

Sérgio Afonso
Mulema¹
Andrés Carrión
García

QUALITY AND PRODUCTIVITY IN AQUACULTURE: PREDICTION OF OREOCHROMIS MOSSAMBICUS GROWTH USING A TRANSFER FUNCTION ARIMA MODEL

Article info:
Received 02.05.2018
Accepted 24.08.2018

UDC – 626.885
DOI – 10.18421/IJQR12.04-03

Abstract: *The cultivation of aquatic species in aquaculture aims at improving fish production, making the activity more dependent on human capacity, especially with what concerns to the application of efficient methods for its management. The weight and standard length are the biometric parameters mostly used to control the growth of tilapia in the cultivation process. In this work there is presented a statistical method based on transfer function ARIMA model to adjust and predict the weight of tilapia with the support of the values of the standard length. The model was adjusted to the data recorded in 21 weeks in the tilapia growing tank of the company Aquapesca de Moçambique, and the results showed that there was a good adjustment (with an explained variability of 97.8%) with which the model can be used to predict the future values of tilapia weight and make the activity more controllable and profitable.*

Keywords: *ARIMA model, Transfer function, predict, Aquaculture, Tilapia.*

1. Introduction

According to the FAO (Food and Agriculture Organization of the United Nations) aquaculture is defined as the production of aquatic organisms, the creation of fish, molluscs, amphibians, reptiles and the cultivation of aquatic plants for human consumption.

Based on its commitment in creating and managing aquatic resources living in a restricted environment, aquaculture is much more related to agriculture and livestock than to fishing.

While in fishing and hunting there are collected animals by free access, in aquaculture, property rights and resources

are required. Ownership of the means of production and property rights are as important in aquaculture as land tenure is in agriculture (Acuña, 2006).

Production in aquaculture requires an intervention of human capacity throughout the cultivation process in order to obtain better results. To this end, modern industrialized aquaculture is an activity with a strong scientific-technical component and is associated to several disciplines such as Biology, Engineering and Economics (Acuña, 2006).

Currently, aquaculture is considered responsible for the production of half of the fish consumed by the world population. Information from Stanford University

Corresponding author: Sérgio Afonso Mulema
Email: sergiomulema@gmail.com

(Stanford University, 2009) indicates that fish production through aquaculture tripled between 1995 and 2007. This aspect may be associated with the fact that aquaculture is the fastest growing zootechnical activity on a global scale with rates averages of expansion of 6.9% between 1970 and 2006. The exponential growth of this activity over the last 50 years enabled an increase from less than one million tonnes in 1950 to 51.7 million tonnes in 2006, with a worldwide contribution of 50% in world-wide consumed aquatic products.

Aquaculture in Mozambique contributes to the family diet, and in addition, the activity contributes significantly to the growth of the country's economy through export trade of fish and job creation. Shrimp and tilapia are the most cultivated species.

The fact that the aquaculture industrialization process is relatively fragile in Mozambique, monitoring methods aimed at controlling key environmental and biometric parameters have not yet been improved for a large-scale production level. Therefore, a field of research is opened to improve this aspect.

Studies related to analysis of biometric parameters in aquaculture are limited in the relationship between weight and length through the growth curves, which determine the form of growth of the species (as is the case of the study conducted by Garcia, Tume and Juárez (Garcia, Tume & Juárez, 2012). These models are static, that is, the models only relate the values of the same moment of the biometric parameters. However, the parameters are recorded throughout the process of cultivation of the tilapia, which should not rule out the hypothesis of autocorrelation in the data, and a dynamic relationship between the parameters, so that their study should be done through a methodology of corresponding time series.

Therefore, this paper seeks to apply a transfer function ARIMA model to analyze the dynamic relationships between the biometric parameters, weight and length, of

oreochomis mossambicus and improve predictions of the species' growth.

2. Literature review

Research on biometric parameters in aquaculture is oriented to the estimation of growth curves, which are based on a function that relates the weight and length of the species in the crop. Such is the case of Garcia, Tume and Juárez (Garcia, Tume & Juárez, 2012) who applies Von Bertalanffy curves to analyse the growth of oreochomis niloticus. Guerra and Manriquez (Guerra & Manriquez, 1979) comments that this method is rigorously applied when analyzing the growth of one or more individuals, weighing and measuring throughout their lives. However, this procedure is rarely possible and, in general, the value of the parameters of the regression is determined by comparing the weights and lengths of a large number of different sized by one or several methods of sampling.

