Universal Journal of Applied Mathematics 11(2): 17-27, 2023
DOI: 10.13189/ujam.2023.110201 http://www.hrpub.org

Modeling Mortality Rates for Botswana

Kago Kebotsamang*, **Thabiso Malomo**, **Oarabile Lekhane**

Department of Statistics, University of Botswana, Botswana

Received November 4, 2022; Revised June 18, 2023; Accepted July 19, 2023

Cite This Paper in the following Citation Styles

***(a)**: [1] Kago Kebotsamang, Thabiso Malomo, Oarabile Lekhane, "Modeling Mortality Rates for Botswana," Universal Journal of Applied Mathematics, Vol.11, No.2, pp. 17-27, 2023. DOI: 10.13189/ujam.2023.110201*

***(b)**: Kago Kebotsamang, Thabiso Malomo, Oarabile Lekhane (2023). Modeling Mortality Rates for Botswana. Universal Journal of Applied Mathematics, 11(2), 17-27.DOI: 10.13189/ujam.2023.110201*

Copyright ©2023 by authors, all rights reserved. Authors agree that this article remains permanently open access under the terms of the Creative Commons Attribution License 4.0 International License

Abstract Botswana has not updated its life tables since 2011. This implies that the current life tables may not reflect the current mortality trends, which could have a negative impact on end users such as insurance and pension fund companies. This study aims to estimate mortality rates and construct new life tables for Botswana. We used the Heligman-Pollard and Lee-Carter models to estimate mortality rates in Botswana for the years 2016-2019. The Heligman-Pollard model parameters were estimated through a Bayesian melding approach with incremental mixture importance sampling. The Lee-Carter model was estimated using a maximum likelihood approach and residual bootstrapping to construct confidence intervals of the estimated mortality rates. The Lee-Carter model was found to produce similar results to the Heligman-Pollard model. The results of the two models estimated life expectancy for males and females in Botswana to be about 68 and 74 years, respectively. The results of this study can be used to update the life tables for Botswana and improve the accuracy of mortality estimates for end users such as insurance and pension fund companies.

Keywords Heligman-Pollard, Lee-Carter, Mortalily Rates, Life Tables, Botswana

1 Introduction

The insurance and pension fund sectors form part of the largest and important sectors in Botswana financial markets. These sectors were first introduced in Botswana around the 1970s and have since shown enormous growth. According to the regulatory authority, the insurance and pension fund contributed about 3.5 percent and 42.0 percent to the Botswana's GDP respectively [1]. In addition, they hold assets worth almost 100 billions of Pula under their management between them as of 2018.

Despite the significant growth in the Botswana's pension and insurance industry, the latest Botswana life tables as published by Statistics Botswana, dates back to 2011. This implies that insurance companies and pension fund managers may be using old life tables or adapting those from neighbouring countries to carry out actuarial calculations. Consequently, the current life tables or mortality models in use may be inappropriate for Botswana's conditions which can lead to costly decisions and misguided public policies. As an example, the market players may overprice their products and services overburdening the consumers or under-price their products risking bankruptcy.

It is against this backdrop that modeling mortality rates for Botswana and subsequently, constructing reliable life tables is critical in facilitating reasonable pricing of products and services offered by the insurance companies and other key users.

Several models, both parametric and non-parametric, used to estimate mortality rates have been developed but with no application to Botswana. We therefore consider the models used mostly in the sub-Saharan African region. For example, [2] used a generalised growth balance (GGB) method to estimate mortality rates in South Africa. The model requires the use of data from two censuses and assumes that the population is closed to migration and that the proportion of deaths reported and completeness of census counts is the same. Although the GGB method has been proved to produce reliable estimates, it is negatively affected by errors and mistakes made when collecting data [2].

In contrast to the above study, [3] used a Heligman-Pollard (HP) model to investigate the sex and age specific changes in mortality for a population affected by HIV in South Africa. They used Bayesian melding with incremental mixture importance sampling to estimate the parameters of the HP model. The HP model has the ability to reflect age-specific mortality and is a basis for age-specific life tables. It also has easily interpretable parameters. In addition, the Bayesian melding en-

ables for the calculation of credible intervals of the estimated parameters and thus captures the uncertainty of the mortality rate estimates. Similarly, [4] used the HP model to construct the life tables of Kenya. The newly constructed tables were found to be consistent with the Kenyan tables already in use.

The Lee-Carter (LC) model and the ARCH model were compared with each to find which model would fit the mortality profile of Zimbabwe [5]. They used a singular value decomposition (SVD) technique to estimate parameters of the LC model whereas the Box Jenkins procedure was used to determine the lag order of the ARIMA model for the ARCH model. The Kolmogorov-Smirnov and root mean square tests were then used to compare the two models and found that the LC model provided a better fit.

The HP and LC models were compared with each other in modeling the mortality rates in Nigeria [6]. The HP model was purported to provide better estimates and subsequently used to construct the abridged life tables for Nigerian male and female populations. However, the HP model was found to overestimate mortality rates for the elderly female population mainly due to incomplete data [6]. On the other hand, the LC model was found to underestimate the mortality rates across all ages.

In this paper, we aim to fit an appropriate model to mortality rates in Botswana and then use the estimates to construct reliable and current life tables for the population of Botswana. More specifically, we use the HP and the LC models to estimate mortality rates in Botswana and then use the estimated mortality rates to construct the complete life tables. The HP model has the ability to capture the increased mid-life mortality rates, which might be common in Botswana due to high HIV prevalence rates whereas the Lee-Carter model can be used to predict future trends of the mortality rates.

This paper is arranged in the following manner. Section 2 introduces the data used for this paper and the initial explanatory data analysis. Section 3 presents the formulation of the Heligman-Pollard and the Lee-Carter models and how they would be fitted to the mortality data. We also give a detailed discussion on how complete life tables are constructed in this section. Section 4 presents the study findings and discussions and lastly, we have the conclusions of the study.

