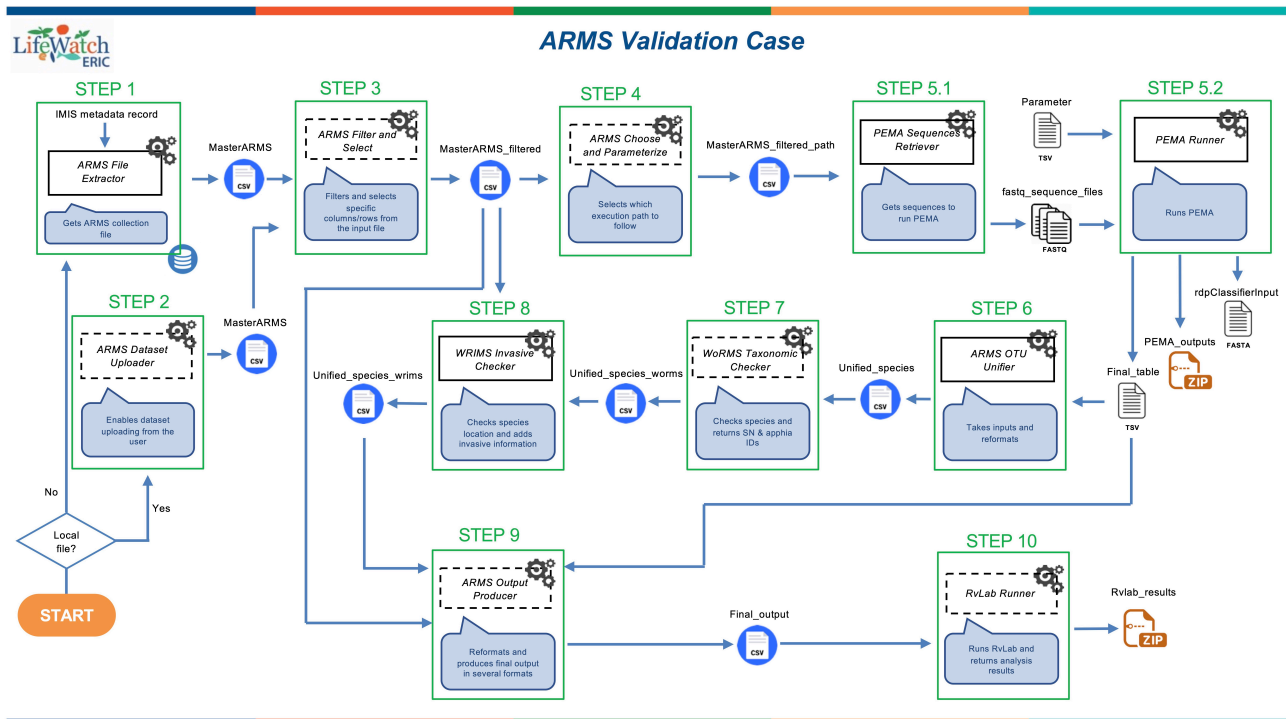


# Autonomous Reef Monitoring Structures (ARMS) Workflow



## Training Guide



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## *Background*

Hard-bottom marine habitats consist of rocks or other hard substrates exposed from the seabed. Whether they are natural (e.g. rocks and coral reefs) or artificial (e.g. shipwrecks and offshore platforms), hard-bottoms feature some of the most diverse biological marine communities on Earth. The genetic, taxonomic and functional diversity of hard-bottom marine communities provides unique ecosystem services.

Unfortunately, such biological communities are undergoing severe changes due to a combination of several anthropogenic pressures including climate change, extraction of natural resources, eutrophication, habitat degradation and invasive species. For such reasons, the design of novel, accurate and efficient diagnostic tools to detect changes in hard-bottom marine communities are needed to identify the cause of the degradation and design the most appropriate conservation approaches to preserve these habitats and their associated biological diversity.

The European network of Autonomous Reef Monitoring Structures (ARMS) is one of these tools and aims at gaining insights into hard-bottom communities and the impact of Non-indigenous and Invasive Species (NIS). A cross-disciplinary team of ASSEMBLE Plus and LifeWatch ERIC scientists and ICT experts have been gathering information from 21 observatories placed in the vicinity of marine stations, ports, marinas, and Long-Term Ecological Research (LTER) sites, distributed over Europe and polar regions, to create an early warning system to monitor the health of hard-bottom marine communities.

ARMS units are passive monitoring systems consisting in stacks of plates that mimic the complex structure of the sea bottom. They are deployed on marine substrates and become quickly colonized by marine organisms. After a few months, they are brought up, so that visual, photographic, and genetic assessments of the lifeforms that settled on them can be made at the Hellenic Centre for Marine Research (HCMR).

The species identified so far by analyzing data collected from these structures include 105 Porifera (sponges), 6 Algae (seaweeds and single-celled life forms), 14 Cnidaria (soft and hard-corals and jellyfish), and 7 Echinodermata (starfish and sea urchins).

Two pilot sites investigated in the first year identified 70 species with only 4-8% overlap between genetic and image-based identification for each site. Of these 70 species, 16 were alien or cryptogenic to the region of detection. In the second year, 35 alien species were detected across 19 different sites, with clear major differences between regions.

Explorative studies across more sites and over more years will give a clear picture of the efficacy of the current European Union monitoring and management procedures.

## *Introduction*

This workflow is a data chaining pipeline that uses genetic data collected by the ARMS network. The analytical workflow produces species occurrence lists and enables to check whether species detected at each site are alien to the location.

The methodological approach for the collection and analysis of samples from ARMS units is standardized across countries and monitoring stations, and the data are made available to the public so that they can be used by other experts to contribute to an increased scientific knowledge.

The ARMS workflow, as presently developed, produces outputs that can then be further analyzed to answer a large spectrum of ecological questions and to highlight changes and trends in community composition of hard-bottom habitats.

An important element embedded in the workflow is P.E.M.A., the Pipeline for Environmental DNA Metabarcoding Analysis. This bioinformatic tool performs a number of analytical steps to clean and filter genetic sequences from ARMS samples. The genetic sequences analyzed will be identified to produce taxonomic lists of organisms detected within each sample.

The workflow can be manually run up to step 9 (out of the 12 steps planned in total).

The LifeWatch ERIC team is currently working towards the integration of standardized tools for downstream statistical analysis (steps 10 and 11) so that the output files of step 9 can be run in the RvLab (step 12) to produce scientific results such as calculation of biodiversity indices and multi-variate analyses results.

## *Learning Objectives*

After this training the user will be able to:

1. Examine the technical requirements of the workflow services;
2. Process the services included in the workflow;
3. Run the workflow successfully;
4. Identify and troubleshoot problems that may arise while running the workflow.

## *Training Materials*

In this training the user will be guided through the workflow steps and ICT services developed in the Tesseract Virtual Research Environment of LifeWatch ERIC.

To do so, on this platform, the user will find the following training material:

1. A guide that illustrates how to read the workflow's diagram and explains the symbols used therein (PDF file);
2. A manual with general information to access and navigate the Tesseract platform. You will

be able to move between the document sections by clicking on items on the table of contents (PDF file);

3. A step-by-step demonstration on how to run the workflow services (video);
4. A series of factsheets (one for each service) that illustrate the technical requirements of each service/step (PDF file);
5. A number of additional resources in case you would like to deepen your knowledge on the case study for which this workflow was developed. In particular, you will find:
  - A link to additional information on the validation case, including an open knowledge map (LifeWatch ERIC website);
  - A scientific presentation of the case study (video);
  - A section where you can post your comments and/or questions for the workflow developers (forum style).