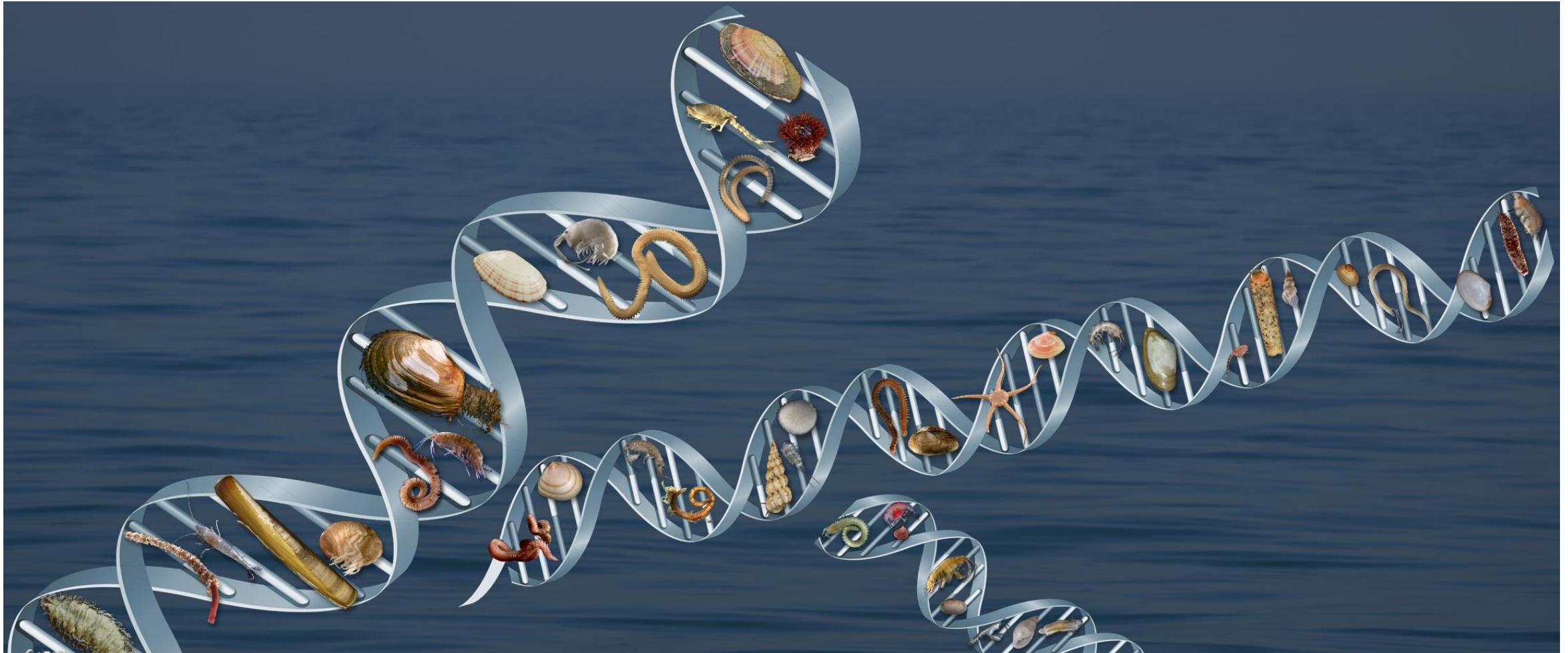
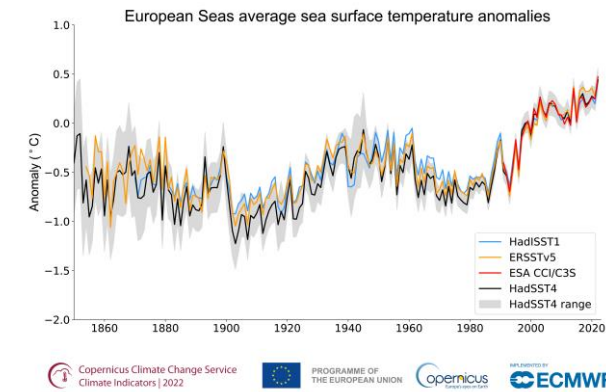


Genetic tools for Ecosystem health Assessment in the North Sea region



GEANS final webinar – 27 June 2023

Why GEANS?



=> Sustainable use and management of the North Sea = grand challenge
=> Fast and accurate monitoring is needed => DNA?

Focus area of GEANS?

North Sea



Interreg VB North Sea Region Programme Area 2014-2020

Regions within the NSR programme area



Target organisms of GEANS?

