Research Experience Placement (REP) Scheme 2025

Supervisor Project Proforma

Project title:	Microbial community and chemical dynamics in a freshwater lake
Host Institution:	University of Warwick
Project supervisor (name, department):	Orkun Soyer, SLS
Project enquiries (supervisor email):	o.soyer@warwick.ac.uk
Co-Supervisor, if any (name, department):	Ryan Mushinski, SLS
Proposed start date and weekly hours: (please note project must be of 6 weeks duration)	June 23, anticipated 30 hours, but needs to be confirmed with the candidate.

Please provide a short paragraph or couple of sentences summarising the project to encourage potential applicants to apply (max 75 words)**:**

Temporal dynamics of microbial communities in Nature remain understudied. In this project, we will analyse 6-month long temporal data on microbial community composition and chemical parameters, collected from the Draycote Reservoir, Dunchurch, UK. In addition, we will collect bi-weekly samples from the same location and at higher temporal resolution over a single day. The former will contribute to our existing long-time data, while the latter will inform us of dynamics over a diel cycle.

Project description (max 700 words, 1-2 figures may be included):

Background and NERC remit. Microbial communities in Nature mediate biogeochemical cycles and contribute to the stability of local and global environments [1]. In turn, disruptions in microbial community composition can result in imbalances or complete collapsing of these environments. An alarmingly familiar example of such disruption are cyanobacterial blooms in lakes, rivers, or coastal waters, which can have significant impact on human and animal life [2]. There is currently limited understanding of the temporal dynamics of microbial community composition in specific environments and their relation to environmental factors. Few recent studies explored temporal collection of meta-genomic and chemical data in tandem from the same environment, revealing seasonal, natural changes in microbial communities [3,4]. Such studies provide "null models" to better spot deviations from natural trends, enabling prediction of larger changes, such as blooms. The analysis of natural microbial communities can also be linked to community culturing in the laboratory, as we and others have done recently [5,6]. These "nature-derived" laboratory communities allow a more direct study of specific interactions among resident microbes, as well as their unique biochemical capabilities. Taken together, the analysis of temporal dynamics of natural communities both *in situ* and through laboratory-based approaches will increase our understanding of their contribution to biogeochemical cycles and further the key strategic NERC goals of "**pushing the frontiers of understanding**" and enabling "**environmental solutions**".

Project objective and context. The objective of this project is to determine microbial community composition over time and in tandem with environmental factors. By doing this, we hope to

identify the relations between the two, and at the same time increase our understanding of dominant microbes in the environment. The proposed project will build on from a previous NERC-funded pilot project conducted at the UoW in 2024, collecting weekly water samples for 6 months from the Dracyote Reservoir, Dunchurch, UK. Sampling was done in a depth-resolved manner, with samples from five different depths filtered through two different mesh sizes to collect eukaryotic and prokaryotic microbial fractions, as well as viruses. In tandem, chemical parameters, including pH, nitrate, and chlorophyll, were collected in a depth-resolved manner. Of the biological samples, the prokaryotic filter fraction for the whole series of the surface samples have been sequenced through short-read metagenomics. This genomic data remains to be fully analysed through our established bioinformatics pipelines [e.g. see 5]. In addition, the chemical data needs processing and analysed for trends.

The proposed project will thus, have two aims;

- Analyse the existing data, using bioinformatics and data analysis pipelines. This task is already ongoing, involving the PI, Orkun Soyer and the staff from the Warwick Bioinformatics Technology Platform. The appointed student would become part of this team, running existing bioinformatics pipelines and analysing resulting outputs.

- Collect additional samples to expand the existing weekly dataset from 2024 with data from 2025. We will collect bi-weekly samples throughout the 6-week placement. In addition, we will perform a high-resolution sampling over a single diel cycle. This will be done only with surface water, limiting logistical complexity.

Student enrichment and freedom. The objectives of the proposed project are well-defined and feasible. For the field-based component, the Soyer group has the appropriate experience, tools, and facilities to undertake the proposed sampling. The student will be helped by the PI, Orkun Soyer, an existing laboratory technician and postdoctoral research assistants in his group. The collected samples will be processed using existing protocols in the Soyer and Mushinsky groups. For the computational component, the student will become part of an experienced group and will be inducted in key bioinformatics tools and methods.
The project also offers freedom to the student. They will be able to develop ideas on the bioinformatics front and explore new aspects of the data that are not currently being analysed. Similarly, on the experimental front, the student will be able to go beyond the main tasks and expand their involvement. For example, it would be possible to setup laboratory cultures from samples, as well as attempt isolation of specific microbes for future physiological studies.

Project timeline:

June 2025 – student recruitment and project start
Week 1 – Training/induction in bioinformatics and sampling methods
Week 2 – Bioinformatic analyses and 1st sampling
Week 3 – Sample processing and bioinformatic analyses
Week 4 – Bioinformatic analyses and 2nd sampling
Week 5 - Sample processing and diel cycle sampling
Week 6 – Write up and 3rd sampling

Candidate requirements:

Ideal candidate should have experience in basic laboratory tasks, such as biological sample handling, sterile work, DNA extraction, and media preparation. The student should also have experience in computer-based analyses and/or bioinformatics. Previous, basic knowledge of command line interface, as well as coding platforms such as Jupyter notebook would be ideal..

Background reading and references:

References:
1. Falkowski, P. G., *et al.* "The microbial engines that drive Earth's biogeochemical cycles" *Science*, 320: 5879 (2008)
2. Schwark M., *et al.* "More than just an eagle killer: The freshwater cyanobacterium *Aetokthonos hydrillicola* produces highly toxic dolastatin derivatives", *PNAS*, 120:40, (2023)
3. Rohwer, R. R. *et al.* "Species invasions shift microbial phenology in a two-decade freshwater time series", *PNAS*, 120 (11), (2023).
4. Rohwer, R. R. *et al.* "Two decades of bacterial ecology and evolution in a freshwater lake", *Nature Microbiology*, 10 (2025).
5. Duxbury S., *et al.* "Niche formation and metabolic interactions result in stable diversity in a spatially structured cyanobacterial community", *bioRxiv*, doi: 10.1101/2022.12.13.520286, (2024), https://www.biorxiv.org/content/10.1101/2022.12.13.520286v2
6. Kust A., *et al.* "Model cyanobacterial consortia reveal a consistent core microbiome independent of inoculation source or cyanobacterial host species", *bioRxiv*, doi: 10.1101/2023.12.09.570939, (2023), https://www.biorxiv.org/content/10.1101/2023.12.09.570939v1