

SEMIPARAMETRIC CONTINUOUS MORTALITY MODELING VIA GAUSSIAN PROCESS RESIDUAL CORRECTION ON TMPI 2023

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Abstract. *The Indonesian Population Mortality Table 2023 (TMPI 2023) provides graduated annual death probabilities at integer ages. This study proposes a semiparametric framework that combines a parametric backbone with a Gaussian Process (GP) correction of log-space residuals to construct continuous mortality functions for male and female populations. Two backbone families are considered: Gompertz and Heligman–Pollard, with fixed eight- and five-parameter variants of the latter. A Matérn $\nu = 5/2$ GP is fitted to residuals of annual cumulative hazards using an interval approximation. Annual death probabilities and survival are derived from a common integrated force, and curtate expectancy is distinguished from complete expectancy restricted to age 111. Evaluation uses 111 annual probabilities per sex and leave-one-age-out cross-validation that refits both the backbone and GP on each training set. Gompertz+GP achieves the lowest LOO RMSE among the evaluated candidates: 3.58881×10^{-5} for males and 3.24246×10^{-5} for females, compared with 0.00648539 and 0.00590577 for Gompertz alone. The absolute birth curtate-expectancy errors are below 0.16% for the three GP-corrected specifications. These results support reconstruction of missing ages within the published table. Conditional pointwise latent-force intervals are provided, while source-estimation uncertainty, active parameter constraints, and within-year approximation limit the interpretation.*

Keywords: Continuous mortality modelling, Gaussian Process, TMPI 2023

1. Introduction

A mortality table is a fundamental actuarial instrument that systematically records the probability of death q_x and survival p_x across age groups within a population. In practice, mortality tables serve as the primary basis for calculating life insurance premiums, determining annuity reserves, and projecting pension fund liabilities [1,2]. Beyond the private insurance sector, mortality tables play a critical role in the

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management of national social security programs. In Indonesia, the National Health Insurance program (Jaminan Kesehatan Nasional, JKN) administered by Social Health Insurance Administration Body (Badan Penyelenggara Jaminan Sosial Kesehatan, BPJS Kesehatan) relies on accurate mortality projections to ensure the long-term actuarial sustainability of the program [3]. The reliability of these projections depends directly on the accuracy and representativeness of the underlying mortality table, making the construction and improvement of mortality models a problem of substantial practical importance.

The Indonesian Population Mortality Table 2023 (Tabel Mortalitas Penduduk Indonesia 2023, TMPI 2023) provides published mortality estimates for both males and females, including a terminal convention at age 111 [4]. Constructed from JKN membership and death information for 2018–2022, it provides graduated estimates of $\hat{q}_x$ at integer ages. Related parametric studies include Gompertz estimation by nonlinear least squares (NLLS) [5], Gompertz–Makeham modelling [6], Heligman–Pollard graduation of a separately constructed participant table [7], and Weibull survival modelling [8]. These studies provide useful representations, but their responses, observation periods, and evaluation windows differ. Their reported errors consequently require their original context.

Classical parametric models are structurally constrained. The Gompertz model, for instance, describes increasing senescent mortality but cannot represent both declining infant mortality and a young-adult accident hump [9,10]. The Heligman–Pollard model introduces components for these age patterns, although departures from a fitted parametric curve may remain. This motivates treating the deviations from the published table as a residual function that can be estimated alongside a parsimonious backbone. The target here is approximation of the graduated TMPI estimates; residual correction is not direct recovery of an error-free underlying population mortality curve.

From an actuarial standpoint, continuous-time life insurance, annuity, and reserve calculations require a force of mortality $\mu(t)$ at continuous ages [2,11]. A discrete table supplies one-year probabilities and therefore requires assumptions about mortality between birthdays [12]. Parametric models can already provide continuous functions. The practical question addressed here is how to combine their global structure with a flexible residual correction while deriving annual probabilities and survival consistently from the resulting force. This construction also supplies mortality inputs at fractional ages within the fitted domain; unrestricted whole-life valuations would require an additional tail specification.

To address this question, this study proposes a semiparametric approach that combines a parametric mortality backbone with a Gaussian Process (GP) correction of log-space residuals. Gaussian Process regression models an unknown function through a mean function and covariance kernel [13]. It provides a continuous residual representation and conditional uncertainty calculations for a table with 111 usable probabilities per sex. Neural-network approaches offer other forms of flexibility in mortality modelling [14,15]; their relative performance is not evaluated here. The GP choice follows existing mortality applications [16,17,18]. Two backbone families are considered: Gompertz and Heligman–Pollard. The latter is evaluated through

fixed HP-8 and HP-5 specifications, producing Gompertz+GP, HP-8+GP, and HP-5+GP for each sex.

This study makes three principal contributions to the analysis of TMPI 2023. First, it constructs continuous forces and survival functions, annual death probabilities, and two explicitly distinguished expectancy measures from a common cumulative hazard. Second, it evaluates the GP corrections against their corresponding independently refitted backbones using absolute annual-probability errors. Third, it implements full-pipeline leave-one-age-out cross-validation (LOO-CV) and examines approximation and boundary errors alongside aggregate scores. This validation concerns missing-age reconstruction within the graduated table. The remainder of this paper is organised as follows. Section 2 presents the theoretical foundations of mortality functions, Gompertz, Heligman–Pollard, and GP regression. Section 3 describes the proposed semiparametric model and evaluation criteria. Section 4 reports and discusses the results. Section 5 concludes with a summary of findings.

2. Theoretical Foundation

2.1. Mortality Functions

Let $t \geq 0$ denote continuous age and T the age at death. The force of mortality is the instantaneous conditional death rate:

$$\mu(t) = \lim_{\Delta t \rightarrow 0^+} \frac{P(t < T \leq t + \Delta t \mid T > t)}{\Delta t}. \quad (2.1)$$

Its unit is per year [1,2]. Define the cumulative hazard $\mathcal{H}(t) = \int_0^t \mu(u) du$. The survival function is:

$$S(t) = \exp[-\mathcal{H}(t)], \quad S(0) = 1. \quad (2.2)$$

The annual death probability beginning at age x satisfies:

$$q(x) = 1 - \frac{S(x+1)}{S(x)} = 1 - \exp \left[- \int_x^{x+1} \mu(t) dt \right]. \quad (2.3)$$

For a published annual probability, define:

$$\hat{h}_x = -\ln(1 - \hat{q}_x), \quad x = 0, 1, \dots, 110. \quad (2.4)$$

This is an annual cumulative-hazard target. If the force is constant over the year, $\hat{h}_x/(1 \text{ year})$ equals that constant force. For a varying force, the transformation specifies its integral and does not identify the instantaneous value at the birthday. The same integral can be generated by different within-year force profiles.

The published TMPI expectancy is curtate [4], denoted here by e_x . With its terminal convention $e_{111} = 0$,

$$e_x = \sum_{k=1}^{111-x} \frac{S(x+k)}{S(x)}, \quad x = 0, 1, \dots, 110. \quad (2.5)$$

The corresponding continuous measure used in this study is the complete expectancy restricted to age 111,

$$\bar{e}_x^{[111]} = \int_x^{111} \frac{S(t)}{S(x)} dt, \quad 0 \leq x \leq 111. \quad (2.6)$$

It differs from curtate expectancy and excludes remaining lifetime beyond age 111. The terminal table entry $q_{111} = 1$ closes the discrete table in the following annual interval; it does not imply $S(111) = 0$. The continuous model covers force and survival on $[0, 111]$ and annual probabilities on starting ages $[0, 110]$.

