UKEOF UKDNA working group conference

13 – 14 May 2025

THE ROYAL SOCIETY

UKEOF

UKDNA WORKING GROUP

Accessibility
The Royal Society is committed to accessibility for our events. If you require assistance please ask a member of staff.

Our lecture hall is fitted with an induction loop for those who are hard of hearing.

Fire alarm
If you hear the fire alarm at any time, it is not a test. Please calmly leave the lecture hall through your nearest fire exit.

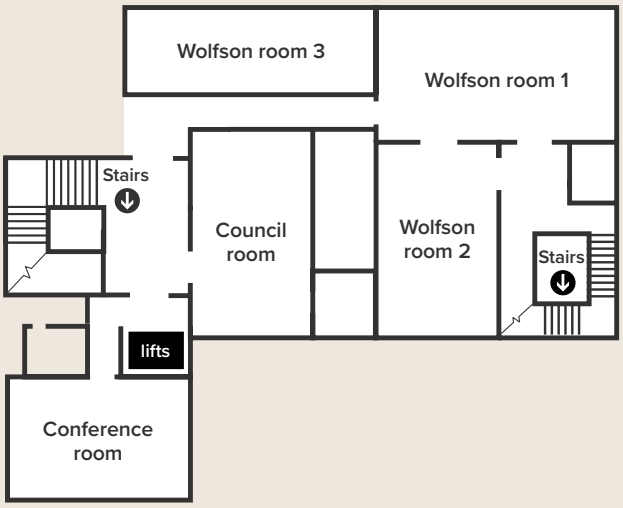
Wifi
Name **RS-Public**
Password **Newton+apple**

@royalsociety

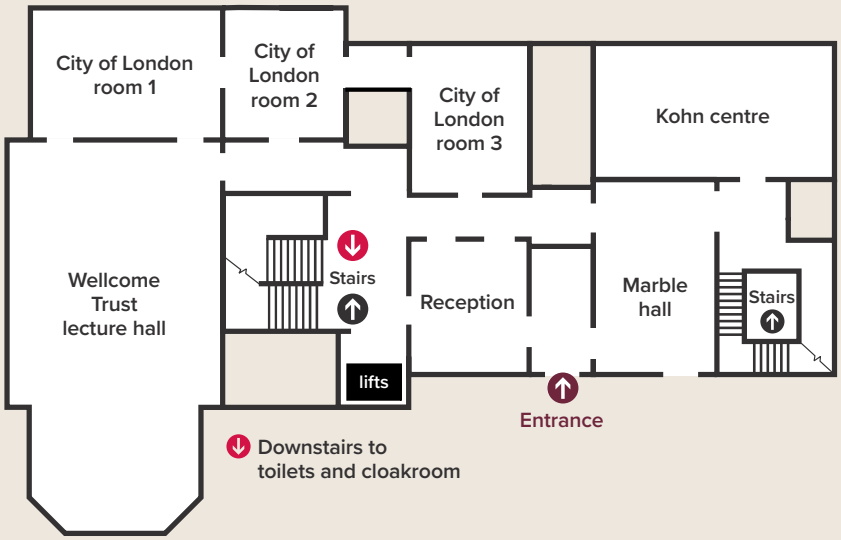
Cover Image:
© iStock.com/onuma Inthapong.

Registered Charity No 207043
Issued: May 2025 DES9038_5

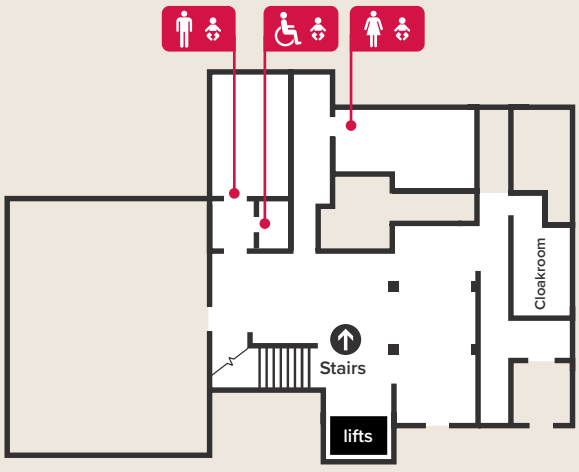
First floor



Ground floor



Basement



Contents

Key Information

The event will be held in the Wellcome Trust Lecture Hall and the adjoining City of London Rooms on the ground floor. Please read the important information below regarding our conference venue.

Royal Society staff will be present throughout the meeting and are identifiable by their red lanyards or gold name badges should you have any questions or need to seek any additional information or support. The conference registration desk will also be staffed.

We hope you enjoy your time with us, and that the conference proves productive and enjoyable.

Fire instructions

In the event of the fire alarm sounding (a continuous alarm) please vacate the building via the marked nearest fire exit sign (please note that this may be behind you).

- **Do not stop to collect your belongings**
- **Do not use the lifts**
- **Do not re-enter the building until authorised**

Please assemble at the emergency point (top of the Duke of York steps to the right of the Royal Society). Fire Wardens will lead the group to the assembly point and report to the roll-call officer.

First Aid

If assistance is required please go directly to the reception desk.

No smoking

Smoking is not permitted in any part of the Royal Society (including terrace, forecourt or balconies).

Toilets

Toilets are located on the lower-ground floor. There is also an accessible toilet behind reception on the ground floor. Please ask staff if you require access to this.

Cloak Room

There is a cloak room available for your use on the lower-ground floor. Please note this will not be staffed so belongings are left at your own risk.

Wi Fi Code

Network: RS-Public

Password: Newton+apple

Welcome and overview

We are delighted to welcome you to the Royal Society for the 11th conference of the UKEOF UKDNA Working Group.

The conference brings together policy makers, end-users, researchers and eDNA service providers, to address application of DNA-based methods for monitoring and policy applications across a range of disciplines. This conference agenda will also cover novel and emerging DNA-based technologies, health and forensic applications as well as opportunities and challenges for operationalising eDNA research, including data standardisation, FAIR principles and data mobilisation.

Sessions will include a combination of full talks, speed talks and panel discussions. Posters will be displayed for the duration of the conference and can be viewed during refreshment breaks.

There is a drinks reception immediately after the first day of conference sessions. During this, there will be the opportunity to book a small group viewing of some items from the Royal Society's archives. These sessions will be available via a sign-up sheet on the registration desk, and on a first come, first served basis. The archive viewing will take place in the library reading room.

Yours sincerely,

UKEOF, the UK DNA Working Group and the Royal Society

About the organisers

UKEOF

The UK Environmental Observation Framework, UKEOF is the coordinating body across the public sector for the UK's environmental observation community. As such it plays a vital role in improving the coordination of the UK's observational evidence needed to understand and manage the changing natural environment. As a partnership of public sector organisations with an interest in using and providing evidence from environmental observations, UKEOF is unique in bringing together the main organisations involved in the field. Together they generate and manage in situ and remote environmental observations across the UK. **Our mission: To work collaboratively to maximise the value of the UK's environmental observations.**

To find out more, visit our website https://ukeof.org.uk/ and follow us on Bluesky at @ukeof.bsky.social.

UKDNA Working Group

The UKEOF, through the UK DNA Working Group (UKDNA-WG), facilitates dialogue and collaboration by providing a forum for the wide community of government agencies, academics and other stakeholders to discuss priorities and emerging developments in the use of DNA for environmental monitoring. The UK DNA Working Group aims to:

1. Link researchers, developers of DNA-based monitoring methods, and end users to ensure that activities are focussed on meeting priority information needs and that knowledge is transferred effectively within the wider community
2. Support and encourage best practice and the development of standards for using DNA-based species monitoring methods
3. Engage and work collaboratively with others nationally and internationally, seeking opportunities to influence research, share best practice and facilitate re-use of samples and data
4. Increase awareness of where and how DNA-based methods can help improve the effectiveness of environmental monitoring.

To find out more about the activities of the UKDNA-WG, and to sign up to our mailing list, see our website https://ukeof.org.uk/our-work/ukdna and follow us on Bluesky at @ukdnawg.bsky.social.

The Royal Society

The Royal Society is the national academy of science for the UK. Its Fellows include many of the world's most distinguished scientists working across a broad range of disciplines in academia, industry, charities and the public sector. The Society draws on the expertise of the Fellowship to provide independent and authoritative advice to UK, European and international decision-makers.

The Society's fundamental purpose, reflected in its founding Charters of the 1660s, is to recognise, promote, and support excellence in science and to encourage the development and use of science for the benefit of humanity. Our strategic priorities therefore are to promote excellence in science; to support international collaboration; and to demonstrate the importance of science to everyone.

The Royal Society recently published a policy report on Environmental DNA, aiming to raise awareness of these technologies among policymakers and other end users. This can be found online here: https://royalsociety.org/news-resources/projects/environmental-dna/

To find out more see our website www.royalsociety.org and follow us on Bluesky at @royalsociety.org.

Agenda: Tuesday 13 May

09:30	**Arrival, registration, refreshments**	
10:00	**Welcome and background**	
	Professor Sheila Rowan CBE FRS	Welcome to the Royal Society
10:05	Dr Sarah Giles	Key findings from the Royal Society's eDNA report
10:15	Andy Nisbet	Welcome from the UK DNA Working Group
10:30	**How can eDNA contribute to policy-related biodiversity monitoring needs?**	
	Chair: Dr Dan Read	
	Professor Gideon Henderson FRS	Opportunities for eDNA to contribute to Defra priorities
10:50	Professor David Bass	A New Strategy for the Defra DNA Centre of Excellence
11:05	Lesley Rippon & Katherine Burgess	How the Natural Capital & Ecosystem Assessment Programme uses DNA for environmental monitoring
11:20	***Break***	
11:45	**Novel and emerging methods for terrestrial DNA-based monitoring**	
	Chair: Dr Andrew Briscoe	
	Dr Joanne Littlefair	Promises and challenges of airborne eDNA for terrestrial biodiversity monitoring
12:05	Professor Matthew Clark	AirSeq: Measuring air metagenomic diversity in agriculture
12:20	Jamie Marsay	Near real-time autonomous airborne pathogen detection sentinel for biodefence, using long read sequencing
12:35	Dr Conor Scott	Sampling airborne fungal DNA to investigate ectomycorrhizal colonisation of former agricultural land
	Speed talks:	
12:50	Dr Kate Denton	Beyond Detection: Deriving Ecological Insights from Terrestrial airDNA
12:55	Lindsay Newbold	Using environmental DNA (eDNA) from leaf washes, to measure changes in arboreal microbial populations linked to host species.
13:00	Lorna Dawson CBE	SCAnDi - Single-cell analysis in forensic science: a collaborative approach to addressing DNA identification
13:05	***Lunch***	
14:00	**eDNA-based monitoring in aquatic ecosystems**	
	Chair: Dr Kerry Walsh	

	Professor Simon Creer	Investigating the ecological relevance of freshwater lotic eDNA: from mesocosm to ecosystem scale.
14:20	Amy Thorpe	National-scale biogeography and function of river and stream bacterial biofilm communities
14:35	Jono Warren	Microbial biofilms as indicators of environmental change in English rivers.
14:50	Dr Joe Taylor	Past, present and future perspectives on integrating DNA monitoring into one of the longest-running freshwater lake time-series
15:05	Dr Tom Wilding	eDNA2IQI – the first regulatory approved eDNA-based monitoring tool in the UK
15:20	***Break***	
15:50	**eDNA-based monitoring in aquatic ecosystems (cont.)**	
	Chair: Dr Kerry Walsh	
	Speed talks:	
	Dr Salla Vartia	PINKTrack - an EU-wide eDNA surveillance programme for pink salmon
15:55	Dr Laura Weldon	The value of eDNA monitoring data in context: the impact of elevated water chemistry on an inland freshwater European eel eDNA survey.
16:00	Sotiris Meletiou	Using eDNA to Detect the Presence of Critically Endangered European Eel in Highly Impacted Freshwater Systems of the Eastern Mediterranean Island of Cyprus
16:05	Milly Jones	More than presence-absence; modelling (e)DNA concentration across time and space from qPCR survey data
16:10	**Panel Discussion – opportunities for cross discipline and cross sector collaboration**	
	Chair: Professor David Bass	
	Dr Joanne Littlefair Professor Davey Jones Jamie Marsay Dr Kerry Walsh Dr Susheel Bhanu Busi	
17:00	**Day 1 Reflections**	
	Andy Nisbet	
17:10	**Drinks Reception** (+ optional private view of the Royal Society's historic archives, via sign-up)	
19:30	**Close**	

Agenda: Wednesday 14 May

08:45	***Arrival, registration, refreshments***	
09:15	**eDNA for marine monitoring**	
	Chair: Dr Katie Clark	
	Dr Kate Wade	UK Marine Monitoring: Working together to enable uptake of biomolecular techniques
09:35	Dr Karen Tait	Comparison of matching morphological and molecular zooplankton time-series data
09:50	Dina-Leigh Simons	Characterising rocky reef biodiversity using environmental DNA from local to national scales
	Speed talks:	
10:05	Dr Kirsten Harper	In Search of the eDNA Bounty: Uncovering Marine Biodiversity in the Mutineers' Seas
10:10	Dr Vera Fonseca	Leveraging eDNA tools for assessing marine diversity: from microfauna to fish
10:15	Dr Margaux Steyaert	Linking ARMS: comparing Autonomous Reef Monitoring Structures (ARMS) and eDNA methods for cryptobenthic reef studies
10:20	Dr Tom Gibson	Environmental DNA Metabarcoding for Biodiversity Monitoring of Ascension Island MPA
10:25	***Break***	
10:55	**Health and forensic applications of eDNA**	
	Chair: Professor David Bass	
	Professor Niamh Nic Daeid FRSE	eDNA as a scientific tool for the criminal justice system – Could we? Should we?
11:15	Professor Davey Jones	Innovations in wastewater-based epidemiology
11:30	Dr Susheel Bhanu Busi	National-scale assessment of antimicrobial resistance in a river surveillance network
	Speed talk:	
11:45	Dr Manisha Gupta	On-site diagnostics for food borne pathogens
11:50	***Lunch***	
12:45	**eDNA for terrestrial ecosystem monitoring, restoration and management**	
	Chair: Holly Broadhurst	
	Professor Bridget Emmett OBE	An overview of ecosystem monitoring by UKCEH and partners and the role of soil eDNA assessment

13:05	Professor Douglas Yu	High quality, granular, timely, trustworthy, and efficient vertebrate species distribution data across a 30,000 km^2 protected area complex
13:20	Professor Julie Lockwood	Use of eDNA in early detection of invasive forest insects
13:35	Buffy Smith	Comparing the iDNA and airDNA sampling methodology for biodiversity monitoring in fragmented forest landscapes.
13:50	Clare Cowgill	Multi-tool monitoring: Comparing and combining non-invasive methods to monitor terrestrial rewilding
	Speed talks:	
14:05	Dr Nadia Barsoum	Comparing different sources of eDNA (water, soil, air, woodland surfaces) for forest mammal detection
14:10	Anna Wood	Metabarcoding to monitor biodiversity in forest restoration projects
14:15	Dr Tamara Schenekar	Monitoring terrestrial vertebrates in savanna ecosystems using environmental DNA of waterholes
14:20	Dr Briony Jones	Leveraging public genomic data repositories for microbial modelling and Soil Health Bioindication
14:25	Dr Penelope Watt	Impact of land management on earthworm diversity
14:30	Dr Claire Carvell	DNA barcoding of a national citizen-led time series from the UK Pollinator Monitoring Scheme reveals potential for large-scale insect community biomonitoring
14:35	***Break***	
14:55	**Standards, best practice, current knowledge gaps and future opportunities**	
14:55	**Chair:** Dr Lori Lawson Handley	
	Professor Florian Leese	From the Wild West to Standards: Unlocking the Power of eDNA for Global Biodiversity Monitoring
15:20	Dr Lyndall Pereira da Conceicoa	BIOSCAN: Insights and Challenges from the First 100K Barcodes in UK Insect Monitoring
15:35	Dr Lynsey Harper	A framework for assessing confidence in metabarcoding assays and results
15:45	Dr Nicholas Dunn	Metadata requirements for the publishing and mobilisation of DNA data
	Speed talks:	
15:55	Dr Caroline Howard	Tree of Life Update: after 2000 genomes the Genome Engine matures

16:00	Dr Tristan Biggs	The use of eDNA metabarcoding for monitoring of UK inshore fish: Current challenges and future recommendations.
16:05	Dr Ben Price	UKBOL: an update on the state of UK DNA reference libraries
16:10	Dr Henrik Cornelisson van de Ven	Establishing a National eDNA Framework in the Netherlands – Insights from the First Dutch National eDNA Workshop

16:15 **Next steps for the UK DNA Working Group**

Dr Lori Lawson Handley and Dr Dan Read

16:25 **Panel discussion: Opportunities and challenges for eDNA research and operationalisation**

Chair: Dr Lori Lawson Handley

Dr Dan Read

Professor Florian Leese

Dr Kate Wade

Professor Simon Creer

Dr Lynsey Harper

16:55 **Day 2 Reflections and Close**

Andy Nisbet

Attendee List

Title	Firstname	Lastname	Organisation
Miss	Meri	Anderson	UKCEH and University of Reading
Dr	Demetra	Andreou	Bournemouth University
Ms	Isna Rasdianah	Aziz	University of Leeds
Professor	Ian	Barnes	Natural History Museum
Dr	Nadia	Barsoum	Forest Research
Professor	David	Bass	Cefas
Dr	Boufana	Belgees	Defra
Dr	Gary	Bending	University of Warwick
Ms	Aurelia	Benhamadouche	University of Plymouth
Mr	Michael	Bennett	UK Centre for Ecology and Hydrology
Mr	Marco	Benucci	Fera Science Ltd
Dr	Justine	Betja	Defra
Mr	Tristan	Biggs	PML Applications Ltd
Dr	Vladimir	Blagoderov	National Museums Scotland
Ms	Eilidh	Boa	Joint Nature Conservation Committee (JNCC)
Ms	Annette	Boniface	Home Office
Dr	Chiara	Borsetto	Resistomap
Dr	Georgina	Brennan	Aarhus University, Department of Ecosciences
Dr	Andrew	Briscoe	NatureMetrics
Dr	Holly	Broadhurst	University of Salford
Dr	Andrew	Brown	National Physical Laboratory
Dr	Katherine	Burgess	Environment Agency
Dr	Susheel Bhanu	Busi	UK Centre for Ecology and Hydrology
Mr	Sean	Butler	Environment Agency
Dr	Lewis	Campbell	Trace Biomonitoring
Dr	Paola	Campos	University College Dublin - School of Biology and Environmental Science
Dr	Claire	Carvell	UK Centre for Ecology & Hydrology
Dr	Sarah	Chordekar	NatureMetrics
Dr	Bethany	Clark	Environment Agency
Professor	Matthew	Clark	Natural History Museum
Dr	Katie	Clark	Natural England
Miss	Milly	Clarke	University of Kent
Ms	Rachel	Coleman Horgan	Marine and Fresh Water Research Center, Atlantic Technological University
Mrs	Clare	Collins	University of Hull
Mr	Michael	Connell	University College Dublin
Dr	Lauren	Cook	UK CEH
Dr	David	Cooke	The James Hutton Institute
Dr	Henrik	Cornelisson van de Ven	TNO

