ICDSOS
The 3rd International Conference
on Data Science and Official Statistics
November 27 - 28, 2025

"From Data to Impact: Leveraging Innovation in Data Science and Official Statistics for Data-Driven Policy Making and Global Competitiveness"

Parameter Estimation in Hierarchical Models: A Comparison of Bayesian and SGD-Adam Approaches on Biomass Data of Lutjanidae

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Abstract. Hierarchical statistical models are widely used to analyse data with nested structures or repeated measurements, allowing variability across levels to be partitioned and providing more accurate parameter estimation than standard regression models. In the Bayesian framework, parameter estimation often uses Markov Chain Monte Carlo (MCMC), which accommodates complex structures and yields full posterior distributions. However, MCMC is computationally intensive, limiting scalability for large datasets. Recent advances in optimization methods, such as Hierarchical Stochastic Gradient Descent (HSGD) with Adaptive Moment Estimation (Adam), offer a faster and more efficient alternative for hierarchical models. This study applies Hierarchical Bayesian and HSGD-Adam approaches to fish biomass data of the family *Lutjanidae* from seven Marine Protected Areas (MPAs) in Raja Ampat, Indonesia. The model incorporates ecological predictors such as hard coral cover, distance to the nearest village and period of monitoring, with random effects for area of MPA. Comparison of predictive performance showed that the Bayesian model performed slightly better in RMSE, indicating its ability to capture extreme biomass variations, while SGD-Adam model achieved a lower MAE, reflecting greater stability in prediction. These findings demonstrate that advanced hierarchical modelling methods can enhance ecological data analysis and provide timely, data-driven insights for sustainable marine conservation policy.

Keyword: Bayesian, HSGD-Adam, Marine Protected Area, MCMC

1. Introduction

The use of hierarchical models is the main approach in handling data that has a multilevel structure or repeats over time [1], [2], [3]. This model allows the separation of variability between levels, such as location, time, and market. In addition, hierarchical models also provide more accurate and informative parameter estimates than simple or multiple regression models. In the Bayesian framework, parameter estimation is often performed using Markov Chain Monte Carlo (MCMC) methods, which can handle complex structures and produce full posterior distributions [4], [5].

However, MCMC suffers from significant computational challenges for large-scale ecological datasets and models with high complexity, limiting its practical applicability for rapid data analysis [6], [7]

Recent advances in stochastic optimization, particularly Stochastic Gradient Descent (SGD) combined with Adaptive Moment Estimation (Adam), offer promising alternatives for scalable and efficient parameter estimation in hierarchical models [7]. Despite their success in machine learning, applications of these methods in ecological hierarchical data remain scarce, particularly for informing conservation management under real-world constraints. This gap is critical because ecological monitoring programs often involve hierarchical data structures across multiple monitoring areas, as in this study with seven Marine Protected Areas (MPAs), and there is growing demand for timely, data-driven insights to support adaptive policy making.

In Raja Ampat, Indonesia, seven Marine Protected Areas (MPAs) host diverse habitats [8] and management systems [9], [10], [11]. Fish biomass, particularly of the family Lutjanidae, serves as a key ecological indicator of coral reef health and fisheries sustainability. This study compares two parameter estimation approaches—Bayesian-MCMC and HSGD-Adam—on longitudinal Lutjanidae biomass data to assess their accuracy, convergence behaviours, and scalability. The findings aim to demonstrate methodological innovations that can enhance official environmental statistics and support evidence-based marine conservation policies at both national and global levels.

2. Research Method

The research methodology applied in this study consists of two approaches for parameter estimation in hierarchical models. The first is the hierarchical Bayesian method, which utilizes the Markov Chain Monte Carlo (MCMC) algorithm with posterior distribution estimation performed using Hamiltonian Monte Carlo (HMC) (hereinafter referred to as the Bayesian model). The second is the Hierarchical Stochastic Gradient Descent (HSGD) method combined with the Adaptive Moment Estimation (Adam) algorithm (hereinafter referred to as the SGD-Adam model). The use of Adam's algorithm is motivated by its ability to accelerate convergence and stabilize parameter updates during optimization.

