Environmental DNA

River University – 3 August 2023

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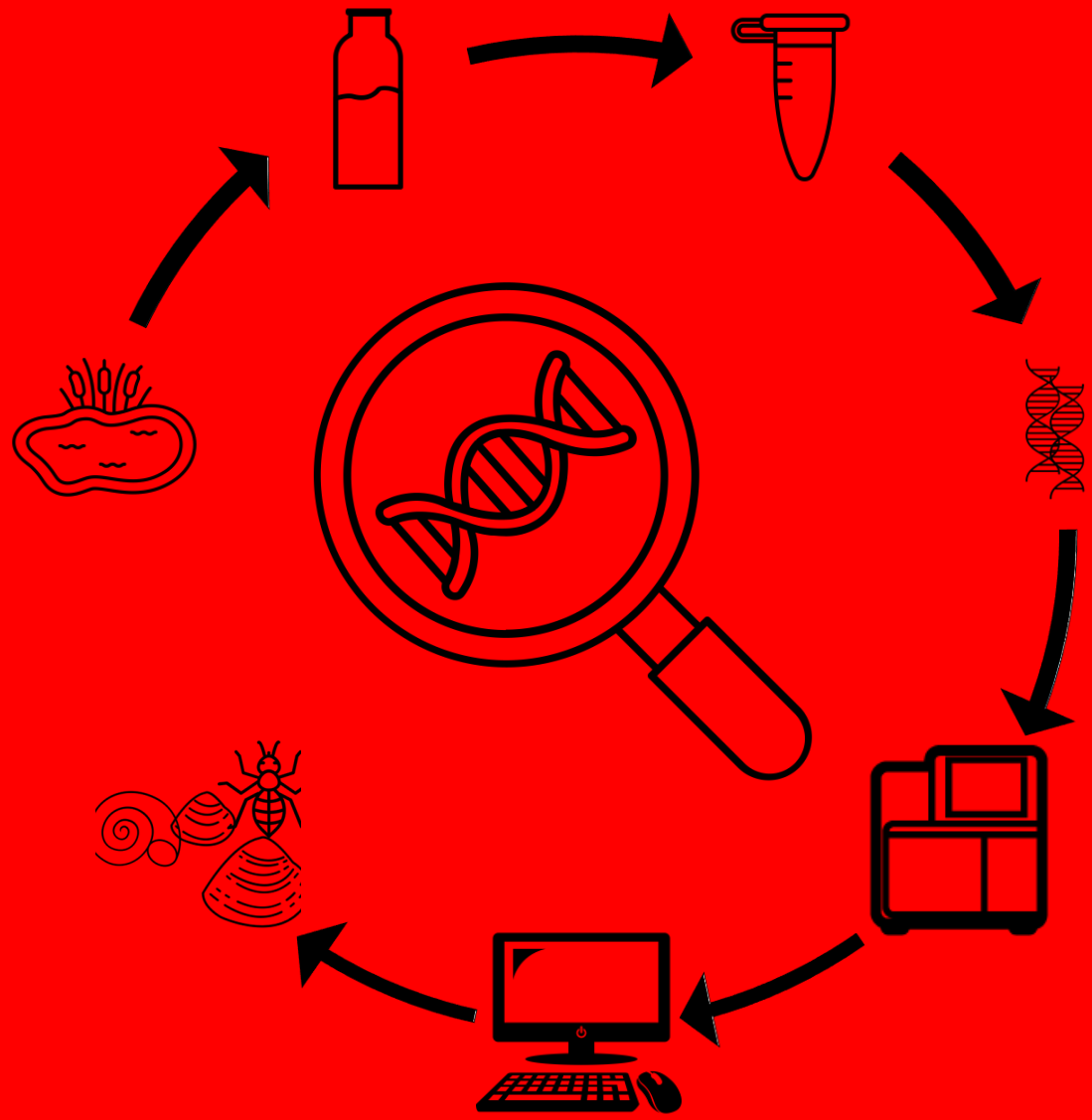
Université de Strasbourg



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www.emysr.cnrs.fr

SENCKENBERG world of biodiversity

Coalition Clean Baltic

Rewilding Oder Delta

Introduction

2012 – 2017: Bachelor Chemistry,

Utrecht University, Netherlands

2017 – 2020: Master Environmental Sciences,

Aquatic Ecology and Water Quality Management,

Wageningen University and Research, Netherlands

Since 2022 : PhD Research **"Ecology of man-made pond networks for wetland biodiversity conservation"**,

