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A proposed stochastic growth model for monitoring the population dynamics in Ghana

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ABSTRACT

Population size modelling offers crucial insights into societal, economic, environmental, and public health dynamics, aiding in informed decision-making and sustainable development efforts. In the absence of suitable population models, complete enumeration (census) would be necessary to track population dynamics. A census may yield erroneous results due to undercounting, even though it is costly, time-consuming, and resource-intensive. A typical human population is susceptible to birth, death, immigration and emigration. Several authors have attempted to model population growth based on these characteristics except that most of them considered some but not all the above characteristics in their models. This study proposed a stochastic growth model to monitor the population dynamics considering; birth, death, immigration and emigration rates. Through the developed model, the expected size of the population and its variability over time was obtained. The study also derived the limiting distribution of the population size and specified its parameters. The long-run probability of zero offspring (probability of ultimate extinction) was also deduced. The results of the study indicates that the long-run probability of zero offspring of the Ghanaian population is approximately 0.21, the net migration and intrinsic growth rates per 1000 Ghanaian population are -0.544 and 22.458 with standard errors of 0.206 and 0.530 respectively. This indicates that although the average birth rate is higher than the average death rate in Ghana, the average emigration rate (rate at which individuals travel out of the population either by the land borders, sea or air ports) is relatively higher than the immigration rate (rate at which individuals come into the population either by the land borders, sea or air ports). The estimated population sizes were almost the same across all bootstrap samples. This indicates that the proposed model is stable. The study therefore recommends the use of the proposed stochastic population growth model to monitor any population that is susceptible to birth, death, immigration and emigration.

Introduction

Population characteristics such as birth, death, immigration and emigration are essential for modelling many real-world problems like queues [1], portfolio management [2], population biology [3], epidemiology [4], production systems [5] among others. It is essential to understand potential changes in future population in order to plan for the fluctuating ages, resources, healthcare needs

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among others. Future population is usually modelled as a function of birth, death and migration rates. The science of describing and understanding changes in population levels over time can be termed as population dynamics [6].

In the absence of suitable population models, complete population enumeration (census) would be necessary to track population changes. However, this approach is costly, time-consuming, resource-intensive, and prone to undercounting, which could lead to inaccurate conclusions. Hence, developing mathematical models to monitor population dynamics is of great importance to population researchers.

Population dynamics and its response to environmental change depend on the balance of birth, death, immigration and emigration, and several authors have attempted to model population dynamics based on these characteristics mathematically [7–12]. Population models can be grouped into deterministic [13,14] and stochastic models [4,15]. Deterministic models' results are strictly determined by their equations, but stochastic models explicitly incorporate randomness and uncertainty into the model. Marrec et al. [16], simulated multiple population growth models and then compared the size averaged over multiple stochastic realizations with the deterministic predictions. The average stochastic population dynamics were demonstrated to be poorly predicted by the deterministic equations in general. Deterministic predictions, in particular, tend to overestimate the sizes of simulated populations, particularly those whose initial population size is small.

In recent times, the stochastic model has received significant attention in literature [4,10,11,17,18]. The stochastic models may be considered ideal for modelling population dynamics because they have the advantage of characterizing the measures of centre (as in the case of the deterministic models) and also address three sources of variability and uncertainty [19];

- temporal or spatial variation in population structure and environmental conditions,
- intra-population variation among individuals and
- uncertainty in parameter estimates.

Stochastic models also allow for the examination of extinction risk, that is, the estimation of extinction probabilities (long-run probability of zero offspring), which are critical for assessing the population's long-term viability. In practice, stochastic models are more realistic than deterministic models when modelling population dynamics, however, they are more complex to work with.

Stochasticity in the case of population dynamics can be categorized into demographic, environmental and individual [19,20]. Demographic stochasticity is due to the random fluctuations in the sequence of birth and death in the population; environment stochasticity arises from the variation in habit, weather and other external factors that may affect the population; and individual stochasticity refers to biological/genetic variability among members of the population [19].

For a given population, the size of the population can fluctuate through:

- *Birth*: an individual producing another individual,
- *Death*: an individual dying,
- *Immigration*: An individual entering the population from outside,
- *Emigration*: An individual moving out of the population.

Even though population size is influenced by birth, death, immigration and emigration, most population modellers consider only birth, death and immigration in their models. To the best of our knowledge, stochastic models that captures birth, death, immigration, and emigration explicitly are limited.

In the work of Tavaré [21], a stochastic model which considered birth, death and immigration process was constructed whiles modelling the dynamics in a population. Matis et al. [22] used birth, death and immigration processes in order to construct a stochastic population model to study the spread of insect population. Matis and Kiffe [23] developed a stochastic logistic population growth model with immigration and multiple births. Furthermore, O'Hara et al. [24] constructed a model which also considered birth, death and immigration processes as the only rates which affect changes in population size. Khodabin et al. [25] proposed a generalized stochastic exponential population growth model based on the assumption that numerous random environmental factors determine the growth rate at any given time t. Additionally, the expectations and variances of the estimates were also obtained. Giorno and Nobile [26] focused on a general linear time-inhomogeneous birth and death process with immigration.

In a recent development, Aghamohammadi and Khorrami [27] studied a simple birth, death and immigration model, in which the birth, death and immigration rates were considered to be linear in the population. KS and Viswanath [4] carried out a study which incorporated birth, death and immigration process, in which they considered two immigration policies; immigration was permissible if and only if the population size is zero, and immigration at a constant rate was allowed irrespective of the population size.

Ultimately the desired model for modelling population dynamics should capture birth, death, immigration and emigration explicitly since these are the characteristics that leads to fluctuation (increase or decrease) in a population. This study proposes a stochastic growth model to monitor the population dynamics considering; birth, death, immigration and emigration rates. Through the developed model, the expected size of the population and its variability would be obtained. The study would also develop the limiting distribution of the population and specify its parameters. The long-run probability of zero offspring (probability of ultimate extinction) would also be derived to monitor the chance of the population going extinction.

It should be noted that, in modelling, the immigration rate can be included in birth and the emigration rate can also be added to the death rate. However, in this study, these processes will be captured explicitly in the mathematical model. That is, the study will assume that the population size at time t, $X(t)$ is controlled from transitions that satisfy the scheme below:

- $n \to n+1$ with rate $\lambda_n(t) = n\lambda(t) + \varepsilon$ for $n = 0, 1, 2, \ldots$.