Ms	Rebecca	Court	University of Leeds
Miss	Clare	Cowgill	University of Hull
Dr	Alex	Crampton-Platt	NatureMetrics
Professor	Simon	Creer	Bangor University
Dr	Lucas	Cunningham	Liverpool School of Tropical Medicine
Dr	Liz	Davidson	NatureMetrics
Other	Vicki	Davison	Environment Agency
Dr	Phil	Davison	Cefas
Dr	Deborah	Dawson	NEOF University of Sheffield
Mr	Jono	Dawson	Environment Agency
Dr	Laura	Dawson	Environment Agency
Professor	Lorna	Dawson CBE	The James Hutton Institute
Dr	Sophie	de Becquevort	Forest Research
Mrs	Ashinsa	de Silva Wijeyeratne	University of Reading
Mr	Aymeric	Degat	University Collège Dublin; Université de Perpignan Via Domitia (France)
Dr	Kate	Denton	NatureMetrics
Miss	Rosie	Dowell	Liverpool John Moores University
Dr	Nicholas	Dunn	Natural England
Dr	Bastian	Egeter	NatureMetrics
Mr	Gwydion	Elliott	University of Sheffield
Professor	Bridget	Emmett	Uk Centre for Ecology and Hydrology
Ms	Ghadah	Fhaid	The University of Sheffield
Professor	Julie	Fitzpatrick OBE	The Scottish Government
Dr	Vera	Fonseca	Cefas
Mr	Leo	Fordham	Royal Holloway, University of London
Ms	Katie	Fort	Defra
Dr	Nathan	Geraldi	NatureMetrics
Dr	Tom	Gibson	CEFAS
Dr	Sarah	Giles	The Royal Society
Mr	Tim	Goodall	UK - Centre for Ecology and Hydrology
Dr	Will	Goodall-Copestake	Royal Botanic Garden Edinburgh
Dr	Gavin	Gouws	University of Sheffield
Dr	Nathan	Griffiths	University of the Highlands and Islands
Dr	Manisha	Gupta	Fera Science Ltd.
Dr	Kirsten	Harper	University of Edinburgh
Dr	Lynsey	Harper	Natural England
Mr	Fred	Hartendorf	TNO
Mr	Jonny	Hazell	The Royal Society
Miss	Xi	He	University of Nottingham
Professor	Gideon	Henderson FRS	Defra
Dr	Helen	Hipperson	University of Sheffield
Mr	Callum	Hobbs	Defra

Mr	Harry	Hosker	Natural History Museum
Dr	Caroline	Howard	Tree of Life, Wellcome Sanger Institute
Mr	Thomas	Hughes	University of Plymouth
Mr	Matthew	Hulse	Queen's University Belfast
Miss	Gozde	Isik	University of Hertfordshire
Mr	Jake	Jackman	University of Salford
Ms	Inez	Januszczak	Natural History Museum
Dr	Tiffany	Jedrecka	NatureMetrics
Miss	Lauryn	Jewkes	SureScreen Scientifics
Dr	Max	John	Natural England
Professor	Davey	Jones	Bangor University
Dr	Briony	Jones	UK Centre for Ecology & Hydrology
Ms	Lucy	Knowles	University of Sheffield
Dr	Urszula	Krzeminska-Ahmadzai	De Montfort University
Dr	Lori	Lawson Handley	UK Centre for Ecology and Hydrology
Mrs	Debbie	Leatherland	Natural England
Mr	Kiran	Lee	University of Sheffield
Professor	Florian	Leese	University of Duisburg-Essen
Dr	Richard	Leggett	Earlham Institute
Dr	Joanne	Littlefair	UCL
Professor	Julie	Lockwood	Rutgers University
Dr	Carolyn	Lovell	NPCC OPCSA
Mr	James	Macarthur	Institute for Biodiversity and Freshwater Conservation, University of the Highlands and Islands
Miss	Abigail	Mackay	Nottingham Trent University
Miss	Sara	Maggini	Danish Technical University
Dr	Katy	Maher	University of Sheffield
Ms	Lucia	Manicom-Smith	Forest Research
Miss	Victoria	Mann	University of Plymouth
Dr	Lucio	Marcello	BioSS (part of the James Hutton Institute)
Mr	Jamie	Marsay	Kromek
Dr	Eleni	Matechou	University of Kent
Ms	Angela	Mayson	Severn Trent Water
Dr	Allan	McDevitt	Atlantic Technological University
Mr	Sotiris	Meletiou	Bournemouth University
Dr	Kirsten	Miller	DEFRA
Dr	Jelena	Mlinarec Novosel	Oikon Ltd.-Institute of Applied Ecology
Mr	Robert	Moise	University College Dublin
Mr	Angus	Monaghan	University of Hull
Dr	Olivia	Mosley	NatureMetrics
Dr	Tom	Myers	Biota Trace Ltd
Mr	Sebastian	Mynott	Applied Genomics
Ms	Lindsay	Newbold	UKCEH

Mr	Tom	Newby	Severn Trent
Professor	Niamh	Nic Daied	University of Dundee
Mr	Andy	Nisbet	Natural England
Miss	Charlotte	Nuyt	Marine and Freshwater Research Centre - Atlantic Technological University
Mr	Matthew	O'Donnell	University of Salford
Dr	Lyndall	Pereira da Conceicoa	Wellcome Sanger Institute
Dr	Kirthana	Pillay	Bournemouth University
Dr	Ben	Price	Natural History Museum
Ms	Madeleine	Quirk	The Royal Society
Dr	Aime	Rankin	UNEP-WCMC (UN Environment Programme World Conservation Monitoring Centre)
Dr	Daniel	Read	UK Centre for Ecology & Hydrology (UKCEH)
Dr	Helen	Rees	RSK ADAS Ltd.
Dr	Luke	Reynolds MBE	The Royal Society
Dr	Alexandra	Richardson	Imperial College London
Ms	Lesley	Rippon	Environment Agency
Dr	Laia	Rovira-Craven	Scottish Environment Protection Agency
Ms	Isabel	Saldanha	Liverpool School of Tropical Medicine
Dr	Naiara	Sales	University of Salford
Ms	Melissa	Saphra	The Royal Society
Dr	Claire	Sarell	Home Office
Miss	Nehlin	Sayed	University College London
Dr	Tamara	Schenekar	University of Graz
Dr	Daniel	Schillereff	King's College London
Dr	Joy	Schmeer	National Physical Laboratory
Dr	Paul	Scholefield	Lancaster University
Dr	Conor	Scott	Forest Research
Dr	Jennifer	Shelton	UK Centre for Ecology & Hydrology
Mr	Nick	Sidwell	University of Oxford
Miss	Dina-Leigh	Simons	University of Liverpool
Ms	Buffy	Smith	The eDNA Consultancy Ltd
Dr	Luke	Spadavecchia	Defra
Mr	Tom	Spencer	University of Hull
Ms	Jennifer	Stagg	University of Sheffield
Dr	Deborah	Steele	Defra
Dr	Martin	Stervander	National Museums Scotland
Dr	Margaux	Steyaert	Imperial College Londn
Dr	Karen	Tait	Plymouth Marine Laboratory
Dr	Joe	Taylor	UK Centre for Ecology and Hydrology (UKCEH)
Ms	Amy	Thorpe	UKCEH
Dr	Joseph	Trafford	University College London
Dr	Chris	Troth	SureScreen Scientifics
Miss	Rachel	Tucker	University of Sheffield

Dr	Hannah	Vallin	Aberystwyth University
Dr	Salla	Vartia	University College Dublin
Dr	Kate	Wade	Joint Nature Conservation Committee (JNCC)
Dr	Kerry	Walsh	Environment Agency
Dr	Penelope	Watt	University of Sheffield
Dr	Laura	Weldon	The eDNA Consultancy Ltd
Dr	James	Whiting	NatureMetrics
Mr	Benedikt	Wiese	Atlantic Technological University Galway
Dr	Tom	Wilding	Scottish Association for Marine Science
Dr	Molly	Williams	University of Warwick
Dr	Zoe	Withey	Forest Research
Miss	Anna	Wood	Bangor University
Dr	Paul	Woodcock	JNCC
Mrs	Panagiota	Xanthopoulou	University of the Aegean; HAO Dimitra-Fisheries Research Institute
Professor	Douglas	Yu	University of East Anglia

Biographies: Organising Committee

Dr Sarah Giles

Senior Policy Adviser, The Royal Society

Sarah is an experienced science policy adviser working at the Royal Society, the UK's Academy of Science, alongside some of the world's leading scientists. Sarah leads the organisations' nature related policy engagement and is currently running programmes of work on environmental DNA, food and oceans. She also recently led the Society's Multifunctional Landscapes programme which explored the competing needs of UK land use and how these may be reconciled. Prior to her career in Science Policy, Sarah worked at the University of Bristol as an assistant lecturer and completed a PhD across the fields of veterinary epidemiology and animal behaviour.

Dr Lori Lawson Handley

Freshwater Molecular Ecologist, UK Centre for Ecology and Hydrology

Lori Lawson Handley is a freshwater molecular ecologist in the Aquatic Ecosystems Group at the UK Centre for Ecology & Hydrology, with over 25 years' experience in research and teaching in ecology. Her research focuses on using environmental DNA (eDNA) for biodiversity monitoring and understanding impact of environmental pressures such as invasive species and restoration practices such as rewilding. Lori has been the Secretariat lead for the UKEOF UKDNA Working Group since January 2025, and member of the steering group since 2015.

Andy Nisbet

UK DNA Working Group Chair and Deputy Director of Monitoring, Natural England

Andy is Deputy Director for Monitoring in Natural England, the government's adviser on the natural environment in England. His background is in ecology with a career centred on environmental monitoring, how we collect data, analyse, apply, and report on it. Within Natural England he sets the strategic direction for NE's work in this area and has oversight of the monitoring of Protected Sites and agri-environment schemes, the People and Nature Survey and the monitoring of long-term ecosystem change. He played a central role in the development and piloting of England's Natural Capital and Ecosystem Assessment programme. In the last decade, his work has also focused on innovation and the development of new techniques. Andy chairs the UKDNA Working Group.

Dr Daniel Read

Associate Science Director, UK Centre for Ecology and Hydrology

Dan is the Associate Science Director for the Environmental Pressures & Responses science area. He provides scientific and people leadership to the five constituent research groups within the science area, contributing to scientific discovery and generating data, insights, and solutions that other researchers, businesses and governments need to solve environmental challenges and respond to the environmental challenges we face. Dan is a member of the UKCEH Executive Committee (ExCo) and the Science Leadership Committee (SLC), contributing to the strategic direction and impact of UKCEH.

Dan's background is in Molecular Ecology, for which he has >17 years of post-Phd research experience as a researcher and a Group Leader at UKCEH. His research interests involve applying molecular methods to understand the structure, function and dynamics of biological communities, environmental DNA (eDNA), freshwater microbiology, focusing on those in rivers and streams, and wastewater management and its role in antimicrobial resistance (AMR) in the environment.

Biographies: Keynote speakers and panelists

Welcome

Professor Sheila Rowan CBE FRS

Physical Secretary and Vice President, The Royal Society

Professor Sheila Rowan FRS is the Chair of Natural Philosophy at the University of Glasgow. Since 2009, Professor Rowan has been Director of the Institute for Gravitational Research at the University of Glasgow's School of Physics and Astronomy. Her research contributed to one of the most significant scientific breakthroughs of this century: the first detection of gravitational waves announced in February 2016. This resulted in a share of the 2016 Special Breakthrough Prize in Fundamental Physics for her and the members of her team in Glasgow. She received the Hoyle Medal and Prize of the IOP in 2016, the Harold Hartley Medal of the Institute of Measurement and Control in 2020 and was made a CBE in 2021.She received the (inaugural) Philip Leverhulme Lifetime Achievement Award in 2023. Sheila served from 2018 - 24 on the Council of the Science and Technology Facilities Council, latterly as its Senior Independent Member and Co-Chair. From 2016 - 21 she was the Chief Scientific Advisor to the Scottish Government, and from 2021 - 23 served as President of the Institute of Physics (IoP). She is currently the Deputy Chair of the Strategic Advisory Board for the UK National Quantum Technology Program and Physical Secretary and Vice-President of the Royal Society.

Day 1 Keynote Speakers

Professor Gideon Henderson FRS

Chief Scientific Adviser, Defra

Professor Gideon Henderson was appointed Chief Scientific Adviser at the Department of Environment, Food and Rural Affairs on 1 October 2019. He is also Director General for Science and Analysis. He is responsible for overseeing the quality of evidence that the Department relies on for policy decisions. He also provides ministers with scientific advice and sets the priorities for scientific research and evidence-gathering.

He has been Professor of Earth Sciences at the Department of Earth Sciences in the University of Oxford since 2006. He has also jointly held positions as Senior Research Fellow at University College, Oxford since 2012 and as Adjunct Associate Research Scientist at the Lamont Doherty Earth Observatory of Columbia University since 1999.

His awards include the 30th Annual Plymouth Marine Science Medal 2016, European Union of Geosciences outstanding young scientist award in 2001, and the Leverhulme Prize Fellowship in 2001. In 2013 he was elected a Fellow of the Royal Society (FRS).

Dr Joanne Littlefair

Lecturer, Genetics, Evolution and Environment, UCL

Joanne Littlefair is a Lecturer and UKRI Future Leaders Fellow working at the People and Nature Lab at UCL East. Her research interests explore new ways to monitor and understand biodiversity, with a particular emphasis on working in habitats that have been heavily altered by human activity and understanding how these areas can be managed to benefit nature. Currently her lab focuses on researching new innovations in terrestrial biomonitoring with airborne eDNA.

Professor Simon Creer

Professor of Molecular Ecology, University of Bangor

I am interested in using contemporary molecular tools to address diverse questions focusing on biodiversity, ecology and evolution. This is a particularly exciting time in the field of molecular ecology, since advances in DNA sequencing throughput have recently offered a paradigm shift in our ability to assess previously intractable functional and taxonomic biodiversity at an unprecedented scale, augmenting existing biodiversity fields and empowering others. Using such technologies, I am testing a range of hypotheses regarding the

alpha and beta functional and taxonomic diversity of macro-, meio- and microbial communities (e.g. microbiomes) in space and time, based on genomic, community and environmental DNA (eDNA). Focal habitats have included estuarine, coastal and deep sea environments with an increasing focus now on freshwater, terrestrial, whole organisms and the aerial biosphere in order to understand the drivers of diversity in natural communities and also how diversity is linked with ecological function, trophic relationships, environmental and human health. Current additional activities include phylogenomics, population genetics, life history evolution, polyploidy, pollination genomics.

Day 1 Panellists

Chair: Professor David Bass

Professor David Bass is a Principal Scientist at Cefas, where he leads the animal and human health science theme. He is Honorary Full Professor in the College of Life and Environmental Sciences, Exeter University, Chair of the Defra DNA Centre of Excellence, serves on the Advisory Board for the UK Microbial Forensics Consortium, and is a Principal Investigator for Defra aquatic animal health R&D programmes and the Defra/UKRI-funded genomics of animal and plant pathogens consortium. Key areas of expertise are genomics, pathogen biology, aquatic animal and plant diseases, molecular biology and ecology, eDNA, biodiversity and phylogenetics, and microbiology. He has developed pathobiome and One Health/systems approaches for better understanding and management of aquatic systems and for coastal ecosystem health.

Professor Davey Jones

Professor in Soil, Environment and Public Health and Associate Pro Vice Chancellor, Bangor University

Davey Jones holds a Professorial Chair in Environmental Science and Public Health at Bangor University. A major focus of his research is on understanding animal pathogen behaviour in the environment and the risk to human health. He has advised UK and Welsh Government on their COVID-19, public health, agriculture, waste and climate change policies. His research is funded via UKRI (NERC, EPSRC, BBSRC), Welsh Government, DHSC, UKHSA, Food Standards Agency, DEFRA and the European Union. He was a member of the SAGE COVID-19 sub-committee 'Transmission of COVID-19 in the Wider Environment Group (TWEG)' and was head of the COVID-19 Technical Advisory Group - Environment (TAG-E) for Welsh Government and reported to the UK Government COVID-19 Public Inquiry. He also collaborates with industry to deliver novel solutions to environmental problems and improve product sustainability. He currently leads the 'Wastewater-based public health surveillance programme for Wales and sits on the UKWIR Substances of Emerging Concern Advisory Group (SECAG).

Dr Susheel Bhanu Busi

Soil Molecular Ecologist, UK Centre for Ecology and Hydrology

Dr. Susheel Bhanu Busi is a molecular ecologist at the UK Centre for Ecology and Hydrology (UKCEH), specialising in multi-omics analysis and workflows. His research experience spans diverse environments, including human and animal health, freshwaters such as alpine streams and rivers, wastewater systems, and soils. Dr. Busi's prior research involves the characterisation of microbial interactions in human and environmental samples such as soils, freshwaters and wastewaters, shedding light on the distribution of composition and functional capacities of microbes within these ecosystems.

