



biodiversa+

European Biodiversity Partnership

Towards a roadmap for implementation of novel biodiversity monitoring methods

Biodiversa+ expert workshop

REC

The recording of the plenary sessions of this workshop are recorded and will be shared on the Biodiversa+ website and Youtube channel

2nd of February – 9am to 12.30pm CET



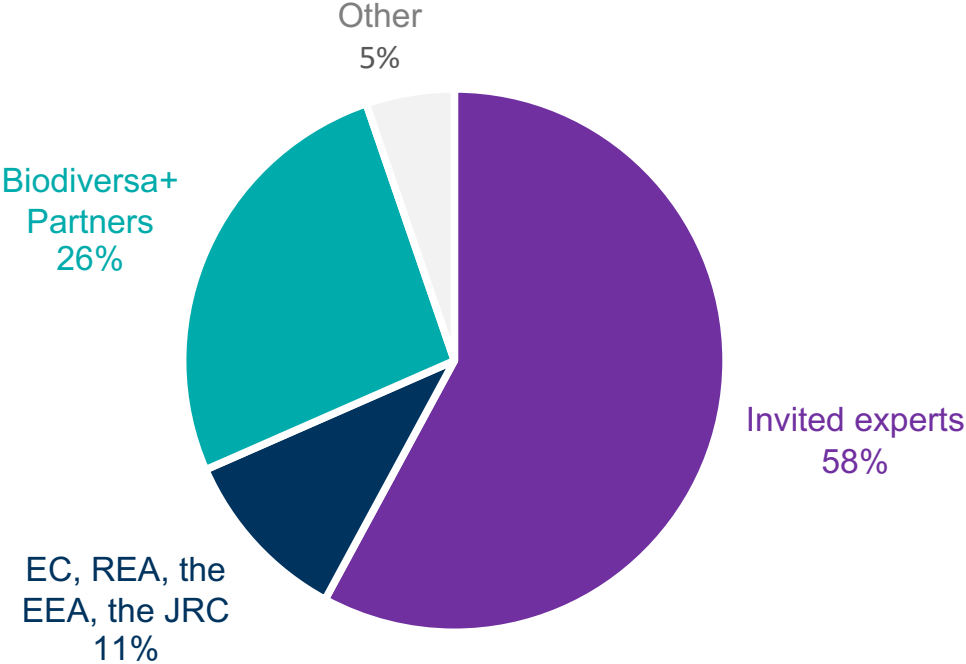
Welcome words

By Lars Dinesen, IFD

Registered participants



Workshop participants



Agenda of the workshop

9.00 – 9.15: Welcome words and aims of the workshop, Lars Dinesen & Hilde Eggermont

9.15 – 10.30: Key presentations of 10 minutes each followed by 5 minutes of Q&A

Break

10.45 – 12.10: Breakout in four thematic groups

Back to plenary

12.10 – 12.20: Plenary and wrap-up

12.20 - 12.30: Next steps and conclusion of the workshop

Aims of the workshop

- Provide input to a roadmap for *implementation* of novel biodiversity monitoring methods
- This roadmap will guide future Biodiversa+ work
- It will promote operationalisation novel monitoring and identify research gaps
- Will build on work undertaken by EuropaBON
- Look into the need and opportunities for standardization
- The work will feed into future activities in the partnership

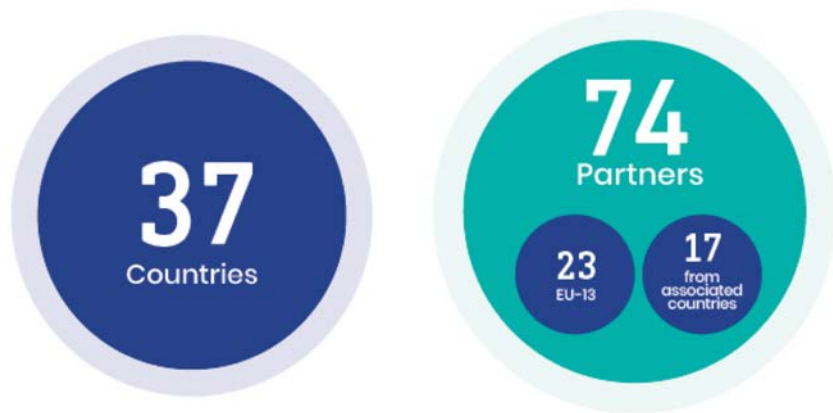
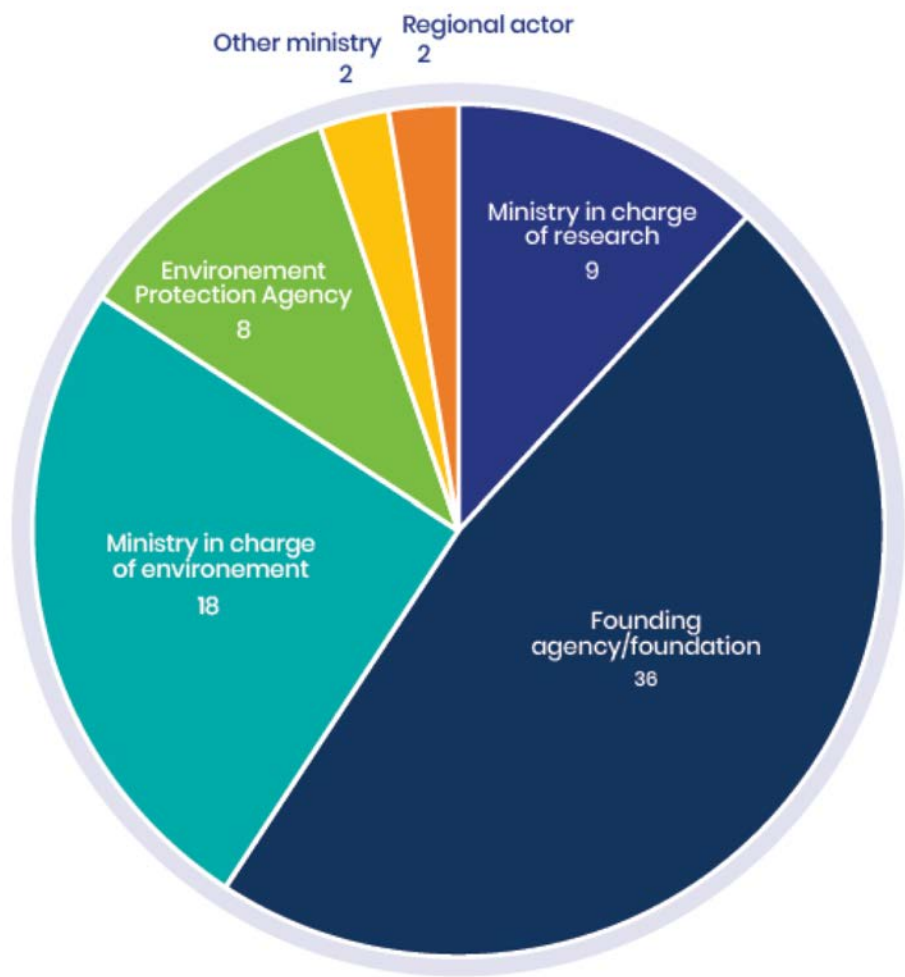
Follow-up of the workshop

- Development of a roadmap guiding the Biodiversa+ activities (by Biodiversa+)
- The experts attending the workshop will have an opportunity to provide feedback

Biodiversa+ introduction

By Hilde Eggermont, BelSPO, Biodiversa+ Chair & Coordinator

Biodiversa+ membership



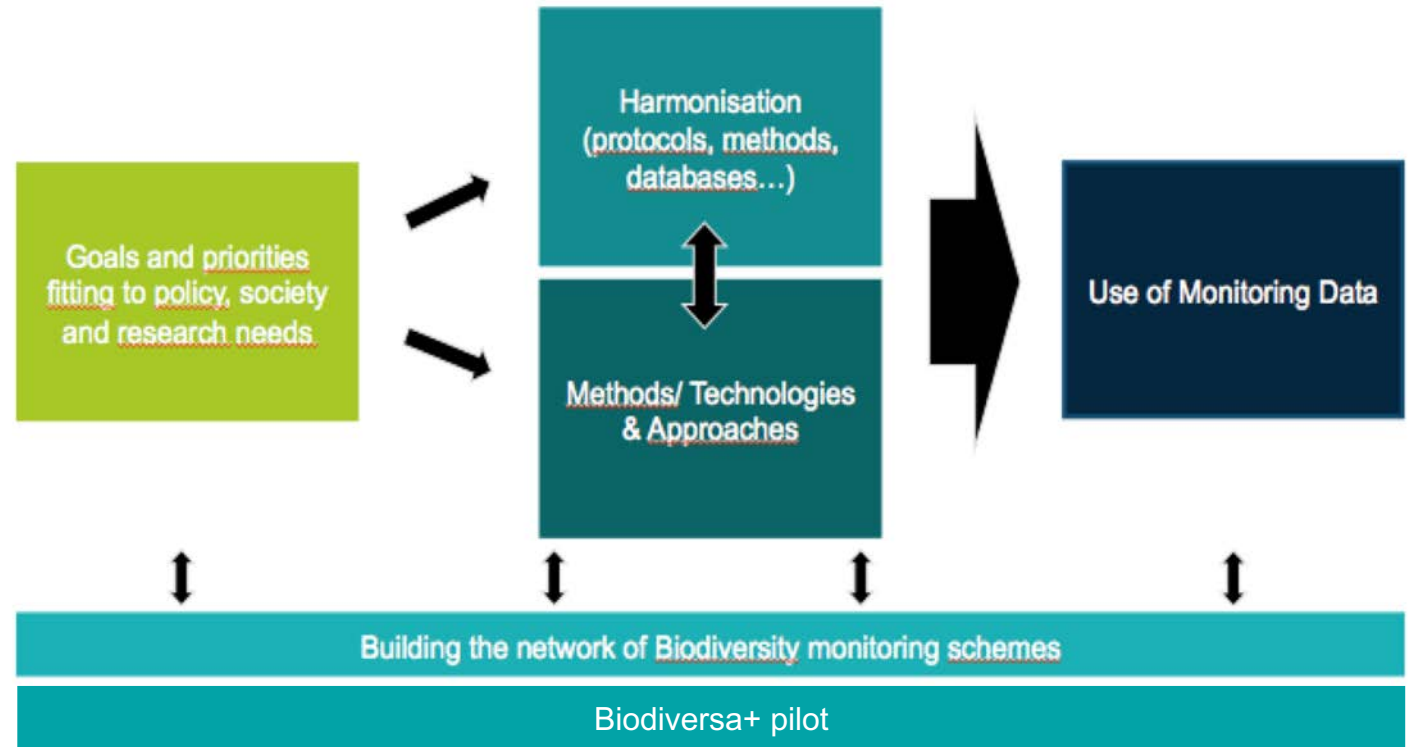
Aligned with the policy context

EU Biodiversity Strategy 2030:

“... making the bridge between science, policy & practice...”



Biodiversity monitoring activities



Setting the scene

Facilitation by Lars Dinesen and Toke Thomas Høye, IFD

Upcoming key presentations

9.15 - 9.30 Cher Chow, EuropaBON – lead author of report on novel technology for biodiversity monitoring

9.30 - 9.45 Elaine van Ommen Kloeke – showcasing ARISE as a large national biodiversity technology infrastructure

9.45 – 10.00 Florian Leese, University of Duisburg-Essen and coordinator of DNAquaNET - developing standards for molecular biodiversity assessments in freshwater ecosystems

10.00 - 10.15 Adrià López-Baucells and Charlotte Roemer - Acoustic monitoring of bats – a showcase of implementation

10.15 - 10.30 Markus Erhard - European Environmental Agency – How to ensure FAIR data in the implementation of novel technologies and data streams for biodiversity monitoring?

Main outcomes of the EuropaBON report on novel technology for biodiversity monitoring

By Cher Chow, EuropaBON – lead author



University of
St Andrews | FOUNDED
1413 |



EUROPABON 

WP 4.2

Novel biodiversity monitoring technologies and methods

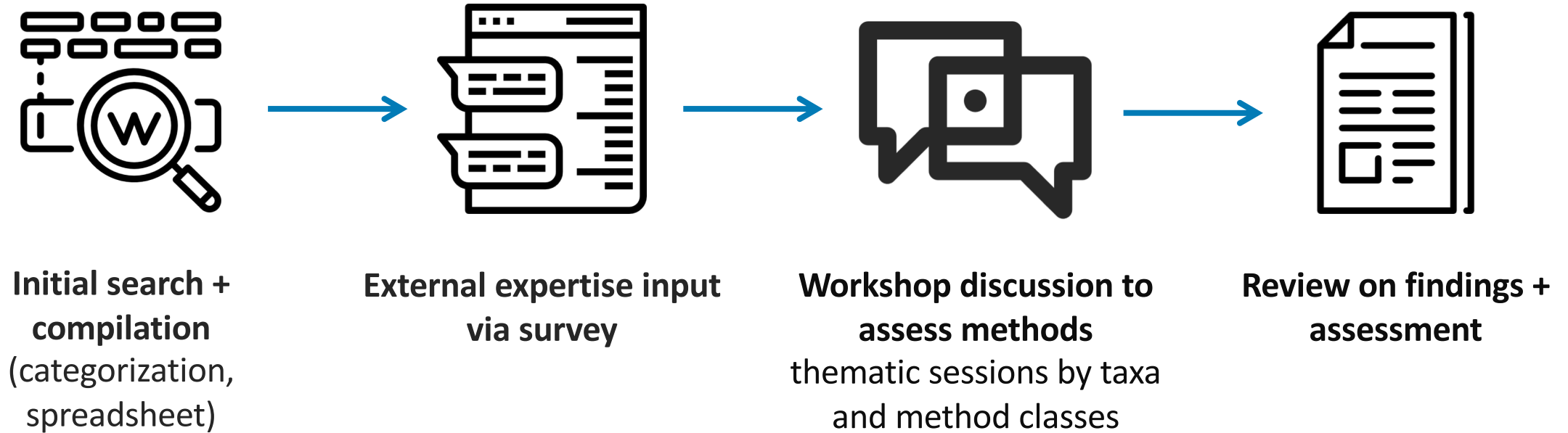
Cher Chow, Rob Patchett & Maria Dornelas

CENTRE FOR BIOLOGICAL DIVERSITY, UNIVERSITY OF ST ANDREWS

Task aims

1. Identify and systematically characterise emergent/novel methodologies, method components, and/or technologies for monitoring biodiversity according to criteria including but not limited to method readiness/maturity, methodology type, taxonomic applicability, addressed Essential Biodiversity Variables (EBVs), and spatiotemporal coverage
2. Assess whether identified novel methods are suitable and ready to implement in EuropaBON's biodiversity monitoring workflow co-design
3. Identify areas in biodiversity monitoring that are not appropriate for novel methods

Task workflow



Novel methods meta-database

- Bottleneck solved
- Method Category
- DevStage
- Est Cost
- EBV classes
- Input data type
- Output data type
- Target habitat
- Target taxa
- Pitfalls
- Main advantages
- Validation
- Temporal resolution
- Temporal extent
- Spatial resolution
- Spatial extent

Preliminary view from literature

285 methods

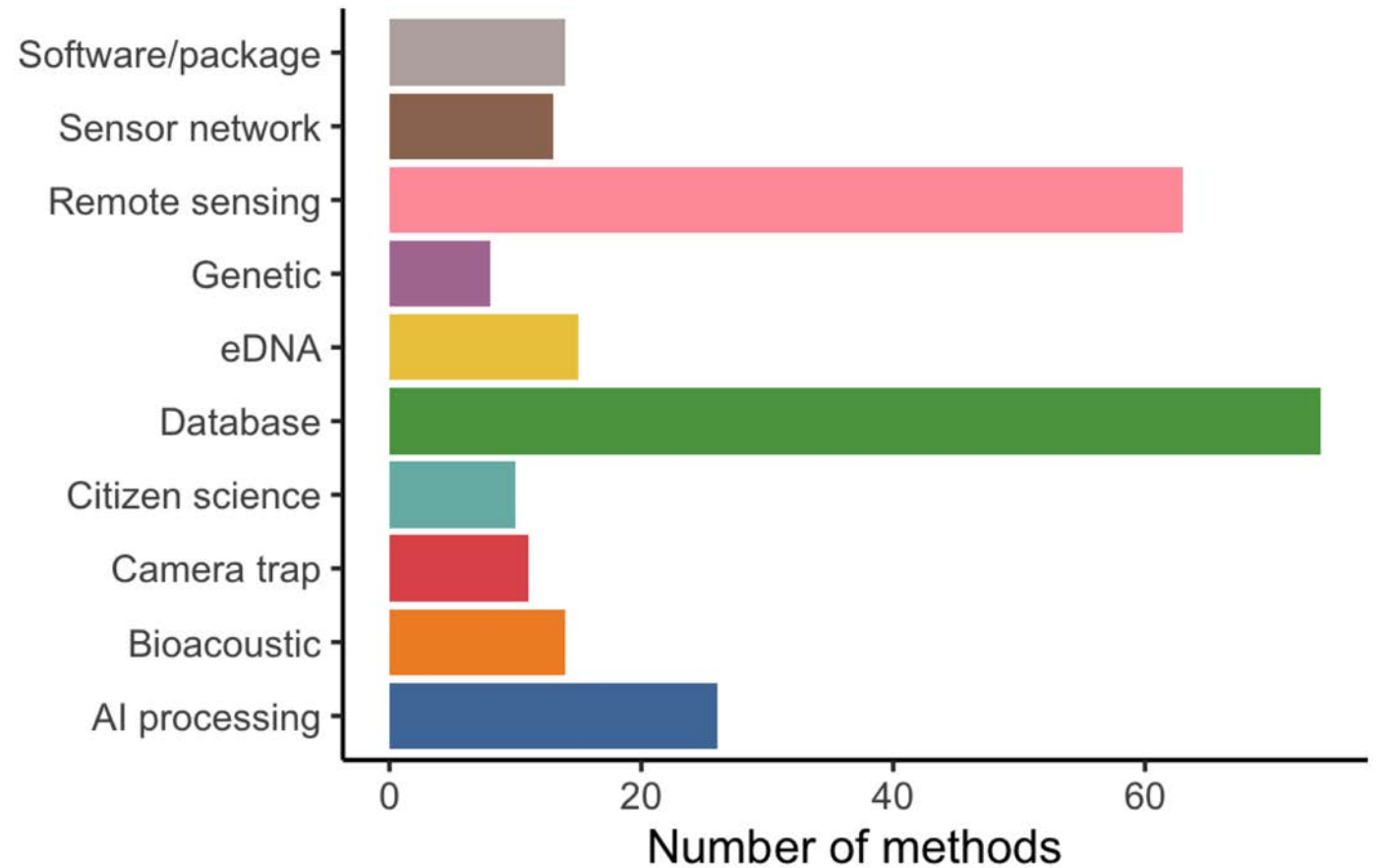
BOTTLENECKS

162 data collection methods

56 analysis methods

60 data integration methods

54 whole pipeline methods





Workshop (May 11-13, 2022)

Discussion focus on critical assessment of implementation

- **Day 1 and 2:** Breakout sessions grouped by taxa expertise and EBV
- **Day 3:** Overarching ideas across all taxa, methodology types, EBVs

Targeted invites to researchers, industry professionals, NGO coordinators, government agencies

207 registrants

111 participants

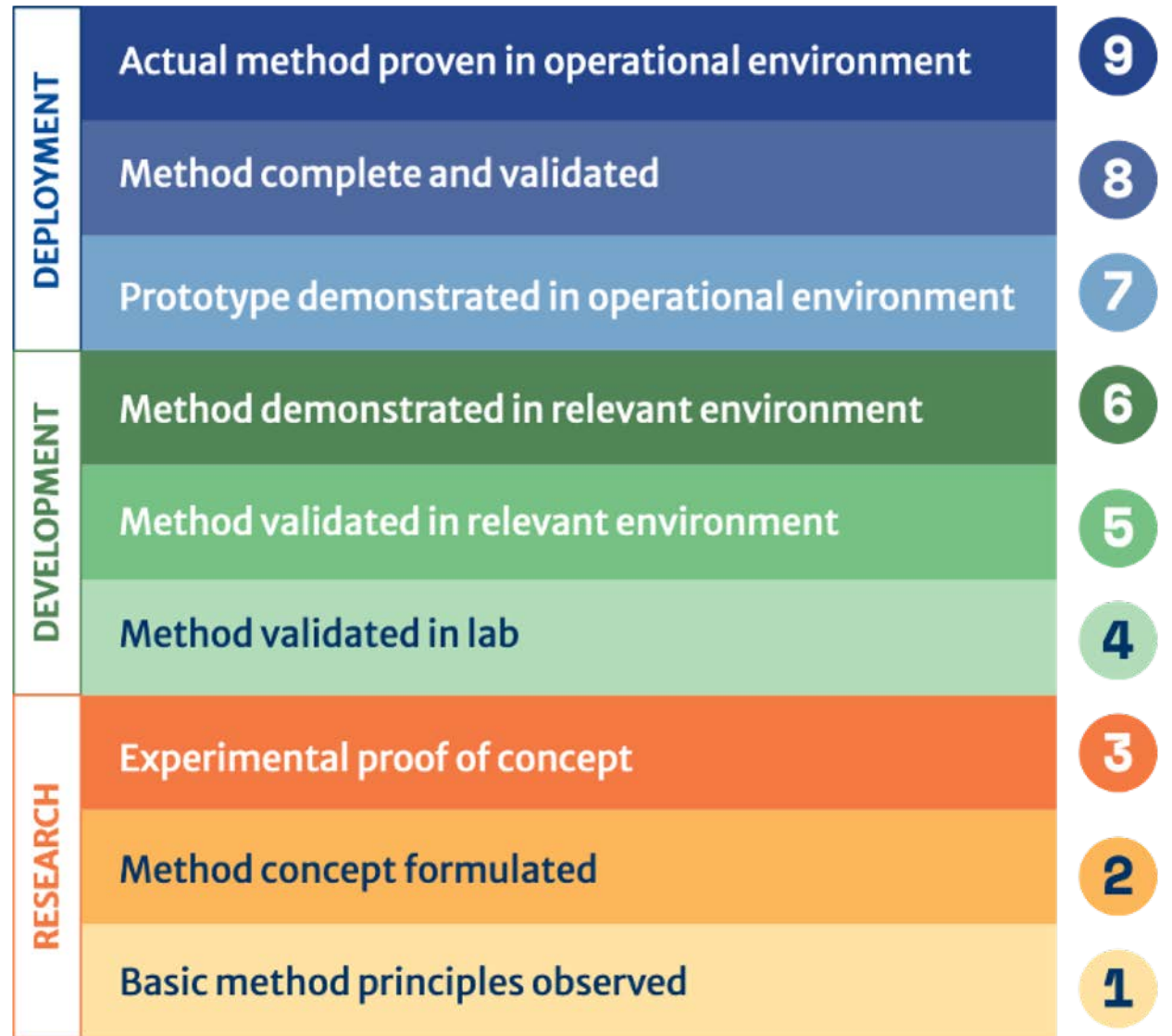
157 potential co-authors

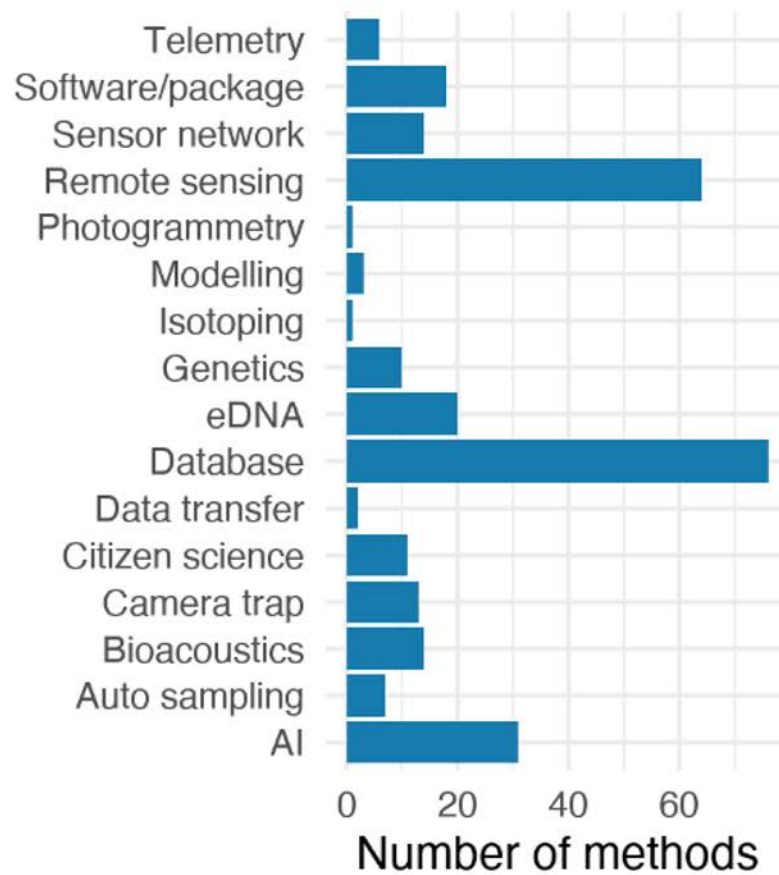
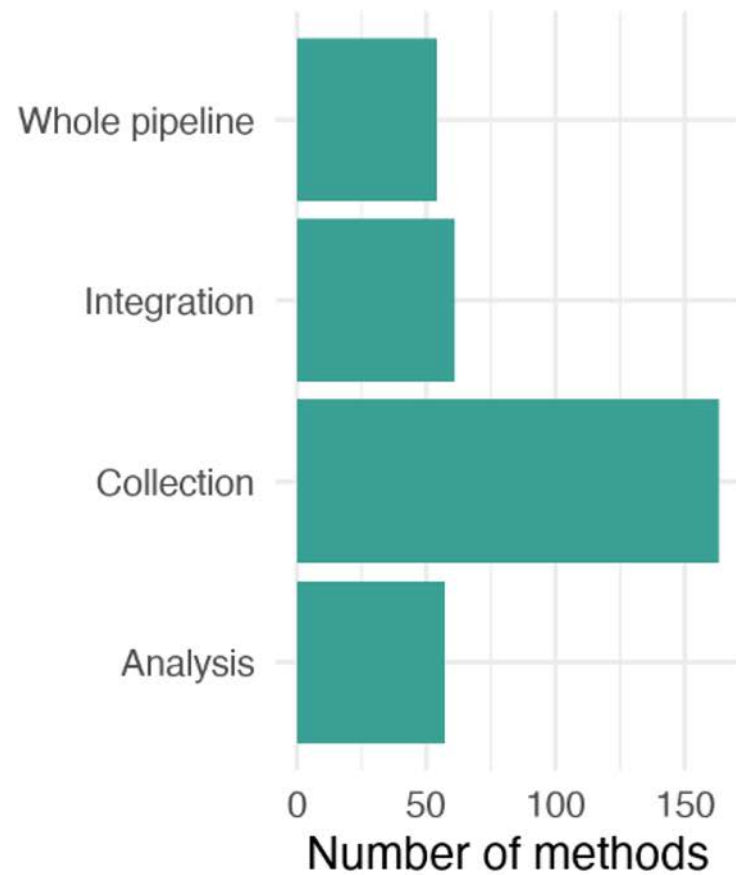
36 countries

