From DNA to diagnostics

The potential of macroinvertebrate metabarcoding to diagnose stressors and assess the effectiveness of restoration measures

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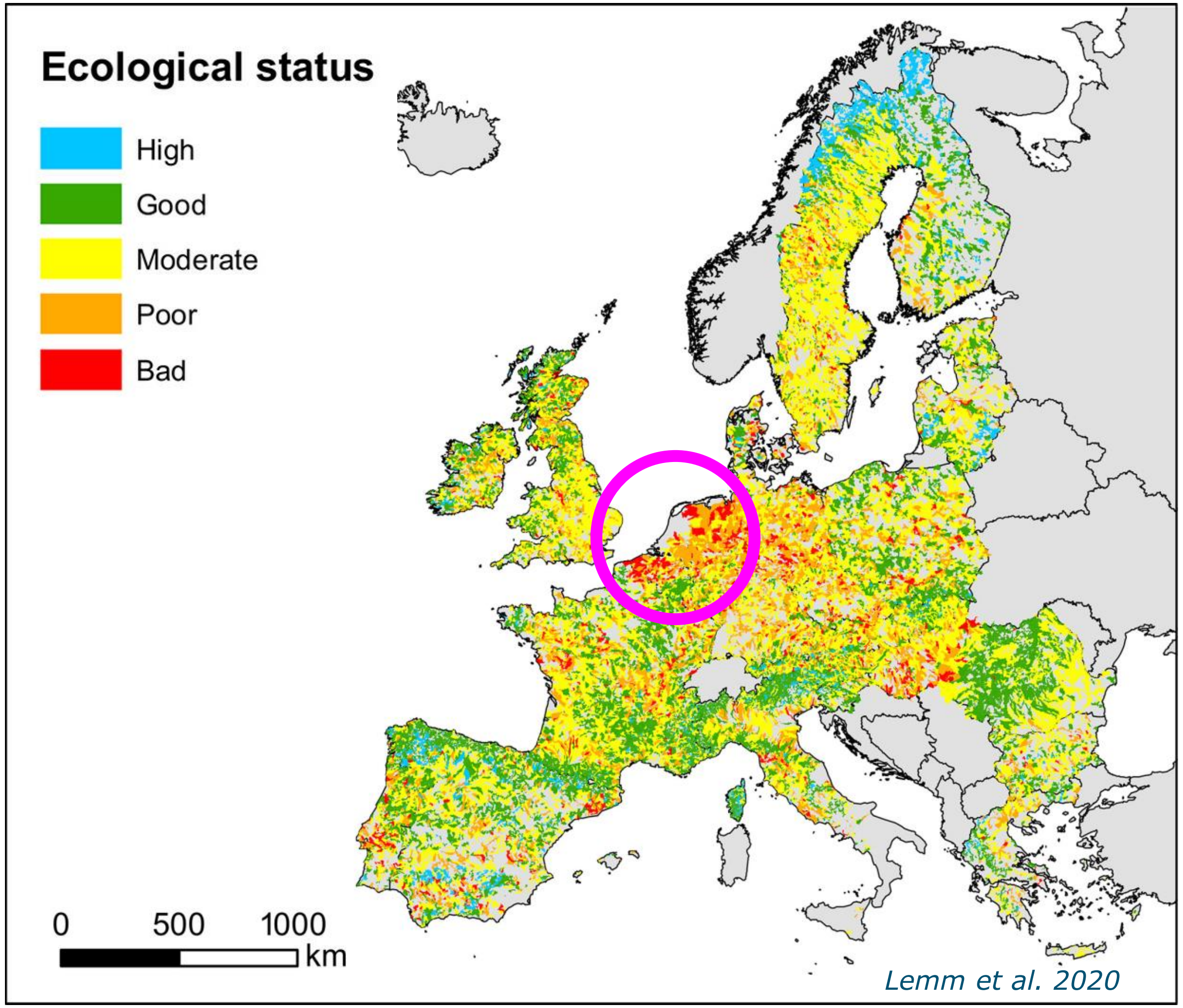
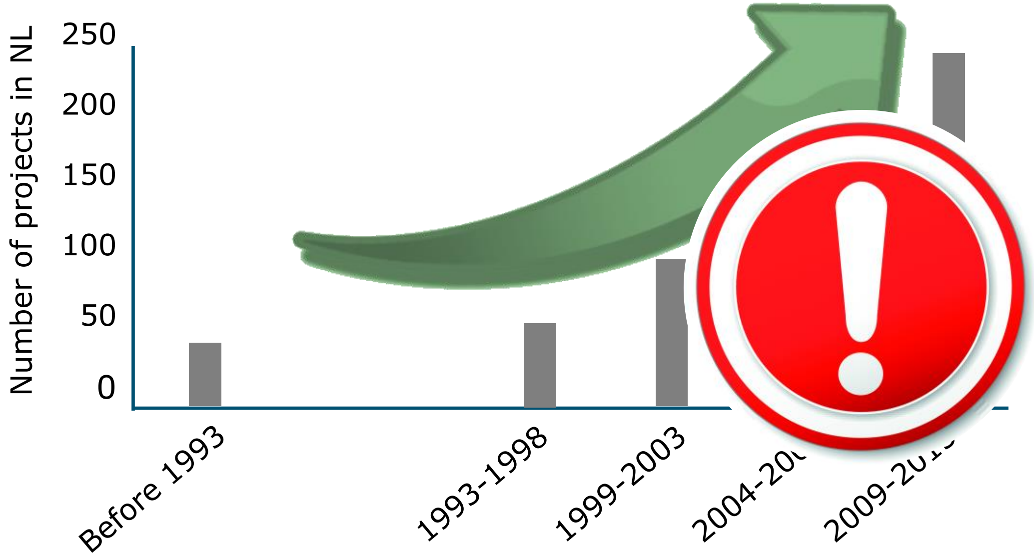
Streams and rivers are under anthropogenic pressure



