

# Amplifying the Power of eDNA by Making it FAIR

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## Abstract

Environmental DNA (eDNA) is a fast-growing biomonitoring approach to detect species and map their distributions, with the number of eDNA publications exponentially increasing in the past decade. While millions of DNA sequences are often generated and assigned to taxa in each publication, these records are stored in numerous locations (e.g., supplementary materials at journals' servers, open data publishing platforms such as [Dryad](#)) and in various formats, which makes it difficult to find, access, re-use and integrate datasets. Making eDNA data [FAIR](#) (findable, accessible, interoperable, re-usable) has vast potential to improve how the biological environment is measured and how change is detected and understood. For instance, it would allow biomonitoring and species distribution modelling studies across extended space and time scales, which is logistically difficult or impossible for individual projects. It would also shed light on "dark" (unassigned) DNA sequences by facilitating their storage and re-analyses with updated ever-growing DNA reference databases. Several challenges are associated with making eDNA FAIR, including how to standardise data formats and bioinformatics workflows, and simplifying the process of post-publication data archiving so that it is acceptable for eDNA practitioners to adopt. Over the next three years, we plan to work closely with biodiversity data platforms such as the Global Biodiversity Information Facility ([GBIF](#)) and Atlas of Living Australia ([ALA](#)), eDNA science journals, and eDNA practitioners, to solve these challenges and enable eDNA to achieve its revolutionary potential as a unified source of information that supports environmental management.

## Keywords

data repository, biodiversity, biosecurity

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## **Conflicts of interest**

The authors have declared that no competing interests exist.