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ORIGINAL ARTICLE

Predicting the distribution of fish community in the Persian Gulf using joint species distribution modelling with a latent variable model

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Abstract
Delineating marine fishes' distribution and home range may help manage and set marine protected areas. While single-species distribution models provide some information about the home range of species, they do not incorporate the interactions among species and may not provide an accurate picture of community distribution in a given habitat. Hence, the present study modeled the distribution of marine fish communities in the Persian Gulf using joint species distribution modeling. In addition, this study converted the predicted presence of every species to dichotomized presence or absence output to facilitate the interpretation of the results. Most species had wide or sporadic distribution across the Persian Gulf, but some indicated contagious distribution mostly confined to coastal areas close to the Hormuz Strait. The presence study showed that joint species distribution has high accuracy and facilitates predicting fish communities across large geographical areas, allowing us to predict such communities simultaneously.

Keywords: Distribution, Modeling, Latent variable model, Persian Gulf. Fish Communities.

INTRODUCTION

The Persian Gulf is a body of water in the Western Asian region, nestled between Iran and the Hormuz Strait. This remarkable gulf is significant for its strategic position and rich and diverse marine ecosystems, particularly its fisheries (Karimpour et al. 2013). The Persian Gulf covers approximately 251,000 square kilometers, making it a relatively shallow and enclosed sea. Its warm and saline waters are influenced by the Indian Ocean, creating a unique and dynamic marine environment. The Persian Gulf is home to a wide range of habitats, including coral reefs, seagrass meadows, mangrove forests, and rocky shores, which provide essential breeding, feeding, and sheltering grounds for numerous marine species (Fatemi & Shokri 2001; Abdelbary & Al Ashwal 2021). The Persian Gulf boasts a remarkable abundance of marine life, making it a vital fishery region. Its waters are teeming with a diverse taxa of fish species, including groupers, snappers, emperor fish, sardines, and mackerel, to name just a few (Eagderi et al. 2019). These species support artisanal and commercial fisheries, providing a source of livelihood for local communities and contributing to the regional economy (Ben-Hasan & Daliri 2023). The fisheries of the Persian Gulf have played a significant role in the culture, history, and economy of the countries bordering the Gulf for centuries (Haiduc-Dale 2018). Despite its importance, the Persian Gulf's fisheries face various challenges. Overfishing, habitat degradation, pollution, and climate change pose significant threats to the sustainability of fish stocks and the overall health of the marine ecosystem (Edmonds et al. 2021). Therefore, conservation efforts are crucial to ensure the long-term viability of the fisheries in the Persian Gulf. Collaborative initiatives between governments, local communities, and scientific organizations should work towards implementing sustainable fishing practices, protecting critical habitats, and promoting responsible fishing techniques.

Species distribution modeling (SDM) is a useful tool for predicting the distribution and abundance of marine fishes (Melo-Merino et al. 2020). SDMs map the probability of occurrence of a species across a landscape by quantifying the relationship between species occurrence or abundance with biotic and abiotic factors (Williams et al. 2009). In the marine environment, SDMs have been used to predict the present and future distribution patterns of marine fish

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by modeling the distribution patterns of marine fish across the ocean using averages of climatic variables such as salinity, chlorophyll, and sea surface temperature (Ghaitaranpour et al. 2019). A critical step in the modeling process is understanding the interplay between the ecological processes that drive the realized species distribution (Cabral et al. 2019). Joint Species Distribution Modeling (JSDM) is a statistical method encompassing interactions among species and is superior to single-species distribution modeling. It is a fast-developing field that promises to revolutionize how data on ecological communities are analyzed and has been increasingly applied in conservation biology. JSDM is a useful tool for explaining or predicting the range and abundance of several species at once. It is becoming an increasingly popular statistical method in conservation biology and is used to explain spatial variation in community composition by contributions of the environment and species interactions.

