The Bogue Research Fellowships

Report for the UCL Friends & Alumni Association Board

March 2026

Pursuing Excellence

We are very pleased once again to share our formal report on the Bogue Research Fellowships with the UCL Friends & Alumni Association (UCLFAA) Board.

Since its inception in 1998, the Bogue Fellowship Scheme has continued to run very successfully. Focused on both postgraduate research students and postdoctoral researchers working in the areas of life and biomedical sciences at UCL, the fellowships provide unique opportunities to undertake research placements in the USA. The scheme was instigated at the bequest of the late Dr James Yule Bogue, a former Research Fellow in UCL's Department of Physiology, and allows the awardees to visit a USA research institution for up to six months, although most visits are shorter than this.

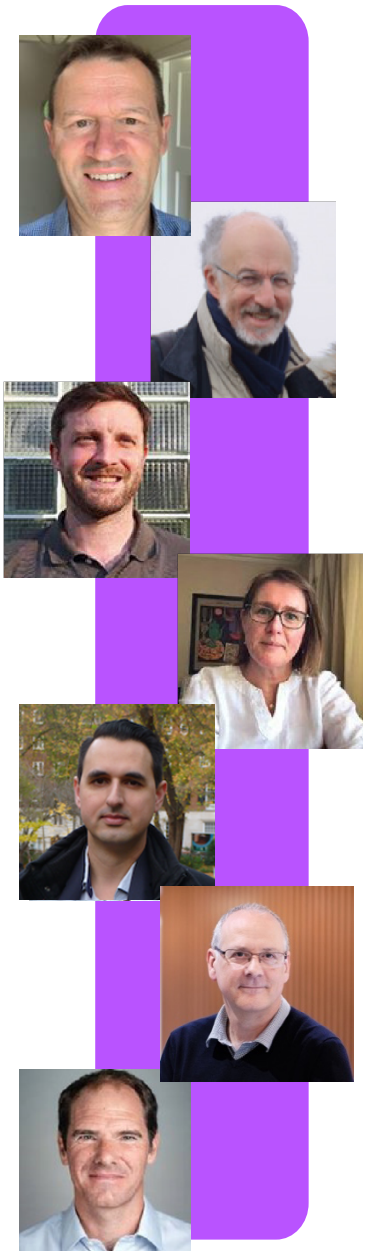
Since 1998, and thanks to the UCLFAA's continued support, UCL has been able to provide around 350 fellowship awards to these exceptional young researchers. The feedback we receive from these fellows clearly shows that opportunities to work with USA teams can make a big difference to their knowledge, research outputs, professional experience and careers. It is also clear that these fellowships continue to generate excellent research outputs and establish numerous, long-lasting, cross-Atlantic collaborations.

The Bogue Fellowships Committee
To be awarded a Bogue Research Fellowship, scholars need to submit a detailed application that fully justifies their planned fellowship project. The Bogue Fellowships Committee reviews these applications and decides on the appropriate funding outcomes within our operating budget. The committee members also discuss the current application rates and patterns and any potential changes needed to the funding guidelines.

The committee has 6–7 members from across UCL's diverse academic departments and institutes. We have enough expertise between us to cover most or all topic areas in each application round. Importantly, all our committee members supervise a range of early career scientists, and we therefore understand their needs and try to fund those applicants who would benefit the most from their proposed placements. At present, the committee members are:

Dr Andrew Stoker (**Chair; on leave June-December 2025**)
Associate Professor with expertise in developmental neurobiology and molecular cell biology of cancer. He is the Faculty Graduate Tutor for research students in Population Health Sciences and has been a committee member for many years and took over being the Chair in 2023. Unfortunately, Dr Stoker has been on medical leave since June 2025 and Professor Duchen kindly took over the role in the interim. Dr Stoker returns in January 2026.

Professor Michael Duchen (**interim Chair June-December**)
A clinically qualified Professor of Physiology who works in cell physiology and cellular energetics in a wide range of disease models. He is the Senior Graduate Tutor for the Department of Cell and Developmental Biology and has been on the committee for 25 years and was our long-standing Chair from 2006-2023. We thank Michael for stepping in as interim Chair.



Professor Chris Barnes
Professor of Systems and Synthetic Biology, with special expertise in mathematical modelling and systems biology. He is UCL Director of the EPSRC Centre for Doctoral Training in BioDesign Engineering.

Professor Paola Pedarzani
Professor of Neurophysiology, with broad expertise in neuroscience. She is the Graduate Tutor for the Department of Neuroscience, Physiology and Pharmacology and Director of the Medical Research Council-funded PhD Doctoral Training Programme.

Dr Pranjal Mehta
Dr Mehta is an Associate Professor in experimental psychology. His research focuses on status hierarchies, stress and their relation to social status and power. He studies these topics using tools and theories from social-personality psychology and behavioural neuroendocrinology.

Professor David Sansom
Professor of Transplant Immunology based at UCL Institute for Immunity and Transplantation. Has wide ranging expertise in immunology focusing on molecular basis of immune regulation and self-tolerance.

Professor Jonathan Rosier (previous member but standing in for Pranjal Mehta at December 2024 meeting)
Professor of Neuroscience and Mental Health, with expertise in cognitive neuroscience, an area strongly represented amongst project proposals. He is Graduate Tutor for the Institute of Cognitive Neuroscience and Director of the UCL-National Institute of Mental Health Joint Doctoral Training Programme in Neuroscience and the UCL PhD programme in mental health.

As a committee we continued to receive excellent and much appreciated support from our long-standing Committee Secretary, Jane Inge.

Selection Process

The committee meets in spring and autumn each year to review the applications. The panel considers the following:

- the novelty and potential impact of the science;
- the quality of the written application itself;
- the likely benefits of the visit for the student or post-doc;
- will the applicant return to UCL with valuable new skills, knowledge to disseminate and new collaborative opportunities?
- are the requested costs justified?

We fund on average 70-80% of applications. The reasons for declining funding include:

- applicants not having at least six months left at UCL upon return (either in employment, or before CRS period for PhD students);
- the science is poorly explained, or the application is poorly constructed;
- the visit's duration or timeline is not justified or appropriate for the planned research;
- the costings are inadequately justified.

The committee is flexible though and it does allow some applicants to re-submit applications. If received, then the Chair requests comments from the other committee members. With the continued increase in costs for these fellowships, the committee is now more frequently requesting some partial financial support from the applicant's supervisor or line manager.

Application Rounds

The applicants continue to be predominantly PhD students, with around 10-15% postdoctoral researchers. Most of our applicants continue to request visits to laboratories, but the excellent courses at Cold Spring Harbour or Woods Hole still attract a small number of applicants. Those visiting laboratories continue to travel to access the technical expertise of hosts, unique datasets (that can only be accessed on-site) or access to human participants or their anonymised data. In some cases, we fund data-gathering visits to museums of national standing, wherein fellows access unique materials for ecological or evolutionary studies.

Most fellowships will either reinforce existing collaborations, or start new ones, providing longer-term added value.

Below is a breakdown of the applications received at the rounds in autumn 2024 and spring 2025. The total provisionally allocated was **£145,530.80**.

Autumn (October) 2024
Number of applications: 22
Total amount requested: £158,697
Amount provisionally allocated: £76,925

Spring (April) 2025

- Number of applications: 10
- Total amount requested: £73,682.80
- Amount provisionally allocated: £68,605.80

Successful applicants

From the autumn 2024 round

Ms Maria Cristina Aparicio De Soto (PhD student, GEE). To spend three weeks with Professor Robert Voss, American Museum of Natural History, New York, to collect data on Caviomorpha not available in the UK or EU institutions and to analyse cranial, mandibular and limb diversity by CT scanning and linear measurements.

Ms Lauren Bennett (PhD student, CDB). To spend six months with Professor Anthony Zador, Cold Spring Harbour Laboratory, to be trained in BarSeq2 genetic sequencing and fluorescent microscopy.

Mr Jai Bhagat, (PhD student, Sainsbury). Six weeks with Jack Lindsey, Anthropic, San Francisco, to apply research techniques in AI to understand how the brain processes information by using SAEs.

Dr Anna-Leigh Brown (Research Fellow, IoN). To spend 21 days with Towfique Raj, Icahn School of Medicine, New York, to gain access to the largest RNA/DNA database from post-mortem neuronal tissue and to establish a remote access data plan.

Miss Sarah Buehler (PhD student, ICN). To spend three months with Professor Xiasou Gu, Icahn School of Medicine, to receive intensive supervision and training in developing and applying the most suitable machine learning analysis pipeline to an existing fMRI dataset.

Ms Yue (Casey) Chen (PhD student, CDB). To spend three months with Professor Ophelia Venturelli, Duke University, to gain expertise in single-cell analysis of natural communities.

Mr Laurence Freeman (PhD student, Sainsbury). To spend two months with Eva Dyer, Georgia Tech, to gain skills in applying large scale AI models to brain activities and to advance research in making these models interpretable.

Mr Benedict Greenwood (PhD student, ICN). To spend three months with Professor James Gross, Stanford, to investigate the neurological mechanisms underlying emotion regulating difficulties in ADHD.

Dr Dejan Mesner (Research Associate, Infection). To spend six weeks with Professor Nevan Krogan, UCSF, San Francisco, to learn CRISPR screen technique in resting primary CDT4 cells. *Note: accepted fellowship but had to withdraw due to loss of grant funding in the host laboratory after recent federal cuts.*

Mr Tom Metherell (PhD student, PALS/Social Research Inst). To spend 31 days with Professor Nilam Ram, Stanford, to be trained in techniques used to analyse the screen captures collected in the Human Screenome Project.

Mr Matthew Jonathan Mitchell (PhD student, CDB). To spend 16 days at the Smithsonian National Museum of Natural History, to collect data from species to increase understanding of how a species interacts with environment and how it has evolved.

Miss Adama Fatima Saccoh (PhD student, Inst Cardiovascular Sci). To spend three months with Dr Catherine Tcheandjieu Gueliatcha, Glastoe Inst, UCSF, to use multi-ethnic genetic datasets to help understand the heart-brain relationship.

Ms Merle Maria Schlief (PhD student, Psychiatry). To spend three months with Professor Dustin Duncan, Columbia University, to learn novel techniques of advanced spatial epidemiology and their application to geographical data. *Unfortunately could not travel due to illness.*

From the spring 2025 round

Dr Jackie Casey, (**Research Fellow, IoN**). To spend 90 days with Professor Bill Skarnes, Jackson Laboratory, Connecticut, to engineer iPSC cells to over express tau.

Mr Quentin Rohan Maria Dercon (PhD student, IoN). To spend 84 days with Professor Yael Niv, Princeton University, to learn about the framework of latent cause inference and its potential application to understanding individual differences in the benefits of psychological interventions.

Miss Natalie Sophie Figueredo Burgos (PhD student, NPP). To spend 10 weeks with Professor Zachary Knight, University of California, to receive extensive surgical training and investigate how *Gipr* neurons are regulated by different post ingestive cues under normal physiology.

Mr Francois Okoroafor (PhD student, GOSICH). To cover two lab visits: two weeks (16th – 29th June) with Dr Rod Scott, University of Delaware, and 11 weeks (30th June – 31st August 2025) with Dr Dario Englot, Vanderbilt University, to deepen understanding of epilepsy and its complex systems behaviour and to create EEG datasets and then apply advanced learning machine tools to model this dataset.

Dr Afolarin Otunla (PhD student, Surgery Dept.). To spend four months with Professor Rolf Barth, University of Chicago, to develop a machine-perfusion pig model of ischaemic kidney injury.

Miss Mengxuan Qiao (PhD student, Experimental Psychology). To spend 47 days with Professor Keith Holyoak, University of Chicago, to gain training in computational modelling within the domain of legal decision-making.

Miss Greta Arancia Sanna (PhD student, Experimental Psychology). To spend 35 days with Dr Briony Swire-Thompson, Northeastern University, to conduct research into the role of memory in misinformation correction.

Ms Yi Yang (PhD student, Crick). To attend the excellent Cold Spring Harbor Neural Data Science course (18 days).

Ms Kathleen (Jia Yue) Zhang (PhD student, CDB). To spend 109 days with Professor James Boedicker, University of Southern California, to explore how engineered bacterial strains arranged in spatial patterns share information and to gain hands-on experience with the ComX system.

Ms Yedi Zhang (PhD student, Gatsby). To spend 17 weeks with Professor James McClelland, Stanford University, to develop a mathematical model to describe empirical findings.

Our fellows are asked to write a report of their experiences on their trips to the USA and these always provide excellent insight into how valuable these visits have been for them. We share our most recent reports on page 9 onwards.

Summary & Future Plans

The autumn 2024 and spring 2025 funding rounds attracted the expected set of diverse applications and we were able to fund the majority of these. The two funding rounds of autumn 2023 and spring 2024 attracted 25 applicants, while the autumn 2024 and spring 2025 attracted 32. Although these were decent numbers, the recent November 2025 round has had only 10 applicants (versus 22 in 2024), so we are again concerned that numbers are reducing. Why might this be? Apart from the ever-increasing costs of these fellowships, the committee also recognise that the current administrative landscape in the USA seems to be negatively affecting some applicants. There have unfortunately been much-publicised cancellations in academic research funding in some USA institutions, and we have had one applicant withdraw their application apparently due to this (see above). Such uncertainty about host laboratory status is therefore a concern. Anxieties have also been expressed by applicants about the increasing scrutiny of international students and researchers, potentially making entry visas a challenge for some. The committee recognises these concerns and will try to reassure applicants where it can with up-to-date and accurate advice. Thus, we will strive to ensure that fellows can continue to

travel successfully and confidently to their chosen hosts.

There had been a plan to organise an alumni event in 2025. However, due to the chair having to take extended leave, this has been postponed. We hope that 2026 may provide the right opportunity to hold such an event. In the coming year we will also update our guidance documents to request of fellows that if they publish work linked to their fellowship, they must remember to include a standard acknowledgement statement in such publications.

Finally, we note with sadness that we are to lose our excellent and longstanding secretary for the Bogue Fellowship Committee, Jane Inge, to retirement. Jane has been a stalwart presence on this committee for many years, and we have benefitted from her wisdom, good humour and common sense. The committee would like to thank Jane profusely, acknowledge her unwavering work in this role, and wish her all the best for the future.

