



Deliverable 5.4

Summary of results on the multi-disciplinary mapping of the alien species distribution and impacts on the European coastal and marine habitats

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Executive Summary

This deliverable summarizes the scientific outputs generated by task T5.4. “Mapping the impacts of Non-Indigenous species (NIS) on European coastal and marine habitats, based on multi-disciplinary approaches”. In this task we integrated species occurrence data with environmental information to produce invasive heat maps and alien forecasts for the European coastline. These were then verified by alien species observations from the genetic observatory network EMO BON. Overall, we used a selection of 35 known marine alien species to predict suitable habitat for individual species as well as to identify potential invasive hotspots. Most of the individual models detected areas with suitable habitat where the species have not yet been reported from. The hotspot models identified regions with elevated risk for establishment and spread of alien species. These were located in the Southern North Sea, the northern Bay of Biscay, the Northern Adriatic Sea, the Northern Skagerrak, the Bay of Gdansk, and the eastern Black Sea. We could match observations of 32 alien species detected by the genetic observatories network ARMS-MBON against the predicted hotspots and found a reasonable overlap between the model predictions and the observations of alien species made by the genetic observatories. We conclude that ARMS-MBON and EMO BON may be used in the future to forecast, detect, and monitor the spread alien species on a continental scale.



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1. Objective

The objectives of this task were to

- (i) integrate conventional species occurrence observations with environmental information to produce invasive heat maps and alien forecasts for the European coastline
- (ii) evaluate alien species forecasts with observations from genetic observatory networks

2. Background

Marine ecosystems are affected by human activities in the sea such as fishing, aquaculture and shipping. These processes often cause invasions of alien species (also called non-indigenous species or NIS), which alter native communities and lead to the global decline of biodiversity. Frazier et al (2013) described the invasion of alien species as one of the major environmental stressors for marine ecosystems, which often results in broad economic and ecological damage. Common approaches to prevent and mitigate marine invasions include risk assessments and early warning programs for alien species. Recently, a number of risk assessments for alien species have been developed based species distribution modelling methods (SDMs). Here statistical models are used to analyze the potential habitat suitability of alien species under a wide range of environmental conditions and thereby predict potential range extensions (Karlsson et al 2019; Leidenberger et al 2015). Such methods may become even more powerful when combined with biodiversity monitoring programs able to detect alien species at an early stage of invasion. To this end, new methods have been proposed recently (Bourlat et al 2013), one of them being DNA metabarcoding. These methods have recently been implemented by the European Marine Biological Resource Center EMBRC into a continental-scale biodiversity observatory network called EMO BON (Santi et al 2023). The programme deploys among others autonomous reef monitoring structures (ARMS) in ports, marinas, and nature reserves along the European coastline with the goal to capture species and genetic diversity across the European regional seas (Obst et al 2020). In this study we tested the potential of combining the predictive approaches offered by SDMs with early warning capabilities provided by DNA-based monitoring programs to improve the early detection and monitoring programs for alien species along the European coastline.

3. Methodology

3.1. Modelling approach

Modelling of hotspots was carried out using Species Distribution Models (SDM). To this end we developed a workflow to identify potential high-risk areas for the establishment and spread of alien species in European coastal waters. The SDM workflow is based on a modeling approach developed by the University of Gothenburg (Karlsson et al 2019; Leidenberger et al 2015) and was further adapted to deal with properties of alien species dynamics, for example identify optimal alien species monitoring sites (Bergkvist et al 2020) and predict transitions between freshwater and brackish and marine habitats (Obst & Andersson 2023). The modelling results not only show potential distribution areas for individual alien species but can also be used to map regions where suitable habitats for known alien species overlap. Such regions with a high overall invasion risk, i.e. high risk of introduction and establishment, can be considered invasive hotspots.





The models are based on a Random Forest machine learning algorithm. A detailed explanation of all analytical steps included in the modeling can be found in Leidenberger et al (2015) and Karlsson et al (2019).

