

Stochastic Multi-State Modeling for Critical Illness Insurance With Integration of Non-Homogeneous Trends and Pandemic Shocks

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Abstract

This study develops a stochastic pricing framework for critical illness insurance using Indonesian population data. The framework captures the joint effects of mortality, morbidity, and longevity across age and sex. A multi-state model is constructed to represent transitions between one healthy state, eleven critical illness states, and death. Benefits are payable upon the first occurrence of a critical illness, upon death, and upon survival to age 95. Using publicly available incidence, prevalence, and mortality data, transition intensities are derived and projected to reflect future health risk patterns. Particular attention is given to the construction of transition intensities for first-time critical illness events under limited data availability. Pandemic-related mortality distortions are addressed through adjustment procedures, and the age domain is segmented to accommodate non-homogeneous mortality trends. Projection models are selected from seven stochastic mortality models based on performance criteria, and additional noise smoothing is applied when cohort-based models produce unstable projections. The results show that total expected costs for males and females are generally comparable. However, differences remain across age groups and benefit components. These findings support the use of age- and sex-specific pricing structures in critical illness insurance.

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1. INTRODUCTION

Accurate pricing of Critical Illness (CI) insurance is actuarially challenging due to the need to model transitions between health states. Unlike traditional life insurance, which focuses on mortality, CI insurance requires explicit modeling of morbidity, defined as transitions from a healthy state to specific disease states. The Multiple-State Model (MSM) is commonly used for this purpose, as it allows individuals to be represented through several health and death states over time [1].

In many applications, transition intensities in the MSM are assumed to follow static or deterministic trends. Such assumptions may not fully capture stochastic changes in morbidity or the presence of structural shocks. The COVID-19 pandemic provides an example of a disruption that affects both mortality and morbidity patterns [2]. Given the long-term horizon of CI insurance contracts, it is necessary to consider models that allow for non-homogeneous trends and sudden changes in health risks.

Several studies have applied MSMs to CI pricing in Indonesia. One study priced cancer-specific CI insurance using claim data from a private insurance company [3]. Another study examined stroke insurance for the Indonesian population using a 33-state model with 1,089 transition probabilities and multiple risk factors [4]. These studies are based on pre-COVID-19 data. To the authors' knowledge, there is no existing study for Indonesian data that incorporates COVID-19-related mortality and morbidity changes into a multiple-state framework.

This study focuses on the actuarial derivation of CI insurance premiums using Kolmogorov's forward equations. The analysis emphasizes data processing and estimation of transition intensities, including the treatment of age-dependent trends and pandemic-related shocks. The model is constructed for a CI product with 11 distinct critical illness states.

Previous work has considered the estimation of transition intensities using prevalence data only, motivated by the limited availability of incidence data [5]. In contrast, incidence data are available for this study. The primary challenge, therefore, lies not in data scarcity but in constructing transition intensities that align precisely with the contractual definition of CI benefits. In particular, the CI benefit is payable only upon the first occurrence of a critical illness, while multiple illness categories are considered.

This paper develops a stochastic multi-state model consisting of one healthy state, one death state, and 11 critical illness states. The critical illness states are chosen according to the definition from the Indonesian Life Insurance Association (AAJI) [6], subject to the availability of historical incidence and prevalence data in Indonesia. The state structure is designed to avoid overlapping illness states for individuals with multiple conditions. Transition intensities are projected using non-homogeneous age trends and pandemic-related adjustments. These projected intensities are then used to calculate CI insurance premiums.

This study differs from existing CI pricing studies in Indonesia in several aspects. First, the model incorporates mortality and morbidity changes observed during the COVID-19 period into the estimation and projection of transition intensities. Second, the multi-state structure is designed to reflect CI contract conditions by allowing benefits only at the first critical illness occurrence, despite the inclusion of multiple illness categories. Third, incidence-based transition intensities are estimated and projected using non-homogeneous age trends, rather than assuming time-homogeneous or deterministic patterns. These features allow the model to reflect recent health shocks and contractual constraints more explicitly than previous Indonesian CI pricing studies.

2. METHODS

The methodology of this study consists of three main steps: estimation of transition intensities, projection of transition intensities, and premium calculation. The insurance provides critical illness coverage for 11 distinct critical illnesses. These illnesses are chosen as the best effort to replicate AAJI's critical illness definition [6], subject to the availability of historical incidence and prevalence data for Indonesia.

The critical illnesses modeled in this study are Alzheimer's disease, chronic kidney disease, ischemic heart disease, rheumatic heart disease, meningitis, neoplasms (cancer), Parkinson's disease, chronic obstructive pulmonary disease (COPD), chronic respiratory diseases, multiple sclerosis, and stroke. To avoid overlapping disease statuses and to reflect the contract condition that benefits are payable only upon the first occurrence of a critical illness, each critical illness state is defined as the state in which that illness is the first critical illness experienced by an individual.

Transition intensities are parameterized using data from the Global Burden of Disease (GBD) study provided by the Institute for Health Metrics and Evaluation (IHME) [7]. The dataset includes incidence, prevalence, mortality, and population counts for Indonesia for each of the 11 critical illnesses. All data are reported in 5-year age groups, ranging from ages 0–4 to 90–94.

The insurance contract provides a fixed lump sum benefit payable immediately upon the first diagnosis of any of the 11 specified critical illnesses, equal to 50% of the sum assured. If the insured subsequently dies after receiving the critical illness benefit, an additional lump-sum benefit of 50% of the sum assured is paid. If death occurs without any prior critical illness claim, a lump-sum benefit of 100% of the sum assured is paid. If the insured survives to age 95, the remaining unpaid sum assured is paid, equal to 100% of the sum assured if no critical illness benefit has been paid, or 50% if a critical illness benefit has already been paid.