His work integrates high-throughput sequencing such as metagenomics and statistical modelling to track the functional contributions of microbial elements. He applies advanced bioinformatics workflows to characterise microbial communities and understand the ecological factors influencing gene mobility in complex systems such as soils. His research informs strategies for soil health, water quality management, pollution mitigation, and One Health initiatives, bridging the gap between molecular ecology and environmental science.

Jamie Marsay

Head of Biotechnology, Kromek

Jamie Marsay is the Head of Biotechnology at Kromek, with over 2 1/2 decades of experience in full product lifecycle, successfully managing the design and development of automated products and equipment, for commercial exploitation.

Specialising in research, development and product delivery of automated platforms for the autonomous detection of airborne and waterborne pathogenic material, he has extensive experience in successfully managing biological detection system development and delivery contracts for both Government and Industrial projects. He is the Principal Investigator for the development of airborne and waterborne detectors for US and UK governmental bio-detection programmes, and has a comprehensive understanding of pathogen detection capabilities using next generation sequencing and bioinformatics.

Dr Kerry Walsh

Senior Specialist, Climate Change and Resource Efficiency team, Chief Scientists Group, Environment Agency.

As the Environment Agency's research lead for DNA, and with over two decades of experience, Kerry has been instrumental in shaping and advancing the operational use of DNA-based technologies to monitor water quality and better understand ecosystem health.

A molecular microbial ecologist by background, Kerry has played a central role throughout her career in developing, coordinating, and managing research projects and strategic partnerships. In 2014, she initiated the formation of the UKDNA Working Group to promote knowledge exchange and support the delivery of practical, relevant research through collaborative engagement between the research community and government stakeholders.

Her earlier research focused on developing DNA methods aligned with taxonomic groups used in Water Framework Directive ecological assessments, such as diatoms and fish. More recently, she has led an Environment Agency research programme investigating the relationships between environmental pressures, microbial community dynamics, and ecosystem health across England's river network. This long-term initiative aims to develop microbial bioindicators of ecosystem health using a large, national-scale dataset derived from river biofilms. The goal is to integrate this knowledge into the Environment Agency's monitoring programmes to provide new insights into environmental change and support more targeted management interventions.

Day 2 Keynote Speakers

Dr Kate Wade

Marine Monitoring Manager, JNCC

Kate Wade is a Marine Monitoring Manager at the Joint Nature Conservation Committee (JNCC), who provide advice to all four Governments of the UK on the natural environment. She has a background in marine and coastal ecology and has worked on a large range of projects including statutory marine reporting, development of biodiversity indicators, natural capital, blue carbon, coastal restoration and Marine Protected Area monitoring. In her current role as part of the Marine Monitoring Team, she is responsible for the development and application of new approaches and technologies for marine monitoring, with a focus on benthic biodiversity. Recognising the potential value of biomolecular approaches for marine monitoring, and the need to bring together members from the marine community to share updates and discuss advances in this area, JNCC have recently established the UK Marine Biomolecular Group, which Kate chairs.

Professor Niamh Nic Daied FRSE

Professor of Forensic Science and Director of the Leverhulme Research Centre for Forensic Science, University of Dundee.

Professor Niamh Nic Daeid is a Professor of Forensic Science and Director of the Leverhulme Research Centre for Forensic Science at the University of Dundee. She has been involved in forensic science education, research and casework for over 30 years. She is a Fellow of the Royal Society of Edinburgh and holds fellowships of the Royal Society of Chemistry, the Chartered Society of Forensic Science, the Institute of Chemistry of Ireland, the Royal Statistical Society and the UK Association of Fire Investigators. She is a registered forensic practitioner with the National Crime Agency and is authorised as a Forensic Chemist under the Criminal Procedure (Scotland) Act 1995. She has worked on many forensic cases particularly in fire investigation.

Niamh holds national and international roles with the Home Office, the Scottish Biometrics Commissioner, the European Network of Forensic Science Institutes, INTERPOL, the International Criminal Court, and the United Nations. She sits on the steering committee of the Judicial primers which produce science primers for Judges led by senior Judiciary in collaboration with the Royal Society and Royal Society of Edinburgh.

Niamh has received awards for her work including the ENFSI distinguished forensic scientist award, the Pete Ganci award for services to fire investigation, The Herald Higher education innovation award, the Royal Society of Edinburgh Senior Medal for Public Engagement and the Stephen Fry Award for public engagement. She has published over 200 peer reviewed research papers and book chapters and holds a research grant portfolio in excess of £30 million.

Professor Bridget Emmett OBE

Principal Scientist, UK Centre for Ecology and Hydrology

Bridget is a Principal Scientist at UKCEH and leads the inter-disciplinary and multi-partner **Environment and Rural Affairs Monitoring and Modelling Programme** (ERAMMP) funded by the Welsh Government since 2012. Bridget is the current president of the British Ecological Society and is a Member of the EU Mission Board for 'A Soil Deal for Europe'.

Bridget was awarded Officer of the Order of the British Empire (OBE) for her Services to Soil and Ecosystem Sciences in 2023 and the Marsh Award for her Climate Change Research by the British Ecological Society in 2016. She has published over 170 articles, has a H index of 64 and has a publication record with over15,000 citations. She sits on a wide range of number of advisory boards both national and international for governments and research organisations and is a Trustee for Rothamsted Research and the Ecological Continuity Trust. She served as the Specialist Adviser for the UK Parliamentary Inquiry into Soil Health in 2016.

Professor Florian Leese

Professor in Aquatic Ecosystem Research, University of Duisburg-Essen, Belgium.

Florian Leese has been Full Professor of Aquatic Ecosystem Research at the University of Duisburg-Essen, Germany, since 2015, where he also serves as Vice Dean of Research. His work focuses on advancing molecular tools for monitoring biodiversity in aquatic ecosystems, particularly under human-induced environmental stressors. He integrates field ecology with genetic and genomic methods to better detect and assess changes in species and community composition. A key aspect of his research involves the development and application of DNA-based techniques for improved aquatic biomonitoring. He played a central role in DNAqua-Net, a European network that brought together scientists and practitioners to promote the implementation of molecular tools in environmental monitoring. Through his work, he aims to bridge the gap between academic research and practical application, fostering international collaboration across science, policy, and industry. He is also actively involved in national (DIN) and international (CEN, ISO) standardization bodies, contributing to the development of standards for DNA-based biomonitoring and FAIR data practices.

Day 2 Panellists

Chair: Dr Lori Lawson Handley

(see above)

Dr Daniel Read

(see above)

Dr Kate Wade

(see above)

Professor Florian Leese

(see above)

Professor Simon Creer

(see above)

Dr Lynsey Harper

Senior Officer, DNA Based Monitoring, Natural England.

I am an ecologist with strong interests in freshwater ecosystems, community ecology, and the development of new tools for biodiversity monitoring. My research to date has ranged in focus from distribution and conservation assessments for single species, dietary profiling for threatened and invasive species, to factors influencing community dynamics using conventional and molecular monitoring tools. I have sought to apply environmental DNA (eDNA) analysis, both targeted single-species and community metabarcoding approaches, to ecological questions in order to better inform biodiversity conservation, management and policy in a changing world. I am currently working in the public sector as a Senior Officer for DNA Based Monitoring with Natural England. I am leading on the development and use of DNA-based approaches for monitoring of habitats and species across Natural England sites to help assess and communicate the state of nature in the UK.

Abstracts

Full talks

(in alphabetical order)

Dr Susheel Bhanu Busi

Title: National-scale assessment of antimicrobial resistance in a river surveillance network

Abstract: Antimicrobial resistance (AMR) represents a global health challenge exacerbated by environmental dissemination. Wastewater treatment plants (WWTPs) act as both reservoirs and conduits for antimicrobial resistance genes (ARGs), yet the dynamics of ARG prevalence due to their influence on river networks is uncharacterised. Our study offers a comprehensive view of ARG diversity, abundance, and dissemination across 450 sites within the nationwide River Surveillance Network (RSN) in the United Kingdom. We assessed the ecological drivers of AMR, where key findings revealed that anthropogenic load in rivers leads to an increase in overall ARGs. WWTPs lead to a discordant increased in ARGs in rivers, with several genes of varying risk categories acting as potential indicators of anthropogenic influence. We observed a distinct resistome associated with the catchment habitats, which further revealed that WWTP load along with manure from agricultural sources are key drivers of AMR abundance, diversity, and composition. Taxa, in close-knit networks are reservoirs of these ARGs, majority of which are known freshwater taxa such as Pseudomonadota, Flavobacteria, Sphingomonodaceae. Furthermore, we found strong correlations between ARG-encoding taxa, catchment characteristics and water chemistry. This research advances our understanding of AMR dynamics, emphasizing the importance of coupling wastewater surveillance with environmental risk assessments. Our approach bridges gaps between environmental microbiology and public health to limit the ecological and societal impacts of AMR, highlighting the critical need for interdisciplinary collaboration and innovation to combat the global challenge of AMR, offering a roadmap for future research and policy implementation.

Dr Katherine Burgess and Ms Lesley Rippon

Title: How the Natural Capital & Ecosystem Assessment Programme uses DNA for environmental monitoring

The Natural Capital and Ecosystem Assessment (NCEA) is Defra's largest Research & Development Programme and will transform environmental decision-making in England. The scale at which DNA is being used for monitoring across Defra Group has increased dramatically since the inception of the NCEA. This talk provides an introduction on how the Environment Agency and Natural England are using DNA to monitor freshwater network and ponds, including preliminary findings and opportunities for further method development.

Professor Matthew Clark

Title: AirSeq: Measuring air metagenomic diversity in agriculture

Abstract: Plant agricultural ecosystems are essential for human nutrition, but modern industrial farming typically uses large monocultures, in which diseases can easily spread and have devastating effects on yield and food security. Thus disease monitoring, chemical treatments, breeding of resistant cultivars etc. are essential for maintaining food security. Importantly disease propagation and outbreaks are not solely based on short distance transmission to neighbouring plants, but also on long distance aerial dispersal of spores over longer ranges. Here we show that the low concentration of airborne DNA from microbes can be recovered, whole genome sequenced and taxonomically classified, including down to the species or even genotype level. Data from wind tunnel microbial release experiments shows the method is reproducible, and that classified reads increase as the released spores levels increase. Monitoring a field growing key crops, we show that AirSeq can quantify agriculturally significant pathogens which are often affected by weather conditions, and generate a profile of native species growing nearby. More recently we have tested our technology against expert disease scoring in the soft fruit industry, and in livestock farming, in both cases generating actionable data for farmers. The results suggest AirSeq could form part of a precision agriculture approach.

Miss Claire Cowgill

Title: Multi-tool monitoring: Comparing and combining non-invasive methods to monitor terrestrial rewilding

Abstract: Rewilding, the facilitation of self-sustaining and resilient ecosystems by restoring natural processes, is an increasingly popular conservation approach. However, outcomes of rewilding can be unpredictable and empirical evidence is lacking. Effective, non-invasive and future-proof monitoring is therefore essential to assess impacts. Our recent review of utilising environmental DNA (eDNA) to monitor terrestrial rewilding suggests that combining eDNA with other non-invasive methods provides the most comprehensive biodiversity assessments. We used this approach to assess vertebrate taxonomic diversity across a rewilding site in Scotland, comparing four types of eDNA samples (water, soil, tree rolling and faecal), with acoustic and camera monitoring. Acoustics detected the highest taxonomic diversity, followed by tree rolling and water sampling. Community composition was similar across methods except acoustics, which primarily detected aerial species. Acoustics also detected the most pronounced community differences between the microhabitats across the site. Conversely, eDNA methods, particularly tree rolling and water sampling, captured the greatest functional diversity. These findings demonstrate the necessity of a multi-method 'toolkit' for rewilding monitoring, emphasising that a diverse array of methods is necessary to comprehensively detect all vertebrate taxa and their functional roles.

Professor Simon Creer

Title: Investigating the ecological relevance of freshwater lotic eDNA: from mesocosm to ecosystem scale.

Abstract: Global biodiversity is under threat from numerous natural and anthropogenic drivers but enumerating ecosystem wide biodiversity using traditional ecological approaches is an impossible task. Destructive sampling, limited resources and limited taxonomic expertise means that we are not assessing ecosystem biodiversity at sufficient temporal and spatial scales to understand global change and support ecosystem services. Environmental DNA based biodiversity analysis provides a cost effective, non-invasive and taxonomically comprehensive solution for assessing biodiversity, but in river ecosystems, how relevant is the eDNA signal? Here, we will overview the key insights leveraged from UK Highlight Topic LOFRESH grant, that deployed field scale experimental mesocosm work, an intensive spatio-temporal investigation of the Conwy catchment in North Wales, expanding through to ecosystem level analyses at the international scale. The results demonstrate the labile nature of the lotic eDNA signal from multiple phyla and taxonomic levels and consequently, the transit, degradation and ecological relevance of eDNA data in relation to the ecological community in temperate lotic ecosystems.

Dr Nicholas Dunn

Title: Metadata requirements for the publishing and mobilisation of DNA data

Currently seen as an innovative technology at Natural England, DNA-based methods are now moving into business as usual for monitoring. To achieve this transition and to ensure that DNA data is Findable, Accessible, Interoperative and Reusable (FAIR), work has been undertaken to identify and develop metadata reporting principles at Natural England. We will present the minimum metadata reporting guideline that we have recently published which, if followed, will enable Natural England to use data provided to it for monitoring and regulation. In line with this, as DNA-based methods are used more widely, mobilising DNA-derived species occurrences requires that sufficient and appropriate metadata is provided to allow the data to be verified. Natural England has been working with the NBN to operationalise the mobilisation of DNA-derived species data to the NBN Atlas and has also been part of a recent collaborative effort to develop a comprehensive FAIR metadata checklist which aims to introduce a standard format for DNA metadata reporting. This talk will introduce Natural England’s minimum metadata reporting guidelines in the context of the new FAIReDNA metadata checklist and show how this integrates into GBIF’s metabarcoding data toolkit (MDT) and the NBN Atlas’ DNA occurrence upload template. Taken together, this talk will demonstrate how best to record DNA metadata so that it can be mobilised onto species occurrence databases with confidence.

Dr Lynsey Harper

Title: A framework for assessing confidence in metabarcoding assays and results

Abstract: DNA-based methods are changing how we monitor and assess ecosystems, but the confidence that can be attributed to these methods can depend on the level to which they have been developed and validated. A validation framework for single species environmental DNA (eDNA) assays was designed to allow end-users to evaluate single species assays for future research and routine monitoring. No such framework exists for metabarcoding assays which are inherently more complex. The many available metabarcoding assays

have been tested to different extents in different environments and applied in various contexts. It is difficult for end-users to understand, interpret, and determine confidence in their results. We constructed a framework for assessing readiness of and confidence in metabarcoding assays through consultation with a steering group comprised of academic, government, non-governmental, and commercial organisations to ensure that the framework can be used by various end-users. A list of 187 variables was compiled, consolidated into 17 thematic blocks (e.g. in silico analysis), and arranged on a 5-level validation scale from “incomplete” to “exemplar” with defined minimum validation criteria and interpretation of results for each level. These variables were evaluated for five widely used, published eDNA metabarcoding assays. The resulting dataset was used to provide an overview of current validation practices and test the wider applicability of the framework to assays targeting different groups in different environments. The framework is a user-friendly tool to evaluate previously published and new metabarcoding assays for future research and routine monitoring, and enables appropriate interpretation of results.

Professor Davey Jones

Title: Innovations in wastewater-based epidemiology

Wastewater-based epidemiology has emerged as a powerful surveillance tool for tracking the prevalence and temporal dynamics of pathogens in communities and healthcare settings. In this talk, I will showcase how this technology can be extended beyond traditional applications to environmental waters for comprehensive public health monitoring. Specifically, I will demonstrate how wastewater surveillance can track the presence of avian influenza in aquatic environments, providing early warning systems for potential outbreaks. Furthermore, I will explain how this approach can predict health risks associated with sewage discharges for recreational water users, enabling evidence-based decisions about water safety. Finally, I will illustrate how wastewater-based epidemiology can monitor organisms responsible for swimmer's itch, highlighting the versatility of this technology in addressing diverse public health challenges.

Dr Florian Leese

Title: From the Wild West to Standards: Unlocking the Power of eDNA for Global Biodiversity Monitoring

Abstract: Environmental DNA (eDNA) analyses are rapidly transforming biodiversity assessment, unlocking the potential for exponentially growing datasets from ecosystems around the globe. Particularly in aquatic environments, eDNA has established itself as a novel and powerful tool to assess ecosystem state and functioning. However, despite its promise, the full potential of eDNA remains underutilized. A major barrier is the lack of comparability across laboratories and between eDNA-based and traditional assessment methods. Moreover, the proliferation of diverse analysis approaches - the current "wild west" of eDNA workflows - poses a significant challenge in particular for end users seeking reliable and standardized services. To ensure eDNA's effective integration into formal biodiversity monitoring frameworks, critical next steps include the development of formal minimum methodological standards and robust quality assurance and quality control (QA/QC) schemes. In this talk, I will draw on insights from international method comparisons to highlight key challenges that currently limit eDNA data quality and reliability to then present the work of the international eDNA Standardization Task Force (iESTF), which is driving the inclusive development of formal standards aimed at the International Organization for Standardization (ISO), with the goal of establishing internationally accepted minimum requirements for eDNA applications. Finally, I will use the Horizon Europe project eDNAqua-Plan as an example, how solutions for FAIR data are being developed within an open, digital ecosystem for eDNA-based biodiversity assessments. Finally, I will argue that embracing international collaboration, open science, and FAIR data principles is essential to fully unlock the transformative potential of eDNA methods for global biodiversity monitoring and conservation.