Statistical methods of prediction were applied in aquaculture. In many studies, these methods have been used to predict water quality in a cropping system. As is the case of Palani, Liong and Tkalich (Palani, Liong & Tkalich, 2008), who applies artificial neural networks to fit a predictive model of water quality characterised by parameters: temperature, oxygen, salinity and chlorophyll-a in the coastal region of Singapore. The study was carried out basically to analyse the linear and nonlinear relationships of the referred environmental parameters.

In 2011 Han, Chen and Qiao (Han, Chen & Qiao, 2011) proposed a methodology that consists of a radical base function of neural networks of flexible structure to predict water quality. The author states that the methodology can vary its structure dynamically in such a way to maintain the accuracy of the forecast. In the same year, West and Dellana (West & Dellana, 2011) performed an empirical analysis on neural

networks in structures with memory. Similarly to the previous cases, West and Dellana study (West & Dellana, 2011) was carried out with the purpose of predicting water quality.

An ARIMA model and artificial neural networks were applied by Faruk (Faruk, 2009) in a study oriented to the prediction of water quality in aquaculture cultivation processes. The author considers that to study the pattern of aquaculture process variability and to obtain good predictions, the two methodologies are necessary, since with ARIMA model we cannot model the nonlinear relation between the variables and, a neural network is not able to model the linear and non-linear relationship between the variables. The results of the study show that the combination of these methods provides better results by comparing each separately.

The studies previously presented are limited to univariate predictive models, leaving out the correlation structure between the parameters that retain relevant information of the process. However, the process in aquaculture is characterized by many parameters correlated with each other, and therefore, a multivariate method is necessary for its coefficient analysis. To overcome this drawback, this paper presents a statistical methodology based on transfer function ARIMA model to analyse the dynamic relationship between biometric parameters (weight and length) and make predictions of the growth of *oreochromis mossambicus*.

Weight is the biometric parameter used as such growth indicator, and due to its strong relationship with the length, this is included in the model to improve its adjustment and obtain better prediction of the growth rate of tilapia.

The proposed model plays an important role both in the characterization of the growth shape of the tilapia (weight-to-length ratio) and the possibility of predicting the size of tilapia at harvest time. The application of this statistical model can improve the

planning of production in the aquaculture industry, ensuring knowledge and control of the production system.

3. Material and methods

The study was carried out at the company Aquapesca de Moçambique, where there was conducted a follow-up three months *oreochromis mossambicus* cultivation, grown in open tank with brackish water, and fed with feed. Throughout the cultivation process, the work was limited to study aspects associated with the growth of *oreochromis mossambicus* males, evaluated through weight and length.

At the beginning of the study, 600 individuals with an average weight of 100g and a standard deviation of 10.71g were allocated in the tank. Therefore, the tank had a total biomass (total weight of the individuals) of approximately 60000g.

The biometric parameters used to evaluate the growth of the individuals (weight and length) were recorded through weekly biometrics, where in each biometry the mortality rate that culminated with the biomass update was analyzed. The individuals extracted and observed in each biometry correspond to 10% of the updated biomass.

3.1. Biometric Parameters

Biometric parameters refer to the variables that characterise the size and fattening of a species in aquaculture cultivation. These parameters are recorded in the species periodically to evaluate their growth and development. Weight and standard length are the most used biometric parameters for tilapia growth control and in this work they were recorded as follows:

(1) Weight

The weight was recorded through the electronic scale, with an accuracy of 0.5g. The measurement consisted of weighing a sample drawn randomly from the tank

corresponding to 10% of the total biomass in each biometry, and estimating the mean weight (MW). Therefore, each weight data, at each time t , corresponds to the mean of the weight estimated from the sample drawn at that time.

(2) Standard length

Standard length of tilapia corresponds to the distance from the tip of the mouth to the peduncle (the beginning of caudal fin) of the individual. After weighing the selected sample in each biometry, the standard length was recorded with a ruler graduated in centimetres.

The standard length data were recorded in each individual; however, to ensure matching in the data, that is, for each data of length to correspond to exactly one weight data, arithmetic mean length (ML) were estimated for each sample drawn.

4. Statistical Forecasting Method

4.1. Stochastic process and time series

In order to define the transfer function ARIMA model which constitutes the basis of the statistical method applied in this work, it is appropriate to first address the concepts of stochastic process and time series on which the model is based.