Premiums are calculated using a Multi-State Model consisting of 23 transitions: 11 transitions from the healthy state to the 11 critical illness states, 11 transitions from each critical illness state to the death state, and one transition from the healthy state to the death state. The structure of the Multi-State Model is shown in **Figure 1**.

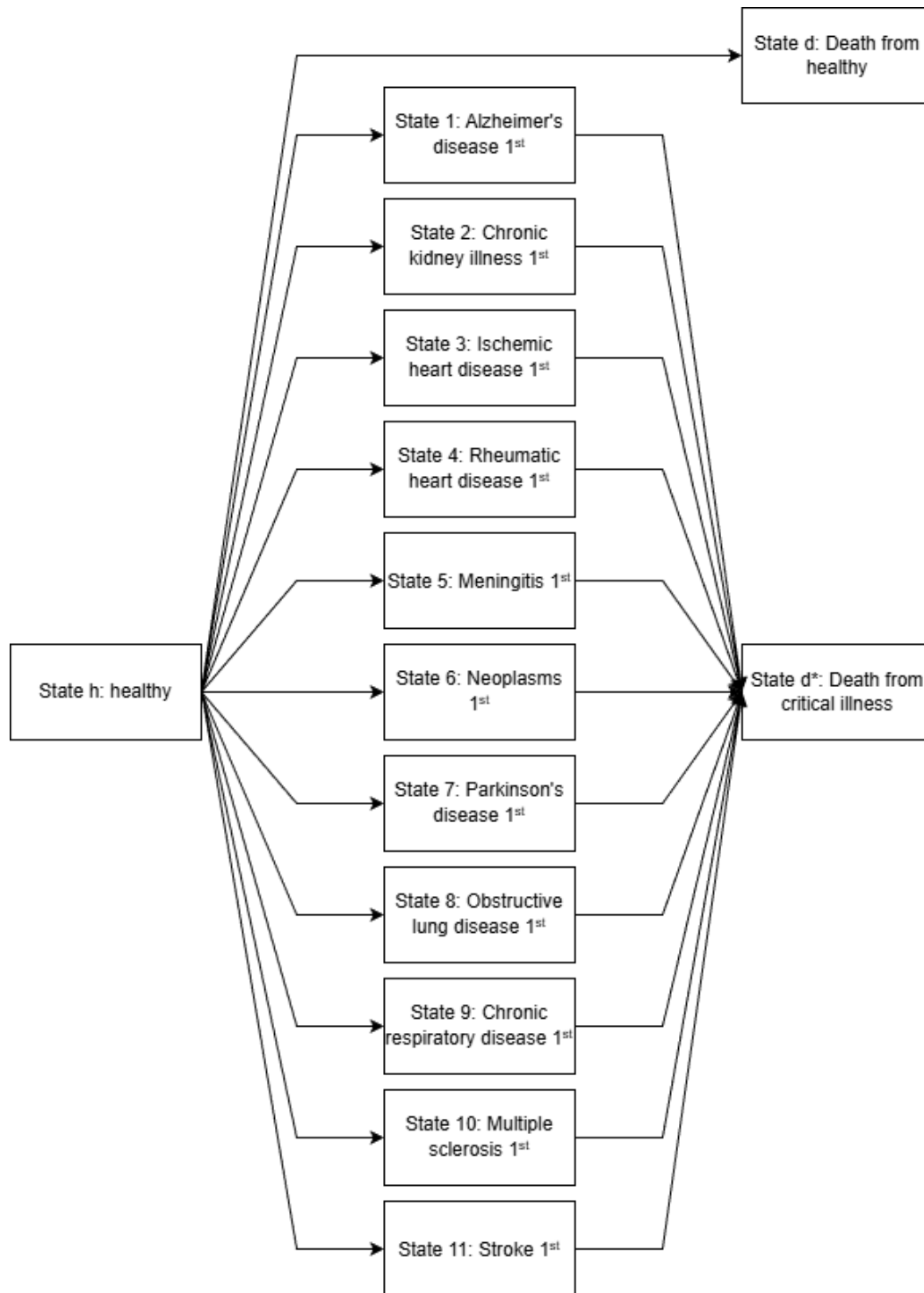


Figure 1. The multiple state model framework.

2.1 Obtaining Transition Intensities

The available data consists of mortality counts, disease prevalence, disease incidence, and population exposures. These data cannot be used directly to estimate transition intensities, as they do not provide information on joint disease prevalence, first-time incidence, or transition rates at single-year ages. As a result, several assumptions and approximations are required, as described below.

The data sources report prevalence for each critical illness separately. In practice, an individual may experience more than one critical illness, but information on the joint prevalence of multiple diseases is not available. To address this limitation, the occurrence of each critical illness is assumed to be independent of the others. The assumption of independence may overestimate the incidence of first critical illness events, as comorbidities and disease correlations are not captured. This overestimation leads to higher expected benefit values and, consequently, higher premiums. As a result, the independence assumption produces conservative premium estimates from a solvency perspective and does not weaken the insurer's ability to meet future liabilities.

The assumptions above are implemented through the following probabilistic formulation. Let disease i denote the i -th critical illness, for $i \in \{1, 2, \dots, 11\}$. Let $X_{x,t,i} = 1$ indicate that an individual aged x in year t is affected by disease i . Under the independence assumption, the joint probability that an individual is affected by multiple diseases is given by

$$P[X_{x,t,i} = 1 \cap X_{x,t,j} = 1 \cap \dots \cap X_{x,t,k} = 1] = P[X_{x,t,i} = 1] \times P[X_{x,t,j} = 1] \times \dots \times P[X_{x,t,k} = 1],$$

where $i, j, k \in \{1, 2, \dots, 11\}$.

