Latin American Journal of Aquatic Research, 54(2): xxx-xxx, 2026
DOI: 10.3856/vol54-issue2-fulltext-3558

Research Article

Models estimating size at maturity in aquatic organisms: a review

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ABSTRACT. Length at mean maturity ($L_{50\%}$) is defined as the length at which 50% of individuals are adults and 50% are juveniles. Estimating size-at-maturity in exploited fish and other aquatic species is important for legal-size catch allocation and for serving as a reference point for adult stock size, spawning stock, and stock-recruitment relationships. When the individuals are separated into mature and immature, the proportion of mature at length is modeled with a logistic function, where there are several models, such as Lysack, Bakhayokho, King, Withe et al., Brouwer & Griffiths, Somerton, or using asymmetric models such as Gompertz, Richards, Weibull, and Gamma distribution. In the multi-model selection approach, several models were used as candidates to fit a dataset of proportions of maturity by length intervals or age, and the best model was selected based on the Akaike information criterion. This estimate contradicts multi-model selection, so it is time to withdraw symmetric logistic models from the multi-model selection approach and rearrange asymmetric models to estimate size-at-maturity at a maturity proportion of 50%.

Keywords: asymmetric model; lobster; crab; sexual maturity

INTRODUCTION

Length at mean maturity ($L_{50\%}$) was defined as the length at which 50% of individuals were adults and 50% were juveniles (Lucano-Ramírez et al. 2023, Vélez-Arellano et al. 2024). In scientific journals, the size-at-maturity is sometimes used as a synonym of $L_{50\%}$.

In fisheries management, the $L_{50\%}$ is an important reference point for setting legal-size limits, as a low $L_{50\%}$ value can indicate high fishing intensity and poor stock health. The mature ogive, or model, for estimating $L_{50\%}$ is important for estimating adult stock size and potential spawning rate (Shertzer et al. 2024). So, it is important to have a good estimate of $L_{50\%}$. For example, an overestimation of the maturity ogive can lead to an underestimation of spawning stock size, and thus to the perception of a less productive stock than in reality.

A simple and fast method to assess the maturity stage of individuals is macroscopic analysis using the morphocromatic gonads scale. However, gonadic maturity varies seasonally, so adult individuals can be immature because their gonads are in a resting stage outside the reproductive season. Histological analyses of gonads are most precise for mature or immature-stage individuals. Domínguez-Petit et al. (2017) suggest that individuals are collected based on reproduction.

When the individuals are separated in mature and immature, the proportion of mature at length is modeled with a symmetric logistic function, which there are several models as: Hill (1910), Lysack (1980), Somerton (1980), Bakhayokho (1983), King (1995), White et al. (2002), and Brouwer & Griffiths (2005). But there are also asymmetric models for estimating size-at-maturity, such as the Gompertz (1825), Weibull (1951), Richards (1959), and Gamma distributions (Aguirre-Villaseñor et al. 2022).

Associate Editor: Leonardo Abitia

In logistics models, the sigmoid curve has an inflection point at Pi = 0.5 (symmetric model), corresponding to the size denoted $L_{50\%}$ or first size-at-maturity. Still, in asymmetric models such as Gompertz, Richards, and Weibull, the sigmoid curve has an inflection point below or above half the maturity proportion, and it is mistakenly assumed to be at $L_{50\%}$. So, the question now is: is it possible to estimate the L_i, like $L_{50\%}$, at half the maturity in asymmetric models?

On the other hand, the multi-model selection approach used several models as candidate models to fit a dataset of the proportion of maturity by length intervals or age, and the best model was selected based on the Akaike information criterion (AIC) (Akaike 1983, Burnham & Anderson 2002, Katsanevakis 2006). However, everyone who used this approach with symmetric logistic models found the same $L_{50\%}$ (Ping-Zhu et al. 2011, Hernández-Covarrubias et al. 2013, Jacob-Cervantes & Aguirre-Villaseñor 2014, García-Rodríguez et al. 2020, Flores-Anaya et al. 2024, Sánchez-Valdez et al. 2024). García-Rodríguez et al. (2020) accepted the same $L_{50\%}$ estimate across those models and suggested that only one should be used in multi-model selection. Then, the question now is, are logistics models a single model?

To answer these questions, the objective of this paper is to rearrange logistics models and fit them to maturity length data of lobster and blue crabs, showing that logistics models are a single model with the same slope, $L_{50\%}$, and AIC values among themselves, and rearrange asymmetric models to estimate L_i like $L_{50\%}$.