2 Data

We use mortality data from Statistics Botswana for analysis in this paper. The data consists of raw data on deaths in Botswana from the year 2016 to 2019. We noticed that the data consists of deaths from other years instead of the year of focus possibly due to late death registrations. The late registered deaths were subsequently excluded from the data of a particular year. Furthermore, the observations with unknown or not stated ages at death and their birth dates were also excluded from the analysis.

For the national population statistics, the population projections complied by Statistics Botswana only consists of projections for single age in years up to the age of 30. As result, we also requested the 2011 census data, the methodology used for the projections and the growth rates and we used them to make projections for the years 2016 to 2019. The formula used for projections is given by

$$P_{n+t} = (1+r)^n \times P_t \tag{1}$$

where P_{n+t} is the population after n years, r is the annual growth rate, P_t is the base or current population at time t.

Statistics Botswana estimated the annual growth to be 1.58 percent. The census data consist of data for ages 0 to 98 and therefore we could only make projections for these. Since the projections and mortality data needs to be consistent, we then combined the number of deaths for ages 98 – 117 to form the 98 and above age-group.

The crude death rates per 1,000 population by sex from the year 2016 to 2019 are presented in Figure 1. The graph shows that the crude death rate increases with age. In particular, the crude death rate is very low for ages less than 80 and it increases sharply after age 80 till it reaches a peak at around age 94 after which then decreases.

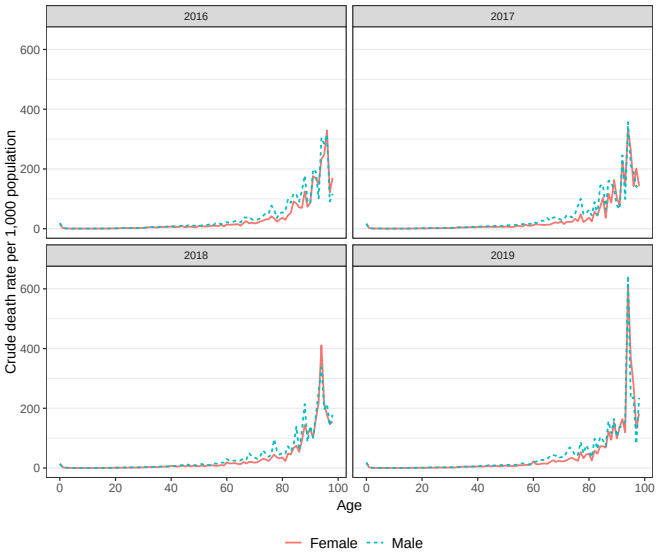

Figure 1. Crude death rates per 1,000 population by sex for the years 2016 – 2019

The plot also shows that the crude death rate was higher for males than for females across all the years. We note that at the crude death rate increases at the age 94 as the years progress. The death rate at age 94 was 35%, 44%, 49% and 70% for the years 2016, 2017, 2018 and 2019 respectively.

We note that the crude death rate reached the highest in the year 2018 at around 7.4 deaths per thousand and the lowest in 2017 at around 6.2 deaths per thousand. The crude death rate was fluctuating across the years and it ranged between 6.0 and 8.0 deaths per thousand. The difference between the crude rates for the different years is minute and it suggests that the population death rate is relatively constant.

3 Methods

3.1 Life Table

A life table is a simple way of representing mortality behaviour of certain groups. The major assumption is that the population is relatively stable and closed, that is, age specific fertility and mortality are constant and there is no migratory flow [7]. Data from population censuses and death registrations are used to construct life tables. The table yields age specific death rates and consists of the following columns:

1. Exact age, x.
2. Separation factor, a_x - represents the average number of years lived in the age interval.
3. Number of people alive, l_x - represents the number of people alive at age x. Usually, the life tables start with a certain number of people l_0. This starting number is called the radix which is usually set to 100,000.
4. Number of deaths, d_x - is the number of deaths at age x. It is the number of people who died before reaching age given by
$$d_x = l_x - l_{x+1} \tag{2}$$
5. Mortality rate, q_x - the probability that a person aged x will die within a year. The crude mortality rate is given by
$$q_x = \frac{d_x}{l_x} \tag{3}$$
6. Person years lived, L_x - the number of years of life lived by the population in the interval $[x, x+1)$. Given the distribution of deaths is uniform over the given interval, it is computed as follows
$$L_x = l_x + 0.5d_x \tag{4}$$
7. Persons years lived after x, T_x - the number of years lived by the population after age x. It is the cumulative sum upward from the last row of the L_x column.
$$T_x = \sum_{y=x}^{w} L_y \tag{5}$$
where w is the maximum age lived.
8. Life expectancy, e_x, is the average number of years lived by a person from age x. It is given by
$$e_x = T_x / l_x \tag{6}$$

The age specific mortality rate, q_x, is needed for the construction of life tables. The number of deaths from death registration data and the number of people at risk of dying from population census data are used to model the age specific probabilities. We assume that individuals within the same age bracket have the same chance of dying and that each death is independent of the other deaths. Below we discuss how probability of death or force of mortality would be estimated using either HP model or LC model respectively.

3.2 Heligman-Pollard Mortality Model

Let d_x be the number of deaths at age x, l_x be the number of people aged x at risk of dying and also let q_x be the probability of death for persons aged x. Then the number of deaths at age x is assumed to Binomial distributed with parameters l_x and q_x. That is, $d_x \sim \text{Bin}(n_x, q_x)$. The mortality rate at age x, q_x, is modeled using the Heligman-Pollard model stated as follows:

$$q_x = A^{(x+B)^C} + D\exp\left\{-E\left[\log(x) - \log(F)\right]^2\right\} + \frac{GH^x}{1+GH^x} \tag{7}$$

where A is a measure of infant mortality, B is the location parameter of infant mortality, C is the decline rate of childhood mortality, D captures the strength of accident hump, E models the spread or width of the accident hump, F is the location parameter of the accident hump, G is a measure of old age mortality and H is the rate of increase in old age mortality [8] .

