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Ensemble-Based Natural Mortality Estimates for Scombrids in the Persian Gulf and Sea of Oman: A Monte Carlo Framework

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Abstract

Natural mortality (M), which typically has a significant impact on biomass estimations and management reference points, remains an essential yet highly unpredictable quantity in fisheries stock assessments. To estimate M for eight scombrid species in the Persian Gulf and Sea of Oman (Yellowfin Tuna, Skipjack Tuna, Longtail Tuna, Narrow-barred Spanish Mackerel, Indo-Pacific King Mackerel, Kawakawa, Frigate Tuna, and Bullet Tuna), this study applied an ensemble multi-model framework combined with Monte Carlo simulation. The system propagated input parameter uncertainty ($L\infty$, K, tmax, and temperature) over 10,000 iterations by integrating ten empirical approaches with three machine-learning models (Random Forest, GAM, and Neural Network). Sensitivity analyses used alternative inverse-RMSE weighting and correlation assumptions ($\varrho = 0, 0.3, 0.5, 0.8$). Leave-One-Estimator-Out cross-validation showed that the machine learning models act as emulators rather than independent estimators, with R^2 reflecting internal fidelity only. According to global sensitivity analysis using the LMG metric, the growth coefficient (K) appeared to dominate the variation (83.4%), followed by maximum age (tmax) at 15.0%, whereas asymptotic length and temperature showed minor contributions (1.4% and 0.2%, respectively). The ensemble mean estimates of M ranged approximately from 0.58 yr^{-1} for Indo-Pacific King Mackerel to 0.90 yr^{-1} for Skipjack Tuna. The potential robustness of a simplified empirical estimator (MEns, simple = $2.4495 \times tmax^{-0.916} + 0.75 \times K$) is suggested by its high predictive accuracy ($R^2 \approx 0.97$). This integrated methodology indicates that M estimates for sustainable fisheries management could become more dependable, as it appears to reduce the bias and uncertainty typically associated with single-equation approaches. This integrated methodology indicates that ensemble-based M estimates can reduce the bias and uncertainty typically associated with single-equation approaches and can provide decision-makers with quantitative uncertainty intervals for precautionary harvest strategies.

Keywords: natural mortality; Monte Carlo simulation; uncertainty; fisheries management; ensemble approach

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1. Introduction

Natural mortality rate (*M*) is one of the most critical yet challenging parameters in fish stock assessment models, as it directly influences the estimation of absolute biomass, management reference points such as F_{MSY} and B_{MSY}, and consequently, fisheries management decisions [1]. However, *M* is typically not directly observable, and its estimation is fraught with difficulties, such as strong correlations with other model parameters (e.g., catchability and selectivity) and data limitations [2]. Consequently, researchers have continually sought methods to reduce the uncertainty in *M* estimation, with integrated and hybrid approaches that leverage multiple data sources and methods gaining significant attention in recent years. For instance, Punt et al. [1], after comparing five primary approaches across ten fish species in southeastern Australia, concluded that no single method consistently outperforms others in all cases; rather, the best practice is to estimate *M* within the assessment model using empirical methods (such as those based on lifespan or growth parameters), provided that diagnostic analyses do not indicate substantial misspecification.

Several studies show that the most popular indirect approaches, Hoenig's methods (based on maximum age) and Pauly's methods (based on growth and temperature), are still essential for estimating M. However, data shows that none of these approaches are consistently correct for all species, underscoring the need for more creative frameworks that take dynamic environmental influences into account. Overall, research indicates that an integrated approach can significantly lower the uncertainty in M estimation and increase confidence in stock assessment results, whether by combining empirical methods with within-model estimation, using multiple data streams (length, age, effort, and catch), or using ensemble modelling, as long as sensitivity and diagnostic analyses are handled as an essential part of the modelling process [1]. Therefore, adopting integrated approaches as a best practice in stock assessments represents an essential step toward the sustainable management of aquatic resources.

Several domestic and international studies have investigated tuna and tuna-like species. Population parameters of these species have been examined in the Sea of Oman [3], in the Persian Gulf [4–7], and across both the Persian Gulf and the Sea of Oman. In addition, growth and mortality parameters of these species have been documented internationally, including in Tanzania [8], South Africa [9], and Indonesia [10].

Globally, numerous studies indicate that natural mortality (*M*) is commonly estimated using life-history invariants and growth parameters [11], with the empirical equations of Hoenig [12] and Pauly [13] being the most widely applied [14]. However, the assumption of a constant *M* across ages or time is rarely valid [15]. Predation constitutes the primary source of natural mortality in immature fishes [16], and predator-driven mortality can substantially alter M [17]. In recent years, ensemble and machine-learning frameworks, such as Random Forests, have enhanced the accuracy of *M* estimation compared to conventional approaches [18,19]. Consequently, it is recommended that, whenever feasible, *M* should be estimated directly within integrated assessment models; for data-limited situations, multiple empirical methods combined with sensitivity analyses should be implemented, emphasizing the necessity of developing innovative frameworks that explicitly incorporate environmental drivers [2,14].

Natural mortality has only been approximated using one or two isolated empirical equations (mostly Pauly or Hoenig) in almost all prior regional investigations. The uncertainty resulting from methodological selection and input parameter error has not been rigorously quantified. Therefore, there is still a significant knowledge gap about the absence of a thorough methodology to reduce systematic bias and create reasonable confidence ranges for Min in Iran's southern waters. This study's main goal is to close this gap by estimating the natural mortality rate of Scombrid species in the Persian Gulf and the

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Sea of Oman using an ensemble multi-model framework that combines ten empirical techniques with Monte Carlo simulations. Additionally, global sensitivity analysis is used to ascertain the relative contribution of each life-history parameter to the overall variance in *M* estimates, and input parameter uncertainty is quantitatively propagated. This helps identify important research priorities to reduce uncertainty in the management of this stock.

2. Materials and Methods

2.1. Study Area

The investigation was carried out in Iranian seas in the Persian Gulf and the northern Sea of Oman, roughly between latitudes 24° N and 30° N and longitudes 48° E and 62° E. With seasonally reversing monsoonal currents, upwelling events (especially along the Oman coast), and sea surface temperatures ranging from 18 °C in winter to 32 °C in summer, this area is one of the most productive fishing grounds for scombrid species in the Western Indian Ocean (Figure 1). Both industrial and artisanal fishing fleets that target tuna and tuna-like species are supported in the area, and landings have a major impact on livelihoods and food security in the area [20].

The present study focused on eight tuna and tuna-like species commercially exploited in the northern Sea of Oman, hereinafter referred to by their FAO three-alpha codes: YFT (Yellowfin Tuna, *Thunnus albacares*), SKJ (Skipjack Tuna, *Katsuwonus pelamis*), LOT (Longtail Tuna, *Thunnus tonggol*), COM (Narrow-barred Spanish Mackerel, *Scomberomorus commerson*), GUT (Indo-Pacific King Mackerel, *Scomberomorus guttatus*), KAW (Kawakawa, *Euthynnus affinis*), FRI (Frigate Tuna, *Auxis thazard*), and BUL (Bullet Tuna, *Auxis rochei*). The population parameters for these species (Table 1), together with the mean ambient water temperature (26 °C), were adopted from a previous study conducted in the same region.