To Conclude

The Bogue Fellowship Scheme is clearly recognised as one of the few routes by which our early-stage researchers can gain key research experience in the USA. We continue to recognise the UCLFAA's generous and invaluable funding of this scheme and can say with confidence that your enduring support provides invaluable opportunities for transatlantic research collaboration. We therefore look forward to another year of exciting research for our fellows.

Reports from our fellows

-

Sandra Lopez Garces, Bogue Fellowship Report
Aug-Dec 2024
Yale School of Medicine

General comments on the experience
Moving from a translational research background to an immunology-focused lab has been an incredible journey. I have learned so much, not just about macrophages and new techniques, but also about the deeper process of scientific thinking. This experience has been transformative, shaping my future as a scientist. I now feel more confident in applying hypothesis testing, working with mouse models, and validating approaches, all of which I hope to bring to a lab focused on understanding scleroderma and discovering new therapies. What truly made this experience special was the people. The lab I joined was full of brilliant and generous researchers who challenged my understanding and encouraged me to grow. They taught me how to ask better questions and helped me develop a more thoughtful and curious approach to science. I have built connections that I know will last a lifetime; people I can turn to for feedback, advice, and collaboration. This community of researchers has been inspiring, and they have had a profound impact on both my work and my confidence. This truly is a once-in-a-lifetime experience that I would recommend to anyone. It has not only expanded my horizons academically but also pushed me to grow as a person. The sense of accomplishment and personal growth I have gained is something I will carry with me forever.

Details of work carried out during the fellowship

Title
Characterising the phenotype of pathogenic macrophages in scleroderma.

Hypothesis
I hypothesise that MERTK expressing macrophages halt the resolution of inflammation by a failure of efferocytosis thus leading to fibrosis.

Background
Scleroderma (SSc) is a severe condition of unknown aetiology in which dysregulated immune responses are linked to vascular damage, inflammation, autoantibody production, and persisting fibroblast activation, leading to skin and organ-based fibrosis [1]. Central to the pathology of SSc are macrophages, versatile immune cells whose malfunction is implicated in the disease's initiation and progression [2]. These cells initially promote inflammation, contributing to tissue damage, and subsequently drive fibrosis through aberrant signalling to fibroblasts. However, the precise mechanisms by which macrophages fail to resolve inflammation, thereby perpetuating fibrosis, remain elusive. Efferocytosis plays a key role in taking apoptotic bodies from the environment. Macrophage efferocytosis has been shown to trigger the change from pro-inflammatory macrophages to a wound healing repair subset [3].

Evidence that efferocytosis is defective in the disease has previously been reported, particularly SSc monocyte derived macrophages have been shown to have lower capabilities at clearing T cells [4]. However, further research is needed to fully elucidate the role of efferocytosis, particularly by MERTK macrophages in inducing fibrosis in SSc. This gap in knowledge forms the cornerstone of my research. Utilising cutting-edge single-cell RNA sequencing, I have shown MERTK is overexpressed in wound healing macrophages from SSc patients. MERTK encodes a tyrosine receptor implicated in the efferocytosis process; the role of this receptor in the context of the diseases is yet to be elucidated. Collaborating with Dr. Rothlin's Lab, renowned for its expertise in macrophage research, particularly the role of efferocytosis and its unique macrophage-specific MERTK knockout mice model, provides an unprecedented opportunity to investigate the role of macrophage MERTK in vivo and in vitro function and to elucidate their exact role in inflammatory fibrosis.

Work carried out

Phase 1: Training and dose optimisation
During the first month, I focused on mastering intradermal bleomycin injections and learning how to induce fibrosis in mice. This training phase also included familiarisation with mouse markers, lab protocols, and the broader research context. Once confident in the technique, we moved to dose-response experiments to optimise the bleomycin dose. Since bleomycin composition can vary between suppliers, we needed to ensure that the dose used would induce measurable fibrosis without overwhelming the system or causing excessive mortality. Using calipers, we determined a dose that reliably produced visible fibrosis without severe adverse effects.

Phase 2: Experimental setup
In the third and fourth months, I conducted the main experiments using 40 mice divided into five groups (n=5 per group). The experimental design included: utilising two mouse models to investigate the role of MerTK in fibrosis, a full knockout model to assess the overall impact of MerTK deficiency, and a CSF-Cre conditional knockout model to deplete MerTK-expressing macrophages. Mice were divided into eight groups, with five mice per group. The groups included wild-type (WT) mice treated with either saline (vehicle control) or bleomycin, full MerTK knockout mice treated with saline or bleomycin, CRE-positive MerTK knockout mice treated with saline or bleomycin, and CRE-negative controls treated with saline or bleomycin. Bleomycin or saline was administered daily via intradermal injections over a 28-day period. During the experiment, skin thickening was measured at regular intervals to monitor fibrosis progression. The goal was to determine whether the absence of MerTK in full knockout mice or macrophage-specific depletion in conditional knockouts would influence the degree of fibrosis in response to bleomycin. At the conclusion of the 28-day treatment period, mice were euthanised and skin biopsies were collected from the treated areas. The collected tissue samples were prepared for histological staining (Trichrome and H&E) to assess structural changes and fibrosis. Additionally, tissue samples were reserved for biochemical analysis to quantify collagen content as a marker of fibrosis severity. These complementary analyses will provide a detailed evaluation of the fibrotic response in each experimental group.

Results

The progression of fibrosis over 28 days, measured as skin thickening using a caliper, is presented in Figure 1. In bleomycin-treated mice, a significant increase in skin thickening was observed in the MerTK full knockout group compared to the wild-type control group.

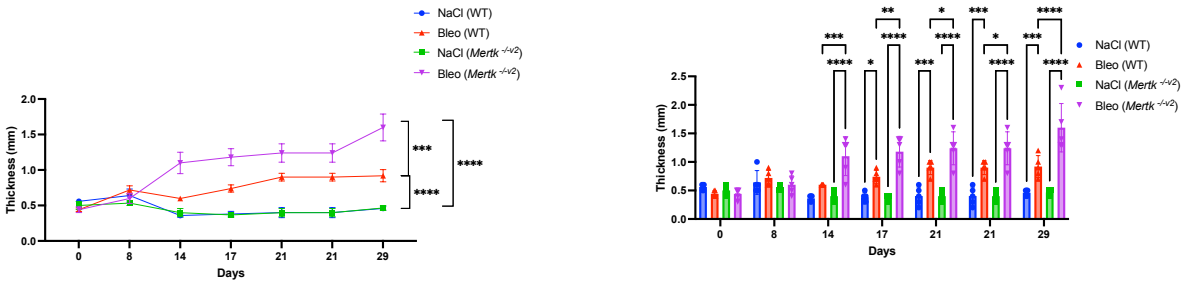


Figure 1 **Skin thickness (mm) was measured in Mertk-/- v2 and C57BL/6 (WT) mice over time after treatment with bleomycin (0.0264mg/injection site) or NaCl.** A) Main effect difference between columns 2way Anova with comparison of means. B) Comparison of means per time point 2way Anova. Significant differences were noted as * p < 0.05, ** p < 0.01, ***, p < 0.001, and **** p > 0.0001.

The right panel of Figure 1 compares skin thickening at specific time points. At day 14, the knockout group exhibited greater fibrosis compared to the wild-type bleomycin treated control, and this disparity is consistent until day 28. Saline-treated groups (both wild-type and knockout) showed minimal to no skin thickening, confirming the specificity of bleomycin-induced fibrosis. These results indicate that MerTK plays a protective role in regulating fibrosis progression, likely by modulating inflammatory and tissue repair processes.

The CSF-Cre conditional knockout model, which specifically targets MerTK expression in macrophages, showed a more gradual progression of fibrosis (Figure 2). Significant differences in skin thickening between the CRE-positive (MerTK knockout in macrophages) and CRE-negative (control) groups treated with bleomycin became apparent at day 17 and continued to increase through day 28. By the end of the experiment, CRE-positive mice exhibited significantly higher levels of fibrosis than their CRE-negative counterparts. The right panel of Graph 2 highlights these differences at specific time points. At day 21 and day 28, there was a pronounced increase in fibrosis in the CRE-positive group compared to the CRE-negative group under bleomycin treatment. Saline-treated controls (both CRE-positive and CRE-negative) displayed minimal skin thickening, indicating that fibrosis was primarily driven by bleomycin administration.

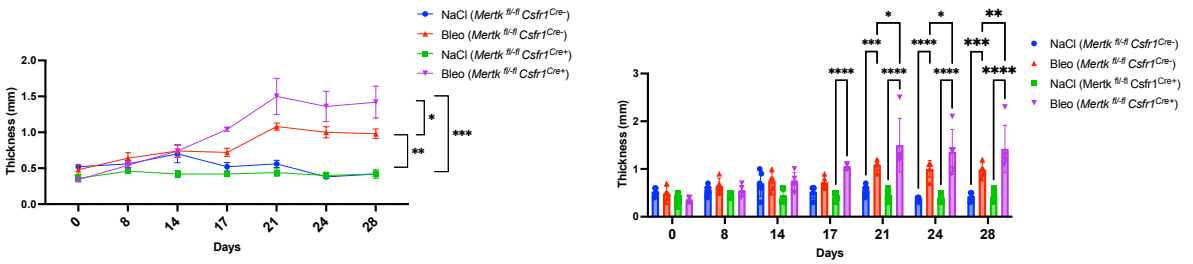


Figure 2 **Skin thickness (mm) measured in Mertk fl/-fl Csfr1Cre+ and Mertk fl/-fl Csfr1Cre- mice over time after treatment with bleomycin (0.0264mg/injection site) or NaCl.** A) Main effect difference between columns 2way Anova with comparison of means. B) Comparison of means per time point 2way Anova. Significant differences were noted as * $p < 0.05$, ** $p < 0.01$, ***, $p < 0.001$, and **** $p > 0.0001$.

Summary of findings

These measurements of skin thickening over time suggest that the absence of MerTK results in a faster establishment and more severe progression of fibrosis. In particular, the findings from the CSF-Cre positive model indicate that MerTK-expressing macrophages may play a protective role in regulating fibrotic responses. The significant increase in fibrosis observed in the macrophage-specific knockout model supports the hypothesis that MerTK expression within macrophages contributes to limiting inflammation and promoting tissue resolution. These results, while promising, will need to be confirmed through histological analysis, particularly by quantifying collagen deposition, which is a hallmark of fibrosis. Collagen measurements have already been collected and are pending analysis to provide a more comprehensive understanding of the fibrotic process in these models. Altogether, these experiments establish a foundation for understanding the role of MerTK in the induction and progression of skin fibrosis. Future studies will be required to delineate the exact mechanisms by which MerTK-expressing macrophages influence fibrosis and to identify the critical time points at which these cells exert their protective effects. Further exploration of signalling pathways and macrophage phenotypes in this context may uncover therapeutic opportunities for fibrotic diseases.

Reflections on the research outcomes

The experiment was well-suited for the four-month timeframe, generating valuable insights and raising new research questions about the role of MerTK in the context of fibrosis. This work has deepened our understanding of MerTK's function, and I am optimistic that we can build upon this data to design experiments with human samples in the future.

There were, naturally, some initial challenges associated with adapting to new techniques and workflows in an unfamiliar lab environment. However, I believe these hurdles are to be expected when starting a new project and transitioning into a different research setting. Despite these challenges, I am confident that the preliminary data we have generated is promising. While the results at this stage are not yet ready for publication, the pending analysis of the histological samples will provide crucial insights that could strengthen the findings and open the door to follow-up experiments and further collaborations.

In summary, I believe this visit has been a resounding success. It has not only generated interesting and impactful results but has also laid the groundwork for further collaboration with the team at Yale. I look forward to continuing this project and I am excited about the potential for meaningful discoveries and eventual publication.

Comments on overall cultural experience

I have greatly enjoyed the opportunity to work in a different lab, and I believe the transition from a translational research lab to an immunology-focused lab has been essential for my

development as a researcher. This experience allowed me to deepen my understanding of macrophages and their phenotypes, and I have learned several new techniques that will be invaluable for my future career. Working with animal models, particularly mice, has enhanced my ability to interpret and digest scientific papers that rely on these models, which has enriched my overall understanding of the field.

Beyond the technical skills, I feel that this experience has also shaped how I approach scientific problems. My experimental techniques have improved, and I have developed a new, more critical way of thinking about challenges in the lab. Networking has been another invaluable aspect of this fellowship. I feel I have built lasting connections with researchers, and I now have a broader network of people I can approach with questions or share results with to gain meaningful feedback. One of the most important lessons I have learned during this time is how to constructively take feedback and use it to refine my data analysis, knowledge, or approach to research questions.

On a personal level, moving abroad for four months was undoubtedly challenging, but it was a positive and enriching experience. Adapting to a new culture, finding accommodation, and learning to navigate a new city pushed me out of my comfort zone and helped me grow. Yale's location in a small, bike-friendly city was a great advantage, as it allowed me to focus on my research while enjoying a walkable, pleasant environment. The city itself is beautiful, with plenty of charming spots to relax, have a coffee, or simply take a stroll.

Living in the U.S. for the first time was exciting and offered new experiences that I truly cherished. Weekends provided the opportunity to explore New York City, where I immersed myself in the museums, walked its iconic streets, and enjoyed activities like comedy performances, which are a personal favourite. I also loved witnessing the change of seasons—from the vibrant colours of fall to the stark beauty of winter.

In summary, this fellowship has been a remarkable experience that I am incredibly thankful for. It has provided me with professional growth, invaluable connections, and personal challenges that have broadened my perspective. I would like to take this opportunity to sincerely thank the committee members, and everyone involved in making this fellowship possible. It has been a transformative experience that I will carry with me throughout my career and life.

Benedict Greenwood, Bogue Fellowship Report
Jan-Mar 2025
Stanford Psychophysiology Laboratory, Stanford University

General comments on the experience

I thoroughly enjoyed my placement in the Psychophysiology Laboratory at Stanford University. I found it incredibly stimulating from a scientific perspective as I developed the theoretical framework underpinning my PhD work and got a lot of hands-on support working through new approaches for analysing cross-sectional datasets. In my spare time I really enjoyed watching the Stanford sports teams competing in elite college sports competitions, spending time with my landlady's family, and exploring the jaw-dropping natural landscapes in California. I really loved experiencing such diverse aspects of life in the USA!