JSDM benefits from Latent Variable Models (LVM), which are statistical techniques used to explain and investigate correlations between large collections of observed variables by incorporating one or more unobserved (latent) variables (Warton et al. 2015). LVMs can be categorized based on various factors, including the nature of response variables (continuous or discrete), the characteristics of the latent variables (discrete or continuous), and the inclusion or exclusion of individual covariates (Tikhonov et al. 2020). LVMs are particularly useful for capturing abstract or complex characteristics of a system that are difficult to measure or describe precisely. They play a crucial role in identifying underlying links and patterns that may not be readily apparent.

LVMs are a subset of latent structure models and are used to explain spatial variation in community composition by contributions of the environment and species interactions. Different statistical analyses are applied to different variables (Wilkinson et al. 2019). For instance, continuous variable distributions are often assumed normal, while categorical variable distributions are assumed to be binomial or multinomial. LVMs find extensive use, particularly when dealing with multilevel, longitudinal panel data and repeated observations. These models are typically used to leverage prior knowledge when defining a model and increase the expressive power of the model. They enable a model design that captures complex relationships and dependencies among variables, making them particularly valuable for analyzing multivariate community data.

The motivation of the present paper is to utilize Latent Variable Models (LVM) to predict the distribution of marine fishes in the Persian Gulf. This approach is motivated by the need for a quantitative method to analyze multivariate community data, particularly in the context of marine fish distribution. Formerly, multivariate community data have been analyzed using descriptive methods like Principal Component Analysis (PCA) and Redundancy Analysis (RDA). However, LVM provides a more quantitative approach, allowing for incorporating interactions among species, which is crucial for understanding the complex ecological relationships in marine ecosystems. The use of LVM is particularly relevant in predicting the distribution of marine fishes, as it allows for considering the intricate interactions and dependencies among species in the marine environment. This approach aims to provide a more comprehensive and accurate understanding of the distribution patterns of marine fishes in the Persian Gulf, considering the complex ecological dynamics that influence their spatial distribution.

MATERIALS AND METHODS

Fishing data: The required data for the present study were obtained from the Institute of Marine and Antarctic Studies of the University of Tasmania, Australia (Watson 2016). The data covered the years 2010 to 2014. The species used for modelling are listed in Table 1. A significant portion of the data was labeled as “Marine fishes not identified” and was excluded from the study. Only the data for 2014 were utilized since it had the highest number of non-duplicated coordinated data across the species.

Environmental data: The environmental data

Table 1. The species used to model their distribution in the Persian Gulf.

ID	Species name
1	*Tenualosa ilisha*
2	*Nemipterus japonicus*
3	*Platycephalus indicus*
4	*Chirocentrus nudus*
5	*Scomberomorus commerson*
6	*Valamugil seheli*
7	*Scomberomorus guttatus*
8	*Epinephelus coioides*
9	*Sardinella longiceps*
10	*Parastromateus niger*
11	*Rastrelliger kanagurta*
12	*Pampus argenteus*
13	*Istiophorus platypterus*
14	*Euthynnus affinis*
15	*Carcharhinus longimanus*
16	*Sphyrna zygaena*
17	*Isurus oxyrinchus*

Table 1. The parameters used as independent variables for modeling the presence of marine fish species in the Persian Gulf.

Parameters	Abbreviated name	Unit	Spatial resolution	Platform
Chlorophyll-a concentration	Chl	mg m^{-3}	0.08° × 0.08°	Aqua
Calcit	PIC	mol m^{-3}	0.08° × 0.08°	Aqua
Particulate organic carbon	POC	mg m^{-3}	0.08° × 0.08°	Aqua
Reflectance at 645 nm	X645	sr^{-1}	0.08° × 0.08°	Aqua
Aerosol optical thickness at 869 nm	AOT869		0.08° × 0.08°	Aqua
Aerosol angstrom exponent (443- 865 nm)	Ac		0.08° × 0.08°	Aqua
Sea surface temperature at day	SSTD	°C	0.08° × 0.08°	Aqua
Sea surface temperature at night	SSTN	°C	0.08° × 0.08°	Aqua
Photosynthetically active radiation	PAR		0.08° × 0.08°	Aqua
Absorption due to phytoplankton at 443 nm	Phy	m^{-1}	0.08° × 0.08°	Aqua

