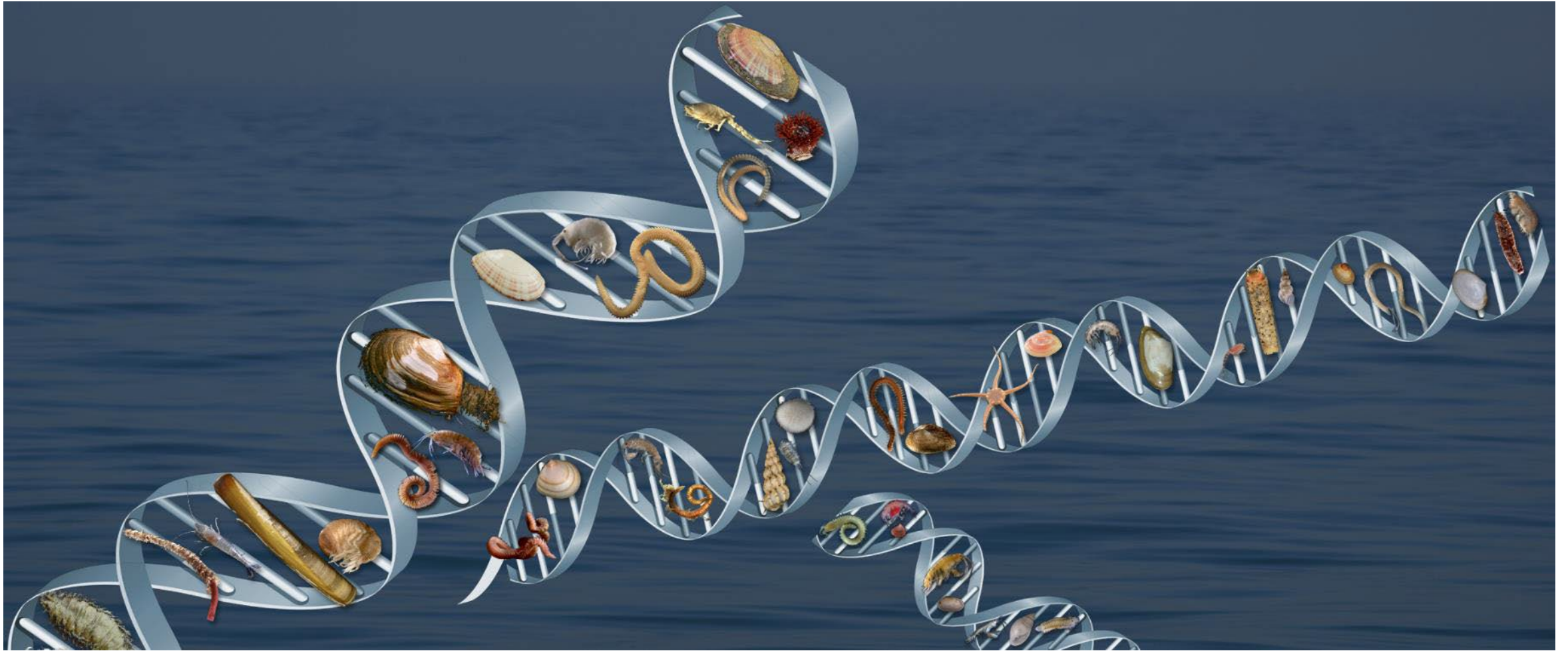
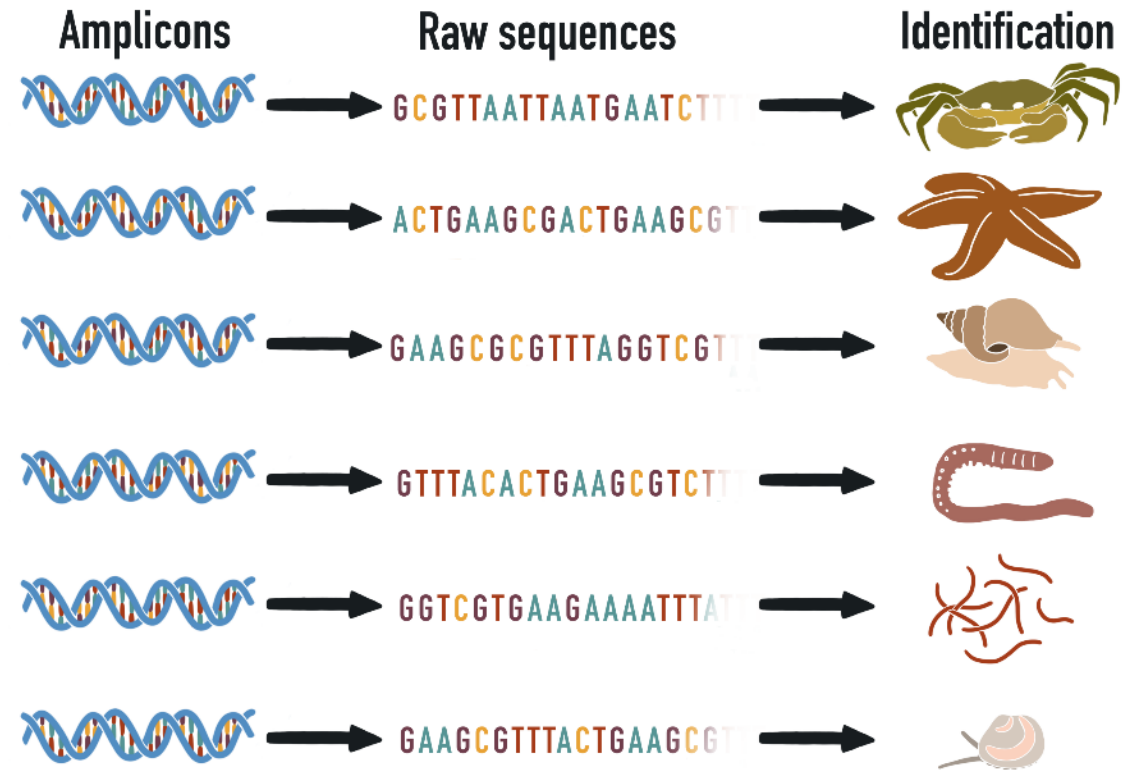
