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# Multi-population modelling and forecasting life-table death counts

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#### Abstract

When modelling the age distribution of death counts for multiple populations, we ought to consider three features: (1) how to incorporate any possible correlation among multiple populations to improve point and interval forecast accuracy through multi-population joint 7 modelling, (2) how to forecast age distribution of death counts so that the forecasts are 8 non-negative and have a constrained integral. (3) how to construct a prediction interval that 9 is well-calibrated in terms of coverage. Within the framework of compositional data analysis, 10 we apply a log-ratio transform to transform a constrained space into an unconstrained space. 11 We apply multivariate and multilevel functional time series methods to forecast period life-12 table death counts in the unconstrained space. Through the inverse log-ratio transformation, 13 the forecast period life-table death counts are obtained. Using the age-specific period 14 life-table death counts in England & Wales and Sweden obtained from Human Mortality 15 Database (2022), we investigate one-step-ahead to 30-step-ahead point and interval forecast 16 accuracies of the proposed models and make our recommendations. 17

Keywords: age distribution of death counts; compositional data analysis; functional principal
 component analysis; log-ratio transformation; multivariate and multilevel functional principal
 component regression

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<sup>22</sup> JEL code: C14, C32, J11

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#### Introduction 1 23

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Actuaries and demographers have been interested in developing methods for mortality fore-24 casting for many years. In particular, actuaries have produced mortality forecasts since the 25 beginning of the 20<sup>th</sup> century in response to the adverse financial effects of mortality improve-26 ments overtime on life annuities and pensions (Pollard 1987). In the literature on human 27 mortality, three functions are generally studied: hazard function, survival function and proba-28 bility density function. These three functions are complementary; knowing any one of them 29 allows us to uniquely derive the other two (for detail on the life table and its indicators, see 30 Preston et al. (2001), Chapter 3, or Dickson et al. (2009), Chapters 2–3). 31

Several authors have proposed new approaches for forecasting the age-specific hazard 32 function (i.e., central mortality rates) using statistical models (see, e.g., Booth 2006, Booth and 33 Tickle 2008, Cairns et al. 2008, Shang et al. 2011, for reviews). Instead of modelling central 34 mortality rates, we consider modelling the life-table death distribution (see, e.g., Basellini et al. 35 2020). Observed over time, we could model and forecast a redistribution of the density of 36 life-table deaths, where deaths at younger ages are shifted towards older ages. In addition 37 to providing a very informative description of the mortality experience of a population, the 38 life-table death counts yield readily available information on 'central longevity indicators' (i.e., 39 mean, median and mode age at death, see Cheung et al. 2005, Canudas-Romo 2010), as well as 40 lifespan variability (for example, standard deviation or inter-quartile range, see Robine 2001, 41 Vaupel et al. 2011, Horiuchi et al. 2013, van Raalte and Caswell 2013, van Raalte et al. 2014, 42 Aburto and van Raalte 2018).

Within the analysis of life-table death counts, we may consider both cohort and period life 44 tables. The period life table represents the mortality conditions in a period (see also Oeppen 45 2008, Bergeron-Boucher et al. 2017, 2018). The cohort life table depicts the life history of a specific 46 group of individuals. Still, it is dependent on projected mortality rates for those cohorts born 47 more recently than around 100 years ago. Cohort mortality developments are observed, and 48 they may differ from those of the synthetic cohorts assumed in period life tables (Goldstein and 49 Wachter 2006). Unlike the period data, the cohort data are partially complete, which presents a 50 challenge. 51

Many methods proposed for completing cohort-based life tables depend on parametric 52 models, which are fitted to the incomplete cohort data and then extrapolated beyond the 53 truncation age. As noted by Booth and Tickle (2008), P-spline regression methods seem to 54 provide a promising approach, and, in this context, one could apply the method of Rizzi et al. 55 (2021) who have proposed a penalised composite link model to complete the mortality profile. 56

With the completed mortality profile, statistical methods used for modelling and forecasting period life-table death counts are applicable. Whether we are considering a period or cohort life table, the age-specific death counts can be naturally viewed as a probability density function, an example of compositional data. Without deviating from our methodological contributions, we focus on period life table results and present cohort life table results in a supplement.

In a novel approach that differs from early work of Bergeron-Boucher et al. (2018), Kokoszka 62 et al. (2019), Shang and Haberman (2020) and Zhang et al. (2022), we jointly model and forecast 63 the age distribution of life-table death counts for multiple populations to capture correlations 64 among multiple series and improve forecast accuracy. Multiple-population modelling and 65 forecasting have attracted increasing attention in actuarial science (see, e.g., Jarner and Kryger 66 2011, Cairns et al. 2011, Dowd et al. 2011, Russolillo et al. 2011, Hatzopoulos and Haberman 67 2013, Villegas et al. 2017) and demography (see, e.g., Li and Lee 2005, Hyndman et al. 2013). Our 68 extension links multiple-population forecasting methods with the compositional data analysis 69 (CoDa) framework (see also, Shang and Kearney 2022, Bergeron-Boucher et al. 2018). In this 70 paper, multiple populations refer to the female and male life-table death counts. 71

We also consider a nonparametric bootstrap method for constructing prediction intervals of life-table death counts. The procedure exploits a univariate autoregressive representation of the time series of principal component scores appearing in the functional principal component analysis of the functional process. Via the CoDa transformation, the bootstrap method generates functional replicates that mimic the temporal dependence of the (original) unconstrained functional time series.

To demonstrate our proposed CoDa methods, we conduct a comprehensive analysis of the 78 age- and sex-specific period life-table death counts from 1841 to 2018 in England & Wales. We 79 evaluate and compare the one- to 30-step-ahead forecast accuracy between the CoDa methods 80 for independently and jointly modelling multiple populations. To evaluate point forecast 81 accuracy, we use the mean absolute percentage error (MAPE), Kullback-Leibler divergence, and 82 two variants of the Jensen-Shannon divergence. The latter three measures are commonly used 83 to evaluate density estimation accuracy. To assess the interval forecast accuracy, we consider the 84 coverage probability difference between the empirical and nominal coverage probabilities and 85 mean interval score of Gneiting and Raftery (2007) and Gneiting and Katzfuss (2014); refer to 86 Section 6.1 for details. To provide reliable recommendations, we additionally evaluate the point 87 and interval forecast accuracy on period life-table death counts in Sweden in Section 7. We also 88 model cohort life-table death counts in both England & Wales and Sweden in the supplementary 89 material. 90

<sup>91</sup> The remainder of this paper is organised as follows: Section 2 describes the age- and sex-

specific period life-table death counts from 1841 to 2018 in England & Wales. Sections 3 and 4 92 couple the CoDa with multivariate and multilevel functional time series forecasting methods of 93 Shang and Kearney (2022) for producing the point and interval forecasts of the age distribution 94 of life-table death counts. Section 5 studies the goodness-of-fit of a CoDa extension. Using the 95 point and interval forecast error criteria in Section 6, we evaluate and compare the one- to 30-96 step-ahead point and interval forecast accuracy among the methods considered. Section 7 also 97 presents the forecasting results on the period life-table death counts in Sweden. Conclusions 98 are summarised in Section 8, along with some reflections on how the methods presented here 99 can be further extended. 100

#### **2** Age-distribution of death counts

We consider age- and sex-specific life-table death counts from 1841 to 2018 in England & Wales, 102 obtained from the Human Mortality Database (2022). We study life-table death counts, where 103 the life table radix (i.e., a population experiencing 100,000 births annually) is fixed at 100,000 104 at age 0 for each year. For the life-table death counts, there are 111 ages, and these are age 105 0, 1, ..., 109, 110+. Due to rounding, there are zero counts for age 110+ at some years. To rectify 106 this problem, we prefer to use the probability of dying and the life table radix to recalculate 107 our estimated death counts (up to 6 decimal places). In doing so, we obtain more precise death 108 counts than the ones reported in the Human Mortality Database (2022). To some extent, the 109 probability of dying relies on smooth rates (see the Human Mortality Database 2022, protocol 110 for detail). 111



**Figure 1:** Rainbow plots of age-specific period life-table death count from 1841 to 2018 in a single-year group in England & Wales. The oldest years are shown in red, with the most recent years in violet. Curves are ordered chronologically according to the colours of the rainbow.

