



Deliverable 5.5

Scientific document summarising the results of the Species distribution modelling and mapping of the alien species impacts on the European coastal and marine habitats

Version 1.0

Date of delivery

2025-06-30

Authors names

*Matthias Obst*¹

Affiliations

¹ Department of Marine Sciences, University of Gothenburg, Box 461, 405 30 Gothenburg, Sweden;

PUBLIC DOCUMENT

Document Information

Grant Agreement	101082021
Project Acronym	MARCO-BOLO
Project Title	MARine COastal BiODiversity Long-term Observations

Deliverable Number	D5.5
Work Package Number	WP5
Deliverable Title	Scientific document summarising the results of the Species distribution modelling and mapping of the alien species impacts on the European coastal and marine habitats
Lead Beneficiary	University of Gothenburg, Partner Number 9
Author(s)	Matthias Obst (University of Gothenburg)
Due Date	30.05.2025
Submission Date	30.06.2025
Dissemination Level	PU
Type of Deliverable	R

Version 0.5	05.05.2025, Matthias Obst
Version 0.6	25.06.2025, Matthias Obst, Carlota Muñiz
Version 1.0	30.06.2025, Matthias Obst



Funded by
the European Union



UK Research
and Innovation



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 modelled 82 species identified by marine genetic monitoring programs in 2020-2024 as occurring outside their native range. Models produced predictions of suitable habitat in current and future climate scenarios for these non-indigenous species (NIS) and can be used to identify regions with elevated risk for establishment and spread of alien species.





Contents

Document Information	2
Executive Summary	3
1. Objective.....	5
2. Background	5
3. Methodology	5
3.1. Modelling approach.....	5
4. Results and Discussion	7
4.1. Modelling trial.....	7
4.2. Shortfalls of the current approach	8
4.3. Future work.....	8
4.4. Conclusion.....	8
5. Research outputs	9
5.1. Summary table.....	9
5.2. Conference contributions	9
6. Appendix	10
6.1. Table 1.....	10
7. References	12





1. Objective

The objective of this task was to run a new analysis with the invasive alien species (IAS) hotspot model for a number of non-indigenous species (NIS) recently detected by genetic monitoring campaigns and produce maps showing areas of potential invasion and ecological impact for these NIS in European coastal waters.

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. Common approaches to prevent and mitigate marine invasions include risk assessments and early warning programs for alien species. Recently, several risk assessment tools for alien species have been developed based on species distribution modelling methods (SDMs). Here statistical models are used to analyse the potential habitat suitability of alien species and thereby predict potential range extensions and areas of potential impact. Here we model the potential distribution of 80 non-indigenous species detected by the genetic monitoring programmes, ARMS-MBON and the Swedish national port monitoring programme (Pagnier et al 2025; Sundberg et al 2024) and their ability to forecast potential range expansions of these species in European coastal waters.

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 spread and establishment of alien species in European coastal waters. The SDM workflow is based on a modelling 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/tree/master/Modelling_trial_2025.

Biological data

The list of target species (Table 1) was obtained from genetic monitoring programs ARMS-MBON (Pagnier et al 2025) program and the Swedish national port monitoring campaign (Sundberg et al 2024).

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 for current and future climate scenario SP119:

Data layer	Description
<i>nos_mean_depthsurf</i>	Mean surface nitrate in mmol per m ³
<i>chl_mean_depthsurf</i>	Mean surface chlorophyll in mg per m ³
<i>O2_max_depthsurf</i>	Maximum surface dissolved molecular oxygen in mmol per m ³
<i>po4_mean_depthsurf</i>	Mean surface phosphate in mmol per m ³
<i>thetao_min_depthsurf</i>	Minimum surface sea water temperature in °C
<i>par_mean_mean_depthsurf</i>	Mean surface photosynthetic available radiation in Einstein per m ² and day
<i>O2_mean_depthsurf</i>	Mean surface dissolved molecular oxygen in mmol per m ³
<i>phyc_mean_depthsurf</i>	Mean phytoplankton concentration at the surface
<i>thetao_mean_depthsurf</i>	Mean surface sea water temperature in °C
<i>thetao_max_depthsurf</i>	Maximum surface sea water temperature in °C
<i>ph_mean_depthsurf</i>	Mean surface PH
<i>O2_mindepthsurf</i>	Minimum surface dissolved molecular oxygen in mmol per m ³
<i>si_mean_depthsurf</i>	Mean surface silicate in mmol per m ³
<i>O2_max_depthmax</i>	Maximum benthic dissolved molecular oxygen in mmol per m ³
<i>O2_mean_depthmax</i>	Mean benthic dissolved molecular oxygen in mmol per m ³
<i>O2_min_depthmax</i>	Minimum benthic dissolved molecular oxygen in mmol per m ³
<i>phyc_mean_depthmean</i>	Mean phytoplankton concentration at mean depth.
<i>thetao_mean_depthmean</i>	Mean midwater sea water temperature in °C
<i>so_mean_depthmean</i>	Mean salinity at mean depth
<i>O2_mean_depthmean</i>	Mean benthic dissolved molecular oxygen in mmol per m ³
<i>po4_mean_depthmean</i>	Mean benthic phosphate in mmol per m ³





