AI-SUPPORTED RECORDING AND FORECASTING OF BIODIVERSITY AND WATER QUALITY IN DRINKING WATER RESERVOIRS

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FEdA

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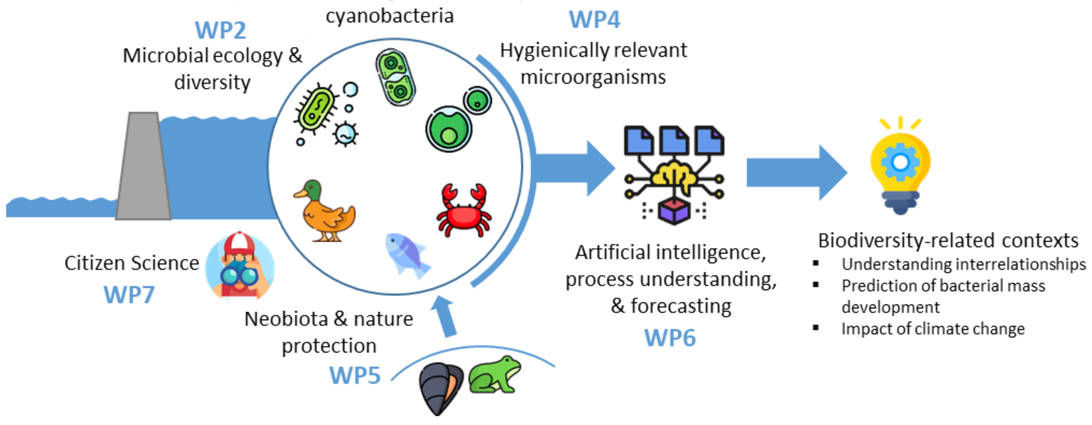
BACKGROUND

Lakes and reservoirs support rich biodiversity and are essential for the natural production of over **12% of Germany's drinking water**. Their biodiversity plays a key role in maintaining water quality but is increasingly threatened by **climate change**, **pollution**, and the spread of **invasive species** (neobiota).

Emerging issues such as **toxic algal blooms**, **faecal contamination**, **antibiotic resistance**, and **shifts in species composition** are already being observed, highlighting the **vulnerability** of these ecosystems and their importance for **drinking water production**.
Water bodies in densely populated or agricultural areas, such as reservoirs in North Rhine-Westphalia, are under greater anthropogenic pressure and often have higher nutrient levels than reservoirs in less populated mountain regions (e.g., the Black Forest or Harz Mountains). However, the vulnerability of these complex ecosystems to climate change, pollution sources, and neobiota remains insufficiently understood.

Standard water quality assessments focus on **physical, chemical, and hygienic parameters** and the **planktonic community**, but the **microbial biodiversity** (bacteria, viruses, protozoa, fungi) is rarely analyzed.

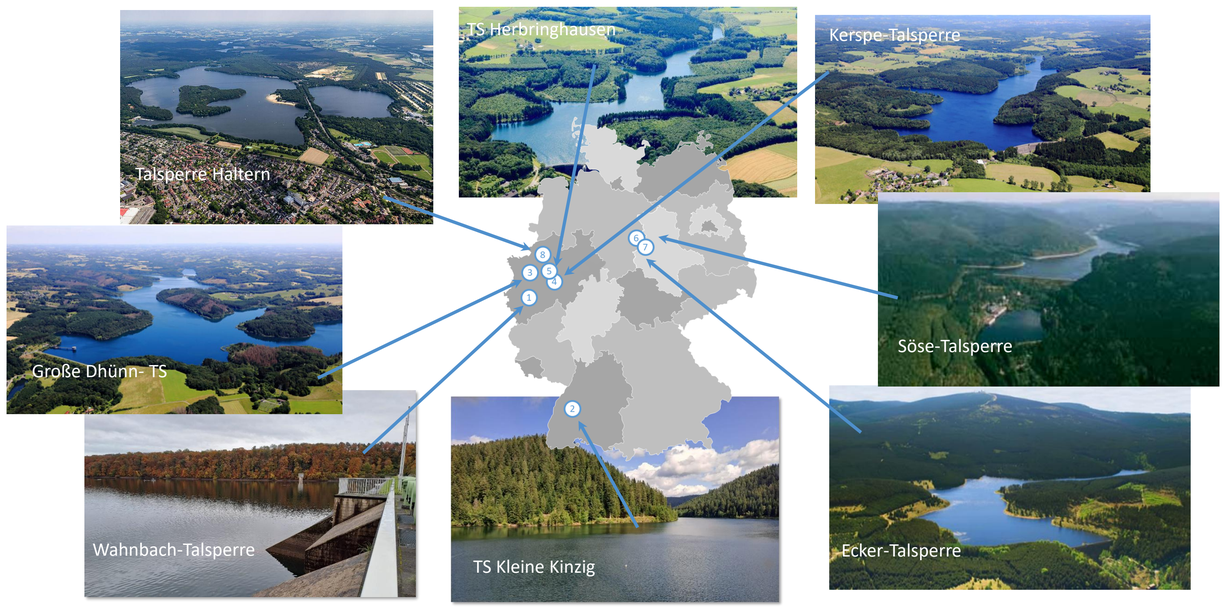
In **IQ Water**, we apply molecular methods to study microbial biodiversity with a focus on **water quality parameters**, such as toxic cyanobacterial blooms, hygienically relevant bacteria, antibiotic resistance genes, and viruses, as well as **invasive species**. **Citizen Science** complements these approaches, enabling **early and broad detection** of biodiversity changes in **water bodies and catchment areas**.