MATERIALS AND METHODS

Lobster females of *Panulirus inflatus* from commercial catches were collected from Mazatlán. Lobsters were classified as mature (stages 2-6) or immature (stage 1) based on a morphochromatic scale of Brione-Fourzán et al. (1981). In blue crab specimens (*Callinectes arcuatus*), sex and maturity were identified by abdominal morphology (Rivera-Velázquez et al. 2018). In both species, carapace length (CL) and carapace width (CW) were measured with a caliper. In total, 2,281 female lobsters and 264 female blue crabs were measured, with CL in lobsters and CW in blue crabs. Data were grouped into 5 mm intervals (Domínguez-Petit et al. 2017), and the maturity proportions were estimated for each species. In the models CL and CW will be used like L_t, $CL_{50,95\%}$ and $CW_{50,95\%}$ like $L_{50,95\%}$ respectively in both species.

A set of logistic models to analyze

Logistic models used to estimate size-at-maturity in aquatic organisms across various papers were analyzed. In the logistic models, PMLt is the proportion of mature individuals in the length class Lt, and $L_{50\%}$ is the size at maturity.

Lysack (1980) model (LM):

$$PM_{Lt} = \frac{1}{1+exp^{-b\left(L_t-L_{50\%}\right)}} \quad (1)$$

where *b* is the slope of the curve.

Bakhayokho (1983) model (BM):

$$PM_{Lt} = \frac{1}{1+exp^{[a-b(L_t)]}} \quad (2)$$

where *a* is the intercept and b is the slope of the curve, and size-at-maturity is $L_{50\%} = \frac{a}{b}$

King (1995) model (KM):

$$PM_{Lt} = \frac{1}{1+exp^{-r\left(L_t-L_{50\%}\right)}} \quad (3)$$

where *r* is the slope of the curve.

White et al. (2002) model (WM):

$$PM_{Lt} = \frac{1}{1+exp^{\left[-Ln(19)\left(\frac{\left(L_t-L_{50\%}\right)}{\left(L_{95\%}-L_{50\%}\right)}\right)\right]}} \quad (4)$$

where $L_{95\%}$ is size-at-maturity in 95%.

Brouwer & Griffiths (2005) model (BGM):

$$PM_{Lt} = \frac{1}{1+exp^{-\left(\frac{\left(L_t-L_{50\%}\right)}{a}\right)}} \quad (5)$$

where *a* is the width of the ogive maturity

Somerton (1980) model (SM):

$$PM_{Lt} = \frac{1}{1+A\times exp^{-(b*L_t)}} \quad (6)$$

where *A* is the parameter of scale and *b* is the slope of the curve, and $L_{50\%} = \frac{Ln(A)}{b}$.

But the SM has an *A* parameter on the scale, so it is very large relative to the *b* parameter, which is difficult to estimate when someone fits it using non-linear methods.

The Hill (1910) model (HM):

$$PM_{Lt} = \frac{1}{1+\left(\frac{L_{50\%}}{L_t}\right)^{b}} \quad (7)$$

where *b* is related directly to the width of the interval.

A set of asymmetric models to analyze

The asymmetric models used to estimate size-at-maturity in aquatic organisms in various papers were analyzed. In the asymmetric models, PMLt is the proportion of mature individuals in the length class Lt, and Li is the inflection point of the curve.

Gompertz model (GM):

$$PM_{Lt} = exp^{-exp^{-b(L_t - L_i)}} \tag{8}$$

where L_i is the length in the inflection point, and b is related directly to the width of the interval.

Richards model (RM):

$$PM_{Lt} = \left[1 - (1 - m) \times exp^{(-b*(L_t - L_i))}\right]^{\left(\frac{1}{1-m}\right)} \tag{9}$$

where L_i is the length in the inflexion point, b is the slope, and m is the shape parameter.

Weibull model (WeM):

$$PM_{Lt} = 1 - exp^{-\left(\frac{L_t}{L_i}\right)^b} \tag{10}$$

where L_i is the length in the inflection point, and b is the shape parameter.

Gamma function (GaM) logistic model (Aguirre-Villaseñor et al. 2022):

$$PM_{Lt} = \frac{1}{b_2^{b_1}\Gamma(b_1)} \int L_i^{(b_1 - 1)}\, e^{-\frac{L_i}{b_2}} dx \tag{11}$$

where: b_1 and b_2 are shape and scale parameters, respectively, and L_i is the length class and $L_{50} = qgamma(0.5, shape = b_1, scale = b_2)$.