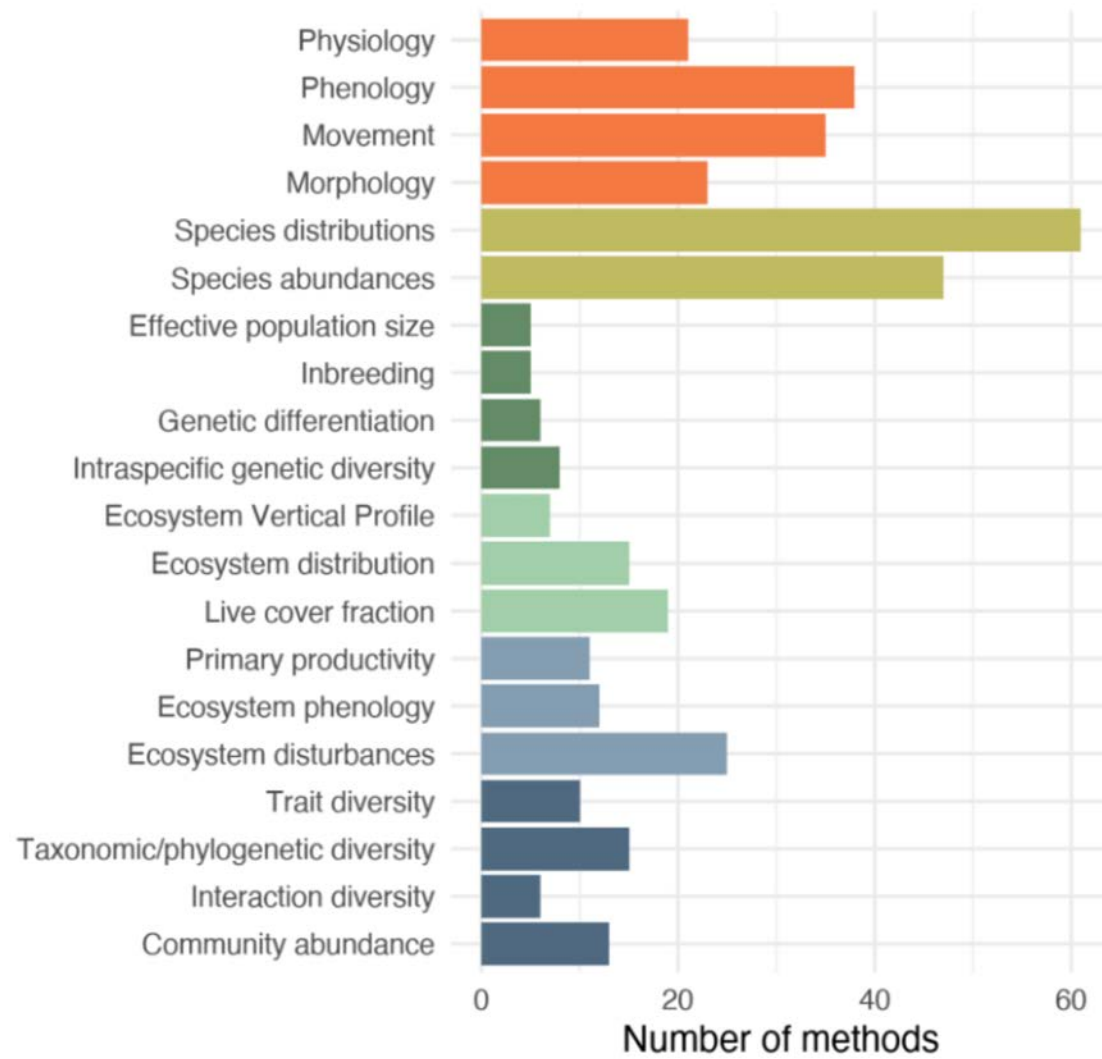
Discussion objectives

- Identify novel methods and technologies (not widely used in monitoring)
- Classify methods by technology readiness (NASA scale)
- Assess main strengths and opportunities in practical implementation
- Understand implementation needs and gaps we cannot yet address
- Scientific and sociological reasons to not change methods

Technology Readiness Scale

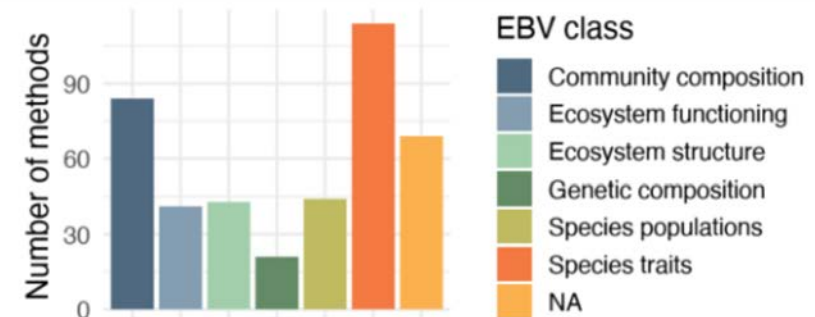






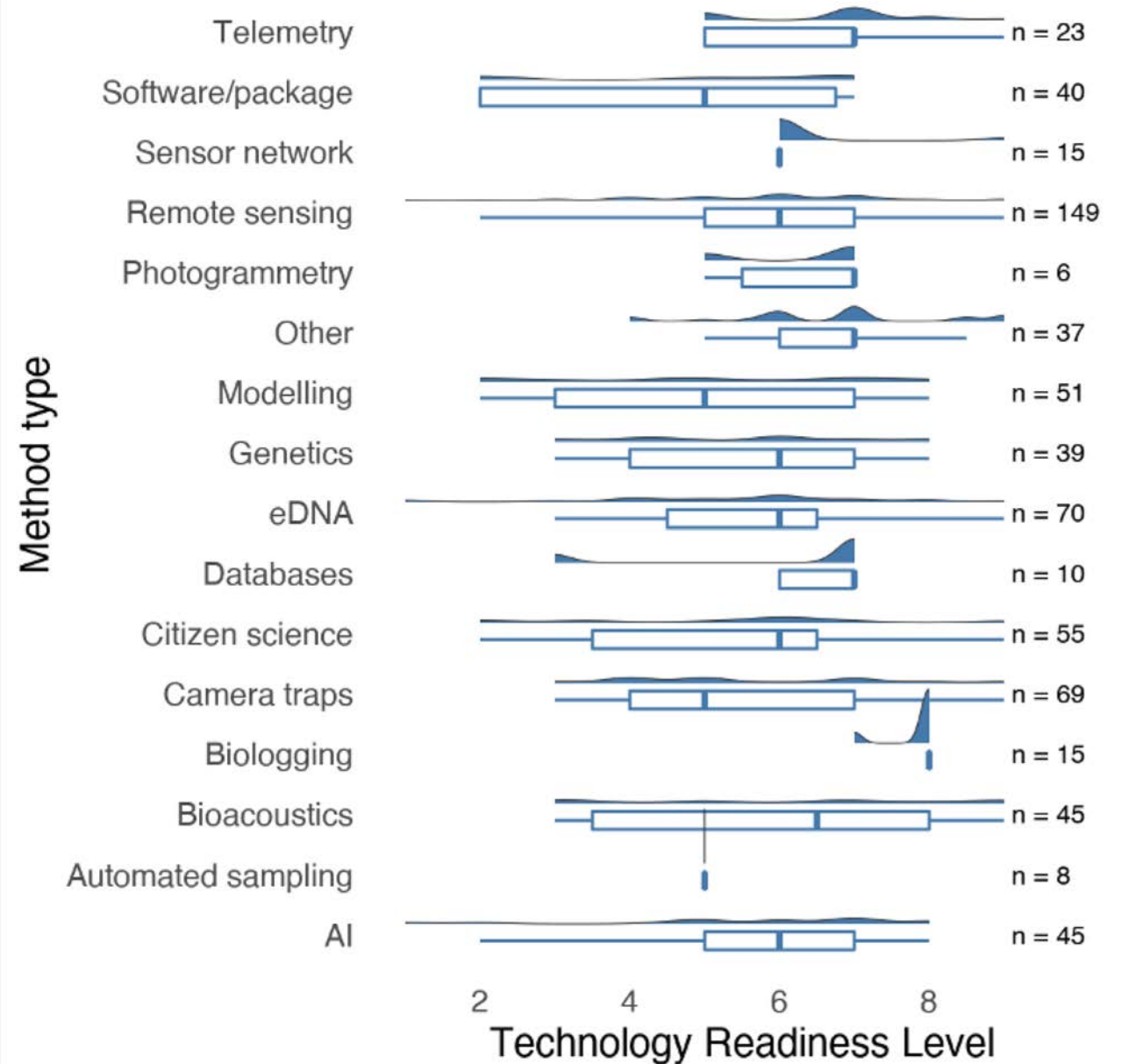
Almost all target monitoring metrics have some novel methods developed

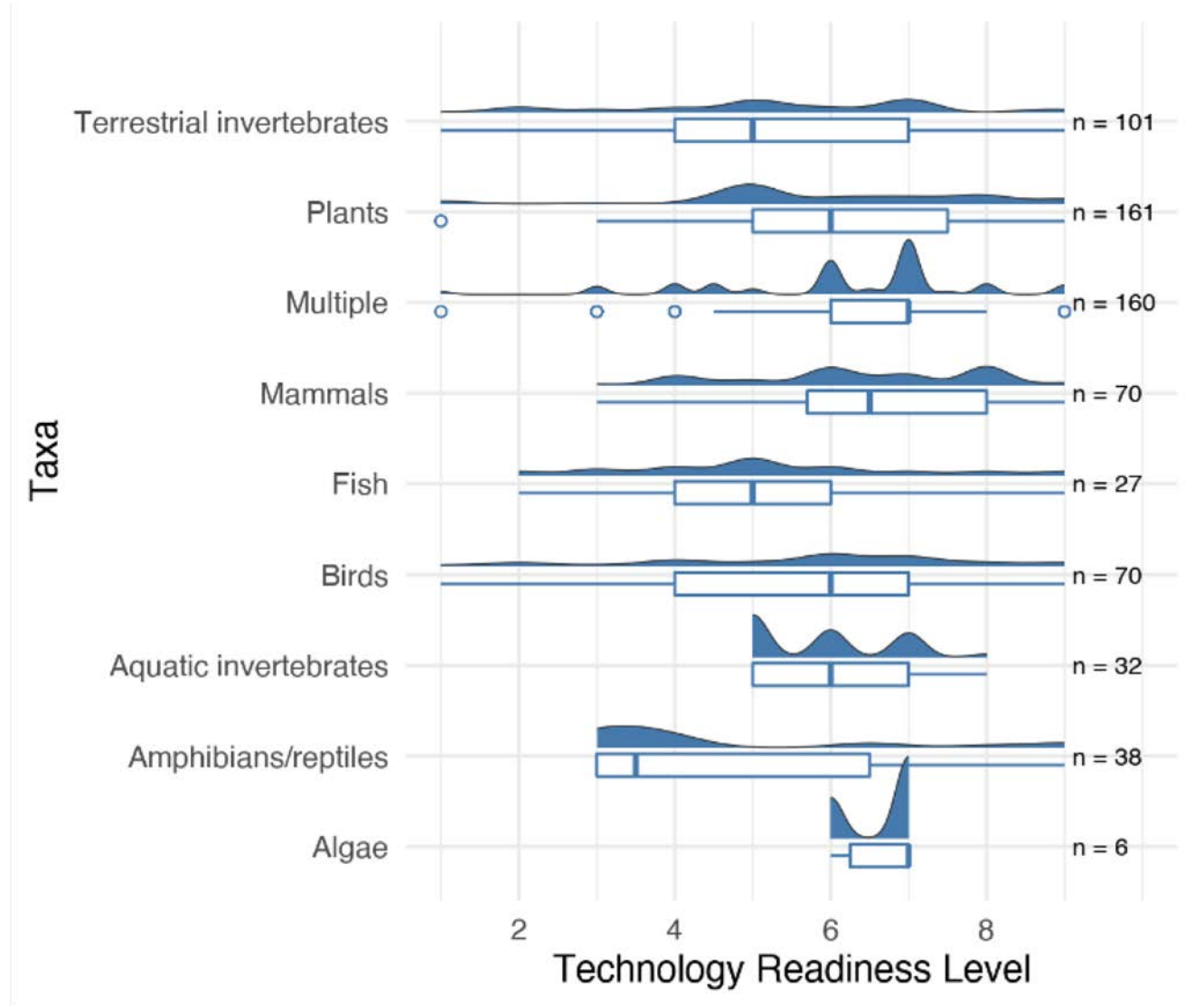
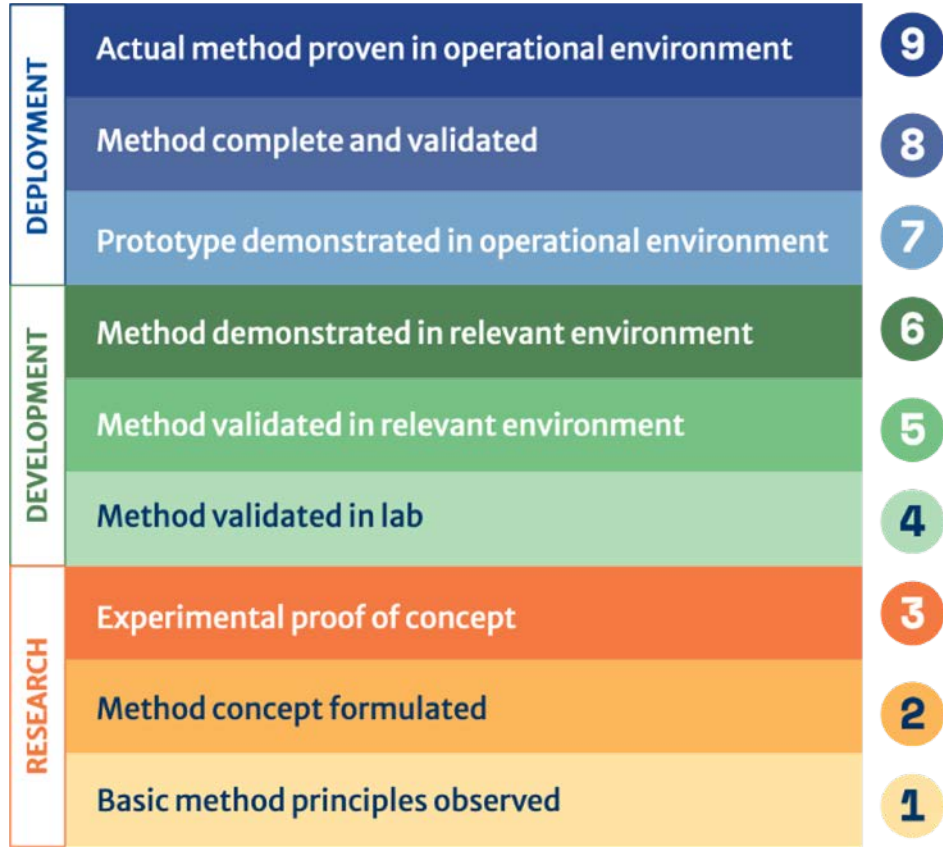
Saturated, well-studied field



Most method classes had some implementations that were definitely ready for more widespread deployments.

Distribution ranges show that readiness is spread widely for most categories with at least 10 methods





Overarching themes

- Need for proper standardisation
 - Interoperable
 - prevents misuse
- Data storage and infrastructure
- Gaps in reference knowledge and databases

Key takeaways

- Validation and testing efforts are largely restricted to a few taxa groups and habitats. Widespread validation is still needed to implement into a Europe-wide workflow
 - Novel tech likely most fit for purpose for specific taxa/EBVs
- The standardisation hurdle: methodology/SOPs, data management and sharing. Common gap
- Longevity as a reason not to change, also initial investments



Next steps

- Synthesising workshop inputs
 - short group session with WP4 members
- Report writing: end of July
- Review manuscript with participants

Showcasing ARISE as a large national biodiversity technology infrastructure

By Elaine van Ommen Kloeke

ARISE

Authoritative and Rapid Identification System for Essential
biodiversity information

Dr. Elaine van Ommen Kloeke
Dr. Chantal Huijbers

Recognize all species on any location
with new technology

National Research Infrastructure

€18 M









Innovate

Cyanistes caeruleus



Pieris rapae

Digital services



Connected

[target list](#)

[about](#)

Welcome to ARISE

We are building a research infrastructure to give you access to advanced identification services for species detection and biodiversity monitoring.

Discover




ARISE tools






Demo Target list

Targetlist

[target list](#)[about](#)



Identify all species

Lorem ipsum dolor sit amet, consectetur adipiscing elit. Integer sit amet faucibus felis. Mauris a vulputate ex, id lobortis eros. Aliquam eleifend cursus. Aenean rutrum, neque eget interdum tristique congue sapient.

Kingdom

Phylum

Class

Order

Family

Genus

family 1

Alcedinidae

genus 2

Alcedoffula

Alcedo

species 2

Alcedoffula alcedinis



[target list](#)

[about](#)

[manage](#)

[Animalia](#) > [Mollusca](#) > [Gastropoda](#) > [Nudibranchia](#) > [Polyceridae](#)

[Clear search](#)

FAMILY
Polyceridae



Netherlands



Global



Total

[Info](#)

[View table](#)



manage

Charts ^

▽

[illegible]



Demo Sampling Tool

Sampling Tool & Admin

samplingtool.nl

Arise Biodiversity Center

Welcome, Hannco!