consisted of satellite remotely sensed data accessible online through the MODIS NASA website (NASA Goddard Space Flight Center, Ocean Ecology Laboratory 2021). The parameters used in the study are listed in Table 2. Turbidity was determined by measuring the reflectance at 645 nm (Chen et al. 2007). All data were in netcdf (.nc) format and were transformed to raster using the raster R package (Hijmans 2021) for data extraction and further analysis. These raster layers were cropped specifically for the Persian Gulf (Fig. 1), and duplicate coordinates were removed using the duplicate function in R. The Pearson correlation coefficient was used to examine the collinearity among the variables to eliminate those being highly correlated to others (≥ 0.95). As no variable was highly correlated with others, all variables were used for modeling. Environmental data were scaled to have a mean of 0 and a variance of 1; therefore, their coefficients in the model (β) were used to examine their importance in the model and, hence, the presence of the species.

Dichotomizing the fishing data: The catch data (y_{ij}) from various coordinates (sites, i) and species (j) were obtained using different fishing methods and types of efforts. Due to this variation and incompatibility between methods, it was impossible to directly convert catch data from one fishing method to another. Consequently, a transformation method was employed. The catch data for a specific coordinate in the Persian Gulf was assigned a value of 1, indicating

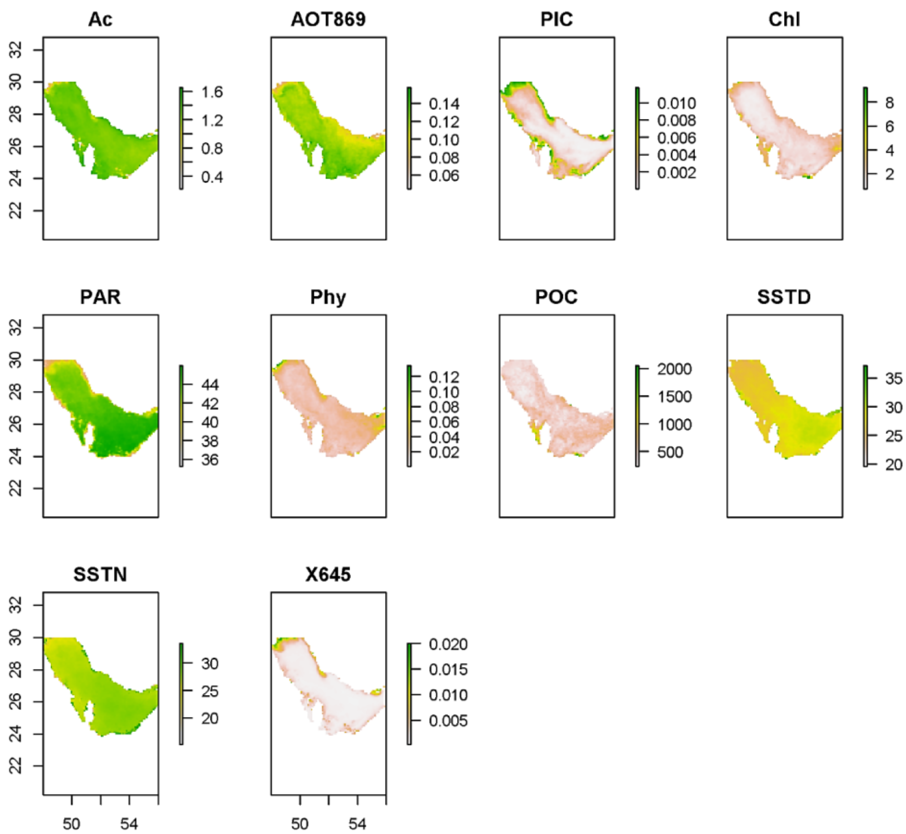

Fig.1. The annually-averaged data of environmental variables across the Persian Gulf in 2014 (NASA Goddard Space Flight Center, Ocean Ecology Laboratory, 2021). To find the full names of the parameters, refer to Table 2.