Dr Joanne Littlefair

Title: Assessing airborne eDNA for surveying British bat roosts in a policy-relevant context

Abstract: Airborne environmental DNA sampling has the potential to offer a comprehensive representation of biodiversity from mixed samples. Enclosed bat roosts could facilitate the long-term preservation and accumulation of DNA within them and are therefore considered an ideal target for terrestrial eDNA collection. Existing studies have already demonstrated the feasibility and effectiveness of using airborne eDNA as a sampling tool to investigate tropical bat roosts which are sometimes enclosed and inaccessible areas. However, there are a number of issues to address before this can be deployed in a policy relevant context. In

the UK, bats are monitored during hibernation, yet the lowered metabolism and movement levels may result in decreasing detectability via lower levels of eDNA being shed. There is also a desire to monitor roosts at a distance to minimise the potential disturbance to bats and negate the need to obtain a license to survey inside the structure. Here we present results from paired airborne eDNA and volunteer surveys within hibernacula, showing that the two approaches have a complementary overlap, in addition to a transect of paired eDNA and ecoacoustics samples on a transect away from a summer bat roost. We discuss the challenges and areas for growth in airborne eDNA sampling.

Professor Julie Lockwood

Title: Use of eDNA in early detection of invasive forest insects

Abstract: Novel approaches to collecting eDNA from terrestrial ecosystems allows close tracking of forest insect pests. Here I illustrate the use of these tools to survey for the presence of spotted lanternfly along major roadways in New York State, USA. This species is a globally important invasive species where successful management depends critically on early detection of satellite populations. Our eDNA surveys elevate probability of detecting this species at a survey site three-fold over conventional traps, and reveal the presence of this species well ahead of the invasion front. Our methods were cost and time efficient, allowing surveys along 1,500km of roadway over 2 weeks, and show promise for use for other forest insect pest surveillance programs.

Professor Niamh Nic Daied FRSE

Title: eDNA as a scientific tool for the criminal justice system – Could we ? Should we?

This presentation provides an exploration of the possible investigative used of eDNA across a variety of applications. In particular we will explore where the advantages may lie and what pitfalls there may be to overcome.

Dr Lyndall Pereira da Conceicoa

Title: BIOSCAN: Insights and Challenges from the First 100K Barcodes in UK Insect Monitoring

Abstract: Insects are fundamental to ecosystem stability and agricultural productivity, yet they face significant threats from habitat loss, climate change, and other human-driven pressures. BIOSCAN contributes to large-scale insect biodiversity monitoring, employing DNA barcoding to address critical knowledge gaps in diversity, abundance, and species interactions. Through monthly sampling of flying insects using Malaise traps, BIOSCAN has generated over 100,000 DNA barcodes, working toward the goal of sequencing more than one million insects in the UK within five years. Using non-destructive DNA extraction methods, the project preserves specimens for integration with phenotypic and genomic data, ensuring a long-term legacy for biodiversity research. Preliminary findings from BIOSCAN include insights into seasonal and habitat-driven biodiversity patterns, species distribution models for underrepresented taxa, detection of cobionts (such as Wolbachia symbionts), and whole genome sequencing. Early datasets suggest relationships between richness, abundance, and species interactions, providing a valuable resource for tracking biodiversity trends. By combining genomic data with ecological frameworks, BIOSCAN enhances our understanding of insect biodiversity and helps establish baselines that will be essential for conservation efforts.

Miss Dina-Leigh Simons

Title: Characterising rocky reef biodiversity using environmental DNA from local to national scales

Abstract: Climate change is reshaping marine ecosystems globally by affecting organism survival and altering species distributions. Efficient and scalable methods for monitoring climate-sensitive systems are critical to address such changes amid limited resources. Environmental DNA (eDNA) metabarcoding has emerged as a promising tool for detecting coastal marine taxa, but the spatial resolution of the method (i.e., the ability to differentiate communities from different locations) remains insufficiently understood, particularly in dynamic intertidal environments. Here, we evaluate the effectiveness and resolution of eDNA in detecting rocky intertidal taxa across three spatial scales – national, regional, and local - in the United Kingdom. We detected 1054 target taxa within 455 families and 19 phyla using two established primers targeting invertebrates (CO1) and macroalgae (18S rRNA). Moderately distinct eDNA signals were found at all spatial scales, indicating local discreteness even between vertical shore heights within the same sites. However, communities were

more discrete at larger scales (i.e. between UK Regional Seas) than smaller scales (i.e. within sites). eDNA signals were more strongly structured by geographic location than by vertical shore height, likely as a consequence of greater mixing and DNA homogenisation at smaller spatial scales. eDNA signals also aligned with established rocky shore ecological patterns, with higher diversity and more taxa observed at lower shore positions, reflecting the limiting effects of environmental extremes in harsher high shore zones. Regionally, detections of cold-water species increased with latitude, while warm-water species declined with latitude. Our work supports emerging evidence that eDNA has strong potential for multi-scale biodiversity monitoring, even in dynamic marine environments. We provide practical recommendations for tailoring eDNA sampling on rocky reefs and integrating the method alongside existing routine ecological monitoring. These insights contribute to the advancement of biodiversity monitoring in temperate marine systems under a changing climate.

Ms Buffy Smith

Title: Comparing the iDNA and airDNA sampling methodology for biodiversity monitoring in fragmented forest landscapes.

Abstract: Environmental DNA (eDNA) presents a scalable and cost-effective alternative to traditional biodiversity monitoring methods, with invertebrate-derived DNA (iDNA) and airborne DNA (airDNA) offering non-invasive approaches to detecting terrestrial vertebrate diversity. This study compares the temporal and spatial sensitivity of iDNA and airDNA for biodiversity assessments in fragmented forest landscapes. We conducted laboratory tests to evaluate the temporal persistence of DNA in each medium, using blowflies fed on brown bear scat and test chambers inoculated with aerosol DNA. DNA degradation was monitored via qPCR to determine detection probability over time. Additionally, we assessed the effectiveness of airDNA and iDNA for biodiversity monitoring by comparing community evenness, species richness, and Shannon diversity obtained from 20 forest fragments in Madagascar's eastern forest belt. Our results indicate that airDNA is less temporally sensitive than iDNA, with detectable DNA persisting for up to 60 hours compared to just 20 hours in iDNA. iDNA exhibited greater spatial sensitivity, suggesting its suitability for fine-scale alpha diversity measurements. Despite these differences, no significant variation was found between methods in diversity, richness, or evenness, indicating that both approaches are effective for beta diversity assessments and broad species coverage. We conclude that while airDNA sampling is more reliable and temporally persistent, iDNA offers finer spatial resolution. A combined approach using both methods could enhance biodiversity monitoring strategies, particularly in fragmented landscapes where species detection remains challenging.

Dr Karen Tait

Title: Comparison of matching morphological and molecular zooplankton time-series data: Strengths, weaknesses and recommendations for integration of molecular data alongside traditional zooplankton monitoring

Abstract: There is currently intense research interest in developing environmental DNA (eDNA) approaches for ecological monitoring. This is especially attractive for understanding changes in plankton, given the declining taxonomic expertise and funding for traditional microscopic analysis of net samples. However, the methods are different, and few studies have intercalibrated over long time periods. The Plymouth L4 shelf site offered an excellent opportunity to compare weekly (415 samples over 11 years) sampling of eDNA alongside nets analysed by microscopy. While the eDNA detected more taxa (427 amplicon sequence variants) than a trained taxonomist (205 taxonomic units), a few major groups present in the nets (e.g. euphausiids and salps) were missed by eDNA. The eDNA and nets often tallied remarkably well for major taxa (including holoplanktonic crustaceans, cnidarians, ctenophores and chaetognaths). Conversely, meroplankton and some of the rarer taxa corresponded very little between the two sampling methods, either in relative dominance or inter-annual occurrence. The common theme, however, was far greater meroplankton diversity in the eDNA, data which helps towards understanding the long-standing question of why meroplankton are increasing at the expense of holoplankton. Net sampling misses these small, delicate, or gelatinous zooplankton and many are hard to identify. Molecular data showed increases over the last decade were driven by the larvae of soft seabed fauna, with increases to Polychaeta specifically driven by increases to meroplankton produced by suspension feeding adults. Our data highlights that the two methods are highly complementary and should be combined for a more holistic understanding of zooplankton.

Dr Joe Taylor

Title: Past, present and future perspectives on integrating DNA monitoring into one of the longest-running freshwater lake time-series

Abstract: The lakes of the UK's Lake District are among the most extensively studied in the world, with Lake Windermere currently at the centre of public concern due to its nutrient status and recurring algal blooms. While monitoring has taken place since the 1940s, recent advances in environmental DNA (eDNA) analysis have provided an unprecedented view of lake biodiversity. Over the past four years, eDNA has been collected alongside traditional biological and chemical data, generating insights into multiple taxonomic groups (phytoplankton, zooplankton, protists, fungi, bacteria, diatoms) and revealing previously hidden biodiversity. DNA-based monitoring has also been conducted across 20 other lakes in the Lake District, offering critical insights into nutrient dynamics and the identification of bioindicator taxa. This work provides an overview of DNA research to date, demonstrating how archived materials (Lugol's-preserved and formalin-fixed samples) and sedimentary DNA can reconstruct past communities and their responses to environmental change, with implications for predicting future lake dynamics in response to anthropogenic change. The presentation will also address key challenges and potential solutions for integrating DNA techniques into long-term monitoring programmes, ensuring these methods complement and enhance traditional ecological assessments.

Dr Amy Thorpe

Title: National-scale biogeography and function of river and stream bacterial biofilm communities

Abstract: River biofilms support diverse microbial communities that form the foundation of aquatic food webs and drive biogeochemical cycles. However, despite their ecological importance, the taxonomic and functional diversity of river biofilm communities and their responses to environmental change across large spatial scales is poorly understood. To address this, we conducted the first national-scale metagenomic assessment of microbial diversity and function in river and stream biofilms. We recovered 1,014 metagenome-assembled genomes (MAGs) from 450 biofilms collected across England's river network, revealing substantial taxonomic novelty, with ~20% of the MAGs representing novel genera. We demonstrated that biofilm communities, dominated by generalist bacteria, exhibit remarkable functional diversity and metabolic versatility, and play a significant role in nutrient cycling with the potential for contaminant transformation. Environmental factors, most notably geology, land cover, and nutrient availability, explained up to 90% of the variation in community composition. These findings highlight the importance of river biofilms and establish a foundation for future research on the roles of biofilms in ecosystem health and resilience to environmental change.

Dr Kate Wade

Title: UK Marine Monitoring: Working together to enable uptake of biomolecular techniques

Abstract: Interest in employing biomolecular techniques, in particular eDNA, for marine habitats has grown rapidly over the past years, however, there have been limited opportunities for marine stakeholders to come together to discuss and share progress. Whilst there is much to be learnt from across ecosystems, marine ecosystems do pose additional questions not currently addressed by other fora. In September 2024, the Joint Nature Conservation Committee (JNCC) established the UK Marine Biomolecular Group (UKMBG) to provide a forum to facilitate discussions and progress ideas to actions. The UKMBG provides a valuable space for those interested in operationalising biomolecular techniques for marine monitoring to 1) share updates on work, 2) identify and prioritise gaps in our knowledge base and 3) seek to work collaboratively to fill these gaps with the potential for collaborative funding bids to develop resource. In March 2025 a workshop saw 38 people from across 27 organisations gather to share current knowledge and challenges on the use of biomolecular methods for marine monitoring, and to discuss and identify key barriers to the uptake of biomolecular methods, developing shared ambitions and actions to enable the application of biomolecular methods within marine monitoring. Key themes identified included communication, coordination, standardisation and guidance, resources and data sharing. This presentation will share details of the key outputs from the workshop, progress to date and future plans.

Mr Jono Warren

Title: Microbial biofilms as indicators of environmental change in English rivers.

Abstract: For over a decade the Environment Agency has been developing DNA based methods for monitoring freshwater ecosystem health. Having developed metabarcoding approaches for the assessment of diatoms in rivers and fish in lakes, focus has now shifted from higher organisms to the recognition of microbes as potential bioindicators of ecosystem health. Microbes play important roles in freshwater ecological processes however, understanding of the environmental drivers that shape their distribution is poor and have not part of routine biomonitoring. Our aim is to enhance understanding of the distribution of microbes, their functional roles and contribution to ecosystem health and resilience. Over time this work could lead to the development and integration of new microbial bioindicators into monitoring programmes to guide more targeted management interventions. We generated a national-scale, metabarcoding dataset capturing the diversity of bacteria (16S), fungi (ITS), phytobenthic algae (rbcL), and microeukaryotes (18S) in over 1642 freshwater biofilm samples, at 699 sites from rivers across England. Landscape characteristics and pressures were identified and mapped using monthly co-located water quality data and spatial datasets of types of landcover. Traditional statistical approaches and random forest regression modelling was applied to the dataset. We will present results of the environmental impacts of pressures on the overall microbial community as well as preliminary results identifying potential microbial bioindicators of specific environmental pressures. We also highlight ongoing areas of data exploration: trends in microbial biogeography, the distribution of pathogens and antimicrobial resistance and linking functional genes and genomes with ecological processes and environmental variables.

Dr Tom Wilding

Title: eDNA2IQI – the first regulatory approved eDNA-based monitoring tool in the UK

Abstract: Scottish farmed salmon is the UK's largest food export sector with a turn-over in excess of £700M. Like any industry, fish-farms alter their receiving environment, and operators are required to assess the seabed condition around their sites towards the end of every production cycle to ensure their environmental impacts are within consented limits. Traditionally, impact assessment is via the analysis of macrobenthic assemblages, used to determine the infaunal quality index (IQI), that characterises farm-proximal sediments. IQI determination is expensive and time-consuming and results are often only available after the site has been harvested, preventing active management. We developed an eDNA-based machine-learning model to predict IQI. Our 'eDNA2IQI' R-package, with sample collection/wet-lab standard operating procedure, extends our previous screening tool model. eDNA2IQI enables users to input bacterial sequence data (fastq) which are then quality checked, and subsequently used to predict the IQI based on 30 independently trained and optimized random-forest models that have been trained on >850 samples taken across the fish-farming sector. Our results show a high degree of congruence between predicted and actual IQI as demonstrated on six full-transect site exemplars. This allows more cost-effective and near real-time assessment of environmental impact enabling superior site management and potentially enhanced regulatory compliance. During this talk I will highlight the challenges and opportunities of embedding eDNA-based monitoring into regulatory and industry sectors and detail how we are taking our model forwards to address other aquaculture impact-related questions.

Professor Douglas Yu

Title: High quality, granular, timely, trustworthy, and efficient vertebrate species distribution data across a 30,000 km^2 protected area complex

Abstract: The Kunming-Montreal Global Biodiversity Framework (KMGBF) needs copious data on species distributions to achieve its targets. However, generating such data at scale remains challenging, impeding effective management and oversight. We used aquatic eDNA metabarcoding to sample vertebrate species across the 30,000 km^2 Gaoligongshan protected-area complex that borders the China-Myanmar border. In just 33 researcher-days, we detected 397 non-human vertebrate species, including 35 Red-Listed species. We introduce the eDNA-aware' OccPlus occupancy model, which accounts for both false-negative and false-positive error, and we recover known species distributions and biogeographic patterns and also find that wild species have higher occupancies inside protected areas while domesticated and non-native species have higher occupancies outside them. In contrast, conventional multi-species occupancy modeling predicts wild species to be distributed widely across Gaoligongshan; this overprediction appears to result from letting rare species borrow information from abundant species, which have different ecologies. In contrast, OccPlus leverages the taxonomic breadth of eDNA datasets by using ordination to estimate species occupancies. Our study demonstrates how eDNA metabarcoding provides a scalable method for obtaining high-quality, granular, timely, and trustworthy species distribution data.

Speed talks

Dr Nadia Barsoum

Title: Comparing different sources of eDNA (water, soil, air, woodland surfaces) for forest mammal detection

Abstract: A wide variety of methods for surveying terrestrial mammals have been developed, including conventional live traps, line transects, thermal imaging, camera traps and track and sign surveys. However, these methods can be invasive and are typically time-intensive, leading to high associated costs per unit sample effort. Environmental DNA (eDNA) shows promise as an alternative method, with some published studies emerging showing that it can detect more terrestrial mammal species at lower costs compared to conventional methods. Forest Research has been trialling forest mammal detection using a range of eDNA sampling methods and comparing these to camera trapping datasets in the same forest areas. Sampling using eDNA metabarcoding approaches have included sampling forest pond water, forest soils, woodland surfaces (standing or fallen trees, stacked logs), vegetation and air samples. Repeat sampling was conducted for all of these sampling methods. The overall number of taxa detected was highest using the woodland surfaces sampling methods. Subterranean mammals (moles) were only detected in soil eDNA samples. Similar mammal species were detected in soil and water samples, with fewer water samples needed to detect the same number of species.

Dr Claire Carvell

Title: DNA barcoding of a national citizen-led time series from the UK Pollinator Monitoring Scheme reveals potential for large-scale insect community biomonitoring

Abstract: Insect samples generated from the UK Pollinator Monitoring Scheme (PoMS) offer novel opportunities to describe UK insect communities and answer longer-term monitoring objectives. In this study we tested the efficacy of the high-throughput individual DNA barcoding pipeline employed on the BIOSCAN project to sequence nearly 10,000 specimens collected in pan traps from across 4 PoMS sites over six years. We employed expert morphological identification on a subset of specimens, including from the hyperdiverse insect groups referred to as dark taxa (eg. the parasitoid wasps and very small flies), to validate existing taxonomy, improve on the taxonomic resolution achieved through existing reference databases and contribute useful new information to DNA databases. Thirdly, we generated a series of DNA-based metrics associated with the abundance, richness and diversity of DNA sequences from our dataset, and compared these to manually-derived measures from the same samples, to investigate the utility of DNA-based biomonitoring for analysing changes in insect community assemblages over time and at scale.

Dr Henrik Cornelisson van de Ven

Title: Establishing a National eDNA Framework in the Netherlands – Insights from the First Dutch National eDNA Workshop

Abstract: Environmental DNA (eDNA) is transforming biodiversity monitoring, ecological research, and regulatory compliance. While well-established in water and soil, the Netherlands is now working toward an integrated national approach covering air, water, soil, and surface domains. The first Dutch National eDNA Workshop brought together experts from academia, industry, and government to address challenges in standardization, infrastructure, and regulatory adoption. Key outcomes included a national roadmap for eDNA, focusing on network development, funding, and community alignment, and discussions on harmonizing methodologies and integrating eDNA into decision-making. The workshop concluded with the formation of the Dutch National eDNA Working Group, which will lead these efforts and organize a second workshop on stakeholder engagement and policy integration.