Lemm et al. 2020

Increasing number of restoration projects but positive effect on biota is limited

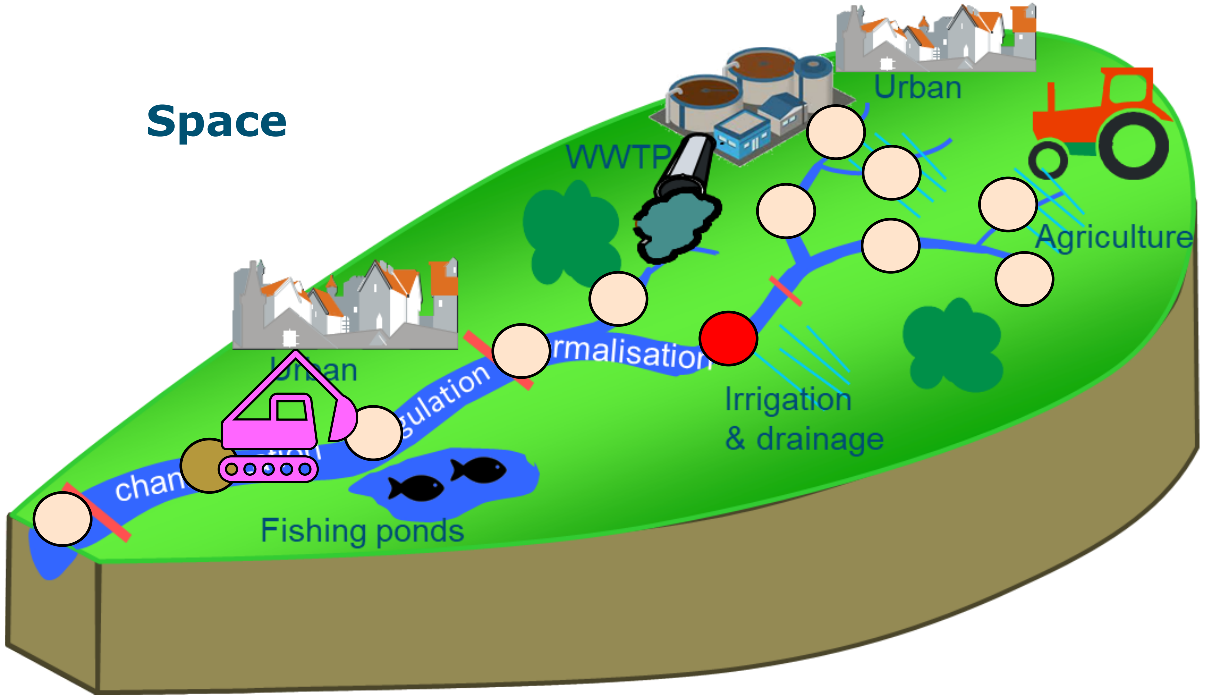


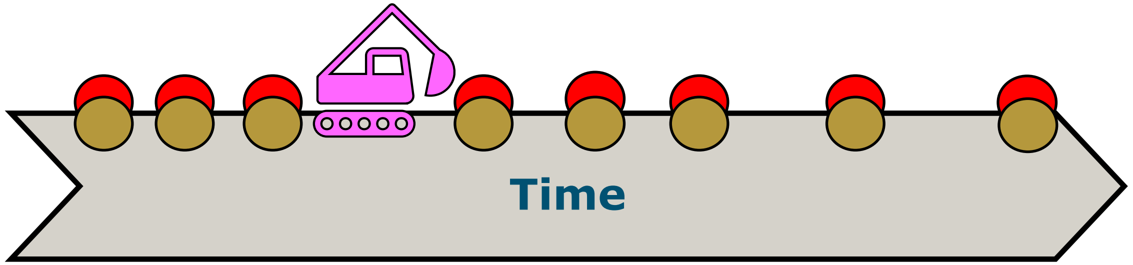
adapted from dos Reis Oliveira et al. 2020

