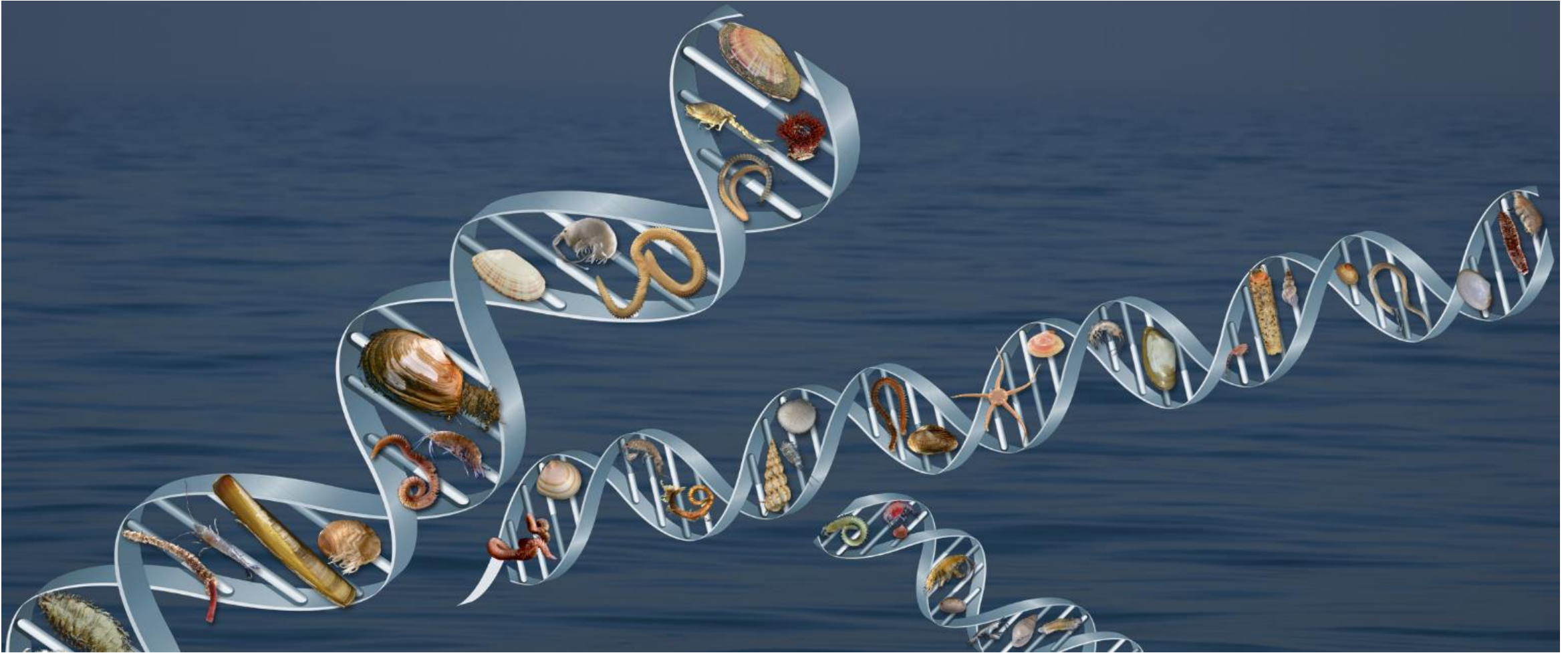


# Introduction to GEANS and main results so far



# Genetic tools for Ecosystem health Assessment in the North Sea region (GEANS)

- EU Interreg North Sea Region project
- Started in March 2019 – will end in June 2023
- Budget: € 3.3 million (50% own contribution)
- 9 partners

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

or: <https://geans.eu>



@GEANS\_Interreg



**Objective: GEANS strives to implement DNA-based tools in routine monitoring programs in support of policy and decision making concerning ecosystem health.**

# Why GEANS?

Sustainable use and management of the North Sea = grand challenge!



⇒ Fast and accurate monitoring needed!