The parameters were estimated by maximizing the log-likelihood function assuming a binomial distribution (Brouwer & Griffiths 2005).

$$LL(\emptyset|data) = \sum_{i=1}^{n}\left[m_i \times Ln\left(\frac{p}{1-p}\right) + n \times Ln(1-p) + Ln\binom{n_i}{m_i}\right] \tag{12}$$

where LL is the log-likelihood, p is the proportion of individuals in class CL_i or CW_i, n_i is the total number in class CLi or CWi, and m_i is the number of mature individuals in class CL_i or CW_i.

Multi-model selection

A statistical method based on information theory was applied, a commonly used approach to model selection. The AIC selects the best model, which is the one with the lowest AIC value, but when the difference between the best model's AIC and that of another model is less than 2, it is considered a good model (Burnham & Anderson 2002). When the AIC value indicates that different models are good, it is necessary to perform an inference across models and obtain a robust inference that does not depend on a single model, unless the best model has an Akaike weight (Wi) higher than 90% (Katsanevakis 2006).

$$AIC = 2 \times (K - LL) \tag{13}$$

where: K is the total number of estimated parameters, and LL is the maximum log-likelihood.

For each model, plausibility was estimated with Akaike weight (Wi).

$$Wi = \frac{e^{(-0.5*\Delta AICi)}}{\sum e^{(-0.5*\Delta AICi)}} \times 100 \tag{14}$$

$$\Delta AICi = AICi - AICmin \tag{15}$$

where $\Delta AICi$ are Akaike differences, $AICi$ AIC is the AIC for each model, and AIC_{min} is the minimum AIC value.

$$GM = \sum_{i=1}^{n} Wi_{i=1}^{n} * Mi_{i=1}^{n} \times 1/100 \tag{16}$$

where GM is the global model, Wi is the Akaike weight for each candidate model, and Mi is the corresponding candidate model.

RESULTS

Rearrangement of logistics models (are logistics models a single model?)

The oldest logistic model used to estimate size-at-maturity is LM, and later, BM proposed another logistic model version with $L_{50\%} = \frac{a}{b}$ but if you replaced this $L_{50\%}$ value in Equation 1. Let's conclude that (1) and (2) are the same model.

$$PM_{Lt} = \frac{1}{1+exp^{-b\left(L_t - \frac{a}{b}\right)}} = PM_{Lt} = \frac{1}{1+exp^{-\left(b*Lt - \frac{b*a}{b}\right)}} = \frac{1}{1+exp^{(a - bL_t)}} \tag{17}$$

Another logistic model version is KM, but it is LM exactly when $r = b$. WM is a more complex version of the logistic model. However, if you replace $\frac{Ln(19)}{(L_{95\%} - L_{50\%})}$ in the b parameter place, (1) has gotten the model (4).

$$PM_{Lt} = \frac{1}{1+exp^{-b(L_t - L_{50\%})}} = PM_{Lt} = \frac{1}{1+exp^{-\frac{Ln(19)}{(L_{95\%} - L_{50\%})} * (L_t - L_{50\%})}} = PM_{Lt} = \frac{1}{1+exp^{\left[-Ln(19)\left(\frac{(L_t - L_{50\%})}{(L_{95\%} - L_{50\%})}\right)\right]}} \tag{18}$$

Another logistic model version is BGM, but $\frac{1}{a}$ is the inverse of the slope, and if you replaced $\frac{1}{a}$ in place of b (1), the model (5) has been obtained.

$$PM_{Lt} = \frac{1}{1+exp^{-b(L_t - L_{50\%})}} = PM_{Lt} = \frac{1}{1+exp^{-\frac{1}{a}*(L_t - L_{50\%})}} = PM_{Lt} = \frac{1}{1+exp^{-\left(\frac{(L_t - L_{50\%})}{a}\right)}} \tag{19}$$

SM is a logistic model version to estimate the mean size-at-maturity in crustaceans, but if you replaced A by exp^{a} in (6) and let's factorize we have gotten the logistic model version (2) and you already saw before that Equation 2 is like (1).

$$PM_{Lt} = \frac{1}{1+A\times exp^{-(b*L_t)}} = PM_{Lt} = \frac{1}{1+exp^{(a)}\times exp^{-(b*L_t)}} = PM_{Lt} = \frac{1}{1+exp^{(a-bL_t)}} \quad (20)$$

The parameter equivalence function for the logistic models is shown in Table 1.