The probability that an individual aged x in year t is affected by disease i is computed as

$$P[X_{x,t,i} = 1] = \frac{PREV_{x,t}^i}{POP_{x,t}},$$

where $PREV_{x,t}^i$ denotes the prevalence of disease i at age x in year t , and $POP_{x,t}$ denotes the corresponding population exposure. Prevalence data are used at this stage to approximate the distribution of individuals across health states, which is required to construct the initial state probabilities in the multi-state model. Consequently, the probability that an individual aged x in year t is healthy, and thus the proportion of healthy individuals at that age and time, is defined as

$$P[X_{x,t} = \text{healthy}] = \prod_{i=1}^{11} \left(1 - \frac{PREV_{x,t}^i}{POP_{x,t}}\right).$$

The mortality data obtained from the IHME report deaths by specific causes, including critical illnesses. However, deaths arising from causes other than critical illnesses are not reported separately. Let $D_{x,t}^\bullet$ denote total deaths at age x in year t , and let $D_{x,t}^i$ denote deaths attributable to critical illness i . The number of deaths originating from the healthy state is therefore defined as

$$D_{x,t}^h = D_{x,t}^\bullet - \sum_{i=1}^{11} D_{x,t}^i.$$

In the insurance product considered, critical illness benefits are payable only upon the first occurrence of any critical illness. Accordingly, the multi-state model includes only transitions corresponding to the first onset of a critical illness, while subsequent occurrences of other critical illnesses are not modeled. The available data report total disease incidence rather than first-time incidence. To address this, the problem is formulated as a multiple-decrement model, in which exits from the healthy state correspond to the first critical illness event.

Let $\varphi'_{x,t}$ denote the probability that an individual aged x in year t contracts disease i , given that the individual was healthy in the previous year. This probability is estimated as

$$\varphi'_{x,t} = \frac{I_{x,t}^i}{H_{x-1,t-1}},$$

where $I_{x,t}^i$ denotes the observed incidence of disease i and $H_{x-1,t-1}$ denotes the number of healthy individuals in the previous year. The quantity $\varphi'_{x,t}$ represents the associated single-decrement probability, as it does not account for competing exits due to other illnesses.

Let $\varphi_{x,t}$ denote the probability that disease i is the first critical illness experienced by an individual, conditional on the individual being healthy in the previous year. This probability is defined as

$$\varphi_{x,t} = \frac{\tilde{I}_{x,t}^i}{H_{x-1,t-1}},$$

where $\tilde{I}_{x,t}^i$ represents first-time incidence. Let $\mu_{x,t}^{hi}$ denote the transition intensity from the healthy state to critical illness i , and let $\mu_{x,t}^{h\bullet}$ denote the total exit intensity from the healthy state, defined as

$$\mu_{x,t}^{h\bullet} = \mu_{x,t}^{hd} + \sum_{i=1}^{11} \mu_{x,t}^{hi}.$$

Under the assumption that transition intensities are constant within each age–time interval, the following relationship holds [1]

$$\varphi_{x,t} = \left(\frac{\mu_{x,t}^{hi}}{\mu_{x,t}^{h\bullet}} \right) \varphi_{x,t}^{h\bullet}. \quad (1)$$

Using the independence assumption across critical illnesses, the total incidence of critical illness at age x in year t is computed as

$$I_{x,t}^{\bullet} = POP_{x,t}(1 - p_{x,t}^{hh}) = POP_{x,t} \left(1 - \prod_{i=1}^{11} (1 - \varphi'_{x,t}) \right). \quad (2)$$

Since the transition intensity from the healthy state to critical illness i satisfies $\mu_{x,t}^{hi} = I_{x,t}^i / H_{x-1,t-1}$, substitution into Equation (1) yields

$$\tilde{I}_{x,t}^i = \left(\frac{I_{x,t}^i}{\sum_{j=1}^{11} I_{x,t}^j} \right) I_{x,t}^{\bullet}. \quad (3)$$

Equations (2) and (3) jointly provide estimates of first-time critical illness incidence for each disease. The multiple-state model adopted in this study follows a permanent disability structure, in which recovery from critical illness is not permitted. The model consists of one healthy state, eleven critical illness states, and death states differentiated by origin.

The transition intensity from the healthy state to death is defined as

$$\mu_{x,t}^{hd} = \frac{D_{x,t}^h}{H_{x-1,t-1}}.$$

The available data are reported in five-year age groups, $[x, x+5)$. As a result, the exposure $H_{[x-1, x+4), t-1}$ is not directly observed. To address this, the following approximation is applied:

$$H_{[x-1, x+4), t-1} = 0.8H_{[x, x+5), t-1} + 0.2H_{[x-5, x), t-1}. \quad (4)$$

The justification for Equation (4) is based on the overlap between adjacent five-year age groups. At time $t-1$, ages x to $x+4$ belong to the age group $H_{[x, x+5), t-1}$ and account for four out of the five ages in the interval

$[x - 1, x + 4)$. The remaining age, $x - 1$, represents one-fifth of the interval and belongs to the age group $H_{[x-5,x),t-1}$. Accordingly, 80% of the exposure in $H_{[x-1,x+4),t-1}$ is approximated by $H_{[x,x+5),t-1}$ while the remaining 20% is approximated by $H_{[x-5,x),t-1}$.