# Ecosystem health indicators

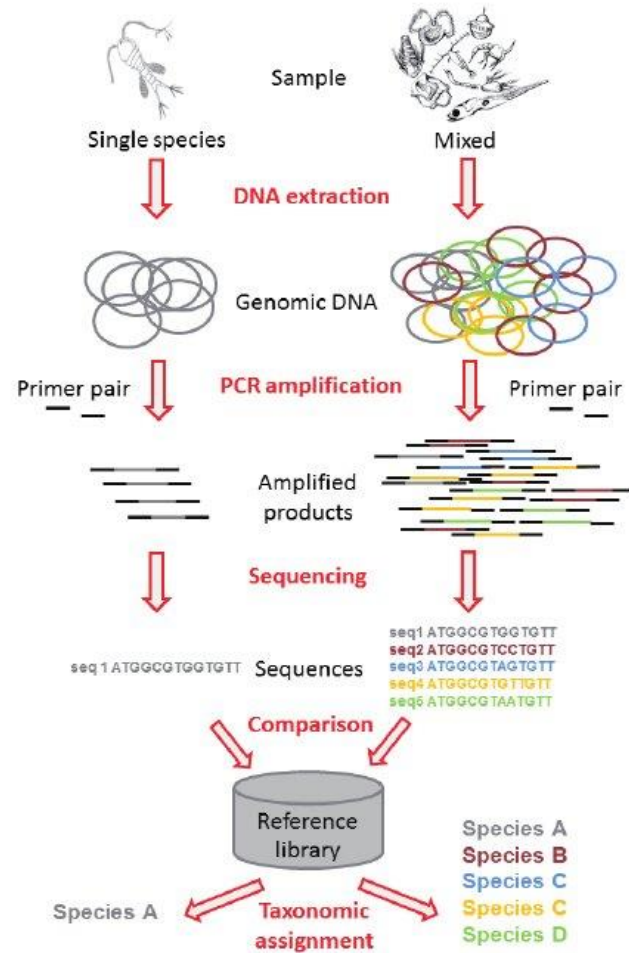


©Hans Hillewaert

# Bulk versus environmental DNA

	Bulk DNA	environmental DNA - eDNA
Definition	<p>Bulk DNA is DNA extracted from the tissue of specimens that have been separated from the sediment/water/substrate by sieving, decantation and manual sorting.</p>  <p>Focus on the (large) animal</p>	<p>Environmental DNA (eDNA) is organismal DNA (bacteria, viruses, plankton) or extra-organismal DNA (skin cells, eggs and sperms, faeces,...) that can be found in the environment.</p>  <p>Focus on free DNA, cells and small floating organisms</p>
Effort to collect a sample	High (trawls, grabs, corers,...)	Low (water, sediment,...)
DNA concentration	High	Low
Geographical precision	GPS location	Range (water) to location (sediment)

# Barcoding versus metabarcoding



- Barcoding:
  - Single species
  - ⇒ *Identification of species OR creating reference sequence*
- Metabarcoding:
  - Multiple species
  - ⇒ *Biodiversity and community structure*

