HIFMB Helmholtz Institute for Functional Marine Biodiversity at the University OLDENBURG

Zooplankton is the perfect candidate for validating eDNA metabarcoding for analyzing North Sea marine fauna

Alica Ohnesorge

S04 (Day 2)

21st March 2024

AWI ALFRED-WEGENER-INSTITUT HELMHOLTZ-ZENTRUM FÜR POLAR- UND MEERESFORSCHUNG

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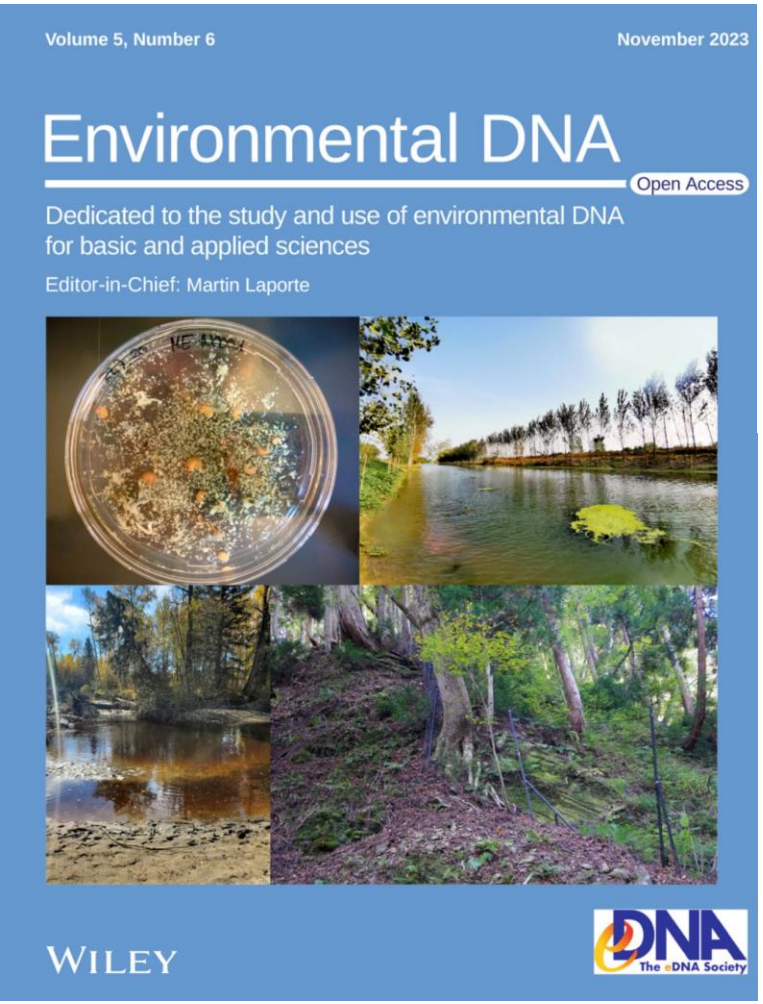

Capturing drifting species and molecules—Lessons learned from integrated approaches to assess marine metazoan diversity in highly dynamic waters

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AIM:

Do we have sufficient reference data & appropriate methods to identify marine fauna in the North Sea?