To understand the principal features of the data, Figure 1 presents rainbow plots of the female and male age-specific period life-table death counts in England & Wales from 1841 to 2018 in a single-year group.

In the male population, there are a few bumps in the death counts between age 20 and 40 for cohorts between 1900 and 1920 due to the First and Second World Wars. Apart from that, both sub-figures demonstrate a decreasing trend in infant death counts and a typical negatively skewed distribution for the life-table death counts, where the peaks shift to higher ages for both females and males. This shift is a primary driver of the longevity risk, which is a major issue for insurers and pension funds, especially in the selling and risk management of annuity products (see Denuit et al. 2007, for a discussion).

The spread of the distribution indicates lifespan variability. A decrease in variability over time can be observed directly. It can be measured, for example, with the interquartile range of life-table ages at death or the Gini coefficient (for comprehensive reviews, see Wilmoth and Horiuchi 1999, Shkolnikov et al. 2003, van Raalte and Caswell 2013, Debón et al. 2017). Figure 2 presents an example where the age-at-death distribution provides important insights on longevity and lifespan variability that cannot be grasped directly from an examination of either the central mortality rate or the survival function.



Figure 2: Gini coefficients for period female and male life-table death count from 1841 to 2018.

From Figure 2, the effects of the first and second World Wars are apparent for the male data based on Gini's coefficient. For the female data, there is a sudden drop around 1918 which possibly relates to the Spanish flu.

### <sup>132</sup> 3 Constrained functional time-series forecasting methods

Density functions are non-negative functions that integrate into one. They naturally share 133 some features with compositional data (see, e.g., Aitchison 1986, Pawlowsky-Glahn et al. 2015). 134 Compositional data arise in many scientific fields, such as geology (geochemical elements), 135 economics (income/expenditure distribution), medicine (body composition), the food industry 136 (food composition), chemistry (chemical composition), agriculture (nutrient balance bionomics), 137 environmental science (soil contamination), ecology (abundance of different species) and de-138 mography (life-table death counts). In statistics, Scealy et al. (2017) use CoDa to study the 139 concentration of chemical elements in sediment or rock samples. Scealy and Welsh (2017) apply 140 CoDa to analyse total weekly expenditure on food and housing costs for households in a chosen 141 set of domains. Delicado (2011), Kokoszka et al. (2019) and Shang and Haberman (2020) use 142 CoDa to analyse density functions and implement dimension-reduction techniques on the 143 constrained compositional data space. In demography, Oeppen (2008) and Bergeron-Boucher 144 et al. (2017) put forward a principal component approach to forecast life-table death counts 145 within a CoDa framework by considering age-specific life-table death counts as compositional 146 data. 147

For a given period *t*, compositional data are defined as a random vector of *I* non-negative components,  $[\mathcal{X}_t(u_1), \ldots, \mathcal{X}_t(u_I)]$ , whose sum is a specified constant, set typically equal to 1 (portion), 100 (percentage) or 10<sup>6</sup> for parts per million (ppm) in geochemical trace element compositions (Aitchison 1986, p.1). Between the positivity and summability constraints, the sample space of compositional data is thereby a simplex

$$\mathcal{S}^{I} = \left\{ \left[ \mathcal{X}_{t}(u_{1}), \ldots, \mathcal{X}_{t}(u_{I}) \right]^{\top}, \quad \mathcal{X}_{t}(u_{i}) > 0, \quad \sum_{i=1}^{I} \mathcal{X}_{t}(u_{i}) = c \right\}, \qquad t = 1, \ldots, n,$$

where *u* denotes a continuum, such as age, *S* denotes a simplex, *c* is a fixed constant,  $^{\top}$  denotes vector transpose, and the simplex sample space is a *I* – 1 dimensional subset of real-valued space  $\mathcal{R}^{I}$ .

In the CoDa framework, the standard approach involves breaking the summability constraint using a transformation of the raw data to remove the constraint before applying conventional statistical techniques to the transformed data in an unconstrained space. Among many possible transformations, the centred log-ratio transformation is commonly used (Aitchison and Shen 1980, Aitchison 1982, 1986). The algorithm for implementing the CoDa method consists of the following steps:

#### 157 1) Compute the geometric mean function

$$\alpha_n^j(u) = \exp\left\{\frac{1}{n}\sum_{t=1}^n \ln[\mathcal{X}_t^j(u)]\right\}, \qquad j = 1, \dots, J,$$
(1)

where  $ln(\cdot)$  denotes natural logarithm, and j denotes a population index in our multiple population setting; here, we consider J = 2 representing the female and male data. We treat age as a continuum  $u \in [0, 110]$  although age is observed at discrete points, and set

$$s_t^j(u) = \frac{\mathcal{X}_t^j(u) / \alpha_n^j(u)}{\int_{\nu=0}^{110} \mathcal{X}_t^j(\nu) / \alpha_n^j(\nu) d\nu}$$

<sup>158</sup> The geometric mean standardises the ranges so that no range dominates the weighting.

<sup>159</sup> 2) Apply the centred log-ratio transformation given by

$$\beta_t^j(u) = \ln\left(\frac{s_t^j(u)}{g_t^j}\right),\tag{2}$$

where  $g_t^j$  is the geometric mean given by

$$g_t^j = \exp\left\{\int_{u=0}^{110} \ln[s_t^j(u)]du\right\}.$$

The log-ratio transformation in (2) removes the constraints on  $\mathcal{X}_t^j(u)$ . For a given population j,  $\beta_t^j(u)$  can be viewed as an unconstrained functional time series, and we present three methods below for modelling and forecasting multi-population functional time series.

<sup>164</sup> 3a) Univariate functional principal component (FPC) decomposition (see, e.g., Kokoszka et al. <sup>165</sup> 2019, Shang and Haberman 2020): Apply functional principal component analysis (FPCA) <sup>166</sup> to the transformed data  $\beta^{j}(u) = {\beta_{1}^{j}(u), ..., \beta_{n}^{j}(u)}$ , i.e., compute the Karhunen-Loève <sup>167</sup> expansion of a functional realisation

$$\beta_t^j(u) = \sum_{\ell=1}^n \widehat{\gamma}_{t,\ell}^j \widehat{\phi}_\ell^j(u) = \sum_{\ell=1}^{L_j} \widehat{\gamma}_{t,\ell}^j \widehat{\phi}_\ell^j(u) + \widehat{\varpi}_t^j(u), \tag{3}$$

where  $\widehat{\varpi}_{t}^{j}(u)$  denotes model residual function for the  $j^{\text{th}}$  population at age u and year t,  $[\widehat{\phi}_{1}^{j}(u), \ldots, \widehat{\phi}_{L_{j}}^{j}(u)]$  are the first  $L_{j}$  estimated FPCs, and  $(\widehat{\gamma}_{t,1}^{j}, \ldots, \widehat{\gamma}_{t,L_{j}}^{j})$  are their scores at year t.

We determine  $L_i$  by three eigenvalue ratio criteria (see Ahn and Horenstein 2013, Li et al.

