Developing new eDNA-based ecological assessment tools for the management of land-based contaminants in coastal environments

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Stressors of different nature are affecting coastal ecosystems. Yet their combined impacts on biodiversity are poorly understood because the majority of studies focus on the impact of a single stressor ignoring interacting effects, and on a restricted number of taxa. In this study, we propose to introduce comprehensive environmental DNA (eDNA) biodiversity surveys into Bayesian Networks Relative Risk Models (BNRRM) to disentangle relative effects of multiple stressors on coastal biodiversity in North Queensland, Australia and to build ecological risk assessment models.

Introducing eDNA biomonitoring data into ecological risk assessment models

eDNA metabarcoding is now recognized as a powerful tool for obtaining comprehensive biodiversity data, while BNRRM have been widely used in ecological risk assessments as they can account for various stressors and response types, over large spatial scale. Recently, Graham et al. (2019) demonstrated the relevance of including eDNA data into such models to predict the relative richness of benthic taxonomic groups. Here, we propose to expand on this work by combining eDNA biomonitoring data with field measures of contaminants into BNRRM to (i) disentangle effects of each contaminant on biodiversity metrics, (ii) identify key stressors and (iii) test management scenarios.

Bayesian Networks for ecological risk assessment models

BNRRM can take into account multiple natural and anthropogenic stressors alike, and can be used to semi-quantitatively assess ecological risks. The model weights the relative importance of each stressor on a set of defined ecological endpoints (here, biodiversity metrics derived from eDNA). The study area is divided into discrete sub-regions to account for the spatial variability of the stressors and biological communities. The relative importance of each stressor and their risks to the system is examined independently for each area (Fig. 1), Collectively, the approach can then be used to test management scenarios.
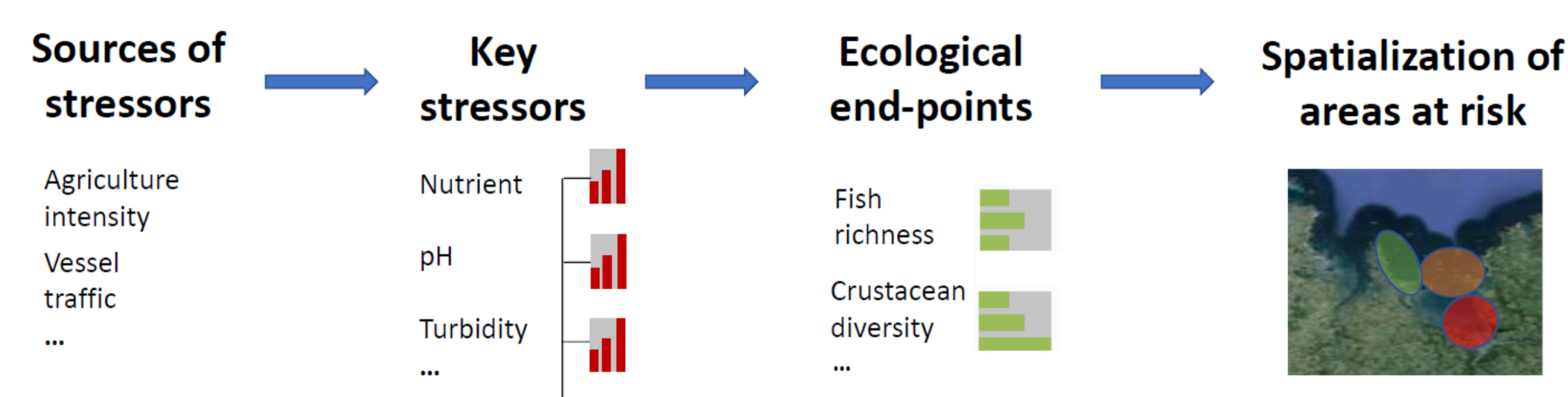

Figure 1: Simplified diagram of the BNRRM approach

Spatially explicit sampling for eDNA biomonitoring and contamination levels

This study is conducted in three estuaries and one harbour, located in North Queensland, Australia (Fig. 2). A total of 34 sites were sampled.