A stochastic process is a family of random variables which, in general, are related to each other and follow a joint probability distribution. It is denoted by:

$$Y_t(\gamma), t = \dots, t - 2, t - 1, t, t + 1, t + 2, \dots$$

For each $t = t_0$, we obtain $Y_{t_0}(\gamma)$ representing each random process characterized by its distribution univariate probability. However, for each $\gamma = \gamma_0$ we obtain a performing process; that is, a sample formed by the set of singular observations at each time t of each of the random variables forming the process:

$$\dots, Y_{t-1}(\gamma_0), Y_t(\gamma_0), Y_{t+1}(\gamma_0), \dots$$

Therefore, for $t = 1, 2, \dots, T$. Temporal series Y_1, Y_2, \dots, Y_T is an accomplishment of the stochastic process $Y_t(\gamma)$.

4.2. Stationary Stochastic Processes

The analysis of time series consists in using stochastic process theory to determine the processes that generated the time series under analysis, in order to characterize its behaviour and to be able to predict the future (Casimiro, 2009). Therefore, for the predictions to be consistent, it is required that the stochastic process is stable, that is, stationary.

The stationarity of a stochastic process can be analysed through a distribution function (stationarity in the strict sense) or through its moments: mean, variance and covariance (second order stationarity or stationarity in covariance) (see details in Casimiro, 2009)).

If we verify that the distribution function of the set of n random variables of the process Y_t does not change for k periods lagged at time t , that means,

$$F[Y_{t_1}, Y_{t_2}, \dots, Y_{t_n}] = F[Y_{t_1+k}, Y_{t_2+k}, \dots, Y_{t_n+k}], \forall (t_1, t_2, \dots, t_n),$$

it is said that the stochastic process is strictly stationary.

We consider the stationarity in covariance when the following three conditions are fulfilled:

If all the process variables have:

(1) The same mean, that is to say:

$$E(Y_t) = \mu < \infty, \forall t$$

(2) The same finite variance:

$$V(Y_t) = E[Y_t - \mu]^2 = \sigma_Y^2 < \infty, \forall t$$

(3) The covariance between two variables does not depend on time t

$$\begin{aligned}
 cov(Y_t, Y_s) &= E[Y_t - \mu][Y_s - \mu] \\
 &= \gamma|t - s| = Y_k \\
 &< \infty, \forall t.
 \end{aligned}$$

4.3. White Noise Process

The white noise a_t is a simpler stochastic process, and corresponds to a sequence of random variables with zero mean, constant variance and null covariance, that is:

$$\begin{aligned}
 E(a_t) &= 0, \\
 V(a_t) &= \sigma^2, \forall t \text{ and,} \\
 Cov(a_t, a_s) &= 0, \forall t \neq s.
 \end{aligned}$$

The main characteristic of a temporal series is the dependence of observations in the time, so the essence of the temporal series models is based on the modelling of this correlation structure that can predict the future pattern of the series in case. However, the previous properties presented show that the observations of a white noise process are not correlated; indicating that for this type of process there is no relevant pattern to be modelled. Nevertheless, the white noise process is very useful in the analysis of time series, since it is the basis of the construction of the ARIMA models.

4.4. Processes AR (p)

It is denominated an autoregressive process of order p, to the stochastic process Y_t from which we can to define a model that relates the current observation with its past until the delay t-p and a white noise term, that is:

$$\begin{aligned}
 Y_t &= \varphi_1 Y_{t-1} + \varphi_2 Y_{t-2} + \dots + \varphi_p Y_{t-p} + a_t \\
 a_t &\sim RB(0, \sigma^2) \quad t = 1, 2, \dots
 \end{aligned}$$

which is equivalent to:

$$(1 - \varphi_1 B + \varphi_2 B^2 + \dots + \varphi_p B^p) Y_t = a_t$$

where, $\varphi(B) = (1 - \varphi_1 B + \varphi_2 B^2 + \dots + \varphi_p B^p)$ is the autoregressive polynomial and B is the delay operator, that is,

$$B_p Y_t = Y_{t-p}$$

The polynomial $\varphi(B)$ is used to test the stationarity of the AR (p) process. An autoregressive process AR (p) is stationary if the autoregressive polynomial $\varphi_p(B)$ has solutions outside of the unit circle, that is, the stationarity is checked by solving the following equation:

$$\begin{aligned}
 \varphi(B) = 0 \Rightarrow & (1 - \varphi_1 B + \varphi_2 B^2 + \dots \\
 & + \varphi_p B^p) = 0
 \end{aligned}$$

Where B is the polynomial variable, and takes positive and greater than one value.

