

Temperate reef assemblages across pollution gradients, what can eDNA reveal compared to ‘traditional’ sampling methods?



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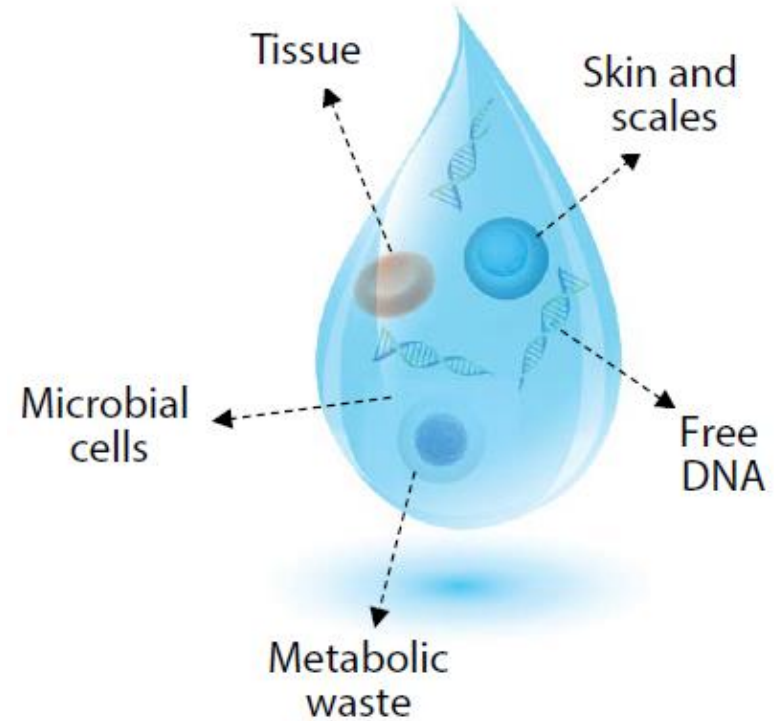
Presenter: Lara Denis-Roy

Supervisors: Prof Graham Edgar, Prof Craig Johnson,
Dr Katrina West

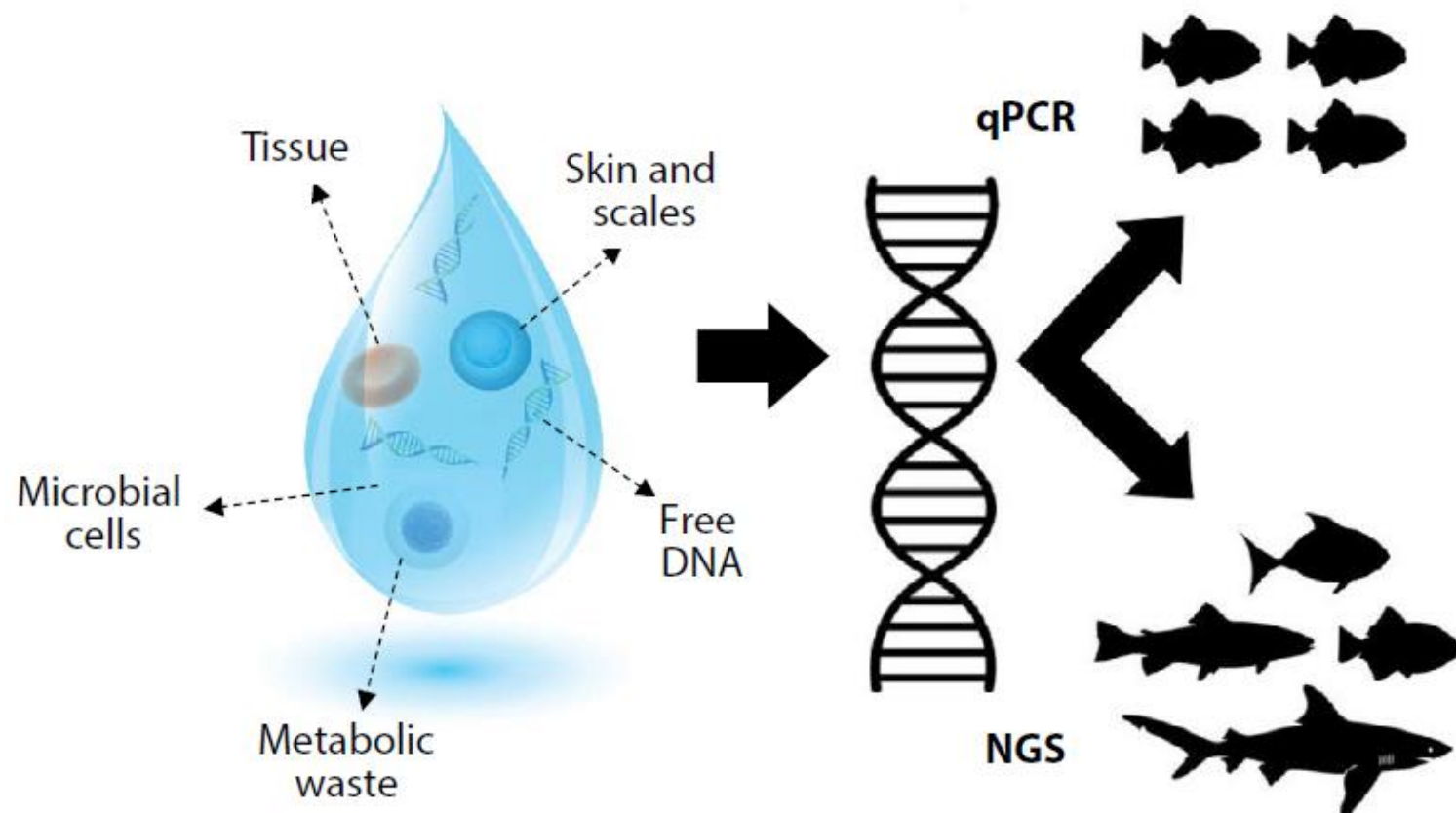
The CSIRO logo, consisting of a blue circle containing a white stylized bar chart with five bars of varying heights, and the word "CSIRO" in white capital letters below it.

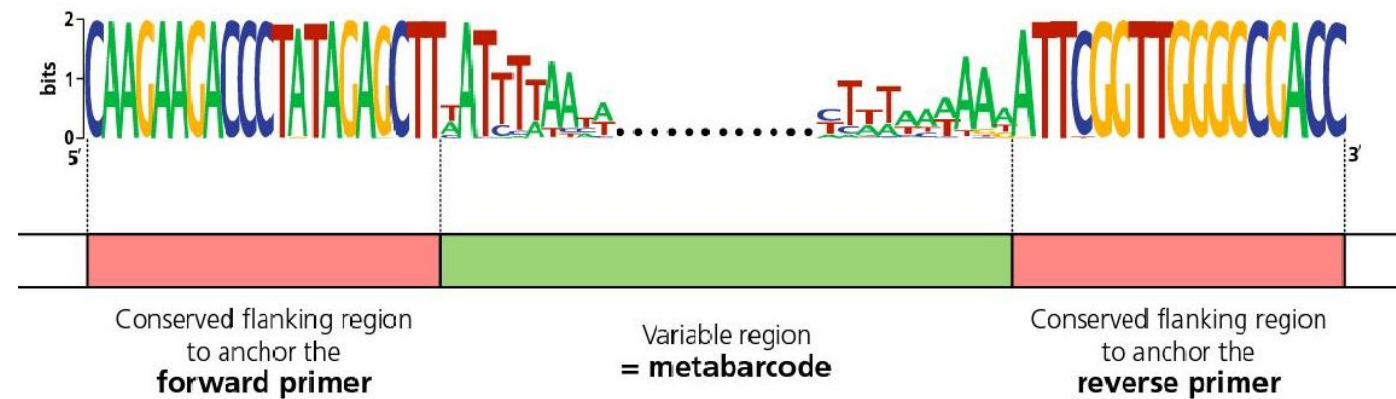
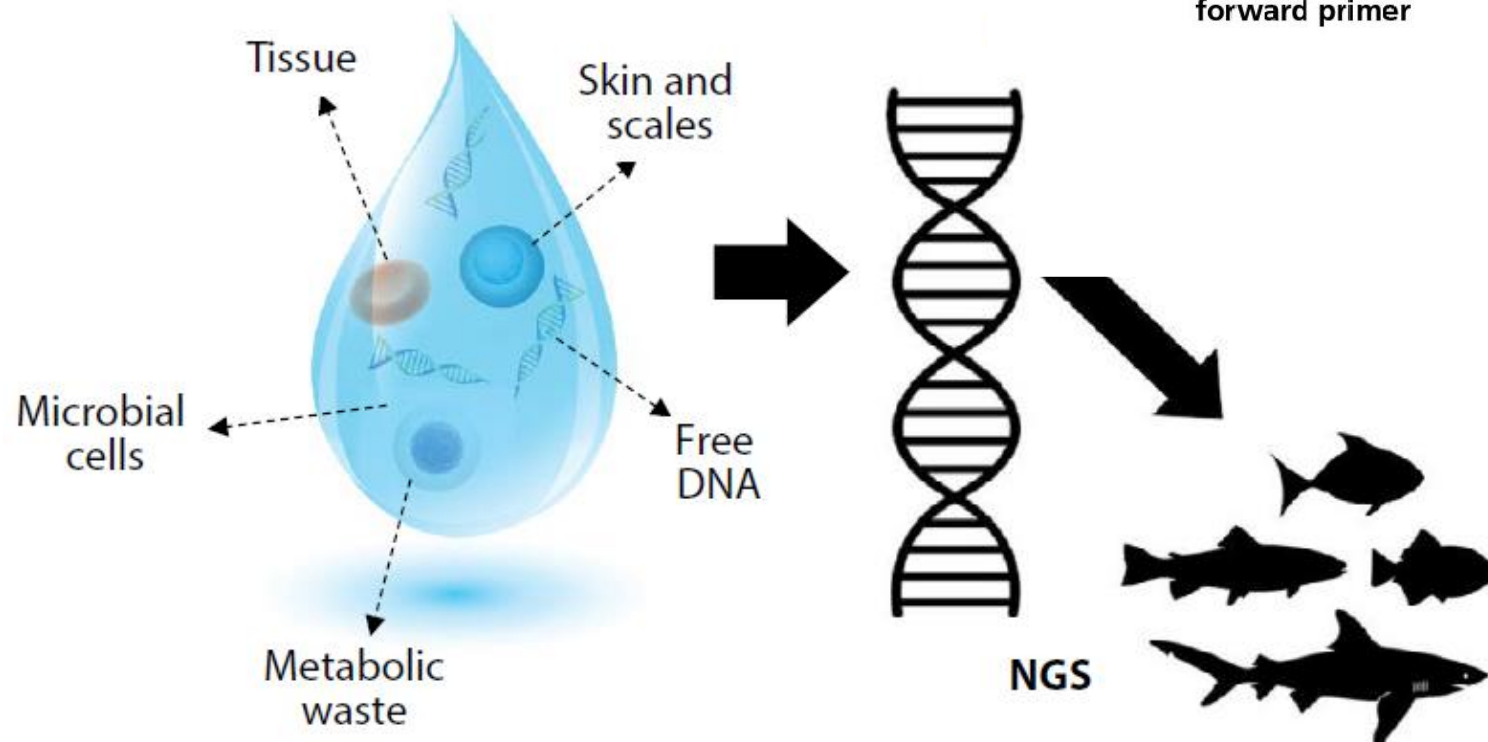
CSIRO

‘Life in a drop’ (Gilbey et al., 2021)



