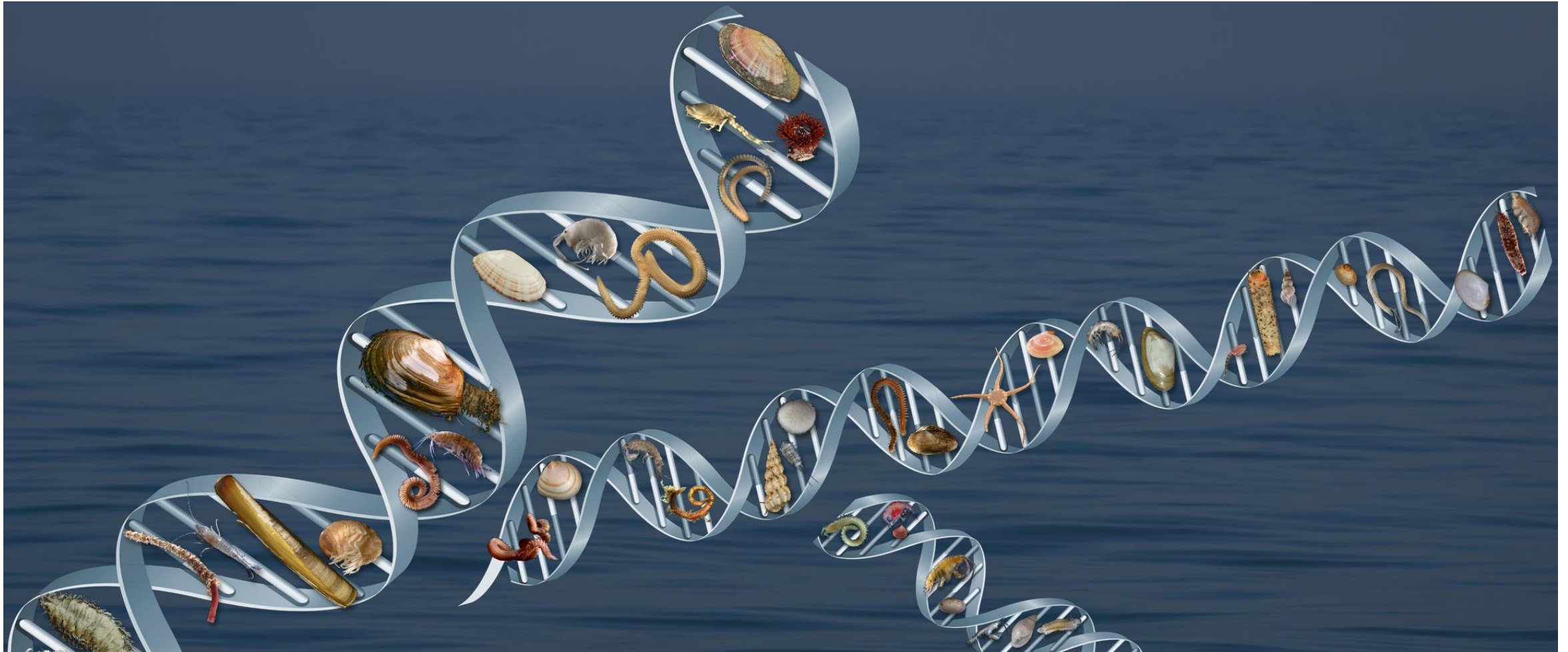


Towards implementation of DNA-based methods



Strengths and weaknesses of DNA-based methods

Faster and cheaper +

High throughput +

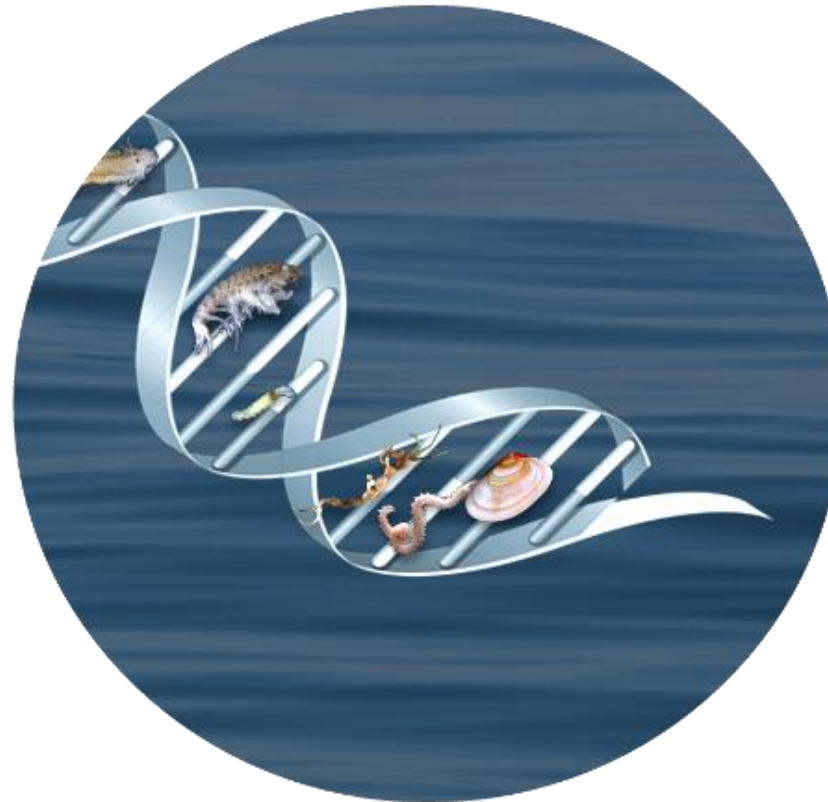
Repeatable & Robust +

Standardisation across regions +

Ecological/community patterns +

Often more species detected +

Early detection of 'new' species +



- No quantitative info

- More prone to technical biases

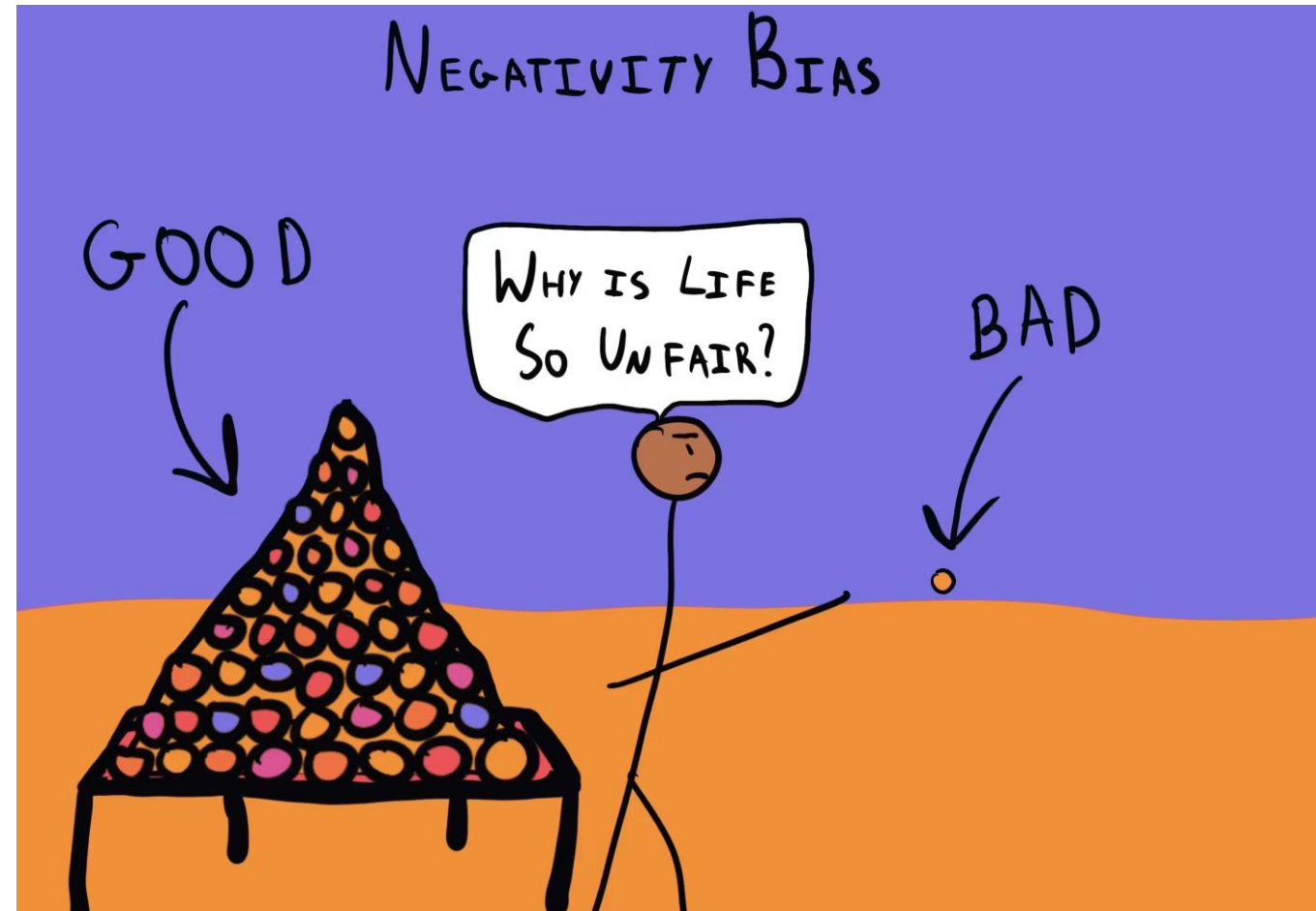
- Reliant on reference libraries

- Interruption of time series
(~legal framework)

- Lack of trust

Minuses hamper routine implementation

- Negative aspects prevail over the positive
- People tend to stick to what they know