Both methods are employed to analyze the relationships between fish biomass and key ecological predictors. The response variable is the biomass of Lutjanidae (kg/ha), an important indicator of fisheries sustainability. Fixed predictors include the distance from each monitoring site to the nearest village, the percentage of hard coral cover, and the monitoring period. Random effects are specified for monitoring areas to account for variability across the seven Marine Protected Areas (MPAs) in Raja Ampat.

Because fish biomass is strictly positive and exhibits considerable variability across locations—many sites have low biomass, but some exhibit high or very high biomass—a Gamma distribution is used for the response variable, formulated as follows:

$$y_{ij} \sim Gamma\ (\mu_{ij}, \alpha) \tag{1}$$

$$\log(\mu_{ij)} = \beta_0 + \beta_1 x_{1ij} + \beta_2 x_{2ij} + \beta_3 x_{3ij} + v_j + \varepsilon_{ij} \tag{2}$$

where y_{ij} is the fish biomass at the *i*-th site in the *j*-th area, μ_{ij} is expected biomass and α is the Gamma shape parameter. $v_j \sim N(0, \sigma_v^2)$ represents the random effect of monitoring areas (MPAs), and $\varepsilon_{ij} \sim N(0, \sigma_\varepsilon^2)$ is the residual error.

The biomass data of the Lutjanidae family were collected from seven conservation areas in Raja Ampat Regency, of which six conservation areas under the management of the Provincial Government of Southwest Papua and one conservation area (West of Waigeo) under the management of the Ministry of Marine Affairs and Fisheries. The data were obtained from Reef Health Monitoring conducted by the Research and Community Service Institute (LPPM), University of Papua, using the Point Intercept Transect (PIT) method for coral data collection and the Long Swim Survey for fish data. Observations were carried out across two periods (2018–2019 and 2021–2022) at 100 monitoring sites, as summarized in table 1.

Model performance is evaluated using Root Mean Square Error (RMSE) and Mean Absolute Error

(MAE) to compare estimation accuracy and convergence behaviour [12]. This methodological framework provides a scalable solution for analysing hierarchical ecological data and supports data-driven marine conservation policies.

Table 1. Number of samples per period in each conservation area.

Number	Conservation Area	Number of Samples (Location)
1	Ayau-Asia	8
2	Misool Islands	18
3	Fam Islands	23
4	Kofiau-Boo Islands	19
5	Dampier Strait	14
6	Mayalibit Bay	11
7	West of Waigeo	7
Total		100

3. Result and Discussion

3.1. Hierarchical Bayesian Inference

3.1.1. Bayesian Model for Hierarchical Data

Suppose the data used in this study consists of responses are y_{ij}. Then the likelihood model is $y_i \sim \text{Gamma}(\mu_i, \alpha)$ with $\log(\mu_{ij)} = \beta_0 + \beta_1 x_{1ij} + \beta_2 x_{2ij} + \beta_3 x_{3ij} + v_j + \varepsilon_{ij}$ The prior for the fixed effect (β) is $\beta \sim N(\mathbf{0}, 25)$. The random effect is $v_j \sim N(0, \sigma_v^2), j = 1, \cdots, J$. The prior for the variance of random effects is $\sigma_v \sim \text{Half} - \text{Cauchy}(0{,}2)$. while the prior for the Gamma shape parameter is $\alpha \sim Exponensial(1)$. The goal of Bayesian estimation is to obtain the posterior distribution:

$$p(\beta, \mathbf{v}, \sigma_v, \alpha | y, \boldsymbol{X}, \boldsymbol{z}), \propto [\textstyle\prod_{i=1}^{n} p(y_i | \mu_i\,, \alpha)] \times p(\beta | \sigma_\beta^2) \times p(\mathbf{v} | \sigma_v) \times p(\sigma_v) \times p(\alpha) \tag{3}$$

with $\sigma_\beta^2 = 25$.

