

Environmental impact assessment 2.0:

Genetic identification as a faster and cheaper method for marine environmental monitoring.

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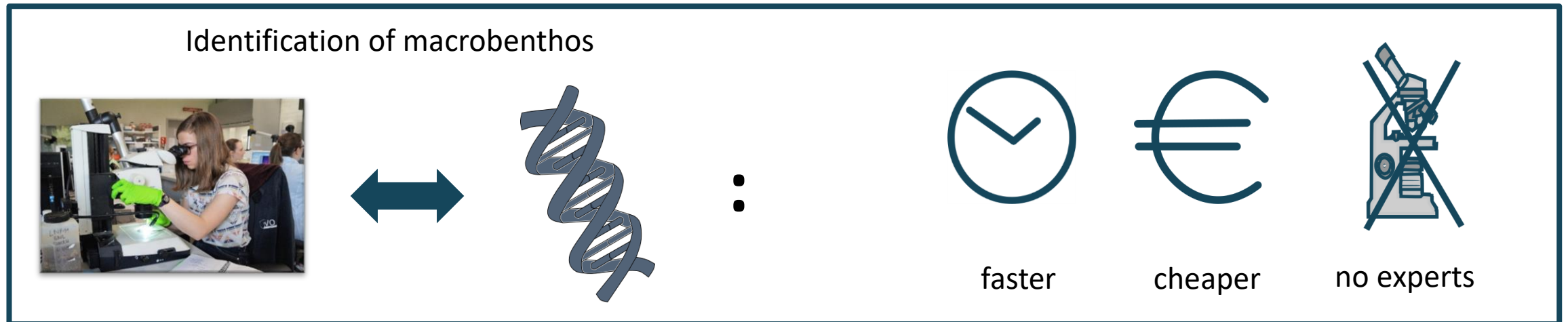
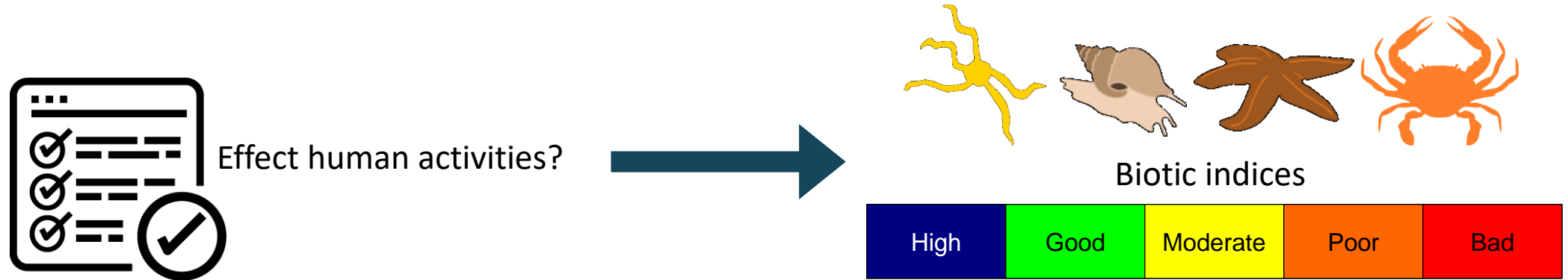


ILVO

 **Interreg**
North Sea Region
GEANS
European Regional Development Fund



Environmental Impact Assessments (EIAs)



Morphological or genetic identification?