2020). The first one is known as the eigenvalue ratio (ER) estimator, which is simply obtained by maximising the ratio of two adjacent eigenvalues of  $\beta^j (\beta^j)^\top / (nI)$  arranged in descending order, where  $\beta^j = [\beta^j(u_1), \dots, \beta^j(u_I)]$  and *I* denotes the total number of discrete grid points:

$$\mathrm{ER}(\ell) = \frac{\tilde{\mu}_{nI,\ell}}{\tilde{\mu}_{nI,\ell+1}}, \qquad \ell = 1, 2, \dots, Lmax.$$

The second criterion function, known as the growth ratio (GR), is given by

$$\mathrm{GR}(\ell) = \frac{\ln(1+\tilde{\mu}^*_{nI,\ell})}{\ln(1+\tilde{\mu}^*_{nI,\ell+1})},$$

where

$$\tilde{\mu}_{nI,\ell}^* = \frac{\mu_{nI,\ell}}{\sum_{s=\ell+1}^{\min(n,I)} \tilde{\mu}_{nI,s}}$$

The optimal number  $L_i$  is selected as

$$L_{j} = \max \Big\{ \underset{1 \le \ell \le Lmax}{\operatorname{argmax}} \operatorname{ER}(\ell), \underset{1 \le \ell \le Lmax}{\operatorname{argmax}} \operatorname{GR}(\ell) \Big\}.$$
(4)

In general, the *Lmax* is a pre-specified positive integer, which can be set as  $Lmax = \#\{\ell | \tilde{\mu}_{nI,\ell} \ge \sum_{\ell=1}^{n} \tilde{\mu}_{nI,\ell} / n, \ell \ge 1\}$ . In other words, *Lmax* counts the number of eigenvalues, which is greater than the sum of all eigenvalues divides by sample size.

The third criterion estimates the number of components as the integer minimising ratios
 of two adjacent eigenvalues given by

$$L_{j} = \operatorname*{argmin}_{1 \le \ell \le Lmax} \left\{ \frac{\tilde{\mu}_{\ell+1}}{\tilde{\mu}_{\ell}} \times \mathbb{1} \left( \frac{\tilde{\mu}_{\ell}}{\tilde{\mu}_{1}} \ge \theta \right) + \mathbb{1} \left( \frac{\tilde{\mu}_{\ell}}{\tilde{\mu}_{1}} < \theta \right) \right\},$$
(5)

where  $\theta$  is a pre-specified small positive number, which can be set as  $\theta = 1/\ln[\max(\tilde{\mu}_1, n)]$ and  $\mathbb{1}(\cdot)$  is the binary indicator function.

- <sup>179</sup> By taking a conservative view, the actual number of retained FPCs is more likely to be <sup>180</sup> within the maximum of the estimated numbers of retained components in (4) and (5).
  - 3b) Multivariate FPC decomposition: We stack the unconstrained data  $[\beta_t^1(u), \beta_t^2(u)]$  into a long vector of functional time series  $\beta_t(u) = [\beta_t^1(u), \beta_t^2(u)]$ . Computationally,  $\beta^j(u)$  is a matrix of  $n \times I$ , then  $\beta(u)$  is a matrix of  $n \times (2I)$ . Then, we apply FPCA to the transformed data matrix  $\beta(u) = [\beta_1(u), \dots, \beta_n(u)]$ , i.e., compute the Karhunen-Loève expansion of a

functional realisation

$$\beta_t^j(u) = \sum_{\ell=1}^n \widehat{\gamma}_{t,\ell}^j \widehat{\phi}_\ell^j(u) \approx \sum_{\ell=1}^L \widehat{\gamma}_{t,\ell}^j \widehat{\phi}_\ell^j(u)$$

<sup>181</sup> where  $[\hat{\phi}_{1}^{j}(u), \dots, \hat{\phi}_{L}^{j}(u)]$  are the first *L* estimated FPCs extracted from the variance-<sup>182</sup> covariance of the *stacked* functional time series, and  $(\hat{\gamma}_{\ell,1}^{j}, \dots, \hat{\gamma}_{\ell,L}^{j})$  are their corresponding <sup>183</sup> scores for the *j*<sup>th</sup> population. For the first population, we truncate the first *I* elements; for <sup>184</sup> the second population, we truncate the second *I* elements. The optimal number of *L* is <sup>185</sup> determined by the eigenvalue ratio criteria in (4).

3c) Multilevel FPC decomposition: We can model  $\beta_t^j(u)$  via a multilevel FPCA. We seek to find a common pattern shared among populations and a series-specific pattern for each *j* series. Mathematically, the multilevel FPC regression can be expressed as

$$\beta_t^j(u) = U_t(u) + R_t^j(u) + e_t^j(u),$$

where  $U_t(u)$  denotes a common trend, such as the average of all series;  $R_t^j(u)$  denotes a series-specific trend, and  $e_t^j(u)$  denotes an error term. The common trend  $U_t(u)$  can be a simple average of  $\beta_t^{(1)}(u)$  and  $\beta_t^{(2)}(u)$  (see, e.g., Li and Lee 2005, Shang 2016). The common trend and series-specific trend can be modelled via a two-stage FPC analyses,

$$U_t(u) = \sum_{k=1}^{K} \widehat{\gamma}_{t,k} \widehat{\phi}_k(u)$$
$$R_t^j(u) = \sum_{l=1}^{L} \widehat{\iota}_{t,l}^j \widehat{\psi}_l^j(u),$$

where *K* and *L* denote the number of retained components,  $[\hat{\phi}_1(u), \ldots, \hat{\phi}_K(u)]$  denotes the estimated FPCs for the common trend, while  $[\hat{\psi}_1^j(u), \ldots, \hat{\psi}_L^j(u)]$  denotes the estimated FPCs for the population-specific trend,  $(\hat{\gamma}_{t,1}, \ldots, \hat{\gamma}_{t,K})$  denotes the estimated principal component score for period *t*, while  $(\hat{i}_{t,1}^j, \ldots, \hat{i}_{t,L}^j)$  denotes the estimated principal component score for period *t*. The optimal numbers of *K* and *L* are determined by the eigenvalue ratio criteria in (4).

An important parameter is the proportion of variability explained by the aggregate data,
 which is the variance explained by the within-cluster variability (Di et al. 2009). A possible
 measure of within-cluster variability is given by

$$\frac{\sum_{k=1}^{\infty} \lambda_k}{\sum_{k=1}^{\infty} \lambda_k + \sum_{l=1}^{\infty} \lambda_l^j} = \frac{\int_{u=0}^{110} \operatorname{Var}[\boldsymbol{R}(u)] du}{\int_{u=0}^{110} \operatorname{Var}[\boldsymbol{R}(u)] du + \int_{u=0}^{110} \operatorname{Var}[\boldsymbol{U}^j(u)] du},\tag{6}$$

where  $\lambda_k$  represents the  $k^{\text{th}}$  eigenvalue of the common trend, and  $\lambda_l^j$  represents the  $l^{\text{th}}$ eigenvalue of the population-specific trend. When the common factor can explain the primary mode of total variability, the value of within-cluster variability is close to 1.

4) Forecast the FPC scores. Using a univariate time series forecasting method, we obtain the *h*-step-ahead forecast  $\hat{\gamma}_{n+h|n,\ell}^{j}$  of the  $\ell^{\text{th}}$  principal component score (see, e.g., Hyndman and Shang 2009, Aue et al. 2015). Conditioning on the estimated principal components and observed data, the forecast of  $\beta_{n+h}^{j}(u)$  is given by

$$\widehat{\beta}_{n+h|n}^{j}(u) = \sum_{\ell=1}^{L_{j}} \widehat{\gamma}_{n+h|n,\ell} \widehat{\phi}_{\ell}^{j}(u).$$
(7)

Similarly, the principal component scores in the multivariate and multilevel FPC decompo sitions can be obtained by a univariate or multivariate time series forecasting method. We
 consider four commonly used univariate time series forecasting methods (see Section 6).
 These methods can model the possible presence of nonstationarity in each set of principal
 component scores.

5) Transform back to the compositional data, i.e., take the inverse centred log-ratio transformation given by

$$\hat{s}_{n+h|n}^{j}(u) = \frac{\exp[\beta_{n+h|n}^{j}(u)]}{\int_{u=0}^{110} \exp[\hat{\beta}_{n+h|n}^{j}(u)]du'},$$

207

where  $\hat{\beta}_{n+h|n}^{j}(u)$  denotes the forecasts in (7).