Table 1
Acquired rates per 1000 population in Ghana.

Year	Birth rate (λ)	Death rate (μ)	Immigration rate (ε)	Emigration rate (δ)
2011	32.96	8.42	31.58	32.35
2012	32.89	8.24	32.08	32.81
2013	32.54	8.09	31.59	32.54
2014	31.83	7.82	29.45	30.91
2015	31.71	7.77	31.05	31.57
2016	30.53	7.46	31.55	32.81
2017	28.98	7.39	32.16	32.77
2018	29.03	7.37	30.98	29.64
2019	28.57	7.14	35.71	35.5
2020	28.04	7.45	11.03	11.39
2021	27.55	7.63	19.09	19.22
2022	27.10	7.60	27.34	28.56

- $n \to n-1$ with rate $\mu_n(t) = n\mu(t) + \delta$ for $n = 1, 2, 3, \ldots$.

The remaining parts of the paper are organized as follows: Section "Methods and materials" (Materials and Methods) presents the data acquisition process, model formulation and specification, derivation of the proposed model with other extensions. In Section "Results and discussion" (Results and Discussion), we validate the proposed model with data obtained from the Ghana Immigration Service and the Birth and Death Registry of Ghana. Section "Conclusions and recommendations" (Conclusion and Recommendation) summarizes the overall achievement of the study with some recommendations and direction for future studies.

Methods and materials

This section of the paper contains a comprehensive motivation of the methodology employed in the study. Specifically, the section discusses the description of the data, presents the proof for the linear growth model with immigration and emigration processes and estimation of the model parameters.

Data acquisition

Secondary data on the total number of immigrants and emigrants (monthly records) through the land borders, sea and air ports from 2011 to 2022 were obtained from the Ghana Immigration Service.

The yearly records of number of births and deaths in Ghana over the period 2011 to 2022 were also obtained from the Birth and Death Registry of Ghana.

The acquired data were used to estimate the parameters:

- rate of immigration (ε),
- rate of emigration (δ),
- birth rate (λ), and
- death rate (μ),

of the proposed stochastic population model.

Table 1 shows the computed rates from the acquired data.

The birth, death, immigration and emigration process

Definition of terminologies

The following are the definitions of some useful terminologies considered in the proposed model.

Birth: This will constitute an increase in the population size by arrival of a new born (offspring).

Death: This will constitute a decrease in the population size by departure through loss of life of an individual in the population.

Immigration: This will constitute an increase in the population size by an arrival of an individual into the population using land borders, seaports or airports.

Emigration: This will constitute a decrease in the population size by a departure of an individual from the population using land borders, seaports or airports.

Now, we consider the linear growth model as a continuous Markov process. It is time-homogeneous because the parameters λ_n, μ_n, ε and δ are independent of time. λ_n, μ_n depends only on the size of the population whereas ε and δ are considered as fixed rates (constant).

To begin specifying the proposed model, the following assumptions should be considered. Given that the population is subject to birth, death, emigration and immigration assume the following in a small time interval of length Δt:

1. The probability of a birth occurring is $\lambda_n \Delta t + o(\Delta t)$.
2. The probability that there is no birth is $1 - \lambda_n \Delta t + o(\Delta t)$.
3. The probability of a death occurring is $\mu_n \Delta t + o(\Delta t)$.
4. The probability that there is no death is $1 - \mu_n \Delta t + o(\Delta t)$.
5. The probability that an event (birth, death, immigration or emigration) occurs more than once is $o(\Delta t)$.
6. The probability that there is an increase in the population size due to immigration is $\varepsilon \Delta t + o(\Delta t)$.
7. The probability that there is a decrease in the population size due to emigration is $\delta \Delta t + o(\Delta t)$.

Model formulation

Given that no more than one event can occur within the interval $(t, t + \Delta t]$, the following cases were considered to derive the proposed stochastic model for birth, death, immigration and emigration.

- An increase in the size of the population may be due to only birth or when there is only immigration.
- No change in the size of the population may be as a result of no birth, no death, no immigration and no emigration.
- A decrease in the population size may be as a result of only death or only emigration.

Suppose that $X(t)$ is the total population size at time t and $P_n(t) = P[X(t) = n]$.

Let $P_{in}(s,t) = P[X(t) = n|X(s) = i]$ which implies $P_n(t) = P_{in}(0,t) = P[X(t) = n|X(0) = i]$, then

$$\begin{aligned} P_{n,n+1}(t, t+\Delta t) &= [\lambda_n \Delta t + o(\Delta t)][1 - \mu_n \Delta t + o(\Delta t)][(1 - \varepsilon \Delta t) + o(\Delta t)][1 - \delta \Delta t + o(\Delta t)] \\ &+ \quad [1 - \lambda_n \Delta t + o(\Delta t)][1 - \mu_n \Delta t + o(\Delta t)][\varepsilon \Delta t + o(\Delta t)][(1 - \delta \Delta t) + o(\Delta t)], \\ &= \lambda_n \Delta t + \varepsilon \Delta t + o(\Delta t). \end{aligned} \tag{1}$$

$$\begin{aligned} P_{n,n}(t, t+\Delta t) &= [1 - \lambda_n \Delta t + o(\Delta t)][1 - \mu_n \Delta t + o(\Delta t)][1 - \varepsilon \Delta t + o(\Delta t)][1 - \delta \Delta t + o(\Delta t)], \\ &= 1 - (\mu_n + \lambda_n + \varepsilon + \delta)(\Delta t) + o(\Delta t). \end{aligned} \tag{2}$$

$$\begin{aligned} P_{n,n-1}(t, t+\Delta t) &= [1 - \lambda_n \Delta t + o(\Delta t)][\mu_n \Delta t + o(\Delta t)][1 - \varepsilon \Delta t + o(\Delta t)][1 - \delta \Delta t + o(\Delta t)] \\ &+ \quad [1 - \lambda_n \Delta t + o(\Delta t)][1 - \mu_n \Delta t + o(\Delta t)][1 - \varepsilon \Delta t + o(\Delta t)][\delta \Delta t + o(\Delta t)], \\ &= [(\mu_n + \delta)\Delta t + o(\Delta t)]. \end{aligned} \tag{3}$$

Note that $\sum_{j \neq n-1,n,n+1} P_{nj}(t, t+\Delta t) = o(\Delta t)$.