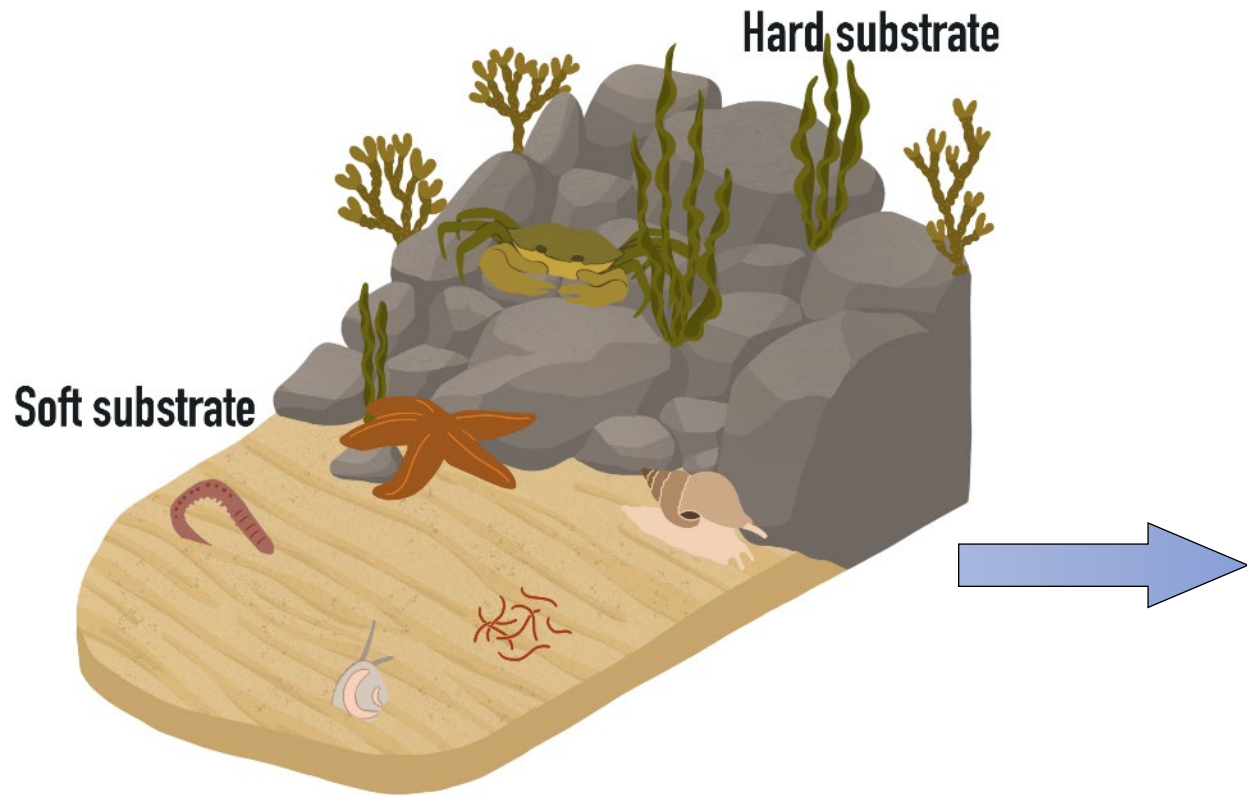
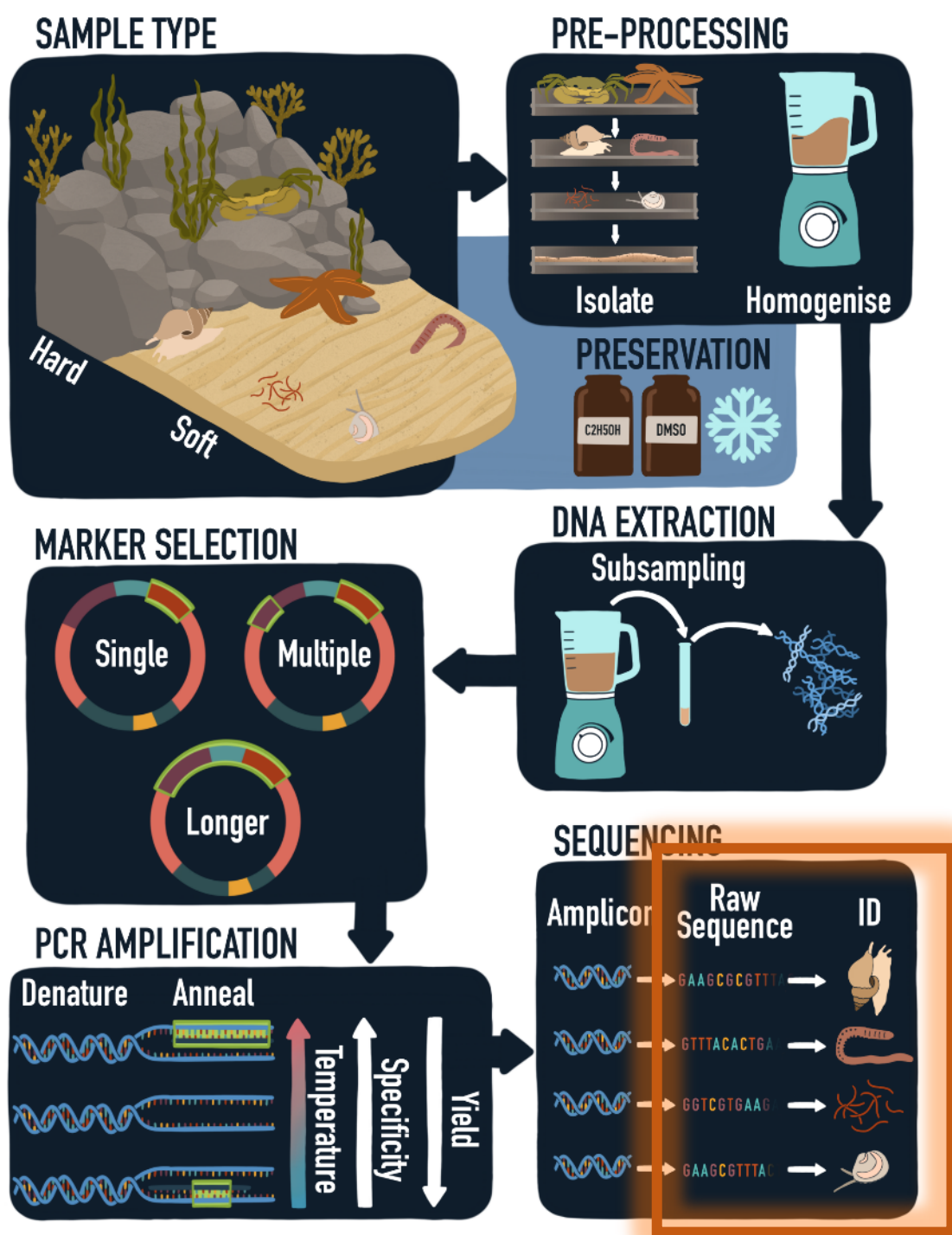