Rearrangement of asymmetric models (is it possible to estimate the L_i like $L_{50\%}$ in half the proportion of maturity of asymmetric models?)

Another sigmoid model used to estimate the maturity ogive with an inflection point in PMLt different from 0.5, like the logistic model, is GM with an inflection point at 0.367 of the proportion of maturity. Still, it has been mistakenly assumed that $L_i = L_{50\%}$. Now, you can estimate $L_{50\%}$ of Equation 8 with:

$$L_{50\%} = Li + (1/-b)\times\ Ln(-Ln(0.5)) \quad (21)$$

The same equation can be used to estimate any LPM% size by replacing 0.5 with PM/100.

A rearrangement Gompertz model (RGM) version that estimates the $L_i = L_{50\%}$ in $PM_{Lt} = 0.5$, has replaced $L_{50\%} = Li + (1/-b)\times Ln(-Ln(0.5))$ in Equation 8 and factorized.

$$PM_{Lt} = 2^{\wedge -exp^{-b(L_t - L_{50\%})}} \quad (22)$$

where $L_{50\%}$ is the length in half the proportion of maturity, and *b* is related directly to the width of the interval.

The general function RGM to estimate whatever size $L_{PM\%}$ of Equation 22.

$$L_{PM} = L_{50\%} - (1/b)\times Ln\left(-\frac{Ln(PM)}{Ln(2)}\right) \quad (23)$$

where PM is the proportion of maturity in whatever size, Ln (2) is the logarithm of half the proportion of maturity in $L_{50\%}$.

In RM, it has also been mistakenly assumed that Li = $L_{50\%}$, but Li is the length at the inflection point, *b* is the slope, and m is the shape parameter.

But you can estimate $L_{50\%}$ of Equation 9 using:

$$L_{50\%} = L_i + (1/-b)\times Ln\left(\frac{1-0.5^{(1-m)}}{1-m}\right) \quad (24)$$

A rearrangement of the Richards model (RRM) version to estimate the L_{50} in $PM_{Lt} = 0.5$.

$$PM_{Lt} = \left[1-(1-0.5^{(1-m)})\times exp^{-b\times(L_t - L_{50\%})}\right]^{\wedge\left(\frac{1}{1-m}\right)} \quad (25)$$

where $L_{50\%}$ is the length in half of the proportion of maturity, *b* is the slope, and *m* is the shape parameter.

General function RRM to estimate whatever size $L_{PM\%}$ of Equation 25.

$$L_{PM} = L_{50\%} - (1/b)\times Ln((1-PM^{1-m})/(1-0.5^{1-m})) \quad (26)$$

Here, PM is the proportion of maturity in whatever size L_{PM}, $L_{50\%}$, *b*, and *m* are model parameters.

In WeM, it has mistakenly assumed that $L_i = L_{50\%}$ too. In this model, the inflection point is 0.632. But it is possible to estimate $L_{50\%}$ of Equation 10 using:

$$L_{50\%} = L_i \times \left(-Ln(0.5)^{\frac{1}{b}}\right) \quad (27)$$

A rearrangement WeM (RWeM) version to estimate the $L_{50\%}$ in $PM_{Lt} = 0.5$.

$$PM_{LT} = 1 - 2^{\wedge -\left[\left(\frac{L_t}{L_{50\%}}\right)^b\right]} \quad (28)$$

where $L_{50\%}$ is the length in half the proportion of maturity, and *b* is the shape parameter.

The general function RWeM to estimate whatever size $L_{PM\%}$ of Equation 28.

$$L_{PM\%} = L_{50\%} \times \left(-\frac{Ln(1-PM)}{Ln(2)}\right)^{\frac{1}{b}} \quad (29)$$

where Ln(PM) is the proportion of maturity in whatever size, Ln (2) is the logarithm of half the proportion of maturity for $L_{50\%}$.

