Peterhouse Biology Newsletter 2025

Peterhouse Biology Newsletter

No. 8

September 2025

This newsletter gives brief summaries of some of the activities undertaken by Peterhouse's biologists (undergraduates, graduates and Fellows) over the past academic year.

Biodiversity surveys

Termly surveys of the college gardens have continued and monthly sampling for BIOSCAN's monitoring of insect abundance. Additional intensive sampling took place in August as part of a survey of the biodiversity of 22 of the Cambridge colleges, a project which came out of the existing surveying in Peterhouse. This added a further 31 species, with quite a lot of material still to be fully identified. We have now recorded 927 animal species in the gardens.

Restoration of the ditch between Scholars' Garden and Coe Fen made a good start in 2024 but this year the ditch was smothered by duck weed. A probable solution has been identified but is not yet in place. Despite the ditch the badgers reappeared and have been enthusiastically expanding their sett in the trees and making new dens in the borders. We also had a number of sighting of grass snakes again this year.

The full list can be found at http://islandbiodiversity.com/petwildlife.htm

Kelvin Club

The Kelvin Club is the scientific society of Peterhouse which hosts a diverse selection of speakers from Biology, Chemistry, Geology, Engineering to Physics.

11-03-2025 – Metal-containing aerosols in the atmosphere: how aqueous chemistry drives health impacts. *Prof. Chiara Giorio*
18-02-2025 – Uncommunicative worlds in our Solar System. *Dr. Saml Cabot*
28-01-2025 – Photovoltaics as Heat Engines. *Dr Louise Hirst*
3-12-2024 – How the need to move has dominated the history of life on Earth. *Dr. Matt Wilkinson*
12-11-2024 – Climate reach of ocean waves from Kelvin to Richardson. *Dr. Ali Mashayek*
21-10-2024 – New materials for the green-energy transition. *Prof. David Fairen-Jimenez*

Peterhouse Biology Symposium

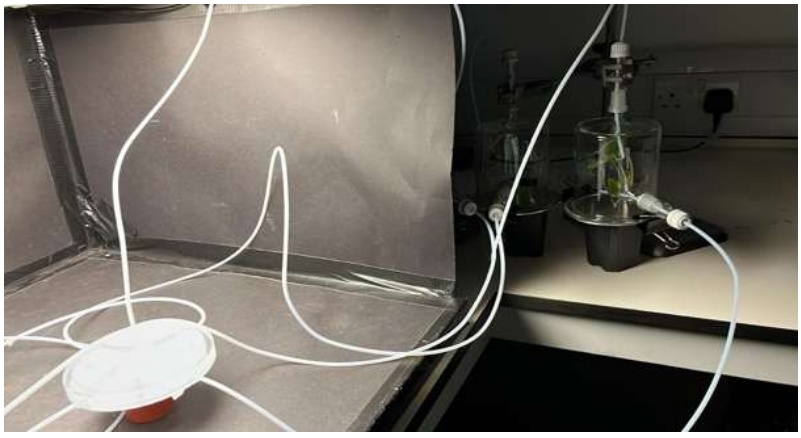
The 5th annual symposium was held on 15th February, abstracts of presentations can be found at https://islandbiodiversity.com/petsymp2025.pdf

Undergraduates

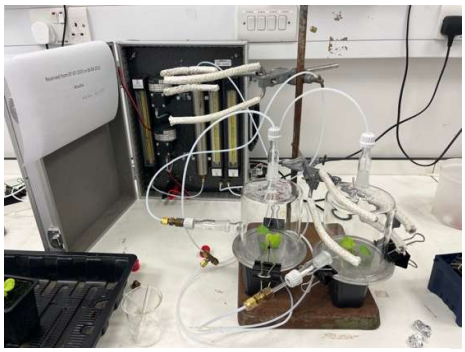
Patrick Collins

During the summer vacation, I spent two months working in the chemical ecology group at Rothamsted Research in Harpenden investigating the role of aphid olfaction in their selection of host plants. Using recognised olfactometry techniques, I tested the behavioural response of two species of aphid (one generalist species, *Myzus persicae,* and one specialist species, *Brevicoryne brassicae*) to plants (Oil seed rape (OSR), lettuce and broad bean) grown either in soil which had been washed of its nutrients or unwashed soil. It was found that where a plant elicited a behavioural response in the aphid, it was the plant grown in the unwashed soil that caused the significant response rather than the plants grown in the washed soil.

To further explore this, I set up 24-hour volatile extractions for OSR plants grown in both the washed and the unwashed soil and ran the concentrated samples on both a gas chromatographer (GC) and a gas chromatographer – mass spectrometer (GC-MS) to identify unique compounds or quantitative differences in compounds which could influence aphid response. The next step for this investigation is to utilise cutting-edge GC-coupled electroantennography (GC-EAG) to determine whether volatile extraction samples from each plant elicit a response in the aphid antennae.