Macrobenthos = invertebrate taxa (body size > 1 mm) living in or near the seafloor



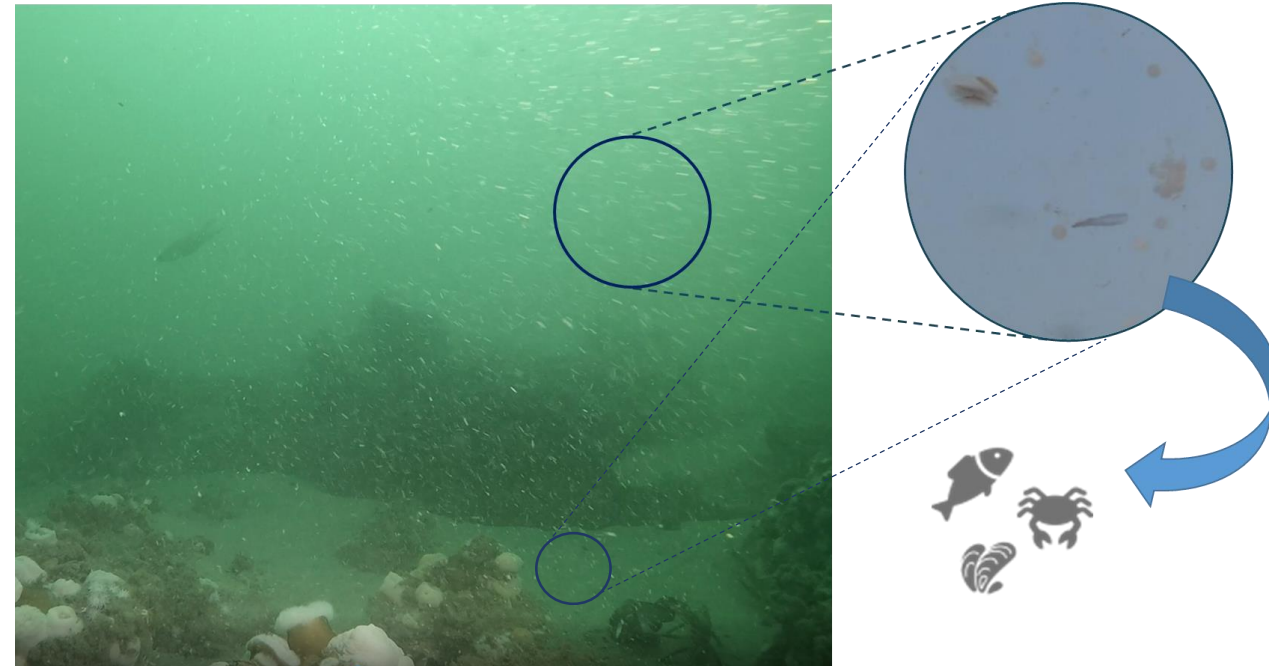
©Hans Hillewaert

What is “DNA-based”?

Bulk DNA



Environmental DNA



Is DNA-based monitoring reliable, accurate, fast and cheap?