so_mean_depthsurf	Mean salinity at the surface
sws_mean_depthsurf	Mean sea water speed at the surface
siconc_mean_depthsurf	Mean benthic sea ice cover in fraction
sithick_	Sea ice thickness in m
siconc_max_depthsurf	Maximum benthic sea ice cover in fraction

4. Results and Discussion

4.1. Modelling trial

Summary of results

The results of the modelling trial are documented on the GitHub project page https://github.com/biomobst/IAS_hotspot_model/tree/master/Modelling_trial_2025 in the folder “results”

https://github.com/biomobst/IAS_hotspot_model/tree/master/Modelling_trial_2025/results.

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 Baltic coast for *Bugula neritina* (Fig. 1). The maps of projected suitable habitat for all the species can be found in the “Plots_species” folder:

https://github.com/biomobst/IAS_hotspot_model/tree/master/Modelling_trial_2025/results/Plots_species.

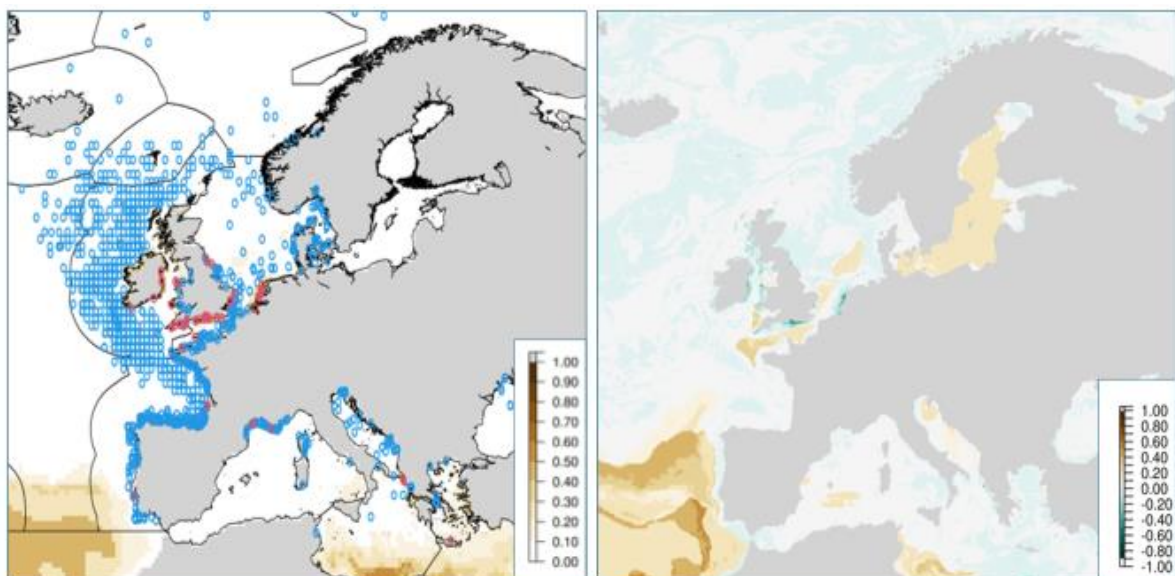


Figure 1. Example of model predictions for *Bugula neritina*. **Left:** currently known distribution indicated by red dots, with pseudo-absence points indicated by blue dots. Colour scale is linear from 0.00 (unsuitable habitat) to 1.00 (highly suitable habitat). **Right:** Difference in suitable habitat between SSP119 scenario prediction for 2100 and current climate scenario. SSP119 refers to a climate scenario within the Shared Socioeconomic



Pathways (SSPs) framework, specifically SSP1-RCP1.9, which is a low-emission scenario. Colour scale is linear from -1.00 (maximum loss of suitable habitat) to +1.00 (maximum gain of suitable habitat).