Scale up monitoring to increase success rates of restoration projects

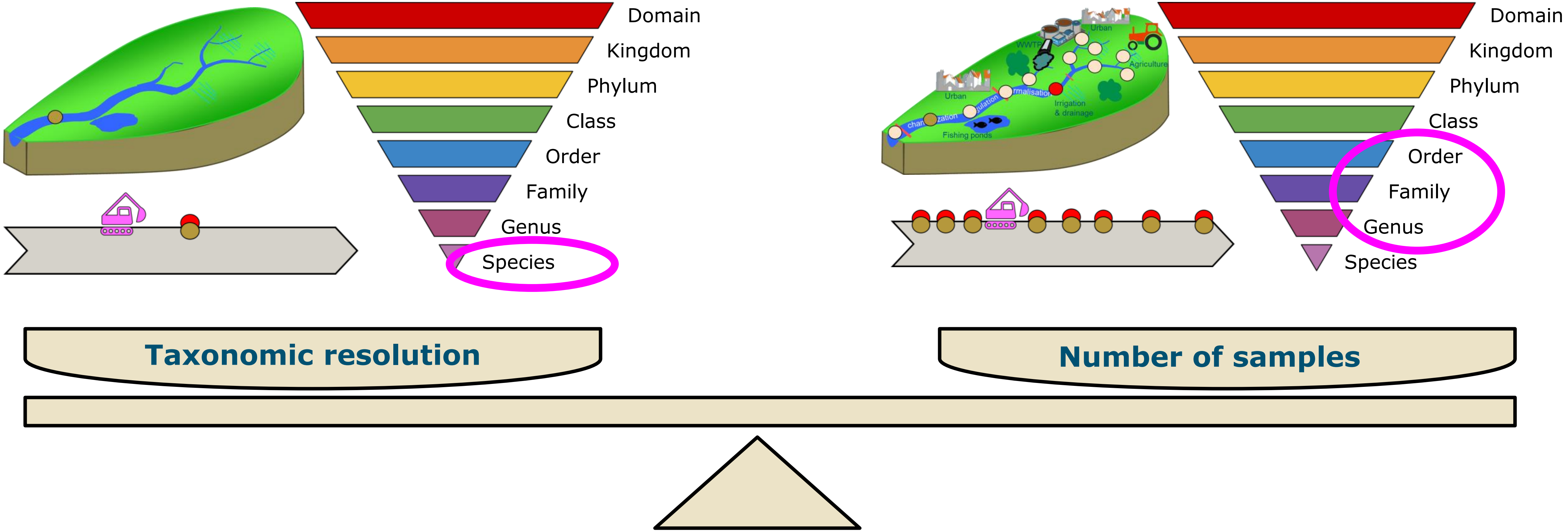
1. Diagnose limiting stressors at catchment scale to plan restoration measures