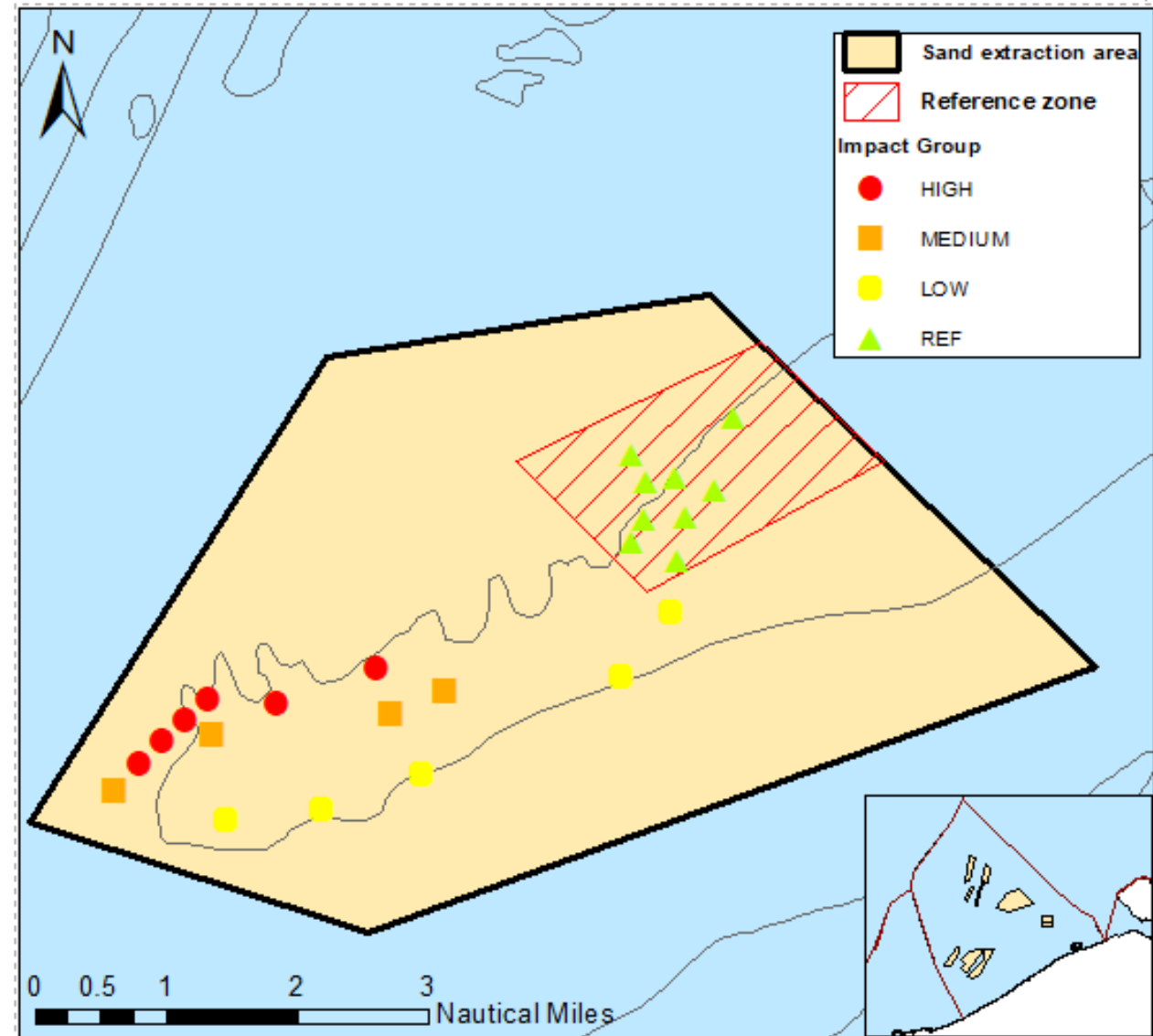


Environmental impact assessment 2.0:

Genetic identification as a faster and cheaper method for marine environmental monitoring.

Pilot project: Impact of sand extraction

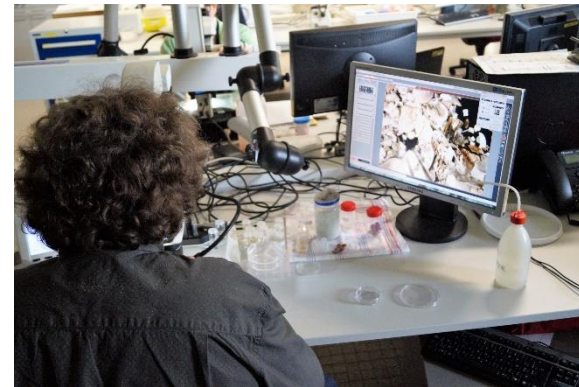
- Belgian Part of the North Sea
- Thorntonbank
- Samples:
 - 9 reference stations
 - 15 impact stations
 - High
 - Medium
 - Low