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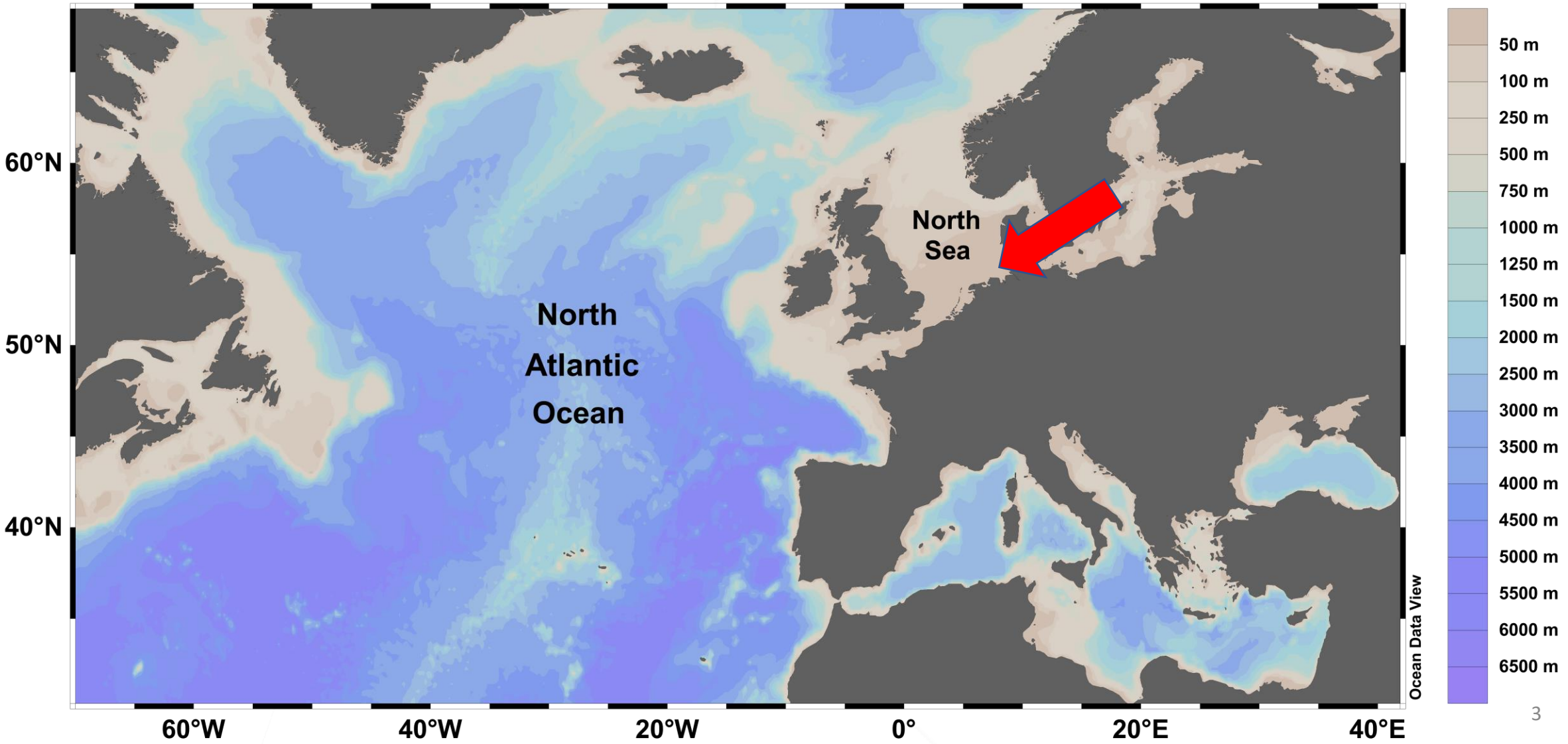
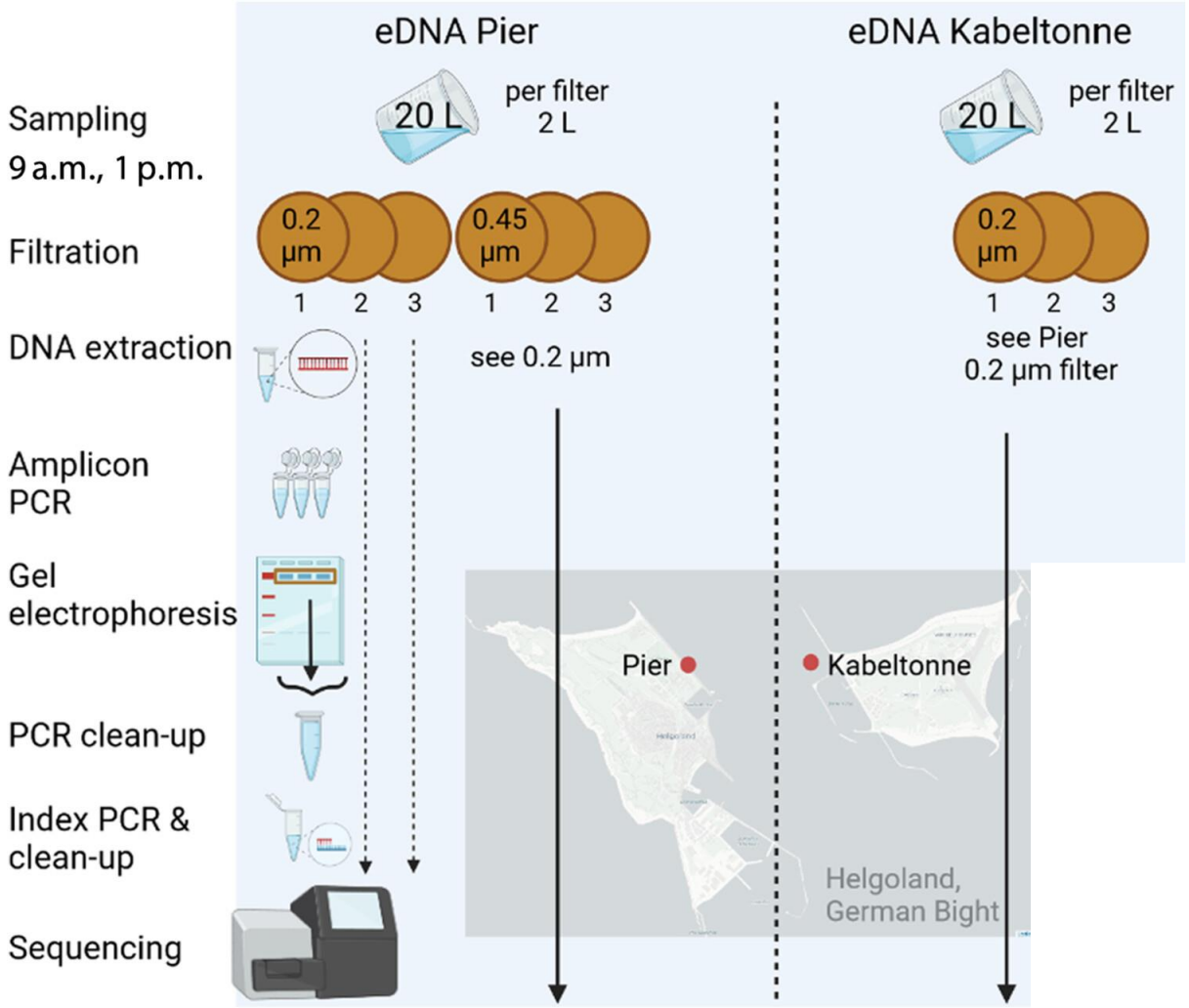
The Approach