the presence of the species at that point. For all other coordinates in the dataset where no catch was reported for a given species in 2014, a value of 0 was assigned. This approach ensures a standardized representation of the presence or absence of a species at different coordinates in the Persian Gulf dataset. In mathematical notation:

$$y_{ij} = \begin{Bmatrix} 0 & \text{if } y_{ij} = 0 \\ 1 & \text{if } y_{ij} > 0 \end{Bmatrix} \qquad \text{Equation 1}$$

Modelling: Any row of the dataset containing missing values for a particular environmental parameter was eliminated using listwise deletion. Therefore, not all coordinates of the Persian Gulf were used for modeling and prediction. Ultimately, a dataset consisting of 557 rows remained. The dataset was divided into training and testing data, with the latter containing 30% of the data. A latent variable model with a probit link function was applied using the R package jSDM (Clément & Vieilledent 2023).

Thresholding to dichotomize the predicted probability: To convert the predicted probabilities of presence (θ_{ij}) of each species (*j*) overfishing sites (*i*; *i* = 1, …, 389) of the training data set to 0 (= absence) or 1 (= presence), the threshold values (t_n) ranging from 0.01 to 1 ($\Delta = 0.01$, $n = 1, \ldots, 100$; *i.e.* $t_1 = 0.01$, $t_{100} = 1$), were examined and if $\theta_{ij} \leq t_n$, 0 was assigned, or 1 if $\theta_{ij} > t_n$; mathematically,

$$\theta'_{ijn} = \begin{cases} 0 & \text{if } \theta_{ijn} \leq t_n \\ 1 & \text{if } \theta_{ijn} > t_n \end{cases} \qquad \text{Equation 2}$$

The quality of the models was attested using accuracy (Kuhn & Johnson 2013). For each threshold value (t_n), the accuracy (ACC) between the binary θ_{ij}s predicted probabilities (θ'_{ij}) and the real 0-1 values (y_{ij}) of a given species (*j*) was calculated ($ACC_{\theta'_{ijn}, y_{ij}}$). The real 0-1 values were those used for training of the model (y_{ij}). Therefore, for each threshold value (t_n), 17 ACCs ($ACC_{\theta'_{jn}, y_j}$) were found that were relevant to