4.2. Shortfalls of the current approach

The models are sensitive to many of parameters, which means that the outputs presented from this trial have to be interpreted with caution. When applied in decision making, these models should be built from a consensus of several algorithms (e.g., not only Random forest) and climate scenarios (e.g., not only SPP119) to be confident about the predictions of suitable habitats and migration trends.

Visualisation of results is challenging as there are many model outputs that need to be inspected simultaneously for interpretation, such as e.g., test statistics, parameter settings, maps in various resolutions (high, low), formats (png, geotiff), and projection settings (present, future scenarios). A visualisation interface (e.g., R-shiny) may be appropriate to solve this problem. But such applications should be developed only after the workflow is consolidated and end users of the models have provided detailed specifications for how and when they would use such an application.

The analytical workflow applied here should be better documented to allow reproducibility and repeatability and thereby enable swift and ad-hoc predictions for relevant species as soon as these are detected in the genetic monitoring programs. This work is currently scheduled for the remainder of the project.

4.3. Future work

The modelling trials need to be better documented and interpreted across different climate scenarios. Also, the individual projections will have to be combined to produce updated maps of the hotspots. These are planned to be used in decision making by Swedish authorities, e.g., when granting exemptions from ballast water treatment in Swedish ports. A workshop is planned for September 2025 to specify the end user demands for output maps.

Furthermore, results from the modelling trial will be presented at the 12th International Conference on Marine Bioinvasions in October 2025.

We currently plan one more scientific manuscript which will focus on the publication of the SDM workflow and results.

Finally, the SDM analysis tool will be added to the EDITO platform (<https://www.edito.eu>) during spring 2026 and thereby become an analytical tool in the Digital Twin of the Ocean (DTO).

4.4. Conclusion

The genetic monitoring programs that donated the alien species lists for this experiment do not yet provide enough species occurrence data to influence the outcome of the model predictions, which means that GBIF and OBIS still provide most of the occurrence data for the modelling. However, the





genetic monitoring programs do provide the list of species detected to be “on the move”. For these species the models provide valuable knowledge on potential alien species impact as they are able to align the presently known distribution with the potential distribution of these species in the future.

5. Research outputs

5.1. Summary table

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. Mol Ecol Res. 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. Mol Ecol Res. In Review.	Molecular Ecology Resources 25 (4), e14073, https://doi.org/10.1111/1755-0998.14073
Data paper presenting the non-indigenous species detected by the ARMS MBON	Pagnier et al (2025) Using the long-term genetic monitoring network ARMS-MBON to detect marine non-indigenous species along the European coasts.	Biological Invasions 27, 77 (2025), https://doi.org/10.1007/s10530-024-03503-2
Conference talk at 12th ICMB, Madeira Island, Portugal	Pagnier et al (2025) Assessing the effectiveness of genetic observatory networks in detecting and monitoring marine non-indigenous species	https://marinebioinvasions.info/program
Conference talk at 12th ICMB, Madeira Island, Portugal	Obst et al (2025) A science-policy interface for non-indigenous species monitoring and management.	https://marinebioinvasions.info/program

5.2. Conference contributions

12th International Conference on Marine Bioinvasions, Madeira Island, Portugal; Dates: 7-9 October 2025





Authors: Pagnier Justine, Nauras Daraghmeh, Obst Matthias. **Title:** Assessing the effectiveness of genetic observatory networks in detecting and monitoring marine non-indigenous species. **Abstract:** The increasing prevalence of non-indigenous species (NIS) in marine ecosystems presents critical challenges for biodiversity conservation and ecosystem management. Advances in molecular techniques, particularly DNA metabarcoding, offer unparalleled opportunities for early detection and long-term monitoring of these taxa. The European ARMS Marine Biodiversity Observation Network (ARMS-MBON) exemplifies this approach, conducting standardized genetic sampling campaigns across Europe. We evaluated the potential of genetic monitoring networks to monitor marine NIS by analyzing ARMS-MBON data for cytochrome c oxidase subunit I (COI) and 18S rRNA markers using a custom bioinformatics pipeline. Screening against reference databases and incorporating manual curation, we detected diverse NIS across multiple locations, including taxa indicative of potential new introductions. This dataset also provides a valuable foundation for modeling NIS distributions and applying machine learning techniques to enhance predictive capabilities. Our findings highlight the efficacy of genetic observatory networks in identifying NIS distributions, mapping range shifts, and functioning as early warning systems. This talk will discuss key insights and future directions for the integration of genetic tools into NIS monitoring frameworks, emphasizing their role in addressing the growing pressures on marine ecosystems.

