ISSN-L: 0798-1015 • eISSN: 2739-0071 (En línea)

REVISTA ESPACIOS

Vol. 43 (01) 2022 • Art. 3

Recibido/Received 02/12/2021 • **Aprobado**/Approved: 05/01/2022 • **Publicado**/Published: 16/01/2022

DOI: 10.48082/espacios-a22v43n01p03

Dynamic life tables and projections for the ecuadorian population using the Lee-Carter model

Tablas de vida dinámicas y proyecciones para la población ecuatoriana utilizando el modelo de Lee-Carter

ARIAS, Wilson A. [1]
ZALDUMBIDE, David A. [2]

Abstract
Static mortality tables underestimate the life expectancy of individuals when used over extended periods of time, since they do not take into account the gradual decrease in mortality due to improvements in living conditions. In light of this, we propose pivot tables that take into account the effect of chronological time on mortality. Our research presents the Lee-Carter model for the construction of pivot mortality tables and the projection for the ecuadorian population. Population death data corresponding to the 1990-2016.
Keywords: Pivot mortality tables, Lee-Carter model, demographics, time series

Resumen
Las tablas estáticas de mortalidad subestiman la esperanza de vida de los individuos cuando se utilizan durante largos períodos de tiempo, ya que no tienen en cuenta la disminución gradual de la mortalidad debido a las mejoras en las condiciones de vida. A la luz de esto, proponemos tablas dinámicas que tienen en cuenta el efecto del tiempo cronológico sobre la mortalidad. Nuestra investigación presenta el modelo de Lee-Carter para la construcción de tablas pivote de mortalidad y la proyección para la población ecuatoriana. Datos de defunciones poblacionales correspondientes al período 1990-2016.
Palabras clave: Tablas pivote de mortalidad, modelo de Lee-Carter, datos demográficos, series temporales

1. Introduction

Issues of demographic dynamics have been the subject of study and constant reflection since the appearance of the world's first urban settlements. Demographic dynamics relates to how the population reproduces and dies, as well as the settlement and depopulation of certain geographic areas. These dynamics were of interest to even the oldest cultures, be it for religious, social, economic, political or military reasons. The importance of quantifying human resources led to population counts among even the most ancient peoples. From the analysis of these data, a set of knowledge and research methods was created. This became a discipline called “Demography” (Ortiz, Serrano, & Vásquez, 2011).

[1] Universidad Católica Andrés Bello. Email: wilsonariasa@yahoo.com
[2] Pontificia Universidad Católica del Ecuador Sede Manabí. PUCE. Email: dzaldumbide@pucem.edu.ec

In demography, mortality is one of the most important components in determining changes in population composition and size. The main conflict faced by a country is population growth. The idea of unstoppable growth has led leaders to question the scope of a certain standard of living for the population. Mortality thus takes on great importance when analyzing aspects related to its levels and its impact on population segmentation by age and gender, which are used as indices of populational health and living conditions (CELADE-CEPAL, 2014)

Mortality studies are usually carried out using mortality tables or life tables. When used over long periods of time, classic (static) mortality tables tend to underestimate life expectancy: they fail to take into account the gradual decrease of mortality over the years, as living conditions improve and population life expectancy increases.

It is therefore important that the effect of calendar time (chronological time) on mortality be taken into consideration, and this gave rise to pivot tables. Hence, the objective of this work is to create a pivot life table for the Ecuadorian population, which will create a projection through 2025 using the Lee-Carter model.

2. Metodology: Lee-Carter Model

The additive-multiplicative model (LC) used in this research was developed in 1992 by Lee Ronald and Lawrence Carter. It used mortality data in the US for a period between 1933 and 1987 and obtained predictions from 1990 to 2065. In their work "Modeling and Forecasting US Mortality", they describe a parametric model in which they adjust a linear function to the logarithms of the central mortality rates observed for each specific age group, and represent the level of mortality through a single intensity index$k(t)$ (dependent on each period t). Hence, the parameters of the function depend on biological time or age x and on chronological or calendar time t (unobserved variable).

2.1. Approach of Model

Lee and Carter propose a model based on the hypothesis of the existence of a linear relationship between the logarithms of the observed central mortality rates.$m(x,t)$ and explanatory factors; age$x$ (biological time) and the independent variable$k(t)$ (not observed) dependent on the chronological time t. The mathematical formulation is expressed as follows:

$$\ln[m(x,t)] = a(x) + k(t)b(x) + \varepsilon(x,t) \quad (1)$$

which, applying properties of logarithms, can be expressed in an equivalent manner as:

$$m(x,t) = e^{a(x)+k(t)b(x)} + \varepsilon'(x,t) \qquad (2)$$

where,$a(x)$ is a constant that depends only on age and describes the general period of the mortality diagram$k(t)$, $b(x)$ is a constant, dependent on age and representing the intensity in the growth or decrease of the mortality rate over time. It also expresses the rate of change of age composition in regard to the time affected by the parameter$k(t)$.

$$\frac{d}{dt}[ln\, m(x,t)] = b(x)\frac{dk(t)}{dt} \qquad (3)$$

Although theoretically this parameter can be negative for certain ages, in practice, the authors determined that this is not possible in the long term. Information errors or specific events such as wars, epidemics, etc., cause changes in mortality.