6) Finally, we add back the geometric means to obtain the forecasts of the density function

$$\widehat{\mathcal{X}}_{n+h|n}(u) = \frac{\widehat{s}_{n+h|n}^{j}(u)\alpha_{n}^{j}(u)}{\int_{u=0}^{110}\widehat{s}_{n+h|n}^{j}(u)\alpha_{n}^{j}(u)du}$$

where  $\alpha_n^j(u)$  is the geometric mean function given in (1).

### **209 4 Nonparametric bootstrap**

Prediction intervals are a valuable tool for assessing the probabilistic uncertainty associated with point forecasts. The forecast uncertainty stems from systematic deviations (e.g., parameter and model uncertainty) and random fluctuations (e.g., due to the model error term). As pointed out by Chatfield (2000, Chapter 7), it is essential in both demographic and actuarial applications to provide interval forecasts as well as point forecasts to (1) assess future uncertainty levels; (2) enable different strategies to be planned for a range of possible outcomes indicated by
the interval forecasts; (3) compare forecasts from different methods more thoroughly; and
(4) explore different scenarios based on various assumptions.

Our aim is to construct a prediction band for the unconstrained functional time series  $\beta_{n+h}$  associated with the predictor  $\hat{\beta}_{n+h}$ . The prediction band, denoted by  $[\hat{\beta}_{n+h}(u) - L_{n,h}(u), \hat{\beta}_{n+h}(u) + U_{n,h}(u)]$ , is given as

$$\lim_{n\to\infty} \Pr\left(\widehat{\beta}_{n+h}(u) - L_{n,h}(u) \le \beta_{n+h}(u) \le \widehat{\beta}_{n+h}(u) + U_{n,h}(u), \quad \forall u \in \mathcal{I} | \beta_{n,k}\right) = 1 - \alpha,$$

where  $\beta_{n,k} = (\beta_n, \beta_{n-1}, \dots, \beta_{n-k+1})$  are the last *k* observations. The crux of the problem is on the estimation of the conditional distribution of the prediction error  $\mathcal{E}_{n+h} = \beta_{n+h} - \hat{\beta}_{n+h}$  given  $\beta_{n,k}$ . The prediction error can be decomposed as

$$\begin{aligned} \mathcal{E}_{n+h} &:= \beta_{n+h} - \widehat{\beta}_{n+h} \\ &= \epsilon_{n+h} + \left[ f(\beta_{n+h-1}, \beta_{n+h-2}, \dots) - g(\beta_{n+h-1}, \beta_{n+h-2}, \dots, \beta_{n+h-k}) \right] + \\ &+ \left[ g(\beta_{n+h-1}, \beta_{n+h-2}, \dots, \beta_{n+h-k}) - \widehat{g}(\widehat{\beta}_{n+h-1}, \widehat{\beta}_{n+h-2}, \dots, \widehat{\beta}_{n+h-k}) \right] \\ &= \mathcal{E}_{I,n+h} + \mathcal{E}_{M,n+h} + \mathcal{E}_{E,n+h}. \end{aligned}$$

 $\mathcal{E}_{I,n+h}$  is the error attributable to the independent and identically distributed innovation,  $\mathcal{E}_{M,n+h}$ is the model mis-specification error, and  $\mathcal{E}_{E,n+h}$  is the error attributable to estimation of the unknown function *g* and of random element ( $\beta_{n+h-1}, \ldots, \beta_{n+h-k}$ ) used for the *h*-step-ahead prediction.

The construction of the prediction interval for CoDa has previously been considered by Bergeron-Boucher et al. (2017) and Shang and Haberman (2020). However, the existing methods do not take into account a model mis-specification error. Our bootstrap method does not only take into account the three sources of uncertainty, but it also considers multi-population modelling of unconstrained data  $\beta^{j}(u) = \{\beta_{1}^{j}(u), \dots, \beta_{n}^{j}(u)\}.$ 

Univariate functional time series method (see Kokoszka et al. 2019, Shang and Haberman 2020): Using a univariate time series forecasting model, we can obtain multi-step-ahead forecasts for the principal component scores,  $\{\hat{\gamma}_{1,\ell}^{j}, \dots, \hat{\gamma}_{n,\ell}^{j}\}$  for  $\ell = 1, \dots, L$ . Let the *h*-step-ahead forecast errors be  $\zeta_{t,h,\ell}^{j} = \hat{\gamma}_{t,\ell}^{j} - \hat{\gamma}_{t|t-h,\ell}^{j}$ , for  $t = h + 1, \dots, n$ . These can then be sampled with replacement to give a bootstrap sample of  $\gamma_{n+h,\ell}$ :

$$\widehat{\gamma}_{n+h|n,\ell}^{j,b} = \widehat{\beta}_{n+h|n,\ell} + \widehat{\zeta}_{*,h,\ell}^{j,b}, \qquad b = 1,\ldots,B,$$

where B = 1,000 symbolises the total number of bootstrap replications and  $\hat{\zeta}_{*,h,\ell}^{j,b}$  are sampled with replacement from  $\hat{\zeta}_{t,h,\ell}^{j}$ .

<sup>229</sup> While the first  $L_j$  principal components approximate the data  $\beta^j(u)$  relatively well, the <sup>230</sup> model residuals should contribute nothing but random noise. We apply a white noise test of <sup>231</sup> Bagchi et al. (2018) to examine whether or not the residuals are white noise. Consequently, we <sup>232</sup> can bootstrap the model fit errors in (3) by sampling with replacement from the model residual <sup>233</sup> term { $\hat{\omega}_1^j(u), \ldots, \hat{\omega}_n^j(u)$ } for a given age u.

Adding both components of variability, we obtain *B* variants for  $\beta_{n+h}^{j}(u)$ :

$$\widehat{\beta}_{n+h|n}^{j,b}(u) = \sum_{\ell=1}^{L_j} \widehat{\gamma}_{n+h|n,\ell}^{j,b} \widehat{\phi}_{\ell}^j(u) + \widehat{\varpi}_{n+h}^{j,b}(u).$$

With the bootstrapped  $\{\widehat{\beta}_{n+h|n}^{j,1}(u), \dots, \widehat{\beta}_{n+h|n}^{j,B}(u)\}$ , we fit a functional time series model, where the retained number of principal components is estimated from the ER and GR tests and is allowed to be different values among the bootstrap samples. By conditioning on the estimated mean function and FPCs in each bootstrap sample, we then obtain the forecasts.

Multivariate functional time series method (see Shang and Kearney 2022): By stacking  $\beta_t(u) = [\beta_t^1(u), \beta_t^2(u)]$  into a long vector of functional time series, we then apply a FPCA to decompose  $[\beta_1(u), \dots, \beta_n(u)]$  into *L* sets of principal components and their associated scores. We apply our bootstrap procedure to construct the bootstrap samples, namely  $\hat{\beta}_{n+h|n}^{j,b}(u)$ .

Multilevel functional time series method (see Shang et al. 2016, Shang and Kearney 2022): By 242 taking a simple average  $U_t(u) = \overline{\beta}_t(u) = \frac{\beta_t^1(u) + \beta_t^2(u)}{2}$ , we obtain a common series between the 243 two populations. First, we apply a FPCA to decompose  $\overline{\beta}(u) = [\overline{\beta}_1(u), \dots, \overline{\beta}_n(u)]$  into *K* sets of 244 FPCs and their associated scores. From the principal component decomposition of the averaged 245 series, we can compute the population-specific residual trend. We again apply a FPCA to 246 decompose the population-specific residual trend into L sets of FPCs and their associated scores. 247 Then, we apply the above bootstrap procedure to construct the bootstrap samples, namely 248  $\widehat{U}^b_{n+h|n}(u) \text{ and } \widehat{R}^{j,b}_{n+h|n}(u). \text{ Then, } \widehat{\beta}^{j,b}_{n+h|n}(u) = \widehat{U}^b_{n+h|n}(u) + \widehat{R}^{j,b}_{n+h|n}(u).$ 249

With the bootstrapped  $\hat{\beta}_{n+h|n}^{j,b}(u)$ , we follow steps 5) and 6) in Section 3, in order to obtain the bootstrap forecast of  $\mathcal{X}_{n+h}^{j,b}(u)$ . At the 100(1 – v)% nominal coverage probability, the prediction bands are obtained by taking v/2 and 1 – v/2 quantiles based on  $\left\{\hat{\mathcal{X}}_{n+h|n}^{j,1}(u), \ldots, \hat{\mathcal{X}}_{n+h|n}^{j,B}(u)\right\}$ .