Sampling and processing



Traditional benthic identification



Sampling and processing



Traditional morphological identification



Genetic identification



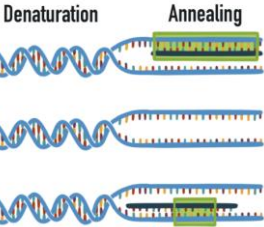
Subsampling



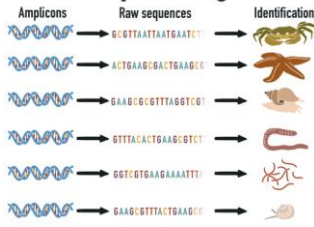
DNA Extraction



PCR Amplification



Sequencing



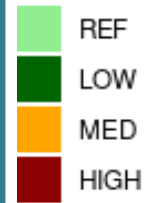
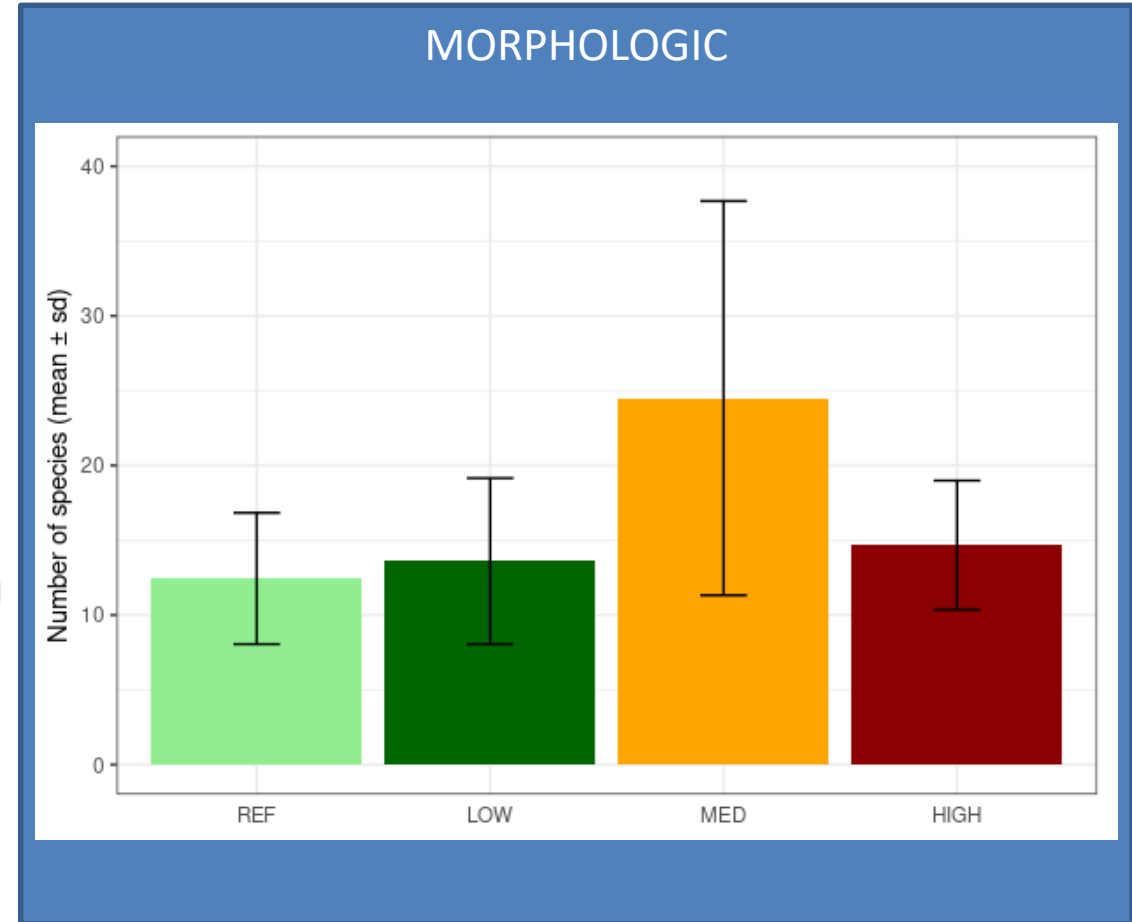
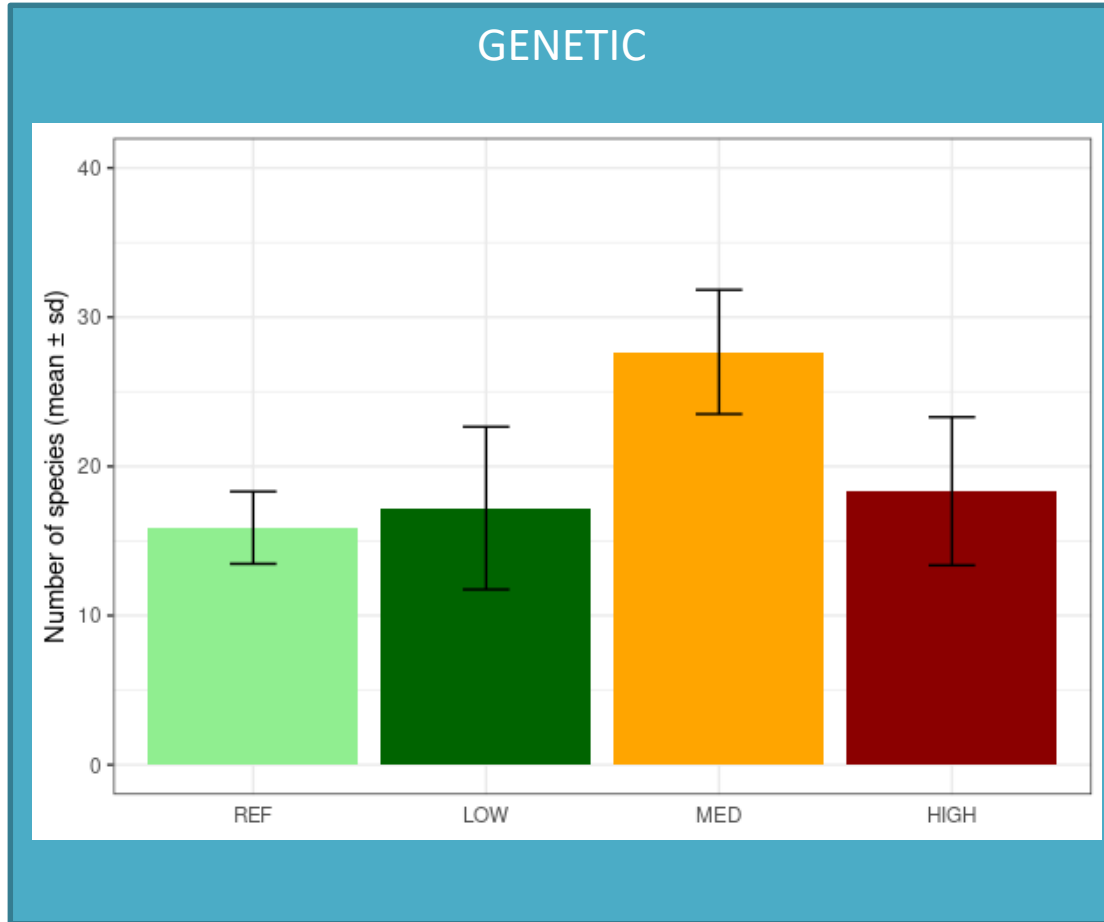
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Reference database