$\varepsilon(x,t)$: represent "white noise" type errors, dependent on time and age. They are interpreted as the specific historical influences of each specific age not explained by the model.

2.2. Model Adjustment

Depending on the proposed model, the next step would be to estimate the parameters$a(x), b(x)\ y\ k(t)$. Therefore, suppose that we have mortality information for a set of ages$x = x_1, x_2, \dots, x_{r-1}, x_r$ and a set of calendar years, $t = t_1, t_2, \dots, t_{n-1}, t_n$.

In this case, model (1) represents a system of rxn equations with $2r + n$ unknowns. It can be written in matrix form as:

$$M_{rxn} = A_{rxn} + K_{rx1}.B_{1xn}$$

As is evident, the system has infinite solutions. To obtain a unique solution to the LC model, the authors propose that the following restrictions be added to model (1):

$$\sum_{x=x_1}^{x_r} b_x = 1 \quad y \quad \sum_{t=1}^{n} k_t = 0 \quad (3.1)$$

To estimate the parameters$a(x)$ and$b(x)$, $\forall x$ and the first estimate of $k(t), \forall t$ the method of least squares is used, with which we obtain:

$$\sum_{x=x_1}^{x_r} a(x) = \frac{\sum_{t=1}^{n}\sum_{x=x_1}^{x_r} \ln[m(x,t)]}{n} \quad (4)$$

That is, the $a(x)$ are the averages of $\ln[m(x,t)]$ over time.

Then, the $a(x)$ are obtained directly from the initial conditions, but we could not obtain the$b(x)$ using normal regression methods. This is because the right side of the expression we have a function in which unknown mortality rates $k(t)$ appear. To adjust the model, other procedures, such as singular value decomposition (SVD), and Newton-Raphson approximation, are used.

2.3. Model Forecast

After having chosen the model that best fits the mortality rates, it is necessary to carry out the mortality rate forecast $k(t)$, using a stochastic time series model. Here, we use the Box-Jenkins methodology, described above.

In their work, Lee and Carter (1992), proposed a model in which the death rate $k(t)$, behaves according to the expression:

$$k(t) = c + k(t-1) + \epsilon(t) \quad (5)$$

where,

c is a constant term and $\epsilon(t)$ is white noise, which responds to the distributed error as a normal random variable with a mean of zero and constant varianceσ^2.

According to the Box-Jenkins methodology, if the mortality rate$k(t)$, behaves as an integrated autoregressive process of moving averages (ARIMA) of order (p, d, q), then;

$$\Psi(B)(1-B)^d k(t) = \Upsilon(\mathrm{B})e(t) \quad (6)$$

where: $\Psi(B)$ and $\Upsilon(\mathrm{B})$ are polynomials of degrees p and q, respectively; B is known as the delay operator and it fulfills that:

$$B^j k(t) = k(t-j) \quad (7)$$

Considering the trends in the model (18), as a deterministic function of time as recommended by the methodology; the equation can be expressed in the form:

$$\Psi(B)(1-B)^d k(t) = \Upsilon_0 + \Upsilon(\mathrm{B})e(t) \quad (8)$$

where the constant term is estimated through:

$$\hat{e}(t) = \frac{\sum_{t=2}^{n} \hat{e}_t}{n-1} = \frac{\sum_{t=2}^{n} \nabla k(t)}{n-1} = \frac{\sum_{t=2}^{n} \big(k(t)-k(t-1)\big)}{n-1} \qquad (9)$$

As a result, we obtain that the mortality rate forecast is carried out by applying the expression (5) or (7), as appropriate.

Using the predicted mortality rate, the value of the central mortality rates is obtained using the expression (1), keeping the estimated vector values constant $a(x)\ y\ b(x)$.

3. Results and Discussion

In this section, a dynamic life table is constructed that allows the behavior of Ecuadorian mortality to be modeled during the 1990-2016 period. Predictions for future years are then made based on the application of the Lee-Carter model.

3.1. Model Forecast

When preparing mortality tables, gross central mortality rates must be obtained $m(x,t)$. This necessitates the collection of empirical data on mortality; thus the importance of obtaining information related to deaths and the population.

To estimate and carry out mortality projections, the time interval 1990-2016 is used as the base period. Data during this period on the Ecuadorian population and deaths, by simple ages and gender, is taken into consideration. This information is available on the website of the Ecuadorian Institute of Statistics and Censuses (INEC, 2019) and in the report "Ecuador: Population estimates and projections 1950-2010 (CONADE, 1993).