Details of work carried out

My PhD is investigating whether ADHD is associated with altered functioning of the autonomic nervous system, and how this impacts emotional reactions. There is a particular emphasis on determining which changes are related to ADHD, and which are driven by comorbid emotional changes. One potentially relevant comorbid emotional factor is alexithymia, a trait comprised of difficulties attending to and appraising emotions. In one of my previous PhD studies, I identified that the positive association between self-reported ADHD traits and self-reported difficulties in regulating emotions is mediated by alexithymia.

The purpose of my visit to Stanford University was to collaborate with Prof*essor* James Gross and Dr David Preece, specialists in emotion regulation and alexithymia, to explore this relationship further. Specifically, I aimed to investigate the following questions:

1. Does alexithymia mediate the relationship between increasing ADHD traits and altered emotion regulation patterns in everyday life?
2. Does alexithymia mediate the relationship between increasing ADHD traits and diminished autonomic emotional reactivity in a lab setting?
3. Does alexithymia mediate the relationship between increasing ADHD traits and more intense subjective emotional reactions in a lab setting?

Research question 1

I analysed data from two of my previous studies on emotional reactions in interpersonal contexts. This was existing data that had not yet been analysed. I first replicated my lab's previous finding, demonstrating that the positive association between self-reported ADHD traits and self-reported emotion regulation difficulties was mediated by alexithymia.

I then used structural equation models (SEMs) to determine whether this mediation relationship was specific to particular aspects of emotion regulation. I found that alexithymia mediated the positive association between ADHD traits and difficulties regulating behaviour; specifically, difficulties suppressing impulsive behaviour and difficulties concentrating/working when upset. However, alexithymia did not mediate the positive association between ADHD traits and non-behavioural emotion regulation difficulties; specifically, feelings of helplessness and negative

self-judgement when upset. These analyses took longer than expected, however they proved an extremely useful learning experience for me. I received hands-on guidance in assessing the reliability of self-report psychometric questionnaire subscales and dealing with reliability issues. I did not have any previous experience in validating assessment scales so this training improved my ability to critically evaluate psychometric questionnaire data. I also received training in implementing and interpreting more complex analysis approaches for cross-sectional self-report data, including Multivariate Mediation SEMs, Network Analyses, Bayesian Directed Acyclic Graphs, and Latent Profile Analysis. Although we opted not to include these more complex analyses in the final manuscript, I really value learning these skills because I will apply them to other cross-sectional data during my PhD.

Based on the limitations and results of the final set of SEMs, we planned another set of SEMs for an independent existing dataset to test whether the mediation relationships between ADHD traits, alexithymia, and emotion regulation difficulties were related to a) specific aspects of alexithymia (difficulty appraising emotions or lack of attention to emotions), or b) emotion valence (i.e. positive or negative emotion). I have pre-registered these analyses and will conduct them on my return to London.

Research questions 2+3

To explore research questions 2+3, I used data from one of my previous studies on emotional reactions in interpersonal contexts. Specifically, I focussed on data from a behavioural task in which pairs of friends viewed each other receiving painful electric shocks. With my supervisors at Stanford, I developed a set of pre-registered hypotheses for testing the relationship between ADHD traits and emotional reactivity while receiving painful electric shocks and while viewing a friend receive painful electric shocks. I developed separate hypotheses and analysis plans were for analysing autonomic emotional reactions (research question 2; focussing on changes in heart rate and skin conductance during the task) and subjective affective reactions (research question 3; focussing on self-reported valence, arousal, and intensity of subjective *effect* on each trial of the task).

Planning these analyses also took longer than expected but again I am pleased with the progress I made *at* Stanford. There were a lot of technical analysis problems to work through during the analysis planning, such as how to analyse the time course of autonomic reactions or the implications of individual differences in shock sensitivity. I enjoyed discussing these practical problems with my supervisors *at* Stanford and working out solutions together. There are no gold standards for analysing psychophysiology data and I had several debates with other PhD students in the Stanford lab about strengths and limitations of different pre-processing and analysis steps. Through these discussions I learnt about different factors to consider and optimised my analysis pipeline. The linear mixed models I need to use to analyse my data are quite complex, so I am grateful for the support I received in refining the models to make them more informative and to reduce the number of tests. I have pre-registered these planned analyses and am excited to conduct them on my return to London. I will present my results at academic conferences in summer 2025 and will publish them in peer reviewed journals. All my planned analyses will be *publishable,* and we plan for at least two publications resulting from this collaboration.

Theoretical understanding

One of the main reasons I wanted to do my Bogue Fellowship in the Psychophysiology lab at Stanford *was* to challenge the way I think as a scientist. From this perspective, I got exactly what I wanted out of the placement. The regular theoretical discussions I had with my supervisors and other members of the lab *at* Stanford about the possible relationships between ADHD, emotion regulation, emotional reactivity, and alexithymia were a real highlight. There are very few studies into the relationships between ADHD and alexithymia so in the past I have found it hard to describe possible mechanisms linking ADHD, emotion regulation, and alexithymia. However, we had wide-ranging discussions on possible genetic, cognitive, neural and behavioural links between them, which will be very useful for my PhD moving forward. By working with David Preece so closely, I developed a much deeper understanding of the different theoretical models of alexithymia and importantly the relative evidence supporting each model. Through this experience, I have changed the way that I interpret different alexithymia measures within my own datasets that are aligned to different theories, and I feel this has already made my research more precise. Furthermore, the lab in Stanford uses a different theoretical framework for researching emotion regulation to my lab at UCL. I now have a more nuanced understanding of this *framework,* and my scientific understanding of emotion regulation has certainly evolved.

Comments on overall cultural experience

I found the different lab environment very helpful. I enjoyed exchanging knowledge with other students and staff and enjoyed having to justify my approaches and scientific beliefs. Sometimes it reassured me that my approach/understanding was correct and other times it helped me learn. The different ways of working also helped me realise what types of support at UCL I find extremely helpful and which types I would like more of. I will return to UCL with a better awareness of the support I need to seek out during the last six months of my PhD to help me progress with my research. During the final year of my *PhD,* I have struggled with feeling overwhelmed and stressed. The experience of spending three months in a different environment with different routines and relationships has helped me change my mindset and view the last six months of my *PhD* in a different way. While this may not be a scientific change, I think it will be very important for my wellbeing going into the final stages of my PhD.

My impression of life in the US has been transformed by spending a prolonged period of time there. I went out of my way to learn as much as I could about the education system, culture, and lifestyle in the Bay Area and wider US. I really enjoyed getting to know more Americans and seeing lots of different parts of California. I visited San Francisco, San Jose, San Diego, Santa Cruz, Monterey and some of the State/National Parks in Northern California so I got a really good insight into life in different cities and the countryside in California. I had many conversations with postdocs about life as an academic in the US, and *I* feel that I now have a much better understanding of the opportunities and challenges at US institutions. My placement covered the first three months of Donald Trump's second *term,* so it was an absolutely crazy time to be in the US from a social and political perspective. It was fascinating to witness peoples' reactions to Trump's actions first-hand and see the impacts of his government on US institutions. I can now make a more informed choice about living and working in the US after my PhD.

Maria Cristina Aparicio De Soto, Bogue Fellowship Report
Jan–Feb 2025
American Museum of Natural History

General comments on the experience

My experience in the US, in the American Museum of Natural History, was a great opportunity to access resources from this institution that were key for my research project. Working in the vast collections of the AMNH will greatly improve my thesis chapter and allows me to include new data and perspectives based on this material. Visiting the US also allowed me to experience a different research environment and meet other people working in similar areas. It was a welcoming circle, where I was able to discuss my project and the research of others. This challenged me to look at my own work in new perspectives and to explore new possibilities with the data I have been gathering. I am most appreciative of these conversations; they have made me very enthusiastic to continue with my work when I came back to the UK. This research trip was a very valuable experience both from a personal and an academic perspective.

Details of work carried out during the fellowship

Adaptive radiations are key evolutionary processes and explain the origins of a major part of our biodiversity. Studying examples of adaptive radiations is key for understanding how biodiversity develops, as well as the internal and external processes that alter it. The evolution of Caviomorpha, a highly diverse infraorder of rodents endemic to the Neotropics, is an example of an adaptive radiation where functional and ecological diversity arise during a period of large-scale environmental change. This key feature of the evolution of Caviomorpha can help us understand how changes in the environment work as the ecological opportunity that drives diversification. Despite this, studies on the relationship between the diversification of the clade and environmental changes have been limited.

The main objective of my thesis' first chapter is to analyse the morphological diversity of caviomorph rodents and its possible relationships with environmental changes through time. For this purpose, cranial, mandibular and limb morphology will be used to compare with two environmental variables of interest: temperature and Andean elevation rates. The skull and mandible will be analysed through 3D geometric morphometrics and therefore will require the scanning of a selection of samples of this group using Computed Tomography (CT-scanning). The appendicular skeleton, on the other hand, will be analysed through linear morphometrics and functional ratios, which will be calculated using measurements collected with callipers.

The data collected through these methods will then be analysed, by creating Principal Component Analyses (PCAs), which allow us to see the main axes of variation in these data. Scans of skulls and mandibles will first have to be processed to create meshes. After this, a Deterministic Atlas Analysis will be used to encompass the overall shape of the skulls, and a PCA will be produced. On the other hand, postcranial measurements can be used directly for the creation of a PCA, given the linear nature of this data. They will also be used to calculate specific functional ratios that can be studied separately. Once the principal components for the data are obtained, these can be used in conjunction with a published evolutionary tree (in this

case, the tree of Álvarez et al., 2017) to estimate morphological diversification rates. Additionally, the rate of disparity through time can be estimated for the different morphologies. Lastly, the principal components can be used to fit different evolutionary models and look for potential patterns in the evolution of shape in Caviomorpha. The fit of multiple models will be tested, including a Brownian Motion model, Early Burst, as well as a traditional Ornstein-Uhlenbeck model and OU models where the long-term tendency of the data is dependent of the temperature or the elevation rates across time.

To accomplish the aims stated above, it is key that the data collected has a good and well dispersed sampling across the evolutionary tree, which is why this visit to the US was vital for my project. While London's Natural History Museum (NHM) has a vast collection of cranial material of caviomorph rodents, there are certain groups that would be underrepresented if the work only relied on this and other European institutions. More specifically, species from the family Echimyidae, one of the most species-rich families, would be noticeably underrepresented. Additionally, to make a well-sampled analysis of caviomorph limb morphology, it would be essential to collect data from other institutions, as the NHM specimens are rarely stored with their skeletal material.

My visits to the American Museum of Natural History (AMNH) and the Field Museum of Natural History (FMNH) were key for the inclusion of more samples from the family Echimyidae, and especially for the inclusion of skeletal samples. If it was not for my data collection in these institutions, the inclusion of appendicular morphology would have not been possible for this part of the project. I considered this aspect particularly important, as caviomorph rodents are especially diverse in their locomotory preference, and the shape of limbs is directly associated with these. It is also of interest to see how different ecologies affect different structures in this group, which makes the comparison between cranial and appendicular morphology valuable.

During my stay in the AMNH, I was able not only to analyse the samples I was expecting to, but I was able to find many other caviomorph rodents that were useful for my project. I was able to find multiple samples from other caviomorph families beyond Echimyidae (such as Ctenomyidae, Octodontidae and Erethizontidae) that were not available in the NHM and therefore would improve my species sampling. I was able to scan more skulls and mandibles than I was anticipating and measure a significantly larger number of skeletons. In total, I was able to scan 22 skulls and mandibles and measure 134 skeletons. I am really satisfied with these additions to my database, and I feel certain that this will greatly improve my work.

Specifically in the case of postcranial measurements, I was expecting to raise my species coverage from 15 to around 34 species with this trip. However, after my visit I can say that my species coverage was raised to 88 species. This improves the research substantially and will make it an exploration of the appendicular morphology of caviomorphs to a degree not seen in the literature before. The selection also has a very good spread across the evolutionary tree, which makes for well-balanced results.

Both the postcranial measurements collected as well as the skull and mandible scans will be part of future publications as part of my research project. While the scan data still has to be

processed and will be included later in my geometric morphometrics analyses, I have already been able to incorporate my postcranial measurements to my database and will be part of the preliminary results I will present during my PhD first year upgrade in March. The data I collected in the US will also be key to making my work better quality and therefore, more likely to be published. I am hopeful about the potential for publication using this data, especially in the case of the postcranial measurements. This will be one of the few projects that analyses these structures in in caviomorph rodents from the last decade, and most definitely one of the first ones to use it against evolutionary models to analyse the impact of the environment on their evolution.

I consider my trip to the US to have been highly successful. I was able to collect all the data that I was anticipating and substantially more. The postcranial measurements taken during this trip will be the base of my analysis of appendicular morphology, and the cranial and mandibular scans will greatly improve the quality of my work. This trip fulfilled its purpose as an opportunity for data collection, as well as a chance to meet colleagues working on similar areas in the US and gaining more experience working in different natural history collections.

Comments on overall cultural experience

Working in the US was a truly great experience for my formation as a researcher and I feel very grateful for it. I think this experience was great for learning about how different museums store their material and categorise their samples. Examining material collected in different times is also very informative of the taxonomic discussions that have been had across the years, which is very useful to keep in mind. Working in the laboratory of Professor Voss in the AMNH truly changed the way I conduct my work within collections for the better, as they have very systematic guidelines for sample management. This helped me to maintain an orderly work with better record keeping than I did before, and with the ability to acquire more useful information from the samples. I am looking forward to continuing my work in the NHM with these new methods of recordkeeping incorporated into my work.

Additionally, meeting other researchers who are working in the AMNH and FMNH was great for expanding my horizons on what can be done with the information I have been collecting. I have met people working in collections with a variety of purposes, some of them completely new to me. It also inspired me to record the information of my samples in more detail and from different perspectives, as I was able to see how all this information can be later useful to conduct research. In the FMNH especially, I felt incredibly welcome by the mammals team, and had great conversations of different possibles areas of research that have not been studied in caviomorph rodents. At the FMNH I was lucky to meet Lázaro Vinola, a post-doctoral fellow in the museum, who was studying not only some samples from this collection, but he was also comparing them with samples from the Florida Museum of Natural History, and with subfossil material directly from Cuba and the Dominican Republic. I was able to look at this material and discuss with him some of his findings, still in process of writing at the time. He was also kind enough to give me some feedback on my thesis project and my methodologies. This conversation motivated me not only to see my work from a different perspective, but also to learn more about the organisms I study, specifically, to learn more about identification through specific anatomical characters such as teeth and jaw anatomy, which is key for the inclusion of extinct species in morphological analyses.