the heart of GEANS: stakeholder driven pilots

Soft sediment



NIS - harbors



Hard substrate



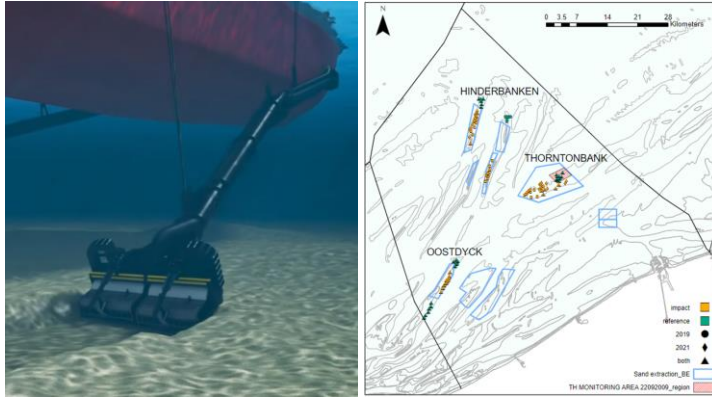
eDNA seawater



Soft sediment pilot

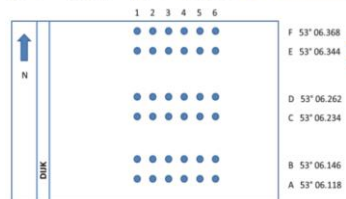
Bulk DNA

Environmental impact assessment



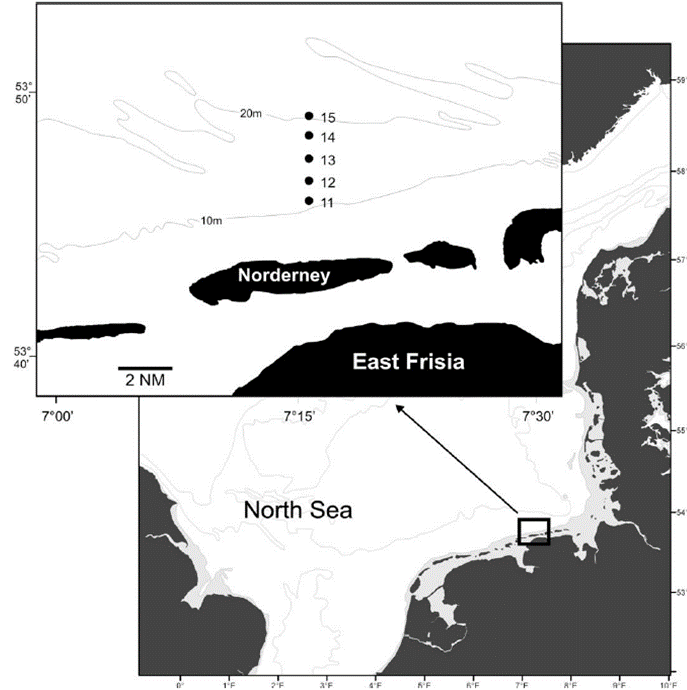
Sampling location and dates

T0	20-3-2016	T9	4-7-2016
T1	21-3-2016	T10	31-8-2016
T2	31-3-2016	T11	14-11-2016
T3	5-4-2016	T12	13-3-2017
T4	11-4-2016	T13	9-5-2017
T5	20-4-2016	T14	23-5-2017
T6	9-5-2016	T15	6-6-2017
T7	23-5-2016	T16	26-6-2017



Bulk DNA

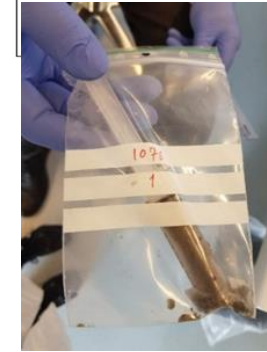
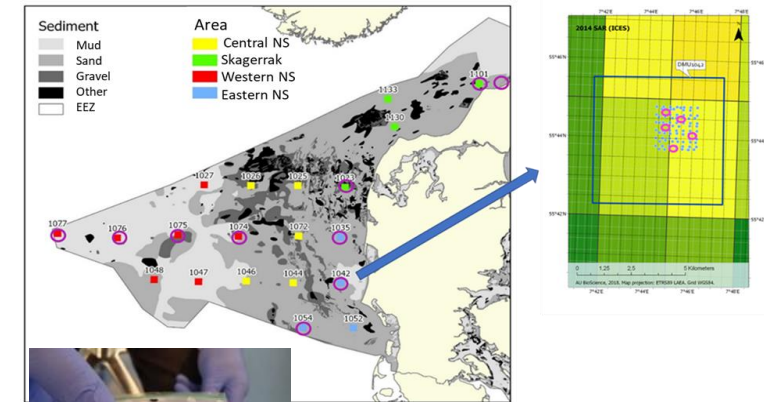
Long term monitoring station (45 years)



Three seasons

Environmental DNA

MSFD monitoring

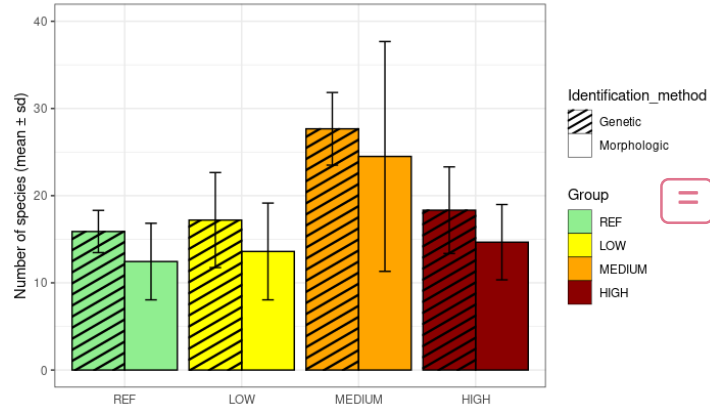


Two depth zones (44m)

