Enhanced Fertility Modelling: Integrating Social Interaction Theories into Differential Equation Models

Qi Cui

q.cui1@lse.ac.uk

London School of Economics and Political Sciences

1. Introduction

The long history of modelling fertility age schedules has always attracted the interest of demographers (e.g., Bloom & Trussell, 1984; Booth, 1984; Coale & McNeil, 1972; Hoem et al., 1981; Peristera & Kostaki, 2007; Schmertmann, 2003). Such models have proven useful for describing fertility patterns by age, correcting flawed fertility data, and forecasting fertility rates. However, the models often overlook the social processes that govern fertility or the diverse components that constitute the total fertility rate (Page, 1977, pp. 85). The underlying fertility behaviours are typically inferred *ex-post* from model parameters such as the mean age at birth, the standard deviation of age at birth, and the mode of age-specific fertility rate, rather than from *ex-ante* behavioural hypotheses.

Among these models, those based on diffusion processes and built upon behavioural postulates using differential equations often appear (Bass, 1969; Hernes, 1972; Pitcher et al., 1978). While first-order ordinary differential equations are regularly used in demography, for example, in the exponential population growth model and the force of mortality function, compartmental differential equation models are rarely featured in demographic literature (Burch, 2018, pp. 79; Willekens, 2011, pp. 175). In fact, compartmental differential equations have a long history, dating back to Alfred J. Lotka (1934/1998), who proposed the Lotka-Volterra equation, a prey-predator model describing the interaction of two species.

While the development of diffusion models has flourished in other disciplines, its advancement has been more limited in demography. Here, only three models, including the Hernes model (Hernes, 1972), the Rosero-Bixby-Casterline model (Rosero-Bixby & Casterline, 1993), and the Gompertz model (Goldstein, 2010), are commonly cited. Though these models have been revisited in recent literature (Billari & Toulemon, 2006; Goldstein & Kenney, 2001; Goldstein, 2010; Li & Wu, 2008; Myrskylä & Goldstein, 2013), their primary application remains forecasting future marriage and fertility rates. Both the behavioural interpretation of model parameters and the theoretical assumptions upon which differential equation models depend have not received sufficient attention, possibly undermining the models' accuracy and predictability. In a recent review, Cui (202X) introduced literature from other disciplines, defined model parameters in terms of fertility behaviour, and underscored the potential for differential equations to bridge micro-level behaviour with aggregated-level patterns, offering an alternative to agent-based models.

Studies have consistently shown that fertility behaviours can spread through social networks, including those of friends, peers, co-workers, and siblings (Balbo & Barban, 2014; Buyukkececi et al., 2020; Hensvik & Nilsson, 2010; Kuziemko, 2006; Lyngstad & Prskawetz, 2010). When deciding on the timing of childbirth, women face a significant trade-off. Delayed motherhood can increase lifetime

earnings; however, postponement is also associated with higher risks of childlessness and adverse health outcomes for both mothers and children. To navigate this dilemma, women might turn to their social environment to acquire information about the cost-benefits associated with the timing of childbearing. They can draw inferences from the experiences of their peers to learn about the advantages and disadvantages of childbearing. Therefore, it is reasonable to posit that fertility behaviours can diffuse through these networks via the operation of underlying diffusion dynamics and are shaped by structural factors. As such, the timing of childbirth can be viewed as the outcome of a diffusion process, illustrating how the decision to have children spreads throughout a population.

In light of these theoretical considerations and recent empirical findings on social interaction, this study aims to develop a fertility model using differential equations based on social interaction theories. The study aims to answer two research questions: (1) Is it feasible to develop a fertility model that describes fertility age schedules using differential equations grounded in social interaction theories? (2) How well can the new model empirically fit (cohort) age-specific fertility data compared with other differential equation models?

The following section provides a theoretical diffusion review, summarising the key diffusion mechanisms, and a methodological review outlining the setting of model parameters. Subsequently, we will present a new diffusion model for fertility and evaluate its performance in terms of fitting accuracy when compared with other differential equation models. Finally, we will discuss the new model and draw conclusions based on the findings.

