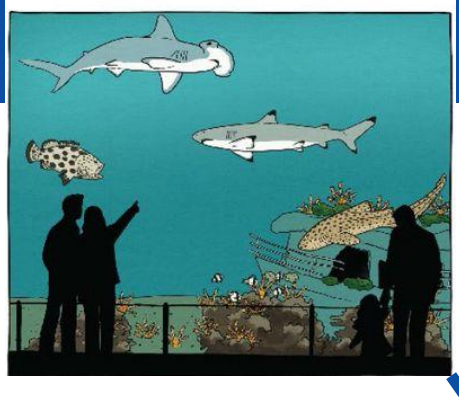
Identifying North Sea fish with nanopore sequencing, using eDNA

Interreg North Sea Region GEANS
European Regional Development Fund
EUROPEAN UNION

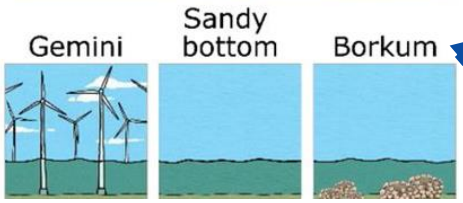
GEANS STORIES

DNA metabarcoding workflows are highly accurate but only give information about a short fragment of the gene of interest (300-500 base pairs). Can Nanopore sequencing overcome this limit? And what would that mean for monitoring of fish diversity?

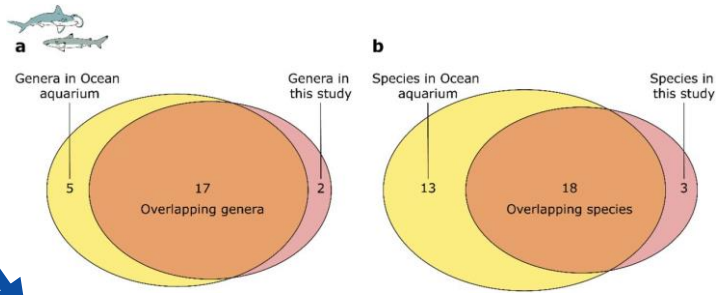
Ocean aquarium



Gemini/Borkum



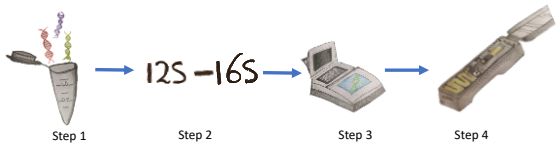
INPUT



Yellow = total amount of taxa in the Ocean aquarium but not found with eDNA.
Orange = the taxa found in both aquarium and eDNA method
Red = the taxa found in the eDNA samples that are not present in the aquarium (false positives).

Step 1: Sample water from aquarium and North Sea and extract DNA

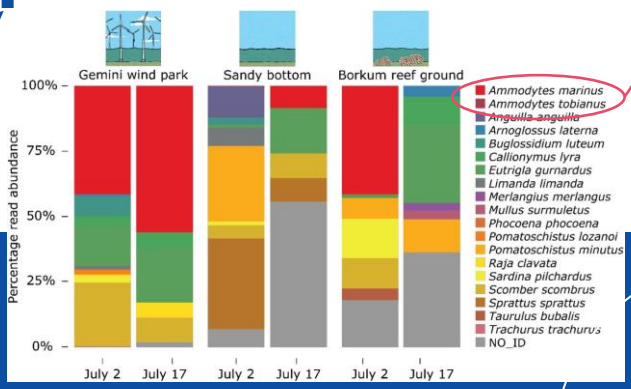
Step 2: Design a primer that covers both the 12s and 16s region of fish mitochondria



Step3: Amplify the DNA with the designed primer

Step 4: Sequence with the MinION and process the data with the new DECONA pipeline

OUTPUT



Sandeel species

(GEANS data 2023, based on samples taken in 2020)

- + **2kb fragments allow 55% of species and 75% of the genera to be identified**
- + **Higher resolution: e.g. different species of sandeel can be detected**
- + **Good representation of the species richness in different locations in the North Sea**

The reference database is not yet complete, and that still hampers correct identification of long reads. Working on it!

ILVO · Cefas · Aarhus University · SEAnalytics AB · Naturalis Biodiversity Center · NORD universitet · Senckenberg world of biodiversity · VLIZ · Wageningen University & Research

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