Supplemental Material

1 Supplemental Tables and Figures

Supplemental Table 1. Predictive deviance for the validation period. Scenario B (trend-based scenario) shows lower values of predictive deviance through the validation period

Supplemental Table 2. Population adjusted (2012 population baseline) **mortality for Coronary Heart Disease and Stroke in 2030, stratified by age and gender with lower (LCrI) and upper (UCrI) credible intervals.** Table 1A – conventional projections, Table 1B – trend-based projections.

2A.

2B.

2 Methods

2.1. Bayesian Age Period Cohort model

The APC model is often regarded as a log-linear Poisson model. Here we model the logit of the probability of death from CHD in age group i in period j as a linear combination of an intercept μ , age effects θ_i $(i = 1, \ldots I)$, period effects φ_j $(j = 1, \ldots J)$ and cohort effects ψ_k $(k = 1, \ldots K)$:

$$
log\left(\frac{p_{ij}}{1-p_{ij}}\right) = \mu + \theta_i + \varphi_j + \psi_k.
$$

I is the total number of age groups and *J* the total number of periods. Cohorts are defined by $k = C(I - i) + j$ and the total number of cohorts is $K = C(I - 1) + J$, where C is the width of the age bands.

To make the model identifiable, the so called "sum to zero" constraints *i.e.* $\sum \theta_i = \sum \varphi_j = \sum \psi_k = 0$ need to be added. The model is only identifiable when it is possible to obtain a unique set of parameters after infinite linear transformations. There is another identifiability problem due to the collinear relationship of age, period and cohort effects which makes it impossible to identify and interpret the separate contributions of each individual effect $\frac{1}{1}$. However, non-linear trends or change points can be interpreted because the non-identifiability only affects linear trends 2 .

Random walk of first and second order

For the Bayesian APC model, it is assumed that effects from adjacent time bands tend to be more alike 3 . There are two types of priors that can represent such relationship: a first difference prior and a second difference prior.

In a first difference prior, used for **scenario A "conventional projections"**, each effect is derived from the immediately preceding effect, thus preventing it from varying much with respect to adjacent estimates. Additionally, a restriction is added to bound those first differences stochastically to zero and preserve a constant trend. This is known as a random walk of first order (RW1) and for the age effect is described by:

$$
\theta_i \sim N\Big(\theta_{i-1}, \kappa^{-1}\Big), i = 2, \dots, I.
$$

$$
p(\theta_1) \propto const.
$$

where the hyperparameter κ is also known as the precision parameter: larger values allow baseline effects to vary only slightly, while small values allow more heavy variation.

In a second difference prior, used for **scenario B "trend-based"**, each effect is derived from its two immediate predecessors. A random walk of second order (RW2) restricts the second differences stochastically to zero, which penalizes deviations from a linear trend:

$$
\theta_i \sim N\Big(2\theta_{i-1} - \theta_{i-2}, \kappa^{-1}\Big), i = 2, \dots, I.
$$

$$
p(\theta_1) = p(\theta_2) \propto const.
$$

For both types of prior, κ is assumed to follow a gamma distribution $G(a,b)$. For RW1 $a=1$ and $b = 0.001$ are set as initial values, and for RW2 initial values are $a = 1$ and $b = 10^{-5}$. Similar priors are given to the period φ and cohort effects ψ with hyperparameters λ and ν , respectively.

Because the non-identifiability only affects linear trends, the RW1 solves the problem by keeping the age, period and cohort effects as constant as possible. However, the RW2 parameters are unidentifiable since the RW2 assumes a linear time trend. Fortunately in a Bayesian framework, it is

not essential to ensure identifiability of age, period and cohort effects because 1 *ij ij p log* $\left(\frac{p_{ij}}{1-p_{ij}}\right)$ is fully

identified ⁴. Additionally, many have considered the problem of identifiability in the APC context as unsolvable $5-7$.

Finally, the model can be easily extended to account for additional unstructured heterogeneity which cannot be explained by the age, period or cohort effects but by unknown and unobserved covariates:

$$
log\left(\frac{p_{ij}}{1-p_{ij}}\right) = \mu + \theta_i + \varphi_j + \psi_k + z_{ij}.
$$

$$
z_{ij} \sim N\left(0, \delta^{-1}\right),
$$

where the hyperparameter δ is assumed to follow a gamma distribution $G(a_{\delta},b_{\delta})$ with the same starting values as K .

Estimation

The models can be implemented in BAMP² which uses Markov chain Monte Carlo (MCMC) simulation for the model estimation. MCMC constructs a Markov chain whose stationary distribution approximates the posterior distribution of interest using a single-component Metropolis-Hastings algorithm 8 for the age, period and cohort effects and a Gibbs sampler algorithm 9 for the hyperparameters.

After it has converged to its stationary distribution, samples from the chain can be used to calculate the parameter estimates. We fitted gamma distributions, using the function mass in R, to the samples of each hyperparameter obtained from the chain to generate new values of *a* and *b.* We used these values as new initial values and the models were recalculated.

The new samples of the posterior distribution were used to calculate credible intervals for the probability of death. A $100(1-2p)$ % credible interval $\lfloor c_p - c_{1-p} \rfloor$ is a Bayesian interval estimate where c_p is equal to the p^{th} quantile of the scalar component and where c_{1-p} is equal to the $(1-p)^{th}$ quantile.

Forecast and comparison

Future rates p_{ij} , $j = J + 1, \ldots, j + T$ can be calculated by projecting the age, period and cohort effects into the future by repeated application of the RW1 or RW2 model definitions. Similarly projected effects z_{ij} , $j = J + 1,... j + T$ can be computed independently from $N(0, \delta^{-1})$.