2.2. Gompertz Mortality Model

The Gompertz model, originally proposed by Gompertz [19], specifies an exponentially increasing force:

$$\mu_G(t) = Be^{\beta t}, \quad B > 0, \quad \beta \geq 0. \quad (2.7)$$

Here B is the baseline force and β the age-gradient parameter. Its annual cumulative hazard and death probability are:

$$h_G(x) = \frac{B}{\beta} e^{\beta x} (e^\beta - 1), \quad q_G(x) = 1 - e^{-h_G(x)}, \quad (2.8)$$

with $h_G(x) = B$ at the continuous limit $\beta = 0$, using one-year age units. For a training age set $\mathcal{I}$, NLLS estimates the parameters through:

$$(\hat{B}, \hat{\beta}) = \arg \min_{B, \beta} \sum_{x \in \mathcal{I}} (h_G(x) - \hat{h}_x)^2. \quad (2.9)$$

This loss uses annual cumulative hazards, consistently with the table's observation interval. The increasing-force restriction prevents Gompertz alone from describing the full early-life age pattern [9].

2.3. Heligman-Pollard Model

Heligman and Pollard [9] proposed an eight-parameter decomposition of mortality odds. The age-offset specification retained in this study is

$$o_8(t; \theta) = A^{(t+B)^C} + D \exp\{-E[\ln(t+0.5) - \ln F]^2\} + GH^t. \quad (2.10)$$

The terms represent childhood decline, an accident-hump component, and senescence [10]. The offset 0.5 makes the logarithm finite at age zero; it also places the second term's maximum at $t = F - 0.5$. The five-parameter variant omits the second component:

$$o_5(t; \theta) = A^{(t+B)^C} + GH^t. \quad (2.11)$$

For either specification, the native odds-based probability is $q_{HP}^{\text{native}}(t) = o(t)/(1 + o(t))$. To retain the log-backbone construction in continuous time, define a continuous force proxy:

$$\mu_{HP}(t) = \frac{\ln[1 + o(t)]}{1 \text{ year}}. \quad (2.12)$$

This is an explicit extension of the odds formulation. Its annual integrated probability generally differs from $q_{HP}^{\text{native}}(x)$ because the proxy varies within the year. Both HP benchmarks and their GP corrections are evaluated with the integrated operator in (2.3).

The HP parameters are calibrated by squared log-error in annual integrated probabilities:

$$\hat{\theta}_{HP} = \arg \min_{\theta \in \Theta} \sum_{x \in \mathcal{I}} [\ln q_{HP}(x; \theta) - \ln \hat{q}_x]^2, \quad (2.13)$$

where $q_{HP}(x; \theta)$ is obtained by integrating (2.12), and Θ is the bounded parameter region specified in Section 3.2. Differential Evolution [20], followed by bounded local refinement, searches this non-convex loss. Its use does not guarantee a global optimum.

2.4. Gaussian Process Regression

A GP is a stochastic process whose finite collections of evaluations are jointly normal [13]. GP regression has been applied to mortality surfaces and multi-population longevity models [16,17,18]. For residuals r_i at inputs u_i , let $z_i = (r_i - \bar{r})/s_r$, where the mean and population standard deviation are computed on the training set only. A zero-mean GP is assigned to the normalized latent residual $g(u)$, with original-scale residual $\delta(u) = \bar{r} + s_r g(u)$.

The signal covariance is Matérn $\nu = 5/2$:

$$k_f(u, u') = \sigma_f^2 \left(1 + \frac{\sqrt{5}d}{\ell} + \frac{5d^2}{3\ell^2} \right) \exp \left(-\frac{\sqrt{5}d}{\ell} \right), \quad (2.14)$$

$$d = |u - u'|.$$

The working observation covariance adds independent residual noise:

$$\mathbf{K}_y = \mathbf{K}_f + \sigma_\epsilon^2 \mathbf{I}. \quad (2.15)$$

Both σ_f^2 and σ_ϵ^2 are variances on the normalized residual scale; ℓ is measured in years. The kernel gives twice mean-square differentiable latent functions [21]. For a test input u^* , the original-scale latent posterior mean and variance are

$$\hat{\delta}(u^*) = \bar{r} + s_r \mathbf{k}_*^\top \mathbf{K}_y^{-1} \mathbf{z}, \quad (2.16)$$

$$v_\delta(u^*) = s_r^2 [k_f(u^*, u^*) - \mathbf{k}_*^\top \mathbf{K}_y^{-1} \mathbf{k}_*]. \quad (2.17)$$

Here $\mathbf{k}_*$ contains signal covariances with training inputs. Test white noise is excluded from the latent variance. The signal and noise variances on the original residual scale are $s_r^2 \sigma_f^2$ and $s_r^2 \sigma_\epsilon^2$, respectively.

For $\phi = (\sigma_f^2, \ell, \sigma_\epsilon^2)$, hyperparameters are estimated by maximizing:

$$\log p(\mathbf{z} | \phi) = -\frac{1}{2} \mathbf{z}^\top \mathbf{K}_y^{-1} \mathbf{z} - \frac{1}{2} \log |\mathbf{K}_y| - \frac{n}{2} \log(2\pi). \quad (2.18)$$

The white-noise component is a working residual-model term. It does not encode a known sampling variance of the graduated TMPI probabilities.

3. Methods

3.1. Data

This study uses TMPI 2023 published by BPJS Kesehatan [3,4]. Its construction uses JKN membership and death information over 2018–2022, linked with civil-registration information from Dukcapil. The source describes age-last-birthday exposure calculation, including a Balducci assumption, partial credibility adjustment with reference to TMI IV, and Whittaker–Henderson graduation with smoothing parameter 0.05 and degree 3 [4, pp. 13–16, 19–22]. These source-construction assumptions are distinct from the continuous residual model fitted here.

The appendices provide published probabilities, curtate expectancy, age-specific exposure, and death counts for each sex [4, pp. 47–50]. The probabilities are printed to six decimal places and expectancy to two. We use $x = 0, 1, \dots, 110$, yielding 111 annual probabilities per sex. The terminal $\hat{q}_{111} = 1$ is excluded from fitting because its cumulative-hazard transform is infinite; $e_{111} = 0$ is retained for curtate calculations. All input probabilities and expectancies were checked against the source appendices.

The input consists of *published graduated estimates*, rather than raw individual records or crude death-to-exposure ratios. No additional pre-fit smoothing is applied. The GP subsequently estimates departures of the parametric backbone from these already-processed probabilities, and therefore supplies an additional residual smoothing step. Source exposure and death counts are available, but they do not by themselves recover the uncertainty of the final credibility-adjusted and graduated probabilities. The two audited source books do not provide sampling standard errors or confidence intervals for every final $\hat{q}_x$, or their cross-age covariance. Their graduation-error summaries are not identified as such sampling variances.