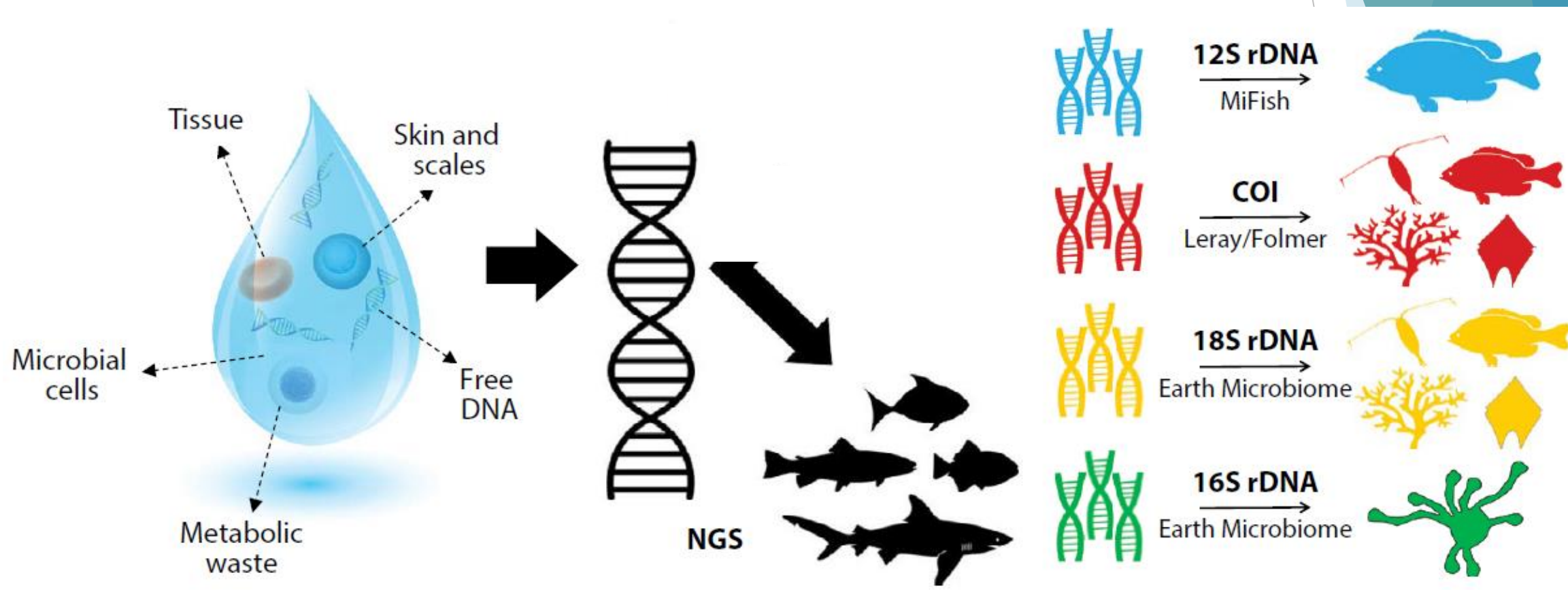
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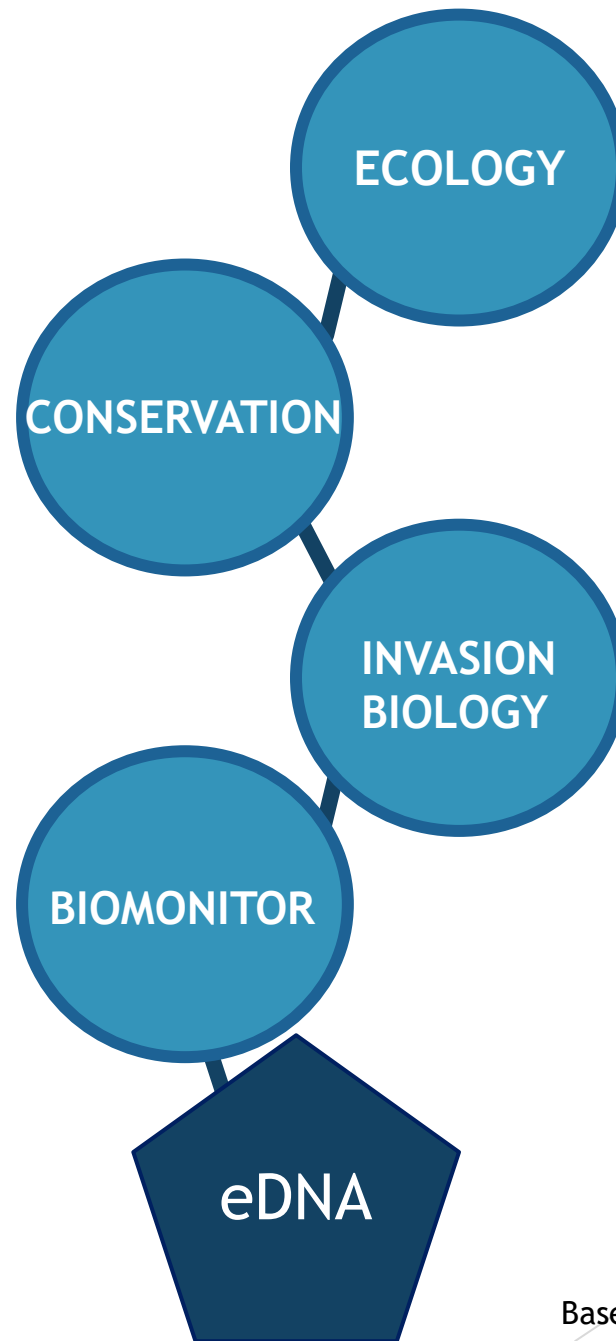