The model assumes that all parameters have a demographic interpretation and that parameters are highly correlated with each other. Therefore the commonly used methods such as maximum likelihood and least squares estimation fail at estimating the parameters because the number of parameters estimated are relatively large compared to the number of data values. As result, we use the Bayesian Melding with Incremental Mixture Importance Sampling (IMIS), see [3] for a more detailed description of the Bayesian Melding with IMIS. An `HPbayes` R package implements this procedure to estimate the HP model parameters which are then be used to create life tables [9].

Briefly, Bayesian Melding with IMIS iteratively constructs an importance sampling distribution by initially drawing N_0 samples of the parameters from their prior distribution then compute their importance weights based on the likelihood function [10]. At each iteration, a multivariate Gaussian distribution centered at the modes is added to the current importance sampling distribution, leading to a well covered target distribution [11].

3.3 Lee-Carter mortality model

Let d_{xt} be the number of deaths at age x and time t, and also let l_{xt} be its matching central exposure. Then a central death rate, $q_{x,t}$, at age x in year t is defined as follows

$$\hat{q}_{xt} = \frac{d_{xt}}{l_{xt}} \tag{8}$$

The Lee-Carter model is then expressed as follows

$$\log(q_{xt}) = \alpha_x + \beta_x\kappa_t + \epsilon_{xt} \tag{9}$$

where α_x is the constant age mortality pattern, β_x measures the age-specific deviations of mortality change from the overall trend, κ_t measures the trend in mortality over time and ϵ_{xt} are

error terms [12]. The parameters β_x and κ_t should however satisfy the following conditions for identifiability;

$$\sum_x \beta_x = 1, \quad \sum_{t=t_1}^{t_n} \kappa_t = 0 \tag{10}$$

The number of deaths, d_{xt}, is assumed to be independent and has a Poisson distribution with the mean being the expected number of deaths under the LC model, $E(D_{xt}) = q_{xt} l_{xt}$. Thus (9), in terms of q_{xt}, corresponds to a generalised linear model (GLM) of the response d_{xt} with log-link and non-linear parameterised predictor given as follows

$$\log(d_{xt}) = \log(l_{xt}) + \alpha_x + \beta_x \kappa_t + \epsilon_{xt} \tag{11}$$

where the number of deaths, d_{xt}, is assumed to follow a Poisson distribution; the parameters, β_x and κ_t still satisfy the constraints in (10); and $\log(l_{xt})$ are treated as offset values during fitting.

The parameters are estimated by minimising the deviance residuals using iterative Newton-Raphson algorithm described in [13], and implemented in R through the `ilc` package [14]. The deviance residuals between observed and the fitted values are given by

$$D = 2\left[\sum_{x,t} d_{xt}\left(\log d_{xt} - \log \hat{d}_{xt}\right) - \sum_{x,t}\left(d_{xt} - \hat{d}_{xt}\right)\right] \tag{12}$$

where $\hat{d}_{xt}$ is expected number of deaths at the age x and time t.

We adopt the residual bootstrapping method considered by [15] to construct the confidence intervals of q_x corresponding to the LC model. The procedure maps the deviance residuals to bootstrapped responses by numerically solving for $d_x^{(j)}$ given that

$$r_x^{(j)} = \text{sign}(d_x^{(j)} - \hat{d}_x)\sqrt{d_x^{(j)} \log\left(\frac{d_x^{(j)}}{\hat{d}_x}\right) - \left(d_x^{(j)} - \hat{d}_x\right)} \tag{13}$$

where $r_x^{(j)}$, $j = 1, 2, \ldots, B$ is the j^{th} bootstrapped deviance residual for age x.

It can then be shown that the j^{th} bootstrapped number of deaths, $d_x^{(j)}$, is the roots of the following function

$$f(d) = d\log(d) - d(1 + \hat{d}) - (0.5r^{*2} - \hat{d}) \tag{14}$$

where $r^* = r_x^{(j)}$ and $\hat{d} = \hat{d}_x$.

Since (14) is highly dimensional, we use the `BB` R package [16], which implements the Newton-Raphson procedure for high dimensional non-linear optimisation problems, to determine the root of this function.

4 Results

This section presents the study findings which include the parameter estimation, model fitting and the estimated life tables.

4.1 Heligman-Pollard Model

The `hp.bm.imis` function from the `HPbayes` R package was used to implement the Bayesian melding with IMIS algorithm in estimating all the eight parameters of the Heligman-Pollard model. The initial values were found through once-off optimisation of the log-likelihood of number of the deaths at age x using the genetic algorithm from the `GA` R package [17].

The estimated parameters and their 95% credible intervals are given in Table A1 for males and females respectively. The parameters A, B and C which captures childhood mortality dynamics [9], have been found to be general higher for males than for females as shown in Figure 2. The higher values of A represent higher intensity of childhood mortality and this implies that males had significantly higher childhood mortality compared to females in 2016 whereas for the other years the intensities were similar between the two sex groups. The rate of mortality decline, represented by parameter C, was higher for males than females as shown in Figure 2.

The parameters D, E and F control the dynamics of young adult mortality with parameter D measuring its intensity. The estimated values of parameter D were all found to be less than 0.01 for both males and females across all the years of study. The small estimates of D imply that there is no sufficient bend on the mortality curves to represent the accident hump for both genders and across the years of study.

The middle component of the Heligman-Pollard model is composed of the product of D and the effects of E and F, and therefore small values of D negate the effect of the spread and the location of the accident hump [9]. This is evident from 4-panel plot representing log-transformed estimated age-specific mortality rates by gender and years presented in Figure A1.

The fitted Heligman-Pollard models in Figure A1 show almost log-linear growth in mortality rates after the lowest points of the childhood mortalities. The plots also reveal that the models fit the data well. The models appear to be similar across the years which implies that the mortality is relatively constant through out the years under study. It can also be noted that the 95% credible intervals are narrow for all the fitted models.