Accordingly, estimation is conditional on the published table. Treating these point estimates as fixed inputs omits uncertainty from source estimation, credibility adjustment, and graduation; it can understate uncertainty about population mortality and does not justify interpreting age entries as independent raw observations. The fitted white-noise variance accounts for departures under the working residual model and is not a calibrated estimate of TMPI sampling uncertainty. Published source uncertainty is not propagated through the fitted curves.

Male and female tables are fitted separately because the objective is to reconstruct each published sex-specific curve with its own backbone and residual scale. This allows their fitted age patterns and length scales to differ without imposing a particular cross-sex covariance. Separate fitting does not assert statistical independence of the underlying populations. It forgoes borrowing information across sexes and does not account for shared source-construction uncertainty in curve differences. A joint or multi-output GP could represent common structure and cross-population covariance [17]. Such a model was not fitted here, so the design does not establish superiority over joint estimation, and differences between the two curves are descriptive rather than significance tests.

3.2. Proposed Semiparametric Model

The proposed model decomposes the log force of mortality into two additive components: a parametric backbone that captures the global mortality trend, and a GP correction that models log-space residuals. The construction proceeds in five steps for each sex and each training set.

- i. **Annual cumulative-hazard targets.** The published annual probabilities are transformed by (2.4):

$$\hat{h}_x = -\ln(1 - \hat{q}_x), \quad x \in \mathcal{I}. \quad (3.1)$$

This exact probability transformation does not assume that the final continuous force is constant within the year.

- ii. **Parametric backbone fitting.** Gompertz, HP-8, and HP-5 are fitted as three fixed specifications within two backbone families. Gompertz uses (2.9); HP-8 and HP-5 use (2.13) with annual integrated probabilities. The fitted backbone is denoted $\mu_0(t)$ and its annual cumulative hazard $h_0(x) = \int_x^{x+1} \mu_0(t) dt$. The two calibration objectives weight errors differently; neither is a direct minimization of the evaluation RMSE in q .

Gompertz has $B \in [10^{-10}, 0.1]$ and $\beta \in [0, 0.3]$. The physical HP-8 bounds are $A \in [10^{-6}, 0.05]$, $B \in [0.01, 2]$, $C \in [0.01, 3]$, $D \in [10^{-6}, 0.03]$, $E \in [0.5, 30]$, $F \in [5, 90]$ years, $G \in [10^{-7}, 0.01]$, and $H \in [1.001, 1.25]$. HP-5 uses the same bounds for A, B, C, G, H and omits D, E, F by specification. Differential Evolution in log parameters uses a maximum of 400 generations, population multiplier 12, and tolerance 10^{-6} . Four bounded least-squares refinements start from its solution and three fixed parameter vectors. The accepted converged solution has the smallest training loss among the starts; global optimality is not asserted.

HP-5 omits D, E, F by specification and is fitted separately for both sexes. HP-8 is never replaced automatically when an optimizer reaches a bound. In particular, boundary convergence of F does not establish structural non-identifiability. An exploratory training-loss profile fixes F at 15 points over $[5, 90]$ per sex and refits the remaining parameters from three starts. This diagnoses constraint dependence rather than supplying a likelihood-based confidence interval or a formal non-identifiability test. All fixed variants remain in the model comparison.

- iii. **Log-space residual computation.** The training residual target is:

$$r_x = \ln \hat{h}_x - \ln h_0(x), \quad u_x = x + 0.5. \quad (3.2)$$

Log-space correction preserves positivity of the reconstructed force [16]. Its interval interpretation follows from:

$$\int_x^{x+1} \mu_0(t) e^{\delta(t)} dt \approx e^{\delta(u_x)} h_0(x), \quad (3.3)$$

$$r_x \approx \delta(u_x) + \epsilon_x.$$

The approximation treats the log-residual correction as approximately constant over one annual interval for constructing the GP target. The backbone itself

may vary within the year. It is a working observation approximation and is not an exact nonlinear integrated-GP likelihood. Where residuals change rapidly, it may transfer within-year approximation error into the fitted GP. Annual observations alone do not identify the within-year shape; final predictions therefore use the integrated force, and midpoint-versus-integral discrepancies are reported in Section 4.3.

- iv. **Gaussian Process fitting on residuals.** A zero-mean normalized GP with the Matérn $\nu = 5/2$ signal kernel and white noise is fitted at u_x . Training-only $\bar{r}$ and s_r restore the original residual scale through (2.16)–(2.17). For Gompertz+GP, the normalized bounds are $\sigma_f^2 \in [10^{-3}, 10^3]$, $\ell \in [1, 60]$, and $\sigma_\epsilon^2 \in [10^{-5}, 0.5]$. For either HP+GP variant, they are $\sigma_f^2 \in [10^{-3}, 10^3]$, $\ell \in [0.5, 40]$, and $\sigma_\epsilon^2 \in [10^{-6}, 0.3]$. No additional diagonal alpha term is added.

Hyperparameters maximize (2.18) using bounded L-BFGS-B from one initial vector and 20 random restarts. The initial normalized vectors $(\sigma_f^2, \ell, \sigma_\epsilon^2)$ are $(1, 15, 0.01)$ for Gompertz+GP and $(1, 10, 0.005)$ for HP+GP. An unsuccessful start may receive one continuation with maximum line-search steps 50 and maximum iterations 2000. Only converged finite candidates are eligible, selected by training marginal likelihood. Base seed 42 is fixed for primary results. Each component seed is the unsigned big-endian integer represented by the first four SHA-256 bytes of the UTF-8 string `base_seed|sex|split|model|formulation|component`; the held-out probability is not used to derive it.

- v. **Continuous mortality function reconstruction.** The plug-in continuous force is:

$$\ln \hat{\mu}(t) = \ln \mu_0(t) + \hat{\delta}(t), \quad 0 \leq t \leq 111. \quad (3.4)$$

For a fixed age it is the marginal lognormal median under the conditional latent model, not the posterior arithmetic mean force. Its integral is not automatically the posterior mean or median of a derived actuarial function. Define $\hat{\mathcal{H}}(t) = \int_0^t \hat{\mu}(v) dv$. The outputs are:

$$\hat{q}(x) = 1 - \exp[-\hat{\mathcal{H}}(x+1) + \hat{\mathcal{H}}(x)], \quad (3.5)$$

$$\hat{S}(t) = \exp[-\hat{\mathcal{H}}(t)], \quad (3.6)$$

$$\hat{e}_x = \sum_{k=1}^{111-x} \exp[-\hat{\mathcal{H}}(x+k) + \hat{\mathcal{H}}(x)], \quad (3.7)$$

$$\hat{e}_x^{[111]} = \int_x^{111} \exp[-\hat{\mathcal{H}}(t) + \hat{\mathcal{H}}(x)] dt. \quad (3.8)$$

Annual $\hat{q}(x)$ covers $0 \leq x \leq 110$, while curtate $\hat{e}_x$ uses integer ages and $\hat{e}_{111} = 0$. Composite Simpson integration uses 160 subdivisions per year, checked against 320; further doubling up to 1280 is available if required. Accepted changes must be at most 10^{-8} in annual q and 10^{-4} years in expectancy. Backbone objective integration uses 32-point Gauss–Legendre quadrature checked against 64 points. A common cumulative hazard enforces the annual- q /conditional-survival identity.