The population data used are the result of the intercensal adjustment, which considers an age range from 0 to 100 years1. In order to purify the database and correct errors arising from age misstatements in the population censuses (an error that significantly affects the data structure, creating peaks on the distribution curve of the population and deaths), smoothing methods are employed that use spline interpolation curves.

Deaths are continuously recorded using death certificates. The data is processed by the National Civil Registry Office of Ecuador (INEC), which is in charge of certifying deaths, and can be found on the INEC website.

3.2. Projections

Once the information was processed, life tables were constructed for the 1990-2016 period. To carry out population projections through the year 2025, mortality rates are adjusted using the Lee & Carter model, as described. The adjustment is made with smoothed data for the period 1990-2016, and using an age range from 0 to 100 years.

Estimation of mortality rates$q(x,t)$. The first step in applying the Lee-Carter model is the calculation of gross mortality rates. Although there are several methods for this, in this work the one proposed by (Debón, Montes,

[1] The population projection for the years 1990-2016 corresponds to estimates based on the 2010 Population Census.

& Sala, 2008) is used. It is based on the ratio between the estimate of the population initially exposed to risk, Ext, and the number of deaths, dxt, for each age x.

$$\hat{q}(x,t) = \frac{d(x,t)}{E(x,t)} = \frac{0{,}5d(x,t)+0{,}5d(x,t+1)}{P(x,t)+0{,}5d(x,t)} \quad (10)$$

Where, $d(\mathrm{x,t})$ is the number of deaths at age x in year t, $d(x,t+1)$ is the number of deaths at age x in the year $t+1$, and$P$ (x, t) is the population that is x years old as of December 31 of year t.

The author also proposes using the expression

$$\hat{q}(x,t) = \frac{\alpha_0 d(x,t)+\beta_0 d(x,t+1)}{P(x,t)+\alpha_0 d(x,t)}$$ for age zero;

due to the high concentration of deaths in the first months of life. In this equation, α_0 represents the proportion of deaths in year t with less than one year of age, among those born that same year, and β_0 the proportion of deaths in year t+1 with less than one year of age among those born in year t. For the Ecuadorian case, we have $\alpha_0 \approx 0.75$ and $\beta_0 \approx 0.25$. Hence, for age zero, the following relationship will be used:

$$\hat{q}(0,t) = \frac{0.75d(x,t)+0.25d(x,t+1)}{P(x,t)+0.75d(x,t)} \quad (11)$$

In the case of advanced ages, some authors use a log-quadratic regression model since the number of deaths and those exposed to risk is low. This is why the expression previously given prevents valid inferences from being drawn. We thus use the methodology described by (Denuit & Goderniaux, 2005) is used for ages over 70 years:

$$\ln(q(x,t)) = a(t) + b(t)x + c(t)x^2 + \varepsilon(x,t);\ \varepsilon(x,t) \sim N(0,\sigma^2)$$

$$\text{s.a:} \begin{cases} q_{max}(x) = 1 \\ \frac{dq_{max}(x)}{dx} = 0 \end{cases}$$

Parameters$a(t), b(t)\ y\ c(t)$ are estimated by least squares, and the cut-off age x_0 will be set using the maximum of the determination coefficient as the optimal criterionR^2.

Considering an Ecuadorian population with a maximum of 100 years of age, the determination coefficients allow 70 to be set as the cut-off point for the male population and 80 for the female population.

Parameter estimation$a(x)$,$b(x)$ and $k(t)$. Once a smoothed mortality surface is obtained, we will estimate the parameters $a(x)$,$b(x)$ and $k(t)$ for the model. To do this, we use “demography” from the R language.

The estimated values of the parameter $a(x)$, in different ages for both sexes, are presented in Figure 1. It shows the high mortality values in the first year of life, which decrease rapidly as the child ages, approximately up to 12 years of age. Then mortality increases again, up to around 20 to 25 years. In the case of the Ecuadorian population, this is the result of deaths caused by external causes, which the authors call an "accident hump". From this age onwards we can see that mortality remains stable until approximately 40 years of age, and then increases exponentially in older adults.