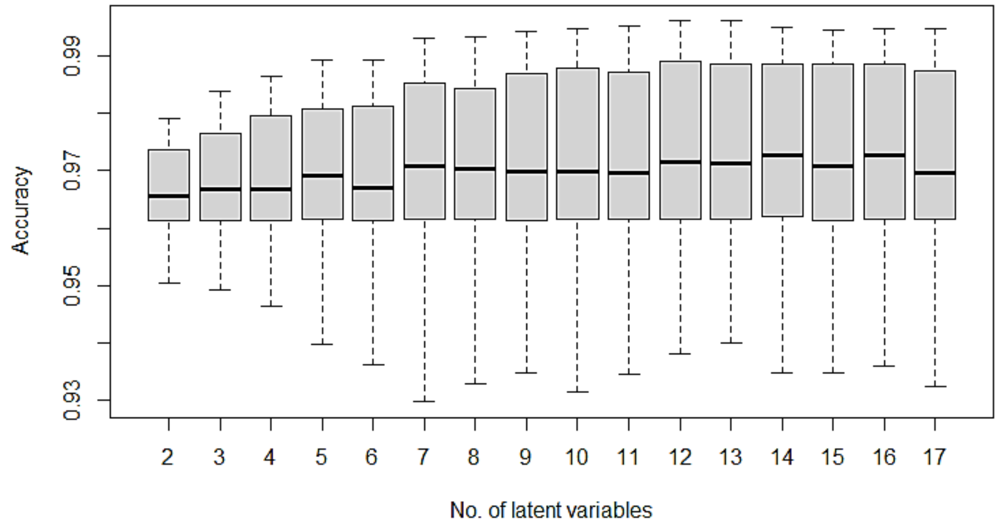

Fig.2. The accuracy between the real training presence data and the dichotomized predicted data from the models with different numbers of latent variables to find the optimal number of latent variables. The variation of the values in each boxplot is a result of different threshold values (t_n). The horizontal line inside the boxes indicates the median of the accuracies.

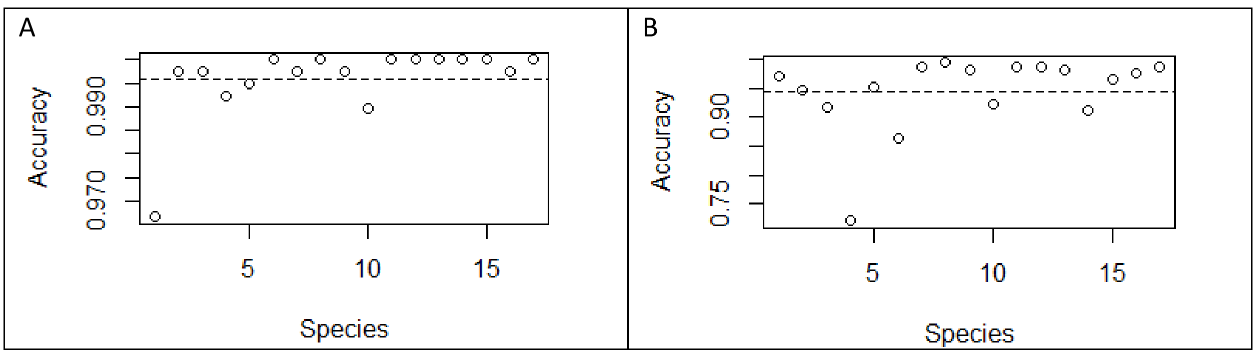

Fig.3. The accuracy between real binary presence data of the training (A) or testing (B) data (θ_j) and the dichotomized predicted probability of the presence of the species (θ'_j) in the model with 12 latent variables model. The dashed line indicates the average of all accuracy values. To find the full names of the species refer to Table 1.

17 species. In total, 1700 ACCs were calculated (17 species [j] × 100 threshold values [n] from 0.01 to 1). The mean of the 17 ACCs of the species was calculated across the 100 t_n s resulting in new 100 mean ACCs ($\overline{ACC}_{ACC_{\theta'_{jn},y_j}}$). The t_n corresponding to the highest $\overline{ACC}_{ACC_{\theta'_{jn},y_j}}$ was considered as the best threshold value (t); mathematically,

$$t = t_n[\max(\overline{ACC}_{ACC_{\theta'_{jn},y_j}})] \qquad \text{Equation 3}$$

To find the best number of latent variables, different values from 2 to 17 were used. The thresholding method was applied for each model with a given latent variable. Finally, the model with the highest $\overline{ACC}_{ACC_{\theta'_{jn},y_j}}$ was considered as the model with the best number of latent variables, and the corresponding best threshold was chosen for that specific model.

RESULTS

A model with 12 latent variables was found to have the maximum accuracy and was hence selected as the best model (Fig. 2). The best threshold value for this model was 0.23.

