-linear phenomenon even at its lowest order, and it can thus generate counter-intuitive results.

Effect of degree of Negative energy balance on hepatic miRna expression in postpartum dairy cattle and their potential targets involved in lipid metabolism

Attia Fatima
Supervisors: Cathal Seoighe, Dermot Morris, Charlie Spillane

Negative energy balance is a metabolic disorder of early post -partum dairy cattle which has pleiotropic effects on liver gene expression. micro RNAs (miRNAs) are small non coding RNA which can regulate gene expression at post transcription level. In this study 5 miRNAs were up-regulated in liver tissues of dairy cattle under severe negative energy balance two weeks postpartum. The up-regulated miRNAs miR-31, miR-17 and miR-140 are implicated in liver diseases. The up-regulated miRNA, miR-2885 is cattle specific and its putative target gene FADS2 (fatty acid desaturase 2) is 6 folds down-regulated under NEB, FADS2 is critical for lipid biosynthesis which is very important to maintain energy balance and normal liver function. This study will help understand better the NEB in cattle.

[1] McCarthy, S., Waters, S., Kenny, D., Diskin, M., Fitzpatrick, R., Patton, J., Wathes, D. and

Morris, D. (2010). Negative energy balance and hepatic gene expression patterns in high-yielding dairy cows during the early postpartum period: a global approach. Physiol Genomics.42A (3): 188Ű199

Bisets and double Burnside algebras.

Brendan Masterson
Supervisor: Götz Pfeiffer

Let G be a finite group and k be a field. A (G,G)-biset is both a left and right G-set, such that the G-actions commute. The double Burnside ring $B(G,G)$ is the Grothendieck ring of the category of finite (G,G)-bisets with respect to disjoint unions and the tensor product of bisets over G. We present recent results in the theory of double burnside algebras, including a method for the decomposition of $kB(G,G)$, complete with worked example.

[1] K. Bauer, D. Sen, P. Zvengrowski. A Generalized Goursat Lemma, 2011. Preprint arXiv:1109.002v1

[2] S. Bouc, R. Stancu, J. Thévenaz. Simple biset functors and double Burnside ring. Journal of Pure and Applied Algebra, 217 (2013) 546-566.

[3] R. Boltje, S.Danz. Ghost algebras of double Burnside algebras via Schur Functors, 2012. Preprint arXiv:1203.1346v1.

Variable Selection Techniques for Multiply Imputed Data

Deirdre Wall
Supervisor: John Newell

Missing data can be a serious problem, in particular in retrospective observational studies where the percentage of subjects with complete data can be of concern. Multiple Imputation (MI) is a popular technique in missing data problems. MI uses models based on observed data to replace missing values with credible values. This process is repeated a number of times to create several imputed datasets. An approach to model selection is to identify the final model based on the imputed datasets. Results will be presented from a simulation study to compare the performance of variable selection techniques in multiple imputed data and a new method of imputation where random forests are used to impute a single dataset.

Recent Developments in Algebraic Statistics

Isaac Zebulun Burke
Supervisor: Dr. Emil Sköldberg

Algebra has traditionally had numerous applications in statistics. However, it is only in recent years that computational algebraic geometry and related combinatorial techniques have been used to examine statistical models and inference problems. Central to this advancement is the fact that polynomials and ratios of polynomials appear frequently in statistical methods, from model representations to inferential procedures. Initial work in this area was concerned with constructing algebraic algorithms for sampling from discrete exponential families conditional on a sufficient statistic [1]. This eventually led to the monograph Pistone et al. [2], where the term "algebraic statistics" was officially coined. Here we present a introduction to this rapidly expanding field from the algebraist's perspective and consider some recent developments.

[1] DIACONIS, P. and STURMFELS, B. (1998). Algebraic Algorithms for sampling from Conditional Distributions. *The Annals of Statistics*, **26**, 363-397

[2] PISTONE, G., RICCOMAGNO, E. and WYNN, H. P. (2000). *Algebraic Statistics (Computational Commutative Algebra in Statistics)*. Chapman and Hall CRC.

Partial matrices whose completions all have the same rank

James McTigue
Supervisors: Dr Rachel Quinlan

A partial matrix over a field $\mathbb{F}$ is a matrix whose entries are either elements of the field $\mathbb{F}$ or independent indeterminates. Let A be an $m \times n$ partial matrix over a field $\mathbb{F}$ whose completions all have the same rank $r \leq \min(m,n)$. We answer the following questions:

[1] What condition on the order of $\mathbb{F}$ is sufficient for A to contain an $r \times r$ partial sub-matrix whose completions are all non-singular?

[2] If the order of $\mathbb{F}$ is not sufficient to guarantee that A contains an $r \times r$ partial sub-matrix whose completions are all non-singular what are the necessary conditions on the dimension of A to ensure that it does contain such a partial sub-matrix?

This is joint work with Dr Rachel Quinlan.

Seasonal migration models

John Donohue
Supervisor: Dr Petri Piiroinen

Population models where two or more species exhibit predator-prey relationships have long been of interest to researchers working on both dynamical systems and ecological modelling [1]. Most of these models have been static where the different species have been constrained to a specific area. However, even though seasonal migration is a common occurrence in nature [2, 3], surprisingly few attempts have been made to model predator-prey systems that incorporate such behaviour. The possibility for predator-prey problems that allow for one or more of the species to undergo mass migration open up a range of new possibilities from a dynamical point of view. Furthermore, systems of this type can be modeled in a variety of different ways. Here we focus on two different approaches, namely, ordinary and partial differential equations, where the former can be seen as a compartment model and the latter a spatial model. In both cases the inclusion of the seasonal periodicity is key in understanding their behaviour. The dynamics arising from the different migration models will be compared, with particular emphasis placed on the stability of periodic solutions and bifurcations.

[1] Murray, J. D., 1989. *Mathematical Biology.* Berlin: Springer.

[2] Egevang, C., Stenhouse, I.J., Phillips, R.A., Petersen, A., Fox, J.W. and Silk, J.R.D., 2009. Tracking of Arctic Terns Sterna paradisaea reveals longest animal migration. *Proceedings of the National Academy of Sciences of the United States of America*, 107(5), pp.2078-2081.

[3] Madsen T. and Shine R., 1996. Seasonal migration of predators and prey - a study of pythons and rats in tropical Australia. *Ecology*, 77(1), pp.149-156.

Topologies as Value Quantales : the ϵ-δ obsession.

Jorge, Bruno
Supervisors: Aisling McCluskey

We present an equivalence of categories $\mathcal{O} : \mathbf{T} \to \mathbf{Top}$ between the category of Value Quantales, $\mathbf{T}$, and the category of topological spaces, $\mathbf{Top}$. We also construct the value quantale equivalent of topological products, coproducts, equalizerers, direct and inverse limits.

[1] R. C. Flagg, *Quantales and Continuity Spaces*. Algebra Universalis, 1997.

[2]

[3]

A Mathematical Model of CENP-A Loading in Mammalian Centromeres

Kevin Doherty
Supervisors: Dr Martin Meere, Dr Petri Piiroinen

The presence of CENP-A at centromeres is vital for the proper construction of the kintechore complex and, in turn, microtubule binding and correct segregation of sister chromatids in mitosis. Loss of CENP-A from centromeres results in defects in chromosome congression to the metaphase plate and missegregation in anaphase which can result in micronuclei [1]. A number of factors play important roles in CENP-A association with and loading into centromeres, for example, HJURP [2] and the Mis18 complex [3]. A mathematical model of CENP-A incorporation in centromeres is presented that uses a dynamical systems approach. The model contains two compartments, one for the nucleoplasm and another for the centromeric binding sites.

[1] V. RÃĭgnier, P. Vagnarelli, T. Fukagawa, T. Zerjal, E. Burns, D. Trouche, W. Earnshaw, and W. Brown, *CENP-A is required for accurate chromosome segregation and sustained kinetochore association of BubR1*, Molecular and Cellular Biology **25** (2005), no. 10, 3967âĂŞ3981.

[2] D.R. Foltz, L.E.T Jansen, A.O. Bailey, J.R. Yates III, E.A. Bassett, S. Wood, B.E. Black, and D.W. Cleveland, *Centromere-specific assembly of CENP-A nucleosomes is mediated by HJURP*, Cell **137** (2009), no. 3, 472âĂŞ484.

[3] Y. Fujita, T. Hayashi, T. Kiyomitsu, Y. Toyoda, A. Kokubu, C. Obuse, and M. Yanagida, *Priming of centromere for CENP-A recruitment by human hMis18Îś, hMis18Îš, and M18BP1*, Developmental Cell **12** (2007), no. 1, 17âĂŞ30.

Extensive variation in DNA diversity patterns in chromosomes of parasite samples from patients

Students of MA216 module on Mathematical Molecular Biology II
Supervisors: Tim Downing

Patterns of DNA variation can describe population history, rates of evolution and highlight mutations associated with disease. In populations, multiple complementary approaches can isolate mutations with differential rates of co-inheritance and contrasting drivers of variability. In 2002-03, 12 Leishmania donovani parasites samples were isolated from patients in Nepal with acute disease. These strains have a unique geographic and genetic profile among leishmaniasis cases, being a distinct lineage all from the uplands of Nepal (aka the ŞYetiŤ strains). Using the DNA sequences for each chromosome, we compared the relative variation, recombination rates and inter-sample genetic distances. Differing patterns of diversity were mirrored by extensive disparities in mutations co-inheritance rates across chromosomes. Linkage between mutations tended not to decline with distance between mutations, which indicated clonal non-sexual reproduction. However, phylogenetic trees were incompatible between chromosomes: each presented differing patterns of relatedness between the 12 strains. This pattern was symptomatic of episodic but rare outbreeding and recombination during co-infection of multiple parasites on the background of clonality. All research presented was performed by students taking this module.

The Pirie-Kieren Theory: a possible framework for exploring growth of mathematical understanding in Metric Spaces

Michelle Duane
Supervisor: Dr Aisling McCluskey

This research seeks to explore how senior Irish undergraduate mathematics students respond to the type of learning required by *Metric Spaces*, a subject both enabling and demanding *advanced mathematical thinking*. It seeks to examine the development of and facility with proof and proving in such students. Data will be collected by means of semi-structured interviews, analysis of studentsâĂŹ written mathematical work and non-participant periodic observation of the classroom.

There are a number of theoretical frameworks within the field of mathematics education that could be ap-

plied to the data collected from this study. The Pirie-Kieren Theory is one such framework that I have chosen to discuss here. It is a dynamical theory for the growth of mathematical understanding that could be utilised to analyse students' understanding of key concepts in Metric Spaces.

[1] Martin, L. (2008). Folding back and the dynamical growth of mathematical understanding: Elaborating the Pirie-Kieren Theory. *The Journal of Mathematical Behavior*, *27*(1), 64-85.

[2] Pirie, S., and Kieren, T. (1994). Growth in mathematical understanding: How can we characterise it and how can we represent it? *Educational Studies in Mathematics*, *26*(2/3), 165-190.

[3] Tall, D. (Ed.). (1991). *Advanced Mathematical Thinking*. Dordrecht: Kluwer Academic Publishers.

Coxeter exponents and flags of root systems

Mohammad Adib Makrooni
Supervisors: John Burns

The exponents of a compact Lie group G (or its Weyl group $W(G)$) can be variously defined in terms of its cohomology, the cohomology of its (full) flag variety or in terms of lattice points in certain associated rational simplices. It seems reasonable therefore (in any of the above settings) to look for descriptions of the exponents related geometrically to important sub-objects (polars and meridians) of G, and this we do. We also apply this new description to compute exponents to certain B-stable ideals (for B a Borel subalgebra) that arise naturally in the study of projective subvarieties of flag varieties.

[1] R. Bott, On Torsion in Lie Groups, Proceedings of the National Academy of Sciences of the United States of America, Vol. 40, No. 7 (1954), pp. 586-588

[2] B. Y. Chen and T. Nagano, Totally geodesic submanifolds of symmetric spaces. II, Duke Math. J. 45 (1978), 405-425.