Species-specific models were created based on each species' maximum distribution within the study area and the environmental variables listed below. Random Forest models were run with 10.000 background points (including input points) drawn from the study area. All models were set to produce a probability rather than binary projection in raster format. The models were tested using confusion matrices and ROC curves, and then projected with the same environmental variables back into the study area. The results were visualized as maps of potential distribution areas, i.e. geographical projections of suitable habitats.

Geographical scope

The study area, i.e., the geographic area where models were trained for, are coastal waters of Europe including the Black Sea, the Mediterranean Sea, the North-East Atlantic and the Baltic Sea. Predictions of the models were generated for the same region.

Documentation

The model's source code, as well as inputs and results with species-specific and group-based projections, are available on GitHub (https://github.com/biomobst/IAS_hotspot_model).

Biological data

The list of target species was obtained from alien species checklists of HELCOM, OSPAR, AquaNIS, and the Swedish Agency for Marine and Water Management and included 35 alien species (Appendix, Table 1). All species were categorized into a series of groupings that make it possible to weight, sort, and compare the species-specific distribution maps according to ecological or risk-based criteria. Groups were assigned according to the biological environment (phytobenthos, phytoplankton, zoobenthos, zooplankton), salinity tolerance (estuarine, freshwater, marine), habitat of adult life stages (benthic, holo-pelagic, symbiotic), potential of invasiveness (based on risk assessments of the Swedish Species Information Center), and taxonomic group (phylum level).

Species observations (presence-only) were obtained for all target species from the Global Biodiversity Information Facility (<https://www.gbif.org/>). All species observations were carefully revised and verified before being used in the models, while unverified records were discarded.

Environmental data

Gridded environmental data available as global marine data layers through the Bio-Oracle website (<http://www.bio-oracle.ugent.be/>) with a resolution of 5 arc-min (Tyberghein et al 2012) were used to generate environmental variables for the SDMs. These data layers are generated from monthly satellite data (Aqua-MODIS and SeaWiFS website <https://oceancolor.gsfc.nasa.gov/>) as well as in-situ measured oceanographic data from the World Ocean Database 2009 (Boyer et al 2009). The following data layers were used: Mean dissolved oxygen in ml/l (Oxy), Mean nitrate [NO₃] [NO₃ + NO₂] in µmol/l (NO₃), Mean phosphate in µmol/l (PO₄), Maximum sea surface temperature in °C (Max SST), Minimum sea surface temperature in °C (Min SST), Sea surface temperature range in °C (Range SST), Mean calcite concentration in mol/m³ (CaCO₃), Maximum chlorophyll *a* concentration in mg/m³ (Max Chl*a*), Minimum chlorophyll *a* concentration in mg/m³ (Min Chl*a*), Range of chlorophyll *a* concentration in mg/m³ (Range Chl*a*), Mean Sea ice concentration in % (Ice).



Analysis of cumulative invasion risk

To calculate the cumulative invasion risk, the following factors were integrated into each ecological group:

- Cumulative probability of encountering suitable habitat, summed for all species in an ecological group (e.g. phytoplankton).
- Weighting of species-specific probability for suitable habitats based on invasive potential, where species with a high risk outcome according to Strand et al (2018) were given more weight, while species with low risk outcomes were given less weight in the aggregate projection (weight factors 1–5).
- Weighting of species-specific probability of suitable habitat based on proximity to shipping traffic, where species with suitable habitat in boxes with shipping traffic were given more weight due to increased introduction risk (weighting factors traffic intensity/5000).
- Cumulative invasion risk maps for ecological groups below are available on the project page (in the folder: results/Raster files GROUPS (GeoTIFF format). Cumulative invasion risk values are expressed with two types of logarithmic scales. Both weighting and scaling are explained in the readme file in the same folder.