3.1.2. MCMC Algorithm

The iterative algorithm used to approximate the posterior distribution using the Metropolis-Hastings algorithm [13] is as follows:

Initiation step: set $\boldsymbol{\beta}^{(0)}, \mathbf{v}^{(t)}, \sigma_v^{(0)}, \alpha^{(0)}$

Iteration step: for each iteration $t = 1, \cdots, T$, $\beta^{(t)} \sim p\left(\beta \middle| \mathbf{y}, \mathbf{X}, \mathbf{v}^{(t-1)}, \alpha^{(t-1)}\right)$, $\mathbf{v}^{(t)} \sim p\left(\mathbf{v} \middle| \mathbf{y}, \boldsymbol{\beta}^{(t)}, \alpha^{(t-1)}, \alpha_v^{(t-1)}\right)$, $\sigma_v^{(t)} \sim p\left(\sigma_v \middle| \mathbf{v}^{(t)}\right)$, $\mathrm{\alpha}^{(t)} \sim p(\alpha | y, \mu^{(t)}$

Final step: save the results of each iteration after *burn-in*.

3.2. SGD-Adam Inference

3.2.1. SGD Model for Hierarchical Data

Based on [7], it is known that there are n observational data $y = (y_1, \cdots, y_n) \in \Upsilon \subset \mathbb{R}^n$ derived from the probability distribution $p(y|\theta)$, where $\theta = (\theta_1, \cdots, \theta_D) \in \Theta \subset \mathbb{R}^D$ is the model parameter. It is known that there is a latent variable, namely $= (v_1, \cdots, v_K) \subset \mathbb{R}^K$. The model structure of the latent variable in general is $v | \vartheta \sim p(v|\theta); y | v, \theta \sim p(y | v, \theta)$. Parameters are estimated using the form $\hat{\theta} = \arg\max_{\theta \in \Theta} \log p(y | v, \theta)$.

The data structure used in this study consists of responses $= (y_1, \cdots, y_n)$ with $n = 7$, dan $y \sim \text{Gamma}(\mu_i, \alpha)$. Based on [14], if $E(Y_i) = \mu_i$ is associated with covariate variables through $\eta_i =$

$g(\mu_i) = x_i'\beta + v_{z[i]}$. The random effect (latent variable) in this study is $v_j \sim N(0, \sigma_v^2)$ with $j = 1, \cdots, K$. The estimated parameters of θ is $\hat{\theta} = \left\{\beta_0, \boldsymbol{\beta}, \alpha, \{v_j\}_{j=1}^{K}\right\}$, where μ_i is the mean of the Gamma distribution for the ith observation, α is the shape parameter of the Gamma distribution, η_i is the linear predictor, x_i is the vector of fixed predictors for the ith observation, β is the fixed regression coefficient, $v_{z[i]}$ is the random effect (latent variable).

3.2.2. Adam's Algorithm

In general, the optimization algorithm is:

Example step: sampling the posterior distribution of the random influence $v^{(t)} = \left(v_1^{(t)}, \cdots, v_K^{(t)}\right)$ based on the fixed parameter values of $\beta^{(t)}$ and the data y, i.e. $v^{(t),1}, \cdots, v^{(t),S} \sim p(v|y, \beta^{(t)})$.

Updating step: update the fixed parameter estimates and model shape by: $\beta^{(t+1)} = f(v^{(t)})$.

In Adam's algorithm [15], [16], the update function f is derived from the gradient of the loss function:

$$\mathcal{L} = -\sum_{i=1}^{n} \log[Gamma(y_i|\mu_i, \alpha) + \lambda \sum_j b_j^2 \tag{4}$$

With parameter updates done via $\theta^{(t+1)} = \theta^{(t)} - lr.\frac{\hat{m}_t}{\sqrt{\hat{v}_t + \epsilon}}$ where $m_t = \beta_1 m_{t-1} + (1 - \beta_1) g_t$ is the first moving average, $v_t = \beta_2 v_{t-1} + (1 - \beta_2) g_t^2$ is the second moving average, and *lr* is the learning rate.