Authors: Obst Matthias, Pagnier Justine. **Title:** A science-policy interface for non-indigenous species monitoring and management. **Abstract:** The rapid accumulation of alien species in marine ecosystems demands urgent, coordinated and cost-effective national management strategies. In Sweden, the Swedish Agency for Marine and Water Management (SwAM) with support from the Swedish Transport Agency (STA) and the local county administrative boards (LST) has established a national monitoring program for marine non-indigenous species (NIS). The aim of the program is to develop a toolbox with effective and scalable methods for early warning for NIS, understanding range shifts, predicting near-future distributions, and identifying origins and vectors of NIS. Methods currently implemented in the program include DNA- based tools (metabarcoding, quantitative PCR), citizen science campaigns, as well as species distribution modelling approaches (SDM). Here we present the results from the first two years of the national monitoring program as well as the associated development of the analytical tools for NIS management. Examples of decision support tools include early warning capabilities, range shift detectors, distribution forecasts, and connectivity maps. We explain further how these tools are used in eradication efforts, prioritization of species or habitats, as well as exemptions from ballast water treatment.

6. Appendix

6.1. Table 1

Table 1. Target species list used for modelling trial.

Species	Records presence	Records absence	Synonyms
<i>Potamopyrgus antipodarum</i>	1620	0	names match
<i>Crepidula fornicata</i>	4007	25345	names match
<i>Cordylophora caspia</i>	108	0	names match
<i>Amphibalanus improvisus</i>	453	8	names match
<i>Austrominius modestus</i>	3297	98	names match
<i>Petricolaria pholadiformis</i>	3991	25390	names match





<i>Hemigrapsus takanoi</i>	239	25189	names match
<i>Mnemiopsis leidyi</i>	2122	7528	names match
<i>Corella eumyota</i>	345	155	names match
<i>Ficopomatus enigmaticus</i>	118	104	names match
<i>Asciidiella aspersa</i>	2083	470	names match
<i>Monocorophium acherusicum</i>	176	0	names match
<i>Bonnemaisionia hamifera</i>	1386	31	names match
<i>Cutleria multifida</i>	676	65	names match
<i>Asparagopsis armata</i>	3687	702	names match
<i>Monocorophium sextonae</i>	309	0	names match
<i>Leptosiphonia brodiei</i>	208	0	<i>Leptosiphonia fibrillosa</i>
<i>Polydora cornuta</i>	294	0	names match
<i>Palaemon elegans</i>	921	32	names match
<i>Halothrix lumbricalis</i>	16	0	names match
<i>Gammarus tigrinus</i>	357	6	names match
<i>Hydroides elegans</i>	77	6	names match
<i>Haloa japonica</i>	20	0	names match
<i>Amphibalanus eburneus</i>	28	0	names match
<i>Rhithropanopeus harrisi</i>	1637	264	names match
<i>Paranthura japonica</i>	9	0	names match
<i>Celleporaria brunnea</i>	5	0	names match
<i>Caprella scaura</i>	52	0	names match
<i>Mytilicola orientalis</i>	40	0	names match
<i>Armadillidium nasatum</i>	189	0	names match
<i>Bugula neritina</i>	264	421	names match
<i>Asparagopsis taxiformis</i>	1148	368	names match
<i>Dasysiphonia japonica</i>	173	370	names match
<i>Acartia tonsa</i>	794	0	names match
<i>Neogobius melanostomus</i>	1901	56	names match
<i>Cercopagis pengoi</i>	117	0	names match
<i>Melanothamnus harveyi</i>	79	0	names match
<i>Herdmania momus</i>	59	0	names match
<i>Ostreopsis ovata</i>	32	10	names match
<i>Amphibalanus amphitrite</i>	496	12	names match
<i>Botrylloides violaceus</i>	708	380	names match
<i>Apionsoma misakianum</i>	5	0	<i>Apionsoma (Apionsoma) misakianum</i>
<i>Caprella mutica</i>	495	332	names match
<i>Pleurosira laevis</i>	8	0	names match
<i>Marenzelleria viridis</i>	9	0	names match
<i>Fenestrulina delicia</i>	10	0	names match
<i>Gonionemus vertens</i>	8	0	names match
<i>Arcuatula senhousia</i>	356	120	names match
<i>Balanus trigonus</i>	91	6	names match
<i>Smittoidea prolifica</i>	5	0	names match
<i>Rangia cuneata</i>	238	1	names match
<i>Perophora japonica</i>	53	129	names match
<i>Corambe obscura</i>	16	0	names match
<i>Juxtacribrilina mutabilis</i>	41	0	names match
<i>Schizoporella japonica</i>	70	12	names match
<i>Streblospio benedicti</i>	383	0	names match
<i>Haminella solitaria</i>	5	0	names match
<i>Sinelobus vanhaareni</i>	5	0	names match
<i>Thalassiosira punctigera</i>	184	0	names match
<i>Ensis directus</i>	322	7	<i>Ensis directus /Ensis leei</i>
<i>Leptosiphonia fibrillosa</i>	10	0	names match
<i>Cephalothrix simula</i>	5	0	names match