First studies illustrating the potential for bulk DNA metabarcoding (e.g. Lejzerowicz et al. 2015, Aylagas et al. 2016,...)

Towards implementation

Ignorance and scepticism at stakeholder level limiting uptake

First studies illustrating the potential for bulk DNA metabarcoding (e.g. Lejzerowicz et al. 2015, Aylagas et al. 2016,...)

Concerted effort across NS countries for 'proof of concept' on what is possible by conducting pilot studies in collaboration with stakeholders

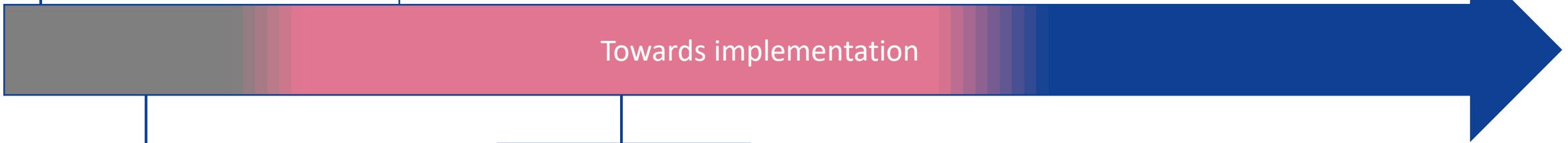
- ✓ Extra 'instrument' in the monitoring toolkit (not abandoning traditional methods)
- ✓ Complementarity is key!

Towards implementation