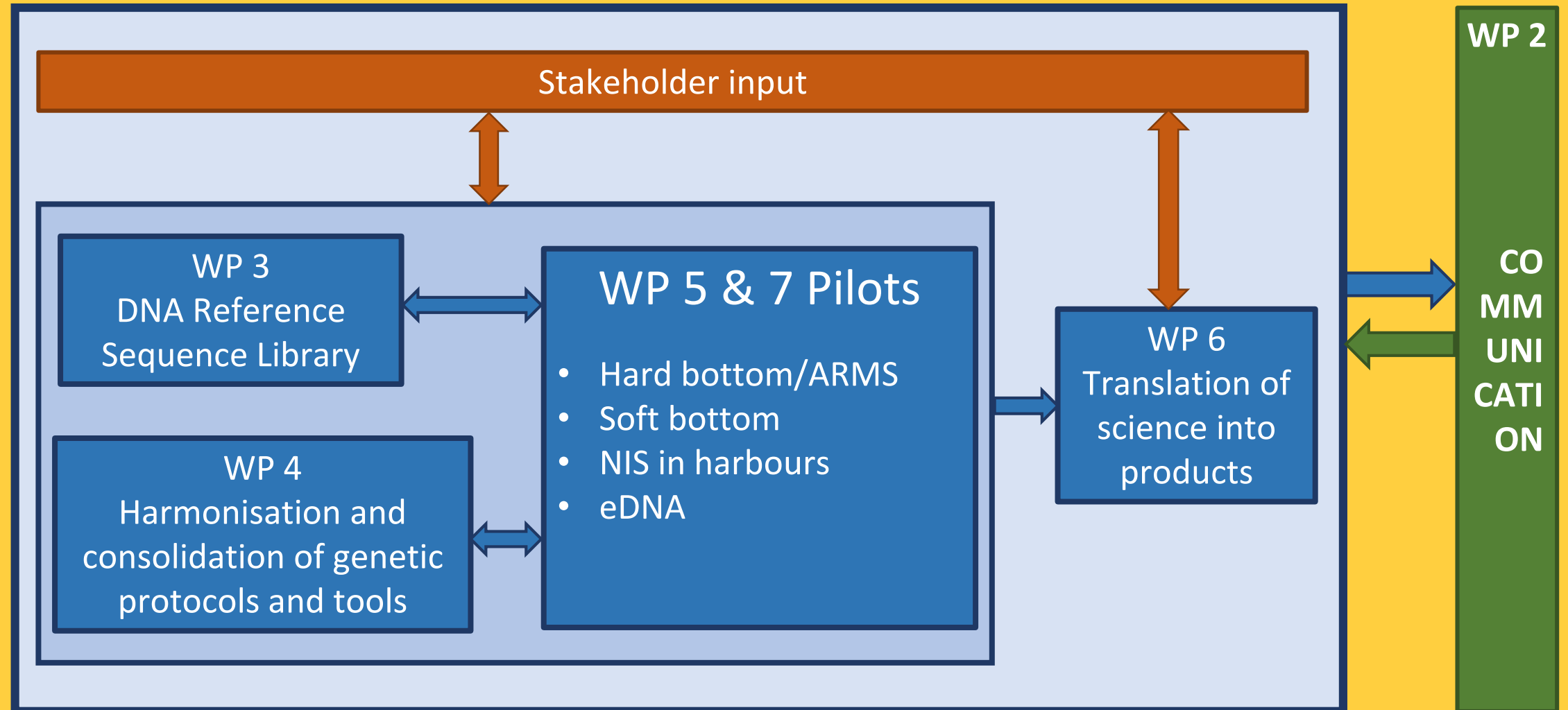
Source: Corell & Rodrigues-Ezpeleta - 2014

# GEANS goals

- Set-up of a reliable and open-source macrobenthic **DNA reference library**
- **Harmonisation and consolidation** of metabarcoding approach across NS countries
- **Real time pilot studies** for validation of genetic tools and methods
  - in close cooperation with (local) managers, policy makers and involved stakeholders
- **Transnational co-operation** will create synergies and assure comparability

# GEANS Project overview

## WP 1 – GEANS Project Management

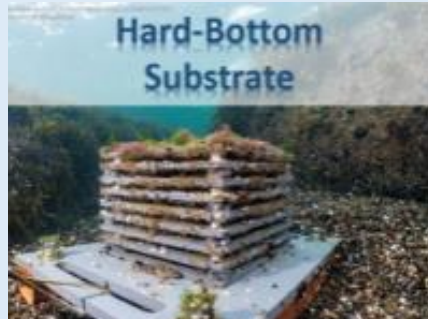
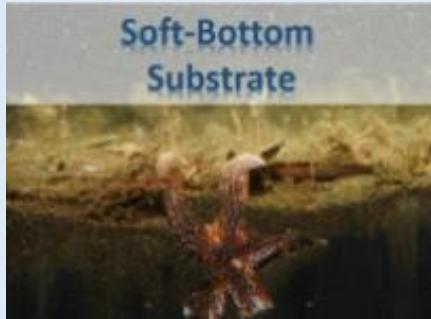