Using Equation (4), the grouped transition intensities are computed as:

$$\begin{aligned}\mu_{[x,x+5),t}^{hd} &= \frac{D_{[x,x+5),t}^h}{(0.8H_{[x,x+5),t-1} + 0.2H_{[x-5,x),t-1})}, \\ \mu_{[x,x+5),t}^{hi} &= \frac{\tilde{I}_{[x,x+5),t}^i}{(0.8H_{[x,x+5),t-1} + 0.2H_{[x-5,x),t-1})}, \\ \mu_{[x,x+5),t}^{id*} &= \frac{D_{[x,x+5),t}^i}{(0.8PREV_{[x,x+5),t-1}^i + 0.2PREV_{[x-5,x),t-1}^i)}\end{aligned}$$

The resulting transition intensities are defined over five-year age intervals. To obtain age-specific transition intensities at single-year ages, these grouped intensities are smoothed using P-spline models. Each transition intensity is modeled separately for each calendar year. Each grouped transition intensity $\mu_{[x,x+5),t}^{ij}$ is assigned to the mid-age, $x + 2.5$, using a midpoint approximation. Observations for ages below five years are excluded, as the insurance product is not intended for individuals under age five, and infant mortality may distort the estimates. The age domain considered is therefore $x \in \{7.5, 12.5, 17.5, \dots, 92.5\}$.

The fitted P-spline curves are evaluated at midpoints, $x + 0.5$, to obtain annual age-specific transition intensities $\mu_{[x,x+1),t}^{ij}$. These age-specific intensities are subsequently used in the valuation of insurance benefits. A similar P-spline approach has been applied in previous studies to address grouped age data in multi-state models [8].

2.2 Stochastic Projection of Transition Intensities

The insurance cost calculation in this study is performed for policies issued in 2026. Accordingly, the transition intensities used in the valuation must reflect future mortality and morbidity conditions rather than relying solely on historical data. To address this, transition intensities are projected forward using stochastic mortality projection models.

The projection framework follows the stochastic mortality models implemented in the StMoMo package in the R programming language [9], including the Lee–Carter (LC), Age–Period–Cohort (APC), Cairns–Blake–Dowd (CBD), Renshaw–Haberman (RH), and the extended models M6, M7, and M8. For each transition intensity, the model with the smallest Mean Absolute Percentage Error (MAPE) over the historical period is selected as the preferred projection model.

The historical data used in this study cover the period 1990–2021. COVID-19 is not classified as a critical illness within the multi-state framework. As a result, the pandemic produced significant outliers in the transition intensity from the healthy state to death during 2020 and 2021, particularly at older ages [10]. This effect is confined to the transition from healthy to death. According to the IHME definition, mortality is recorded by specific cause. Deaths attributable to COVID-19 are therefore classified separately and are not included among the defined critical illnesses. Consequently, the pandemic affects only the healthy-to-death transition intensity, while the other transition intensities remain unaffected.

Figure 2. illustrates the mortality spike at age 80 in 2021, together with the projected mortality path if no adjustment is applied. The pandemic-related spike distorts the underlying mortality trend and results in unrealistically increasing projected mortality rates in subsequent years. To reduce this distortion, one approach is to extend the dataset beyond the pandemic period so that the projection model can incorporate post-pandemic mortality patterns. For this purpose, additional total mortality data up to 2023 are obtained from the United

Nations [11]. However, the model requires mortality from the healthy state rather than total mortality. Therefore, the following approximation is applied for the years 2022 and 2023:

$$\mu_{x,t}^{hd} = \left(\frac{D_{x,t}^{\bullet}}{D_{x,2019}^{\bullet}} \right) \mu_{x,2019}^{hd}, \quad t = 2022, 2023. \quad (5)$$

The justification for Equation (5) assumes that the transition intensity from the healthy state to death is proportional to the total number of deaths in a given year. The year 2019 is used as a benchmark, as it represents the last pre-pandemic year and reflects baseline mortality conditions. Under this assumption, the healthy-to-death transition intensity for 2022 and 2023 is adjusted proportionally to the corresponding total mortality levels. Consequently, the dataset used to project the healthy-to-death transition intensity covers the period 1991–2023. For all other transitions (healthy to illnesses or illnesses to death), the projection period remains 1991–2021, since these transitions are not affected by COVID-19-related mortality.

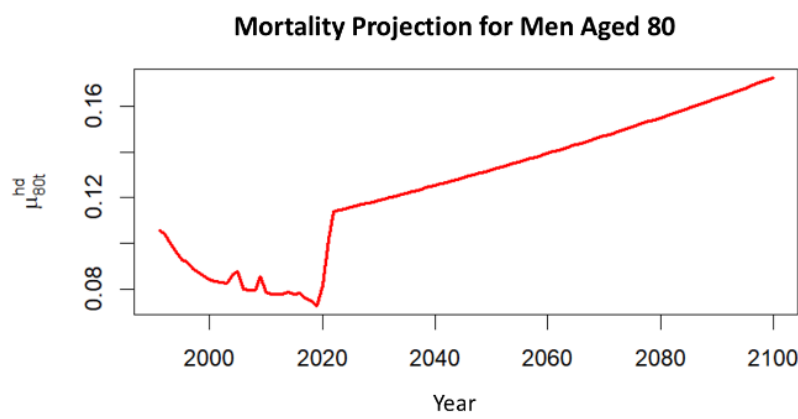


Figure 2. Effect of the COVID-19 pandemic on mortality projections for males aged 80.

After correcting for the COVID-19 outliers, the projection models still exhibit suboptimal performance, as indicated by systematic patterns in the residuals. Further examination suggests that this issue arises from non-homogeneous mortality trends across age groups. For example, the transition intensity from chronic kidney disease to death for females decreases by 23.13% for ages 5–9 during 1991–2021, while increasing by 79.95% for ages 90–94 over the same period. Such heterogeneous age-specific trends make it difficult for a single projection model to capture mortality dynamics uniformly across all ages.

