

## 2024\_79\_UKCEH\_DR: Predicting chemical impacts on environmental microbiomes using species sensitivity distributions

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The environmental microbiome, a complex consortium of microorganisms including bacteria, archaea, fungi, and viruses, underpins the stability and functionality of diverse ecosystems, facilitating critical processes such as nutrient cycling, organic matter decomposition, and plant growth promotion. These microorganisms play a pivotal role in sustaining life, biogeochemical processes, and environmental health.

Chemical pollution in the environment is a growing global concern, and is characterized by the near ubiquitous presence of anthropogenic contaminants including pesticides, heavy metals, pharmaceuticals, and industrial chemicals. This pollution presents a substantial threat to biodiversity<sup>1</sup>, including microbes, potentially leading to alterations in community structure, composition, and functionality. Understanding the impacts of chemicals on microbial communities is challenging. Traditional approaches to performing ecotoxicological assays, taking one species at a time and exposing them to concentration gradients of different chemicals, is not applicable to environmental microbes. This is because most environmental microbial taxa are uncultured, and they naturally live in complex interacting communities that are challenging to replicate in lab cultures.

In this PhD, you will seek to address this problem by applying the latest methodologies in microbial ecology to metabolically label, sort and identify (by amplicon and metagenomic DNA sequencing) active members of soil and freshwater environmental microbiomes<sup>2</sup>. This approach will be used to identify ecotoxicological responses to chemical (antibiotics, biocides and metal) exposure for whole communities<sup>3</sup>, and create species sensitivity distributions (SSDs) for hundreds of microbial taxa simultaneously. Chemical exposures will be performed on microbiomes from both short-term (lab exposures) and long-term (contaminated field sites) chemical exposures. This novel approach will be a step towards developing a framework to predict how microbial communities respond to chemical exposure in the environment.

The project will address the following key research questions:

1. Do microbial communities respond to chemical stressors in a predictive manner based on phylogeny?
2. Can functional traits (e.g., genome size, ribosomal copy number, mobile genetic elements) be used to predict responses to chemical exposure?
3. Are microbiome responses to short-term (acute) chemical exposures predictive of microbiome responses under long-term chemical stress?

### References:

1. Sigmund, G. *et al.* Addressing chemical pollution in biodiversity research. *Glob. Chang. Biol.* **29**, 3240–3255 (2023).
2. Kasteren, S. van & Rozen, D. E. Using click chemistry to study microbial ecology and evolution. *Isme Commun* **3**, 9 (2023).
3. Wang, K.-L. *et al.* Detection and Quantification of Antimicrobial-Resistant Cells in Aquatic Environments by Bioorthogonal Noncanonical Amino Acid Tagging. *Environ Sci Technol* **56**, 15685–15694 (2022).

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