Left Image: Equipment used to pump and control the volume of air passing through each plant jar and into the olfactometer. Right Image: General olfactometry set-up with all tubes attached to the olfactometer in their respective positions.



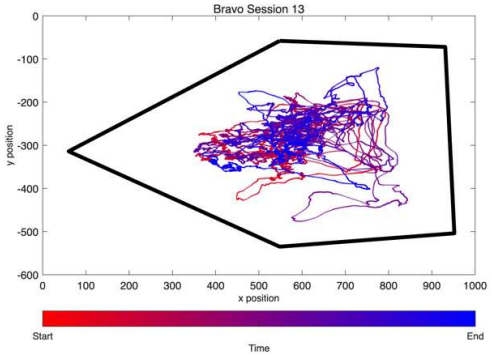
Volatile extraction equipment and set-up.

Function Fang

This summer I have been lucky enough to work at the comparative cognition lab at Cambridge. The focus of this lab is to investigate and compare cognitive abilities between different animals (including humans) through behavioural experiments. The two main clades in non-human animals are corvids and cephalopods – corvids are known as the smartest birds among all, while cephalopods, with their independent evolutionary route, can provide us insights into the organization of the nervous system.

The research project I was involved in was to adapt the GoFish system to the cuttlefish cognition experiments, so as to automate the process. Automation is important in comparative cognition studies, because it enables standardized methods to reduce temporal variability and observer effects, and thus increase replicabilities and reliabilities. Automated experimental designs have been widely used in primates and avian studies, while GoFish was the first platform designed for aquatic animals (originally used in goldfish experiments). The design is to have an over-tank camera to capture the scene and feed into Bonsai platform, where cuttlefish position would be acquired. An electronic feeder is also controlled by Bonsai, which would reward the cuttlefish when it completes the task.

In the last two weeks we also visited the Marine Biology Association in Plymouth, where the cuttlefish experiments were done. Based on what I learned from the analysis of the previous data, we improved the experimental settings to prepare for the coming experiments. I also learned the husbandry of cuttlefish (they are still very small, and very cute!!)

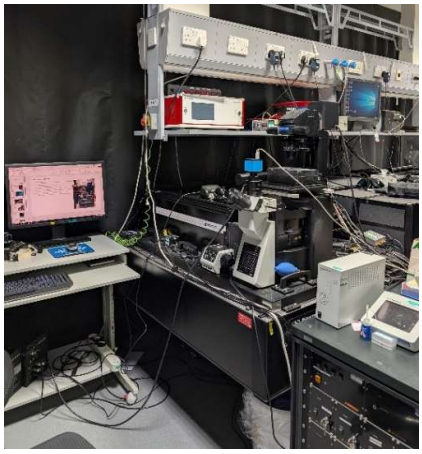


Louisa Fricker

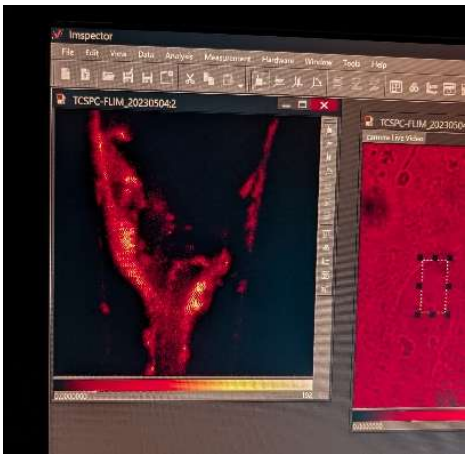
This summer I had the opportunity to take on a summer studentship with the Cambridge Neuroscience group at the Department of Chemical Engineering and Biotechnology. The specific group I joined are interested in primarily Alzheimer's disease (but other neurodegenerative diseases also) and researching the mechanisms, impacts and treatments related to protein aggregation. In most common neurodegenerative diseases, it is the aggregation of proteins within the neurones due to inconsistent protein repair and removal pathways that causes cell death and subsequent short circuiting in the brain, leading to the common symptoms known.

My research focused on Tau; a protein found in the brain that is a commonly seen to aggregate in Alzheimer's patients. I used *C. elegans*, a common model organism nematode, under different conditions to enable me to image Tau tagged with mScarlet via FLIM (fluorescence lifetime imaging microscopy). I maintained populations of *C. elegans* with both wild type and mutated forms of Tau protein on both high and normal cholesterol agar dishes, allowing me to investigate two conditions with both the impact of cholesterol and the mutation on protein aggregation. I maintained these populations through synchronizations and transfers using a platinum rod, and subsequently imaged worms on days 4, 7 and 10 of their life cycle. Imaging required the use of TCSPC (time correlated single photon counting) microscopy, which uses lasers to excite the fluorophore attached to my protein of interest, causing it to appear as a red colour. I have subsequently used my data to undertake statistical analysis of the degree of aggregation under the different conditions using a range of software, allowing me to present my findings to the research group I joined.