University of Strasbourg, France

Supervised by Isabelle Combroux, Kathrin Theissinger and Corinne Grac

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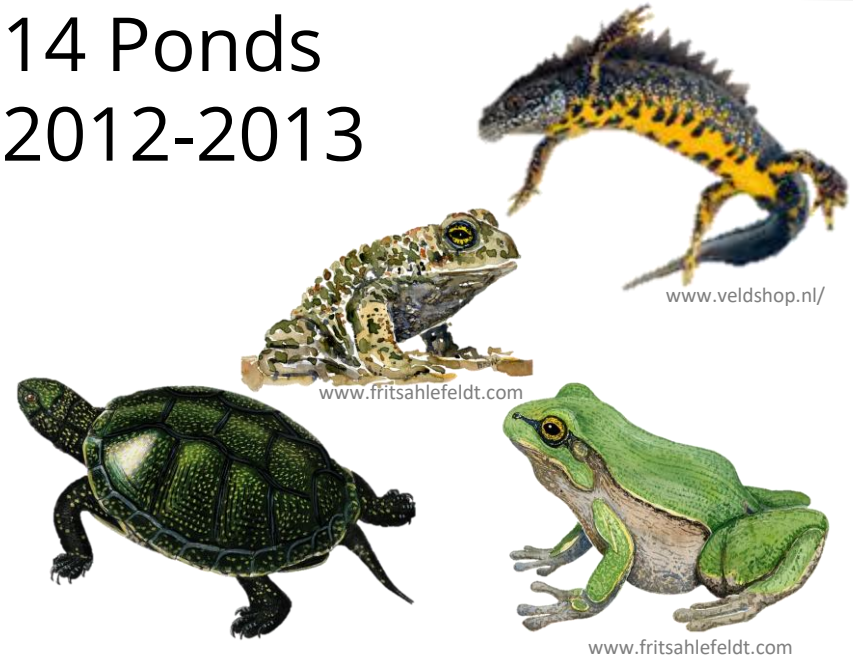
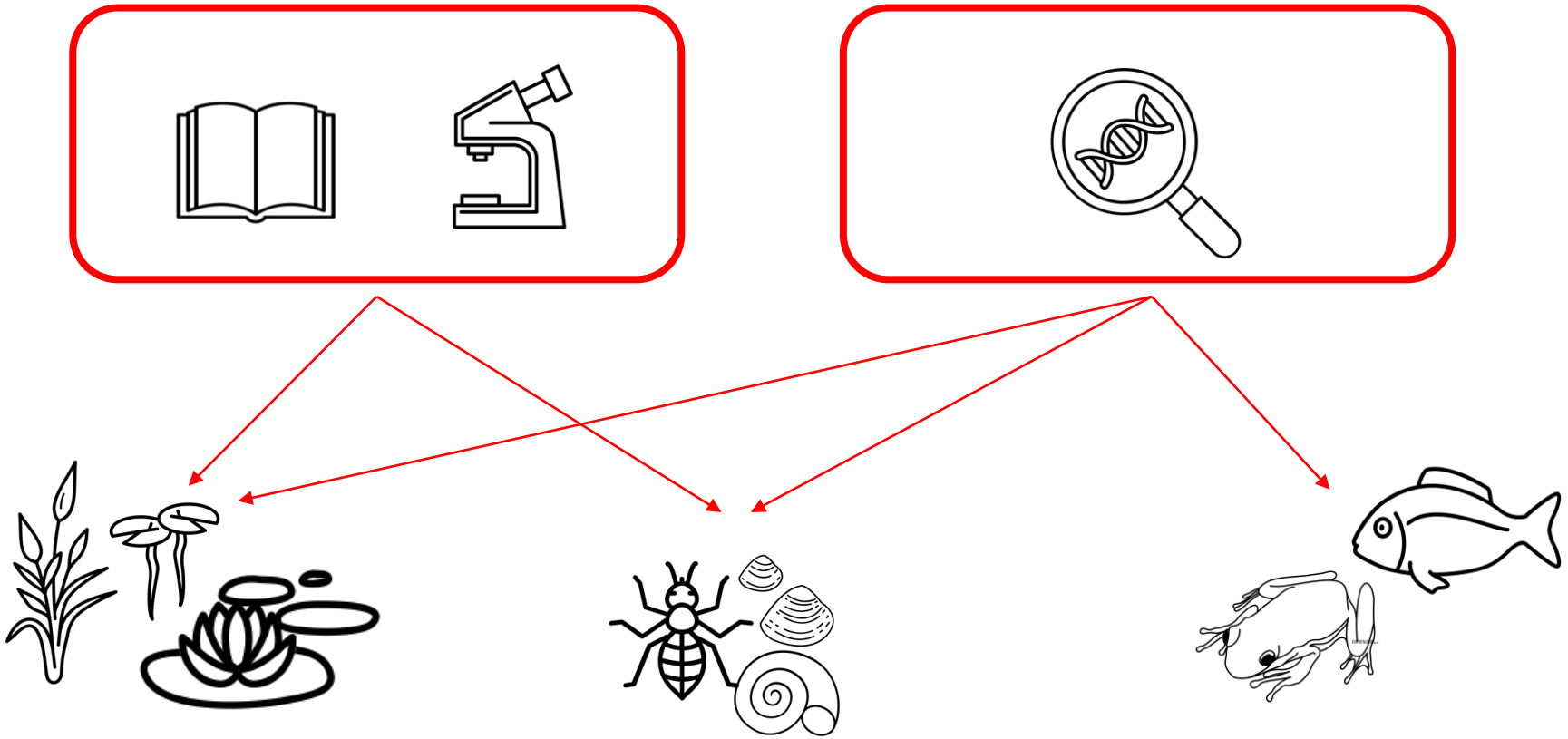
	Woerr, France	Neuburg, Germany	Silene,Latvia
Actions	6 Ponds, 2 lagunas 2011-2012 or 2015 + 2 basins and gravel pit rehabilitations	14 Ponds 2012-2013	27 ponds 2013 or 2018
Target species			
Example of pond			

My project

What variables determine the **biodiversity** and **habitat provisioning function** of **created pond networks**?