3.2. Observations of alien species with genetic observatories

We used the derived species observation data from the European ARMS-MBON sampling campaigns 2018-19 to evaluate the alien species forecasts made by the models. The data set encompasses samples collected by 15 observatories distributed across 12 countries, which deployed (and continuously deploy) ARMS units in the vicinity of marinas, ports, marine protected areas (MPAs), and long term ecological research sites (LTERs) - from Svalbard in the north to the Red Sea in the south (Figure 2). For the analysis, 56 ARMS units were included in total, which were deployed between 2018 and 2019 and retrieved between 2018 and 2020 (Obst et al 2020; Daraghmeh et al 2024; Santi et al 2023). The duration of sampling events (i.e., deployment duration of individual ARMS units) ranged from 37 to 649 days. ARMS units were deployed, retrieved, photographed, and processed by individual partners in the ARMS-MBON network following the ARMS-MBON protocols (accessible through the ARMS-MBON GitHub repository at <https://github.com/arms-mbon>). Details on data analyses can be found in Daraghmeh et al (2024).

We performed a scan against reference checklists for ecological key species. Species occurrences with at least two sequence reads were scanned against the World Register of Introduced Marine Species (WRiMS; Costello et al 2024) for species with alien status at the place of observation. The WRiMS checks can be replicated using the Jupyter notebook on <https://www.github.com/vliz-be-opsci/lw-iji-invasive-checker>.

4. Results and Discussion

4.1. Hotspot model

Summary

All modelling results are documented on the GitHub project page https://github.com/biomobst/IAS_hotspot_model in the folder Results/Confusion matrices and





Results/Test results. A total of 260 model results are available on the project page. All models showed good test results with regard to predictive performance and are presented according to groupings, weightings, and scalings. Overall, the modelling produced 48 species-specific predictions (28 marine and 20 freshwater species) as well as 11 group-specific marine predictions, delivered as TIFF files, which can be analyzed individually or in concert in a GIS environment to investigate the influence of different parameters on the aggregate invasion risk.

Individual projections

Species specific projections can be used to identify areas of suitable habitat where species have not yet been observed or areas where species may migrate to in the near future. For example, the German and Danish North Sea coasts for *Bugula neritina* and *Ficopomatus enigmanticus*, the large Baltic estuaries for *Rhithropanopeus harrisii*, the Bay of Biscay for *Hydroides dianthus*, and the Northern Adriatic Sea for *Austrominius modestus* (Fig. 1).