4.2 Lee-Carter Model

The Lee-Carter model was fitted to the observed number of deaths by age for the years 2016 through 2019 using the `ilc` R package [14]. The model was fitted to both the female and male mortalities but separately.

We present parameter estimates for the main-age effects on mortality pattern and age-specific deviations from the overall trend and their corresponding bootstrapped 95% confidence intervals for males and females in Figure 3. The figure shows that main-age effects on mortality, α_x, decrease from birth to their lowest between ages 5 to 15 thereafter generally increase with

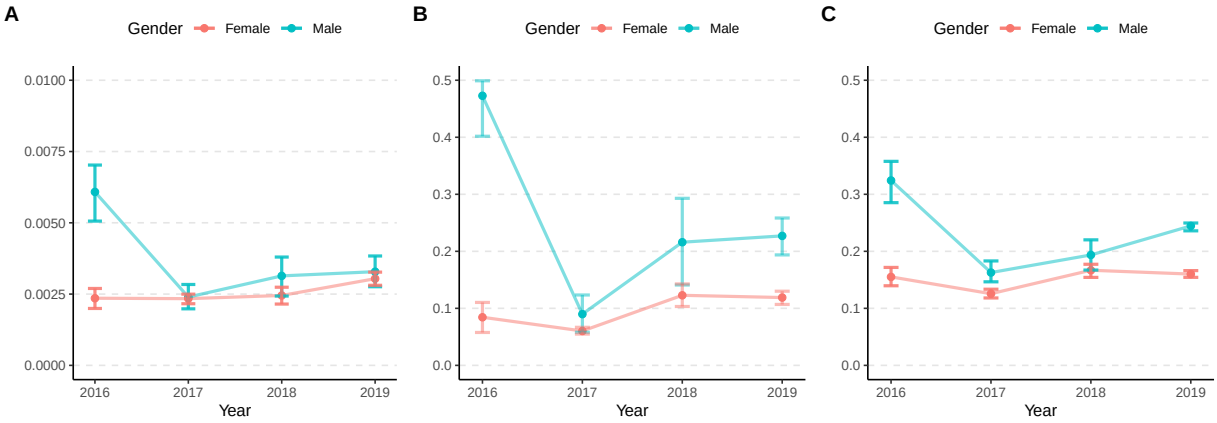

Figure 2. Childhood mortality parameters – A, B and C, of the Heligman-Pollard model and their corresponding 95% credible error bars by sex for the years 2016 – 2019

age until the last years of age recorded for the data. In addition, the main-age effects of the female are generally lower than those of their males counterparts for almost all the ages.

As for the age-period interaction effects, β_x, Figure 3 shows that these fluctuate around zero across most ages for both sexes. The fluctuations are however different for males and females. The females' age-period interaction effects appears to be volatile, as evidenced by wide confidence intervals compared to those of their male counterparts. This is evident during the early ages effects where there appears large deviations on the females series compared to the males series.

The parameter estimates of the period effects, κ_t, from 2016 through 2019 for both females and males are presented in Table 1. The results show that mortality rates were relatively high in 2016 compared to other years for both males and females. The lowest rate were however occurred at different points. For males, the lowest mortality rates occurred in 2018 compared to female rates which were at their lowest in 2017. It should also noted that the bootstrapped 95% confidence intervals of period effects for female contains zero. We therefore conclude that the period effects for the female population are not significantly different from zero. Henceforth, the female mortality rates are largely dependent only age only.

Table 1. Mortality trend estimates and their 95% bootstrapped confidence intervals for males and females from the year 2016 to 2019

	2016	2017	2018	2019
Male	2.79	0.41	-2.06	-1.14
	(1.50 – 3.95)	(0.19 – 0.74)	(-2.93 – -1.04)	(-1.68 – -0.72)
Female	1.86	-0.94	-0.25	-0.67
	(-0.61 – 4.10)	(-2.05 – 0.23)	(-0.57 – 0.31)	(-1.47 – 0.17)

4.3 Life tables

We constructed two life tables, one using the HP model while the other was constructed from the LC model. The HP model life tables for both sexes were constructed through the `hp.lifetab` function from the `HPbayes` package [9]. The function uses the posterior samples of the parameters obtained in Table A1. The expected life expectancy at birth for both sexes from 2016 – 2019 are presented in Table 2. The results show that the females are expected to live longer at birth (about 74 years) compared to the their male counterparts (about 69 years) across the years 2016 – 2019.

We also present the life expectancy at birth for sexes estimated through the LC model in Table 2. Similarly, females were expected to live longer at birth (about 74 years) than the males whose estimated life expectancy was around 68.5 years across the years of study. It can also be noted from Table 2 that the models considered for this study produced almost identical results and therefore there is little to choose between the two models.

Table 2. Estimated life expectancy at birth and their corresponding 95% credible and confidence intervals by gender for the years 2016 – 2019 using the Heligman-Pollard and Lee-Carter models respectively

Model	Sex	2016	2017	2018	2019
HP	Male	68.4 (67.3 - 69.3)	69.8 (69.0 - 70.4)	69.0 (67.9 - 70.1)	69.2 (68.0 - 69.9)
	Female	73.9 (73.1 - 74.7)	74.9 (73.9 - 75.8)	74.4 (73.6 - 75.2)	73.8 (72.8 - 74.8)
LC	Male	68.0 (66.8 - 69.5)	68.5 (67.7 - 69.2)	68.6 (67.6 - 69.8)	68.6 (67.8 - 69.5)
	Female	73.6 (72.9 - 75.4)	74.3 (73.6 - 75.2)	74.3 (73.7 - 75.0)	74.3 (73.7 - 75.2)

The age-specific estimated life expectancy for males and females by the years 2016 – 2019 are presented in Figure A2 and Figure A3 for the HP and LC models respectively. The two figures show that across almost the ages, the estimated life expectancy of the females was greater than that of their male counterpart across the years 2016 – 2019. There was however no much differences across the four year period in the estimated life expectancy of both males and females. The detailed estimated abridged life-tables for both sexes across the years 2016 – 2019 are given in the supplementary material of this article.