Finally, a general model is the Gamma function (GaM) with an inflection point in PM_{Lt}= 0.5, but this is different from the logistic model, and the approximation for size-at-maturity ($L_{50\%}$) is:

$$L_{50\%} = (b_1 \times b_2) - (b_2/3) \quad (30)$$

Tables 2-3 show that the models LM, BM, KM, WM, BGM, and SM have the same slope, $L_{50\%}$, and AIC values; this was also observed in the Akaike weights. In contrast, the models GM, RM, WeM, HM, and GaM differ from one another. On the other hand, the rearranged RGM, RRM, and RWeM estimated Li at half the maturity proportion, while the other parameters remained unchanged from the original models.

The logistics models fitted for both species are shown in Figure 1; all curves have the same shape, and the last plot is the yellow line. In contrast, the models LM, RGM, RRM, RWeM, HM, and GaM have different curve shapes (Fig. 2).

In the multi-model selection, the RRM was better for lobster data, while the RWeM was better for blue crab data. The RRM had strong support on the blue crab data, but, due to parameter penalties, ranked second (Tables 4-5).

Table 1. Equivalence functions of parameters in logistic models, Lysack (LM), Bakhayokho (BM), King (KM), White (WM), Brouwer and Griffiths (BGM), and Somerton (SM). The double asterisk sign indicates a parameter estimate by the model.

Model	Intercept	Slope	$L_{50\%}$	$L_{95\%}$
LM	$L_{50} \times b$	**	**	$L_{50} + \frac{Ln(19)}{b}$
BM	**	**	a/b	$\frac{a + Ln(19)}{b}$
KM	$L_{50} \times b$	**	**	$L_{50} + \frac{Ln(19)}{b}$
WM	$\frac{Ln(19) \times L_{50}}{L_{95} - L_{50}}$	$\frac{Ln(19)}{L_{95} - L_{50}}$	**	**
BGM	L_{50}/a	$1/a$	**	$L_{50} + a \times Ln(19)$
SM	$Ln(A)$	**	$Ln(A)/b$	$Ln(19 \times A)/b$

Table 2. Lysack (LM), Hill (HM), Rearrangement Gompertz (RGM), Rearrangement Richards (RRM), Rearrangement Weibull (RWeM) and Gamma (GaM) models, slope (b), shape (m), size-at-maturity ($L_{50\%}$), confidence interval (CI), likelihood (LL), and Akaike information criterion (AIC) of the mature data of *Panulirus inflatus*.

Model	b (CI)	m (CI)	$L_{50\%}$ (CI)	LL	AIC
LM	0.087 (0.08-0.094)		68.048 (66.606-69.572)	-93.638	191.276
HM		6.328 (5.845-6.888)	66.147 (64.771-67.443)	-63.224	130.447
GMR	0.067 (0.063-0.072)		65.906 (64.61-67.03)	-59.212	122.424
RRM	0.052 (0.043-0.062)	0.378 (0.029-0.944)	63.449 (61.619-65.304)	-48.376	100.751
RWeM		3.444 (3.192-3.715)	68.134 (66.293-69.678)	-111.154	226.308
GaM	5.53 (4.761-6.392)	12.469 (10.689-14.472)	67.117 (66.209-67.324)	-77.046	158.092

DISCUSSION

Several papers have used multi-model selection but mistakenly evaluated multiple versions of the logistic model, which, as seen above, are the same LM. The logistic models used in the multi-model inference violate the principles of multi-model selection and inference (Burnham & Anderson 2002, Katsanevakis 2006). The papers that did selection and inference multi-model with several logistic models had the same L_{50} estimations (Ping-Zhu et al. 2011, Hernández-Covarrubias et al. 2013, Jacob-Cervantes & Aguirre-Villaseñor 2014, García-Rodríguez et al. 2020, Flores-Anaya et al. 2024, Sánchez-Valdez et al. 2024), and this was confirmed by adjusting these models on lobster and blue crab maturity data, because different algorithms used in the multi-model selection approach describe the same sigmoid maturity function; therefore, the size-at-maturity lengths are the same, since rearranging logistic functions embeds the intercept and slope parameters of the logistic model into equivalent parameters, as demonstrated previously. Repeated models in multi-model selection result in Wi being divided by the number of model repeats, giving the impression of minor importance to the model. It is observed in papers that used logistic models in multi-model selection and inference, whereas inference with a single logistic model and asymmetric models does not. On the other hand, the generalized linear model (GLM) function in R statistical software for estimating ogive maturity uses the BM, so GLM is a logistic model; however, this one does not require grouped data in size intervals.