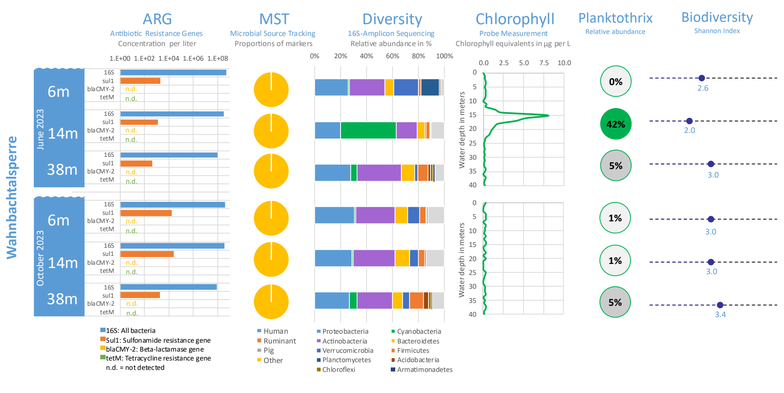
PROJECT GOALS

(1) Use of molecular methods for AI-supported microbial biodiversity monitoring
(2) Development of eDNA-based methods for detecting invasive species
(3) Advancement of sensor technologies for rapid detection of algae and cyanobacteria
(4) Identification of sources of microorganisms relevant to hygiene and antibiotic resistance
(5) Creation of an AI-based tool for data analysis and forecasting
(6) Integration of a Citizen Science–AI approach for biodiversity monitoring