Lastly, the solo travel experience was especially edifying for me, and I hope I get to have such an experience again in the future. Before this trip, I had never travelled alone. Living by myself in the US while working in the museum, taking the time to do some touristic activities and contemplating the city in solitude, was a great moment of self-reflection as well as a great source of self-confidence. Both New York and Chicago are incredibly rich in culture; I particularly enjoyed the art, architecture, and the regional pizza preparations of both cities.

Tom Metherell, Bogue Fellowship Report
April–May 2025
The Change Laboratory, Stanford University

General comments on the experience

I had an enjoyable six week visit to the San Francisco Bay Area to learn from the Change Lab at Stanford University. Under the guidance of Professor Nilam Ram, I learned about the analysis of the content of screenshots taken from participants' mobile phones to understand how they use their devices. The visit supports my PhD aim to use the latest developments in methodology to improve our understanding of how social media use is related to adolescent mental health.

My visit allowed me to gain hands-on experience of analysing data in this new paradigm, including harnessing the latest developments in machine learning. In the process, I was able to develop my programming skills and my understanding of the pros and cons of intensive longitudinal data collection. Furthermore, I have expanded my professional network and attended many seminars that broadened my horizons as a psychological researcher. On my return to UCL, I can use my newfound knowledge to guide how the Centre for Longitudinal Studies collects data about technology use, as well as integrating insights from my visit into my PhD research.

I made the most of the opportunity to see the sights and the nightlife of San Francisco, took a road trip to Yosemite National Park, and learnt about the history and collections of Stanford University. My fellowship gave me the opportunity to experience a way of life that I previously hadn't considered. I came back to London with new connections and a renewed drive to make a difference with my PhD research.

Details of work carried out

Background

Social media platforms serve as an important facilitator of social interaction for adolescents, and social interaction has a pervasive impact on mental health, particularly in adolescence when one is especially susceptible to social influence [1]. It follows that there exists a plethora of potential mental health impacts of social media. However, there is little convincing evidence that social media pose a pressing threat to the mental health of the adolescent public. At the population level, Orben & Przybylski (2019) demonstrated that a practically meaningful overall association between digital technology use and mental health symptoms in adolescents is unlikely [2], and a number of reviews of the literature have described the evidence around this relationship as 'weak' or 'inconsistent', with fewer opting for a more concrete negative interpretation [3].

The field has been hindered by difficulties in measuring social media use. In most studies, especially those with large samples which are not specifically focusing on social media (e.g. the CLS' Millennium Cohort Study), self-reported weekly duration or frequency of screen time or time spent on social media is the primary measure available. The concordance of these measures with objective measures of screen time or time spent on social media has been

shown to be moderate to poor [4], [5], which limits the inferential utility of the data. In addition, since these measures consider screen time or social media use in the aggregate, the results are often non-significant or small associations without practical implications for public health or clinical practice. Attempts to use more detailed measures of social media use have been hindered by a lack of collaboration from controllers of social media platforms, and a lack of action by regulators to force these companies to share data with accredited researchers. Since 2023, Meta and TikTok have established collaborations with researchers with varying degrees of restrictions applied [6], [7], while X (formerly known as Twitter) has withdrawn free access to its API for researchers [8]. To circumvent these obstacles, researchers are now turning to passive collection of data from study participants' smartphones, ecological momentary assessment (EMA) or other forms of intensive data collection [9], [10].

One such paradigm is used by the Human Screenome Project [11], [12], which measures social media use (and smartphone use in general) through periodic screen capturing. This has two key advantages over the self-reported screen time measure that is commonly used. Firstly, it allows for the derivation of substantially more accurate predictors of overall screen use. Secondly, it gives a huge wealth of detail about the activities that participants undertake using their devices, including within individual social media platforms. The latter quality distinguishes Screenomics even from other methods of passive data collection, such as EMA and app usage logs. Accordingly, I see this paradigm as an opportunity to gain a more thorough understanding of the online behaviours connected to adolescent mental health risk and resilience.

The *Human Screenome Project* protocol involves installing an app onto participants' phones that records screenshots every five seconds for the duration of the study. In addition, foreground app and event logs are collected continuously to provide context to the screenshot data. At baseline and every two weeks, participants are prompted to fill in a survey to ask about mental health symptoms, COVID-19-related questions, eating behaviours etc. Currently there are two datasets available for analysis. One is of a sample of adults, who contributed their data for a period of one year. The other comprises teenagers and parents for a period of six months. Given the focus of my PhD project on advancements in the investigation of the relationship between social media and adolescent mental health, my work with the Screenomics data will focus on this latter adolescent dataset.

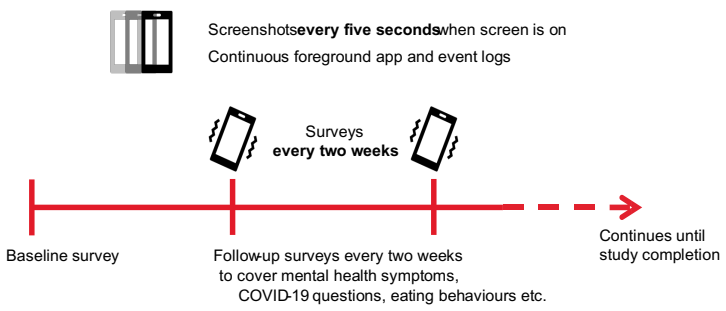


Figure 1. The *Human Screenome Project* data collection paradigm.

My work at Stanford

I applied for a Bogue Fellowship with the stated aim of developing a hands-on understanding of how to process the complex data collected in the *Human Screenome Project*. On my arrival,

I was rapidly inducted into the Change Lab, and I discussed with Professor Ram the array of machine learning assays that have been applied to the raw screenshots. We identified the object detection algorithm outputs as an area of opportunity given the lack of existing analysis undertaken by the lab using these data and the potential relevance of detections of people, the phone keyboard and certain objects to mental-health-related research questions.

The object detection assay comprises the outputs of the Ultralytics YOLOv5 computer vision model [13]. The model was trained on the Common Objects in Context dataset, which includes a set of more than 200,000 images annotated with instances of 80 common objects (where "objects" also includes people, certain animals and keyboards). Therefore, the outputted object detections are of these 80 object categories only. Alongside an identification of each detected object, the algorithm also gives a confidence estimate and a bounding box that describes the location of the object in the image.

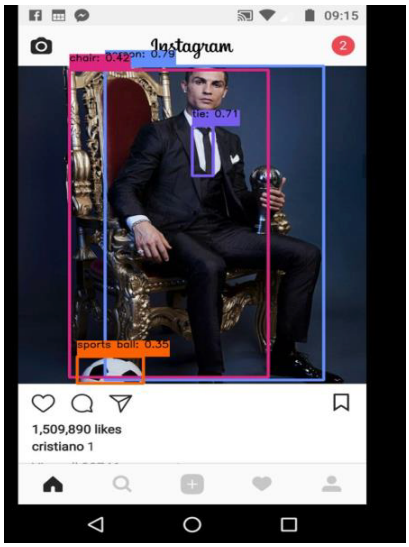


Figure 2: YOLOv5 object detect ion outputs in a screenshots from a specimen dataset, mapped back onto the screenshot itself.

Once I was onboarded, I proceeded to review specimen datasets produced by previous researchers in the lab. My initial impression on viewing and performing some basic descriptive analyses on the sample data was that the detection of people is more reliable than the detection of most other objects. However, Professor Ram and I agreed that additional validation work would be necessary to provide the necessary credence to the YOLOv5 outputs. Accordingly, I curated a set of images that could be presented to human raters recruited from the general population in order to compare their annotations with those generated automatically. I also established that it is possible to compute a number of summary metrics that describe participants' exposure to depictions of people on their devices. We began to discuss the possible implications of these metrics, noting for example that estimates of waking hours spent in the presence of other people are in the 50-70% range for working-age adults, but an initial estimate for one participant of the proportion of screen time in which a person was visible on the screen was below this range. We also discussed possible complicating factors, for example the possibility of an ethnic bias in YOLOv5's detections of people, which we agreed it would also be important to test. I also reviewed the detections of the phone keyboard, noting that the sensitivity of this varied widely depending on the exact phone model because some designs were not detected as a keyboard by the YOLOv5 algorithm.

During my visit, I attended various meetings alongside affective and cognitive psychology seminars. I also attended the Communication Department Colloquium. Overall, the visit exceeded my expectations in supporting my PhD progress. The connections that I have built and skills that I have gained will make it much easier to work with the *Human Screenome Project* data, and I have gained a new perspective on the investigation of social media use that will guide the overall direction of my thesis and potential future research career.

Subsequent work

Based on the analytical skills that I developed during my visit, along with the discussions about practical considerations and the relevant theory, I am now in the process of putting together a plan to conduct a full research study using the adolescent Screenomics dataset. Since my return, and in collaboration with my supervisors and Lived Experience Advisors, I have been studying the literature to compile a theoretical framework on which I can base my research and prioritise the most important research questions. Ultimately, I aim to publish this work, in addition to presenting it at conferences and including it as a major component of my PhD thesis.

In addition, I will be using the knowledge I have gained of mobile sensing and other data collection methods to help inform the Centre for Longitudinal Studies' strategy for measuring technology use by birth cohort participants.

References

[1] S.-J. Blakemore, "Avoiding Social Risk in Adolescence," Curr. Dir. Psychol. Sci., vol. 27, no. 2, pp. 116–122, Apr. 2018, doi: 10.1177/0963721417738144.

[2] A. Orben and A. K. Przybylski, "The association between adolescent well-being and digital technology use," Nat. Hum. Behav., vol. 3, no. 2, pp. 173–182, Feb. 2019, doi: 10.1038/s41562-0180506-1.

[3] P. M. Valkenburg, A. Meier, and I. Beyens, "Social media use and its impact on adolescent mental health: An umbrella review of the evidence," Curr. Opin. Psychol., vol. 44, pp. 58–68, Apr. 2022, doi: 10.1016/j.copsyc.2021.08.017.

[4] P. Coyne, J. Voth, and S. J. Woodruff, "A comparison of self-report and objective measurements of smartphone and social media usage," Telemat. Inform. Rep., vol. 10, p. 100061, Jun. 2023, doi: 10.1016/j.teler.2023.100061.

[5] T. Verbeij, J. L. Pouwels, I. Beyens, and P. M. Valkenburg, "The accuracy and validity of self reported social media use measures among adolescents," Comput. Hum. Behav. Rep., vol. 3, p. 100090, Jan. 2021, doi: 10.1016/j.chbr.2021.100090.

[6] Center for Open Science, "Meta Partners with the Center for Open Science to Share Data to Study Well-being Topics." Accessed: Aug. 05, 2024. [Online]. Available: https://www.cos.io/about/news/meta-partners-with-cos-to-share-data-to-study-well-being-topics.

[7] TikTok, "Expanding TikTok's Research API and Commercial Content Library," Newsroom | TikTok. Accessed: Aug. 05, 2024. [Online]. Available: https://newsroom.tiktok.com/en-gb/tiktoks-researchapi-and-commercial-content-library.

[8] J. Calma, "Scientists say they can't rely on Twitter anymore," The Verge. Accessed: Aug. 05, 2024. [Online]. Available: https://www.theverge.com/2023/5/31/23739084/twitter-elon-musk-api-policychilling-academic-research.

[9] M. J. Dreier et al., "Adolescents' daily social media use and mood during the COVID-19 lockdown period," Curr. Res. Ecol. Soc. Psychol., vol. 7, p. 100196, Jan. 2024, doi: 10.1016/j.cresp.2024.100196.

[10] I. Beyens, J. L. Pouwels, I. I. van Driel, L. Keijsers, and P. M. Valkenburg, "The effect of social media on well-being differs from adolescent to adolescent," Sci. Rep., vol. 10, no. 1, p. 10763, Jul. 2020, doi: 10.1038/s41598-020-67727-7.

[11] B. Reeves, T. Robinson, and N. Ram, "Time for the Human Screenome Project," Nature, vol. 577, no. 7790, pp. 314–317, Jan. 2020, doi: 10.1038/d41586-020-00032-5.

[12] N. Ram, N. Haber, T. N. Robinson, and B. Reeves, “Binding the Person-Specific Approach to Modern AI in the Human Screenome Project: Moving past Generalizability to Transferability,” Multivar. Behav. Res., pp. 1–9, doi: 10.1080/00273171.2023.2229305.

[13] Ultralytics, “*YOLOv5*: A state-of-the-art real-time object detection system,” 2021, URL: https://docs.ultralytics.com/, Accessed: 2 Jun. 2025.

Comments on overall cultural experience

The Change Lab spans the Communication and Psychology Departments at Stanford, which marks a departure from my environment at UCL, where the specialisation is in the methodology of longitudinal social science research. As such, visiting the lab was an opportunity to discuss psychological theory and research in greater depth than I typically do at UCL. I found the lab very welcoming, with comprehensive procedures in place to support its students. Visiting the lab in person made it much easier to integrate into the lab’s culture and identify whom to turn to with specific issues and therefore will facilitate my ongoing collaboration with the group.

Outside of the university, I took the opportunity most weekends to visit San Francisco and experience its sights and nightlife. I was also able to explore the Stanford campus and its museums and surrounding nature. Additionally, I rented a car and took a two-night excursion to Yosemite National Park. Overall, I had an enjoyable visit and feel satisfied that I have made the most of the time I had in California.

Francois Okoroafor, Bogue Fellowship Report
August 2025
Nemours Children's Hospital & Vanderbilt University Medical Centre

General comments
The Bogue Fellowship provided a wonderful opportunity to engage in cutting-edge quantitative research in the field of Epilepsy Surgery and neurostimulation. I was able to join two very welcoming research labs, where I was able to build significantly upon my base understanding of brain network dynamics, dynamic systems mathematical theory, and advanced machine learning.

From a work culture perspective, the labs were very different; the Rod Scott lab was a pre-clinical, hypothesis-driven laboratory. This was the environment where I spent more time intellectually curating my hypotheses surrounding epilepsy and brain network dynamics. Whereas the BIEN lab was, on balance, more data-driven, using heavy machine learning techniques in their analytical work. I learnt to build state-of-the-art machine learning models in the BIEN lab, along with robust methods for curating and preprocessing multimodal datasets, including EEG and brain imaging datasets.