GEANS products helping to improve molecular marine environmental monitoring in the North Sea region



GEANS final webinar – 27 June 2023

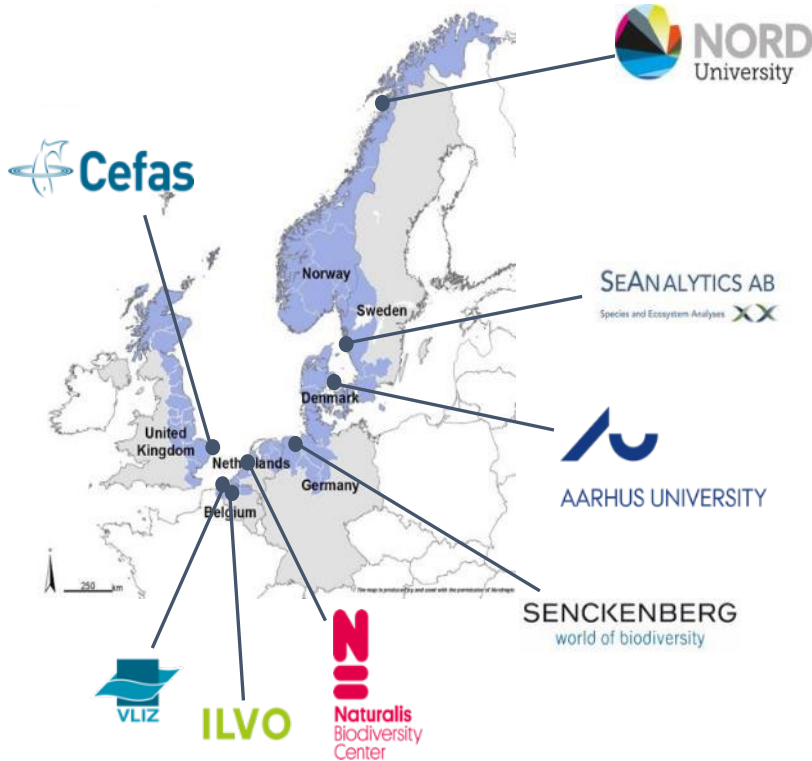




GEANS products to improve molecular monitoring

Target species for the GEANS reference library

First Key list : targeted 802 species (96 NIS species) found in monitoring stations of GEANS partners.



New sampling campaigns






In-house sequence databases

Two screenshots of the BOLD SYSTEMS Barcode of Life Data System interface. The top screenshot shows the 'BNSEP Barcoding North Sea Epimeriidae' project with 75 specimens and 83 sequences. The bottom screenshot shows the 'BNSDE Barcoding North Sea Decapoda' project with 529 specimens and 537 sequences. Both screens display project details, progress bars, and a 'Calculate the Data' button.

Lab workflow

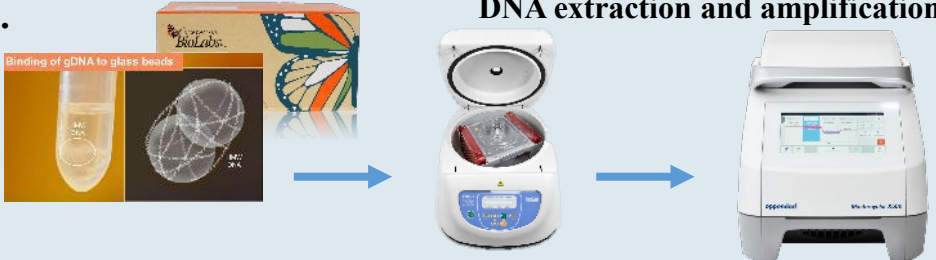
1. Selection of the barcode marker

The mitochondrial genome

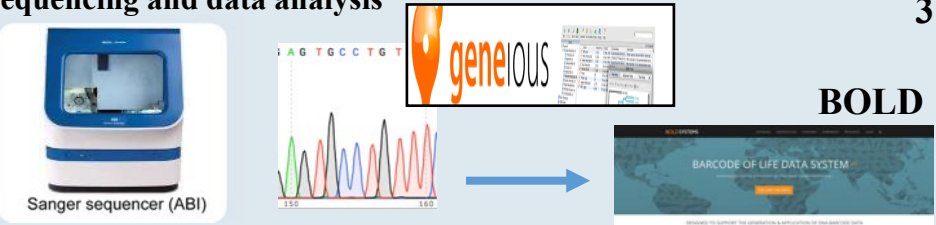




658 bp
(Folmer region)

2. DNA extraction and amplification



3. Sequencing and data analysis



Sanger sequencer (ABI)

geneIOUS

BOLD

4. Photos and collection data in BOLD



Pagurus bernhardus (Linnaeus, 1758)



Ophiecten affinis (Lütken, 1858)



Sinelobus vanhaareni Bamber, 2014



Pycnogonum litorale (Strøm, 1762)



Pseudoprotella phasma (Montagu, 1804)



Epitonium clathrus (Linnaeus, 1758)