© Aline Joustra

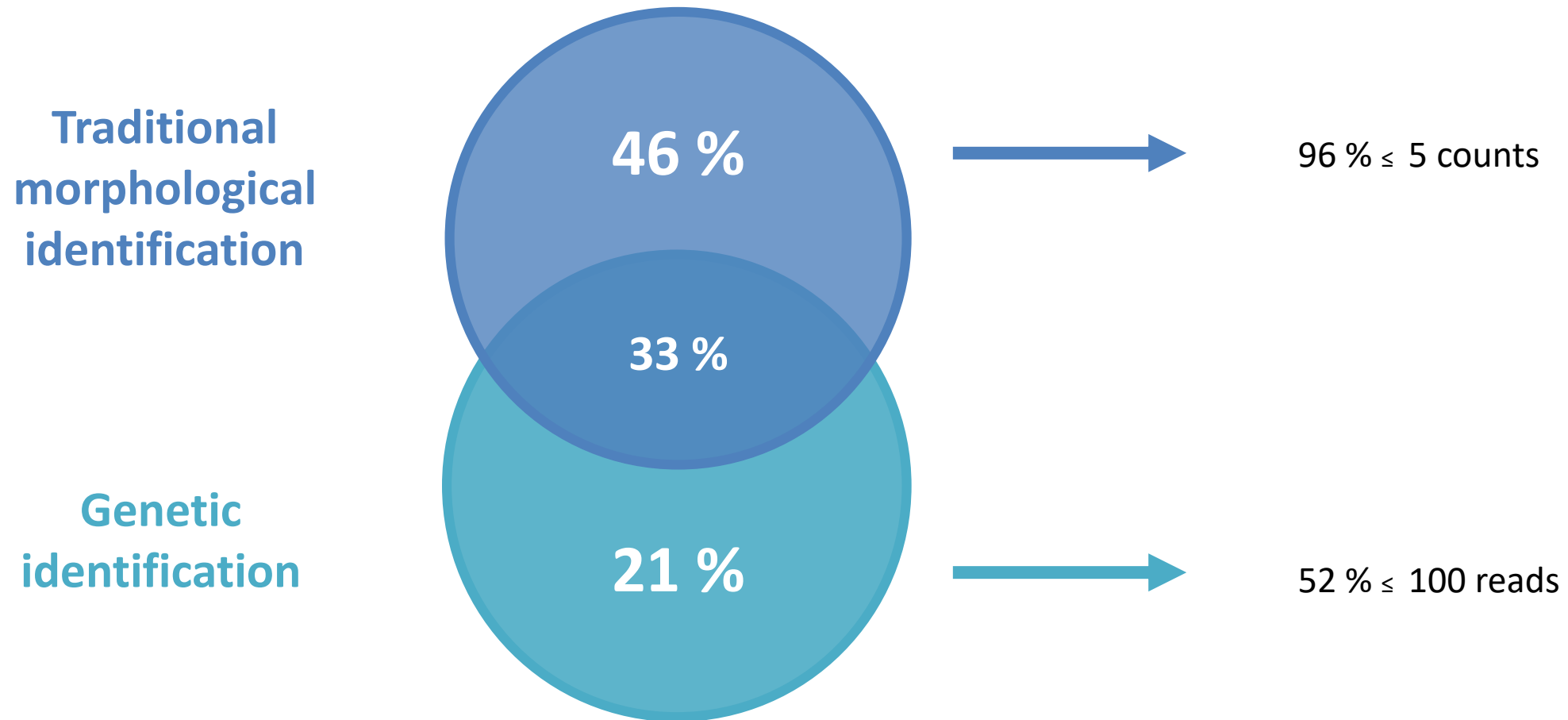
Comparison of genetic and morphologic identification