Figure 3 presents the accuracies of the best-selected model, the one with 12 latent variables and a threshold value of 0.23, across the species. The model

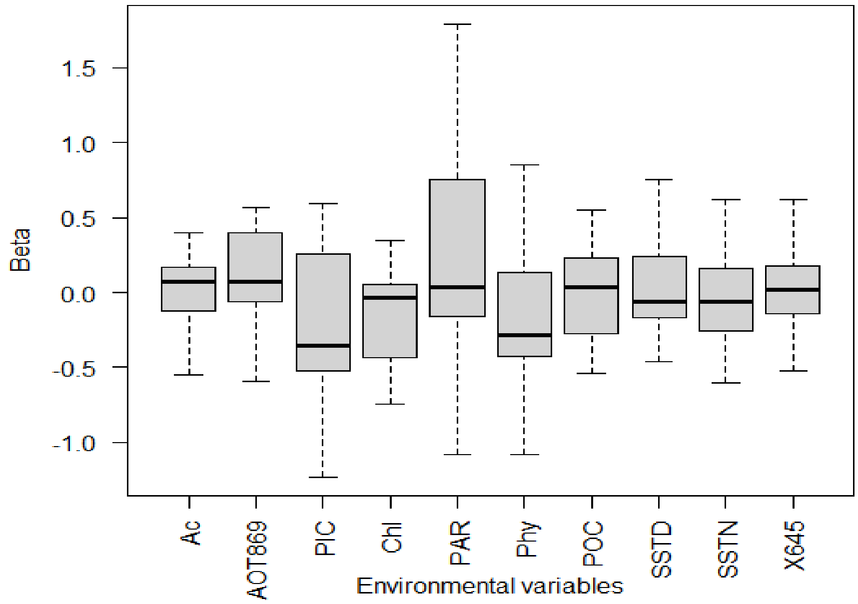

Fig.4. The coefficients (β) of environmental parameters for the best model with 12 latent variables. To find the full names of the parameters, refer to Table 2.

accurately predicted the presence of most species.

The variation of the coefficients (β) of the environmental parameters in the model during training has been demonstrated in Figure 4. All environmental variables have almost similar importance for the presence of the species; however, based on the median of β, PIC and AOT869 were the least and most important variables for the presence of the species, respectively.

The predicted presence of species in the Persian Gulf has been presented in Figure 5. Among the species, *Chirocentrus nudus*, *Euthynnus affinis*, *Carcharinus longimanus*, *Isurus oxyrinchus*, *Epinephelus coioides,* and *Rastrelliger kanagurta* had sporadic wide distributions across the Persian Gulf. *Platycephalus indicus*, *Scomberomorus guttatus*, *Parastromateus niger*, and *Sardinella longiceps* were mostly limited to the west of the Hormuz Strait in the eastern part of the Gulf. *Tenualosa ilisha* was predicted to have limited distribution west of the Hormuz Strait. *Pampus argenteus*, *Sphyrna zygaena*, *Istiophorus platypterus*, and *Nemipterus japonicus* were mostly limited to the southeastern part of the Gulf. *Valamugil seheli* was mostly found in the southern and western coastal waters.

DISCUSSION

Predicting fish distribution in the Persian Gulf is necessary for understanding and managing marine ecosystems, especially in the context of environmental changes and anthropogenic impacts. In this study, we employed satellite remotely sensed data and applied JSDM to predict the spatial distribution of various fish species across the Persian Gulf. JSDM proved to be an effective tool for predicting the distribution of multiple fish species simultaneously (Cabral et al. 2019). Unlike traditional single-species models, JSDM allowed us to predict the distribution of the communities at once.

One significant aspect of our study involves incorporating a thresholding method to convert the continuous predicted values, indicating the presence probability of fish species generated by JSDM, into binary outcomes. This post-processing step holds considerable importance in translating model outputs into actionable information with practical applicability. Though discouraged, such conversion of predicted presence probability is sometimes necessary to create community maps (Scherrer et al. 2020). Hence, several thresholding methods have been suggested (Scherrer et al. 2018). The decision to employ a thresholding method stems from the need for