At each site, 3 water and 3 sediment samples were collected for eDNA analyses (total N = 204). After DNA extraction, multiple DNA metabarcodes were PCR amplified to characterize groups of ecological interests: eukaryote, bacteria, metazoa, diatoms, fish and crustacea. Three PCR replicates per sample were conducted using tagged primers, and sequencing is ongoing on Illumina platforms. Biodiversity metrics will then be derived, and used as endpoints in the model (Fig.3).
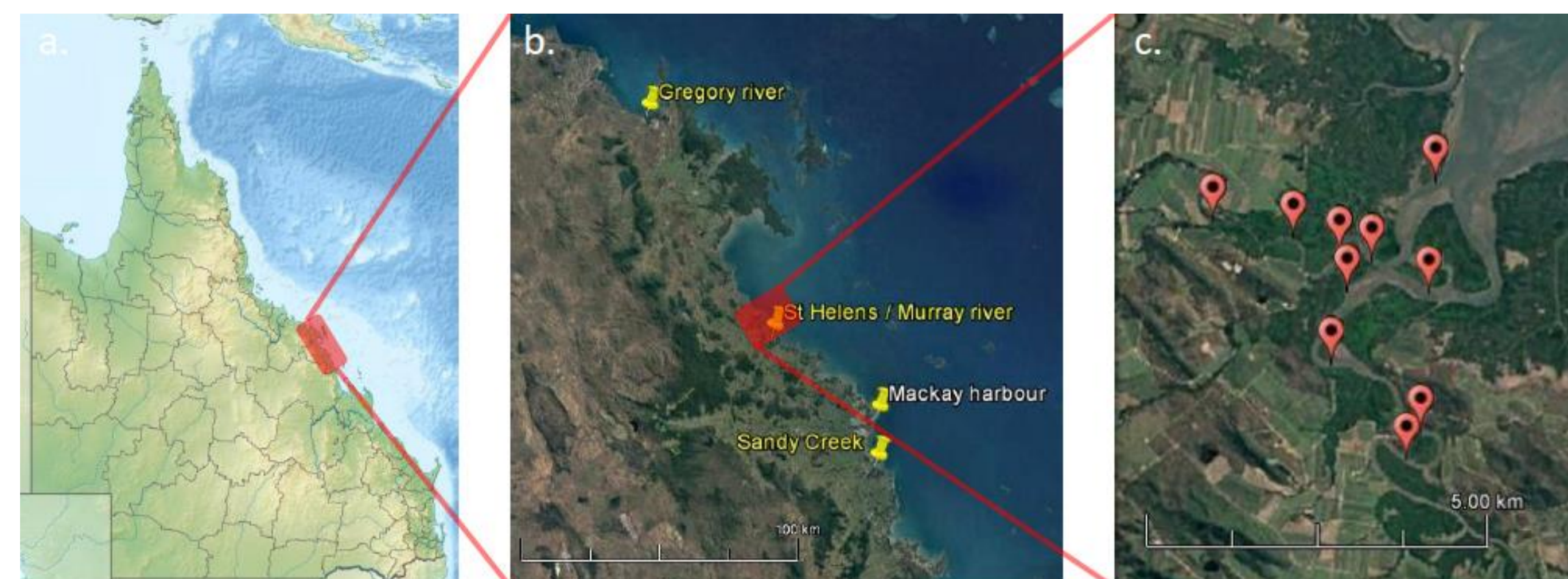

Figure 2: Study area. a) Location of the study area in Queensland, Australia, b) Location of the 3 estuaries (Gregory, St Helens/Murray and Sandy Creek) and of Mackay harbour, c) Sampling sites within one of the estuary (St Helens/Murray).