Add specimen

Add bulk

Overview

Wishlist

Tasks

samplingtool.nl

Add specimen

Step 1 of 4

Registration ID

Scanned code

RMNH.0548621

Species or taxonomic group

☐ I am uncertain the species I picked is correct

Cancel < Prev Next >

Home Overview Wishlist Tasks

samplingtool.nl

Add specimen

Polycera quadrilineata

Step 2 of 4

Location

Date and time

20/07/2022 10:28AM

Location

Zeelandbrug, Zierikzee

51.63189933615488 3.9151651051361123

Biotope

Sandy beach

Cancel < Prev Next >

Home Overview Wishlist Tasks

samplingtool.nl

Overview

Search

All registrations Pending Sent

Amphorina linensis
Status: pending
25/06/2022 10:30AM Oostnol, Burghsluis

Tergipes tergipes
Status: sent to Arise
Sample status: received by Arise and waiting for sequencing
25/06/2022 10:30AM Zeelandbrug, Zierikzee

Myxilla rosacea
Status: pending
25/06/2022 10:30AM Zeelandbrug, Zierikzee

Polycarpa scuba Monniot
Status: pending
25/06/2022 10:30AM Zeelandbrug, Zierikzee

Botrylloides violaceus Oka
Status: sent to Arise
Sample status: sequencing
30/06/2022 11:45AM Vliete polder, Wissenkerke

Home Overview Wishlist Tasks

Home Overview Wishlist Tasks



Demo digital species recognition



ARISE – Digital Species Identification

Dashboard

Sensors

Media Browser

Datasets

Algorithms

Start Analysis

Analysis Jobs

Admin

Algorithm
browser

Logout

Recent Analysis Jobs

Job Name	Status	Action
Diopsis Inference Server-From Last June	Completed	
Diopsis Inference Server-15 Diopsis images.	Completed	

Analysis job details

Job Name
Diopsis Inference Server-From Last June

Job Status
Completed

Created at
Tuesday, 17 January 2023 at 11:03

Dataset Name
From Last June

Algorithm Name
Diopsis Inference Server

Job Run Details
Instance brave_keldysh run on port 6000 with batch size 1

Show Detections

Show Logs

Recent Datasets

Name	Item count	Actions
15 Diopsis images.	15	
From Last June	88	



Demo Sensor dashboard

ARISE MDS Home Viewer Statistics Help

ARISE-MDS Home

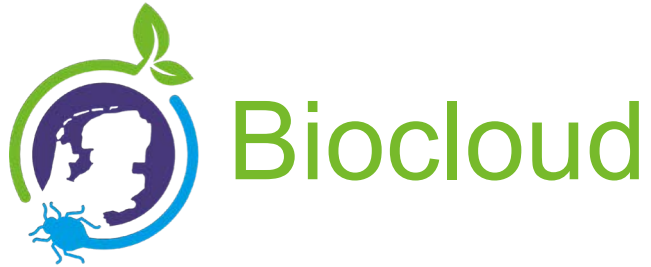


Data viewer
Monitor devices

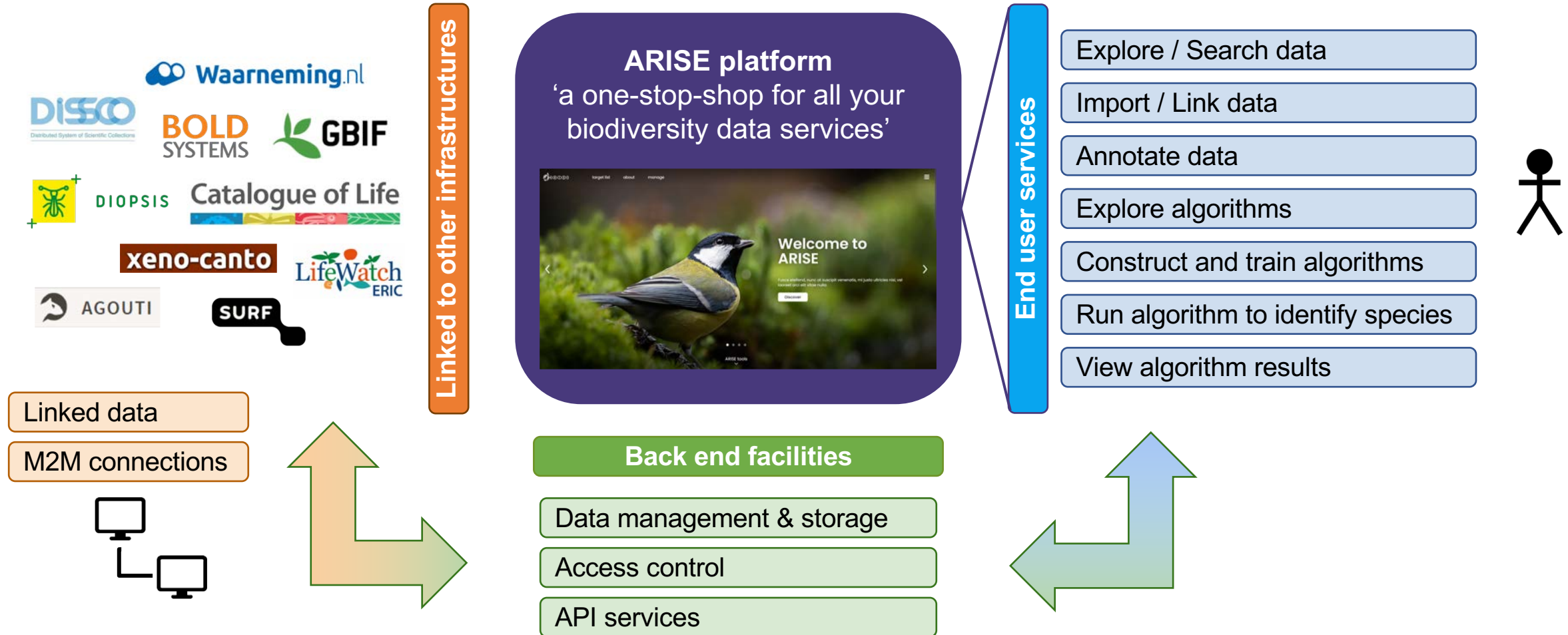


Data importer

arisemdsvm.science.uva.nl/



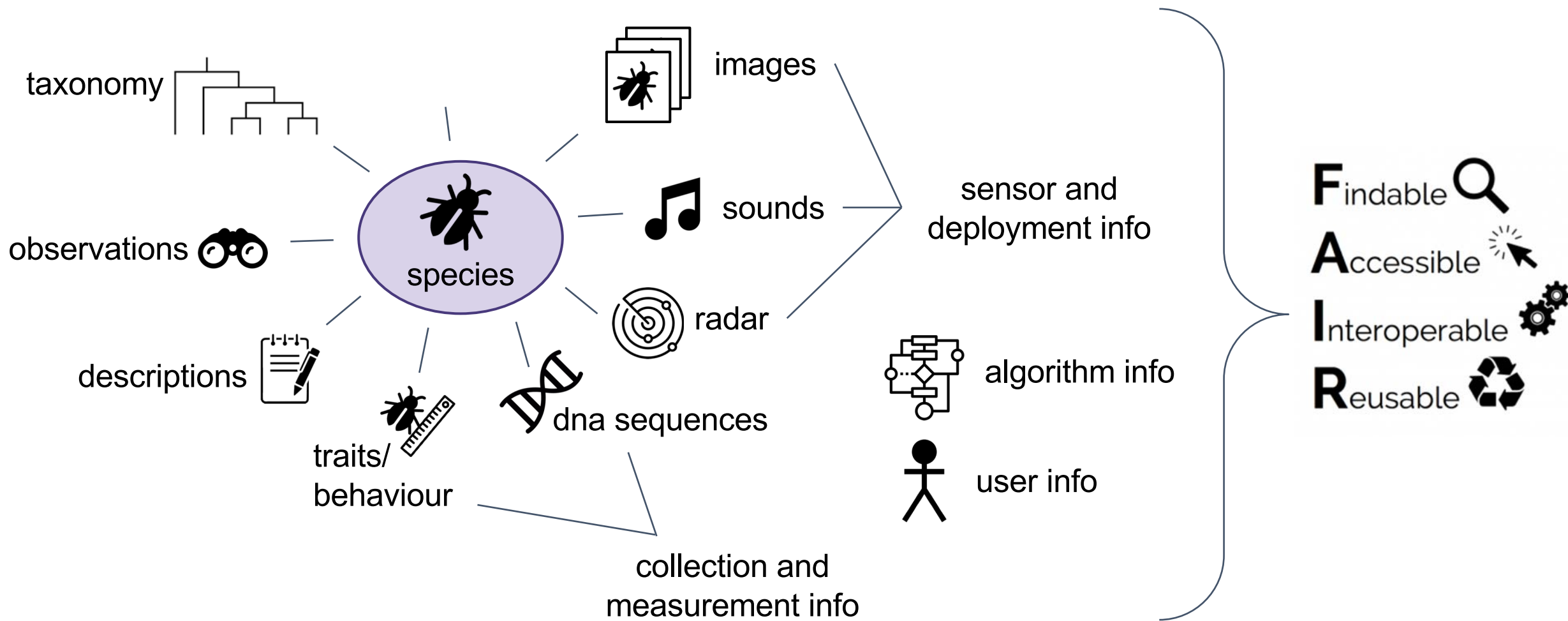
Building the underlying infrastructure of ARISE and an interactive platform for access to data and services

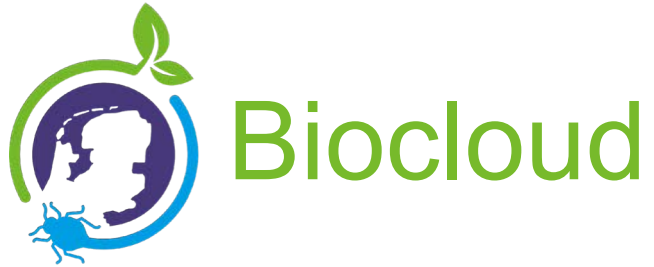




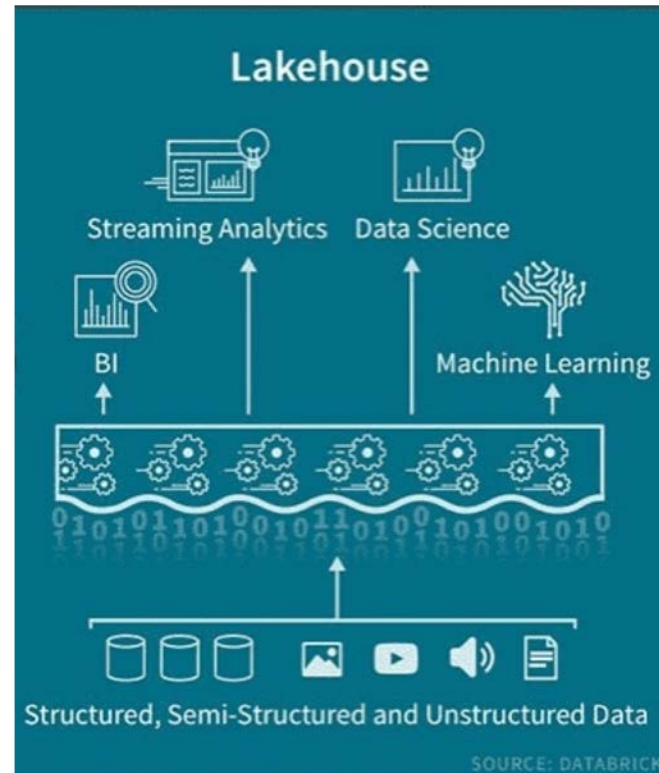
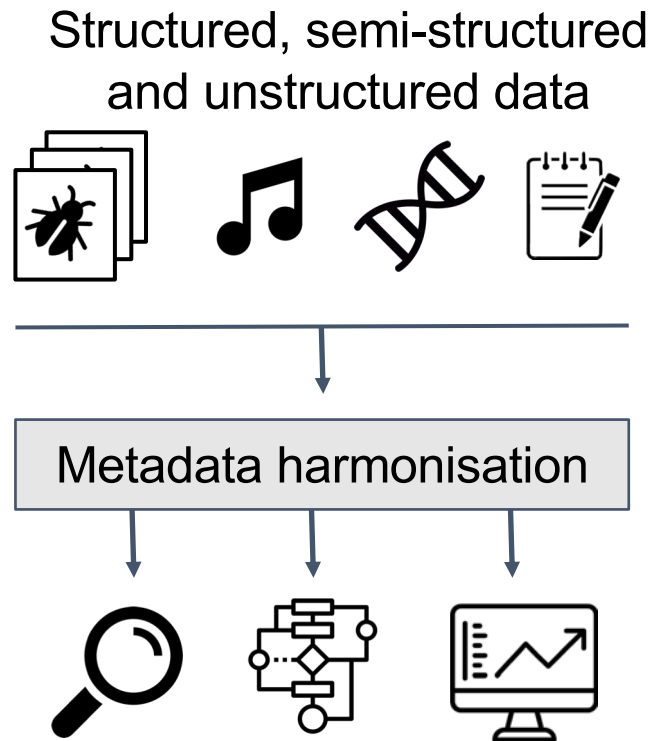
Biocloud

A data management system for petabytes of data
of various kinds with linked metadata





Work in progress:
architectural design and development of data management system



Open-source storage framework that
enables building a Lakehouse architecture

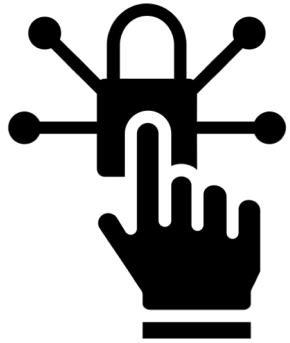
> schema evolution: allows changing data
structures and adding new use cases

> time travel: keep track of changes (e.g.
update of species identification, taxonomic
name change) and keep provenance trail



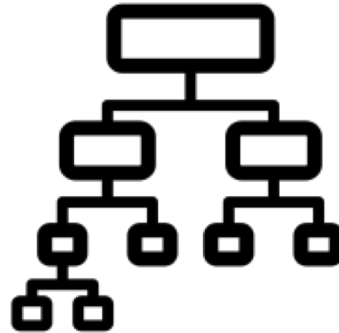
Biocloud

More than 'just' data management



Identity and Access Management

- user roles and permissions
- integration with other systems
- GDPR compliance



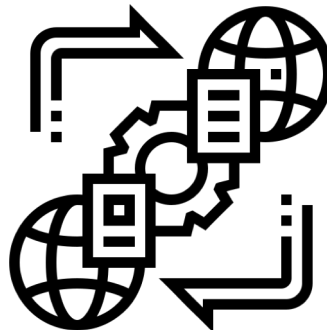
Taxonomic backbone

- all data is linked to a taxon name
- up to date list of taxon names + synonyms needed to link data from different sources



Persistent Identifiers (PID)

- uniquely identifiers for each data object
- identifiers must be persistent



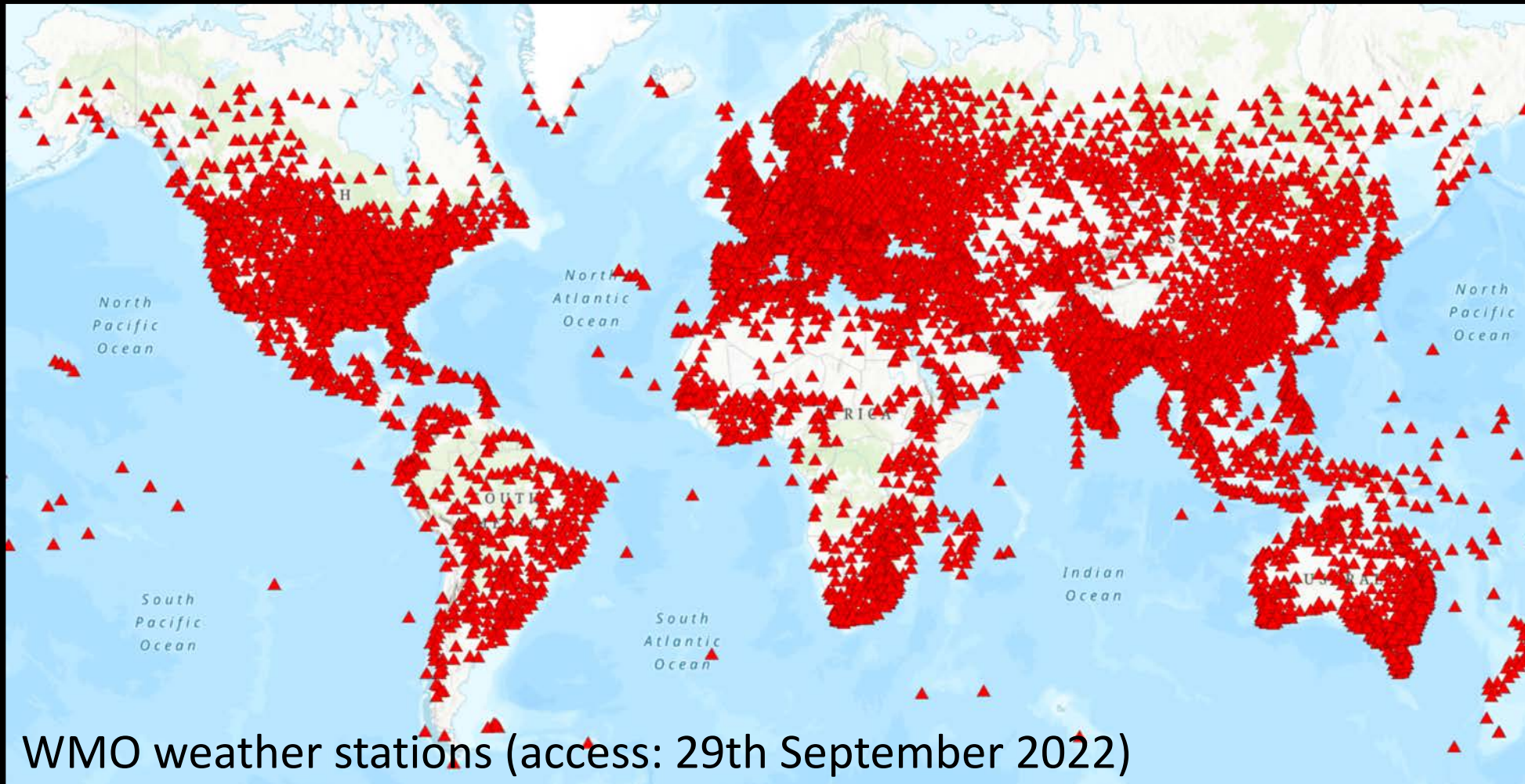
Data strategies

- Data storage: what, where, for how long?
- Data sharing: user agreements
- Data standards: enable interoperability with other infrastructures

Developing standards for molecular biodiversity assessments in [freshwater] ecosystems

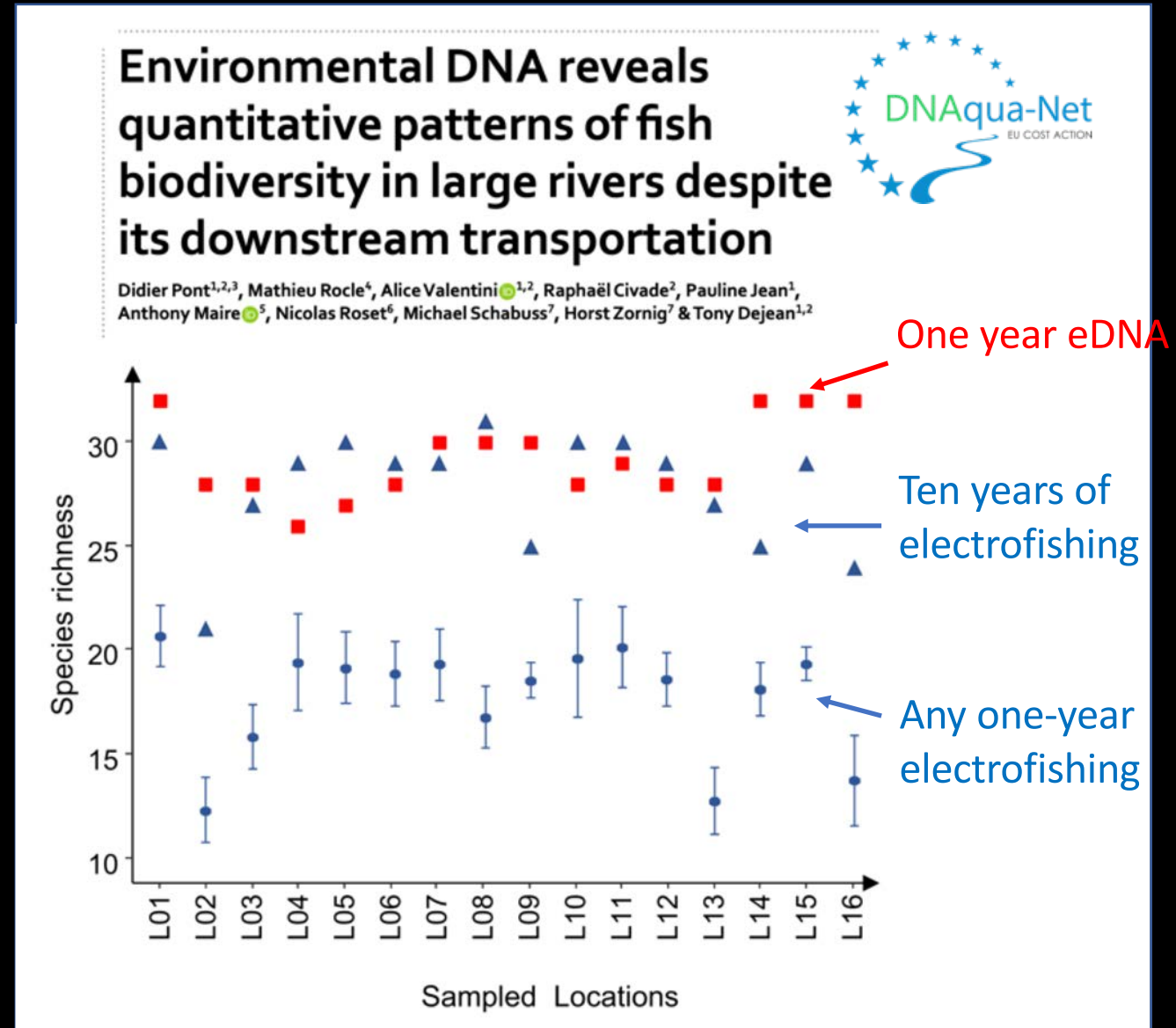
By Florian Leese, University of Duisburg-Essen and coordinator of DNAquaNET

Proposition 1: We need biodiversity 'weather stations' & DNA methods can help here



DNA & eDNA based methods: "more with less"

- great performance of eDNA for biodiversity assessments, e.g. fish community detection
- Many such studies reported from many different countries!
- Errors remain (like with all methods)



Also beyond water applied & capable

DOI: 10.1002/edn3.372

METHOD

Environmental DNA
WILEY

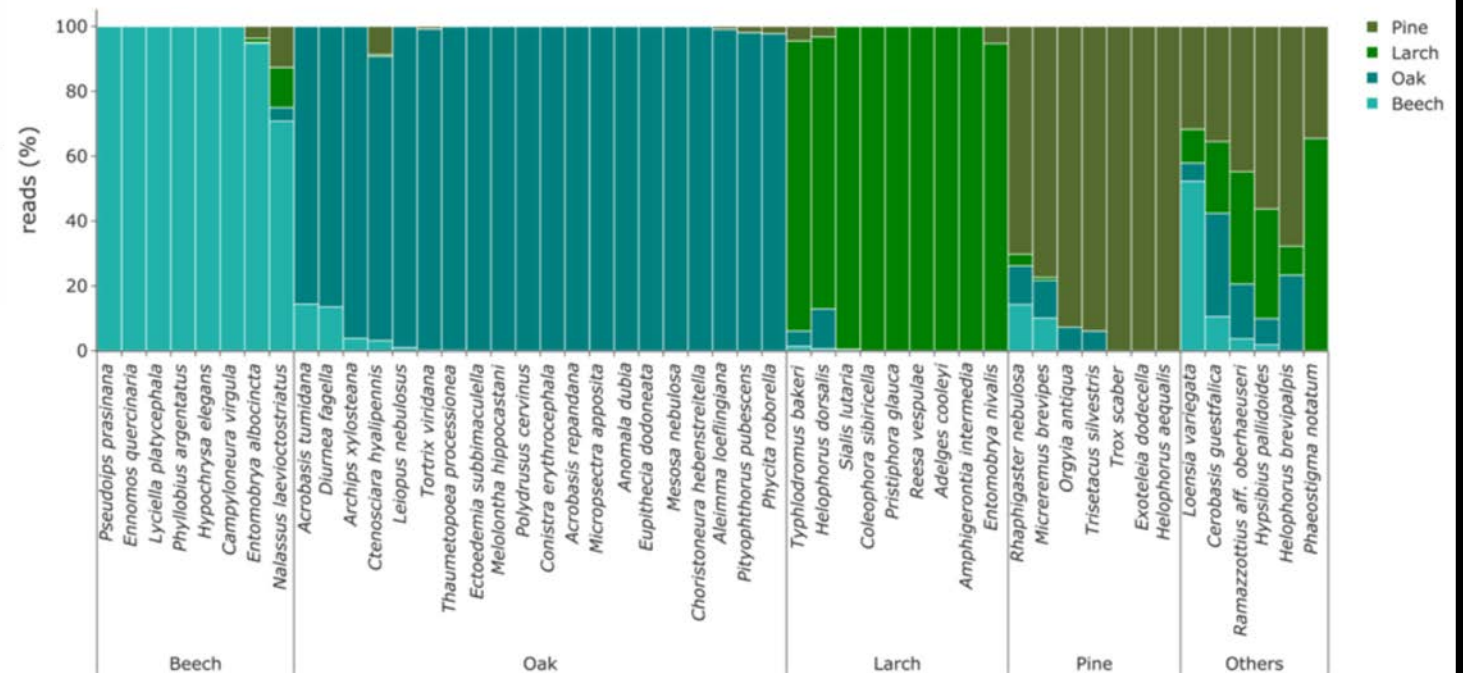
It's raining species: Rainwash eDNA metabarcoding as a minimally invasive method to assess tree canopy invertebrate diversity

Till-Hendrik Macher¹ | Robin Schütz¹ | Thomas Hörren^{2,3} | Arne J. Beermann^{1,4} | Florian Leese^{1,4}

- Rainwash eDNA
- Non-invasive, simple, low-risk biodiversity assessment



Supplementary Figure 1: Schematic overview of the rain sampler prototype.



