

Inferring the allometric growth coefficient of juvenile African mud catfish, *Clarias gariepinus* (Burchell, 1822), using Bayesian and Frequentist regression models

Oluwale, F. V.¹

¹Department of Zoology, Faculty of Science, University of Ibadan, Ibadan, Oyo State, Nigeria

Corresponding author: Femi Oluwale. wale_femi@yahoo.com

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Abstract

Statistics is essential in biological and ecological scientific research. However, the default Frequentist statistics based on p-value and null hypothesis testing is often misused and misinterpreted, hence causing reproducible crises. The p-value concept deserved further examination because it has been irretrievably lost. Therefore, there is dire need for reform in the default Frequentist statistics as practiced by researchers because of the perils of p-values. Bayesian statistics, using the tools of Bayes Factors and posterior distributions derived from priors and likelihood function; rooted in Bayes' Theorem is one of the suggested alternatives. Frequentist (least square) and Bayesian (specifying uniform Jeffreys-Zellner-Siow prior, r-scale =0.35) regression models, a standard statistical protocol in fisheries were applied to determine the allometric growth coefficient based on length (mm) and weight (g) measurements of juvenile African mud catfish, *Clarias gariepinus* from Epe Lagoon. The growth coefficient, $b=3.20$, 95% Confidence Interval [3.07, 3.34], $t(96)=47.55$, $p<0.001$ was significant with 96% explanatory power ($R^2=0.96$). While Bayesian method, with 96% explanatory power ($R^2=0.96$), also estimated, $b=3.20$, (with Credible Interval between 3.06 and 3.32). The Bayes Factor (>100) suggested the data is more plausible under the alternative model than the null model, but p-value cannot quantify evidence in support of alternative hypothesis, since p-value can only reject or fail to reject a null hypothesis. These findings suggested that juvenile *C. gariepinus* thrived in Epe Lagoon. Therefore, Bayesian inference is a robust substitute for Frequentist regression model in fisheries.

Introduction

Bayesian statistics is experiencing a renaissance in the fields of biological and environmental sciences including fishery. It is a different statistical framework (contrary to the common statistics paradigm learnt in introductory statistics courses probably when getting a first degree in the sciences, technically called Frequentist statistics unknown to many) involving the principles of conditional probability rooted in the Bayes Theorem that provides a mathematical framework for updating and revising beliefs about hypotheses and parameter estimates conditional on observed data with prior knowledge by using the Bayes Factor (*BF*) (Kruschke 2010; Doll and Jacquemin 2018; Faulkenberry 2018; Faulkenberry *et al* 2020; Millar 2022). Bayesian statistics allows researchers to incorporate their prior knowledge into a formal model (Morris *et al* 2014) which is conceptually and practically impossible in the default Frequentist statistics. A notable difference between the Bayesian and the Frequentist statistical paradigms is rooted in the concept of probability, a central dogma in statistics describing the inherent uncertainty and randomness of events in the natural realm. While the frequentist envisages probability as the long-run relative frequency of a particular outcome/event occurring in many trials,

the Bayesian statistics views probability as subjective measures of uncertainty about events based on previous knowledge associated with it (Kruschke 2010; Morris *et al* 2014; Hackenberger 2019).

The use of descriptive and inferential statistics is essential in biological and ecological scientific research, but the widespread use of the Frequentist statistics, based on the p-value and Null Hypothesis Significance Testing (NHST) is mostly misinterpreted and abused, fueling the reproducibility crisis (Hu *et al* 2016). This abuse is not only reflected in p-hacking, which describes hypothesizing after the results are known, but also cherry-picking statistical significant (Fraser *et al* 2018); as in all scientific fields, of which fish and fisheries biologists are no exception to this pervasive trend hindering the ability to corroborate or nullify results. A number of problems with conventional Frequentist techniques have also been found. The American Statistical Association gave the clarion call that the terms p-value and NHST, as well as variations like "statistically significant," "nonsignificant" and " $p\leq 0.05$ " be immediately abandoned in the 2019 Special Edition Editorial titled "*Moving to a World beyond $p<0.05$* " (Wasserstein *et al* 2019). The initial intent of statistical significance as revealed by Fisher (1952), was simply to