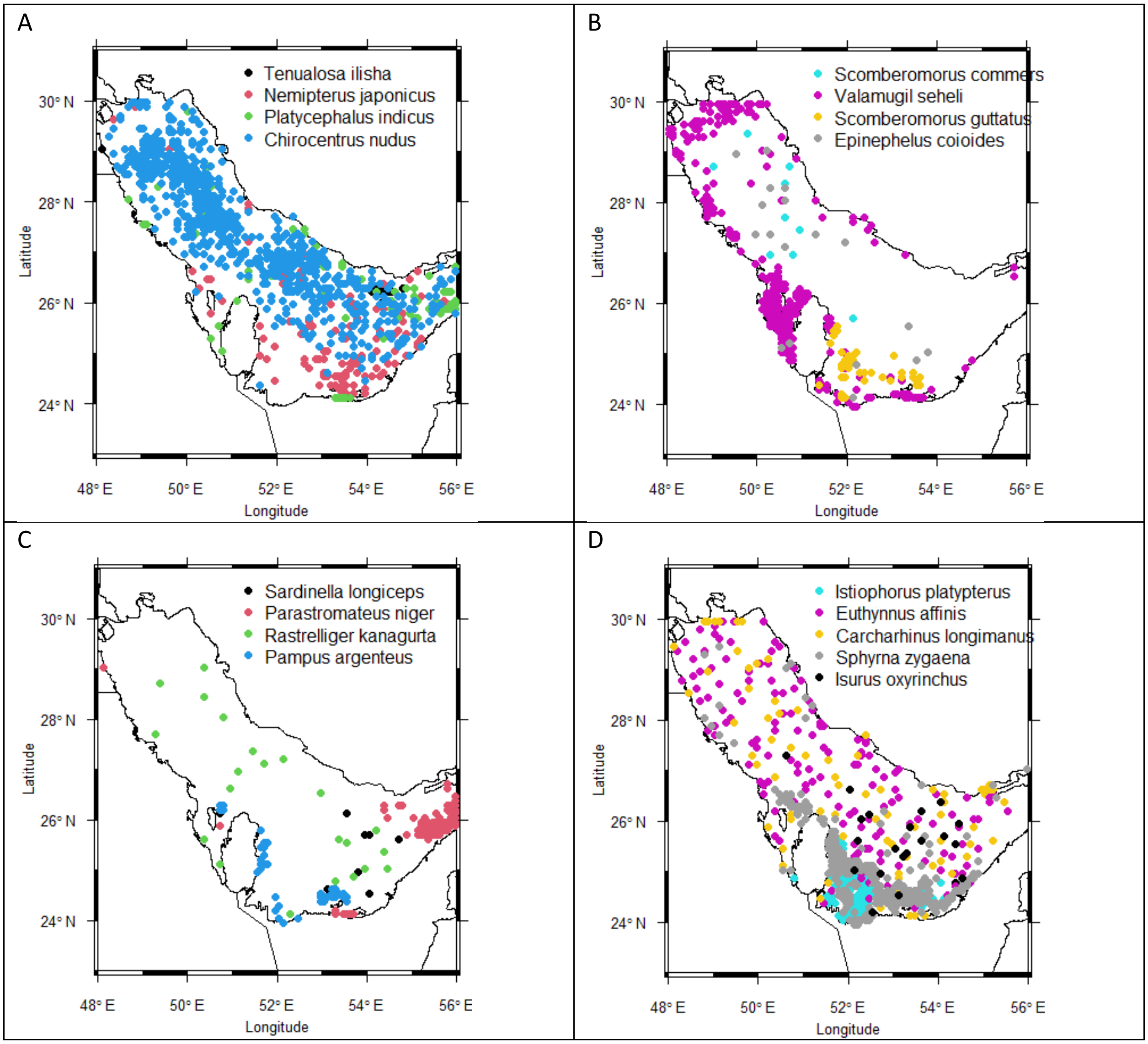

Fig.5. The predicted presence coordinates of various species in the Persian Gulf for 2014.

a clear delineation between the presence and absence of fish species, simplifying the interpretation and implementation of our predictive model. By converting the predicted probabilities to binary outcomes, we created a straightforward framework for decision-making in conservation and resource management. The selection of an optimal threshold is a nuanced process, balancing the sensitivity and specificity of our predictions. This approach allowed us to define a cutoff point that aligns with the ecological significance of the presence or absence of a given fish species in a particular region of the Persian Gulf. Fine-tuning the threshold provides flexibility, accommodating variations in the ecological context and management priorities.