Using the Chapman–Kolmogorov equation for Markov process with discrete state space and the Yule's process [27–29], $\lambda_n = n\lambda$ and $\mu_n = n\mu$, we obtain;

$$\begin{aligned} P_n(t+\Delta t) &= P_{n-1}(t)[(\lambda_{n-1} + \varepsilon)\Delta t + o(\Delta t)] + P_n(t)[1 - (\mu_n + \lambda_n + \varepsilon + \delta)(\Delta t) + o(\Delta t)] \\ &+ P_{n+1}(t)[(\mu_{n+1} + \delta)\Delta t + o(\Delta t)], \\ &= P_n(t) - (\mu_n + \lambda_n + \varepsilon + \delta)(\Delta t)P_n(t) + (\lambda_{n-1}(t) + \varepsilon)(\Delta t)P_{n-1}(t) + (\mu_{n+1} + \delta)(\Delta t)P_{n+1}(t) + o(\Delta t). \end{aligned} \tag{4}$$

Dividing through (4) by Δt and taking the limit as $\Delta t \to 0$, gives;

$$\lim_{\Delta t \to 0} \frac{P_n(t+\Delta t) - P_n(t)}{\Delta t} = -(\mu_n + \lambda_n + \varepsilon + \delta)P_n(t) + (\lambda_{n-1} + \varepsilon)P_{n-1}(t) + (\mu_{n+1} + \delta)P_{n+1}(t) + \lim_{\Delta t \to 0} \frac{o(\Delta t)}{\Delta t},$$

$$P_n'(t) = -(\mu_n + \lambda_n + \varepsilon + \delta)P_n(t) + (\lambda_{n-1} + \varepsilon)P_{n-1}(t) + (\mu_{n+1} + \delta)P_{n+1}(t), \tag{5}$$

where $\lim_{\Delta t \to 0} \frac{o(\Delta t)}{\Delta t} = 0$.

For special case, we adopt the Yule's Process such that $\lambda_n = n\lambda$ and $\mu_n = n\mu$ and (5) becomes;

$$P_n'(t) = -(n\mu + n\lambda + \varepsilon + \delta)P_n(t) + (n-1)\lambda P_{n-1}(t) + \varepsilon P_{n-1}(t) + (n+1)\mu P_{n+1}(t) + \delta P_{n+1}(t). \tag{6}$$

Considering the initial conditions;

$$P_n(0) = P(X(0) = n) = \begin{cases} 1 & , \quad n = i, \\ 0 & , \quad n \neq i. \end{cases}$$

The expected size of the population at time t given that the initial population size $X(0) = i$, $E[X(t)|X(0) = i]$ is given by

$$
\begin{aligned}
E[X(t)|X(0)=i] &= \sum_{n=0}^{\infty} nP_n(t), \\
\frac{d}{dt}E[X(t)|X(0)=i] &= \sum_{n=0}^{\infty} \frac{d}{dt} nP_n(t), \\
&= \sum_{n=0}^{\infty} nP'_n(t), \\
&= \sum_{n=0}^{\infty} n[-(n\mu+n\lambda+\varepsilon+\delta)P_n(t)+(n-1)\lambda P_{n-1}(t)+\varepsilon P_{n-1}(t)+(n+1)\mu P_{n+1}(t)+\delta P_{n+1}(t)]. \qquad (7)
\end{aligned}
$$

Setting $n-1=n$ and $n+1=n$ in (7) gives;

$$
\begin{aligned}
\frac{d}{dt}E[X(t)|X(0)=i] &= -(\mu+\lambda)\sum_{n=0}^{\infty} n^2P_n(t)-(\varepsilon+\delta)\sum_{n=0}^{\infty} nP_n(t)+\lambda\sum_{n=1}^{\infty}(n+1)nP_n(t) \\
&+ \quad \varepsilon\sum_{n=0}^{\infty}(n+1)P_n(t)+\mu\sum_{n=1}^{\infty}(n-1)nP_n(t)+\delta\sum_{n=0}^{\infty}(n-1)P_n(t), \\
&= (\lambda-\mu)\sum_{n=0}^{\infty} nP_n(t)+\varepsilon-\delta, \\
&= (\lambda-\mu)E[X(t)]+\varepsilon-\delta. \qquad (8)
\end{aligned}
$$

Solving the differential equation in (8), gives expected size of the population (with birth, death, immigration and emigration) at time t given an initial size, $X(0)=i$ as;

$$
E[X(t)|X(0)=i] = \begin{cases} (\varepsilon-\delta)t+i, & \lambda=\mu, \\ \dfrac{(\varepsilon-\delta)}{(\lambda-\mu)}\left\{e^{(\lambda-\mu)t}-1\right\}+ie^{(\lambda-\mu)t}, & \lambda\neq\mu. \end{cases} \qquad (9)
$$

Now the second non-central moment of the population is given as;

$$
\begin{aligned}
E[X(t)^2] &= \sum_{n-0}^{\infty} n^2P_n(t), \\
\frac{d}{dt}E[X(t)^2] &= \sum_{n=0}^{\infty} n^2P'_n(t), \\
&= \sum_{n=0}^{\infty} n^2[-(n(\lambda+\mu)+(\delta+\varepsilon))P_n(t)+(n-1)\lambda P_{n-1}(t)+\varepsilon P_{n-1}(t)+(n+1)\mu P_{n+1}(t)+\delta P_{n+1}(t)].
\end{aligned}
$$