<i>Fibrocapsa japonica</i>	19	0	names match
<i>Torquigener flavimaculosus</i>	1	0	names match
<i>Boccardia proboscidea</i>	3	0	names match
<i>Pseudocalanus mimus</i>	255	0	names match
<i>Pseudocalanus acuspes</i>	1333	0	names match
<i>Paracerceis sculpta</i>	6	3	names match
<i>Oithona davisae</i>	32	0	names match
<i>Pseudodiaptomus marinus</i>	35	0	names match
<i>Polydora websteri</i>	2	0	names match
<i>Xenostrobus securis</i>	28	67	names match
<i>Aurelia solida</i>	1	0	names match
<i>Evadne anonyx</i>	48	0	names match
<i>Parathalestris harpactoides</i>	6	35	names match
<i>Stylochus ellipticus</i>	1	0	names match
<i>Marenzelleria neglecta</i>	40	0	names match
<i>Marenzelleria arctica</i>	1	0	names match
<i>Aporrectodea caliginosa</i>	8	0	<i>Aporrectodea trapezoides</i>
<i>Polycerella emertoni</i>	2	0	names match

7. References

Bergkvist J, Magnusson M, Obst M, et al (2020) Provtagningsdesign för övervakning av främmande arter. Övervakning i marin miljö. Havs- och vattenmyndighetens rapport 2020:22. ISBN 978-91-88727-86-2. In Swedish.

Boyer TP, et al (2009). World ocean database 2009. In: Levitus S (ed) NOAA Atlas NESDIS 66. U.S. Government Printing Office, Washington, DC, 216 pp.

Daraghmeh, Exter K, Pagnier J, et al (2025) A long-term ecological research data set from the marine genetic monitoring programme ARMS-MBON 2018-2020. Molecular Ecology Resources 25 (4), e14073 <https://doi.org/10.1111/1755-0998.14073>

Karlsson R, Obst M, Berggren M (2019) Analysis of potential distribution and impacts for two species of alien crabs in Northern Europe. Biological Invasions. <https://link.springer.com/article/10.1007/s10530-019-02044-3>

Leidenberger S, Obst M, Kulawik R, et al (2015) Evaluating the potential of ecological niche modelling as a component in non-indigenous species risk assessments. Marine Pollution Bulletin. 97: 470-487. <https://www.sciencedirect.com/science/article/pii/S0025326X15002350>

Obst M, Andersson G (2023) Hotspot modell för invasiva arter i Bottniska viken - Övervakning i marin miljö. SeAnalytics rapport 2023-03. På uppdrag av Havs- och vattenmyndigheten. In Swedish.

Pagnier J, Daraghmeh N, Obst M (2024) Using the long-term genetic monitoring network ARMS-MBON to detect marine non-indigenous species along the European coasts. Biological Invasions 27, 77 (2025). <https://doi.org/10.1007/s10530-024-03503-2>

Sundberg P, Obst M, Panova M (2024) DNA-baserad övervakning av arter i akvatisk miljö - verifiering och tillämpning. Naturvårdsverket rapport. pp 44. Rapport 7157. ISBN 978-91-620-7157-8





Tyberghein L, Verbruggen H, Pauly K, et al (2012) Bio-ORACLE: a global environmental dataset for marine species distribution modelling. *Global Ecology and Biogeography* 21:272–281.





Project Coordinator

Nicolas Pade | nicolas.pade@embrc.eu

Project Manager

Giulia Vecchi | giulia.vecchi@embrc.eu

Press and Communications

Mathilde Vidal | mathilde@erinn.eu

Website: MarcoBolo-Project.eu