3.3. Empirical Study

3.3.1. Data Description

Figure 1 and table 2 show that the distribution of Lutjanidae biomass data has many values clustered very close to small values, around 0 to 100 kg/ha with an average of 285, 84 kg/ha. There are some very large biomass values approaching 20,000 kg/ha, but in very small numbers (elongated right tail). The distribution is *positively* skewed to the right, which can also be seen from the comparison of the mean and median values. The small median value (72.69 kg/ha) compared to the mean value indicates that 50% of the data is at values not exceeding 72.69 kg/ha.

Table 2. Descriptive statistics of Lutjanidae biomass distribution.

Statistics	Values (kg/ha)
Average	285.84
Median	72.69
Skewness	12.16

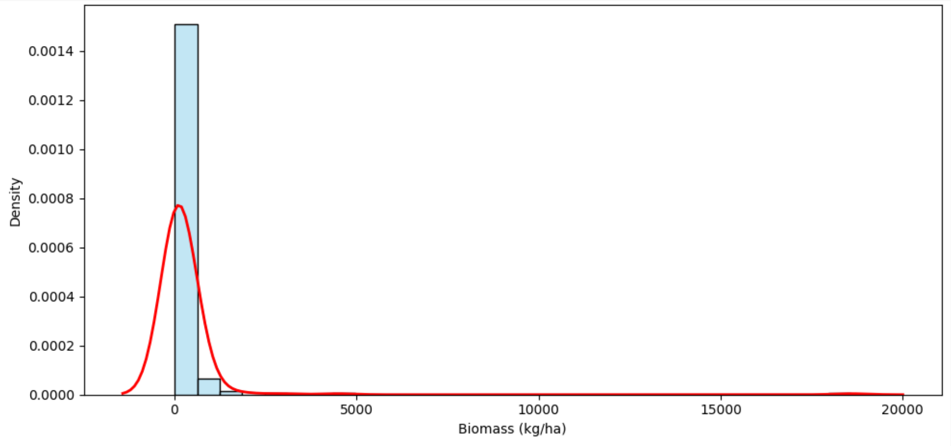


Figure 1. Biomass distribution of Lutjanidae.

Skewness values greater than 2 are considered highly skewed. This result shows that the distribution of data is not normal, so in this study the distribution used for the Bayesian prior model and SGD model is gamma distribution.

3.3.2. Parameter Estimation of Hierarchical Bayesian Model

The results of the analysis using the Hierarchical Bayesian Method with Gamma spread show that all parameters have reached convergence with the R Hat value around the value of 1, and the Effective sample size (ESS) value is sufficient, where the bulk ESS value > 750 and tail ESS > 1000 for all parameters. The intercept parameter has a posterior mean value of 5.112 (HDI 97% 4.187-6.055) indicating a high log base value of biomass under reference conditions. The parameterα of Gamma distribution was estimated to be 0.827 (HDI 97% 0.696-0.956) indicating that the biomass distribution of the Lutjanidae family has a heavy-tailed distribution.

Table 3. Posterior estimates of the Hierarchical Bayesian *m*odel.