This was a fantastic experience, both from a research and cultural perspective. In addition to my research experience, I visited some of my close friends who were working in Palo Alto in the tech industry – one of my friends builds driverless car software for a living, and he drove us around San Francisco, driverless, using his own AI model downloaded into his car! This and other extra-curricular experiences made my research fellowship in the US a very special and memorable experience.

Details of work carried out during the fellowship

Background
Epilepsy is a chronic neurological disorder characterised by an increased propensity for spontaneous seizure generation, affecting approximately 65 million people globally. Despite clinical and technical advancements, about 30% of patients are medication resistant. Epilepsy increases the risk of mortality, including sudden unexpected death (SUDEP), particularly in those with drug-resistant epilepsy (DRE), who have a 4- to 7-fold higher risk. People with epilepsy are at increased risk of mental health issues, such as depression and stress, which are also key risk factors for reduced quality of life, in addition to poor seizure control.

Given the limitations of conventional treatment and the significant morbidity burden associated with DRE, neuromodulation has emerged as a promising treatment strategy aim*ed* at controlling seizures in selected epilepsy patients. Neuromodulation refers to manipulating neural activity through the delivery of electromagnetic, thermal, optic, acoustic, or ultrasound-based stimulation. This includes technologies such as Vagal Nerve Stimulation (VNS), Deep Brain Stimulation (DBS), Responsive Neurostimulation (RNS), Transcranial Electrical Field Stimulation (TEFS), Transcranial Magnetic Stimulation (TMS) and Focussed Ultrasound (FUS), with some of

these therapies already licensed for treatment, while others remain under investigation. Unfortunately, long-term clinical outcomes remain unpredictable with neuromodulation despite attempts to standardise neuromodulation strategies for epilepsy diagnoses.

There are multiple hurdles to overcome for people with drug-resistant epilepsy (DRE) who are surgical candidates. Heterogeneity in healthcare provision infrastructures presents geographical and financial barriers. Lack of public awareness around changing attitudes toward epilepsy surgery as an early intervention rather than a last-chance intervention presents an information barrier. The stress of living with a chronic intractable disease, and anxieties surrounding surgery, especially the dread of surgery potentially being unsuccessful, present a significant psychological barrier. Indeed, long-term clinical outcomes remain unpredictable *for* resective surgery and invasive neurosurgical neuromodulation, despite significant advances in epilepsy surgery management.

The development of biomarkers that offer early predictive information on long-term seizure outcomes could greatly help address the infrastructural, information and psychological issues, through streamlining presurgical and early post-surgical care and decision-making.

Biomarkers

The modern view of epilepsy considers this group of diseases as a disorder of dynamic brain networks. Such a complex pathology is not easily tackled from a purely physiology-driven biomarker approach, firstly, because of the overwhelming number of biological processes in the pathophysiological pathways that lead to seizure, making it difficult to identify critically important biomarkers. Secondly, empirical evidence in the literature shows that it is a challenge to distil biomarkers that are predictive of relevant clinical outcomes from biomarkers that are simply surrogate measures of current seizure severity. A phenomenologically driven approach might be a more appropriate strategy for biomarker development in drug-resistant epilepsy.

Phenomenological models use mathematical principles to analyse brain imaging or brain electrographic activity, with the objective of analysing the brain as a complex mathematical system and describing the properties of the system, such as its stability, its behaviours, and its functions. These models operate without needing to understand the underlying biological processes of the system under investigation. In the context of epilepsy, this is particularly valuable because these models don't fall into the trap of being linked to a single disease mechanism pathway, but provide a macro-level analysis of the essential dynamics of the system from a mathematical perspective.

The phenomenological approach, regardless of the method used, involves the following essential steps: collecting biological data such as brain imaging or EEG/SEEG (electroencephalography and stereotactic-electroencephalography, respectively); performing mathematical abstraction of the data; and analysing the mathematical abstraction to answer the research question of interest. Today, the analysis step is significantly helped by state-of-the-art machine learning tools.

Literature Review

Rationale
Epilepsy is increasingly conceptualised as a disorder of brain network dynamics, where seizures and cognitive impairments may result from network dysregulation. Traditional thinking emphasises seizures as the primary cause of cognitive deficits, but emerging evidence suggests that deviations from near-critical brain dynamics may be a more fundamental mechanism. This review was motivated by the need to explore epilepsy through the lens of dynamic systems theory, integrating mathematical models with empirical data to better understand the relationship between seizures, cognition, and brain network stability.

Methods
To develop this perspective, I conducted an extensive literature review and visited Prof*essor* Rod Scott at Nemours Children's Hospital. During this visit, I studied landmark preclinical studies published by his group, observed classic animal behavioural experiments, and received training in interpreting preclinical data in the context of human research design. This experience enabled me to intellectually refine a hypothesis that epilepsy and its cognitive consequences stem from failures in regulatory mechanisms that stabilise brain networks near criticality. The review synthesizes theoretical frameworks—including criticality theory, bifurcation theory, and dynamic systems *modelling*—with findings from both preclinical and clinical studies.

Results
The literature and observational studies revealed that cognitive deficits in epilepsy can be rescued independently of seizure reduction through interventions that restore spatiotemporal patterns in brain networks—hallmarks of critical dynamics. Environmental enrichment and medial septal nucleus deep brain stimulation (MSN DBS) in animal models demonstrated recovery of behavioural performance, suggesting that these treatments may repair regulatory mechanisms governing quasi-criticality. Clinical studies further support the link between proximity to criticality and cognitive function, with metrics such as long-range temporal correlation and avalanche spreading distinguishing drug-resistant epilepsy from other states. These findings support the hypothesis that cognition may serve as a biomarker for stable brain dynamics.

Conclusion
There is empirical and theoretical evidence to suggest that epilepsy reflects a destabilised brain system unable to maintain near-critical dynamics, possibly due to failure of control parameters governing self-organising quasi-criticality. Treatments that restore these dynamics—rather than merely suppress seizures—could offer dual benefits for seizure control and cognitive recovery. Cognition, as an emergent property of critical brain dynamics, may serve as a biomarker for network stability. Future therapeutic strategies might be guided by surrogate measures of chaos and resilience, with neurostimulation tailored to restore regulatory mechanisms. This paradigm offers a promising direction for advancing epilepsy management and understanding broader neurological disorders.

The output of my visit to Professor Rod Scott's laboratory was a detailed understanding of brain

dynamics from the dynamic systems theory paradigm, which shaped subsequent research projects carried out at Vanderbilt University's BIEN lab. Immediately, I wrote an authoritative review called The Edge of Chaos in Epilepsy: A Hopf, skip and jump into the unknown, which we are preparing for submission to an IF20 high-impact neuroscience journal.

Pre-surgical biomarker

Rationale
Accurate presurgical biomarkers that predict 12-month seizure outcomes after responsive neurostimulation (RNS) or focal resection could improve patient selection and counselling for drug-resistant epilepsy. We evaluated whether neural-avalanche–derived transition matrices (Fig. 1), analysed with Random Forest, Decision Tree and a matrix-adapted LeNet-5, predict one-year outcomes and generalise across therapy types.

Methods
Retrospective resting-state SEEG (20 min, bipolar montage) from RNS (n=24) and resection (n=39) cohorts were pre-processed (0.5–119 Hz band-pass, 60 Hz notch), thresholded to detect neural avalanches, and converted into per-patient avalanche transition matrices. Models were trained and optimised via normalisation, seed-grid search and hyperparameter optimisation. Our performance metrics included accuracy, sensitivity, specificity and ROC AUC. Engel class stratification exploratory analyses were performed to determine their influence on model performance. External validation of the trained RNS models allowed comparison of the RNS-trained models applied to the resection dataset with the resection-trained models on the same dataset.

Results
For the RNS cohort the top model was LeNet-5 (seed-grid) achieving accuracy of 91.7%, sensitivity of 87.5%, specificity of 94.4% and ROC AUC 0.75; Random Forest reached 75% accuracy, sensitivity of 68.8%, specificity of 72.2% and ROC AUC 0.5.
Engel group stratification analysis demonstrated heterogeneous behaviour: e.g., "1a vs rest" showed RF accuracy of 55.0% with sensitivity ~22% and specificity ~82%; broader groupings such as "1+2 vs rest" and "1+2+3 vs 4" yielded high accuracy driven by sensitivity ≈1.0 and specificity ≈0.0 for several models, indicating class-imbalance or tendency to predict only the responder class. "1a+1b vs rest" grouping was used for downstream resection analysis.
In the resection cohort, the best single-model performances were modest: Random Forest (seed-grid) accuracy of 65.0% and LeNet-5 peaked at 60.0% with high sensitivity but low specificity; many resection ROC AUC metrics were not computable in the supplied output.
The external validation analysis confirmed that the top RNS-trained model demonstrated better accuracy, specificity and AUC ROC scores, when tested on resection data, compared to resection-trained models tested on resection data (Fig. 2).

Conclusion
Neural-avalanche transition matrices combined with machine learning models can achieve strong within-cohort predictive performance for RNS outcomes, but cross-modality generalisability is limited. Further work should prioritise larger, balanced multi-centre datasets,

explicit calibration to improve specificity, and prospective external validation before clinical translation.

This project is being prepared for submission as a manuscript to a peer-reviewed journal. It has been submitted as an abstract to the annual AES (American Epilepsy Society) conference, as a late-breaking abstract.

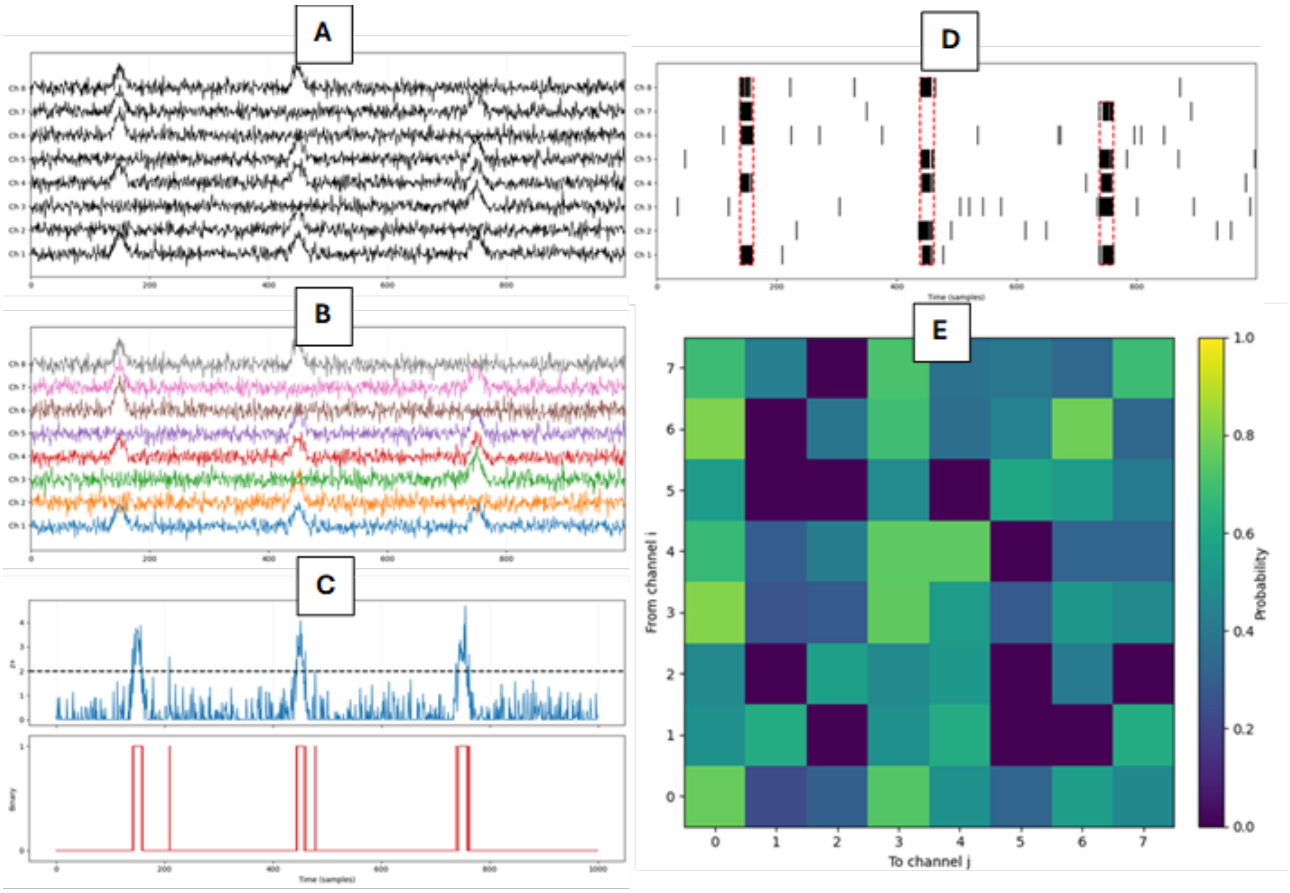


Figure 1: Neural avalanche transition matrix pipeline. A: Raw multichannel EEG trace. B: Z-scored version of each EEG (per-channel mean removed and scaled by per-channel standard deviation). C: Positive rectified z-scored signal for one channel. The thick dashed line marks the threshold at +2 standard deviations. Bottom panel shows the corresponding binarised activity (1 = activated when z+ ≥ 2, 0 = quiescent). D: Raster plot of binarised activity across all 8 channels over time. Each tick indicates an activation event within a time bin. Red dashed rectangles highlight three identified neural avalanches, bounding their temporal extents and participating channels. E: Avalanche Transition Matrix (ATM) heatmap for the 8 channels showing P(j | i): the probability that channel j activates at time t+1 given channel i was active at time t. The colourbar indicates probability values.

