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## New eDNA-modelling approach accurately maps biodiversity of rivers



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Carraro, L., Mächler, E., Wüthrich, R., and Altermatt, F. (2020) Environmental DNA allows upscaling spatial patterns of biodiversity in freshwater ecosystems. *Nature Communications*, 11: 3585. <https://doi.org/10.1038/s41467-020-17337-8>

**Contact:**

[luca.carraro@eawag.ch](mailto:luca.carraro@eawag.ch)  
[florian.altermatt@ieu.uzh.ch](mailto:florian.altermatt@ieu.uzh.ch)

**Researchers have shown how accurate, fine-scale maps of riverine biodiversity can be obtained using a method combining the trace genetic material (eDNA) found in rivers and streams and modelling based on hydrological principles.** This non-invasive method can identify biodiversity hotspots to inform their management and conservation and could provide information on locations that are inaccessible (and therefore very difficult to monitor).

With global freshwater biodiversity in alarming decline, detailed monitoring is needed to inform conservation measures. The researchers behind a new study note that most current monitoring practices rely on localised estimates based on samples collected from water bodies, and instead show how a novel, non-invasive method can indicate aquatic insect populations over a whole river basin<sup>1</sup> (while remaining accurate down to 1-kilometre-long sections). The approach combines environmental DNA (eDNA) from stream water — traces of organismic DNA found in environmental samples, in this case stream water — with hydrological modelling and offers an efficient way of identifying biodiversity hotspots.

As genetic material is transported downstream, analysing eDNA in river water samples may also offer information about the upstream catchment. While making direct inferences on biodiversity from eDNA data is complex, this study demonstrates how it is possible to derive precise estimates of spatial distribution of aquatic insect density from eDNA data collected in a 740-km<sup>2</sup> river basin in northeastern Switzerland. The study focused on mayflies, stoneflies and caddisflies — which are highly sensitive to pollutants, and therefore indicators of water quality — and used a genetic sequencing platform to analyse water samples from 61 sites along the Thur River network.

The eDNA analysis identified 50 different genera (groups of animal or plants more closely related than a family, but less similar than a species), to which the researchers then applied a modelling framework to predict the abundances and source locations of insect material, using variables such as water velocity and eDNA decay rate. This permitted detailed mapping of species distribution (expressed as relative abundance or detection probability) in the study area, which revealed patterns of species richness.

According to the model, the insect-richest areas were the central headwaters (around the source),



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## New eDNA-modelling approach accurately maps biodiversity of rivers (continued)

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indicating that insects in the downstream portions of the catchment and tributaries are negatively affected by factors such as pollution. Such findings agree with recognised features and aspects of water quality in these areas. Importantly, the researchers also identified biodiversity hotspots that were identified by the model — not by a combination of eDNA and kicknet sampling.

To validate the method, they compared the mapped insect presence with actual observations obtained via standard sampling (using a net to collect insects from the water). On average, modelled estimates matched this data 82% of the time, indicating high accuracy.

The researchers emphasise that this method allows the non-invasive and efficient detection of endangered or invasive organisms, or even pathogens, to inform freshwater ecosystem management. Importantly, the method could be applied in highly biodiverse but inaccessible ecosystems, and could also be used for fish, crustaceans or molluscs.

Further studies are needed, however, to investigate how the positioning of eDNA sampling sites within a catchment influences the model's predictive power, they acknowledge. Another key challenge is honing the predictive relationship between eDNA detection and species abundance. Although the method could, therefore, be refined, this case study shows how eDNA and hydrology-based modelling allows prediction of aquatic biodiversity across whole river networks at a fine resolution, based on a relatively small number of sampling sites. This creates opportunities to map river biodiversity worldwide — even in inaccessible locations.

1. The area over which surface runoff is transported by a [single drainage system](#).