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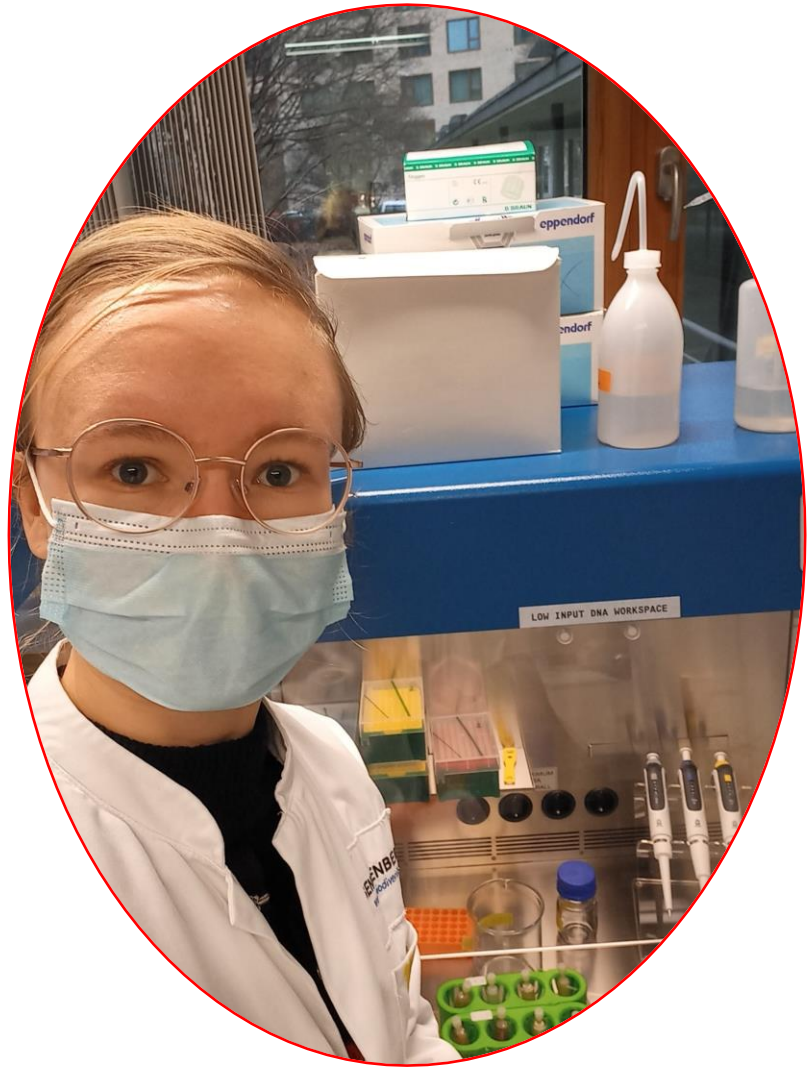
eDNA work in my project



