

Effective biodiversity monitoring of river rewilding projects using eDNA modelling

Clare E. Collins^a

Primary supervisor: Dr Jon Bolland^a

Supervisory team: Dr Lori Lawson Handley^a, Dr Bernd Hänfling^b, Dr Robert Dorrell^a, Professor Dan Parsons^c

Contact: C.Collins-2019@hull.ac.uk

^aUniversity of Hull, ^bUniversity of the Highlands and Islands, ^cLoughborough University



Link to GitHub poster & contact

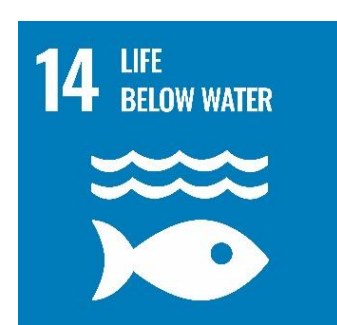
The issue

- Freshwater biodiversity is declining faster than any other ecosystem¹
- Rivers function as ecological connectors, biodiversity corridors linking both aquatic and terrestrial habitats
- Only 14% of English rivers meet good ecological status²
- Rewilding is an important tool for tackling the biodiversity crisis
- Monitoring the change that rewilding brings to ecosystems is important if we are to understand the costs and benefits
- 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



Project aims

- Using existing research on the spatial³, temporal⁴, mechanical⁵ and hydromorphological⁶ dynamics of eDNA dispersal, can we further develop existing models to accurately predict the distribution of river diversity from an eDNA signal?
- Can we apply these models to different river systems?
- Do these models help us understand rewilding (species reintroduction, river restoration or natural recolonization) impacts on the wider ecosystem?



Rewilding projects



Alosa fallax (shad)
© Jack Perks,



Lota lota (burbot)
© Dillen, A. (Fishbase Collab ID 1015)

- Catchment-wide migration of diadromous fishes, *Alosa fallax* and *Petromyzon marinus*, in response to reconnection of the River Severn.
- Whole community biodiversity in response to re-introducing a keystone predator, *Lota lota*, in the River Wissey.

References

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

² Environmental Audit Committee, *Water quality in rivers* HC 2021-22, 74-IV

³ Hänfling, B., Lawson Handley, L., Read, D. S., Hahn, C., Li, J., Nichols, P., Blackman, R. C., Oliver, A., & Winfield, I. J. (2016). Environmental DNA metabarcoding of lake fish communities reflects long-term data from established survey methods. *Molecular Ecology*, 25(13), 3101–3119. <https://doi.org/10.1111/mec.13660>

⁴ Lawson Handley, L., Read, D. S., Winfield, I. J., Kimbell, H., Johnson, H., Li, J., Hahn, C., Blackman, R., Wilcox, R., Donnelly, R., Szitenberg, A., & Hänfling, B. (2019). Temporal and spatial variation in distribution of fish environmental DNA in England's largest lake. *Environmental DNA*, 1(1), 26–39. <https://doi.org/10.1002/edn3.5>

⁵ Harrison, J. B., Sunday, J. M., & Rogers, S. M. (2019). Predicting the fate of eDNA in the environment and implications for studying biodiversity. *Proceedings of the Royal Society B: Biological Sciences*, 286(1915), 20191409. <https://doi.org/10.1098/rspb.2019.1409>

⁶ Carraro, L., Stauffer, J. B., & Altermatt, F. (2021). How to design optimal eDNA sampling strategies for biomonitoring in river networks. *Environmental DNA*, 3(1), 157–172. <https://doi.org/10.1002/edn3.137>