4.5. Processes MA (q)

The moving averages model of order q expresses the value of Y_t pursuant to the noise and their respective delays up to the q order, y is represented by:

$$\begin{aligned}
 Y_t &= a_t - \theta_1 a_{t-1} - \theta_2 a_{t-2} - \dots - \theta_q a_{t-q}, \\
 a_t &\sim RB(0, \sigma^2)
 \end{aligned}$$

in an equivalent way:

$$\begin{aligned}
 Y_t &= (1 - \theta_1 B - \theta_2 B^2 - \dots - \theta_q B^q) a_t \\
 a_t &\sim RB(0, \sigma^2)
 \end{aligned}$$

where

$$\theta_q(B) = (1 - \theta_1 B - \theta_2 B^2 - \dots - \theta_q B^q)$$

is the polynomial moving averages and

$$B^q a_t = a_{t-q}.$$

The MA(q) model is stationary if it satisfies the condition: $\sum_{i=1}^q \theta_i^2 < \infty$, and since the number of parameters θ_i is finite, that is: $i = 1, \dots, q$, then this condition is always fulfilled, so that it can be said that an MA (q) model is always stationary.

A process with characteristics of both AR(p) and MA(q) is called autoregressive moving average, and is represented by ARMA (p,q).

The analytical expression of an ARMA (p, q) process is given by:

$$\begin{aligned} \varphi_p Y_t &= \theta_q a_t \\ a_t &\sim RB(0, \sigma^2) \end{aligned}$$

where φ_p and θ_q are defined in a similar way as in the previous cases. It is commonly assumed that ARMA processes are stationary. In every way, the stationarity of the process can be tested through the $\varphi_p(B)$ in an analogous way as in the AR(p) model.

The present research is oriented to non-stationary processes. The biometric parameters (weight and length) mentioned above, besides being dependent on the time, they present a continuous evolution, which adds to the model the trend component.

In this type of process, where in addition to the autoregressive and the moving average structure, also has a component trend that may be modelled by the polynomial $\nabla^d = (1-B)^d$ of order d (d = root number of non-stationary units) is called integrated, and is represented by: ARIMA (p, d, q).

The order d indicates the number of differences necessary to achieve the stationary process mean. Therefore, if Y_t is an integrated process of order d, the model $(1-B)^d Y_t = ARMA(p-d, q)$ is stationary and invertible.

In general, the ARIMA model (p, d, q) can be represented as:

$$\begin{aligned} \varphi_p \nabla^d Y_t &= k + \theta_q a_t \\ a_t &\sim RB(0, \sigma^2) \end{aligned}$$

where p is the order of the stationary autoregressive polynomial, d is the number of differences necessary to make it stationary (integration of the series), q is the order of the invertible moving average polynomial, and k is the constant of model.

4.6. ARIMA model with transfer function

As previously commented, this research

aims at modelling the autocorrelation structure in the biometric parameters in order to predict the growth of oreochromis mossambicus. Associated with commercial interests, weight was taken as the main indicator of such growth (fattening), and on this parameter the ARIMA model is adjusted. However, considering the high correlation between weight and length, it is relevant to include this parameter in the study in order to increase the variability explained in the model and to improve predictions about the growth rate. To achieve this, a transfer function ARIMA model is required.

According to Tsay (Tsay, 2005) the transfer function is a statistical model describing the dynamic relationship between a y_t variable response and one or more explanatory variables x_t . On the other hand, Yaffee and McGee (Yaffee & McGee, 1999) considers that the transfer function is a functional relationship between a response series y_t and an explanatory series x_t in a dynamic system.

In this work, the transfer function is applied to model the weight values of the tilapia through their past values and with the aid of the standard length values. Therefore, the length is used, in this case, as a variable that increases information in the model.

Consider p_t and l_t the weight and standard length, respectively. The transfer function adjusted for these two variables is given by:

$$p_t = k + v(B)l_t + N_t$$

where $v(B) = v_0 + v_1B + v_2B^2 + \dots$ is the coefficient of the transfer function, B is the delay operator, that is $B^m l_t = l_{t-m}$; and N_t is the model residual, which may be strongly correlated with l_t .

Therefore, the transfer function consists of two components: $v(B)$ and N_t .