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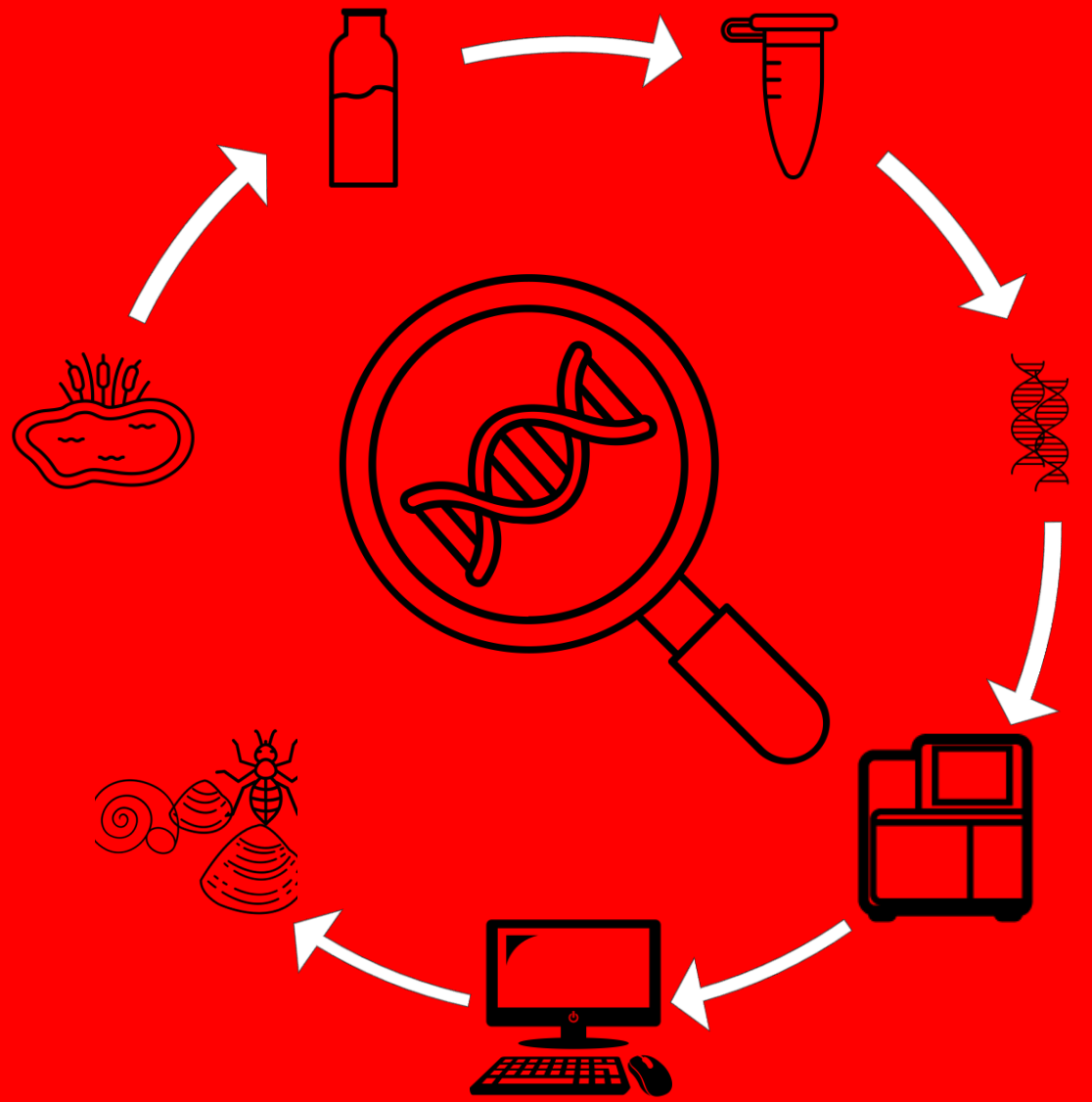
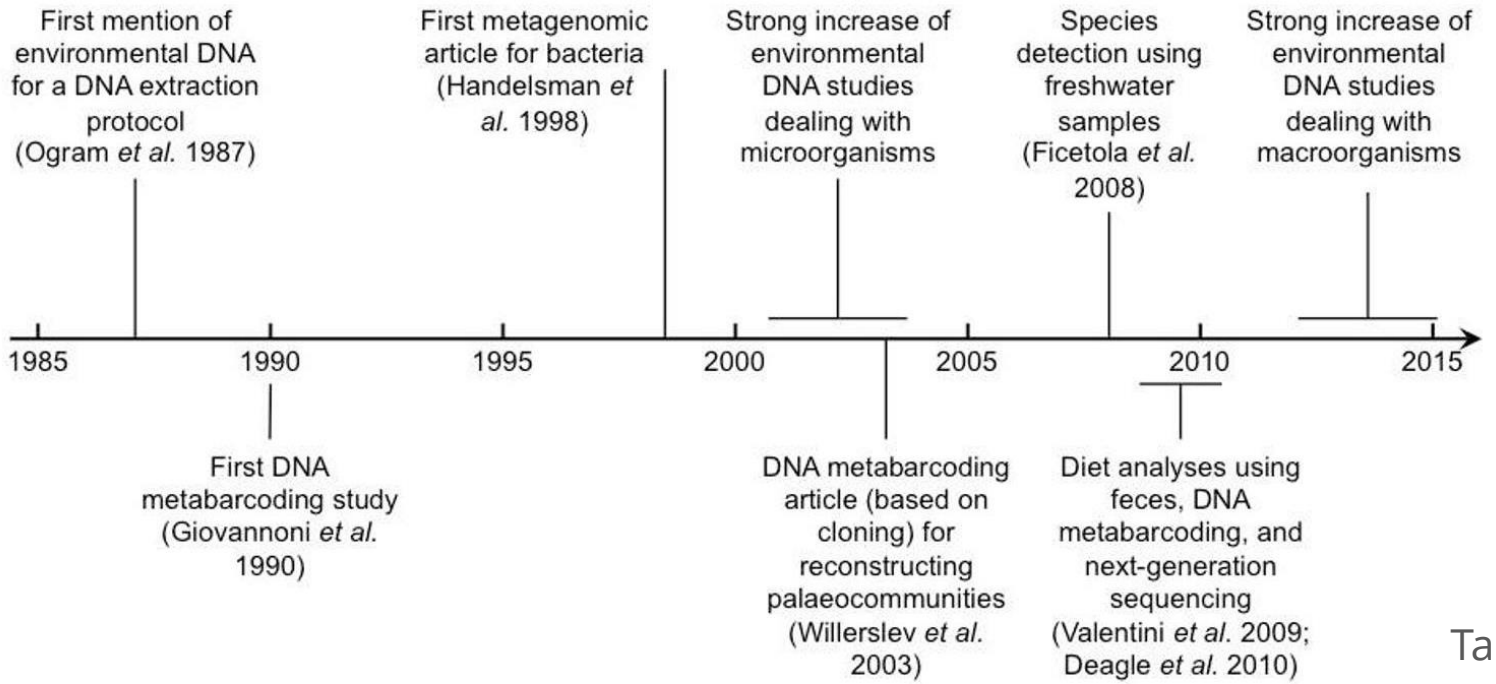
Freshwater Environmental DNA



What is environmental DNA?

Mixture of DNA in the environment

Soil | Sediment | Water | Biofilms | Faeces

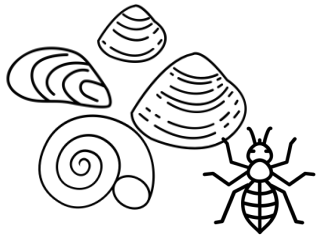


A young field

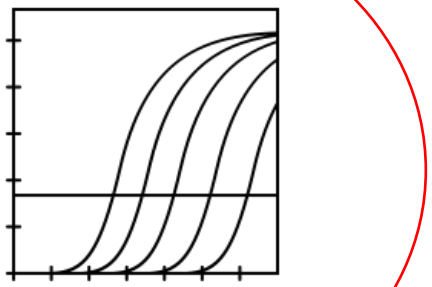
Taberlet et al. (2018)

Barcoding and metabarcoding

Single species



Whole community



qPCR

HTS

Example barcoding: Great Crested Newt survey

Traditional survey:

4 to 6 visits between mid-March and mid-May

eDNA qPCR:

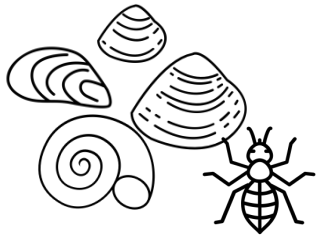
1 visit between March and August

Triturus cristatus

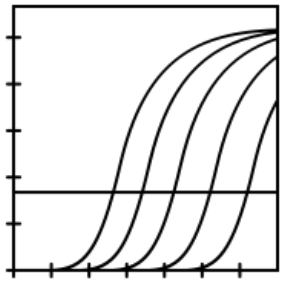
Rees et al. (2014), Rees et al. (2017)