### **253 5 CoDa model fitting**

We examine the goodness-of-fit of the CoDa model for multiple populations. In Section 6, the 254 CoDa with the multivariate and multilevel functional time series methods are our recommenda-255 tion for producing the point and interval forecasts for multiple populations. For example, we 256 consider the CoDa model fitting by the multilevel functional time series method for the female 257 and male life-table death counts. The number of retained components, K and L are determined 258 by the ER and GR criteria in the common and residual trends, respectively. For the common 259 trend between the female and male data in England & Wales, the chosen number of components 260 is 1. For the population-specific trend between the female and male data in England & Wales, 261 the chosen numbers of components for the residual trend is 1 and 4, respectively. From (6), 262 we compute the within-cluster variability. The common trend accounts for 96.16% of the total 263 variation for the female series, and it accounts for 93.63% of the total variation for the male 264 series. 265





**Figure 3:** Elements of the CoDa with the multilevel functional time series method for analysing female and male age-specific life-table death counts in England & Wales from 1841 to 2018.

From the observed death counts from 1841 to 2018 (i.e., 178 observations), in Figure 3, we 266 present the geometric mean of female and male period life-table death counts, given by  $\alpha_x^j$ , 267 the transformed data matrix  $\beta^{j}(u) = {\beta_{1}^{j}(u), \dots, \beta_{n}^{j}(u)}$ , the reconstructed female and male 268 life-table death counts using a multilevel FPCA, and one- to 30-step-ahead forecasts of female 269 and male life-table death counts. From the unconstrained data  $\beta^1(u)$  and  $\beta^2(u)$ , we notice that 270 the series are nonstationary. Therefore, our bootstrap procedure for constructing prediction 271 intervals must be tailored to handle nonstationary functional time series. These forecast life-272 table death counts are obtained by multiplying the estimated principal components with the 273 forecast principal component scores using the random walk with drift (RWD) for the years 274 between 2019 and 2048. RWD is one of the four univariate forecasting methods employed in 275 the example, and which will be discussed in Section 6.4. 276

## 277 6 Comparisons of point and interval forecast accuracy

#### **6.1** Expanding window

An expanding window analysis of a time series model is commonly used to assess model 279 and parameter stability over time and prediction accuracy. The expanding window analysis 280 determines the constancy of a model's parameter by computing parameter estimates and their 281 resultant forecasts over an expanding window of a fixed size through the sample (for details 282 Zivot and Wang 2006, pp. 313–314). Using the first 148 observations from 1841 to 1988 in 283 the female and male age-specific life-table death counts, we produce one- to 30-step-ahead 284 forecasts. Through an expanding window approach, we re-estimate the parameters in the time 285 series forecasting models using the first 149 observations from 1841 to 1989. Forecasts from 286 the estimated models are then produced for one- to 29-step-ahead forecasts. We iterate this 287 process by increasing the sample size by one year until we reached the data period in 2018. 288 This process produces 30 one-step-ahead forecasts, 29 two-step-ahead forecasts, ..., and one 289 30-step-ahead forecast. We compare these forecasts with the holdout samples between 1989 and 290 2018 to determine the out-of-sample forecast accuracy. 291

#### 292 6.2 Point forecast error criteria

To evaluate the point forecast accuracy, we consider the MAPE that measures how close the forecasts are to the holdout observations being forecast, regardless of the direction of forecast errors. This error measure can be written as

$$MAPE(h) = \frac{1}{111 \times (31 - h)} \sum_{\xi=h}^{30} \sum_{i=1}^{111} \left| \frac{\mathcal{X}_{n+\xi}(u_i) - \widehat{\mathcal{X}}_{n+\xi|n}(u_i)}{\mathcal{X}_{n+\xi}(u_i)} \right| \times 100, \qquad i = 1, \dots, 111,$$

<sup>293</sup> where  $\mathcal{X}_{n+\xi}(u_i)$  denotes the holdout sample for the  $u_i^{\text{th}}$  age and  $\xi^{\text{th}}$  forecasting year, while <sup>294</sup>  $\hat{\mathcal{X}}_{n+\xi|n}(u_i)$  denotes the point forecasts for the holdout sample.

Since age-specific life-table death counts can be considered a probability density function, we also consider some density evaluation measures. These measures include the discrete version of the Kullback-Leibler divergence (Kullback and Leibler 1951) and the square root of the Jensen-Shannon divergence (Shannon 1948). The Kullback-Leibler divergence is intended to measure the loss of information when we choose an approximation. For two probability density functions denoted by  $\mathcal{X}_{n+\xi}(u)$  and  $\hat{\mathcal{X}}_{n+\xi|n}(u)$ , the discrete version of the Kullback-Leibler divergence is

$$\begin{split} \text{KLD}(h) &= D_{\text{KL}}[\mathcal{X}_{n+\xi}(u_i)||\widehat{\mathcal{X}}_{n+\xi|n}(u_i)] + D_{\text{KL}}[\widehat{\mathcal{X}}_{n+\xi|n}(u_i)||\mathcal{X}_{n+\xi}(u_i)] \\ &= \frac{1}{111 \times (31-h)} \sum_{\xi=h}^{30} \sum_{i=1}^{111} \mathcal{X}_{n+\xi}(u_i) \cdot \left[\ln \mathcal{X}_{n+\xi}(u_i) - \ln \widehat{\mathcal{X}}_{n+\xi|n}(u_i)\right] + \\ &= \frac{1}{111 \times (31-h)} \sum_{\xi=h}^{30} \sum_{i=1}^{111} \widehat{\mathcal{X}}_{n+\xi|n}(u_i) \cdot \left[\ln \widehat{\mathcal{X}}_{n+\xi|n}(u_i) - \ln \mathcal{X}_{n+\xi}(u_i)\right], \end{split}$$

<sup>295</sup> which is symmetric and non-negative.

An alternative is given by the Jensen-Shannon divergence, defined by

$$JSD(h) = \frac{1}{2}D_{KL}[\mathcal{X}_{n+\xi}(u_i)||\delta_{n+\xi}(u_i)] + \frac{1}{2}D_{KL}[\widehat{\mathcal{X}}_{n+\xi|n}(u_i)||\delta_{n+\xi}(u_i)],$$

<sup>296</sup> where  $\delta_{n+\xi}(u_i)$  measures a common quantity between  $\mathcal{X}_{n+\xi}(u_i)$  and  $\widehat{\mathcal{X}}_{n+\xi|n}(u_i)$ . We consider <sup>297</sup> simple mean and geometric mean, given by  $\delta_{n+\xi}(u_i) = \frac{1}{2}[\mathcal{X}_{n+\xi}(u_i) + \widehat{\mathcal{X}}_{n+\xi|n}(u_i)]$  or  $\delta_{n+\xi}(u_i) = \sqrt{\mathcal{X}_{n+\xi}(u_i)\widehat{\mathcal{X}}_{n+\xi|n}(u_i)}$ . We denote JSD<sup>*s*</sup>(*h*) for the Jensen-Shannon divergence with the simple <sup>298</sup> mean, and JSD<sup>*g*</sup>(*h*) for the Jensen-Shannon divergence with the geometric mean. To make the <sup>300</sup> Jensen-Shannon divergence a metric between two probability densities, we take the square root <sup>301</sup> of the Jensen-Shannon divergence (see, e.g., Fuglede and Topsoe 2004).