A conditional pointwise 95% interval for the latent force is

$$\hat{\mu}^{\pm}(t) = \exp \left[\ln \mu_0(t) + \hat{\delta}(t) \pm 1.96 \sqrt{v_{\delta}(t)} \right]. \quad (3.9)$$

Backbone and kernel estimates are held fixed, and test white noise is excluded. These intervals omit source, backbone-parameter, and hyperparameter uncertainty; they are neither simultaneous bands nor propagated intervals for q, S, e . They describe conditional uncertainty under the fitted working model rather than sampling uncertainty in TMPI 2023. The resulting corrected models are consistently named Gompertz+GP, HP-8+GP, and HP-5+GP.

3.3. Model Evaluation

3.3.1. In-sample metrics

Full-fit accuracy at integer ages is assessed using four criteria computed on the annual integrated $\hat{q}(x)$:

$$\text{MSE} = \frac{1}{n} \sum_{x=0}^{110} (\hat{q}(x) - \hat{q}_x)^2, \quad (3.10)$$

$$\text{RMSE} = \sqrt{\text{MSE}}, \quad (3.11)$$

$$\text{MAE} = \frac{1}{n} \sum_{x=0}^{110} |\hat{q}(x) - \hat{q}_x|, \quad (3.12)$$

$$\text{MAPE} = \frac{100\%}{n} \sum_{x=0}^{110} \left| \frac{\hat{q}(x) - \hat{q}_x}{\hat{q}_x} \right|, \quad (3.13)$$

where $n = 111$ per sex and all included source probabilities are positive. MSE has probability-squared units; RMSE and MAE have probability units. These scores describe goodness-of-fit to the training table. Small errors are expected from fitting the GP to residuals of those same observations and do not establish predictive superiority.

3.3.2. Leave-One-Out Cross-Validation

LOO-CV assesses reconstruction of each missing age using the other 110 annual probabilities of the same sex. For every $i = 0, 1, \dots, 110$, the backbone is fitted anew on $\mathcal{I}_{-i}$. Residual targets, training normalization, initialization, and GP hyperparameters are then recomputed using only this set. The held-out probability enters scoring after the fitted force has been integrated over $[i, i + 1]$:

$$\varepsilon_i^{\text{LOO}} = \hat{q}^{(-i)}(i) - \hat{q}_i. \quad (3.14)$$

The absolute LOO RMSE is:

$$\text{RMSE}_{\text{LOO}} = \sqrt{\frac{1}{111} \sum_{i=0}^{110} (\varepsilon_i^{\text{LOO}})^2}. \quad (3.15)$$

The other metrics use the same held-out predictions. This is full refitting, rather than analytical LOO with full-sample residuals or fixed full-sample hyperparameters. There are no full-sample warm starts, adaptive HP substitutions, observed-target replacements, or silently discarded failed folds. A failed fit would stop the final summary and remain in the diagnostics.

All six candidates use identical held-out ages and the annual integrated- q operator. Each standalone backbone is independently calibrated on training data; its corresponding GP model adds the training-fitted residual correction to that backbone. Absolute held-out errors are compared directly with held-out benchmark errors. The LOO/in-sample RMSE ratio is not used as evidence of good generalization or absence of overfitting, particularly when the training denominator is small. The configuration was developed using full-fit and five-age pilot diagnostics at ages 0, 1, 20, 60, and 110, then frozen before complete LOO. The final scores consequently evaluate the fixed developed procedure, not an independent test of configuration selection. Moreover, source graduation can induce dependence among neighboring age estimates. The validation supports missing-age reconstruction within TMPI 2023 and does not assess new populations, calendar years, cohorts, contiguous missing-age blocks, or extrapolation beyond the modeled age range.

4. Results and Discussion

4.1. Parameter Estimation

The estimated Gompertz and Heligman–Pollard backbone parameters are reported in Table 1. Gompertz’s fitted age-gradient parameter is lower for males than for females, while its baseline parameter is larger for males. These are whole-table calibration parameters under the increasing-force specification; they should not be interpreted as accurate infant mortality estimates. Both HP variants are reported for both sexes, so their performance can be examined without a data-dependent replacement rule.

For male HP-8, the second component has $F = 8.5234$ and $E = 0.5$, the lower bound. It therefore need not correspond directly to a conventional young-adult accident hump [9,10]. For females, $F = 90$ reaches the upper bound, while B and E reach their lower bounds. The exploratory profile’s female training loss decreases toward the upper F constraint. This indicates sensitivity to the feasible region; it does not determine statistical non-identifiability or justify eliminating that component automatically. HP-5 provides a separate fixed comparison, and the fitted HP parameters are interpreted as descriptive curve parameters.

The GP hyperparameters and training residual scales are reported in Table 2. Gompertz+GP has longer fitted length scales than either HP correction, consistent with a more broadly varying correction of its restricted backbone. Its signal variance reaches the normalized upper bound 1000 and its noise variance the lower bound 10^{-5} for both sexes. The same constraints are active in all 111 Gompertz+GP LOO folds of each sex. The resulting smooth curves and narrow conditional intervals remain dependent on these bounds; convergence under the specified constraints does not establish an unconstrained optimum.

Table 1. Full-fit backbone parameters for the three fixed specifications

Model	Parameter	Male	Female
Gompertz	B	2.6974×10^{-5}	2.1861×10^{-6}
Gompertz	β	9.385×10^{-2}	1.1616×10^{-1}
HP-8	A	7.2557×10^{-3}	2.4746×10^{-3}
HP-8	B	4.392×10^{-1}	1×10^{-2L}
HP-8	C	3.4479×10^{-1}	1.6206×10^{-1}
HP-8	D	2.7593×10^{-4}	9.4382×10^{-4}
HP-8	E	5×10^{-1L}	5×10^{-1L}
HP-8	F	8.5234×10^0	9×10^{1U}
HP-8	G	1.1553×10^{-4}	6.2548×10^{-5}
HP-8	H	1.0826×10^0	1.0854×10^0
HP-5	A	2.8248×10^{-3}	2.2637×10^{-3}
HP-5	B	1×10^{-2L}	1×10^{-2L}
HP-5	C	1.6179×10^{-1}	1.5733×10^{-1}
HP-5	G	1.3342×10^{-4}	1.2359×10^{-4}
HP-5	H	1.0806×10^0	1.077×10^0

Each backbone is shared with its corresponding +GP fit. Superscripts L and U indicate active lower and upper constraints. HP-8 and HP-5 are reported separately for both sexes. Gompertz uses $\mu_0(t) = B \exp(\beta t)$.

All three corrected models follow $\ln \hat{\mu}(t) = \ln \mu_0(t) + \hat{\delta}(t)$. Table 2 distinguishes normalized kernel variances from their original-scale values and separates them from residual standard deviations. Small fitted noise describes the working residual model, rather than proving that the published probabilities are error-free or that the correction exactly interpolates annual probabilities.