Again setting $n-1=n$ and $n+1=n$ gives;

$$
\begin{aligned}
\frac{d}{dt}E[X(t)^2] &= -(\lambda+\mu)\sum_{n=0}^{\infty} n^3P_n(t)-(\delta+\varepsilon)\sum_{n=0}^{\infty} n^2P_n(t)+\lambda\sum_{n=0}^{\infty}(n+1)^2nP_n(t) \\
&+ \quad \varepsilon\sum_{n=0}^{\infty}(n+1)^2P_n(t)+\mu\sum_{n=0}^{\infty} n(n-1)^2P_n(t)+\delta\sum_{n=0}^{\infty}(n-1)^2P_n(t), \\
&= 2(\lambda-\mu)\sum_{n=0}^{\infty} n^2P_n(t)+(\lambda+\mu+2\varepsilon-2\delta)\sum_{n=0}^{\infty} nP_n(t)+\varepsilon+\delta, \\
&= 2(\lambda-\mu)E[X(t)^2]+(\lambda+\mu+2\varepsilon-2\delta)E[X(t)]+\varepsilon+\delta. \qquad (10)
\end{aligned}
$$

Solving the differential equation in (10), gives;

$$
E[X(t)^2|X(0)=i] = \begin{cases} \left(\dfrac{\varepsilon+\delta}{2(\mu+\varepsilon-\delta)}\right)\left(e^{2(\mu+\varepsilon-\delta)t}-1\right)+i^2e^{2(\mu+\varepsilon-\delta)t}, & \lambda=\mu, \\[2ex] \left(\dfrac{(\lambda+\mu+2\varepsilon-2\delta)(\varepsilon-\delta)}{2(\lambda-\mu)^2}\right)\left(e^{(\lambda-\mu)t}-1\right)^2+\left(\dfrac{\lambda+\mu+2\varepsilon-2\delta}{\lambda-\mu}\right)ie^{(\lambda-\mu)t}\left(e^{(\lambda-\mu)t}-1\right) & \\ \qquad +\left(\dfrac{\varepsilon+\delta}{2(\lambda-\mu)}\right)\left(e^{2(\lambda-\mu)t}-1\right)+i^2e^{2(\lambda-\mu)t}, & \lambda\neq\mu. \end{cases} \qquad (11)
$$

The second central moment (variance) of the proposed stochastic population model at a specified time t given the initial size of the population (with birth, death, immigration and emigration), $X(0) = i$ can easily be deduce from Eqs. (9) and (11) as;

$$Var[X(t)|X(0)=i] = \begin{cases} \left(\dfrac{\varepsilon+\delta}{2(\mu+\varepsilon-\delta)}\right)\left(e^{2(\mu+\varepsilon-\delta)t}-1\right)+i^2e^{2(\mu+\varepsilon-\delta)t}-\left((\varepsilon-\delta)t+i\right)^2, & \lambda=\mu, \\ \left(\dfrac{(\lambda+\mu+2\varepsilon-2\delta)(\varepsilon-\delta)}{2(\lambda-\mu)^2}\right)\left(e^{(\lambda-\mu)t}-1\right)^2+\left(\dfrac{\lambda+\mu+2\varepsilon-2\delta}{\lambda-\mu}\right)ie^{(\lambda-\mu)t}\left(e^{(\lambda-\mu)t}-1\right) & \\ +\left(\dfrac{\varepsilon+\delta}{2(\lambda-\mu)}\right)\left(e^{2(\lambda-\mu)t}-1\right)+i^2e^{2(\lambda-\mu)t}-\left(\dfrac{(\varepsilon-\delta)}{(\lambda-\mu)}\left\{e^{(\lambda-\mu)t}-1\right\}+ie^{(\lambda-\mu)t}\right)^2, & \lambda\neq\mu. \end{cases} \tag{12}$$

The limiting distribution for the linear growth (birth and death) model with immigration and emigration

A limiting distribution (asymptotic distribution), describes the behaviour of a statistical distribution as a certain parameter or variable tends to a specified limit [30]. This helps to determine behaviour of a statistic as the sample size increase or some relevant parameter changes. In this study, we derive the limiting distribution of the size of the population as time, t gets infinitely large.

Mathematically, let

$$\begin{aligned} &\lim_{t\to\infty} P_n(t) = \Pi_n, \\ &\lim_{t\to\infty} P_n'(t) = 0, \end{aligned} \tag{13}$$

where Π_n is the limiting distribution [30].

For $n = 0$, we deduce the limiting distribution of the proposed stochastic population model from Eq. (5) as follow;

$$\begin{aligned} 0 &= -(\mu_0+\lambda_0+\varepsilon+\delta)\Pi_0+\lambda_{-1}\Pi_{-1}+\varepsilon\Pi_{-1}+(\mu_1+\delta)\Pi_1, \\ &= -\varepsilon\Pi_0+(\mu_1+\delta)\Pi_1, \\ \Pi_1 &= \left\{\frac{\varepsilon}{\mu_1+\delta}\right\}\Pi_0, \end{aligned} \tag{14}$$

since at $n = 0$, $\mu_0 = 0$, $\lambda_0 = 0$, $P_{-1}(0) = \Pi_{-1} = 0$ and $\delta = 0$.

When $n = 1$, Eq. (5) with Eq. (13) becomes;

$$\begin{aligned} 0 &= -(\mu_1+\lambda_1+\varepsilon+\delta)\Pi_1+(\lambda_0+\varepsilon)\Pi_0+(\mu_2+\delta)\Pi_2, \\ \Pi_2 &= \left\{\frac{(\lambda_1+\varepsilon)\varepsilon}{(\mu_1+\delta)(\mu_2+\delta)}\right\}\Pi_0. \end{aligned} \tag{15}$$

When $n = 2$, Eq. (5) with Eq. (13) becomes;

$$\begin{aligned} 0 &= -(\mu_2+\lambda_2+\varepsilon+\delta)\Pi_2+(\lambda_1+\varepsilon)\Pi_1+(\mu_3+\delta)\Pi_3, \\ \Pi_3 &= \left\{\frac{\varepsilon(\lambda_1+\varepsilon)(\lambda_2+\varepsilon)}{(\mu_1+\delta)(\mu_2+\delta)(\mu_3+\delta)}\right\}\Pi_0. \end{aligned} \tag{16}$$

Proceeding iteratively, the limiting distribution, Π_n is given as;

$$\Pi_n = \left\{\frac{\varepsilon(\lambda_1+\varepsilon)(\lambda_2+\varepsilon)\dots(\lambda_{n-1}+\varepsilon)}{(\mu_1+\delta)(\mu_2+\delta)(\mu_3+\delta)\dots(\mu_n+\delta)}\right\}\Pi_0. \tag{17}$$