2. Assess the effectiveness of restoration measures over longer time periods





Morphological identification to species-level is time consuming and costly!



Taxonomic resolution

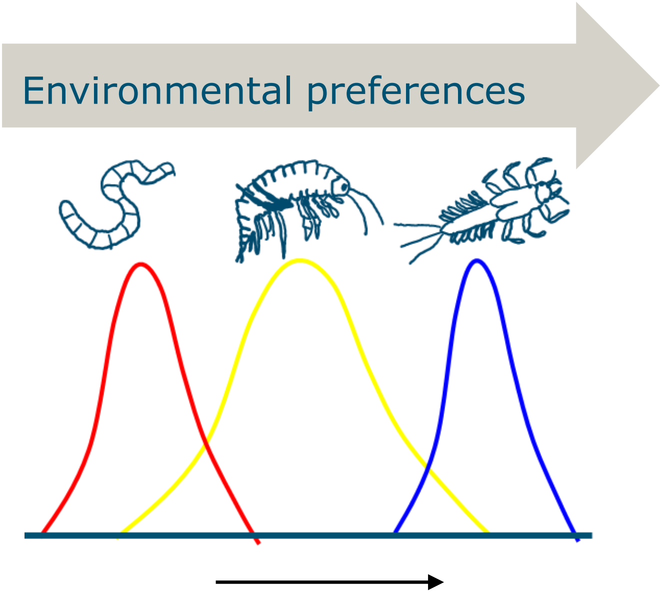
Number of samples

- ➢ DNA metabarcoding may overcome trade-off between number of samples and taxonomic resolution

DNA metabarcoding can be used to determine degree of degradation

Ecological status

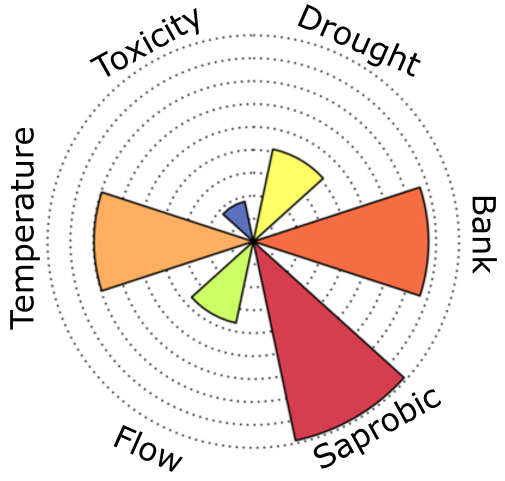
- 🟦 High
- 🟩 Good
- 🟨 Moderate
- 🟧 Poor
- 🟥 Bad