Also beyond water applied & capable: Airborne eDNA analysis



Figure 1. The sampling sites and airborne eDNA detections of vertebrate species

Report

Airborne environmental DNA for terrestrial vertebrate community monitoring

Christina Lynggaard,^{1,6,*} Mads Frost Bertelsen,² Casper V. Jensen,³ Matthew S. Johnson,^{3,4} Tobias Guldberg Froslev,⁵ Morten Tange Olsen,¹ and Kristine Bohmann^{1,7,8,*}

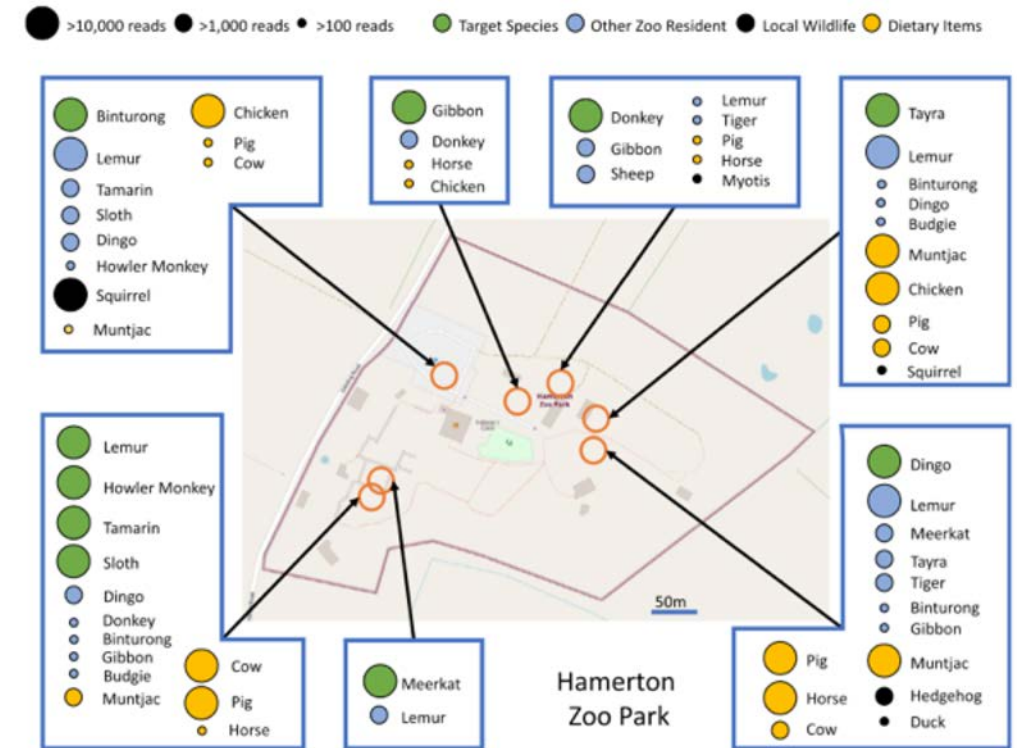
¹Section for Evolutionary Genomics, Globe Institute, Faculty of Health and Medical Sciences, University of Copenhagen, 1353 Copenhagen, Denmark

²Center for Wild Animal Health, Copenhagen Zoo, 2000 Frederiksberg, Denmark

³Department of Chemistry, University of Copenhagen, 2100 Copenhagen, Denmark

⁴Airlabs Denmark, 2200 Copenhagen, Denmark

⁵Section for GeoGenetics, Globe Institute, Faculty of Health and Medical Sciences, University of Copenhagen, 1353 Copenhagen, Denmark



Current Biology

CellPress
OPEN ACCESS

Report

Measuring biodiversity from DNA in the air

Elizabeth L. Clare,^{1,2,4,6,*} Chloe K. Economou,¹ Frances J. Bennett,¹ Caitlin E. Dyer,¹ Katherine Adams,³ Benjamin McRobie,³ Rosie Drinkwater,¹ and Joanne E. Littlefair^{1,5}

¹School of Biological and Chemical Sciences, Queen Mary University of London, London E1 4NS, UK

²Department of Biology, York University, Toronto, ON M3J 1P3, Canada

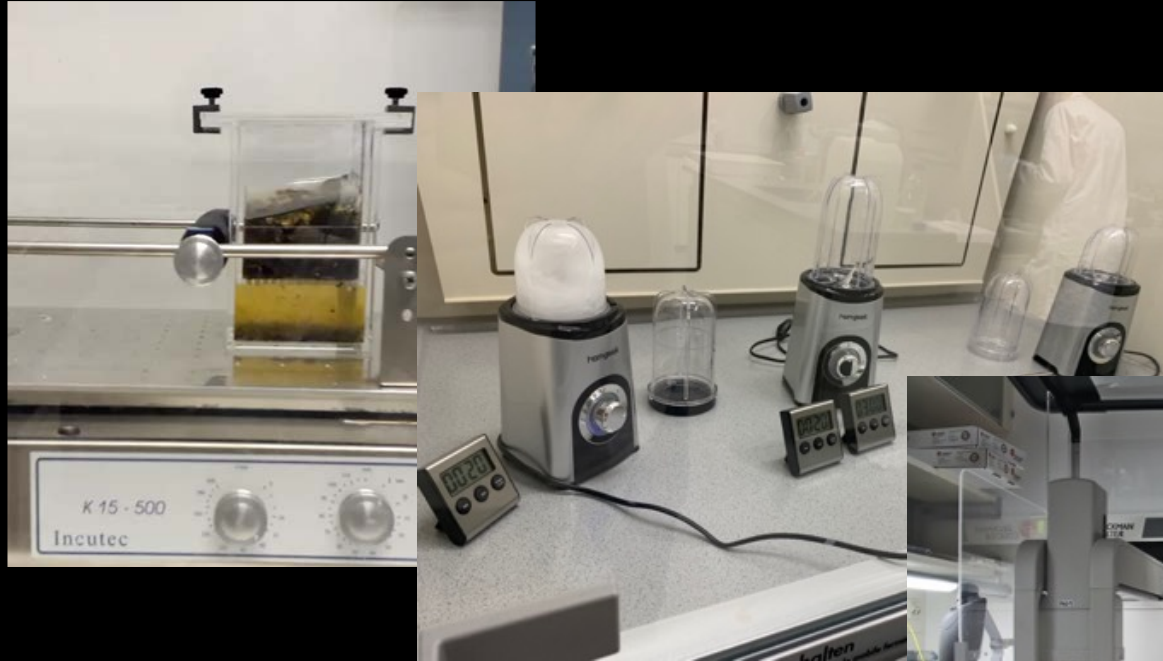
³Hamerton Zoo Park, Huntingdon PE28 5RE, UK

⁴Twitter: @Dr_bat_girl

⁵Twitter: @JELittlefair

⁶Lead contact

Scalable & affordable




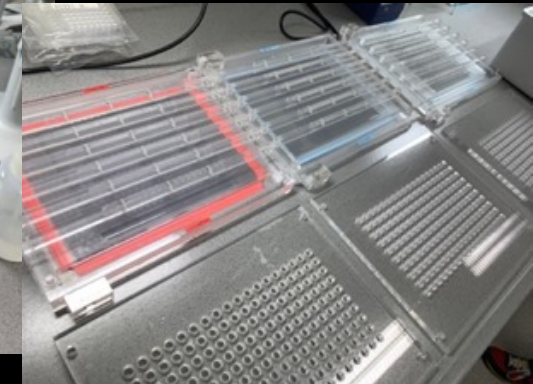
- 4000 samples (whole German insect monitoring LTER-D [Haase, Frenzel]) analysed within ~3 months

Original Research
Standardized high-throughput biomonitoring using DNA metabarcoding: Strategies for the adoption of automated liquid handlers

Dominik Buchner ^{a,1}, Till-Hendrik Macher ^{a,1}, Arne J. Beermann ^{a,b}, Marie-Thérèse Werner ^a, Florian Leese ^{a,b,*}

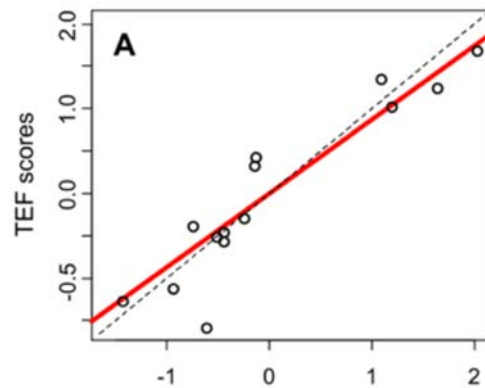
^a University of Duisburg-Essen, Aquatic Ecosystem Research, Universitätsstr. 5, 45141, Essen, Germany
^b University of Duisburg-Essen, Centre for Water and Environmental Research (ZWE), Universitätsstr. 3, 45141, Essen, Germany



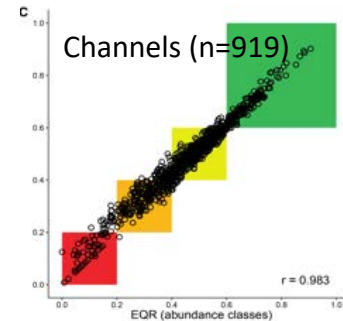


Elbrecht & Leese (2015) PLoS One, Elbrecht & Leese (2017) Front. Ecol. Env.; Vamos et al. (2017) MBMG; Macher et al. (2018) Mol. Ecol. Res. Buchner et al. (2019) PLoS ONE, Leese et al. (2018) Adv. Ecol. Res.; Buchner et al. 2021 MBMG; Buchner et al. (2021) Ecol & Evol, Buchner et al. (2021) ESE, Macher et al. (2021)....

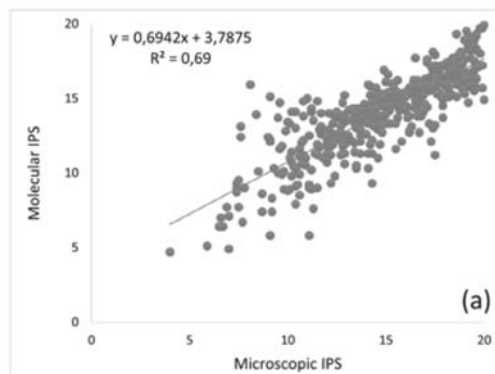
Comparable monitoring data to traditional methods (taxa lists partly)



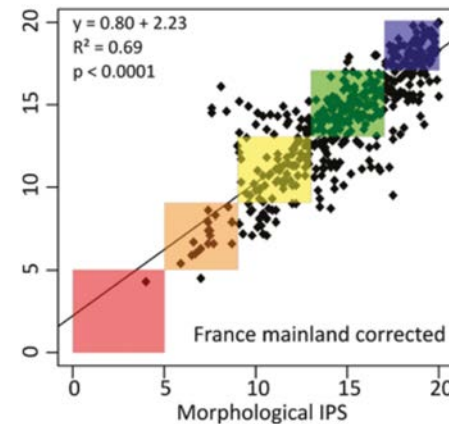
Pont et al. 2018



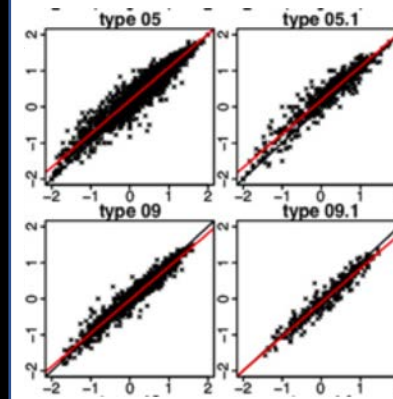
Beentjes et al. (2018)



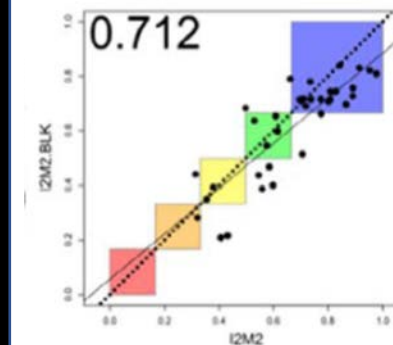
Rivera et al. (2020)



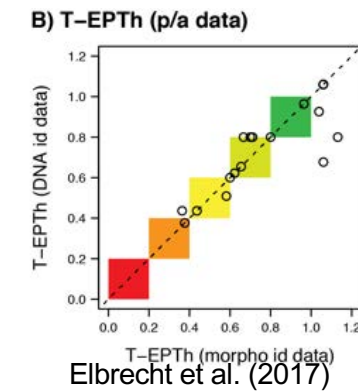
Vasselon et al. (2019)



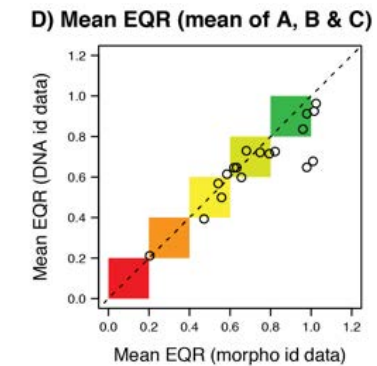
Buchner et al. (2019)



Meyer et al. (2021)



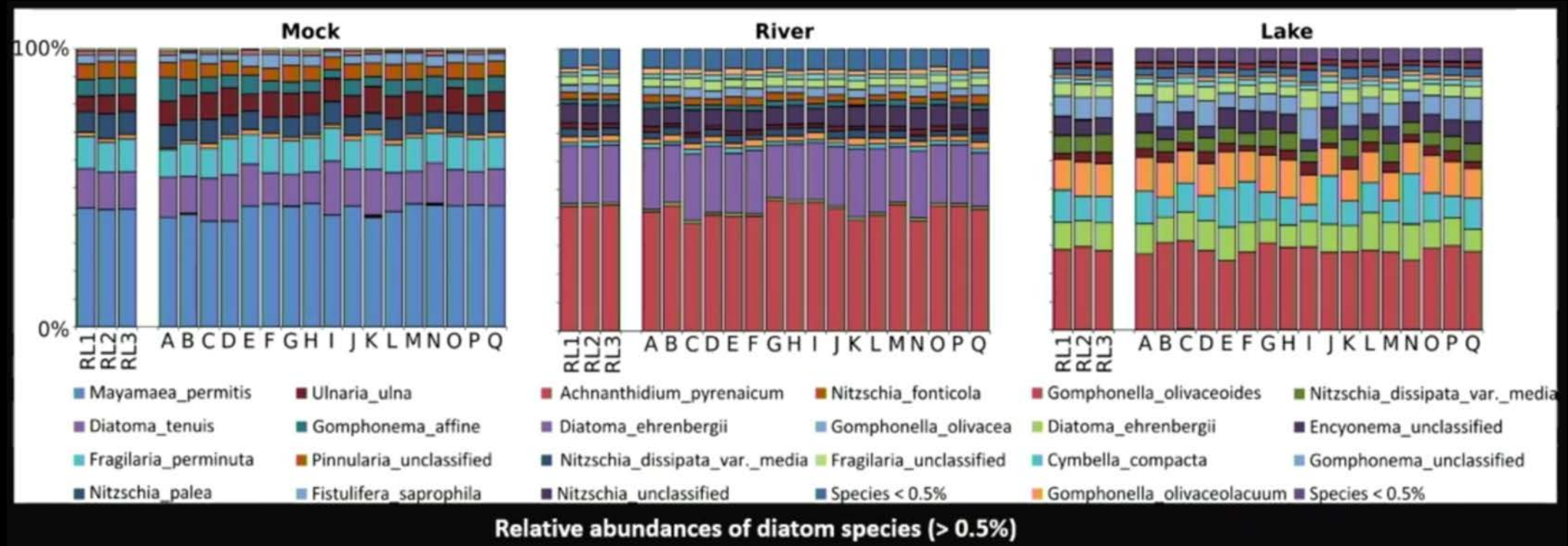
Elbrecht et al. (2017)



Elbrecht et al. (2017)

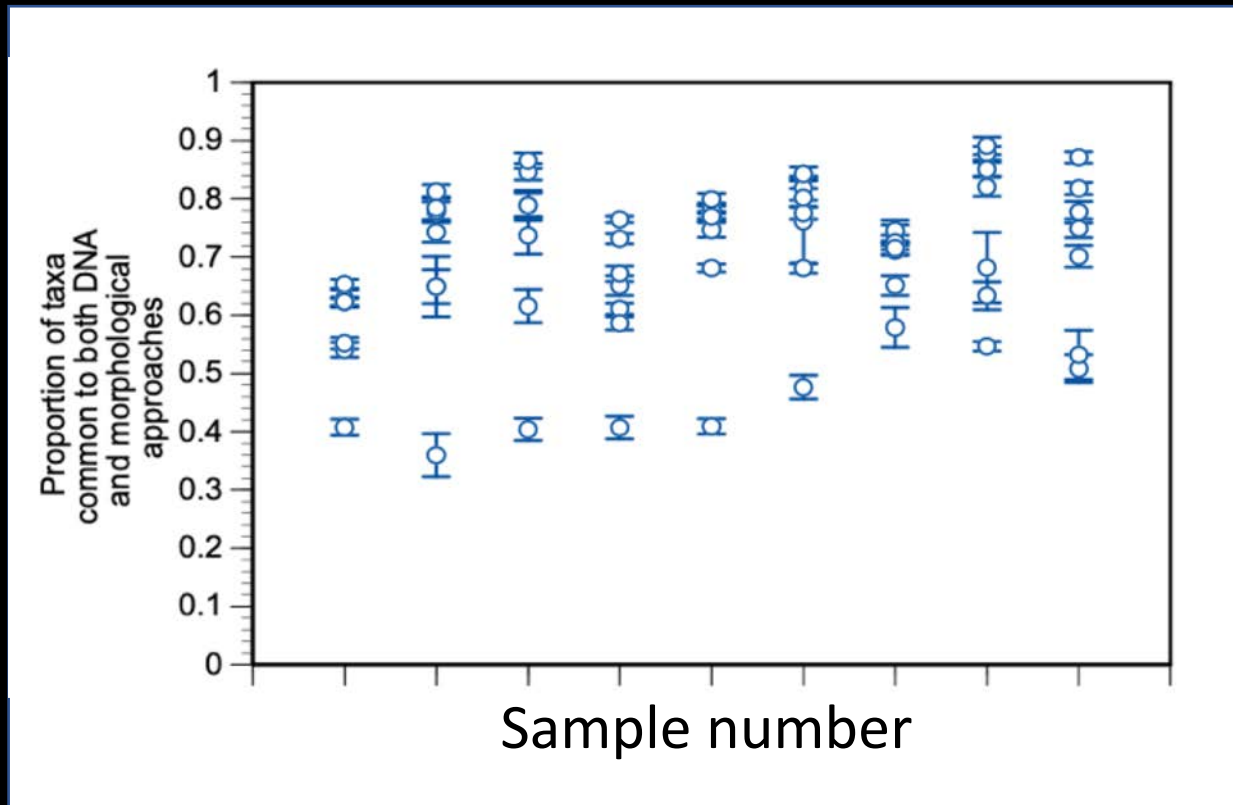
Methods deliver very comparable results

Diatom ring tests



Data: Valentin Vasselon et al. (DNAqua-Net)

But: strong method biases (extraction, primers) & inter-lab variation exist



- Several parameters can have strong impacts on the results
- **They won't vanish if we don't act**

→ Standards + QA/QC

Data: DNAqua-Net ring-test MZB, data: Jones, Blackmann, Buchner et al. (in prep.)

Proposition 2: eDNA data can complicate biodiversity monitoring frameworks!



ELSEVIER

Contents lists available at SciVerse ScienceDirect

Ecological Indicators

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



thousand

~~Three hundred~~ ways to assess Europe's surface waters: An almost complete overview of biological methods to implement the Water Framework Directive

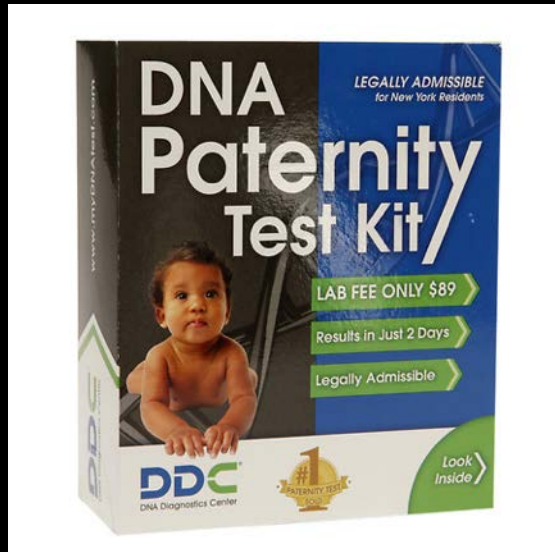
Sebastian Birk^{a,*}, Wendy Bonne^b, Angel Borja^c, Sandra Brucet^b, Anne Courrat^d, Sandra Poikane^b, Angelo Solimini^e, Wouter van de Bund^b, Nikolaos Zampoukas^b, Daniel Hering^a

- We need standards and guidance (revolution -> constitution)
- We need central coordination (e.g. linked to ECOSTAT)
- We need FAIR data and (meta-) data standards



Propositions 3: Solutions exist!

- Standardized assessment of ingredients (species detection)
- References, reference material
- SOPs, QA/QC



<https://www.foodnavigator.com/Article/2020/05/12/Beef-fraud-Counterfeit-products-the-biggest-threat-to-supply-chain>

Standards: Basis for accurate measurements

Berlin, Jan 17th, 2020

Diagnostic detection of 2019-nCoV by real-time RT-PCR

-Protocol and preliminary evaluation as of Jan 17, 2020-

Victor Corman, Tobias Bleicker, Sebastian Brünink, Christian Drosten
Charité Virology, Berlin, Germany

Olfert Landt, Tib-Molbiol, Berlin, Germany

Marion Koopmans
Erasmus MC, Rotterdam, The Netherlands

Maria Zambon
Public Health England, London

Additional advice by Malik Peiris, University of Hong Kong

Users looking for a workflow protocol consult the last three pages of this document

All assays can use SARS-CoV genomic RNA as positive control. Synthetic control RNA for 2019-nCoV E gene assay is available via EVAg. Synthetic control for 2019-nCoV RdRp is expected to be available via EVAg from Jan 21st onward.

First line screening assay: E gene assay
Confirmatory assay: RdRp gene assay

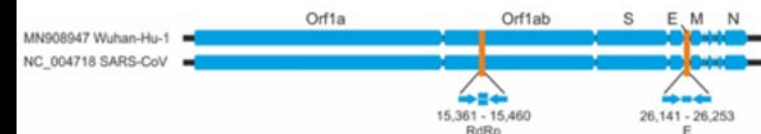


Figure 1 relative positions of amplicon targets on SARS-CoV and 2019-nCoV genome. ORF: open reading frame; RdRp: RNA-dependent RNA polymerase. Numbers below amplicon are genome positions according to SARS-CoV, NC_004718.

Table 1. Primers and probes

Optimized concentrations are mol per liter of final reaction mix.

(e.g., 1.5 microliters of a 10 micromolar (μM) primer stock solution per 25 microliter (μl) total reaction volume yields a final concentration of 600 nanomol per liter (nM) as indicated in the table)

-note that standard, non-optimized reaction conditions as indicated by suppliers of one-step RT-PCR kits will generally yield sufficient sensitivity-

Assay/Use	Oligonucleotide ID	Sequence (5'-3')	Comment
RdRP gene	RdRP_SARSr-F2	GTGARATGGTCATGTGTGGCGG	use 600 nM per reaction
	RdRP_SARSr-R1	CARATGTTAAACACTATTAGCATA	use 800 nM per reaction
	RdRP_SARSr-P2	FAM-CAGGTGGAACTCATCAGGAGATGC-BBQ	Specific for 2019-nCoV, will not detect SARS-CoV use 100 nM per reaction and mix with P1
	RdRP_SARSr-P1	FAM-CCAGGTGGWACATCATCMGGTGATGC-BBQ	Pan Sarbeco-Probe, will detect 2019-nCoV, SARS-CoV and bat-SARS-related CoVs use 100 nM per reaction and mix with P2
E gene	E_Sarbeco_F1	ACAGGTACGTTAATAGTTAATAGCGT	use 400 nM per reaction
	E_Sarbeco_R2	ATATTGCAGCAGTACGCACACA	use 400 nM per reaction
	E_Sarbeco_P1	FAM-ACACTAGCCATCCTACTGCGCTTCG-BBQ	use 200 nM per reaction

W is A/T; R is G/A; M is A/C; FAM, 6-carboxyfluorescein; BBQ, blackberry quencher

Standards don't hinder innovation, they enable these



Example:

In the medical sector many devices are not perfect (x-ray devices, ultrasonication etc.) and undergo constant improvements. Still they are very successfully applied for medical diagnoses.

