Effective biodiversity monitoring of river rewilding projects using eDNA modelling

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Link to GitHub poster & contact

Background

- **Freshwater biodiversity** is **declining faster** than any other ecosystem[1]
- Long-term, regular **monitoring** of restoration and **rewilding** projects will inform how best to tackle the **biodiversity crisis**
- **eDNA metabarcoding** provides **whole community** inventories
- …but **dispersal** in **river** systems affects our understanding of **community distribution**
- Improving our understanding of eDNA dispersal will **lead** to **effective biodiversity monitoring** of **river rewilding projects**

How has the shad (*Alosa fallax*) spawning migration responded to reconnection in the River Severn?

What we did:

Citizen science sample collection - three years **(FIG1)**; 2023 sites to see distance shad travel upstream of reconnection work **(FIG2)**

What we found:

Shad are passing all the reconnected parts of the River Severn, but are not going further and total river reads are low

FIG1: Inter-annual comparison of species relative abundance at three sites across four years of sampling for monitoring.

FIG2: 2023 Citizen science monitoring across six sites over four occasions. Site three is upstream of the most upstream navigation weir.

Can we model eDNA transport in river systems and apply this to eDNA results to improve the effectiveness of biodiversity monitoring?

What we did:

1. Used the transport equation to explore the effect of variables on eDNA concentration downstream **(FIG3)**.
2. Bathymetry and flow measurements taken at the top and bottom of model area **(FIG4A & 4B)**.
3. Water samples at 1.5km intervals along model area **(FIG5)**.

What we found:

The theoretical model shows various explanations for an eDNA concentration at a particular location.

With a slow decay rate, our example eDNA concentration could have come from a smaller amount of eDNA 600m upstream, or from a large concentration of eDNA 2600 metres upstream.

With a faster decay rate, the source of the eDNA would be much closer.

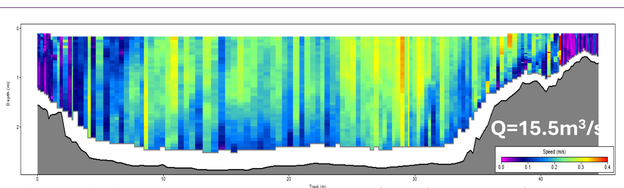

FIG4A: ARCBoat bathymetry and flow rate data, including average discharge (Q) (n = four crossings) across the most upstream model area cross section.

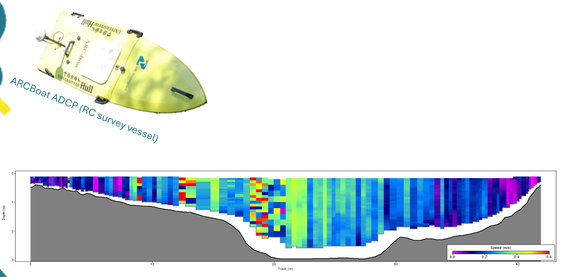

FIG4B: ARCBoat bathymetry and flow rate data, including averag discharge (Q) (n = four crossings) across the most downstream model area cross section.

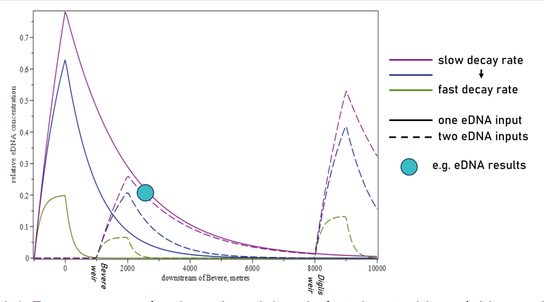

FIG3 (right)**:** Transport equation-based model exploring changeable variables such as eDNA input and decay rate.