Finally, when different BAPC models need to be compared (e.g. RW1 versus RW2), the Deviation Information Criterion (DIC)¹⁰ provides a simple yet powerful way of evaluating different models. DIC is the sum of two components: a term that measures goodness of fit known as posterior expectation of the deviance and a penalty term for increasing model complexity. Models with smaller DIC should be preferred.

2.2. Validation

We used observed data from 1979-2002 to project CVD mortality for 2003-2012 using both RW1 and RW2 and calculated predictive deviance. The predictive deviance at time *t* is defined as

$$
D_t = 2\sum_j l(\widehat{y_{jt}}) - l(y_{jt})
$$

Where $\widehat{l(\hat{y}_{jt})}$ is the log-likelihood of predicted number of cases in age *j* and period *t* and $\widehat{l(y_{jt})}$ is the maximum log-likelihood achievable. Likewise, models with smaller predictive deviance are preferred.

2.3. Lee-Carter Model

As we discussed in the result section of the manuscript, our trend-based scenario underestimated the number of deaths during 2003-2012. Therefore, we alternatively used the well know Lee-Carter to project mortality over the same period.

Lee and Carter¹¹ developed a method commonly used in actuarial science, that combines a demographic model with time-series methods of forecasting. The model uses a single parameter (mortality index) governs the dynamics of a mortality trend.

Let $m_{x,t}$ be the central mortality rate for age x in year t , the model states

 $\ln(m_{xt}) = \alpha_x + \beta_x k_t + \varepsilon_{xt}$

Where k_t the mortality index is at time t, α_x is the average pattern of mortality by age, β_x is the

relative change with respect to the mortality index at age x and $\varepsilon_{x,t}$ is the residual at age x and year t.

Generally, Lee-Carter models are most suitable for forecasting mortality trends characterised by strong period effects, such as infectious respiratory disease¹². Period effects might capture temporal change in factors associated with medical and broader societal development.

We fitted the basic Lee-Carter model to the 1979-2002 data and projected 2003-2012. Because Lee-Carter produces mortality rates m_{ij} , we transformed these into probabilities of death p_{ij} using the next formula ¹³ to allow for comparison with our BAPC scenarios:

$$
p_{ij} = \frac{m_{ij}}{1 + \frac{m_{ij}}{2}}
$$

Lee-Carter model was implemented using the R package demography 14 , using monotonic regression spines for smoothing, due to having data available only in 5-year age group bands¹⁵

2.4. Race CVD mortality disparities

The BAMP software allows saving the samples of the posterior distribution of the outputs generated during the estimation process. We used these samples to calculate population-adjusted and ageadjusted rate ratios to compare CVD mortality in Blacks and Hispanic with Whites.

For the age-adjusted rate ratios, we obtained the age and gender adjusted probability of death using each iteration of the BAMP software and the 2012 US standard population. We then used bootstrapping to estimate the age and gender adjusted relative risk of mortality and 95% bootstrapped CI.

For the population-adjusted rate ratios, we obtained probability of death standardised by gender, age and race group for each iteration of the BAMP software in years 2012 and 2030. We then used bootstrapping to estimate the relative risk of mortality and 95% bootstrapped CI.

2.5. Age-Period and Cohort Analysis

Random walks models of first order are useful to explore the contributions of age, period and cohort effects on CHD and stroke mortality. More specifically, the hyperparameters of the model gives an idea of the size of the effects. Larger values of the hyperparameters allow baseline effects to vary only slightly, while small values allow more heavy variation.

Supplemental Table 3: Hyperparameter estimates

By far, the most important factor for both sexes in CHD and stroke was age, followed by period and cohort. However for CHD, cohort effects were as important as period effects, especially for men. This is an interesting finding since there is contradictory evidence whether CHD mortality has a cohort effect. APC models built for Australia 16 and New Zealand 17 and other descriptive analyses conducted for Poland and Hungary¹⁸ suggested the absence of any cohort effect. However cohort effects were found in Singapore¹⁹ and Norway²⁰. While a descriptive study in Hong Kong 21 found cohort effects for women but not for men

Looking at the analysis by ethnicity (supplemental table 3), we found only for white men and women the same phenomena. For the rest of the ethnicities cohort has a very small effect in comparison with age and period.

The next graphs show the age, period and cohort effects. Because of some assumptions imposed to the model, we can only interpret non-linear trends or change points. For example, for CHD and for both men and women there is a distinctive peak at the beginning of the $20th$ century. Then, we can observe a less steep slope for men born around 1955, which can be interpreted as a slowing of the effect. Finally, women and men born after 1955 and 1978 respectively experience an increasing trend.

For stroke, we can see series of peaks before and around the First World War. This distinctive peak was also reported by Doll et al. 22 , who reported that those birth cohorts were associated with an historical excess mortality associated with cigarette smoking. Women born around 1955-1960 experience an increasing slope. But, generations born just before 1970-1980 experiment a sharply decreasing slope. New generations born after 1975 (for men) and 1980 (for women) experience an increasing trend

Supplemental Figure 1: Age effects by ethnicity, sex and cause of death

Supplemental Figure 2: Period effects by ethnicity, sex and cause of death

Supplemental Figure 3; Cohort effects by ethnicity, sex and cause of death

Supplemental Figure 4. Validation of mortality projections 2003-2012: Observed rates, Lee-Carter, 'trend-based' and conventional projections. 1A CHD Men, 1B, CHD Women, 1C Stroke Men, 1D Stroke Women

1A.

1B.

1C.

Year

Supplemental Table 4: Hyperparameter estimates by ethnicity

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