



OPEN Modelling the global invasion potential of *Pelagia noctiluca* under climate change

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Invasive species are recognised as a major driver of global biodiversity loss. In marine ecosystems, blooms of non-native jellyfish species are widely perceived to be increasing globally, with impacts on food webs, ecosystem services, biogeochemical cycles, and coastal livelihoods. *Pelagia noctiluca* (Forsskal, 1775) is a jellyfish native to the Mediterranean Sea and the northeastern Atlantic Ocean, but has been increasingly associated with recurrent bloom events in non-native regions, which cause adverse ecological and socio-economic impacts. Here, we use an ensemble species distribution modelling framework implemented in the biomod2 package in R to assess the global habitat suitability of *P. noctiluca*, and to evaluate its present-day and future invasion potential across non-native marine ecosystems. Based on species occurrence records and eight environmental variables, our results indicate that *P. noctiluca* exhibits high habitat suitability in temperate and subtropical coastal waters, driven primarily by salinity, primary productivity, and sea surface temperature. Ultimately, by projecting a substantial future habitat contraction, our findings strongly contradict the general perception that jellyfish blooms and distribution will universally increase under global climate change.

Keywords Species distribution modelling, Species invasion, Jellyfish, Climate change, biomod2, Shared socioeconomic pathways

Invasive non-native species are recognised among the primary drivers of global biodiversity loss, exerting severe ecological and socio-economic impacts by altering ecosystem functioning and services^{1–8}. Driven by climate change and rapid human-mediated introductions, non-native species are increasingly spreading into previously inaccessible regions^{9–14}. Managing species invasions is inherently more challenging in highly interconnected marine ecosystems, where oceanic currents and shipping pathways enable continuous dispersal and complicate monitoring and eradication efforts^{15–17}. Within these marine environments, invasive species can have erratic population explosions. In jellyfish, these sudden increases are commonly referred to as blooms^{18,19}. When driven by non-native invasive jellyfish, these bloom events can severely disrupt trophic structures, ecosystem stability and environmental conditions, as demonstrated by *Mnemiopsis leidyi* and *Rhopilema nomadica* in the Mediterranean Sea^{20–22}.

*Pelagia noctiluca*²³ is a pelagic jellyfish native to the northeast Atlantic and the west Mediterranean, and is known for blooms characterised by large aggregations of individuals^{24–29}. The species has also been reported from non-native regions, including the Gulf of Mexico³⁰ and the northern Indian Ocean along the Indian coast³¹, Hari^{32–35}. Bloom events of *P. noctiluca* have pronounced social-ecological consequences due to the presence of potent stinging cells in the tentacles and bell, which can remain active even after death or stranding until desiccation occurs²⁶.

P. noctiluca exhibits a generalist feeding strategy, shifting between omnivory and carnivory in response to prey availability and seasonal variability³⁶. Due to its limited swimming capability, the species is frequently transported by winds and ocean currents beyond its typical temperature range, occasionally forming large blooms with concentrations up to 500 individuals/m³^{37,38}. The absence of a benthic larval stage, resulting in a shorter larval phase, combined with a predominantly pelagic life cycle, continuous wave-mediated dispersal and an opportunistic zooplanktivore diet, confers high ecological adaptability and strong invasive potential to *P. noctiluca*^{36,39}. Despite this, significant knowledge gaps remain in understanding the global invasion potential

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of *P. noctiluca*, particularly in the absence of detailed dispersal models. Improved understanding of its suitable habitat could therefore provide critical information for ecosystem managers, international organisations, and policy makers worldwide during bloom events.

Species distribution models (SDM) are algorithms that relate species occurrence records to environmental conditions to build models based on ecological niche theory^{40–42}. These models generate spatial predictions of current and future species distribution⁴³ and are widely applied in ecology, biogeography, conservation planning and biosecurity⁴⁴. SDM-based projections provide scientifically robust information that can support informed conservation and management decisions⁴⁵, particularly for invasive species risk assessments and climate-change impact forecasting^{46,47}. Incorporating global datasets into both regional and large-scale SDMs has been shown to improve the accuracy of invasion-risk predictions^{48,49} (Jones et al. 2010). Numerous studies have successfully applied SDMs to predict global habitat suitability and assess invasion potential of non-native species^{50,51}. Integrating such global-scale assessments with continuous monitoring can significantly enhance management effectiveness⁵².

In this study, we aimed to map the global environmental niche of *P. noctiluca* using an ensemble species distribution modelling (SDMs) framework, with the primary objective of assessing its global invasion potential across non-native marine ecosystems under current and future climate conditions. Here, we define “invasion potential” as a proxy derived from reclassified habitat suitability; it indicates the vulnerability of regions to potential invasion if the species is introduced and does not imply actual dispersal or realized invasion. Within the biomod2 package in R⁵³, individual SDMs were combined to build an ensemble SDM with improved transferability, predictive accuracy and overall model performance compared to single-algorithm approaches^{54–56}. We further examined projected shifts in species distribution under multiple Shared Socioeconomic Pathways (SSPs) consistent with IPCC climate scenarios across near-, mid-, and end- century temporal scales. This approach provides insights into climate-driven changes in geographic range and habitat suitability, supporting risk forecasting and adaptive management strategies for *P. noctiluca*. Additionally, we identify key environmental variables influencing the global distribution of *P. noctiluca* and highlight potential range shifts by comparing future projections of the species’ habitat suitability against its current distribution. Overall, this study provides the first global-scale evaluation of the distribution and invasion potential of *P. noctiluca* using a multi-algorithm ensemble modelling framework that integrates diverse environmental predictors and future climate scenarios.

Materials and methods

The modelling framework of this study was structured into three major methodological phases, as visualised in our schematic workflow (Fig. 1). The first phase, Data preparation, involved the acquisition, spatial thinning, and preprocessing of the species occurrence records and the selection of environmental variables based on the ecology of the species and statistical analyses. The second phase, Modelling Procedure, encompassed the generation of pseudo-absences, model building across multiple algorithms, statistical evaluation, and final ensemble model construction. The last phase, Projection and Analysis, involved the mapping of the predicted habitat suitability, invasion potential classification and assessing the species range shifts under future climate scenarios.

Species data

Occurrence records for *P. noctiluca* were extracted from the Global Biodiversity Information Facility⁵⁷ using the scientific name as search term, yielding 5929 raw occurrence records for the period 2010–2024 (<https://www.gbif.org/occurrence/download/0068545-240506114902167>). To match the temporal resolution of our sourced environmental data (see below), only records from 2010–2020 were retained for further processing, resulting in 2093 records. Occurrence records were spatially thinned using a minimum distance threshold of 5.5 km with a single replicate, corresponding to the spatial resolution of the environmental layers, to reduce spatial autocorrelation. Spatial thinning was performed using the thin function within the spThin R package⁵⁸. The function applies a randomisation algorithm to generate a dataset in which occurrence locations are separated by at least the specified minimum distance. The thinned dataset was subsequently plotted in QGIS to identify and remove erroneous records (occurrences located on land) and duplicate entries, thereby minimising pseudo-replication⁵⁹. Following data filtering and quality control, a total of 211 occurrence records were retained for model building. The workflow for occurrence data preprocessing is illustrated in Supplementary Fig. 2.

Environmental data

Environmental data for the current decade (2010–2020) and the future climate scenarios based on Shared Socioeconomic Pathways (SSP) were obtained from the Bio-Oracle database at a spatial resolution of 3 arcminutes (approximately 5.5 km at the equator)⁶⁰. The SSPs are climate change scenarios defined by the IPCC that incorporate projected socioeconomic pathways and predicted radiative forcing up to 2100⁶¹. The selected SSP scenarios represent low-emission (SSP1-1.9, intermediate (SSP3-7.0, and high-emission (SSP5-8.5 futures, reflecting contrasting trajectories of greenhouse gas emissions and socioeconomic development. We utilised the SSP-based climate layers provided by Bio-ORACLE, these pre-processed layers were generated by Assis et al.⁶⁰ using a multi-model ensemble of CMIP6 Earth System Models and the change-factor (delta change) method to reduce biases and improve the confidence of climate projections^{62,63}.