1) Alpha diversity



Comparison of genetic and morphologic identification

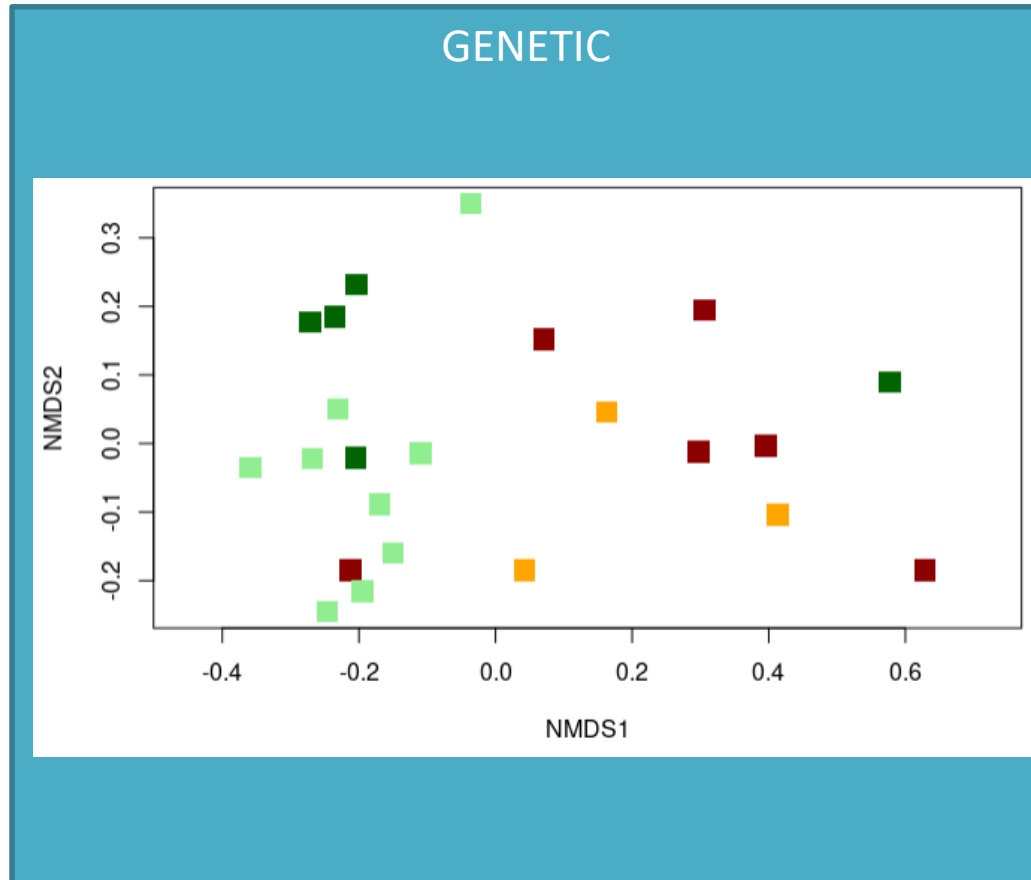
1) Alpha diversity



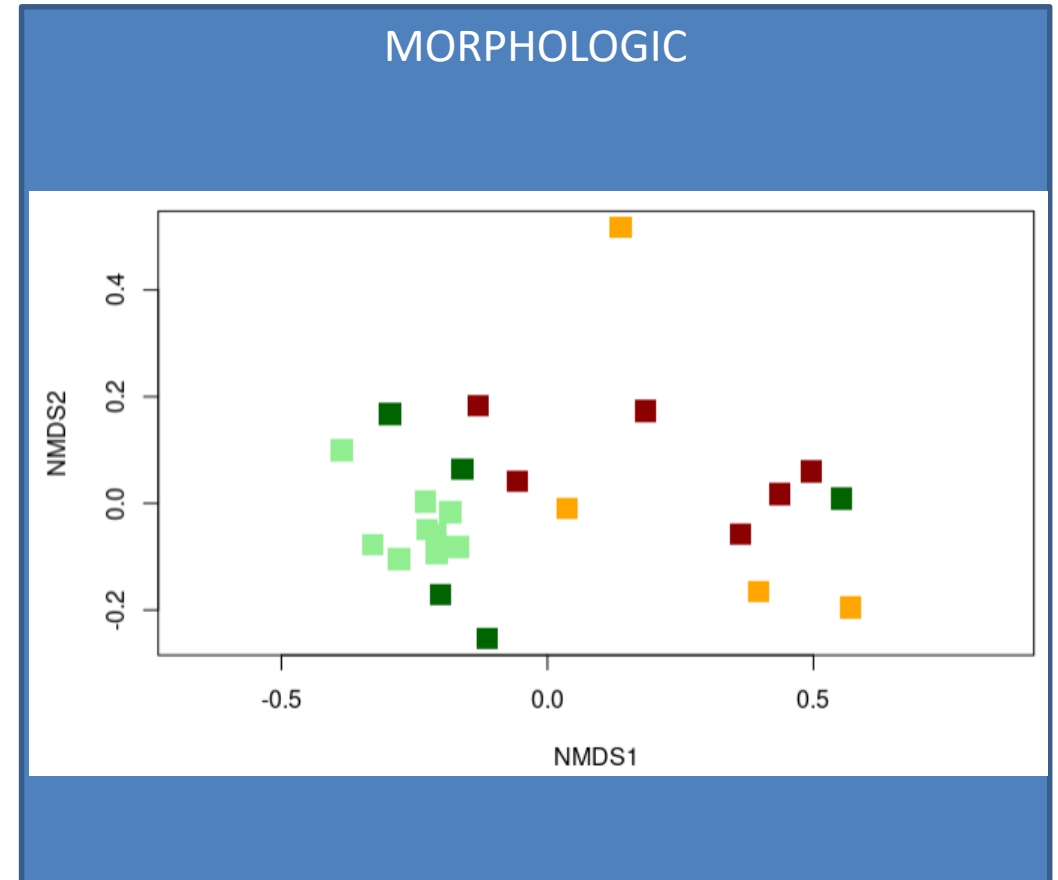
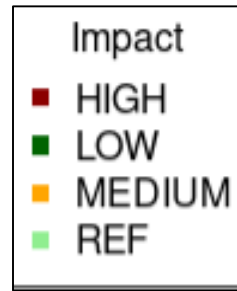
- High number of species detected only by one method, but the abundant species are found by both methods.

Comparison of genetic and morphologic identification

2) Beta diversity




Bray-Curtis

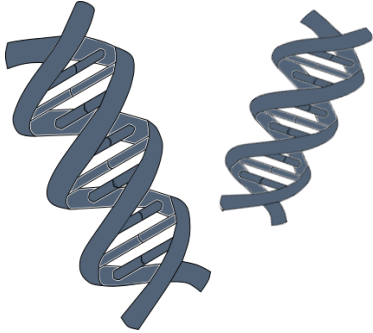