4.2. Continuous Mortality Function

For the male population, Figure 1 compares published annual probabilities with the three backbones and their GP corrections. Gompertz alone cannot reproduce the initial decline in mortality, while the HP specifications allow a childhood component. The GP corrections bring the annual curves closer to the published age pattern. Agreement is evaluated through the integral over each complete annual interval; proximity of a fitted midpoint residual to its target does not ensure identical annual probability.

For the female population, Figure 2 retains both HP-8+GP and HP-5+GP alongside Gompertz+GP. The comparison treats inclusion of the HP hump component as a fixed modeling alternative, rather than declaring the component unnecessary from its boundary fit. Curves for the two sexes are descriptive reconstructions of their respective published tables; their differences are not tests based on a joint population-uncertainty model.

Table 2. Full-fit Gaussian-process hyperparameters and residual scales

A. Normalized residual scale						
Sex	Model	$\bar{r}$	s_r	σ_f^2	ℓ	σ_ϵ^2
Male	Gompertz+GP	8.4158×10^{-1}	9.6252×10^{-1}	1×10^3	4.5687×10^1	1×10^{-5}
Male	HP-8+GP	1.1536×10^{-2}	1.6208×10^{-1}	1.1836×10^0	5.4438×10^0	1×10^{-6}
Male	HP-5+GP	1.4046×10^{-2}	1.7654×10^{-1}	8.9347×10^{-1}	3.3981×10^0	9.16×10^{-4}
Female	Gompertz+GP	1.8597×10^0	1.6835×10^0	1×10^3	5.7894×10^1	1×10^{-5}
Female	HP-8+GP	1.3345×10^{-2}	2.1519×10^{-1}	9.7125×10^{-1}	5.4702×10^0	7.1442×10^{-3}
Female	HP-5+GP	1.7342×10^{-2}	2.3921×10^{-1}	1.0151×10^0	5.2611×10^0	4.2122×10^{-3}

B. Original residual scale			
Sex	Model	$s_r^2 \sigma_f^2$	$s_r^2 \sigma_\epsilon^2$
Male	Gompertz+GP	9.2644×10^2	9.2644×10^{-6}
Male	HP-8+GP	3.1096×10^{-2}	2.6271×10^{-8}
Male	HP-5+GP	2.7847×10^{-2}	2.8549×10^{-5}
Female	Gompertz+GP	2.8343×10^3	2.8343×10^{-5}
Female	HP-8+GP	4.4974×10^{-2}	3.3082×10^{-4}
Female	HP-5+GP	5.8083×10^{-2}	2.4103×10^{-4}

The kernel is $\sigma_f^2 k_{\text{Matérn } 5/2} + \sigma_\epsilon^2 I$. Panel A uses normalized residuals; Panel B restores the original log-hazard-ratio scale. Both sigma terms are variances; length scale is in years. Training normalization uses the population SD and alpha=0. Gompertz+GP reaches the signal-variance upper and noise lower bounds for both sexes; male HP-8+GP reaches its noise lower bound.

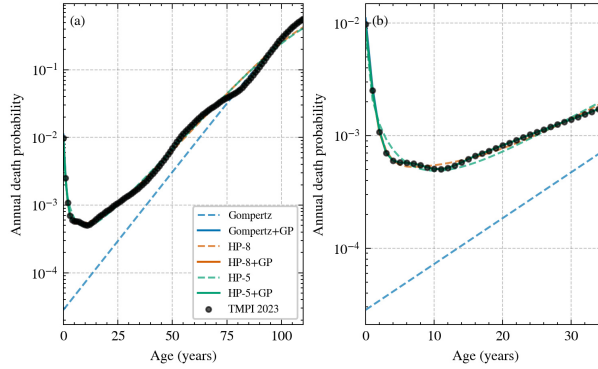


Figure. 1. Annual death probabilities for male lives: (a) ages 0–110; (b) ages 0–35. Points are published TMPI probabilities; dashed lines are backbones and solid lines include GP residual corrections. All predictions integrate the fitted force over a complete one-year interval. The log scale reveals low-age differences

4.3. Model Evaluation

Table 3 reports full-fit goodness-of-fit for all six candidates. Every GP correction has lower annual- q RMSE than its corresponding backbone. Male HP-8+GP has the lowest male full-fit RMSE, 3.28402×10^{-5} , whereas Gompertz+GP has the lowest

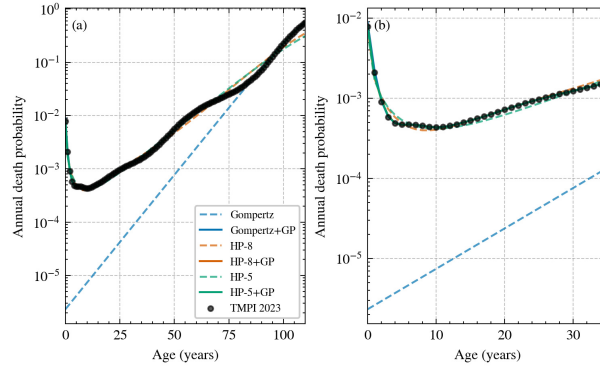


Figure. 2. Annual death probabilities for female lives: (a) ages 0–110; (b) ages 0–35. Points are published TMPI probabilities; dashed lines are backbones and solid lines include GP residual corrections. All predictions integrate the fitted force over a complete one-year interval. The log scale reveals low-age differences

female full-fit RMSE, 9.17813×10^{-5} . These scores quantify reconstruction of the training table and are not independent predictive evidence.

Table 3. Full-fit errors in annual death probabilities at ages 0–110

Sex	Model	MSE	RMSE	MAE	MAPE (%)
Male	Gompertz	3.9069×10^{-5}	6.2505×10^{-3}	4.7328×10^{-3}	4.5194×10^1
Male	HP-8	1.0139×10^{-3}	3.1841×10^{-2}	1.3261×10^{-2}	1.1761×10^1
Male	HP-5	1.2433×10^{-3}	3.526×10^{-2}	1.434×10^{-2}	1.3525×10^1
Male	Gompertz+GP	1.5399×10^{-8}	1.2409×10^{-4}	2.2621×10^{-5}	2.61×10^{-1}
Male	HP-8+GP	1.0785×10^{-9}	3.284×10^{-5}	1.343×10^{-5}	5.8×10^{-2}
Male	HP-5+GP	1.0396×10^{-8}	1.0196×10^{-4}	2.4643×10^{-5}	1.10×10^{-1}
Female	Gompertz	3.4437×10^{-5}	5.8683×10^{-3}	4.266×10^{-3}	6.2164×10^1
Female	HP-8	1.6331×10^{-3}	4.0411×10^{-2}	1.5023×10^{-2}	1.5463×10^1
Female	HP-5	2.4184×10^{-3}	4.9178×10^{-2}	1.785×10^{-2}	1.6618×10^1
Female	Gompertz+GP	8.4238×10^{-9}	9.1781×10^{-5}	1.5282×10^{-5}	2.60×10^{-1}
Female	HP-8+GP	1.5849×10^{-7}	3.9811×10^{-4}	7.606×10^{-5}	3.30×10^{-1}
Female	HP-5+GP	1.1334×10^{-7}	3.3666×10^{-4}	6.5811×10^{-5}	2.64×10^{-1}

All six candidates use the same annual integrated-q operator and 111 ages per sex. Terminal q111=1 is excluded. MSE is in probability squared; RMSE and MAE are in probability units; MAPE is a percentage. These are training goodness-of-fit scores.