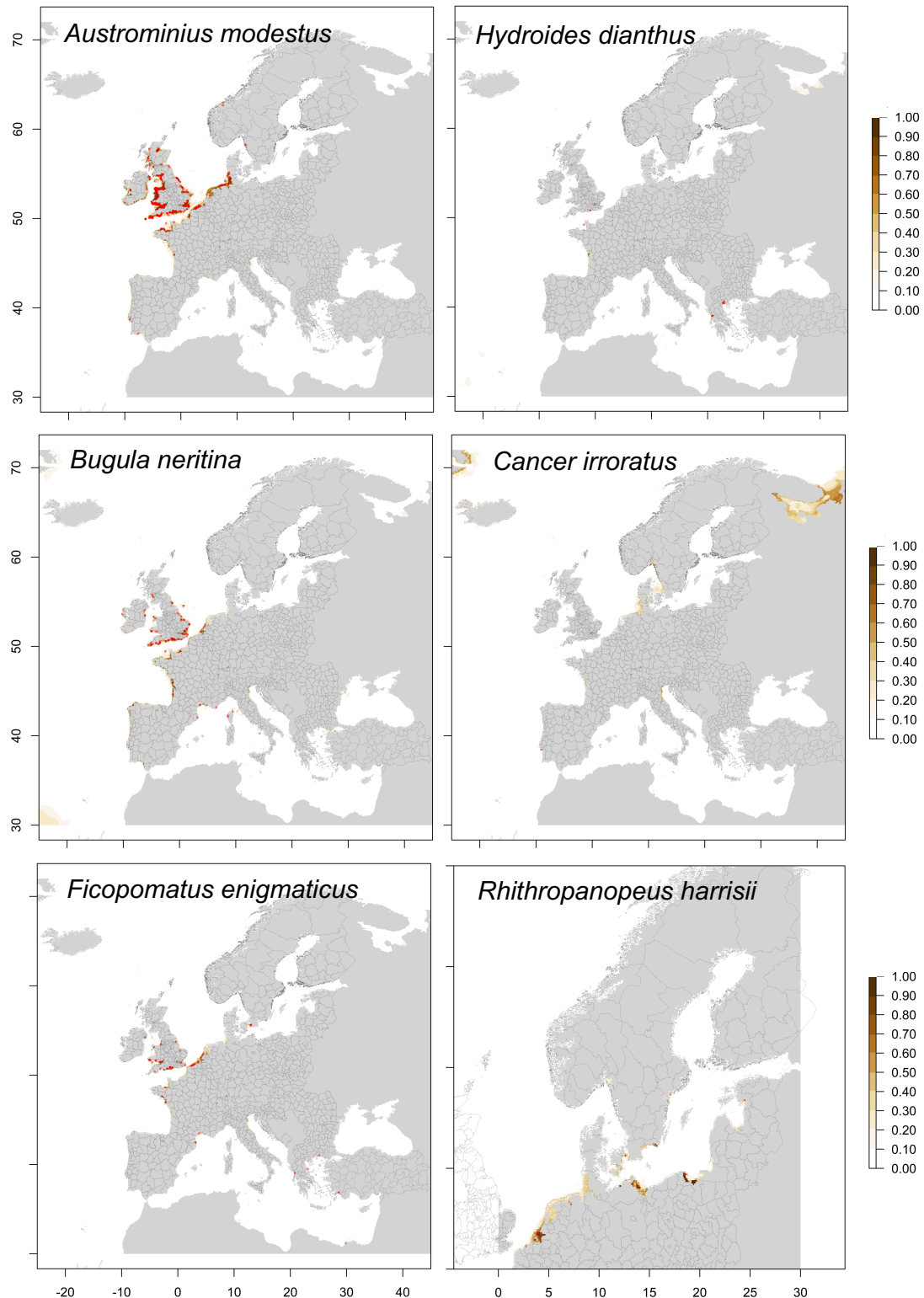


Figure 1. Example of model predictions for 6 alien species. The colour scale is linear from white to dark brown, with 0 indicating lowest probability to find suitable habitat, and 1 indicating highest probability to find suitable habitat. Red circles indicate training points for the models based confirmed observations of the species.

Invasive hotspots

Predictions of accumulated risk for establishment and spread of alien species along the European coastline indicated that the most eminent invasive hot spot is located the southern coast of the North Sea, stretching from the Netherlands to Denmark and here specifically the estuarine areas which provide suitable habitat for both freshwater tolerant and brackish water as well as marine species, while they also boast numerous large ports (Fig. 2). Additional areas of high invasive pressure include the coastal stretches from the English channel to the Bay of Biscay, the Northern Adriatic Sea, the Northern Skagerrak, the Bay of Gdansk, and the east coast of the Black Sea (Fig. 2).