“Ultrasonication – more indications through new techniques”


Minimum standards, reporting standards



→ DNAqua-Net WG3 (2021)


Pawłowski et al. 2020: Available in 3 languages!

Help eDNA monitoring tools to bridge the science x policy gap!


 CEN
CEN/TR 17244:2018 (MAIN)
SIST-TP CEN/TR 17244:2019

Water quality - Technical report for the management of diatom barcodes

This technical report specifies the data and metadata necessary to validate the identity of a diatom barcode used for ecological assessment along with recommendations for storage of the barcode and metadata to ensure access to this information.


 **Technical report 11 pages** ⓘ
English language

sale 10% off
€ 45.98

 **e-Library read for 1 day** ▼


€ 5.00

12-Sep-2018 # 13.060.70 CEN/TC 230


 CEN
CEN/TR 17245:2018 (MAIN)
SIST-TP CEN/TR 17245:2019

Water quality - Technical report for the routine sampling of benthic diatoms from rivers and lakes adapted for metabarcoding analyses

This technical report specifies a method for the field sampling of benthic diatoms which will be then analysed by subsequent metabarcoding techniques for ecological status and water quality assessments. Data produced by this method are suitable for production of taxonomical diatom lists.


 **Technical report 8 pages** ⓘ
English language

sale 10% off
€ 38.72

 **e-Library read for 1 day** ▼


€ 5.00

12-Sep-2018 # 13.060.70 CEN/TC 230


 CEN
FprEN 17805 (MAIN)
kSIST FprEN 17805:2022

Water quality - Sampling, capture and preservation of environmental DNA from water

Water sampling for capture of environmental DNA (eDNA) in aquatic environments. eDNA stems from organisms which are or have recently been living in the water body and does not include eDNA found in sediments or similar sample types. Covers procedures for avoiding sample contamination and ensuring DNA quality, key properties of the filtering procedure and equipment, and reporting standards.

 **Draft 15 pages** ⓘ
English language

sale 10% off
€ 53.24

 **e-Library read for 1 day** ▼

€ 5.32

30-Sep-2023 # 13.060.70 2000/60/EC CEN/TC 230

CEN
CEN/TC 230/WG 28 - DNA AND EDNA METHODS

ABSTRACT SLOVENIAN

GENERAL INFORMATION

Status	Active
Work Field	Information technology
Parent	CEN/TC 230 - Water analysis

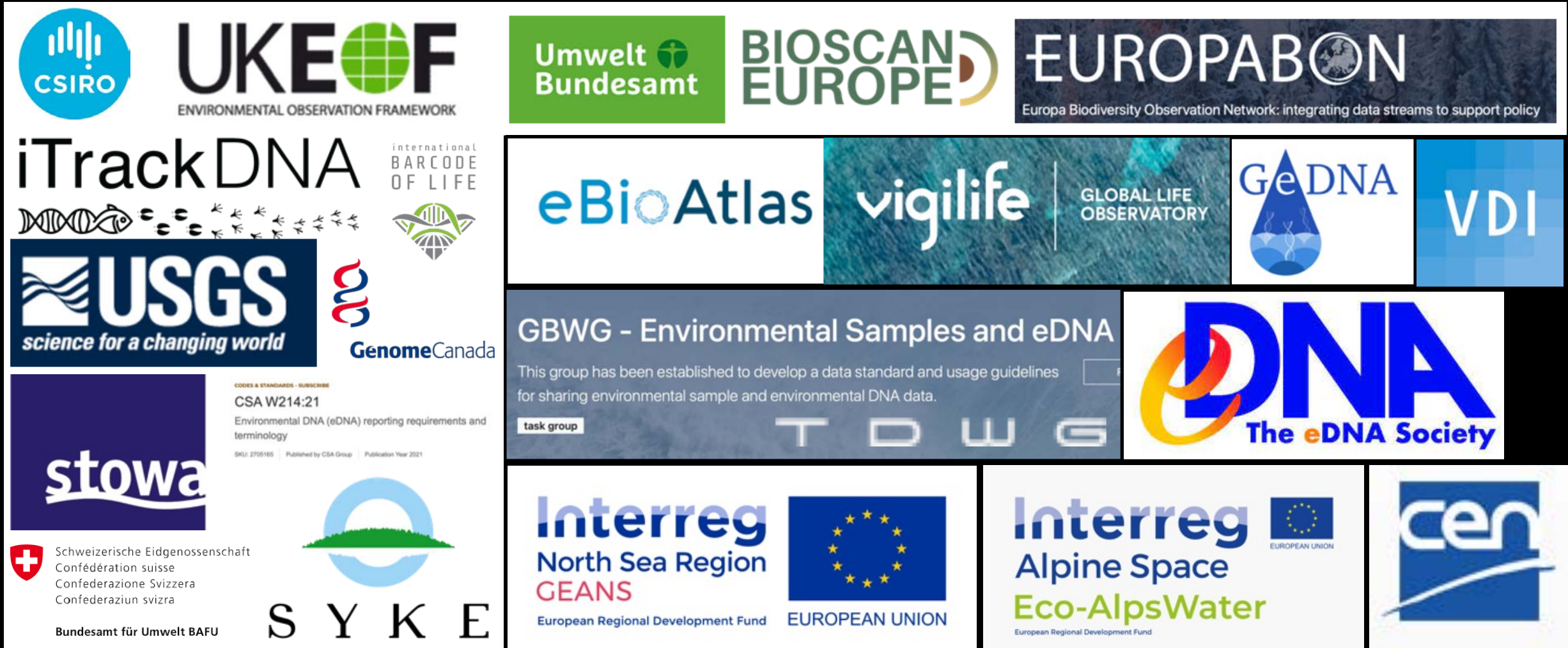


Harmonized intern. biomonitoring 2.0

UNIVERSITÄT
DUISBURG
ESSEN

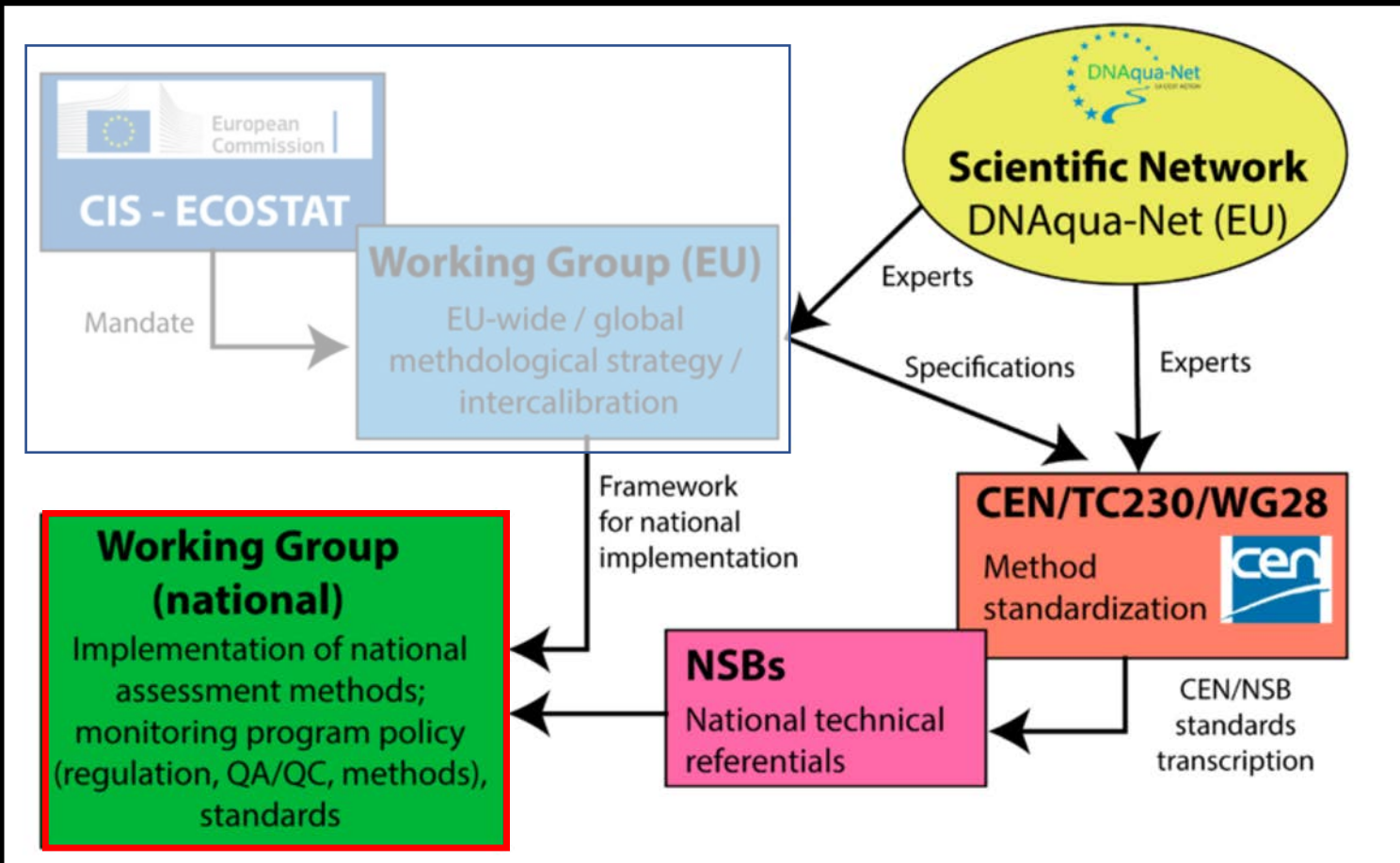
Open-Minded

- Mostly academic sector at international level, but academic intern. networks!



Harmonized biomonitoring 2.0...

- At the moment: National level discussions, no EU JCR mandate group
- KCBD monitoring group, int. networks, projects (eDNAqua-Plan)



Beyond Europe

UNIVERSITÄT
DUISBURG
ESSEN

Open-Minded

Key messages:

The necessity of creating minimum requirement standards

First, we need to internationally agree on minimum requirements for frontend methods to collect, handle and store samples for molecular analysis. This is a matter of high urgency, as many countries are already developing their national approaches. Due to the sensitivity of molecular methods, a lack of common frontend standards will result in a plethora of different national approaches, varying results and incompatible data. Only international molecular method standards will enable global assessments of biodiversity or genetic diversity and stimulate markets and industry to produce products to do so. ***We recommend to decide on the inclusion of method standards into the CBD policy frameworks and its work programme.***

The need to create standards inclusively

Second, to be effective, standards need to be developed inclusively, taking into consideration the requirements of the methods themselves as well as the need and possibilities of developing countries. Currently participation from developing countries in standardization is minimal. ***We recommend that developing countries are actively involved in the standardization work and that the international standardization bodies CEN and ISO formally conduct the standardization process.***

The need for dedicated funding

Third, in both developed and developing countries there is no separate funding available to facilitate the production of standards. ***We recommend that dedicated funding is available to encourage participation in inclusive method standardization especially by developing countries.***

Expert opinion

To be considered at COP 15 and the UN Summit of the Future 2023

September 2022

We, the experts representing contributing organizations from 4 continents of the side-event "The key for a successful UN's Post-2020 Global Biodiversity Framework - standards for measuring biodiversity with molecular tools" organized by the Science Summit at the UN general Assembly 77 in New York propose the following key messages to be considered in the preparation of the COP 15 and UN Summit of the Future, 2023 meetings.

The observed global loss of biodiversity has serious implications for human wellbeing and can amplify several of the negative aspects of climate change and impact adversely on achieving several of the SDG's. **We need international standards to enable the use of novel molecular techniques to extend and improve current biodiversity and genetic monitoring in all types of habitats.** Standards are needed because data from biological monitoring is the primary source of information to quantify biodiversity loss, as well as to evaluate the effectiveness of biodiversity management actions such as ecological restorations. The current motivation to standardize biodiversity methods stems mainly from policy demands of mandatory national legislation. This approach is ineffective in producing internationally agreed upon standards quickly. Continuing as usual will lead to long delays in the reporting of genetic diversity, reduce the intercomparability of country-wise reports and delay urgently needed management action to secure biodiversity. **Standardization of both backend (data standards), but especially frontend molecular method minimum requirements (sampling, laboratory procedures) is paramount to avoid error propagation and ensure global comparability of results.**



Science Summit at UNGA77
13-30 September 2022

Conclusion: (e)DNA biodiversity monitoring is not / will never be is not perfect, but...

- great chances to extend / scale-up biodiversity monitoring
- highly complementary to other monitoring approaches
- an option we should not miss





THANK YOU! Let's identify next steps



Acoustic monitoring of bats – a showcase of implementation

By Adrià López-Baucells and Charlotte Roemer

Passive
Remote
Automatic
Non-invasive
Relatively economic
Appropriate for +habitats +seasons



Standardization???

Repositories???

Passive
Remote
Automatic
Non-invasive
Relatively economic
Appropriate for +habitats +seasons



EUROBATS



Publication Series
No.

5



Guidelines for Surveillance and Monitoring of European Bats

Compiled by Jessamy Battersby

Monitoring protocols database:
shorturl.at/yLT09



UNEP EUROBATS

Bat Monitoring protocols						
Fitxer Edita Mostra Inserir Format Dades Eines Extensions Ajuda La darrera modificació es va fer el dia 20 de novembre de 2022						
D9						
March 1st - October 30th						
	A	B	C	D	E	F
1	Country	Bat cycle period	Method	Period	Periodicity	Video camera model
2	Spain (Catalonia)	Hibernation	Visual / Photography	15 November - 28 February	1 survey/yr roost	
3	Spain (Catalonia)	Migration	Visual / Photography	September 1st - November 1st & February 1st - May 15th	1 survey every 15 days	
4	Spain (Catalonia)	Migration	Emergence with infrared video / Acoustic	September 1st - November 1st & February 1st - May 15th	1 survey every 15 days	
5	Spain (Catalonia)	Migration	Clicker + handheld detector	September 1st - November 1st & February 1st - May 15th	1 survey every 15 days	
6	Spain (Catalonia)	Maternity	Visual / Photography	May 16th - August 31st	1 survey	
7	Spain (Catalonia)	Maternity	Emergence with infrared video / Acoustic	May 16th - August 31st	1 survey	
8	Algeria	Hibernation	Visual / Photography	November 1st to March 1st	1 survey/yr roost	Canon D600
9	Algeria	Maternity	Visual / Photography / Acoustic	March 1st - October 30th	Survey	Canon D600
10	Slovakia	Maternity	Visual / Emergence	May 15th - June 30th	1 survey	
11	Slovakia	Hibernation	Visual / Photography	January 15th - February 28th		
12	Slovakia	Swarming	Mist-netting	August 15th - October 15th		
13	Slovakia	Maternity	Emergence with infrared video / Acoustic	May 15th - June 15th	1 survey	
14	Ireland	Hibernation	Visual / Photography	January - February ±1week	1 survey/yr roost	
15	Ireland	Maternity	Visual / Photography or Visual / Emergence	May 23rd - July 7th	1 survey	Sony HandyCam FDR-AX33 and FDR-AX53
16	Ireland	Maternity	Visual / Photography or Visual / Emergence	16 May to 15 June / 16 June to 31 July / August to 30 August	3 surveys	Sony HandyCam FDR-AX33 and FDR-AX53
17	Basque Country	Hibernation	Visual / Photography	January	1 survey/yr roost	
18	Basque Country	Migration	Emergence with infrared video / Acoustic	01-31 May	1 survey/yr roost	
19	Basque Country	Maternity	Emergence with infrared video / Acoustic	June 25th - July 15th	1 survey/yr roost	
20	Germany	maternity	manual bat box checking	10th July until mid August	once per site	
21	Germany	hibernation	Visual / Photography	January	1 survey/yr roost	
22	Bulgaria	Maternity	Visual / Photography or Visual / Emergence	15 May - 15 June	once per site	Canon
23	Bulgaria	Hibernation	Visual / Photography	January, February, March	1 survey/yr roost	Canon
24	Romania	Maternity	Visual / Photography, at one site Emergence	June - July	once per site	Nikon D7000 mostly
25	Romania	Hibernation	Visual / Photography	January - March	1 survey/yr roost	Nikon D7000 mostly
26	Romania	Swarming	Mistnetting, harptrapping	Autumn	once per area (always includes the two standard caves)	-
27	United Kingdom	Hibernation	Visual / Photography	December - March	2 survey/yr roost	-
28	United Kingdom	Maternity	Visual / Acoustic	June - July	twice per site	-

Bat Monitoring Programme

Citizen science programme to monitor bat populations



Choose your protocol!

This initiative includes 4 different protocols: the **ChiroRivers**, the **ChiroHabitats**, the **ChiroBoxes** and the **ChiroRoosts**. Each one of them has been specifically designed for monitoring a certain group of bat species, either forest-dwelling, cave-dwelling or urban-dwelling species. The combination of all 4 monitoring programmes provides a complete image of the health status of all bat species populations. If you would like to participate chose a protocol and [contact us](#) for further information!



ChiroHabitats

Monitoring of bat species in all kind of habitats using passive acoustic monitoring.

[Read more ...](#)



ChiroRivers

Monitoring of bat species present in aquatic ecosystems, used as ecological indicators of water and riparian forest quality.

[Read more ...](#)



ChiroBoxes

Monitoring of bat species that use artificial roosts such as bat boxes.

[Read more ...](#)



ChiroRoosts

Monitoring of bat colonies in natural or artificial roosts such as caves, mines, tunnels, churches or buildings.

[Read more ...](#)



www.batmonitoring.org



Pallerols Obert

GENERAL DATA	
Sun	Sunrise at 07:08 and sunset at 17:08 (UTC)
Geographic coordinates	42.391, 1.273
UTM coordinates	31T 4694585 357823
Elevation	1624
Municipality	Montferrer i Castelló
Habitat	Coniferous forest
Typology	Permanent
Open/Closed	Open
Sessions	5
Species and sonotypes	15
Pictures	2
Atlas of mammals of Catalonia	No
User	Maria Mas
Data de creació	2019-01-01 00:00:00

Sessions 5

Pictures 2

Resultats públics

Pictures



Resultats per sessió (5)

Period	Start	End	Days	Detector	Passes / night	Tags
Summer	2022-07-08	2022-07-21	13	SM4 (02)	4900	Hypsav-m, NycSp-m, Myo50-m, Barbar-m, Pippip-m, Pkuhnat-m, EptNycVes-m, PleSp-m, PpygMin-m, Rhihip-m, Myo30-m, Rhifer-m, TadNyc-m
Summer	2021-07-02	2021-07-14	12	SM4 (14)	827	Pippip-m, Myo50-m, EptNycVes-m, Hypsav-m, PpygMin-m, Pkuhnat-m, PleSp-m, Barbar-m, NycSp-m, Myo30-m, MyoSp-m, Rhihip-m
Summer	2020-07-09	2020-07-21	12	SM4 (07)	1138	Myo50-m, Hypsav-m, Pippip-m, PpygMin-m, PleSp-m, Barbar-m, Pkuhnat-m, MyoSp-m, EptNycVes-m, Myo30-m, TadNyc-m, Rhieur-m, Rhihip-m
Summer	2019-07-01	2019-07-09	8	SM4 (02)	1803	Barbar-m, EptNycVes-m, EptNycVes-m, Hypsav-m, Myo30-m, Myo50-m, MyoSp-m, NycSp-m, Pkuhnat-m, Pippip-m, PpygMin-m, PleSp-m, Rhihip-m, TadNyc-m
Summer	2018-07-04	2018-07-13	9	SM4 (10)	1236	Hypsav-m, MyoSp-m, Barbar-m, PpygMin-m, Myo50-m, Pippip-m, Pkuhnat-m, EptNycVes-m, PleSp-m, MyoSp-m

Evolution of counts of

All bat species



Each bar represents the average of counts (or bat passes) detected per night in each sampling point. A bat pass is defined as a recording of a maximum of 5 seconds with a minimum of 2 bat calls identified to species level or as a phonic group. Through the menu, it is possible to visualize the average of total bat activity (including all bat species) or the total count for each species. The bar colours correspond to each season.

Summary of accumulated bat activity

Species / Sonotype	Passes / night
Pipistrellus pipistrellus	55.2
Myotis 50	26.6
Pipistrellus kuhlii / P. nathusi	22.9
Hypsugo savii	20.3
Barbastella barbastellus	12.0
Pipistrellus pygmaeus / Miniopterus sp.	8.9
Eptesicus / Nyctalus / Vespertilio	5.1
Nyctalus sp.	5.2
Plecotus sp.	3.3
Myotis sp.	3.4
Myotis 30	3.6
Rhinolophus hipposideros	3.3
Tadarida teniotis / Nyctalus lasiopterus	3.2
Rhinolophus euryala	3.1
Rhinolophus ferrumequinum	3.1

Summary of accumulated bat activity for each bat species on the sampling locality. The bars indicate the average of contacts (or bat passes) detected per night, including all samplings carried out within the year.