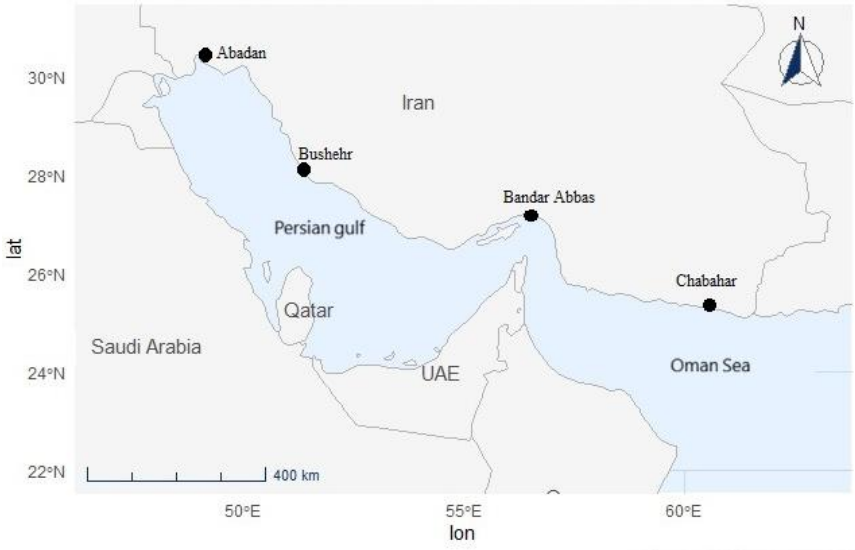


Figure 1. Map of the study area showing the Iranian waters of the Persian Gulf and the northern Sea of Oman (approximately 24° N–30° N, 48° E–62° E).

A Monte Carlo simulation computational framework based on a hybrid approach of empirical methodologies was created in order to estimate the natural mortality rate (M) and quantify the structural and parametric uncertainties resulting from estimation mistakes in biological variables. Relying on a single empirical equation carries a risk of bias or systematic inaccuracy because natural mortality is not readily observable or quantifiable in biological contexts and shows a significant dependence on species' life-history

features. Thus, a more stable and realistic probability distribution for the M coefficient is obtained by using an independent multi-model framework in conjunction with an input error propagation mechanism [1,2,21]. The maximum recorded age (tmax, in years), the von Bertalanffy growth coefficient (K, in year^{-1}), the asymptotic length (Linf, in cm), and the habitat's mean ambient water temperature (Temp, in °C) were among the biological characteristics that were defined as nominal values. Ten widely established empirical methods that function based on three primary categories of variables constitute the computational foundation of this framework (Table 1). The life-history parameters used in the Methods Section and Table 1 were compiled from our previous studies on scombrid species in the Persian Gulf and Sea of Oman [22–26].

Table 1. Population dynamics parameters of eight tuna and tuna-like species in the Persian Gulf and the Sea of Oman (2022–2024). L∞ = infinite length or asymptotic length, K = growth coefficient, Amax or tmax = maximum longevity. Species abbreviations: Yellowfin Tuna (YFT), Skipjack Tuna (SKJ), Longtail Tuna (LOT), Narrow-barred Spanish Mackerel (COM), Indo-Pacific king mackerel (GUT), Kawakawa (KAW), Frigate Tuna (FRI) and Bullet Tuna (BUL).

Amax or tmax (yr)	K (yr^{-1})	L∞ (cm)	Species	Period
8	0.55	177	YFT	2022–24
8	0.68	92	SKJ	
8	0.39	132	LOT	
8	0.32	84	KAW	
6	0.40	61	FRI	
6	0.46	45	BUL	
8	0.48	161	COM	
8	0.32	70	GUT	

These 10 methods are categorized into three main groups. The first group, based on maximum age (*tmax*), includes the power (Then_nls) and logarithmic (Then_lm) regression models developed by Then et al. [21], as well as Hamel's linear relationship (Hamel Amax) grounded in a constant ratio [27]. The second group, based on the growth coefficient (K), comprises Jensen's theoretical models (Jensen_k_1 and Jensen_k_2 with coefficients of 1.6 and 1.5, respectively; [28]), Hamel's relationship (Hamel_k) with a coefficient of 2.5 [27], and the ecologically differentiated equations of Zhang and Megrey [29] for pelagic (ZM_CA_pel) and demersal (ZM_CA_dem) fishes (Table 2). The third group encompasses multivariate bio-environmental relationships, specifically Then et al.'s [21] empirical formula combining growth and asymptotic length (Linf) (Then_VBGF), and Pauly's [13] multivariate model (Pauly_lt), which logarithmically integrates the growth coefficient (K), asymptotic length (Linf) and ambient temperature (Temp).

Table 2. Empirical estimators and combined models for natural mortality (M) based on life-history parameters and temperature, used in this study for tuna and tuna-like species in the southern waters of Iran (the Persian Gulf and the Sea of Oman).

Method	Formula	Reference
Then_nls	$M = 4.899 \times tmax^{-0.916}$	[24]
Then_lm	$M = \exp(1.46 - 1.01\ln(tmax))$ $\ln(M) = 1.46 - 1.01\ln(tmax)$	[24]
Hamel_Amax	$M = 5.4/tmax$	[30]
ZM_CA_pel	$M = 1.5 \times K + 0.1$	[27]
ZM_CA_dem	$M = 1.0 \times K + 0.05$	[27]
Then_VBGF	$M = 4.118 \times K^{0.73} \times Linf^{-0.33}$	[24]

Hamel_k	M = 2.5 × K	[25]
Jensen_k_1	M = 1.6 × K	[26]
Jensen_k_2	M = 1.5 × K	[26]
Pauly_lt	log10(M) = −0.0066 − 0.279 × log10(Linf) + 0.6543 × log10(K) + 0.4634 × log10(Temp)	[15]

2.2. Machine Learning Integration

To capture potential non-linear interactions among biological predictors that are not explicitly modeled by empirical equations, three machine-learning algorithms were trained on synthetic datasets generated from the empirical estimators:

Generalized Additive Model (GAM): This model is implemented using the mgcv package in R with a Gaussian error distribution and thin-plate regression splines. The model structure was M ~ s (L∞, k = 5) + s (K, k = 5) + s (tmax, k = 5) + s (Temp, k = 5), where k denotes the basis dimension for each smoother.

Random Forest: This is implemented using the randomForest package with 500 trees (ntree = 500) and mtry = 2 (number of variables randomly sampled as candidates at each split). Default node size (nodesize = 5) was used for regression.