Table 4 reports absolute errors from full-pipeline LOO. Gompertz+GP achieves RMSE 3.58881×10^{-5} for males and 3.24246×10^{-5} for females, compared with 0.00648539 and 0.00590577 for the corresponding refitted Gompertz benchmarks. HP-8+GP gives 0.000787188 and 0.00214314, while HP-5+GP gives 0.00175582 and 0.00223946. Thus, each correction improves on its own specified backbone under this reconstruction protocol, and Gompertz+GP has the lowest LOO RMSE among

the evaluated candidates for each sex. These are descriptive comparisons under the stated calibration objectives and bounds, not evidence of superiority over all possible parametric fits.

Table 4. Full-pipeline leave-one-age-out errors in annual death probabilities

Sex	Model	MSE	RMSE	MAE	MAPE (%)
Male	Gompertz	4.206×10^{-5}	6.4854×10^{-3}	4.8812×10^{-3}	4.5282×10^1
Male	HP-8	1.0698×10^{-3}	3.2707×10^{-2}	1.3673×10^{-2}	1.2930×10^1
Male	HP-5	1.2981×10^{-3}	3.603×10^{-2}	1.4684×10^{-2}	1.4227×10^1
Male	Gompertz+GP	1.288×10^{-9}	3.5888×10^{-5}	1.409×10^{-5}	1.87×10^{-1}
Male	HP-8+GP	6.1967×10^{-7}	7.8719×10^{-4}	1.2613×10^{-4}	9.41×10^{-1}
Male	HP-5+GP	3.0829×10^{-6}	1.7558×10^{-3}	2.7474×10^{-4}	1.186×10^0
Female	Gompertz	3.4878×10^{-5}	5.9058×10^{-3}	4.3079×10^{-3}	6.2216×10^1
Female	HP-8	1.7579×10^{-3}	4.1927×10^{-2}	1.5555×10^{-2}	1.6157×10^1
Female	HP-5	2.5271×10^{-3}	5.027×10^{-2}	1.8276×10^{-2}	1.7422×10^1
Female	Gompertz+GP	1.0514×10^{-9}	3.2425×10^{-5}	1.0931×10^{-5}	2.06×10^{-1}
Female	HP-8+GP	4.593×10^{-6}	2.1431×10^{-3}	3.277×10^{-4}	1.527×10^0
Female	HP-5+GP	5.0152×10^{-6}	2.2395×10^{-3}	3.3243×10^{-4}	1.287×10^0

All six candidates use the same annual integrated-q operator and 111 ages per sex. Terminal q111=1 is excluded. MSE is in probability squared; RMSE and MAE are in probability units; MAPE is a percentage. Each held-out age is absent from backbone fitting, residual construction, normalization and GP optimization. The task is missing-age reconstruction within the published graduated table.

The complete LOO calculation comprises 666 training-only backbone/GP pairs, corresponding to three backbone specifications, two sexes, and 111 held-out ages. Each pair supplies a backbone and corrected prediction, yielding 1332 held-out predictions over the six candidates. Saved-model audits confirmed training inputs, residual reconstruction, normalization, and optimizer acceptance. No fit bundle failed. Targeted checks with base seeds 2026 and 1729 were also run at the selected additional diagnostic age 109; they assess repeatability under the fixed procedure, rather than providing a bound-sensitivity experiment.

The annual LOO RMSE is smaller than annual full-fit RMSE for Gompertz+GP. This is compatible with GP fitting by an approximate midpoint-residual likelihood, which does not directly minimize annual integrated-q RMSE. Each refit changes both the backbone and residual curve, so there is no required ordering between the two annual scores. For male age 0 in the full fit, the published probability is 0.009791. The constant-midpoint-residual diagnostic yields 0.00977790, whereas integration of the fitted force yields 0.01106861, an error of about 0.001278. The full-fit midpoint diagnostic RMSE is about 1.606×10^{-6} , compared with the scored annual-integral RMSE 0.000124093. The principal scores retain the latter operator. This example shows that the interval approximation is consequential at infancy and should not be hidden by an aggregate error measure.

Figure 3 shows signed full-fit and LOO errors for all three GP corrections.

The largest male Gompertz+GP held-out error occurs at age 1, with magnitude 0.000237147; the largest female error occurs at age 0, with magnitude 0.000227961. HP corrections have larger boundary errors: for female HP-8+GP and HP-5+GP at age 110, their absolute errors are 0.0207017 and 0.0221113. These local discrepancies qualify the aggregate accuracy gains and motivate caution at both ends of the age range.

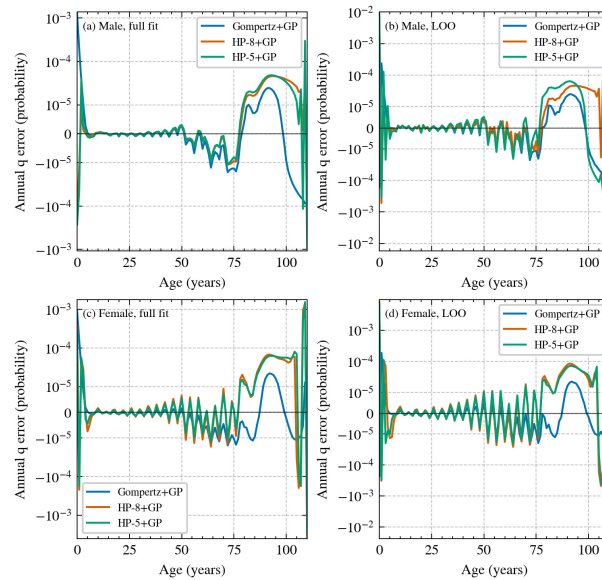


Figure 3. Signed annual- q errors for the three +GP candidates: (a,b) male and (c,d) female lives. Left panels show full-fit errors; right panels show training-only leave-one-age-out errors. The symmetric logarithmic scale is linear within ± 0.00001 . Boundary errors are retained

4.4. Survival Function and Life Expectancy

Figure 4 displays annual probability, force, survival from birth, and complete expectancy restricted to age 111. The positive force produces decreasing survival through the common cumulative hazard. Annual probabilities satisfy the conditional-survival identity to numerical precision. This internal actuarial coherence is a property of the construction; it does not imply exact agreement with every published annual probability or uniquely identify mortality between birthdays.

Table 5 compares curtate expectancy with the published curtate reference. For males, Gompertz+GP yields 73.625 years, HP-8+GP 73.752 years, and HP-5+GP 73.757 years, against 73.74 years. Their signed errors are -0.156% , $+0.017\%$, and $+0.022\%$. For females, the corresponding values are 78.281, 78.348, and 78.354 years, against 78.37 years, with errors -0.113% , -0.027% , and -0.020% .