Even for the model with the lowest MAPE (the RH model), as shown in **Figure 3.**, the residuals display systematic patterns, particularly at older ages. The magnitude of residuals at older ages is noticeably larger than at younger ages, indicating a poorer fit in the higher age range.

To address this issue, the age domain is partitioned into separate groups for projection purposes. Previous studies indicate that mortality patterns differ substantially across age ranges: younger ages are often characterized by accident-related humps, working-age adults exhibit relatively stable mortality dynamics, and older ages display distinct and rapidly changing mortality patterns [12], [13], [14]. Based on these findings, the data are projected separately for three age groups: 5–34 (young ages), 35–64 (working ages), and 65–94 (older ages). Ages below 5 are excluded, as the insurance product does not cover individuals younger than 5 years, and ages above 94 are excluded due to data limitations.

This age segmentation substantially improves projection performance. In certain transitions, such as the transition from chronic kidney disease to death for females, the Mean Absolute Percentage Error (MAPE) is reduced by up to 85%.

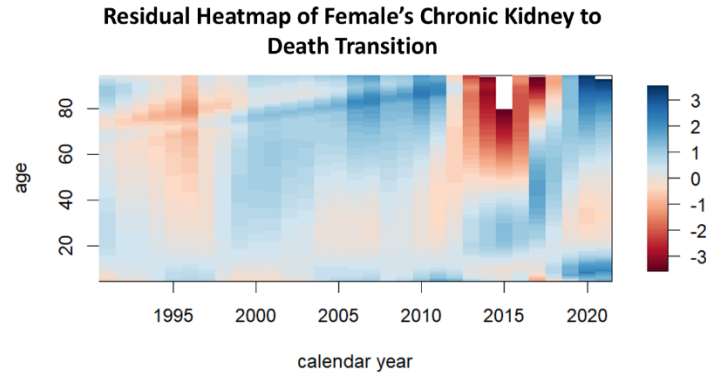


Figure 3. Heatmap of residuals for the chronic kidney disease–to–death transition intensity in females.

After projection, the resulting transition intensities are evaluated to determine whether further adjustment is required before use in insurance cost calculations. Among the projection models considered, the LC and CBD models do not include cohort effects, whereas the APC, RH, M6, M7, and M8 models incorporate cohort components. Although cohort effects can improve model fit by capturing birth-cohort-related mortality patterns, they introduce a large number of additional parameters. This increased complexity reduces the stability of the fitting procedure and increases sensitivity to random fluctuations in the data. Consequently, cohort-based models may generate unrealistic jumps or spikes in projected transition intensities. For example, in the projection of the transition intensity from first ischemic heart disease to death for young males, the RH model produces an implausible spike. In this study, all projections requiring additional smoothing originate from models that include cohort effects, suggesting reduced robustness of these models in the presence of random noise.

To mitigate this issue, a noise smoothing model is applied using a P-spline. The smoothing parameter cannot be selected using cross-validation, as cross-validation results do not adequately remove projection noise. The smoothing parameter lies in the interval $[0,1]$, where values close to 0 correspond to a tight fit and values closer to 1 produce a smoother curve. In the absence of a formal selection criterion, the parameter is chosen based on visual inspection and actuarial judgment. Given that the observed projection spikes are considered unrealistic, a smoothing parameter of 0.6 is selected to prioritize noise reduction while preserving the overall projection trend.

2.3 Deriving Pricing Formula

This section derives the pricing formula for the critical illness insurance product using the multiple-state framework introduced previously. The sum insured is normalized to one, so that the resulting premium can be scaled linearly. The total expected present value (EPV) of benefits consists of four components: death from the healthy state (first component), first occurrence of critical illness (second component), death following a critical illness (third component), and survival benefit at age 95 (fourth component). All expectations are calculated for an individual aged x at calendar time t , with benefits payable up to age 95.

Let $f_{x,t}^{hd}(s)$ denote the probability density function of the time s to death from the healthy state, without experiencing any critical illness. Let the continuous discount rate be δ , so that the discount factor is $v^s = e^{-\delta s}$. The EPV of the benefit payable upon death from the healthy state is

$$\mathbb{E}[B_{x,t}^{(1)}] = \int_0^{95-x} f_{x,t}^{hd}(s) v^s ds.$$

Using Kolmogorov's forward equations, the density function can be written as

$$f_{x,t}^{hd}(s) = {}_s p_{x,t}^{hh} \mu_{x+s,t+s}^{hd},$$

where the survival probability in the healthy state is

$${}_s p_{x,t}^{hh} = \exp \left(- \int_0^s \left(\mu_{x+u,t+u}^{hd} + \sum_{i=1}^{11} \mu_{x+u,t+u}^{hi} \right) du \right).$$

Substituting yields

$$\mathbb{E}[B_{x,t}^{(1)}] = \int_0^{95-x} \exp \left(- \int_0^s \left(\mu_{x+u,t+u}^{hd} + \sum_{i=1}^{11} \mu_{x+u,t+u}^{hi} \right) du \right) \mu_{x+s,t+s}^{hd} v^s ds.$$

Let $f_{x,t}^{hi}(s)$ denote the density of transition from healthy to critical illness i . The benefit payable upon first diagnosis is 0.5. The EPV of this component is

$$\mathbb{E}[B_{x,t}^{(2)}] = \sum_{i=1}^{11} \int_0^{95-x} 0.5 f_{x,t}^{hi}(s) v^s ds.$$