After being taught the relevant techniques and being cleared to use the microscope, I completed the majority of experiments by myself, with full autonomy of number of repeats and the specific protocols I used for my experiments. This experience has been an amazing opportunity to work alongside PhD students and gain an insight into the life of a researcher.



The very overwhelming microscope set up in the dark lab!



The appearance of tau as red (mScarlet) during imaging.

The beginning of my analysis using Flimpa determining the average fluorescence life time of different photons to determine the aggregation level of the protein in different areas of each image.

PhD students

Lina Yousry

I'm Lina, a first-year PhD student in the Marine Behavioural Ecology group supervised by Dr James Herbert-Read in the Department of Zoology. My research uses a coral reef predator, the trumpetfish (*Aulostomus maculatus*), to study predator–prey interactions and the effects, mechanisms and drivers of different stealthy hunting strategies.

Trumpetfish occur in three colour morphs (yellow, blue, and brown) and use various strategies to hunt stealthily and approach prey undetected. One of these strategies, called "shadowing", involves the trumpetfish swimming closely aligned to a larger "host" species to conceal their approach. However, the underlying mechanism is not well understood. This year, I used model fish to investigate whether the relative positions of the shadowing trumpetfish, host, and prey influence the chance of detection of the trumpetfish by a prey species (damselfish). Two possible explanations are that trumpetfish either blend in with the host species (background matching) or actively hide behind them (occlusion).

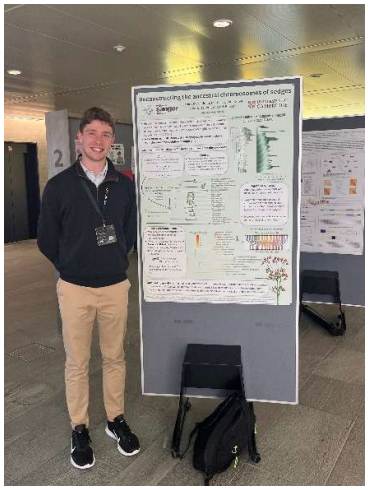
I spent three months in Curaçao running the model experiments while on SCUBA, as well as carrying out surveys to explore whether individual trumpetfish or particular colour morphs specialise in certain hunting strategies. Because trumpetfish have unique spot patterns, they can be individually recognised, making a mark–recapture style approach possible. In addition, I conducted focal follows of different individuals and morphs to compare the success rates of their hunting tactics.

At the moment, I am analysing the data, but next spring I'll return to the field to investigate the ecological drivers of hunting strategies, the social structure of both predator and prey, and the potential role of dynamic camouflage in trumpetfish.

James McCulloch

Last October saw me start my PhD at the Wellcome Sanger Institute. The first eight months of the programme comprise 3 rotations, providing a flavour of the science being carried out and the working environment in different faculty groups. My first rotation of the programme was in the group of Professor Mark Blaxter, investigating chromosomal rearrangements in the sedge family (in the grass order) by reconstructing ancestral linkage groups (i.e. ancestral chromosomes and their gene content at internal nodes of the phylogeny). Sedges have a very high number of rearrangements (like chromosome fusions and fissions) compared to other taxonomic groups, so reconstructing their ancestral genomes is algorithmically complicated, but I was still able

to glean insights into their chromosomal evolution. I was able to present these early results at a conference in Neuchâtel, Switzerland, in April, and then a revised version at the large conference of the European Society for Evolutionary Biology (ESEB) in Barcelona in August. I am going to continue this research for the first chapter of my PhD.



The plans for the rest of my PhD, however, are quite different. My second and third rotations involved research into the genus *Dicyrtomina*, which are globular springtails (insect-like invertebrates). Firstly, I was working in the group of Kamil Jaron, collecting specimens of this genus from Oxford, Edinburgh, and the Sanger campus, and devising a new method of quantifying their colour pattern variation to integrate these data with the results of short-read genome sequencing. For my final rotation I was working in the group of Leopold Parts in the Generative and Synthetic Genomics programme at Sanger, applying machine learning and deep learning methods such as convolutional neural networks to try to classify this same phenotypic variation in a way that was unsupervised and therefore relatively unaffected by my intrinsic bias. I look forward to comparing these results to those from the genome sequencing; preliminary analyses of the sequences indicate patterns of cryptic speciation, global movement, and hybridisation in these springtails, which I've already been able to share at the meeting of the Soil Invertebrate Genome Initiative in Strasbourg this September.