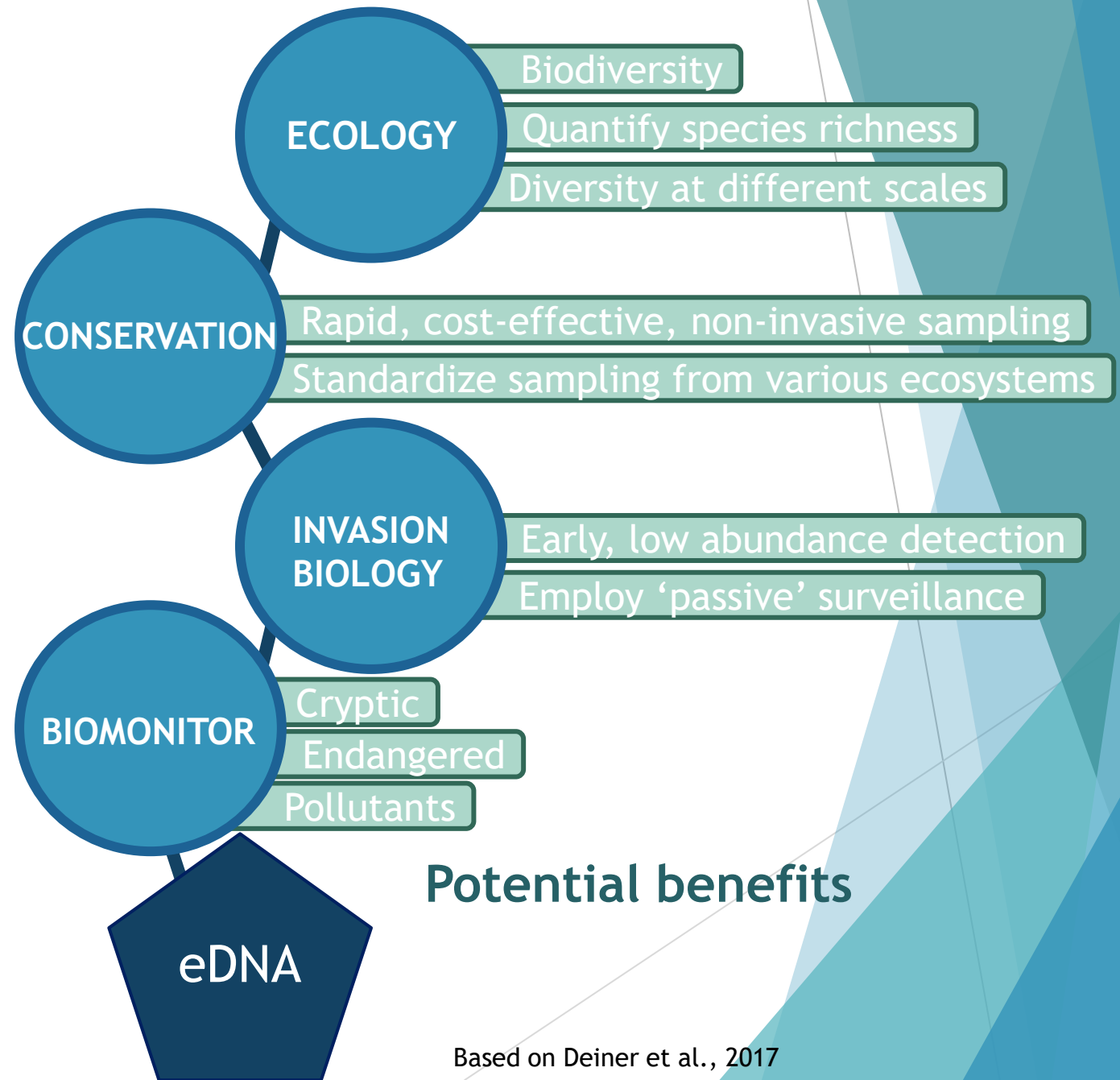


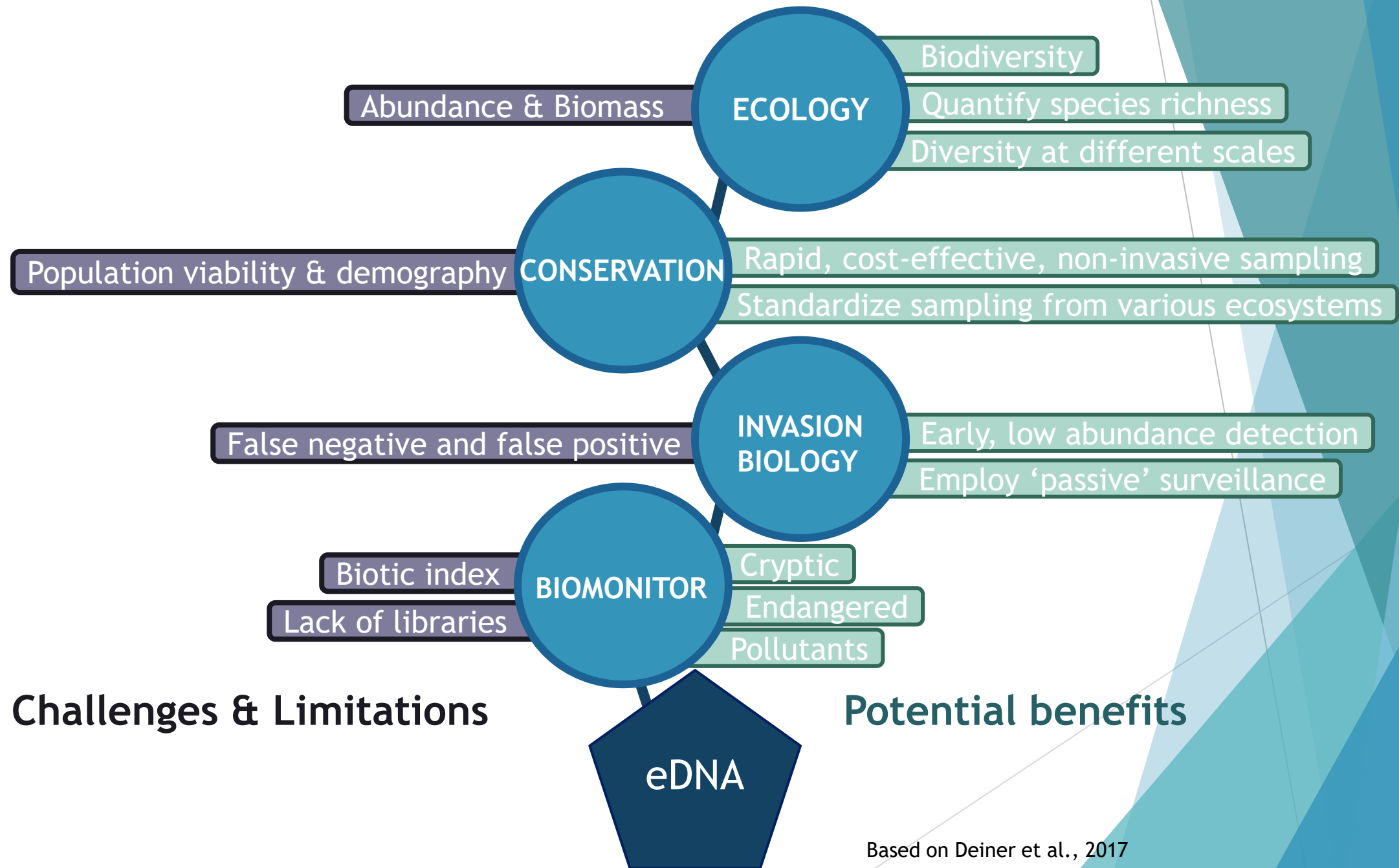
Taberlet et al., 2018

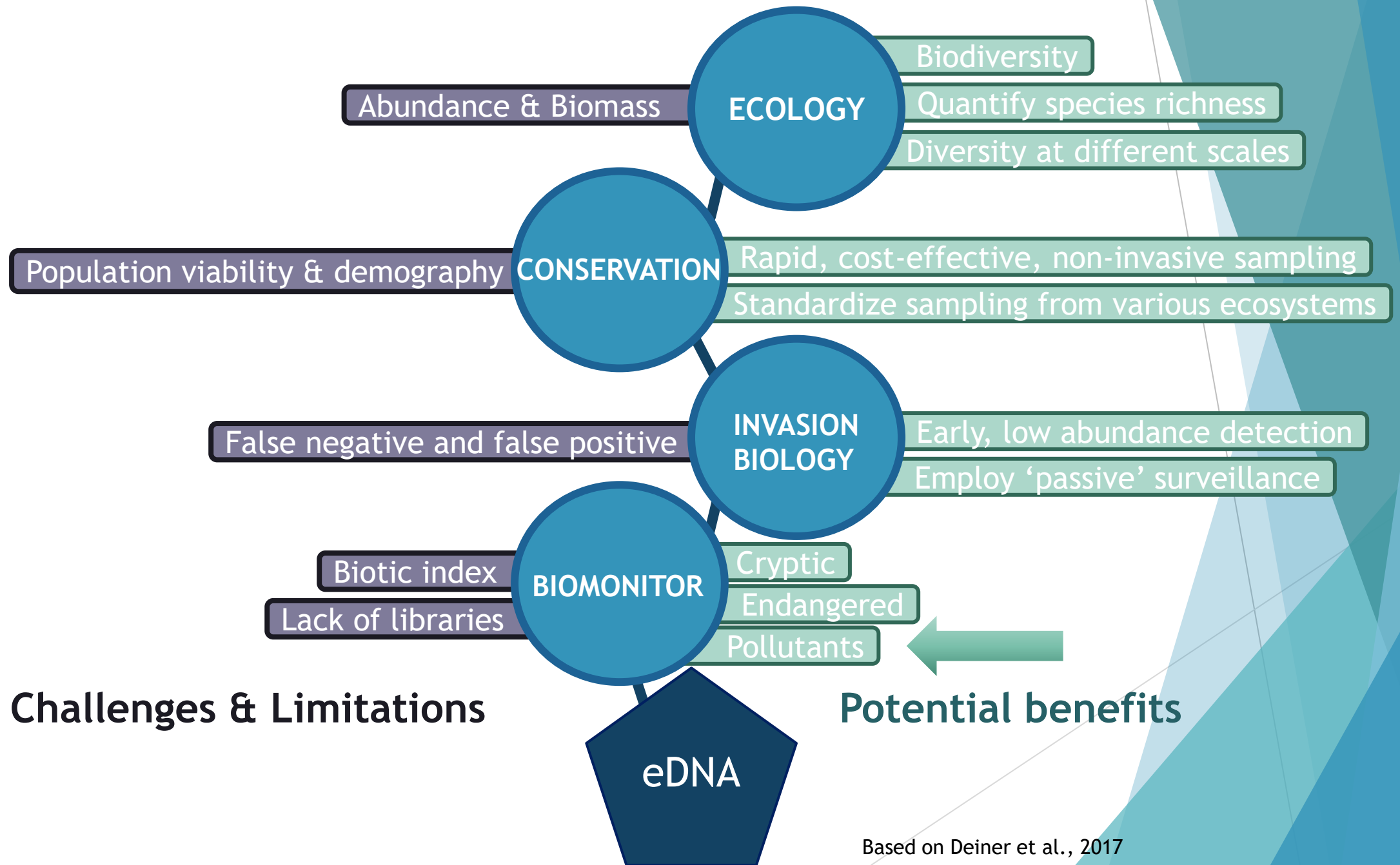
Chavez et al., 2021





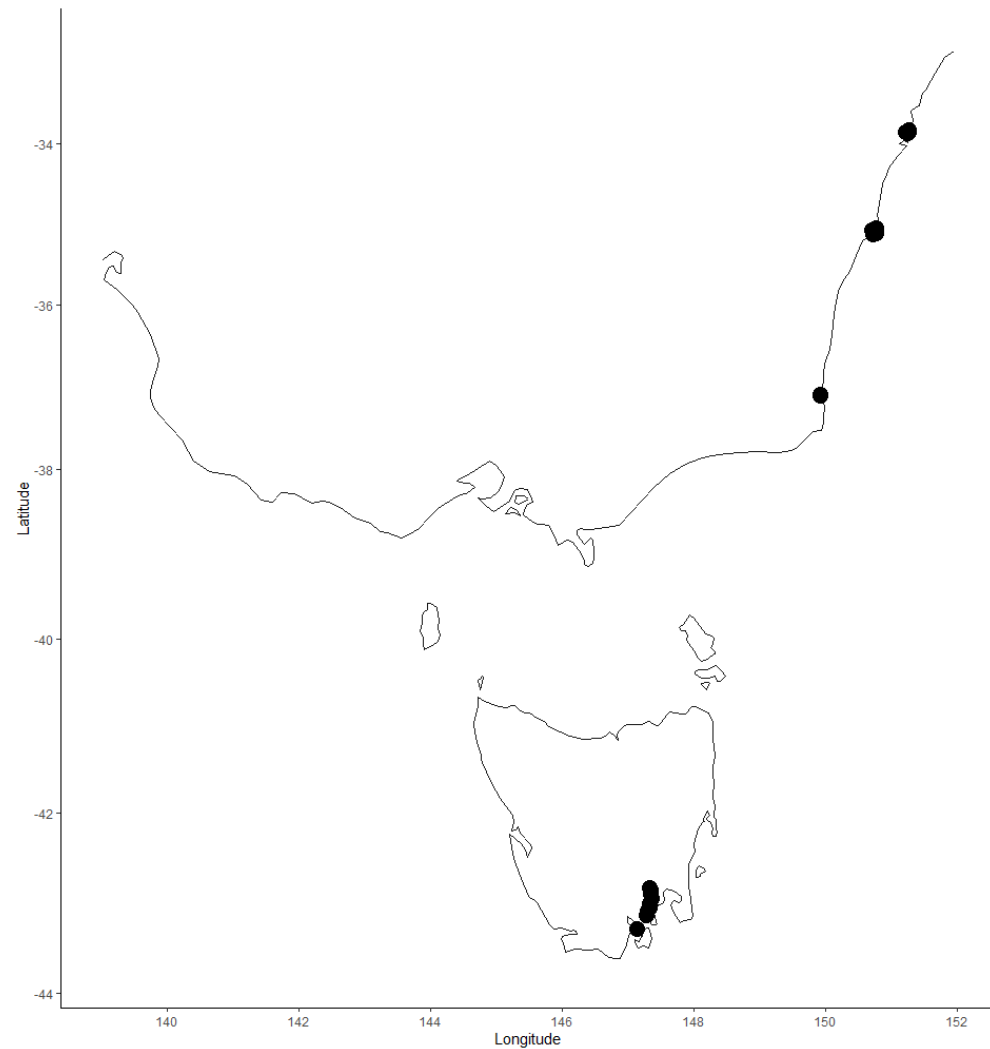




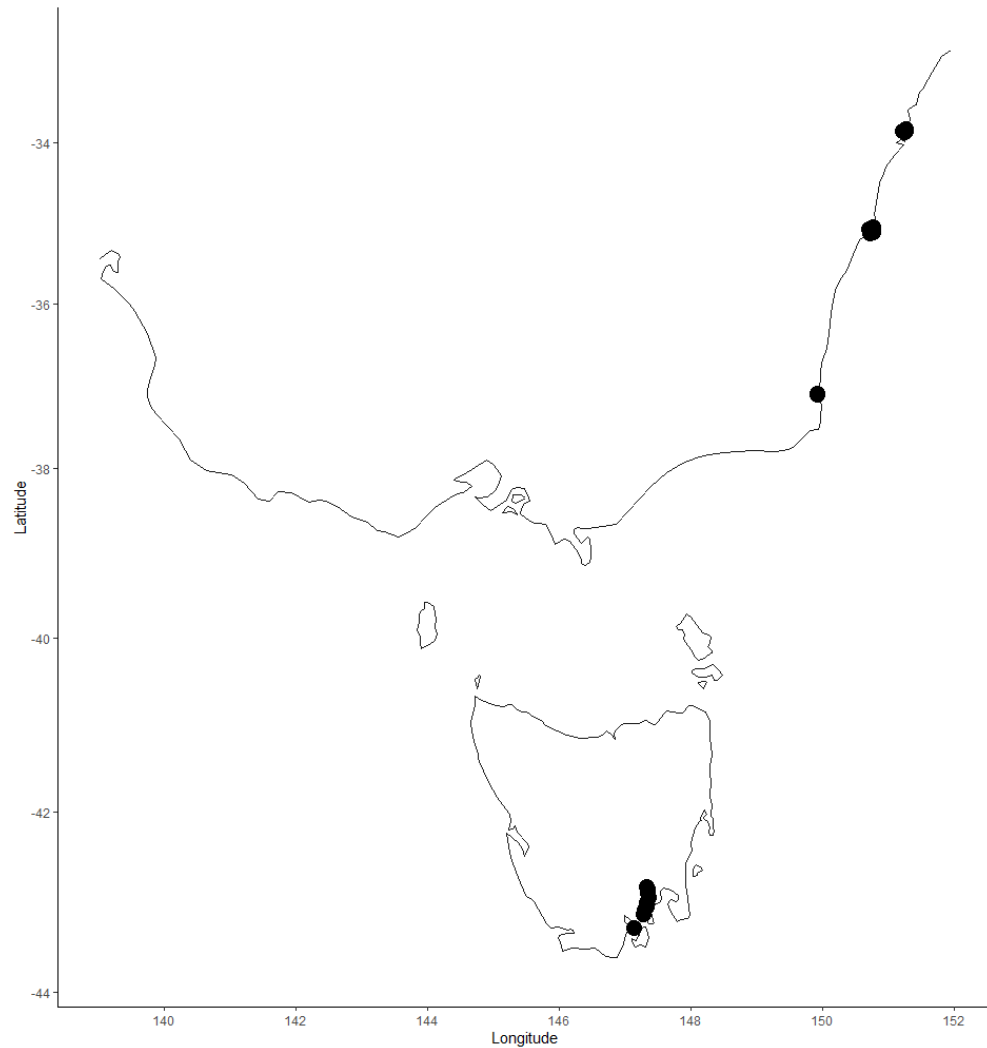


Questions

- ▶ How consistent is the detection of effects of natural and pollutant factors on the temperate reef by eDNA and traditional methods?
- ▶ How much more information does the holistic approach of using eDNA provide compared with more traditional methods?