The asymmetric models, such as the Gompertz, Richards, and Weibull distributions, are distinct func-

Table 3. Lysack (LM), Hill (HM), Rearrangement Gompertz (RGM), Rearrangement Richards (RRM), Rearrangement Weibull (RWeM), and Gamma (GaM) models, slope (b), shape (m), size-at-maturity ($L_{50\%}$), confidence interval (CI), likelihood (LL), and Akaike information criterion (AIC) of the mature data of *Callinectes arcuatus*.

Model	b (CI)	m (CI)	$L_{50\%}$ (CI)	LL	AIC
LM	0.377 (0.288-0.479)		79.512 (78.094-80.704)	-8.706	21.412
HM		30.317 (22.814-38.872)	79.367 (78.127-80.605)	-9.26	22.521
GMR	0.245 (0.194-3.05)		78.206 (76.955-79.421)	-12.632	29.264
RRM	0.615 (0.303-1.202)	4.012 (1.179-8.532)	80.403 (74.433-82.147)	-7.261	20.522
RWeM		18.558 (15.168-23.415)	80.206 (78.811-81.543)	-7.256	18.512
GaM	283.194 (185.352-462.01)	0.28 (0.172-0.423)	79.201 (78.263-79.408)	-8.582	21.164

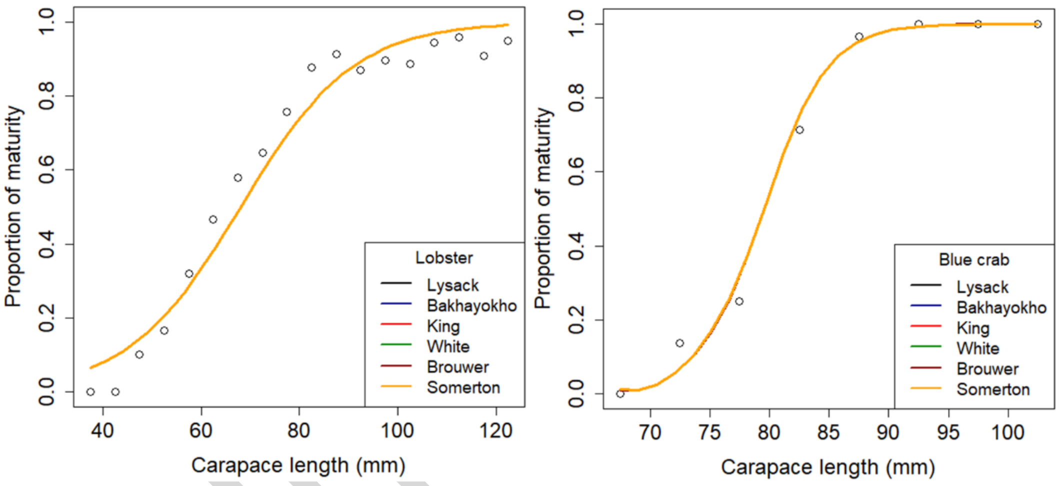

Figure 1. Logistics models fitted to the maturity data of lobster and blue crab.

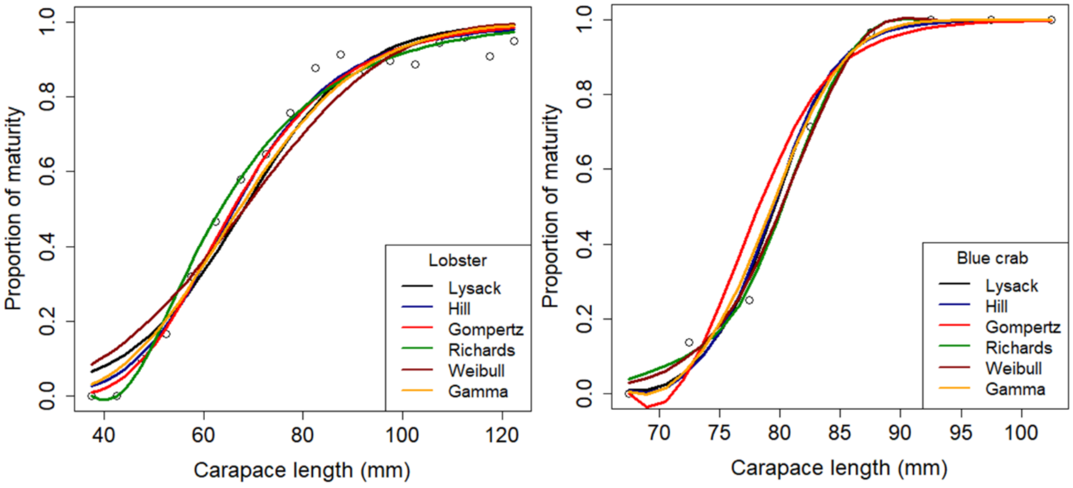

Figure 2. Multi-model selection for the maturity data of lobster and blue crab.