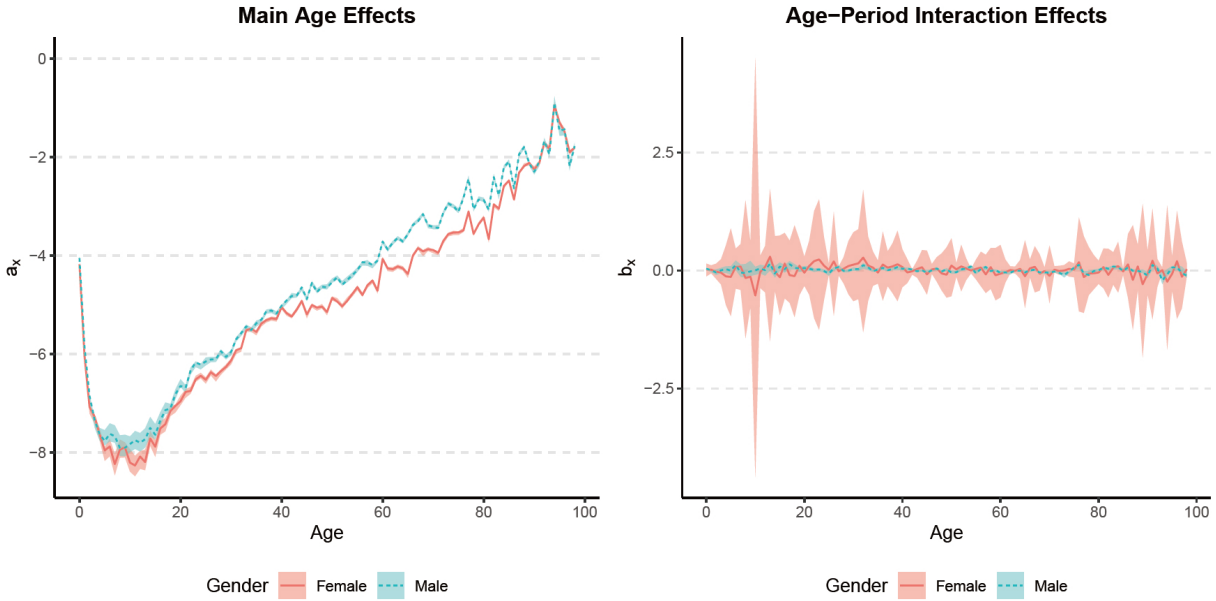

Figure 3. The main-age effects on mortality pattern and age-specific deviations from the overall trend for males and females.

5 Conclusions

This study was concerned with estimating mortality rates and constructing life tables for Botswana. The mortality data and population projections from 2016 through 2019 sourced from Statistics Botswana, were used to estimate mortality rates and then construct life tables using the Heligman-Pollard and Lee-Carter models.

The two models produced identical results across the different years considered in this study. The two models estimated the life expectancy at birth for males living in Botswana to be about 69 years compared to the life expectancy of 74 years for estimated for the females. These results, are however not consistent with the more conservative life expectancy estimates from the World Bank. During the same period, the World Bank estimated the life expectancy for males in Botswana to be around 63 years compared to 68 years for their female counterparts [18]. However, the World Bank estimates should be treated with care as they based on interpolated data from 5-year period.

A major limitation of this study was that the data from Statistics Botswana was not in the desired format and was erroneous. We had to discard a significant number of data points due to missing values or erroneous entries which may had contained valuable information that could have been insightful to this study. Another limitation was that the population projection data only allowed us to explore ages up to 98 whereas the death data contained deaths up to ages 117.

Acknowledgements

We are very grateful to Statistics Botswana for providing the authors with their mortality data and for informative average growth rate of Botswana's population. This study was not funded by any organisation.

REFERENCES

[1] Non-Bank Financial Institutions Regulatory Authority. 2019 Annual Report: continuing to rise. Online available from https://www.nbfira.org.bw/annual-report-2019

[2] R. Dorrington, T.A. Moultrie, I. Timaeus. Estimation of mortality using the South African census 2001 data, Centre for Actuarial Research, University of Cape Town, 2004.

[3] D. Sharrow, S. Clark, M. Collinson, K. Kahn, S. Tollman. The age-pattern of increases in mortality affected by HIV: Bayesian fit of the Heligman-Pollard model to data from Agincourt HDSS field site in the Northeast South Africa, Demographic Research, 29, 1039-1096, 2013.

[4] F.N. Mbugua. Kenyan Mortality and Survivorship tables, MSc dissertation, University of Nairobi, 2019, Online available from http://erepository.uonbi.ac.ke/handle/11295/2

[5] R. Taruvinga, W. Gachira, W. Chiwanza, D.J. Nkomo. Comparison of the Lee-Carter and ARCH model in modelling and forecasting mortality in Zimbabwe, Asian Journal of Economic Modeling, Vol 5(1), 11–22, 2017.

[6] Y.H. Umar, U.J. Chukwudi. Modeling mortality rates using Heligman-Pollard and Lee-Carter models in Nigeria, American Journal of Theoretical and Applied Statistics Vol 8 (6), 221-239, 2019.

[7] I. Etikan, S. Abubakar, R. Alkassim. A review of life table construction, Biometry and Biostatistics International Journal, Vol 5(3), 132, 2017.