Our environmental predictor selection for *P. noctiluca* followed a rigorous two-step process. Initially, we downloaded the mean value of 18 out of 24 available environmental variables (Supplementary Table 1) for the current period and three future decadal periods (2020–30, 2050–60, and 2090–100). To avoid the repetition of proxy variables and exclude predictors with limited ecological relevance for the species, we omitted six of the available variables from Bio-ORACLE at this stage: diffuse attenuation, photosynthetically available radiation, cloud cover, terrain ruggedness index, sea-ice cover, and sea-ice thickness. Even prior to statistical filtering, we explicitly ensured the initial inclusion of wave dynamics, sea surface temperature, salinity and primary

Modelling Framework of Ensemble Species Distribution Modelling of *P. noctiluca*

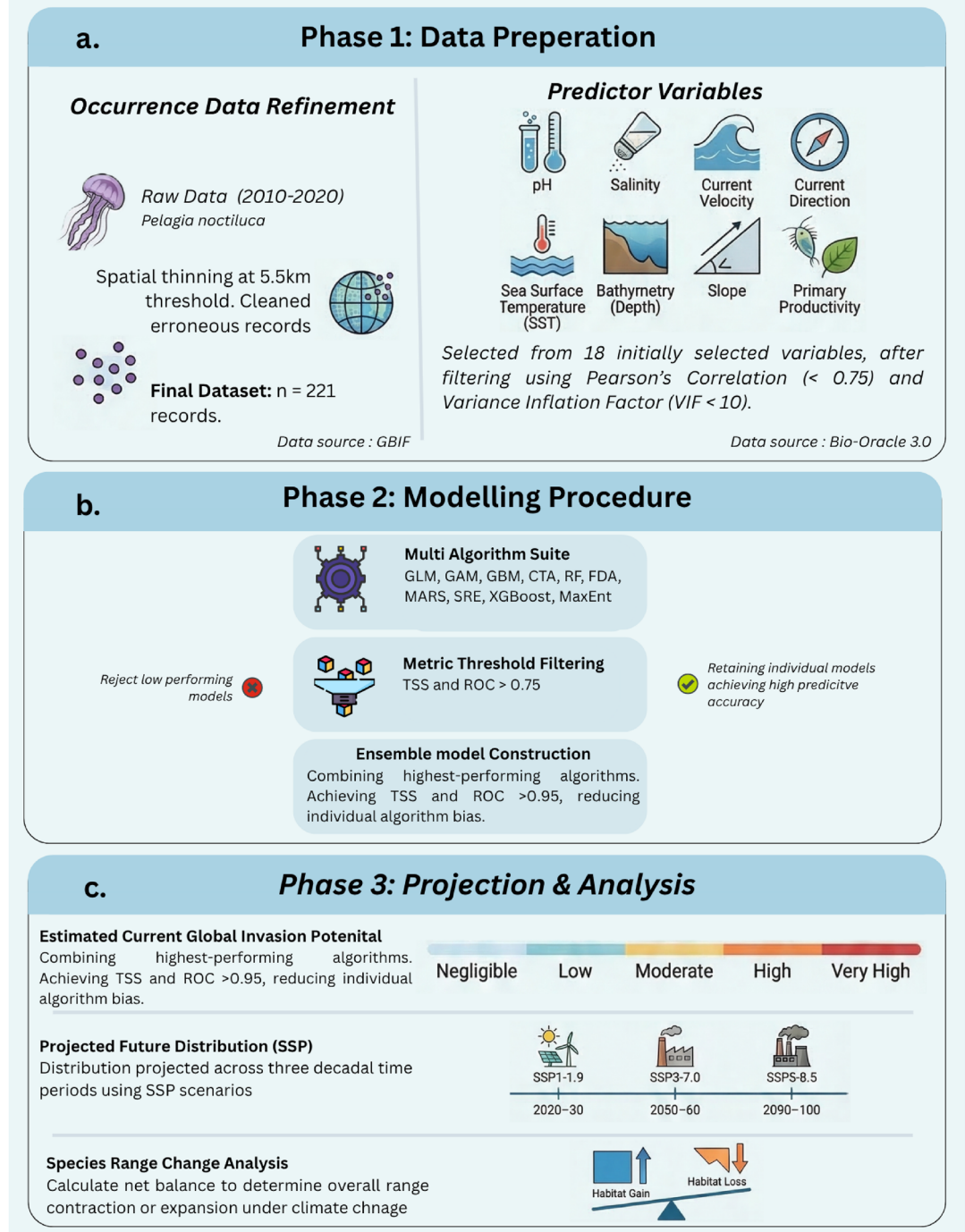


Fig. 1. Modelling framework of the ensemble species distribution modelling of *P. noctiluca*. The workflow is structured into three major phases: (a) Data preparation, including preprocessing and analyses of the data; (b) Modelling, encompassing model calibration, evaluation, and ensemble construction; and (c) Projection & Analysis, involving habitat suitability mapping and range-change assessment under current and future SSP climate scenarios.

productivity among our 18 variables. Retaining these variables was an intentional means of testing the inferences of existing literature^{64–66} against the results of our modelling to see if both conform with the established ecological findings for the species.

To assess the inter-variable correlation and multicollinearity among the 18 initially retained variables, Pearson's correlation coefficients and Variance Inflation Factor (VIF) scores were computed using the *vifcor* function within the *usdm* package in R. Thresholds of 0.75 for Pearson's correlation and 10 for VIF were applied, and variables exceeding these thresholds were excluded before model construction (Supplementary Table 2). Following the statistical elimination of highly correlated predictors, our final predictor set comprised seven variables: five environmental variables (pH, salinity, current velocity, current direction, and sea surface temperature), one terrain variable (slope), and one biological variable (primary productivity). The inclusion of these statistically selected variables is ecologically justified: slope accounts for the species' known coastal blooms, while pH represents physiological limits within the marine environment.

Modelling procedure

Following the data preparation phase (Fig. 1), the modelling procedure was initiated to estimate the realised niche of *P. noctiluca*. Consistent with the standard SDM framework, these models estimate the realised niche of *P. noctiluca*, representing environmental conditions favourable for the species based on current occurrence data. As true absence data were unavailable, pseudo-absences (PAs) were generated using the BIOMOD_FormatingData function in the biomod2 package to meet the input requirements of some algorithms (GAM, GBM, ANN, RF, CTA, and FDA) requiring both presence and absence data. PAs were generated using the Surface Range Envelope (SRE) strategy. This method calculates the environmental boundaries of the species' known occurrences. The PA points were sampled exclusively from areas strictly outside this defined environmental niche envelope. A total of 2110 PA points were generated at a ratio of 10:1 to presence data, following the recommendation for SDM development⁶⁷.

To reduce bias of individual models, we employed a highly diverse set of nine correlation based, machine-learning, regression and profile-based algorithms, representing the subset of models available within the biomod2 package. Instead of relying on a single model approach, we incorporated models from distinct statistical branches to most accurately capture the complex relationships between occurrence of *P. noctiluca* and environmental predictors. The modelling framework included:

Regression based models

Generalised additive model (GAM) to capture both linear and complex smoothed relationships.

Machine learning and tree-based models

Random forest (RF), Classification tree analysis (CTA), Generalised boosting model (GBM), Artificial neural network (ANN) and XGBoost (eXtreme Gradient Boosting Training) to offer high predictive accuracy and to capture complex, non-linear relationships through iterative decision-tree partitioning.

Classification and maximum entropy models

Flexible discriminant analysis (FDA) and maximum entropy (MaxEnt) to estimate the probability of occurrence by contrasting species presence data with environmental background conditions.

Profile based models

Surface range envelope (SRE) to define the multidimensional bounding box of known occurrences and project this spatially.

Each algorithm was used to build individual SDMs using default parameter settings. We evaluated model performance using a repeated cross-validation approach, randomly splitting the dataset into 80% training and 20% testing subsets across 10 independent iterations. We selected True Skill Statistic (TSS) and Area Under the Receiver Operating Characteristic Curve (ROC) to evaluate the models. The computation of these metrics was done natively within the biomod2 package using the BIOMOD_Modeling function. ROC is calculated to assess the overall discriminatory ability of the models across all probability thresholds. TSS is calculated by finding the optimal cut-off threshold that maximises the score when the continuous probability of the models are converted to binary predictions. These are widely used metrics for evaluating species distribution models. TSS values range from −1 to 1 (where a value ≤ 0 indicates performance no better than a random model and a value of 1 represents perfect predictive accuracy), while ROC values range from 0 to 1 (with greater values indicating greater discriminatory ability).

To ensure predictive robustness, only individual models achieving a TSS and ROC ≥ 0.75 were retained. These high performing models were subsequently combined into a final ensemble model using the probability mean method (EMmean), which calculates the unweighted average of the predicted habitat suitability probabilities across the retained single models. All of the above was implemented using the BIOMOD_EnsembleModeling function within the biomod2 package in R.

To identify areas of extrapolation uncertainty in the ensemble outputs, a clamping mask was generated during the model projection phase within the BIOMOD_Projection function (Setting: build.clamping.mask = TRUE, Package: biomod2). Computationally, this mask generates a raster layer with pixel values corresponding to the exact number of environmental variables that fall outside of the calibration and validation range. Regions flagged with higher values by this mask are considered less reliable, as the model is forced to extrapolate predictions beyond the environmental conditions it was trained on.

Variable importance scores (VIS), ranging from 0 to 1, were estimated within the BIOMOD_Modeling function (Setting: var.import, Package: biomod2). The VIS data was extracted using the get_variables_

importance function (Package: biomod2) from the modelling output to assess the relative predictive influence of each variable on the habitat suitability of *P. noctiluca*. Computationally, the algorithm estimates the importance through a randomisation process, where the data for each variable is randomly shuffled, and the model's predictive correlation is compared to the original prediction. A higher VIS indicates that the variable is highly influential, as shuffling its values heavily disrupts predictive accuracy.

Response curves were computed using the `bm_PlotResponseCurves` function (Package: biomod2) to evaluate changes in habitat suitability across the observed range of predictor values. To compute the response curve of a specific environmental predictor, the algorithm sets the value of all the other predictors constant. The predictor of interest is then forced to vary across its entire range, and the model predicts habitat suitability, thereby identifying the sensitivity of the model to that particular variable.