For the special case of $\lambda_n = \lambda$, $\mu_n = \mu$ along with the constraint $\sum_{n=0}^{\infty}\Pi_n = 1$ we have,

$$\begin{aligned} &\Pi_0+\sum_{n=1}^{\infty}\Pi_n = 1, \\ &\Pi_0\left\{1+\left(\frac{\varepsilon}{\lambda+\varepsilon}\right)\sum_{n=1}^{\infty}\left(\frac{\lambda+\varepsilon}{\mu+\delta}\right)^n\right\} = 1. \end{aligned} \tag{18}$$

For $0 < \left(\dfrac{\lambda+\varepsilon}{\mu+\delta}\right) < 1$, Eq. (18) becomes;

$$\begin{aligned} &\Pi_0\left(1+\frac{\varepsilon}{(\mu+\delta)-(\lambda+\varepsilon)}\right) = 1, \\ &\Pi_0\left(1-\frac{\varepsilon}{(\lambda-\mu)+(\varepsilon-\delta)}\right) = 1, \end{aligned}$$

$$\Pi_0 = \left(1 - \frac{\varepsilon}{\mathcal{G} + \mathcal{M}}\right)^{-1}. \tag{19}$$

Now for $\left(\frac{\lambda + \varepsilon}{\mu + \delta}\right) > 1$, then

$$\begin{aligned} \Pi_0 &= \left(1 + \frac{\varepsilon}{(\lambda - \mu) + (\varepsilon - \delta)}\right)^{-1}, \\ &= \left(1 + \frac{\varepsilon}{\mathcal{G} + \mathcal{M}}\right)^{-1}. \end{aligned} \tag{20}$$

where $\mathcal{G} = \lambda - \mu$ is the intrinsic growth rate and $\mathcal{M} = \varepsilon - \delta$ is the net migration rate.

From Eqs. (19) and (20),

$$\Pi_0 = \begin{cases} \left(1 - \frac{\varepsilon}{\mathcal{G} + \mathcal{M}}\right)^{-1}, & 0 < \left(\frac{\lambda + \varepsilon}{\mu + \delta}\right) < 1, \\ \left(1 + \frac{\varepsilon}{\mathcal{G} + \mathcal{M}}\right)^{-1}, & \left(\frac{\lambda + \varepsilon}{\mu + \delta}\right) > 1, \end{cases} \tag{21}$$

where $\mathcal{G} = \lambda - \mu$ is the intrinsic growth rate and $\mathcal{M} = \varepsilon - \delta$ is the net migration rate.

Now from Eqs. (17) and (21), the limiting distribution or the steady state distribution for the population (with birth, death, immigration and emigration) exist and is given as;

$$\Pi_n = \begin{cases} \left(\frac{\varepsilon}{\lambda + \varepsilon}\right)\left(1 + \frac{\varepsilon}{\mathcal{G} + \mathcal{M}}\right)^{-1}\left(\frac{\lambda + \varepsilon}{\mu + \delta}\right)^n, & \left(\frac{\lambda + \varepsilon}{\mu + \delta}\right) > 1, \quad n = 0, 1, 2, 3 \ldots \\ \left(\frac{\varepsilon}{\lambda + \varepsilon}\right)\left(1 - \frac{\varepsilon}{\mathcal{G} + \mathcal{M}}\right)^{-1}\left(\frac{\lambda + \varepsilon}{\mu + \delta}\right)^n, & 0 < \left(\frac{\lambda + \varepsilon}{\mu + \delta}\right) < 1, \quad n = 0, 1, 2, 3 \ldots . \end{cases} \tag{22}$$

From Eq. (22), the long-run probability of zero offsprings (probability of ultimate extinction) can be deduced as;

$$\kappa = \begin{cases} \left(\frac{\varepsilon}{\lambda + \varepsilon}\right)\left(1 + \frac{\varepsilon}{\mathcal{G} + \mathcal{M}}\right)^{-1}, & \left(\frac{\lambda + \varepsilon}{\mu + \delta}\right) > 1, \\ \left(\frac{\varepsilon}{\lambda + \varepsilon}\right)\left(1 - \frac{\varepsilon}{\mathcal{G} + \mathcal{M}}\right)^{-1}, & 0 < \left(\frac{\lambda + \varepsilon}{\mu + \delta}\right) < 1. \end{cases} \tag{23}$$

It worth noting that for the purpose of this study, ultimate extinction can only be caused by death or emigration.

The probability generating function of the birth, death, immigration and emigration model

Let the probability generating function (pgf) be denoted as, $\psi(Z)$.

$$\begin{aligned} \psi(Z) = \sum_{n=0}^{\infty} P_n(t) Z^n = \sum_{n=0}^{\infty} \Pi_n Z^n, \\ &= \Pi_0 + \sum_{n=1}^{\infty} \Pi_n Z^n, \\ &= \Pi_0 \left\{ 1 + \left(\frac{\varepsilon}{\lambda + \varepsilon}\right) \sum_{n=1}^{\infty} \left[Z \left(\frac{\lambda + \varepsilon}{\mu + \delta}\right) \right]^n \right\}. \end{aligned} \tag{24}$$

From Eq. (24) the probability generating function for the random variable (the size of a population with birth, death, immigration and emigration) is given by;

$$\psi(Z) = \begin{cases} \Pi_0 \left\{ 1 + \left(\frac{\varepsilon}{\lambda + \varepsilon}\right) \left[\frac{\left(\frac{\lambda+\varepsilon}{\mu+\delta}\right) Z}{1 - \left(\frac{\lambda+\varepsilon}{\mu+\delta}\right)} \right] \right\}, & 0 < \left(\frac{\lambda+\varepsilon}{\mu+\delta}\right) Z < 1, \\ \Pi_0 \left\{ 1 + \left(\frac{\varepsilon}{\lambda + \varepsilon}\right) \left[\frac{\left(\frac{\lambda+\varepsilon}{\mu+\delta}\right) Z}{\left(\frac{\lambda+\varepsilon}{\mu+\delta}\right) - 1} \right] \right\}, & \left(\frac{\lambda+\varepsilon}{\mu+\delta}\right) Z > 1. \end{cases} \tag{25}$$

Table 2
Estimates of probability of ultimate extinction using the proposed stochastic population model.