Professor Lorna Dawson CBE

Title: SCAnDi - Single-cell analysis in forensic science: a collaborative approach to addressing DNA identification

Abstract: The analysis and evaluation of evidential samples arising from multiple contributors remains a significant hurdle in forensic science, often requiring computational deconvolution of the mixed DNA profile after it is generated. The Single-Cell Analysis for DNA identification collaborative project brings together expertise in single-cell genomics, microfluidics and AI with forensic researchers and stakeholders from across

the criminal justice scene system to explore how single-cell approaches may be used in forensic casework. We are using single-cell approaches to isolate and amplify individual cells to address low-cell-number samples and study DNA transfer and persistence and link cell-of-origin information with the DNA profile of the same cell. This information could be critical in deconvoluting complex mixed samples, potentially ascertaining where a DNA molecule came from, when it was transferred and by whom. We are developing AI-based approaches to classify cell types based on imaging data acquired during cell sorting, e.g. sperm cells and seminal/vaginal epithelial cells, enabling linkage between cell-of-origin. We aim to also apply to samples of human and non-human DNA profiles, such as in soil or dust for future impact. In this presentation, we provide an overview of the project, vital roles of collaboration and cooperation with stakeholders, promising initial findings and anticipated outcomes.

Dr Kate Denton

Title: Beyond Detection: Deriving Ecological Insights from Terrestrial airDNA

Abstract: The invisible world of DNA floating through our air represents an unprecedented opportunity to revolutionise terrestrial biodiversity monitoring. While environmental DNA (eDNA) methods have gained traction in aquatic monitoring, the application and interpretation of airborne DNA (airDNA) opens new windows into understanding terrestrial ecosystems. NatureMetrics' airDNA technology demonstrates a power to capture material across taxonomic and ecological boundaries, revealing dimensions inaccessible to traditional monitoring techniques. Beyond generating species lists, airDNA data illuminates functional relationships and ecological associations between organisms. These molecular snapshots differentiate community compositions between habitats, revealing patterns that indicate ecosystem resilience, functional redundancy, and vulnerability. By simultaneously capturing diverse taxonomic groups—from microorganisms to invertebrates and to vertebrates—airDNA provides integrated insights into ecological networks that underpin ecosystem processes. This approach offers new opportunities to analyse multiple ecological complexities from single samples, helping to address challenging questions in terrestrial monitoring. airDNA enhances our capacity to understand not only species exist in terrestrial systems but providing additional context about their ecological relationships—creating new pathways to monitor and protect biodiversity across landscapes.

Dr Vera Fonseca

Title: Leveraging eDNA tools for assessing marine diversity: from microfauna to fish

Abstract: Environmental DNA (eDNA) and environmental RNA (eRNA) have transformed marine biodiversity monitoring, offering non-invasive methods to detect species from microfauna to macrofauna, including fish. These tools provide valuable insights into marine ecosystem diversity and status. This talk will explore the use of eDNA, eRNA, and traditional techniques such as trawl surveys and acoustic methods to assess marine diversity across various trophic levels. CEFAS' initiatives (national and international programmes of work) have advanced the application of eDNA in diverse marine environments. Some, integrating eDNA with trawl and acoustic data to enhance species detection and biodiversity assessments. This presentation will attempt to highlight how these combined methods could improve our ability to monitor marine ecosystems and detect changes in biodiversity. We will aim to discuss the challenges and successes of these projects/ data, focusing on the benefits of integrating eDNA with traditional monitoring approaches. Opening discussions on how to move forward with eDNA existing data, experimental design and harmonisation.

Dr Tom Gibson

Title: Environmental DNA Metabarcoding for Biodiversity Monitoring of Ascension Island MPA

Abstract: The deep sea, below 200m, is the largest ecosystem on Earth. Although relatively pristine, the biodiversity within this region is increasingly threatened by industrial fishing, sea floor mining, and climate change. In 2019, the Ascension Island Government designated 445,000 km² of the waters around the island, 95% of which are below 200m, as a Marine Protected Area. Monitoring the biodiversity of such a vast area is challenging, and eDNA is one potential method. However, the application of eDNA metabarcoding to monitor deep sea fish and invertebrate communities is currently understudied. This study aimed to utilize eDNA to characterize teleost and invertebrate communities, assessing the potential effectiveness of eDNA as a monitoring tool for the Ascension Island MPA. In 2022, eDNA was collected as part of a multidisciplinary habitat characterization survey of the MPA. Water samples were taken at multiple stations at seven depth layers up to 3000 m deep and subjected to two metabarcoding assays using 12S rRNA and 18S ribosomal

markers for fish and invertebrates, respectively. Our results revealed the presence of numerous deep-sea and oceanic fish species, including Lantern Fishes and Bristlemouths, as well as a diverse array of invertebrate taxa, such as Copepods, hydrozoans, and thaliaceans. These findings demonstrate that eDNA can detect species and family-level biodiversity. The ecological analysis of how sampling depth influences eDNA assemblages will be presented, along with lessons learned, to inform the application of this technology for MPA monitoring in the open sea.

Dr Manisha Gupta

Title: On-site diagnostics for food borne pathogens

Abstract: On-site diagnostics for foodborne pathogens play a crucial role in safeguarding public health and ensuring food safety. Rapid detection methods for pathogens such as Salmonella, Escherichia coli, and Listeria at critical points in the food supply chain can prevent contaminated products from reaching consumers. These methods also facilitate faster shipment releases at border control points, promoting smoother trade. Within PATH-SAFE WS3a, Fera scientists explored on-site diagnostic technologies in two phases. In the first phase, a horizon scanning literature review identified promising technologies for foodborne pathogen detection. These technologies were evaluated using a customised Technology Readiness Level (TRL) framework to select technologies suitable for real-world piloting. Stakeholder interviews further identified practical applications within the food sector. Two technologies were chosen for pilot studies: portable real-time PCR for detecting E. coli in irrigation water, tested by agronomists and farmers, and LAMP for Salmonella detection in high-risk foods at ports, conducted by Port Health Authority officials. Laboratory validation established full testing procedures, including sample preparation, DNA extraction, and molecular assays suitable for non-laboratory environments. Technology transfer to end-users involved training and on-site testing. The performance of these technologies was evaluated through user feedback, assessing feasibility and identifying implementation challenges. In second phase of WS3a, recommendations for the development and implementation of on-site diagnostic tests for detecting foodborne pathogens were developed. A deployment readiness level (DRL) framework was designed that provides a roadmap for test developers to determine if a test is fit for purpose.

Dr Kirsten Harper

Title: In Search of the eDNA Bounty: Uncovering Marine Biodiversity in the Mutineers' Seas

Abstract: The Pitcairn Islands, a UK Overseas Territory, is the 12th largest Marine Protected Area (MPA) on Earth. Located in an isolated area of the Pacific, the MPA covers 841,910 square kilometres which includes an Exclusive Economic Zone as well as the territorial seas of Pitcairn, Henderson, Ducie, and Oeno Islands. The MPA is one of the most pristine ecosystems on the plant with approximately 1,249 identified marine species, including five endemic fish species: Henderson squirrelfish Sargocentron megalops, Henderson triplefin Enneapterygius ornatus, Pitcairn sandlance Ammodytoides leptus, many-spined butterfly-fish Hemitaurichthys multispinosus, and an undescribed species of combtooth blenny Alticus sp. Given the MPA's isolated location, environmental DNA will enable baseline biodiversity data to be rapidly generated against which future changes can be measured. In February 2023, a total of 58 1L water samples were collected from three sites (Adams Seamount, Henderson Island and Oeno Atoll) at five depths (2, 30, 60, 120 and 200m), while in February 2024 a total of 28 1L water samples were collected from three additional sites around Pitcairn Island (Bounty Bay, Down Rope, and Matt's Rocks) at three depths (30, 60, and 120 m). Six primer pairs covering four gene regions (12S, COI, 16S and 18S) were used to characterise biodiversity present. Results indicate communities differ between sites and depths due to species' life histories, while preliminary results indicate that there is high overlap in species detected by eDNA analysis and Baited Remote Underwater Vehicles (BRUVs).

Dr Caroline Howard

Title: Tree of Life Update: after 2000 genomes the Genome Engine matures

Abstract: The Tree of Life programme at the Wellcome Sanger Institute has created a genome engine - a pipeline that generates reference-level genome assemblies for eukaryotic species. Since 2019 work has been in progress to enable all parts of this engine, to optimise and streamline data generation, and genome assembly & curation for species spanning a broad sampling of biodiversity. Currently, over 2,000 chromosomally-resolved assemblies have already been released and data are in place for the assembly of

over 2,000 more. The laboratory protocols used to facilitate this have been made available via protocols.io and efficient pathways to data production embedded. These are described here, along with the different workflows we have developed to successfully process a wide variety of species, covering plants, fungi, chordates, protists, arthropods, meiofauna and other metazoa for sequencing. These genomes and the data generated to provide them are made available publicly through INSDC and are also accessible via a suite of online portals, each of which is described. Applications of these data are described, along with some of our more surprising findings. The community as a whole are invited to use these data, provide feedback as to their usefulness in their fields of expertise, and consider what we can do to enable the full incorporation of these data. The Genome Engine is now a well oiled machine and we welcome taxonomic experts, researchers, Agencies and others to provide samples for which knowledge of the full genome sequence would benefit their work.

Dr Briony Jones

Title: Leveraging public genomic data repositories for microbial modelling and Soil Health Bioindication

Abstract: Public DNA repositories consist of vast quantities of microbial marker gene data obtained from soils capturing broad geographical coverage. Yet these repositories remain an underutilized resource for the purposes of molecular data synthesis as well as the development of bioindicators for Soil Health. Coupling genomic data with associated information on soil and environmental measures is essential to answer environmentally relevant questions using public data sources. Here we develop a querying pipeline between the three International nucleotide database collaboration (INSDC) databases (ENA, SRA and DDBJ) and their associated environmental metadata repositories (Biosample databases). We assess the availability and accessibility of soil microbial genomic data and soil health metrics (pH, organic matter and salinity) to derive key soil health indicators as part of the EU HORIZON project AI4SoilHealth. We highlight methodological variation (e.g primer type, marker gene region and sequencing platform) within publically deposited soil datasets and the need for effective data harmonization and synthesis. Finally, we emphasize the potential of applying previously developed predictive taxonomic response modelling approaches to publically available microbial data to derive continental or global scale soil health indicators.

Miss Milly Jones

Title: More than presence-absence; modelling (e)DNA concentration across time and space from qPCR survey data

Abstract: Environmental DNA (eDNA) surveys offer a revolutionary approach to species monitoring by detecting DNA traces left by organisms in environmental samples, such as water and soil. These surveys provide a cost-effective, non-invasive, and highly sensitive alternative to traditional methods that rely on direct observation of species, especially for protected or invasive species. Quantitative PCR (qPCR) is a technique used to amplify and quantify a targeted DNA molecule, making it a popular tool for monitoring focal species. Modelling of qPCR data has so far focused on inferring species presence/absence at surveyed sites. However, qPCR output is also informative regarding DNA concentration of the species in the sample, and hence, with the appropriate modelling approach, in the environment. We introduce a modelling framework that infers DNA concentration at surveyed sites across time and space, and as a function of covariates, from qPCR output. Our approach accounts for contamination and inhibition in lab analyses, addressing biases particularly notable at low DNA concentrations, and for the inherent stochasticity in the corresponding data. Additionally, we incorporate heteroscedasticity in qPCR output, recognizing the increased variance of qPCR data at lower DNA concentrations. We validate our model through a simulation study, comparing its performance against models that ignore contamination/inhibition and variance heterogeneity. Further, we apply the model to a case study involving aquatic species surveys in the UK. Our findings demonstrate improved accuracy and robustness in estimating DNA concentrations, offering a refined tool for ecological monitoring and conservation efforts.

Mr Sotiris Meletiou

Title: Using eDNA to Detect the Presence of Critically Endangered European Eel in Highly Impacted Freshwater Systems of the Eastern Mediterranean Island of Cyprus

Abstract: The European eel (Anguilla anguilla) is critically endangered, with severe population declines across its range. EU legislation mandates Eel Management Plans (EMPs) for conservation, yet Cyprus has been

exempt due to a lack of data. The island's freshwater systems are heavily modified, with dams constructed primarily for water supply, potentially restricting eel migration. To address this gap, we conducted eDNA surveys in both winter and summer across diverse freshwater habitats, assessing seasonal variation in eel presence and the use of summer refugia. Our findings confirmed eel distribution in high-elevation catchments and even within reservoirs, challenging previous assumptions about their absence in these systems. Subsequent multi-method surveys, revealed the presence of all life stages, indicating a more established population than previously recognised. These results provide important evidence to support the future development of an EMP for Cyprus, aligning with broader European conservation efforts. Further research will focus on population genetics to investigate potential structuring within Mediterranean eel populations and question the long-standing assumption of panmixia.

Dr Lindsay Newbold

Title: Using environmental DNA (eDNA) from leaf washes, to measure changes in arboreal microbial populations linked to host species.

Abstract: Forests, woodlands and trees are an integral component of the Earth's biogeochemistry and are estimated to harbour 80% of the world's terrestrial biodiversity. Crucial to understanding the impacts of climate change upon our existing forest ecosystems, are an understanding their associated arboreal communities. Yet, inventories of these communities can be time taking and requires expert knowledge. Emerging molecular technologies have advanced methodologies for organism detection, quantification, and monitoring yet the much of existing work focuses upon limited taxa. This study presents a new sampling methodology for the environmental DNA (eDNA) of leaf dwelling arboreal communities on two tree species; The English Oak (Quercus robur) and Scots Pine (Pinus sylvestris). Through the use of multi-kingdom taxonomic markers this study demonstrates that microbial communities are distinctly linked to their source tree species. eDNA derived from Q. robur leaves suggests a higher diversity of invertebrate species than on P. sylvestris, yet our data would indicate that bacterial and fungal diversity was higher in P. sylvestris needles. In this study we suggest that multi-kingdom monitoring of arboreal communities through their eDNA, would act as a rapid and cost-effective way of monitoring arboreal communities. When eDNA inventories of invertebrates are combined with those of rapidly changing and sensitive microbial communities such approaches will enhance our understanding of forest ecosystem response to climate change.

Dr Ben Price

Title: Using environmental DNA (eDNA) from leaf washes, to measure changes in arboreal microbial populations linked to host species.

Abstract: This talk will outline the current state of UK DNA reference libraries reflecting on the progress since UKBOL's initiation in 2020 and next steps.

Dr Tamara Schenekar

Title: Monitoring terrestrial vertebrates in savanna ecosystems using environmental DNA of waterholes: Insights from eDNA metabarcoding and camera trapping

Abstract: Environmental DNA (eDNA) metabarcoding of waterhole samples offers a promising method for monitoring terrestrial vertebrates in semi-arid and arid ecosystems, such as the southern African savannas. However, little guidance exists on key sampling design parameters. The first part of this study investigated the effects of sampled substrate, sampling season, and metabarcoding primer pair on species richness and taxonomic group detection of vertebrates, using eDNA samples from waterholes in Botsalano Game Reserve, South Africa. A total of 725 eDNA samples were collected from 94 sampling events across wet and dry seasons, detecting 95 species (45 birds, 42 mammals, 4 amphibians, 3 reptiles, and 1 fish). Based on the received results, we propose recommendations for optimizing eDNA metabarcoding study designs in similar systems, such as substrate choice or sampling season, and discuss potential sources of false positives, including secondary eDNA input, incomplete genetic reference databases, and low genetic resolution of metabarcoding markers. In the second part of this study, camera traps were deployed in parallel to eDNA sampling to document mammal visitations events, their behavior, and interactions with the waterbody. The combined dataset of camera trapping and eDNA enables a quantifiable comparison between those two monitoring approaches and provides preliminary insights into how animal behavior at waterholes influences eDNA shedding rates.

Dr Connor Scott

Title: Sampling airborne fungal DNA to investigate ectomycorrhizal colonisation of former agricultural land

Abstract: To achieve the ambitious UK goals of new woodland creation it is likely that former low-grade agricultural land will be utilised. However, the history of physical and chemical alterations often means that these soils are highly disturbed and potentially lacking in many of the woodland rhizosphere microbial communities that typically support tree establishment, health and growth. Ectomycorrhizal (EcM) fungi form vitally important symbiotic relationships with many UK woodland species; they provide access to nutrients and protection against pathogens and drought in exchange for photosynthetically captured carbon. Yet, the ability of EcM fungi to colonise the roots of trees on former agricultural land is not well understood. Sampling airborne fungal DNA has emerged as an alternative method for capturing fungal diversity and is particularly advantageous in the context of fungal colonisation due to the capture of reproductive spores. The fungal spore profiles at the boundary between an established woodland and former agricultural land were investigated through metabarcoding of the airborne fungal eDNA captured on filters attached to air sampling vacuum units. At the same locations, above-ground sporocarps were sampled and classified based on morphology and with metabarcoding to compare the communities of spore dispersing structures with the airborne presence of their reproductive cells. Additionally, profiling both these communities at four time points throughout autumn allowed temporal variation in fungal communities to be investigated at the frontier between woodland and former farmland. By exploring these increasingly ecologically relevant gradients with sampling techniques that depict dispersal, the ability of EcM fungi to colonise new disturbed environments will be elucidated to educate the process of former agricultural land afforestation.