Fig. 1
Estimation of the parameter ax
using the 1990-2016 period

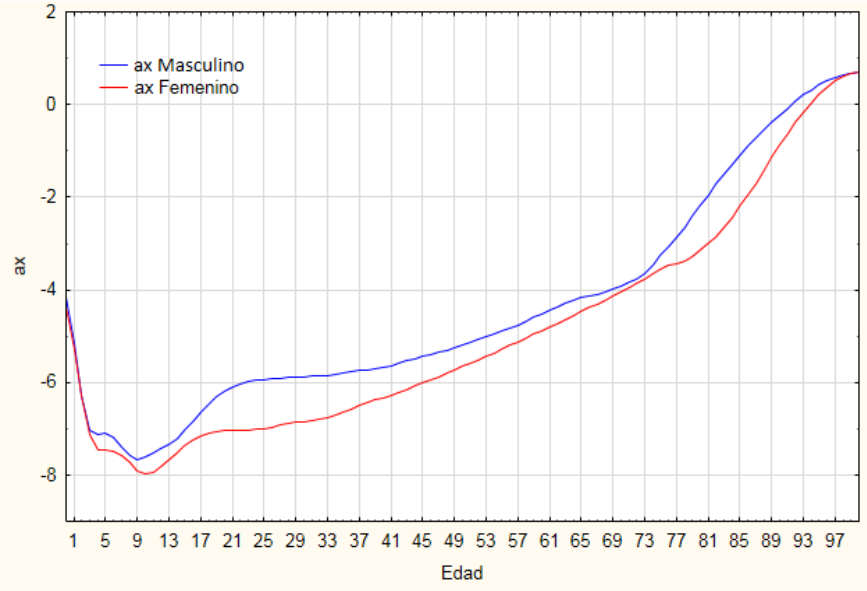
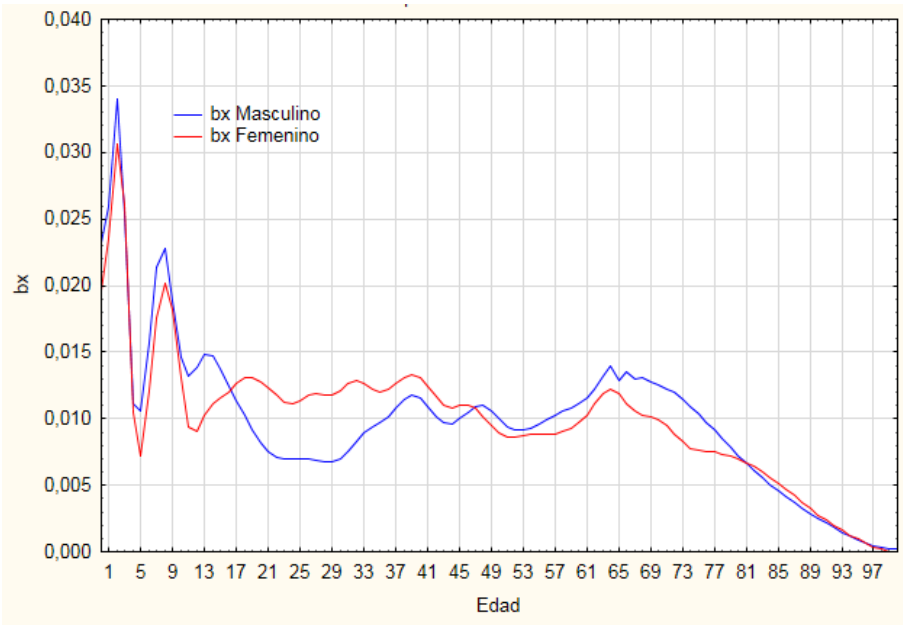


Figure 2 describes the estimation of the parameter b (x); that is, the variation in mortality at age x, where the changes in general mortality levels at each age can be observed. In the first years of life, variation reaches high values that decrease sharply, arriving to a minimum at 5 years of age. In adulthood, the impact of the reduction oscillates, presenting a relative maximum at 65 before decreasing again from approximately from 65-70, up until 100 years of age.

Fig. 2
Estimation of the parameter bx
using the 1990-2016 period



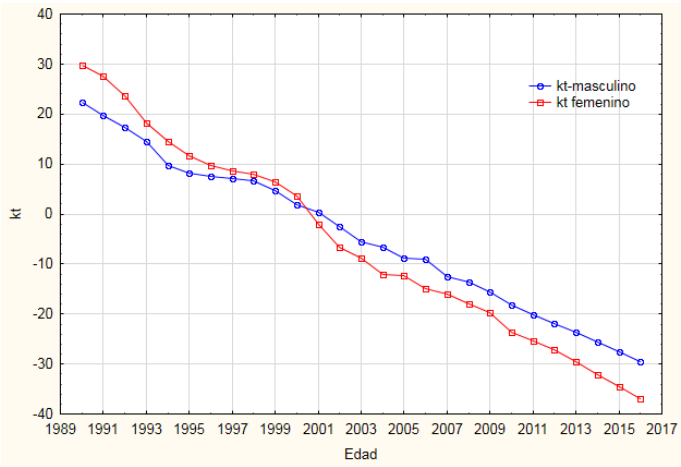
Next, the values of the adjusted mortality pattern $k(t)$ are given for the 1990-2016 period.

Table 1
Adjusted mortality
pattern for both sexes.