Map of 20 sample sites across NSW & Tas



Map of 20 sample sites across NSW & Tas

Factors

Environment

- Region
- SST

Pollutant

- Heavy Metals
- Dichloroethane
- Bromofluorobenzene
- Nitrogen
- Nutrients
- Kelp¹⁵N
- Population index

Marine community

Sampling

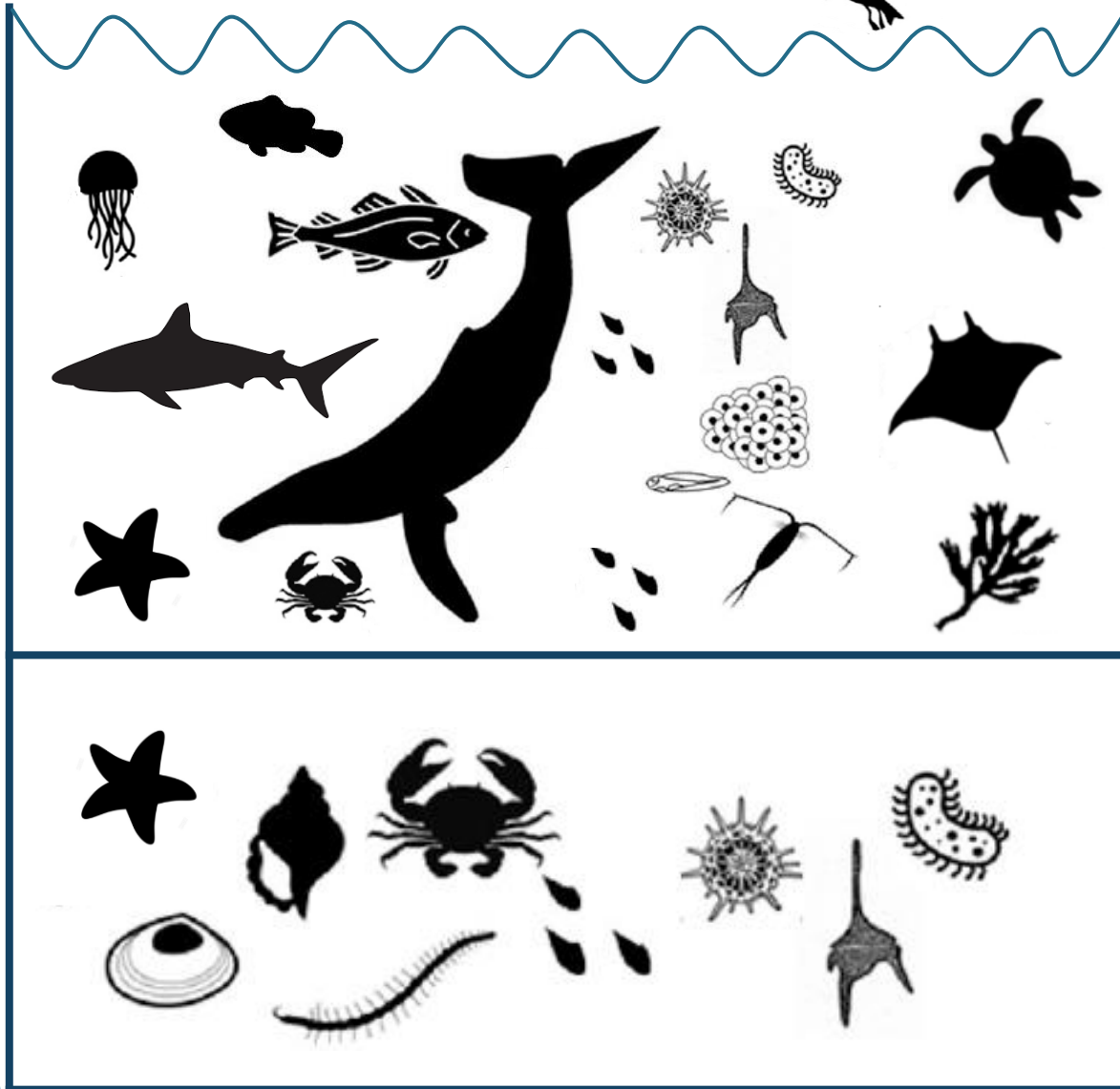
Sample

Processing

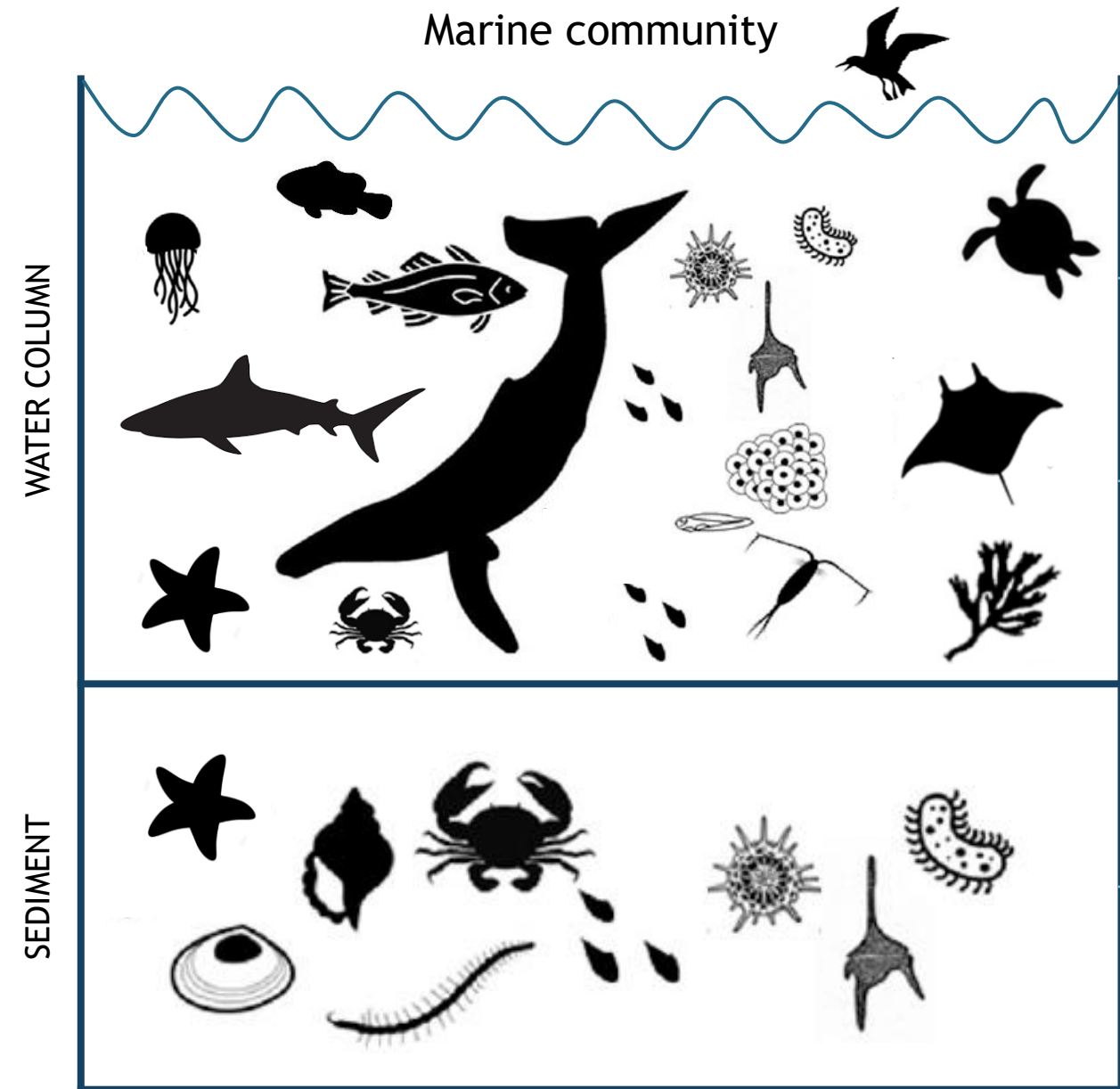
Data

WATER COLUMN

SEDIMENT



Local biota



Sampling

Sample

Processing

Data

Underwater Visual Surveys
 → Reef Life Survey Method

UVS: transect

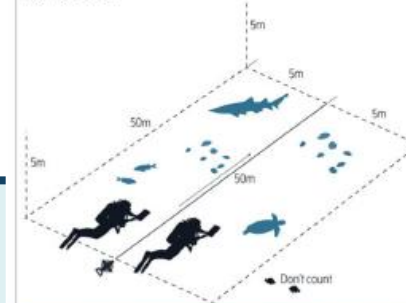
In situ
Observation

RLS dataset

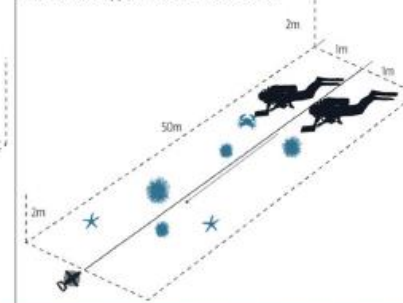


Species
 -Fish
 -Megafauna
 -Invertebrates

Method 1: Fish



Method 2: Cryptic fish & invertebrates



Method 3: Photo-quadrats

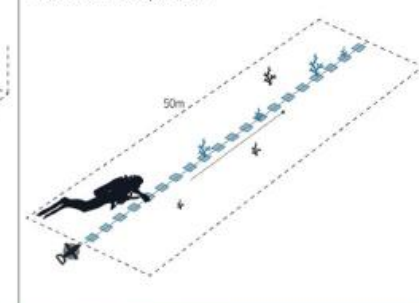


Fig. 1. Diagrammatic depiction of survey methods.