Scepticism and ignorance at stakeholder level

First studies illustrating the potential for bulk DNA metabarcoding (e.g. Lejzerowicz et al. 2015, Aylagas et al. 2016,...)

Concerted effort across NS countries for 'proof of concept' on what is possible by conducting pilot studies in collaboration with stakeholders



Scepticism and ignorance at stakeholder level

Reach consensus on methodology (protocols, workflow)

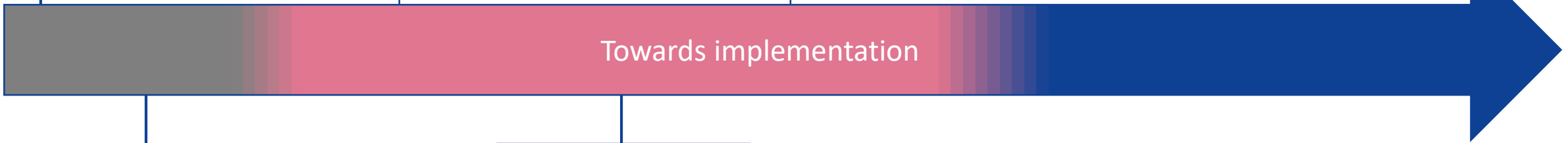
- ✓ Mature standardized bulk metabarcoding methodology
- ✓ Increased standardization of biodiversity data at regional level

First studies illustrating the potential for bulk DNA metabarcoding (e.g. Lejzerowicz et al. 2015, Aylagas et al. 2016,...)