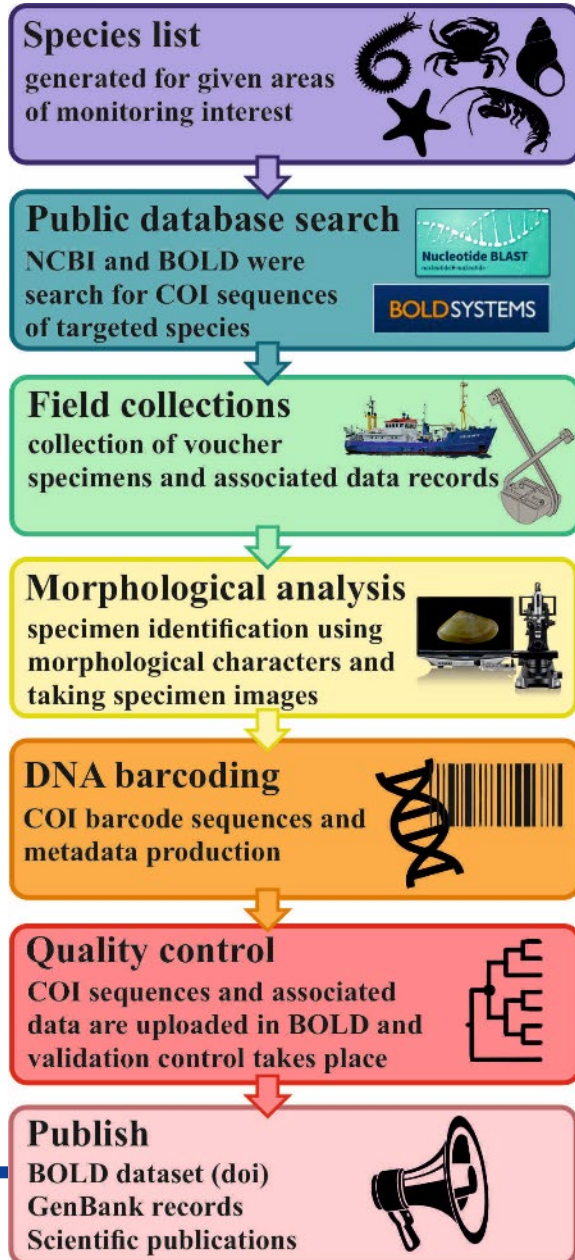


Loimia ramzega Lavesque et al. 2017



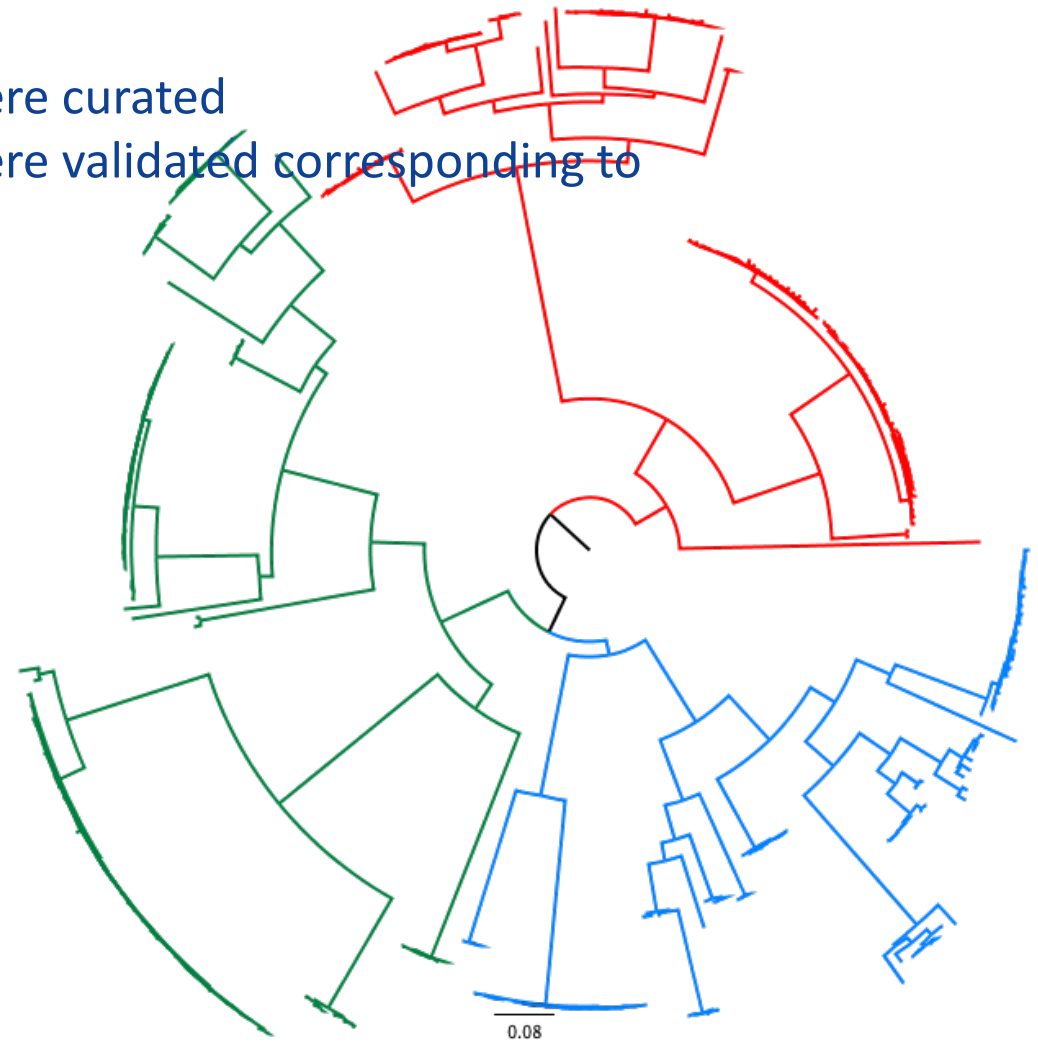
Macoma balthica (Linnaeus, 1758)

Curation workflow



- over 4500 sequences were curated
- over 4000 sequences were validated corresponding to over 700 species

- 1 NJ trees were constructed and obvious mistakes (i.e. contaminations) were excluded
- 2 Barcodes assigned to one species were validated when attributed to one BIN cluster exclusive for the species
- 3 Barcodes were validated when attributed to more than one BIN cluster but all of them were nearest neighbour to each other
- 4 When conflict was detected between barcode clustering and morphological identification the specimen morphological identification was revised to search for missidentification or cryptic species
- 5 Taxonomy constantly updated (i.e. synonyms, new species)
- 6 Cross-referencing of sequences among research groups
- 7 Curating new record entries and control of old entries



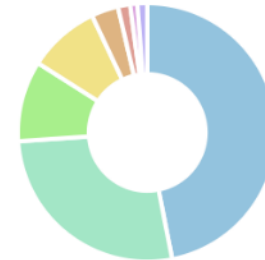
GEANS barcode reference library in BOLD

Dataset – DS-GEANS1 GEANS Reference Library

- 4005 specimens
- 712 species (743 BINs)
- 15 Phyla
- 4005 COI sequences



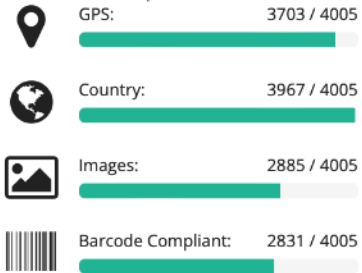
Taxonomy



- Arthropoda (phylum): 1879
- Mollusca (phylum): 1081
- Echinodermata (phylum): 405
- Annelida (phylum): 359
- Cnidaria (phylum): 135
- Chordata (phylum): 61
- Bryozoa (phylum): 36
- 8 others (phylum): 49