Barcoding and metabarcoding

Single species



Whole community

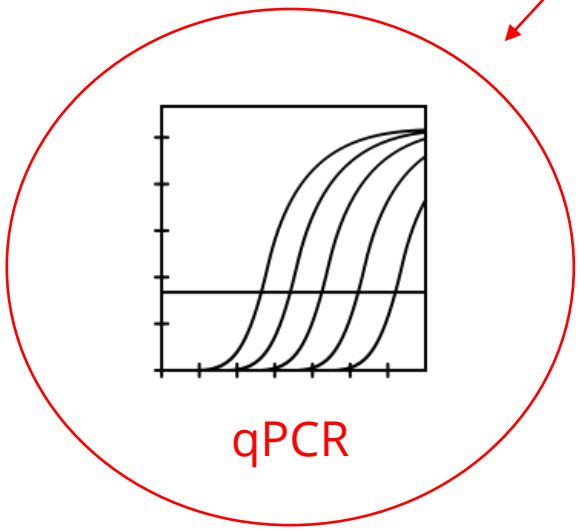


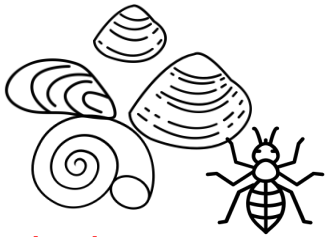
qPCR

HTS

Barcoding and metabarcoding

Single species





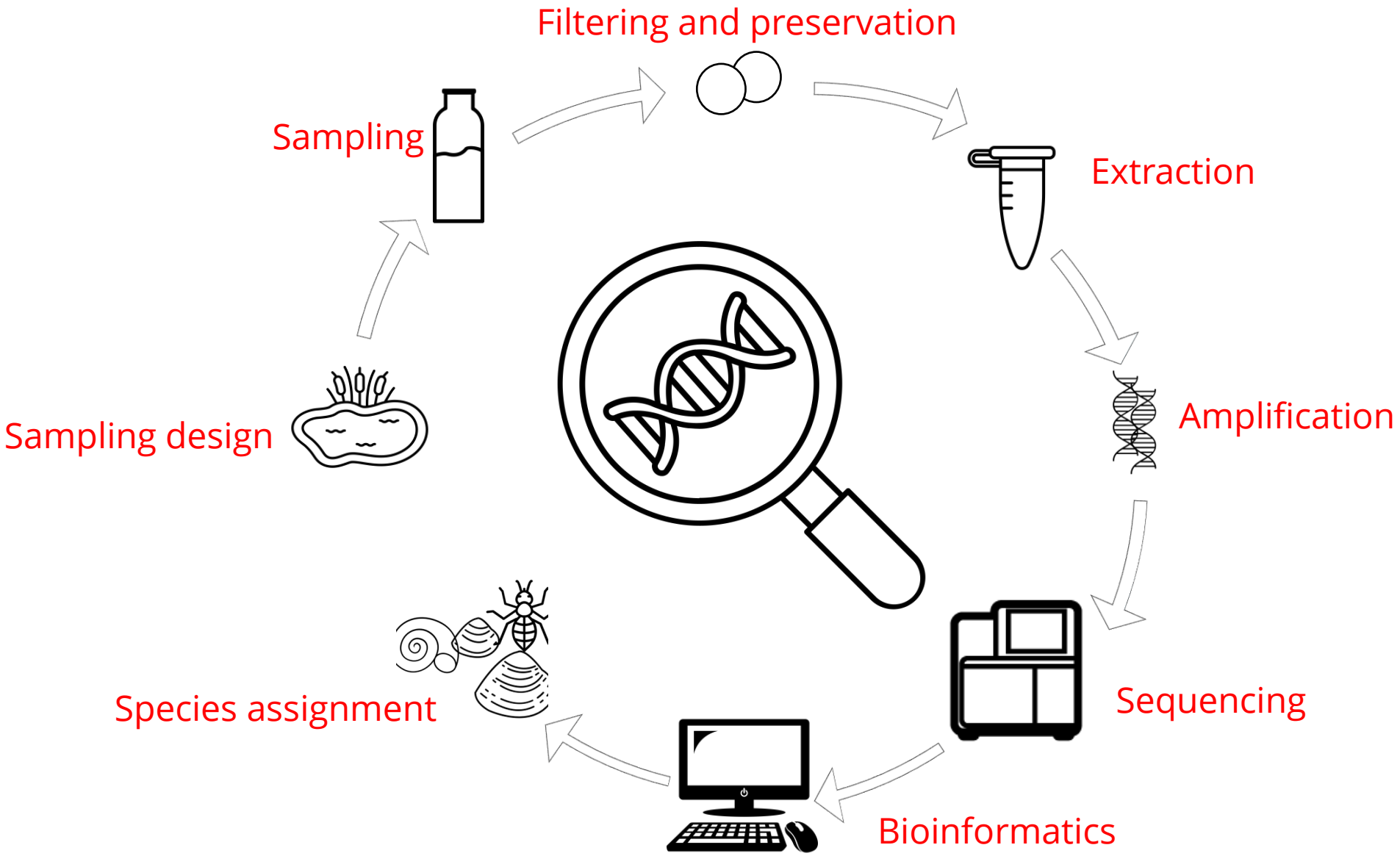
Whole community

Conserved region

Variable region
=metabarcode

Conserved region

Aquatic eDNA metabarcoding workflow



Comparison with traditional methods

Keck et al. (2022)