Sample (n)	$\hat{\lambda}$	S.e ($\hat{\lambda}$)	$\hat{\mu}$	S.e ($\hat{\mu}$)	$\hat{\varepsilon}$	S.e ($\hat{\varepsilon}$)	$\hat{\delta}$	S.e ($\hat{\delta}$)	$\hat{\Pi}_0$	$\hat{\mathcal{G}}$	S.e ($\hat{\mathcal{G}}$)	$\hat{\mathcal{M}}$	S.e ($\hat{\mathcal{G}}$)
50	30.201	0.449	7.708	0.087	28.874	1.982	29.435	1.996	0.2109922	22.492	0.395	−0.560	0.177
100	30.218	0.572	7.696	0.098	28.676	1.852	29.235	1.853	0.2111806	22.522	0.502	−0.559	0.213
500	30.157	0.584	7.696	0.102	28.591	1.978	29.132	1.980	0.2111985	22.461	0.506	−0.541	0.212
1000	30.159	0.610	7.701	0.104	28.682	1.914	29.226	1.938	0.2111227	22.458	0.530	−0.544	0.206

Bootstrap resampling

The next process after specifying the model parameters is to estimate the parameters. Due to the limited or small size of the available data (shown in Table 1), the bootstrap technique was employed to estimate the average (mean) birth, death, immigration and emigration rates.

The Bootstrap algorithm is a resampling technique used to estimate a statistic of interest such as mean, median and standard error by repeatedly resampling the data with replacement. It is particularly useful when you desire to make inference about a population parameter but the available sample data is limited. The bootstrap procedure operates as follows:

Resampling: Suppose the observed data is $\mathcal{X} = (x_1, x_2, \dots, x_n)$. Draw n random sample, with replacement from the observed data $\mathcal{X}$ to obtain a bootstrap sample $\mathcal{X}^* = (x_1^*, x_2^*, \dots, x_n^*)$.

Generate large number of independent bootstrap samples, say $\mathcal{B}$, each of size n: $\mathcal{X}^{*1}, \mathcal{X}^{*2}, \dots, \mathcal{X}^{*\mathcal{B}}$.

Computation: Let $S(\cdot)$ denote the average rate, calculate bootstrap replication of $S : S\left(\mathcal{X}^{*b}\right), b = 1, 2, \dots, \mathcal{B}$.

Now, the bootstrap estimate of the mean is given as;

$$\hat{\hat{X}}_{boot} = \frac{1}{\mathcal{B}} \sum_{b=1}^{\mathcal{B}} S(\mathcal{X}^{*b}), \tag{26}$$

and the associated standard error (the standard deviation of the bootstrap replication) is

$$\hat{se}_{boot}(\hat{\hat{X}}) = \sqrt{\frac{1}{(\mathcal{B}-1)} \sum_{b=1}^{\mathcal{B}} \left[S\left(\mathcal{X}^{*b}\right) - \hat{\hat{X}}_{boot}\right]^2}. \tag{27}$$

In this study, we would consider bootstrap samples of size $n = 50, 100, 500, 1000$. Booth and Sarkar [31] demonstrated that at least 800 resamples are required so that conclusion of statistical analysis utilizing bootstrap variance estimates remain unaffected by Monte Carlo error. Following the above recommendation and for brevity of presentation we would discuss the results for the $n = 1000$ bootstrap samples for all inferences in this study although the results for the remaining bootstrap sample $n = 50, 100, 500$ are also presented in Tables 2 and 3.

Results and discussion

Table 2 contains the estimates of the model parameters (rates), the long-run probability of zero offspring, the intrinsic growth rate and the net migration rate per 1000 Ghanaian population.

From Table 2, the average birth ($\hat{\lambda}$), death ($\hat{\mu}$), immigration ($\hat{\varepsilon}$) and emigration ($\hat{\delta}$) rates per 1000 Ghanaian population for a bootstrap sample of size $n = 1000$ were 30.159, 7.701, 28.682 and 29.226 respectively. Their respective standard errors were 0.610, 0.104, 1.914 and 1.938.

The intrinsic growth ($\hat{\mathcal{G}}$) and the net migration ($\hat{\mathcal{M}}$) rates per 1000 population for a bootstrap sample of $n = 1000$ was 22.458 and -0.544 respectively. It can be inferred from the results above that, the Ghanaian population over the surveyed period has recorded more average birth than death per 1000 population (Intrinsic growth rate greater than 0). The net migration rate values indicate that the population has recorded more emigration (people moving out) than immigration (people coming in) over the surveyed period.

In order to better understand reproductive behaviours, inform policy decisions, address societal needs, and advance research agendas pertaining to population dynamics, family formation, and individual well-being, it is useful to estimate the long-run probability of zero offspring. The Long-run Probability of zero offspring (Probability of Ultimate Extinction) of the Ghanaian Population was about 0.21 across all the bootstrap samples ($n = 50, 100, 500$ and 1000) considered. This indicates that the Ghanaian population has about 21% chance of being extinct (or achieving a generation with zero offspring). It is evident from the results that, the estimated rates and probability of ultimate extinction are stable across all bootstrap samples.

Table 3 shows the estimated population size, $E[X(t)]$ and the standard deviation of the population size estimate, S.D$[\hat{X}(t)]$ across all the bootstrap samples ($n = 50$, 100, 500 and 1000) considered.

The reported population sizes 24,658,823 and 30,832,019 from the 2010 and 2021 Population and Housing Census (PHC) in Ghana were used as the initial population sizes $X(0) = i$, for the periods 2011 to 2021 and 2022 to 2025 respectively.

From Table 3, the estimated population size for the years 2011 and 2022 using the proposed stochastic growth model for $n = 1000$ bootstrap samples were 25,218,876 with standard deviation 993.65 and 31,532,278 with standard deviation 1111.09 respectively. These were estimated using the initial population sizes of 24,658,823 and 30,832,019 drawn from 2010 and 2021 PHC in Ghana

Table 3
Estimates of the Ghanaian population size across the bootstrap samples using the proposed stochastic population model.