Marine community

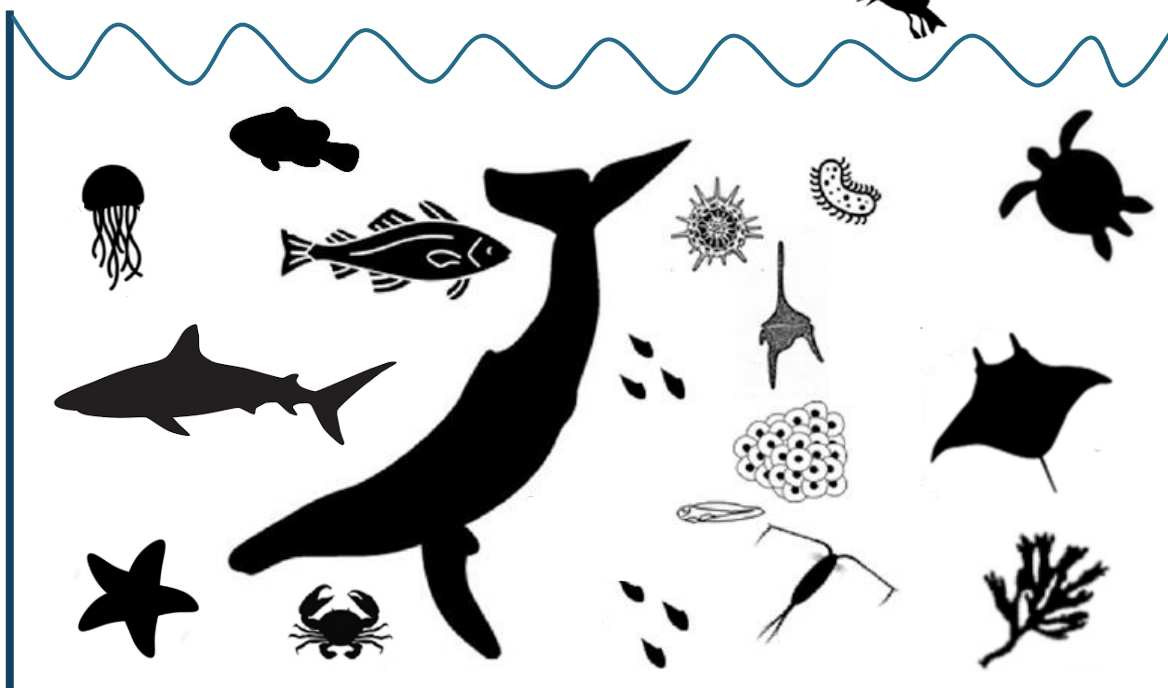
Sampling

Sample

Processing

Data

WATER COLUMN



Whole Algae



Community



Microscope ID

Species:
- Epifauna

SEDIMENT

Van Veen
Grab

Community



Microscope ID

Species:
- Infauna

Marine community

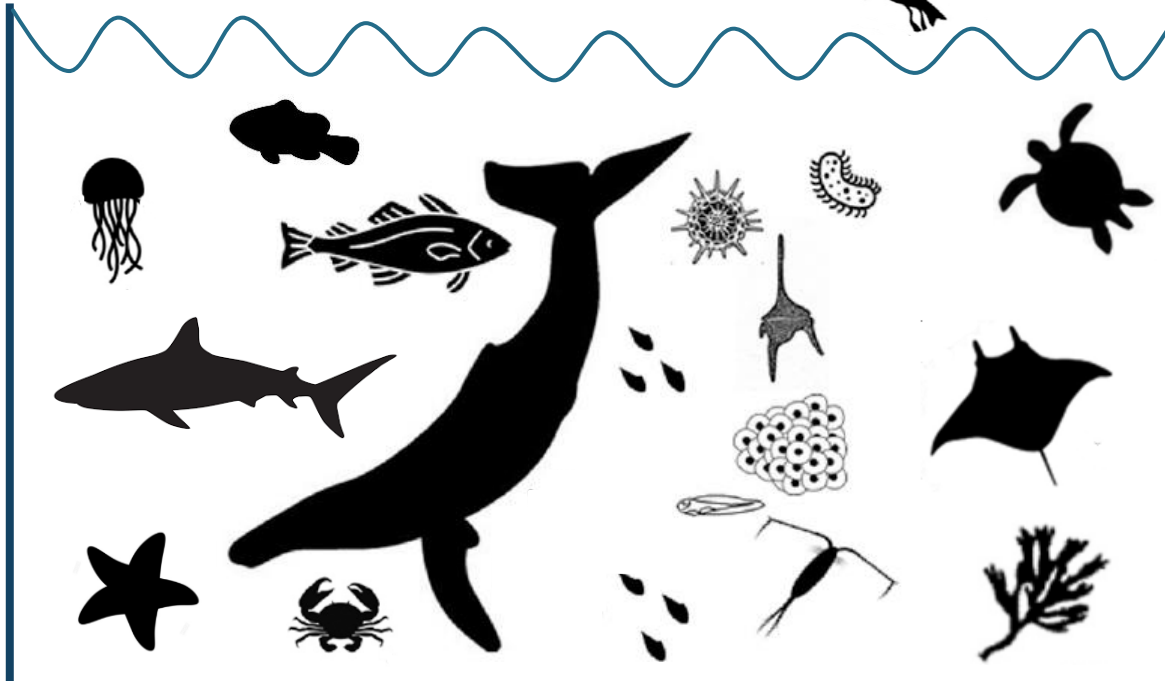
Sampling

Sample

Processing

Data

WATER COLUMN



Swab



eDNA

eDNA
extraction &
sequencingOTUs:
18S: eukaryote/phyto
16S: microbes
COI: invert/phyto

- OTUs: sequences clustered if <3% dissimilarity.
- In the process of redoing the analysis with ASVs.

SEDIMENT



Swab

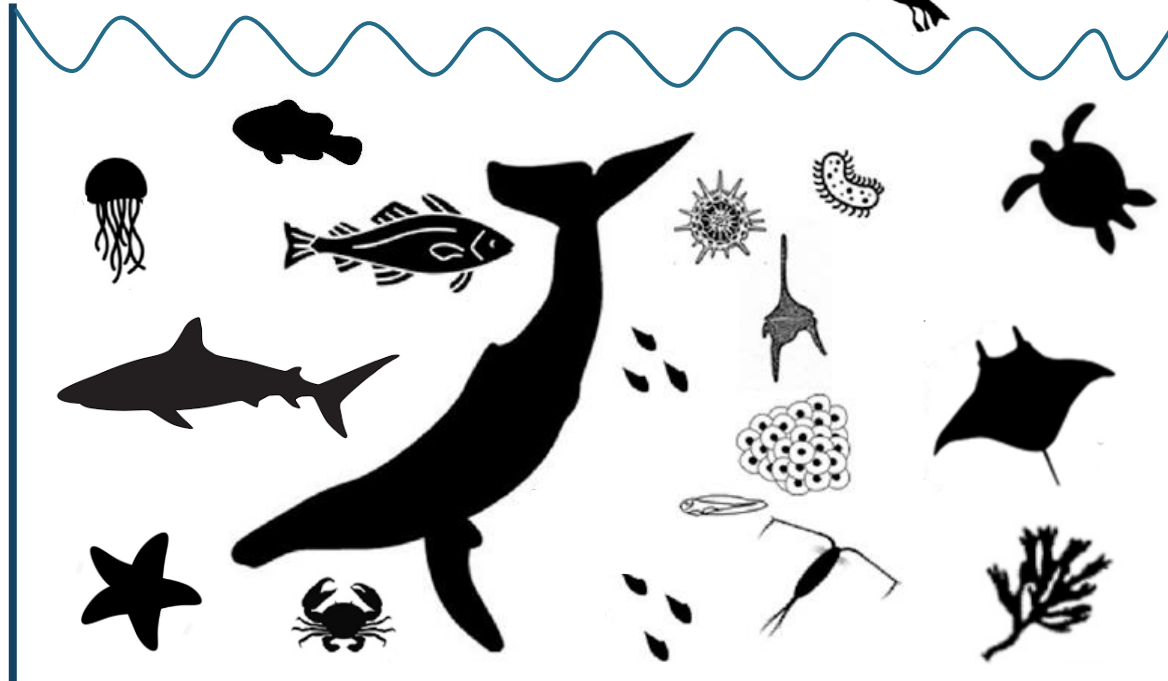


eDNA

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Marine community

WATER COLUMN



SEDIMENT



Sampling

Sample

Processing

Data

Swab



eDNA

eDNA
extraction &
sequencing

OTUs:

18S: eukaryote/phyto
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UVS: transect

In situ
Observation

RLS dataset



Species
- Fish
- Megafauna
- Invertebrates

Whole Algae



Community



Microscope ID



Species:
- Epifauna

Swab

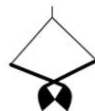


eDNA

eDNA
extraction &
sequencing

OTUs:

18S: eukaryote/phyto
16S: microbes
COI: invert/phyto

Van Veen
Grab

Community



Microscope ID



Species:
- Infauna

- **DistLM**: Distance based Linear Model → « (Primer) routine for analysing [...] the relationship between a multivariate data cloud (resemblance matrix) and one or more predictor variables »

Assemblages
(OTUs/infauna/epifauna/
RLS)

Environmental &
Pollutants variables

→ Based on the **null hypothesis of no relationship** = detects the **potential effect of an environmental/pollutant variable** on a community, gives the **% of variation** within the community explained by that **variable (R^2)**.

100% variability observed

Region

Pollutant x

1

2

X% variability
explained

Y% variability
explained

→ From the remaining
variability observed

→ Only sequential

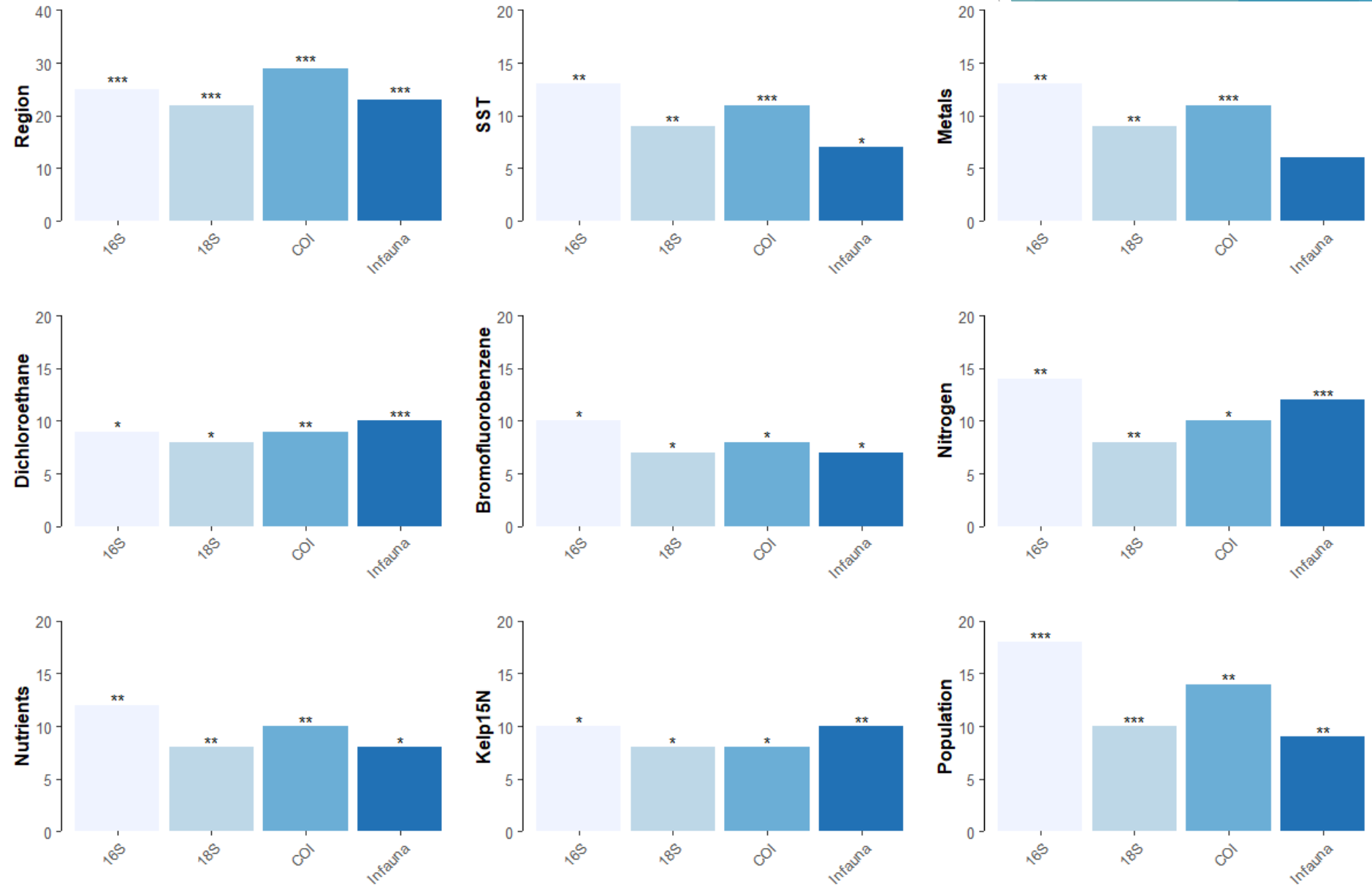


Figure 2: DISTLM results for temperate sediment community assemblage assessed through four methods: COI, 18S and 16S metabarcoding (OTUs) & infauna (species)