#### 302 6.3 Interval forecast error criteria

To evaluate the interval forecast accuracy, we consider the coverage probability difference (CPD) between the empirical and nominal coverage probabilities and mean interval score of Gneiting and Raftery (2007). For each year in the forecasting period, the *h*-step-ahead prediction intervals are calculated at the 100(1 - v)% nominal coverage probability. We consider the common case of the symmetric 100(1 - v)% prediction intervals, with lower and upper bounds that are predictive quantiles at v/2 and 1 - v/2, denoted by  $\hat{X}_{n+\xi}^{\text{lb}}(u_i)$  and  $\hat{X}_{n+\xi}^{\text{ub}}(u_i)$ . The CPD is defined as

$$CPD_{h} = \frac{1}{111 \times (31-h)} \sum_{\xi=h}^{30} \sum_{i=1}^{111} \left[ \mathbb{1}\{\mathcal{X}_{n+\xi}(u_{i}) > \widehat{\mathcal{X}}_{n+\xi}^{ub}(u_{i})\} + \mathbb{1}\{\mathcal{X}_{n+\xi}(u_{i}) < \widehat{\mathcal{X}}_{n+\xi}^{lb}(u_{i})\} \right].$$

For different ages and years in the forecasting period, the mean CPD is defined by

$$\overline{\text{CPD}} = \frac{1}{30} \sum_{h=1}^{30} \text{CPD}_h.$$

As defined by Gneiting and Raftery (2007), a scoring rule for the prediction intervals at time

point  $\mathcal{X}_{n+\xi}(u_i)$  is

$$\begin{split} S_{v,\xi} \Big[ \widehat{\mathcal{X}}_{n+\xi}^{\mathrm{lb}}(u_i), \widehat{\mathcal{X}}_{n+\xi}^{\mathrm{ub}}(u_i), \mathcal{X}_{n+\xi}(u_i) \Big] &= \Big[ \widehat{\mathcal{X}}_{n+\xi}^{\mathrm{ub}}(u_i) - \widehat{\mathcal{X}}_{n+\xi}^{\mathrm{lb}}(u_i) \Big] \\ &+ \frac{2}{v} \Big[ \widehat{\mathcal{X}}_{n+\xi}^{\mathrm{lb}}(u_i) - \mathcal{X}_{n+\xi}(u_i) \Big] \mathbbm{1} \Big\{ \mathcal{X}_{n+\xi}(u_i) < \widehat{\mathcal{X}}_{n+\xi}^{\mathrm{lb}}(u_i) \Big\} \\ &+ \frac{2}{v} \Big[ \mathcal{X}_{n+\xi}(u_i) - \widehat{\mathcal{X}}_{n+\xi}^{\mathrm{ub}}(u_i) \Big] \mathbbm{1} \Big\{ \mathcal{X}_{n+\xi}(u_i) > \widehat{\mathcal{X}}_{n+\xi}^{\mathrm{ub}}(u_i) \Big\}, \end{split}$$

where  $1\{\cdot\}$  represents the binary indicator function and v denotes the level of significance, customarily v = 0.2 or 0.05. The interval score rewards a narrow prediction interval, if and only if the true observation lies within the prediction interval. The optimal interval score is achieved when  $\mathcal{X}_{n+\xi}(u_i)$  lies between  $\widehat{\mathcal{X}}_{n+\xi}^{\text{lb}}(u_i)$  and  $\widehat{\mathcal{X}}_{n+\xi}^{\text{ub}}(u_i)$ , and the distance between  $\widehat{\mathcal{X}}_{n+\xi}^{\text{lb}}(u_i)$  and  $\widehat{\mathcal{X}}_{n+\xi}^{\text{ub}}(u_i)$  is minimal.

For different ages and years in the forecasting period, the mean interval score is defined by

$$\overline{S}_{v}(h) = \frac{1}{111 \times (31-h)} \sum_{\xi=h}^{30} \sum_{i=1}^{111} S_{v,\xi} \Big[ \widehat{\mathcal{X}}_{n+\xi}^{\text{lb}}(u_i), \widehat{\mathcal{X}}_{n+\xi}^{\text{ub}}(u_i), \mathcal{X}_{n+\xi}(u_i) \Big]$$

where  $S_{v,\xi} \left[ \hat{\mathcal{X}}_{n+\xi}^{\text{lb}}(u_i), \hat{\mathcal{X}}_{n+\xi}^{\text{ub}}(u_i), \mathcal{X}_{n+\xi}(u_i) \right]$  denotes the interval score at the *i*<sup>th</sup> age and  $\xi^{\text{th}}$  curve in the forecasting period. Averaged over all forecast horizons, we obtain the overall mean interval score

$$\overline{S}_v = \frac{1}{30} \sum_{h=1}^{30} \overline{S}_v(h).$$

#### **308** 6.4 Forecast results

Using the expanding window scheme, we compare the one-step-ahead to 30-step-ahead forecast 309 errors between the CoDa with the functional time series methods in Table 1. We consider 310 forecasting each set of the estimated principal component scores by four distinct univariate 311 time series forecasting methods. These forecasting methods are the autoregressive integrated 312 moving average (ARIMA), exponential smoothing (ETS), naïve random walk (RW) and RWD. 313 While these methods are widely applied to analyse linear time series, ETS can be tailored to fit 314 a nonlinear time series. We aim to identify which one of the four methods produces the most 315 accurate forecasts through an empirical comparison. 316

**Table 1:** A comparison of the point forecast accuracy, as measured by the overall MAPE, KLD and JSD with simple and geometric means, among the CoDa with independent and joint modelling approaches and several benchmark methods using a holdout sample of the period life-table death counts for the female and male data in England & Wales. Further, we consider four univariate time series forecasting methods for our functional time-series forecasting methods within the CoDa. ETS denotes the automatic exponential smoothing method. ARIMA denotes the automatic autoregressive integrated moving average method of Hyndman and Khandakar (2008). FTS denotes the univariate functional time series method. MFTS denotes the multivariate functional time series method. MLFTS denotes the multilevel functional time series method. The smallest errors are highlighted in bold.

Modelling	Forecasting		Fem	ale	Male				
method	method	MAPE	KLD	JSD <sup>s</sup>	JSD <sup>g</sup>	MAPE	KLD	JSD <sup>s</sup>	JSD <sup>g</sup>
CoDa									
FTS	ARIMA	29.900	0.041	0.010	0.010	42.737	0.130	0.031	0.033
	ETS	33.405	0.032	0.008	0.008	47.223	0.153	0.037	0.038
	RW	31.422	0.070	0.017	0.017	47.077	0.152	0.036	0.038
	RWD	29.914	0.042	0.010	0.010	43.175	0.127	0.031	0.032
MFTS	ARIMA	18.966	0.021	0.005	0.005	38.318	0.099	0.024	0.025
	ETS	32.214	0.044	0.011	0.011	52.609	0.123	0.030	0.031
	RW	33.953	0.041	0.010	0.010	54.951	0.118	0.029	0.029
	RWD	18.031	0.018	0.004	0.004	38.096	0.092	0.022	0.023
MLFTS	ARIMA	22.988	0.034	0.008	0.008	27.499	0.055	0.013	0.014
	ETS	32.837	0.054	0.013	0.013	39.211	0.079	0.019	0.020
	RW	34.762	0.054	0.013	0.013	39.797	0.078	0.019	0.019
	RWD	20.833	0.028	0.007	0.007	27.049	0.053	0.013	0.013
RW		34.209	0.042	0.010	0.010	43.151	0.086	0.021	0.021
LC	VECM	29.020	0.046	0.011	0.011	43.110	0.140	0.034	0.035
LL	RWD-AR	33.451	0.076	0.019	0.019	36.668	0.075	0.018	0.019
PR	ARIMA	35.114	0.062	0.015	0.016	40.699	0.108	0.026	0.027
<u>CBD-M6</u>	VAR	43.422	0.161	0.039	0.040	60.407	0.178	0.042	0.045
CBD-M6	VECM	31.029	0.088	0.022	0.022	41.486	0.107	0.026	0.027

317

From the aggregated error measures over the forecast horizon, we present the forecast errors obtained from the CoDa and a number of single- and multi-population benchmark models in Table 1, namely,

- <sup>321</sup> 1) the naïve random walk model.
- 2) two-population Li-Carter model (LC) with a vector error correction model (VECM) for the
   evolution of period effects, discussed by Zhou et al. (2014).
- 324 3) Li-Lee model (LL) with RWD for common PC scores and autoregressive (AR) of order 1 for
   population-specific PC scores, considered by Li and Lee (2005).
- 4) product-ratio model (PR) with the FPC scores forecasted by ARIMA, which was introduced
  by Hyndman et al. (2013).
- <sup>328</sup> 5) two-population Cairns-Blake-Dowd model with cohort effect (CBD-M6) with population <sup>329</sup> specific coefficients jointly predicted by vector autoregressive model (VAR) of order 1 or
   <sup>330</sup> VECM (see, e.g., Li et al. 2015).