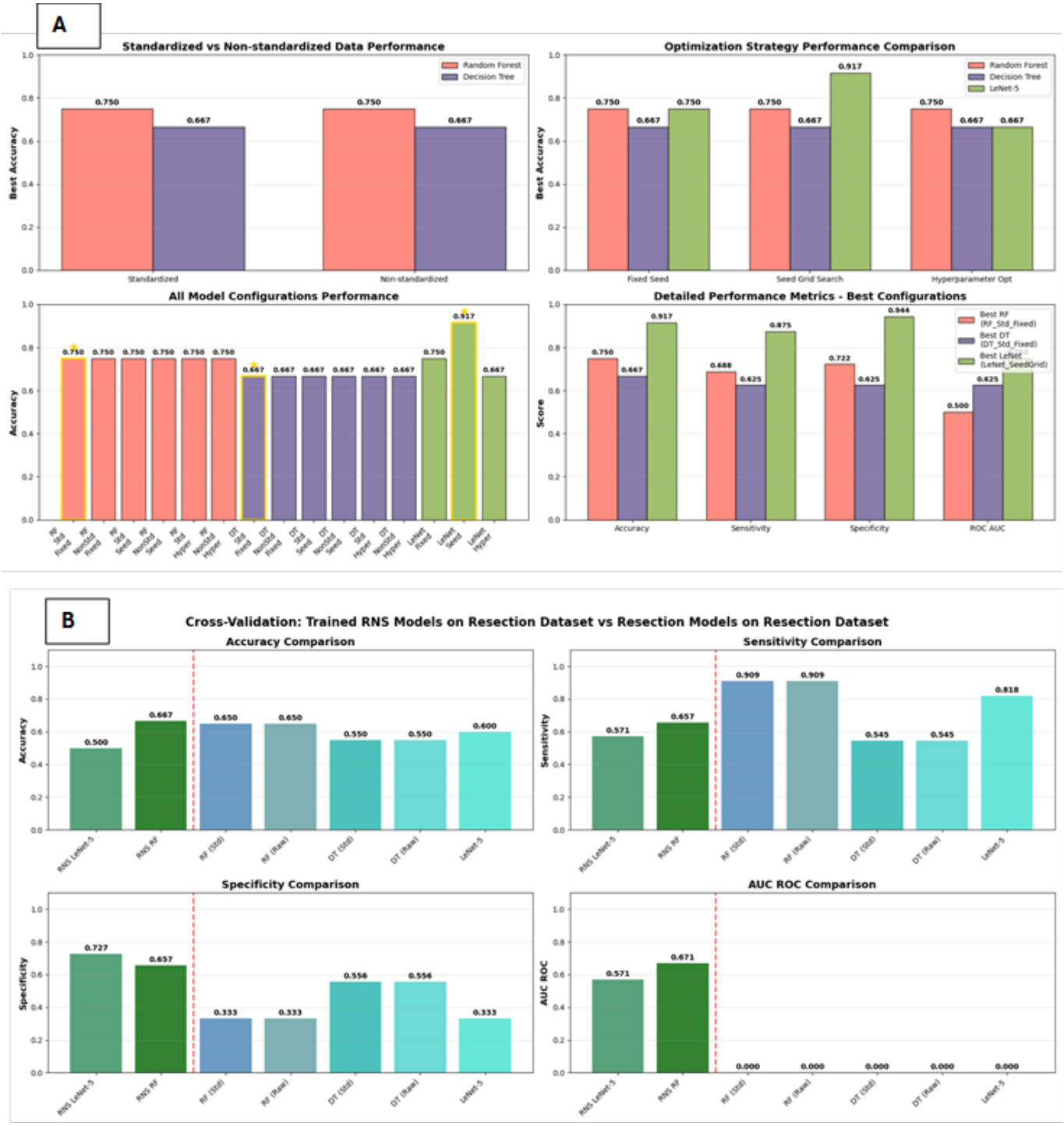


Figure 2: Results. A: RNS Machine Predictive Model Performances. B: External validation of RNS models versus resection models, comparing each model's performance when both tested specifically on resection datasets.

A further project, which aims to identify which signal frequencies are significant drivers of communication between seizure onset zones and the non-ictogenic zones, using transfer entropy, is underway but incomplete. The output of this study would be the identification of the hallmark signatures of epileptogenic brain regions, allowing focused and consistent identification of these regions for resective and ablative epilepsy surgery planning.

Learning
In addition to the aforementioned projects, which are either completed or ongoing, several important learning milestones were achieved during the Bogue Fellowship, which I will endeavour to share with my development neurosciences research group at the Institute of Child Health:

1. Building Advanced Machine Learning Models
    a. Building neural network models and large language models from scratch, such as BERT, and simple logistic regression neural networks;
    b. Modifying pre-implemented deep learning models for novel applications i.e. developing a deep learning model that receives multi-channel time series data as input;
    c. Building deep ensemble models which use the weights of multiple individual trained deep learning and traditional models in combination to create a meta-model with advanced pattern recognition capabilities;
    d. Using cloud computing services such as google collab to train models which are compute intensive outside of the capabilities of local CPU and RAM capacity;
2. Image and Signal Processing
    a. Contributing to SEEG pre-processing at the BIEN lab. The lab has a standardised pre-processing approach for EEG, SEEG, evoked potential and fMRI data.
    b. Studying their lab's approach, which uses automation algorithms and MATLAB, I designed an automated SPES/CCEPS pre-processing pipeline for their lab in Python because their existing SPES/CCEPS pre-processing pipeline was out of date and no longer functioning.
    c. I subsequently studied their pre-processing pipelines and designed automated pre-processing pipelines for the UCL GOSH ICH paediatric epilepsy datasets, which enable standardised pre-processing which is scientifically robust and will streamline data-driven research in my research group.

Comments on the overall cultural experience

I had a very useful experience working in the US this summer. *Professor* Scott's lab was a hypothesis-driven preclinical laboratory, where I observed and was able to finally understand the significance of behavioural studies in animal disease models, and I was able to intellectually curate a more comprehensive hypothesis of the brain's network dynamics through mathematical dynamic systems theory, through multiple theoretical paradigms. It allowed me to ask more powerful research questions and changed somewhat the direction of my data-driven work at Vanderbilt University's BIEN lab.

Dr Englot's BIEN lab was an AI-focused research placement. The placement began with attending a lecture by a physician and AI researcher, who introduced important paradigms concerning emergent behaviour in AI, state-of-the-art AI models, and current and potential future applications of AI in medicine. During my placement debrief, Dr Englot strongly recommended that I continue to pursue heavy machine learning methods in my epilepsy research.

I think the main differences between my UK research experience and my US research placements are:

1. Knowledge: In general, I was working with US researchers who had stronger training in mathematics and machine learning.
2. Translation: In the UK, researchers had a stronger grasp of clinical translation and posed research questions with a more clinically impactful focus.
3. Team culture: In Vanderbilt in particular, the group was much more hierarchical than research labs I've worked in in the UK. But the team also had relatively stronger interpersonal relationships and engaged in more informal, spontaneous outside work social activities and interactions.
4. All individuals within the lab were expected to submit abstracts to major epilepsy conferences and were also expected to be involved in securing personal and group-level research grants on a cyclical basis.

From a broader perspective, visiting San Francisco, Delaware, and Tennessee gave a broad glimpse into the regional differences across the US in terms of economics, politics and diversity. San Francisco was *the* most interesting, because it seemed the most culturally diverse region, and also the most economically successful.

Dr Englot's BIEN lab – Me, Bruno, Derek, Anas, Dr Englot, Ghassan, Addison, Emily, Kate

References

1. Kalilani L, Sun X, Pelgrims B, Noack-Rink M, Villanueva V. The epidemiology of drug-resistant epilepsy: a systematic review and meta-analysis. Epilepsia. 2018;59(12):2179-2193.

2. Rugg-Gunn F, Miserocchi A, McEvoy A. Epilepsy surgery. Pract Neurol. 2020;20(1):4-14.

3. Devinsky O, Spruill T, Thurman D, Friedman D. Recognizing and preventing epilepsy-related mortality: A call for action. Neurology. 2016;86(8):779-86.

4. Rheims S, Sperling MR, Ryvlin P. Drug-resistant epilepsy and mortality: why and when do neuromodulation and epilepsy surgery reduce overall mortality? Epilepsia. 2022;63(12):3020-36.

5. Ryvlin P, Rheims S, Hirsch LJ, Sokolov A, Jehi L. Neuromodulation in epilepsy: state-of-the-art approved therapies. Lancet Neurol. 2021;20(12):1038-47.

6. Jarosiewicz B, Morrell M. The RNS System: brain-responsive neurostimulation for the treatment of epilepsy. Expert Rev Med Devices. 2021;18(2):129-38.

7. Toth R, Zamora M, Ottaway J, Gillbe T, Martin S, Benjaber M, et al. DyNeuMo Mk-2: An Investigational Circadian-Locked Neuromodulator with Responsive Stimulation for Applied Chronobiology. Conf Proc IEEE Int Conf Syst Man Cybern. 2020;2020:3433-40.

8. Denison T, Morrell MJ. Neuromodulation in 2035: The Neurology Future Forecasting Series. Neurology. 2022;98(2):65-72.

9. Rugg-Gunn F, Miserocchi A, McEvoy A. Epilepsy surgery. Pract Neurol. 2020;20(1):4-14.

10. Nair DR, Laxer KD, Weber PB, et al. Nine-year prospective efficacy and safety of brain-responsive neurostimulation for focal epilepsy. *Neurology*. 2020;95(9):e1244-e1256. doi:10.1212/WNL.0000000000010154.

11. Ghatan S. Pediatric Neurostimulation and Practice Evolution. *Neurosurg Clin N Am*. 2024;35(1):1-15. doi:10.1016/j.nec.2023.09.006.

12. Shi J, Lu D, Wei P, Yang Y, Dong H, Jin L, et al. Comparative Efficacy of Neuromodulatory Strategies for Drug-Resistant Epilepsy: A Systematic Review and Meta-Analysis. World Neurosurg. 2024;193:373-96.

13. Sancetta BM, Matarrese MAG, Ricci L, et al. Altered neural avalanche spreading in people with drug-resistant epilepsy. Neuroimage. 2025;311:121188. doi:10.1016/j.neuroimage.2025.121188.

Lauren Bennett, Bogue Fellowship Report
Apr-Oct 2025
Cold Spring Harbor Laboratory

General comments on the experience

Undertaking the Bogue experience in 2025 at CSHL has given me the valuable opportunity to build my professional network in the US and learn and upskill my scientific capacity at a speed and depth I did not previously believe was possible. During my six months visit to the Zador and Banerjee labs at CSHL, I was able to make the transition from computational neuroscience at UCL to experimental spatial transcriptomics - a burgeoning branch of neuroscience pioneered by Tony Zador and his laboratory. Having access to the scale of resources and pool of expertise in CSHL has allowed me to jump start my transition into this new and exciting field, all the while being mentored by the very scientists who have invented the technology.

Details of work carried out

During my six-month visit to Tony Zador and Arka Banerjee's labs at CSHL, I have made significant progress towards the goal of being able to perform BARseq spatial transcriptomics on a model organism that demonstrates a unique and innate behaviour. In 2024, members of the Zador and Banerjee labs at Cold Spring Harbour, led by Emily Isko, performed MAPseq on a new model organism: Alston's Singing Mouse, with the aim to understand the heritable connection signature that confers the mouse's innate singing ability (Isko et al., 2025).

MAPseq is a high-throughput spatial transcriptomics pipeline that was developed at CSHL by alumni of the Zador lab (Kebschull et al., 2016), in which Sindbis virus particles are modified to deliver high-diversity RNA barcodes to individual neurons through injections in the brain. These barcodes are then efficiently transported down the axon terminals, after which the animal is sacrificed and the brain is thinly sliced. MAPseq then involves dissecting selected 'target regions' of the brain, which are then combined with probes, which are designed against the primer region of the transfected barcodes. After amplification, RNA sequencing reveals the relative abundance of these probes at the target site, which has been shown to correlate to projection strength from the source region to this target area.

Emily's recent work performing MAPseq on the singing mouse highlighted that the connection between two regions of the brain, the PAG and OMC, were significantly expanded in the model organism compared to the lab mouse. My work at CSHL involves preparing to perform the next level of experiment, BARseq, on the singing mouse in order to understand what neuronal types underpin this expanded connection that is connected to its novel innate behaviour. BARseq is an extension of MAPseq, in which in situ transcriptomics is additionally performed at the source (injection) location in order to identify the location and cellular types of the individual projecting neurons.

In BARseq, the injection site is cryofrozen and cut into thin slices, over which newly designed padlock probes are washed. These padlock probes bind to either end of the random RNA barcodes in situ and can then undergo gap filling by dNTP addition in order to bind fully over each barcode. As these padlock probes form a circle including the unknown barcode, the addition of a

specialised polymerase over multiple washes with cross-linkers, allows the barcode to be amplified in situ into what is referred to as a 'rolony'. These rolonies, located at the site of gene expression in each of the neurons in situ, then undergo a series of washes with fluorescent bases under a spinning disk confocal to reveal each rolony's hidden barcode. In addition, BARseq also includes a series of padlock probes designed against the mRNA transcripts of 100 cell-type marker genes, which can be used to deduce the cellular identity of each barcoded neuron in the injection site, and later coupled with what target regions that barcode projected to throughout the brain.

The first major hurdle for me performing BARseq on the singing mouse, is that there is no fully annotated and high-quality genome or transcriptome for the new model organism. In order to perform BARseq on the singing mouse, we require a detailed and complete transcriptome that will allow us to find the analogous transcripts for each of the 100 genes in the singing, versus lab mouse. Therefore, my first task upon arriving at CSHL was to undertake a de novo transcriptome assembly in order to understand how this panel of 100 genes (referred to as the 'M1 panel') was different between the two species in terms of both sequences and expression level.

In BARseq, 10-12 padlock probes are designed against each of these 100 genes of interest, and these probes have been optimised for the transcripts of lab mice. In 2024, Emily had performed one round of short-read Illumina bulk sequencing on the signing mouse, and from this I began to read and learn about bioinformatics enough to be able to assemble these short-read transcripts into longer 'contigs' using an algorithm referred to as 'Trinity'. I was then able to align these longer assembled contigs to the consensus lab mouse transcriptome in order to begin to find the panel of 100 genes and to quantify how they differed in terms of base substitution, indels and alternative splicing, between the two species of mouse.

Perhaps unsurprisingly, I was able to locate the aligned contigs for all 100 genes of the M1 panel, however the base substitution rate and incidence of indels between the singing and lab mouse was significant enough that we concluded that the original padlock probes that were designed to ligate to the lab mouse transcripts of the 100 genes would have to be redesigned for the signing mouse (Figure 1).

Alongside this line of investigation, Emily and I applied for an open call by Oxford Nanopore Technologies for researchers interested in using two of their long-read flow cells for free with a supervised team. Luckily, our application was successful and we were granted two flow cells on which we ran RNA that we extracted from the brains of four singing mice. Waiting for these long reads to come back, we expect that these results will give us greater confidence in the assembled transcriptome for the singing mouse and will give us greater clarity on regions of the transcriptome that are highly repetitive, including non-coding regions, that are therefore difficult to distinguish using short read sequencing.

