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Biomonitoring in rivers adopting environmental DNA (eDNA)

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1. Introduction

A monitoring technique capable of assessing the status of an aquatic ecosystem is needed for reversing negative trends in river biodiversity. Recently, an innovative technique for detecting the degree of biodiversity based on environmental DNA traces (mucus, shed skins etc.) has been proposed (Carraro et al., 2020). This eDNA-based biomonitoring relies on the collection and processing of water samples containing genetic material released by organisms. In recent years, the research community has made significant efforts to advance the identification of species from biological samples, for instance by expanding genetic reference databases. However, eDNA technique implementation is hampered by a lack of knowledge about the dynamics of biological traces in rivers. Here, the aim is to investigate the transport of eDNA in water streams, while considering processes such as degradation and spreading.

2. Transport of eDNA traces in rivers

The mathematical description of the phenomena governing the presence of the eDNA traces along a 1D channel can be described by the equation (Sansom & Sassoubre, 2017):

$$\frac{\partial C}{\partial t} + u\frac{\partial C}{\partial x} = S\text{-}k\,C \qquad (1)$$

where C is the concentration of eDNA, t is time, u is the water velocity in the streamwise (x) direction, S is the production of traces in the system and k is a first-order decay constant. The term C can be modeled as a first-order reaction, through a logarithm function (Sansom & Sassoubre, 2017):

$$C = C_0 e^{-kt}$$

with C_0 the initial eDNA concentration.

3. Results

At the Department of Hydraulics Engineering of TU-Delft, we are currently working on eDNA dynamics in water systems both numerical and experimental approaches. The spreading is evaluated numerically through a 1D simulation adopting Sobek. The decay of eDNA is investigated experimentally.

In Fig 1 we present the results of a simulation run in Delft 3D aiming at evaluating the spreading of eDNA, assuming three points of release of genetic material. The selection of the type of species, initial concentration, and point of release is made by referring to the open-source database of Carraro et al. 2020. Genetic material released from different sections located at branches of different stream orders I to III is simulated (Fig 1a). We have investigated the temporal change of eDNA concentration (Fig 1b) in a downstream section (order IV, see the purple dot in Fig 1a). As expected, the traces released from order-I will arrive at a later time than the ones of higher order. At the downstream section, there is a mixing of eDNA material coming from the different branches of varying stream order.

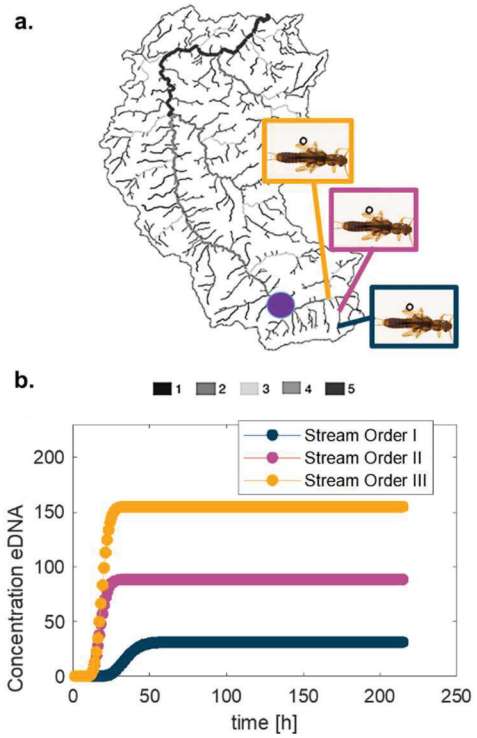

Figure 1. Spreading of eDNA in a river basin. a) basin and location of the 3 points of constant release of eDNA (genus *Leuctra*); b) relation of eDNA concentration (in number of reads of genetic material) in time at the river section depicted in (a) with a purple dot.

3. Conclusions

The modelling of the eDNA spreading helps in identifying a downstream location where traces are accumulated. Biological samples taken in this section could provide a complete picture of the river biodiversity.

References

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