Dr Margaux Steyaert

Title: Linking ARMS: comparing Autonomous Reef Monitoring Structures (ARMS) and eDNA methods for cryptobenthic reef studies

Abstract: Coral reef cryptobenthic communities are intrinsically linked to complex but fragile reef matrix. To limit the impact of scientific exploration of such communities, non-destructive sampling methods are vital. Benthic image analysis, Autonomous Reef Monitoring Structures (ARMS) and environmental DNA (eDNA) are three ways to non-destructively sample the cryptic coral reef, but communities retrieved from each method have yet to be critically compared. Here, we determined the extent of genetic overlap between ARMS and ambient seawater using community and eDNA multi-marker metabarcoding, across two reefs of the Chagos Archipelago Marine Protected Area (MPA) (Central Indian Ocean). Additionally, we investigated how sessile recruitment and diversity patterns on ARMS compare with those on in-situ dead Acropora sp. tabular coral using image-analysis. As expected, we find that communities across ARMS and eDNA samples recovered using metabarcoding are different, and that more cryptobenthic taxa are detected within ARMS communities. More importantly, we show how eDNA can increase the number of cryptobenthic taxa detected from in-situ reef communities, and when integrated with ARMS, provide a valuable tool for the detection of key sessile groups such as sponges. Findings from our image analysis highlight how ARMS may bias or under-report the recruitment of certain groups (including fleshy and crustose coralline algae, bryozoans, and calcified tube worms), whilst accurately reflect abundance patterns of others (brown algae, sponges, bivalved molluscs) found on natural reef substrate. Our findings show that non-destructive methods can be powerful analysis tools for recovering patterns of cryptobenthic abundance and diversity across reef ecosystems and highlight the importance of combining image and DNA-based approaches for studying cryptobenthos. With artificial materials, such as ARMS, increasingly used to survey and monitor marine benthic ecosystems across the globe, studies comparing and ground truthing associated analysis methods are warranted.

Dr Salla Vartia

Title: PINKTrack - an EU-wide eDNA surveillance programme for pink salmon

Abstract: PINKTrack programme is an EU-wide, coordinated environmental DNA (eDNA) surveillance programme for pink salmon. The spread and establishment of non-native pink salmon in the North Atlantic is an emerging threat to native Atlantic salmon which is a species with a huge social, economic and cultural value in the EU and the wider North Atlantic region.Native to the northern Pacific, pink salmon has been introduced outside its range throughout the 20th century, including the White Sea basin of North-western

Russia. Since 2017, pink salmon has been observed in the northern Atlantic all throughout the range of the Atlantic salmon. Due to its two-year life cycle with the odd-year population dominating, most sightings take place in the odd-years. Since 2019, pink salmon has showed exponential population growth in Norway as well as in the White Sea basin of North-western Russia where it has established self-sustaining populations leading to a growing concern that pink salmon will continue to spread and establish populations in the waters of EU member states southward from Norway.The PINKTrack programme aims to develop standardised protocols for eDNA sampling and analyses for the detection of pink salmon. Secondly, the project will use the developed methods to understand the extent of occurrence of pink salmon in EU waters, which will enable it to elucidate temporal and geographic patterns of spread and provide an 'early warning system' of their presence to inform appropriate management responses.

Dr Penelope Watt

Title: Impact of land management on earthworm diversity

Abstract: Soil degradation and erosion is a worldwide problem. Intensive agriculture has led to the loss of soil carbon and a destruction of aggregates, causing drainage issues, flooding and nutrient loss, and, as a result, inefficient crop production. Soil is a living ecosystem, and it is important to understand how to maintain its health and protect it, whilst ensuring it can support crop growth. Earthworms are essential for soil functioning since they improve soil aggregation, water infiltration and carbon stabilisation and sequestration, and build in resilience. They are key soil health indicators, such that an increased presence leads to better plant growth. Conventional monitoring of earthworms involves hand-sorting from soil pits and is highly labour intensive. Furthermore, it can only reliably identify adults and may under-record some species. We compared soil eDNA metabarcoding using two different primer sets and next-generation sequencing, with earthworm hand-sorting from standard soil-pits in a series of arable and ley plots. The eDNA method found the same earthworm species as hand-sorting but had greater power for detecting deep burrowing earthworms and quantifying local species richness. In addition, the leys enhanced earthworm populations depleted by arable farming. Use of eDNA can improve earthworm diversity monitoring and can be used to better understand soil management effects on earthworm populations and to guide agricultural policy decisions affecting soil health.

Dr Laura Weldon

Title: The value of eDNA monitoring data in context: the impact of elevated water chemistry on an inland freshwater European eel eDNA survey.

Abstract: Baseline surveys were completed to assess the present-day distribution of the freshwater European eel (Anguilla anguilla) population in the South west of England. The 46 km2 project area project lies on the Somerset levels, within the Brue valley which also encompasses part of the Avalon Marshes. Traditionally the area supported an abundant freshwater eel population and conservation organisations locally support species recovery efforts. Baseline single species eDNA surveys were undertaken alongside surveys to record barriers to fish movement, evaluate water quality and describe ditch habitat so that subsequent habitat improvements result in quantifiable increases to the inland eel population. A comprehensive data set was generated that described seasonal eel eDNA distribution in the project area. By collecting water samples for the eDNA survey in spring and repeating the survey in late summer. The eDNA data suggests that eel use the ditches and rhynes to move in and out of the project area, retreating to the larger watercourses in summer as water chemistry and the quality of ditch habitats decline. These surveys provide additional context to previous eel eDNA surveys by describing seasonal differences in inland eel distribution, whereby eel eDNA is less frequently detected in summer surveys amongst the smaller ditches and rhynes. It highlights the importance of interpreting eDNA data alongside other ecological data to provide context to the eDNA findings. The data also provides evidence that elevated water chemistry directly affects European eel eDNA distribution.

Miss Anna Wood

Title: Metabarcoding to monitor biodiversity in forest restoration projects

Abstract: Forests cover about one-third of land on earth and provide valuable ecosystem services and habitats for biodiversity (FOA, 2020). Forests and their associated soils can act as carbon sinks with Europe's forests

sequestering about 115 million tonnes of carbon per year, providing possible climate change mitigation (FOREST EUROPE, 2020). However, forest ecosystems are increasingly under threat from anthropogenically driven pressures, and the health of Europe's forests and the biodiversity that rely on them are at risk (Dirzo et al., 2014; FOREST EUROPE, 2020; Muys et al., 2022). The SUPERB project is a large trans-national project funded by Horizon 2020 to restore thousands of hectares of forest landscape across Europe. The success of forest restoration can be judged by collecting biodiversity data to detect changes in communities compared to a "target" or predicted forest ecosystem progression (Gann et al., 2019). Chrono-sequences of forest progression have been determined at six "Demonstration" forests across Europe and are being monitored using metabarcoding and remote sensing.The poster will present the preliminary data produce by SUPERB and ongoing PhD and the goals of the SUPERB project on using metabarcoding to monitor the success of the forest restoration programs using forest chrono-sequences and over 3000 aerial arthropod and soil samples.

Posters

(in alphabetical order)

Ms Meri Anderson

Title: Comparing Bacterial Diversity in UK Rivers Using Short-Read Illumina and Long-Read Pacific Biosciences Sequencing.

Abstract: Accurately characterising bacterial diversity in freshwater ecosystems is crucial for understanding microbial ecology, water quality, and ecosystem health. High-throughput sequencing technologies, such as Illumina short-read and Pacific Biosciences (PacBio) long-read sequencing, offer different advantages in microbial community analysis. In this study, we compared these two sequencing approaches to assess bacterial diversity in 42 river biofilm samples across 7 freshwater sites in the United Kingdom, targeting the 16S rRNA gene. Our findings demonstrate that PacBio sequencing provides higher taxonomic resolution, enabling the classification of taxa that remained unassigned in Illumina datasets. This enhanced resolution is particularly beneficial for biodiversity assessments, as it improves species-level identifications crucial for ecological monitoring. Despite these differences, both sequencing methods produced comparable bacterial community structures in terms of relative taxa abundances, suggesting that sequencing approach does not profoundly affect overall community composition. However, while Illumina offers higher throughput and cost-efficiency, PacBio's ability to resolve complex microbial communities highlights its potential for studies requiring precise taxonomic identification.

Dr Demetra Andreou

Title: Tracking invasive parasites and their hosts: can eDNA be an effective epidemiological tool?

Abstract: Environmental DNA can be a powerful tool in detecting environmental stages of parasites whilst also co-detecting hosts. Here, a specific assay was used to determine the extend of the distribution of the non-native parasite – Sphaerothecum destruens- across two river systems in the UK. Sphaerothecum destruens is a generalist parasite (infects multiple hosts) and in this work the utility of DNA based metabarcoding for determining the host distribution as well as the potential of some hosts acting as reservoirs was investigated.

Professor David Bass

Title: Microbial, holobiont, and Tree of Life eDNA/ eRNA for enhanced ecological assessment

Abstract: Microbial environmental DNA and RNA (collectively 'eNA') originate from a diverse and abundant array of microbes present in environmental samples. These eNA signals, largely representing whole organisms, serve as a powerful complement to signals derived from fragments or remnants of larger organisms. Integrating microbial data into the toolbox of ecosystem assessments and biotic indices therefore has the potential to transform how we use eNA data to under- stand biodiversity dynamics and ecosystem functions, and to inform the next generation of environmental monitoring. Incorporating holobiont and Tree of Life approaches into eNA analyses offers further holistic insight into the range of ecological interactions between microbes and other organisms, paving the way for advancing our understanding of, and ultimately

manipulating ecosystem properties pertinent to environmental management, conservation, wildlife health, and food production.

Ms Eilidh Boa

Title: Application of eDNA techniques for offshore statutory monitoring: pilot work

Abstract: The Joint Nature Conservation Committee (JNCC) plays a pivotal role in delivering scientific advice to the UK governments for Marine Protected Areas (MPAs) located in the UK's offshore waters. Through the UK MPA Monitoring Programme, JNCC collects empirical data to monitor, assess, and understand the health of the UK offshore seabed. The programme aims to detect and monitor change over time in the habitats and features within each MPA, attributing changes to causes where possible, and to assess the effectiveness of current management strategies. Traditional monitoring methods frequently employed include video and still imagery, infaunal grab data and collection of environmental variables. Environmental DNA (eDNA) is emerging as a powerful method for monitoring marine biodiversity and JNCC are keen to understand how we can employ this to enhance our existing offshore monitoring activities. Three eDNA sampling methods were piloted during an offshore survey on the Scottish Continental Shelf in September – October 2024: 1) metaprobes attached to a towed camera sledge, 2) metaprobes towed behind a vessel, 3) water samples collected in Niskin bottles filtered through Sterivex filters. Samples were analysed by a contractor using primers targeting marine vertebrates, fish, and invertebrates. In addition to presenting our results from this survey, we will share and discuss the challenges we encountered from a logistical and technical standpoint, providing recommendations for future work, including for refining methods and reducing contamination risk. We will also explore how we can use eDNA data to complement existing indicators and policy frameworks.

Dr Chiara Borsetto

Title: An advanced platform for quantitative monitoring and management of environmental antimicrobial resistance from eDNA analysis

Abstract: The escalating threat of Antimicrobial Resistance (AMR) across clinical, animal, and environmental settings necessitates the ongoing development of innovative eDNA-based monitoring and management tools for rapid mitigation strategies. As pioneers in AMR SmartChip qPCR service, Resistomap has leveraged advancements in SmartChip qPCR and data science, empowering researchers to investigate the resistome of diverse environments—spanning water, soil, animal manure, etc—through eDNA analysis. To further harness the potential of eDNA data science via Smartchip qPCR, we have developed a cutting-edge Platform for quantitative AMR monitoring and management in aquatic settings. This platform translates AMR gene (ARGs) Smartchip data from eDNA analysis into actionable insights, facilitating longitudinal and spatial tracking of AMR trends across various locations. The Platform features advanced visualization tools for identifying AMR hotspots, pathogen and resistance marker analysis, and indices for monitoring the prevalence of clinically and environmentally significant resistance factors. Indeed, we developed a new standardised metric, the Antibiotic Resistance Gene Index (ARGI), which is key to evaluating and comparing resistance gene abundance across samples. Additional metrics in development include Comparative Risk Assessment Scores and Gene Reduction, designed to assess ARG risks across multiple water environments and gauge the efficacy of interventions or treatments in eliminating ARGs within specific systems. The Platform design ensures its applicability in optimizing AMR management strategies for a broad array of applications and diverse stakeholders. The continued utilization and development of strategic eDNA analysis tools like our Platform will foster cross-sectoral collaborations to deliver comprehensive and sustainable solutions to the AMR crisis.

Dr Susheel Bhanu Busi

Title: Integrating Large-Scale Genomics and Environmental Data Using Cloud-Based Services

Abstract: Integrating large-scale genomics and environmental data is essential for advancing biodiversity monitoring and assessment. However, accessibility and interoperability challenges remain significant barriers to effectively leveraging these datasets. Building on the NERC DataLabs, a cloud-native collaborative analysis platform, we are developing workflow services to process, quality-assure, and integrate national-scale DNA sequencing data from bacterial, fungal, eukaryotic, and plant communities with environmental datasets. By leveraging JASMIN's high-performance computing infrastructure, our cloud-based services will enable seamless access to genomic and environmental data centres. This approach enhances scalability, reproducibility, and adherence to FAIR data principles. However, limitations in accessibility and data

integration present key obstacles. To illustrate this, we highlight these challenges and introduce BOOST as an example of how cloud-based workflows can improve data accessibility, streamline analysis, and facilitate robust biodiversity monitoring. In collaboration with the BBSRC Decode Biodiversity programme and EMBL-EBI this work will support the development of national-scale biomonitoring frameworks, informing policy and conservation efforts. BOOST is a step toward overcoming the current limitations of genomic-environmental data integration, namely, data accessibility and interoperability, including the lack of harmonisation across data analysis methods. By demonstrating the potential of cloud-based solutions, we aim to engage researchers, policymakers, and end-users in shaping the future of DNA-based environmental monitoring.

Dr Lewis Campbell

Title: Whole-Community Microbial Source Tracking: Identifying Sewage Pollution in the River Loddon Catchment

Abstract: Understanding the sources of organic pollution in river systems is critical for effective water quality management. Traditional approaches to pollution monitoring do not routinely distinguish between different pollution sources, precluding targeted mitigation efforts. Whole-community microbial source tracking (WC-MST) makes use of bacterial metabarcoding to determine the bacterial community composition of a river sample. By statistically comparing these microbiome “signatures” with those of potential pollution sources it is possible to determine the origin of organic pollution, and gain a holistic picture of the bacteria present at a given location. In this study, we applied WC-MST to assess the extent sewage-derived pollution in the River Loddon catchment. Forty water filter samples were collected across the catchment. Quantitative PCR was used to measure bacterial load, and high-throughput sequencing identified the full spectrum of bacterial taxa present in each sample. By comparing these communities to reference sewage microbiomes, we determined where human-derived organic pollution was occurring. Our results identified key pollution hotspots, some located near sewage treatment infrastructure and others in areas without known wastewater inputs, suggesting contamination from septic tanks and surface water drainage. These findings demonstrate that WC-MST provides a cost-effective, scalable, and high-resolution method for identifying pollution sources at the catchment scale. This approach enables more informed decision-making for water quality management, facilitating targeted remediation efforts. Our study highlights the potential of WC-MST to revolutionise pollution source tracking and drive evidence-based management for cleaner rivers.

Ms Rachel Coleman Horgan

Title: Using eDNA to monitor a critically endangered coastal skate – the white skate (Rostroraja alba)

Abstract: At least 37.5% of all chondrichthyan species are threatened by human activities, and for coastal species this rises to over 50%. Innovative monitoring approaches are needed to support policy and management, particularly for rare and elusive species which can be undetectable through traditional surveys.The white skate (Rostroraja alba), a Critically Endangered coastal species, has disappeared from much of its former habitats in the Northeast Atlantic. Today, only small populations persist on the West coast of Ireland and Portugal, with potentially isolated groups in the Mediterranean and South Africa. In Ireland, little is known about its current distribution and movement patterns where evidence is primarily gathered through citizen science-led coastal eggcase surveys, and occasional survey captures. This project will develop a species-specific environmental DNA (eDNA) assay to detect white skate. We will evaluate the feasibility of shore-based monitoring, comparing active filtration and passive sampling methods, as well as quantitative and digital PCR techniques. To aid assay design and validation, we will first sequence mitogenomes of local elasmobranchs, then test the assay on control mock communities before applying it to environmental samples collected via metaprobes and 0.45µm Sterivex filters along the Galway Bay coastline.Our overall aim is to produce a non-invasive, eDNA-based tool to monitor this critically endangered species and to help build baseline data for future marine conservation planning in the white skate’s remaining refugia. If successful, this could serve as an important additional tool for monitoring this and for other endangered coastal elasmobranchs across their distribution ranges.

Mrs Clare Collins

Title: Biodiversity monitoring of fish in rivers using eDNA metabarcoding: modelling on the River Severn

Abstract: Community-wide, spatially-explicit biodiversity monitoring is essential in assessing priorities, progressing nature recovery and providing evidence for policy, action and advice. Environmental DNA

(eDNA) sampling of rivers for metabarcoding is a non-invasive biomonitoring tool that is highly sensitive to detect even elusive and rare species. However, the stochastic nature of eDNA and river systems can lead to spatial uncertainty. Using transport models, we explored the effect of decay rate and species location on the eDNA concentration downstream and attempted to predict the signal origin upstream. We also took water samples from the River Severn to explore eDNA concentration in a model area related to species' behaviour, with a particular focus on the twaite shad (Alosa fallax). Here we present results modelled in an idealised system along with eDNA concentration related to predictions from species' behaviour.

Mr Michael Connell

Title: Phytobenthos as a passive collector of eDNA in riverine environments

Abstract: Phytobenthos (benthic algae) plays a crucial role in aquatic ecosystems and is a key biological quality element required for assessment under the Water Framework Directive (WFD). Many European countries, including Ireland, use diatoms (Bacillariophyceae) to fulfil this requirement, as diatoms are a dominant component of phytobenthos, and well-established methods exist for assessing water quality based on their community composition. Traditionally, diatom-based monitoring relies on labour intensive morpho-taxonomic identification using light microscopy. However, advances in high throughput sequencing technologies, particularly DNA metabarcoding, offer new opportunities for more efficient biodiversity assessments in addition to water quality monitoring. Phytobenthos forms a biofilm matrix that may be able to passively capture environmental (e)DNA from other organisms inhabiting the river ecosystem. This raises the potential for phytobenthos-based eDNA sampling to complement traditional methods such as kick sampling and electrofishing. In this study, we will apply DNA metabarcoding to phytobenthos samples collected from forty sites across the Republic of Ireland to assess diatom community composition present and explore the ability of phytobenthos as an eDNA filter for fish and macroinvertebrates. We will compare these results to those obtained from eDNA metabarcoding of water samples, electrofishing surveys and kick net sampling conducted at the same site.