Additional samples were collected at each site for determining local levels of metals, nutrients (N, P…), and pesticides (diuron, atrazine…), as well as local physico-chemical parameters (pH, turbidity, T°...).
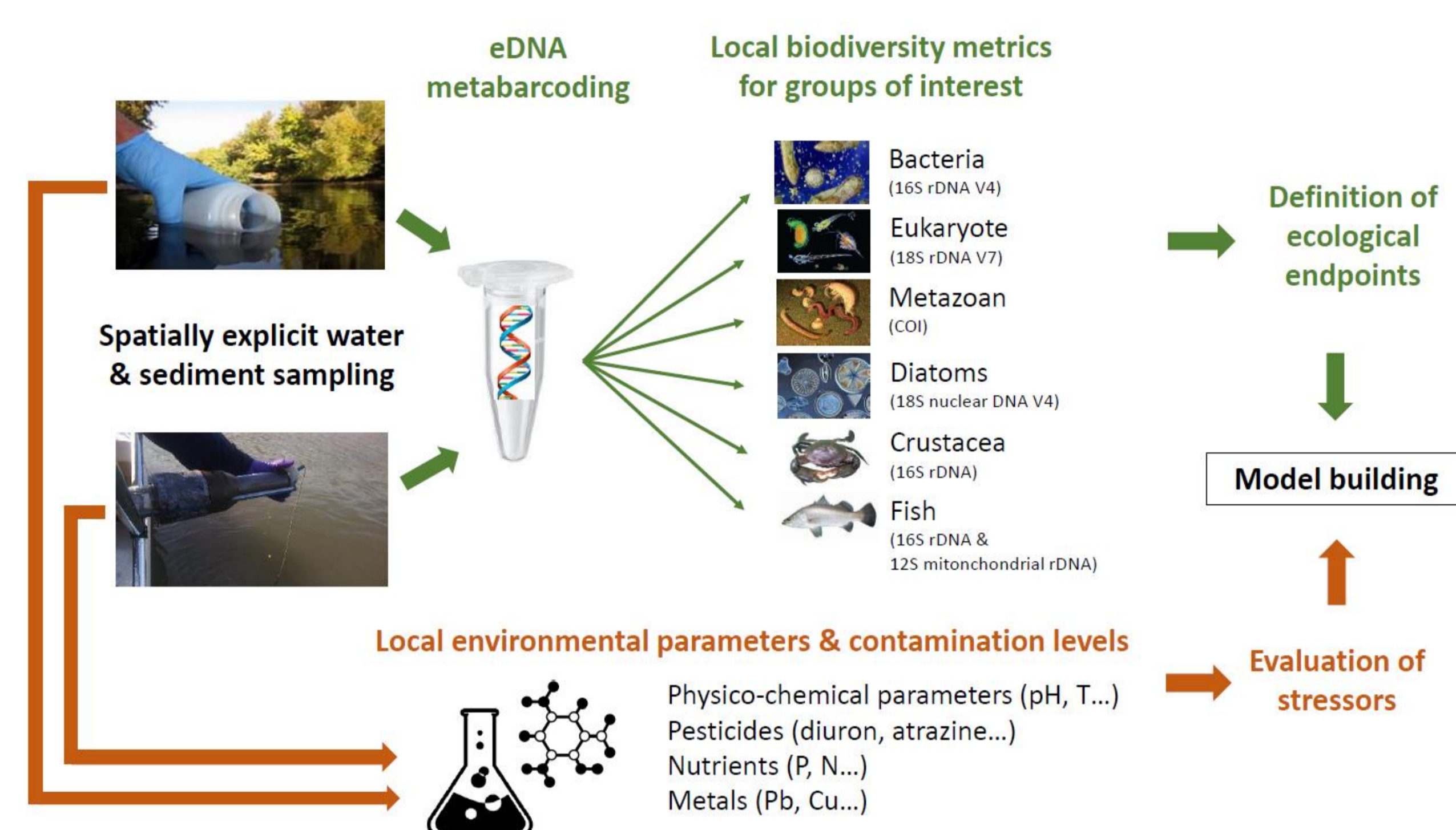