Soft sediment pilot

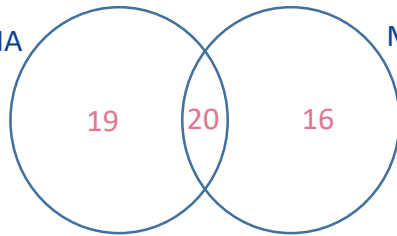
Bulk DNA

Environmental impact assessment



Bulk DNA

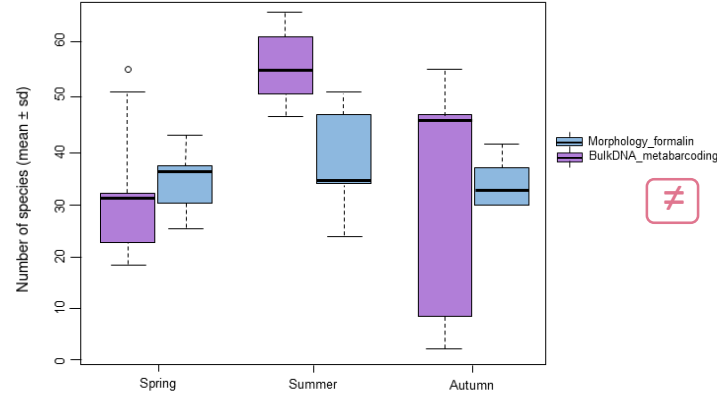
Morphology



- Main characteristic species for each impact zone were similar for both methods
- Bulk DNA: 46 % faster, 26 % cheaper

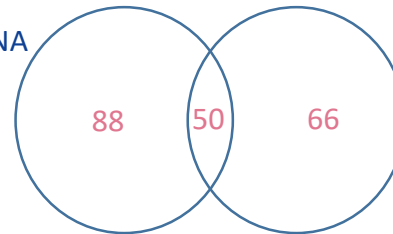
Bulk DNA

Long term monitoring station (45 years)



Bulk DNA

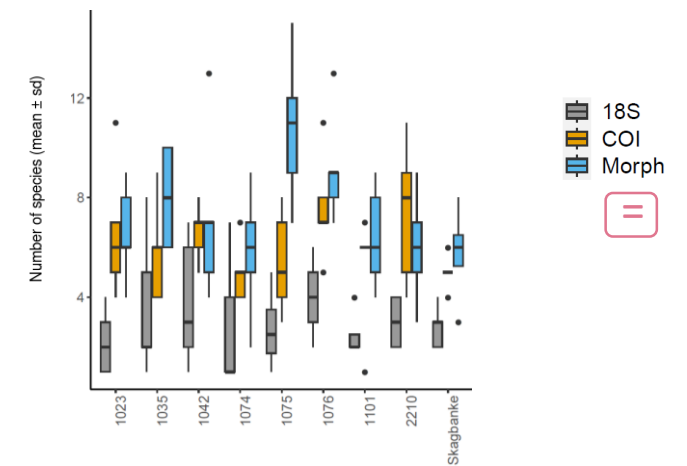
Morphology



- Characteristic species for each season different between both methods
- Bulk DNA: 66 % faster, 27 % cheaper