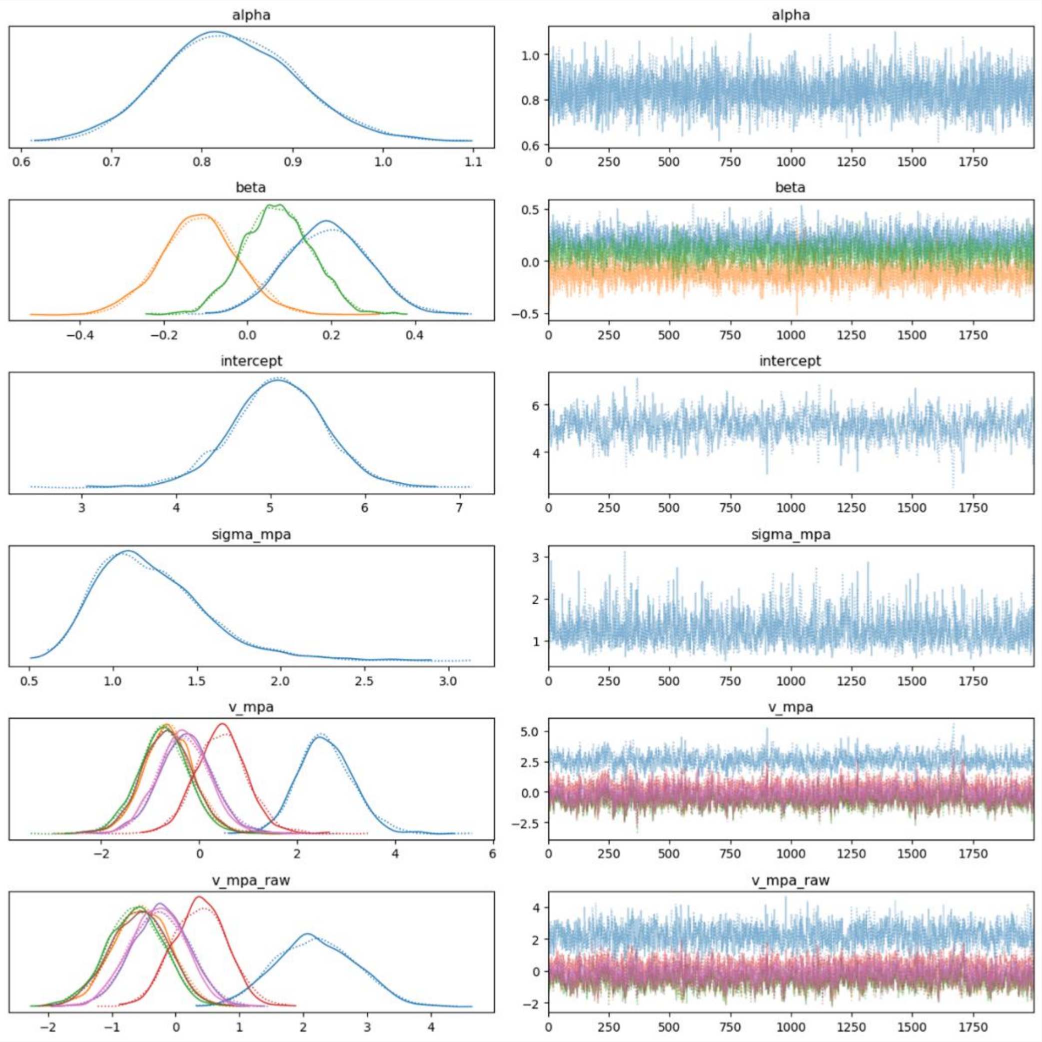
Parameter	Mean	SD	HDI 3%	HDI 97%	Mean MCSE	SD MCSE	ESS Bulk	ESS Tail	R-Hat
α	0.827	0.07	0.696	0.956	0.001	0.001	3711	2596	1
β[Distance]	0.188	0.099	-0.002	0.372	0.002	0.002	3252	2891	1
β [Percentage of Hard Coral Cover]	-0.118	0.09	-0.282	0.055	0.002	0.001	2927	2402	1
β [period]	0.076	0.082	-0.067	0.239	0.001	0.001	3497	2716	1
Intersep	5.112	0.503	4.187	6.055	0.018	0.013	749	1067	1
σ MPA	1.238	0.345	0.701	1.906	0.01	0.01	1115	1791	1
v [Ayau]	2.541	0.557	1.535	3.633	0.018	0.012	941	1433	1
v [Fam Islands]	-0.644	0.529	-1.675	0.312	0.019	0.013	804	1083	1
v [Misool Islands]	-0.758	0.535	-1.84	0.204	0.019	0.012	806	1139	1
v [Kofiau-Boo Islands]	0.418	0.526	-0.573	1.414	0.019	0.013	801	1177	1
v [West of Waigeo]	-0.265	0.575	-1.402	0.807	0.019	0.012	959	1407	1
v [Dampier Strait]	-0.686	0.54	-1.763	0.274	0.018	0.012	863	1147	1
v [Mayalibit Bay]	-0.316	0.548	-1.356	0.715	0.019	0.012	869	1215	1
v raw [Ayau]	2.179	0.646	0.947	3.355	0.018	0.013	1227	1734	1
v raw [Fam Islands]	-0.561	0.449	-1.426	0.252	0.016	0.009	756	1071	1
v raw [Misool Misool]	-0.658	0.463	-1.551	0.198	0.017	0.009	784	1086	1