Finally, continuous habitat suitability projection for the current environmental setting was reclassified into five categories of invasion potential: Negligible (0–200), Low (200–400), Medium (400–600), High (600–800), and Very high (800–1000). These thresholds were finalised by linearly partitioning the continuous suitability scores (0–1000) into equal intervals. Invasion potential is defined here as habitat suitability for *P. noctiluca*, such that areas of higher suitability are considered to face a greater risk of invasion if the species is introduced. Species range shift analysis was performed to measure distributional shifts under future climate scenarios relative to the projected current distribution. Net percentage range shift was calculated as Percentage Gain minus Percentage Loss, where Percentage Gain represents the proportion of newly suitable pixels in future projection, and Percentage Loss corresponds to currently suitable pixels projected to become unsuitable under future conditions.

Results

Key environmental drivers

Among the environmental predictors used in our species distribution model (SDM), salinity emerged as the most influential variable governing the distribution of *P. noctiluca* (Fig. 2). Habitat suitability increased sharply with rising salinity, exhibiting an exponential response from 35 PSU and reaching an optimum at approximately 38 PSU, beyond which suitability declined as salinity approached 40 PSU (Fig. 3). Primary productivity and sea surface temperature were identified as the second and third most influential variables, respectively, whereas pH exerted the weakest influence on the model prediction. Collectively, our results underscore salinity as the dominant environmental driver shaping the distribution of *P. noctiluca*, with additional variables contributing progressively lesser effects.

Predicted current habitat suitability of *P. noctiluca*

Our modelled projections indicate that *P. noctiluca* exhibits a highly structured spatial pattern of habitat suitability, which serves as a baseline for evaluating its invasion potential across non-native marine regions (Fig.

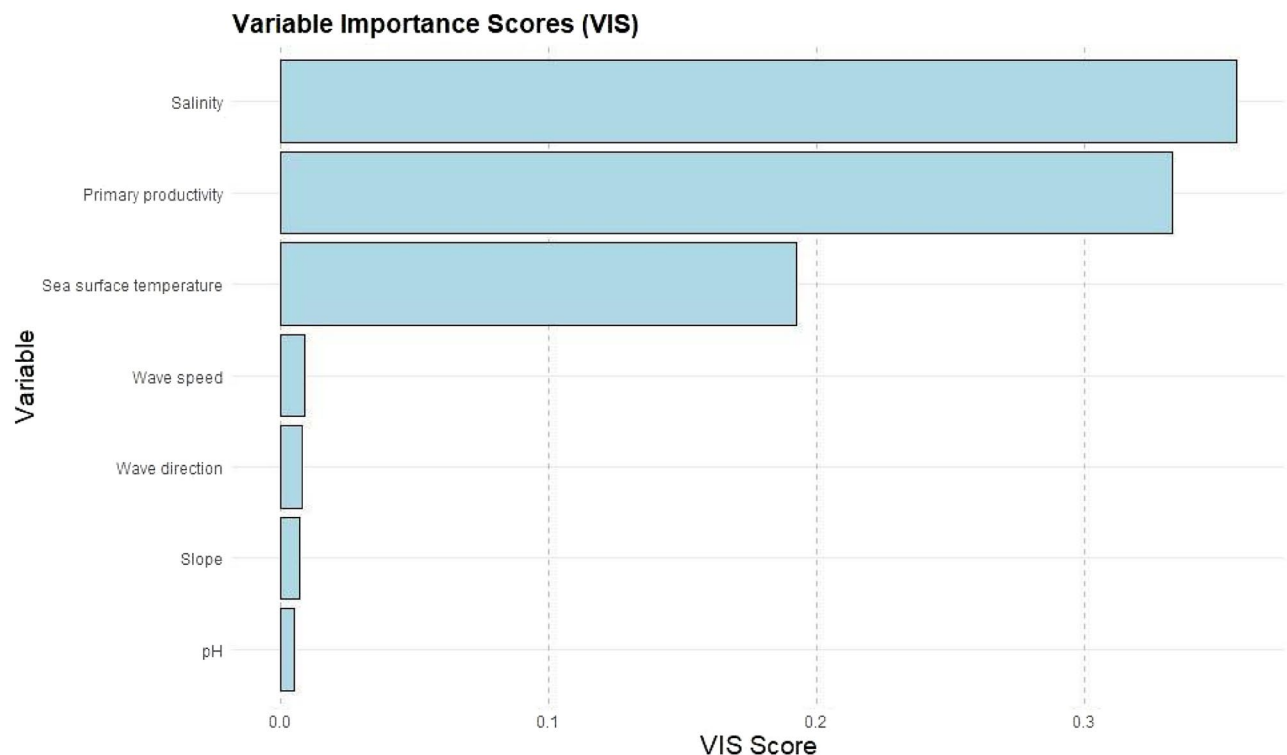


Fig. 2. Variable importance scores (VIS) of predictor variables used in the species distribution model of *P. noctiluca*. The x-axis represents the VIS values, indicating the relative contribution of each predictor, while the y-axis lists the environmental variables included in the model.

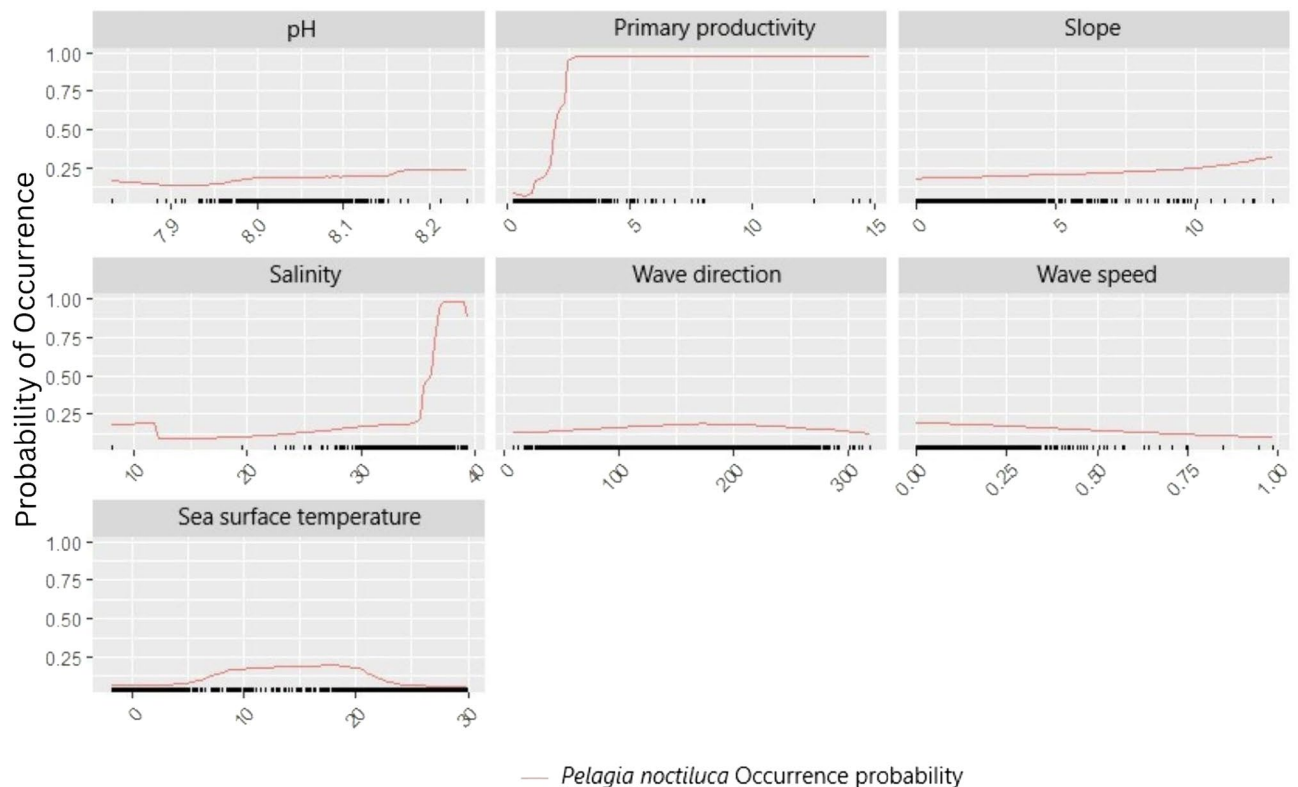


Fig. 3. Response curves of predictor variables illustrating the influence of each environmental predictor on the predicted invasion potential of *P. noctiluca* across its modelled environmental gradients.

4). Areas classified as high invasion potential correspond to regions of high habitat suitability characterised by favourable environmental conditions for the species. Within the native range, particularly the Northeast Atlantic and the Mediterranean Sea, the modelled high habitat suitability highlights core areas of environmental suitability that support established populations.

Beyond the native range, large coastal regions across multiple ocean basins were found to exhibit high to very high invasion potential, indicating potential for establishment and spread of *P. noctiluca* into these temperate and subtropical marine ecosystems. Continental margins consistently emerged as high-potential zones, suggesting a substantial coastal preference and widespread environmental suitability across both hemispheres. These regions may represent areas with conditions conducive to bloom formation.