[3] B. Kostant, The Principal Three-Dimensional Subgroup and the Betti Numbers of a Complex Simple Lie Group, American Journal of Mathematics, Vol. 81, No. 4 (Oct., 1959), pp. 973-1032

Incomplete-LU preconditioning for a singularly perturbed problem

Nhan Anh Thai
Supervisor: Niall Madden

I am studying the iterative solution of linear systems arising from the finite difference discretization of singularly perturbed two-dimensional reaction-diffusion problems on a layer adapted mesh. Our model problem is:

$$-\varepsilon^2 \Delta u + b(x,y)u = f(x,y), \quad \text{on } \Omega = (0,1)^2, \qquad \text{and } u(\partial\Omega) = 0. \tag{1}$$

Discretization of (1) for a mesh with N interval in each direction leads to a linear system to be solved:

$$AU = F, \tag{2}$$

where A is banded, symmetric and positive definite $(N-1)^2 \times (N-1)^2$ matrix. These systems can be solved by direct methods. However, the computational cost becomes prohibitively large as the degrees of freedom grow. Also, they don't necessarily behave well for small ε [1]. Alternatively, one can use a iterative scheme. There are many possible schemes, but perhaps the most widely used is the method of Conjugate Gradient (CG) [3]. However, unpreconditioned CG behaves badly since the condition number of symmetrized problem (2) depends badly on ε [2]. To overcome this constraint, we consider Incomplete-LU factorization preconditioning. I present some numerical results demonstrating the suitability of this approach for (1), and provide an outline of some of the mathematical analysis for ILU(0).

[1] Scott MacLachlan and Niall Madden. Robust solution of singularly perturbed problems using

multigrid methods. *Submitted for publication,* August 2012.

[2] Hans-Görg Roos. A note on the conditioning of upwind schemes on Shishkin meshes. *IMA J. Numer. Anal.*, 16(4):529–538, 1996.

[3] Yousef Saad. *Iterative methods for sparse linear systems.* Society for Industrial and Applied Mathematics, Philadelphia, PA, second edition, 2003.

Summarising Microarray Probes Using A Statistical Learning Approach

Paul K. Korir
Supervisors: Prof. Cathal Seoighe, Dr. Tim Downing

Microarrays are an affordable and flexible high-throughput technology that simultaneously measure the abundance of thousands of genes. Each gene on a microarray is represented by tens to hundreds of probes, which have to be summarised into a single measure. Numerous summarisation algorithms have been developed with varying success. We present an alternative approach to summarisation that uses statistical learning algorithms instead of functional models. Our approach builds gene-specific models from gold standard estimates, such as those obtained using high-throughput sequencing (HTS) technology, then uses the learned models to predict the expression for a new set of probes.

We show that this strategy not only outperforms conventional summarisation algorithms but also extends the the reach of microarrays. Furthermore, it easily lends itself to estimating the abundance of individual transcript isoforms. Two biological applications are also presented that show how this technique increases statistical power in genome-wide experiments.

[1] Irizarry, Rafael A., et al. "Exploration, normalization, and summaries of high density oligonucleotide array probe level data." *Biostatistics* 4.2 (2003): 249-264.

[2] Hoheisel, Jörg D. "Microarray technology: beyond transcript profiling and genotype analysis." *Nature Reviews Genetics* 7.3 (2006): 200-210.

[3] Marioni, John C., et al. "RNA-seq: an assessment of technical reproducibility and comparison with gene expression arrays." *Genome Research* 18.9 (2008): 1509-1517.

The impact of the Aire gene on alternative splicing

Peter Keane
Supervisors: Cathal Seoighe, Rhodri Ceredig

The Autoimmune Regulator gene (Aire) is a transcription factor that induces the expression of otherwise tissue specific genes in the thymus. Mutations in this gene lead to APECED, a severe multi-organ specific autoimmune disease. Although Aire has been shown to influence the alternative splicing of a tissue specific gene (Zumer et al. 2011), the global impact of Aire on alternative splicing and the degree to which this contributes to Aire's function remains unknown. Using data in the public domain, we present evidence for a widespread impact of Aire on alternative splicing in the thymus.

[1] Zumer. K, Plemenitas. A, Saksella. K, Peterlin. B. M. (2011). Patient mutation in AIRE disrupts P-TEFb binding and target gene transcription. Nucleic Acids Research. 39(8), 7908-7919

Cocyclic Development of Pairwise Combinatorial Designs

Ronan Egan
Supervisors: Dane Flannery

A design for us is a square matrix over some ring, satisfying explicit combinatorial constraints. A PCD

(*pairwise combinatorial design* [1]) is a design whose rows taken pairwise satisfy a balance condition such as orthogonality. For example, Hadamard matrices and their generalizations are PCDs. The most effective method known to date of generating PCDs is *cocyclic development*. An $n \times n$ $\{\pm1\}$-matrix M is *cocyclic* over a group G with cocycle $\psi : G \times G \mapsto \{\pm1\}$ if $M = [\psi(g,h)\phi(gh)]_{g,h \in G}$ for some set map ϕ. The cocycles from a group G to an abelian group U form a group $Z(G,U)$ under pointwise composition. Unfortunately cohomological equivalence does not preserve orthogonality. We are investigating the relatively new idea of *shift representations*, which are derived from an action of G on $Z(G,U)$ (discovered by Horadam [2]) that preserves both cohomology and orthogonality.

[1] Warwick de Launey and Dane Flannery, *Algebraic design theory*, Mathematical Surveys and Monographs, vol. 175, American Mathematical Society, Providence, RI, 2011.

[2] K.J. Horadam, *The shift action on 2-cocycles*, Journal of Pure and Applied Algebra, vol. 188, pp. 127-143, Elsevier, 2003.

An Energetic/Impulsive formulation of the Impact Law

Shane Burns
Supervisor: Petri Piiroinen

Impact Mechanics is concerned with the reaction forces and impulses which develop during a collision and the governing dynamics which ensue [1]. We derive an impact law for a general 2D rigid body using the *Amontons-Coulomb* friction law. The law relates the tangential and normal components F_T and F_N, respectively, of the reaction forces occurring at impact using a coefficient of friction μ_f, which gives the relation $F_T = \hat{s}\mu_f F_N$, where $\hat{s}$ is given by the sign of the tangential velocity [1]. By integrating out the time dependance we arrive at an Impulsive interpretation of the *Amontons-Coulomb* friction law [2].

This work analyses the impact law in an effort to give scientists and engineers informative predictions on collision dynamics. The limitations of this approach are discussed and bounds on the Impulse ratio μ are derived and analysed. This is an extension of the work of [3].

[1] W.J.Stronge, *Impact Mechanics*, Cambridge University Press 2000, pp: 1–3 .

[2] R.M. Brach, *Formulation Of Rigid Body Impact Problems Using Generalized Coefficients*, Int. J. Impact Engng Sci Vol 36, No. 1, pp. 61-71, 1998.

[3] R.M. Brach, *Friction, Restitution and Energy Loss in Planar Collisions*, J. Appl. Mech. , ASME, Vol. 51, 1984, pp. 164–170.

Harnessing related species and samples data to create and optimise a draft genome sequence for Leishmania colombiensis

Simone Coughlan
Supervisors: Tim Downing, Cathal Seoighe

Advances in DNA sequencing technologies require genome assembly strategies that exploit related species and sample data to develop and improve new draft sequences. The majority of current DNA sequencing methods create large volumes of short overlapping sequences: for de novo assembly, these require either long DNA sequences, or guidance (contiguation) using related species information. Contiguation uses related genomes to align, order and orient genome assemblies in development: here we apply this approach to a paired-end short read library to create a draft genome sequence for Leishmania colombiensis. Initial de novo assemblies and sequence alignments with other Leishmania indicated that this new species was genetically distinct, and was approximately equidistant from L. tarauntolae and the L. braziliensis complex. The Leishmania colombiensis genome sequence was sampled from a dog in Colombia (MCAN/CO/1986/CL223) and was improved with a sample from the same species (MCAN/CO/1985/CL085). We improved these assemblies by correcting miscalled bases, closing gaps

and clarifying repetitive regions by examining the differences during re-mapping of sample DNA sequences to the reference genome sequences. Using information from multiple subspecies identifies chromosomal differences unique to L. colombiensis that would have been incorrectly aligned data from a single sample alone. This efficient scheme produces draft genome sequences that reflect more accurately intra-species variation and also allows the improved comparison of nucleotide and structural diversity. Discovering the genetic basis for phenotypic variability is crucial for tackling the acute global disease burden caused by leishmaniasis.

[1]

[2]

[3]

Genomics of the human nucleolar organizer region

Sofia Barreira
Supervisors: Brian McStay Cathal Seoighe

Nucleolar Organiser Regions, NORs, comprised of tandem arrays of ribosomal DNA and responsible for the formation of a major functional domain of the nucleus dedicated to ribosome biogenesis, the nucleolus, are positioned on the short arms of the five human acrocentric chromosomes (13, 14, 15, 21 and 22). These regions and those adjacent to the NORs are missing from the current human genome assembly. The identification and characterisation of these sequences is of critical importance, as nucleoli have a central role in growth-regulation and a long-established connection to tumorigenesis, and more importantly, ribosomes serve as the primary site of biological protein synthesis. My work focuses in the organisation of rDNA repeats, in extending and characterising the sequences on the distal side (DJ) of the NORs and establishing the organisation of DJ chromatin.

[1] McStay, B., and Grummt, I. (2008). The Epigenetics of rRNA Genes: From Molecular to

Chromosome Biology. Annual Review of Cell and Developmental Biology 24, 131157.

[2] Data from the ENCODE Project: Rosenbloom KR, Sloan CA, Malladi VS, Dreszer TR, Learned K, Kirkup VM, Wong MC, Maddren M, Fang R, Heitner SG, Lee BT, Barber GP, Harte RA, Diekhans M, Long JC, Wilder SP, Zweig AS, Karolchik D, Kuhn RM, Haussler D, Kent WJ. ENCODE Data in the UCSC Genome Browser: year 5 update. Nucleic Acids Res. 2012;

[3] McCord RP, Nazario-Toole A, Zhang H, Chines PS et al. Correlated alterations in genome organization, histone methylation, and DNA-lamin A/C interactions in Hutchinson-Gilford progeria syndrome. Genome Res 2013 Feb;23(2):260-9.

Multiscale Sparse Grid Methods for Singularly Perturbed Reaction-Diffusion Problems

Stephen Russell
Supervisors: Dr. Niall Madden

Standard finite element methods for partial differential equations, such as the Galerkin finite element method, are often impractical for high-dimensional problems: for fixed accuracy, the computational complexity grows exponentially with the dimension of the problem. Sparse grid methods were designed to overcome this difficulty; even for two-dimensional singularly perturbed problems, research has shown they can match the accuracy of standard FEMs but are much more efficient.

The "classic" sparse grid methods are classified as multiscale, whereas recent studies [1,2] use simpler, but still effective, two-scale methods. The focus in this poster will be on the more sophisticated multiscale approach. The main ingredient in designing and analysing such methods is the construction of a special interpolation operator.

For Poisson's equation, we present a new, simple proof of a standard result: that the multiscale fi-

nite element method has the same order of accuracy as the standard Galerkin method but with significantly lower computational cost. We conclude with numerical results indicating that the sparse-grid method achieves the same accuracy as the full Galerkin method, and demonstrating the savings in computational effort.

[1] Franz, S., Liu, F., Roos, H.-G., Stynes, M., and Zhou, A. (2009). The combination technique for a two-dimensional convection-diffusion problem with exponential layers. *Appl. Math.*, 54(3):203–223.

[2] Liu, F., Madden, N., Stynes, M., and Zhou, A. (2009). A two-scale sparse grid method for a singularly perturbed reaction-diffusion problem in two dimensions. *IMA J. Numer. Anal.*, 29(4):986–1007.

Integrative analysis of gene expression and half-life data reveals *trans*-acting genetic variants that affect RNA stability in human populations

Thong T. Nguyen
Supervisors: Andrew Flaus, Cathal Seoighe

Genetic variation in gene expression makes an important contribution to phenotypic variation and susceptibility to disease. Recently, a subset of *cis*-acting expression quantitative loci (eQTLs) has been found to result from polymorphisms that affect RNA stability.

Here we carried out a search for *trans*-acting variants that influence RNA stability. We first demonstrate that differences in the activity of *trans*-acting factors that stabilize RNA can be detected by comparing the expression levels of long-lived (stable) and short-lived (unstable) genes in high-throughput gene expression experiments. Using gene expression microarray data generated from eight HapMap3 populations, we calculated the relative expression ranks of long-lived RNAs versus short-lived RNAs in each sample. Treating this as a quantitative trait, we applied genome-wide association and identified a single

nucleotide polymorphism (SNP), rs6137010, on chromosome 20p13 with which it is strongly associated in two Asian populations ($p = 4 \times 10^{-10}$ in CHB Ű Han Chinese from Beijing; $p = 1 \times 10^{-4}$ in JPT Ű Japanese from Tokyo). This SNP is a cis-eQTL for SNRPB in CHB and JPT but not in other six HapMap3 populations. SNRPB is a core component of the spliceosome, and has previously been shown to affect the expression of many RNA processing factors. We propose that a *cis*-eQTL of SNRPB is directly responsible for inter-individual variation in relative expression of long-lived versus short-lived genes in Asian populations. In support of this hypothesis, knockdown of SNRPB results in a significant reduction in the relative expression of long-lived versus short-lived genes. Samples with higher relative expression of long lived genes also had higher relative expression of coding compared to non-coding RNA and of RNA from housekeeping compared to non-housekeeping genes, due to the lower decay rates of coding RNAs, particularly those that perform housekeeping functions, compared to non-coding RNAs.