# Pilots are @ the heart of GEANS

- Goals:
  - Investigate effectiveness of DNA-based methods for different monitoring questions
  - Remove barriers for implementation
  - Establish harmonized protocols for DNA-based monitoring
- Four '*sensu lato*' pilots – often comparison conventional with DNA-based methods
- Mostly steered through stakeholders and/or in parallel with existing conventional monitoring programs

## WP5 – bulk DNA



## WP7 – eDNA



# Cost and time efficiency

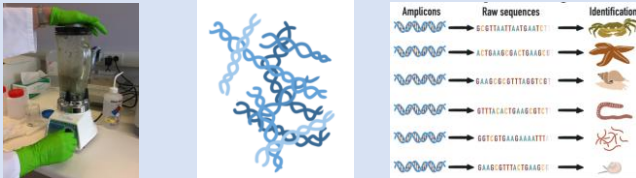
- Cost and time tracking in:
1. Soft sediment EIA sand extraction (Belgian NS)
  2. NIS harbor Ostend
  3. Soft-bottom LTER monitoring (Norderney, GE)

## Morphology based analysis



1. 2,7h – 271 € /sample
2. 11,25h – 369 €/sample
3. 19h/sample

## DNA-based analysis (bulk metabarcoding)



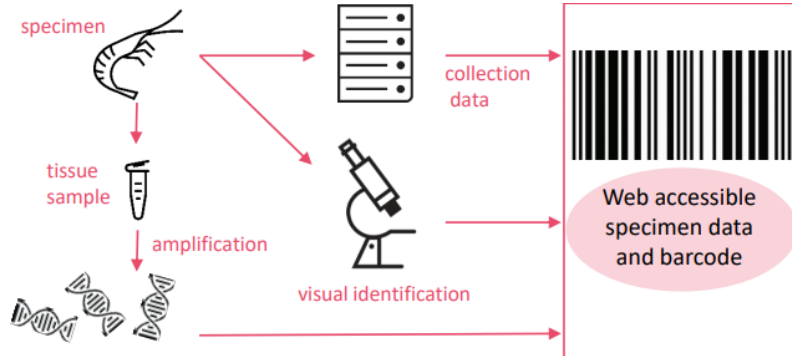
1. 1,5h – 198€/sample
2. 1h – 157€/sample
3. 2,3h/sample

**DNA-based ID on average  
75% faster  
&  
42% cheaper**

# WP3 Reference library



species in pilot areas = target list for reference library (+/- 800 macrobenthic species)



Pilot list supplemented with existing vouchered barcodes => expanding list to +/-1000 species

## Example: *Microprotopus maculatus* (Norman, 1867)

GEANS00142 - Genetic tools for Ecosystem health Assessment in the North Sea region [GEANS]

A screenshot of the GEANS00142 specimen details page. The page shows a photograph of the specimen, a scale bar (1000µm), and various metadata fields. The 'Specimen Details' section includes fields for Sample ID, Process ID, Project, Institution, Field ID, Museum ID, Collection Code, Reference Link, Voucher Status, Tissue Descriptor, Sex, Reproduction, Life Stage, Extra Info, Associated Taxa, and Associated Specimens. The 'Taxonomy' section shows the classification: Phylum: Arthropoda, Class: Malacostraca, Order: Amphipoda, Family: Microprotopidae, Subfamily: Microprotopinae, Genus: Microprotopus, Species: Microprotopus maculatus. The 'Barcode Index Numbers' section shows the BOLD ID: ABW2067, Type: Member, Max Divergence in BIN: 1.87% (p-dist), Distance to NIN: 20.71% (p-dist), and the Phylum, Class, Order, Family, Subfamily, Genus, and Species for the BIN.