- Similar beta diversity patterns

Comparison of genetic and morphologic identification

3) Cost / Time calculation

Traditional benthic identification		
	TIME	COSTS
	67 hours 1 minutes	6 514,37 euro

Genetic identification		
	TIME (hands-on)	COSTS
	38 hours 7 minutes	4 848,39 euro

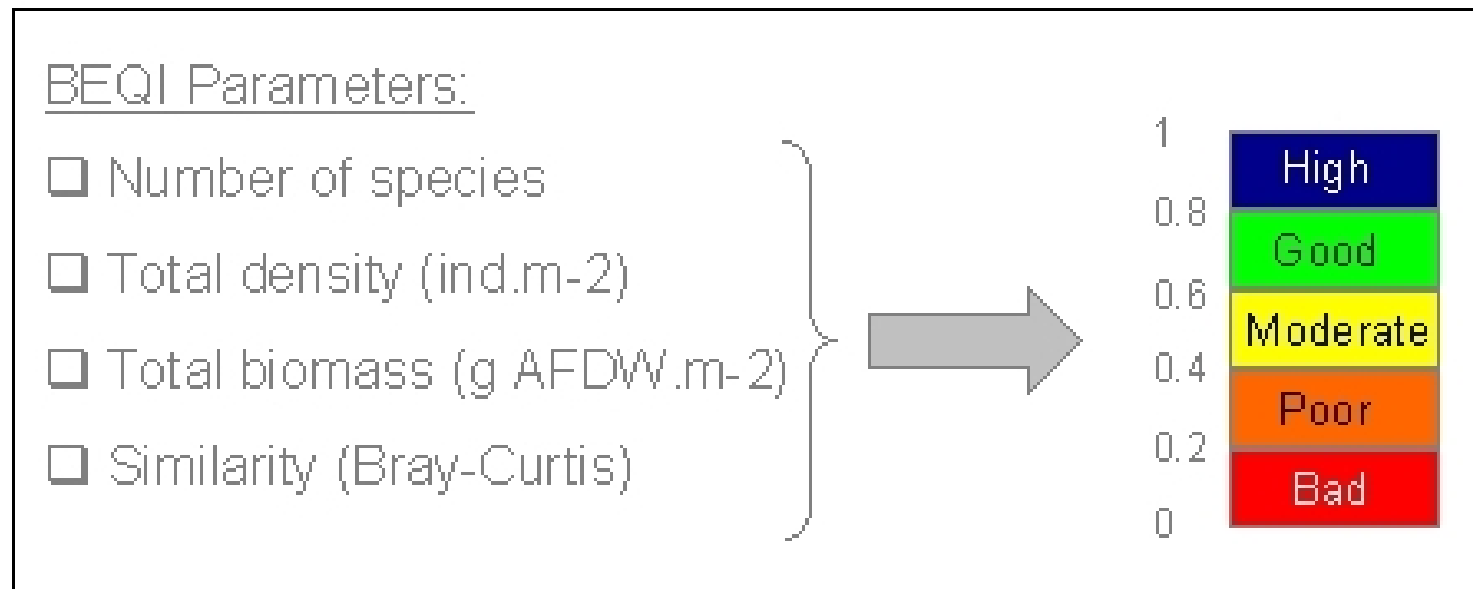
The genetic identification is 45% **faster** and 27% **cheaper** when processing 24 samples!