Higher Genus Aspects of Vertex Operator Algebras

Thomas Gilroy
Supervisors: Michael Tuite

This year I have been working towards finalising the recursion theory for the genus 2 correlation functions for Vertex Operator Algebras. The approach has been to build genus 2 correlation functions from genus 1 functions and sewing procedures on tori and then using Zhu's recursion formulae for genus 1 functions on each of the sewn tori. Complete formal recursion formulae for the general quasiprimary recursion of genus 2 n-point correlation functions have been found. These formulae allow for explicit calculation of genus 2 Ward identities for n primary vectors and Virasoro n-point correlation functions. The convergence of these formulae is currently being studied using geometric methods and the connection between the algebraic and geometric aspects of the recursion theory are being explored.

[1] Yongchang Zhu, *Vertex Operator Algebras, Elliptic Functions, and Modular Forms,* Ph.D thesis, Yale University (1990), appeared as: *Modular Invariance of Characters of Vertex Operator Algebras* J. Amer. Maths. Soc **9** (1996)

[2] Geoffrey Mason and Michael P. Tuite, *On Genus Two Riemann Surfaces Formed from Sewn Tori*, Commun. Math. Phys. **270** (2007), 587–634.

[3] Geoffrey Mason and Michael P. Tuite, *Free Bosonic Vertex Operator Algebras on Genus Two Riemann Surfaces I*, Commun. Math. Phys. **300** (2010), 673–713.

[2] M.Crainic, "On the perturbation lemma, and deformations", arXiv:math/0403266v1 (2004), pp 13.

[3] G. Ellis and L.V. Luyen, "Computational homology of n-types", *J. Symbolic Computation* 47(11): 1309-1317 (2012).

Computational homology of n-types

Van Luyen Le
Supervisors: Graham Ellis

Let G_* be a simplicial group. By treating each group G_i as a category with one object and constructing the nerve $\mathcal{N}G_i$ one obtains a bisimplicial set $\mathcal{N}G_*$. The diagonal $\Delta\mathcal{N}G_* = \{(\mathcal{N}G_i)_i\}_{i\geq 0}$ is a simplicial set whose geometric realization is a CW-space $B(G_*)$. The condition on the Moore complex of G_* is sufficient to ensure that $B(G_*)$ is an n-type. The functor B induces an equivalence of categories

$$Ho(\text{Simplicial groups with Moore complex trivial in degrees } \geq n) \xrightarrow{\simeq} Ho(n\text{-types})$$

where $Ho(C)$ denotes the category obtained from a category C by localizing with respect to those maps in C, termed *quasi-isomorphisms*, that induce isomorphisms on homotopy groups. We define the integral homology of a simplicial group G_* to be

$$H_i(G_*, \mathbb{Z}) = H_i(B(G_*), \mathbb{Z}), \quad i \geq 0.$$

In this report, we describe an algorithm for computing the integral homology of a simplicial group and illustrate an implementation on simplicial groups arising as the Eilenberg-Mac Lane space and the nerve of a cat^1 group.

[1] G. Ellis, "Homology of 2-types", *J.* London Math. Soc. (2) 46 (1992), no. 1, 1–27.

5 Abstracts of PhD Theses

Analysis of gene regulation using high throughput genomics

Geeleher, Paul
Supervisor: Prof. Cathal Seoighe

The recent development of high-throughput genomics techniques and their subsequent applications have completely transformed the study of biology. The analysis, interpretation and storage of the resulting large volumes of data have created a wide range of computational challenges and opportunities that have driven the majority of recent bioinformatics research. In this thesis we focus on four research questions grounded in functional genomics and epigenomics, yielding novel methodologies and biological insights. The first research question relates to whether miRNA activity, as a general regulatory effect, is a heritable trait. To do this, we used Affymetrix Human Exon Microarray and RNA-seq data from the International HapMap project. We confirmed such an association in humans using the regulatory effect score (REscore) of a miRNA, which has previously been defined as the difference in the gene expression rank of targets of the miRNA compared to non-targeted genes. We also identified a SNP in the miRNA processing gene DROSHA, which is associated with inter-individual difference in miRNA regulatory effect. During this analysis we noted that correlations between gene expression measures from RNA-seq and gene expression microarray platforms were often relatively poor. This led us to develop a method to improve the estimation of gene expression from microarrays. Our method uses samples for which there is both microarray and RNA-seq data available and builds statistical models which learn the relationship between probe level gene expression, as measured by the microarrays, and gene level expression, as measured by RNA-seq. These models can then be used to estimate gene expression on separate sets of microarray samples. We have assessed the performance of our method in comparison to Affymetrix Power Tools (APT). To do this, we fitted models for all genes on a training set of the HapMap YRI samples and tested performance on the HapMap CEU (both microarray and RNA-seq data are available for all of these samples). Overall, our method improves within sample correlations with RNA-seq substantially, but does not achieve the same level of performance as APT in terms of across sample correlations. The third research question aimed to determine whether or not it was possible to ascertain a consistent pattern of differential methylation in a limited number of ulcerative colitis (UC) biopsies, using data generated with the Agilent Human CpG Island microarray. Although there were no statistically significant differences between the sample groups at CpG island or probe level, we did uncover evidence of overall CpG island hypermethylation in UC. Subsequently, gene set analysis (GSA) revealed highly significant results for several GO biological processes. It became apparent that these results were a consequence of a sampling effect, which stems from the large differences in numbers of probes (targeting CpG sites) associated with genes in different gene sets. The fourth and final research question consisted of the development of a method to correct the bias in GSA analysis of these data. We applied our method to both the UC microarray dataset and a previously published genome-wide CpG island study of DNA methylation in lung cancer. We obtained novel biological insights into both of these conditions, consistent with their respective pathologies. Finally, we showed that this bias is also found with next generation sequencing based methylation assays, which we demonstrated using a HELP-seq dataset. In conclusion, this thesis presents novel analytical strategies encompassing gene expression and genome-wide methylation, and it also introduces methodologies that link microarray and RNA-seq measures of expression. It documents for the first time a correction for an intrinsic bias in GSA associated with many CpG island methylation platforms, and yields results of biological consequence with regard to endogenous RNAi regulatory processes and the epigenetic characterization of several human diseases.

Evolutionary Models for the Human Immunodeficiency Virus with Applications to Epitope Prediction and the Natural Selection of Escape Variants

Lacerda, Miguel
Supervisor: Prof. Cathal Seoighe

The rapidity with which the human immunodeficiency virus (HIV) adapts to its host environment presents huge challenges for the development of a fully protective vaccine. However, important insights have been gained from studying the characteristic footprints that the immune response and drug treatment leave on the virus. In this thesis, evolutionary models are developed and applied to study immune escape and drug resistance, and to predict epitopes. The first phylogenetic model of immune escape that allows the codon substitution rates to depend on an arbitrary environmental parameter is developed. The model is applied to identify sequence positions in an HIV Gag alignment that correlate with host human leukocyte antigen (HLA) genotypes across the phylogeny and which therefore provide evidence of escape from the cell-mediated immune response. T cell epitopes are then identified by combining this novel evolutionary model with a hidden Markov model that accounts for the sequence length and HLA binding motifs of known epitopes. This phylogenetic hidden Markov model is found to perform well in identifying documented T cell epitopes and can be combined with any other sequence- or structure-based epitope prediction tool to further enhance its performance.

The model above is then extended to identify B cell epitopes based on the antibody neutralisation sensitivities of a panel of viruses. In particular, the model is adapted to allow the distribution of amino acids at each site to depend on neutralisation titre. Sites that influence neutralisation sensitivity across the phylogeny are identified by comparing the fit of this model to a null model in which the amino acids evolve independently of titre. The model is applied to a large panel of HIV envelope sequences with ID50 titres measured against the broadly neutralising sera of seven HIV-infected women. The predictions are shown to identify many amino acid positions that are known to be targeted by the antibodies in these and other broadly neutralising sera. Conformational B cell epitopes are successfully identified with a Markov chain Monte Carlo algorithm that searches the tertiary envelope structure for three-dimensional clusters of sites that influence neutralisation sensitivity.

After considering HIV adaptation at the host population level, the focus then shifts to viral evolution within a host. The characteristics of transmitted viral variants are examined by analysing the breakthrough sequences from 96 monkeys experimentally infected with the simian immunodeficiency virus (SIV). It is shown that most infections are homogenous and that the proportion of multiple founders is not significantly different for the animals that received a vaccine compared to those that did not, despite the vaccine having a significant protective effect against infection with one of the two challenge stocks. Sieve analyses are also performed to determine whether certain viral variants were selectively blocked from establishing infection by the vaccine-primed immune response. No evidence for such a sieve effect is found at the sequence, epitope or amino acid levels in this study.

Finally, the population genetics parameters of HIV escape mutants within a host are estimated from longitudinal sequence data using maximum likelihood. The procedure is an extension of that of Bollback et al. [1], who assumed that mutants evolve according to the Wright-Fisher model. For computational reasons, this discrete model is commonly approximated by a diffusion process which assumes that selection and mutation are weak and is therefore inappropriate for modelling the evolution of HIV escape mutants. Here, the mutant frequency distribution is instead approximated by a Gaussian distribution with the mean and variance specified by a system of recurrence equations obtained with the *delta* method of statistics. Simulation studies are used to compare its performance to that of the standard diffusion approximation and the less well-known Gaussian diffusion approximation of Norman [2]. For large populations, the *delta* method is found to provide a much better approximation to the mutant frequency distribution when selection is strong, while all three methods perform comparably when selection is weak. Importantly, maximum likelihood estimates of the selection coefficient are severely attenuated when selection is strong under the two diffusion models, but not when the *delta* method is used. To demonstrate the utility of the approach, the method is applied to estimate the selection and effective population size of drug resistant mutants in temporal samples of next-generation HIV protease sequences.

key references

[1] Bollback, J. P., York, T. L., and Nielsen, R. (2008). Estimation of 2Nes from temporal allele frequency data. *Genetics*, 179(1):497-502.

[2] Norman, F. (1975). Approximation of stochastic processes by Gaussian diffusions, and applications to Wright-Fisher genetic models. *SIAM Journal of Applied Mathematics*, 29(2):225-242.

Automorphisms of Pairwise Combinatorial Designs

Ó Catháin, Padraig
Supervisor: Dr. Dane Flannery

In this thesis, we investigate group actions on certain families of pairwise combinatorial designs, in particular Hadamard matrices and symmetric 2-$(4t-1, 2t-1, t-1)$ designs.

A Hadamard matrix H is called cocyclic if a certain quotient of its automorphism group contains a subgroup acting regularly on the rows and columns of H. Cocyclic Hadamard matrices (CHMs) were first investigated by de Launey and Horadam in the early 1990s. We develop an algorithm to construct all CHMs of order $4t$, based on a well-known relationship between CHMs and relative difference sets. We apply the algorithm to classify all CHMs of order less than 40. This extends and completes work by de Launey and Ito.

Non-affine groups acting doubly transitively on a Hadamard matrix have been classified by Ito. Implicit in Ito's work is a list of Hadamard matrices with non-affine doubly transitive automorphism group. We give this list explicitly, in the process settling an old research problem of Ito and Leon. We then use our classification to show that the only CHMs with non-affine automorphism group are those that arise from the Paley Hadamard matrices. As a corollary, we show that twin prime power difference sets and Hall sextic residue difference sets each give rise to a unique CHM.

If H is a CHM developed from a difference set then the automorphism group of H is doubly transitive. We classify all difference sets which give rise to Hadamard matrices with non-affine doubly transitive automorphism group. A key component of this is a complete list of difference sets corresponding to the Paley Hadamard matrices. As part of our classification we uncover a new triply infinite family of skew-Hadamard difference sets. To our knowledge, these are the first skew-Hadamard difference sets to be discovered in non-abelian p-groups with no exponent restriction.