Dr Lauren Cook

Title: Translating eDNA for biodiversity monitoring in policy and practice: stakeholder consultation

Abstract: Recent environmental policies highlight the need for accurate, scalable biodiversity data to inform conservation and resource management. However, monitoring demands often exceed available resources. Environmental DNA (eDNA) offers a promising solution for rapid, cost-effective biodiversity assessment. Considering the urgency of filling biodiversity data gaps, the social process of 'translating' eDNA from research into policy and practice should be proactive and co-developed alongside stakeholders. Through 40 interviews across government, non-profit and private sectors, the challenges and opportunities regarding the ongoing translation of eDNA are determined. Improved communication tools emerged as the top priority for policy integration, with effective storytelling, clear summarisation, and spatial visualisation of results being critical for engaging diverse stakeholders. Standardisation and validation frameworks are highly prioritised by regulators and end-users. In particular, standardising data reporting with universal templates is needed to improve integration across studies. Transitioning to new methods requires substantial resources, and while eDNA methods are cost-effective at large scales, the high cost at smaller scales and the perceived riskiness of investment hinder broader uptake. These findings highlight the necessity of continuous dialogue to integrate eDNA methods appropriately, where methods have reached operational maturity, e.g., as early warnings of invasive and pathogenic species, or as sandbox studies for ongoing development, e.g., for ecological health metrics. This study is anticipated to be a valuable resource for regulators and researchers, providing a roadmap to facilitate the translation of eDNA into policy and practice.

Dr Henrik Cornelisson van de Ven

Title: Catchment area modeling for airborne eDNA

Abstract: Recent regulatory advancements, such as the acceptance of eDNA assays for bat detection in wall cavities, signal growing policy recognition. This presentation outlines the next steps in transitioning eDNA from research to applied decision-making in biodiversity, public health, agriculture, and regulatory compliance.

Dr Phil Davison

Title: Using eDNA surveys to detect marine non-native species in ports and marinas

Abstract: Marine non-native species are largely under-monitored in British waters, hindering early detection of new invaders and mapping of range expansions, so long-term monitoring programmes combining traditional and molecular methods are needed. In 2023 and 2024, we conducted surveys at 19 ports and marinas in England and Wales which directly compared the results of eDNA analysis with Rapid Assessment Surveys (RAS; one-hour expert searches). Three one-litre samples collected from each location during the survey were analysed using both metabarcoding and single-species targeted qPCRs (for six key species of animal and macroalgae). The targeted PCRs proved sensitive for detecting those species at sites at which they were observed during the survey. The metabarcoding detected a wider suite of non-native species than the Rapid Assessment Surveys, including planktonic species, but was outperformed by the RAS for detecting the species which encrust hard substrates (e.g. barnacles, bryozoans and tunicates) for which the RAS methodology is designed. Further analysis of these results demonstrates the potential for molecular methods to complement morphological surveys, but also demonstrates the cautionary approach that would need to be applied if relying on the technique as a stand-alone surveillance method.

Dr Deborah Dawson

Title: Are you an environmental researcher needing help and training in genetic techniques?

Abstract: Are you an environmental researcher needing help and training in genetic techniques? The NEOF Visitor Facility at Sheffield supports UK-based researchers using molecular analyses to answer environmental questions. We provide:

Project-specific expert training and support in wet lab methods;

- Access to all necessary facilities, clean rooms, equipment and free consumables;

- Next-generation sequencing (funded to a maximum of £10k);

- Bespoke training and assistance in data processing, analysis and interpretation.

Researchers (PhD students/technicians/postdocs/fellows) can apply for up to 6 months access to facilities and training. We can advise on project design and technical requirements, if required. Apply any time of year. Applicants do not have to be NERC-funded.

NEOF also funds pilot schemes and provides free training courses in bioinformatics, see https://neof.org.uk/opportunities/

We are always happy to discuss your project, the support you need and new ideas. Questions, general or project-specific, can be submitted via https://neof.org.uk/contact/

Dr Sophie de Becquevort

Title: Effects of preservation methods and storage duration on the effectiveness of non-destructive metabarcoding for arthropod species identification

Abstract: Although Forest Research (FR) uses Lindgren funnel traps and non-destructive DNA metabarcoding in multiple biodiversity assessment projects, protocol adjustments may be needed, and further research is required to validate the benefits of methodological refinements. This project aimed to assess various preservation methods and storage durations for arthropod samples collected in large-scale monitoring programs and processed using non-destructive DNA metabarcoding for species identification. Low and high diversity insect mock communities were assembled using similar proportions of insect orders as is typically recovered in Lindgren canopy traps. Three different preservation methods were tested to evaluate their comparative influence on species detection. These included: (1) absolute ethanol (99.9%) stored at -18°C, (2) 100% monopropylene glycol (MPG) stored at 5°C, and (3) ‘rainwater’-diluted monopropylene glycol (DMPG: 40% MPG and 60% distilled water) stored at 5°C. Samples were stored for 2 weeks, 2 months, and 4 months before non-destructive DNA extraction and metabarcoding. The composition of the recovered communities was significantly influenced by community diversity and preservation methods. Conversely, the effects of storage time and transfer were significant only in samples with low diversity communities, and detection rates varied across species. Overall, the findings align with existing literature and confirm that monopropylene glycol is a promising alternative to ethanol as a fixative and preservative for samples prior to non-destructive DNA extraction and metabarcoding, particularly for short- to medium-term storage at 5°C.

Mrs Ashinsa de Silva Wijeyeratne

Title: Evaluating the Effectiveness of Sodium Hypochlorite for Genomic DNA Decontamination

Abstract: Environmental DNA (eDNA) is an increasingly popular, sensitive, and cost-efficient method for studying biodiversity and detecting species. This non-invasive approach involves collecting environmental samples that contain genetic material shed by organisms into their surroundings. Due to the method's sensitivity, robust decontamination strategies are crucial, with sodium hypochlorite, commonly known as bleach, frequently employed. Despite its widespread use, there is no consensus on the most effective bleach concentration, leading to inconsistencies in how the chemical is used in research. This study aimed to determine the minimum concentration of bleach needed for effective decontamination. Genomic DNA of signal crayfish was treated with various concentrations of bleach, ranging from 0.01% to 5% (w/w). Results were observed using Qubit High Sensitivity reagents, quantitative PCR, agarose gel electrophoresis, and the Agilent TapeStation. Our results indicate that a minimum concentration of 0.5% (w/w) bleach is sufficient to prevent the detection of genomic DNA by the techniques tested. These results provide important insights into the use of bleach for decontamination in eDNA research. Establishing a standard bleach concentration for decontamination protocols will help to reduce inconsistencies and enhance the reliability of eDNA studies.

Miss Rosie Dowell

Title: Using tree-of-life eDNA metabarcoding to investigate trophic changes due to seabird-derived nutrients on coral reefs

Abstract: Environmental DNA (eDNA) metabarcoding has quickly become a common tool for documenting biodiversity and informing the conservation and management of coral reefs. The Chagos Archipelago is a remote no-take marine protected area, situated in the Central Indian Ocean, that provides an opportunity to study coral reefs facing few anthropogenic pressures. This study aims to use tree-of-life metabarcoding of eDNA to assess divergent trophic structuring across sites in the archipelago, and over time. Benthic seawater samples were collected over 4 years and analysed using four metabarcoding assays, targeting bacteria, metazoans, fish, and elasmobranchs (16S, COI, 18S and 12S). Samples were collected above coral reefs next to islands that host healthy seabird populations and those next to rat-infested islands. The reduction of bird derived nutrients due to the presence of invasive rats has been shown to alter fish behaviour, reduce coral growth, resilience to heat stress and fish biomass on these neighbouring reefs. However, studies have yet to explore these impacts on the diversity and structuring of whole reef communities. Here, we investigate biodiversity patterns across major taxonomic groups and functional roles of key taxa, showing that fish, elasmobranch and bacterial communities were found to differ between sites with rats and birds. Further, the was significantly more herbivorous fish and elasmobranch taxa found to be differentially abundant at sites receiving seabird-derived nutrients. This work resulted in a large dataset, already available open access and provides a thorough example of tree-of-life metabarcoding from a hyper diverse environment.

Mr Tim Goodall

Title: Deciphering landscape-scale plant cover and biodiversity from soil eDNA

Abstract: Biodiversity surveys are critical for detecting environmental change; however, undertaking them at scale and capturing all available diversity through observation is challenging and costly. This study evaluated the potential of soil-extracted eDNA to describe plant communities and compared these findings to traditional, observation-based, field surveys. We analysed 789 soil samples using high-throughput amplicon sequencing and compared DNA-based diversity metrics, indicator taxa, predicted vegetation class, and plant cover in a comparison with co-located field survey data. The results indicated that taxonomically aggregated (genus) eDNA-derived data, while showing slightly reduced Shannon’s diversity scores, yielded remarkably similar overall richness and composition estimates. However, the DNA indicator taxa and predictive power for vegetation community classification were also lower overall than those recorded by the field survey. However, in many cases plant cover could be inferred from amplicon abundance data with some accuracy despite widely differing scales of sampling – 0.25 g crumb of soil versus a 1 m2 quadrat. Overall, results from eDNA demonstrated lower sensitivity but were broadly in accordance with traditional surveys, with our findings revealing comparable taxonomic resolution at the genus level. We demonstrate the potential and limitations of

a simple molecular method to inform landscape-scale plant biodiversity surveys, a vital tool in the monitoring of land use and environmental change.

Mr Harry Hosker

Title: Hydrocyclone Filtration: Enhancing Precision in eDNA Research & Application

Abstract: Filter clogging is one of the most frequently reported challenges in environmental DNA (eDNA) sampling, affecting both practitioners and researchers. This issue initially inspired the development of an inline filtration device designed to effectively remove sediment. However, as the project evolved, it became evident that fundamental questions remain about the origins and transport of eDNA—questions that, when answered, could significantly improve sampling efficiency. Questions that, with our developed device, can be investigated. The poster for UKDNAWG25 will cover: The device: What it is and how it works. Development progress: Completed tests, ongoing experiments, and future plans. The broader vision: The long-term goals of the project. Opportunities for collaboration: Areas where input, discussion, and partnerships are welcomed. CURRENT DEVELOPMENT STATUS A field-ready prototype has been constructed, and we are refining a repeatable filtration setup to ensure it is operationally effective across different environments. The device is currently being tested in various field and lab settings to assess its performance, limitations, and potential improvements. CALL FOR COLLABORATION To advance this project, we seek to deepen our understanding of eDNA capture through targeted experiments in both controlled and real-world conditions. We welcome ideas, discussions, and collaborations from across the community—whether in device development, experimental design, or practical application. If you are interested in contributing to this effort, we would love to connect.

Mr Matthew Hulse

Title: Advancing Frog Non-invasive Dietary Analysis with DNA Metabarcoding

Abstract: Dietary analyses are crucial for understanding species interactions, providing insights into ecological networks, competition, resource partitioning, and trophic roles — factors that shape ecosystems and inform conservation strategies. This is particularly important for globally threatened amphibians, which are vital to ecosystem stability and sensitive to change, yet remain poorly understood and lack baseline dietary data. Techniques traditionally used to acquire dietary sampling in amphibians are very invasive, and in many cases even fatal. Faecal samples have become a less invasive alternative which is gaining popularity, albeit with certain challenges (e.g. tiny samples in amphibians, presence of inhibitors, DNA degradation and fragmentation). In addition to these, very little is known and understood about the DNA that is digested and how much it can still be used for biodiversity classification purposes. This project aims to gain a better understanding of amphibian dietary techniques and analyses using faecal samples from captive collections and their controlled dietary sources. Key experiments made on ~100 samples (spanning 3 amphibian families) include comparing sample preservation strategies, optimising extraction methods, assessing degradation, and testing multiple molecular markers for optimal arthropod and invertebrate prey identification. By improving the ability to retrieve dietary DNA from faecal samples, this project aims to establish a practical, non-invasive workflow that aligns with the 3Rs (Replacement, Reduction, and Refinement) principles. The resulting improved methods will be useful in field-based research and it will advance DNA-based methodologies for ecological monitoring while promoting ethical, non-invasive sampling strategies which contributes to the standardisation of dietary analysis techniques.

Dr Laura Hunt

Title: Exploring ecosystem dynamics using ecological network analysis

Abstract: From microbes to invertebrates, interactions within and between different trophic levels are fundamental to ecosystem processes and the delivery of ecosystem services. Approaches from the field of ecological network science are able to identify interactions between taxa and construct networks from ecological data. Different properties of these ecological networks, such as network robustness, complexity, and resilience provide insight into the fundamental structure of ecosystems. However, ecological network science has not been extensively applied to microbial datasets because the interactions between microbes cannot be directly observed, requiring microbial ecological networks to be inferred. New Environment Agency monitoring programmes have utilised DNA metabarcoding approaches to generate a spatio-temporally comprehensive dataset of microbes in biofilms (bacteria, fungi, microeukaryotes, and diatoms) along with

conventional invertebrate community data in English rivers. These data, combined with new advances in techniques for inferring interactions between microbes, provides an exciting opportunity to understand the dynamics of microbial communities and their interactions within riverine ecosystems. Working with leading academics in the field of ecological network science we have explored how we can apply ecological network science to this dataset to understand both microbial communities and wider ecosystem dynamics. Next we aim to begin developing new metrics of ecosystem health and function using these techniques.

Dr Dimitrious Kaloudis

Title: The use of eDNA metabarcoding for monitoring of UK inshore fish: Current challenges and future recommendations.

Abstract: The monitoring of UK coastal fish populations is vital to support sustainable fishing practices and policies, protect coastal ecosystems, and understand the impacts of climate change. However, there is currently a lack of information surrounding their biodiversity and condition, which limits the confidence in management and conservation measures. The current methods used, limit regular monitoring as they are often time and cost intensive; invasive and extractive; as well as species, habitat, and life stage selective. The use of environmental DNA (eDNA) offers a non-invasive, non-selective and potentially cost-effective method to monitor a wide range of fish species. Yet, eDNA is a relatively novel technique and methodologies vary in levels of scientific rigour, transparency, and reporting of results. As part of the Environment Agency's goal to address evidence gaps in the use of eDNA for monitoring UK inshore fish, we performed a UK and metabarcoding focused scoping literature review, the results of which were used to develop a roadmap that lists recommendations for research that is essential for a robust eDNA monitoring plan. Our meta-analyses emphasises that further development of methodologies is vital, as well as a comprehensive understanding of its efficacy compared with traditional methods, particularly in terms of abundance or biomass estimations. Our report highlights a lack of standardisation and best practise guidelines, as well as knowledge gaps in each part of the workflow, from sampling and laboratory processes to bioinformatics and reporting. We recommend actions for further research that will ultimately advance the application of eDNA metabarcoding for fish population monitoring in the UK.

Miss Abigail Mackay

Title: Restoring tidal freshwater zones: The use of environmental DNA to monitor fish communities

Abstract: Upper estuarine tidal freshwater zones (TFZs) are unique habitats which are often overlooked in scientific literature because their distinctive characteristics exclude them from studies on non-tidal freshwater rivers or brackish estuaries (Jones et al. 2020; Little et al. 2022). TFZs could play an important role in the functioning of estuarine and riverine ecosystems by providing trophic subsidies and serving as important habitats for fish species, including those of conservation concern (Pihl et al. 2002). These habitats are under threat from climate change and human intervention (Little et al. 2022; Prandle and Lane 2015). Restoring these zones, particularly their intertidal marshes, could help offset losses while delivering multiple ecosystem benefits. The dynamic nature of TFZs makes monitoring fish communities and habitat use across tidal cycles challenging. Environmental DNA is a promising tool for monitoring estuaries as sampling is non-invasive and requires minimal set-up which makes it easier to identify changes in fish communities throughout the tidal cycle or before and after habitat restoration (Yao et al. 2022). Here we present the findings of a systematic review evaluating how eDNA has been used to survey fish in estuaries, in particular TFZs and the current knowledge of fish presence and habitat use in TFZs in NW Europe. We conclude by providing recommendations for how eDNA surveys can be improved to deal with the issues arising from the transport of DNA in tidal systems.

Ms Lucia Manicom-Smith

Title: Passive colonisation of vital tree fungal symbionts: Assessing the ectomycorrhizal fungal communities on tree roots in commercial nurseries, woodland creation sites and mature woodlands

Abstract: Improving tree establishment success rates is crucial if we are to meet the UK's target to plant 30,000 hectares of new woodland annually by 2050. Much of this woodland will be planted on low-quality agricultural land, which differs significantly from established woodland soils, including in the presence of ectomycorrhizal fungi (EMF). EMF benefit trees by exchanging nutrients found in the soil for photosynthetic compounds, enhancing the success of many commonly planted tree species such as English oak (Quercus

robur) and silver birch (Betula pendula). As part of a wider Fungi4Restor project, we explore the EMF communities colonising tree fine roots in commercial tree nursery settings and how these communities evolve following planting in former agricultural soils using a chronosequence approach. We compare these EMF fungal communities with those on trees in adjacent mature woodland. Metabarcoding revealed significant variation in EMF communities within and across these groups. Notably, drivers of EMF community such as the growing method implemented by commercial nurseries are identified. Our findings offer initial insight into the development of tree-EMF relationships across afforestation stages, and highlight the potential for interventions, such as EMF inoculation or mixed species planting, to enhance afforestation success.