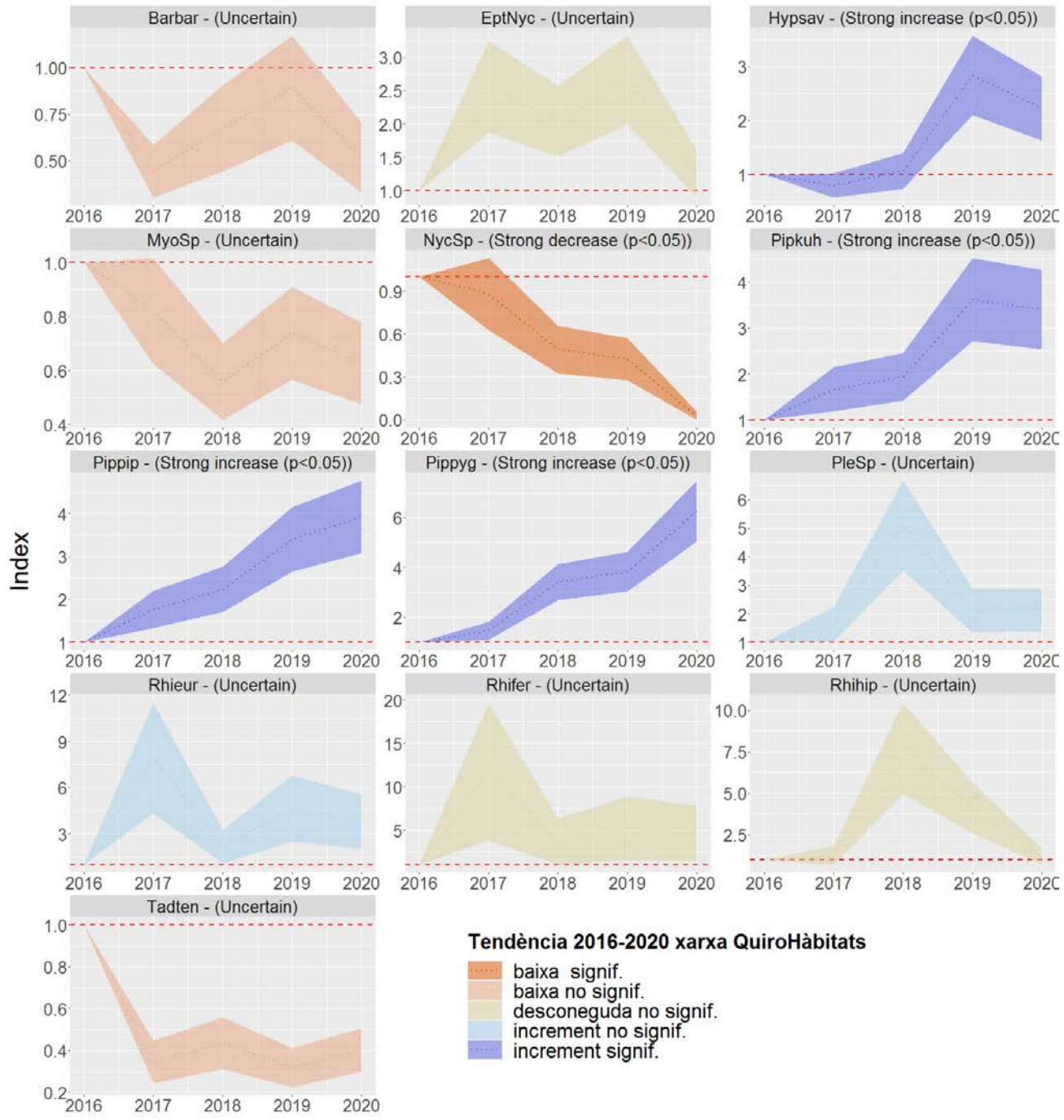
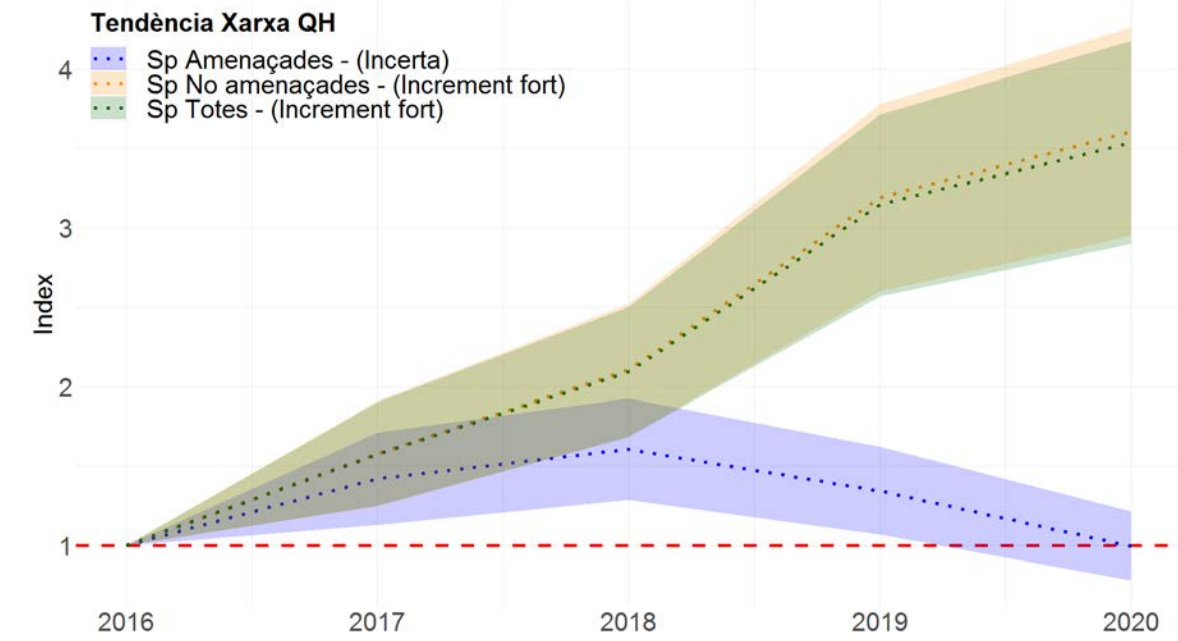
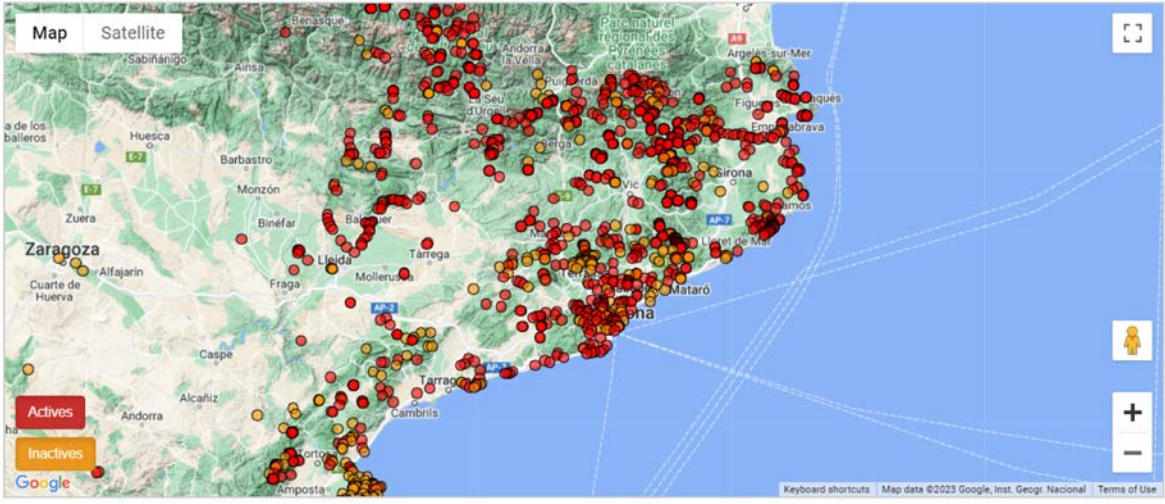
Species and/or phonic group identified in this locality



Explore data

Filtres

Habitat All Tipus All



ChiroRoosts

Bat monitoring in natural and artificial roosts

Bat roost monitoring protocol, including natural roosts (such as caves, rock shelters, trees etc.) as well as artificial roosts (mines, tunnels, roofs, stone cabins etc.). It is the simple protocol for following bat populations, mainly cave-dwelling, such as rhinolophid bats (*Rhinolophus sp.*), the Schreiber's Bent-winged bat (*Miniopterus schreibersii*) and (*Myotis sp.*), that are otherwise difficult to detect.

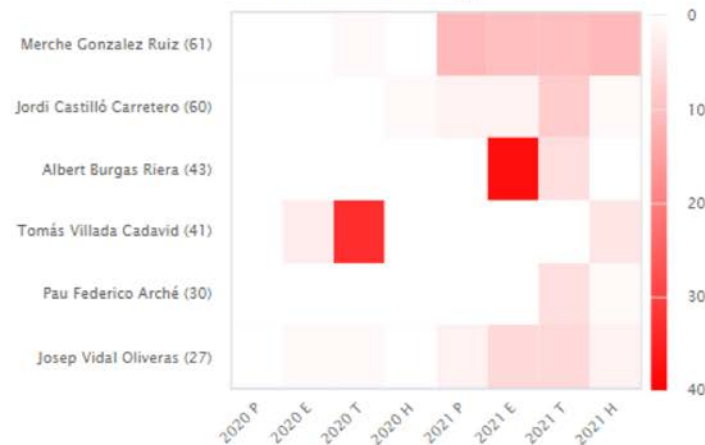
Throughout the monitoring of bat populations in roosts, we can extrapolate the population trends of these species, and thus prevent the local extinctions caused by negative effects of human activities on the landscape. For this monitoring, the Natural Science Museum of Granollers adapts the protocol to the specific characteristics of each roost.



📍 Roosts: 567

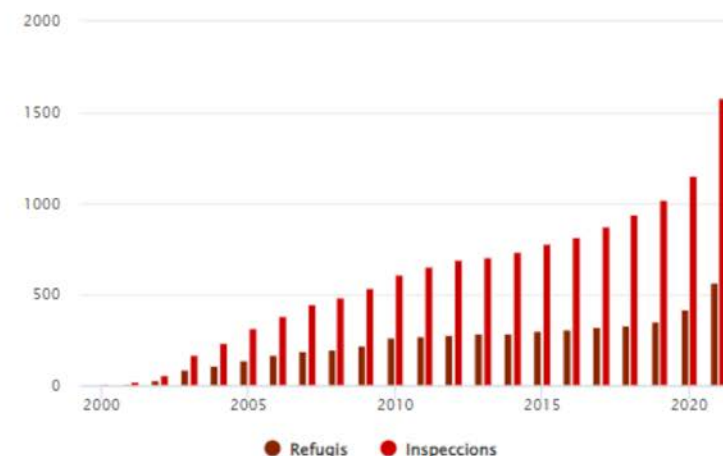
👁️ Inspections: 1583

Volunteer ranking



Volunteer ranking with the maximum number of roosts' inspections per year and season.
(P=spring, E=summer, T=autumn, H=winter)

Evolution in the number of roosts and inspections



Evolution of the number of roosts and inspections acumulated through the years





2500

2000

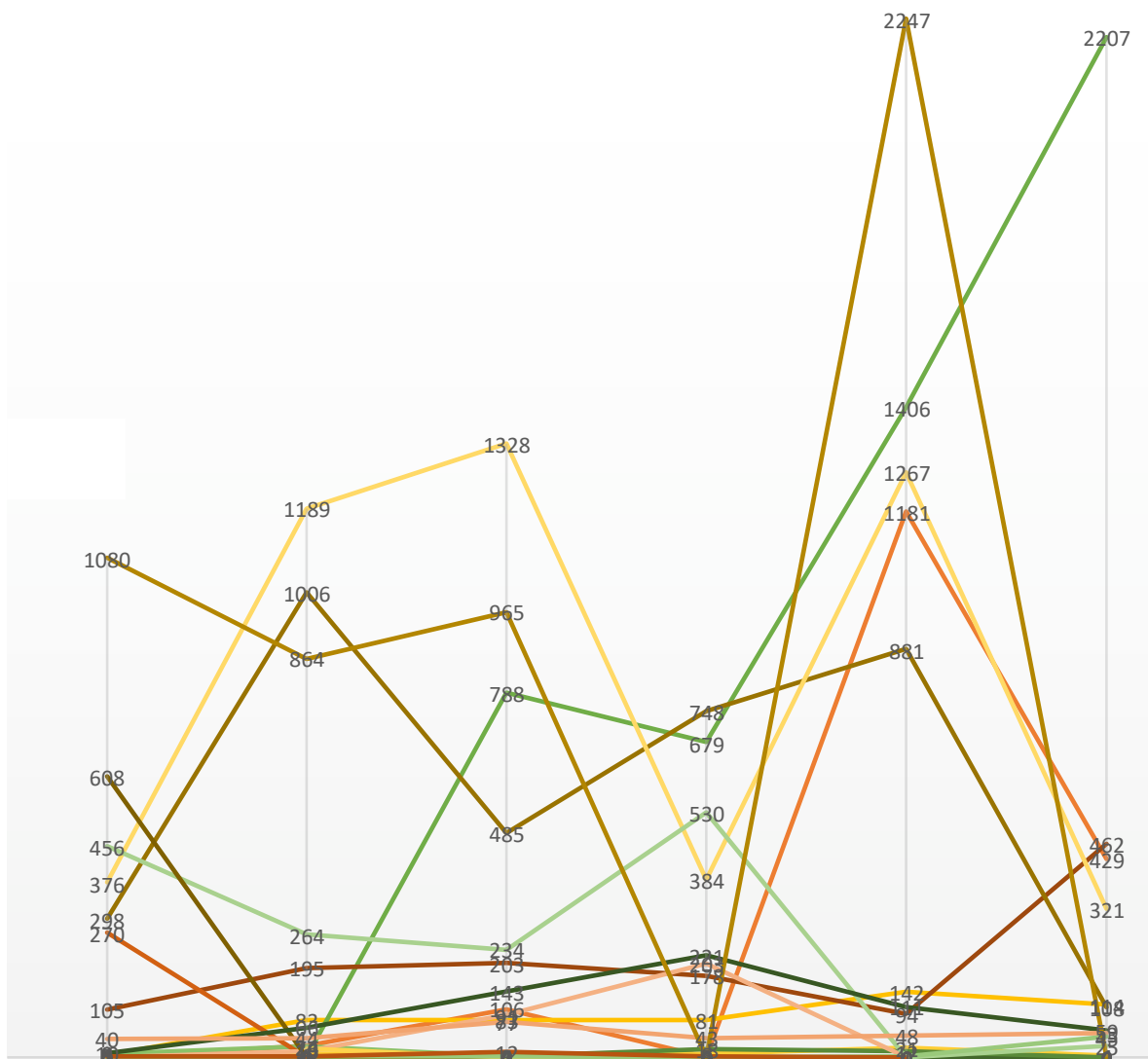
1500

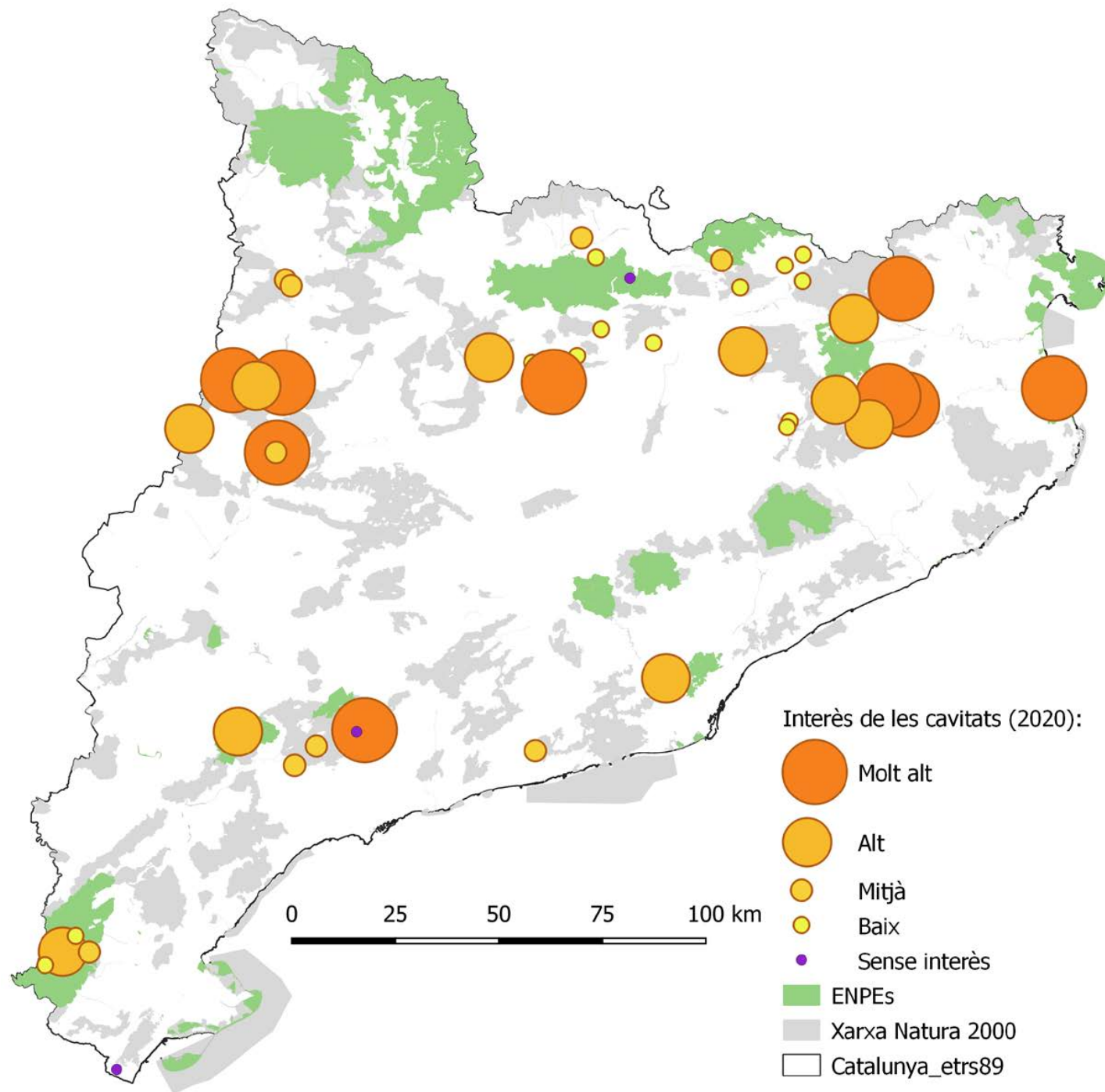
1000

500

0

1r cens 2n cens 3r cens 4t cens 5è cens 6è cens







Bat Migration routes in Europe

[Get involved!](#)

[Apply for an Audiomoth!](#)

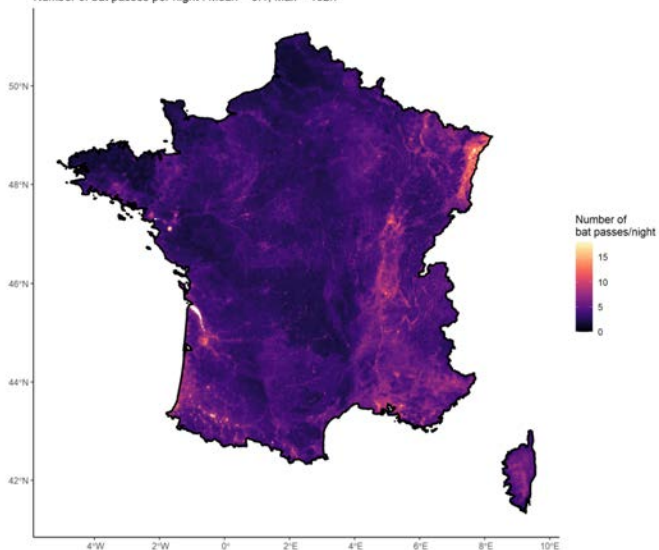


Funding and support

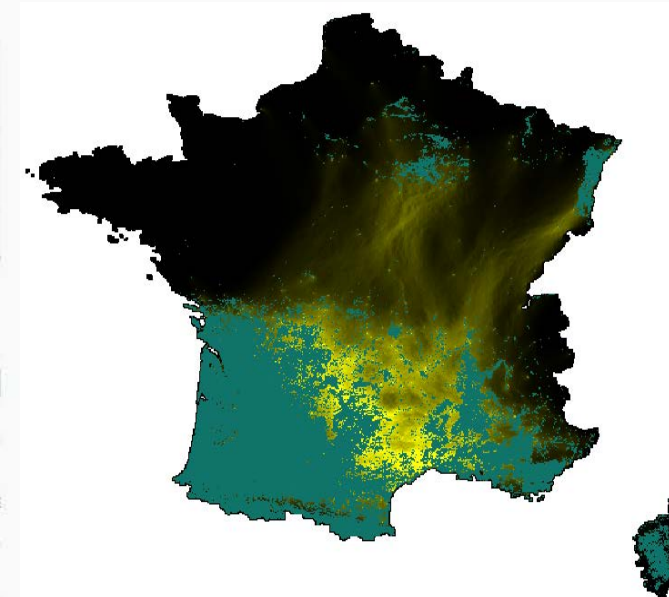
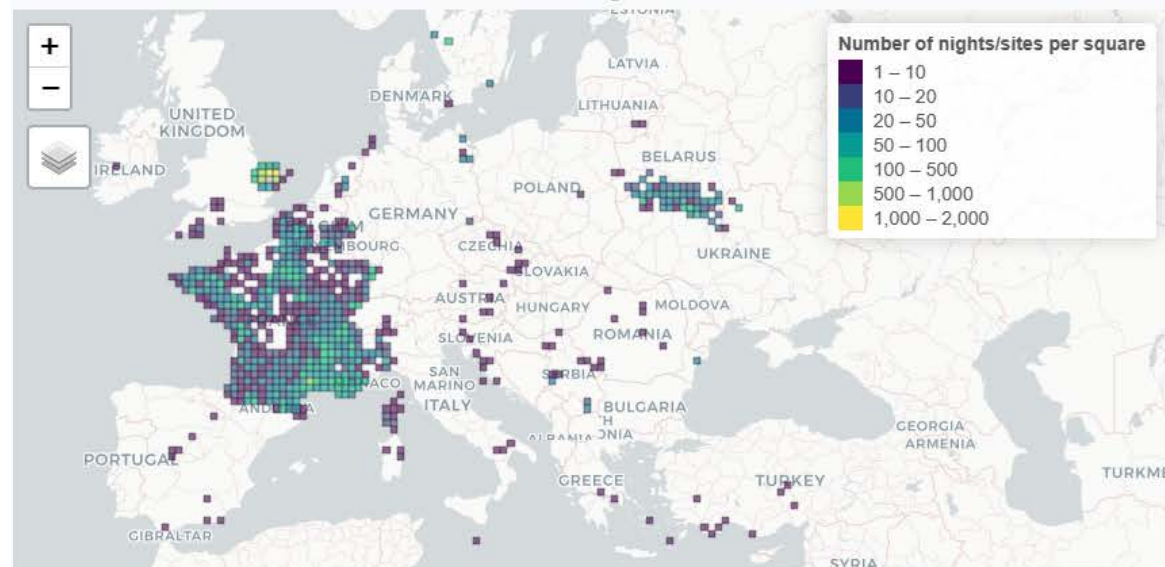


Participation map

Nyctalus leisleri
January
Number of bat passes per night : Mean = 5.1, Max = 132.7



50 km grid



- **Opportunity: first review of the most common uses of settings and machines in Europe**
- **Define which possibilities exist to aggregate data from different machines/settings**
 - Field tests to define which settings/machines give similar results
 - Larger time interval to count bat passes (e.g. positive minute of activity, Miller 2001, Haquart 2012)
→ eliminates a lot of variability due to material used
 - Use setting and machine as input in models to take the variability into account



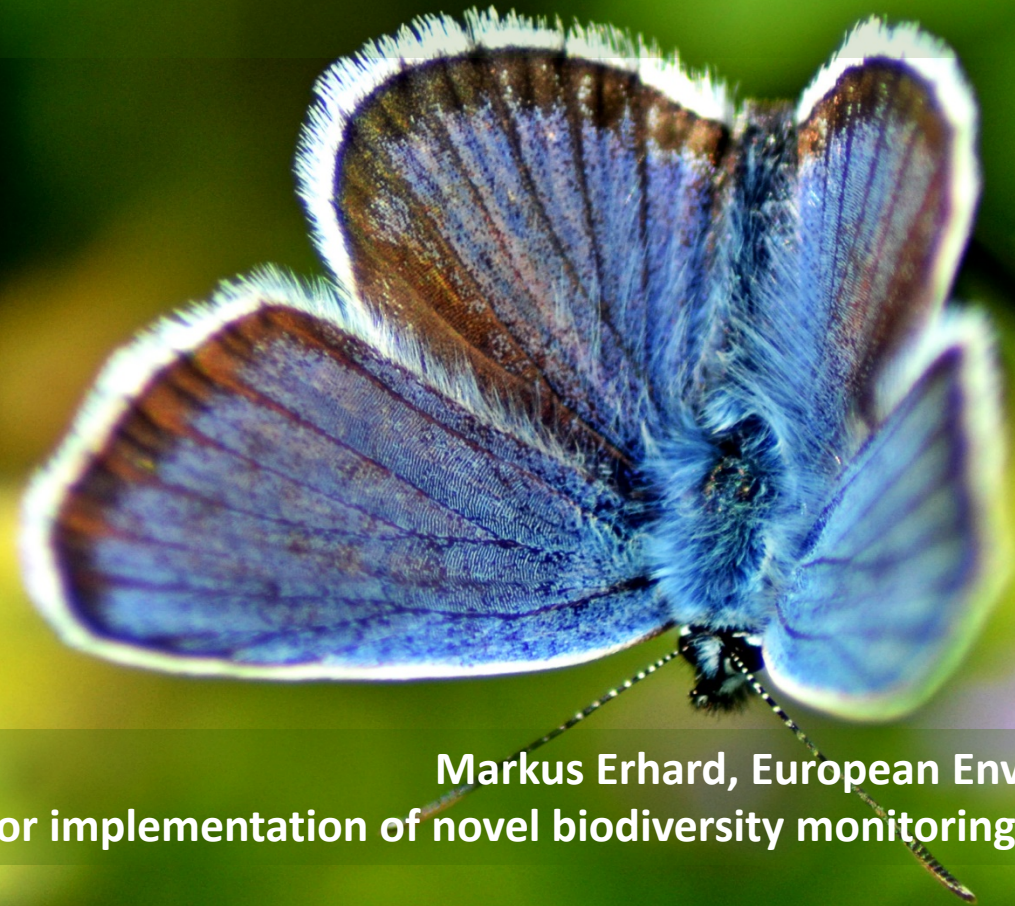
A European database for full-night recordings of bats?