The Approach

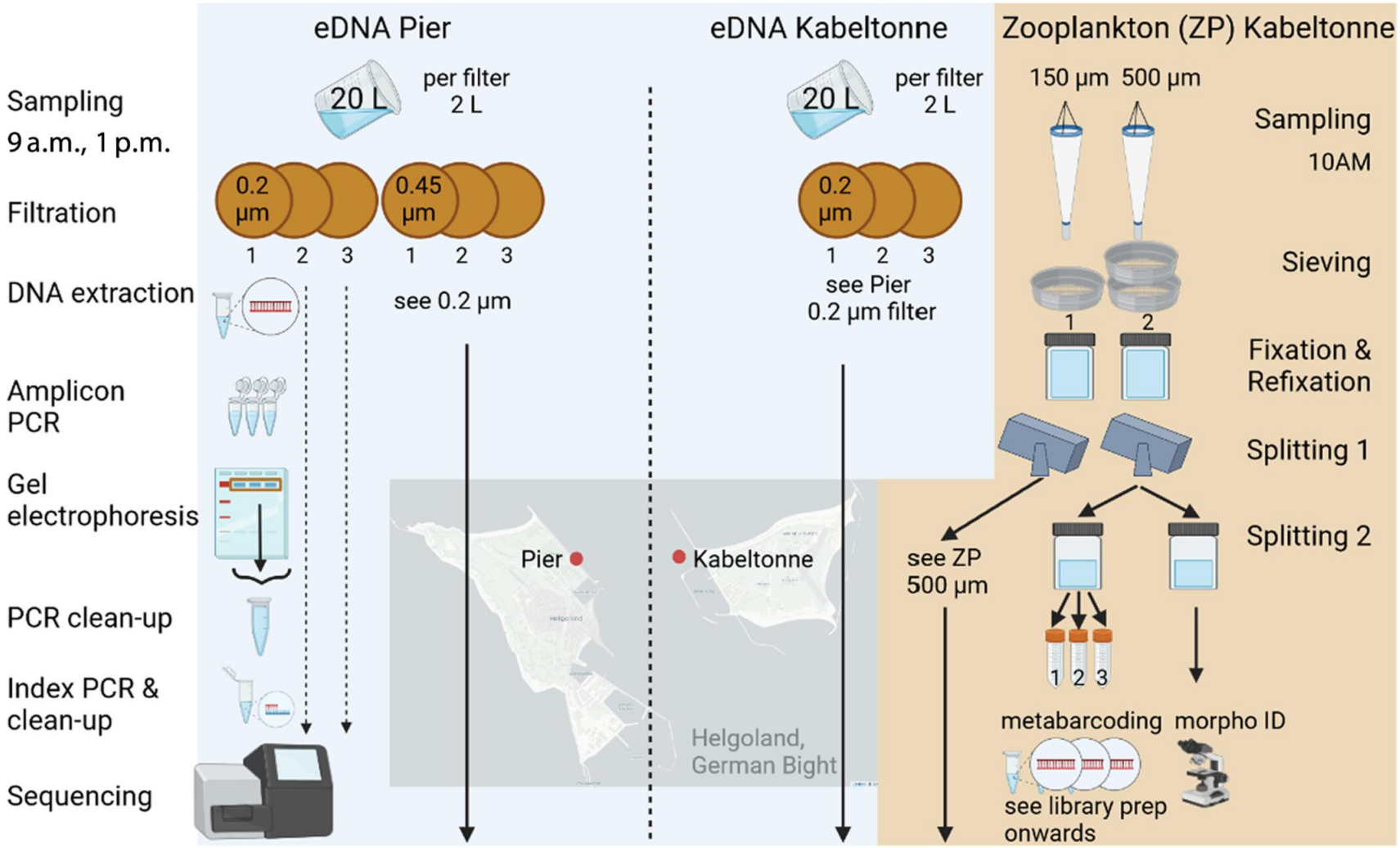


Sampling
Helgoland (North Sea, German Bight)
19-27 June 2019

eDNA: ca. 260 L

Metabarcoding:
a) COI: MetaZooGene db
b) 18S V4: SILVA & PR2

The Approach



Sampling
Helgoland (North Sea, German Bight)
19-27 June 2019

eDNA: ca. 260 L
ZP net: ca. 120,000 L (150 & 500 µm)

Metabarcoding:
a) COI: MetaZooGene db
b) 18S V4: SILVA & PR2

Validation of metabarcoding

ZP net catches: metabarcoding vs. taxa identified by morphological characteristics:

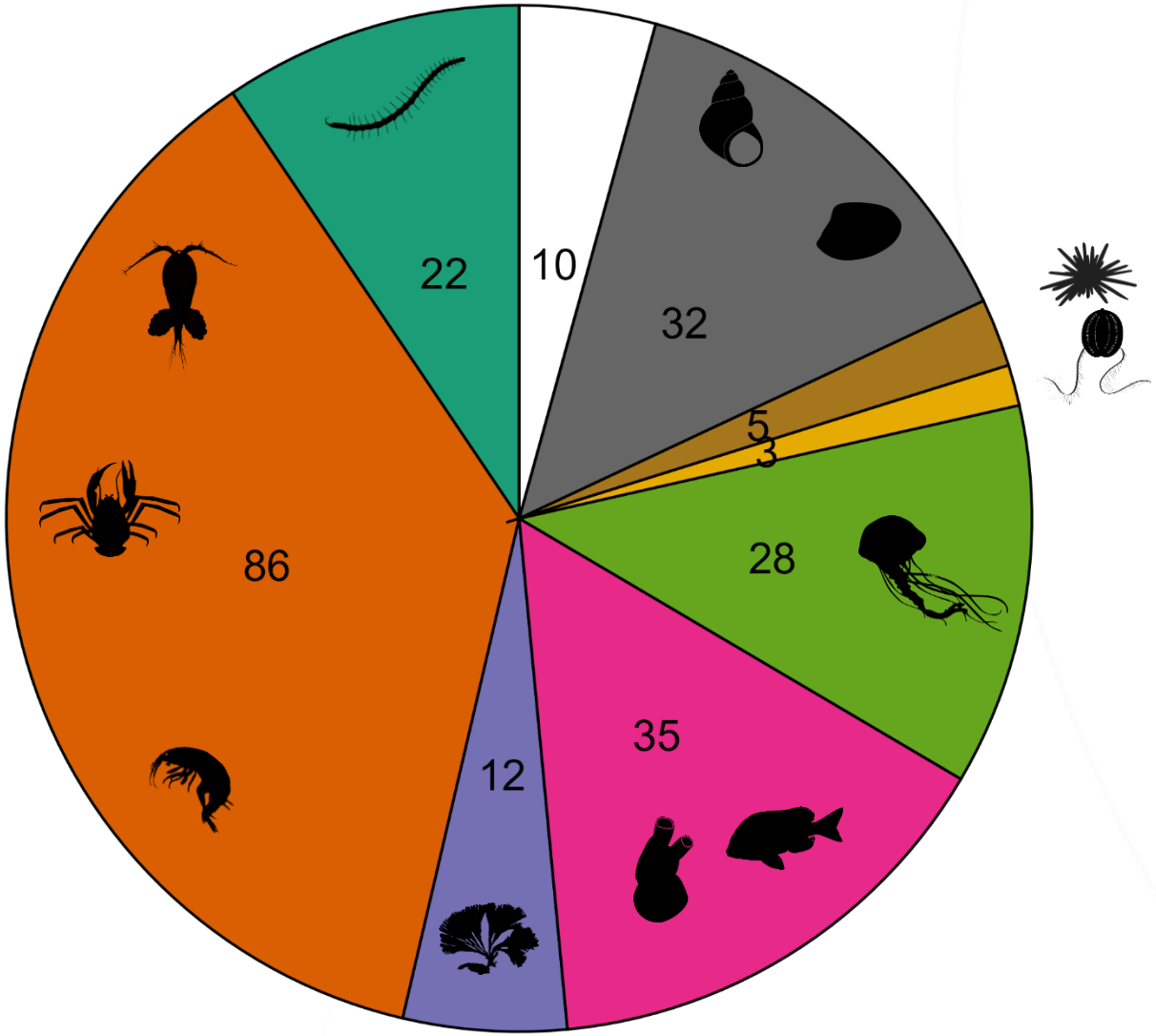
Which taxa do we **miss** by metabarcoding?

- Phoronida
- Asteroidea
- (Chaetognatha)

Which phyla are **additionally** recovered by metabarcoding?