[8] L. Heligman, J.H Pollard. The age pattern of mortality, Journal of the Actuaries, 107 (1), 49-80, 1980. https://doi:10.1017/S0020268100040257

[9] D. Sharrow. HPbayes: Heligman-Pollard mortality model parameter estimation using Bayesian Melding and Incremental Mixture Importance Sampling, 2012. https://CRAN.R-project.org/package=HPbayes

[10] B.J Stojkova, D.A Campbell. Incremental Mixture Importance Sampling With Shotgun Optimization, Journal of Computational and Graphical Statistics, Vol 28 (4), 806-820, 2019. https://doi.org/10.1080/10618600.2019.1592756

[11] A.E Raftery, L. Bao. Estimating and Projecting Trends in HIV/AIDS Generalized Epidemics Using Incremental Mixture Importance Sampling, Biometrics, Vol 66 (4), 1162-1173, 2010. https://doi.org/10.1111/j.1541-0420.2010.01399.x.

[12] R.D. Lee, L.R. Carter. Modeling and forecasting US mortality, Journal of the American Statistical Association, Vol 87(419), 659-671, 1992.

[13] A.E. Renshaw, S. Haberman. A cohort-based extension to the Lee–Carter model for mortality reduction factors, Insurance: Mathematics and Economics, Vol 38(3), 556-570, 2006.

[14] Z. Butt, S. Haberman, H.L. Shang. ilc: Lee-Carter Mortality Models using Iterative Fitting Algorithms, 2014. https://CRAN.R-project.org/package=ilc

[15] A.E. Renshaw, S. Haberman. On simulation-based approaches to risk measurement in mortality with specific reference to Poisson Lee–Carter modelling, Insurance: Mathematics and Economics, Vol 42, 797-816, 2008.

[16] R. Varadham, P.D Gilbert. BB: An R Package for solving a large system of nonlinear equations and for optimizing a high-dimensional nonlinear objective function, Journal of Statistical Software, Vol 32(4), 1-26, 2009. https://doi.org/10.18637/jss.v032.i04

[17] L. Scrucca. On some extensions to GA package: hybrid optimisation, parallelisation and islands evolution. The R Journal, Vol 9 (1), 187-206, 2017. https://doi.org/10.32614/RJ-2017-008

[18] The World Bank. World Development Indicators: Life expectancy at birth, total (years) - Botswana, 2022. Retrieved from https://data.worldbank.org/indicator/SP.DYN.LE00.IN?locations=BW

Appendices

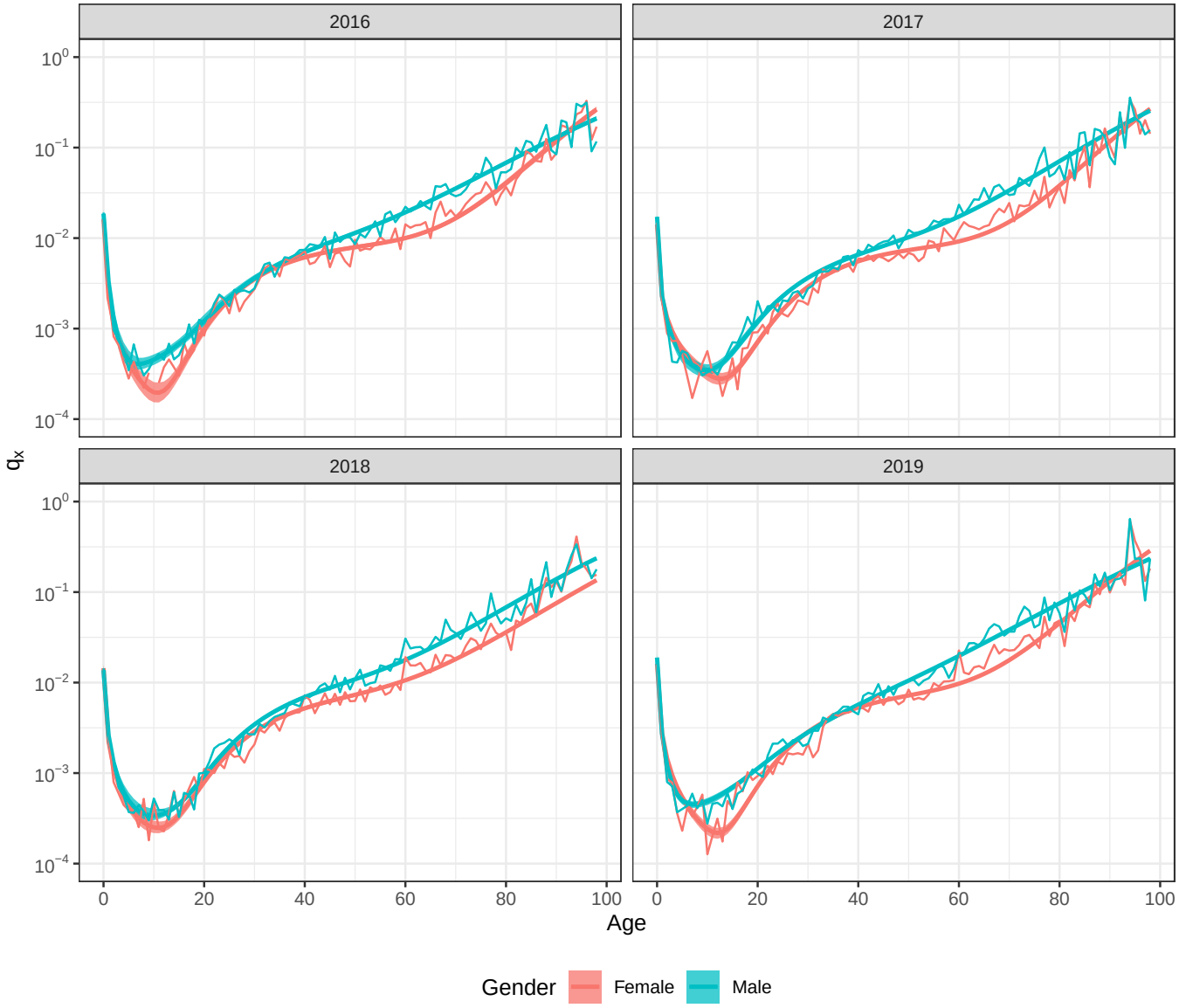

Figure A1. The Heligman-Pollard log-transformed estimated age-specific mortality rates by gender for the years 2016 – 2019.