- Secured and standard storage
- Confidentiality management
- Remote access for:
 - Raw data processing
 - Download of processed data
 - Dynamic tools for results

How to ensure FAIR data in the implementation of novel technologies and data streams for biodiversity monitoring?

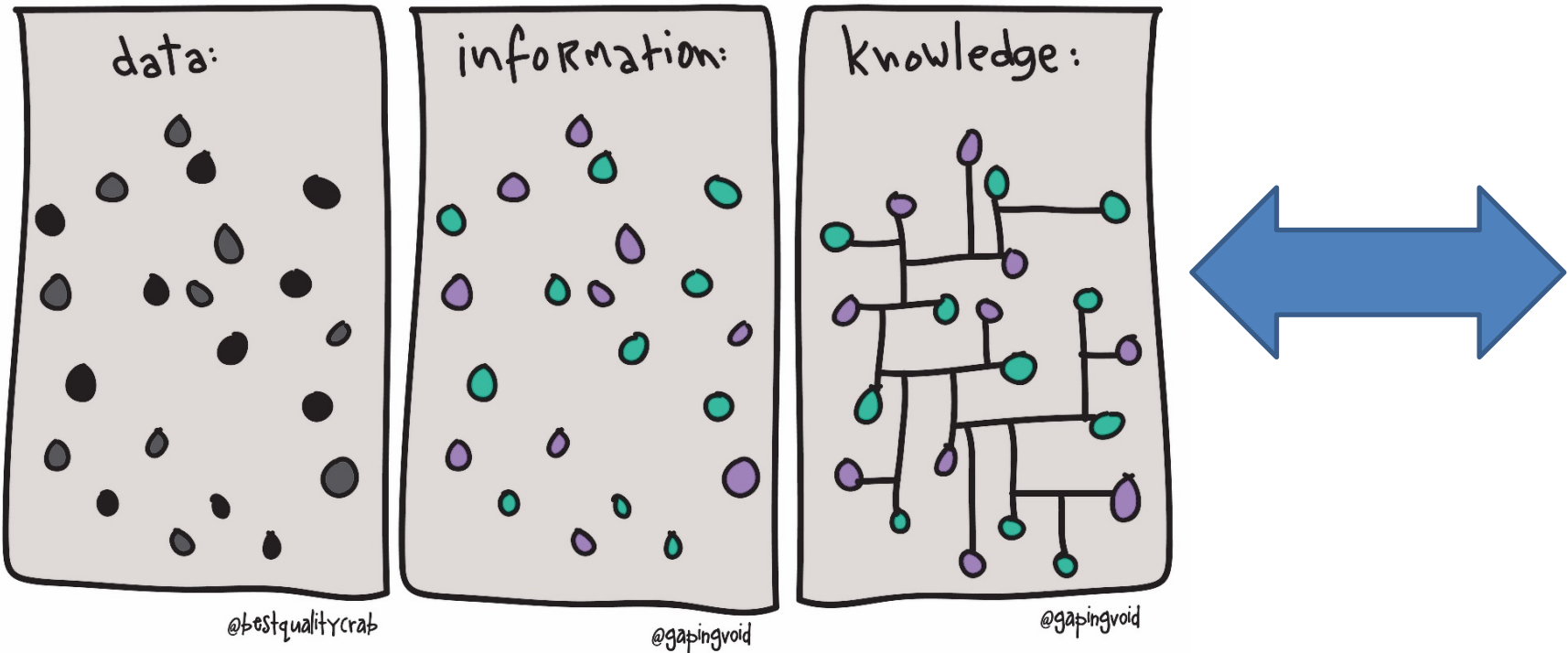
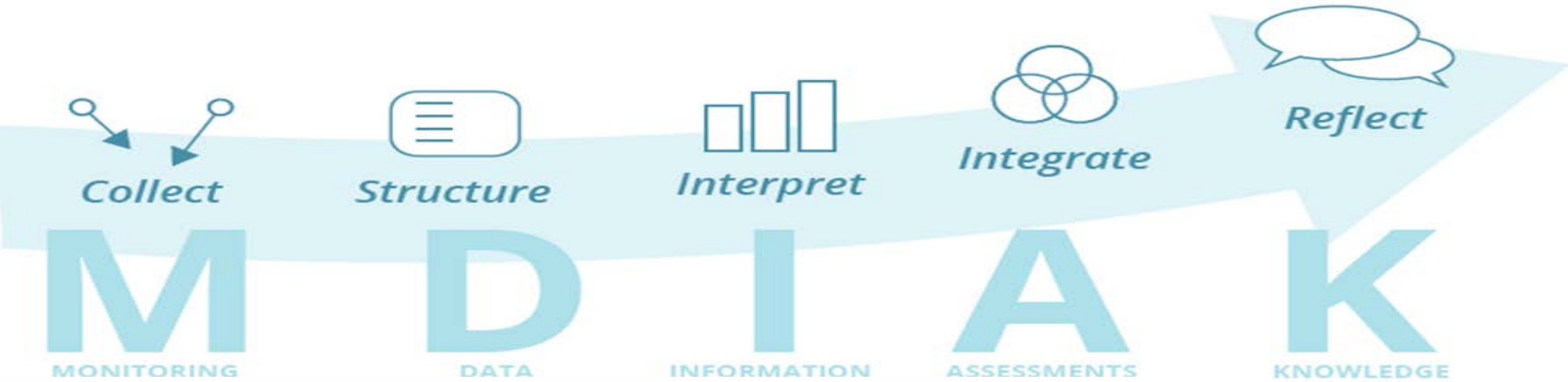
By Markus Erhaard, EEA

How to ensure FAIR data in the implementation of novel technologies and data streams for biodiversity monitoring?



Markus Erhard, European Environment Agency (EEA)
Towards a roadmap for implementation of novel biodiversity monitoring methods, 02 Feb. 2023

Knowledge integration



Policy Targets

A Union that strives for more

‘Europe must lead the transition to a healthy planet and a new digital world.’

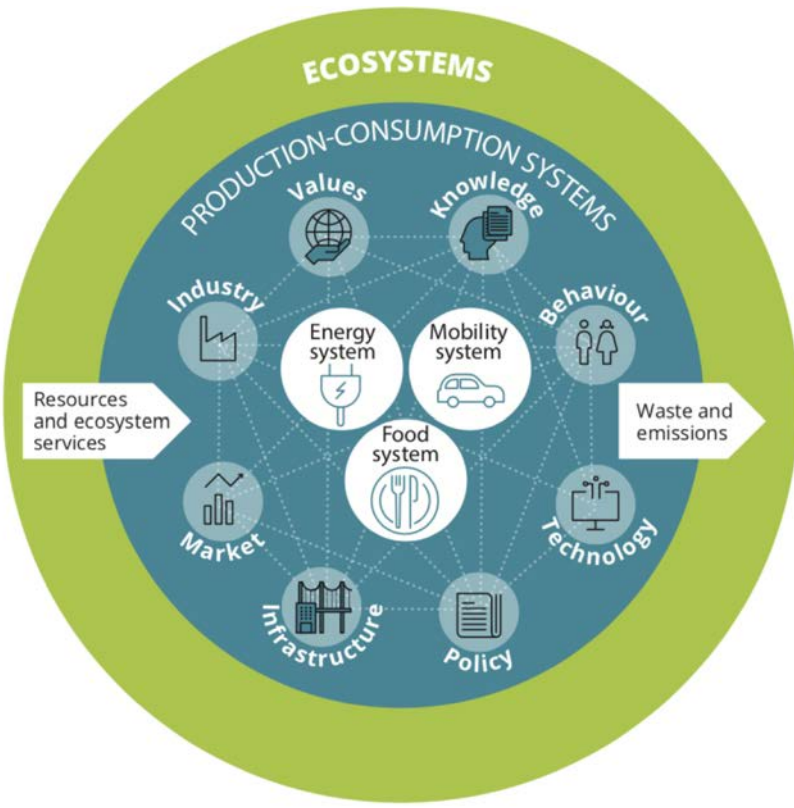
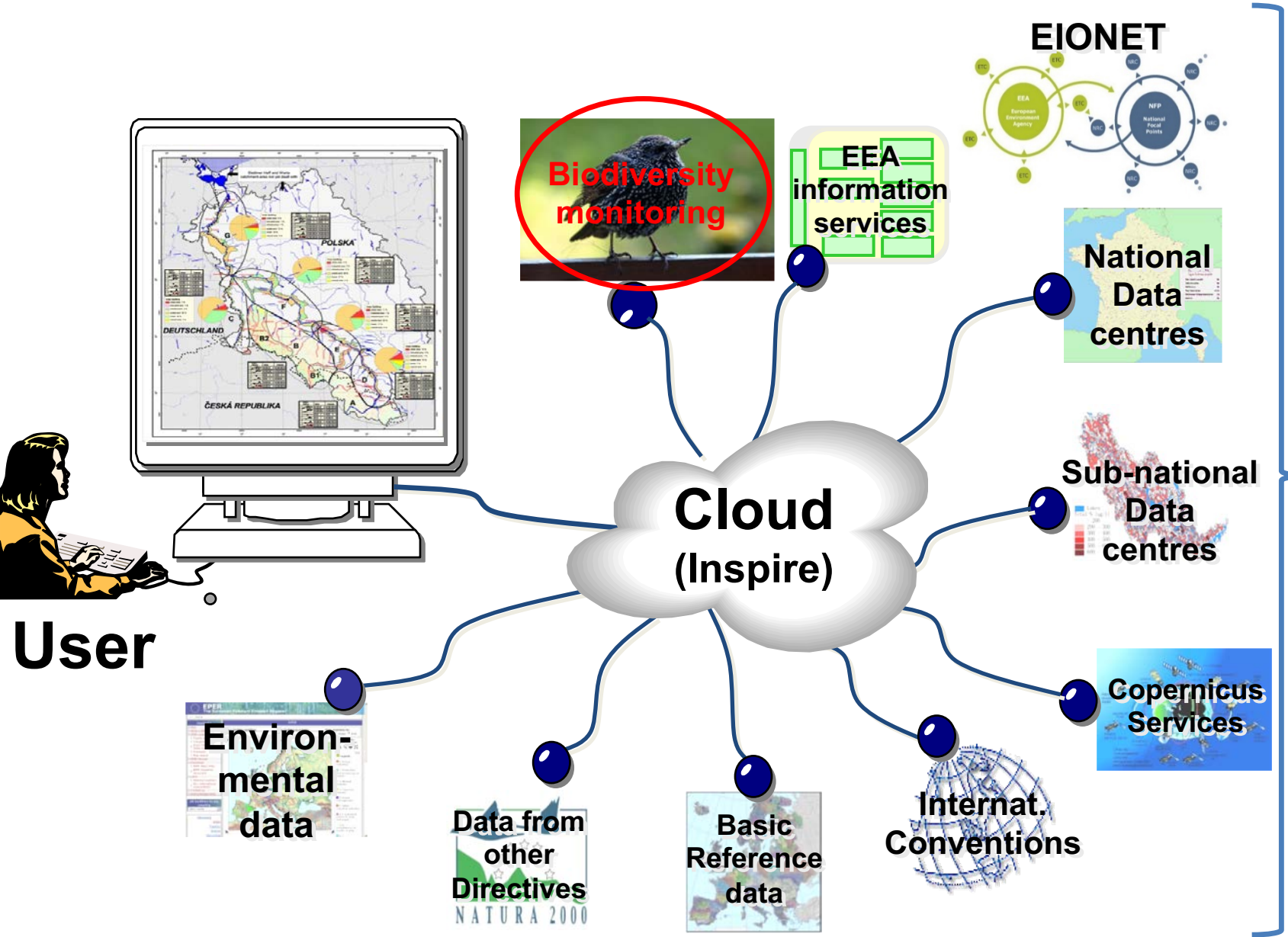
By candidate for President of the European Commission

Ursula von der Leyen

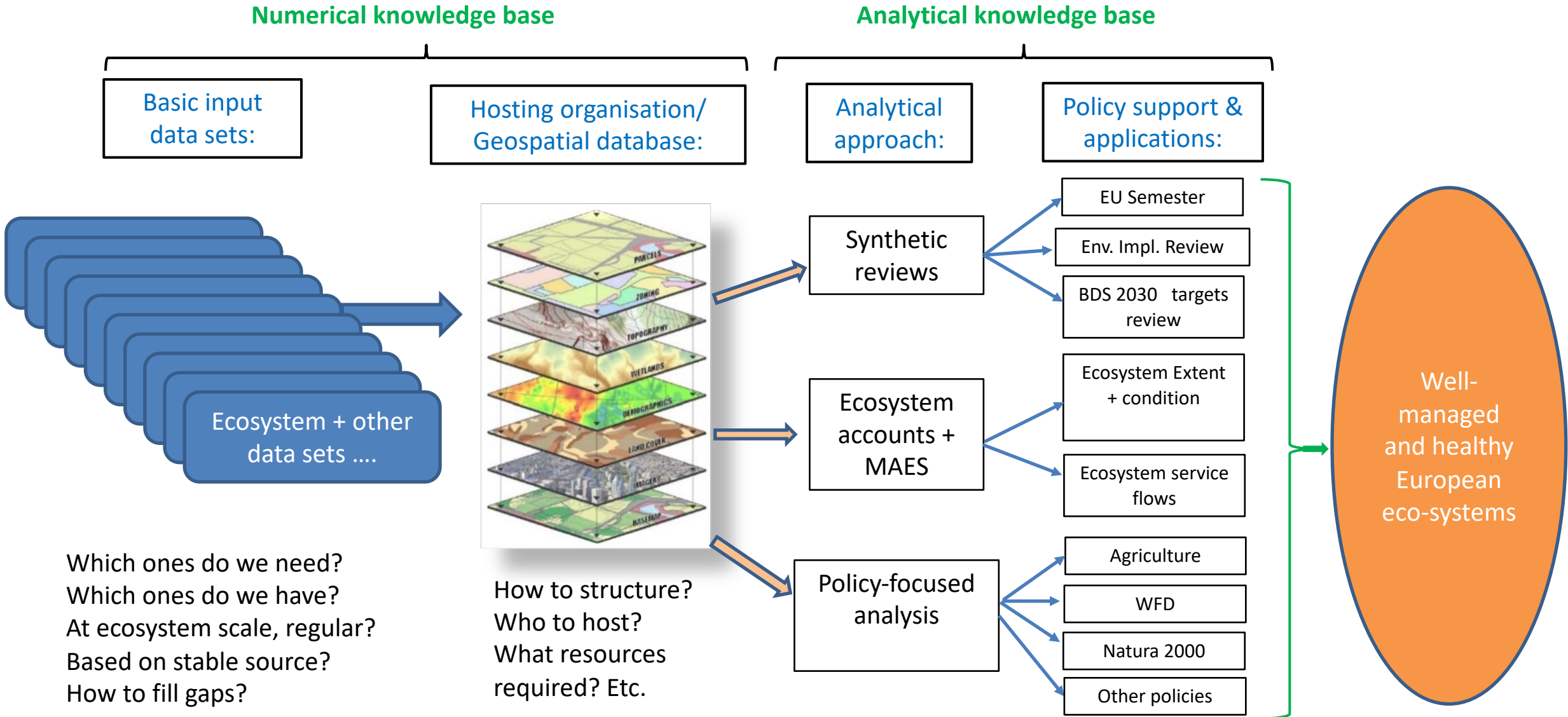


POLITICAL GUIDELINES FOR THE NEXT EUROPEAN COMMISSION 2019-2024

Data integration for assessments



Review of knowledge chain for ecosystem assessment

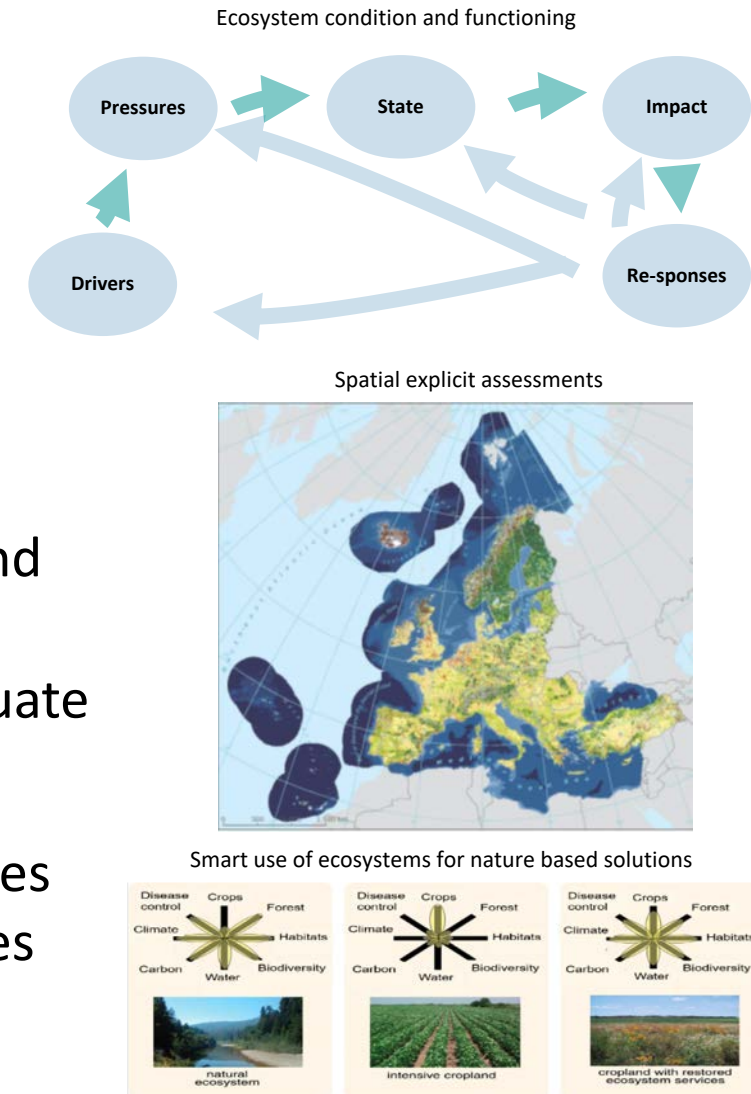


Biodiversity data – the challenge

- Biodiversity data tend to be limited and biased
 - taxonomically
 - spatially
 - temporally
 - ecologically
 - Not representative for overall biodiversity – biased towards charismatic species and presence/absence, lack of data on abundance
 - Not fit for purpose, skewing management decisions and policy
 - Policy making needs aggregated indicators – how to monitor, indicate and aggregate?
 - There is an institutional gap at EU level for gathering, compiling and hosting (biodiversity) data.
- Urgent need for more and better data to enhance our knowledge base

Way forward with FAIR data

- Novel technologies provide new opportunities to improve
 - Harmonise and standardise methods of monitoring, data storage and architecture also for re-calculation of time series and integration of existing monitoring schemes
 - Robust change detection needed, not single data point inventories
 - Towards ecosystem monitoring - contextualisation of biodiversity monitoring with environmental conditions in appropriate temporal and spatial scales
drivers, pressures, condition, impacts to provide knowledge for adequate responses (policy decision)
- **Co-development** with respective institutions to develop joint capacities no simple handing over of data bases / platforms / products / websites etc. without prior agreement and follow-up resourcing

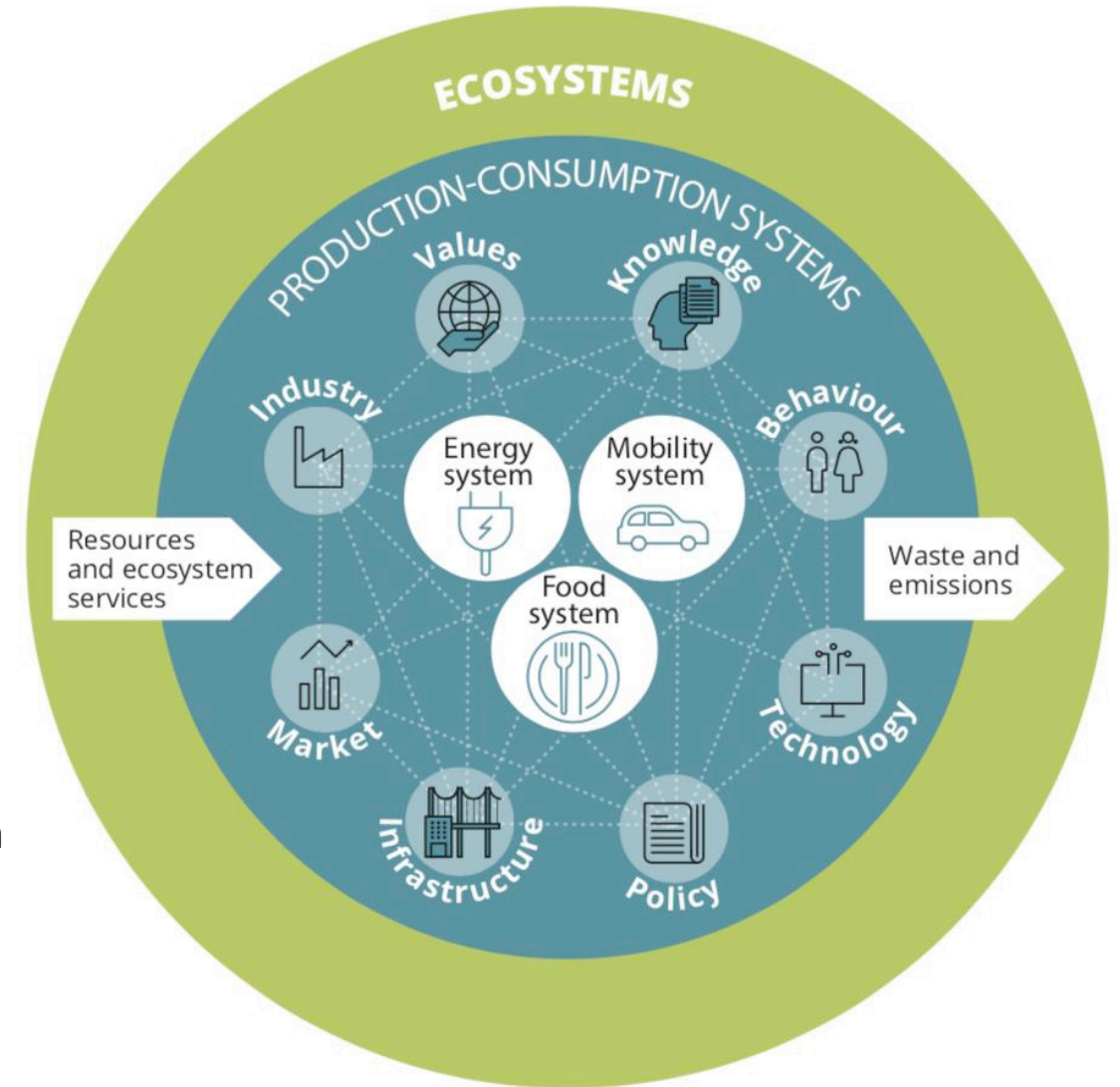


Thank you

**“We can only manage
what we have measured”**

Virginijus Sinkevičius

Commissioner for Environment, Oceans and Fisheries, European
Commission



Any questions?