As in the univariate case, these two components can be written as:

$$v(B) = (w(B)/\delta(B))B^b$$

where B is a non-negative integer number,

$$\begin{aligned} w(B) &= w_0 - w_1B - w_2B^2 - \dots \\ &\quad - w_sB^s \text{ and } \delta(B) \\ &= 1 - \delta_1B - \delta_2B^2 - \dots \\ &\quad - \delta_rBr. \end{aligned}$$

On the other hand, N_t can be modelled as:

$$\varphi(B)N_t = \theta(B)a_t$$

which corresponds to an ARIMA(p,q) model, where $\varphi(B) = 1 - \varphi_1B - \varphi_2B^2 - \dots - \varphi_pB^p$, $\theta(B) = 1 - \theta_1B - \theta_2B^2 - \dots - \theta_qB^q$ and $a_t \sim N(0, \sigma^2)$. Assuming stationary and invertibility of the model, N_t can be presented as:

$$N_t = (\theta(B)/\varphi(B))a_t$$

Then:

$$p_t = k + (w(B)/\delta(B))B^b l_t + (\theta(B)/\varphi(B))a_t$$

The fit of the transfer function will follow the modelling strategy of Box and Jenkins (Box & Jenkins, 1976), and in this case we will use the following steps:

- (1) fit an ARMA model for the time series length l_t ;
- (2) Use the same filter, that is, the same polynomials of the l_t model and fit an ARMA model for p_t ;
- (3) Let a_t denote the white noise from the fitted model in step (1) and a_t^* the corresponding noise obtained in (2) (which is not necessarily a white noise), determining a function of cross-correlation between a_t and a_t^* ;
- (4) Through the graph of the correlation function obtained in (3), identify the orders b, r, s of the transfer function;
- (5) The first estimation of the transfer function model is to determine the

coefficients $v(B)$ with the orders r, s, b estimated in (4) and the polynomials p and q of the fitted ARMA model for N_t , identified from the model of p_t .

5. Results and Discussion

In this section there are presented the results of the transfer function ARIMA model adjusted to the biometric parameters recorded in 21 weeks in the tilapia tanks at the company Aquapesca de Moçambique.

Figure 1 shows the evolution of weight (figure 1 (a)) and standard length (figure 1 (b)) over the considered cultivation period. The trend is obvious component in the parameters whereby a regular difference $d = 1$ in both cases is considered, and the differences of weight and standard length values (the difference between value of an instant and the first previous time) are presented in Figure 1 (c) and Figure 1 (d), respectively.

The oscillation of the differences obtained from the two parameters indicates, on one hand, that the growth of tilapia is not linear, and on the other hand, that this aspect may be associated with the randomness which is subject to sampling (it may happen that in a given biometry, individuals relatively smaller than those of the previous biometry are observed). However, Figure 1 show the original data of the parameters and their respective differences, where it can be observed that the stationarity was obtained in the mean.

The graphs in Figure 2 show successive decreases of simple correlations (Figure 2 (a) and (c)) and only a significant partial correlation (Figure 2 (b) and (d)), indicating that both parameters come from an autoregressive process of order 1 (AR (1)).

Following the modelling strategy of Box and Jenkins presented in section 3, an ARIMA (1,1,0) model was adjusted for standard length l_t , and its parameters were used to fit the ARIMA model (1,1,0) * for weight p_t . Then, it was regarded as a cross-correlation

function between residues at and a_t^* resulting from the two models (Figure 3) where it can be observed that the most important cross-correlation (significant) is Lag=0, indicating

that the correlation between weight and standard length is instantaneous (observations of the same instant).

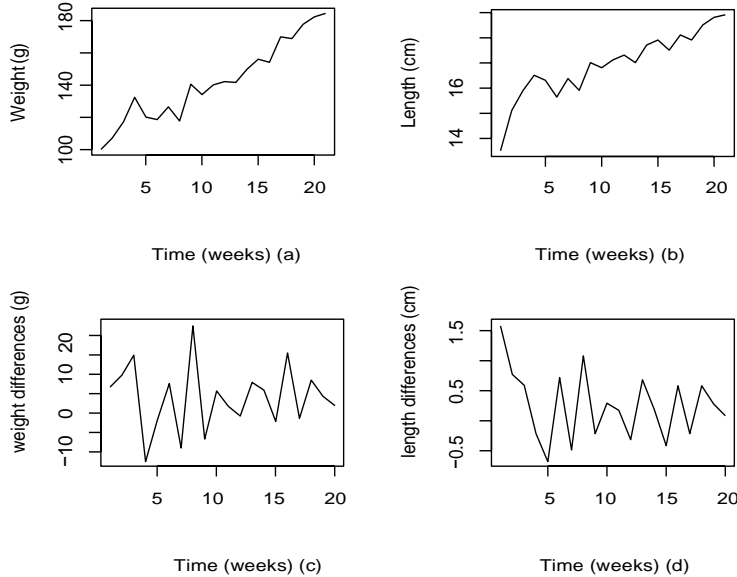


Figure 1. Representation of the biometric parameters and their respective differences

In the transfer function:

- b indicates the first significant Lag, and represents the first delay of the input variable (in this case the standard length) to enter in the model;
- s represents the number of increasing Lags after b ;
- r indicates the number of exponential falls in the increasing Lags.