serve as a tool to signal when a result merited further examination (Edgeworth 1885), but this idea has been irretrievably lost. Also, the null hypothesis of no difference between treatments (parameter values) is known *a priori* to be false, invalidating the premise of the test (White *et al* 2014). Consequently, the fields of science would benefit from drastic reform in the prevailing statistical inference involving the p-value. One of the proffered solutions is a number called the Bayes Factor (*BF*), a centrepiece in Bayesian statistics, and an essential replacement for the Frequentist p-value (Kass and Raftery 1995). The *BF* is a principled Bayesian tool for model selection and hypothesis testing, interpreted as the strength for both the Null hypothesis (H_0) and the Alternative Hypothesis (H_1) based on the current data (Kass and Raftery 1995).

In the burgeoning literature, Bayesian inference has been increasingly adopted in fisheries sciences due to its ability to incorporate uncertainty and prior knowledge, as well as provide information for risk analysis and decision-making (Kinas 1992; André *et al* 1997; White *et al* 2014; Hilborn and Walters 2015). Several workers emphasized that statistical and biological significance differ, and p-values are useless without measures of effect size and statistical power (Yoccoz 1991; Johnson 1999; Hurlbert and Lombardi 2009; Beninger *et al* 2012). Despite the perils of the p-values and NHST, the use of Bayesian statistics stays incipient among workers, especially in the developing nations, because formal

educational institution implicitly train students and researchers to “discover by p-value” using hypothesis tests. To advance our knowledge, regression modelling using linear models, a standard statistical protocol in fisheries, was used to infer the growth coefficient (*b*) of juvenile African mud catfish, *Clarias gariepinus* (a commercially important species), in the context of default Ordinary Least Square (OLS) Frequentist statistics and Bayesian methods (using uniform Jeffreys-Zellner-Siow prior for parameter estimate and models comparison). This will reinforce the increasing use of Bayesian inferential methods for data analysis, concurrent with addressing the growing concerns with regards to the widespread mishandling of p-values.

Materials and methods

Study area

Epe Lagoon is a shallow (6m depth) freshwater lagoon measuring 243 square kilometers and located in Lagos State, Nigeria (Figure 1). This body of water provides a highly significant habitat area for a wide array of fish species, also, serving as a breeding ground and nursery. Therefore, it is an important water body for sustenance of the local fish industry. Artisanal fishing, with predominantly passive and active fishing gears thrive in the lagoon. The major vegetation around the lagoon comprised freshwater swamp forest and secondary forest (Adeonipekun *et al* 2019).