Environmental preferences

e.g. flow velocity

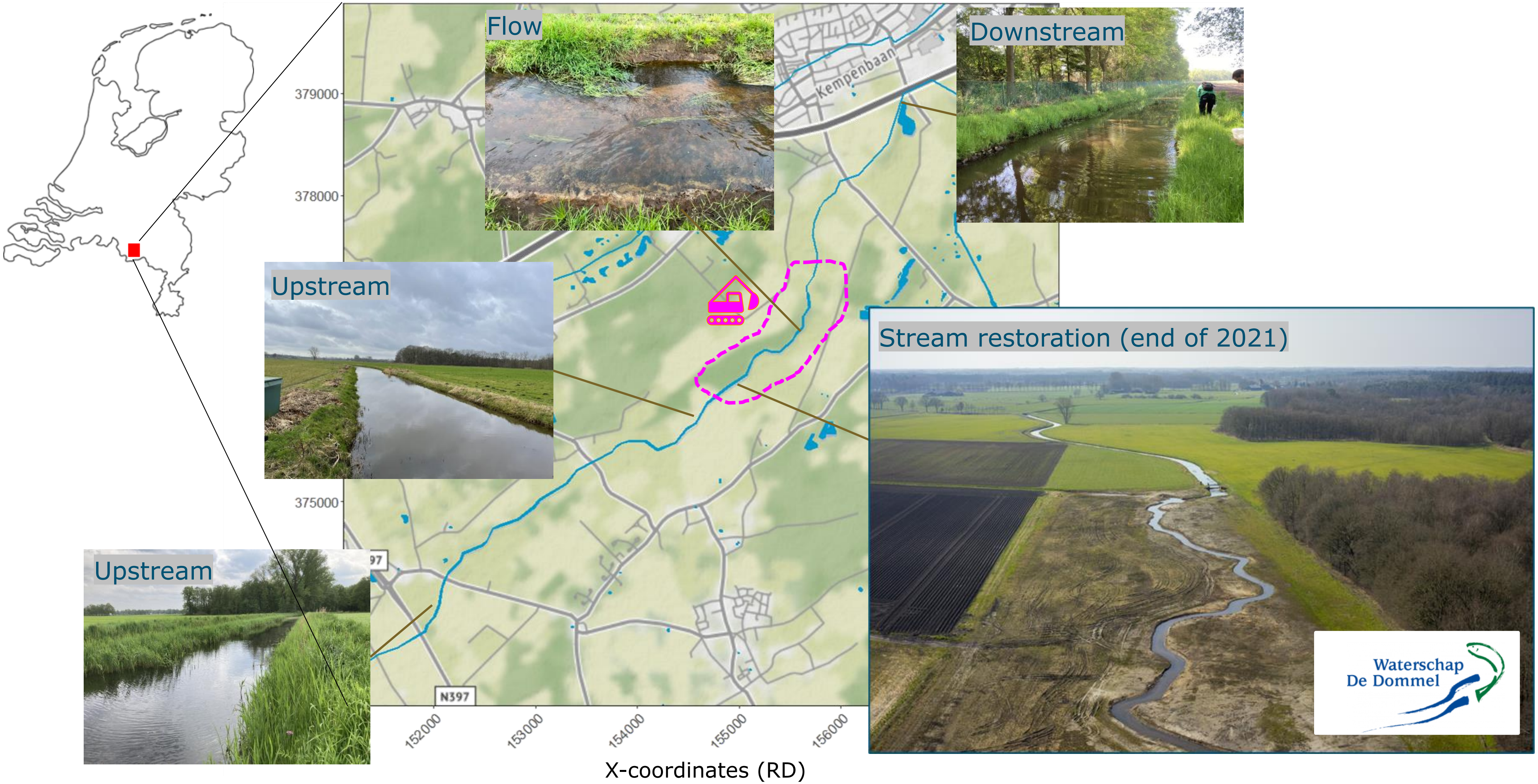
Diagnostics?



