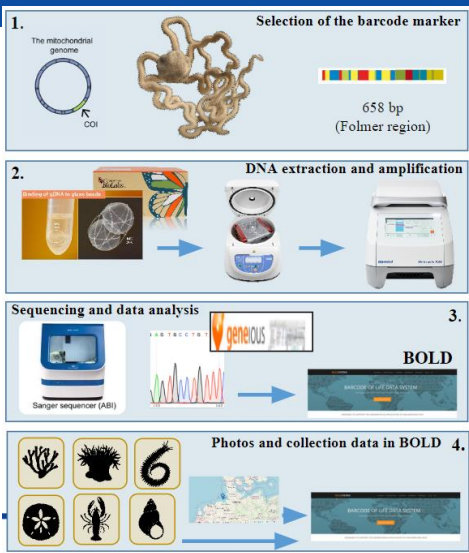


# The GEANS reference library of North Sea macrobenthos

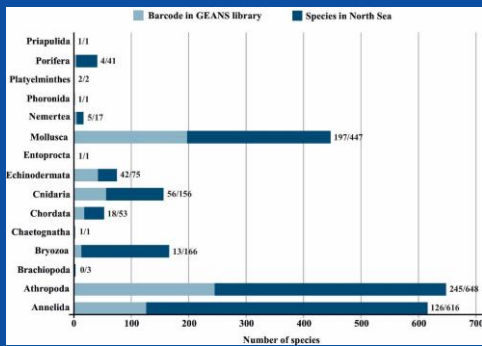
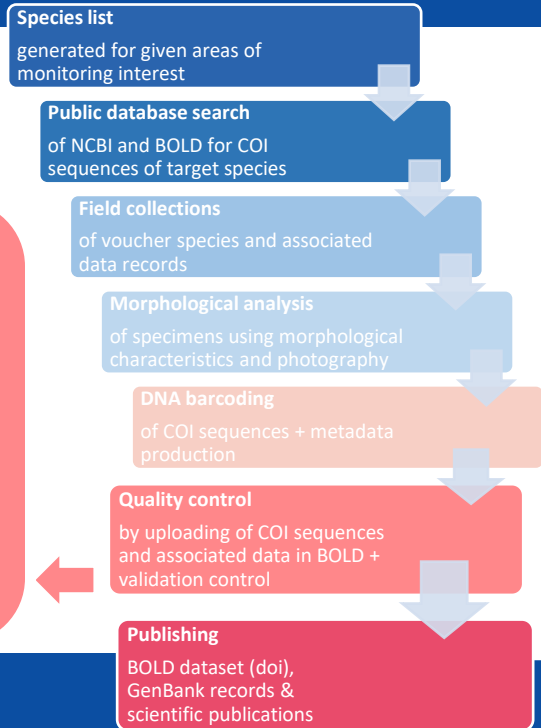
The set-up of a reliable and curated **DNA sequence library** together with preservation of taxonomically validated vouchers is essential for the development of DNA based tools. Linking DNA sequences and existing taxonomy (species names) is one of the strengths of GEANS.



## Lab flow

## Curation flow

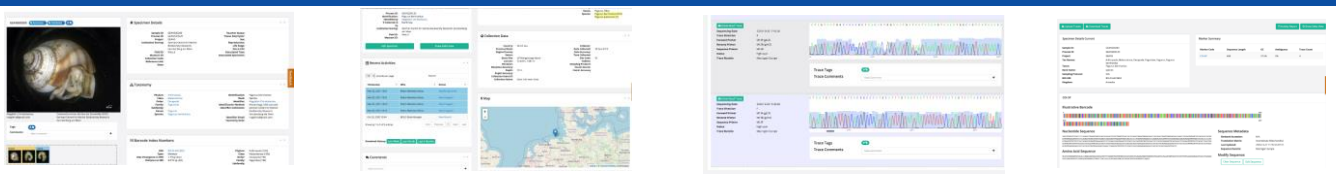
- ✓ NJ trees were constructed and obvious mistakes (i.e. contamination) were excluded
- ✓ Barcodes assigned to one species were validated when attributed to one BIN cluster exclusive for the species
- ✓ Barcodes were validated when attributed to more than one cluster but all of them were nearest neighbor to each other
- ✓ When conflict was detected between barcode clustering and morphological ID, the identification of the specimen was revised for misidentification or cryptic species
- ✓ Taxonomy was constantly updated (synonyms, new species)
- ✓ Cross-referencing of sequences among research groups was organized
- ✓ New record entries were curated and old entries controlled



## The GEANS reference library d.d. 2023

- 4005 specimens
- 712 species (743 BINs)
- 12 phyla
- 4005 COI sequences

- **72 NIS**
- **Covering 32% of North Sea macrobenthos**
- **89 species barcoded for the first time**



The GEANS reference library is the first curated DNA-library covering the full spectrum of macrobenthos in the North Sea, and includes validated sequences compared within and across research institutes. This DNA-library supports the implementation of fast, cost-efficient and reliable DNA-based identifications and subsequently environmental health assessments in the North Sea.