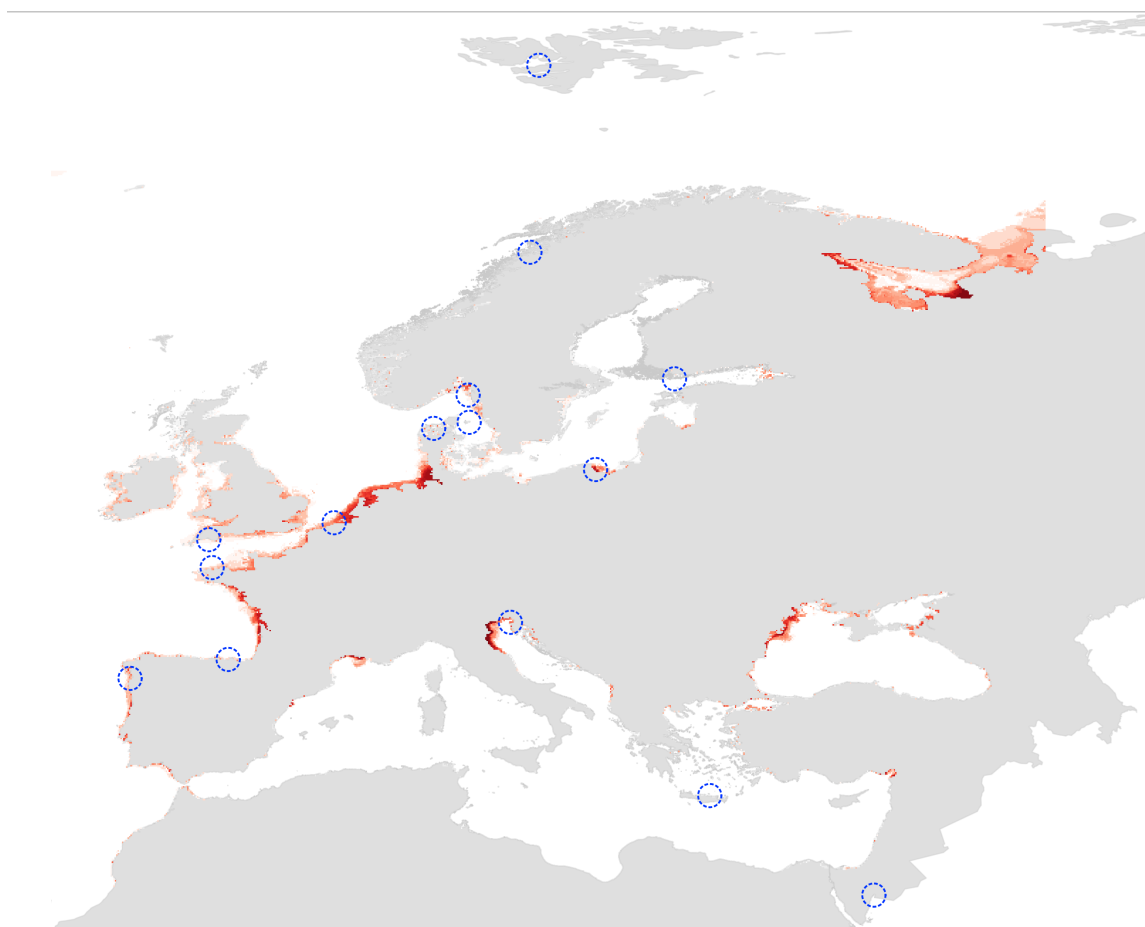


Figure 2. Prediction of cumulative risk for introduction and spread of marine invasive species. Colour scale reaches from white (lowest cumulative probability) to dark red (highest cumulative probability) to find suitable habitats for all marine benthic species. Blue dotted circles indicate the location of ARMS-MBON observatories included for analysis in this report.

4.2. Alien species observations from the ARMS-MBON network

Overall, we observed 32 species listed as “alien” in WRiMS at the location of occurrence across the European coastline. Most alien species were detected by the observatories in Limfjord (Denmark), Koster (Sweden), and Gdansk (Poland). Four observatories did not detect any alien species, while for numerous locations the prediction of cumulative risk for introduction and spread of marine invasives and the number of observed alien species matched (Fig. 3).