Our study revealed significant overlap in fish distributions, though dissimilar patterns of distributions across the studied species, shedding light on the key ecological drivers in the Persian Gulf. Identifying specific factors influencing these fish species' spatial distribution is vital for informed conservation and management strategies. Utilizing satellite remotely sensed data afforded us the ability to incorporate a wide range of environmental variables. This comprehensive dataset enabled a more thorough exploration of the ecological factors influencing fish distribution. Using satellite data to delineate marine species distribution has attracted much attention and has been widely used in various studies (Lenoir et al. 2011; Mugo et al. 2011).

Such studies may help define protected areas for endangered species, as the predictive capabilities of our model have substantial implications for fisheries management and conservation efforts in the Persian Gulf. By identifying areas of high species richness and potential ecological hotspots, our findings can inform the design and implementation of marine protected areas and sustainable fishing practices. This proactive approach is crucial in facing ongoing environmental changes and anthropogenic pressures on marine ecosystems. While our study provides valuable insights, it is essential to acknowledge certain limitations. The resolution of satellite data and potential biases in the sampling of fish distribution may influence the accuracy of predictions. Future research could refine these aspects and explore additional environmental variables to further enhance the predictive power of JSDM in the Persian Gulf.

In summary, our methodology applies a thresholding method to convert JSDM-predicted presence probabilities into binary outcomes. This approach enhances our model's interpretability and practical applicability, aligning our findings with the needs of conservation and management practices in the dynamic and ecologically significant context of the Persian Gulf.

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مقاله کامل

پیش‌بینی پراکندگی جامعه ماهیان در خلیج فارس با استفاده از مدل‌سازی توزیع گونه‌های مشترک با مدل متغیر پنهان

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چکیده: تعیین پراکنش ماهیان دریایی و محدوده زیست ممکن است به مدیریت و تنظیم مناطق حفاظت‌شده دریایی کمک کند. در حالی‌که مدل‌های توزیع تک گونه‌ای اطلاعاتی را در مورد محدوده زیستگاه گونه‌ها ارائه می‌کنند، اما تعاملات بین گونه‌ها را در بر نمی‌گیرند و ممکن است تصویر دقیقی از توزیع جامعه در یک زیستگاه معین را ارائه نکنند. از این‌رو، پژوهش حاضر، پراکنش جوامع ماهیان دریایی در خلیج فارس را با استفاده از مدل‌سازی توزیع گونه‌های مشترک مدل‌سازی نمود. علاوه بر این، این مطالعه حضور پیش‌بینی‌شده هر گونه را به خروجی حضور یا عدم حضور دوگانه تبدیل نمود تا تفسیر نتایج را تسهیل کند. بیشتر گونه‌ها پراکنش گسترده یا پراکنده در سراسر خلیج فارس داشتند، اما برخی از آنها پراکندگی همزمان را بیشتر در مناطق ساحلی نزدیک به تنگه هرمز نشان دادند. مطالعه حاضر نشان داد که توزیع گونه‌های مشترک دقت بالایی دارد و پیش‌بینی جوامع ماهی را در مناطق بزرگ جغرافیایی تسهیل می‌کند و به ما این امکان را می‌دهد چنین جوامعی را به‌طور همزمان پیش‌بینی کنیم.

کلمات‌کلیدی: توزیع، مدلسازی، مدل متغیر پنهان، خلیج فارس. جوامع ماهی.