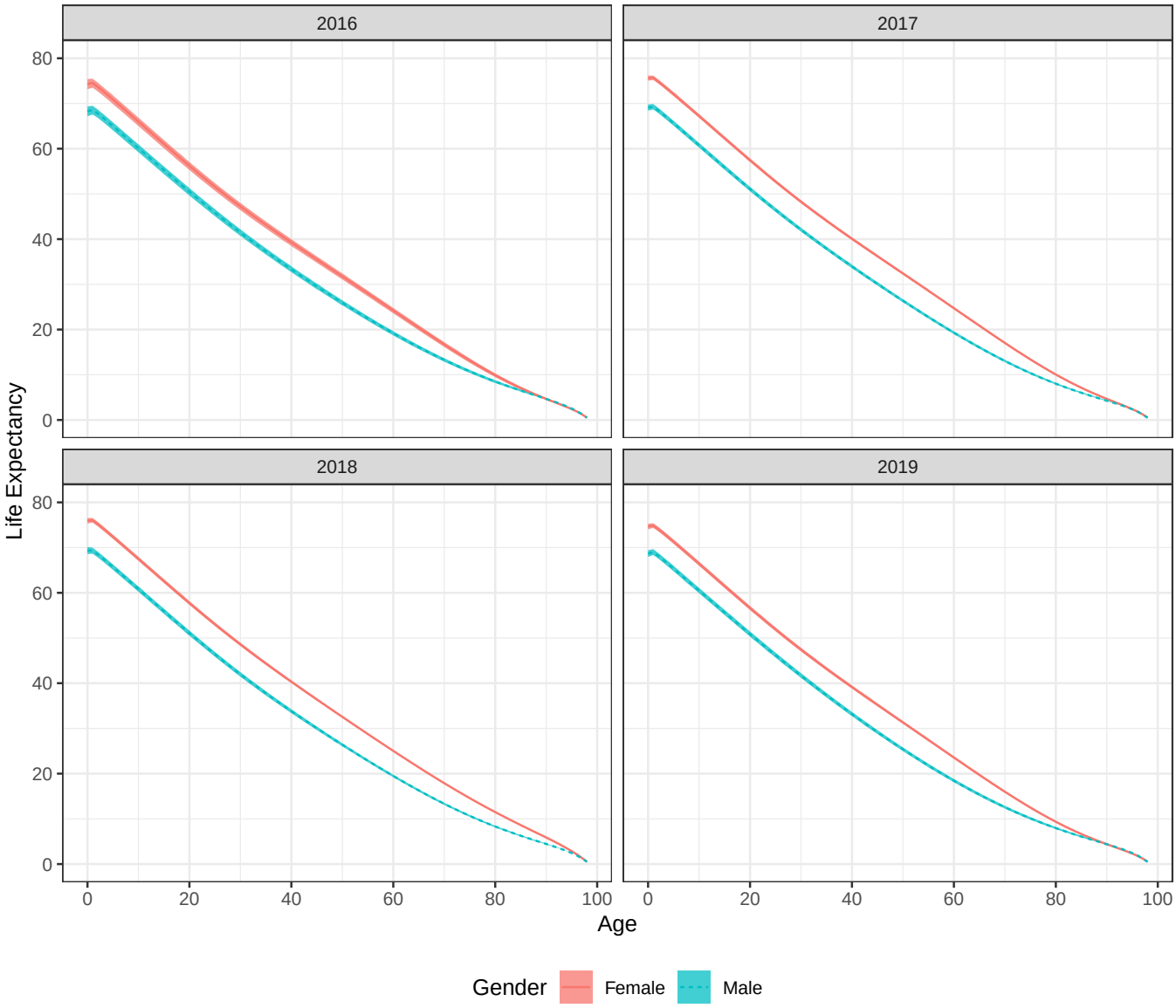

Figure A2. The Heligman-Pollard model expected age-specific life expectancy by gender for the years 2016 – 2019