v raw [Kofiau-Boo Islands]	0.356	0.422	-0.448	1.134	0.014	0.008	863	1422	1
v raw [West of Waigeo]	-0.231	0.471	-1.155	0.61	0.015	0.009	960	1654	1
v raw [Dampier Strait]	-0.598	0.463	-1.49	0.248	0.016	0.009	826	1095	1
v raw [Mayalibit Bay]	-0.277	0.449	-1.118	0.562	0.015	0.009	864	1424	1

The three fixed effect parameters,$\beta_{[Distance]}$,$\beta_{[Percentage\ of\ Hard\ Coral\ Cover]}$, and $\beta_{[period]}$, showed that the effect values varied. Of the three parameters, only$\beta_{[Jarak]}$ is close to significant with a mean value of 0.188 and an HDI of 97%: -0.002 to 0.372. This indicates that the farther away a site is from human settlements, the biomass of the Lutjanidae family tends to increase. This effect supports the suggestion that sites close to human settlements may experience higher fishing pressure. The insignificance of hard coral cover percentage on the biomass of the Lutjanidae family may be due to various factors, including other habitat factors that are more dominant or due to spatial interactions that were not explicitly modeled in this study. The period variable was also not significant. This indicates that there is no consistent trend of change in Lutjanidae biomass from 2018-2019 to 2021-2022.

The diversity between areas in the Raja Ampat Islands Regional Conservation Area can be seen from the random effectσ of MPA, which is 1.238 with a 97% HDI of 0.701-1.906, indicating considerable differences between areas. Of the 7 areas, Ayau-Asia Area and Kofiau-Boo Area have a positive effect, especially in Ayau-Asia Area which is very strong (2.541), while other areas show a negative effect. This result can serve as a basis for the importance of considering spatial structure as well as institutions in fisheries management. The varying influence of these areas could be due, in part, to differences in habitat conditions.

The Bayesian inference results from this data can also be seen visually in Figure 2, which shows that the entire Markov Chain Monte Carlo (MCMC) chain has reached convergence as indicated by a stable trace with no upward or downward trend and a smooth and unimodal posterior distribution. The posterior distributions of the parameters , intercept, as well as each β show a centered density, with sample values evenly distributed throughout the iterations. This indicates sampling stability. The σ MPA parameter indicates the existence of inter-area diversity within the conservation area. The random effect between areas and their base values shows considerable differences between spatial units. Overall, Figure 2 supports the reliability of the hierarchical Bayesian model estimation results.



(a) **(b)**

Figure 2. Bayesian sampling posterior graphs, (a) posterior scatter, (b) MCMC chain trace plot (values and iterations)

The random effect of area in more detail can be seen in Figure 3. The Ayau-Asia Area is the highest area in maintaining or increasing the biomass of Lutjanidae.