Year	$k(t)$- male	$k(t)$- female
1990	22.301263	29.704865
1991	19.689281	27.665478
1992	17.412899	23.686444
1993	14.460630	18.281796
1994	9.785869	14.598014
1995	8.125081	11.737452
1996	7.486419	9.684929
1997	7.017409	8.581664
1998	6.654981	7.949272
1999	4.625118	6.469571
2000	1.784073	3.611668
2001	0.435236	-1.972476
2002	-2.506757	-6.642082
2003	-5.617076	-8.850184
2004	-6.674812	-11.984252
2005	-8.703796	-12.265755
2006	-9.052265	-14.830417
2007	-12.542810	-16.004875
2008	-13.706592	-17.910271
2009	-15.647146	-19.786184
2010	-18.286590	-23.681760
2011	-20.205803	-25.367592
2012	-21.845880	-27.079200
2013	-23.593410	-29.559350
2014	-25.491240	-32.039490
2015	-27.476360	-34.519640
2016	-29.448600	-36.999790

Figure 3 shows the variations in the mortality pattern for the 1990-2016 period, which reflect a decreasing linear trend in mortality for both sexes. We can therefore conclude that mortality among the Ecuadorian population has decreased over this period.

Fig. 3
Variation of the parameter k (t)
in the period 1990-2016



Forecast. To obtain the projections, we must adjust a time series model to the estimated sequence of mortality rates, $\{k(t)\}$. Here, we will use the "automatic forecasts" procedure in the Statgraphics processing package. This procedure tests several models and selects the one with the best performance according to the criteria specified.

Males. Comparing the results from five tests and adjusting different models to the data for males, we can deduce that ARIMA is the most appropriate model (0,2,1) (= 0.998835), since it has the lowest value of the Akaike Information Criterion (AIC).

Forecast Summary. The Table2 summarizes the statistical significance of the terms in the forecasting model and the model performance. The P-value for the MA (1) term is less than 0.05, so it is statistically different from 0. The estimated standard deviation of the input white noise is equal to 1.0051. Each of the performance statistics is based on the one-step ahead forecast errors, which are the differences between the data at time t and the predicted value at time $t-1$. The first three statistics measure the magnitude of the errors. The last two statistics measure the bias.

Table 2
ARIMA Model Summary

Parameter	Estimated	Std. Error	t	P-value
MA (1)	1.06272	0.0138314	76.8336	0.000000

Statistical	Estimate
Root mean square error (RMSE)	0.998835
Mean absolute error (MAE)	0.725357
Mean absolute percentage error (MAPE)	
Mean error (ME)	0.0211036
Mean percentage error (MPE)	

Estimated autocorrelations for residuals. The

Table shows the estimated autocorrelations between the residuals at different lags and the 95% probability limits. The lagged autocorrelation coefficient k measures the correlation between the residuals at time t and at time $t-k$. If the probability limits at a particular lag do not contain the estimated coefficient, there is a statistically significant correlation to that lag, at the 95.0% confidence level. In this case, none of the 24 autocorrelation coefficients is statistically significant, meaning that the time series may well be completely random (white noise).

Table 3
Estimated autocorrelations for residuals.

Lag	Autocorrelation	Std. Error	Limit at 95.0% Lower	Limit at 95.0% Upper
1	0.0798702	0.2	-0.391994	0.391994
2	-0.0202401	0.201272	-0.394486	0.394486
3	-0.227828	0.201353	-0.394646	0.394646
4	-0.340191	0.211413	-0.414363	0.414363
5	-0.121613	0.23228	-0.455261	0.455261
6	-0.114535	0.234813	-0.460226	0.460226
7	0.0542306	0.237037	-0.464585	0.464585
8	0.238775	0.237533	-0.465557	0.465557

Estimated partial autocorrelations for residuals. The

Table 4 shows the estimated partial autocorrelations between the residuals at different lags and the 95% probability limits. The partial autocorrelation coefficient at lag k measures the correlation between the residuals at time t and at time t+k, discounting all minor lags for the correlation. It can be used to judge the order of the autoregressive model necessary to fit the data. If the probability limits at a particular lag do not contain the estimated coefficient, there is a statistically significant correlation to that lag, with a confidence level of 95.0%. In this case, none of the 24 partial autocorrelation coefficients is statistically significant with a 95.0% confidence level.

Residual Randomness Test. Table 5 shows the results of the randomness tests for the residuals and the normal probability for the residuals. Three tests have been run to determine whether or not the residuals form a random sequence of numbers (white noise). The first test counts the number of times the sequence was above or below the median. The number of such runs equals 13, compared to an expected value of 13.0 if the sequence were random. Since the P-value for this test is greater than or equal to 0.05, the hypothesis that the residuals are random cannot be rejected with a confidence level of 95.0% or greater. The second test counts the number of times the sequence rose or fell. The number of such runs equals 14, compared to an expected value of 16.3333 if the sequence were random. Since the P-value for this test is greater than or equal to 0.05, the hypothesis that the series is random cannot be rejected, with a confidence level of 95.0% or greater. The third test is based on the sum of squares of the first 24 autocorrelation coefficients. Since the P-value for this test is greater than or equal to 0.05, the hypothesis that the series is random cannot be rejected, with a confidence level of 95.0% or greater.

