

# MARCO-BOLO WP2

## Validating the use of eDNA

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Station Biologique  
de Roscoff



**Objective:** To enable eDNA-based approaches for biodiversity monitoring across trophic and functional groups (i.e. from microbes to vertebrates) in marine, terrestrial and freshwater systems.



### Specific objectives:

- Validate the performance of eDNA-based approaches through meta-analysis of already existing studies and by comparing eDNA-based with traditional observations using a large collection of data.
- Tuning and integration of available resources necessary for eDNA-based biomonitoring.
- Derive eDNA-based measures/variables in line with the EBV, MSFD and WFD frameworks.
- Develop standard operating procedures for eDNA across ecosystems and ecological/taxonomic groups in line with the requirements of biodiversity observation networks.





35.5 Person-months  
Lead T2.2  
Contact: Kim Præbel



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13 Person-months  
Lead T2.5  
Contact: Fabrice Not



28 Person-months  
Lead T2.3  
Contact: Lucie Zinger



11 Person-months  
involved in: T2.2, T2.3, T2.4  
Contact: Ward Appeltans



26 Person-months  
Lead T2.4  
Contact: Mike Cunliffe



8 Person-months  
involved in:  
T2.2, T2.3, T2.4, T2.5  
Contact: Daniele Iudicone



20 Person-months  
Lead T2.1  
Contact: Iveta Matejusova



6 Person-months  
involved in: T2.3, T2.4  
Contact: Klaas Deneudt



## Five tasks:

**T2.1: Meta-analysis of technical and practical aspects of current eDNA approaches (lead: MS)**

**T2.2: Tuning and integration of current resources and technologies for metabarcoding-based monitoring (lead: UiT)**

**T2.3: Comparison of spatial and temporal eDNA-based vs traditional observations (lead: MBA)**

**T2.4: Defining eDNA-based variables for the EV, MSFD and WFD frameworks (lead: CNRS)**

**T2.5: Developing a framework of guidelines/protocols for eDNA-based biodiversity observations (lead: SU-Roscoff)**

## Five deliverables:

**D2.1 Report on meta-analysis of the performance of eDNA-based approaches and associated optimal diversity indices for biodiversity observations. (Month 15) Lead: Iveta Matejusova, MS**

**D2.2 Set of databases and software/pipelines facilitating the implementation of eDNA-based monitoring in terms of study design, data analysis and sharing. (Mo. 36) Lead: Kim Præbel, UiT**

**D2.3 Report on the congruence between traditional and eDNA-based biodiversity observations, and their robustness across bioinformatics issues and diversity metrics. (Mo. 36) Lead: Mike Cunliffe, MBA**

**D2.4 Report on the definition of eDNA-based EBVs with associated eDNA-based EBVs datasets and efficiency of eDNA for detecting/quantifying taxa/species of interest. (Mo. 36) Lead: Lucie Zinger?, CNRS/Naturalis/Brazil?**

**D2.5 Report on a framework of guidelines and protocols for eDNA-based biodiversity observations (Mo. 48) Lead: Fabrice Not, SU/Roscoff**

## **Task 2.1: Meta-analysis of technical and practical aspects of current eDNA approaches**

**Lead:** MS, **Contributors:** CNRS, UiT, MBA

- Evaluate the performance of eDNA approaches for (i) detecting species presence, (ii) quantifying species abundances, and (iii) estimating taxonomic diversity
- Across taxa (from microbes to vertebrates), environments (marine, freshwater, terrestrial), and molecular protocols (qPCR, metabarcoding, metagenomics...)
- Review current diversity metrics and statistical tools to identify those that best complies with eDNA data characteristics

**D2.1 Report on meta-analysis of the performance of eDNA-based approaches and associated optimal diversity indices for biodiversity observations. (Month 15) Lead: Iveta Matejusova, MS**

## **Task 2.2: Tuning and integration of current resources and technologies for metabarcoding-based monitoring**

**Lead: UiT, Contributors: CNRS, MBA, SU, MS, SZN, UNESCO**

- (1) Assess the robustness of current databases of DNA sequences, eDNA-based occurrences, and ecological/functional information, as well as of available resources such as of currently available metabarcoding primer sets
- (2) Tune, define and intercalibrate bioinformatics pipelines according to different molecular protocols
- (3) Test recently proposed standards for eDNA occurrence data integration in biodiversity databases
- (4) Integrate all these into existing bioinformatic workflows to facilitate MBO downstream analyses and increase scientific community and professionals' access to eDNA data

**D2.2 Set of databases and software/pipelines facilitating the implementation of eDNA-based monitoring in terms of study design, data analysis and sharing. (Mo. 36)**

**Lead: Kim Præbel, UiT – Assistance: Owen Wangenstein (U-BCN)**

## **Task 2.3: Comparison of spatial and temporal eDNA-based vs traditional observations**

**Lead:** MBA, **Contributors:** CNRS, UiT, VLIZ, SU, MS, SZN, UNESCO

- Compare different datasets of eDNA-based observations vs. traditional counts data
- Comparing the ability of both kinds of data to retrieve different biodiversity facets (e.g. communities taxonomic/functional diversity, taxa abundances, etc.)
- In space or time, across taxa and ecosystems.
- Using already existing data, that will be completed in this task with some new eDNA data (e.g. for fish and invertebrates)

**D2.3 Report on the congruence between traditional and eDNA-based biodiversity observations, and their robustness across bioinformatics issues and diversity metrics. (Mo. 36) Lead: Mike Cunliffe, MBA**



## **Task 2.4: Defining eDNA-based variables for the EV, MSFD and WFD frameworks**

**Lead: CNRS, Contributors: UiT, MBA, VLIZ, SU, MS, SZN, UNESCO**

- Standardise eDNA data and evaluate their robustness to retrieve higher taxa and/or species groups prioritised by the MSFD, WFD, Habitats Directive, IUCN Red List, etc.
- Define and produce new EBVs, either species-centred (i.e. related to the EBV class Species Population) or ecosystem-centred (i.e. EBV classes Taxonomic Composition and Ecosystem Functions)

**D2.4 Report on the definition of eDNA-based EBVs with associated eDNA-based EBVs datasets and efficiency of eDNA for detecting/quantifying taxa/species of interest. (Mo. 36) Lead: Lucie Zinger?, CNRS/Naturalis/Brazil?**

## **Task 2.5: Developing a framework of guidelines/protocols for eDNA-based biodiversity observations**

**Lead:** SU-Roscoff, **Contributors:** CNRS, UiT, MBA, MS, SZN

- Develop a modular framework of optimised protocols and guidelines for all steps of the eDNA data production process, from sampling to data sharing.
- This framework will encompass all current eDNA-based applications, focus taxa, ecological groups, or ecosystems
- Flexible enough to allow integration of short/long-term evolutions of the eDNA field (e.g. metagenomics, long-reads sequencing, eDNA-based population genetics...
- It will be an important contribution to the Ultimate Handbook of Observation (D7.1)

**D2.5 Report on a framework of guidelines and protocols for eDNA-based biodiversity observations (Mo. 48) Lead: Fabrice Not, SU/Roscoff**

*“I did not write half of what I saw,  
for I knew I would not be believed”*

Marco Polo, on his deathbed

**THANK YOU!**