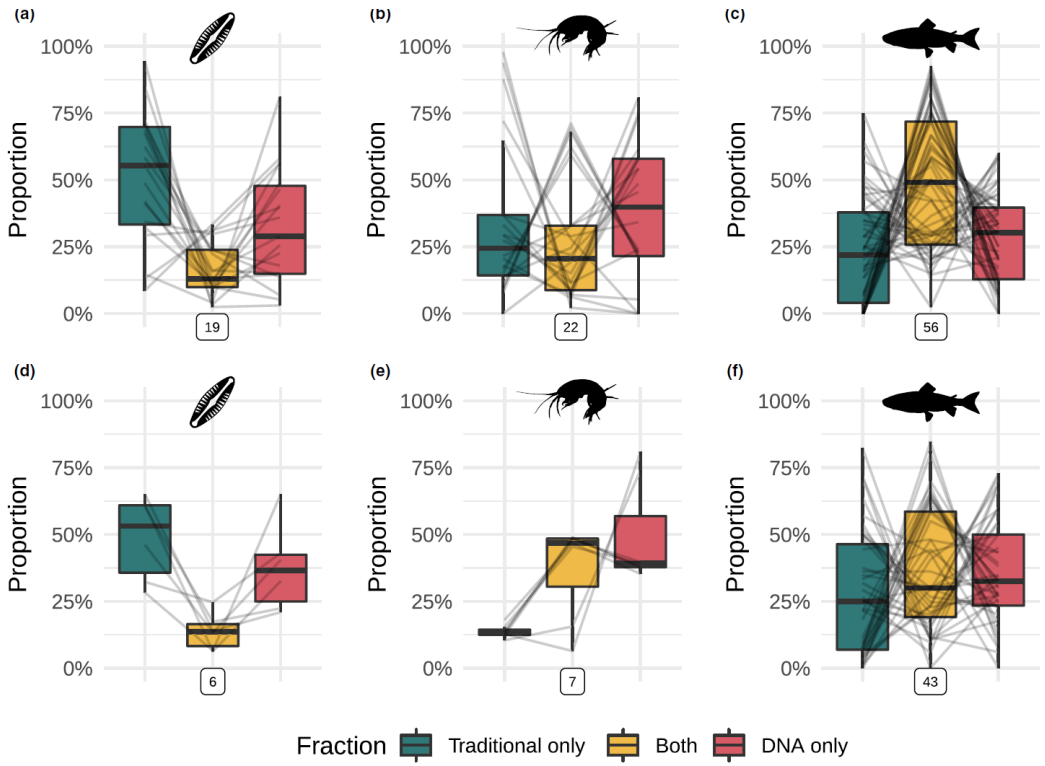


FIGURE 4 Relative fraction of diversity detected by the traditional method only, by DNA metabarcoding only and by both methods. Data are presented for different groups of organisms identified at species level only. Boxplots show medians, first and third quartiles, and full ranges (limited to 1.5 × interquartile range). Grey lines connect values from the same comparison. Framed numbers below each panel indicate the number of comparisons represented. (a–c) Gamma diversity for plankton and microphytobenthos, macroinvertebrates and fish. (d–f) Alpha diversity for plankton and microphytobenthos, macroinvertebrates and fish

Fish: as good as or better than traditional methods

Results plankton, microphytobenthos and macroinvertebrate communities very different from traditional methods

Plant aquatic eDNA metabarcoding

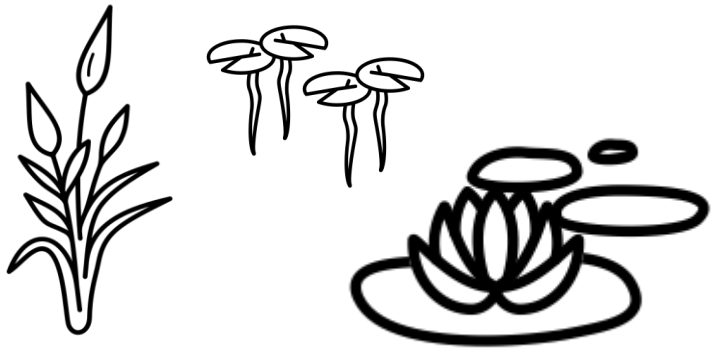
Traditional survey :

When plants flower

Overestimate floating leaved big plants

eDNA metabarcoding :

When plants are present



Need multiple metabarcodes

Espinosa Prieto et al. (2023)