Therefore, Figure 3 indicates that $b = 0$, $s = 1$ and $r = 0$.

On the other hand, the simple and partial correlation functions, and the regular difference considered, suggest an ARIMA model (1,1,0) for the weight parameter p_t (model fitted for weight without resorting to

pre-whitening method). Hence, a first estimation of the analytic expression of the transfer function for p_t and it is:

$$p_t = (w_0 - w_1B)l_t + (1/(1 - \varphi_1B)) a_t$$

that is

$$p_t = \varphi_1 p_{t-1} + w_0 l_t - (w_1 + w_0 \varphi_1) l_{t-1} + w_1 \varphi_1 l_{t-2} a_t$$

where $a_t \sim RB(0, \sigma^2)$. This model indicates that the weight value of the tilapia at a given moment is influenced by the weight of the previous time, and the values of the length of the same instant and of the two previous times.

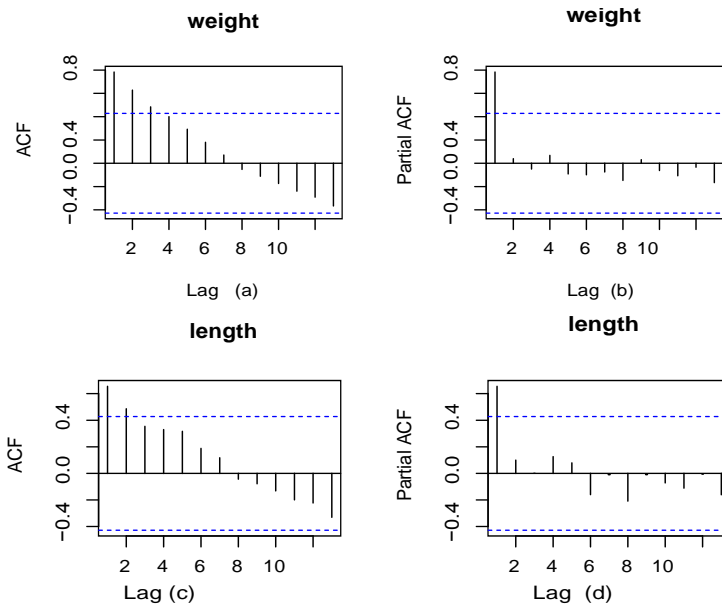


Figure 2. Simple and partial correlation function for the biometric parameters

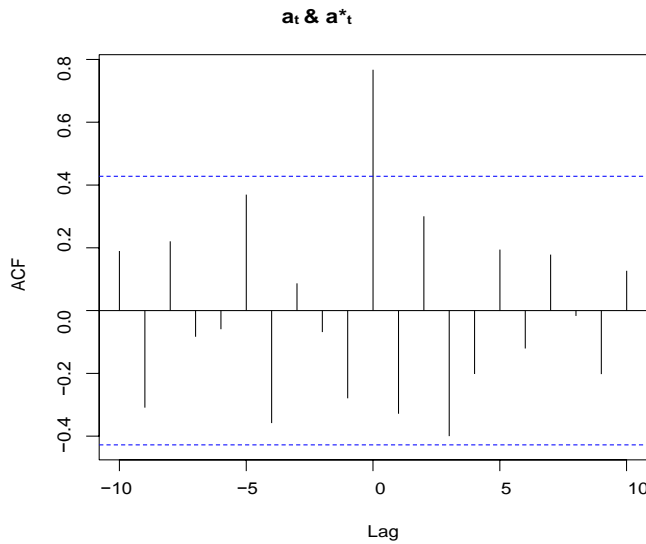


Figure 3. Cross-correlations between a_t and a^*_t

The estimated values of the coefficients are: $\varphi_1 = -0.50, w_0 = 17.08$ and $w_1 = -0.40$. And the final model is defined as follows:

$$p_t = -0,50p_{t-1} + 17,08l_t + 8,94l_{t-1} + 0,2l_{t-2} + a_t$$

The future values of the weight can be estimated as follows:

$$p_{t+h} = -0,50p_{t+h-1} + 17,08l_{t+h} + 8,94l_{t+h-1} + 0,2l_{t+h-2}$$

where h is a positive integer number.