The transition from the healthy state to a critical illness is assumed to be independent of the subsequent transition from critical illness to death. Under this assumption, the multi-state structure shown in **Figure 1**. can be reduced to a multiple-decrement model with exits from the healthy state to 11 critical illness states and one death state. Within this multiple-decrement framework, the density of transition from the healthy state to critical illness i is given by:

$$f_{x,t}^{hi}(s) = {}_s p_{x,t}^{hh} \mu_{x+s,t+s}^{hi}.$$

Hence,

$$\mathbb{E}[B_{x,t}^{(2)}] = \int_0^{95-x} \sum_{i=1}^{11} 0.5 \exp \left(- \int_0^s \left(\mu_{x+u,t+u}^{hd} + \sum_{j=1}^{11} \mu_{x+u,t+u}^{hj} \right) du \right) \mu_{x+s,t+s}^{hi} v^s ds.$$

Let $\mu_{x,t}^{id*}$ denote the transition intensity from critical illness i to death. The unconditional density of death following critical illness i , is obtained by integrating over the possible times of disease onset. Omitting the intermediate derivations for brevity, the EPV of death after critical illness is given by:

$$\begin{aligned} \mathbb{E}[B_{x,t}^{(3)}] &= \int_0^{95-x} \sum_{i=1}^{11} \int_0^s \exp \left(- \int_u^s \mu_{x+v,t+v}^{id*} dv \right) \mu_{x+s,t+s}^{id*} \\ &\quad \times \exp \left(- \int_0^u \left(\mu_{x+v,t+v}^{hd} + \sum_{j=1}^{11} \mu_{x+v,t+v}^{hj} \right) dv \right) \mu_{x+u,t+u}^{hi} du v^s ds. \end{aligned}$$

If the insured survives to age 95, a maturity benefit is paid. The benefit equals 1 (in proportion to the sum assured) if the insured remains in the healthy state, and 0.5 if the insured is in any critical illness state at age 95. EPV of the survival benefit is given by:

$$\mathbb{E}[B_{x,t}^{(4)}] = {}_{95-x} p_{x,t}^{hh} v^{95-x} + 0.5 \sum_{i=1}^{11} {}_{95-x} p_{x,t}^{hi} v^{95-x},$$

where

$${}^{95-x}p_{x,t}^{hi} = \int_0^{95-x} {}^u p_{x,t}^{hh} \mu_{x+u,t+u}^{hi} du.$$

Substituting gives

$$\begin{aligned} \mathbb{E}[B_{x,t}^{(4)}] &= \exp\left(-\int_0^{95-x} (\mu_{x+u,t+u}^{hd} + \sum_{i=1}^{11} \mu_{x+u,t+u}^{hi}) du\right) v^{95-x} \\ &+ 0.5 \sum_{i=1}^{11} \left(\int_0^{95-x} \exp\left(-\int_0^u (\mu_{x+v,t+v}^{hd} + \sum_{j=1}^{11} \mu_{x+v,t+v}^{hj}) dv\right) \mu_{x+u,t+u}^{hi} du\right) v^{95-x}. \end{aligned}$$

The total EPV of benefits for an individual aged x at time t is obtained by summing up all benefit components:

$$\mathbb{E}[B_{x,t}] = \mathbb{E}[B_{x,t}^{(1)}] + \mathbb{E}[B_{x,t}^{(2)}] + \mathbb{E}[B_{x,t}^{(3)}] + \mathbb{E}[B_{x,t}^{(4)}]. \quad (6)$$

3. RESULT AND DISCUSSION

3.1 Obtaining Transition Rates and Their Projections

The procedures described in Subsection 2.1 are applied to obtain the transition intensities. However, since the available data are reported in five-year age groups, the estimated transition rates are also defined over five-year intervals. As explained in Subsection 2.1, P-spline models are employed to derive single-year age-specific transition intensities.

The P-spline smoothing is applied to all 23 transition intensities for each gender, resulting in 46 datasets in total. Across these datasets, the Mean Absolute Percentage Error (MAPE) of the P-spline fit is below 15% in all cases. Higher MAPE values occur in transitions that exhibit irregular patterns across age.

An example is shown in **Figure 4.**, which presents the transition intensity from meningitis to death for females. This transition yields the highest MAPE among female transitions (12%). The grouped transition intensities at ages 72.5, 77.5, and 82.5 display an inconsistent increasing and decreasing pattern. As a result, the P-spline model underestimates the transition intensities at ages 72.5 and 82.5, where sharp increases are observed, and overestimates the transition intensity at age 77.5, where a sharp decline occurs.

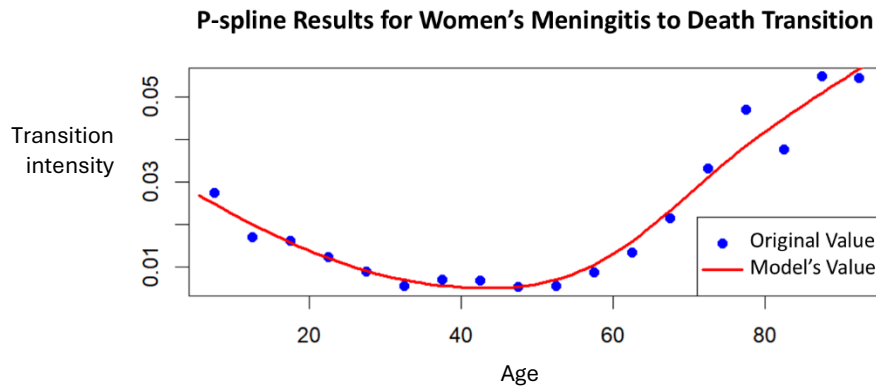


Figure 4. P-spline fit for the meningitis-to-death transition intensity in females.

After obtaining age-specific transition intensities, the projection is performed using stochastic mortality models. As described in Subsection 2.2, the transition intensity from the healthy state to death is adjusted to

account for pandemic-related outliers using the procedure outlined in that subsection. The adjusted transition intensities are shown in **Figure 5**.