➔ Similar

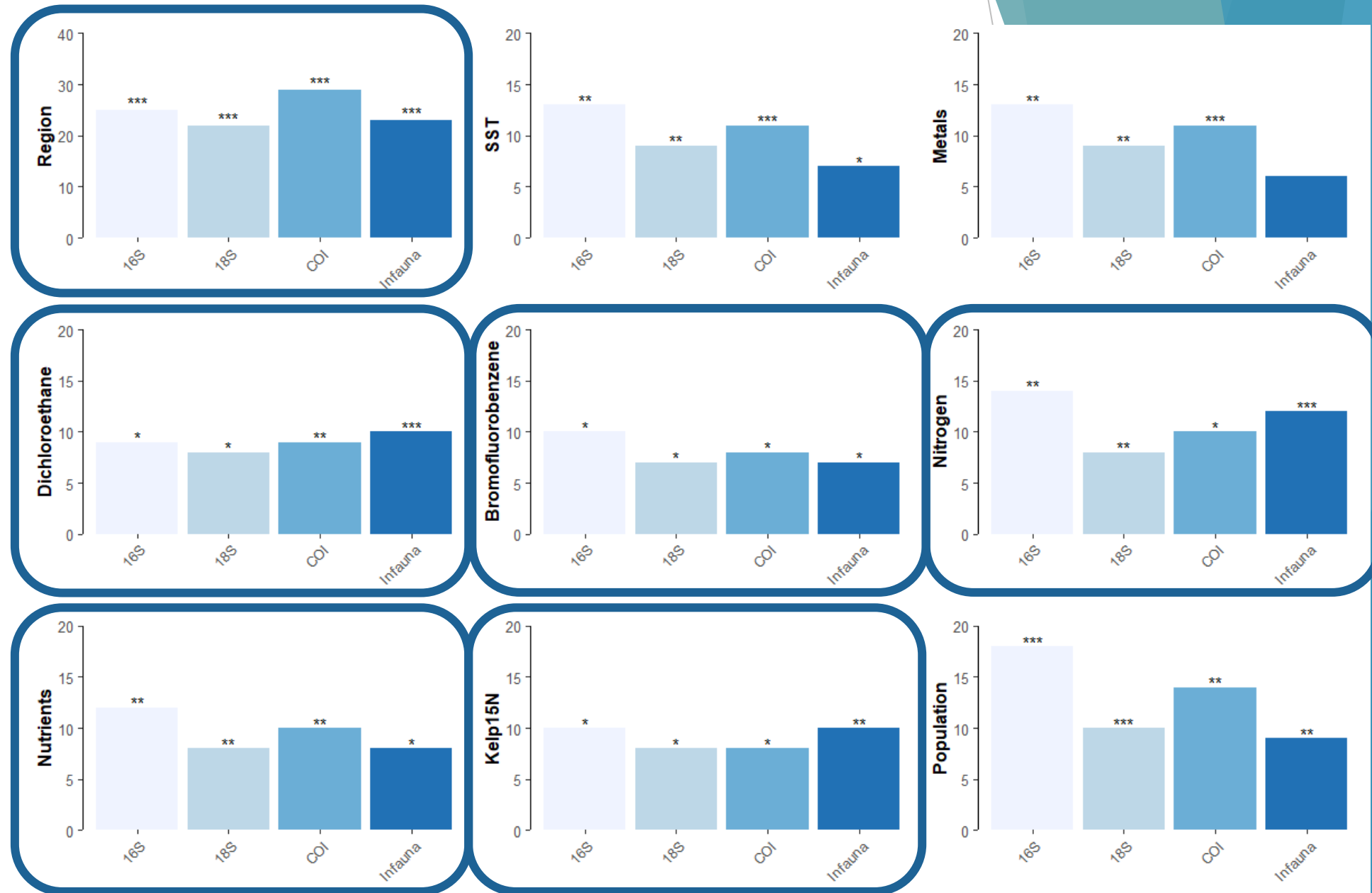


Figure 2: DISTLM results for temperate sediment community assemblage assessed through four methods: CO1, 18S and 16S metabarcoding (OTUs) & infauna (species)

➔ Similar

➔ Better

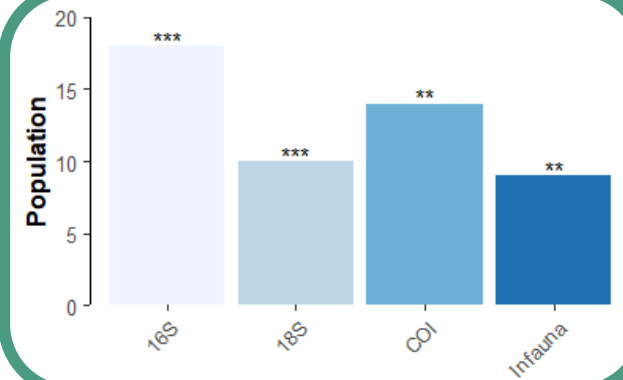
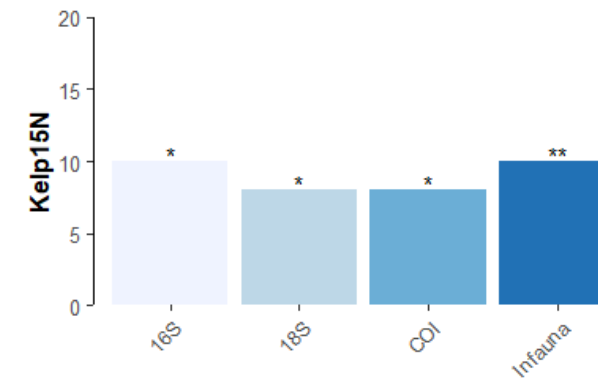
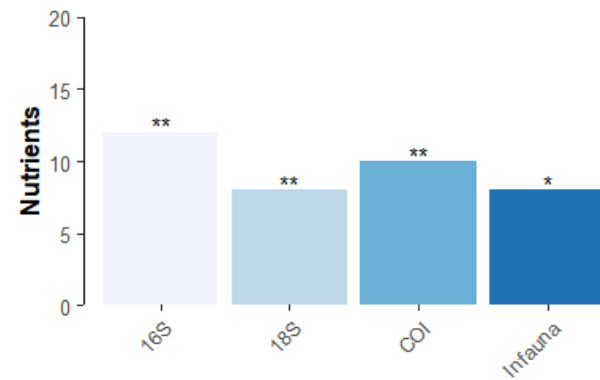
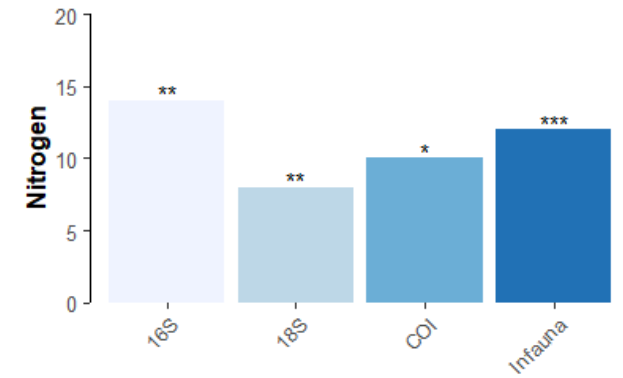
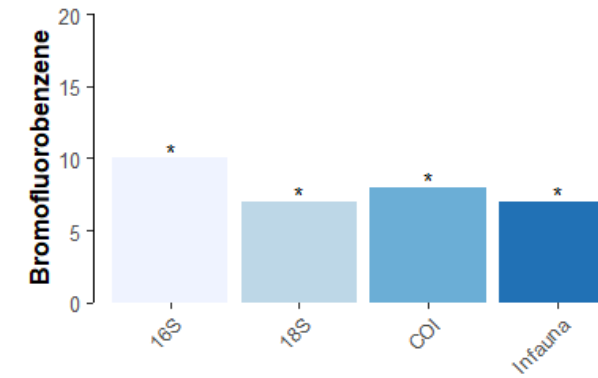
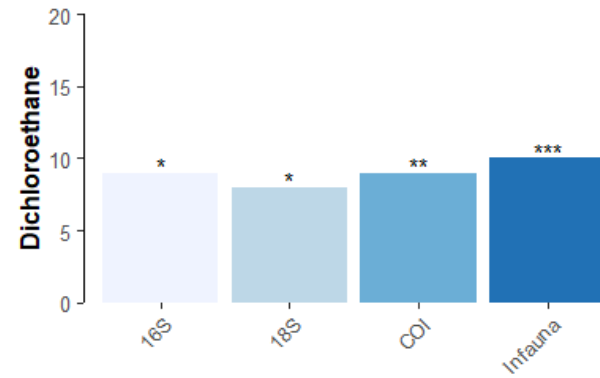
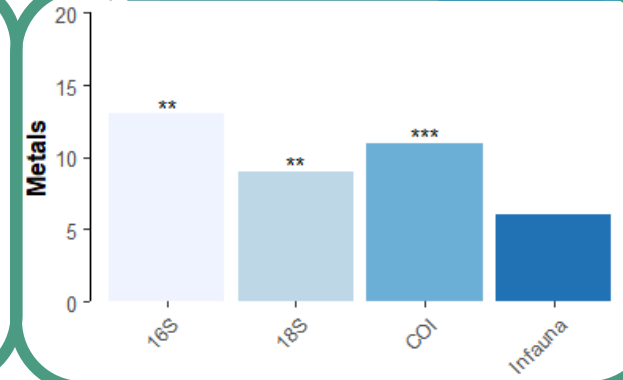
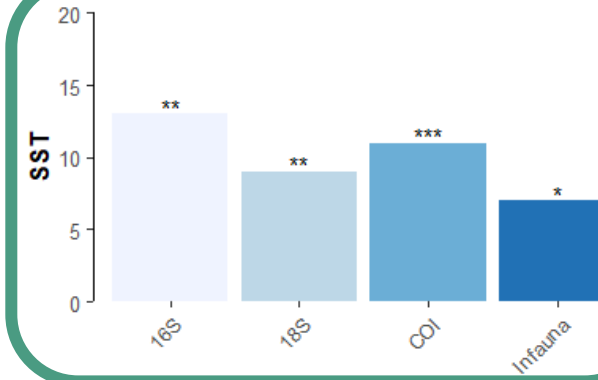
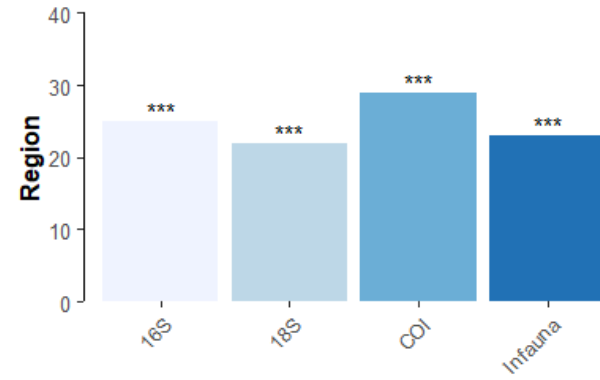