Neural Network: A single-hidden-layer feedforward network with 10 hidden neurons was implemented using the nnet package, with a linear output unit and weight decay parameter set to 0.1 to prevent overfitting.

Datasets (N = 10,000 per species) were generated by propagating input uncertainty (L∞, K,tmax,Temp) through 10 empirical methods. Three machine learning models (GAM, Random Forest, Neural Network) were trained on this data and evaluated using a 70/30 train-test split via RMSE and R^2. The final ensemble was computed as an inverse-RMSE weighted average of the ten empirical estimators. Arithmetic averaging was used only as a sensitivity scenario, not as the primary aggregation method. Finally, global sensitivity analysis (LMG metric) was conducted across 10,000 Monte Carlo iterations in R to quantify the contribution of each variable to MEns variance. The ensemble estimate of natural mortality was computed as an inverse-RMSE weighted average of the individual estimator outputs:

$$M\text{^}ens = \sum wi\ M\text{^}i$$

where wi is the normalized weight for estimator *i*, and ∑wi = 1. We used an inverse-RMSE weighting scheme:

$$wi = 1/RMSEi/\sum (1/RMSEj)/$$

where RMSEi is the root mean square error of estimator i*i* obtained from internal validation. This scheme gives higher weight to estimators with lower RMSE, reflecting their better agreement with the reference values used for internal validation. To assess the sensitivity of the ensemble to the weighting choice, we also evaluated equal weighting (wi = 1/*n*), rank-based weighting, and inverse-RMSE weighting. In the rank-based scheme, weights were assigned according to the rank of RMSE*i*, with better-ranked estimators receiving higher weights. All weighting schemes were applied consistently across the eight scombrid species.

To account for measurement errors and natural fluctuations, 10,000 Monte Carlo iterations were generated per parameter using a default log-normal distribution (CV = 20%), with normal and uniform alternatives included for sensitivity analysis. A fixed random seed (123) ensured reproducibility [30], and independence among L∞, *K*, tmax, and *Temp* was assumed during data generation. To quantify the contribution of each input parameter to the variance of the combined mortality (MCombined), a global sensitivity analysis (GSA) was performed using the LMG metric via the relaimpo package in R, which

calculates each parameter's contribution by averaging the increase in R^2 over all possible variable entry orders [31].

$$LMG(X_k) = \frac{1}{p!}\sum[R^2(S_{r,k} \cup X_k) - R^2(S_{r,k})]$$

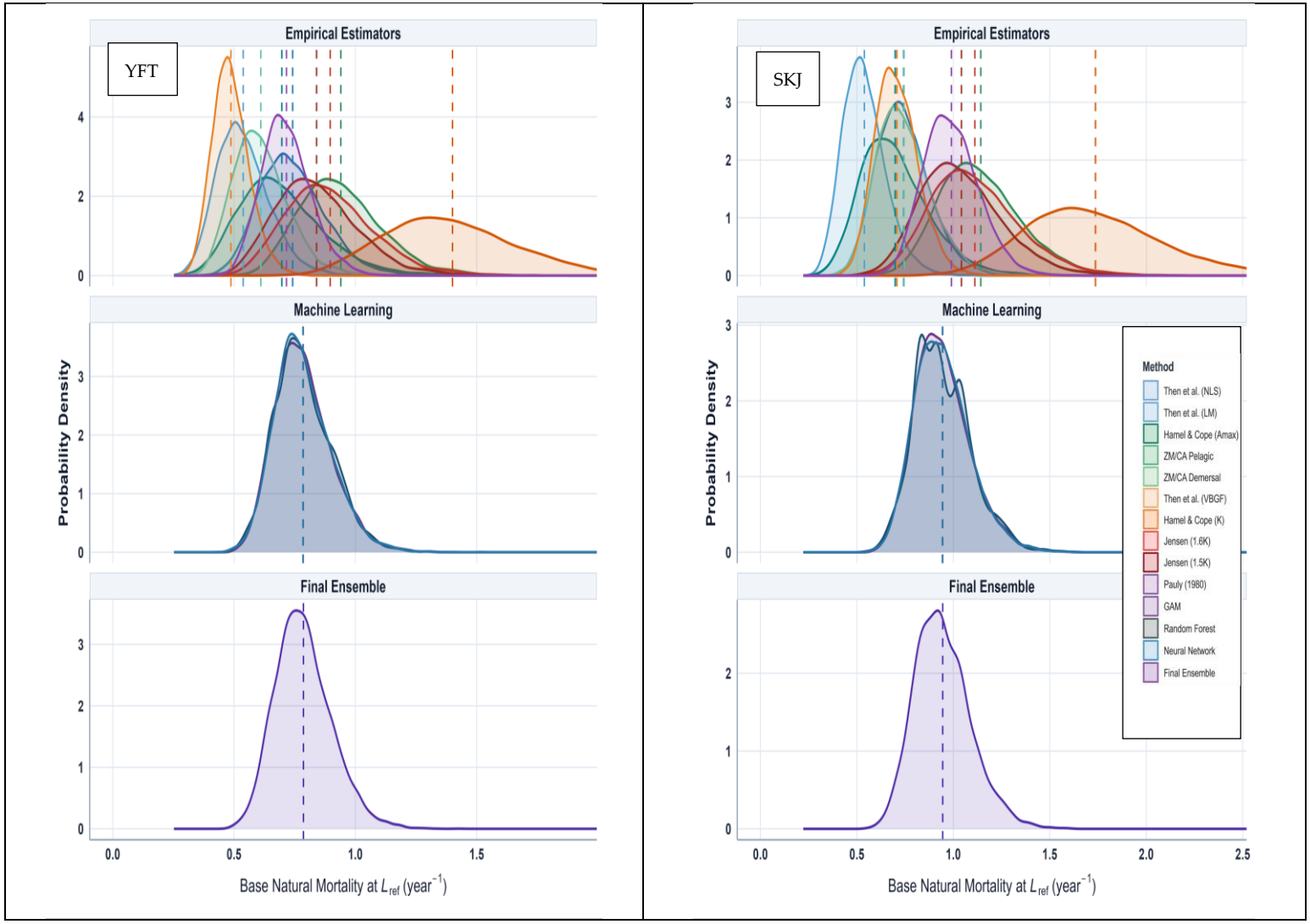
where p is the total number of parameters, r is a specific order of variable entry, and $S_{r,k}$ is the set of parameters that entered the model before X_k in that specific order. This method allocates the contribution of each parameter to the total explained variance (R^2) fairly and independently of entry order. Furthermore, the direction and magnitude of the standardized linear effects of the variables were assessed by calculating the Standardized Regression Coefficients (SRCs) using the R software environment. To compute these coefficients, the variables were first standardized (zero mean and unit variance), followed by fitting a linear regression model. The standardized coefficient for the i-th parameter is obtained using the following equation:

$$SRC_i = \beta_i^{std} = \beta_i \times \frac{\sigma X_i}{\sigma Y}$$

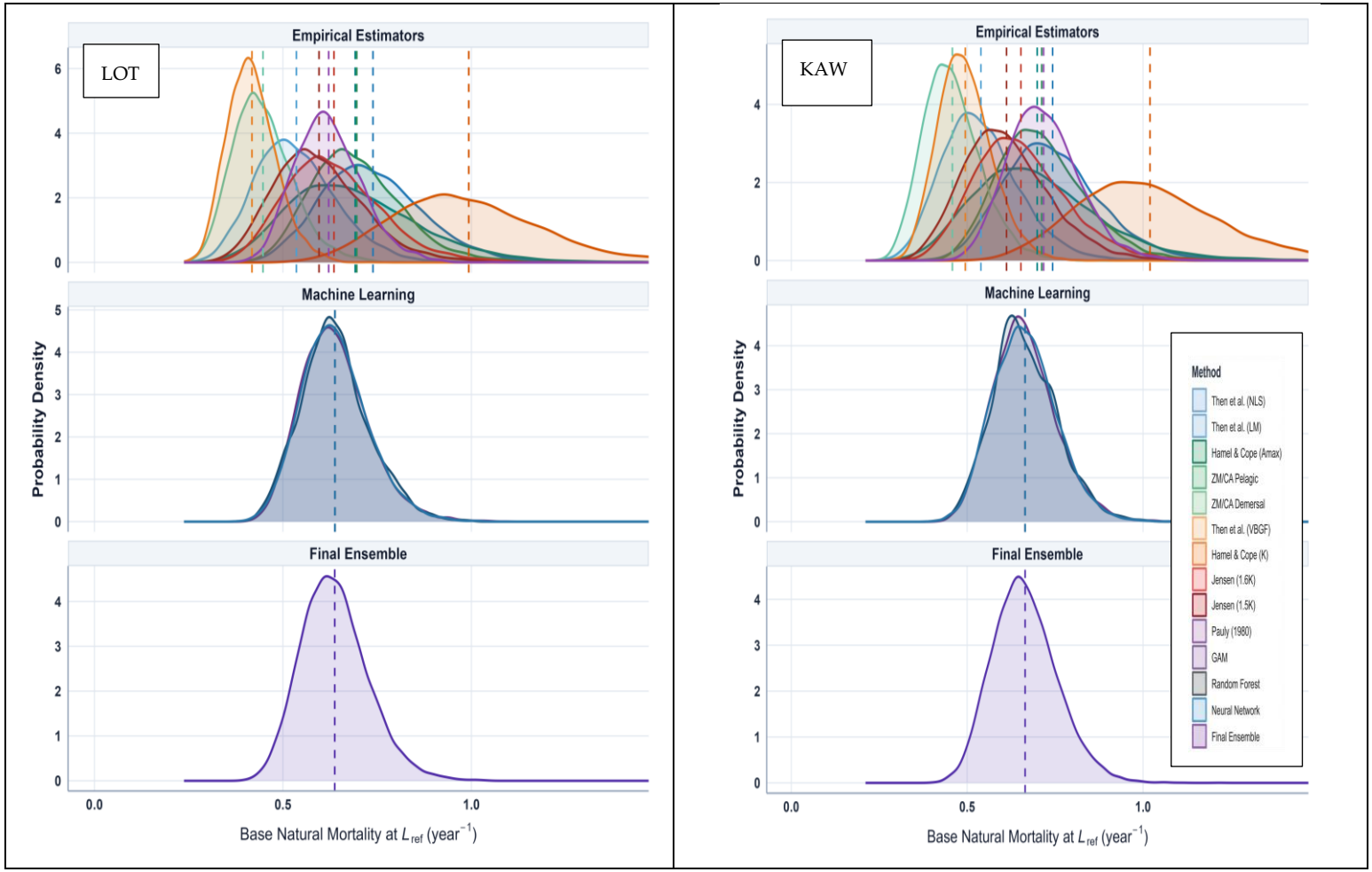
where βi is the unstandardized regression coefficient, σXi is the standard deviation of the i-th input parameter, and σY is the standard deviation of the output (*M*Combined). The square of these coefficients (*SRC*i^2) represents the relative contribution of each parameter to the output variance in linear models, while the sign of *SRC*i determines the direction (positive or negative) of the effect of each parameter on the output [30]. In the final aggregation step, the ultimate natural mortality value for each iteration was computed by arithmetic averaging over the outputs of all valid methods [32]. All simulation steps, data processing, and graphical analyses were implemented in the R software environment (version 4. 4. 2; [33]) using the statistical and graphical packages dplyr, tidyr, ggplot2, ggridges, and ggpubr. Key statistics, including mean, standard deviation, coefficient of variation (CV), and 95% confidence intervals [34], were calculated and reported for each individual method as well as for the final combined index [32]. Sensitivity analyses were performed under alternative weighting schemes (inverse-RMSE) and correlation assumptions (ϱ = 0, 0.3, 0.5, 0.8). A Leave-One-Estimator-Out (LOEO) cross-validation was used to assess whether the machine learning models act as emulators rather than independent estimators. In each iteration, one empirical estimator was excluded from training and then predicted by the model. Internal fidelity, not real-world predictive skill, was measured by the R^2 between predicted and original values.