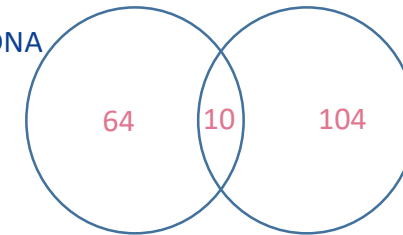
Environmental DNA

MSFD monitoring



eDNA

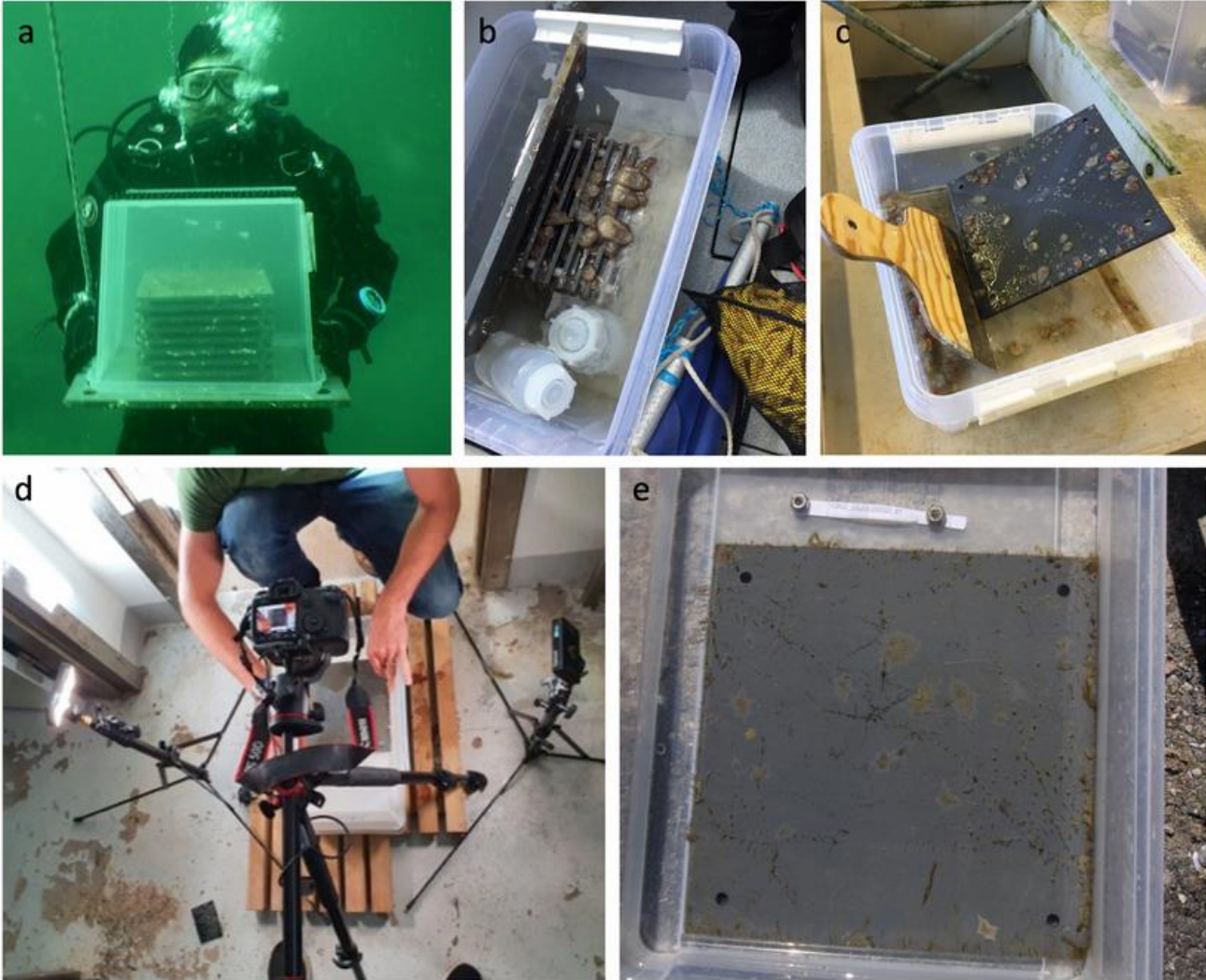
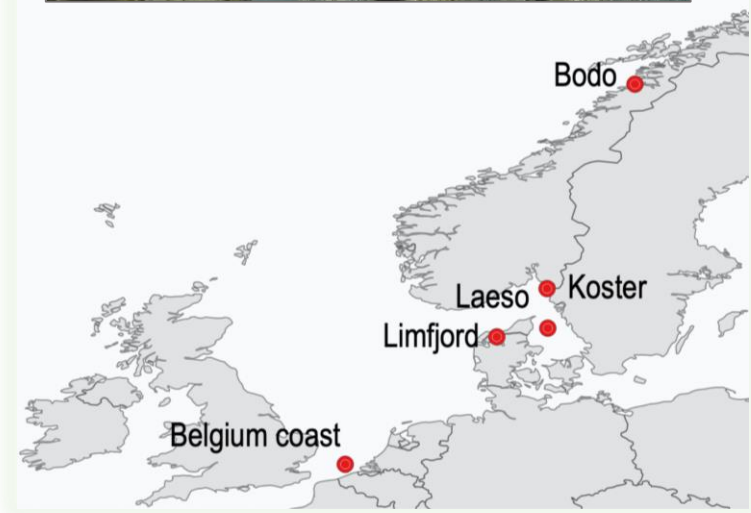
Morphology



- Characteristic species for each depth different between both methods
- 43 % faster, 9 % cheaper