Table 4. Summary of multi-model selection for size-at-maturity of Lysack (LM), Hill (HM), Rearrangement Gompertz (RGM), Rearrangement Richards (RRM), Rearrangement Weibull (RWeM), and Gamma (GaM) models, number of parameters (k), Likelihood (LL), Akaike information criterion (AIC), Differences AIC (Δ AIC), and Akaike weight of *P. inflatus*.

Model	k	LL	AIC	Δ AIC	Wi
LM	2	-93.638	191.276	88.525	0.000
HM	2	-63.224	130.447	27.696	0.000
RGM	2	-59.212	122.424	19.673	0.005
RRM	2	-48.376	102.751	0.000	99.995
RWeM	3	-111.154	226.308	123.557	0.000
GaM	2	-77.046	158.093	55.341	0.000

Table 5. Summary of multi-model selection for size-at-maturity of Lysack (LM), Hill (HM), Rearrangement Gompertz (RGM), Rearrangement Richards (RRM), Rearrangement Weibull (RWeM), and Gamma (GaM) models, number of parameters (k), Likelihood (LL), Akaike information criterion (AIC), Differences AIC (Δ AIC), and Akaike weight of *Callinectes arcuatus.*

Model	k	LL	AIC	Δ AIC	Wi
LM	2	-8.706	21.412	2.901	11.694
HM	2	-9.260	22.521	4.009	6.719
RGM	2	-12.632	29.264	10.753	0.231
RRM	3	-7.261	20.522	2.010	18.250
RWeM	2	-7.256	18.512	0.000	49.868
GaM	2	-8.582	21.164	2.652	13.239

tions. The GM or RGM and WeM or RWeM have the characteristic that the inflexion points in the curve always occur at the same proportions of maturity, 0.367 and 0.6321, respectively. RGM suggests that the organisms show maturity signals (reproductive capacity) before the half-proportion maturity, whereas RWeM suggests that the maximum reproductive capacity occurs after half the proportion of maturity. Therefore, it is expected that organisms with an early size at maturity (RGM) will fit the data better than those with a late size at maturity (RWeM).

On the other hand, the RM or RRM has additional parameters that allow the inflexion point to be flexibly shifted to fit different maturity patterns in the population. In the three cases (RGM, RWeM, RRM), the inflexion point occurs at the same proportion across parameter estimation methods, as demonstrated by the results for lobster and blue crab. Those papers that used GM, RM, and WeM (Eqs. 8-10) before this manuscript estimated length at the inflection point, whilst they can estimate $L_{50\%}$ with Equations 21, 24, and 27, respectively. As for the Gamma model, it has an integral expression, and the solution is complex; however, we proposed an analytical approximation for estimating size at maturity.

RRM was the best model for the lobster data, with a Wi of 99%. Still, RWeM was in blue crab data with Wi of 49.868%, so this one does not make a clear winner (Katsanevakis 2006). In blue crab, it is necessary to do a multi-model inference to estimate size-at-maturity using models with Δ AIC minor of 7, because their sum ΔAIC gets a Wi major of 90%.

CONCLUSION

There is a single logistic model with different versions. Still, in a multi-model selection procedure, it is recommended to use only the LM version, which includes the $L_{50\%}$ parameter, and to compare it with other models such as RGM, RRM, RWeM, and GaM, since these models have different curve shapes but also estimate the $L_{50\%}$ parameter in their functions.

Credit author contribution

G. Rodríguez-Domínguez: conceptualization, methodology, formal analysis and review; J. Payán-Alejo: original draft, writing, methodology, formal analysis, review and editing.

Conflict of interest

The authors declare no potential conflict of interest in this manuscript.

ACKNOWLEDGMENTS

Thanks to the Cooperative Societies of C.V. Punta Tiburón and José María Canizales for the facilities granted to carry out the sampling. Martín Borrego and Luis Miguel Valadez, staff of the lobster laboratory FACIMAR-UAS.

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Received: October 29, 2025; Accepted: December 18, 2025