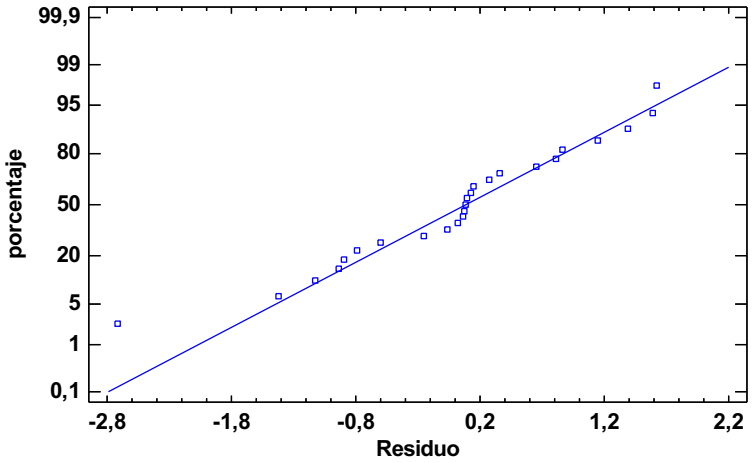
Table 4
Estimated partial autocorrelations for residuals.

Lag	Autocorrelation	Std. Error	Limit at 95.0% Lower	Limit at 95.0% Upper
1	0.0798702	0.2	-0.391994	0.391994
2	-0.0267903	0.2	-0.391994	0.391994
3	-0.225629	0.2	-0.391994	0.391994
4	-0.323688	0.2	-0.391994	0.391994
5	-0.120114	0.2	-0.391994	0.391994
6	-0.20916	0.2	-0.391994	0.391994
7	-0.137991	0.2	-0.391994	0.391994
8	0.0575542	0.2	-0.391994	0.391994

Table 5
Residual randomnes tests

Tests	Z statistic for large samples	P-value
Runs above or below the median	-0.208712	1.0
Runs up and down	0.902975	0.366537
Box-Pierce Test	6.55718	0.476393

Fig. 4
Normal probability for residuals

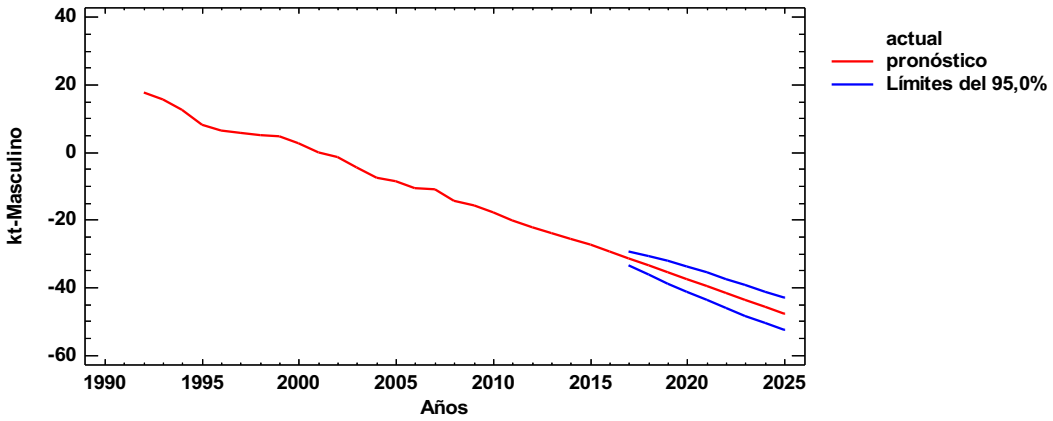


Finally, the Table 6 shows the mortality rate estimates for the 2017-2025 period for males, as well as the confidence intervals, assuming only the error in the prediction of the mortality rate k (t) obtained from the ARIMA model adjusted to the time series.

Table 6
Prediction of the mortality rate for males

Period	Forecast $k(t)$	Limit at 95.0% Lower	Limit at 95.0% Upper
2017	-31.5103	-33.5847	-29.4358
2018	-33.572	-36.4151	-30.7288
2019	-35.6336	-39.0063	-32.2609
2020	-37.6953	-41.4651	-33.9255
2021	-39.757	-43.8345	-35.6795
2022	-41.8187	-46.1377	-37.4997
2023	-43.8804	-48.389	-39.3717
2024	-45.942	-50.5984	-41.2856
2025	-48.0037	-52.7735	-43.234

Fig. 5
Projections for k(t). Males



Females. Comparing the results from five tests and adjusting different models to the data for females, we can deduce that ARIMA is the most appropriate model (1,2,1) (= 0.998835), since it has the lowest value of the Akaike Information Criterion (AIC).