Initial Pop. $\hat{X}(0) = i$	Year	Time (t)	$n = 50$ Est. Pop. size		$n = 100$ Est. Pop. size		$n = 500$ Est. Pop. size		$n = 1000$ Est. Pop. size	
			$E[\hat{X}(t)]$	S.D$[\hat{X}(t)]$	$E[X(t)]$	S.D$[\hat{X}(t)]$	$E[\hat{X}(t)]$	S.D$[\hat{X}(t)]$	$E[\hat{X}(t)]$	S.D$[\hat{X}(t)]$
24,658,823										
	2011	1	25,219,759	994.43	25,220,490	994.53	25,218,952	993.65	25,218,876	993.65
	2012	2	25,793,455	1005.67	25,794,951	1005.79	25,791,804	1004.87	25,791,649	1004.87
	2013	3	26,380,201	1017.05	26,382,496	1017.18	26,377,669	1016.22	26,377,431	1016.22
	2014	4	26,980,295	1028.55	26,983,424	1028.70	26,976,841	1027.70	26,976,518	1027.69
	2015	5	27,594,039	1040.18	27,598,040	1040.35	27,589,624	1039.31	27,589,210	1039.30
	2016	6	28,221,745	1051.95	28,226,656	1052.13	28,216,327	1051.04	28,215,819	1051.03
	2017	7	28,863,729	1063.85	28,869,589	1064.05	28,857,265	1062.91	28,856,659	1062.90
	2018	8	29,520,318	1075.88	29,527,167	1076.10	29,512,762	1074.92	29,512,053	1074.91
	2019	9	30,191,842	1088.05	30,199,723	1,088.28	30,183,148	1087.06	30,182,333	1087.04
	2021	10	30,878,643	1100.35	30,887,599	1100.61	30,868,763	1099.34	30,867,837	1099.32
30,832,019										
	2022	1	31,533,382	1111.96	31,534,296	1112.07	31,532,373	1111.09	31,532,278	1111.09
	2023	2	32,250,699	1124.53	32,252,570	1124.66	32,248,635	1123.64	32,248,442	1123.63
	2024	3	32,984,334	1137.25	32,987,204	1137.40	32,981,168	1136.33	32,980,871	1136.32
	2025	4	33,734,658	1150.11	33,738,571	1150.28	33,730,340	1149.16	33,729,935	1149.15

respectively. It is worth noting that, the estimated population size for year 2021 (from bootstrap sample $n = 1000$) based on the proposed stochastic model is 30,867,837 with a standard deviation of 1099.32. This figure is very close to the actual Ghanaian population size (30,832,019) from 2021 PHC reported by the Ghana Statistical Service.

The estimated population sizes for years 2023, 2024 and 2025 from $n = 1000$ bootstrap samples were 32,248,442, 32,980,871 and 33,729,935 with standard deviations of 1123.63, 1136.32 and 1149.15 respectively using the 2021 PHC as the base population size. It is evident from Table 3 that, the estimated population sizes for specified times were almost equal across all the bootstrap samples considered. This indicates that the proposed model is stable. The estimated Ghanaian Population sizes in Table 3 are consistent with estimates from the United Nations, Department of Economic and Social Affairs, Population Division. World Population Prospects: The 2022 Revision. *(https://www.worldometers.info/world-population/ghana-population/)*. These estimated population sizes provide a quick, easy, and economical way to get demographic data for planning, research, and policy. Additionally, they support well-informed interventions and evidence-based decision-making to address societal issues and advance human welfare.

The added advantage of using the proposed stochastic model is that, other population parameters (Long-run probability of zero offspring, Net migration rate, intrinsic growth rate) as well as the limiting distribution and the probability generating function of the population size can also be estimated. This makes it easier to monitor the population dynamics to inform policy decisions.

Conclusions and recommendations

Most of the existing population models in literature consider some but not all the relevant population characteristics (birth, death, immigration and emigration) in modelling. A typical human population is susceptible to birth, death, immigration and emigration. It is therefore important to incorporate all the characteristics in any human population model to achieve more realistic estimates of population parameters.

The study sought to develop a stochastic population model to monitor the population dynamics considering the birth, death, immigration and emigration rates of the surveyed population. The study succeeded in developing a stochastic population growth model, estimated population moments (expected size and variance) at specified time t, derived the limiting distribution of the population size and deduced the probability of ultimate extinction of the population. The probability generation function of the limiting distribution was also obtained.

As indicated earlier, these estimates aid in understanding populations change over time by predicting trends which helps in managing resources sustainably, and addressing challenges related to overpopulation or population decline in different regions.

The proposed stochastic population growth model was validated with bootstrap samples of data obtained from the Ghana Immigration Service and the Birth and Death Registry of Ghana. The results shown in Tables 2 and 3 indicates that the long-run probability of zero offspring of the Ghanaian population is approximately 0.21 (This is characterized by death and emigration). It is also evident from the study results that, the net migration and intrinsic growth rates per 1000 Ghanaian population are −0.544 and 22.458 with standard errors of 0.206 and 0.530 respectively. This indicates that although the average birth rate is higher than the average death rate in Ghana, the average emigration rate (rate at which individuals travel out of the population either by the land borders, sea or air ports) is relatively higher than the immigration rate (rate at which individuals come into the population either by the land borders, sea or air ports).

The estimated population sizes shown in Table 3 were almost same across all bootstrap samples at any specified time. This signifies that the proposed model is stable. Also, the estimated population size for year 2021 (from bootstrap sample $n = 1000$) based on the proposed stochastic model is 30,867,837 with a standard deviation of 1099.32. This figure is very close to the actual Ghanaian Population size (30,832,019) from 2021 PHC reported by the Ghana Statistical Service. The estimated Population sizes are also consistent with other global estimates from international sources such as United Nations, Department of Economic and Social Affairs, Population Division. World Population Prospects: The 2022 Revision. *(https://www.worldometers.info/world-population/ghana-population/)*.

Based on the above, the study recommends the use of the proposed stochastic population growth model to monitor any population that is susceptible to birth, death, immigration and emigration. Future studies would consider applying the developed model to non-human population or to processes whose transitions mimic the birth, death, immigration and emigration. Also future works would consider relaxing some of the model assumptions (such as constant immigration and emigration rates) to make them random and more realistic as it is in natural populations.