2. Previous methods

In this section, we explore three well-established demographic models: the Bass model, the Hernes model, and the Gompertz model. For a comprehensive review of additional differential equation models, readers are referred to the recent work by Cui (202X). These differential equation models have analytical solutions that can be derived using a variety of methods, such as the variable separable method, Laplace transform, and Riccati equation, once the initial conditions are set. To simplify the analytical expression and later estimation process, we integral the differential equations from time 0 to the time of interest instead of the covering the entire reproductive period.¹

2.1 Hernes model

The Hernes model is used to estimate the process of entry into the first marriage and is established based on two hypotheses – marriageability and social pressure. Specifically, as age increases, marriageability declines but social pressure increases. For the marriageability assumption, Hernes assumed that an individual starts from a certain level of marriage potential, but this potential declines with a constant proportion for each time unit. Thus, the expression of marriageability, Ab^x , is a geometric function, decreasing with a constant proportion for each time unit (A > 1 and 0 < b < 1). For the social pressure assumption, Hernes (1972) assumed that as more people get married, the likelihood of unmarried people making the transition will also increase (ceteris paribus). The "social pressure" force in essence can be considered an imitation (or internal-force-driven) process. The Hernes model is defined as,

 $\frac{dF(x)}{dx} = Ab^{x}F(x)[1 - F(x)], \qquad 0 < b < 1 \text{ and } A > 1$ (1)

¹ Mathematically, both integrations (from 15 to 45 and from 0 to 30) are equal.

In the fertility context, F(x) indicates the cumulative first ordered age-specific fertility rate (or the proportion of females who have given the first birth). x means the time of adoption (in the case of fertility, this indicates age of giving firth birth. $f(x) = \frac{dF(x)}{dx}$ represents the age-specific fertility rate. A is the initial fecundity and b is defined as the speed of fecundity deterioration. Insert $lna = \frac{A}{lnb}$ and $k = \frac{F(0)}{a[1-F(0)]}$ into the solution, then the equation can be simplified as the original Hernes model, $F(x) = \frac{1}{1+\frac{1}{u-b^{X}}}$.

2.2 Gompertz model

The Gompertz model (Hendry, 1972) can be considered as an expression of the internal-forces diffusion model. The model takes the logarithm transformation for the maximum proportion of adopters, c, and the proportion of females who have given the first birth, F(x). Mathematically, it is described as:

$$\frac{dF(x)}{dx} = qF(x)\{\ln(c) - \ln[F(x)]\}, \qquad q > 0 \text{ and } 0 < c < 1$$
(2)

where q represents internal forces (i.e., social interaction among individuals). Insert $m = \ln \frac{c}{F(0)}$ into

Eq. 2, we can get a simplified version, $F(x) = e^{\ln(c) - me^{-qt}}$. By using different parameters, the model can be transformed into the method without infertility term proposed by Goldstein (2010) (for a detailed comparison see Appendix A1).

3. New model

We define the model as follows,

$$\begin{cases} \frac{dF_1(x)}{dx} = \left\{ p_1 + \frac{1}{c} [q_1 F_1(x) + q_2 F_2(x)] \right\} [c_1 - F_1(x)] \\ \frac{dF_2(x)}{dx} = \frac{1}{c} [q_3 F_1(x) + q_4 F_2(x)] [c_2 - F_2(x)] \end{cases},$$
(3)

where, c equals the sum of c_1 and c_2 and F(x) equates to $F_1(x) + F_2(x)$. The parameters satisfy $0 \le c_1 \le 1$, $0 \le c_2 \le 1$, $0 \le c_1 + c_2 \le 1$, and $p_1 \ge 0$. p_1 symbolizes the external forces (e.g., intergenerational transmission, education, income, etc). c_1 and c_2 represent the maximal proportions of each subgroup within a birth cohort, respectively. The parameters q_i represent the internal forces (i.e., social interaction among individuals), with subscript *i* referring to one of the four interaction forces, where i = 1, 2, 3, 4. Notably, q_2 and q_3 gauge the cross-group social interaction forces, while q_1 and q_4 measure the within-group social interaction forces.

4. Data

The data utilized in this study were sourced from the Human Fertility Database (HFD 2023), an expansive resource for historical fertility data, compiling vital statistics, census counts, and official population estimates. The application of standardized methods across all populations over time ensures the comparability of the data (Jasilioniene et al., 2015).

To mitigate fluctuation, we calculated first-order fertility data from five-year birth cohorts, employing age-specific births and cohort exposure data. This strategy permits us to focus on the timing of adoption among peer groups, providing more age-related accuracy than period data. Specifically, we used age-specific fertility rate (ASFR) and factored in the first-order total fertility rate (TFR) calculated from age 15 to 45 (i.e., $TFR = \sum_{15}^{45} ASFR(x)$). This age range encompasses almost all first births and mitigates potential fluctuations caused by assisted reproductive technology (ART) at later ages. Countries with fewer than five available cohorts, lacking full ASFR information covering ages 15 to 45, and with a total population of less than five million in 2020 were excluded to avoid random fluctuations. In total, our study incorporates 19 countries with 93 birth cohorts. The selected countries and cohorts are detailed in Table 1.