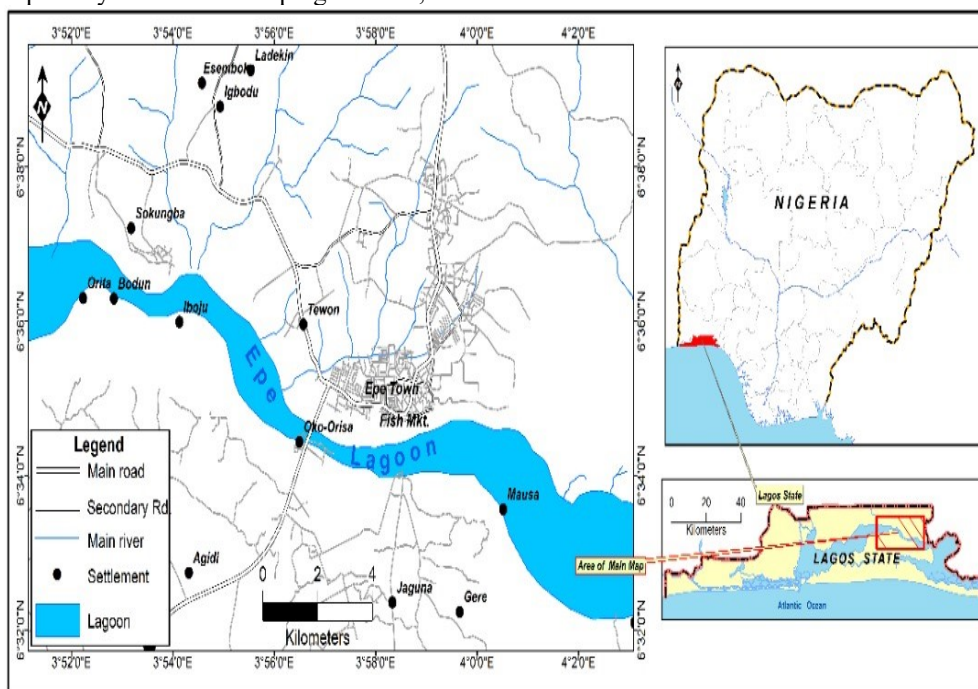


Figure 1. Map of Epe Lagoon with inserts of map of Lagos State showing location of study area and map of Nigeria showing location of Lagos State

Collection of fish samples

Random samples of 98 juvenile African mud catfish, *Clarias gariepinus* were obtained monthly (December to May 2021) from Chief Market, a landing site for artisanal fishermen from Epe Lagoon. These samples

were preserved in ice-filled vessels and transported to the Hydrobiology and Fisheries Laboratory in the Department of Zoology at the University of Ibadan for further preservation by deep freezing prior to biological data collection.

Species identification and biometric measurements

Individual fish were mopped dry with tissue paper after thawing, and identified using standard guide (Idodo-Umeh, 2003). Two biometric characters, namely body length and weight were measured. Total body length (L) was measured in millimeter using Vernier Caliper (0.1 mm), and body weight (W) was measured in gram on a digital scale (0.1g precision).

Allometric power model body length–weight relationship

The allometric growth relationship between fish body length (L) and body weight (W) was represented by the power function model (Eq 1), originally proposed by Huxley (1924), which explains the variations in body forms with size. According to the equation, body dimensions increase relative to each other according to a constant defined as b termed the allometric coefficient, while the constant a is the proportionality coefficient between the two variables

$$W = aL^b \tag{1}$$

Hypothesis testing for the regression coefficient

Regression tests two hypotheses about the effect of the regression slope (where β = regression slope in concerning model error (Chen and Jackson 2000).

$$Y = mX + c \tag{2}$$

$$Y = \beta_0 + \beta_1 X + \epsilon \tag{3}$$

Several regression cases exist in fish and fishery biology (Ricker, 1973), and a regression model proved ideal for estimating the exponent in equation 1 after logarithmic transformation (Le Cren 1951; Ricker 1973) by linear regression as illustrated in Equ. 4.

$$\text{Log}(W) = a + b \text{Log}(L) \tag{4}$$

Frequentist framework of simple linear regression by Ordinary Least Square (OLS)

The default regression estimation method use in fisheries and ecology is ordinary least squares which is based on the Gauss-Markov assumption of the model error (Chen and Jackson 2000), by minimizing residual sum of square. The popularity of the OLS method may be due to the tradition and its ease of computation by commercially available point-and-click computer software.

Bayesian framework of simple linear regression by the Bayes' Theorem

Bayes' Theorem

Bayes' Theorem is a mathematical formula used to calculate the probability of a hypothesis being true based on prior knowledge or information. It involves using the prior probability distribution and the likelihood of the data to generate a posterior probability distribution. This probability is found by applying the Bayes' Theorem (Bayes 1763) modified as Equ. 5 for ease of understanding where p represents probability,

statistics, but termed allometric growth coefficient in fisheries):

- i. Null hypothesis $H_0 = \beta_1 = 0$
- ii. Alternative hypothesis $H_1 = \beta_1 \neq 0$

The null hypothesis, H_0 states that there is no relationship between the dependent variable $Y=W$ and the independent variable $X=L$. In this case, the regression coefficient i.e., slope, β_1 is zero, while the alternative hypothesis, H_1 represents a two-tail (directionless) state of an association between W and L , which is not zero.