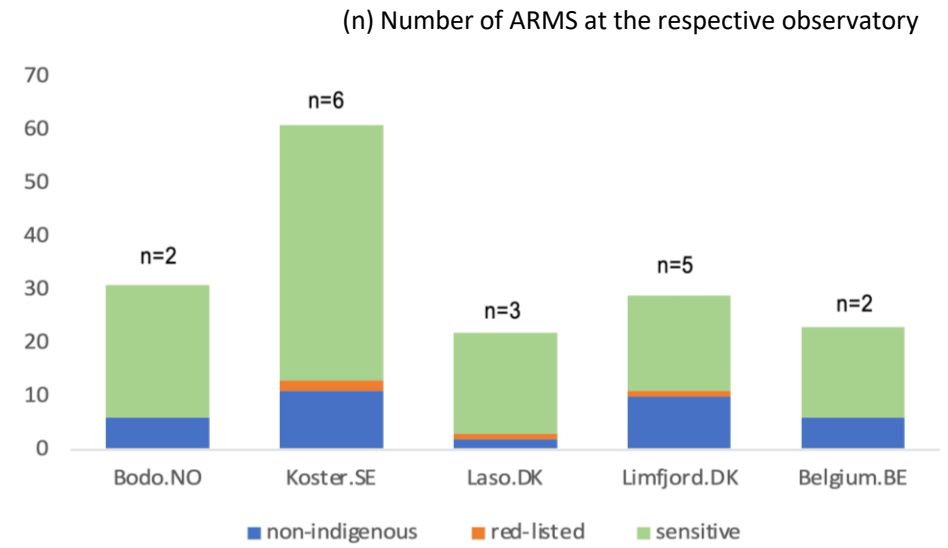
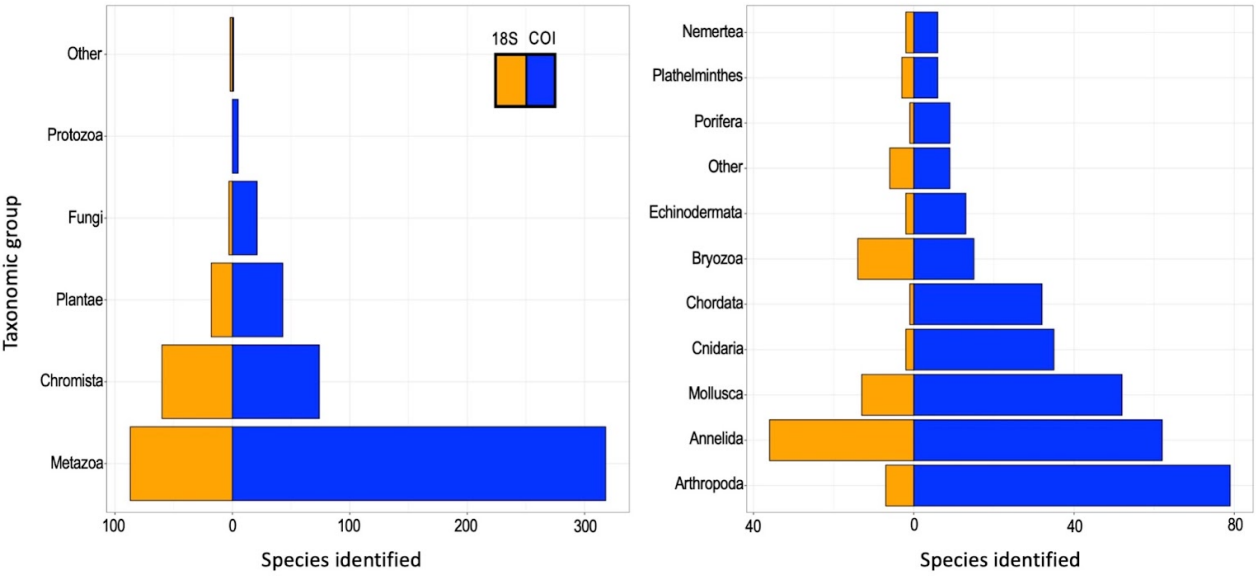
Hard substrate pilot

Autonomous Reef Monitoring Structures (ARMS)



© Maria Asplund and Matthias Obst

Hard substrate pilot



Standardised method allowing large scale comparisons of hard sub fauna

NIS pilot in harbors



© Rune Lagaisse

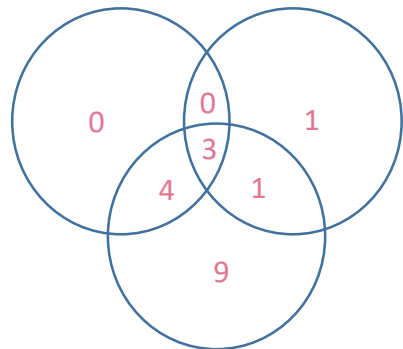


NIS pilot in harbors

Belgium

Plate + zooplankton

Bulk DNA plate Morphology plate



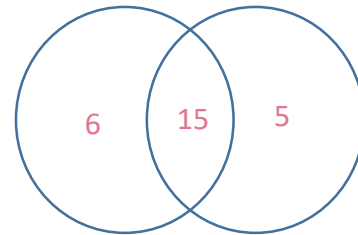
Bulk DNA zooplankton

- DNA-based method detects more NIS
- 93 % faster, 65 % cheaper
- bulk DNA to detect NIS

Germany

Plate + grab

Bulk DNA Morphology

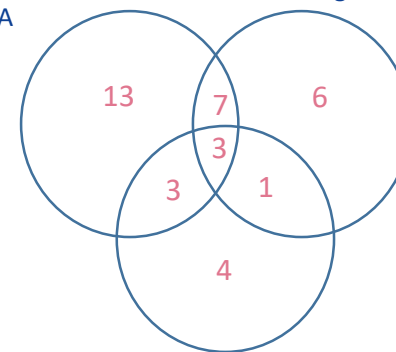


- DNA- and morphology based methods detect about equal number of NIS
- bulk DNA + morphology to detect NIS