Country	Birth Cohorts	Country	Birth Cohorts	
Belarus	1950-1969	Poland	1960-1969	
Bulgaria	1935-1959	Portugal 1945-1974		
Canada	1930-1969	Russia	1945-1969	
Czechia	1935-1969	Slovakia	1935-1964	
Denmark	1955-1974	Spain	1960-1974	
Finland	1970-1974	Sweden	1955-1974	
Hungary	1940-1974	Taiwan	1965-1969	
Japan	1955-1974	Ukraine	1945-1964	
Netherlands	1935-1969	USA	1920-1974	
Norway	1955-1974			
		Total	93	

Table 1 Countries, birth cohorts, and periods of data used in the analysis

Source: HFD (2023)

5. Results

This section is divided into two parts. The first part tests the fitting accuracy of our proposed models against empirical data, employing USA 1960-1964, Japan 1965-1969 and Sweden 1970-1974 birth cohorts as case studies. Then, we present a table summarizing the performance of the models across various indices for the 93 birth cohorts. The final part investigates the predictive power of our models by fitting the data from ages 15 through 30, 31, up to 44, and then extrapolating the curve to age 45.

Figure 2 depicts the fertility rates estimated by the Gompertz and Hernes models (in the first column), the full model (in the second column), and the simplified model (in the third column) for the selected three birth cohorts. Our full model (Eq. 3) successfully captures most characteristics of the age-related fertility schedule (e.g., the fertility humps at different ages), while the other models can generate a unimodal pattern.





Source: Calculated by authors based on HFD (2023).

In assessing the performance of our model's fitness, we utilized four key indices: the Sum of Squared Errors (SSE), the Mean Absolute Percentage Error (MAPE), the Mean Squared Error (MSE), and the Bayesian Information Criterion (BIC). Both the BIC and MSE serve to penalize models that incorporate a larger quantity of free parameters. Typically, models exhibiting lower values of SSE, MAPE, MSE, or BIC are favoured due to their superior accuracy and fit. An overview of the results for all countries and five-year birth cohorts is encapsulated in Table 2. As evident from the data, our model excels in comparison to its counterparts and significantly curtails errors. The simplified model demonstrates impressive results as well. Results pertaining to other models are detailed in Appendix A3.

6	Gompertz	0 002280 (2)	0.000700 (2)		
		0.002280 (2)	0.030793 (3)	0.000081 (2)	-286.413542 (2)
Diffusion models	Hernes	0.011890 (3)	0.013902 (2)	0.000424 (3)	-255.825959 (3)
N	ew model	0.000071 (1)	0.001109 (1)	0.000003 (1)	-390.249654 (1)

Source: Calculated by authors based on HFD (2023).

Figure 3 compares the predictive power of our models to the above differential equation models

and two frequently cited approaches: the Coale-McNeil model and the freeze rate approach. It's worth noting that the freeze rate approach was considered as the benchmark model in a recent fertility model survey (Bohk-Ewald et al., 2018). In our analysis, to systematically examine model predictive performance, we fitted the data with varying ranges starting from age 30 to age 44. As illustrated in Figure 3, our models outperform the rest, substantially reducing the SSE. The freeze rate does not yield as promising results as those found by Bohk-Ewald and her colleagues. It only outperforms the full model after age 42, where the age-fertility rates have already reached low levels. Freezing these ages until 45 inevitably produces negligible residuals. Further comparisons with other models are presented in Appendix A4.





6. Conclusion

In conclusion, our paper introduces a novel differential equation model designed to scrutinize fertility diffusion behaviour. Our model acknowledges population heterogeneity, postulating two latent groups with fertility behaviours triggered by distinct forces. The differential evolution approach is employed to estimate the model parameters. The efficacy of our model is tested using the Human Fertility Database, covering 19 countries (93 cohorts), with both the complete and simplified versions of our model outperforming other diffusion and conventional demographic parametric models. It's important to remember that the conclusions drawn in this paper are influenced by the nature of the databases used and may vary in different contexts. Nevertheless, we believe our innovative model contributes valuable insights into the diffusion process in fertility analysis.