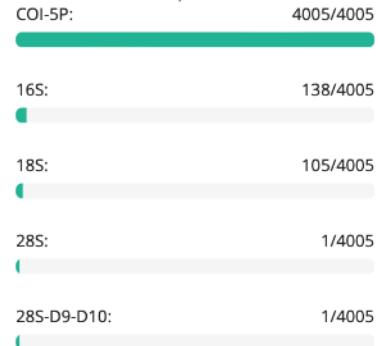
Specimens

4005
Specimens



Sequences

4250
Sequences

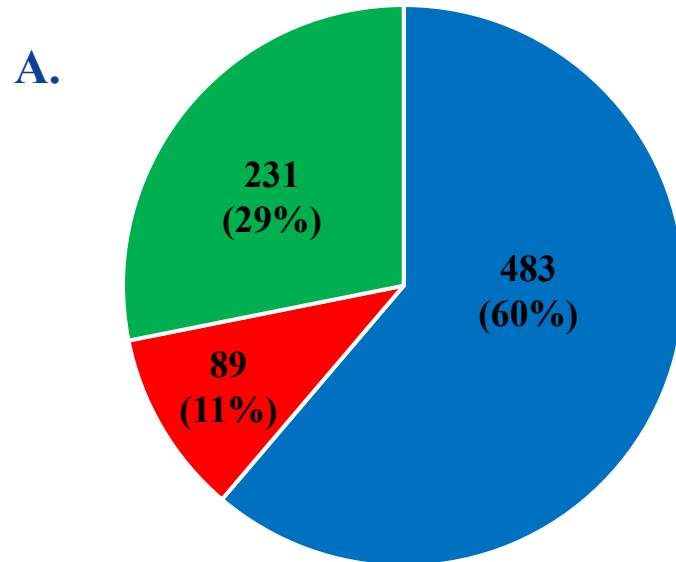


- http://www.boldsystems.org/index.php/Public_SearchTerms?query=DS-GEANS1

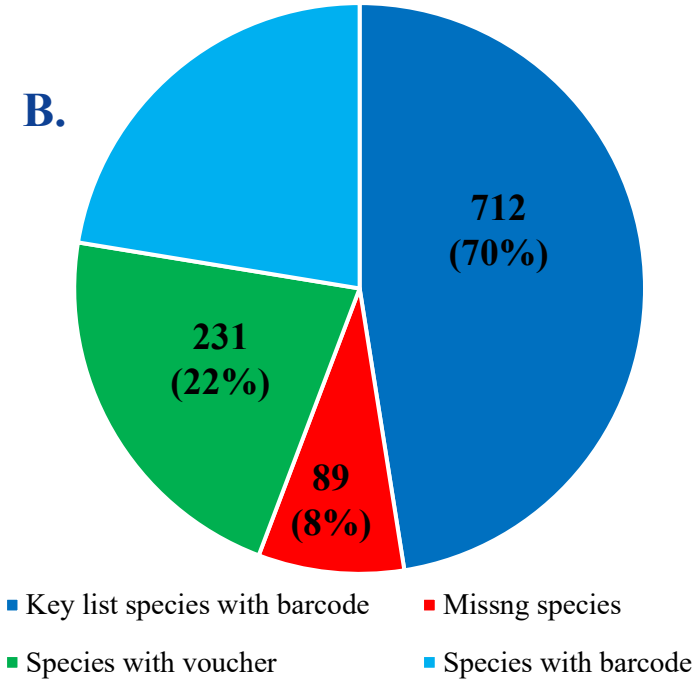
GEANS barcode reference library

Original list (A): 802 species

Expanded list (B): 1017 species



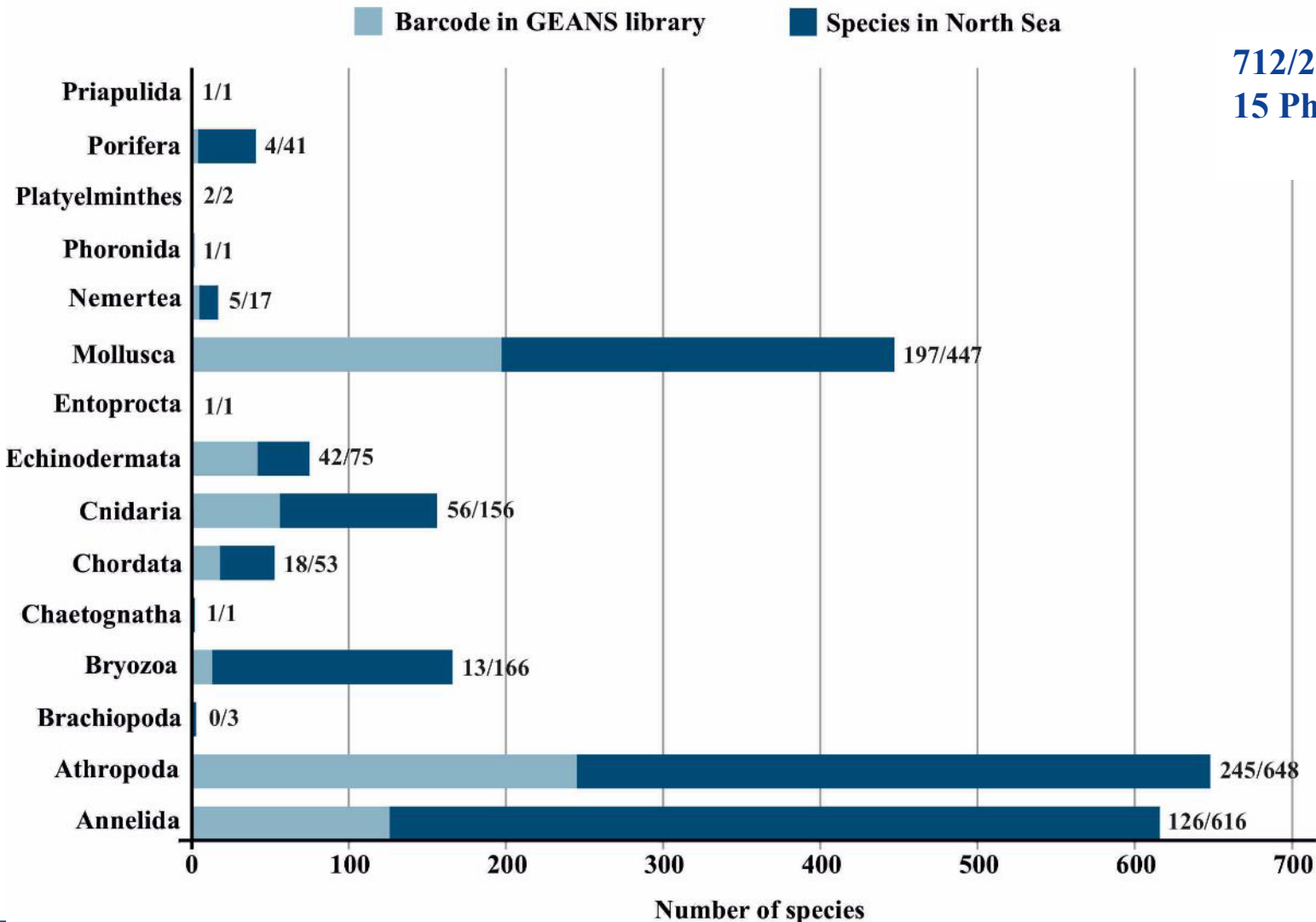
■ Key list species with barcode ■ Missing species ■ Species with voucher