Figure 2: DISTLM results for temperate sediment community assemblage assessed through four methods: CO1, 18S and 16S metabarcoding (OTUs) & infauna (species)

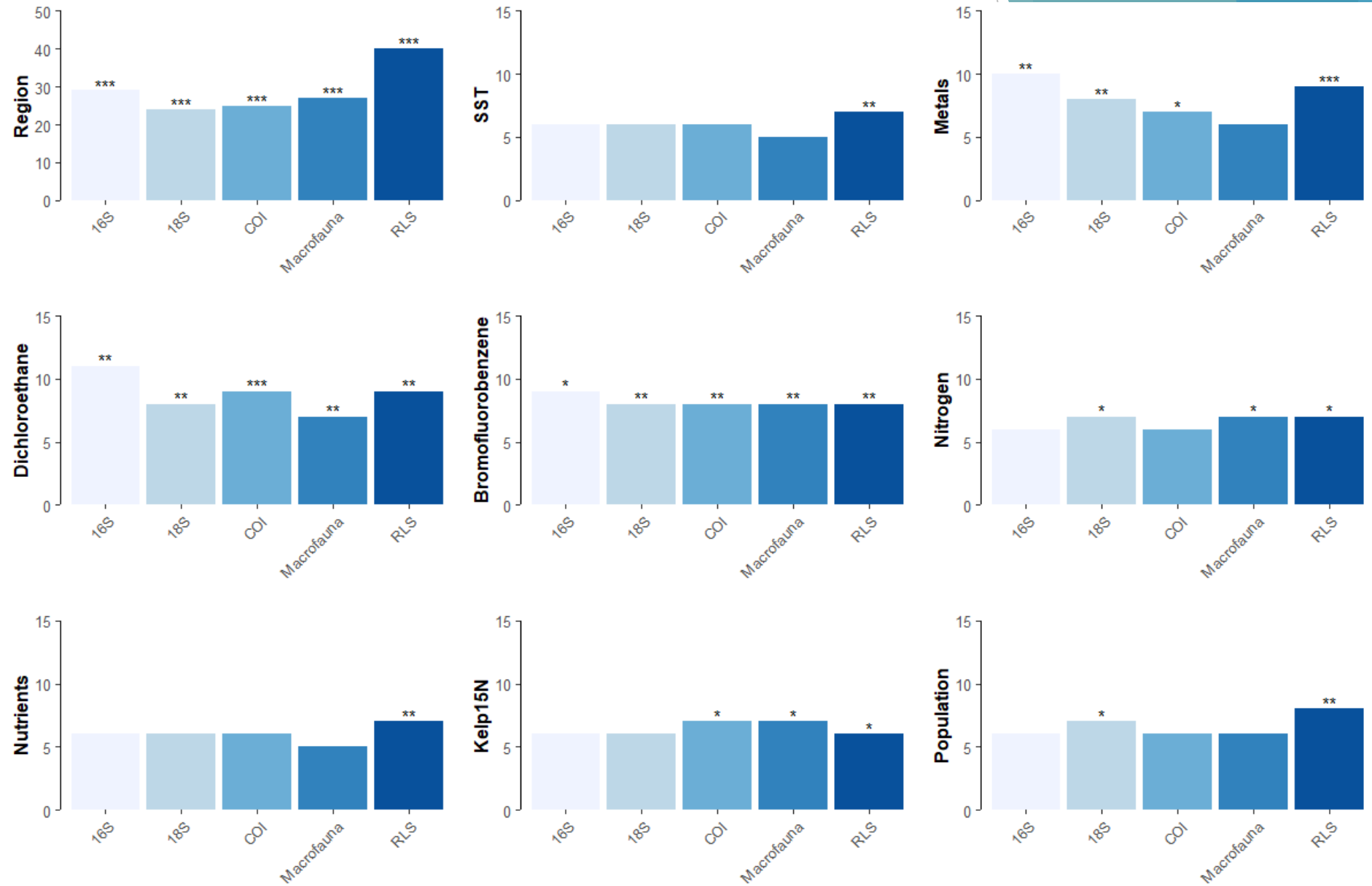


Figure 3: DISTLM results for temperate reef community assemblage assessed through five methods: COI, 18S and 16S metabarcoding (OTUs), UVS (RLS, species) & epifauna (species)