Figure 4 shows that there is not a large discrepancy between observed and predicted weight values using the fitted transfer function ARIMA model, indicating a good fit of the model (AIC = 112.23).

The residuals of the fitted model follow a

normal distribution (see figure 5) from the Ljung-Box test ($W = 18.437$, $p\text{-value} = 0.362$) found that there is no significant evidence to reject the hypothesis that the residues are independent and identically distributed.

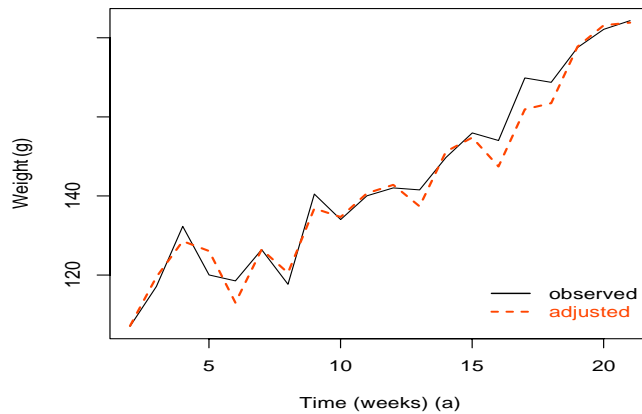


Figure 4. Adjustment of the transfer function ARIMA model for weight of tilapia

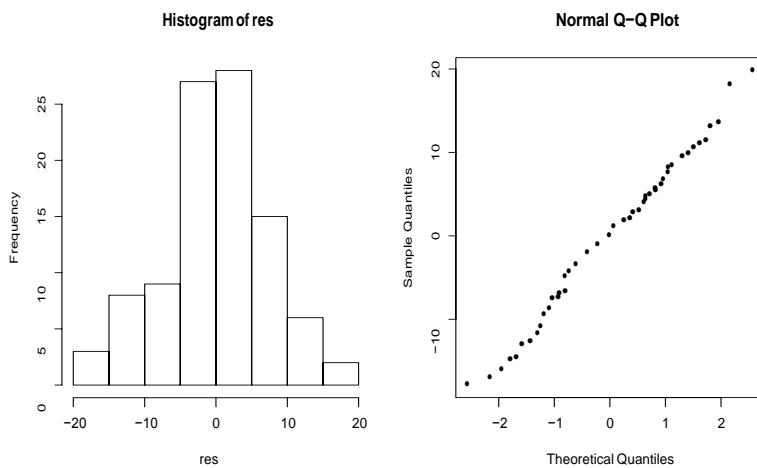


Figure 5. Model Diagnosis

With these findings, the fitted transfer function ARIMA model can be used to predict the weight of tilapia in the next weeks of cultivation. Such prediction depends on the recorded historical values of weight and length.

The use of this model may help in the monitoring process, with regard to the

growth rate of tilapia, and with the biometric parameters considered, it will be possible to carry out forecasts of the level of growth, from which the expected yield can be evaluated in the crop, giving possibilities to make early changes in the process in case of anomalies.

Table 1 shows the predictions of the next ten (10) weeks of culture (with their respective confidence intervals of 80 and 90%). The model indicates that if the cultivation period was extended for a further 10 weeks, that is, up to week 31, tilapias with an average weight of approximately 250g would be

obtained (corresponding to 36.6% of the average weight at week 21) with a weekly growth rate of 6.9g end of the current section. It is recommended that footnotes be avoided. Instead, try to integrate the footnote information into the text.

Table 1. Estimated weight values for the next 10 weeks (LL=Lower limit, UL=Upper limit)

Time(weeks)	Weight	IC80 %		IC95 %	
		LL	UL	LL	UL
22	188,2	179,3	197,2	174,6	201,9
23	195,1	185,9	204,2	181,1	209,1
24	201,9	192,3	211,5	187,2	216,6
25	208,8	198,4	219,2	192,8	224,7
26	215,6	204,1	227,1	198,0	233,2
27	222,4	209,5	235,4	202,6	242,3
28	229,3	214,6	244,0	206,8	251,8
29	236,1	219,4	252,9	210,5	261,7
30	243,0	224,0	262,0	213,9	272,0
31	249,8	228,4	271,2	217,1	282,6

6. Conclusions

The profitability of fish farming activity in aquaculture is measured by the levels of fattening obtained at the end of the crop, which is interpreted in monetary values. Therefore, several strategies are used in aquaculture aimed at improving such yield. However, some non-controllable factors may influence in a way that hinders the expectation of the final crop result. In this aspect, the transfer function ARIMA model was applied in this work in order to improve the prediction of tilapia growth levels throughout its cultivation process.