Medium invasion potential was observed over tropical and subtropical regions of the Indian, Pacific and Atlantic Oceans, as well as parts of the Southern Ocean and sub-Arctic Zones. Although these locations may possess certain near-optimal environmental conditions, overall habitat suitability is constrained by the species' multi-dimensional environmental niche; specifically, the interacting limits of key predictors (Salinity, Primary Productivity and Sea Surface Temperature) that prevent these areas from being classified as highly suitable. Nevertheless, the species may still thrive in localised microhabitats or during periods of favourable conditions that occasionally align with its environmental niche. On the other hand, regions of low and negligible invasion potential exhibited limited habitat suitability and are considered to be under minimal ecological threat within the scope of this study.

In general, our results reveal a clear invasion potential gradient, ranging from highly suitable core regions to moderately suitable environments, with substantially high-potential zones existing beyond the native range of the species. Despite local-scale geographic variability, the global pattern depicts that invasion potential is predominantly concentrated within temperate and subtropical marine systems worldwide.

Species range shifts under future climate scenarios

Under the future climate scenarios, the projected range shifts for *P. noctiluca* were highly dependent on the emission pathway and the time period, driven mostly by habitat loss rather than gain (Fig. 5). Although the near-future projections (2020–2030) showed minimal net range shifts across all Shared Socioeconomic Pathways (SSPs), mid- and end- century projections displayed increasingly high habitat contractions.

Under the low emissions scenario (SSP1-1.9), range shifts were marked by moderate habitat loss that was partially offset by relatively higher habitat gains, leading to a relatively minor net contraction across decadal ranges. Conversely, the intermediate (SSP3-7.0) and high emission (SSP5-8.5) scenarios displayed a sharp, progressive increase in habitat contraction beyond the near-future periods. By the end of the century (2090–

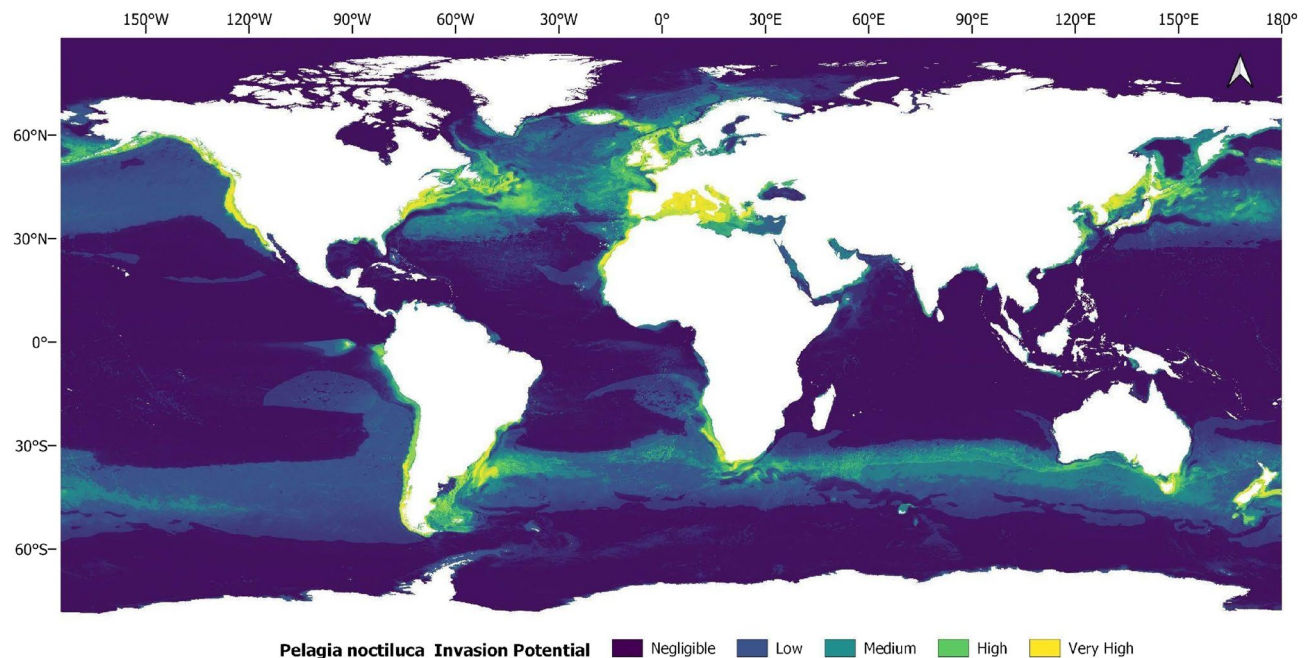


Fig. 4. Habitat suitability of *P. noctiluca* classified into invasion potential categories: negligible (0–200), low (200–400), medium (400–600), high (600–800), and very high (800–1000), based on the model-derived suitability index.

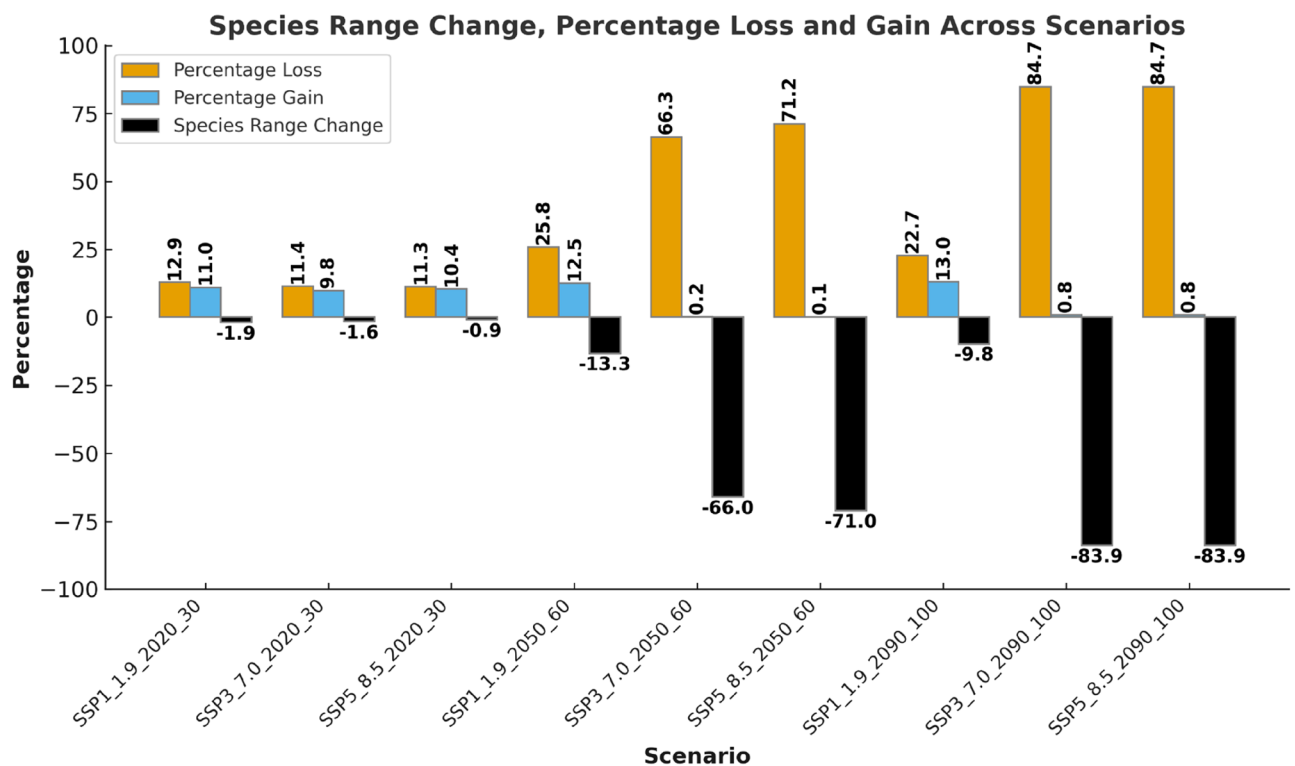


Fig. 5. Species range shift of *P. noctiluca* under different Shared Socioeconomic Pathway (SSP) climate scenarios relative to the predicted current distribution. Percentage loss indicates the proportion of currently suitable areas projected to become unsuitable, Percentage Gain represents the proportion of newly suitable areas relative to the current range size, and species range shift corresponds to the net balance between gain and loss (Percentage Gain – Percentage Loss), reflecting overall range contraction or expansion.

2100) under SSP5-8.5, the species is projected to experience its most severe net range contraction, driven by extensive habitat loss and nominal gains (Fig. 5).

Spatially, these projected range shifts are not uniformly distributed. Mapping the future habitat loss and gain reveals a severe loss of suitable environments across tropical and subtropical regions, especially under the intermediate and high emission scenarios by 2050–2060 and 2090–2100 (Fig. 6; Supplementary Figure 3,4,5,6,7,8,9,10,11). Therefore, the future distribution of *P. noctiluca* is projected to undergo a poleward contraction, with stable presence and newly gained habitats becoming increasingly restricted to higher latitudes (Fig. 6).