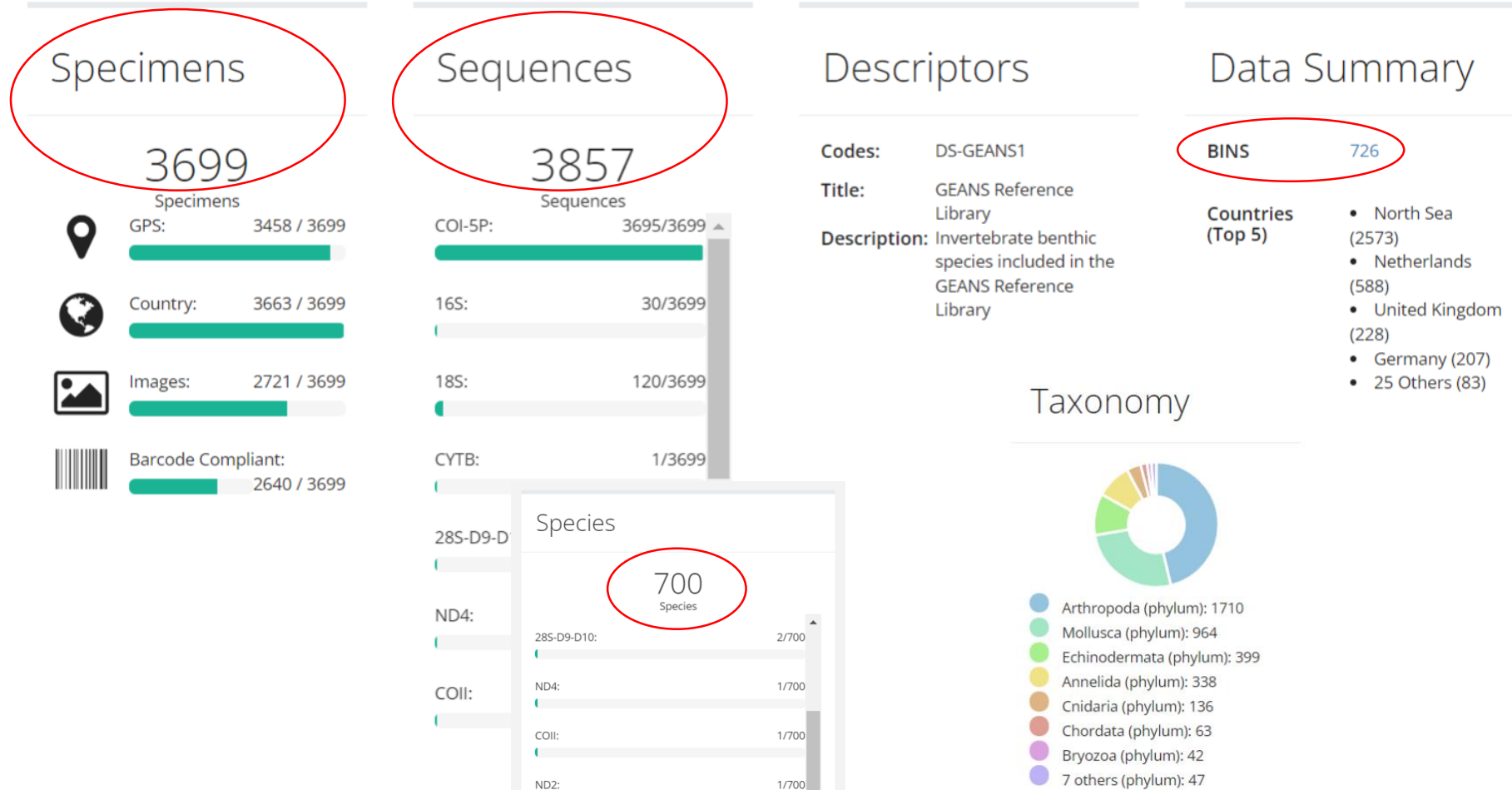
A screenshot of the GEANS00142 collection data page. The page shows a map of the North Sea region with a location pin. The 'Collection Data' section includes fields for Country, Province/State, Region/Country, Sector, Exact Site, Loc/Loc, Elevation, Elevation Accuracy, Depth Accuracy, Collection Event ID, Collection Notes, Collector, Date Collected, Date Accuracy, Time Collected, Site Code, Habitat, Sampling Protocol, Coord. Source, and Coord. Accuracy.