Mathematical analysis of some models for drug delivery

Tuoi, Vo Thi Ngoc
Supervisor: Martin Meere and Yury Rochev

This thesis is concerned with the mathematical modelling of controlled drug release from a number of delivery systems. There are two major strands to the work: (i) modelling release from affinity-based systems, and, (ii) modelling release from thermoresponsive films. A model that is related to the affinity models is also considered, and used to evaluate the effect of reversible binding on drug release in vivo. In Chapter 1, the topic is introduced by briefly discussing some commonly used drug delivery systems and the mathematical models that have been developed to describe them. In Chapters 2 and 3, two affinity-based delivery systems composed of modified fibrin matrices are analysed. The model equations are reduced, and the non-dimensional parameters governing the release rate identified. For both models, a parameter regime that minimises the passive leakage of growth factor from the system is found. In Chapter 4, a reaction-diffusion model for drug redistribution in tissue is considered, and some generic problems to evaluate drug penetration and persistence in tissue are analysed. In Chapter 5, a model for pulsatile drug release from the thermoresponsive polymer poly(N-isopropylacrylamide) is developed. Theoretical pulsatile release profiles are compared with experimental profiles generated by colleagues working at the National Centre for Biomedical and Engineering Sciences, and the correspondence between theory and experiment is found to be good. In Chapter 6, a mathematical model is developed to evaluate the feasibility of an in vivo implanted drug delivery system based on a thermoresponsive polymer and a cooling device, and it is found that the system may be realised for realistic parameter values and materials. Finally, in Chapter 7, an evaluation of the modelling work of the thesis is presented, and strengths and weaknesses of some of the models are identified.

6   Abstracts of MSc Theses

Dynamic Asymmetric Networks

Richard, Burke

Supervisor: Dr. Petri Piiroinen

In this study we are investigating nonlinear dynamical systems, represented as complex networks. We have built robust mathematical models of interacting nodes of integrators, chaotic oscillators and flocking agents. We are drawing heavily on a technique called *Edge Snapping* to create networks that evolve (themselves) naturally to a static steady state. The hope is to analyse the emergent topologies of these networks using appropriate graph-theoretic metrics. We also aim to understand the influence of key parameters and initial conditions on the network evolutions. Finally, we want to undertake a rigorous investigation of the stability of the dynamic networks.

[1] P.DeLellis, M. diBernardo, F. Garofalo and M. Porfiri, "Evolution of Complex Networks via Edge Snapping", IEEE Transactions on circuits and systems-1: regular papers, vol. 57, 2010, pp.$\sim$ 2132-2143.

[2] L.M. Pecora and T.L. Carroll, "Master Stability Functions for Synchronized Coupled Systems", Phys. Rev. Lett., vol. 80, 1998, pp.$\sim$ 2109-2112.

[3] M. E. J. Newman, "The structure and function of complex networks", SIAM Rev.45, 25 March 2003, pp.$\sim$ 167-256.

Discontinuity Geometry for Periodically-forced Impact Oscillators

Humphries, Neil

Supervisor: Dr. Petri Piiroinen

In this thesis I am developing a geometric framework, termed Discontinuity Geometry, for use in the analysis of periodically-forced impact oscillators which was first described in 2002 [1], and is not yet well known. The basis of this framework is the definition of an $\mathbb{R}^n$ representation space ($\mathbb{R}^3$ for all the systems illustrated here) and some system-specific codimension-one fundamental geometric objects embedded within that space. The fundamental objects are all defined without reference to impacts or the impact rule.

All methods within the discontinuity geometry framework work in the same way. A correspondence is established between a particular dynamical behaviour being manifested in a particular instance of a system and certain geometric relationships being found within the corresponding fundamental objects for that system. These relationships are here termed *Discontinuity Geometry Interactions*, or DGIs for short, and can take many forms; a particular detail appears on an object, a particular intersection between objects does (or does not) occur, . . .

Some of the DGIs presented here were first described in [1] and the rest are being presented for the first time. Among the new DGIs are a method to determine the existence of $(1, n)$-orbits (i.e. a periodic orbit which contains **1** impact and has period of **n** forcing periods) that can be extended to more general (m, n)-orbits, and a method to determine if a saddle-node bifurcation will be manifested in the neighborhood of a grazing bifurcation or not.

For all the DGIs used here (both the inherited and the original) programs within the software package MATLAB were written to enact them. These programs are used to illustrate the DGIs with reference to three specific instances of a periodically-forced, damped, harmonic oscillator with impacts modelled by a coefficient of restitution.

In addition to this, some of the framework was extended to be applied to the analysis of one specific periodically-forced impact oscillator with two impact surfaces that arose from modelling a rattle problem in a gearing system. This work was in collaboration with Dr. J.F. Mason and the results of this analysis are presented in detail in [2], with a selection of the results and some discussion of how the extension was achieved given here.

As this is a relatively new technique there is considerable scope for further development. Not only are there dynamical behaviours of these systems for which no DGI has yet been found, some of the existing DGIs need further establishment of their theoretical foundations.

References:

1 Chillingworth D.R.J., Discontinuity geometry for an impact oscillator, *Dynamical Systems*, vol.4, 2002, pp. 389–420.

2 Mason J.F., Humphries N. and Piiroinen P.T., Numerical analysis of codimension-one, -two and -three bifurcations in a periodically-forced impact oscillator with two discontinuity surfaces, in submission to *Mathematics and Computers in Simulation*

7 Research Activity from 1 Jan 2012 to 31 Dec 2012

Permanent and Contract Staff

Aramayona, Javier

Current Research Interests

Mapping class groups, Teichmüller spaces and their various combinatorial models. Spaces of nonpositive curvature and their isometry groups.

Publications

Most significant publications in last 5 years.

[1] Finite rigid sets in curve complexes (with C. J. Leininger). To appear in *Journal of Topology and Analysis*.

[2] Homomorphisms between mapping class groups (with J. Souto). Geometry and Topology 16 (2012).

[3] Simplicial embeddings between pants graphs. Geometriae Dedicata 144 (2010).

[4] Injections of mapping class groups (with C. J Leininger and J. Souto). Geometry and Topology 13 (2009).

Research Activities

Two preprints, three papers in the last stages of preparation (all papers available from my website). Co-organiser of Groups in Galway 2013; co-organiser of the William Rowan Hamilton Geometry and Topology Workshop (Dublin, September 2013). Invited speaker at *Surface groups in Paris* (Paris, March 2012), *Group actions and applications in geometry, topology and analysis* (Kunming, China, July 2012), *Summer school on automorphisms of free groups*, (Barcelona, September 2012), *Automorphisms of free groups* (Barcelona, November 2012). Invited researcher at CRM, Barcelona (3 months). Shorter research visits (of over a week) to University of British Columbia (2 weeks), and Technion (Israel). Seminar talks in France (Marseille), Israel (Haifa and Jerusalem), Spain (Barcelona and Zaragoza),

Switzerland (Fribourg)

Burns, John

Current Research Interests

My current research interests are Algebra (Lie algebras, Lie groups, Weyl groups) and Differential Geometry (Homogeneous manifolds, Symmetric spaces, manifolds with multiple conjugate points). Research in all of the above areas is ongoing with various authors:

Adib Makrooni and I are applying our new description of Lie Algebra exponents,to certain B-stable ideals (for B a Borel subalgebra) that arise naturally in the study of projective subvarieties of flag varieties.

David Wraith (NUIM), Eoghan Staunton (NUIG) and I have been studying manifolds with multiple conjugate points. (See: On the Jacobi equation and manifolds with multiple conjugate points. (to appear in Mathematical Proceedings of the R.I.A.)

Goets Pfeiffer and I are finishing work on the geometry of maximal order Abelian subgroups of Coxeter groups and their applications, ranging from branching rules for Lie algebra representations, to the geometry of -1 curves on del Pezzo surfaces.

Publications

Research Activities

Journal submissions: Power sums of Coxeter exponents (with R. Suter), Adv. Math. 231 (2012) 1291-1307
Invited talks: The Irish geometry conference NUI Maynooth in June 2013 Refereeing: 1 paper. Conferences and workshops: Marseille, Paris and Zurich. Postgraduate supervision: 1 Ph.D. student. conferences, visits, invited talks, research visits, papers refereed, math reviews, editorships, memberships, external posts, etc

---

Cruickshank, James

Current Research Interests

- Rigidity and flexibility of frameworks and linkages.

- Linear algebra, in particular spaces of matrices with bounded rank properties and spaces of nilpotent matrices.

- Automorphisms of directed graphs.

7.1 Publications

- None appeared in 2012

7.2 Other Outputs

7.2.1 Preprints

- J.Cruickshank, A. Herman, R. Quinlan, F. Szechtman. *Unitary Groups over local rings.* Available at http://arxiv.org/pdf/1303.5106.pdf

- J. Cruickshank, R Quinlan. *On a theorem of Gerstenhaber*

7.2.2 Conference presentations

- IMS meeting, September 2012.

- De Brun Workshop, December 2012.

Destrade, Michel

Current Research Interests

I am currently mostly interested in applying the principles of Continuum Mechanics to the modelling of soft matter, including biological tissues and gels. The equations of motion can be written down to take into account all physical characteristics of these materials, including coupling with other fields such as electromagnetism or fluid dynamics. However great care must be taken when large deformations are envisaged, especially in the elaboration of adequate boundary conditions, with crucial repercussions in the correct formulation of numerical simulations. I am mainly working in problems and application of elastic wave

propagation, elastic stability, and proper computational solid mechanics.

Keywords: Stability of soft solids; Acousto-elasticity with application to soft tissues; Mechanical modelling of Human Skin and of Brain Tissue, Numerical implementation.

Publications

Numbers of publications appearing in calendar year 2012: 12

Four significant publications

[1] M. Destrade, Y. Liu , J.G. Murphy , G.S. Kassab. Uniform transmural strain in prestressed arteries occurs at physiological pressure, Journal of Theoretical Biology 303 (2012) 93-97.

[2] A. Ni Annaidh, K. Bruyere, M. Destrade, M.D. Gilchrist, C. Maurini, M. Ottenio, G. Saccomandi. Automated estimation of collagen fibre dispersion in the dermis and its contribution to the anisotropic behaviour of skin, Annals of Biomedical Engineering, 40 (2012) 1666-1678.

[3] Z. Abiza, M. Destrade, R.W. Ogden. Large acoustoelastic effect, Wave Motion, 49 (2012) 364-374.

[4] M. Destrade, J.G. Murphy, G. Saccomandi. Simple shear is not so simple, International Journal of Non-Linear Mechanics, Special Issue on Nonlinear Continuum Theories [invited contribution], 47 (2012) 210-214.

Research Activities

Research grants: NUI and Ile-de-France Mobility Grants for A. Ni Annaidh (co-I), 2 Postgraduate IRC-SET Fellowships (co-I), NUI Galway start-up grant, NUI Galway Hardiman Scholarship, Italian Institute of Higher Mathematics (INdAM) Visiting Professor Programme, INdAM Marie Curie COFUND Fellowship for L. Vergori, Royal Society International Joint Project (co-I), New Foundations Grant from the Irish Research Council;
Numbers of graduate students: 3;
Conferences/Seminars: 4;
Outreach talks: 8;

Guest Visits: 3; Host Visits: 3;
Papers/Grants refereed: 20;
Editorships: Quarterly Journal of Mechanics and Applied Mathematics, International Journal of Applied Mechanics, International Journal of Non-Linear Mechanics, Proceedings of the Royal Society A;
Memberships: Acoustical Society of America, Society for Industrial and Applied Mathematics, International Society for the Interaction of Mechanics and Mathematics;
External positions: Adjunct Professor of Mechanical Engineering, University College Dublin; Directeur de Recherche, Institut d'Alembert, CNRS, Paris, France (on leave).

Detinko, Alla

Current Research Interests

Computational group theory; linear groups, permutation groups, algebraic groups.

Publications: in calendar year 2012

Four significant publications

[1] A. Detinko, D. Flannery, E. O'Brien, 'Recognition of finite matrix groups over infinite fields', Journal of Symbolic Computation, 50 (2013), 100-109.

[2] A. Detinko, D. Flannery, E. O'Brien, eds. 'Probabilistic Group Theory, Combinatorics, and Computing', Lectures from the Fifth de Brún Workshop, Lecture Notes in Mathematics, Vol. 2070, Springer, 2013, 114 pp.

[3] A. Detinko, D. Flannery, E. O'Brien, 'Algorithms for linear groups of finite rank', 2013, submitted.

Research Activities

[1] Selected talks (2012).

(i) Computational aspects of infinite linear groups. University of Auckland, April 2012.

(ii) Algorithms for finitely generated linear groups. University of Sydney, May 2012.

(iii) Computing with infinite linear groups: results and challenges. University of Western Australia, June 2012.

[2] Selected research visits (2012).

(i) University of Auckland (supported in part by the Marsden Fund of New Zealand).

(ii) University of Sydney (supported in part by University of Sydney).