Across all integer starting ages 0–110, curtate MAE for the six corrected sex/model cases ranges from 0.00274644 to 0.0041294 years. The largest absolute rel-

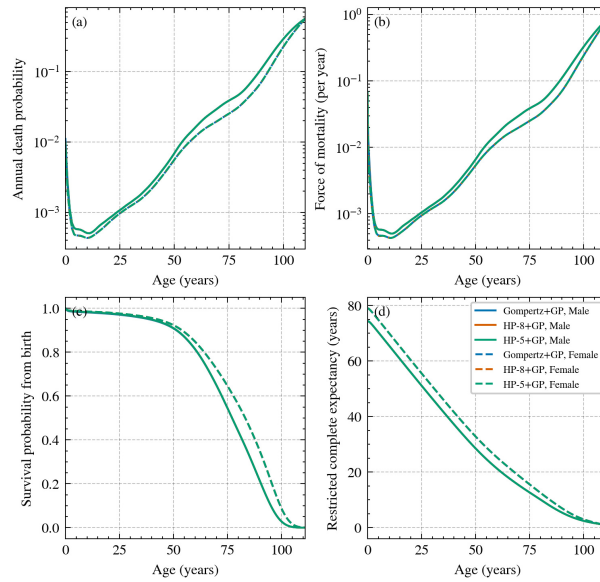


Figure. 4. Actuarial functions from each fitted cumulative hazard: (a) annual death probability; (b) force of mortality; (c) survival from birth; (d) complete expectancy restricted to age 111. Solid lines denote male lives and dashed lines female lives. Panel (d) is a restricted continuous integral, distinct from the curtate expectancy in Table 5. All curves are plug-in estimates; no continuous tail is assumed

Table 5. Curtate life expectancy compared with the published TMPI 2023 values

Male					
Age	TMPI	Gompertz+GP	HP-8+GP	HP-5+GP	
0	73.74	73.625 (-0.156)	73.752 (+0.017)	73.757 (+0.022)	
20	55.38	55.384 (+0.007)	55.382 (+0.004)	55.382 (+0.004)	
40	36.68	36.684 (+0.012)	36.683 (+0.008)	36.683 (+0.007)	
60	20.71	20.709 (-0.003)	20.708 (-0.010)	20.708 (-0.011)	
80	9.62	9.618 (-0.017)	9.618 (-0.026)	9.617 (-0.028)	
100	1.98	1.978 (-0.095)	1.978 (-0.116)	1.978 (-0.113)	
Female					
Age	TMPI	Gompertz+GP	HP-8+GP	HP-5+GP	
0	78.37	78.281 (-0.113)	78.348 (-0.027)	78.354 (-0.020)	
20	59.81	59.816 (+0.010)	59.811 (+0.002)	59.811 (+0.002)	
40	41.06	41.061 (+0.003)	41.057 (-0.007)	41.057 (-0.008)	
60	24.73	24.732 (+0.008)	24.728 (-0.008)	24.728 (-0.009)	
80	12.06	12.060 (+0.003)	12.057 (-0.022)	12.058 (-0.020)	
100	2.53	2.527 (-0.110)	2.527 (-0.129)	2.527 (-0.134)	

Expectancies are in years. Parentheses contain signed percentage errors computed before rounding. The source publishes curtate expectancy to two decimals; model values use $e_x = \sum_{k=1}^{111-x} S(x+k)/S(x)$, with $e_{111} = 0$. Complete expectancy restricted to age 111 is a separate quantity.

ative error is 1.093%, for male HP-5+GP at age 110. Short remaining lifetimes make relative errors sensitive to the source's two-decimal expectancy precision. Reconstructing source expectancy from rounded published probabilities gives birth values 73.73641 and 78.36765 years, already slightly different from the printed values. Differences in Table 5 consequently combine model discrepancy and publication rounding; they should not all be attributed to residual smoothing. Nor should the selected-age table be read as a universal bound on errors.

The framework also evaluates mortality at non-integer ages within its defined domain. For illustration, male Gompertz+GP yields $\hat{q}(50.5) = 0.0073219$ for the complete interval $[50.5, 51.5]$. This is a model-implied probability, not an observed fractional-age TMPI datum. Such inputs can support actuarial calculations over the covered ages $[1, 11]$; use beyond age 111 would require a continuous-tail assumption.

4.5. Comparison with Existing Studies

Table 6 retains the four cited TMPI studies and their reported evaluation contexts. Putra et al. [5] fit central death rates with terminal-inclusive ranges, so their reported RMSE is not a matched reconstruction score for the present integrated annual- q target. Amalia et al. [6] report a response plotted as m_x over ages 30–90, with a transformation insufficiently specified for an exact matched comparison. Sari et al. [7] construct a separate 2018–2021 participant table before comparison with TMPI; its reported MSE values were verified through the publisher-deposited abstract, without access to the full publisher PDF. Alibazah and Prabowo [8] evaluate survival over ages 59–111, which differs from annual-probability evaluation over ages 0–110.

Table 6. Verified reported literature results and their evaluation contexts

Study	Metric	Ages	Male	Female
Putra et al. [5]	RMSE(q)	0-111; also 35-100	7.461×10^{-3}	Not verified
Amalia et al. [6]	RMSE(m_x)	Figure: 30-90	2.959×10^{-3}	1.777×10^{-3}
Sari et al. [7]	MSE (abstract)	Not verified	5.6×10^{-2}	5.5×10^{-2}
Alibazah and Prabowo [8]	RMSE(S)	59-111	1.77192×10^{-2}	3.08751×10^{-2}

These are reported source values, not reproduced or matched benchmarks. Putra fits central death rates and includes the terminal age; its exact female RMSE is not numerically tabulated. Amalia plots ages 30–90 with a response labelled m_x , whose transformation is under-specified. Sari constructs a separate 2018–2021 participant table; only its publisher-deposited abstract was accessible. Alibazah and Prabowo fit survival over ages 59–111. These metrics do not establish superiority over the cited studies; the controlled comparison is in Tables 3–4.

The source audit does not certify an exact female Putra RMSE from its unlabelled figure bars. That entry is marked unverified rather than replaced with

an inferred number. These results provide literature context and are not presented as reproduced benchmarks or ranked against our LOO scores. Controlled accuracy comparisons use Tables 3–4, where the same data, age splits, and output operator apply. The cited studies remain relevant to parametric modelling of Indonesian mortality without supporting universal cross-study improvement ratios.

4.6. Assumptions and Limitations

The results depend on three distinctions. First, the published table is already credibility-adjusted and graduated. Conditioning on its point estimates permits reproducible curve reconstruction, but omits source-estimation and cross-age covariance uncertainty. Second, the interval-residual observation approximation and chosen continuous HP proxy impose within-year structure that annual data do not identify uniquely. Third, LOO measures reconstruction in this same table under a developed, frozen configuration. It does not establish generalization to new population experience or assess the complete configuration-selection process.

The fixed bounds and separate-sex design also affect interpretation. Active HP and GP constraints limit claims about optimal parameters and interval robustness; the seed checks do not quantify uncertainty under alternative bounds. Separate fits neither borrow cross-sex information nor estimate the covariance of sex differences. A joint model could address sharing, and source-aware uncertainty would require an observation model for the graduated estimates. These extensions have not been evaluated, and their gains cannot be inferred from the present curves.