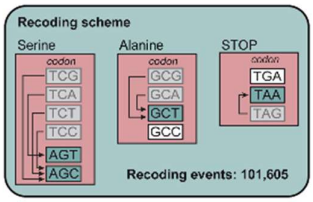
Outside of the current focus of my PhD, I've taken on the role of national recorder for springtails, meaning that I collate and verify records of these invertebrates from various sources in the UK. This has been a fascinating endeavour. Already this year there have been records of at least five species of springtail not previously recorded in the country, which may represent small native populations or imports from elsewhere (probably both). The highlight, however, has been the description of a new species of springtail based on specimens collected in Edinburgh, which I named *Entomobrya petri*: https://soil-organisms.org/index.php/SO/article/view/476/454. Springtails harbour a wealth of potential discoveries, even among the British fauna: I am currently preparing the description of a new genus and two further new species, one of which was found at the Cambridge University Botanic Garden. Look out for these publications in a few months' time!

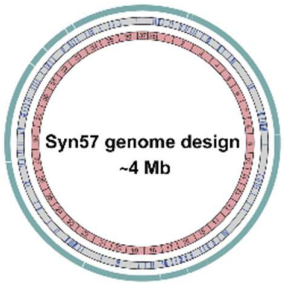
McCulloch, J. (2025). *Entomobrya petri* sp. nov.: A new species of springtail found in the British Isles. *Soil Organisms*, *97*(2), 199–209. https://doi.org/10.25674/476

Research Associates

Wesley Robertson

It's been about one year since I started my own synthetic biology research group, developing novel tools for generating synthetic genomes for gut bacteria. Our goal is to reprogram the gut microbiome to help us better understand the relationship between bacteria and health and disease. Thus far with a small team we're setting up the framework to do this at the Medical Research Council Laboratory of Molecular Biology (MRC LMB). To reprogram bacteria, we engineer the genetic code - this endows our synthetic strains with new-to-nature properties such as complete resistance to phage. To push the limits of genetic code minimalism, this past summer I've published the last of my work as a postdoc at the LMB - we synthesized a recoded genome for *E. coli* which harbours only 57 codons. The near universal 64-codon genetic code was thought to be a 'frozen accident,' as Crick posited, but we don't know if this is an historical accident or is hard-wired into all organisms on earth for a biological reason. Our synthetic 57-codon strain, Syn57, removes 7 codons and still sustains life. In other words, 'life still works,' as I told Carl Zimmer in an interview for an article in the *New York Times.* This strain is now the foundation for reassigning 7 open codons to new meaning as unnatural monomers, thus providing increased chemical diversity available for the synthesis of proteins and polymers in our recoded cells. This is only the 3rd synthetic genome ever made, and now in my lab we're using these genome engineering experiences to facilitate the synthesis of the 4th (and maybe more afterwards!). Meanwhile, to make sure our synthetic organisms don't take over the world, I've just attended a safeguarding synthetic life conference. In a nutshell, synthetic biology isn't the problem but it's part of the solution for ensuring that we don't irresponsibly end the world with mirror world bacteria. Anyway, no reason to worry, the recoded bacteria are biosecure - we engineer them to allow for the precise control of their genetic material and moreover their growth. With that in mind, ideally by next year's newsletter our work with recoded bacteria in mouse gut models will demonstrate how recoded bacteria are more safe than conventional biotherapeutic bacteria.





Alia dos Santos

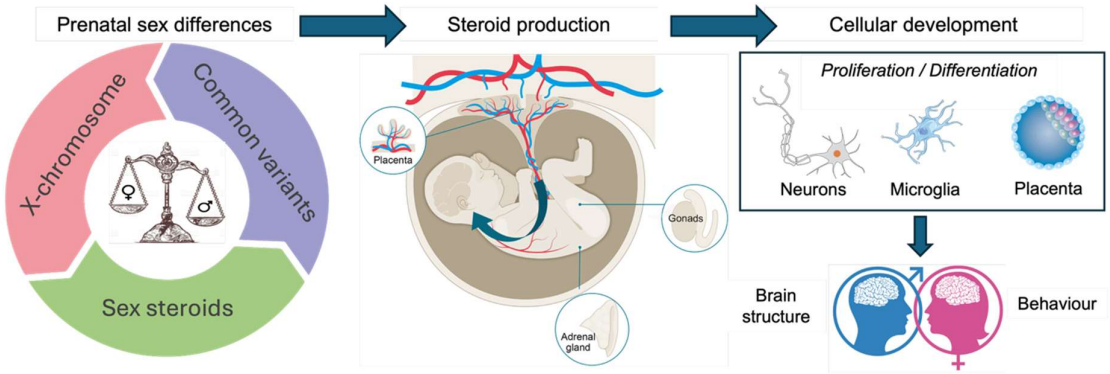
This year I had the chance to attend the EMBO Workshop on *In situ* Structural Biology at EMBL in Heidelberg - my first visit both to the city and EMBL. I presented my ongoing work on the *in situ* structure of nuclear pore complexes (NPCs) in human sperm cells, and on nuclear transport during human sperm cell differentiation. The conference was an excellent opportunity to hear about exciting new research and technologies that promise to make the coming years in cryo-electron tomography transformative.