➔ Similar

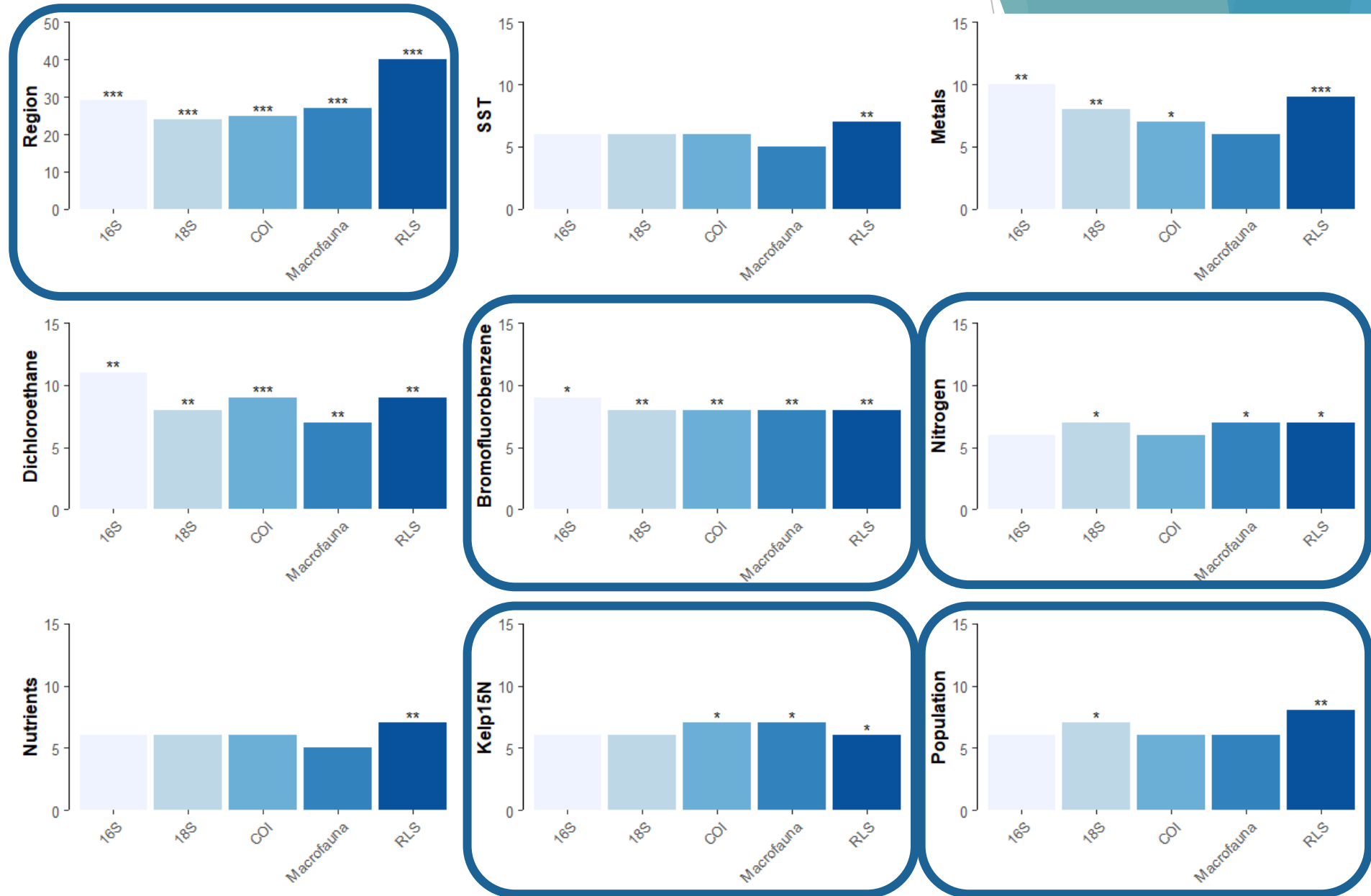


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➔ Similar

➔ Better

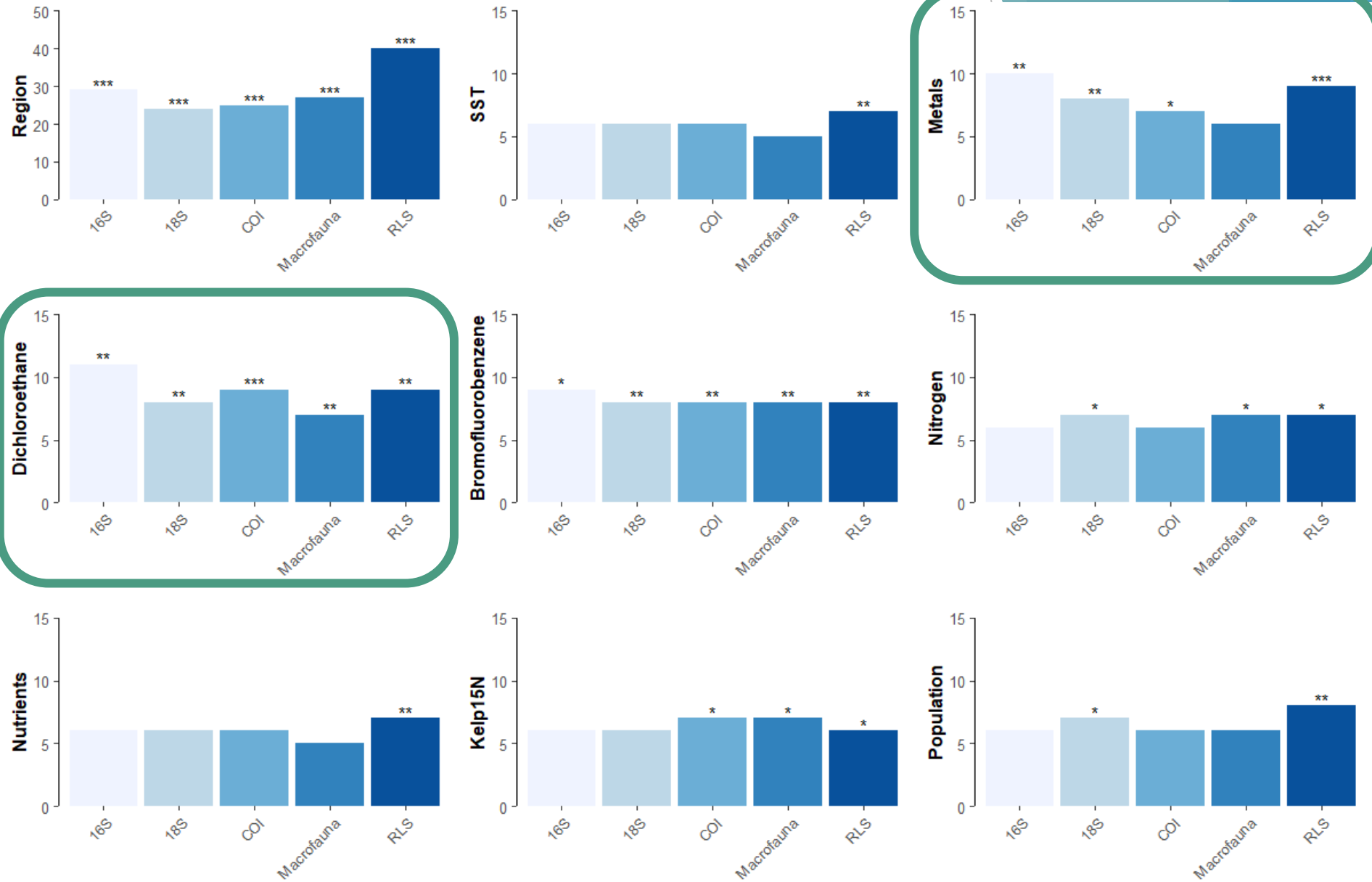


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➔ Similar

➔ Better

➔ Not as good

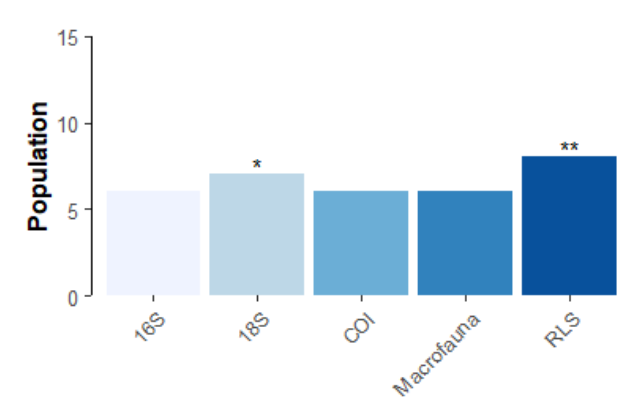
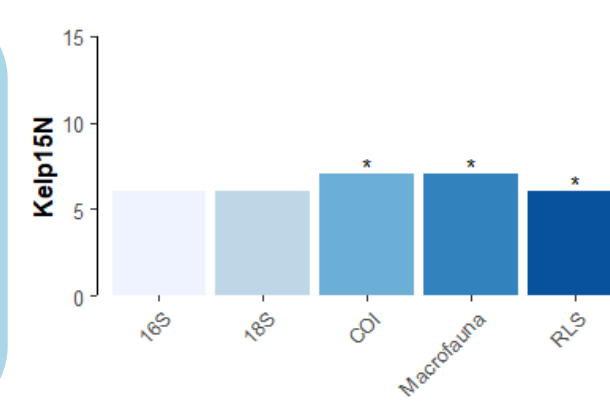
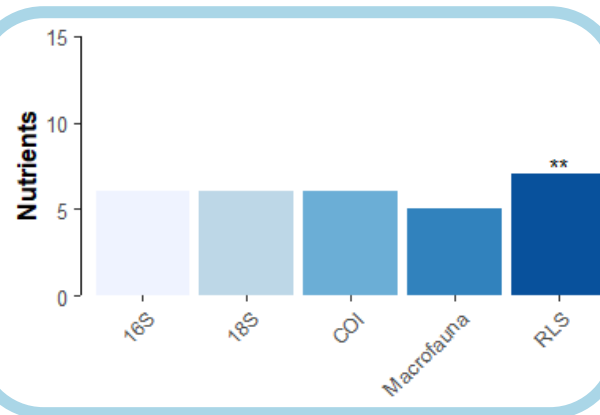
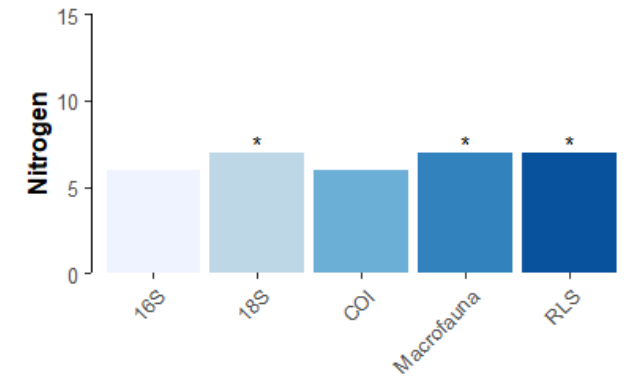
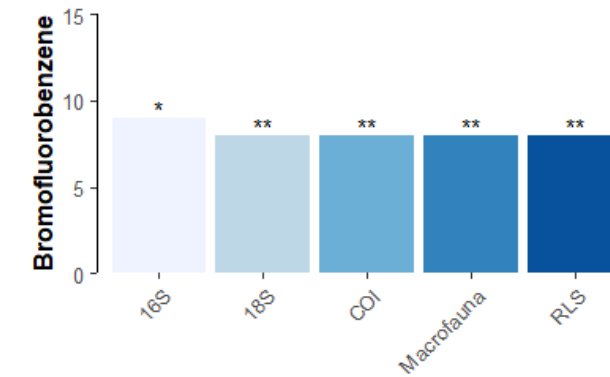
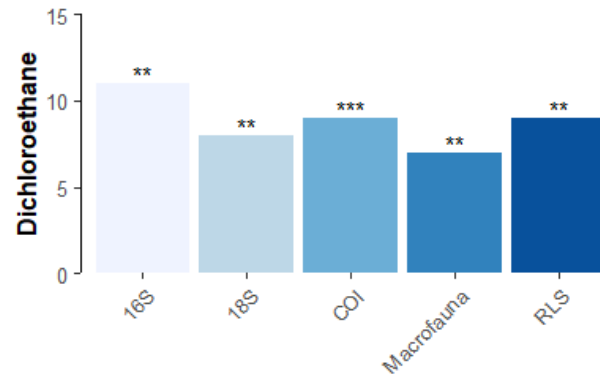
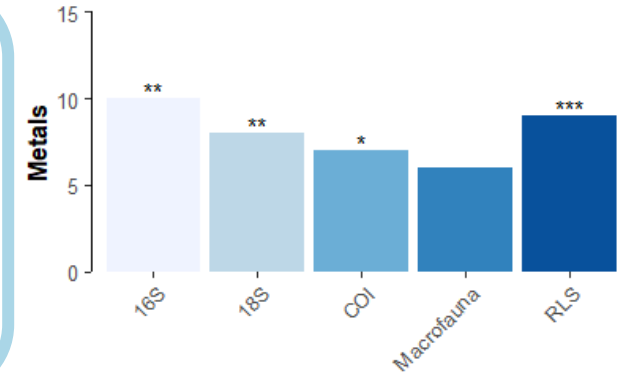
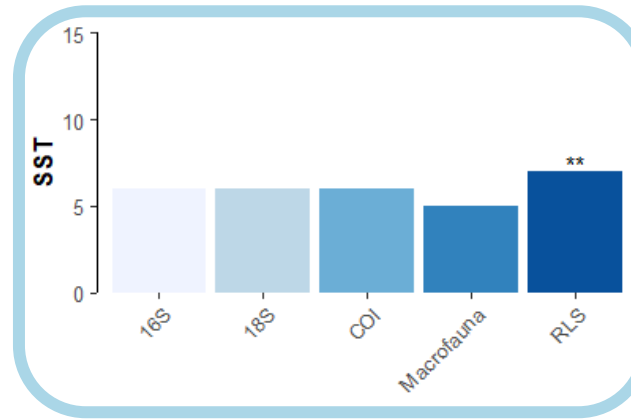
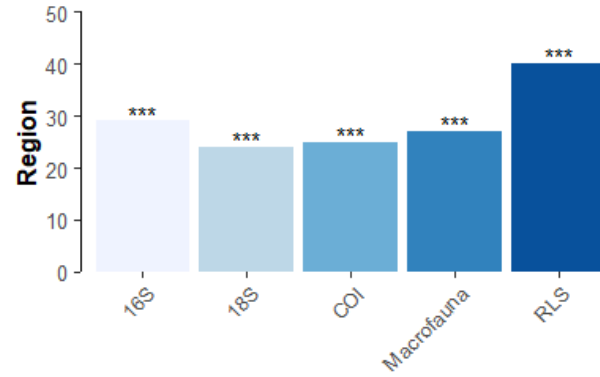


Figure 3: DISTLM results for temperate reef community assemblage assessed through five methods: COI, 18S and 16S metabarcoding (OTUs), UVS (RLS, species) & epifauna (species)

Assemblages

18S

16S

COI

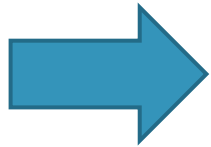
UVS

Epifauna

Infauna

eDNA

'Traditional methods'



Sensitive to potential impact of pollutants and environmental factors

Assemblages

18S

16S

COI

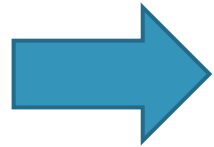
UVS

Epifauna

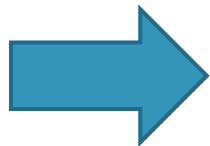
Infauna

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Sensitive to potential impact of pollutants and environmental factors



Discrepancy in reef vs sediment results

Assemblages

18S

16S

COI

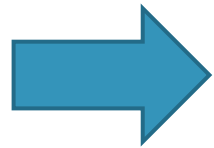
UVS

Epifauna

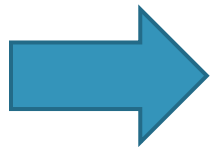
Infauna

eDNA

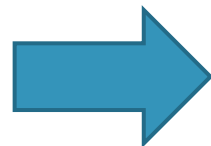
'Traditional methods'



Sensitive to potential impact of pollutants and environmental factors



Discrepancy in reef vs sediment results



Analysis to be redone but likely to show same results

And then?

- ▶ “It is expected that the new method is “safe to use” only if it provides the same or almost same results as the conventional one. However, obtaining such perfect congruence is often impossible because the character of data is very different ” Pawlowski et al., 2021
- ▶ Future of biomonitoring as noted back in 2015 by Thomsen et Willersev
- ▶ Efforts in standardization, building reliable databases and inter-calibration have been made since, successfully establishing eDNA as a revolutionising tool.


Received: 7 June 2021 | Accepted: 10 June 2021
DOI: 10.1111/mec.16023

SPECIAL ISSUE

Editorial

MOLECULAR ECOLOGY WILEY

Environmental DNA for biomonitoring

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Special Issue Article: Environmental DNA

Environmental DNA – An emerging tool in conservation for monitoring past and present biodiversity

Philip Francis Thomsen, Eske Willerslev *

Centre for GeoGenetics, Natural History Museum of Denmark, University of Copenhagen, Øster Voldgade 5-7, DK-1350 Copenhagen, Denmark





Thank you

And a big thanks to:

- Prof. Graham Edgar
- Dr Sharon Appleyard
- A/Prof Scott Ling
- Dr Jodie van de Kamp
- Dr Andrew Bissett
- Dr Lev Bodrossy
- Dr Stephen Bent
- Ms Safia Maher
- Dr Kate Fraser

- Mr Adam Davey
- Mr Simon Reeves
- Prof Emma Johnston
- Dr Beth Strain
- A/Prof Jeff Ross
- Dr Ana Bugnot
- Ms Amanda Scholes
- Mr Paul Hallam



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