(iii) University of Western Australia (supported by SFI Short Term Travelling Fellowship grant, and by the Australian Research Council).

[3] Reviewing: 4 reviews for Mathematical Reviews.

[4] Membership: member of the American Mathematical Society.

Downing, Tim

Studying the evolution of drug-resistance and immune response evasion in human pathogens offers insights into the genetic diversity of virulence factors and mechanisms of treatment tolerance. I am examining the genomes of pathogens to identify mutations associated with outbreaks of disease. Primarily this is to combat leishmaniasis using DNA data from patient samples, experimentally evolution of drug-resistant strains, and samples from wider sources, including sandfly vectors and animals. I also interested in developing improved genomic approaches to mutation discovery, data comparison between species, and hybridisation of genetically distinct types.

Current Research Interests

My priniciple interests are the population genetics and adaptive evolution of pathogens: single-cell parasites, bacteria and related systems.

Publications

Most significant publications

[1] Adaptive mechanisms in pathogens: universal aneuploidy in Leishmania. Mannaert A, Downing T, et al. Trends Parasitol. 2012 28(9):370-6. PMID: 22789456

[2] Genetic markers for SSG resistance in Leishmania donovani and SSG treatment failure in visceral leishmaniasis patients of the Indian subcontinent. Vanaerschot M, Decuypere S, Downing T, et al. J Infect Dis. 2012 206(5):752-5. PMID: 22753945.

[3] Genome-wide SNP and microsatellite variation illuminate population-level epidemiology in the Leishmania donovani species complex. Downing T, et al. Infection, genetics and evolution. 2012 12(1):149-169. PMID: 22119748.

Research Activities

I supervised one PhD student funded by the NUIG fellowships. I applied as a partner on a FP7 research proposal. I have active collaborations with the Wellcome Trust Sanger Institute, the Institute of Tropical Medicine Antwerp, Strathclyde University, Charite University Berlin and the Institute of Tropical Medicine Amsterdam. I am developing research collaborations with Prof. Martin Cormican and Dr. Thomas Barry here in NUIG. I refereed for a variety of journals and gave 5 talks at conferences in 2012.

Ellis, Graham

Current Research Interests

My research interests lie in *homotopical algebra*, particularly nonabelian algebra related to low-dimensional integral homotopy types of spaces. Much of my recent research activity has focused on developing practical algorithms for computing algebraic homotopy invariants of spaces. The algorithms are being implemented as part of an officially refereed, and ever growing, *Homological Algebra Package (HAP)* for the computer algebra system GAP. The algorithms were initially aimed at spaces arising theoretically as classifying spaces of algebraic objects such as groups, Lie algebras and crossed modules. Recently my focus has broadened to include spaces modelling real-life data from medical images, bioinformatics and dynamical systems.

Publications

4 publications appeared in 2012

Most significant publications

[1] G. Ellis & F. Hegarty, "Computational homotopy of finite regular CW-spaces" , *J. Homotopy and Related Structures*, DOI 10.1007/s40062-013-0029-4.

[2] Computational homology of *n*-types (with Le Van Luyen). J. Symbolic Computation, Vol 47 (11) (2012), 1309-1317.

Research Activities

I supervised three PhD students and one postdoctoral researcher. One PhD submitted his thesis in September. I was on the editorial boards of three journals: Homology, Homotopy and Applications; Journal of homotopy and related structures; Applicable Algebra in Engineering, Communications and Computing. A gave innvited lectures at: *Dynamics, Topology and Computations*, Bedlewo, Poland, June 24-30 2012; *Groups in Galway*, Galway, May 11-12, 2012; . Jagiellonian University, Computer Science Seminar, December 2012; University College Cork, Mathematics Seminar, January 2013.

Dane Flannery

Current research interests

Group theory, linear groups, algebraic design theory, computational algebra.

Publications

[1] Books

    (a) W. De Launey and D. Flannery, *Algebraic Design Theory*, Mathematical Surveys and Monographs **171**, American Mathematical Society.

    (b) A. Detinko, D. Flannery, E. O'Brien, *Probabilistic Group Theory, Combinatorics, and Computing*, Lecture Notes in Mathematics **2070**, Springer.

[2] Refereed journal papers

    (a) A. Detinko, D. Flannery, E. O'Brien, Recognition of finite matrix groups over infinite fields, Journal of Symbolic Computation **50** (2013), 100-109.

    (b) A. Detinko, D. Flannery, Integrality and arithmeticity of solvable linear groups, 2013, submitted.

Research activities

[1] Talks, research visits, funding.

- Invited lectures at The University of Auckland (April 2012), The University of Sydney (May 2012), and The University of Western Australia (May 2012).

- Research visits to E. O'Brien at The University of Auckland, J. Cannon of the MAGMA Development Team, and C. Praeger of the Centre for the Mathematics of Symmetry and Computation.

- Financial support received from the Research Frontiers Programme of Science Foundation Ireland, the Marsden Fund of New Zealand, The University of Sydney, and the Australian Research Council.

[2] Supervisor of PhD student Ronan Egan.

[3] Referee for Archiv der Mathematik; Communications in Algebra; Groups Complexity Cryptology; Journal of Algebra; Journal of Combinatorial Designs; Journal of Combinatorial Theory, Series A; LMS Journal of Computation and Mathematics.

[4] Reviewer for Mathematical Reviews.

Hayes, Michael

Research Interests

Up to 2006 my research interests were in fluid mechanics mainly using lubrication and perturbation techniques. These techniques were applied to the governing (Navier Stokes and conservation) equations. The resulting partial differential equations were solved to establish the fluid and subsequent solute thickness in the phosphor coating of TV screens.

My current/ future research interests are in the analysis of stochastic differential equations.

Publications

Below are listed a number of publications including a publication in the Physics of Fluids journal.

1. The fluid profile of a gravity driven film over any small two dimensional object, M.A. Hayes, S.B.G. O'Brien & J.H. Lammers, (1999), in Advances in coating and drying of thin films, (Ed. F. Durst, H. Raszillier), Shaker Verlag, 253-258.

2. Models for flows over non-flat substrates, S.B.G O'Brien, M. Hayes, J. Lammers, (2000), in Trends in the application of mathematics to mechanics, 147-155, Elsevier (ISBN 2842992458).

3. Green's function for flow over a small two dimensional topography, M.Hayes, S.B.G. O'Brien, J. Lammers, (2000), Phys. Fluids, 12, 2845-2861.

4. Evaporative and topographical effects in coating flows, S.B.G. O'Brien, M. Hayes, (2001), Mathematics in industry 2001.

5. A model for dip-coating of a two liquid mixture, M. Hayes, S.B.G. O'Brien, (2002), Int. J. Math. Math. Sci., 29, 313-325.

6. M.A. Hayes, S.B.G.O 'Brien. 2004. Spincoating over a small sinusoidal topography,. Int. J. Math. Math. Sci. 43, 2279-2298.

7. S.B.G. O'Brien, M. A. Hayes. 2005. A model for gravity driven flow of a thin liquid solid suspension with evaporation effects. Z. angew. Math. Phys. 56, 1-22.

Current Activities

From 2007, I have been passing the Institute and Faculty of Actuaries examinations. In 2008 I was awarded an interim qualification.

Hinde, John

Current Research Interests

Statistical modelling, particularly generalized linear models and random effects models; statistical computing and statistical software; likelihood theory and inference; applications of statistics in biological, medical and social sciences.

Publications

Most significant recent publications

[1] Papageorgio, G, and Hinde, John (2012) Multivariate Generalized Linear Models with Semi- and Smooth Nonparametric Random Effects. *Statistics and Computing*, **22**, 1, pp 79-92.

[2] Coffey, Norma, Hinde, John and Holian, Emma (2013) Clustering longitudinal profiles using P-splines and mixed effects models applied to time-course gene expression data. Accepted *Computational Statistics and Data Analysis.*

[3] Urbano, Mariana Ragassi, Hinde, John and Demétrio, Clarice Garcia Borges (2013) Bioassays with natural mortality: handling overdispersion using random effects. Final revision for *Journal of Agricultural, Biological and Environmental Statistics.*

Research Activities

Current research grants:

SFI Mathematics Initiative — Bio-statistics and Informatics (BIO-SI) with Prof. Mackenzie, University of Limerick (€500,000)

Medicines for Malaria Venture — Screening the Malaria Box for Novel Drug Interactions with Prof. Anus Bell, TCD (PI), ($ 50,000)

Graduate students: 2; .

Journal submissions: 2 accepted, 1 under review

Conferences: Chair Scientific Programme Committee 1; Invited Speaker 1; Attended 3.

Invited talks:

Mixtures and Random Effects — University of Pau, France, February, 2012

Mixtures and Random Effects — Universitat Autonoma de Barcelona, Spain, March, 2012

Mixtures and Random Effects — 57th Reunião Anual da RBras, Brazil, April, 2012

Random Effects, Mixtures and NPMLE — Federal University of Brasilia, Brazil, April 2012

Mixtures and Random Effects — RSS Northeastern Local Group, UK, May, 2012

GLMs 40 years on: A Personal Perspective —- British and Irish Region, IBS, Presidential Address, November 2012

Editorships: Statistics and Computing (Associate); Computational Statistics and Data Analysis (Associate); Statistical Modelling (Advisory Board).

President of the British and Irish Region of the International Biometric Society (2010-2012);

Elected President of the International Biometric Society (2013-2017)

Review Panel Member for Group Biomedical Sciences/ L-BioStat Cluster, K. U. Leuven, Belgium (2013)

Holian, Emma

Current Research Interests

Mixture modelling to cluster longitudinal data profiles and to model the group features via generalized linear mixed models and penalized smoothing models, leading to the formulation of the Regression Cluster Model (RCM). Analysis into capability of the RCM to handle missing data within profiles or profiles measured at variable time-points. Extension of the RCM to longitudinal profiles measured on discrete or categorical scales. Applications in microarray analysis.

Publications

Recent publications pending review

[1] N. COFFEY, J.P. Hinde, E.L. HOLIAN. Clustering longitudinal profiles using p-splines and mixed effects models applied to time-course gene expression data. *Computational Statistics and Data Analysis. Accepted for publication April 2013.*

[2] M.J. MARTINEZ, E.L. HOLIAN. An alternative estimation approach for the heterogeneity linear mixed model. *Communications in Statistics - Simulation and Computation. Accepted for publication Dec 2012.*

Research Activities

Memberships: Irish Statistical Association - Executive committee member.
Collaborative work with Marie-José Martinez, Team MISTIS, INRIA Rhône-Alpes & Laboratoire Jean Kuntzmann, and University of Grenoble II, FRANCE, on an alternative estimation approach for the heterogeneity linear mixed model and cluster analysis of discrete and categorical response profiles - supported by NUIG Millenium Fund for travel.

Jennings, Kevin

Current Research Interests

Algebra, finite fields, difference sets.

Publications

None. Most significant publications N/A

Research Activities

Krnjajić, Milovan

Current Research Interests

Bayesian model specification, Bayesian non-parametric modelling, Inverse problems. Applications in engineering, science, medicine.

Madden, Niall

Current Research Interests

I am interested in the design and mathematical analysis of numerical methods for solving ordinary and partial differential equations, particular those whose solutions feature boundary and interior layers. I am especially interested in highly efficient algorithms, such

as operator splitting finite difference schemes, sparse grid finite element methods, and fast linear solvers.

Recent Publications

[1] Catherine G. Enright, Michael G. Madden, and Niall Madden. Bayesian networks for mathematical models: Techniques for automatic construction and efficient inference. *International Journal of Approximate Reasoning*, 54(2):323 – 342, 2013.

[2] Niall Madden. John Todd and the development of modern numerical analysis. *Irish Math. Soc. Bull.*, 69(2):11–23, 2012.

[3] Niall Madden and Martin Stynes. A curious property of oscillatory fem solutions of one-dimensional convection-diffusion problems. In J. Brandts, J. Chleboun, S. Korotov, K. Segeth, J. Šístek, and T. Vejchodský, editors, *Applications of Mathematics 2012 (Proc. of Conference in Honour of 60th birthday of Michal Křížek, 2–5 May 2012)*, pages 188–196, Prague, 2012. Czech Academy of Sciences.

Research Activities

During 2012, I submitted four papers, including [1] and [2] above. The other two were on the topics of linear solvers for singularly perturbed problems, and hp-finite elements methods for fourth-order problems, and are still under review. My collaborators on these projects, Scott MacLachlan (Tufts University, MA) and Christos Xenophontos (University of Cyprus) visiting NUI Galway during 2012, thanks to generous support from the de Brún Centre.