Heidelberg, Germany (2025).

For this project, the next steps will take this work beyond spermatogenesis, asking what happens to sperm NPCs after fertilisation. I plan to explore this both in zygotes and in artificial fertilisation systems, with a new Part III student joining me to tackle this question in the starting academic year.

Alex Tsompanidis

As an Assistant Research Professor at the Department of Psychiatry, I study the causes of autism and other neurodevelopmental conditions that start in the womb. These conditions, while increasingly prevalent in both men and women, consistently feature a biased sex ratio in diagnosis. This is why my research aims to understand sex differences in humans, during prenatal development, at the clinical, cellular and molecular levels. To achieve this, I collaborate with researchers in Cambridge and abroad, as part of a consortium funded by the Simons Foundation and led by Sir Simon Baron-Cohen. As part of this endeavour, I am conducting clinical projects that involve the creation and analysis of biobanks of samples, such as cord blood and placenta, in the UK, Israel and Norway. In addition, I co-ordinate the work of the geneticists and molecular biologists of our consortium, who study brain development using stem-cell-derived brain organoids. Independently to this consortium, I also study sex differences in brain structure at birth and their effects on toddler behaviour, together with researchers at King's College London. Finally, I integrate all these findings in the context of human evolution, having recently published a new article on the matter in the journal *Evolutionary Anthropology*, together with eminent experts in the field.



Tsompanidis, A et al. The placental steroid hypothesis of human brain evolution. Evolutionary Anthropology; 20 June 2025; DOI: 10.1002/evan.70003

Hugo Fleming

I'm a postdoctoral researcher in the Mental Health Neuroscience Lab at the MRC Cognition and Brain Sciences Unit, and my work explores how the brain and body interact, and how this goes wrong in mental illness.

This year has been exciting, as several long-term projects are approaching the finish line at once. Early in the year, we finally wrapped up a three-year experiment we called the 'juice study', because it involved participants tasting various sweet drinks, to see whether the presence/absence of calories influenced their motivation on a task. I spent the summer analysing the data and writing it up, and the paper is now under review – fingers crossed it will be published by the year's end.

With that milestone behind me, I've turned now to another experiment, looking at somatic anxiety. Summer was quiet for testing (as most of our participants are students, who have gone home for the summer) but we're almost finished, with just ten more participants to recruit. With a bit of a push, I hope this project will also be finished and written up within a few months.

Finally, a personal highlight this year was the Ergodicity Economics conference in Lisbon. This was a conference about a radical new theory of economic decision-making, which I think could overhaul how neuroscientists think about effort allocation and motivation. Two days of discussions with scientists and thinkers from an unusually broad range of disciplines left me inspired and energised, and eager to apply these ideas in my own work.

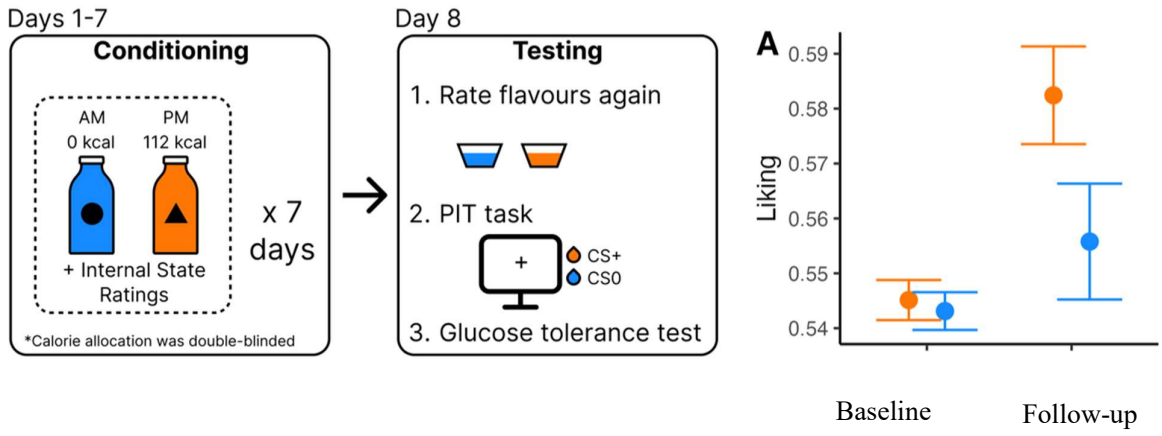
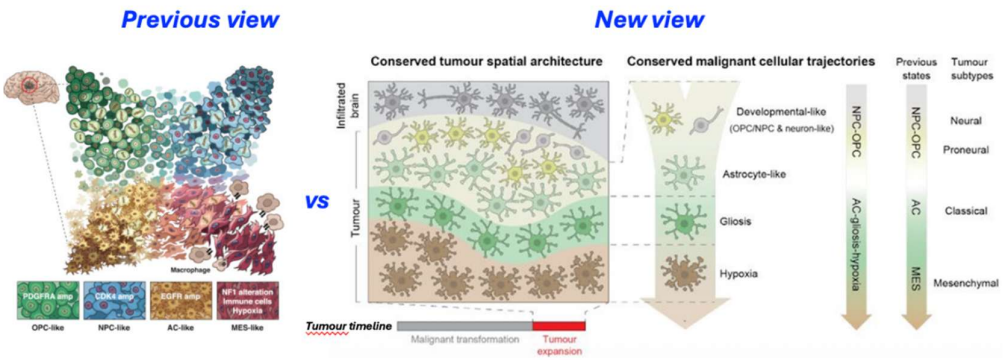