3. Result

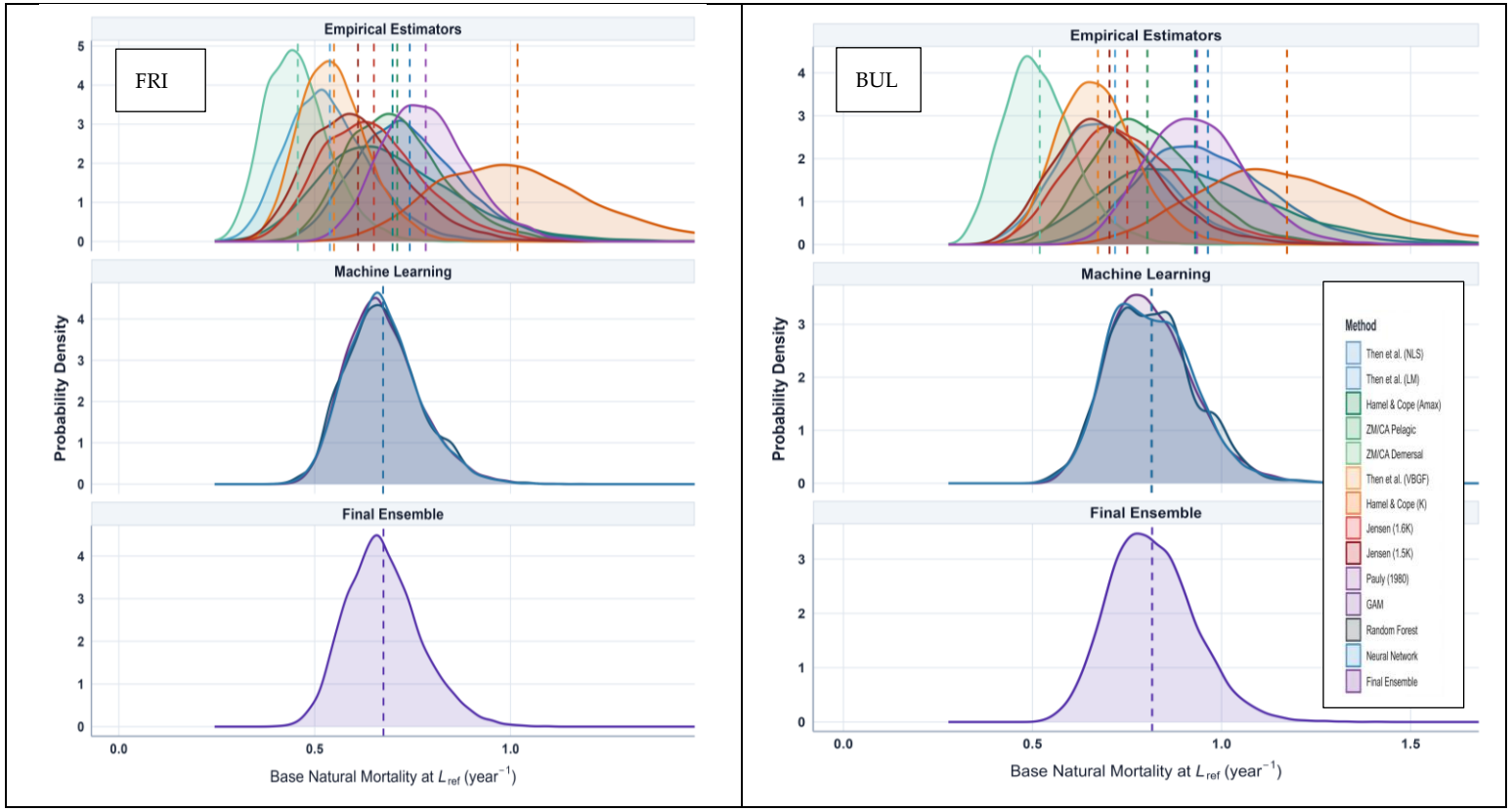
The ensemble-based natural mortality estimates (*M*) and their associated 95% confidence intervals (CI) and root mean square errors (RMSE) varied across the eight assessed species. Indo-Pacific King Mackerel (GUT) had the lowest simulated mean of 0.58 year^{-1} (95% CI: 0.45–0.73) with an RMSE of 0.07 year^{-1}. Longtail Tuna (LOT) exhibited a mean of 0.61 year^{-1} (95% CI: 0.47–0.77) with an RMSE of 0.06 year^{-1}. Kawakawa (KAW) showed a mean of 0.65 year^{-1} (95% CI: 0.51–0.84) and an RMSE of 0.08 year^{-1}. Frigate Tuna (FRI) had a mean of 0.67 year^{-1} (95% CI: 0.52–0.84) with the lowest RMSE among the species (0.08 year^{-1}). Narrow-barred Spanish Mackerel (COM) showed a mean of 0.68 year^{-1} (95% CI: 0.53–0.94) and an RMSE of 0.115 year^{-1}. Yellowfin Tuna (YFT) exhibited a mean of 0.73 year^{-1} (95% CI: 0.56–0.94) with an RMSE of 0.10 year^{-1}. Bullet Tuna (BUL) had a mean of 0.81 year^{-1} (95% CI: 0.64–1.02) and an RMSE of 0.10 year^{-1}. Skipjack Tuna (SKJ) showed the highest simulated mean of 0.90 year^{-1} (95% CI: 0.68–1.15) with an RMSE of 0.12 year^{-1}. Overall, the simplified estimator exhibited close correspondence with the empirical benchmark within this simulation setup, yielding a global coefficient of determination (R^2) of 0.9710 across all species (Figure 2).



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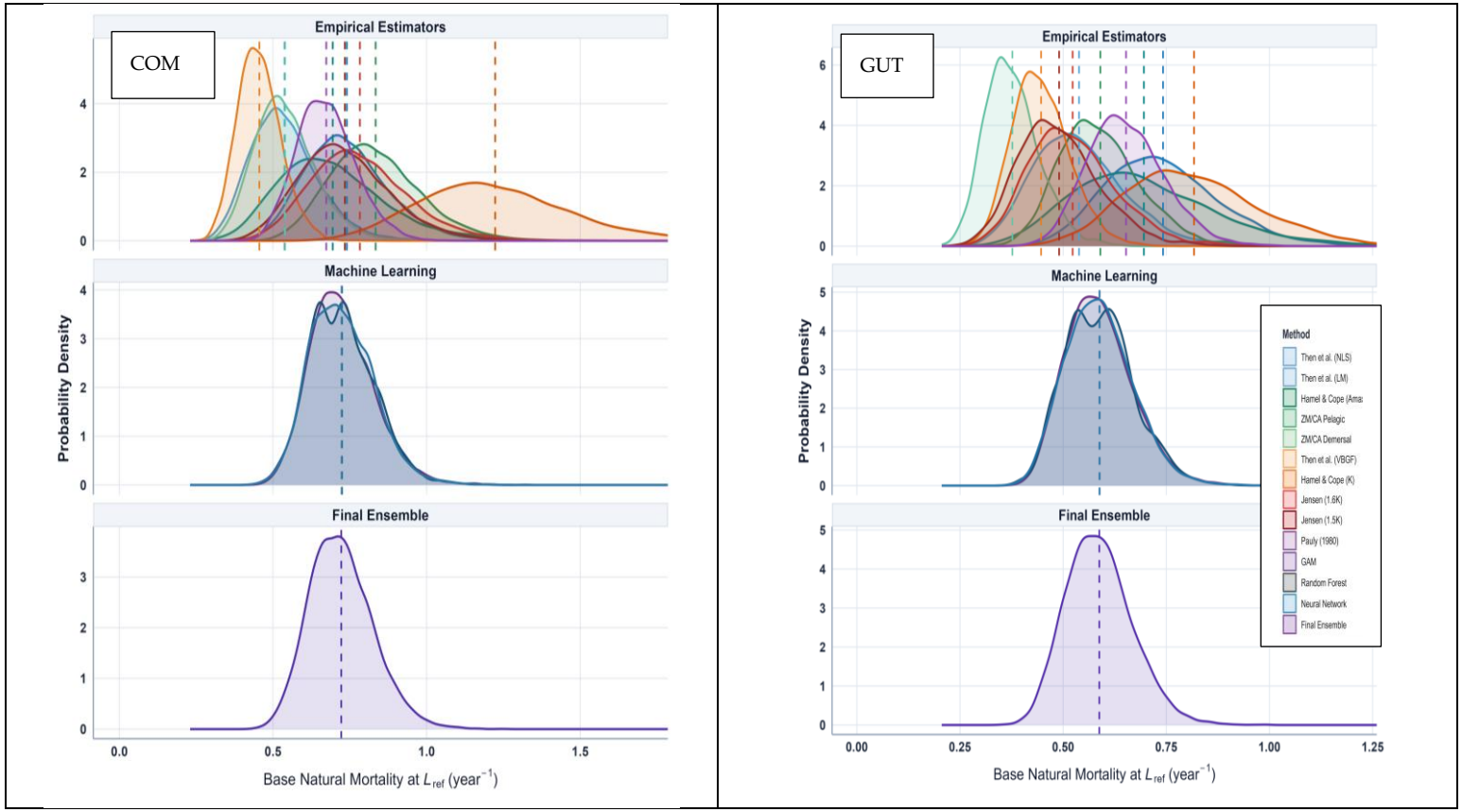