+ Rotifera
+ Nemertea

Detections ZP net catches

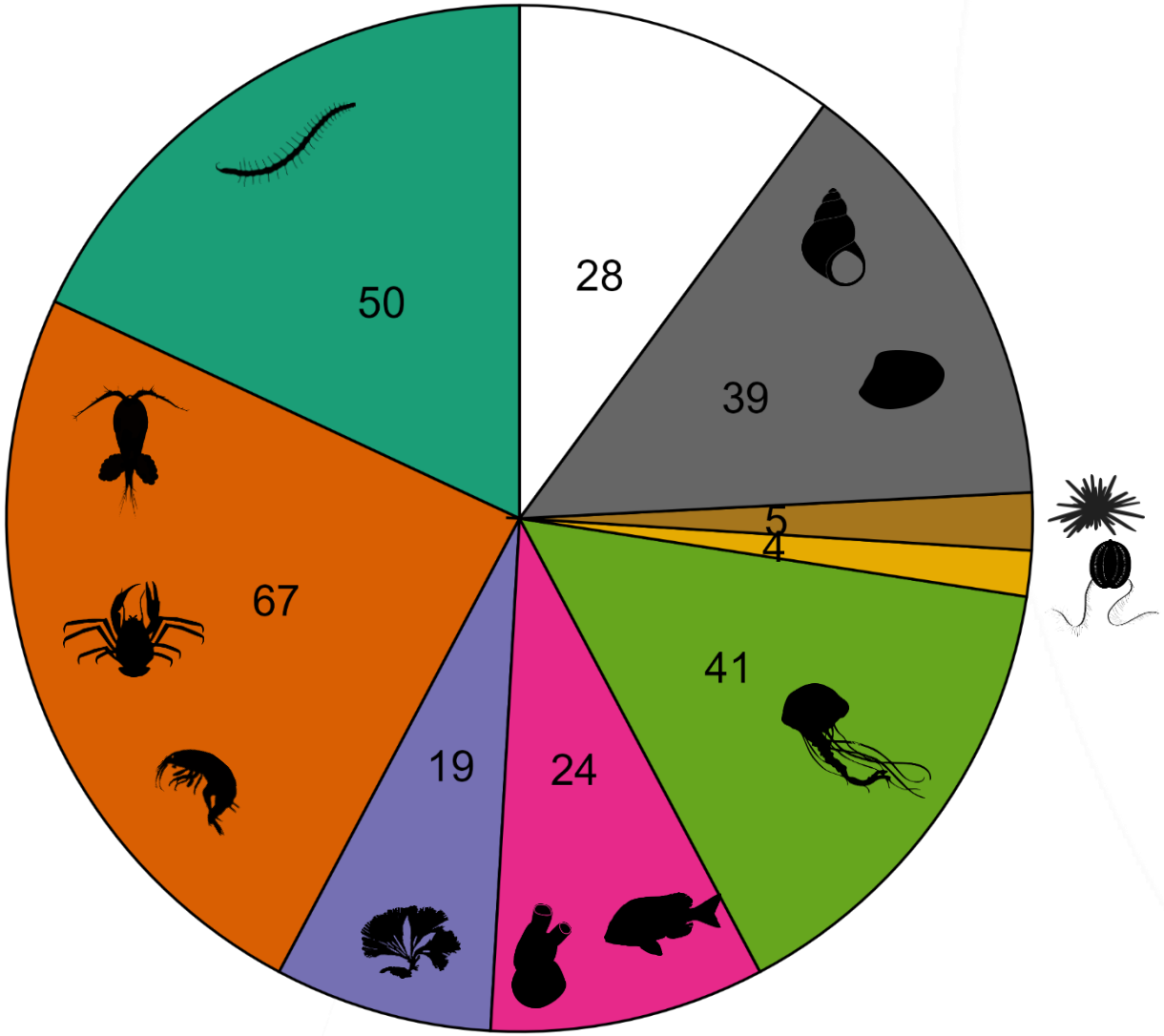


Phylum

- Annelida
- Arthropoda
- Bryozoa
- Chordata
- Cnidaria
- Ctenophora
- Echinodermata
- Mollusca
- other : Entoprocta: 1
  Nematoda: 1
  Nemertea: 5
  Platyhelminthes: 1
  Rotifera: 2