Figure 1. The 'juice study', a major milestone for our lab this year. (left) Study design – participants spent a week drinking calorific and calorie-free drinks, then did several tasks in the lab; (right) Participants developed an unconscious preference for the flavour that was previously paired with calories (orange) over one that had been calorie-free (blue).

Fani Memi

The past year marked the completion of a 3-year long project I led as a Senior Staff Scientist at the Sanger Institute, funded by Wellcome LEAP, which aimed to build the deepest multi-modal cell atlas of Glioblastoma (GBM), the deadliest form of brain cancer. The idea of this project was to leverage all the different technologies available, including single cell and spatial omics, and put these together using computational tools to take a holistic look at the biology of these tumours. We found that the different cancer cell states in these tumours have a very particular spatial organisation which stems from tractable cellular trajectories – cells move from a developmental like state to a hypoxic state, all of which is spatially patterned. This creates the architecture of these tumours. Better understanding of the fundamental biology of these tumours will enhance the development of new drugs.

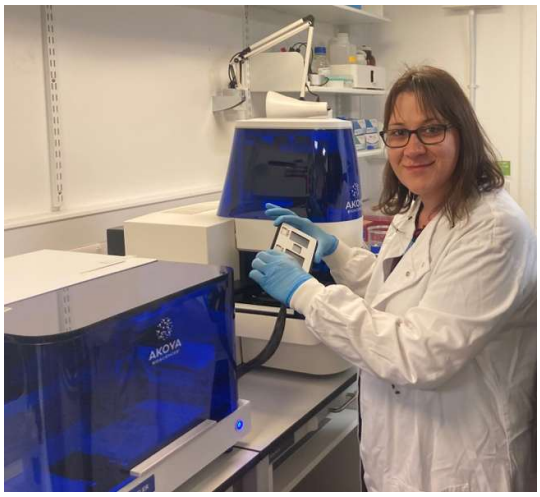
We report our findings in this manuscript, which is now under peer-review process: https://www.biorxiv.org/content/10.1101/2025.05.13.653495v1



Comparison between the current model for the cellular states of glioblastoma and our updated model (new view), depicting the tumour tissue architecture and cellular trajectories.

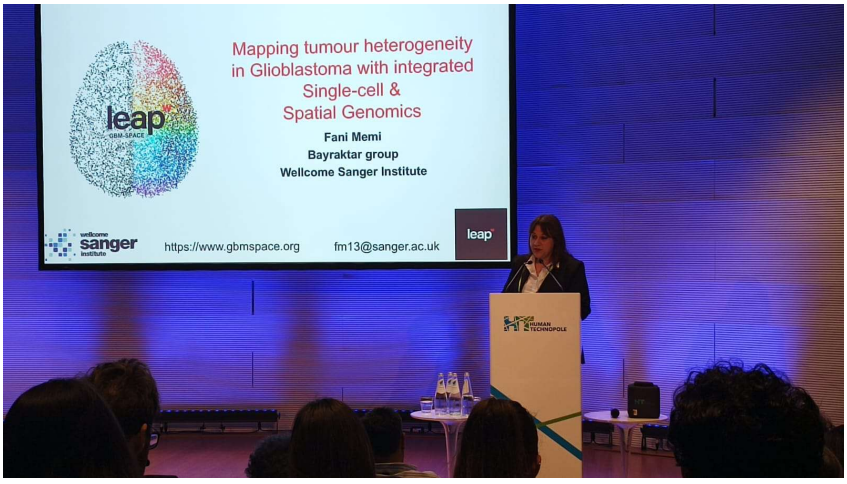
Another exciting adventure I embarked last year was starting a collaboration with researchers from the Africa Health Research Institute (South Africa) to study the evolution of granulomas-areas of tightly clustered immune cells forming around infectious pathogens to "wall them off" from the rest of the body– in the lungs of individuals infected with tuberculosis (TB), using spatial transcriptomics (ST). To date, we still do not understand what determines whether granulomas resolve, progress or disseminate; using ST we are currently mapping the molecular profiles of the different lesions and the cellular crosstalk in play hoping that we will gain new insights into the pathways involved in the transitions between the disease states and provide new therapeutic avenues.