Model evaluation and uncertainty

Performance evaluation of individual and ensemble models using the True Skill Statistic (TSS) and Receiver Operating Characteristic (ROC) metrics indicated high predictive accuracy across models. Among the individual models, XGBoost achieved the highest performance, whereas the Surface Range Envelope (SRE) model exhibited the lowest performance (Fig. 7). The ensemble model showed strong predictive capability, with both TSS and ROC values exceeding 0.95, underscoring its superior performance. Furthermore, analysis of the clamping mask indicated the model projections were reliable and accurate in most regions, while the extrapolation uncertainty, due to the environmental predictor values falling outside the calibration range, was largely confined to upper temperate and polar environments, and a few localized coastal areas (Supplementary Fig. 1).

Discussion

By combining species occurrence records with bioclimatic predictors using an ensemble species distribution modelling framework, this study assessed the global habitat suitability of *P. noctiluca* under current environmental conditions and across three future SSP scenarios over three decadal periods. In our interpretation of the invasion potential maps and subsequent discussions, we focussed on regions classified as very high to medium invasion potential, as these areas represent environments with conditions most conducive to establishment and spread.

Under current climatic conditions, *P. noctiluca* exhibits high habitat suitability primarily within temperate marine regions between 25° and 60° in both hemispheres. However, habitat suitability alone does not guarantee invasion success; rather, it represents only one component of a complex invasion process. Introductory pathways, dispersal mechanisms, species-specific traits, and biotic interactions all influence invasion dynamics^{68–72}. Nevertheless, our predictions provide a robust baseline for identifying environmentally suitable regions susceptible to invasion following species introduction, which can be further refined in future works by incorporating dispersal dynamics and introduction pathways.

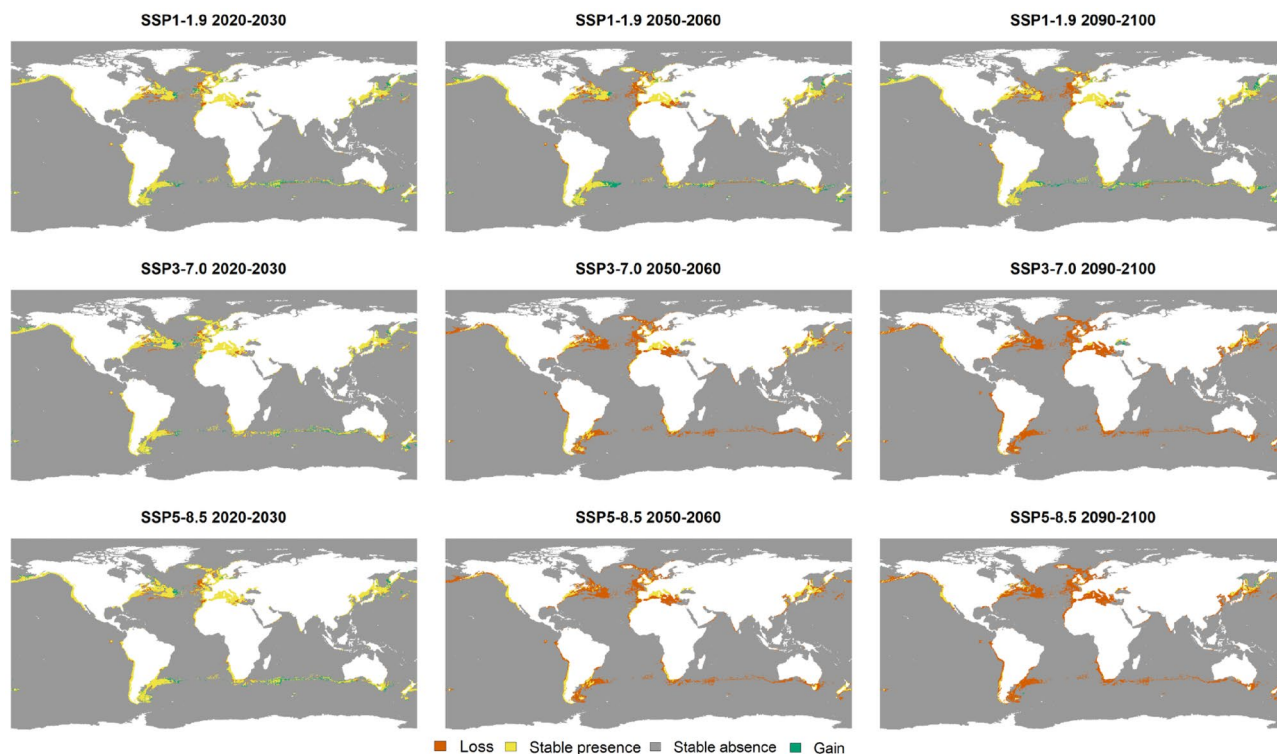


Fig. 6. Map depicting habitat loss and gain for *P. noctiluca* under three Shared Socioeconomic pathways (SSP1-1.9, SSP3-7.0 and SSP5-8.5) across three decadal periods (2020–2030, 2050–2060 and 2090–2100). Areas of projected habitat loss (orange), stable absence (grey), stable presence (yellow) and habitat gain (green) are shown compared to the current modelled distribution. Individual high-resolution maps for each specific scenario and time period are provided in the Supplementary materials for further reference.

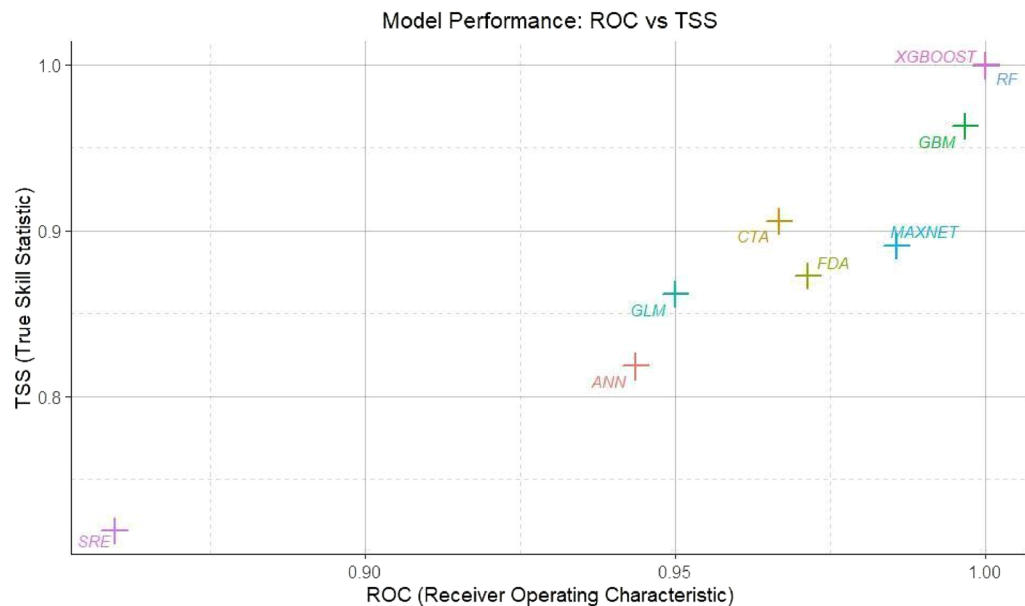


Fig. 7. True skill statistic (TSS) and receiver operating characteristic (ROC) scores of individual models, illustrating the performance of each modelling algorithm used in constructing the ensemble species distribution model for *P. noctiluca*.

Our model prediction of very high habitat suitability in the Mediterranean Sea and the northeast Atlantic is consistent with established knowledge, as these regions represent the native range of *P. noctiluca*^{65,73–76}. However, beyond this native range, bloom occurrences reported from the northern Indian Ocean^{32,34,35} (Hari), North Atlantic^{77–80}, North Sea⁸¹, the Strait of Messina⁸², the Moroccan Mediterranean coast⁸³, and the North Adriatic Sea⁸⁴, and other regions closely align with areas identified by our model as having high invasion potential. This concordance between model outputs and documented bloom records reinforces the predictive validity of the approach.

Our future projections indicate a significant poleward shift in the distribution of *P. noctiluca*, accompanied by an overall contraction of suitable habitat. Such poleward redistribution has been documented in marine taxa, including fish⁸⁵, plankton⁸⁶, benthic invertebrates⁸⁷ and other jellyfish species^{88–90}. Under high-emission climate scenarios, particularly SSP5-8.5, projections for 2090–2100 indicate an estimated reduction of approximately 85.4% in suitable habitats relative to current conditions. Our projections indicate that *P. noctiluca* will experience significant habitat loss in the tropical regions, with suitable conditions for the species becoming increasingly restricted to higher latitudes.

The response of the occurrence probability of *P. noctiluca* to salinity closely matches experimental observations by Catalano et al.⁶⁴, who reported optimal preference at salinity levels of 37 ± 1 PSU, with deviations impairing pulsation and motility. The strong concordance between the physical evidence and modelled response supports the ecological realism of the predictions. Furthermore, our model's identification of primary productivity and sea surface temperature as influential predictors is corroborated by previous studies that highlighted their importance in regulating population dynamics in *P. noctiluca*, particularly during early life stages^{65,66}. Anticipated climate-driven alterations in these variables may therefore have cascading effects on the future distribution and survival of the species^{91–94}.