Concerted effort across NS countries for 'proof of concept' on what is possible by conducting pilot studies in collaboration with stakeholders

Tools to help for implementation and communication with stakeholders

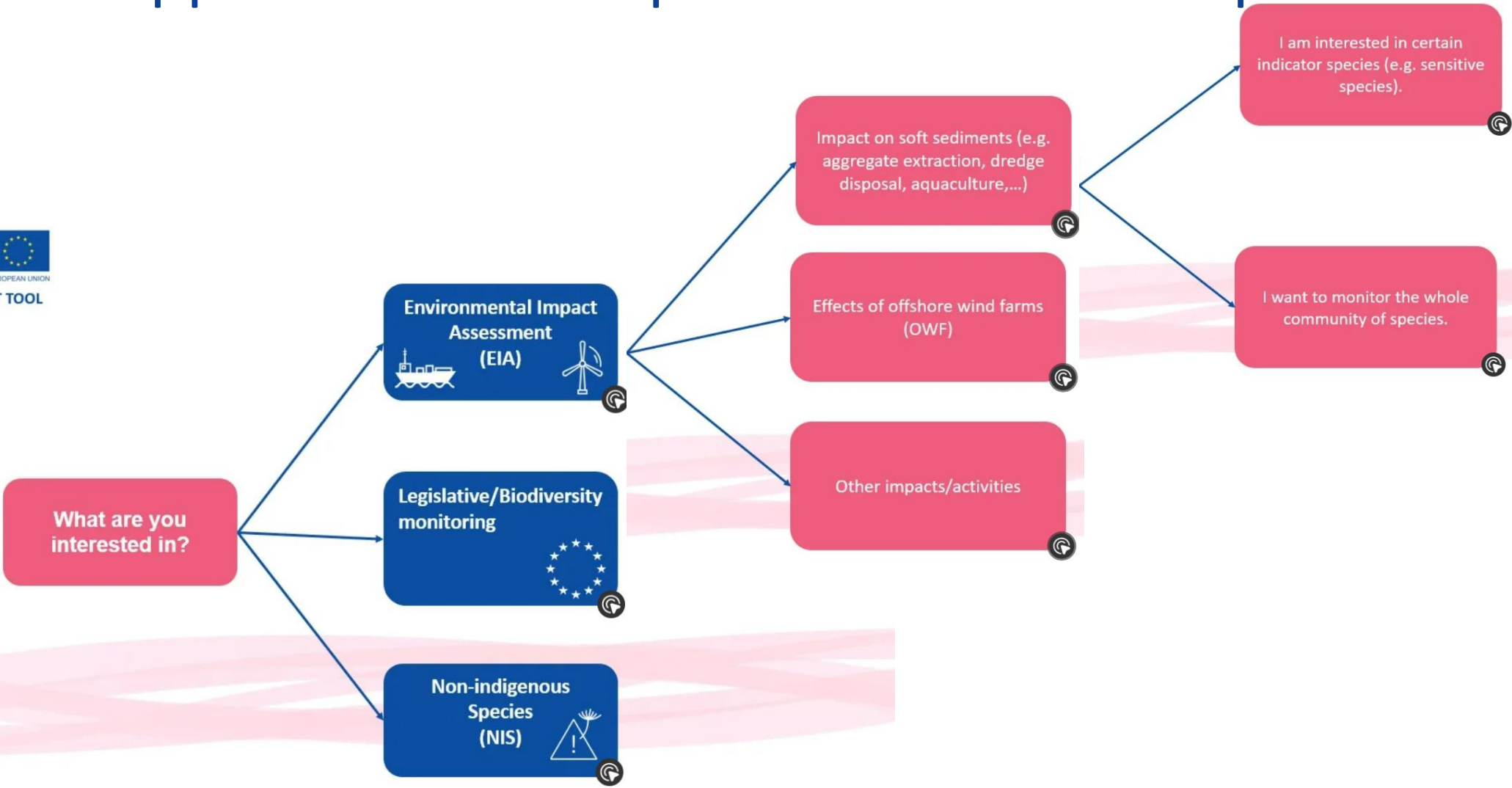
- ✓ Reference library
- ✓ Protocols
- ✓ Interactive decision tree



Scepticism and ignorance at stakeholder level

Reach consensus on methodology (protocols, workflow)

Decision support tree - example soft sediment impact



<https://www.geans.eu/decision-support-tool-0>



Decision support example – soft sediment impact

I want to monitor the whole community of species

I am mainly interested in general benthic community patterns or trends, without need for information on life stages, abundance or biomass.