Denmark

Plate + eDNAwater

metabarcoding Bulk DNA plate + eDNA Morphology Plate, grab, scrape



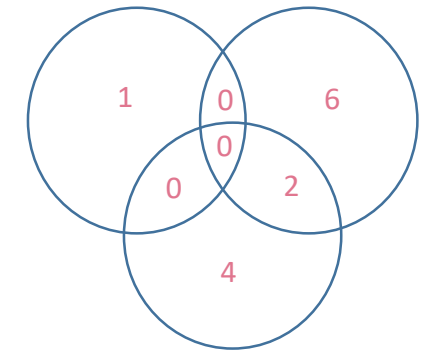
qPCR Bulk DNA plate + eDNA

- DNA-based metabarcoding detects more NIS
- 20 % faster, 28% more costly
- Bulk DNA + morphology to detect NIS

Sweden

Plate + eDNAwater + zooplankton

Bulk DNA ARMS Bulk DNA zooplankton

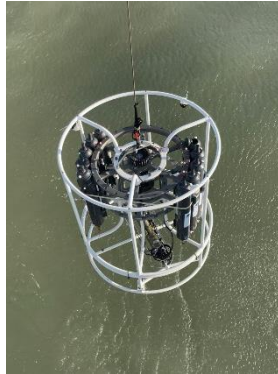
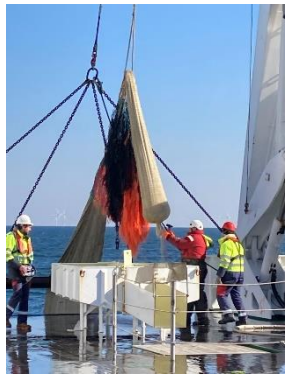


eDNA water

- No NIS with morphology
- Bulk DNA plankton + eDNA water to detect NIS

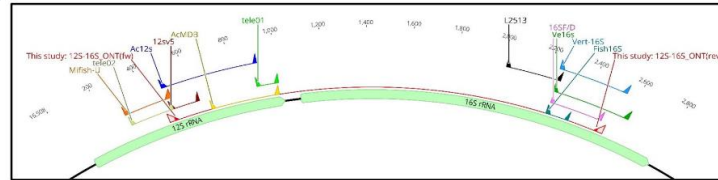
eDNA seawater pilot

EIA offshore wind farms



Belgium

Reef monitoring

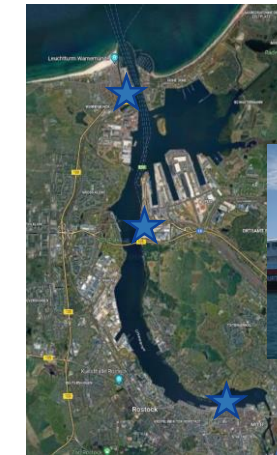
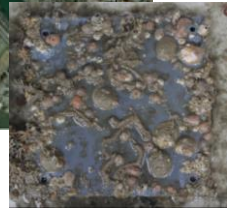


2000 bp long fragment



The Netherlands

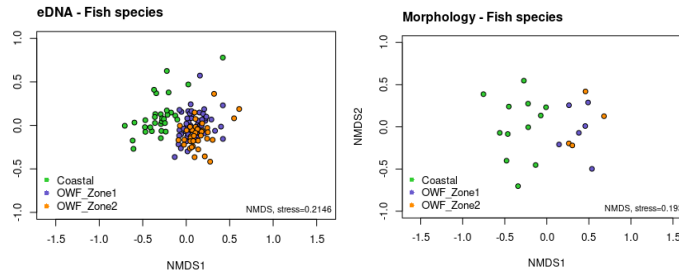
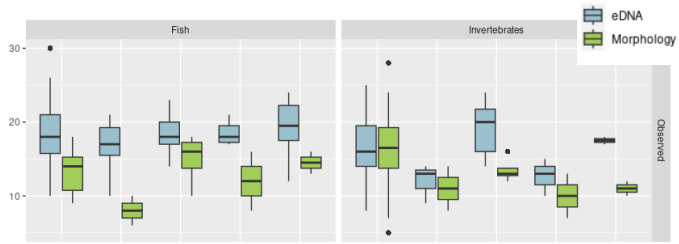
NIS monitoring