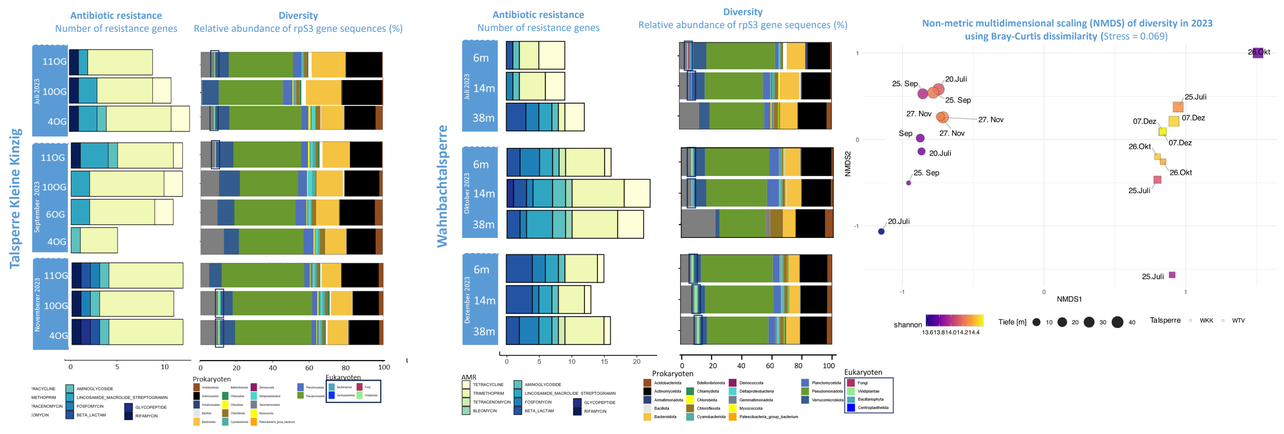
WORKING AREAS



Molecular Analysis and Biodiversity



Metagenomic Analysis and Biodiversity

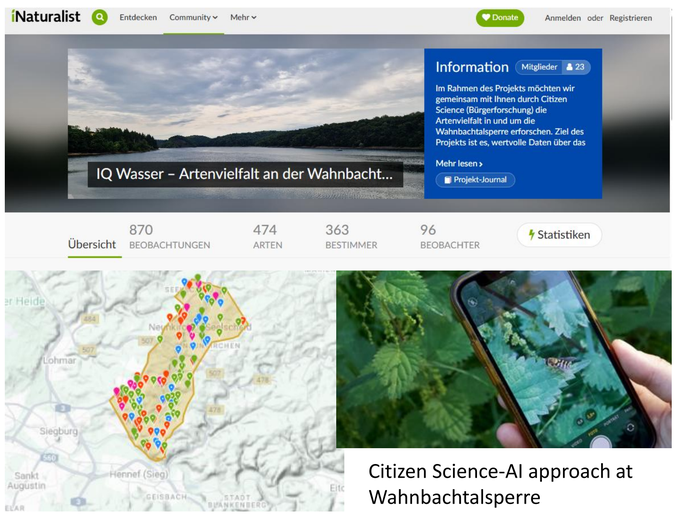


Data Analysis, Evaluation and AI

PRELIMINARY RESULTS

- **Seasonal, dam- and depth-dependent variation in microbial biodiversity**
- **Distinct biodiversity patterns among different reservoirs**
- **Low abundance and diversity of antibiotic resistance genes**
- **Non-specific MST markers detected (no link to humans, pigs, or ruminants)**
- **Seasonal variation observed in viral contigs**
- **Cyanobacterial blooms associated with reduced microbial biodiversity**
- **Eukaryotes (e.g., diatoms, green algae, fungi) identified via metagenomic analyses**
- **Raman spectroscopy shows promise for detecting toxic cyanobacteria**
- **Citizen Science–AI activities implemented at Wahnbach-talsperre**

Citizen Science and AI



Citizen Science-AI approach at Wahnbachtalsperre

eDNA analysis for invasive species

→ Development & implementation of eDNA methods for the detection of relevant species (neobiota and nature protection)

Monitoring Cyanobacteria and Cyanotoxins

→ Direct measurements through fluorescence probes
→ Application of Raman spectroscopy for relevant species

ACKNOWLEDGEMENTS

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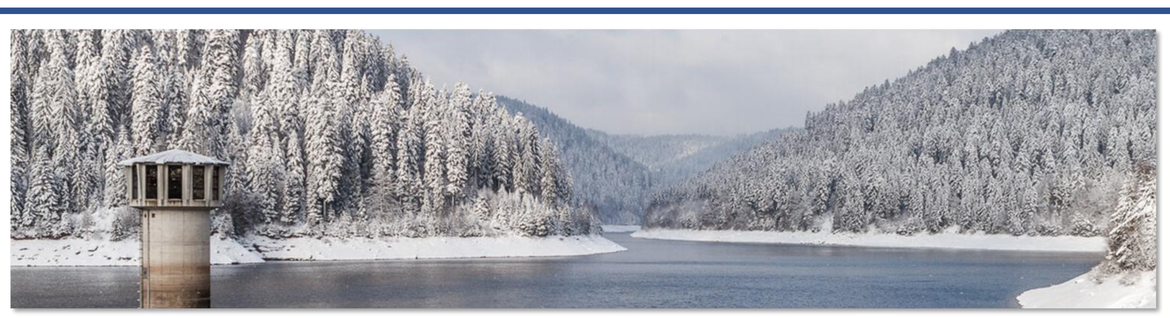

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