A screenshot of the GEANS00142 map page. The page shows a map of the North Sea region with a location pin. The 'Map' section includes a zoom in/out button and a map of the North Sea region with a location pin.

A screenshot of the GEANS00142 nucleotide sequence page. The page shows a 'Nucleotide Sequence' section with a 'Sequence Metadata' table. The 'Sequence Metadata' table includes fields for Sequence Accession, Translation Matrix, Last Updated, and Sequence Run(s). The 'Modify Sequence' section includes buttons for 'Clear Sequence', 'Edit Sequence', 'Identify Sequence', 'Full DB', 'Species DB', 'Published DB', and 'Full Length DB'.

# WP3 Reference library

Dataset - DS-GEANS1 GEANS Reference Library





# WP4 – Protocols and tools

Review of existing methods and potential biases

further testing and finetuning in our different pilots



Molecular Standard Operating Procedure (MSOP)  
for  
Marine Biodiversity Observation network for genetic  
monitoring of hard-bottom communities  
(ARMS-MBON)



Received: 21 March 2020 | Accepted: 28 July 2020  
DOI: 10.1111/mec.15592

SPECIAL ISSUE

MOLECULAR ECOLOGY WILEY

**Biases in bulk: DNA metabarcoding of marine communities and the methodology involved**

Luna M. van der Loos | Reindert Nijland

Research Article Metabarcoding and Metagenomics 5: e71107  
<https://doi.org/10.3897/mbmg.5.71107> (29 Dec 2021)

**Towards harmonization of DNA metabarcoding for monitoring marine macrobenthos: the effect of technical replicates and pooled DNA extractions on species detection**

\* Laure Van den Bulcke, Annelies De Backer, Bart Ampe, Sara Maes, Jan Wittoeck, Willem Waegeman, Kris Hostens, Sofie Derycke

frontiers  
in Marine Science

ORIGINAL RESEARCH  
published: 10 June 2021  
doi: 10.3389/fmars.2021.637959

**Detection of Macrobenthos Species With Metabarcoding Is Consistent in Bulk DNA but Dependent on Body Size and Sclerotization in eDNA From the Ethanol Preservative**

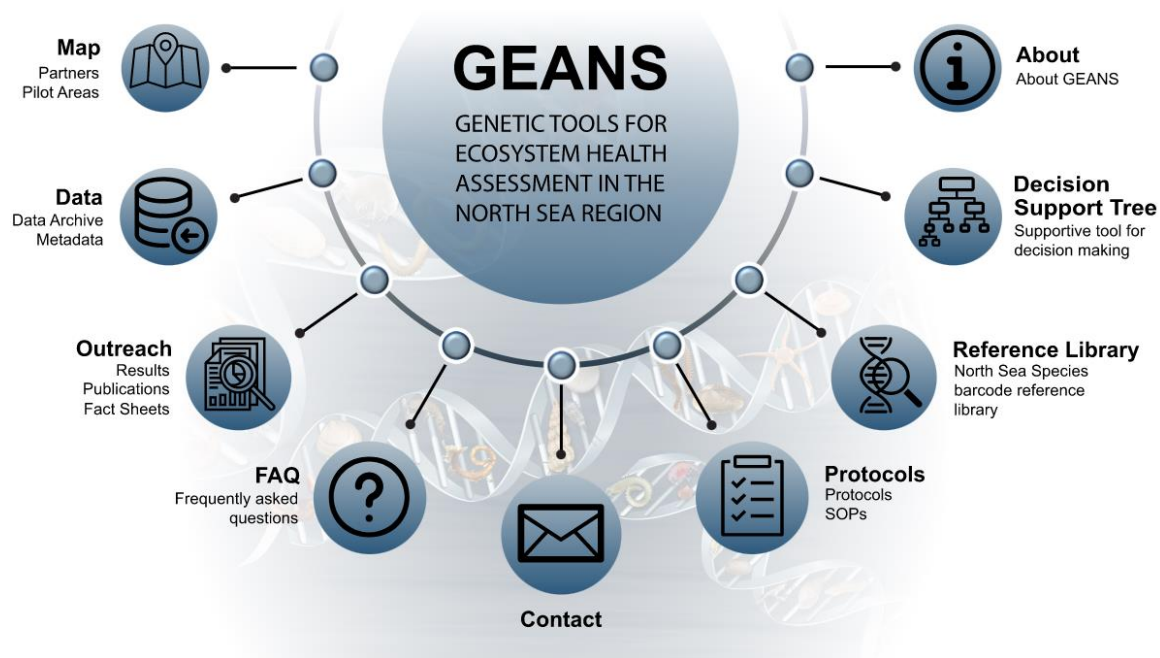
Sofie Derycke<sup>1,2\*</sup>, Sara Maes<sup>1</sup>, Laure Van den Bulcke<sup>1</sup>, Joran Vanhollenbeke<sup>1</sup>, Jan Wittoeck<sup>1</sup>, Hans Hillewaert<sup>1</sup>, Bart Ampe<sup>3</sup>, Annelies Haegeman<sup>4</sup>, Kris Hostens<sup>1</sup> and Annelies De Backer<sup>1</sup>