In December 2012, I was one of the organisers of the 6th de Brún Wrokshop: *Linear Algebra and Matrix Theory: connections, applications and computations.*

I refereed papers for various journals, including IMA J. Numer. Anal., J. Comput. Appl. Math., and Appl. Numer. Math.

I presented a talk on Schwarz methods for coupled systems (based on joint work with Meghan Stephens) at the International Conference on Boundary and Interior Layers, at POSTECH, Korea, as well as giving local seminars in the School and in the Ryan Institute.

Stephen Russell, working under my supervision, was a awarded a Masters in Applied Mathematics for his thesis titled *Sparse grid methods for the two-dimensional Poisson problem.*

I am currently supervising two Ph.D. students: Nhan Anh Thai and Stephen Russell.

McCluskey, Aisling

Current Research Interests

My research interests reside primarily within analytic topology, with a particular fascination in how order theoretic structures mesh with topology. The fusion between order and topology arises naturally in the following question: for a non-empty set X, the collection $Top(X)$ of all topologies on X sits inside the Boolean lattice $\mathcal{PP}(X)$ (when ordered by set-theoretic inclusion) which in turn can be naturally identified with the Stone space $2^{\mathcal{P}}(X)$. Via this identification then, $Top(X)$ naturally inherits the subspace topology from $2^{\mathcal{P}}(X)$. This suggests the possibility of applying lattice-theoretic methods in pursuit of fundamental topological questions, not the least of which is just how complex a set $Top(X)$ is in terms of the Borel hierarchy. Considerable insight into the structure of $Top(X)$ has been accomplished by my graduate student Jorge Bruno, whilst new avenues of research, with a categorical flavour, have unfurled in collaboration with Ittay Weiss (University of South Pacific). Other ongoing research concerns continua theory in the context of both a natural associated order (a notion of "betweenness"), and of discrete dynamical systems.

Additionally, my research interests also encompass research in undergraduate mathematics education. Specifically, and in collaboration with Hardiman scholar Michelle Duane, I am interested in the development of and facility with proof and proving in abstract analysis-based mathematical subjects typically taken in mathematics-major degree programmes.

Publications

Most significant publications

[1] A. E. McCluskey and R. W. Knight, "A consistent counterexample in P(R)", Topology Appl.

156 (11) (2009), 1943 - 1945.

[2] Aisling E. McCluskey, "What are our Senior Undergraduates in Mathematics Learning? A Mathematician's Hope", Proceedings of Volcanic Delta 2011, 278 - 291.

[3] S. Bayhan, A. Kanibir, A. McCluskey and I. L. Reilly, "On almost z-supercontinuity", Filomat (2012).

[4] J. L. Bruno and A. E. McCluskey, "Topologies on X as points within $2^P(X)$", Topology Appl. 159 (13) (2012), 3027 - 3032.

[5] J. L. Bruno and A. E. McCluskey, "Topologies as points within a Stone space: lattice theory meets topology", Topology Appl. 160 (2) (2013), 273 - 279.

Research Activities

Publications: 3 peer reviewed Journal Articles Published; 3 peer reviewed Articles in Conference Proceedings published; 2 further journal articles submitted.

Visiting research fellow at the University of Auckland: two seminars presented, one to research mathematicians and one to mathematics education researchers.

Visiting research fellow at Queen's University Belfast. Invited speaker at 15th Galway Topology Colloquium (GalTop15) in Oxford; principal organiser of GalTop16 at NUI Galway in July 8 - 10, 2013.

Research funding applications: Hardiman scholar (Michelle Duane) awarded to carry out research in the field of mathematics education; two further Hardiman applications made; one Empower IRCSET postdoctural application made re Oxford graduate. Funding awarded (Ǎ4000 - various sources) to host GalTop16.

Details of research collaborations initiated or ongoing in Calendar Year 2012: Jiling Cao, Auckland University of Technology New research

Ivan Reilly, University of Auckland New research

Ittay Weiss, University of South Pacific New research

Paul Bankston, Marquette University New research

Bill Barton/Greg Oates, University of Auckland New research

Judy Paterson, University of Auckland New research

Brian McMaster, Queen's University Belfast Ongoing

Máire Ní Ríordáin, NUI Galway Ongoing

M. Meehan (UCD, S. Breen (St. Pat's), A. O'Shea (NUI Maynooth) and J.Odonovan(CIT) Ongoing.

Invited to be Irish representative on the International Steering Committee of DELTA 2013

Invited by Science advisory committee of the annual General Topology and its Applications conference to host the event in 2015.

External examiner of PhD theses: University of Birmingham and NUI Maynooth.

Reviewer of papers submitted to Topology and its Applications and Central European Journal of Mathematics.

Mc Gettrick, Michael

Current Research Interests

My current research interests are mainly in the area of Quantum Computation (an interdisciplinary research area involving mathematics, physics and computer science). In particular, I work mostly on studying properties of Quantum Random Walks and Quantum Game Theory.

In the last year, we have initiated (with Colm O'Riordan in IT) studies on a new model called Quantum Evolutionary Computation, which fuses ideas from Evolutionary Computation and Quantum Game Theory. Other interests are in Computer Algebra and using mathematics and computational techniques to analyze and compose music.

Number of publications in 2012

Numbers of publications appearing in calender year 2012: 0. Most significant publications:

[1] "One dimensional quantum walks with memory", Mc Gettrick, M., **Quantum Information and Computation** Volume: 10 Issue: 5-6 (2010)

[2] "Alternate two-dimensional quantum walk with a single-qubit coin", Di Franco, C., Mc Gettrick, M., Machida, T., Busch, Th. **Physical Review A** Volume: 84 Issue: 4 (2011)

Research Activities

- I participated in the 2012 LMS Midlands Regional Workshop & Meeting in September at the University of Aberystwyth, where I gave a talk on Quantum Evolutionary Game Theory.

- In June 2012, Jarek Miszczak came as a De Brun Centre visitor to collaborate for 2 weeks on quantum random walks.

- In late 2012 we submitted a joint paper "Quantum walks with memory on cycles" to the journal **Quantum Information and Computation**. This work is available on the arXiv at arXiv:1301.2905.

- I am a member of the Irish Mathematical Society and the American Mathematical Society.

- A potential PhD student from Uruguay (Marcelo Forets) was given a College of Science Scholarship to work with me: But after originally accepting it, he changed his mind and went to study in France.

Meere, Martin

Current Research Interests

Centromere modelling. The aim of this project is to build a mathematical model that describes the stable propagatin of human centromeres from one generation to the next.
Drug release modelling. Some work remains to be completed on stent modelling and on the analysis of affinity based drug delivery systems.
Modelling diffusion in crystals. This is ongoing work with colleagues at the University of Nottingham.
Modelling wave/structure interactions. This work is in collaboration with colleagues in the department of Civil Engineering at NUI Galway.

Publications

[1] Tuoi Vo T. N. & M.G. Meere, Minimizing the passive release of heparin-binding growth factors from an affinity-based delivery system, *Mathematical Medicine & Biology*, doi:10.1093/imammb/dqs027 (2012)

[2] Rongbing Yang, Tuoi Vo T. N., Alexander V. Gorelov, Fawaz Aldabbagh, William M. Carroll, Martin G. Meere, Yury Rochev, A mathematical model for pulsatile release: controlled release of rhodamine B from UV-crosslinked thermoresponsive thin films, *International Journal of Pharmaceutics*, 427:320-327 (2012)

Research Activities

Current graduate students: I co-supervise (with P. Piiroinen) one PhD student.
Completed projects: In the past year, one student has successfully graduated with a PhD, and one student successfully completed a Summer internship.
Research visits: I visited the University of Nottingham for one week in January 2013.

Newell, John

Current Research Interests

Statistical modelling, statistical computing, survival analysis and the application of statistics in Clinical Research and Sports Science.

Publications

Numbers of publications appearing in calendar year 2012:

Four significant publications

[1] Byrne, M., Newell J., Coffey N., OŠ Hara M.C., Cooke E., Dinneen SF (2012). Predictors of quality of life gains among people with type 1 diabetes participating in the Dose Adjustment for Normal Eating (DAFNE) structured education programme. Diabetes Research and Clinical Practice, Volume 98, Issue 2, 243-248, ISSN 0168-8227, 10.1016/j.diabres.2012.09.017.

[2] Waters PS, McDermott AM, Wall D, Heneghan HM, Miller N, Newell J, Kerin MJ and Dwyer RM. Relationship between circulating and tissue microRNAs in a murine model of breast cancer. PloS One 2012; 7(11):e50459 Epub Nov 30 PMID: 23226290.

Research Activities

Current research grants (2012):

Health Research Board Interdisciplinary Capacity Enhancement Grant. ŞATLANTIC DIP 2: Gestational Diabetes Mellitus (GDM) Screening, Follow up and Intervention in the CommunityŤ (Co-Principal Investigator). Funding awarded: Ă674,950.

SPHERE(Secondary Prevention of Heart Disease in General Practice) follow up study (Co-applicant). Funding awarded: Ă190,669.

Health Research Board Interdisciplinary Capacity Enhancement Grant ŞChronic pain in Ireland: Population prevalence, clinical management and professional educationŤ (Co applicant). Funding awarded: Ă705,300.

Numbers of graduate students:2;

Journal submissions: 4;

Conferences: 3;

Visits: 4;

Invited talks: 2;

Research visits: 2;

Papers refereed: 4;

Memberships: President of Irish Statistical Association;

External posts: Senior Research Fellow, Department of Mathematics and Statistics, University of Canterbury, Christchurch, New Zealand.

Nolan, Louise

Current Research Interests

General relativity; examining solutions to the field equations for cylindrically symmetric spacetimes using dynamical systems analysis, self-similar gravitational collapse of a spacetime with different matter content, matching spacetimes to investigate the existence of physical solutions.

Mathematical aspects of gravitational lensing; using weighted projective spaces to investigate caustic singularities and gravitational lensing, (in collaboration with Dr. Patrick Browne).

Publications

[1] L. NOLAN, B. NOLAN. 'Global structure of self-similar cylindrically symmetric spacetimes', In preparation.

[2] L. NOLAN, B. NOLAN. 'On isotropic cylindrically symmetric stellar models', Class. Quantum Grav., Vol 21. (2004).

Research Activities

Research grants: NUIG University Fellow Annual Grant; Conferences: 2; Invited talks: 1; Research visits: 2; Memberships: Institute of Physics;

O'Regan, Donal

Current Research Interests

Differential Equations, Nonlinear Analysis and Fixed Point Theory.

47 publications in 2011. Four most significant publications

[1] Hernández, E. and O'Regan, D., *On a new class of abstract neutral differential equations*, J. Funct. Anal. **261** 3457-Ű3481 (2011).

[2] O'Regan, D., *A note on fixed point theory for extension type maps*, Nonlinear Stud. **18** 587-Ű593 (2011).

[3] Agarwal, R., O'Regan, D. and Taoudi, M-A, *Fixed point theorems for general classes of maps acting on topological vector spaces*, Asian-Eur. J. Math. **4** 373-Ű387 (2011).

[4] Banas, J., O'Regan, D., Agarwal, R., *Measures of noncompactness and asymptotic stability of solutions of a quadratic Hammerstein integral equation*, Rocky Mountain J. Math. **41** 1769Ű-1792 (2011).

Pfeiffer, Götz

Current Research Interests

Computational algebra, representations of finite groups and associative algebras, combinatorics and geometry of finite Coxeter groups.

Publications

Numbers of publications appearing in calendar year 2012: 2

Four significant publications

[1] (with Liam Naughton)
Computing the Table of Marks of a Cyclic Extension.
Math. Comp. **81** (2012), no. 280, 2419–2438.

[2] (with J. Matthew Douglass and Gerhard Röhrle)
An Inductive Approach to Coxeter Arrangements and Solomon's Descent Algebra.
J. Algebraic Combin. **35** (2012), no. 2, 215–235.

Research Activities

Research grants: Numbers of graduate students: 2; Journal submissions: 3; Conferences: 2; Visits: 3; Invited talks: 2; Research visits: 3; Papers refereed: 7; Math review: 2; Editorships: Mathematical Proceedings of the Royal Irish Academy; Memberships: Irish Mathematical Society, American Mathematical Society;

Piiroinen, Petri T

Current Research Interests

My main research interests are in the area of discontinuous dynamical systems with application to rigid-body mechanics, economics, psychology and biological systems. I am also involved in a few projects that deal with the analysis of evolving networks. An overarching aim of my research is to bridge the gap between mathematics and numerical analysis on one hand and biology, engineering and social sciences on the other to make mathematical theories more applicable to non-theoreticians.