There is a widespread perception of a globally increasing trend in jellyfish blooms, however our global-scale projections contradict this narrative. As demonstrated by Sanz-Martín et al.⁹⁵, the assumption of a universal jellyfish proliferation is largely unsubstantiated and perpetuated by flawed citation practices, a critique that our results directly corroborate. By applying a global-scale ensemble modelling framework across a suite of environmental variables and multiple climate scenarios, our study extends beyond earlier assessments of *P. noctiluca* that were previously constrained to regional extents^{96,97}. Through this comprehensive, global perspective, we indicate that climate change may negatively influence the future distribution of *P. noctiluca* under projected future climate scenarios. Ultimately, the influence of climate change on invasive species is inherently complex and context-dependent, with potential outcomes including range expansion, contraction or redistribution^{98–101}.

High TSS and ROC values for both individual models and the ensemble model indicate strong model performance, supporting the predictive accuracy and real-world relevance of the projections. However, despite this high predictive performance of the model, several limitations should be acknowledged. Occurrence records sourced from GBIF are subject to strong spatial sampling bias, particularly within the native range where monitoring intensity is greatest. Spatial thinning was therefore applied using the *spThin* R package with a 5.5 km minimum distance threshold, matching the environmental data layers, to reduce this bias. Additionally, pseudo-absence data were used instead of true absences to meet the algorithm requirements, a practice widely

adopted in SDM studies and shown to yield reliable outcomes^{102,103}. Regions identified by the clamping mask as having higher uncertainty should be interpreted cautiously, as predictions in these areas involve environmental extrapolation. Furthermore, while the ensemble modelling approach reduced individual algorithm bias, habitat suitability alone cannot account for biotic resistance, dispersal vectors or oceanographic transport processes. The spatial-resolution paradox may also lead to an underestimation of local refugia and an overestimation of regionally suitable habitat^{104,105}. In particular, coarse-resolution environmental layers aggregate fine-scale environmental variations, causing the model to overlook small, localised refugia while simultaneously artificially expanding the species' estimated environmental tolerance and overestimating habitat suitability at larger scales.

P. noctiluca is widely recognised for its capacity to form intense blooms with ecological and socio-economic impacts. However, contrary to the prevailing assumption that climate change will universally enhance jellyfish proliferation, our projections indicate a substantial contraction of suitable habitats under future climate scenarios, potentially indicating a risk to the long-term survival of the species. It is important to note that SDMs may underestimate survival in microrefugia and do not explicitly account for physiological acclimation or adaptive capacity under suboptimal conditions^{106–108}. Because our results provide a spatial projection of the species' realised niche across global marine environments, these results should be interpreted as predictions of habitat suitability rather than a definitive map of its existing distribution or active invasion success. Future studies integrating dispersal modelling, oceanographic connectivity and anthropogenic introduction pathways would further enhance predictive accuracy. Nonetheless, the projections offer valuable early insights into potential habitat contraction and shifting invasion potential, providing a useful foundation for long-term monitoring and management.

In conclusion, though *P. noctiluca* is widely known for its ability to form dense blooms with severe ecological and socio-economic impacts, our global-scale projections contradict the prevailing assumption that climate change will globally enhance jellyfish proliferation. Instead, our projections indicate a contraction of suitable habitats for this jellyfish species, estimating an 85.4% reduction under high-emission SSP scenarios, accompanied by a significant poleward shift in suitable habitats. These findings have broader implications for understanding the ecology of jellyfish and their impacts. Ecologically, the estimates indicate a severe habitat contraction for the species within tropical and warm temperate regions. However, from a global biosecurity and management perspective, the poleward shift in habitats signals a newly emerging invasion potential in higher-latitude environments. Ultimately, mapping these non-native hotspots provides foundational knowledge that can guide proactive, targeted management strategies to mitigate future *P. noctiluca* invasions globally.

Data availability

The data used is available online and can also be shared on request.

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References

- Gallardo, B., Clavero, M., Sánchez, M. & Vilà, M. Global ecological impacts of invasive species in aquatic ecosystems. *Global Chang. Biol.* <https://doi.org/10.1111/gcb.13004> (2016).
- Gallardo, B. et al. Risks posed by invasive species to the provision of ecosystem services in Europe. *Nat. Commun.* **15**(1), 2631 (2024).
- Hejda, M., Pyšek, P. & Jarošík, V. Impact of invasive plants on the species richness, diversity and composition of invaded communities. *J. Ecol.* <https://doi.org/10.1111/j.1365-2745.2009.01480.x> (2009).
- Holmes, T., Aukema, J., Holle, B., Liebhold, A. & Sills, E. Economic impacts of invasive Species in Forests. *Ann. Sci. New York Acad.* <https://doi.org/10.1111/j.1749-6632.2009.04446.x> (2009).
- Pyšek, P. et al. A global assessment of invasive plant impacts on resident species, communities, and ecosystems: the interaction of impact measures, invading species' traits, and environment. *Glob. Chang. Biol.* **18**, 1725–1737. <https://doi.org/10.1111/j.1365-2486.2011.02636.x> (2012).
- Rai, P. & Singh, J. Invasive alien plant species: Their impact on environment, ecosystem services and human health. *Ecol. Indic.* **111**, 106020–106020. <https://doi.org/10.1016/j.ecolind.2019.106020> (2020).
- Roy, H., Pauchard, A., Stoett, P., Renard Truong, T., Bacher, S., Galil, B. & Vandvik, V. Summary for policymakers of the thematic assessment report on invasive alien species and their control. In *IPBES Invasive Alien Species Assess.* 1–56 (2023).
- Shackleton, R., Shackleton, C. & Kull, C. The role of invasive alien species in shaping local livelihoods and human well-being: a review. *J. Environ. Manag.* **229**, 145–157. <https://doi.org/10.1016/j.jenvman.2018.05.007> (2019).
- Chase-Lubitz, J. Anthropocene briefing: Invasive species could replace native species in extreme weather. *Nature* (2023).
- Hulme, P. Climate change and biological invasions: evidence, expectations, and response options. *Biol. Rev.* <https://doi.org/10.1111/brev.12282> (2017).
- Lockwood, J. L., Hoopes, M. F. & Marchetti, M. P. *Invasion ecology* (John Wiley & Sons, 2013).
- Pyke, C. et al. Current practices and future opportunities for policy on climate change and invasive species. *Conserv. Biol.* <https://doi.org/10.1111/j.1523-1739.2008.00956.x> (2008).
- Rahel, F. & Olden, J. Assessing the effects of climate change on aquatic invasive species. *Conserv. Biol.* <https://doi.org/10.1111/j.1523-1739.2008.00950.x> (2008).
- Ward, N. & Masters, G. Linking climate change and species invasion: an illustration using insect herbivores. *Global Chang. Biol.* <https://doi.org/10.1111/j.1365-2486.2007.01399.x> (2007).
- Gorenz, J., Klarl, M., Nehring, S., Pander, J. & Geist, J. Passage denied: the potential of dispersal barriers to limit the spread of aquatic invasive species through shipping canals. *J. Environ. Manage.* **389**, 126075 (2025).
- Keller, A. G., Counihan, T. D., Grosholz, E. D. & Boettiger, C. The transition from resistance to acceptance: managing a marine invasive species in a changing world. *J. Appl. Ecol.* **62**(3), 715–725 (2025).
- Simberloff, D. Maintenance management and eradication of established aquatic invaders. *Hydrobiologia* <https://doi.org/10.1007/s10750-020-04352-5> (2020).
- Ceh, J., Gonzalez, J., Pacheco, A. S. & Riascos, J. M. The elusive life cycle of scyphozoan jellyfish—metagenesis revisited. *Sci. Rep.* **5**(1), 12037 (2015).