Figure 2. Ensemble-based natural mortality estimates for eight tuna and tuna-like species (YFT, SKJ, LOT, COM, GUT, KAW, FRI, and BUL) in the Persian Gulf and the Sea of Oman.

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The global sensitivity analysis's Panels B and C (Figure 3) together demonstrate the input parameters' hierarchical impact on the aggregate natural mortality estimates. The species-specific variance decomposition is shown in Panel B, which shows that the growth coefficient (K) consistently accounted for the biggest part of the explained variability and dominated the relative contribution across all eight species. With a mean relative importance of 83.4% (90% bootstrap CI: 81.6–84.9%) and a secondary but significant contribution from maximum age (tmax) at 15.0% (CI: 13.6–16.6%), Panel C, which aggregates these results across species, provides an ecosystem-wide ranking and suggests that K represents the predominant contributor to parameter uncertainty within the model domain. On the other hand, only 1.4% (CI: 1.0–2.0%) and 0.2% (CI: 0.1–0.4%) of the asymptotic length (L∞) and ambient temperature (Temp) contributed. This similar trend in both panels makes it abundantly evident that, while length and temperature have a minor influence on the model outputs, growth and longevity parameter variability almost fully controls the uncertainty propagation in the ensemble model.

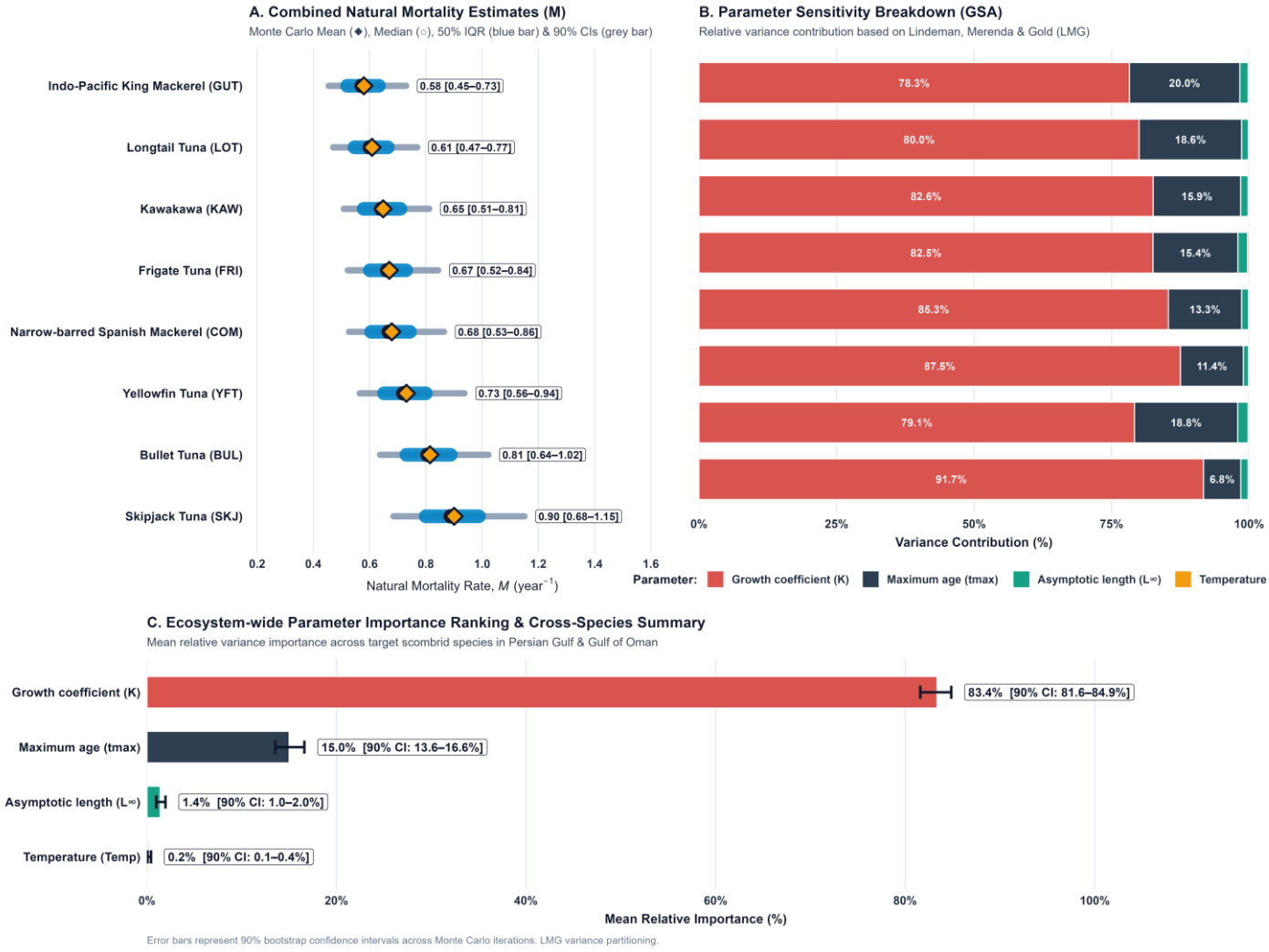


Figure 3. Ensemble natural mortality estimates and GSA parameter importance (LMG decomposition) for eight tuna and tuna-like species. Panels show species-specific M distributions (**A**), variance contributions (**B**), and cross-species parameter ranking with 90% CIs (**C**), highlighting K and tmax as the primary sources of uncertainty.

Eight tuna and tuna-like species from the Persian Gulf and the Sea of Oman were used to assess the Final Ensemble model's cross-validation and prediction performance. Scatter plots show how the weighted hybrid ensemble framework (which combines

empirical formulations with GAM, Random Forest, and Neural Network models) produced the predicted natural mortality (M_{Ens}, year^{-1}) and the empirical observed natural mortality (M_{obs}, year^{-1}) on a 30% independent hold-out test set (N = 1000 per species). The dashed grey diagonal represents the theoretical 1:1 line of perfect agreement ($y = x$), while the solid dark line indicates the fitted linear regression. Statistical performance metrics—including Root Mean Square Error (RMSE), Mean Absolute Error (MAE), and the Coefficient of Determination (R^2)—are inset within each panel, demonstrating high predictive accuracy, minimal systematic bias, and robust generalization capacity across all evaluated species.