■ Key list species with barcode ■ Missing species
■ Species with voucher ■ Species with barcode

DNA barcode coverage for marine macroinvertebrate species occurring in North Sea in the original key list (A) and in the expanded list (B).

GEANS barcode reference library



712/2229 species
15 Phyla

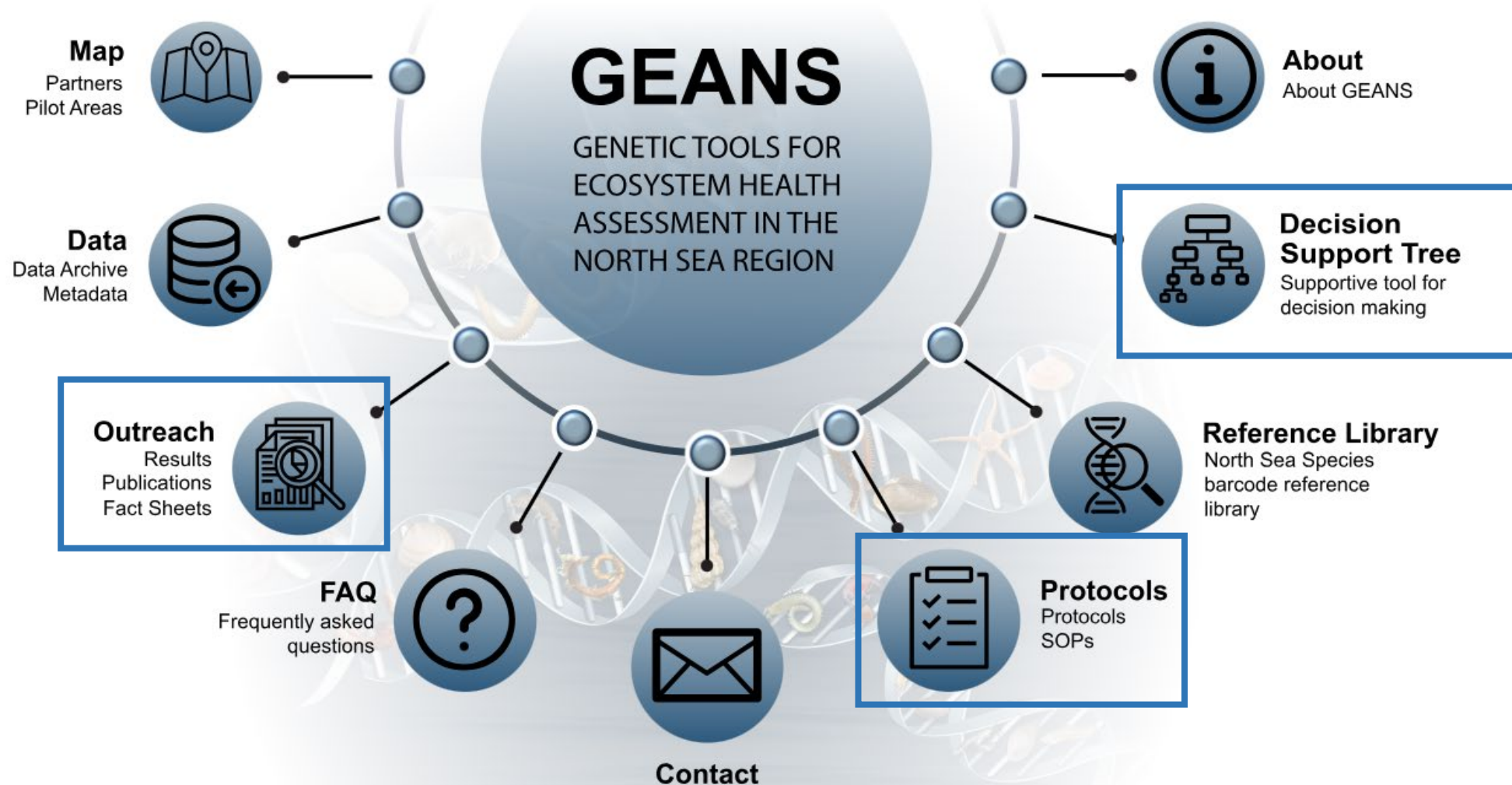
Barcode coverage of marine macrobenthic species of the North Sea in the GEANS DNA reference library. Numbers on bars refer to the species barcoded in comparison to the North Sea species.

GEANS barcode reference library

Take home message:

- Reference libraries are **critical** for the implementation of DNA-based environmental assessments
- Currently GEANS Reference Library holds **4005 COI sequences** belonging to **712 species** (743 BINs), of which **69 NIS**, covering **32%** of the North Sea macrobenthos and continues to grow. A barcode for **89 species** found in the North Sea was given for the first time.
- The GEANS reference library is the first curated DNA-library covering all the spectrum of macrobenthic animals in the North Sea that includes validated sequences **compared within and across research institutes**.
- This DNA-library **supports** the implementation of fast, cost-efficient and reliable DNA-based identifications and subsequently environmental health assessments in the North Sea.