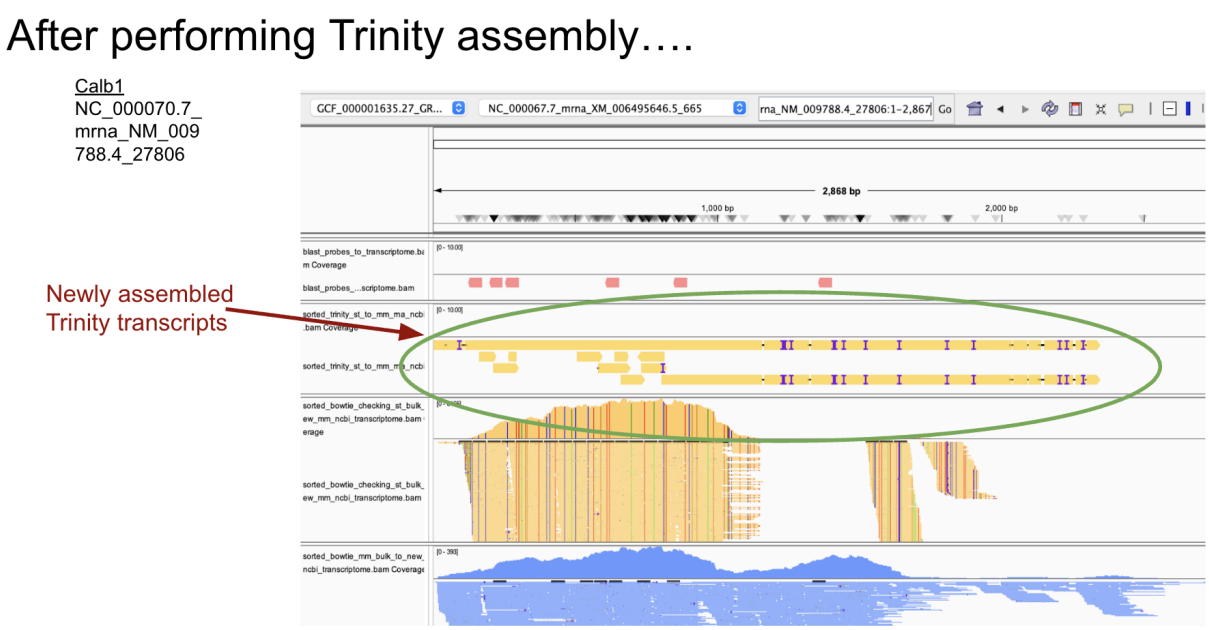


Figure 1. An example of one gene (Calb1) transcript in the lab mouse (top track of length 2868 bp) and 6 padlock probes that were designed against it in the original MAPseq panel. The following track (circled) shows the contigs that I assembled from the short bulk reads of the singing mouse to the lab mouse transcript. The singing mouse short bulk RNA reads also aligned to the lab mouse transcript are shown on the second to bottom track, with each vertical coloured stripe representing a base substitution event from the singing to the lab mouse transcript. The final track shows the bulk RNA reads for the lab mouse as also aligned to the consensus lab mouse transcript. The circled contigs that I constructed are able to align to a significantly greater proportion of the lab mouse transcript than the bulk reads below, which allows us to identify homologous regions of the transcripts to design probes against, that would otherwise be absent from our alignment (including the portion of the transcript covering the 6th and final probe that is missing from the singing mouse bulk alignment).

The next piece of the puzzle is to ensure that the 100 genes that are used to differentiate neuronal cell type in lab mice are also expressed in large and correct proportions to enable use in differentiating cell types in the singing mouse. To answer this question, we need information on single nuclei sequencing in the singing mouse. At the beginning of my stay at CSHL, Emily was generous in training me in the process of single nuclei sequencing, from the initial extraction of brain tissue to its slicing and sample preparation. From there, we collaborated with the core cell sorted facility at CSHL, who enabled us to design gates on our homogenised tissue samples in order to sort the nuclei from other ambient RNA and junk material. After collecting on the order of 100,000 nuclei from the cell sorter, we then transported the material to CSHL's core sequencing facility, who ran the library preparation in order to determine the quality and quantity of the genetic material within the nuclei before they are sent to Illumina sequencing.

Unfortunately, the first round of single nuclei sequencing returned a high degree of 'ambient RNA' that led to the loss of single nuclei behaviour and low-quality sequencing (Figure 2). Given that not many other labs were working on single nuclei extraction, Emily and I worked closely together over the following months to troubleshoot the protocol. This process was incredibly rewarding as we

had very much the feeling of pushing ourselves into unknown scientific territory in the pursuit of a clear and measurable aim - to increase the quality of our neuronal single nuclei RNA. Throughout this process and in discussions with many other researchers in the Zador lab, at others labs in CSHL and at Columbia University, we learnt much about the behaviour and stability of RNA and some of the tricks to stabilise nuclei when they are extracted from neurons.

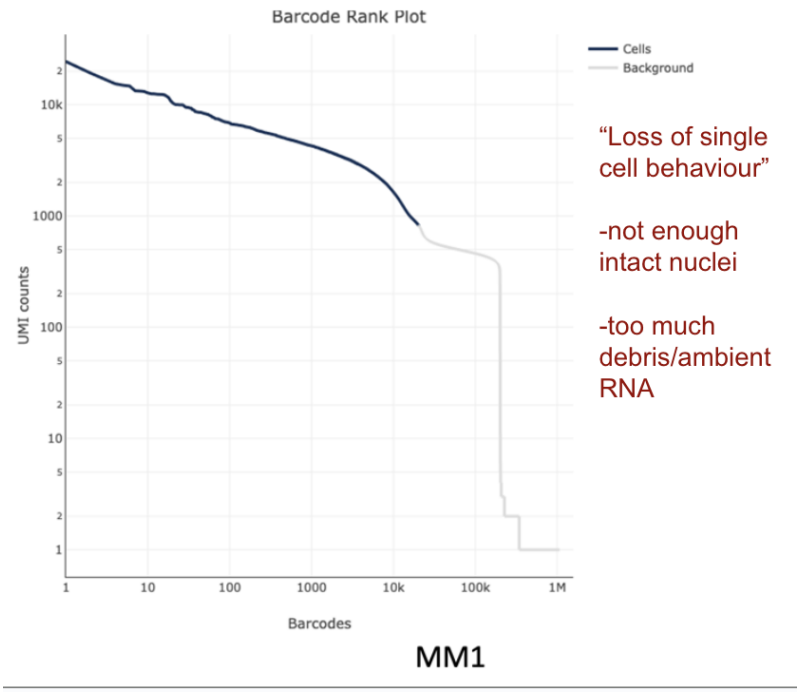


Figure 2. Loss of single cell behaviour in the first round of attempted single nuclei RNA extraction in the lab mouse.

Also, throughout this process, we were lucky enough to be trained by members of the MAPseq and BARseq core, including Professor Ching Zhan and Dr Diana Ravens, on how to analyse the quality of the RNA we were extracting at various stages of our single nuclei protocol. We began to troubleshoot our own experiment as we intermittently extracted RNA after different methods of tissue preparation and analysed its quality and quantity using Nanodrop and Bioanalyser analysis tools. In this way, we were able to discover the method of nuclei extraction that provides the best quality and quantity of RNA - a discovery that not only taught us so much along the way, but will also be invaluable when we next turn our efforts towards attempting to extract single nuclear RNA from the singing mouse. Most recently, I was accepted into CSHL's High Throughput Neuroanatomy training course and have just formally completed the intensive two-week training program on MAPseq and BARseq which qualifies me to perform both of these protocols.

I am so deeply grateful to have had the opportunity to work so closely with all of the passionate and talented people at CSHL, particularly Emily Isko, Ching Zhan, Diana Ravens and Arka Banerjee, who have donated so much of their time and passion to train me up from a completely

computational neuroscientist who had never used a pipette into a proficient and confident experimentalist. My project that I started at CSHL will be an ongoing collaboration when I return to UCL, as we continue to move closer towards a redesigned BARseq probe panel that will allow us to understand what neuronal cell types underpin the expanded projection in singing mice that supports their innate, and beautiful, singing behaviour.

Comments on overall cultural experience

2025 in the US represented a unique and challenging time within a broader cultural movement. Upon arriving at CSHL in April, conversations at the institute were almost entirely dominated by anxieties regarding the upcoming cuts to NIH funding at the termination of vital research projects. As April progressed into May, we watched colleagues and PIs of Iranian descent fear for their imminent deportation and witnessed the termination of CSHL's 'prep scholar' programme for students from diverse and disadvantaged backgrounds. From May to June, many PIs began to vocalise their contingency plans to move their laboratories too, if their funding was suddenly removed and, later that month, international students who arrived from Harvard as CSHL summer interns were gripped to their computers in anticipation of their visas being cancelled.

In July and August, we received notice from CSHL on how to respond to the presence of "ICE" agents, including the importance of denying knowledge of specific international researchers, students and academics at the institute. By September, CSHL announced dramatic cuts in its "Women in STEM" and "Diversity Initiative for the Advancement of STEM" and the mood at the institute became one of grave concern. Being in the US at such a challenging time has shown me how institutes, like CSHL, come together to protect their values, fight for every member of their community, and most importantly, act as an exemplar to other organisations about what it means to take a stance against misinformation and fear.

References

1. Kebschull, Justus M., et al. "High-throughput mapping of single-neuron projections by sequencing of barcoded RNA." *Neuron* 91.5 (2016): 975-987.

2. Isko, Emily C., et al. "Selective expansion of motor cortical projections in the evolution of vocal novelty." *bioRxiv* (2024).

Matthew Mitchell, Bogue Fellowship Report
January 2025
Smithsonian Museum of Natural History, American Museum of Natural History, and Yale Peabody Museum

General comments on the experience

The Bogue Fellowship provided me with an invaluable opportunity to work in the US during a very interesting time in its history. My trip enabled me to conduct successful data collection, taught me a lot about the preparation and conservation of the museum specimens that I use in my research, and also put me in contact with many interesting people with whom I could potentially work in the future. As well as advancing the academic aims of my PhD and additional projects, the fellowship has helped me grow personally and professionally by teaching me new skills, providing me with new experiences and enabling me to explore the cultural side of a fascinating country.

Details of work carried out during the fellowship

My work in the US on the Bogue Fellowship featured visits to three natural history museums: Yale Peabody Museum, the Smithsonian Natural History Museum and the American Museum of Natural History. Between them, these institutions contained 180 specimens that were useful for the project I went out to complete.

The goal of my research is to understand how captivity influences evolution. To achieve this, my PhD focusses on the effects of long-term captivity on phenotype, specifically in extinct in the wild (EW) birds, in the context of understanding the need for post-release support and longer-term recovery potential. In this additional, PhD-adjacent project, I aim to compare the changes that have occurred in an EW species to those that may have occurred in congeneric species that have persisted in the wild, without the additional pressures of population bottlenecks and captivity. This should provide insight into the role of captivity in the morphometric traits of modern individuals of EW species and enable me to determine whether phenotypic differences between modern day EW individuals, and their pre-extirpation counterparts, are also present in congeneric species that have not undergone these population level effects.

When managed ex-situ, species are exposed to different pressures than those experienced in their natural environment (Bryant and Reed, 1999; Williams and Hoffman, 2009). This includes reduced selection pressures and, where traits are beneficial to the captive environment, adaptation to captivity (Frankham, 2008; Schenekar & Weiss, 2017). These effects can manifest as morphological changes (Collar, 2020), with examples found in ecological traits such as wing shape and feeding morphology (Siciliano-Martina et al., 2021; Stojanovic et al., 2021). I study these effects in three EW species; the sihek (Guam kingfisher, Todiramphus cinnamominus), Socorro dove (Zenaida graysoni) and Vietnam pheasant (Lophura edwardsi), in which I use morphometric data to investigate phenotypic change potentially resulting from population bottlenecks and captivity. All three of my study species have existed exclusively in captivity for between 40 and 100 years and have captive population sizes of between 100 and 1000. Comparing modern and pre-extirpation specimens of these species helps me understand how

population bottlenecks and ex-situ management may affect phenotypic traits and how these changes may impact a species post-release.

While studying captive populations and their differences to historic populations can help us prepare for the release of captive populations back into the wild, additional context is useful to understand the exact extent to which captivity may influence phenotype. When studying this in EW species, no wild individuals are available for comparison, so similar species must be chosen. For this additional research question, I selected four species with which to carry out this comparison. To help distinguish between captivity-induced changes and natural evolution in the sihek, I selected the Palau kingfisher (Todiramphus pelewensis) and the Pohnpei kingfisher (Todiramphus reichenbachii), both species previously classified as conspecific with the sihek. For the Vietnam pheasant and Socorro dove, I have chosen the silver pheasant (Lophura nycthemera) and mourning dove (Zenaida macroura) respectively, both species that are known to have successfully hybridised with their EW counterparts (in the wild in some historic cases). By using the same measuring protocol to measure both modern day and historic specimens of these species, I will be able to compare the changes that have taken place in captivity to those that have taken place in the wild, as well as studying differences in variation between those groups.

The methodology I used to gather data during this trip included the standard measures used by the AVONET database (Tobias et al., 2022). These measurements were originally selected to be used for my wider project because they capture as much ecological data as possible without damaging the specimen or causing unnecessary stress to live animals. Gathering these data is particularly important when conducting a comparative study because they capture aspects of morphology that can be most variable and adaptable. Beak shape, for example, is highly adaptable and is therefore closely associated with food availability, a variable likely to be inconsistent between a captive and wild environment. A bird's wings, tail and legs are all essential in allowing locomotion through its environment and expressing natural behaviours and, thus, are suitable measures for determining effects of changed environmental pressures (Leisler & Winkler, 1985; Miles & Ricklefs, 1984; Pigot et al., 2020; Ricklefs & Travis, 1980). The hand-wing index (HWI) is a metric of flight efficiency in birds that can be used to estimate dispersal ability and is important to consider when studying birds that have been unable to carry out natural functions such as flying long distances for many generations spent in captivity (Claramunt, 2021).