Linear regression model

The regression model (Eq. 3) is a variant of the general equation of a straight line (Eq. 2) where m is the slope or gradient of the line and c is the intercept on y-axis, that is the value of y when $x = 0$, but with standard statistical notation (where Y and X are defined in Equ. 2, β_0 = intercept, β_1 = slope, and ϵ = error term; Equ. 3) quantifying changes in the response variable as a function of one or more explanatory variables. It is termed simple linear regression if the explanatory variable is one, as in this context. Parameters (slope and intercepts) regression models are estimated by fitting the model to observed data with assumptions made and “|” indicates conditional upon, and H is a generic term mostly depicted by theta (θ), which indicates parameter(s) or models to perform inference on a statistical context. In Bayesian regression model, H is either the regression slope, or the hypothesis being tested, technically term models (Null Hypothesis, H_0 , and Alternative Hypotheses, H_1) are tested in regression, but Bayesian inference can test more than two hypotheses) or a combination of both in multiple regression,

$$p(H|data) = \frac{p(data|H) X p(H)}{p(data)} \tag{5}$$

Therefore, quantity $p(H|data)$, or the probability of the hypothesis given the data, is called the posterior probability distribution, or simply the posterior. The quantity $p(data|H)$ is the likelihood. The quantity $p(H)$ is called the prior probability distribution, or just the prior, and reflects information available about the hypothesis independent of (and hence prior to) conducting the experiment. The denominator $p(data)$ is simply a normalizing constant, the marginal probability density of the data across all possible hypotheses and is equal to the integration; rescaling the equation back to probability. Consequently, the Bayes Theorem is conceptually represented as shown in Equ. 6

$$p(H|data) \propto p(H) x p(data|H) \tag{6}$$

Model comparison and the Bayes Factor (BF)

The Bayes Factor represents summary of the evidence provided by the data in favour of one scientific theory, represented by a statistical model, as opposed to another (Kass and Raftery, 1995). Bayes Factor (BF) indexes support for regression models (Null Hypothesis, H_0 and

Alternative Hypothesis, H_1) by directly comparing their posterior probabilities called posterior odd. (Odd is simply a ratio of probability). The posterior odds in favour of H_1 over H_0 can be computed as $p(H_1|data) \div p(H_0|data)$. Using Bayes' Theorem, Eq. 5 becomes Eq. 7 and further simplified in Eq. 8, where the *Bayes Factors (BF)* are the marginal likelihood of the two models (the integral of the probabilities of the data given the parameters under all models being considered), and the subscript 1 or 0 denotes the model in either the numerator or denominator respectively.

$$\frac{p(H_1|data)}{p(H_0|data)} = \frac{p(H_1)}{p(H_0)} \times \frac{p(data|H_1)}{p(data|H_0)} \quad (7)$$

$$\text{Posterior odds} = \quad (8)$$

$$\text{Prior odds} \times \text{Likelihood}$$

Specifically, the posterior odds are equal to the prior odds multiplied by an updating factor. This updating factor is equal to the ratio of likelihoods $P(D|H_1)$ and $P(D|H_0)$, and is called the Bayes factor (*BF*) (Jeffreys 1961).