All output available on: www.geans.eu



Protocols <https://www.geans.eu/protocols>

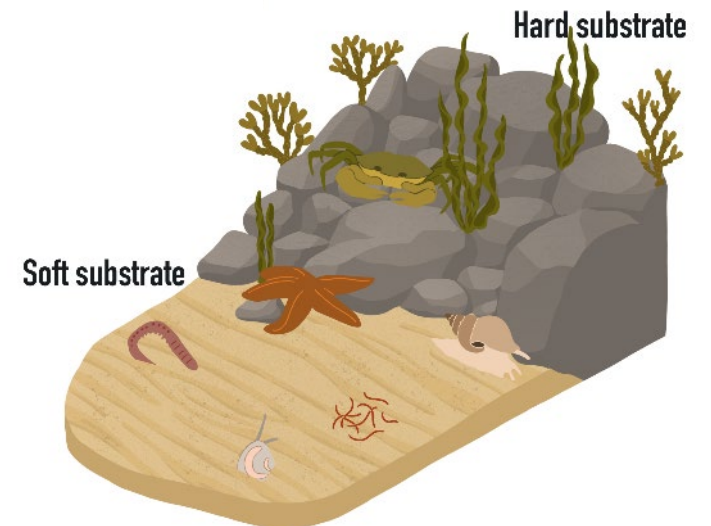
Soft Bottom
Substrate

Hard Bottom
Substrate

Non Indigenous
Species

eDNA

Unsuccessfull
Protocols



Quality assurance of soft sediment protocol

Ecological Indicators 150 (2023) 110207



Contents lists available at [ScienceDirect](#)

Ecological Indicators

journal homepage: www.elsevier.com/locate/ecolind



Original Articles

DNA metabarcoding on repeat: Sequencing data of marine macrobenthos are reproducible and robust across labs and protocols

Laure Van den Bulcke^{a,f,*}, Annelies De Backer^a, Jan Wittoeck^a, Kevin Beentjes^d, Sara Maes^a,
Magdalini Christodoulou^{b,h}, Pedro Martinez Arbizu^b, Rumakanta Sapkota^e,
Berry Van der Hoorn^{d,g}, Anne Winding^e, Kris Hostens^a, Sofie Derycke^{a,c}

^a Flanders Research Institute for Agriculture, Fisheries and Food – Marine Research, Jacobsenstraat 1, 8400 Oostende, Belgium

^b Senckenberg am Meer, German Centre for Marine Biodiversity Research, Südstrand 44, 26382 Wilhelmshaven, Germany

^c University of Ghent, Department of Biology - Marine Biology Research Group, Krijgslaan 281, 9000 Gent, Belgium

^d Naturalis Biodiversity Center, Darwinweg 2, 2333 CR Leiden, The Netherlands

^e Aarhus University, Department of Environmental Science, Frederiksborgvej 399, 4000 Roskilde, Denmark

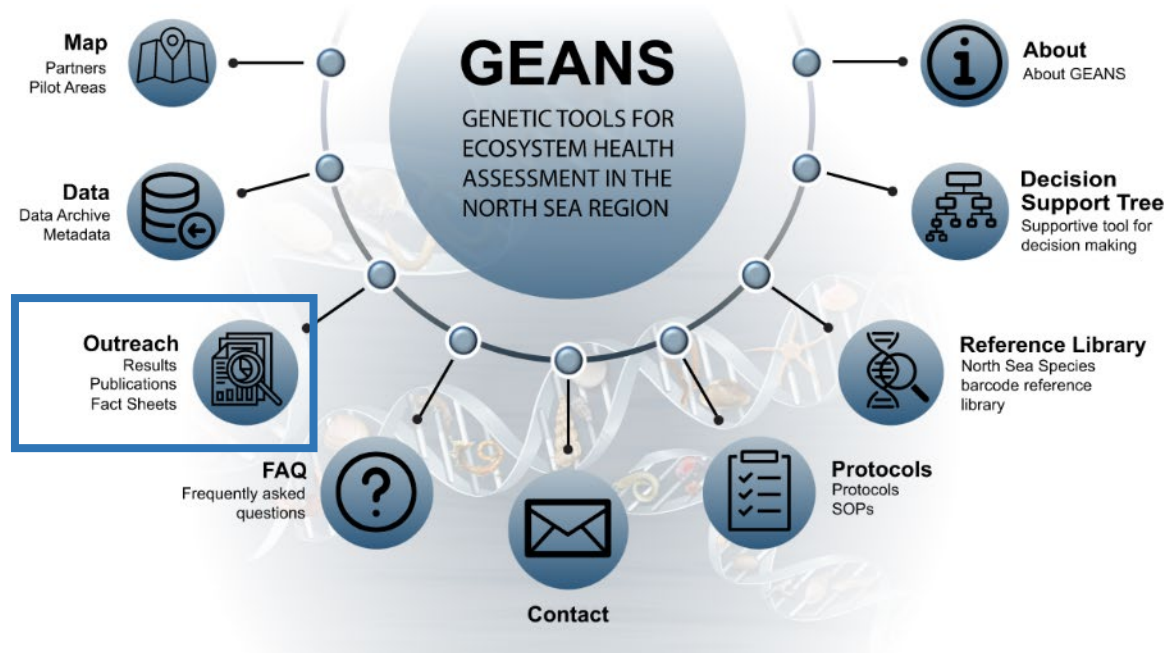
^f University of Ghent, Department of Data Analysis and Mathematical Modelling - Knowledge-based Systems Research Group, Coupure Links 653, 9000 Gent, Belgium

^g Inholland University of Applied Sciences, Landscape and Environment Management, Rotterdamseweg 141, 2628 AL Delft, The Netherlands

^h OÖ Landes-Kultur GmbH, Biologiezentrum, Johann-Wilhelm-Klein-Straße 73, 4040 Linz, Austria



Compilation and integration of info and results



<https://www.geans.eu/>

Fact sheets and stories

Biofouling on recreational vessels: metabarcoding for rapid screening of NIS
The connectivity of maritime and inland waterways promotes the risk of unnoticed distribution of non-indigenous species (NIS) in the form of biofouling on ship hulls or by ballast water. Screening of biofouling requires scraping the hull of bryozoans, cnidarians and small annelids are hard to identify. A test case was using metabarcoding as screening technique.

eDNA supplements scuba diver observations in hard substrate monitoring
Hard substrates that are protected by the EC Habitats Directive need long term monitoring to understand responses in species composition, coverage and diversity in relation to changes in environmental conditions. Traditionally, reef monitoring is done by divers equipped with underwater video and radio communication. While this approach is robust, it is of interest to explore the usefulness of modern techniques that are less expensive and/or provide more detailed information on plants, animals and microorganisms associated with the reefs.