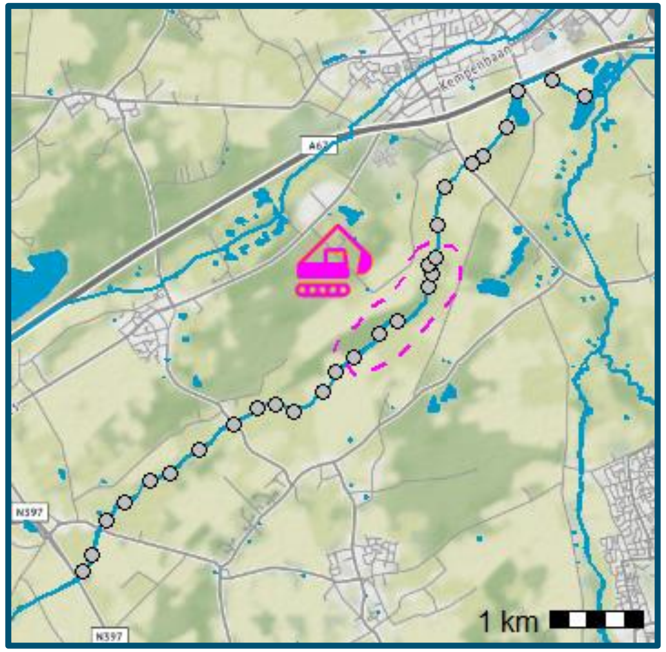
Elbrecht et al. 2017, Fernández et al. 2019,
Kuntke et al. 2020, Ji et al. 2022

Can DNA metabarcoding of macroinvertebrates be used for diagnostic purposes to assess the effectiveness of restoration measures?

Study area: stream restoration in the Run, the Netherlands



Study design: comparison of three different methods of identification



28 sites

Invertebrate sampling

Morphological identification
(genus/family/order)

Morphology bulk

DNA Metabarcoding*

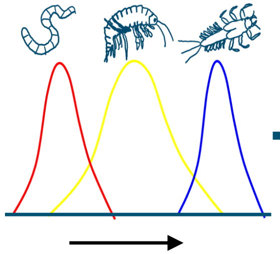
DNA bulk

Water filtration (Sylphium)

DNA Metabarcoding*

eDNA water

Diagnose effect of flow



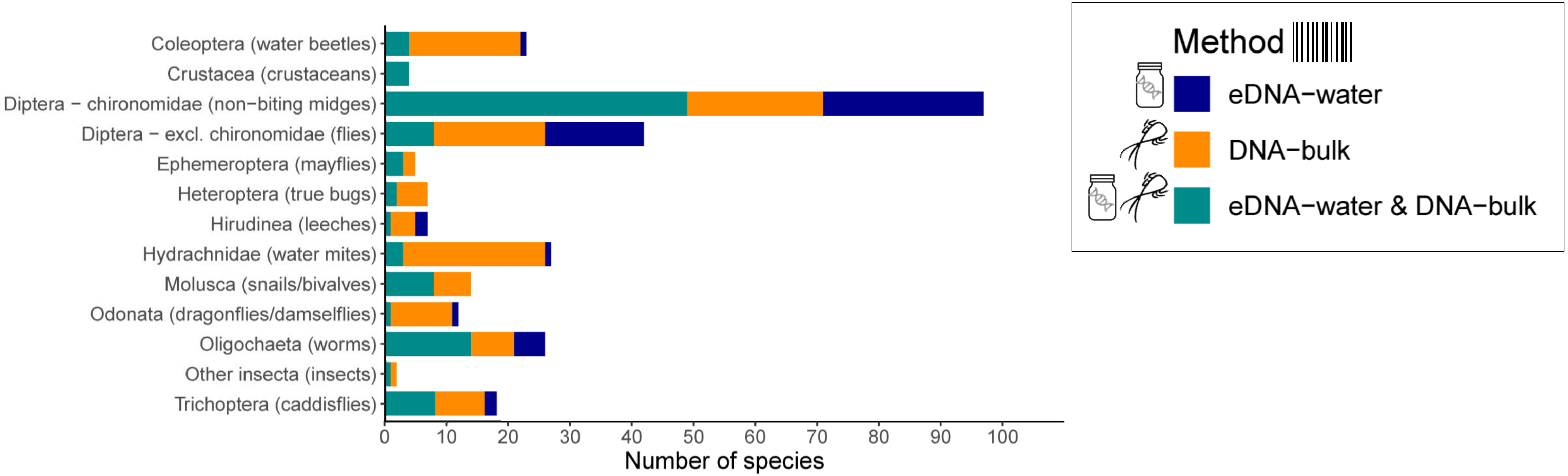
Preference flow velocity

Verberk et al. 2012

Stress-score
- ● 0.0–0.1
- ● 0.1–0.2
- ● 0.2–0.3
- ● 0.3–0.4
- ● 0.4–0.5
- ● 0.5–0.6
- ● 0.6–0.7
- ● 0.7–0.8
- ● 0.8–0.9
- ● 0.9–1.0