19. Rupp, F. & Scheurle, J. The dynamics of the jellyfish joyride: mathematical discussion of the causes leading to blooming. *Math. Method. Appl. Sci.* **38**, 3408–3420. <https://doi.org/10.1002/mma.3347> (2015).
20. Guy-Haim, T. et al. The effects of decomposing invasive jellyfish on biogeochemical fluxes and microbial dynamics in an ultraoligotrophic sea. *Biogeosci. Discuss.* **2020**, 1–37 (2020).
21. Purcell, J. E., Uye, S. I. & Lo, W. T. Anthropogenic causes of jellyfish blooms and their direct consequences for humans: a review. *Mar. Ecol. Prog. Ser.* **350**, 153–174 (2007).
22. Roohi, A., Fazli, H., Rowshantabari, M., Rahmati, R. & Khodaparast, N. Effect of an invasive species *Mnemiopsis leidyi* on the zooplankton community structure in the Caspian Sea. *J. Great Lakes Res.* **50**(6), 102420 (2024).
23. Forsskål, P. Descriptiones animalium, avium, amphibiorum, piscium, insectorum, vermium. ex officina Mölleri (1775).
24. Canepa, A., Fuentes, V., Sabatés, A., Piraino, S., Boero, F. & Gili, J. M. Pelagia noctiluca in the Mediterranean Sea. In *Jellyfish blooms* 237–266 (2014).
25. Franc, A. Classe des Scyphomeduses (Scyphozoa Goette, 1887)(Acraspeda Gegenbaur, 1856). *Traité de Zoologie. Anatomie, Systematique, Biologie.* Publié sous la direction de Pierre-P. Grassé. Tome III. Cnidaire, Cténaires. Fascicule, **2** (1993).
26. Mariottini, G. L., Giacco, E. & Pane, L. The Mauve Stinger *Pelagia noctiluca* (Forsskål, 1775). Distribution, ecology, toxicity and epidemiology of stings. *Mar. Drug.* **6**(3), 496–513 (2008).
27. Sabatés, A. et al. Planktonic cnidarian distribution and feeding of *Pelagia noctiluca* in the NW Mediterranean Sea. *Hydrobiologia* **645**(1), 153–165 (2010).
28. Spallanzani, L. Voyages dans les deux Siciles et dans quelques parties des Apennins Vol. 1 Chez Emanuel Haller (1795).
29. Tibballs, J. Australian venomous jellyfish, envenomation syndromes, toxins, and therapy. *Toxicon* **48**(7), 830–859 (2006).
30. Greer, A. T., Chiaverano, L. M., Luo, J. Y., Cowen, R. K. & Graham, W. M. Ecology and behaviour of holoplanktonic scyphomedusae and their interactions with larval and juvenile fishes in the northern Gulf of Mexico. *ICES J. Mar. Sci.* **75**(2), 751–763 (2018).
31. Baliarsingh, S. K., Srichandan, S., Sahu, K. C. & Lotliker, A. A. Occurrence of a new species of toxic Cnidaria (*Pelagia noctiluca* Forskål, 1775) from estuarine waters of Rushikulya River, Western Bay of Bengal. *Indian J. Geo-Mar. Sci.* **44**(4), 580–582 (2015).
32. Praved, H. P. et al. Report of Mauve Stinger *Pelagia cf. noctiluca* (Cnidaria: Scyphozoa) bloom from Northeastern Arabian Sea (NEAS). *Thalass. Int. J. Mar. Sci.* **37**(2), 569–576 (2021).
33. Lakshmanan, R. et al. Occurrence of the non-native Mauve Stinger, *Pelagia cf. noctiluca*, in coastal waters off Cape Comorin, Southern Bay of Bengal. *J. Coast. Res.* **40**(6), 1103–1110 (2024).
34. Ramesh, C. H., Koushik, S., Shunmugaraj, T. & Ramana Murthy, M. V. Occurrence of a Scyphozoan jellyfish, *Pelagia noctiluca* (Forskål, 1775) bloom in the Gulf of Mannar Marine National Park, Southern India. *Indian J. Geo-Mar. Sci. (IJMS)* **50**(02), 161–164 (2022).
35. Milisenda, G. et al. Seasonal variability of diet and trophic level of the gelatinous predator *Pelagia noctiluca* (Scyphozoa). *Sci. Rep.* **8**(1), 12140 (2018).
36. Ferraris, M. et al. Distribution of *Pelagia noctiluca* (Cnidaria, Scyphozoa) in the Ligurian Sea (NW Mediterranean Sea). *J. Plankton Res.* **34**, 874–885. <https://doi.org/10.1093/PLANKT/FBS049> (2012).
37. Zavodnik, D. J. M. B. Spatial aggregations of the swarming jellyfish *Pelagia noctiluca* (Scyphozoa). *Mar. Biol.* **94**(2), 265–269 (1987).
38. Helm, R. R., Tiozzo, S., Lilley, M. K., Lombard, F. & Dunn, C. W. Comparative muscle development of scyphozoan jellyfish with simple and complex life cycles. *EvoDevo* **6**, 1–10 (2015).
39. Hutchinson, G. E. Concluding remarks. In *Cold Spring Harbor symposia on quantitative biology* 22, 415–427 (Cold Spring Harbor Laboratory Press, 1957).
40. Lechner, A. M., Langford, W. T., Bekessy, S. A. & Jones, S. D. Are landscape ecologists addressing uncertainty in their remote sensing data? *Landsc. Ecol.* **27**(9), 1249–1261 (2012).
41. Riva, F. & Nielsen, S. E. A functional perspective on the analysis of land use and land cover data in ecology. *Ambio* **50**(5), 1089–1100. <https://doi.org/10.1007/s13280-020-01434-5> (2021).
42. Guisan, A. & Zimmermann, N. E. Predictive habitat distribution models in ecology. *Ecol. Model.* **135**(2–3), 147–186 (2000).
43. Sofaer, H. R. et al. Development and delivery of species distribution models to inform decision-making. *Bioscience* **69**(7), 544–557 (2019).
44. Elith, J. & Leathwick, J. R. (2009). Species distribution models: ecological explanation and prediction across space and time. *Annu. Rev. Ecol. Syst.* **40** (1), 677–697.
45. Franklin, J. Species distribution models in conservation biogeography: developments and challenges. *Divers. Distrib.* **19**(10), 1217–1223 (2013).
46. Jiménez-Valverde, A. et al. Use of niche models in invasive species risk assessments. *Biol. Invasion.* **13**(12), 2785–2797 (2011).
47. Barbet-Massin, M., Rome, Q., Villemant, C. & Courchamp, F. (2018). Can species distribution models really predict the expansion of invasive species? *PLoS ONE*, **13** (3), e0193085.
48. Mainali, K. P. et al. Projecting future expansion of invasive species: comparing and improving methodologies for species distribution modeling. *Global Chang. Boil.* **21**(12), 4464–4480 (2015).
49. Lee, W. H., Song, J. W., Yoon, S. H. & Jung, J. M. Spatial evaluation of machine learning-based species distribution models for prediction of invasive ant species distribution. *Appl. Sci.* **12**(20), 10260 (2022).
50. Lewis, J. S. et al. Biotic and abiotic factors predicting the global distribution and population density of an invasive large mammal. *Sci. Rep.* **7**(1), 44152 (2017).
51. Jones, M. C., Dye, S. R., Pinnegar, J. K., Warren, R. & Cheung, W. W. Modelling commercial fish distributions: prediction and assessment using different approaches. *Ecol. Model.* **225**, 133–145 (2012).
52. Thuiller, W. et al. biomod2: ensemble platform for species distribution modeling. *R. Packag. Vers.* **4**, 2–5 (2023).
53. Breiner, F. T., Nobis, M. P., Bergamini, A. & Guisan, A. Optimizing ensembles of small models for predicting the distribution of species with few occurrences. *Method. Ecol. Evol.* **9**(4), 802–808 (2018).
54. Erickson, K. D. & Smith, A. B. Modeling the rarest of the rare: A comparison between joint species distribution models, ensembles of small models, and single-species models at extremely low sample sizes. In *bioRxiv* 2022–06 (2022).
55. Grenouillet, G., Buisson, L., Casajus, N. & Lek, S. Ensemble modelling of species distribution: the effects of geographical and environmental ranges. *Ecography* **34**(1), 9–17 (2011).
56. GBIF.org GBIF Occurrence Download <https://doi.org/10.15468/dl.wsbxxn> (2024).
57. Aiello-Lammens, M. E., Boria, R. A., Radosavljevic, A., Vilela, B. & Anderson, R. P. spThin: an R package for spatial thinning of species occurrence records for use in ecological niche models. *Ecography* **38**(5), 541–545 (2015).
58. QGIS Development Team, QGIS Geographic Information System. *Open Source Geospatial Foundation Project.* <http://qgis.org> (2024).
59. Assis, J. et al. Bio-ORACLE v3.0. Pushing marine data layers to the CMIP6 earth system models of climate change research. *Glob. Ecol. Biogeogr.* **33**(4), e13813 (2024).
60. Masson-Delmotte, V. et al. Climate change 2021: the physical science basis. *Contrib. Work. Gr. I to the sixth Assess. Rep. Intergov. Panel. Climat. Chang.* **2**(1), 2391 (2021).
61. Hall, A. Projecting regional change. *Science* **346**(6216), 1461–1462 (2014).
62. Schoeman, D. S. et al. Demystifying global climate models for use in the life sciences. *Trend. Ecol. Evol.* **38**(9), 843–858 (2023).
63. Catalano, G., Avian, M. & Zanelli, R. Influence of salinity on the behaviour of *Pelagia noctiluca* (Forskål)(Scyphozoa, Semaestomeae) (1985).