Community trends can be assessed solely **using bulk metabarcoding** of grab samples. Bulk metabarcoding provides a species inventory for the DNA sequences present in the bulk sample. There will be differences between species lists generated from traditional methods, but the general trends are similar. This has advantages over morphological identification because it is less expensive and faster (46 up to 66%), requires less taxonomic expertise, and enables accurate identification of difficult species groups.

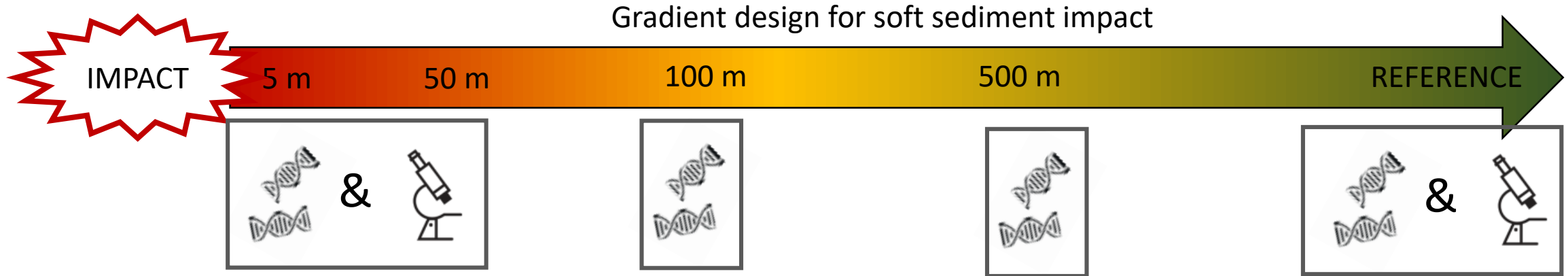
I need the full suite of benthic community data, including species diversity and community patterns, and information on life stages, abundance or biomass.

You will need to take a **combined approach of traditional morphological analysis with bulk metabarcoding**. DNA metabarcoding cannot give information on life history or biomass and can give only qualitative information on abundance. Traditional morphological analysis cannot identify hard-to-identify specimens (eg juveniles, or taxonomic groups with few diagnostic characters) Metabarcoding of the bulk samples, when combined with morphology, can improve resolution of identification (particularly in hard-to-identify species groups), therefore providing a more accurate species list, while traditional morphology provides more detailed quantitative information.

I want data for multimetric indicators to assess environmental health status

<https://www.geans.eu/decision-support-tool-0>

What could a combined approach look like?

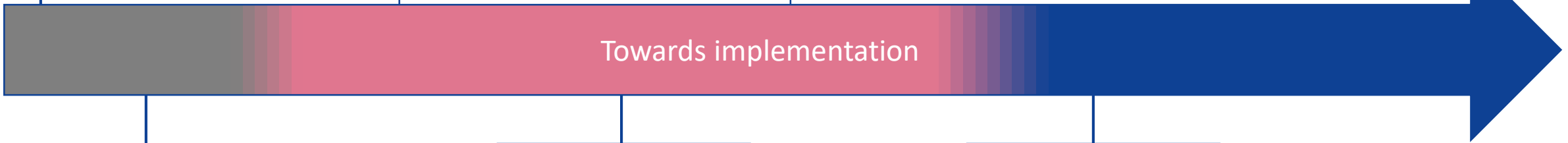


- ✓ Rapid assessment to detect changes using DNA-based method
- ✓ More comprehensive species list
- ✓ No loss of quantitative information at 'crucial' location
- ✓ Increased effort possible for similar budget (e.g. 4/5 instead of 3 morphological replicates)

First studies illustrating the potential for bulk DNA metabarcoding (e.g. Lejzerowicz et al. 2015, Aylagas et al. 2016,...)

Concerted effort across NS countries for 'proof of concept' on what is possible by conducting pilot studies in collaboration with stakeholders

Tools to help for implementation and communication with stakeholders



Scepticism and ignorance at stakeholder level

Reach consensus on methodology (protocols, workflow)

Continued collaboration to close remaining gaps

Further actions needed for implementation

- ✓ Centralised and standardized reliable reference libraries
- ✓ Regional guidelines and methodological standards
- ✓ Proper data management – FAIR and including provenance tracking
- ✓ Trained people
- ✓ Continued communication with stakeholders
- ✓ Include local taxonomic/ecological knowledge

First studies illustrating the potential for bulk DNA metabarcoding (e.g. Lejzerowicz et al. 2015, Aylagas et al. 2016,...)