This is my first time working on a project outside of Neuroscience, and I'm absolutely loving it! I'm discovering fascinating aspects of lung biology and pathogen–host immune interactions, while also drawing parallels between tumours and granulomas in the strikingly similar ways they both exploit and reshape the immune system to their advantage.



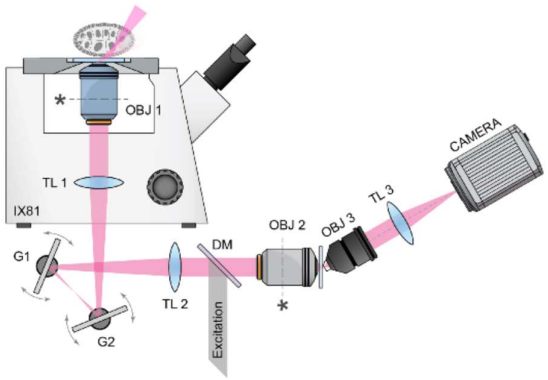
Additionally, last summer we got a new addition to our spatial omics platform at Sanger, the PhenoCycler-Fusion, a fluidics system that allows ultrahigh-plex automated cycling staining (protein) and iterative imaging of 100+ biomarkers across the whole slide in 24hrs. For reference, until a few years ago one could only stain with antibodies and image only up to 4 markers on a tissue section so doing hiplex is very exciting! I have already used it to stain glioblastoma tumours and brain slices with 60 different antibodies detecting the different immune cells present in the tumour microenvironment as well as the difference cancer cells, glia and neurons at the same time!

Finally, I was fortunate to attend a couple of conferences to present my work, with the most recent being the Neurogenomics conference in Milan last May.



ByeFellows

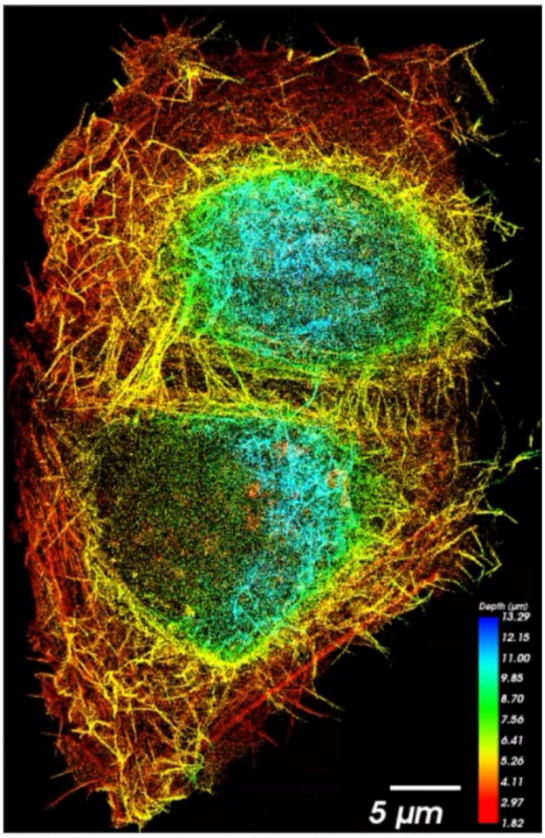
Daniel St Johnston



Design of an oblique plane lightsheet microscope for 3D super-resolution imaging

The highlight of my year was the invention by my team of optical engineers of a new microscope that can perform super-resolution imaging in 3 dimensions.