Publications

Numbers of publications appearing in calender year 2012: Most significant publications

[1] Mason, J., Humphries N. and Piiroinen, P.T., *Numerical analysis of codimension-one, -two and -three bifurcations in a periodically-forced impact oscillator with two discontinuity surfaces*, Accepted for publication in MATCOM, 2012. (DOI: 10.1016/j.matcom.2012.08.010)

[2] Humphries, N. and Piiroinen, P.T., *A discontinuity-geometry view of the relationship between saddle-node and grazing bifurcations*, Physica D 241, pp. 1911–1918, 2012.

[3] Alzate, R., Piiroinen, P.T. and di Bernardo, M., *From complete to incomplete chattering: a novel route to chaos in impacting cam-follower systems*, International Journal of Bifurcation and Chaos 22(5), 2012. (DOI: 10.1142/S0218127412501027)

Research Activities

During 2012 I supervised or co-supervised 3 PhD students. Two MSc students, Richard Burke and Neil Humphries, graduated in the autumn of 2012. I attended 2 conferences and gave 1 academic seminar (University of Naples Federico II (Italy). I am guest editor for the Special Issue *Discontinuous Dynamical Systems: Theory and Numerical Methods* of the journal Mathematics and Computers in Simulation (MATCOM), and I organised a three-day meeting at NUIG in July 2012 in collaboration with an EU COST action.

Quinlan, Rachel

Current Research Interests

My current research is primarily situated in the area of linear algebra and its interactions with combinatorics, field theory, group theory and representation theory. One specific recent focus of attention involves characterization of partial matrices whose completions all have the same rank (a *partial matrix* is a matrix in which some entries are specified and some

are free to assume any value from a field). This topic is particularly interesting in the case of finite fields. Other recent and current projects involve linear spaces of nilpotent matrices, and unitary groups over finite local rings. I also have research interests in mathematics education at university level.

Publications

Most significant publications

[1] James McTigue and Rachel Quinlan. Partial matrices whose completions all have the same rank. Linear Algebra and its Applications, Vol. 438 (2013), no. 1, 348–360.

[2] James McTigue and Rachel Quinlan. Partial matrices whose completions have ranks bounded below. Linear Algebra and its Applications, Vol. 435 (2011), no. 9, 2259–2271.

[3] Rachel Quinlan. Spaces of matrices without non-zero eigenvalues in their field of definition, and a question of Szechtman. Linear Algebra and its Applications, Vol. 434 (2011), no. 6, 1580–1587.

[4] Rod Gow and Rachel Quinlan. Galois extensions and subspaces of alternating bilinear forms with special rank properties. Linear Algebra and its Applications, Vol. 430 (2009), no. 8–9, 2212âĂŞ-2224.

Research Activities

Invited talks at the following conferences in 2012

- Canadian Mathematical Society Summer Meeting, University of Regina, June 2012

- Women in Mathematics Day Ireland, University of Limerick, April 2012

- Irish Mathematics Students Association Conference, UCD, March 2012

Journal submissions

- (with J. McTigue) Partial matrices whose completions all have the same rank. (appeared in 2013 in *Linear Algebra and its Applications*

- (with J. Cruickshank, A. Herman, and F. Szechtman) Unitary groups over local rings. (submitted to *Journal of Algebra and its Applications*, August 2012)

Co-organizer of the 6th De Brún Workshop (Linear Algebra and Matrix Theory), NUI Galway, December 2012.
Supervision of the research of one PhD student, James McTigue.
Internal examiner for the PhD thesis of Barry Hurley
Memberships : Irish Mathematical Society, American Mathematical Society, International Linear Algebra Society.

Röver, Claas

Current Research Interests

Group Theory

Publications

Ryan, Ray

Current Research Interests

Functional Analysis: multilinear, polynomial and holomorphic functions on Banach spaces. Tensor products of Banach spaces and Banach lattices. Regular polynomial and holomorphic functions on Riesz spaces and on Banach lattices.

Publications

Most significant publications

[1] "Introduction to tensor products of Banach spaces", Springer Monographs in Mathematics, Springer-Verlag, London, 2002.

[2] with C. Boyd, "Geometric theory of spaces of integral polynomials and symmetric tensor products", J. Functional Analysis 179 (2001), no. 1, 18–42.

[3] with B. Grecu, "Polynomials on Banach spaces with unconditional bases",

Proc. Amer. Math. Soc 133 (2005), no. 4, 1083–1091.

[4] with C. Boyd, "The norm of the product of polynomials in infinite dimensions", Proc. Edinburgh Math. Soc. (2) 49 (2006), no. 1, 17–28.

Research Activities

Refereeing papers for journals, membership of editorial board of journal, hosting of visiting researcher, preparation of papers for submission to journal.

Seoighe, Cathal

Research in my group spans several areas of bioinformatics/computational biology: Genomics and epigenetics, including gene expression analysis, mRNA splicing and analysis of chromatin structure using deep sequencing data. Development and application of probabilistic models of evolution, especially the use of evolutionary models to identify immune epitopes in HIV-1. Bioinformatics is interdisciplinary and I collaborate with several other research groups on campus. A major focus of recent collaborations involves the analysis of data from ultradeep sequencing technologies. These technologies can be used to sequence genomes or for studying gene expression or the binding of proteins to DNA, which is critical for the control of gene expression.

Current Research Interests

The focus of my research is on modeling molecular biological data, including epigenetic data, gene expression, alternative mRNA splicing and molecular evolution, including the evolution of viruses such as HIV-1.

Publications

Three journal articles appeared in 2012.

Most significant publications

[1] The regulatory effect of miRNAs is a heritable genetic trait in humans. Geeleher P, Huang SR, Gamazon ER, Golden A, Seoighe C. BMC Genomics. 2012 Aug 10;13:383.

[2] Semi-supervised Nonnegative Matrix Factorization for gene expression deconvolution: A case study. Gaujoux R, Seoighe C. Infect Genet Evol. 2012 Jul;12(5):913-21

Research Activities

My research group consisted of seven PhD students in 2012. Research is currently supported by SFI (Stokes Programme); IRCSET, through a graduate education programme in collaboration with UCD; PRTLI, through a graduate programme in simulation science and the EU, through an international training network coordinated by Leeds University (to commence in 2013). Continued development and establishment of new research collaborations across NUIG took place in 2012. Academic community service included memberships of editorial boards of Bioinformatics and Trends in Evolutionary Biology and refereeing for a wide range of journals, as well as membership of the Programme Board for RECOMB Comparative Genomics workshop, held in Rio de Janeiro in October, 2012.

Sheahan, Jerome

Current Research Interests

Combinatorial techniques to unify apparently different enumeration problems in various areas of scientific endeavour

Publications

1 publication in an international refered journal

Research Activities

Statistical consulting service to researchers in most of the College on Campus. Problems solved run the gamut of statistical methods. Currently particularly involved in, for example, the design of social surveys for Department of Marketing and School of Education.

Sköldberg, Emil

Current Research Interests

I am interested in combinatorial methods in algebra, in particular for studying the structure of free resolutions in both commutative and non-commutative algebra. I am also interested in computational aspects of resolutions and homology, and related techniques, such as Gröbner bases.

Publications

Most significant publications

[1] G. Ellis, E. Sköldberg, *The K(π,1) conjecture for a class of Artin groups.* Comment. Math. Helv. **85** (2010), no. 2, 409âĂŞ-415

[2] E. Sköldberg, *Morse theory from an algebraic viewpoint*, Trans. Amer. Math. Soc. **358** (2006), 115–129

[3] E. Sköldberg, *The Hochschild homology of truncated and quadratic monomial algebras*, J. London Math. Soc. (2), **59** (1999), 76–86.

Research Activities

During 2012 Isaac Burke started his PhD studies under my supervision.

My travels and talks included

[1] Talk at Université de Luxembourg.

[2] Lecturing at "Summer school on discrete Morse theory and commutative algebra", Institut Mittag-Leffler

[3] Participating at conference "Combinatorial commutative algebra and applications" at MSRI.

[4] Research visit at Trinity College, Dublin.

Tuite, Michael

Current Research Interests

Vertex operator algebras (VOAs), Riemann surfaces, elliptic and modular functions in number theory and combinatorics. I am particularly interested in computing partition and correlation functions on higher genus Riemann surfaces for various VOAs. I am also interested in exceptional VOAs and their relationship to Virasoro constraints. I also have a growing interest in applying vertex operator algebras to number theory such as understanding Ramanujan congruences in a new way.

Publications

2 publications in calendar year 2012 and two other papers in press.

[1] D. Hurley and M.P. Tuite, Virasoro correlation functions for vertex operator algebras, International Journal of Mathematics **23**, 1250106 (2012).

[2] 36. M.P. Tuite and A. Zuevsky, A generalized vertex operator algebra for Heisenberg intertwiners, Journal of Pure and Applied Algebra **216** 1442–1453 (2012).

Research Activities

- I currently hold one SFI RFP grants and one IRCSET Embark Studentship.

- I supervised 1.5 PhD students in 2012.

- I refereed 2 papers.

Ward, James

Current Research Interests

Permutability and subnormality criteria in certain classes of infinite soluble groups.
The study of $\mathcal{N}_1$ groups (groups with all subgroups subnormal).
History of Mathematics: Transmission of Greek and Arabic Mathematics in the early medieval era.
Reception of Galois Theory in 19th century University Mathematics teaching.
Professors of Mathematics in Queen's College, Galway.

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.

Publications

Most significant recent publications

[1] Pierre C. Havugimana, G. Traver Hart, TamÃąs Nepusz, Haixuan Yang, Andrei L. Turinsky, Zhihua Li, Peggy I. Wang, Daniel R. Boutz, Vincent Fong, Sadhna Phanse, Mohan Babu, Stephanie A. Craig, Pingzhao Hu, Cuihong Wan, James Vlasblom, Vaqaar-un-Nisa Dar, Alexandr Bezginov, Gregory W. Clark, Gabriel C. Wu, Shoshana J. Wodak, Elisabeth R.M. Tillier, Alberto Paccanaro, Edward M. Marcotte, Andrew Emili. A census of human soluble protein complexes. Cell 150 (5), 1068-1081, 2012.

[2] Haixuan Yang, TamÃąs Nepusz, Alberto Paccanaro. Improving GO semantic similarity measures by exploring the ontology beneath the terms and modelling uncertainty. Bioinformatics 28 (10), 1383-1389, 2012.

[3] Prajwal Bhat, Haixuan Yang, Laszlo BÃűgre, Alessandra Devoto, Alberto Paccanaro. Computational Selection of Transcriptomics Experiments Improves Guilt-by-Association Analyses. PloS one 7 (8), e39681, 2012.

[4] Haixuan Yang, Michael R Lyu, Irwin King. A volume-based heat-diffusion classifier. IEEE Transactions on Systems, Man, and Cybernetics, Part B 39(2),417-430, 2009.

Research Activities

I was an international referee for a PhD thesis in Department of Mathematics, University of Messina, Italy. I worked as Program Committee of the following three conferences: the 7th Pattern Recognition in Bioinformatics Conference, the 2012 IEEE/WIC/ACM International Conference on Web Intelligence, and the 4th Asian Conference on Machine Learning. Moreover, I reviewed papers for Bioinformatics, Pattern Recognition, IEEE Transactions on Neural Networks and Learning Systems. I submiited a proposal for Science Without Border project.

Visitors

Demétrio, Clarice, ESALQ/USP, Piracicaba, Brazil

Dates of visit: March 2013

Research Interests

The purpose of this short visit was to continue collaborative work with Professor John Hinde on overdispersion modelling and its application in entomology. A new research project on quasi-likelihood estimation for Poisson-Tweedie regression models was also initiated.

Mason, Geoffrey, University of California Santa Cruz

Dates of visit: 6-16 June 2012

Research Interests

Vertex operator algebras, number theory and group theory. Discussions on joint research on vertex operator algebras on genus two Riemann surfaces and exceptional vertex operator algebras.

Miszczak, Jarosław Adam

Dates of visit: 10/6/2012 to 24/6/2012

Research Interests

Dr. Miszczak (from the Institute of Theoretical and Applied Informatics, Polish Academy of Sciences) visited for two weeks as a guest of the De Brun Centre for Computational Algebra. He collaborated with Dr. Mc Gettrick on the asymptotics of Quantum Random Walks with memory and on ideas in Quantum Evolutionary Game Theory.

Ogden, Ray

Dates of visits: 22-31 October 2012 and 09-20 April 2013

Research Interests

Visit to collaborate with Michel Destrade and Luigi Vergori on computational solid mechanics and on straightening wrinkles. Funded by the Royal Society.

Otténio, Mélanie

Dates of visit: 11-16 March 2013

Research Interests

Visit to collaborate with Michel Destrade on the mechanics of brain matter. Funded by a "New Foundations" grant from the Irish Research Council.