Table 1: Classification scheme for interpreting the Bayes Factor

Bayes Factor	Evidence
1–3.2	Anecdotal
3.2–10	Substantial
10–100	Strong
> 100	Decisive

Source: Jeffrey (1961)

Prior distribution for estimation and model comparison
Prior specification is an important aspect in Bayesian analysis, where prior represent background knowledge about the unknown parameter ($\theta = \beta_1$ and β_0) and the compared regression models compared (null and alternative models). Jeffreys-Zellner-Siow (JZS) priors were applied, both on the parameter estimates and model comparison. A uniform prior is true, non-informative since it provides equal support over the space of candidate distributions and leads to closed-form posterior, and when the data-generating distribution is unknown (Rademacher and Doroslovacki 2019; Karadavut 2020)

Data analysis

Data analytics were performed using R programming language and statistical environment (version 4.3.1) and JASP (version 0.17.2) statistics. Distributions and numerical descriptive statistics as well as Frequentist regression model were performed in R programming environment. Bayesian regression model using Uniform JZS prior (r scale = 0.35) was done in JASP statistics.

Results

Describing the biometric traits

Biometric traits (namely body weight and total length) of juvenile *C. gariepinus* in the samples ranged from 201.00–102.0mm (59.68±26.81) in total length, while

the body weights varied between 57.8–8.40g (2.74±15.03). The biometric traits exhibited bi-modal, skewed distribution (Figure 2A and B) in Epe Lagoon. The juveniles exhibited greater variations in weight than length, as indicated by the coefficient of variation (Table 2).

Describing linear regression parameter using Frequentist statistics

The Frequentist linear regression model (Figure 2C) using Ordinary Least Square (OLS) explained a statistically significant and substantial proportion of variance ($R^2 = 0.96$, $F(1, 96) = 2260.54$, $p < 0.001$, adj. $R^2 = 0.96$). The model intercept, corresponding to $\log L = 0$, is at -5.58 (95% CI $[-5.88, -5.29]$, $t(96) = -37.70$, $p < .001$). Within this model, the effect of $\log L$ is statistically significant and positive ($\beta = 3.20$, 95% CI $[3.07, 3.34]$, $t(96) = 47.55$, $p < 0.001$; Std. $\beta = 0.98$, 95% CI $[0.94, 1.02]$) and reliably different from zero, that is, rejecting the null hypothesis. In fisheries, the growth parameter, $b = 3.30$ indicates positive allometric growth for juvenile *Clarias gariepinus* in Epe Lagoon. Therefore, the results show that the juvenile *C. gariepinus* that inhabits the Epe Lagoon exhibited positive allometric growth ($p < 0.05$) with an exponent parameter between 3.07 and 3.34.

Bayesian regression models comparison and parameter estimates

Models' comparison

The alternative model (H_1) remains best predictor of the observed data using Jeffreys-Zellner-Siow (JZS, (r scale = 0.35) prior, evidenced by the increased and updated posterior probability after observing the data; the *Bayes Factor (BF₁₀)* > 100 indicates decisive evidence against the null hypothesis (Table 3). The allometric growth coefficient for juvenile *C. gariepinus* = 3.20, indicating positive allometric growth for the species in Epe Lagoon ($b = 3.20$, $BF_{inclusion} = 3.24 \times 10^{+64}$) as shown in Table 4.

Discussion

Positive allometric growth coefficient ($b =$ regression slope) was found by the Frequentist and Bayesian statistics for the juvenile African mud catfish, *Clarias gariepinus*, suggesting that this vulnerable early life stage thrived in this natural habitat, Epe Lagoon, during the study period. Intensive search of literatures on the web revealed scarcity of allometric data for these vulnerable early life stages in Nigeria's natural water. This critical biological trait remains understudied because most fisheries studies focus on commercial and/or adult populations. Fry and juvenile stages are predominantly examined under feeding trials in culture enclosures, because of the species aquaculture importance. Several workers reported that juvenile fish had different values for b and growth types from adults (Safran 1992; Peyton *et al* 2016; Possamai *et al* 2020).