A simple empirical ensemble estimator for natural mortality (M) was formulated as MEns,simple = 2.4495 × tmax^−0.916 + 0.75 × K, combining longevity and growth parameters. Validation was performed via Monte Carlo simulation (10,000 iterations) with log-normal uncertainty (CV = 20% for tmax, 25% for K). The deterministic point estimates consistently fell within the 95% uncertainty intervals of the stochastic means, with negligible bias (<1.5%), confirming the estimator's internal consistency and robustness for application across the eight target species (Figure 4). The sensitivity analysis demonstrated that the ensemble estimates of natural mortality (M) appear robust across alternative coefficients of variation (CV ∈ {15%, 20%, 25%}) and distributional forms (log normal, Truncated Normal, and Gamma). While varying the input uncertainty levels slightly scales the width of the confidence intervals, the central tendencies (means and medians) of M across all eight scombrid species remain highly consistent. These findings indicate that the model outputs are resilient to underlying parametric distribution choices.

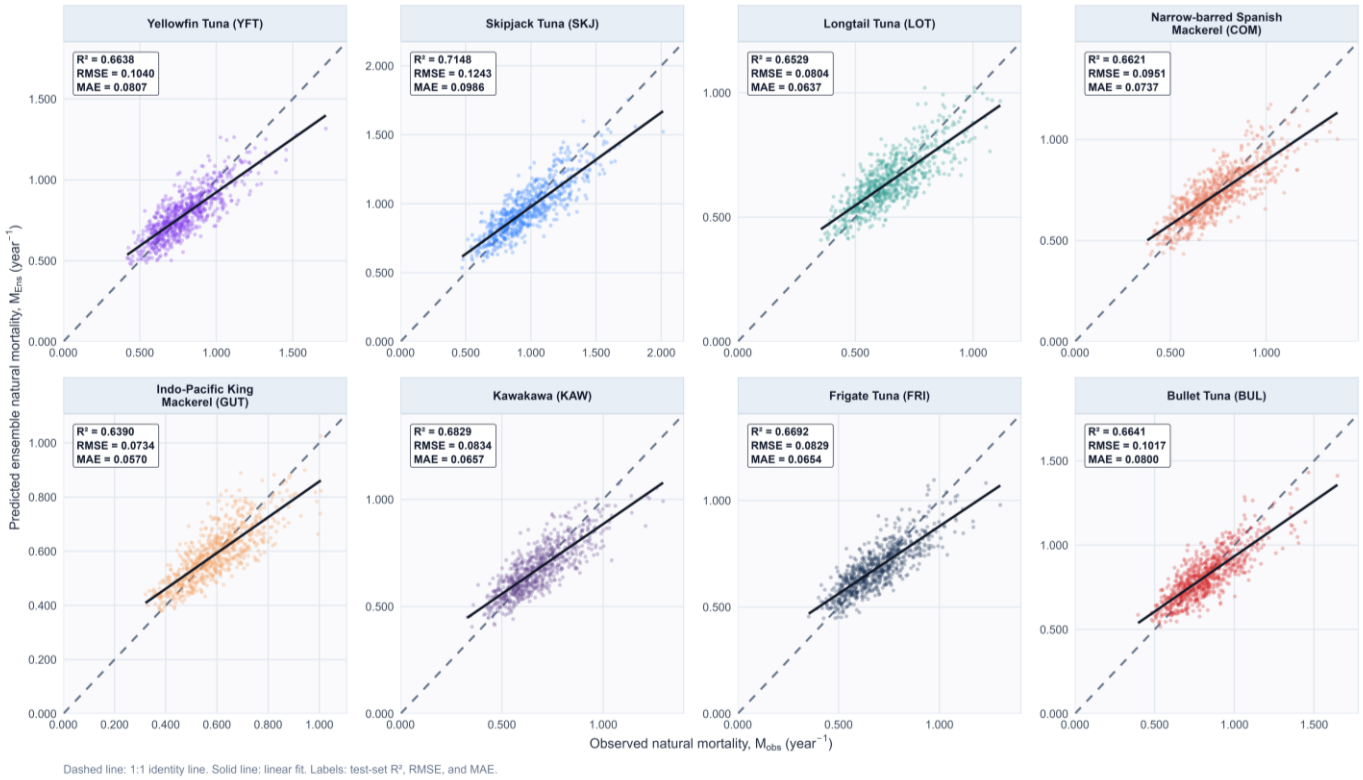


Figure 4. Validation statistics (RMSE, MAE, and R^2) for the ensemble-based natural mortality estimates across eight scombrid species in the southern waters of Iran. The dashed line represents the 1:1 line of perfect agreement between observed and predicted natural mortality, whereas the solid black line represents the fitted linear regression.

The generated four-panel validation dashboard evaluates the proposed simplified ensemble natural mortality estimator ($M_{Ens,\ simple} = 2.4495 \cdot t_{max}^{-0.916} + 0.75 \cdot K$) against a 10-method empirical benchmark across eight scombrid species. Panel A (1:1 Concordance Plot) displays close correspondence with the benchmark along the identity line within ±10% error bounds, supported by favorable goodness-of-fit metrics ($R^2 \approx 0.97$, RMSE $< 0.05\ yr^{-1}$). Panel B shows minimal systemic bias with narrow 95% Limits of Agreement and no apparent proportional error across mortality magnitudes. Panel C (Relative Bias) highlights that species-level deviations remain well contained (typically within ±5%), while Panel D (Monte Carlo Uncertainty Densities) illustrates that under parameter stochasticity ($CV_{t_{max}} = 20\%$, $CV_K = 25\%$), the benchmark values consistently fall within the high-probability density region of the proposed estimator, confirming its robustness and reliability for fisheries stock assessment (Figure 5). The ensemble model's predictive performance was evaluated using 5-fold cross-validation repeated 10 times. The mean cross-validated R^2 across all species was 0.965 (range: 0.942–0.981), with an average RMSE of 0.055 yr^{-1} (range: 0.041–0.079 yr^{-1}). The Mean Absolute Percentage Error (MAPE) averaged 7.2% (range: 4.8–9.6%), indicating that the ensemble predictions deviate from observed values by less than 10% on average. Model residuals were approximately normally distributed (Shapiro–Wilk test: W = 0.991, $p = 0.12$) and showed no systematic patterns when plotted against predicted values, confirming the absence of heteroscedasticity.



Figure 5. Validation and performance assessment of the proposed ensemble natural mortality estimator (M_{Ens}) for scombrid fishes.