Figure 3: Overview of the workflow

Model building

A conceptual model (Fig. 4) is built linking sources of stressors to endpoints based on causal relationships between the variables in the system. In this series of causal networks, interactions between the nodes are described by conditional probability tables. Using prior knowledge and field data, Bayesian Networks then calculates the probability of a specific response (e.g. high diatom richness) occurring, and the associated uncertainty, according to the state of stressors influencing it. In this case, eDNA-based biodiversity metrics will be used as endpoints. Physico-chemical data will allow for the most important stressors to be identified. A conceptual model will be later built accordingly, and parametrized from field data.
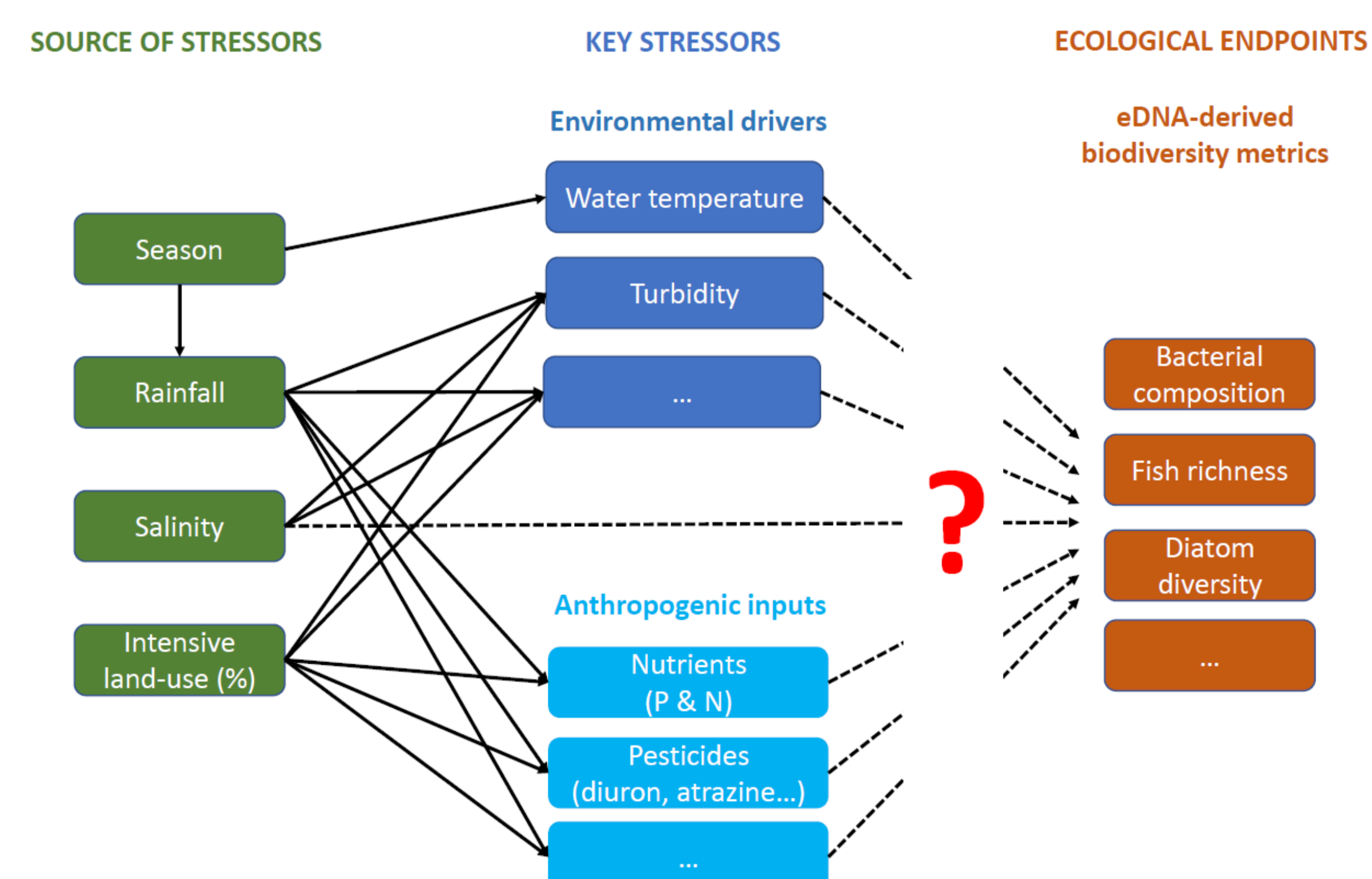

Figure 4: Simplified conceptual model, derived from Graham et al. 2019

Perspectives

The notion of studying a single stressor on a small number of taxa is now out-dated. This research aims to provide a proof-of-concept for the integration of eDNA biodiversity data into ecological risk assessment models at a scale relevant for managers. This approach can provide comprehensive information on biological communities and key information for developing effective management strategies and guiding mitigation actions.

REFERENCES
Chariton et al. (2016) Emergent technologies and analytical approaches for understanding the effects of multiple stressors in aquatic environments. Marine Freshwater Research, 67, 414-428.
Graham et al. (2019) Using Bayesian networks to predict risk to estuary water quality and patterns of benthic environmental DNA in Queensland. Integrated Environmental Assessment and Management, 15, 93-111.