Monitoring NON-INDIGENOUS SPECIES (NIS) in the marine environment
WHAT are non-indigenous species and WHY do they need to be monitored?
As a result of human activities such as shipping (with biofouling and ballast water transfer), non-native species find access to ecosystems outside their natural range. Due to the absence of predators or other control mechanisms, they have the potential to become invasive and harm the local ecosystem. Consequently, early detection is key and monitoring a must.

	Water column	Soft seafloor	Hard seafloor
Adult individual/colony	<ul style="list-style-type: none"> Plankton or shrimp net Video 	<ul style="list-style-type: none"> Grab or corer Video 	<ul style="list-style-type: none"> Diver census Scrape samples Settling panels (ARMS)
Larvae	Plankton net	Plankton net	Plankton net

A curated SEQUENCE LIBRARY: the fundament of all DNA-based monitoring
WHY is a sequence library necessary for DNA-based monitoring?
Comprehensive and taxa specific barcode libraries are integral to monitoring and conserving aquatic biodiversity. The reference library is what allows the identification of the species found in metabarcoding analyses.

Articles, Reports & Publications

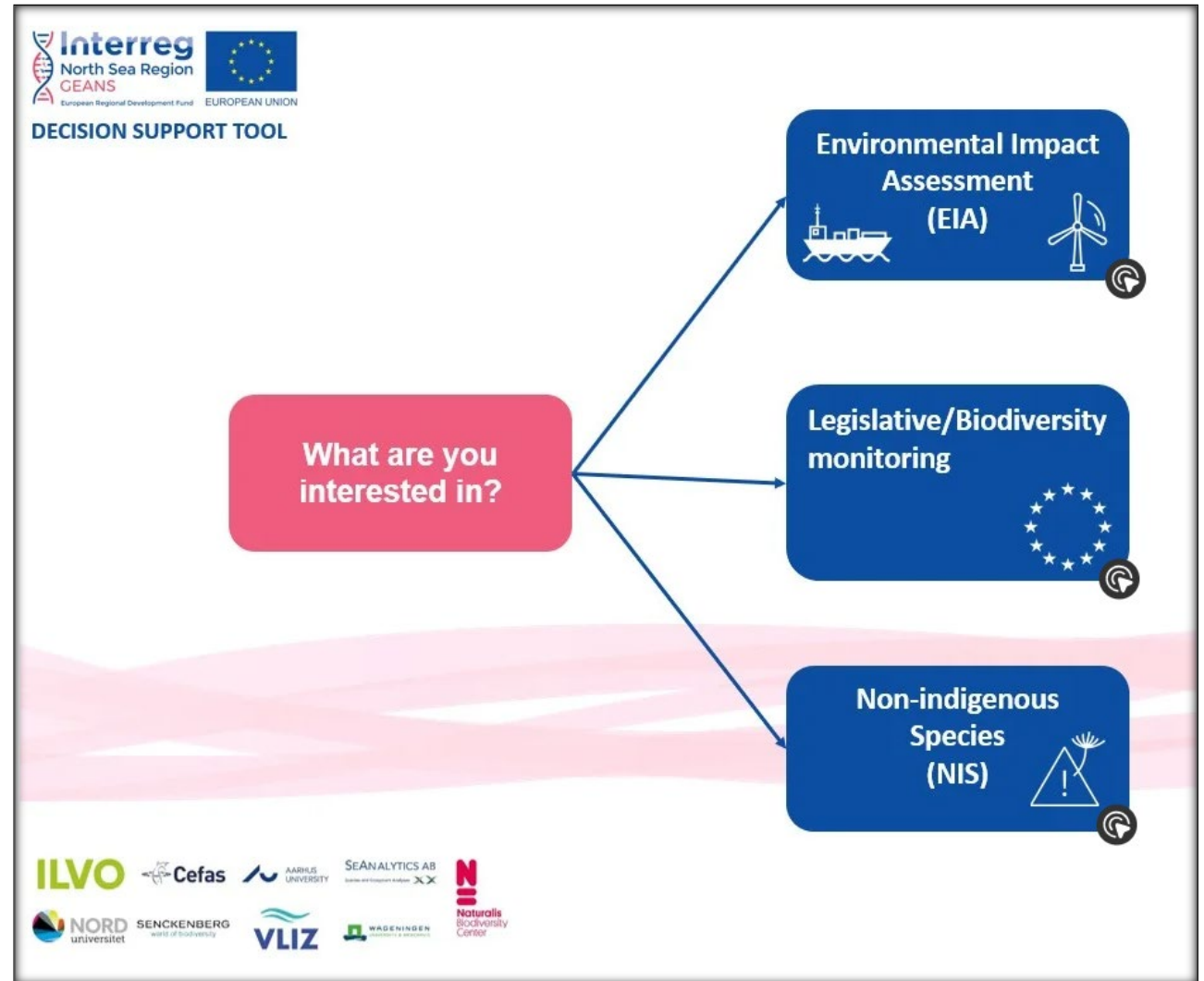
Home > Outreach > Articles, Reports & Publications

Peer-reviewed publications

- [Biases in bulk: DNA metabarcoding of marine communities and the methodology involved](#)
- [A Marine Biodiversity Observation Network for Generic Monitoring of Hard-Bottom Communities](#)
- [Detection of Macrobenthos Species With Metabarcoding Is Consistent in Bulk DNA but Depends From the Ethanol Preservative](#)
- [Environmental DNA Monitoring of Biodiversity Hotspots in Danish Marine Waters](#)
- [Towards harmonization of DNA metabarcoding for monitoring marine macrobenthos: the effect of extraction methods and DNA extractions on species detection](#)
- [Phylogeographic study using autonomous reef monitoring structures indicates fast range expansion](#)

Decision support tool

- Integration of all knowledge gained in GEANS
- Help on choosing best workflow for monitoring/management question
- Can be found through www.geans.eu



THANK YOU!
QUESTIONS?

CONTACT US

annelies.debacker@ilvo.vlaanderen.be



<https://www.geans.eu/>
<https://northsearegion.eu/geans/>