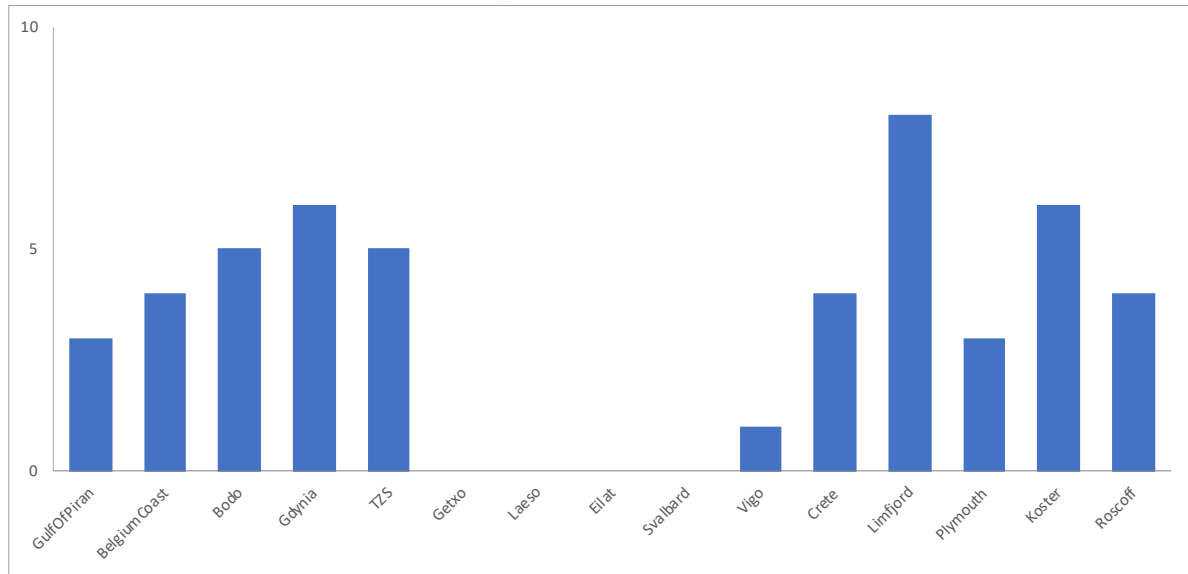


Figure 3. Number of identified species registered as alien in WRiMS at the location of occurrence across ARMS-MBON observatories. Observatories are ordered from left to right by increasing number of ARMS units deployed ($n = 1$ for GulfOfPiran, $n = 8$ for Roscoff).

4.3. Shortfalls of the current approach

The modelling results have their limitations. First, the selection of modelled species focussed on northern Europe while less emphasis was placed on species recently migrated from the Red Sea into the Mediterranean. Hence the Eastern Mediterranean has relatively few hotspots given our results, which may not reflect the actual situation. However, the modelling can also be done for Lessepsian migrant species in the future.

Another shortfall of the current approach that combined modelling with DNA-based sensing is that it was based on known alien species only, while unknown aliens (i.e., species not registered in WRiMS) remain undetected. Future projects should develop analytical workflows for detecting species yet unregistered in WRiMS.

Although ARMS-MBON covers many of the predicted invasive hotspots and also detects alien species, it captures only a small fraction of the actual alien species currently establishing and migrating along the European coastal waters. In order to increase the rate of detection it is important to increase the spatio-temporal sampling (e.g., in ports and marinas), add similar sampling campaigns from other habitats (e.g., water column and soft bottom), and establish new observatories in predicted hotspot areas such as e.g., the Atlantic coast, the Black sea, and the Eastern Mediterranean.

At this stage the models could only be used to inform about the placement of the observatories. In the future, the genetic monitoring data may be used to update the models and thereby generate more dynamic predictions of suitable areas for invasive species. This could be implemented as soon large number of alien species observations data are becoming available through genetic observatory programs, such as e.g. EMO BON.

5. Conclusion

- ARMS-MBON (and EMO BON) is a monitoring program able to detect new aliens and monitor known aliens along the European coastline.
- The intensity of spatio-temporal sampling can be improved as well as the diversity of habitats sampled by the genetic observatory networks. EMO BON is a promising initiative delivering the backbone for such a coordinated sampling effort.
- Interaction between Species distribution models (SDM) and genetic observatory networks can be improved and made more dynamic in the future to obtain dynamic forecasts when species are observed outside their known range.
- We still lack a detection mechanism for unknown alien species.

6. References

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7. Appendix

6.1. Summary of research outputs produced by task 5.4

Output description	Reference	Documentation
Species distribution model (SDM) workflow to predict potential high-risk areas for introduction, establishment and spread of invasive species	Bergkvist et al (2020); Obst & Andersson (2023)	https://github.com/biomobst/IAS_hotspot_model/
Script-based workflow to identify known alien species from genetic observation data sets using WRiMS	Daraghmeh et al (2024) A long-term ecological research data set from the marine genetic monitoring programme ARMS-MBON 2018-2020. <i>Mol Ecol Res.</i> In Review.	https://github.com/vliz-be-opsci/lw-iji-invasive-checker
Data paper presenting the first batch of genetic observatory data from EMO BON	Daraghmeh et al (2024) A long-term ecological research data set from the marine genetic monitoring programme ARMS-MBON 2018-2020. <i>Mol Ecol Res.</i> In Review.	Molecular Ecology Resources (In review)
Data paper presenting the non-indigenous species detected by the ARMS MBON	Pagnier et al (in prep) Broad-Scale Detection of Non-Indigenous Species in Marine Ecosystems using Autonomous Reef Monitoring Structures and DNA Metabarcoding	To be submitted