**Metabarcoding based on COI marker (Leray et al. 2013) & taxonomy assignment using BOLD (Buchner & Leese 2020)*

Results (1): identification of species using DNA-metabarcoding

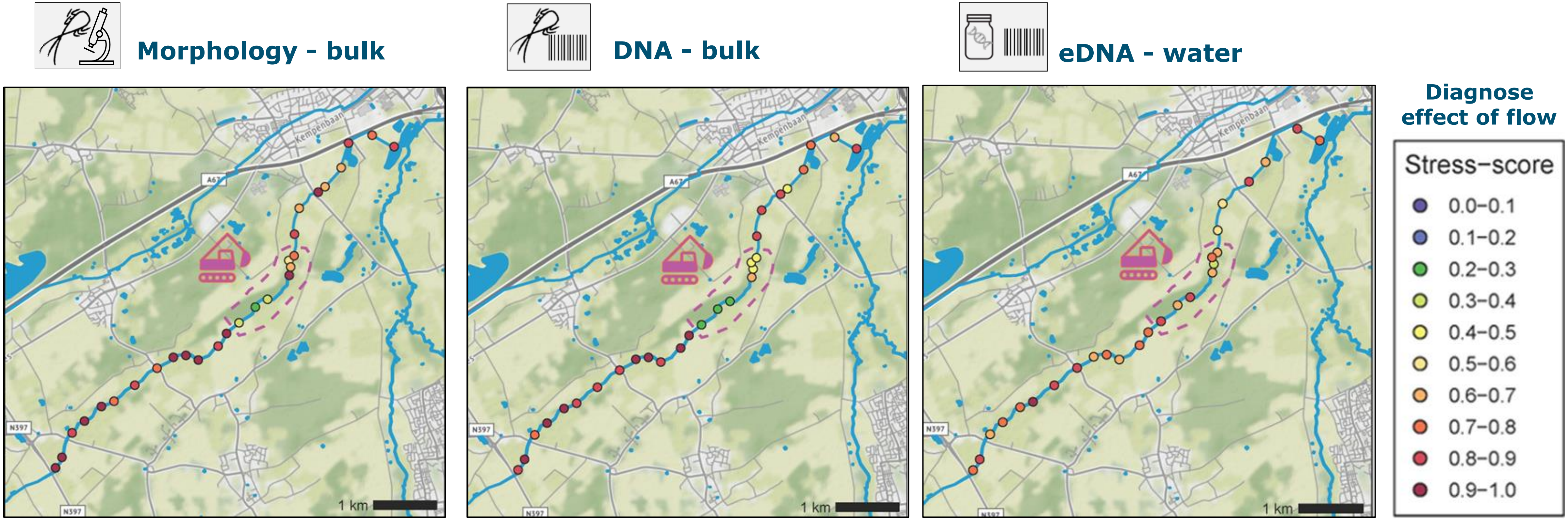


DNA-bulk samples detected 230 species, representative for the community in the stream

eDNA-water samples detected less species (160 species, mostly diptera)

**animals with exoskeleton shed less eDNA? eDNA settles in sediment? Effect of filter or primer set? (Gleason et al. 2021)*

Results (2): comparison of methods to diagnose effect stream restoration



Morphology-bulk and DNA-bulk samples indicated better flow at restored section of the stream

eDNA-water samples did not distinguish differences in flow, as indicative species were not detected

Gea van der Lee

Conclusions

DNA metabarcoding of invertebrate bulk samples was a cost-effective method to gain a complete picture of the species present at multiple sampling points, which can facilitate diagnosing the effectiveness of restoration measures.