Moral, Rafael, ESALQ/USP, Piracicaba, Brazil

Dates of visit: April 17th to June 14th

Research Interests

Rafael de Andrade Moral visited NUI Galway for a 2-month period in 2013 as part of his Master's studies to work under the supervision of Prof. John Hinde. His research involves statistical modelling of the ecological interactions among species of agricultural significance, including pests and natural enemies. His supervisor at ESALQ/USP is Prof. Clarice G. B. Demétrio.

Szechtman, Fernando

Dates of visit: July 2012

Research Interests

Fernando Szechtman is an Associate Professor at the University of Regina, Canada. During a two week visit in July 2012, he worked with James Cruickshank and Rachel Quinlan on an investigation of properties of unitary groups over finite local rings. This has resulted in a submission to the *Journal of Algebra and its Applications.*

Valdes, Teofilo, Complutense University, Madrid, Spain

Dates of visit: September to November 2012

Research Interests

Professor Valdes spent a part of his sabbatical leave as a research visitor in the School. While in Galway he worked on algorithmic approaches for sequential analysis of variance with imprecise observations and completed two research papers. He took part in the regular discussion sessions of the Statistics Group including presenting his own work.

Zuevsky, Sasha, Prague

Dates of visit: 19-25 Feb 2012

Research Interests

Vertex operator algebras and Riemann surfaces. Discussions on joint research on vertex operator super algebras on genus two Riemann surfaces.

Postdoctoral Researchers

Vergori, Luigi

In collaboration with Proff. K.R. Rajagopal (Texas A&M University, USA) and G. Saccomandi (Università di Perugia, Italy), I worked on the mechanics of fluids with variable viscosity. In particular, we studied in detail the flows in fluids whose viscosity depends on the pressure and shear-rate.

In collaboration with Dr. Napoli (Università del Salento, Italy), I derived mathematical models for the free energy density of a liquid crystal coating a rigid surface and studied the resulting equilibrium equations.

I started a collaboration with Proff. M. Destrade (NUIG), R.W. Ogden (University of Glasgow, UK) and I. Sgura (Università del Salento, Italy) to work on stability problems in nonlinear elasticity. Moreover, in collaboration with Proff. Destrade and Ogden, and

Dr. P. McGarry (NUIG), I worked on the incorrect implementation of models for anisotropic materials in the current finite element codes.

Current Research Interests

- Mechanics of fluids with variable material parameters.

- Mechanics of liquid crystals.

- Nonlinear Elasticity.

Publications

Number of publications appearing in calender year 2012: 4 Most significant publications

[1] G. Napoli, L. Vergori, *Curvature-induced ordering in cylindrical nematic shells.* International Journal of Non-Linear Mechanics, doi: 10.1016/j.ijnonlinmec.2012.09.007.

[2] K.R. Rajagopal, G. Saccomandi, L. Vergori, *Flow of fluids with pressure-and shear-dependent viscosity down an inclined plane.* Journal of Fluid Mechanics 706, 173-189.

[3] G. Napoli, L. Vergori, *Surface free energies for nematic shells.* Physical Review E - Statistical, Nonlinear, and Soft Matter Physics 85 (6), art. no. 061701.

[4] G. Napoli, L. Vergori, *Extrinsic curvature effects on nematic shells.* Physical Review Letters 108 (20), art. no. 207803.

Rahm, Alexander D.

Current Research Interests

Analyzing the invariants of infinite discrete groups of isometries. A technique herefore developed by Rahm is Torsion Sub-complex Reduction, which has been successfully applied to the Bianchi groups as well as to the tetrahedral Coxeter groups. In both cases, general formulae for the homological torsion have been established, and for the former class of groups, they are expressed in terms of elementary number-theoretic information. Application of this technique

have been elaborated for equivariant K-homology, as well as for Chen–Ruan quantized orbifold cohomology of Bianchi orbifolds.

Publications

Most significant publications in 2012/2013 :

[1] *On level one cuspidal Bianchi modular forms.* Joint work with Mehmet Haluk Sengun, accepted for publication in LMS J. Comp. & Math.

[2] *On a question of Serre.* Published in the Comptes Rendus Mathématique of the Académie des Sciences - Paris, 2012, presented by Jean-Pierre Serre.

[3] *The homological torsion of SL_2 of the imaginary quadratic integers.* Transactions of the AMS, volume 365 (2013), pp. 1603–1635.

[4] *The subgroup measuring the defect of the Abelianization of* $SL_2(\mathbf{Z}[i])$, published in the Journal of Homotopy and Related Structures, February 2013.

Postgraduate Researchers

Current Postgraduate Research Students

Student	Degree	Supervisor	Supervisor
Nhan Anh Thai	PhD	Niall Madden	
Bui Anh Tuan	PhD	Graham Ellis	
Alan Barnicle	PhD	Cathal Seoighe	Laurence Egan
Sofia Barreira	PhD	Cathal Seoighe, Brian McStay	
Jorge Bruno	PhD	Aisling McCluskey	
Isaac Burke	PhD	Emil Sköldberg	
Shane Burns	PhD	Petri Piiroinen	
Simone Coughlan	PhD	Tim Downing	Cathal Seoighe
Kevin Doherty	PhD	Martin Meere	Petri Piiroinen
John Donohue	PhD	Petri Piiroinen	
Cara Dooley	PhD	John Hinde	
Liam Doonan	PhD	Uri Frank	Cathal Seoighe
Michelle Duane	PhD	Aisling McCluskey	
Ronan Egan	PhD	Dane Flannery	
Attia Fatima	PhD	Cathal Seoighe	Dermot Morris
Thomas Gilroy	PhD	Michael Tuite	
Artur Gower	PhD	Michel Destrade	
Peter Keane	PhD	Cathal Seoighe	Rod Ceredig
Paul Korir	PhD	Cathal Seoighe	Tim Downing
Adib Makrooni	PhD	John Burns	
Brendan Masterson	PhD	Götz Pfeiffer	
Nur Fatihah Mat Yusoff	PhD	John Hinde	
James McTigue	PhD	Rachel Quinlan	
Thong Nguyen	PhD	Cathal Seoighe	Andrew Flaus
Stephen Russell	PhD	Niall Madden	
Le Van Luyen	PhD	Graham Ellis	
Deirdre Wall	PhD	John Newell	
Rachel Wallace	PhD	Götz Pfeiffer	

Seminars

[1] <u>Alexander Rahm</u>, NUI, Galway **Torsion subcomplex reduction and conjugacy classes graphs** 12/1/2012

[2] <u>Conor Houghton</u>, Trinity College, Dublin **The temporal structure of spike train noise** 19/1/2012

[3] <u>Barry Hurley</u>, NUI, Galway **Classification problems for finite linear groups** 23/1/2012

[4] <u>Alan Rogerson</u>, Poland **Developing Quality in Mathematics Education** 24/1/2012

[5] <u>Colin Wilmott</u>, Masaryk University (Brno) **Quantum sign permutation polytopes** 9/2/2012

[6] <u>Michael Mackey</u>, University College Dublin **Local triple derivations** 23/2/2012

[7] <u>Kevin Hutchinson</u>, University College Dublin **Polylogarithms and linear groups** 1/3/2012

[8] <u>Jesús Hernández</u>, Universidad Veracruzana (Mexico) **Simplicial maps between non-separating curve graphs** 8/3/2012

[9] <u>Liam Naughton</u>, NUI, Galway **Computing the Table of Marks of a Cyclic Extension** 22/3/2012

[10] <u>Oliver O'Reilly</u>, University of California at Berkeley **The Dynamics of a Novel Ocean Wave Energy Converter** 28/3/2012

[11] <u>Lloyd Bridge</u>, University of Bristol **Mathematical and computational modelling of cell signalling dynamics** 29/3/2012

[12] <u>Aylwyn Scally</u>, Sanger Institute, Cambridge **The gorilla genome and the evolution of the great apes** 12/4/2012

[13] <u>Ivan Marin</u>, Université Paris 7 **Complex reflection groups, braid groups and Hecke algebras** 16/4/2012

[14] <u>José Burillo</u>, Universitat Politècnica de Catalunya (Barcelona) **On groups with polynomial geodesic growth** 17/4/2012

[15] <u>Tim Downing</u>, NUI, Galway **Deciphering genetic networks of drug resistance in parasites** 19/4/2012

[16] <u>Dick Hamlet</u>, Portland State University **Computer Science is Mathematics, not Science** 24/4/2012

[17] <u>Christian Lehn</u>, Université Joseph Fourier (Grenoble) **Lagrangian subvarieties and Hodge theory**

[18] <u>Miguel Lacerda</u>, NUI, Galway **Epitope Discovery in HIV-1 using Evolutionary Models** 4/5/2012

[19] <u>Anthony G. O'Farrell</u>, NUI, Maynooth **Reversibility and factorisation in power series groups** 10/5/2012

[20] <u>Padraig Ó Catháin</u>, NUI, Galway **Skew difference sets** 17/5/2012

[21] <u>Luigi Vergori</u>, NUI, Galway **Convection and viscous dissipation in piezoviscous fluids** 7/6/2012

[22] <u>John Cosgrave</u>, St. Patricks College, Drumcondra **Gauss primes, a new class of primes intimately related to quarter Gauss factorials** 11/6/2012

[23] <u>Ciara Morgan</u>, National University of Singapore **Quantum Shannon theory and channel capacities** 14/6/2012

[24] Geoff Mason, University of California at Santa Cruz **Conformal Flow for Vertex Operator Algebras** 15/6/2012

[25] David Liberles, University of Wyoming **Computational Approaches for Linking Comparative Genomics to Biochemistry and Evolution** 28/6/2012

[26] Matthias Wendt, Universität Freiburg **On homology of linear groups over polynomial rings** 30/7/2012

[27] Rob de Jeu, Vrije Universiteit Amsterdam **Algebraic K-theory and arithmetic** 16/8/2012

[28] Ethan Berkove, Lafayette College, Pennsylvania **L2 homology and clean complexes** 22/8/2012

[29] Vladimir Dotsenko, Trinity College Dublin **Pattern avoidance in permutations** 20/9/2012

[30] Petri Piiroinen, NUI, Galway **Twists and turns during my sabbatical** 27/9/2012

[31] Thomas Huettemann, Queens University Belfast **From toric varieties to finite domination** 4/10/2012

[32] Conor Lawless, Newcastle University **Quantifying and comparing fitnesses of yeast cultures to uncover biological function** 11/10/2012

[33] Paul Geeleher, NUI, Galway **Analysis of gene regulation using high throughput genomics** 16/10/2012

[34] Ernesto Spinelli, Università di Roma **Lie identities for skew and symmetric elements of group algebras** 18/10/2012

[35] Bernd Kreussler, Mary Immaculate College, Limerick **Means, Braids and Triangle Equations** 1/11/2012

[36] Klaus Lux, University of Arizona **Modular Representation Theory: Algorithms and Applications** 8/11/2012

[37] Aisling McCluskey, NUI, Galway **Extending a notion of betweenness** 15/11/2012

[38] Alberto Alvarez, NUI, Galway **Extensions and applications of survival trees in medical data** 19/11/2012

[39] Paul Bankston, Marquette University **A Road System Interpretation of Betweenness** 22/11/2012

Specialist seminar series

- Representation Theory of the Symmetric Groups (Organizer: **Goetz Pfeiffer**)

- Bioinformatics journal club (Organiser: **Cathal Seoighe & Tim Downing**);

- Statistics Reading Group (Organiser: **John Hinde**);

- MathSoc seminar series (Organisers: **MathSoc**.

Conferences and Workshops

- 6th de Brun Workshop: Linear Algebra and Matrix Theory - connections, applications and computations
  (Organisers: Graham Ellis, Niall Madden, Rachel Quinlan)
  Date: December 3–7, 2012

- 1st Irish Meeting for Linear Algebra Research
  Organisers: Niall Madden, Rachel Quinlan
  Date: December 8, 2012

- COST Action MP0801: Physics of competition and conflict annual meeting 2012
  Organiser: Petri Piiroinen (Maths), Srinivas Raghav (Economics)
  Date: July 11–13, 2012

- Statistical Analysis with Missing Data using Multiple Imputation
  (Organiser: John Newell, delivered by Jonathan Bartlett)
  Date: December 10–11, 2012

- Summer School in Biostatistics (Introduction)
  (Organiser: John Newell, delivered by John Newell and George McCabe)
  Date: June 18–22, 2012

  Title: Summer School in Biostatistics (Advanced) (Organiser: John Newell, delivered by John Newell and Tom Aitchison)
  Date: June 11–15 2012