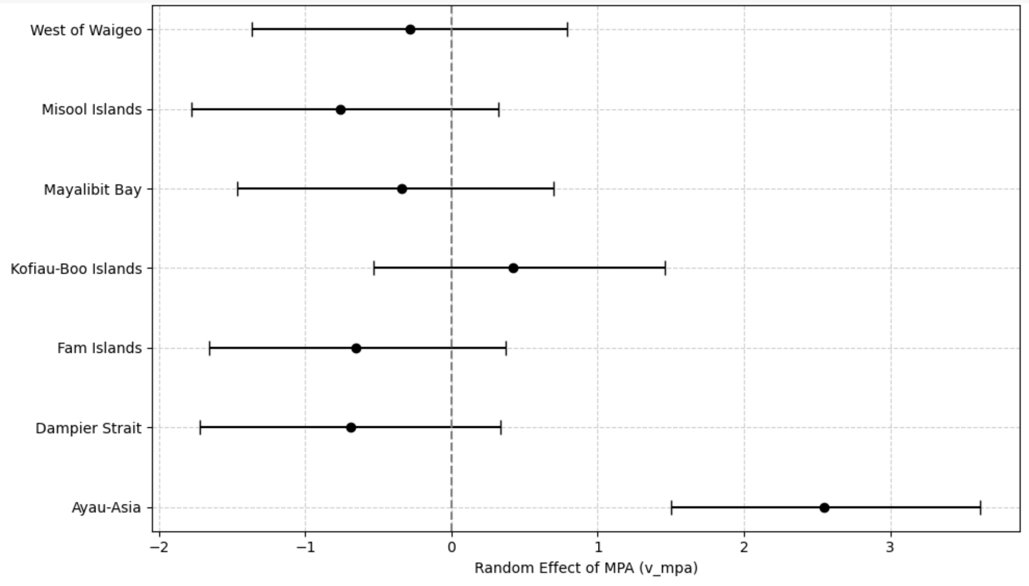


Figure 3. Graph of randomized influence of each area on the biomass of Lutjanidae family

3.3.3. Parameter Estimation of SGD-Adam Model

The results of estimating the SGD model with Adam's algorithm on the Lutjanidae family biomass data can be seen in Table 3. Some estimation results with this model are somewhat different from the estimation results with the Bayesian approach, namely the estimated values $\beta_{[Jarak]}$ and $\beta_{[Persentase\ tutupan\ karang\ keras]}$. The estimation results with the Bayesian method for distance produced a positive estimated value while the SGD method produced a negative value, and vice versa with the parameter for the percentage of hard coral cover, where the Bayesian method was negative while the SGD method was positive. Only the parameter for period has the same direction between the two methods. The random effects were all positive, indicating that all areas in the conservation area contributed positively to the biomass of the Lutjanidae family. The low value of the Gamma shape reinforces the notion that the model captures the asymmetry of the biomass distribution well, as is its nature.

Table 4. Formatting sections, subsections and subsubsections.

Parameter	Estimation Value
Beta [Distance]	-0.124
Beta[Percentage of Hard Coral Cover]	0.326
Beta[period]	0.283
Random Effect [Ayau]	0.623
Random Effect [Fam Islands]	0.890
Random Effect [Misool Islands]	0.924
Random Effect [Kofiau-Boo Islands]	0.911
Random Effect [West of Waigeo]	0.911
Random Effect [Dampier Strait]	0.903
Random Effect [Mayalibit Bay]	0.917
Gamma Shape	0.444

3.3.4. Comparison of Bayesian Model and SGD-Adam Model

It is visually shown that the estimated values of random effects per area on the biomass of the Lutjanidae family by the hierarchical Bayesian and hierarchical SGD-Adam methods are different. The

Bayesian model shows greater variability between areas than the SGD-Adam method. This indicates that the Bayesian method more explicitly captures uncertainty. The SGD-Adam method's almost identical estimated values between areas indicates a strong penalty in the model and also a possible underestimation of the variance between areas.

The Ayau-Asia area is very different from other areas. Judging from the results of the Bayesian model, Ayau-Asia has a very positive and significant effect. In contrast to the results of the SGD-Adam model, which provides a lower estimated value and is almost the same as the estimated value in other areas. This indicates that the SGD-Adam model is unable to capture important spatial outliers in the case of the Ayau-Asia area.

