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Reconstructing species distribution and abundance patterns in rivers with environmental DNA

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Environmental DNA (eDNA) is an innovative technique allowing the detection of DNA fragments of target species in environmental samples. The use of eDNA as a noninvasive, rapid and cost-effective tool for monitoring biodiversity in freshwater ecosystems has gained substantial popularity over the last decade. Despite the immediate benefits of eDNA-based detection, the localization of the target species and the assessment of its density based on eDNA surveys in rivers remains challenging. In fact, the measured eDNA concentration at a river's cross-section is the outcome of decay processes from distributed species densities at any point upstream, connected by the hierarchical drainage network. Here, we present a hydrology-based eDNA transport modelling framework, which enables us to unravel such upstream species distribution subsumed by downstream eDNA measurements. In our framework, eDNA transport dynamics are coupled with a species distribution model relating eDNA production to environmental covariates, allowing us to infer the potential effect of hydromorphological and geological drivers in determining the distribution of target species. We provide two examples of the capabilities of our method. In a first case study, we used eDNA data obtained by quantitative polymerase chain reaction (qPCR, a single-species detection technique) to derive the catchment-wide distribution of two target species: the freshwater bryozoan *Fredericella sultana* and its myxozoan parasite *Tetracapsuloides bryosalmonae*, the latter being the causative agent of PKD, a lethal disease of salmonids. These results are instrumental to identify the portions of the catchment at highest risk for fish. In a second application, we calibrated our model against data obtained via eDNA metabarcoding (a multispecies detection method) on 50 genera belonging to the orders Ephemeroptera (mayflies), Plecoptera (stoneflies) and Trichoptera (caddisflies). Being highly sensitive to pollutants, these taxa are commonly used as indicators of water quality in stream environments. The spatial distributions of the target genera produced by our model are in agreement with data obtained by kicknet samples, historical records and experts' knowledge.