Defining Algal Communities and their Ecological Functions using eDNA and AI

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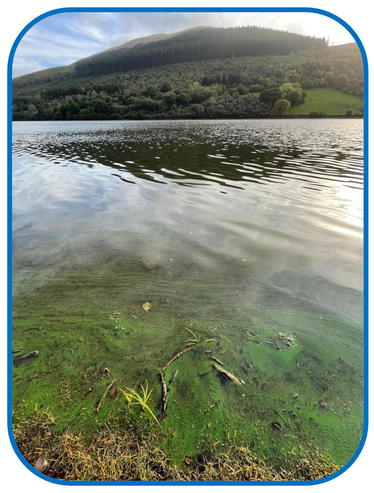
1: Background

- **Algae** found in **reservoirs** can cause various issues, including **toxin** production [1], **taste and odour** events [2] and **clogging** of water treatment infrastructure [3].
- **Biomonitoring** via **microscopy** alone, can be **erroneous** and **biased** [4].
- **AI modelling** may eliminate operator bias.
- **eDNA analysis** enables **cost effective** [5], **high throughput community quantification** [6], as well as **gene function identification** [7].

2: Project Aims



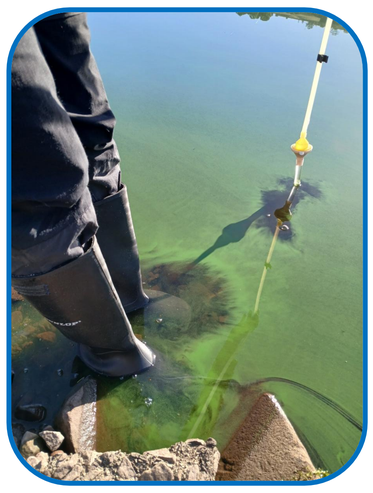


Figure 1: Cyanobacteria blooms at Talybont Reservoir

- **Quantify** the **taxonomic compositions** of **algae communities** using metabarcoding to **validate AI** results.
- **Quantify abundances** of indicator algae taxa and calculate **diversity indices** per reservoir.
- **Identify genes of interest** and the **ecological functions** of **indicator taxa**, using metagenomics**.**

3: Methodology

1 Paired eDNA and reservoir water sampling

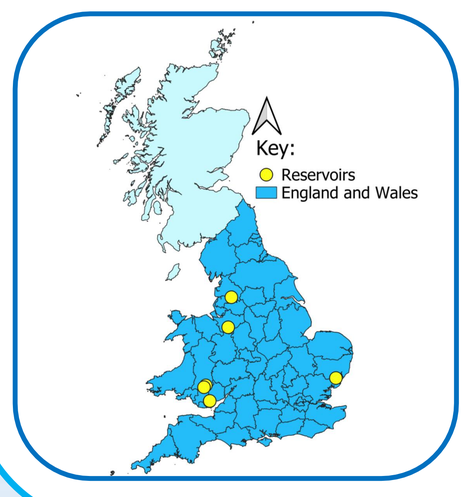


Figure 2: Sampling sites within DCWW, Anglian Water and United Utilities catchments

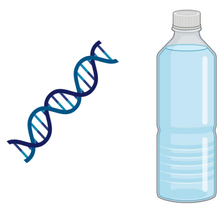
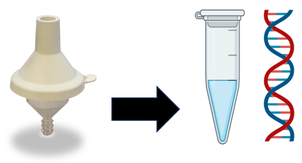


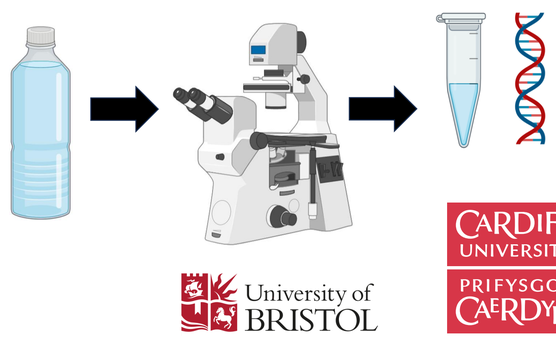
Figure 3: eDNA sampling at Pontsticill Reservoir

2 High throughput DNA extractions

2a) eDNA Filters



2b) Lugol's iodine-Stained Reservoir Water



4: Priorities and Successes

1 Data Collection

- **Analyse** the **pilot study's samples** (Oct – Nov 2024).
- **Talybont 2024** case study.
- Sampling: Mar – Oct **2025**.

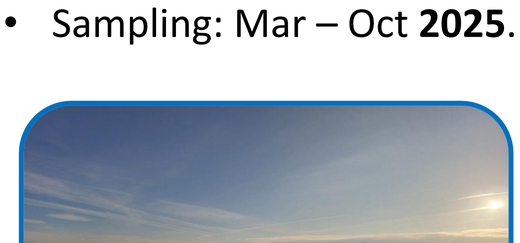


Figure 4: Lisvane Reservoir, Cardiff

2 DNA Extraction Optimisation

- **Aim**: **Genetic analysis** of **Lugol's iodine-stained reservoir water** samples, to describe algal and bacterial communities.
- **Aim: eDNA screening** of ~1000 Kugol's-stained samples (2024) to **validate AI models**.
- Comprehensive evaluation and trials of laboratory methods, to overcome issues.
- **Benefit:** Same sample used for microscopic and genetic identification.
- **Benefit:** Cost effective, high-throughput genetic analysis.

- **Success #1: Optimised DNA extraction**.
- **Success #2: Amplified** the **bacteria genetic marker** (*16S*).
- **Success #3: Amplified** the **green algae** and **diatom genetic marker** (*RbcL*).
- Next: Optimising DNA sequencing methods.

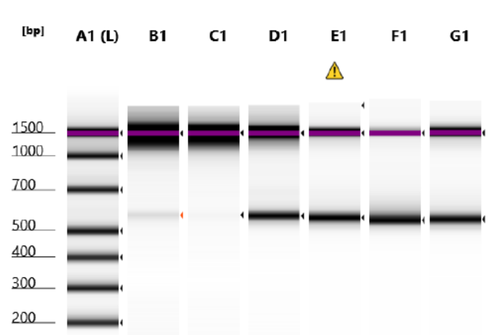


Figure 5: Successful amplification of *RbcL* from Lugol's-stained samples

References: 1) Lyon-Colbert, A., et al. (2018). Toxins (Basel) 10(7): 1-18. **2)** Hooper, A. (2023). Cardiff University. PhD thesis: 463. **3)** Nwankwegu, A. S., et al. (2019). 3 Biotech 9(12): 449. **4)** Esenkulova, S., et al. (2020). Facets 5(1): 784-811. **5)** Krehenwinkel, H., et al. (2017). Scientific Reports 7(1): 17668. **6)** Rivera, S. F., et al. (2017). Hydrobiologia 807(1): 37-51. **7)** Pael, H. K., et al. (2024). M. P. Shah. London, Academic Press: 21-40.