Belgium + Germany

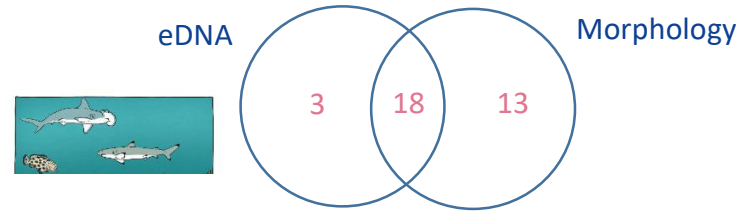
eDNA seawater pilot

EIA offshore wind farms

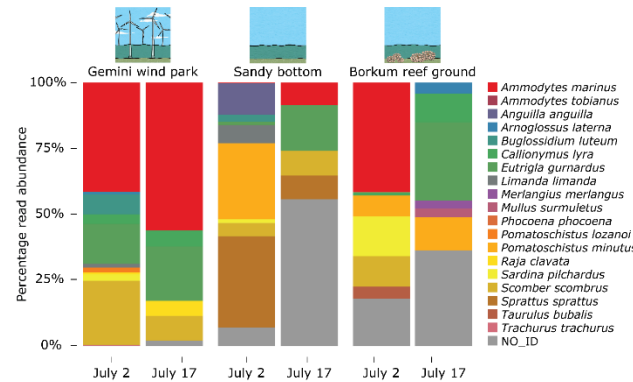


- 83% of fishes and 27% of epibenthic invertebrates from the catches were detected with eDNA
- beam trawl analyses are 42.5% faster and 53% cheaper than eDNA metabarcoding

Reef monitoring

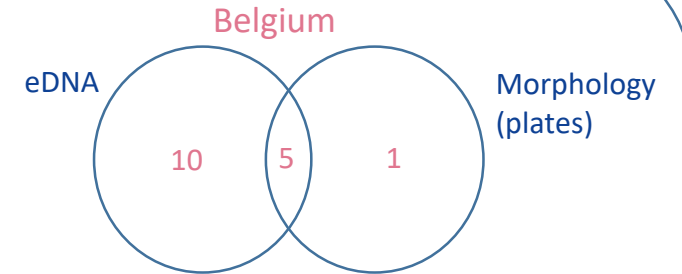


- 58% of fishes detected with long fragment

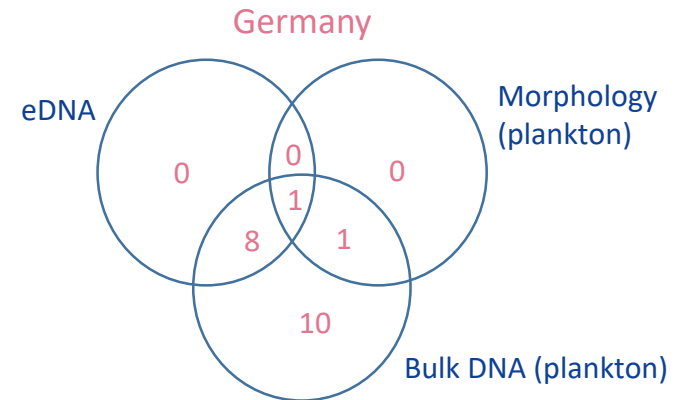


- Broad diversity of fishes detected
- Reference database incomplete + comparison with short read data needed

NIS monitoring



- twice as many NIS detected with eDNA
- Time of sampling may bias results!



- Twice as many NIS detected with bulk DNA than with eDNA

Is DNA-based monitoring reliable, accurate, fast and cheap?

GEANS recommendations

Soft sediment monitoring

- Bulk DNA >> eDNA_{sediment}
- Bulk DNA protocol: validated with ringtest
- Curated reference database
- Faster + cheaper

BUT

- Sample preservation is key: switch to ethanol
- No abundance/biomass information
- No life history information
- Species identity
- No good indicators available

Integration of bulk DNA + morphology = highest resolution for a similar cost

NIS monitoring

- Bulk DNA > eDNA_{water} > morphology
- Each method detects unique NIS
- Faster, not always cheaper

BUT

- Reference databases incomplete
- No abundance/biomass information
- Sampling design: temporal + spatial replication

Bulk DNA + eDNA + morphology = highest number of NIS

Bulk DNA plankton + eDNA if resources are limited

eDNA monitoring

- eDNA_{water} = beamtrawl fish
- eDNA_{water} ≠ beamtrawl epibenthic invertebrates
- Non-destructive and non-invasive
- Automatisation and high throughput

BUT

- No abundance/biomass information
- Eggs/adults?
- Not cheaper or faster
- Method development ongoing
- Further harmonisation needed

eDNA for fish monitoring, but further standardisation needed

Hard sub monitoring

ARMS:

- Standardised method for inventory of hard sub species
- DNA-based analyses allows streamlining of sample processing

BUT

- Long deployment time
- No abundance/biomass information
- Similar time/costs as morphology

Bulk DNA of ARMS for cross regional monitoring

THANK YOU!
QUESTIONS?

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