Because of diffraction, most light microscopy can only resolve objects that are further than 200nm apart. This limit can be overcome by imaging single molecules in a Nobel prize winning approach called Single Molecule Localisation Microscopy (SMLM), because one can calculate the centre of the diffraction limited spot produced on the camera by light from a single molecule with much greater accuracy. The technique we use is called DNA-PAINT, where the protein of interest is labelled with a DNA oligonucleotide and then imaged with the complementary oligonucleotide with a fluorescent dye attached. When the two single-stranded pieces of DNA hybridise, the fluorescent probe is held stationary, producing a blink of light that can then be localised. Previous techniques to perform SMLM in 3D have been very slow and require an extremely complicated microscope. Our new technique is much simpler and is 100x faster. This allows us to visualise protein localisation in large tissue samples with a resolution of 20nm in the x and y dimensions and 60nm in z in less than a couple of hours. Since one can label many different proteins with different oligonucleotides and then image them sequentially, this paves the way for spatial proteomics at the nanoscale. We are now in the process of founding a company to develop this technology further.



A projection of a 3D image of the actin cytoskeleton in a pair of HeLa cells. Depth is encoded by colour

Fellows

Justin Gerlach

It has been a rather varied year once again, and ending in a particularly intense few months. A couple of projects came to conclusion, seeing two papers accepted for publication and one in print. This was a revision of a genus of extinct snails from St. Helena, including the description of one new species. This was an interesting group to work on as it involved trying to track down some of Charles Darwin's specimens, which proved far harder than anticipated. Darwin noted their extinction and attributed it to forest clearance in the very first attribution of an extinction to human agency (180 years ago). I am also slowly trying to work out diversity in the 'St. Helena blushing snail', yes that really is its name.

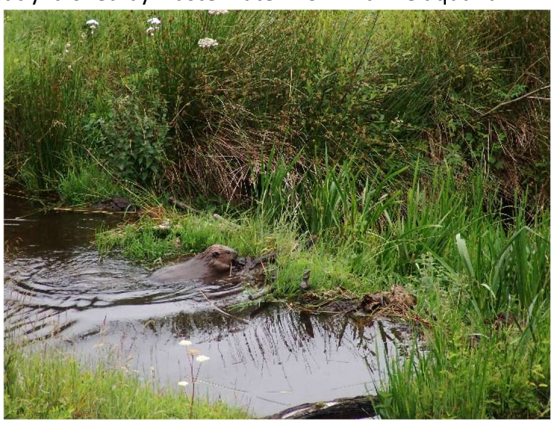
More extinct snail material followed and I have a load of Mauritian species to describe when I find some time. Stopping snails from going extinct has been the focus of the past few months. In July I was asked to lead a mission to rescue the last survivors of the Wallis & Futuna Islands tree snail *Partula obesa* (I've only come across two people who claimed to know where those islands are – right and up a bit from Fiji, if that's any help). When we got there (four days of travelling) we found them almost everywhere we looked. Far from needing rescuing this is a species bouncing back from near extinction, now that its predators have died out.

July was a distraction from snails with a survey of the biodiversity of Cambridge college gardens. 22 colleges signed up so I had a busy few weeks sampling as much as possible. I was ably assisted by Polina Yakushev throughout, and by Function Fang while she wasn't playing with cuttlefish (my interpretation). The enormous amount of material has all been identified to morphospecies level, but full identification will take a while longer with 7,685 terrestrial invertebrate specimens collected (plus an uncounted number of aquatic ones). We should be able to get an interesting publication out of this as the long grass habitats look like have interesting patterns within them, differing in age and management in each college. I'm hoping that we can also come up with recommendations of how best to manage these sites, or how best to recreate meadows in college settings.

Then September was back to saving snails. I run the field conservation programme for the *Partula* tree snails of French Polynesia, and for the third year running spent my September leading a team to reintroduce zoo bred animals back into the wild. Last year was a major breakthrough when we were able to demonstrate the first successful re-establishment of a snail species, in fact only the 13th species of animal or plant returned to wild successfully. There was a lot riding on this year and I feared that it would be a let-down in comparison. We didn't top that success, but we did have many very positive signs in that we found evidence of breeding in the wild for several species (the first wild births for 40 years); the first step to re-establishment. We also were able to open the new *Partula* reserve on Moorea island. This was a wild idea I had two years ago, and it was fantastic to see

it come to fruition so quickly. This predator-free space is surrounded by a salt-water moat that the predators (carnivorous snails and flatworms) cannot cross. Very neatly it is fed by waste-water from marine aquaria.

Down-time over the summer was just three days, but that was spent staying in wooden cabin by a beaver lodge in Scotland. This was the first place to bring beavers back and over the past couple of decades what they have done to restore the landscape is astounding.



Gerlach, J., Griffiths, O., Hume, J. P., Louchart, A., Sorrel, P., & Cairns-Wicks, R. (2025). Diversity of the extinct land snail genus *Chilonopsis* of St Helena (Mollusca: Gastropoda: Achatinidae). *European Journal of Taxonomy*, *1007*(1), 176–210. https://doi.org/10.5852/ejt.2025.1007.3007