233 species
13 phyla

Detections eDNA

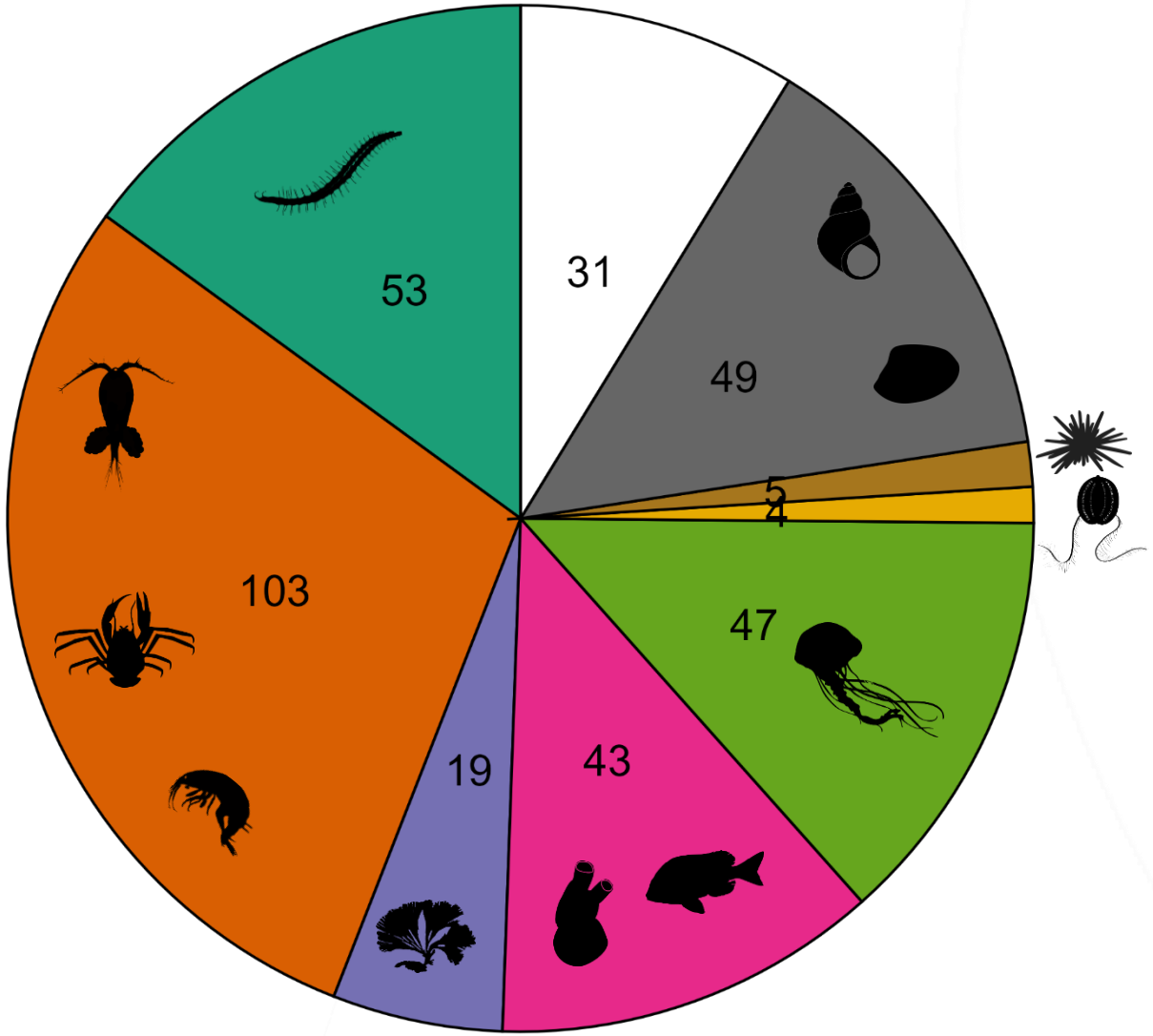


Phylum

- Annelida
- Arthropoda
- Bryozoa
- Chordata
- Cnidaria
- Ctenophora
- Echinodermata
- Mollusca
- other : Gastrotricha: 2
  Nematoda: 8
  Nemertea: 5
  Platyhelminthes: 9
  Porifera: 1
  Rotifera: 1
  Xenacoelomorpha: 2

277 species
15 phyla

Detections eDNA + ZP net catches



Phylum

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- Chordata
- Cnidaria
- Ctenophora
- Echinodermata
- Mollusca
- other

other:
Entoprocta: 1
Gastrotricha: 2
Nematoda: 8
Nemertea: 6
Platyhelminthes: 9
Porifera: 1
Rotifera: 2
Xenacoelomorpha: 2

354 species
16 phyla

→ ½ shared

Validation of metabarcoding

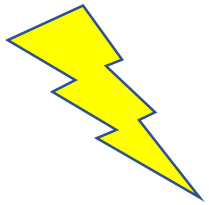
Are the detected species by metabarcoding known from the North Sea?

	total	Very likely	Likely	Unlikely
COI	269	238 (88.5 %)	20 (7.4 %)	11 (4.1 %)

Validation of metabarcoding

Are the detected species by metabarcoding known from the North Sea?

	total	Very likely	Likely	Unlikely
COI	269	238 (88.5 %)	20 (7.4 %)	11 (4.1 %)
18S V4	127	84 (63.0%)	20 (15.7 %)	23 (18.1 %)



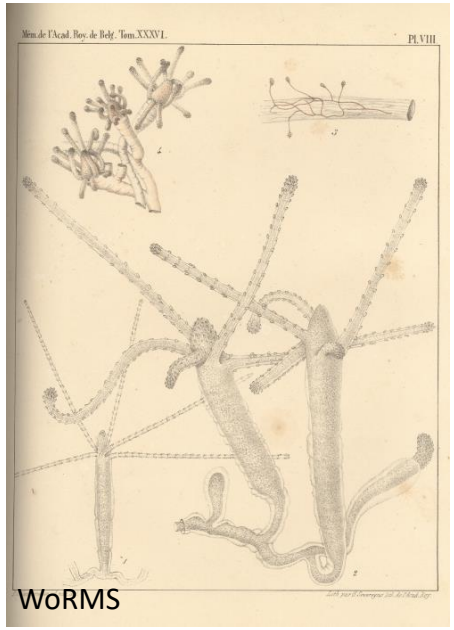
congeneric species

Potentially new in German Seas?

- *Acartia (Acartiura) hudsonica*
  North Sea: this study: eDNA & ZP, COI & 18S
  Baltic Sea: study submitted

Re-discovered species

Dicoryne conferta
Hydrozoa
before 1950



WoRMS

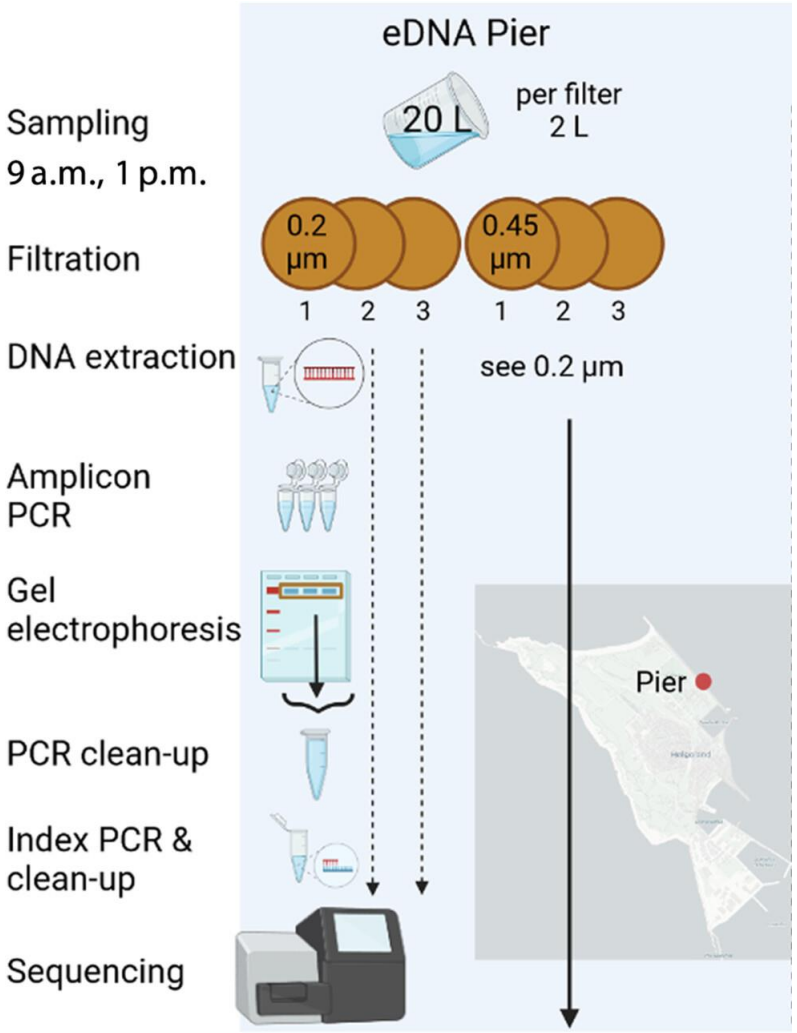
Sagartia (Cylista) viduata
Anthozoa
before 1950

eol.org

Megadrilus purpureus
Polychaeta
before 1900

Drew, D. J.