Unlike the methods commonly used in aquaculture to relate biometric parameters, such as the weight-length growth curves and linear regression models, the ARIMA model with transfer function considers the dynamic relationship between biometric parameters, as shown by the previous results presented. This method allows that both instantaneous relations and the effect of the relationships between lagged values from the parameters are included in the model. This strategy increases the explained variability of the

model compared to the usual methods mentioned, this aspect can be justified by the good result of adjustment capacity obtained (97.8%).

Therefore, the ARIMA model with transfer function can be considered a relevant methodology to control and predict the growth of tilapia. This model may make the activity more controllable and accessible to implement strategies for improving the final product.

In future investigations, the model can be extended considering the environmental parameters in the transfer function model as regressors to quantify the impact of each environmental parameter on the growth of the cultivated species, as well as improvements in the predictive capacity of the model.

Acknowledgment: I would like to thank the *Universidade Pedagógica de Moçambique, Delegação de Quelimane* for funding this research and the the company *Aquapesca de Moçambique* for guaranteeing the experimental phase of this work.

References:

- Acuña, C. (2006). Biotechnology applied to aquaculture. *ArgenBio, Argentine Council for the information and development of biotechnology*, 1(1), 1-6.
- Box, G. E. P., & Jenkins, G. M., (1976). Time series analysis: forecasting and control. *San Francisco, CA: Holden-Day*, 1(44), 976-575.
- Casimiro, M. P. G. (2009). Análisis de series temporales: Modelos ARIMA. *Universidad del País Vasco*, 1(1), 1-169. ISBN: 978-84-692-3814-1.
- Faruk, D. O. (2009). A hybrid neural network and ARIMA model for water quality time series prediction. *Engineering Applications of Artificial Intelligence*, 23(4), 586-594.
- García, A., Tume, J., & Juárez, V. (2012). Determination of growth parameters of Nile tilapia (*Oreochromis niloticus*) in a Magazine with geomembrane pond stocked with water and subsoil. *Ciencia y Desarrollo*, 15(2), 47-55.
- Guerra, A., & Manriquez, M. (1979). Parámetros biométricos de *Octopus vulgaris*. *Instituto de Investigaciones Pesqueras de Vigo*, 1(44), 177-198.
- Han, H. G., Chen, Q. L., & Qiao, J. F. (2011). An e-scientific self - organizing RBF neural network for water quality prediction. *Neural Netw.*, 7(24), 717-725. doi: 10.1016/j.neunet.2011.04.006.
- Palani, S., Liang S. Y., & Tkalich, P. (2008). An ANN application for water quality forecasting. *Marine Pollution Bulletin*, 56(1), 1586-1597.
- Tsay, R. S. (2005). Analysis of Financial Time Series. *Wiley series in probability and statistics*. Second Edition, 1(1), 1-638.
- Stanford University. (2009). *Half of Fish Consumed Globally Is Now Raised on Farms, Study Finds*, *Science New*. Retrieved from www.sciencedaily.com. (Accessed: September, 09, 2015)
- West, D., & Dellana, S. (2011). An empirical analysis of neural network memory structures for basin water quality forecasting, *International Journal of Forecasting, Elsevier*, 27(3), 777-803.
- Yaffee, R. A., & McGee, M. (1999). Introduction to Time Series Analysis and Forecasting with Applications of SAS and SPSS. *ACADEMIC PRESS, INC, San Diego London Boston New York Sydney Tokyo Toronto*, 1(1), 1-555.

Sérgio Afonso Mulema

Departamento de Ciências
Naturais e Matemática,
Universidade Pedagógica de
Moçambique-Delegação de
Quelimane, Campus
Coalane,nr.106,
Quelimane,
Moçambique
sergiomulema@gmail.com

Andrés Carrión García

Departamento de Estadística
e Investigación Operativa
Aplicadas y Calidad,
Universitat Politècnica de
Valencia, Camiño de Vera,
Valencia,
España,
acarrion@eio.upv.es