The benchmark models do not consider the constraints. Therefore, to obtain a fair comparison with our proposed methods, we slightly modify the benchmark approaches by applying them to the unconstrained  $\beta_t^j(u)$  after the centred log-ratio transformation to adapt the positivity and summability constraints in the age-specific life table.

We consider the RW method for each sub-population for the single-population benchmark 335 separately, where the one-step-ahead forecast density is the same as the most recently observed 336 density. While this method does not consider temporal changes, it does not require the CoDa 337 transformation and thus is computationally fast. Regarding the coherent forecasting of mortality 338 rates for multiple sub-populations, most such models extend the well-known single-population 339 models, such as the Lee-Carter model and Cairns-Blake-Dowd (CBD) model, by specifying the 340 correlation and interaction between the involved populations (Villegas et al. 2017). The LC, LL 341 and PR methods are extensions of the Lee-Carter model, while CBD-M6 is the extension of the 342 CBD model. Li et al. (2015) proposed several two-population extensions of the CBD model, 343 among which the CBD-M6 model is the final recommended one. 344

We find that the CoDa with the multivariate functional time series method using the RWD method produces the smallest point forecast errors for females. The CoDa with the multilevel functional time series method using the RWD method produces the smallest point forecast errors for males. While Table 1 presents an aggregated measure, we present horizon-specific forecast errors in Figure 4. In general, as the forecast horizon increases, the differences in forecast errors among the CoDa variants become more apparent.

The overall interval forecast error results of the CoDa method with various functional time series methods are presented in Table 2, where we average over the 30 forecast horizons. We find that the CoDa with the multivariate functional time series method using the automatically



Figure 4: A comparison of point forecast accuracy between the CoDa with functional time series methods using the holdout samples of the England & Wales period data. In the CoDa variants, we use the RWD forecasting method. The six benchmark methods are the random walk method, two-population Lee-Carter method of Zhou et al. (2014), Li-Lee method of Li and Lee (2005), the product-ratio method of Hyndman et al. (2013), two-population CBD-M6 model with VAR (or VECM) forecast of Li et al. (2015).

selected ARIMA of Hyndman and Khandakar (2008) produces the smallest interval forecast errors for females. In contrast, the CoDa with the multilevel functional time series method with the RWD produces the smallest interval forecast errors for male period data. Among the four univariate time series forecasting methods and three functional time series methods, the multilevel functional time series method with RWD produces the smallest interval forecast errors averaged over females and males, and thus is recommended to obtain both the point and interval forecasts.

**Table 2:** A comparison of the interval forecast accuracy, as measured by the overall CPD and mean interval scoreamong the CoDa methods using the holdout sample of the female and male data in England & Wales.Further, we consider four univariate time series forecasting methods for the CoDa.

Modelling	Forecasting	CPD (Fe	emale)	$\overline{S}_{\alpha}$ (F	emale)	$\overline{\text{CPD}}$ (Male)		$\overline{S}_{\alpha}$ (Male)	
method	method	$\alpha = 0.2$	0.05	0.2	0.05	0.2	0.05	0.2	0.05
FTS	ARIMA	0.288	0.164	829.766	1267.737	0.339	0.241	1830.273	3954.051
	ETS	0.247	0.107	718.468	931.781	0.292	0.234	1958.649	4437.786
	RW	0.118	0.070	926.145	1437.361	0.284	0.229	1942.471	4306.580
	RWD	0.163	0.034	797.098	994.477	0.308	0.201	1781.903	3393.862
MFTS	ARIMA	0.079	0.037	421.524	657.474	0.331	0.293	2022.347	4731.384
	ETS	0.080	0.041	480.040	676.078	0.309	0.282	2120.377	5435.254
	RW	0.112	0.045	459.755	673.594	0.273	0.261	2037.320	5095.628
	RWD	0.158	0.049	443.686	796.824	0.215	0.148	1503.861	2344.673
MLFTS	ARIMA	0.094	0.045	650.225	866.905	0.139	0.045	941.893	1221.611
	ETS	0.139	0.046	701.098	949.348	0.119	0.047	1009.098	1330.439
	RW	0.141	0.045	711.635	918.514	0.122	0.046	1000.434	1327.669
	RWD	0.195	0.050	655.530	1056.286	0.115	0.044	738.543	1077.238

In contrast to the point forecasts, the RW method does not provide a prediction interval. For the multi-population benchmark models, there is no established prediction interval under the CoDa framework in the literature. Thus, we report the interval forecast accuracy based on the functional time series methods using the nonparametric bootstrap approach described in Section 4 in Table 2.

While Table 2 presents the average over 30 forecast horizon, we show the one-step-ahead to 368 30-step-ahead interval forecast errors in Figure 5. The differences in forecast accuracy among 369 the CoDa methods become wider as the forecast horizon becomes longer. In the relatively





**Figure 5:** A comparison of interval forecast accuracy between the CoDa with functional time series methods using the holdout samples of the England & Wales period data. We use the ARIMA forecasting method for females and the RWD forecasting method for males.

Among the four univariate time series forecasting methods, the RWD is generally recom-372 mended for producing point forecasts. For producing interval forecasts, the RWD is recom-373 mended for males but not so for females. The difference is how well the forecasts generated 374 from a statistical model capture the holdout data. For females, we found the ARIMA method 375 produces the smallest interval scores using the holdout samples of the England & Wales data 376 set. The ARIMA method can include higher-order lags than the RWD counterpart, the latter 377 method being a special case of AR(1). Since we don't know the underlying data generating 378 process, the most accurate method is data-driven, subject to the fitting period. Although a 379 model is better when it is a good proxy of the data generating process, it can not be gener-380 alised. To facilitate reproducibility, the 🗬 code for implementing all the methods is available at 381 https://github.com/hanshang/LTDC. 382

### **7** Results on Swedish period life-table death counts

To check the robustness of our proposed methods, we perform the point and interval estimation on age- and sex-specific period life-table death counts from 1861 to 2018 in Sweden, obtained from the Human Mortality Database (2022). The comparison of the point and interval forecast accuracy are presented in Table 3 and 4, respectively. In addition, we present horizon-specific point and interval forecast errors in Figures 6 and 7, respectively. As the forecast horizon increases, the differences in forecast errors among the CoDa variants become more apparent.

**Table 3:** A comparison of the point forecast accuracy, as measured by the overall MAPE, KLD and JSD with simple and geometric means, among the CoDa with independent and joint modelling approaches and several benchmark methods using a holdout sample of the period life-table death counts for the female and male data in Sweden. Further, we consider four univariate time series forecasting methods for our functional time-series forecasting methods within the CoDa. ETS denotes the automatic exponential smoothing method. ARIMA denotes the automatic autoregressive integrated moving average method of Hyndman and Khandakar (2008). FTS denotes the univariate functional time series method. MFTS denotes the multivariate functional time series method. The smallest errors are highlighted in bold.