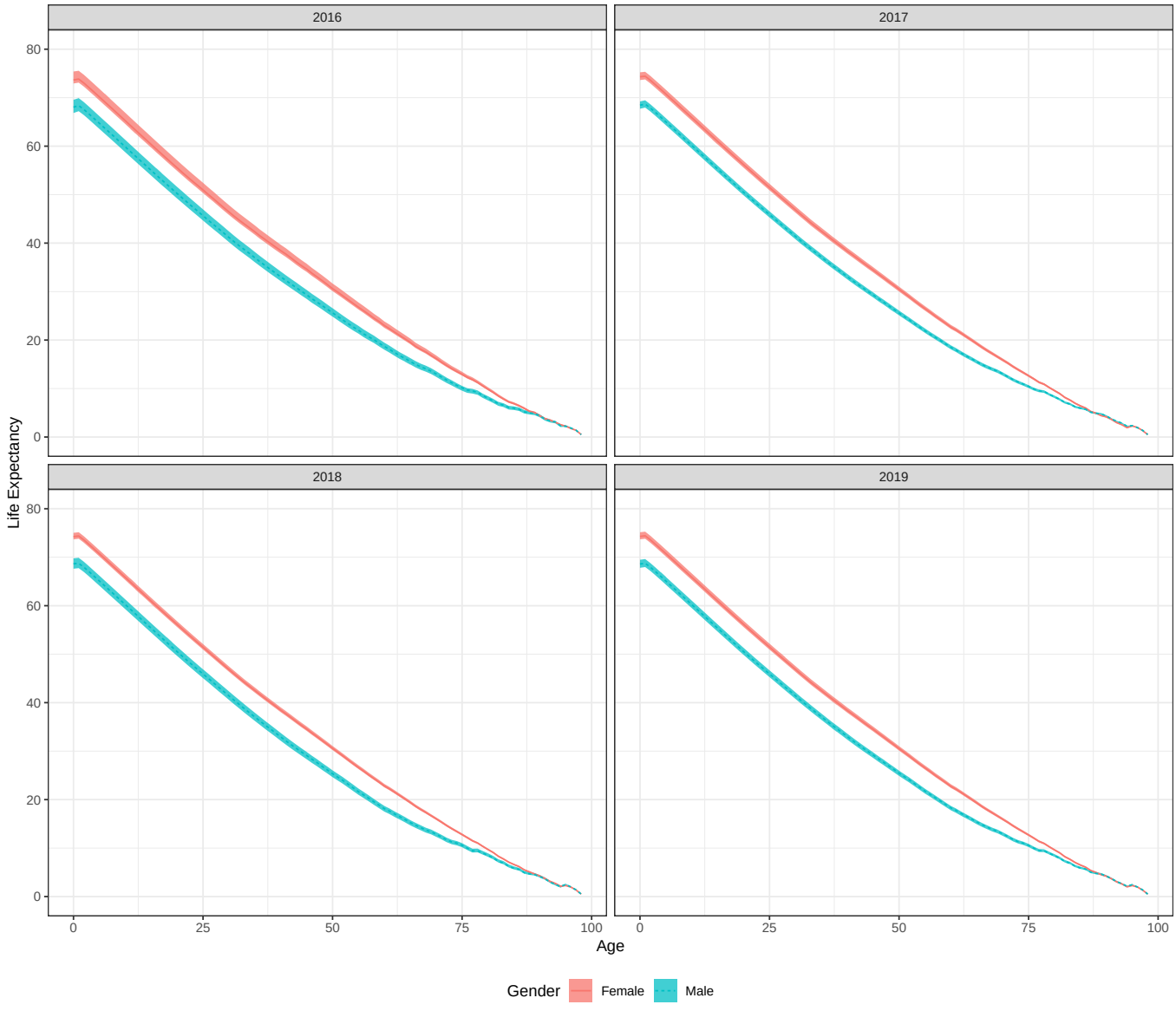

Figure A3. The Lee-Carter model expected age-specific life expectancy by gender for the years 2016 – 2019

Table A1. Heligman-Pollard parameter estimates with their corresponding 95% credible intervals by gender for 2016 - 2019

Parameter	Gender	2016	2017	2018	2019
A	Male	6.08×10^{-3} $(5.06 - 7.03) \times 10^{-3}$	2.40×10^{-3} $(1.98 - 2.84) \times 10^{-3}$	3.14×10^{-3} $(2.43 - 3.80) \times 10^{-3}$	3.29×10^{-3} $(2.76 - 3.84) \times 10^{-3}$
	Female	2.35×10^{-3} $(2.00 - 2.70) \times 10^{-3}$	2.34×10^{-3} $(2.16 - 2.50) \times 10^{-3}$	2.45×10^{-3} $(2.15 - 2.74) \times 10^{-3}$	3.04×10^{-3} $(2.81 - 3.27) \times 10^{-3}$
B	Male	0.473 (0.402 – 0.499)	0.090 (0.058 – 0.123)	0.216 (0.141 – 0.293)	0.227 (0.194 – 0.258)
	Female	0.084 (0.058 – 0.110)	0.060 (0.055 – 0.067)	0.123 (0.103 – 0.143)	0.119 (0.107 – 0.130)
C	Male	0.324 (0.285 – 0.358)	0.163 (0.147 – 0.183)	0.194 (0.167 – 0.220)	0.245 (0.236 – 0.250)
	Female	0.155 (0.140 – 0.172)	0.126 (0.118 – 0.134)	0.167 (0.154 – 0.177)	0.160 (0.154 – 0.166)
D	Male	3.54×10^{-3} $(2.79 - 4.26) \times 10^{-3}$	4.65×10^{-3} $(4.32 - 4.95) \times 10^{-3}$	4.96×10^{-3} $(4.44 - 5.45) \times 10^{-3}$	2.02×10^{-3} $(1.47 - 2.57) \times 10^{-3}$
	Female	7.19×10^{-3} $(6.79 - 7.62) \times 10^{-3}$	6.78×10^{-3} $(6.61 - 6.94) \times 10^{-3}$	4.46×10^{-3} $(4.10 - 4.83) \times 10^{-3}$	6.27×10^{-3} $(6.00 - 6.54) \times 10^{-3}$
E	Male	3.177 (2.165 – 4.118)	2.264 (2.043 – 2.514)	3.062 (2.735 – 3.432)	2.413 (2.261 – 2.495)
	Female	2.067 (1.901 – 2.215)	2.458 (2.333 – 2.595)	2.608 (2.330 – 2.880)	2.284 (2.191 – 2.382)
F	Male	48.3 (43.2 – 53.3)	49.8 (49.2 – 50.0)	49.7 (49.0 – 50.0)	54.3 (53.0 – 55.0)
	Female	54.7 (54.3 – 55.0)	54.9 (54.7 – 55.0)	49.8 (49.2 – 50.0)	54.9 (54.8 – 55.0)
G	Male	2.08×10^{-4} $(1.77 - 2.43) \times 10^{-4}$	7.77×10^{-5} $(7.42 - 8.13) \times 10^{-5}$	9.73×10^{-5} $(9.51 - 9.95) \times 10^{-5}$	2.11×10^{-4} $(1.87 - 2.36) \times 10^{-4}$
	Female	1.54×10^{-6} $(1.39 - 1.70) \times 10^{-6}$	9.93×10^{-7} $(9.47 - 10.3) \times 10^{-7}$	4.48×10^{-5} $(4.46 - 4.50) \times 10^{-5}$	2.12×10^{-6} $(2.02 - 2.23) \times 10^{-6}$
H	Male	1.076 (1.074 – 1.078)	1.089 (1.089 – 1.090)	1.086 (1.085 – 1.086)	1.132 (1.132 – 1.132)
	Female	1.134 (1.134 – 1.134)	1.140 (1.140 – 1.140)	1.087 (1.087 – 1.087)	1.132 (1.132 – 1.132)