Concerted effort across NS countries for 'proof of concept' on what is possible by conducting pilot studies in collaboration with stakeholders

Tools to help for implementation and communication with stakeholders

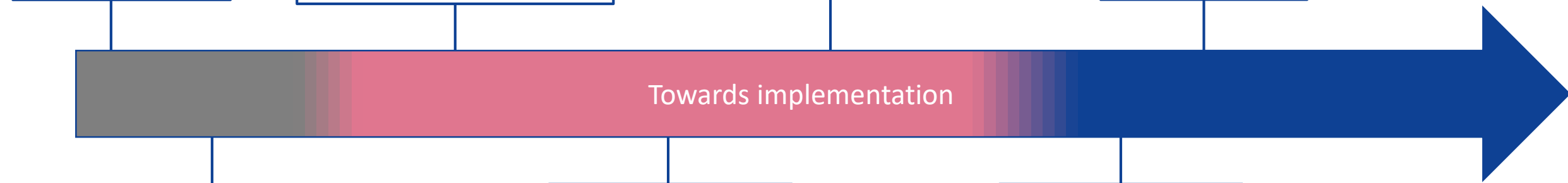
Keep it on agenda and lobby by funding agencies

Towards implementation

Scepticism and ignorance at stakeholder level

Reach consensus on methodology (protocols, workflow)

Continued collaboration to close remaining gaps



First studies illustrating the potential for bulk DNA metabarcoding (e.g. Lejzerowicz et al. 2015, Aylagas et al. 2016,...)

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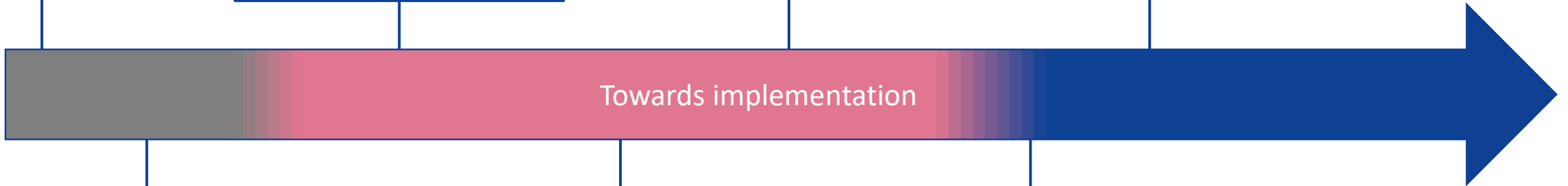
Routine application leading to high resolution biodiversity monitoring of our seas and oceans

Towards implementation

Scepticism and ignorance at stakeholder level

Reach consensus on methodology (protocols, workflow)

Continued collaboration to close remaining gaps

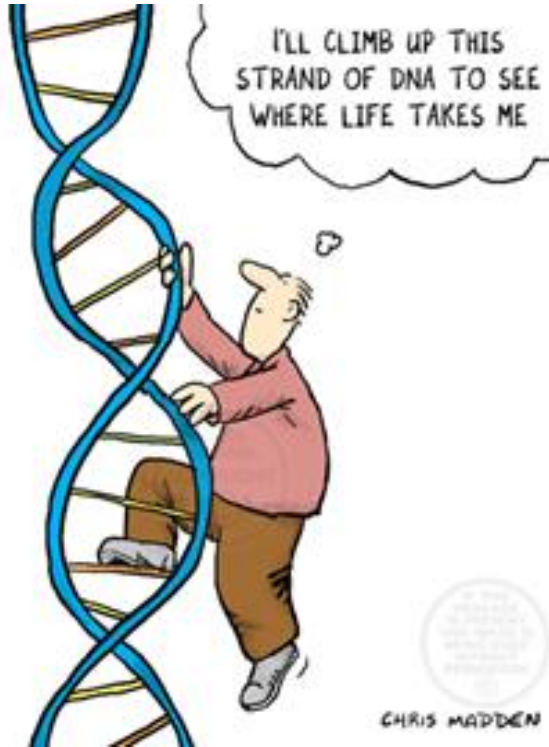


Concluding message

Integrate DNA-based methods in your (national) monitoring programmes!

- ✓ Fastest way to routine application
- ✓ Construction of time series in parallel with traditional ones
- ✓ Make use of the available GEANS outputs 😊

THANK YOU!
QUESTIONS?



CONTACT US

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