Modelling	Forecasting		Fem	ale		Male				
method	method	MAPE	KLD	JSD <sup>s</sup>	JSD <sup>g</sup>	MAPE	KLD	JSD <sup>s</sup>	JSD <sup>g</sup>	
CoDa										
FTS	ARIMA	26.721	0.028	0.007	0.010	28.625	0.041	0.010	0.010	
	ETS	28.385	0.020	0.005	0.011	29.431	0.042	0.011	0.011	
	RW	37.155	0.061	0.015	0.018	48.421	0.073	0.018	0.018	
	RWD	27.587	0.032	0.008	0.011	30.020	0.043	0.011	0.011	
MFTS	ARIMA	26.085	0.032	0.008	0.014	34.673	0.058	0.014	0.014	
	ETS	24.070	0.029	0.007	0.009	29.891	0.038	0.009	0.009	
	RW	42.589	0.049	0.012	0.018	54.852	0.072	0.018	0.018	
	RWD	22.285	0.019	0.005	0.009	29.806	0.036	0.009	0.009	
MLFTS	ARIMA	26.737	0.020	0.005	0.008	26.521	0.033	0.008	0.008	
	ETS	24.597	0.017	0.004	0.004	22.568	0.017	0.004	0.004	
	RW	48.286	0.054	0.013	0.015	48.987	0.062	0.015	0.015	
	RWD	25.907	0.025	0.006	0.007	26.678	0.028	0.007	0.007	
RW		43.945	0.028	0.007	0.007	51.057	0.061	0.015	0.015	
	VECM	27.022	0.029	0.007	0.007	27.216	0.035	0.009	0.009	

Continued on next page

**Table 3:** A comparison of the point forecast accuracy, as measured by the overall MAPE, KLD and JSD with simple and geometric means, among the CoDa with independent and joint modelling approaches and several benchmark methods using a holdout sample of the period life-table death counts for the female and male data in Sweden. Further, we consider four univariate time series forecasting methods for our functional time-series forecasting methods within the CoDa. ETS denotes the automatic exponential smoothing method. ARIMA denotes the automatic autoregressive integrated moving average method of Hyndman and Khandakar (2008). FTS denotes the univariate functional time series method. MFTS denotes the multivariate functional time series method. The smallest errors are highlighted in bold.

Modelling	Forecasting		Fem	ale		Male				
method	method	MAPE	KLD	JSD <sup>s</sup>	JSD <sup>g</sup>	MAPE	KLD	JSD <sup>s</sup>	JSD <sup>g</sup>	
LL	RWD-AR	30.137	0.048	0.012	0.012	26.932	0.027	0.007	0.007	
<u>PR</u>	ARIMA	26.373	0.027	0.012	0.012	31.226	0.048	0.012	0.012	
CBD-M6	VAR	39.356	0.118	0.029	0.030	39.349	0.079	0.019	0.020	
CBD-M6	VECM	23.890	0.026	0.006	0.007	26.002	0.017	0.004	0.004	

390

**Table 4:** A comparison of the interval forecast accuracy, as measured by the overall CPD and mean interval score among the CoDa methods using the holdout sample of the female and male data in Sweden. Further, we consider four univariate time series forecasting methods for the CoDa.

Modelling	Forecasting	$\overline{\text{CPD}}$ (Fe	emale)	$\overline{S}_{\alpha}$ (F	emale)	$\overline{\text{CPD}}$ (Male)		$\overline{S}_{\alpha}$ (Male)	
method	method	$\alpha = 0.2$	0.05	0.2	0.05	0.2	0.05	0.2	0.05
FTS	ARIMA	0.142	0.098	555.147	729.946	0.164	0.057	727.857	828.368
	ETS	0.103	0.074	536.641	739.982	0.166	0.072	807.424	967.387
	RW	0.097	0.044	748.397	947.080	0.195	0.111	957.126	1408.082
	RWD	0.056	0.028	575.866	900.978	0.038	0.036	666.834	934.014
MFTS	ARIMA	0.031	0.022	466.119	629.841	0.176	0.103	919.075	1198.767
	ETS	0.054	0.027	455.101	640.374	0.096	0.036	676.307	770.708
	RW	0.034	0.023	478.209	625.414	0.178	0.082	865.841	1003.854
	RWD	0.101	0.036	553.178	1007.872	0.023	0.032	668.155	860.760
MLFTS	ARIMA	0.095	0.027	545.464	840.192	0.084	0.039	619.514	810.734
	ETS	0.099	0.030	547.777	837.673	0.110	0.039	544.588	822.576
	RW	0.112	0.040	595.128	865.717	0.103	0.037	664.062	835.116
	RWD	0.152	0.044	717.787	1244.656	0.155	0.047	724.160	1169.407



**Figure 6:** A comparison of point forecast accuracy between the CoDa with functional time series methods using the holdout samples of the Swedish period data. In the CoDa variants, we use the ETS forecasting method. The six benchmark methods are the random walk method, two-population Lee-Carter method of Zhou et al. (2014), Li-Lee method of Li and Lee (2005), the product-ratio method of Hyndman et al. (2013), two-population CBD-M6 model with VAR (or VECM) forecast of Li et al. (2015).



**Figure 7:** A comparison of interval forecast accuracy between the CoDa with functional time series methods using the holdout samples of the Swedish period data. In the CoDa variants, we use the ETS forecasting method.

For the point estimates, our proposed CoDa methods outperform the all the benchmark models except CBD-M6 model with VECM forecasts, which performs on par with our proposed methods for the male group. Among our proposed CoDa method, the CoDa with the multilevel functional time series and ETS generally produces the smallest forecasting error for Swedish period data. The multivariate functional times series model generally performs best regarding the interval forecast accuracy. At the same time, there is no universally best univariate timeseries forecasting method to forecast the FPC scores.

### **399 8 Conclusion**

We extend the CoDa from univariate to multivariate and multilevel functional time series methods for modelling multiple populations. Within the CoDa framework, we take the log-ratio transformation to obtain unconstrained data. Then, we apply the multivariate and multilevel functional time series methods to model the unconstrained data for multiple populations. After <sup>404</sup> applying the back-transformation, we obtain the age-specific life-table death counts for multiple
 <sup>405</sup> populations.

We compare our proposed CoDa methods with six benchmarks in the single-population 406 forecast (simple random walk) and multi-population forecasts (two-population Lee-Carter 407 model, Li-Lee method, product-ratio method and two-population CBD model with cohort 408 effects using VAR/VECM for prediction) on both period and cohort life-table death counts 409 in England & Wales and Sweden. Our proposed CoDa methods outperform the existing 410 benchmarks in most cases. In contrast, the product-ratio method and CBD-M6 (with VECM 411 forecasts) perform on par or with a slight edge under certain error measurements for the 412 Swedish male life-table death counts. Among our proposed methods, it is difficult to single out 413 a universal univariate time-series forecasting method that outperforms the rest in all cases. 414

There are a few ways in which this paper could be extended, and we briefly discuss four. 415 1) To obtain more stable forecasts, simple averaging forecasts from three functional time series 416 models may result in improved forecast accuracy. In addition, we recommend selecting the 417 univariate time series forecasting method via an information criterion before fitting the model. 418 2) A robust CoDa method proposed by Filzmoser et al. (2009) may be utilised in the presence 419 of outlying years. These outlying years are from a different data generating process than the 420 non-outlying observations. 3) We could consider some of the other methods in the literature for 421 extending data sets for non-extinct cohorts (e.g., Basellini et al. 2020) and suggest examining 422 the sensitivity of the results to the choice of method. 4) We could also extend from considering 423 two populations in the current paper to considering life-table data for multiple populations and 424 for multiple subsets of a population (for example, subdivided by socio-economic status). In 425 these scenarios, the number of populations could exceed the number of functional curves in a 426 population, and this then leads to the high-dimensional functional time series analysis (see, e.g., 427 Gao et al. 2019, Tang and Shi 2021). 428

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