Comparison of genetic and morphologic identification

4) Benthos Ecosystem Quality Index (BEQI)

Ysebaert & Herman (2004)

- Multilevel approach
- Show changes from a certain reference state
- More information: <http://www.beqi.eu/background.php>

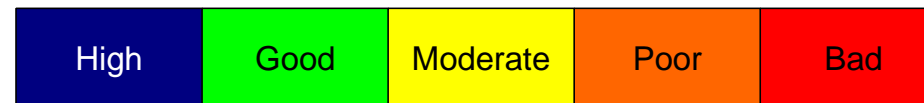


Comparison of genetic and morphologic identification

4) Benthos Ecosystem Quality Index (BEQI)

GENETIC				
Low impact:				
Ecotope	Similarity EQR	No. of species EQR	Density EQR	Final EQR Default
ECOTOPE thornnton	GOOD (0.671)	HIGH (1)	GOOD (0.627)	0.766
Medium impact:				
Ecotope	Similarity EQR	No. of species EQR	Density EQR	Final EQR Default
ECOTOPE thornnton	GOOD (0.656)	HIGH (1)	MODERATE (0.518)	0.725
High impact:				
Ecotope	Similarity EQR	No. of species EQR	Density EQR	Final EQR Default
ECOTOPE thornnton	MODERATE (0.499)	HIGH (1)	MODERATE (0.425)	0.641