Forecast Summary. Table 7 summarizes the statistical significance of the terms in the forecasting model and the model performance. The P-value for the MA (1) term is less than 0.05, meaning that it is statistically different from 0. For the AR (1) term it is greater than or equal to 0.05, meaning that it is not statistically significant. We should therefore consider reducing the order of the AR term to 0. The estimated standard deviation of the input white noise is equal to 1.22695. Each of the performance statistics is based on the one-step ahead forecast errors, which are the differences between the data at time t and the predicted value at time $t-1$. The first three statistics measure the magnitude of the errors. The last two statistics measure the bias.

Table 7
ARIMA Model Summary

Parameter	Estimated	Std. Error	t	P-value
AR (1)	0.384722	0.197158	1.95133	0.063301
MA (1)	1.07807	0.00801377	134.527	0.000000

Statistical	Estimate
Root mean square error (RMSE)	1.22037
Mean absolute error (MAE)	0.888924
Mean absolute percentage error (MAPE)	
Mean error (ME)	-0.0863268
Mean percentage error (MPE)	

Estimated autocorrelations for residuals. The Table 8shows the estimated autocorrelations between the residuals at different lags and the 95% probability limits for females. The lagged autocorrelation coefficient k measures the correlation between the residuals at time t and at time $t-k$. If the probability limits at a particular lag do not contain the estimated coefficient, there is a statistically significant correlation to that lag, at the 95.0% confidence level. In this case, none of the 24 autocorrelation coefficients is statistically significant, meaning that the time series may well be completely random (white noise).

Table 8
Estimated autocorrelations for residuals.

Lag	Autocorrelation	Std. Error	Limit at 95.0% Lower	Limit at 95.0% Upper
1	0.0491866	0.2	-0.391994	0.391994
2	0.114086	0.200483	-0.392941	0.392941
3	-0.290196	0.203064	-0.397998	0.397998
4	-0.230809	0.219025	-0.429282	0.429282
5	-0.323291	0.228547	-0.447945	0.447945
6	-0.0547692	0.246161	-0.482467	0.482467
7	0.0154633	0.246648	-0.483421	0.483421
8	0.278373	0.246686	-0.483497	0.483497

Estimated partial autocorrelations for residuals. The Table 9 shows the estimated partial autocorrelations between the residuals at different lags and the 95% probability limits. The partial autocorrelation coefficient at lag k measures the correlation between the residuals at time t and at time t+k, discounting all minor lags for the correlation. If the probability limits at a particular lag do not contain the estimated coefficient, there is a statistically significant correlation to that lag, with a confidence level of 95.0%. In this case, none of the 24 partial autocorrelation coefficients is statistically significant with a 95.0% confidence level.

Residual Randomness Test. Table 10 shows the results of the randomness tests for the residuals, and figure 6, the normal probability for the residuals. Three tests have been run to determine whether or not the residuals form a random sequence of numbers (white noise). In the first test the number equals 12, compared to an expected value of 13.0 if the sequence were random. Since the P-value for this test is greater than or equal to 0.05, the hypothesis that the residuals are random cannot be rejected with a confidence level of 95.0% or greater. For the second tests the number of runs equals 14, compared to an expected value of 16.3333 if the sequence were random.

Table 9
Estimated partial autocorrelations for residuals.

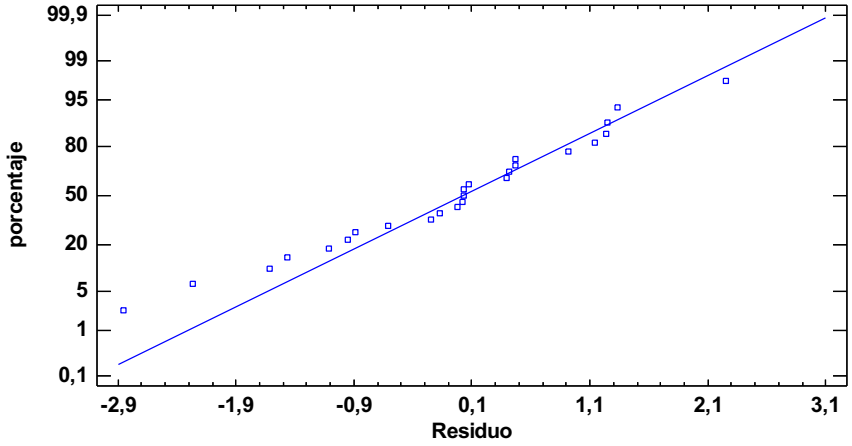
Lag	Autocorrelation	Std. Error	Limit at 95.0% Lower	Limit at 95.0% Upper
1	0.0491866	0.2	-0.391994	0.391994
2	0.111937	0.2	-0.391994	0.391994
3	-0.305239	0.2	-0.391994	0.391994
4	-0.23228	0.2	-0.391994	0.391994
5	-0.275356	0.2	-0.391994	0.391994
6	-0.111382	0.2	-0.391994	0.391994
7	-0.0814796	0.2	-0.391994	0.391994
8	0.0889909	0.2	-0.391994	0.391994

Since the P-value for this test is greater than or equal to 0.05, the hypothesis that the series is random cannot be rejected, with a confidence level of 95.0% or greater. In the third test, the P-value is greater than or equal to 0.05, so the hypothesis that the series is random cannot be rejected, with a confidence level of 95.0% or greater.