Split in sub-groups

By Lars Dinesen, IFD and Cécile Mandon, FRB

4 sub-groups

GROUP 1: Remote sensing

(Satellites, Lidar, and drones for habitat status and condition)

Facilitator: Petteri Vihervaara
Support: Cécile Mandon

GROUP 2: Image-based approaches

(Species monitoring such as camera trapping, drones and thermal cameras)

Facilitator: Toke Høye
Support: Lars Dinesen

GROUP 3: Acoustic sensors (Permanently deployed for birds, bats, some marine mammals and terrestrial insects)

Facilitator: Hilde Eggermont
Support: Daniela Hamidovic

GROUP 4: Molecular methods (species and communities)

Facilitator: Florian Leese
Support: Ola Inghe and Guillaume Body

Potential cross-cutting topics which can be considered in the breakout groups

- What are the barriers (anchors) and opportunities (winds) for *implementation* (sail boat)
- Need for standardisation
- How to do this in practice (spatial and temporal sampling regimes)
- Need for reference libraries and training data
- Make sure to capture synergies among technologies
- Link to EU monitoring requirements for business and financial sectors?
- Use of Artificial Intelligence to improve monitoring

How to join your sub-group?

You will automatically join your sub-group and be invited to click on [join](#)

Join Breakout Room

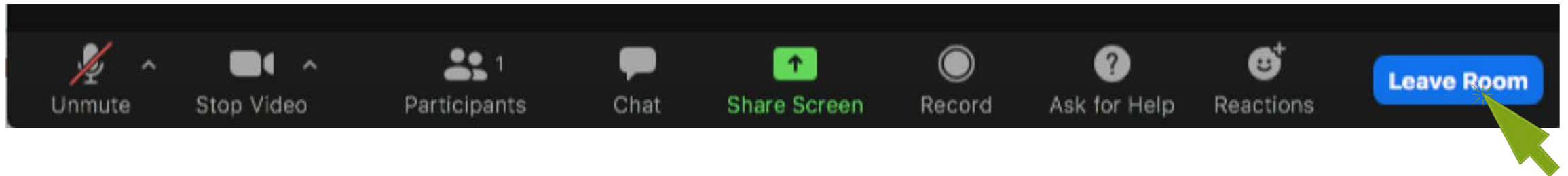
Biodiversa+ is inviting you to join Salle 1

Not Now

Join

At the end of the sub-group discussions

You will either be automatically brought back in plenary or you will have the possibility to click on [leave room](#)



Let's take a break!

**Be back at 10.50am
in sub-groups**



Welcome back!

Sub-group objectives

- Quick round table
- Sailboat brainstorming session

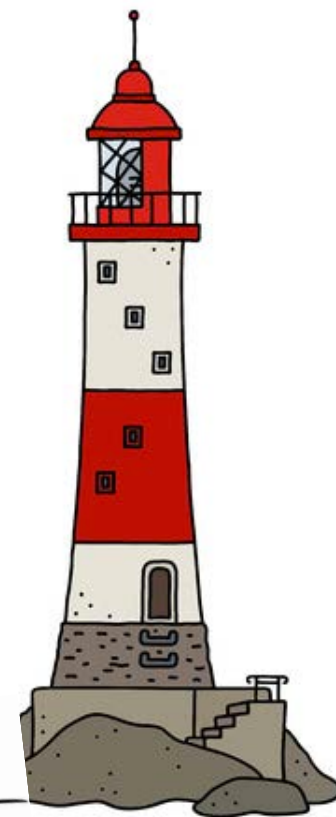
SailBoat

Boat = our group/ Biodiversa+

Winds: What
contributes,
as of now



Anchors: What
hinders, as of now



Lighthouse: Enhance
the upscale and
operationalisation of
biodiversity monitoring
novel methods and
approaches in Europe

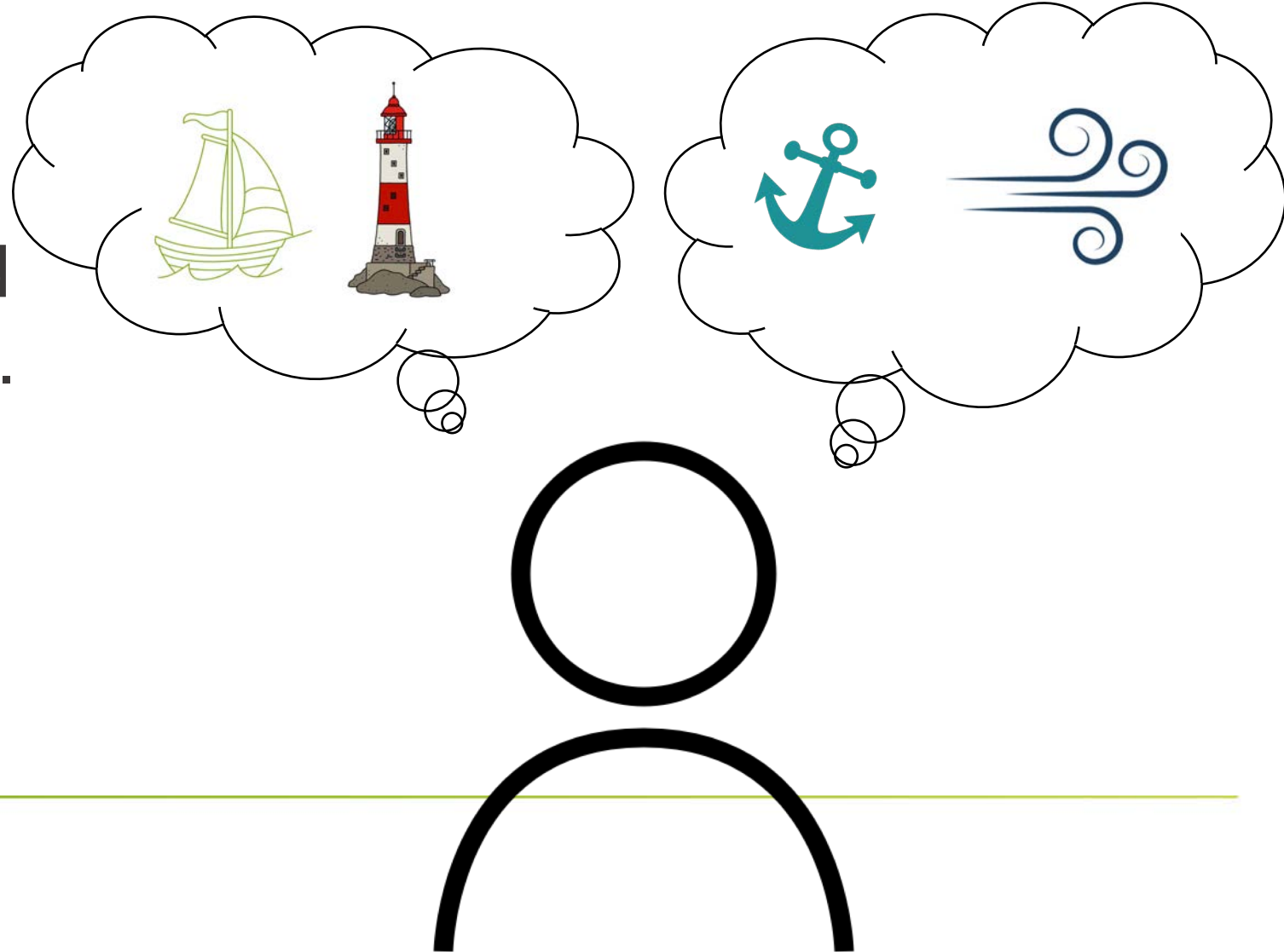
First Step : Individual Work

During 10 minutes :

→ Identify « winds » and « anchors » in Jamboard.

Winds: blue post-its

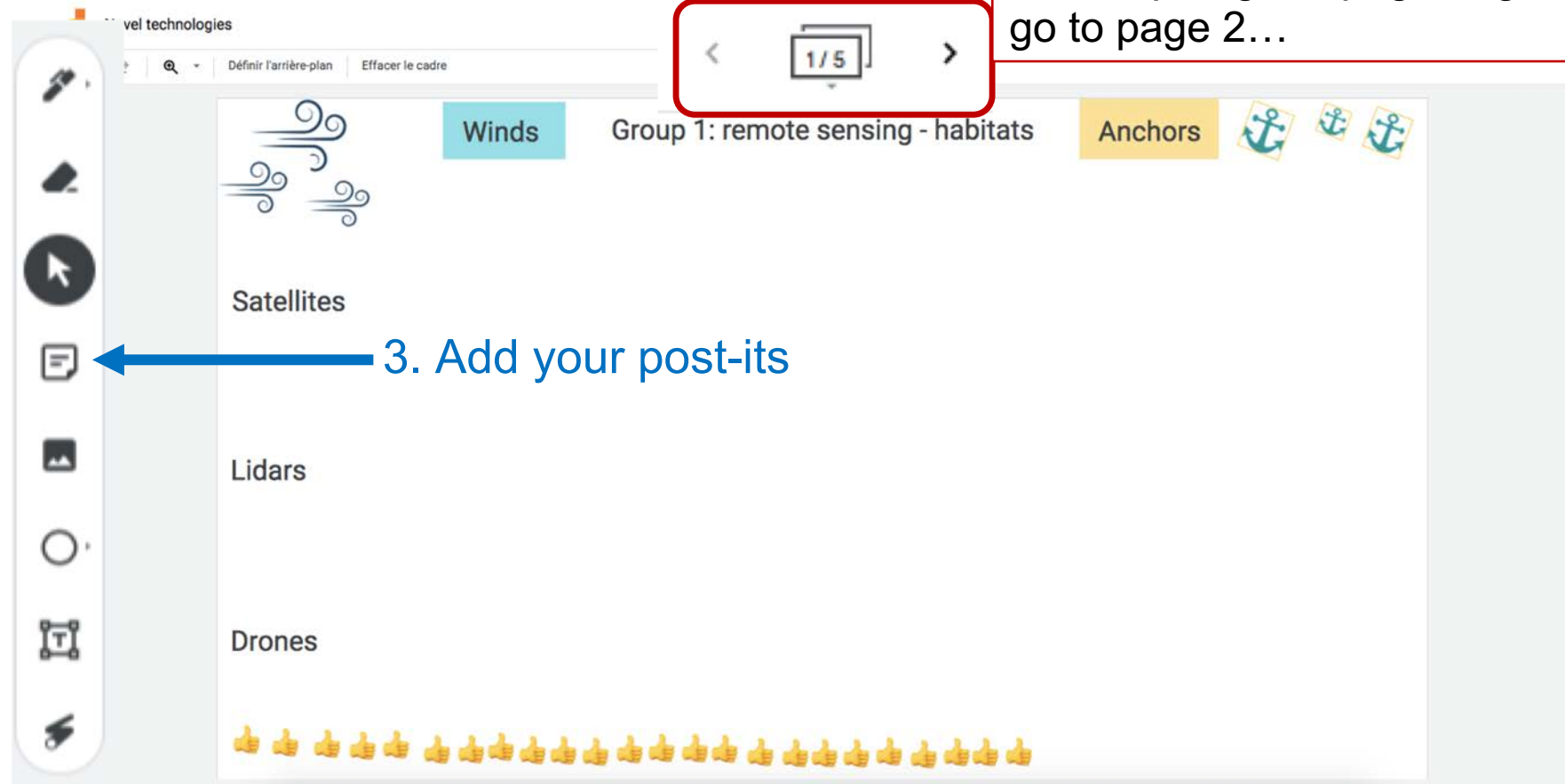
Anchors: yellow post-its



First step: on Jamboard, how does it work?

1. Click on the link: <https://jamboard.google.com/d/1i32YNdLOwzQ0raibx4PYx--ppwd37Aor8vJ5PC7Peyg/edit?usp=sharing>

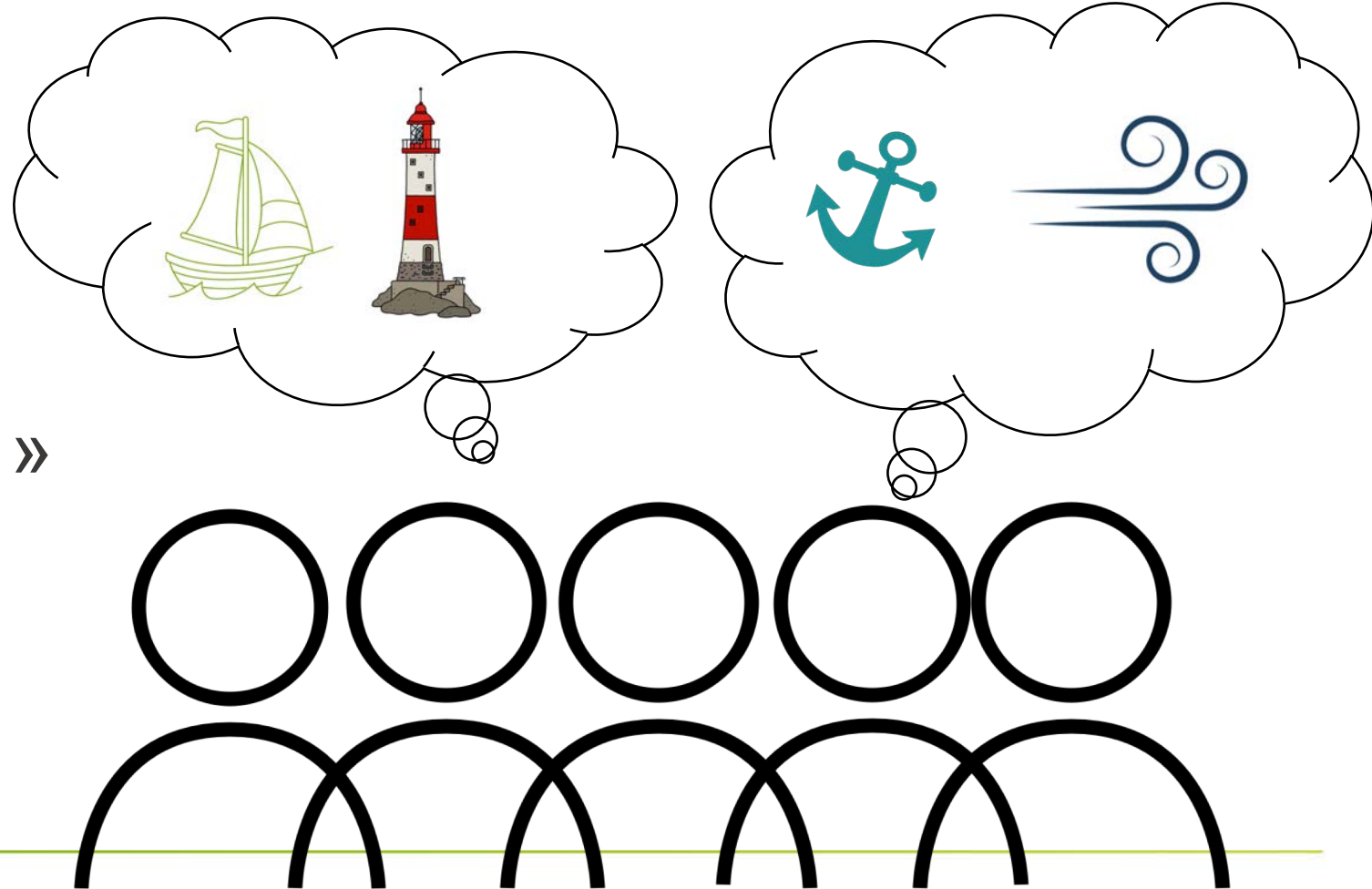
2. Group 1: go to page 1, group 2 go to page 2...



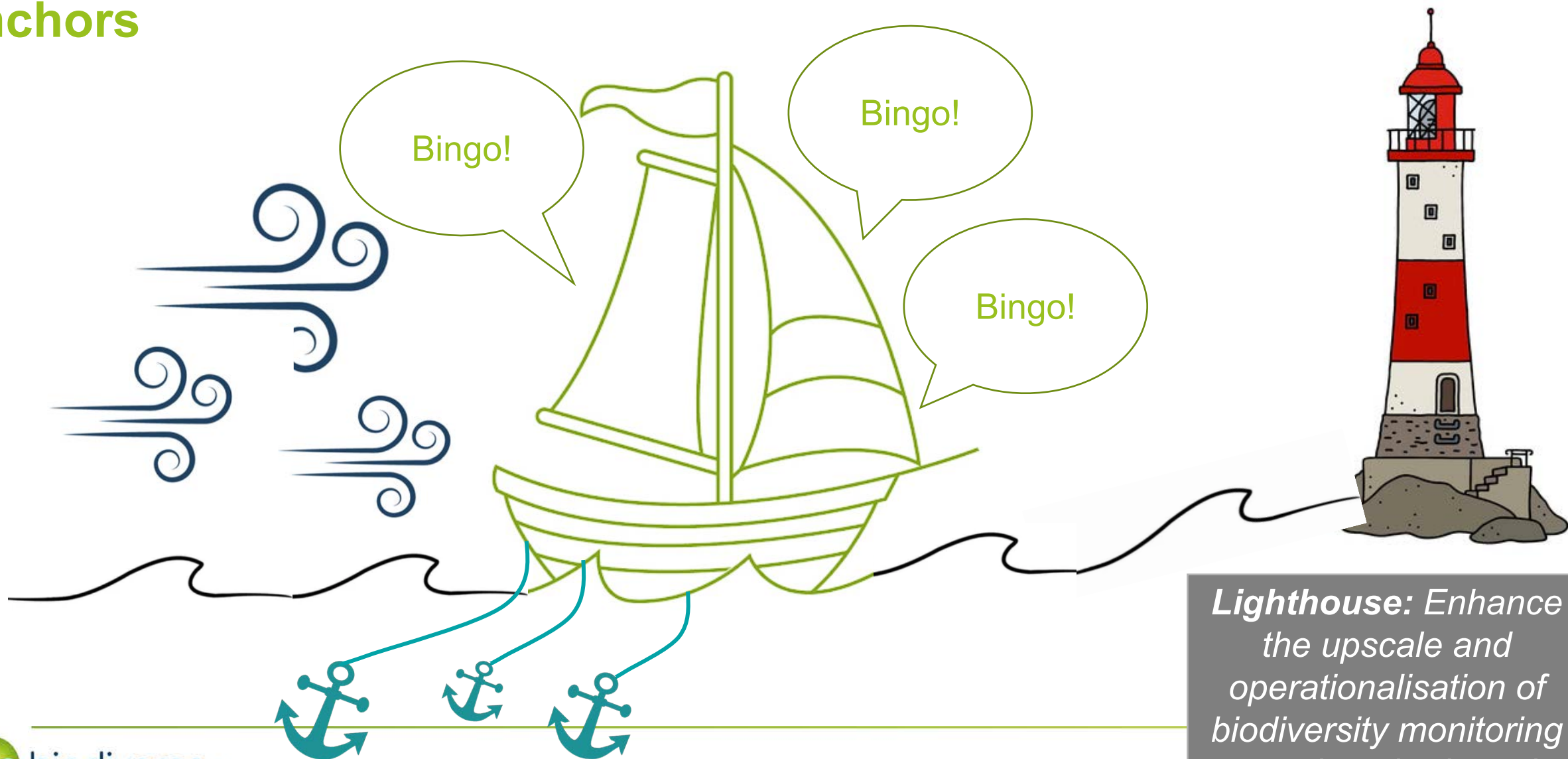
Second Step : Group Work

During 30 minutes :

→ Share and pool the
« **winds** » and « **anchors** »
individually identified

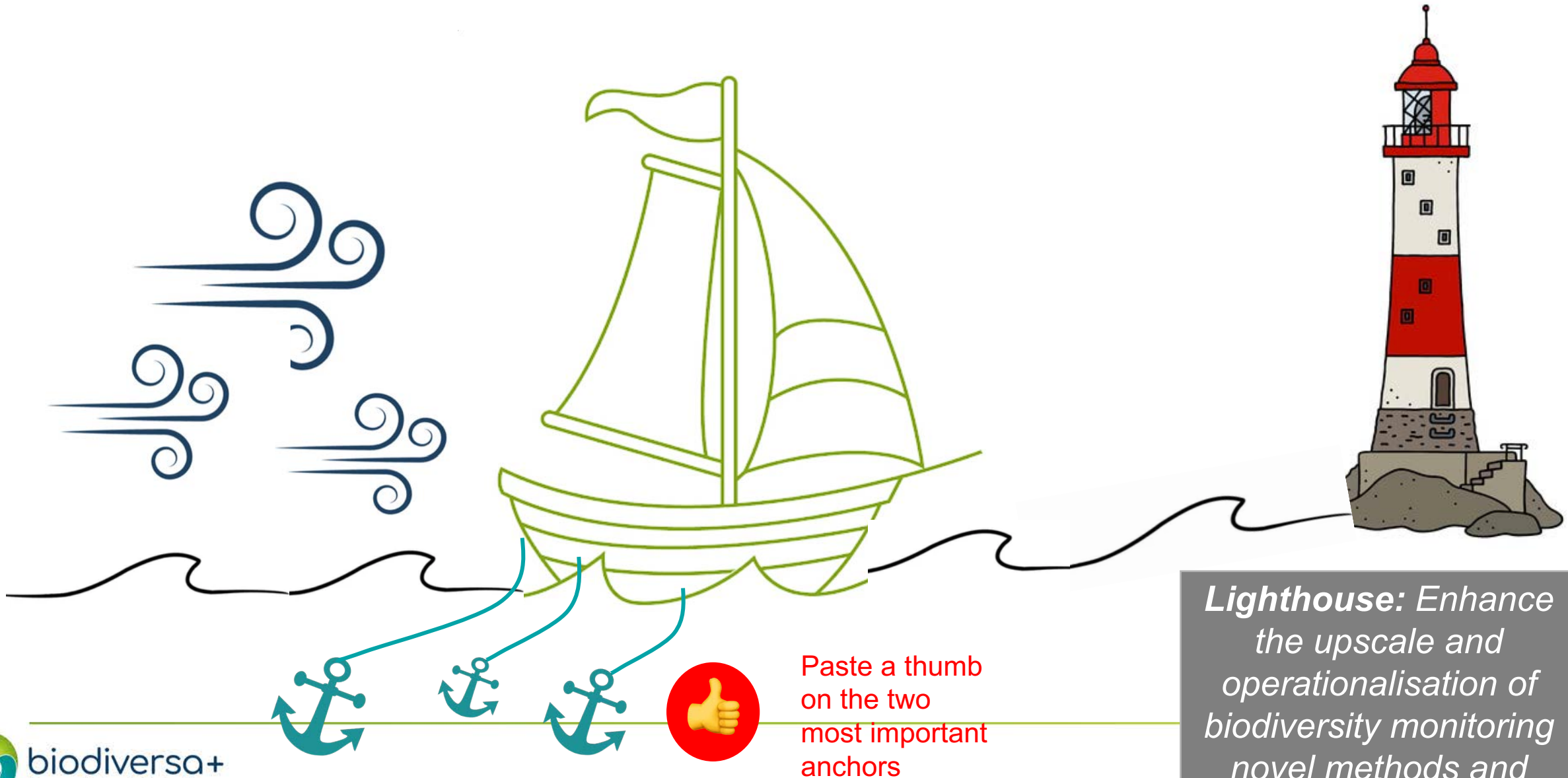


Third step: present and articulate groups' winds and anchors



***Lighthouse:** Enhance the upscale and operationalisation of biodiversity monitoring novel methods and approaches in Europe*

Fourth steps: Prioritize the anchors: what are the biggest anchors?



***Lighthouse:** Enhance the upscale and operationalisation of biodiversity monitoring novel methods and approaches in Europe*

Fifth step: dig into the anchors in groups

Guidelines :



- For the biggest anchor
- 15 min
 - > Discuss **3 first steps** that could help to address the anchor
 - > Discuss **how Biodiversa+ could help** in achieving these steps
 - > Discuss **who else** needs to “be on the boat”.

Plenary wrap-up

Conclusion of the workshop and next steps

Follow-up of the workshop

- Development of a roadmap guiding the Biodiversa+ activities (by Biodiversa+)
- The experts attending the workshop will have an opportunity to provide feedback



biodiversa+
European Biodiversity Partnership

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