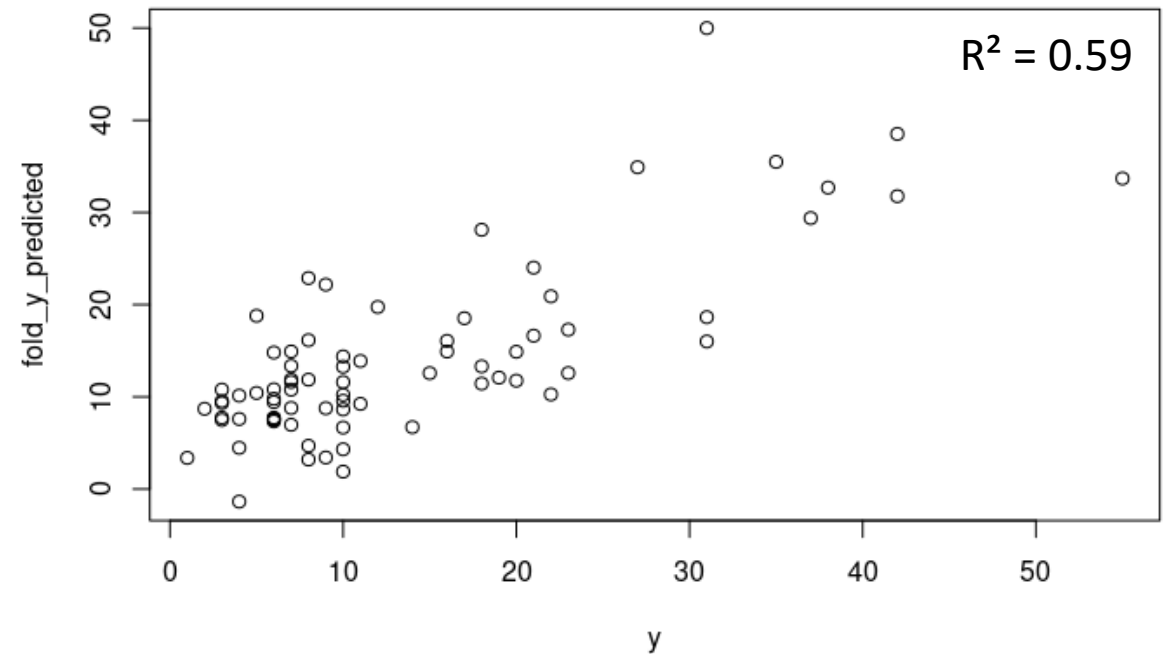
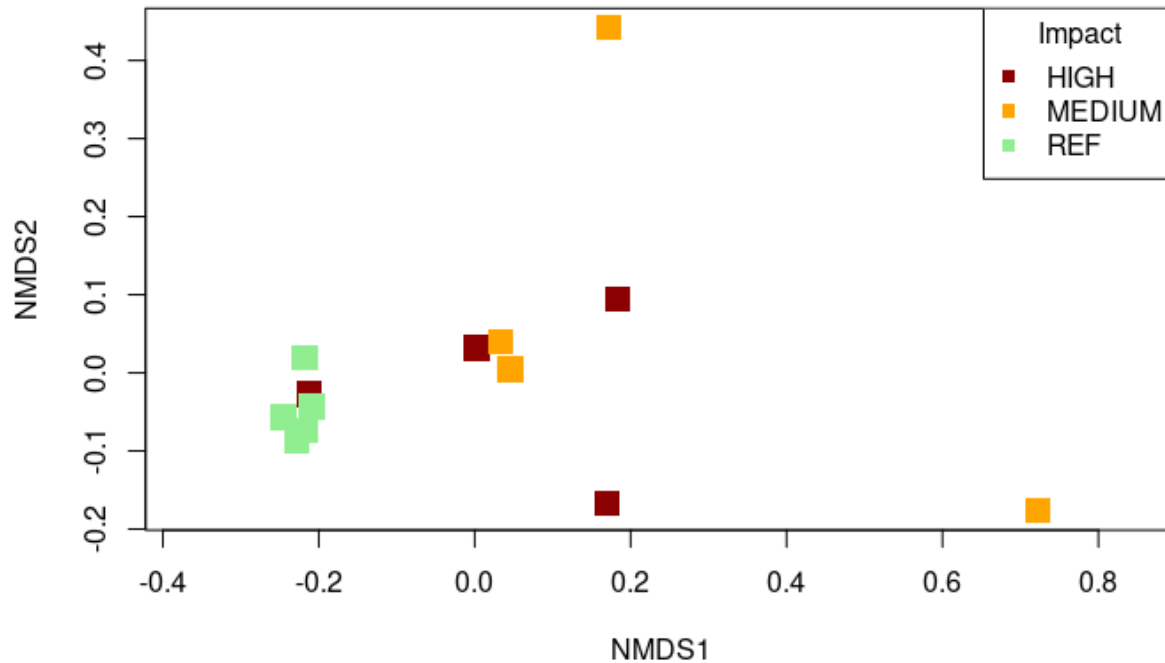
MORPHOLOGIC					
Low impact:					
Ecotope	Similarity EQR	No. of species EQR	Density EQR	Biomass EQR	Final EQR Default
ECOTOPE thornnton	MODERATE (0.477)	HIGH (1)	GOOD (0.725)	MODERATE (0.45)	0.663
Medium impact:					
Ecotope	Similarity EQR	No. of species EQR	Density EQR	Biomass EQR	Final EQR Default
ECOTOPE thornnton	MODERATE (0.499)	HIGH (1)	GOOD (0.64)	POOR (0.357)	0.624
High impact:					
Ecotope	Similarity EQR	No. of species EQR	Density EQR	Biomass EQR	Final EQR Default
ECOTOPE thornnton	MODERATE (0.42)	HIGH (1)	GOOD (0.715)	BAD (0.056)	0.548



- A decrease in the final EQR value can be seen in both methods when increasing the impact, but this results in different statuses for the impacted areas.

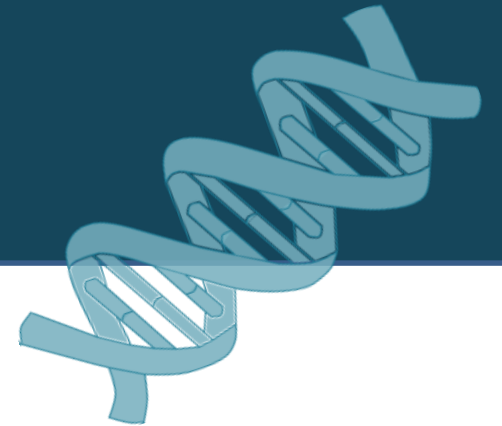
Future research

- We want to apply **machine learning algorithms** on this genetic data to predict the environmental status, independent of the reference database.
- Using **bacterial communities**, we can optimize also the processing time in the lab, as we can extract DNA directly from the samples.



Conclusions

This study shows that **DNA metabarcoding** gives **comparable** results of alpha and beta diversity patterns to the **traditional morphological identification**. As the genetic method is also **faster** and **cheaper**, this supports the suitability of DNA metabarcoding for monitoring of marine macrobenthos. However, before implementation in EIAs, the possibility of a **genetic Biotic Index** or **the use of machine learning algorithms** need to be investigated.



Thank you!

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



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