

EEES Project Proposal Form – 2023 entry

Project Title	A deep dive into biogeochemical cycling in Icelandic Hot Springs
Key words	Bioinformatics; biogeochemistry; microbiology
Supervisory team (including email address)	PI: Michael Macey. OU Michael.macey@open.ac.uk Co-I: Mark Fox-Powell. OU Mark.fox-powell@open.ac.uk Karen Olsson-Francis. OU karen.olsson-francis@open.ac.uk Dan Read. CEH Wallingford. dasr@ceh.ac.uk
Is the PhD suitable for part time study?	Yes <input checked="" type="checkbox"/> No <input type="checkbox"/>

Project Highlights:

- Analysing unique datasets from a set of Icelandic hot springs
- Training in state-of-the-art techniques in bioinformatics.
- Identifying key metabolic process, adaptations and inter-organism relationships that sustain life in extreme conditions.

Overview:

Studying extremophiles and extreme environments is important to: 1) characterise the physical and chemical boundaries of life on Earth; 2) identify the keystone biogeochemical processes that fuel this life; 3) understand the impact of these extreme selection boundaries on the taxonomic and functional diversity of microbial communities. However, understanding of biogeochemical cycles and inter-organism relationships is hindered by the presence of uncultivated microbes and unidentified pathways [1,2]. Extreme environments such as hot springs are ideal for exploring such organisms and pathways, as their comparatively reduced taxonomic diversity greatly empowers bioinformatic approaches [3].

Metagenomics is a powerful nucleic acid sequencing technique that enables analysis of the full taxonomic and functional diversity of the microbial community of an environment. Prior applications of metagenomics to extreme environments have provided valuable insight into the metabolic diversity of the resident microbiomes [4]. However, many metagenomic studies only scratch the surface of their datasets. Diving deeper into metagenomic data using novel search functions has revealed novel pathways overlooked in established metagenomics datasets [5]. Metagenomic data from extreme environments such as geothermal springs would benefit greatly from further mining to provide targeted analysis of biogeochemical pathways and the potential role of uncultivated taxa.

The environments to be investigated in this project are a series of acid and alkaline geothermal hot springs from Iceland's active volcanic rifting zone, and sediment samples from the surrounding geothermal gradient. Localised input from volcanic gases and geothermal heating results in chemical and physical conditions that range dramatically over small spatial scales, with the potential to drive major variations in biology across relatively short distances. This studentship is bioinformatics-focused and will identify 1) the biogeochemical cycles that are present and fuelling survival using a metagenomics approach; 2) how the microbial communities fluctuate with the physicochemical

parameters of the geothermal sites 3) the potential role of the uncultivated in influencing biogeochemical cycling.



Figure 1: A neutral-acidic geothermal spring system near Hveragerði, Southern Iceland, that will be studied in this PhD.

Alt-text: A photograph of a landscape in Iceland that captures a geothermal spring system and three Open University researchers gathering samples from it.

Methodology:

A combination of bioinformatics approaches will be applied to investigate the sequencing data generated from the samples across the geothermal gradient of the Icelandic hot springs. This will involve: 1) screening of metagenomes for genes involved in biogeochemical cycling, 2) comparing the taxonomic and functional diversity across the geothermal gradient, and 3) using iterative search functions to mine for potential novel genes, pathways, and taxa within the sediment. This will be supported by modelling of the geochemistry of the sites to understand the relationship between the microbial communities and the environment. The student will have access to a range of additional techniques at the partner organisations that can be used to identify microbial interactions.

Training and skills:

The student will be trained extensively in the bioinformatic analysis of amplicon, genomic and metagenomic datasets, with a focus on the identification of genes and pathways involved in biogeochemical cycling and the identification of uncultivated taxa. The student will also be trained in modelling and the analysis of geochemical datasets, to contextualise their findings with regards to the specific chemistry of the environments. A short placement with the project partners will enable access to laboratory facilities and training in specific laboratory techniques. The student will also be trained in microbial systematics and taxonomy.

Partners and collaboration:

Sophie Nixon (Manchester University) has expertise in environmental microbiology and analysis of environmental metagenomics data and Icelandic hot springs.

Possible timeline:

Year 1: Perform a literature review on biogeochemical cycling in thermophilic environments. Complete initial training in bioinformatic analysis of sequence data, statistical analysis, and modelling. Set up initial geochemical analyses of Icelandic samples. Begin analysis of metagenomic datasets generated from the Icelandic samples across the geothermal gradient to identify the metabolisms fuelling survival

Year 2: Continue with the geochemical analyses and metagenome analysis. Explore the metagenome for genes encoding enzymes involved in biogeochemical cycling and novel taxonomic groups using iterative search functions. Start modelling the relation between the physicochemical parameters of the site to the taxonomic and functional diversity identified. Present results at a national conference (e.g. MMEG).

Year 3: Prepare and submit manuscript regarding the metagenomic work and related geochemical work. Present data at an international conference (e.g. Gordon Applied and Environmental Microbiology). Write and submit thesis.

Further reading:

1. Hug LA, Thomas BC, Sharon I, Brown CT, Sharma R, Hettich RL, et al. 2016;18:159–73.
2. Pratscher J, Vollmers J, Wiegand S, Dumont MG, Kaster AK. Environ Microbiol. 2018;20(3):1016–29.
3. Merino N, Aronson HS, Bojanova DP, Feyhl-Buska J, Wong ML, Zhang S, et al. Front Microbiol. 2019;10(MAR).



4. Martin-Cuadrado AB, Senel E, Martínez-García M, Cifuentes A, Santos F, Almansa C, et al. Environ Microbiol. 2019;21(10):3577–600.
5. Lannes R, Cavaud L, Lopez P, Bapteste E. Genome Biol Evol. 2021;13(1):1–7.

Further details:

Please contact Michael Macey (Michael.macey@open.ac.uk) for further information and informal discussion about this project.

Applications should include:

- A covering letter that includes:
 - Your motivation to study for a PhD in general
 - Your interest in this project in particular
 - The project-specific skills, aptitude and experience you bring to the project
- an academic CV containing contact details of three references, one of whom should be able to comment on your academic abilities.
- and an Open University application form.
 - If you are living in the UK and have residency rights then use the [Home form](#)
 - If you are living abroad then use the [International form](#)

Applications should be sent to STEM-EEES-PHD@open.ac.uk by the end of the day on Wednesday 11th January 2023.