6.2. List of modelled species

Scientific name	Source	Ecotype	Salinity tolerance	Habitat
<i>Alexandrium tamarense</i>	AquaNIS	phytoplankton	marine	holo-pelagic
<i>Thalassiosira punctigera</i>	AquaNIS	phytoplankton	marine	holo-pelagic
<i>Eriocheir sinensis</i>	AquaNIS	zoobenthos	estuarine/freshwater	benthic
<i>Fucus evanescens</i>	WRiMS	phytobenthos	estuarine/freshwater	benthic
<i>Hemigrapsus sanguineus</i>	WRiMS	zoobenthos	estuarine/freshwater	benthic
<i>Hemigrapsus takanoi</i>	WRiMS	zoobenthos	estuarine/freshwater	benthic
<i>Marenzelleria viridis</i>	WRiMS	zoobenthos	estuarine/freshwater	benthic
<i>Sargassum muticum</i>	WRiMS	phytobenthos	estuarine/freshwater	benthic
<i>Undaria pinnatifida</i>	SwAM	phytobenthos	marine	benthic
<i>Chaetoceros seiracanthus</i>	SwAM	phytoplankton	marine	holo-pelagic
<i>Dissodinium pseudocalani</i>	SwAM	phytoplankton	marine	holo-pelagic
<i>Fibrocapsa japonica</i>	SwAM	phytoplankton	marine	holo-pelagic
<i>Alexandrium ostenfeldii</i>	SwAM	phytoplankton	marine	holo-pelagic
<i>Arcuatula senhousia</i>	SwAM	zoobenthos	marine	benthic
<i>Austrominius modestus</i>	SwAM	zoobenthos	marine	benthic
<i>Bugula neritina</i>	SwAM	zoobenthos	marine	benthic
<i>Cancer irroratus</i>	SwAM	zoobenthos	marine	benthic
<i>Ficopomatus enigmaticus</i>	SwAM	zoobenthos	marine	benthic
<i>Mytilopsis leucophaeata</i>	SwAM	zoobenthos	estuarine/freshwater	benthic
<i>Ocenebra inornata</i>	SwAM	zoobenthos	marine	benthic
<i>Penaeus japonicus</i>	SwAM	zoobenthos	marine	benthic
<i>Rangia cuneata</i>	SwAM	zoobenthos	estuarine/freshwater	benthic
<i>Rapana venosa</i>	SwAM	zoobenthos	estuarine/freshwater	benthic
<i>Rhithropanopeus harrisii</i>	SwAM	zoobenthos	estuarine/freshwater	benthic
<i>Ruditapes philippinarum</i>	SwAM	zoobenthos	marine	benthic
<i>Urosalpinx cinerea</i>	SwAM	zoobenthos	marine	benthic
<i>Conchoderma auritum</i>	SwAM	zoobenthos	marine	symbiotic/parasitic
<i>Palaemon macrodactylus</i>	SwAM	zooplankton	marine	holo-pelagic
<i>Neogobius melanostomus</i>	WRiMS	zoobenthos	estuarine/freshwater	benthic
<i>Admete viridula</i>	OSPAR	zoobenthos	marine	benthic
<i>Amphibalanus eburneus</i>	OSPAR	zoobenthos	marine	benthic
<i>Hydroides dianthus</i>	OSPAR	zoobenthos	marine	benthic
<i>Acipenser gueldenstaedtii</i>	OSPAR	zoobenthos	estuarine/freshwater	benthic
<i>Asterias amurensis</i>	OSPAR	zoobenthos	marine	benthic
<i>Styela clava</i>	OSPAR	zoobenthos	marine	benthic

Table 1. Target species list used for modelling invasive hotspots with information on source database, ecotype, salinity tolerance, and habitat. Swedish Agency for Marine and Water Management (SwAM), World Register of introduced Marine Species (WRiMS).





MARCO-BOLO

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