Using environmental DNA to study species distributions in river networks

Luca Carraro (1), Hanna Hartikainen (2,3), Jukka Jokela (2,3), Enrico Bertuzzo (4), Andrea Rinaldo (1,5)

(1) École Polytechnique Fédérale de Lausanne, Laboratory of Ecohydrology (ECHO), Lausanne, Switzerland (luca.carraro@epfl.ch), (2) Institute of Integrative Biology, ETH Zürich, Zurich, Switzerland, (3) Aquatic Ecology Group, Eawag, Dübendorf, Switzerland, (4) Dipartimento di Scienze Ambientali, Informatica e Statistica, Università Ca' Foscari Venezia, Venice, Italy, (5) Dipartimento di Ingegneria Civile, Edile e Ambientale, Università di Padova, Padua, Italy

Environmental DNA (eDNA) is a relatively new and widely used technique for detecting rare or invasive species in freshwater environments. The exact localization of the target species and assessment of its density based on eDNA surveys remain a demanding task, but would be highly valuable for management and monitoring. Here, we propose a general framework for using downstream eDNA measurements to reconstruct the upstream location and density of a target species across a river basin. This framework, based on mass conservation principles and simple hydrological transport concepts, can be coupled with other population and ecological models in order to detect the spatial location of the target species and its local biomass, as well as their correlations with environmental variables. We tested the framework using quantitative eDNA measurements of both myxozoan *Tetracapsuloides bryosalmonae* and freshwater bryozoan *Fredericella sultana* at various locations within the Wigger watershed (Switzerland). The myxozoan is the causative agent of a highly virulent fish disease (proliferative kidney disease - PKD) and is released both from a fixed source (infected bryozoans) and a mobile source (infected fish). This aspect poses further challenges from a modelling perspective, as the two sources must be singled out. The examined case represents a paradigm of the potentiality of our framework, as predicting the spatial pattern of bryozoan density is crucial for the assessment of the spatial distribution of PKD prevalence in fish and, ultimately, for the implementation of disease mitigation strategies.