The conditional intervals describe uncertainty in the latent residual function with fitted backbone and kernel parameters fixed. They should not be used as population confidence intervals or as uncertainty bounds for integrated probabilities, survival, or expectancy. Actuarial use therefore requires the same age-domain and tail qualifications as the point estimates, together with a separate treatment of uncertainty relevant to the application.

5. Conclusion

This study proposed a semiparametric framework for constructing continuous mortality functions from TMPI 2023. The framework combines a Gompertz or Heligman–Pollard backbone with a Gaussian Process correction of log-space residuals. Fixed HP-8 and HP-5 variants are evaluated for both sexes. The resulting Gompertz+GP, HP-8+GP, and HP-5+GP curves supply a positive continuous force and coherent survival on $[0, 111]$, annual probabilities on starting ages $[0, 110]$, curtate expectancy, and complete expectancy restricted to age 111.

Four principal conclusions are drawn. First, all three GP corrections reduce absolute LOO RMSE relative to their own training-refitted backbones. Gompertz+GP achieves the lowest LOO RMSE among the evaluated candidates, 3.58881×10^{-5} for males and 3.24246×10^{-5} for females. These comparisons concern the specified calibration objectives, parameter bounds, and missing-age reconstruction task.

Second, refitting the backbone, residual targets, normalization, and GP hyperparameters for each held-out age provides a validation procedure consistent with the stated training pipeline. Small in-sample errors and near-one LOO/in-sample ratios do not establish predictive superiority. Source graduation, configuration development on the same table, and boundary errors limit the interpretation of the held-out scores.

Third, survival and expectancy calculations share the same cumulative hazard. Birth curtate-expectancy errors are below 0.16% in absolute value for all six corrected sex/model cases, while the largest all-age relative error is 1.093%. The comparison distinguishes curtate from restricted complete expectancy and accounts for the published precision of the reference values.

Fourth, the framework supplies mortality inputs at fractional ages within its domain, with conditional pointwise intervals for the latent force. Within-year residual approximation, active constraints, and omitted source and parameter uncertainty prevent interpreting these intervals as complete mortality uncertainty. A joint multi-population extension, source-aware uncertainty modelling, and an exact integrated observation model are natural directions for future research. Their evaluation would complement the bounded reconstruction evidence presented here.

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Bibliography

- [1] Bowers, N.L., Gerber, H.U., Hickman, J.C., Jones, D.A., Nesbitt, C.J., 1997, *Actuarial Mathematics*, 2nd, Society of Actuaries, Schaumburg, IL
- [2] Dickson, D.C., Hardy, M.R., Waters, H.R., 2020, *Actuarial Mathematics for Life Contingent Risks*, 3rd, Cambridge University Press, Cambridge
- [3] Ruby, M., Simanjuntak, B.S.P., Falihin, M.M.A., Setiawan, A., Mansur, R., Yenny, Cerinda, M., Rusanti, F., Hasibuan, W.S., Sormin, S., Magfirah, A.C., Kalla, M.I., Prabaswara, R., 2023, *Pengantar Tabel Mortalitas dan Morbiditas Penduduk Indonesia: Volume 1*, 2023, BPJS Kesehatan, Jakarta, Indonesia, ISSN 3046-5664; edited by RR. Kurnia Novita Sari and Antokalina Sari Verdiana
- [4] Ruby, M., Simanjuntak, B.S.P., Falihin, M.M.A., Setiawan, A., Mansur, R., Yenny, Cerinda, M., Rusanti, F., Hasibuan, W.S., Sormin, S., Magfirah, A.C., Kalla, M.I., Prabaswara, R., 2023, *Tabel Mortalitas Penduduk Indonesia: Volume 1*, 2023, BPJS Kesehatan, Jakarta, Indonesia, ISSN 3032-4017; edited by RR. Kurnia Novita Sari and Antokalina Sari Verdiana
- [5] Putra, M.R.A., Nurjannah, N., Kurniawaty, M., 2025, Estimation of Gompertz Mortality Parameter Models on Indonesian Population Mortality Table 2023, *CAUCHY: Jurnal Matematika Murni dan Aplikasi*, Vol. 10: 545-555
- [6] Amalia, S., Siallagan, C.J., Maulana, B., 2025, Dekomposisi Kesenjangan Harapan Hidup Laki-laki dan Perempuan dan Pemodelan Mortalitas Gompertz-Makeham pada TMPI-23, *Reliability: Journal of Industrial Statistics*, Vol. 1: 79-90

- [7] Sari, K.N., Arfan, N., Dzakiya, A., Rusli, J.G., 2025, Construction of Mortality Rate Using Heligman Pollard Model, in ITM Web of Conferences, Vol. 75, p. 04003, EDP Sciences
- [8] Dei Alibazah, T., Prabowo, A., 2025, Comparison of Estimation Methods for the Weibull Distribution in Indonesian Life Tables, *Indonesian Actuarial Journal*, Vol. 1: 185–202
- [9] Heligman, L., Pollard, J.H., 1980, The Age Pattern of Mortality, *Journal of the Institute of Actuaries*, Vol. 107: 49–80
- [10] Tabeau, E., van den Berg Jeths, A., Heathcote, C., eds., 2001, *Forecasting Mortality in Developed Countries: Insights from a Statistical, Demographic and Epidemiological Perspective*, Vol. 9 of *European Studies of Population*, Springer, Dordrecht
- [11] Promislow, S.D., 2014, *Fundamentals of Actuarial Mathematics*, 3rd, John Wiley & Sons
- [12] London, D., 1988, *Survival Models and Their Estimation*, ACTEX Publications
- [13] Williams, C.K., Rasmussen, C.E., 2006, *Gaussian Processes for Machine Learning*, Adaptive Computation and Machine Learning, MIT Press, Cambridge, MA
- [14] Deprez, P., Shevchenko, P.V., Wüthrich, M.V., 2017, Machine learning techniques for mortality modeling, *European Actuarial Journal*, Vol. 7: 337–352
- [15] Nascimento, J.D., Escovedo, T., 2021, Construction of mortality tables using LSTM neural networks, in Simpósio Brasileiro de Sistemas de Informação (SBSI), SBC
- [16] Ludkovski, M., Risk, J., Zail, H., 2018, Gaussian process models for mortality rates and improvement factors, *ASTIN Bulletin: The Journal of the IAA*, Vol. 48: 1307–1347
- [17] Huynh, N., Ludkovski, M., 2021, Multi-output Gaussian processes for multi-population longevity modelling, *Annals of Actuarial Science*, Vol. 15: 318–345
- [18] Risk, J., Ludkovski, M., 2024, Expressive mortality models through Gaussian process kernels, *ASTIN Bulletin: The Journal of the IAA*, Vol. 54: 327–359
- [19] Gompertz, B., 1825, On the nature of the function expressive of the law of human mortality, and on a new mode of determining the value of life contingencies, *Philosophical transactions of the Royal Society of London*, Vol. 115: 513–583
- [20] Storn, R., Price, K., 1997, Differential evolution—a simple and efficient heuristic for global optimization over continuous spaces, *Journal of global optimization*, Vol. 11: 341–359
- [21] Stein, M.L., 1999, *Interpolation of Spatial Data: Some Theory for Kriging*, Springer Series in Statistics, Springer, New York