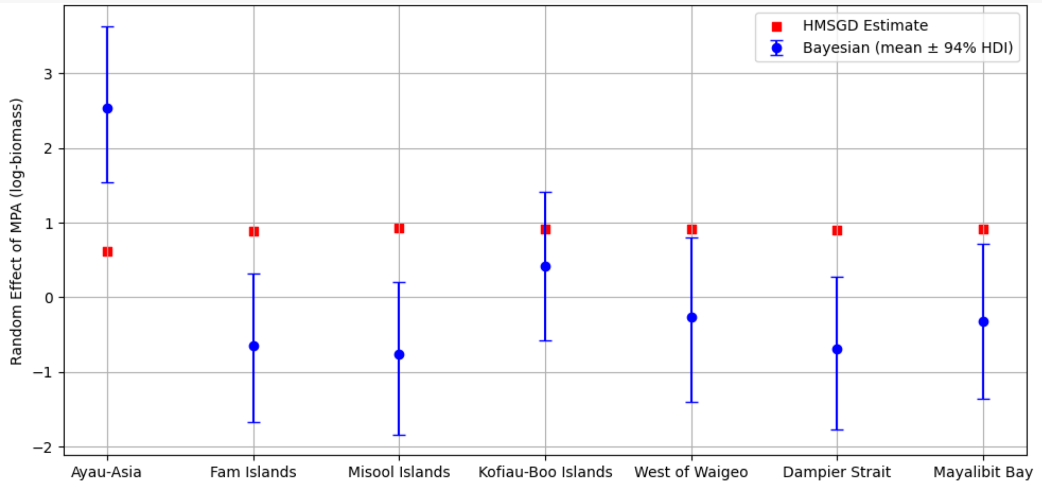


Figure 4. Comparison Graph of Random Area Influence with Bayesian Method and Hierarchical SGD Method with Adam's algorithm.

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Comparison of the two models is also done by comparing the RMSE and MAE values. The results of the RMSE and MAE calculations can be seen in Table 4

Table 5. MSE and MAE Values for the Bayesian Model and the SGD-Adam Model

Model	RMSE	MAE
Bayesian Hierarchy	1296.82	302.39
SGD-Adam	1395.78	280.08

The RMSE results show that the Bayesian Hierarchy method is better at handling large outliers than the SGD-Adam method. When viewed from the MAE value, the SGD-Adam method is more stable in predicting the average biomass value but is less sensitive to outliers.

4. Conclusion

The hierarchical Bayesian and SGD-Adam methods successfully estimated the parameters of the Gamma model with random effects at the area level, but showed differences in predicted values, sensitivity, spatial variability, and prediction accuracy. The results of the Bayesian method showed that distance to the village had a positive, albeit weak, influence on the biomass of the Lutjanidae family (mean 0.188 kg/ha HDI 75% -0.002-0.372), while hard coral cover and observation period were not significant. In contrast, results from the SGD-Adam method suggested that hard coral cover was the most positive predictor, followed by observation period and distance to village. Random effects between areas from model I showed greater spatial variability than the SGD-Adam model.

Comparison of predictive performance illustrated that the Bayesian model was slightly superior in terms of RMSE, i.e., the Bayesian model was better able to capture extreme differences in biomass. The SGD-Adam model had a lower MAE value, reflecting the stability of the model in predicting biomass values of the Lutjanidae family.

Although the Bayesian model showed a lower RMSE, HMSGD provided a smaller MAE value, indicating that the model tends to be more robust to fluctuations in intermediate biomass values. The choice between these two methods can be tailored to the objectives of the study, i.e. whether to focus on the precision of the average estimate or the control of extreme errors.

The results of the Bayesian model show that there is variability between areas, with the Ayau-Asia Area having a highly positive and significant effect, in contrast to other areas. These results can inform the importance of considering spatial structure as well as institutions in fisheries management in conservation areas in Raja Ampat.

Acknowledgement

Thank you to the Science for Conservation Program of LPPM UNIPA for allowing the use of data in this study, BLUD UPTD KKP Raja Ampat, the Papua Bird's Head Seascape Reef Health Monitoring team, Blue Abadi Fund, KEHATI Foundation, Indonesian Conservation Foundation, Nusantara Nature Conservation for cooperation in collecting data used in this study.

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