As illustrated in **Figure 5**, the projection continues the long-term declining mortality trend. However, this adjustment does not completely eliminate the influence of the pandemic, since the 2020–2021 observations remain included in the projection dataset.

Following the pandemic adjustment, the issue of non-homogeneous age trends is addressed by dividing the data into three age groups, as described in Subsection 2.2. As a result, the projection is performed separately for each age group. In total, 138 transition intensity datasets are projected ($23 \text{ transitions} \times 2 \text{ genders} \times 3 \text{ age groups}$).

For females, 53 out of the 69 projected transition intensities select the Renshaw–Haberman (RH) model as the best-performing model based on MAPE. The highest MAPE among the 69 female transitions is 2.8%, corresponding to the transition from healthy to rheumatic heart disease in the 35–64 age group.

For males, 41 out of 69 transition intensities select the RH model as the preferred model. The highest MAPE among male transitions is 8.58%, observed for the transition from Parkinson’s disease to death in the 5–34 age group. One contributing factor to this relatively higher MAPE is the absence of observed Parkinson’s prevalence below age 20. Consequently, the projection for the 5–34 age group is effectively driven by data from ages 20–34 only.

The dominance of the RH model across both genders indicates the relevance of incorporating cohort effects in modeling mortality and morbidity dynamics in Indonesia. Overall, the MAPE values across all projected transitions remain below 10%, suggesting that the selected models adequately capture the historical trends in the transition intensities.

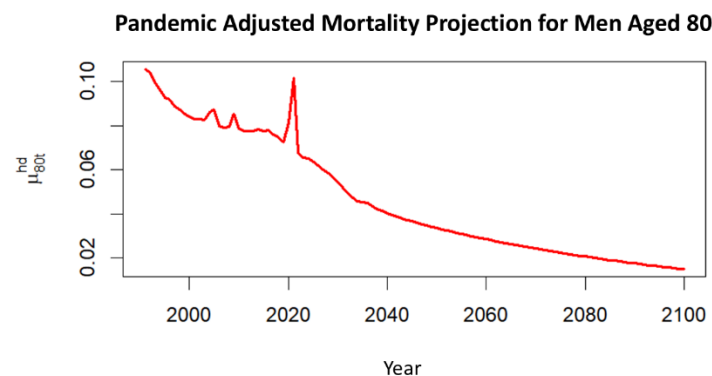


Figure 5. Mortality projection for men aged 80 after pandemic adjustment.

After the transition intensities were projected, eight transition intensity groups required additional noise smoothing, as described in Subsection 2.2. All eight projections were generated by models incorporating cohort

effects: seven were based on the RH model and one on the M7 model. An example of the projection noise and the corresponding smoothing results is presented in **Figure 6**.

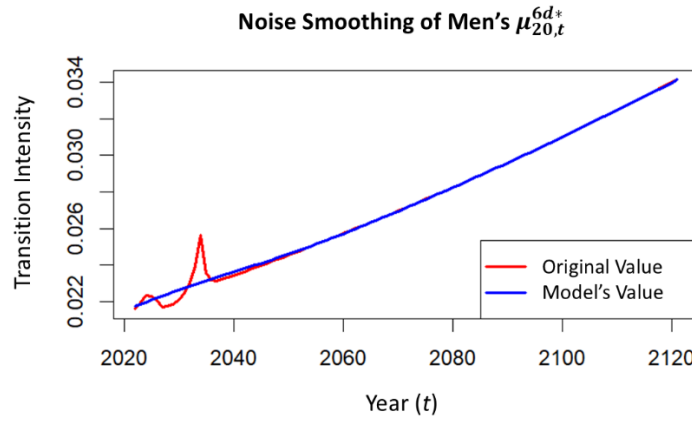


Figure 6. Example of noise smoothing applied to projected transition intensities.

3.2 Premium Calculation Results

Using the formulas presented in Section 2.3, the single premium results are shown in **Figure 7**. The expected present values of the four cost components are displayed separately in the four panels of the figure: $B_{x,2026}^{(1)}$ appears in the top-left panel, $B_{x,2026}^{(2)}$ in the top-right panel, $B_{x,2026}^{(3)}$ in the bottom-right panel, and $B_{x,2026}^{(4)}$ in the bottom-left panel.

For the first cost component, $B_{x,2026}^{(1)}$, males exhibit higher expected values at younger ages, whereas females exhibit higher expected values at older ages. This pattern suggests that males have a higher probability of death from the healthy state at younger ages, but a lower probability at older ages compared to females.

In contrast, the second cost component, $B_{x,2026}^{(2)}$, shows the opposite pattern. This indicates that, when aggregated across the 11 critical illnesses, females have a higher probability of experiencing a first critical illness at younger ages, but a lower probability at older ages relative to males.

The third cost component, $B_{x,2026}^{(3)}$, shows consistently higher expected values for males across all ages. This suggests that, conditional on the occurrence of any of the 11 critical illnesses, males have a shorter expected remaining lifetime than females.

For the fourth cost component, $B_{x,2026}^{(4)}$, the expected values for males and females are nearly identical up to age 45. Beyond age 45, females exhibit higher expected values. This pattern indicates that, conditional on reaching age 45, females have a higher probability of surviving to age 95 compared to males, reflecting a longer remaining life expectancy for females.