Do we need replicates?



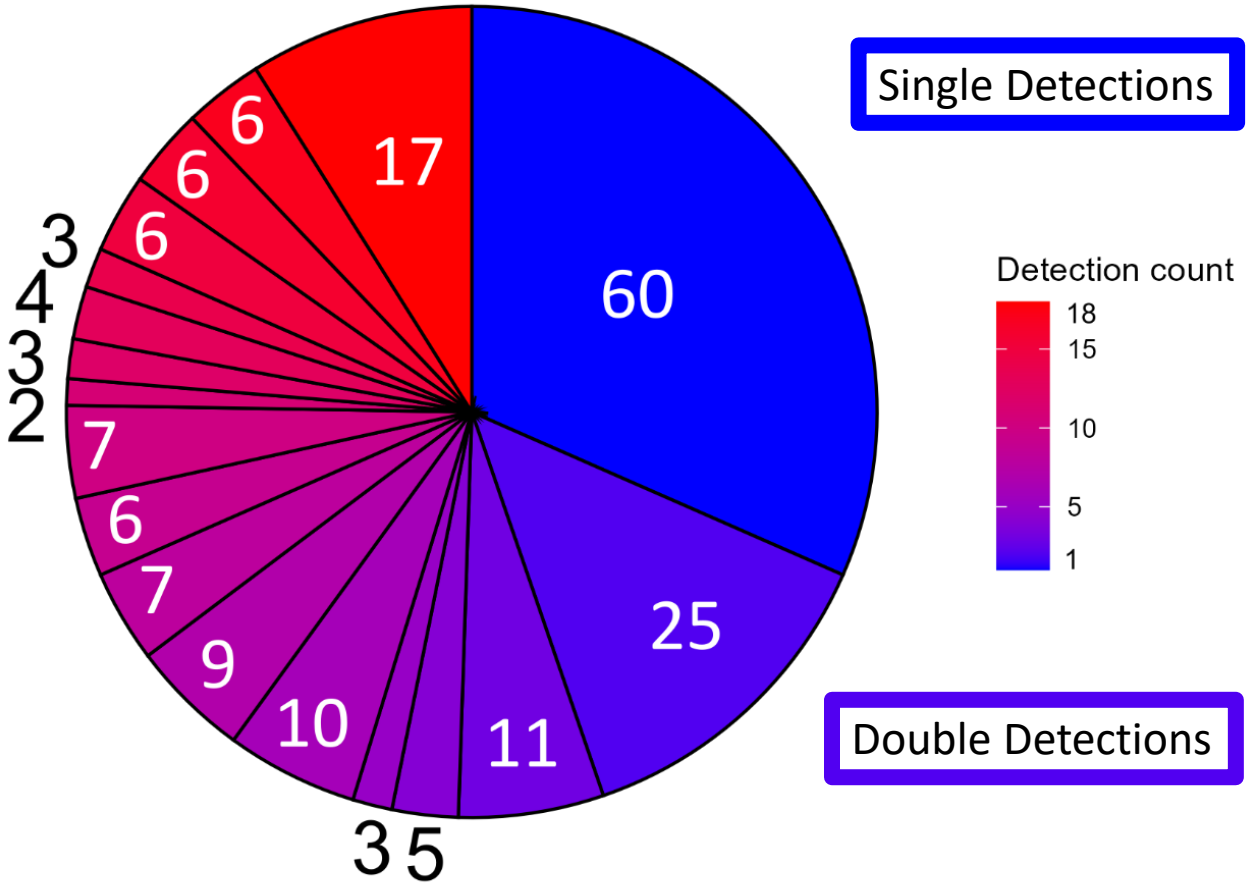
2x / day
over 9 days
→ **18** sampling events

6 replicates à 2 L/ sampling event

→ 108 filter replicates in total

(following results based on **COI** only)

Do we need replicates: repetitive sampling



✓ Almost half of the species (44.7 %) was detected only during one or two sampling events

Do we need replicates: repetitive sampling

Core Community: 17 sp.