Comparable regression coefficients by Frequentist ($\beta = 3.20$, 95% confidence interval $[3.07, 3.34]$, and Bayesian (3.20 credible interval 3.06 – 3.32) statistics were found in this study. Several works have affirmed

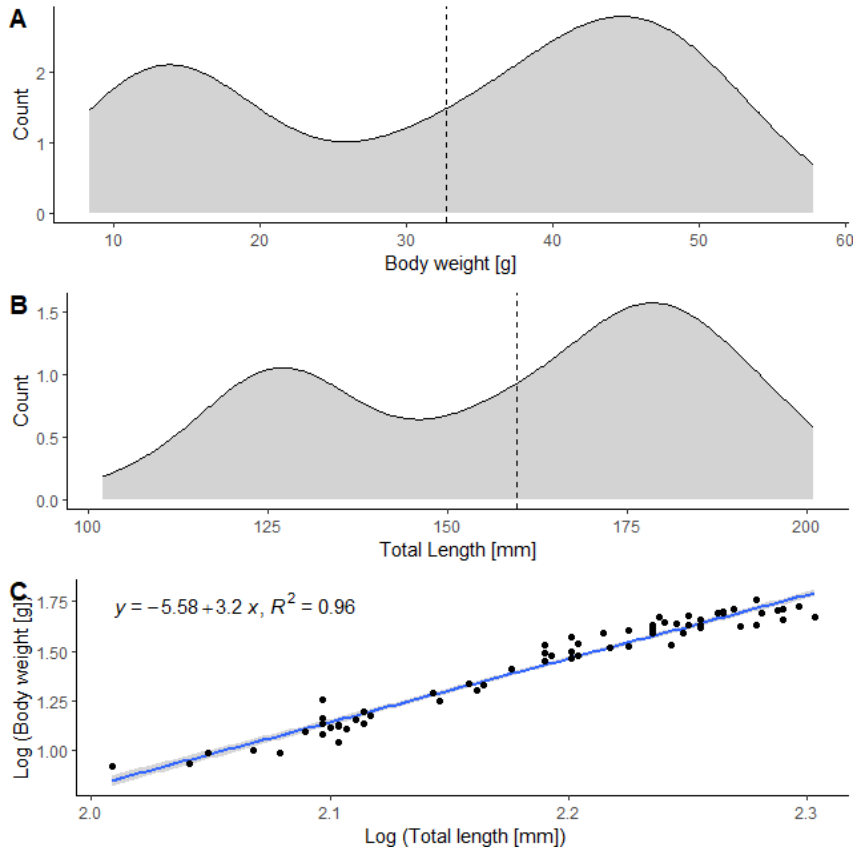


Figure 2. Characteristics of length and weight of juvenile *Clarias gariepinus* from Epe Lagoon. A and B: Density plots showing distributions of total length and body weight, dotted vertical lines show the means. C: Scatter plot showing linear association between logarithmic transformed total length and body weight superimposed with best-fit of linear regression line.

Table 2: Descriptive characters of juvenile *Clarias gariepinus* from Epe Lagoon

Characteristics	<i>Clarias gariepinus</i>	
	Total length (mm)	Body weight (g)
n	98.00	98.00
Mean ± SD	159.68 ± 26.81	32.74 ± 15.03
CI (Upper - Lower)	164.99 – 154.38	35.72 – 29.77
CV	16.80%	45.90%
Median	168.00	38.25
Skewness	-0.36	-0.28
Kurtosis	-1.20	-1.46
R (Max - Min)	99.0 (201.00 – 102.0)	49.40 (57.8 – 8.40)
Shapiro-Wilk	0.92	0.89

Note: n = sample size, CI = confidence interval, CV = Coefficient of Variation, CI = Confidence Interval, Min = minimum, Max = maximum value

Table 3: Bayesian Linear Regression: Model Comparison

Model	P(M)	P(M/data)	BF _M	BF ₁₀	R ²
Null model	0.50	3.089 × 10 ⁻⁶⁵	3.089 × 10 ⁻⁶⁵	1.0	0.00
Log L	0.50	1.00	∞	3.238 × 10 ⁺⁶⁴	0.96

Note: Prior probability = P(M), Posterior probability = P(M), Model Bayes' Factor = BF_M, BF₁₀ = Bayes Factor with respect to the alternative hypothesis.