64. Ottmann, D. et al. Abundance of *Pelagia noctiluca* early life stages in the western Mediterranean Sea scales with surface chlorophyll. *Mar. Ecol. Prog. Ser.* **658**, 75–88 (2021).
65. Rosa, S., Pantera, M., Granata, A. & Guglielmo, L. Interannual variability, growth, reproduction, and feeding of *Pelagia noctiluca* (Cnidaria: Scyphozoa) in the Straits of Messina (Central Mediterranean Sea): Linkages with temperature and diet. *J. Mar. Syst.* **111**, 97–107. <https://doi.org/10.1016/j.jmarsys.2012.10.001> (2013).
66. Barbet-Massin, M., Jiguet, F., Albert, C. H. & Thuiller, W. Selecting pseudo-absences for species distribution models: how, where and how many?. *Method. Ecol. Evol.* **3**(2), 327–338 (2012).
67. Clarke Murray, C. et al. Spatial distribution of marine invasive species: environmental, demographic and vector drivers. *Divers. Distrib.* **20**(7), 824–836 (2014).
68. Lindgren, M., Gabellini, A. P., Munk, P., Edelvang, K. & Hansen, F. T. Identifying key processes and drivers affecting the presence of non-indigenous marine species in coastal waters. *Biol. Invasions.* **24**(9), 2835–2850 (2022).
69. Marks, L. M., Reed, D. C. & Holbrook, S. J. Niche complementarity and resistance to grazing promote the invasion success of *Sargassum horneri* in North America. *Diversity* **12**(2), 54 (2020).
70. McKnight, E., García-Berthou, E., Srean, P. & Rius, M. Global meta-analysis of native and nonindigenous trophic traits in aquatic ecosystems. *Glob. Change Biol.* **23**(5), 1861–1870 (2017).
71. Stachowicz, J. J., Whitlatch, R. B. & Osman, R. W. Species diversity and invasion resistance in a marine ecosystem. *Science* **286**(5444), 1577–1579 (1999).
72. Bergamasco, A. et al. Observing and modeling long-term persistence of *P. noctiluca* in coupled complementary marine systems (Southern Tyrrhenian Sea and Messina Strait). *Sci. Rep.* **12**(1), 14905 (2022).
73. Marambio, M. et al. Unfolding jellyfish bloom dynamics along the Mediterranean Basin by transnational citizen science initiatives. *Diversity* **13**(6), 274 (2021).
74. Montesanto, F., Albano, M., Ayaş, D., Betti, F. & Yapıcı, S. New records of rare species in the Mediterranean Sea (December 2022) (2023).
75. Tilves, U. et al. Natural diet and predation impacts of *Pelagia noctiluca* on fish eggs and larvae in the NW Mediterranean. *J. Plankton Res.* **38**(5), 1243–1254 (2016).
76. Kennerley, A., Wood, L. E., Luisetti, T., Ferrini, S. & Lorenzoni, I. Economic impacts of jellyfish blooms on coastal recreation in a UK coastal town and potential management options. *Ocean Coast. Manag.* **227**, 106284 (2022).
77. Long, A. P. et al. Regular widespread aggregations of the oceanic jellyfish *Pelagia noctiluca* in the Northeast Atlantic over 11 years. *Estuar. Coast. Shelf Sci.* <https://doi.org/10.1016/j.ecss.2024.108805> (2024).
78. Miller, B. J., Von der Heyden, S. & Gibbons, M. J. Significant population genetic structuring of the holoplanktic scyphozoan *Pelagia noctiluca* in the Atlantic Ocean. *Afr. J. Mar. Sci.* **34**(3), 425–430 (2012).
79. Rapp, J. et al. Microplastic ingestion in jellyfish *Pelagia noctiluca* (Forsskal, 1775) in the North Atlantic Ocean. *Mar. Pollut. Bull.* **166**, 112266 (2021).
80. Baxter, E. J., Walne, A. W., Purcell, J. E., McAllen, R. & Doyle, T. K. Identification of jellyfish from continuous plankton recorder samples. In *Jellyfish Blooms: New Problems and Solutions* 193–201 (2010).
81. Milisenda, G. et al. Reproductive and bloom patterns of *Pelagia noctiluca* in the Strait of Messina, Italy. *Estuar. Coast. Shelf Sci.* **201**, 29–39 (2018).
82. Mghili, B., Analla, M. & Aksissou, M. Estimating the economic damage caused by jellyfish to fisheries in Morocco. *Afr. J. Mar. Sci.* **44**(3), 271–277 (2022).
83. Kogovšek, T., Bogunović, B. & Malej, A. Recurrence of bloom-forming scyphomedusae: wavelet analysis of a 200-year time series. In *Jellyfish blooms: new problems and solutions* 81–96 (2010).
84. Perry, A., Low, P., Ellis, J. & Reynolds, J. Climate change and distribution shifts in marine fishes. *Science* **308**, 1912–1915. <https://doi.org/10.1126/SCIENCE.1111322> (2005).
85. Beaugrand, G., Reid, P., Ibañez, F., Lindley, J. & Edwards, M. Reorganization of North Atlantic marine copepod biodiversity and climate. *Science* **296**, 1692–1694. <https://doi.org/10.1126/SCIENCE.1071329> (2002).
86. Hiddink, J., Burrows, M. & Molinos, J. Temperature tracking by North Sea benthic invertebrates in response to climate change. *Global Chang. Biol.* <https://doi.org/10.1111/gcb.12726> (2015).
87. Brodeur, R. et al. Rise and fall of jellyfish in the Eastern Bering Sea in relation to climate regime shifts. *Prog. Oceanogr.* **77**, 103–111. <https://doi.org/10.1016/j.pcean.2008.03.017> (2008).
88. Holst, S. Effects of climate warming on strobilation and ephyra production of North Sea scyphozoan jellyfish. *Hydrobiologia* **690**, 127–140. <https://doi.org/10.1007/s10750-012-1043-y> (2012).
89. Lynam, C. et al. Have jellyfish in the Irish Sea benefited from climate change and overfishing?. *Global Biol. Chang.* <https://doi.org/10.1111/j.1365-2486.2010.02352.x> (2011).
90. Doney, S. et al. Climate change impacts on marine ecosystems. *Annu. Rev. Mar. Sci.* **4**, 11–37. <https://doi.org/10.1146/ANNUREV-MARINE-041911-111611> (2012).
91. Häder, D. & Gao, K. Aquatic productivity under multiple stressors. *Water* <https://doi.org/10.3390/w15040817> (2023).
92. Nagelkerken, I. & Connell, S. Global alteration of ocean ecosystem functioning due to increasing human CO₂ emissions. *Proc. Natl. Acad. Sci. U. S. A.* **112**, 13272–13277. <https://doi.org/10.1073/pnas.1510856112> (2015).
93. Röthig, T. et al. Human-induced salinity changes impact marine organisms and ecosystems. *Glob. Change Biol.* **29**, 4731–4749. <https://doi.org/10.1111/gcb.16859> (2023).
94. Sanz-Martín, M. et al. Flawed citation practices facilitate the unsubstantiated perception of a global trend toward increased jellyfish blooms. *Glob. Ecol. Biogeogr.* **25**(9), 1039–1049 (2016).
95. Doyle, T. K. et al. Widespread occurrence of the jellyfish *Pelagia noctiluca* in Irish coastal and shelf waters. *J. Plankton Res.* **30**(8), 963–968 (2008).
96. Kennerley, A., Lorenzoni, I., Luisetti, T., Wood, L. E. & Taylor, N. G. H. Mapping habitats for the suitability of jellyfish blooms around the UK and Ireland. *Hydrobiologia* **848**(7), 1535–1552 (2021).
97. Bellard, C. et al. Will climate change promote future invasions?. *Global Chang. Biol.* <https://doi.org/10.1111/gcb.12344> (2013).
98. Bradley, B., Oppenheimer, M. & Wilcove, D. Climate change and plant invasions: restoration opportunities ahead. *Global Chang. Biol.* <https://doi.org/10.1111/j.1365-2486.2008.01824.x> (2009).
99. Clements, D. & DiTommaso, A. Climate change and weed adaptation: can evolution of invasive plants lead to greater range expansion than forecasted?. *Weed Res.* **51**, 227–240. <https://doi.org/10.1111/J.1365-3180.2011.00850.X> (2011).
100. Ihlow, F. et al. Impacts of climate change on the global invasion potential of the African Clawed frog *xenopus laevis*. *PLoS ONE* <https://doi.org/10.1371/journal.pone.0154869> (2016).
101. Iturbide, M. et al. A framework for species distribution modelling with improved pseudo-absence generation. *Ecol. Model.* **312**, 166–174. <https://doi.org/10.1016/j.ecolmodel.2015.05.018> (2015).
102. Schickele, A. et al. Modelling European small pelagic fish distribution: methodological insights. *Ecol. Model.* <https://doi.org/10.1016/j.ecolmodel.2019.108902> (2020).
103. Lenoir, J., Hattab, T. & Pierre, G. Climatic microrefugia under anthropogenic climate change: implications for species redistribution. *Ecography* **40**(2), 253–266 (2017).
104. Meineri, E. & Hylander, K. Fine-grain, large-domain climate models based on climate station and comprehensive topographic information improve microrefugia detection. *Ecography* **40**(8), 1003–1013 (2017).

105. Melo-Merino, S. M., Reyes-Bonilla, H. & Lira-Noriega, A. Ecological niche models and species distribution models in marine environments: A literature review and spatial analysis of evidence. *Ecol. Model.* **415**, 108837 (2020).
106. Muhling, B. A. et al. Predictability of species distributions deteriorates under novel environmental conditions in the California Current System. *Front. Mar. Sci.* **7**, 589 (2020).
107. Robinson, N. M., Nelson, W. A., Costello, M. J., Sutherland, J. E. & Lundquist, C. J. A systematic review of marine-based species distribution models (SDMs) with recommendations for best practice. *Front. Mar. Sci.* **4**, 421 (2017).
108. Thuiller, W., Georges, D., Engler, R. & Breiner, F.T. biomod2: ensemble platform for species distribution modelling (version R package version 3.3–7.1) (2019).

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During the preparation of this work, the authors used ChatGPT and NotebookLM to check the grammar and other lexical errors. After using this tool/service, the author(s) reviewed and edited the content as needed and take full responsibility for the content of the published article.

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