2 Annelida

4 Arthropoda

3 Bryozoa

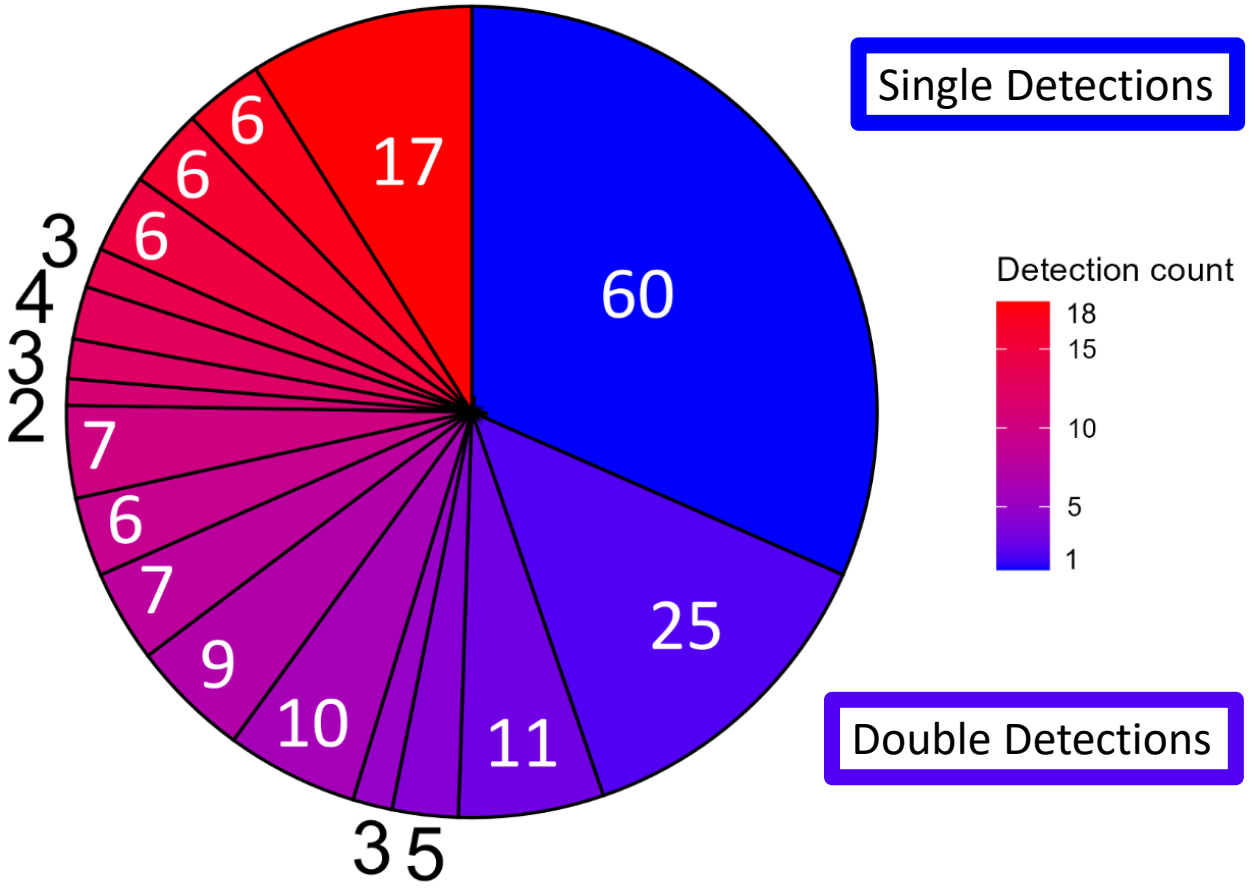
1 Chordata

4 Cnidaria

1 Echinodermata

1 Mollusca

1 Rotifera



- ✓ Almost half of the species (44.7 %) was detected only during one or two sampling events
- ✓ 17 species (‘Core Community’) were always detected (ca. 9 %)

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Summary

- YES - We are ready to use molecular identification methods to monitor North Sea zooplankton and marine fauna

- eDNA and zooplankton net catches identify slightly different communities:
  - **eDNA**
    ++ benthic-associated taxa (i.e. polychaetes)
  - **ZP net catches**
    ++ Arthropoda (i.e. holo- and meroplankton)
    ++ identification of reproductive state based on mero- and ichthyoplankton

- Core community identified by low replication; comprehensive community identified by high replication

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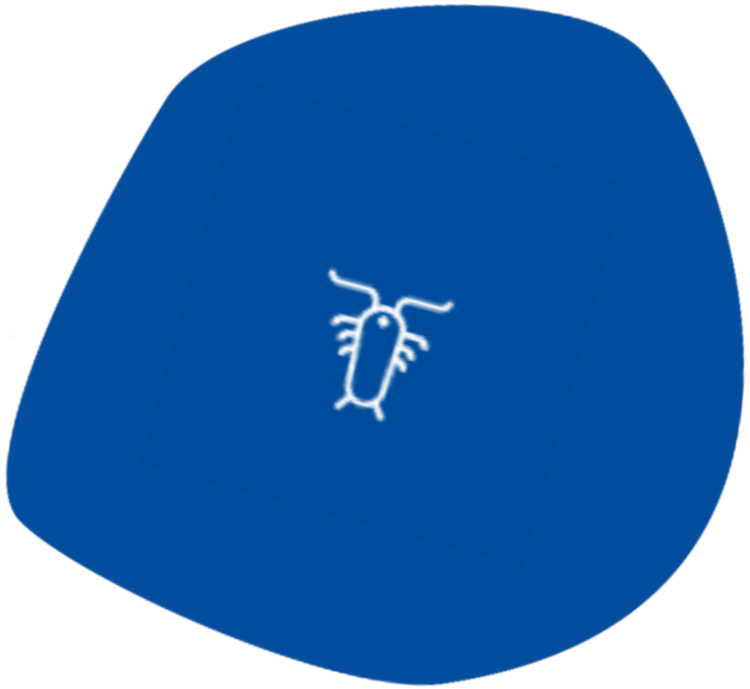

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