Table 4: Bayesian linear regression parameter estimates

Coefficient	Mean	SD	P(incl)	P(incl data)	BF _{Inclusion}	95% Credible Interval	
						Lower	Upper
Intercept	1.45	0.001	1.00	1.00	1.00	1.44	1.46
Log L	3.20	0.067	0.50	1.00	3.24 × 10 ⁺⁶⁴	3.06	3.32

Note: SD = Standard Error, P(incl) = Probability of Inclusion, BF = Bayes Factor

that Frequentist and Bayesian regression estimates could be similar, but Bayesian regression allows incorporating prior information and uncertainty in the parameter estimates (Korner-Nievergelt *et al* 2015; Kabaila and Dharmarathne 2015). Credible intervals and confidence intervals are two different ways to quantify uncertainties of parameter estimates in statistics. Credible intervals are the Bayesian version of classical confidence intervals and do not require the existence of a pivotal quantity. Bayesian credible intervals frequently produce results with precision greater than or equal to frequentist confidence intervals (Gray *et al* 2015), as shown in this study. Bayesian inference could be a compelling alternative to default Ordinary Least Square (OLS) regression in fisheries and ecological models using a uniform prior. The choice of prior is critical in Bayesian data analysis, which is beyond the scope of the present study. Comparable estimates of b may also be attributed to the common methodological likelihood between the Frequentist and Bayesian frameworks: The frequentist Maximum Likelihood Estimate (MLE) functions similarly to the Bayes theorem likelihood. Consequently, the likelihood functions in the Frequentist regression and a prior form the posterior distribution in Bayesian inference.

The Bayes Factor > 100 quantifies decisive evidence that the observed data in this study favour the alternative model than the null model, but p -value cannot quantify evidence in support of alternative hypothesis; since p -value can only reject or fail to reject a null hypothesis. This functional ability to quantify evidence either in support or against of all possible models under the data space underscore the superiority of Bayesian inference over the Frequentist statistics. The p -values quantify the discrepancy between the data and a null hypothesis, indicating the probability of observing the data under the assumption of no difference or no effect, which is the major peril with frequentist regression, as in other frequentist methods. Inference is not based on the actual data but on a long-run chance of infinite sampling.

Furthermore, the p -value produced in standard (i.e., classical, orthodox, or frequentist statistics) is strongly influenced by sampling size (< 30) and composition of the sample (Baran and Warry 2008; Edwards *et al* 1963; Ho *et al* 2019). Therefore, researchers using these methods may be tempted to stop data collection early, and draw conclusions based on incomplete data if a preliminary result is compelling, meaning that the p -value are very low ($p < 0.05$). This can lead to biased or inaccurate results, as the p -value may change as more data is collected. In contrast, if a known sample size result is ambiguous (meaning that the p -value is not low enough to reject the null hypothesis but also not high enough to accept it), researchers may be tempted to continue data collection in search of a more definitive result (otherwise termed p -hacking).

Conclusion

Estimated positive allometric growth coefficient were comparable by the Frequentist and the Bayesian

inferential statistics for the juvenile African mud catfish, *Clarias gariepinus* inhabiting Epe Lagoon, indicating the vulnerable early life stages thrived in this habitat during the study period. In addition, the uncertainty in parameter estimates was identical between paradigms. Nevertheless, Bayesian inference does not reflect p -values and test statistics, thereby highlighting the fundamental difference between these two statistical frameworks. While a p -value is the probability of observing a test statistic as high or more extreme as the data given that the null hypothesis is true. Bayesian determines the plausibility and true range values for population parameters that would give rise to observed data. Unlike the p -value, the interpretation of Bayesian inference is intuitively meaningful because the credible interval reveals the plausibility that observed range contains the parameter true value rather than the boundaries like confidence intervals. Therefore, Bayesian methods adopted in this study make it possible to make inferences about the actual values of the parameter.

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