Constraints

Exact location, life stages, number not known

Incomplete reference databases

Only species detection

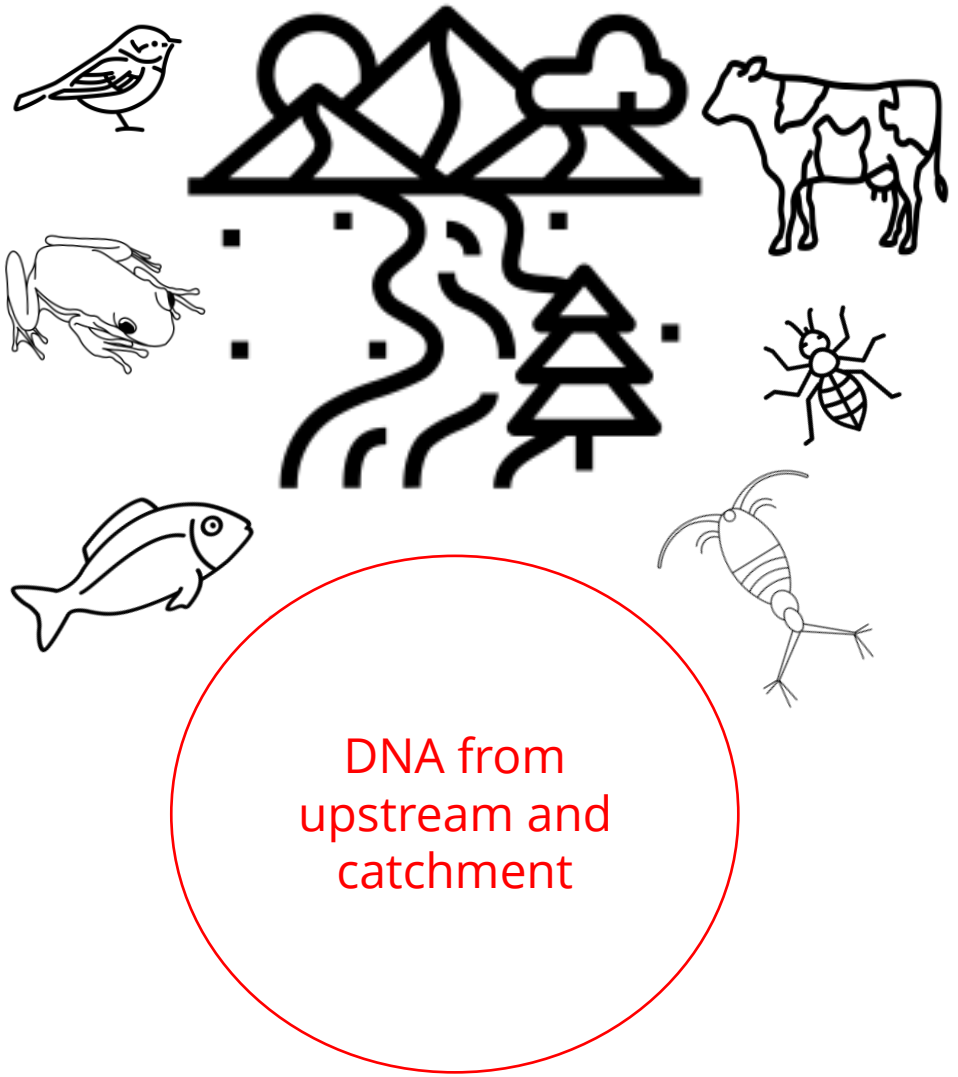
Methods not standardised

Plastic waste

Example: whole river biodiversity assessment

Cannon et al. (2016)

Group	Primer pair	No. species detected
Mammals	16Smam	17
Insects+Arachnids	COI_ZBJ_Art	15
Birds	Aves12S	8
Fish	FishCB	8
Copepods	Cop28S	4
Amphibians and reptiles	AmpCB	2
Vascular plants	trnL	-
Algae	23SrDNA	-
Fungi	FungusITS	-
Bryophytes	BryoTrnL	-
Diatoms	Diatom18S	-
Archaea	Archaea16S	-



Example: bivalve biodiversity

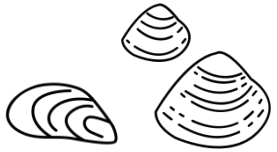
Traditional surveys:

Difficult to find

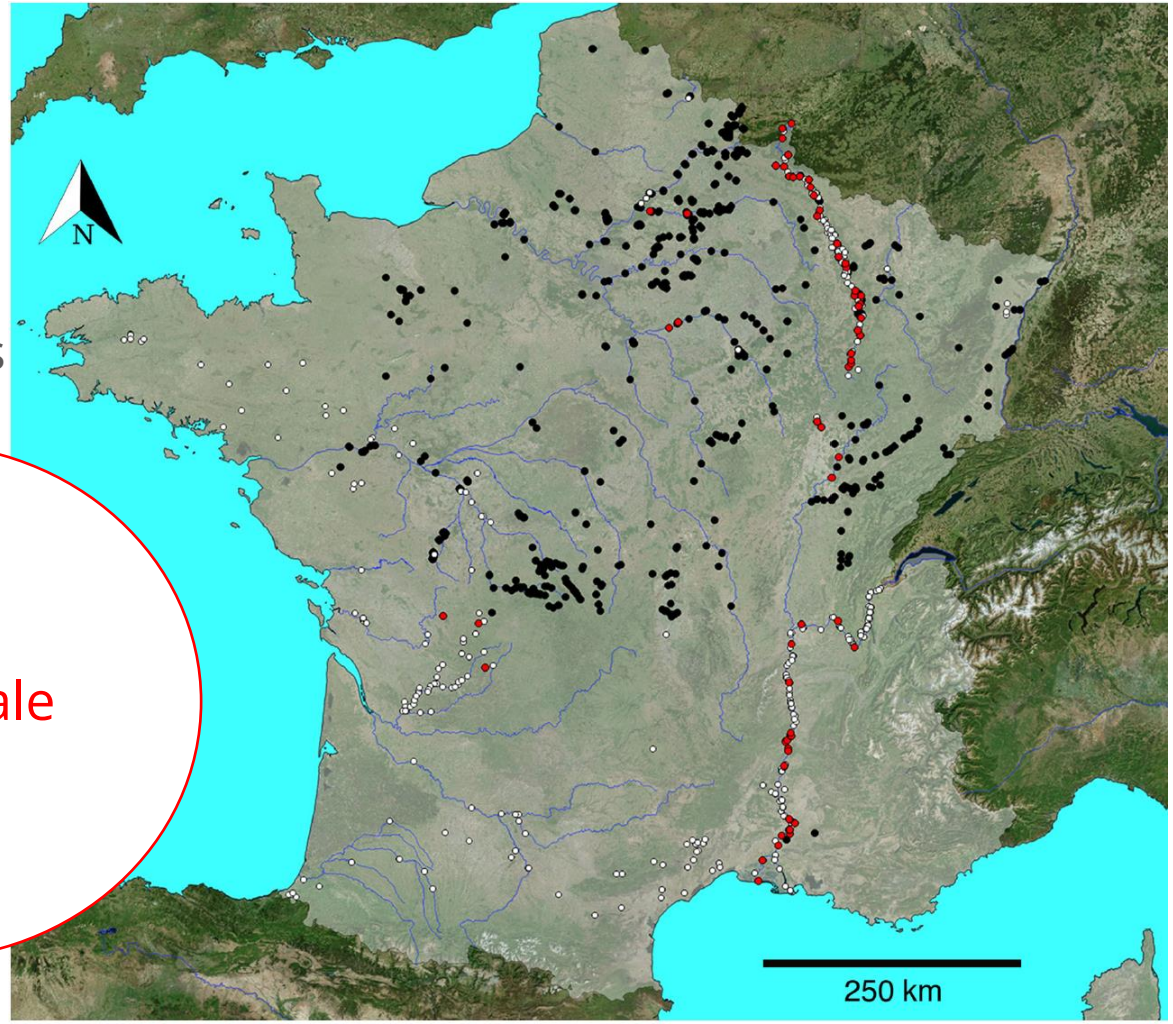
Difficult to identify

Differnt methods (scuba divers) different species

Often need to kill



Large scale



Prié et al. (2020)

Fig. 6 *Unio crassus* in France. White dots: eDNA sampling sites with absence; red dots: eDNA sampling sites with presence; black dots: all available data prior to eDNA deployment, with no limit of time. The data acquireddown stream the Rhône River and in the south-west is completely nev

Conclusions

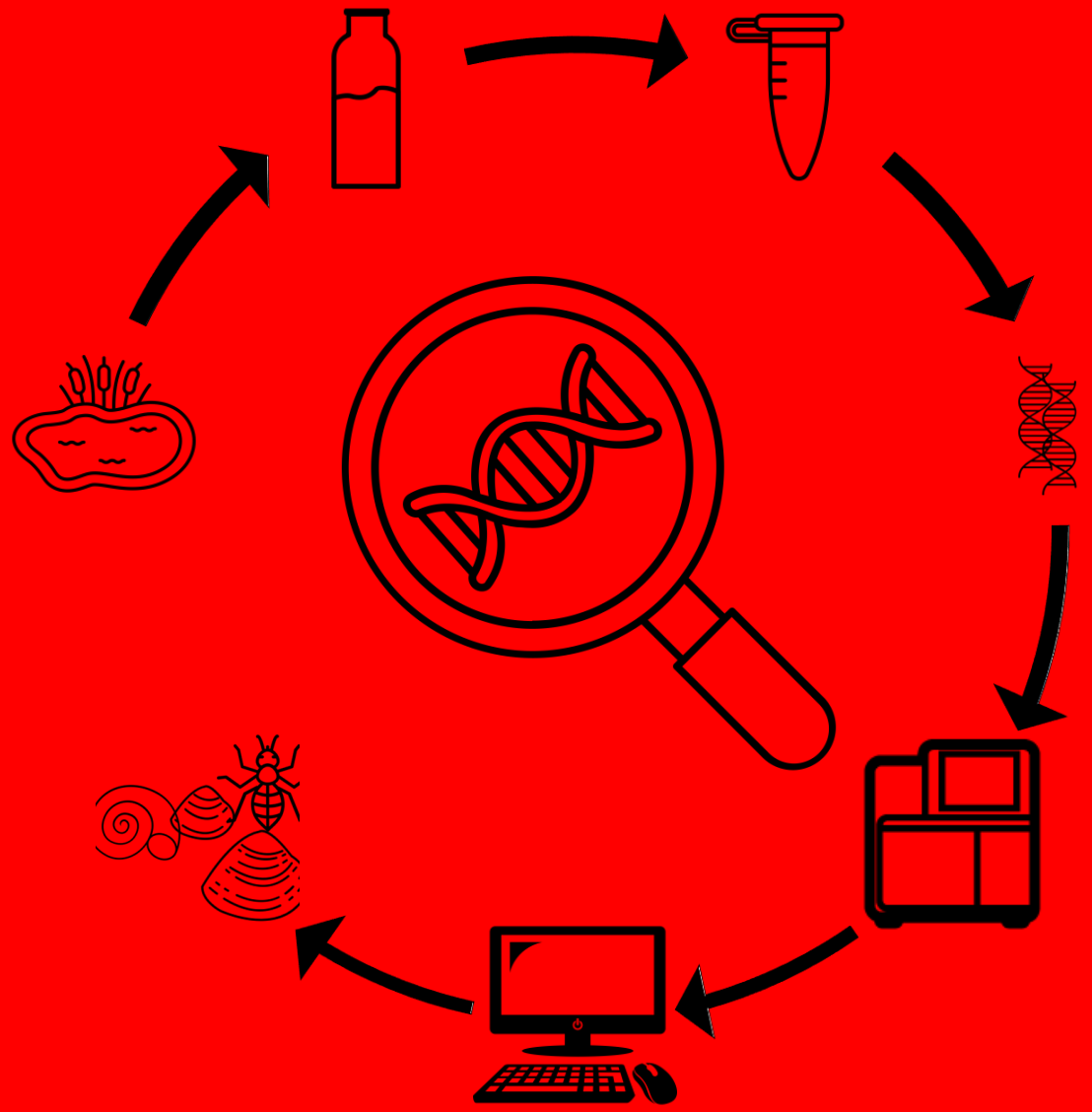
Applied for detection of invasive and rare species

Works well for fish, amphibian and bivalve communities

Results plankton, microphytobenthos and macroinvertebrate communities very different from traditional methods

“Another tool in the toolbox”

Questions?



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