CRediT authorship contribution statement

Richel O. Attafuah: Conceptualization, Methodology, Writing – original draft. **Eric Ocran:** Data curation, Formal analysis. **Enoch Sakyi-Yeboah:** Data curation, Formal analysis. **Edward Acheampong:** Conceptualization, Supervision, Validation, Reviewing and editing. **Louis Asiedu:** Conceptualization, Supervision, Validation, Reviewing and editing.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Data availability

The data used to support the findings of this study are available from the corresponding author upon request.

References

[1] B.K. Pradhan, P. Dash, et al., A note on generalization of the simplest time-dependent discrete Markov process: Linear growth process with immigration-emigration, J. Stat. Theory Appl. 20 (1) (2021) 111–131.
[2] T.R. Padi, C. Gudala, Linear birth, death and migration processes for portfolio management modelling, IOSR J. Math. (IOSR-JM) 11 (2015) 29–36.
[3] F. Brauer, C. Castillo-Chavez, C. Castillo-Chavez, Mathematical Models in Population Biology and Epidemiology, vol. 2, Springer, 2012.
[4] S. KS, N.C. Viswanath, Study of birth-death processes with immigration, Croatian Oper. Res. Rev. 13 (1) (2022) 49–63.
[5] F. Azizi, N. Salari, A novel condition-based maintenance framework for parallel manufacturing systems based on bivariate birth/birth–death processes, Reliab. Eng. Syst. Saf. 229 (2023) 108798.
[6] S. Engen, B.-E. Sæther, Stochastic population models: some concepts, definitions and results, Oikos (1998) 345–352.
[7] W. Feller, et al., An introduction to probability theory and its applications, 1971.
[8] K. Mehata, S. Duraiswamy, A parity-dependent immigration-birth-death-emigration process, Math. Biosci. 109 (2) (1992) 177–199.
[9] L.S.T. Ho, J. Xu, F.W. Crawford, V.N. Minin, M.A. Suchard, Birth/birth-death processes and their computable transition probabilities with biological applications, J. Math. Biol. 76 (2018) 911–944.
[10] C.R. Doss, M.A. Suchard, I. Holmes, M. Kato-Maeda, V.N. Minin, Fitting birth-death processes to panel data with applications to bacterial DNA fingerprinting, Ann. Appl. Stat. 7 (4) (2013) 2315.
[11] S. Sindayigaya, N.L. Kennedy, A.A. Wasike, The population mean and its variance in the presence of genocide for a simple birth-death-immigration-emigration using the probability generating function, 2016.
[12] D.G. Kendall, On the generalized“ birth-and-death” process, Ann. Math. Stat. 19 (1) (1948) 1–15.
[13] S. Benzekry, C. Lamont, A. Beheshti, A. Tracz, J.M. Ebos, L. Hlatky, P. Hahnfeldt, Classical mathematical models for description and prediction of experimental tumor growth, PLoS Comput. Biol. 10 (8) (2014) e1003800.
[14] S. Tabassum, N.B. Rosli, M.S.A. Binti Mazalan, Mathematical modeling of cancer growth process: a review, in: Journal of Physics: Conference Series, Vol. 1366, IOP Publishing, 2019, 012018.
[15] J.F. Speer, V.E. Petrosky, M.W. Retsky, R.H. Wardwell, A stochastic numerical model of breast cancer growth that simulates clinical data, Cancer Res. 44 (9) (1984) 4124–4130.
[16] L. Marrec, C. Bank, T. Bertrand, Solving the stochastic dynamics of population growth, Ecol. Evol. 13 (8) (2023) e10295.
[17] J. Fieberg, S.P. Ellner, Stochastic matrix models for conservation and management: a comparative review of methods, Ecol. Lett. 4 (3) (2001) 244–266.
[18] R. Lande, S. Engen, B.-E. Saether, Stochastic Population Dynamics in Ecology and Conservation, Oxford University Press, USA, 2003.
[19] M. Borsuk, D. Lee, Stochastic population dynamic models as probability networks, in: Handbook of Ecological Modelling and Informatics, WIT Press, 2009, p. 199.
[20] G.C. White, Population viability analysis: data requirements and essential analyses, in: Research Techniques in Animal Ecology: Controversies and Consequences, Columbia university Press, New York, New York, USA, 2000, pp. 288–331.
[21] S. Tavaré, The genealogy of the birth, death, and immigration process, Math. Evol. Theory 41 (1989) 56.
[22] J. Matis, T. Kiffe, G. Otis, Use of birth–death–migration processes for describing the spread of insect populations, Environ. Entomol. 23 (1) (1994) 18–28.
[23] J.H. Matis, T.R. Kiffe, On stochastic logistic population growth models with immigration and multiple births, Theor. Popul. Biol. 65 (1) (2004) 89–104.
[24] R. O'Hara, S. Lampila, M. Orell, Estimation of rates of births, deaths, and immigration from mark–recapture data, Biometrics 65 (1) (2009) 275–281.
[25] M. Khodabin, K. Maleknejad, M. Rostami, M. Nouri, Interpolation solution in generalized stochastic exponential population growth model, Appl. Math. Model. 36 (3) (2012) 1023–1033.
[26] V. Giorno, A.G. Nobile, Bell polynomial approach for time-inhomogeneous linear birth–death process with immigration, Mathematics 8 (7) (2020) 1123.
[27] A. Aghamohammadi, M. Khorrami, On a model for death, birth, and immigration, Phys. A 599 (2022) 127405.
[28] L.J. Allen, E.J. Allen, A comparison of three different stochastic population models with regard to persistence time, Theor. Popul. Biol. 64 (4) (2003) 439–449.
[29] B. Mehta, P. Khurana, D. Kumar, Deterministic and stochastic models-population growth models population models, in: 2020 8th International Conference on Reliability, Infocom Technologies and Optimization (Trends and Future Directions), ICRITO, IEEE, 2020, pp. 212–216.
[30] G. Grimmett, D. Stirzaker, Probability and Random Processes, Oxford University Press, 2020.
[31] J.G. Booth, S. Sarkar, Monte Carlo approximation of bootstrap variances, Amer. Statist. 52 (4) (1998) 354–357.