Table 10
Residual randomness tests.

Tests	Z statistic for large samples	P-value
Runs above or below the median	0.208712	0.834669
Runs up and down	0.902975	0.366537
Box-Pierce Test	8.45421	0.206678

Fig. 6
Normal probability for residuals

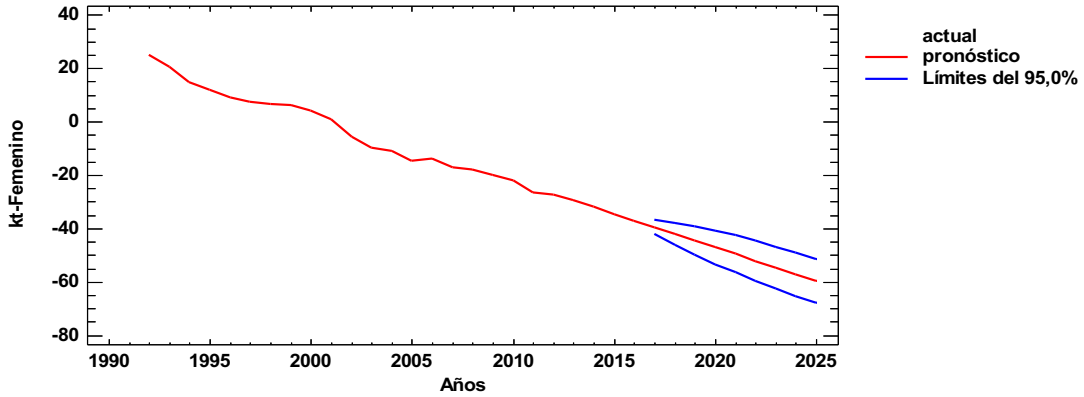


Finally, table 11 shows the mortality rate estimates for the 2017-2025 period for females, as well as the confidence intervals, assuming only the error in the prediction of the mortality rate k (t) obtained from the ARIMA model adjusted to the time series.

Table 11
Prediction of the mortality rate for females

Period	Forecast $k(t)$	Limit at 95.0% Lower	Limit at 95.0% Upper
2017	-39.5114	-42.0496	-36.9733
2018	-42.0352	-46.2115	-37.859
2019	-44.5637	-49.9602	-39.1671
2020	-47.0939	-53.3979	-40.7899
2021	-49.6248	-56.6059	-42.6437
2022	-52.156	-59.6415	-44.6705
2023	-54.6873	-62.5447	-46.8299
2024	-57.2186	-65.3441	-49.0931
2025	-59.75	-68.0616	-51.4383

Fig. 7
Projections for k(t). Females.



4. Conclusions

According to the results obtained, the following conclusions can be arrived to:

Pivot life tables allow us to identify the true mortality levels for the male and female population of Ecuador up to the present year. This information is fundamental for the country, since it allows policies to be advanced that will improve the population's living standards.

The mortality tables present certain limitations in terms of the bias in data and ages and mortality records (resulting from the process of information gathering).

The results show that women are longer-lived than men: they show higher residual life expectancy values. This is particularly due to activities aimed at reducing pregnancy and childbirth risks, among other factors related to female mortality.

Bibliographic references

CELADE-CEPAL. (2014). *Los datos demográficos: Alcances, limitaciones y métodos de evaluación.* Santiago de Chile: Naciones Unidas.

CONADE. (1993). *Ecuador: Estimaciones y proyecciones de población 1950-2010.* Quito: CONADE.

Debón, A., Montes, F., & Sala, R. (2008). *Tablas de mortalidad dinámicas para España. Una aplicación a la hipoteca inversa.* Valencia.

Denuit, M., & Goderniaux, A. (2005). Closing and projecting life tables using log-linear models. *Bulletin de L´ássociation Suisse des Actuaries*, 29-49.

INEC. (2019, 9 6). *Ecuador en cifras.* Retrieved from http://www.ecuadorencifras.gob.ec/nacimientos-defunciones/

Ortiz, A., Serrano, T., & Vásquez, G. (2011). *Antología de demografía y de estudios de población.* Hidalgo: Univesidad Autónoma del Estado de Hidalgo.