Data collection on the trip was successful, with a total of 180 specimens measured across the three different institutions; this constituted the majority of relevant specimens that were present in their collections. The remaining specimens were housed at the Smithsonian, and the biggest difficulty in collecting the remaining data was an illness I contracted preceding my visit and the funeral of Jimmy Carter causing the museum to close on one of my three measuring days. The majority of the data will be used for a manuscript complementary to my PhD, analysing the difference between phenotypic changes that have taken place in captivity versus any that have taken place in the wild. The trip also enabled me to gather additional material relevant to the final chapter of my PhD, therefore contributing to two potential future publications.

I also made the decision not to measure certain specimens due to their unsuitability for my study. The silver pheasant is currently classified into 15 sub-species, spread out across central and south-east Asia. Any differences between more historical and recent specimens of individuals from this whole range are not comparable to changes that may have taken place in individuals from the much more restricted range of the Vietnam pheasant. Similarly, the range of the mourning dove spreads from South America all the way up to Canada, a significantly wider range than the single island of Socorro that the Socorro dove inhabited. As a result, I chose to focus only on individuals of these species that matched certain criteria and allowed a fairer comparison, mostly based on their geography. I chose subspecies of Lophura nycthemera that also reside in Annam, the same location where the Vietnam pheasant was found. These include L. nycthemera annamensis, L. nycthemera beli, L. nycthemera beauleaui and some specimens of L. nycthemera ripponi. For mourning doves, I selected Z. macroura clarionensis, a subspecies that lives on an island not far from Socorro, Z. macroura macroura and Z. macroura marginella, subspecies that occur only in Central and South America. A complexity that arose from this approach was that in many cases, individuals had no assigned subspecies. In these cases, I used their location of collection to guide whether or not they should be included. In cases where these data were also unavailable, I took measurements as usual but made a note that its metadata was unknown.

In addition to data collection, I was also able to take advantage of the other benefits of working in the collections I visited. At the Smithsonian, I was invited to attend a lecture by Professor Edward L Braun who, whilst visiting from the University of Florida, gave a talk on bird phylogenetics that I thoroughly enjoyed. Also at the Smithsonian, I was also able to spend an afternoon in a specimen preparation lab, learning about the whole process of how the study skins I use are created from deceased birds through the preparation of two pheasant specimens: one into a full skin and one into a partial skin and skeleton. Insight into these processes was extremely valuable to my personal and professional development as it gave me a clearer understanding of how much time and precision goes into creating the specimens that I use and specifically into the steps taken by museum specialists to enable scientific study such as ensuring easy access to oft-measured parts of specimens such as bills and tarsi.

Specimen acquisition was also a topic that I spent time discussing at all three of the institutions that I visited. At both the Smithsonian and the American Museum of Natural History, I learned much about collecting licences at both state and federal level and collecting laws, guidelines and processes from other countries in which they procure individuals. At the Peabody Museum in Yale, I learned about projects based at the museum that use birds that had died naturally to enhance their collections, including collecting birds that had suffered from window strikes or similar accidental deaths.

In conclusion, my trip to the USA using the Bogue Fellowship was academically successful in many different ways. I was able to take linear measurements from 180 museum skins, which contribute to the additional manuscript as well as my main PhD; I attended a lecture from a visiting professor; had informative and interesting conversations with museums specialists regarding the logistics of specimen collection; and was able to watch the preparation of two specimens from deceased individuals all the way through to fully prepared study skins.

Together, these experiences benefited me as a professional and an individual as they provided context to my work as well as allowing me to learn more about potential careers suitable to my skillset.

References

1- Claramunt S. 2021. Flight efficiency explains differences in natal dispersal distances in birds. Ecology 102: e03442.

2 - Collar NJ. 2020. Preparing captive-bred birds for reintroduction: the case of the Vietnam Pheasant Lophura edwardsi. Bird Conservation International 30: 559-574.

3 - Frankham R. 2008. Genetic adaptation to captivity in species conservation programs. Molecular Ecology 17: 325-333.

4 - Leisler B, Winkler H.1985. Ecomorphology. Current Ornithology, 2, 155–186. Miles D.B, Ricklefs RE. 1984. The correlation between ecology and morphology in deciduous forest passerine birds. Ecology 65: 1629–1640.

5 - Pigot AL, Sheard C, Miller ET, Bregman T, Freeman B, Roll U, Seddon N, Trisos H, Weeks BC, Tobias JA. 2020. Macroevolutionary convergence connects morphological form to ecological function in birds. Nature Ecology & Evolution 4: 230–239.

6 - Ricklefs RE, & Travis J. 1980. A morphological approach to the study of avian community organization. The Auk, 97, 321–338.

7 - Schenekar T and Weiss S. 2017. Selection and genetic drift in captive versus wild populations: an assessment of neutral and adaptive (MHC-linked) genetic variation in wild and hatchery brown trout (Salmo trutta) populations. Conservation Genetics 18: 1011-1022.

8 - Siciliano-Martina L, Light JE, Riley DG, Lawing AM. 2021. One of these wolves is not like the other: morphological effects and conservation implications of captivity in Mexican wolves. Animal Conservation 25: 77-90.

9 - Stojanovic D, Neeman T, Hogg CJ, Everaardt A, Wicker L, Young CM, Alves F, Magrath MJL, Heinsohn R. 2021. Differences in wing shape of captive, critically endangered, migratory Orange-bellied Parrot Neophema chrysogaster relative to wild conspecifics. Emu – Austral Ornithology 121: 178-186.

10 - Tobias JA, Sheard C, Pigot AL, Devenish AJM, Yang J, et al. 2022. AVONET: morphological, ecological and geographical data for all birds. Ecology Letters 25: 581-597.

Comments on overall cultural experience

Working in a different lab with staff in different roles was extremely valuable and eye-opening. I was able to fully integrate during my visit and was invited to a guest lecture on bird phylogenetics and to eat lunch with the curatorial staff working in the bird collections (during which they shared with me homemade treats known as ‘buckeyes’). It was fascinating to hear about the day-to-day lives of the staff, their views on the museum and its current direction and to hear about their backgrounds and career trajectories. During my observation of the pheasant skin preparation, I was able to have an in-depth discussion with one of the specialists about life in America and her opinions on the cultural and political direction the country was taking. To make the most of my time in Washington DC, I spent the Saturday afternoon chatting to a British academic who had been awarded a three-year post-doctoral grant at the Smithsonian and had been living in the US with her husband for that time. As well as learning about her role within the department and the differences she had experienced between academia in the UK and US, it was interesting to hear her insights into the cultural differences that she hadn’t expected. Staff I spoke to had also immigrated from both Europe and South America, and hearing their reasons for first moving to the US were also very valuable to me as a visitor from another country and one that will soon be job-searching.

Spending time in the US during January of 2025 was particularly interesting due to the

current political climate. The nature of my work provided me the opportunity to spend significant time discussing current affairs with a variety of people, from those I shared a train carriage with to taxi drivers and those I worked with at the museums I visited. I found the American people very friendly and forthcoming; simply asking a member of staff at an airport where I could find a quiet place to work during a connection led to an engaging conversation about her upbringing in New York and her reasons for moving a little way out of the city. Taxi rides from airports gave me the opportunity to learn about cities and get advice about what less well-known attractions I should add to my itinerary. During my time in DC, the funeral took place for Jimmy Carter, which brought with it a wide range of views regarding the need for a national holiday and the cost of celebrations. My time in DC also directly proceeded the presidential inauguration, which gave me the unusual opportunity to witness military parade preparations on the Mall and observe the tightening of security and increased tension in the city. On my final day in DC whilst taking a picture of a bird near the Capitol car park I was accused of photographing someone's number plate. I tried to use my free time as productively as possible whilst in the US, making visits to the White House (sadly surrounded in fencing due to the impending inauguration), the many memorials and monuments on the Mall and eating in a range of restaurants when I could. I ate New Haven-style pizza in New Haven, New York-style pizza in New York, and also experienced New York cheesecake at American diner Junior's before watching a Broadway show. To celebrate the completion of measuring in DC I treated myself to a sandwich at the Old Ebbitt Grill, Washington's oldest restaurant. In New York, I spent a day exploring and bird watching in Central Park, making a friend who was there to do the same.

Travelling between cities by train was vastly different in the US to in the UK. Trains are often delayed even more than in the UK and the Amtrak Acela 'fast train' is still slower than the average cross-country train in the UK. However, the travelling experience is considerably better, with every train I used having a dining/café carriage and seats considerably roomier even in economy class, which allowed me to get on with work. Travelling to and from New York City by train provided fantastic views of the New York skyline, which I was lucky to see several times (and at different times of day) due to my visit to Yale Peabody Museum at the beginning of the trip.

Jackie Casey, Bogue Fellowship Report
Jun-Aug 2025
Cellular Engineering, The Jackson Laboratory

General comments on the experience

I am extremely grateful to the Bogue Fellowship for supporting my visit to The Jackson Laboratory (JAX) in Connecticut to generate new induced pluripotent stem cell (iPSC) models of Frontotemporal Dementia (FTD). This incredible opportunity enabled me to establish a key collaboration with the Skarnes lab, internationally recognised leaders in the development of iPSC models for neurodegenerative diseases.

I developed valuable skills in CRISPR/Cas9 editing and clone validation in a collaborative and fast-paced environment. By training directly in a lab with world-leading expertise in CRISPR/Cas9-mediated genome editing in iPSCs, I am now well equipped to use these tools in my home institution. Now back at UCL, I am implementing a similar workflow to generate additional iPSC lines, leveraging the tools, protocols, and insights I gained at JAX. This will directly enhance the efficiency and reproducibility of our disease models.

Details of work carried out during the fellowship

Human induced pluripotent stem cells (iPSCs) are an excellent resource for studying neurodegenerative diseases. However, a major limitation in iPSC-based disease modelling is the heterogeneity of genetic backgrounds between patient and control lines. The development of isogenic iPSC models, in which specific disease-causing mutations are introduced or corrected on an identical genetic background, is critical for overcoming this limitation and identifying mutation-specific effects with greater accuracy. To address this, the iPSC Neurodegenerative Disease Initiative (iNDI), a large-scale genetic engineering project led by Professor Bill Skarnes at JAX, has pioneered the creation of isogenic iPSC lines carrying common neurodegenerative disease mutations, on the well-characterised Kolf2.1J control background. This initiative has transformed the field by enabling researchers worldwide to work with consistent, standardised models. An additional issue we face when studying tau is that some isoforms (such as 4R tau) are only present in miniscule amounts. This hinders the study of mutations that affect these isoforms, resulting in FTD in patients. The primary aim of my visit was to generate new isogenic iPSC models of FTD on the Kolf2.1J background that expressed different levels of 4R tau. This work forms a crucial part of my research, which focuses on FTD caused by mutations in the MAPT gene, encoding the tau protein. During my time at JAX, I produced ten new lines, with two additional lines in progress. I generated an additional model that had not been part of the original plan, gaining experience with deletion and knock-in model generation as well as plasmid design. I also contributed work to another project in the lab, which is being prepared for publication.

This visit has been extremely successful. I gained hands-on experience with CRISPR/Cas9 gene-editing techniques using a streamlined and highly efficient workflow, significantly expanding my technical expertise in genetic engineering. These skills have already proven invaluable to the progress of my project and to my broader development as a scientist.

Comments on overall cultural experience

Spending time in a US-based lab was an enriching experience, both professionally and personally. Working in the Skarnes lab allowed me to engage with a different research culture and observe first-hand how large-scale collaborative projects like iNDI are executed.

During my time in Connecticut, I experienced beautiful hikes, fun new activities with the lab and a trip to a nature reserve. At the end of the trip, I spent a few days in New York visiting museums and enjoying incredible food. This exchange has been the highlight of my professional career; thank you so much for making it possible.

Anna-Leigh Brown, Bogue Fellowship Report
May 2025
Icahn School of Medicine at Mount Sinai

General comments on the experience
The Bogue fellowship gave me the opportunity to network with important labs across the US and strengthen and create new collaborative opportunities.

Details of work carried out during the fellowship
In the neurodegenerative diseases amyotrophic lateral sclerosis (ALS) and frontotemporal dementia (FTD), the protein TDP-43 plays a central role. Under normal conditions, TDP-43 resides in the cell nucleus, but in ALS and FTD, it mislocalizes and forms toxic clumps outside the nucleus, disrupting RNA processing. This leads to the emergence of abnormal RNA sequences known as “cryptic exons,” which only appear when TDP-43 function is compromised. TDP-43 is also associated with more severe symptoms in Alzheimer’s disease, yet its involvement in other dementias remains poorly understood.

In 2024, I won a postdoctoral fellowship to investigate key questions: How common is TDP-43 dysfunction across different forms of dementia? Is it widespread or limited to specific conditions? Are certain individuals genetically predisposed to this pathology?

At the Icahn School of Medicine, my host lab has compiled an extensive dataset containing over 11,000 post-mortem RNA sequences and genetic profiles from 4,900 individuals, both with and without neurodegenerative diseases. My research focused on using this resource to quantify cryptic exons as indicators of TDP-43 malfunction and combine splicing data with large-scale genetic analysis. I was able to mine this dataset for TDP-43 splicing and now have been able to set up a remote access plan for this dataset, that I can still access and am actively still undergoing analyses on.

In addition to setting up remote data access, I was also an invited speaker at three different institutions, the Icahn School of Medicine, New York University, and the New York Genome Center. I gave seminars at each of these institutions and had the opportunity to start new collaborations and receive crucial feedback on my work. I was also able to attend departmental talks and specialised seminars across the Icahn School of Medicine, from which I gained insights into novel methods, one of which directly inspired a recently successful grant application I submitted since returning. From my in-person visit to Mount Sinai, I also joined an active Slack network of geneticists and now participate in monthly Zoom lab meetings, ensuring sustained collaboration.

In all, the time spent was perfect to set up the necessary groundwork and connections to complete my project, which will be crucial to the success of my current post-doctoral fellowship.

Comments on overall cultural experience

New York City is an amazing place to live and travel. I was able to leave the city to go on hikes in the Hudson River Valley, which is an area of beauty that I never expected to find so very close to the city. I enjoyed being in America, and the lab environment at the Icahn School of Medicine was a remarkably collaborative place where I was able to interact with scientists across the clinical and basic biology spectrum. In particular, I was struck by the way the Raj lab organises both dry lab and wet lab meetings. As a bioinformatician working in a wet lab, I found that putting together all the dry lab students and post-docs helped people discuss common problems in a way that might be glanced over when doing a whole lab meeting.