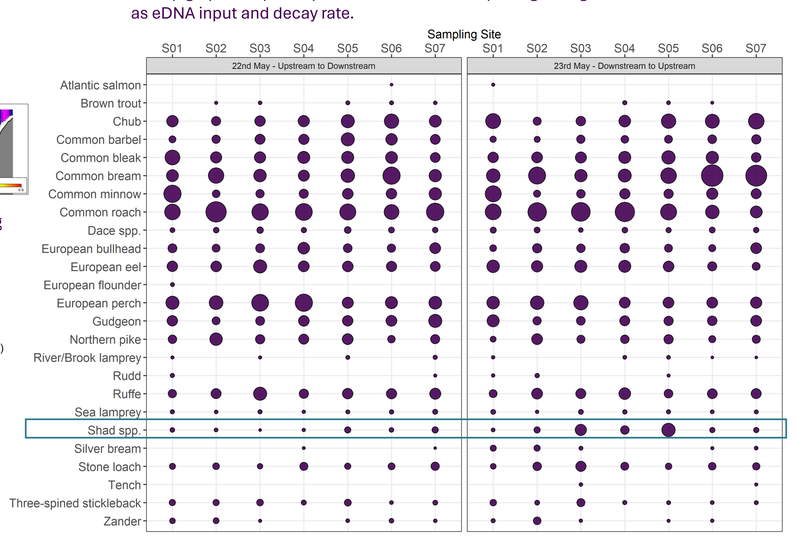

FIG5: Relative fish species reads at seven sites (see river map, purple pentagons) between downstream of Diglis weir and upstream of Bevere weir (ordered numerically downstream to upstream) on 22 (sampled consecutively starting upstream, travelling downstream) and 23 (sampling starting downstream, moving consecutively upstream) May 2023.

How do events like spawning affect eDNA read counts in metabarcoding results?

What we did:

Sampled water in one location every two hours over a 24hr period (plus an extra 2am sample just in case!).

What we found:

Temporal sampling data shows the expected rise in shad (Alosa spp.) eDNA concentration on a day we were expecting some spawning, but not the following day at 2am.

We will also analyse AudioMoth data used to identify spawning upstream.

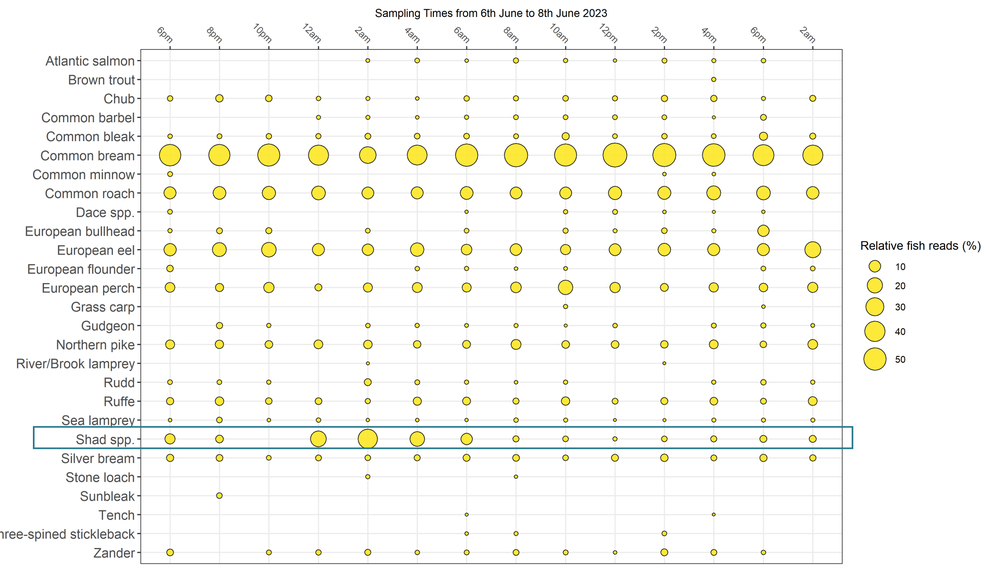

FIG6: Relative fish species reads at Lower Lode (see river map, yellow star), downstream of Upper Lode weir, between 6pm on 6 June and 2am on 8 June 2023 (2 hr sampling interval for first 24 hrs).

Next steps

- **Place a point source of eDNA at the top of our 9km study area to flood the system and sample at regular intervals downstream to understand decay rate.**
- **Explore source and decay effects on eDNA transport within our theoretical models.**
- **Use the point source data to refine our models and then interpret the actual eDNA metabarcoding data.**

References

[1] IUCN Freshwater Species https://www.iucn.org/our-work/topic/freshwater-species Accessed: 2023-02-10

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