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

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

# WP6 – Compilation and integration of info and results

## Webpage



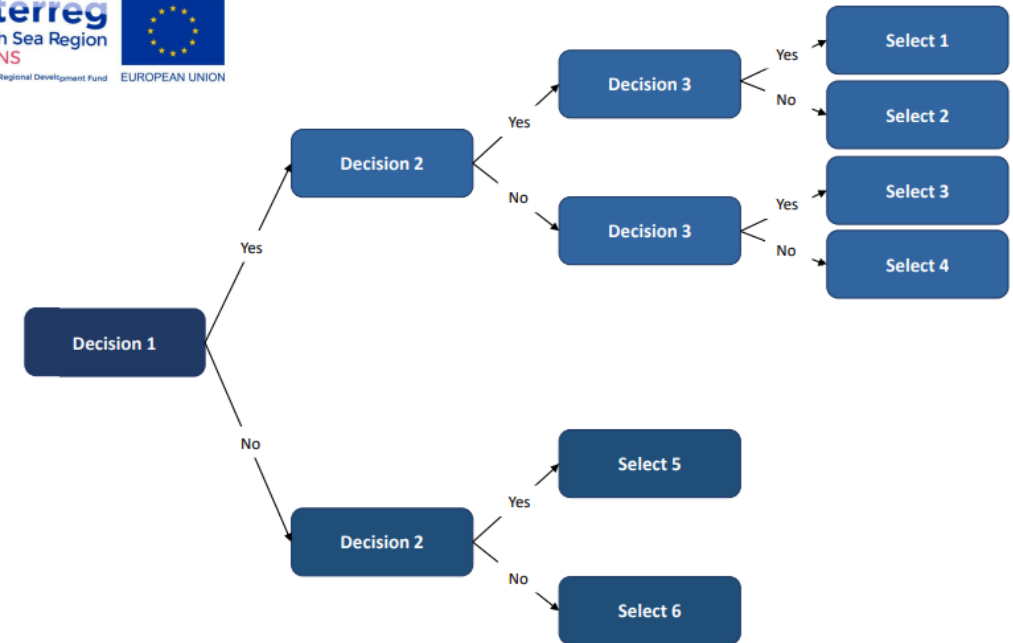
<https://www.geans.eu/>

## Fact sheets and stories



# WP6 – Decision support tree

- Integration of knowledge gained from other WPs
- Help on choosing best workflow for monitoring/management question
- Work in progress
  - If you have ideas/specific needs, let us know and we will try to include them



THANK YOU!  
QUESTIONS?  
REMARKS? SUGGESTIONS?

CONTACT US

[annelies.debacker@ilvo.vlaanderen.be](mailto:annelies.debacker@ilvo.vlaanderen.be)

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

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# WP4 – Quality assurance of soft sediment protocol

- Same 4 samples processed @different labs using the exact same protocol to test reproducibility
- Patterns are highly similar! => protocol = reliable!