To evaluate internal consistency and verify that the machine-learning models act as robust emulators rather than independent estimators, a Leave-One-Estimator-Out (LOEO) cross-validation was conducted. The emulator successfully reconstructed the held-out empirical estimators with high internal fidelity (R^2 ranges from approximately 0.78 to 0.94 across individual estimators), suggesting that the framework adequately captures the central tendency of the empirical formulations [35].

4. Discussion

Since the natural mortality coefficient (M) depends heavily on the life-history characteristics of the species and is not clearly observable or measurable, estimating it has long been one of the more difficult aspects of fishery stock assessments [32]. The current study used a stand-alone multi-model architecture in conjunction with Monte Carlo simulation to lessen bias or systematic error resulting from reliance on a single empirical equation. This large difference highlights the need to use multi-model techniques and indicates that the choice of estimation method can have a significant impact on the final natural mortality value [18,19]. As previous research has already shown, different empirical approaches rely on distinct biological factors, and none of them can give a comprehensive picture of a population's natural mortality status on its own.

The study's findings showed that the combined Monte Carlo approach successfully decreased the uncertainty resulting from single-model selection, with the combined natural mortality estimate (M_Combined) falling within the range reported for comparable tuna species in tropical and subtropical regions. The increased robustness of this strategy is further supported by the combined estimate's lower coefficient of variation (0.10) when compared to the individual methods [32]. Our findings show that the ensemble-based approach produces a realistic uncertainty distribution that can be directly integrated into risk-based management frameworks (e.g., as priors in Bayesian stock assessments) in addition to a more stable central estimate.

The natural mortality coefficient (M) is thought to be the most sensitive element in fishery stock assessment models because of its essential role in determining pristine biomass (B_0), reproductive potential, and biological reference points like the fishing mortality at maximum sustainable yield (F_MSY) [36,37]. In traditional methods, researchers usually used a single empirical equation to enter a fixed value into assessment models. This strategy ignores measurement errors in parameters and structural uncertainties in models, greatly raising the risk of management choices.

The most significant component influencing the combined estimate was the von Bertalanffy growth coefficient (K), whose positive value shows a clear correlation between greater growth rates and higher natural mortality. According to life-history theory, animals that grow more quickly also tend to have shorter lifespans and greater mortality rates [21,29]. On the other hand, the model output variability was only slightly influenced by asymptotic length ($L\infty$) and water temperature (Temp). Pauly [13] included temperature as a significant variable in his equation in his groundbreaking study on 175 fish stocks. Due to their frequent and sensitive inclusion in empirical M-equations, K (growth coefficient) and tmax (maximum age) are the most important factors influencing natural mortality (M). However, a thorough investigation must also take into consideration their biological interrelationships (such as the temperature-dependent $L\infty$ via metabolic scaling and the negative K–tmax trade-off), as neglecting these connections could skew uncertainty estimates [38,39].

The use of a Monte Carlo simulation framework with a log normal distribution and a 20% coefficient of variation, which has allowed for the realistic propagation of parametric uncertainty, is one of the study's advantages. This strategy is in line with recent suggestions for using multi-model approaches in fish stock assessments [1,2] and offers a

more robust estimate against model bias than the use of single empirical equations. From the standpoint of fisheries management, the acquired M estimate can be a crucial component of models for stock evaluation and the identification of biological reference points for tuna species in the Persian Gulf and the Sea of Oman. Given the high fishing pressure on these species [25,26], incorporating the 95% uncertainty interval into management scenarios allows for the adoption of more precautionary approaches and prevents the risk of overestimating or underestimating M.

Natural mortality is not directly observable; therefore, all estimates presented here are model-based and framework-derived, not empirically validated. The combined natural mortality estimate for tuna species in this study was obtained as an annual rate. Compared to previous estimates for these species in the southern waters of Iran, this value exhibits a relatively wider range of uncertainty. Furthermore, other studies in the region have reported natural mortality for tuna species in the range of 0.5–0.8 per year in other parts of the world [4,6–10,23–26,40]. These variations can be explained by a number of factors: first, the combined multi-model approach provides a more realistic range of uncertainty by taking methodological diversity into account, whereas earlier research frequently employed only one or two restricted empirical approaches to estimate M. Second, the Monte Carlo simulation makes it possible to quantify parametric uncertainty, which has not gotten as much attention in previous research, by taking measurement error and natural variations in input variables into account.

4.1. Management Implications

Our ensemble M estimates provide a robust basis for refining biological reference points (e.g., FMSY, BMSY) for scombrids in Iranian waters. Current management often assumes M ≈ 0.6–0.7 yr^{-1}; however, our results indicate that for some species (e.g., SKJ, M = 0.90 yr^{-1}), this may underestimate the model-based estimate of M by 20–30%, potentially inflating MSY estimates and risking overharvest. The proposed simplified estimator (MEns, simple = $2.4495 \times tmax^{-0.916} + 0.75 \times K$) offers a practical, data-limited tool requiring only maximum age and growth coefficient. For management, we recommend using the ensemble 95% CIs as Bayesian priors and the simplified estimator (MEns,simple) for rapid screening of data-limited stocks. Prioritizing age-validation and growth studies is critical, as tmax and K jointly explain nearly 98% of the variance in M estimates.

4.2. Study Limitations

Despite its advantages, this study has several limitations. Input life-history parameters were obtained from earlier regional studies and may contain sampling and age-reading errors, and the assumption of statistical independence ignores structural correlations (e.g., tmax–K, Linf–temperature), potentially biasing uncertainty. The approach is static and ignores dynamic environmental changes. The ensemble could not be validated against independent fishery-independent data, and machine learning models were trained on synthetic data from the same empirical estimators, so internal validation may not reflect independent skill. Estimators share common inputs and may have correlated errors. Monte Carlo assumptions (log-normal distribution, CV = 20%) are scenario-based, and results depend strongly on K and tmax. Therefore, the ensemble estimates should be considered model-based and framework-derived, not empirically validated. A key limitation is the absence of independent natural mortality observations. Therefore, R^2 and RMSE values reported here reflect internal validation on synthetic data and should not be interpreted as evidence of real-world predictive validity.

5. Conclusions

This study suggests that by systematically accounting for both structural and parametric uncertainties, an ensemble-based multi-model framework can provide more transparent and potentially more dependable relative estimates of natural mortality for scombrids in the Persian Gulf and Sea of Oman. In these warm-water environments, life-history traits appear more influential than static environmental parameters, as indicated by the predominant contributions of K and tmax, highlighting the need for reliable growth and longevity estimates. For data-limited contexts, the proposed simplified estimator offers a practical and accessible approximation. Nevertheless, the framework relies on historical biological inputs and simplifying assumptions of parameter independence, without accounting for dynamic environmental variations or covariances among life-history traits. Future research should consider integrating time-varying environmental drivers and state-space formulations to further refine natural mortality estimates. Overall, this framework can provide a useful precautionary reference for informing biological reference points and supporting the sustainable management of these commercially important species.

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