Dr Jelena Mlinarec Novosel

Title: Temporal and Spatial Dynamics of the Lotic Fish Communities: A Comparison of Coffee Filter-Based Passive eDNA Collection Versus Active eDNA Filtering

Abstract: The integration of novel eDNA-based methods into current monitoring practices is not straightforward and require standardization of methodological approaches. We investigated spatial and temporal variation in fish assemblages within two lotic systems in Croatia. Six sampling stations were located alongside the middle section of the river Sava upstream and downstream of Zagreb, and one location in the stream Okićnica. We compared traditional field surveys with two eDNA sampling methodologies: active eDNA filtering and passive eDNA collection. We showed that passive eDNA collection using coffee filters detected fish composition as effectively as active eDNA filtration, providing comparable results in terms of local species richness and spatial variation in fish assemblages. Generally, our eDNA approach detected a greater fish species richness per site than electrofishing. Each single sample captured an average of 18.3 species, from a total of 30 species encountered in the 78 samples. The sites upstream of Zagreb showed significant differences in species read abundance in comparison to the sites downstream. Nonmetric multidimensional scaling (nMDS) plot based on read abundance appeared to be structured according to the type of lotic system, with a clear separation in the two-dimensional space between samples from the river Sava and stream Okićnica and between seasons. A substantial increase in read abundance during spawning periods of certain species was observed, emphasizing the method's utility in unraveling ecological complexities. Altogether, this study exemplifies how eDNA metabarcoding is a powerful tool for community monitoring, providing standardized information that will be valuable for environmental management.

Mr Robert Moise

Title: Exploring DNA-Based Pollinator Detection: A Comparative Molecular Approach

Abstract: Pollinators play a crucial role in maintaining ecosystem stability and biodiversity, yet their monitoring remains challenging due to their mobility and the limitations of traditional survey methods. To address these issues, this study explores the potential of DNA-based techniques for pollinator detection through three complementary approaches: floral water washing, DNA extraction from flowers, and airborne environmental DNA (eDNA). Each method was evaluated for its ability to detect pollinators and other taxa using high-throughput sequencing and metabarcoding. The study was conducted at an urban farm in Dublin, Ireland, where samples were collected from various areas hosting different plant and animal species. By assessing the feasibility and sensitivity of each approach, the findings contribute to the development of non-invasive molecular techniques for pollinator monitoring. These results highlight the potential of DNA-based methods to complement traditional surveys, offering a scalable and efficient alternative for assessing pollinator biodiversity. Further research will refine these approaches to improve their accuracy and applicability across diverse ecological settings.

Mr Angus Monaghan

Title: Understanding European Eel Distribution and Habitat Requirements with eDNA and Drainage Management Data to Guide Eel Regulation Compliance and Conservation in Pumped River Catchments

Abstract: In response to the European eel's (Anguilla anguilla) population decline and critically endangered status, European Commission Regulation No. 1100/2007 mandates eel management plans, including safe eel passage at hazardous intakes, such as pumping stations. England and Wales eel regulations require screening or alternative passage measures at many hazardous intakes. Pumping stations are a threat to seaward migration of spawning stage eels via entrainment mortality and delayed migration. Additionally, they impede upstream eel migration. River modifications for drainage can also degrade habitat. Environmental

DNA (eDNA) metabarcoding offers an effective alternative to traditional fish sampling, providing comprehensive vertebrate community data. Four eDNA sampling campaigns were conducted across 144 pumping station catchments in the Anglian Fens, UK, detecting eels in 43 (30%) of them. Eel presence correlated with better connectivity to the downstream river and higher fish species richness with a significantly higher fish species richness at eel-positive sites ($p<0.01$). Remote sensing, physical habitat data and technical metadata from drainage authorities are being integrated with eDNA community data to assess eel habitat suitability and quantify suitable habitat in catchments. These findings are guiding pumping station management for costly less damaging downstream passage modifications and upstream passage remediation for juvenile eels to increase migration success and reduce habitat fragmentation. The Environment Agency will use these findings to provide Best Available Eel Protection across the Fens, ensuring effective funding allocation. The extensive eDNA sampling effort of the project also provides insight into rare and invasive species distribution in the fens.

Miss Charlotte Nuyt

Title: Environmental DNA in fisheries management: future horizons for bycatch monitoring

Abstract: Elasmobranch (sharks and rays) populations have declined worldwide since the mid-1900s due to the industrialisation of fisheries. Their life-history traits, characterised by strategies such as late maturity, slow growth with a long lifespan, and low fecundity – do not allow them to rapidly recover from population decline, caused by overexploitation, bycatch and habitat loss. In particular, the real impact of bycatch on these group of iconic species is likely underestimated. Interest in the applications of environmental DNA (eDNA) for bycatch monitoring is increasing, highlighting its potential to supplement traditional methods like fisheries observers or fisheries logbooks. Accurate information of catch and bycatch composition and size are essential to inform fisheries management and to allow sustainable exploitation of marine resources. However, quantifying multiple species simultaneously in the bycatch, remains particularly challenging. This project aims to develop innovative environmental DNA (eDNA) protocols for different types of fishing gear, using both metabarcoding and species-specific digital PCR approaches, to enable elasmobranch bycatch quantification directly from the catch. This eDNA-based monitoring method will be tested in gillnets and bottom trawls in Irish and Icelandic waters to optimise samples collection and subsequent processing. The first insights of the methodology will be presented. If successful, this will become part of a toolset for bycatch monitoring that will improve our understanding of the distribution and abundance of elasmobranchs as well as the level in which they interact with fisheries.

Mr Matthew O’Donnell

Title: Perfect primers for finding frogs

Abstract: Amphibians are at the forefront of biodiversity declines globally, with 41% of known species classified into a threatened category during the second Global Amphibian Assessment, conducted by the IUCN Red List. Driven by a toxic cocktail of factors including climate change, habitat loss and disease, many species have been pushed to the brink of extinction. However, recently isolated populations of rare frogs have been found clinging on in remote regions, offering hope for their survival. eDNA metabarcoding has been successfully implemented to detect and monitor amphibians. However, comparative studies have demonstrated significant differences between the performance of different primers. This study compares the universal vertebrate primer 12S-V5 against two amphibian specific primers, Amph16S and Batra12S using 96 samples collected in Costa Rica and Vietnam. These two topographically diverse countries with high levels of amphibian diversity and endemism represent the frontline of threatened status amphibians globally. After sequencing and bioinformatics stages, each primer retained between 2.5 and 4 million amphibian reads. Amph16S performed best with 6 threatened frogs out of 37 detected to species level, whereas 12S-V5 detected 3 threatened species out of a total of 31 and Batra12S detected 2 threatened species out of 24 frogs in total. Notably, we detected three critically endangered frogs, Oreolalax sterlingae, Leptobrachella botsfordi in Vietnam and Isthmohyla tica in Costa Rica. These results will inform further analysis of over 400 samples collected from both countries amid ongoing conservation efforts in collaboration with ZSL, Manchester Museum and local institutions and researchers.

Dr Paul Scholefield

Title: Assessing eDNA Across a Forest Restoration Gradient: The SUPERB Project Approach

Abstract: The SUPERB project (Systemic solutions for upscaling of urgent ecosystem restoration for forest-related biodiversity and ecosystem services) is a €20 million initiative funded by the European Union's Horizon 2020 research and innovation programme (grant agreement No 101036849), aiming to restore forest landscapes across Europe. Within this framework, we developed a robust eDNA pipeline (DADA, QIIME) to assess biodiversity changes along a forest restoration gradient in six countries (Romania, Spain, Sweden, Serbia, Czech Republic, and France). Over 1651 soil samples targeting plants, fungi, and eukaryotes, and 1591 malaise trap samples targeting arthropods (CO1 primer set from the BOLD database) were analysed. The pipeline employs parallel processing for primer trimming, quality filtering, and error learning, followed by taxonomic classification using naive Bayes classifiers trained at 97% OTU clustering on curated reference databases (CHEN, SILVA, UNITE, and BOLD). Each sample's metadata, including stand, country, and year, is integrated into comprehensive multi-format reports that capture primer hit counts, filtering summaries, and error rate profiles. By mapping these eDNA-derived biodiversity metrics against restoration gradients, we provide useful insights into how different forest management interventions influence community composition and ecosystem functioning. This standardised, cluster-based approach enables efficient detection of key taxa, supporting data-driven decision-making for large-scale ecological restoration efforts. The work underscores the value of eDNA-based monitoring in tracking biodiversity responses, informing adaptive strategies that foster forest resilience and enhance ecosystem services across Europe.

Dr Margaux Steyaert

Title: Environmental DNA as an effective tool for the assessment of hard coral (Scleractinia) composition in lagoonal and exposed reef habitats (Poster Presentation)

Abstract: Human-induced global warming has triggered a persistent decline in the health of marine ecosystems, particularly coral reefs, in part due to increasingly frequent and severe high-mortality bleaching events. Refining cost-effective and precise monitoring tools, such as environmental DNA (eDNA) metabarcoding, is essential to supplement future coral reef monitoring programs, with ongoing efforts focused on improving methods, validating results, and understanding limitations. Although eDNA has been widely used in aquatic ecosystem studies, its application to Scleractinian corals remains underexplored. Here, we investigate the use of eDNA metabarcoding with molecular markers targeting the ITS2 region for monitoring coral communities in a remote and relatively undisturbed atoll system. We show that integrating multiple taxonomic assignment methods can improve taxonomic resolution and robustness, with approximately 70% of the eDNA-detected sequences recovered classified within Anthozoa, encompassing 27 Scleractinian genera. Considerable overlap in coral identification is observed between eDNA and traditional benthic transect surveys, giving support to the ability of eDNA to assess coral community composition. Importantly, cryptic genera, such as Cycloseris, Cyphastrea, Hydnophora, Merulina, Oxypora, and Turbinaria were identified solely through an eDNA approach. Conversely, we identify genera present in natural communities which an eDNA approach fails to detect, and we put forward possible explanations. Our findings also demonstrate how an eDNA approach recovers distinct coral community structures between our lagoonal and seaward reef habitat type and identifies potential characteristic taxa. This study supports the utility of eDNA metabarcoding as a non-invasive, cost-effective and complementary tool for coral biodiversity monitoring and provides insights into how to improve eDNA techniques for use as a coral biodiversity monitoring tool.

Dr Joseph Trafford

Title: Selecting and optimising an airborne environmental DNA sampling asset for terrestrial biodiversity monitoring

Abstract: Global biodiversity continues to decline at an alarming rate, and will continue to do so without significant and ambitious changes in approach. Recent proof-of-concept studies provide tantalising evidence that airborne environmental DNA technology will provide novel, scalable, high-throughput terrestrial biomonitoring capabilities. Airborne eDNA reveals a remarkable taxonomic breadth of species' DNA and offers the possibility of a previously unachievable volume of data collection from all trophic levels of terrestrial ecosystems. A variety of air sampling assets have been used in initial studies with little justification of choice of instrument beyond accessibility or 'best-guess' justification. Given that most modern air sampling instruments were designed for capturing particulates, gases and microbes for air pollution monitoring and healthcare applications, the suitability of particular instruments to a biomonitoring application remains a key unknown to end-users. We surveyed potential end-users from across government, industry and research fields to gather the needs for airborne eDNA applications. We used our responses to inform which air sampling instruments to evaluate and what outputs to deliver. We are comparing a range of active and

passive samplers and sample media for sampling efficacy across taxon specific regions for plants, fungi, invertebrates and vertebrates. Samplers are evaluated for both taxonomic diversity and relative abundance of sequences captured by each combination of sampling method/material.

Dr Hannah Vallin

Title: What's on the Menu? Investigating Dolphin Diets & Population Dynamics in Cardigan Bay.

Abstract: Amidst increasing global pressures from climate change, resource exploitation, anthropogenic disturbance, and pollution, monitoring marine biodiversity is essential to mitigate species decline and shifts in ecosystem dynamics. Understanding how top apex predators, such as bottlenose dolphins (Tursiops truncatus), respond to these changes is key to marine conservation efforts. Diet is a fundamental factor influencing animal populations. Where and what an animal chooses to eat, along with the nutritional value of its diet, directly impacts health, survival, reproduction, and overall population dynamics. However, studying the diets of wild animals, particularly marine species, has long been a challenge. Traditional approaches, such as stomach content analysis and observational studies, often lack taxonomic precision and provide only snapshots of feeding behaviour. This project focuses on Cardigan Bay's semi-resident bottlenose dolphin population, combining eDNA metabarcoding and ecological monitoring to assess diet composition, resource availability, habitat use, and population dynamics. By analysing DNA from seawater and faecal samples, we can identify prey species composition with greater taxonomic accuracy. This is complemented by Baited Remote Underwater Video Surveys (BRUVs) to assess prey availability and habitat use. Additionally, genetic analysis will be applied to investigate population dynamics, including sex ratios, relatedness, and connectivity within the population. By integrating genetics, ecology, and citizen science, this project aims to advance our understanding of bottlenose dolphin ecology, contributing to evidence-based conservation strategies to safeguard the bottlenose dolphin population of Cardigan Bay.

Mr Benedikt Wlese

Title: Understanding the Dietary Ecology of Overabundant Deer using non-invasive genetics: The Roles of Density and Competition

Abstract: Overabundant deer populations pose significant ecological and economic challenges. In Ireland, the three most abundant species—fallow (Dama dama), sika (Cervus nippon), and red deer (Cervus elaphus)—coexist in sparsely forested hotspot areas with overlapping ranges, creating substantial intra- and interspecific competition. This PhD project aims to provide insights into the dietary preferences of these populations under varying ecological pressures through genetic analysis of non-invasive faecal samples. Seasonal sampling will be conducted along density gradients within these hotspot areas. Species and sex identification, along with hybridisation estimates (e.g. sika and red deer), will be determined via qPCR and microsatellite markers, while dietary composition will be analysed using DNA metabarcoding of the trnL chloroplast intron. Integrating this data with faecal DNA-based spatial capture-recapture models and extensive camera trap data from parallel PhD projects will allow us to examine dietary patterns across seasons, sites, sexes, and species composition, identifying preferred vegetation types, niche overlap, and dietary shifts. We hypothesise that deer in low-density areas will preferentially consume highly palatable plants, whereas competition in high-density areas will drive dietary shifts towards less preferred species. These feeding patterns are expected to exert variable pressures on tree and grassland species, shaping habitat availability. By combining dietary data with deer population densities and forest damage assessments from parallel PhD projects, this study aims to provide crucial insights into the ecological impacts of deer browsing in Ireland. Findings will support evidence-based management strategies to mitigate the pressures of overabundant deer on Irish and other ecosystems.

Dr Molly Williams

Title: Using eDNA to map signal crayfish and crayfish plague in Coventry

Abstract: White-clawed crayfish are under significant threat in UK freshwaters due to the introduction of the non-native North American signal crayfish. This invasive species not only outcompetes white-clawed crayfish for habitat but also carries crayfish plague (Aphanomyces astaci) for which our indigenous crayfish has no natural resistance. Working alongside Warwickshire Wildlife Trust, Coventry City Council and the Canal and River Trust, this project aims to map the distribution of signal crayfish and crayfish plague within Coventry and surrounding areas using eDNA technology. Water sampling was carried out at two time points (winter and autumn), across 48 sites, with assistance from local volunteers. eDNA extracts were analysed using

previously published targeted qPCR approaches for signal crayfish (COI) and crayfish plague (ITS), and a generalist COI metabarcoding approach to detect invertebrates. The results show a wide distribution of signal crayfish across the Coventry region, whilst also highlighting regions currently uninhabited by the species. This data has enabled our partners to pursue the creation of a new site where white-clawed crayfish can be translocated and hopefully thrive without the impact of the invasive crayfish.

Dr Zoe Withey

Title: Ecological Function of Trees Outside Woodlands: Insights from Canopy Arthropod and Soil Metabarcoding Studies

Abstract: Trees outside of woodlands (ToW) account for approximately 30% of England's tree cover and may play a crucial role in ecological networks across fragmented landscapes. However, their biodiversity contributions remain understudied. This study assessed the biodiversity associated with oak and sycamore ToW using eDNA by sampling 28 sites across southern and eastern England, each containing pasture and adjacent woodland. Two mature sycamore and two English oak trees were selected per site. Canopy arthropods were collected six times over six months using Lindgren funnel traps and analysed via COI metabarcoding. Soil samples were collected at ordinal points around each tree at one time point and metabarcoded for fungi (ITS) and invertebrates (18S, COI). Soil chemical properties, including pH and nutrients, were also assessed. Tree species significantly influenced community composition across the taxonomic groups studied but only significantly affected species richness in fungal and Nematoda communities. While oak and sycamore supported similar numbers of arthropoda taxa, many taxa were unique to a given tree species. Habitat influenced richness, with soil Insecta taxa being more diverse in pastures. Seasonality strongly affected canopy arthropod communities, while soil properties such as pH and nutrients were key predictors of soil invertebrate composition. These findings highlight the ecological role of ToW in supporting biodiversity and may facilitate species movement across fragmented landscapes. Protecting ToW through conservation policies and sustainable management will enhance biodiversity conservation and ecosystem resilience in the face of environmental change.

Mrs Panagiota Xanthopoulou

Title: Fishes in seaports: the good, the bad, and the invisible

Abstract: Coastal areas encompass diverse habitats and communities, from the microscopic to the macroscopic world, and contribute to ecosystem functioning and health. They function as refuges and nurseries to numerous species, including endemic, endangered and/or rare species. However, they form attractive areas for human settlement, such the establishment of large cities and ports, which magnifies the anthropogenic pressure that marine populations receive. Understanding the complexity of coastal ecosystems is crucial for their sustainable management. Environmental DNA (eDNA) metabarcoding is a novel and promising technique for non-invasive biomonitoring of aquatic communities, including endangered, cryptic, rare and invasive species. The aim of this study was to provide useful insight on how the establishment of large ports affects fish distribution in coastal areas and how different sampling techniques may influence species detection. Two gulfs (Thermaikos and Saronikos) where two major ports are located, were sampled in Greece during summer 2024. Six locations and two depth zones (sea surface and the end of the euphotic zone or just above the seabed) were sampled. Three sampling techniques were tested, including vacuum pump filtering, inline filtering (sterivex), and passive samplers (rolls of gauze). The fish-specific MiFish primer pair was used to amplify a hypervariable region of the mitochondrial 12S rRNA gene. While numerous studies have proved the method's potential against traditional monitoring methods, the complexity of coastal areas and their dynamics are still to be fully understood.