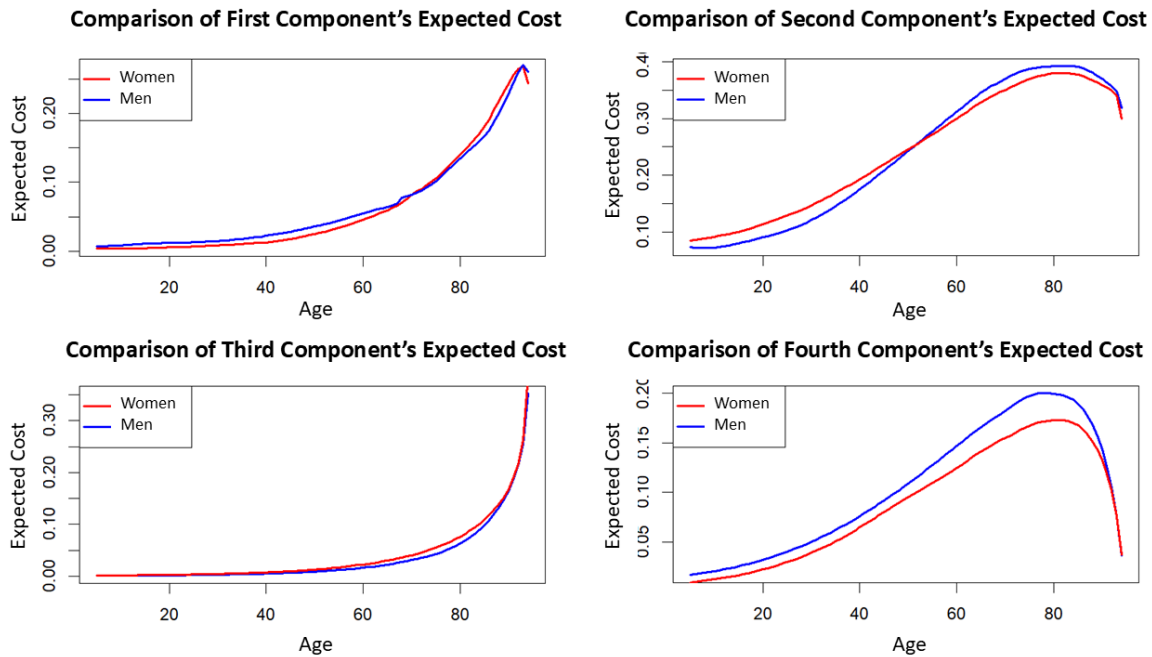


Figure 7. Each component's cost comparison by gender.

A comparison of total expected costs, as defined by Equation (6), is presented in **Figure 8**. The figure shows that males have lower total expected costs at ages below 40, but higher total expected costs at ages above 40.

The lower expected costs for males at younger ages are primarily driven by lower values of the second and fourth cost components. In contrast, at older ages, males exhibit higher total expected costs mainly due to higher values of the third cost component.

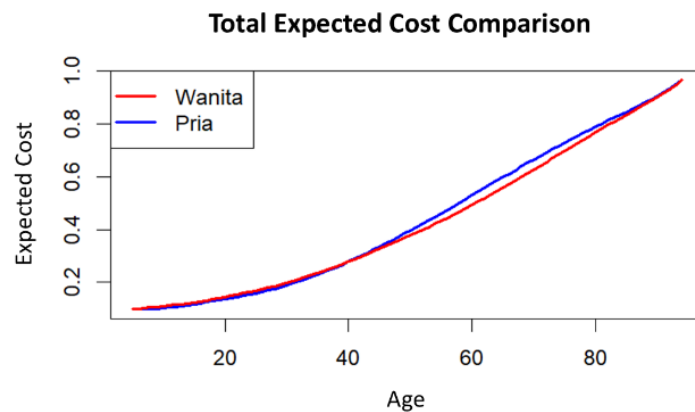


Figure 8. Total expected present value of benefits by gender.

4. CONCLUSIONS

This study examines how mortality, morbidity, and longevity jointly influence the pricing of critical illness insurance using Indonesian population data. Although total expected costs for males and females are broadly similar, differences arise across age groups and benefit components. Males exhibit higher expected costs related to death following a critical illness, reflecting shorter post-diagnosis survival. In contrast, females show higher expected costs associated with critical illness incidence at younger ages and survival benefits at older

ages. These results indicate the importance of modeling both disease incidence and post-illness survival when pricing critical illness products.

A key contribution of this study is the construction of transition intensities from aggregated population data. First-time critical illness incidence is approximated within a multiple-decrement framework under data limitations. The findings also demonstrate that structural shocks, such as the COVID-19 pandemic, must be explicitly addressed, as unadjusted mortality spikes can distort long-term projections and affect pricing results. In addition, projection models incorporating cohort effects require further smoothing to mitigate instability and unrealistic fluctuations. Overall, the results support the use of age- and sex-specific pricing structures to reflect underlying health risks and longevity patterns in the Indonesian context.

This study also provides practical implications for actuarial practice in Indonesia. In practice, critical illness products are often modeled by aggregating all illnesses into a single state for computational simplicity. While this approach is efficient, it does not provide information on disease-specific incidence or expected survival following each illness. The multi-state framework adopted in this study allows for a more detailed assessment of both aspects. This information can assist insurers in evaluating how changes in claim definitions or coverage conditions affect expected cash flows. It may also support claim management strategies by identifying illnesses with higher financial impact. Furthermore, estimates of expected remaining lifetime following each illness can improve liability modeling by incorporating the health-state composition of the insured portfolio.

This study has several limitations. The analysis relies on aggregated population-level data and simplifying assumptions required to construct transition intensities under data constraints. In particular, the assumption of independence among critical illnesses and the approximation of first-time incidence within a multiple-decrement framework may not fully capture dependence across diseases. In addition, pandemic adjustments and projection smoothing are based on actuarial judgment rather than a structural epidemiological model, which may affect long-term projections. Future research may address these limitations by incorporating dependence modeling between diseases, using individual-level longitudinal data when available, and developing formal pandemic-adjustment or regime-switching frameworks to enhance projection robustness.

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