Epidemiological Models in Actuarial Mathematics

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Abstract

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The emergence of the worldwide SARS epidemic in 2003 led to a revived interest in the study of infectious diseases. Mathematical models have become important tools in analyzing transmission dynamics and measuring effectiveness of controlling strategies. In hope of further applying them to design insurance coverage against infectious diseases, the author makes an attempt to build a bridge between epidemiological modelling and actuarial mathematics.

Based on classical compartment models of ordinary differential equation systems, the first part of this thesis is devoted to developing insurance policies among susceptible and infected participants and then formulating their financial obligations using actuarial notation. For the purpose of practical applications, the thesis employs a variety of parameter estimation techniques and numerical methods of calculating premiums and reserves. The theory is later demonstrated to design insurance products for the Great Plague in Eyam and the SARS Epidemic in Hong Kong.

In the second part, the thesis also investigates a stochastic model by incorporating the theory of comonotonicity and copulas. The idea of approximating a random vector indicating infectivity levels is developed by two approaches. While one is to find its closest conditional random vector in stochastic orders, the other examines the dependency structure of its component variables through copulas and then constructs a new random vector by transforming uniform random variables.

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謹以此文獻給我的父母

Dedicated to my dear parents.

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Chapter 1

Introduction

1.1 Background

One beneficial side of the Severe Acute Respiratory Syndrome (SARS) epidemic in 2002 has been to draw tremendous attention to the treatment and prevention of infectious diseases and to their deep impact on general social welfare. The adverse economic impact caused by SARS in East Asia has been compared with its 1998 financial market crisis in that area. From a social point of view, an effective protection against diseases depends not only on the improvement of medical technology but also on a well-designed healthcare system, which reduces the financial impact of medical costs and prevention measures such as vaccination and quarantine. Therefore, as actuaries are urged to expand their expertise to deal with epidemics in healthcare systems, infectious disease modelling is very likely to play a more important role in actuarial science.

In some Asian countries, health insurers start to provide coverage designed to compensate for medical costs due to SARS, in spite of inadequate clinical data and

unsophisticated techniques. The disease is simply listed as an extended liability to a regular health insurance policy with an additional charge proportional to its death rate. But problems arose - not only were such premiums inaccurate and unfair, but maximum benefits were also too low to cover the high treatment expenses that SARS patients require. Insurers fear to increase the benefit amount due to insecure funding and the possibility of an unprecedentedly large number of claims.

These problems reveal that traditional actuarial approaches to model life insurance might lack the flexibility and sophistication required to model infectious diseases, which are significantly different from natural causes of death in many aspects. One of the many remarkable differences is that in a population exposed to an epidemic outbreak there are always several mutually dependent groups involved. How fast a disease spreads within a population relies on the number of susceptible individuals, the number of infectious individuals and the social structure between these two groups. To be more specific in the context of a health insurance for an initially complete susceptible group, the number of insureds bearing premiums would actually decrease, whereas the number of insureds claiming benefits due to infection increases as the epidemic breaks out. Applying traditional life table methods, based on mortality of the whole population, overlooks epidemiological dynamics and dependence between insurance payers and beneficiaries. It consequently violates the fair premium principle used in the industry.

Therefore, the idea of bringing in epidemiological models to take account of several interacting populations in an actuarial context is suggested in this thesis.

1.2 Overview

Over the last century, many contributions to the mathematical modelling of communicable diseases have been made by a great number of public health physicians, epidemiological mathematicians and statisticians. Their brilliant work ranges from empirical data analysis to differential equation theory. Many have achieved successes in clinical data analysis and effective predictions. For a complete review of a variety of mathematical and statistical models, the interested readers are referred to Hethcote [19] and Mollison *et al.* [22]. However, because of the fact that clinical data only become available after an epidemic breaks out and also it is often difficult to estimate parameters accurately, people are questioning whether the study of mathematical modelling is really of practical value. Brauer [6] answers that mathematical modelling provides us with quantitative inferences on the epidemiological dynamics, and helps us choose control strategies by measuring their effectiveness in terms of adjustable parameters, like vaccination proportion.

As this thesis advocates applications in actuarial mathematics, the value of research on epidemiological modelling is further confirmed in a socio-economic context. Standing on the shoulders of giants, actuaries could incorporate economic factors into epidemiological models and make financial and medical arrangements to protect the public against infectious diseases. For an account of co-operative opportunities for actuaries and epidemiologists, we refer to a report by Cornall *et al.* [10].

To make the thesis self-contained with complete reference, Chapter 2 is devoted to a brief review of two well-known compartment models in the mathematics of infectious diseases and actuarial methodologies that are used in this work.

For the purpose of applications in the context of insurance, in Chapter 3 we formulate epidemiological models in actuarial notation and analyze the quantitative relations among the insurance related concepts induced from the models. An account

of statistical inference methods for model parameters is presented in Chapter 4. As an alternative to commonly used estimations, we propose a least square estimator based on Runge-Kutta method. In the main part of Chapter 4, several premium calculation methods for deterministic models are presented to achieve our initial goal of infectious disease insurance modelling. To ensure that benefit reserve is positive or negative within an acceptable range throughout an insurance duration, we develop a numerical method to determine safety-loaded premium levels. As examples to demonstrate the theory, we analyze numerically the dynamics of the Great Plague in Eyam and illustrate insurance policies with the aim to reduce financial impact on the disease-ravaged village. One might argue that nobody can ever change history. For that reason we also give an example of possible financial coverage against the more recent SARS outbreak in Hong Kong that could still make a difference today.

As a continuation of discussion in deterministic models, in Chapter 5 we look into a stochastic model studied by Lefèvre [20], in which the probability of infection is considered as a moment generating function of random variables indicating infectivity levels. By using a technique of conditioning on random variables from the theory of comonotonicity, we could stochastically order a group of random variables and the smallest one in the sense of moment generating function order is believed to be the best for approximating the probability of infection. However, since it is difficult in practice to directly obtain information of conditional distributions and in turn the above approach might not be easily applied, we introduce the concept of copulas to exam dependency structure of random variables. Then we employ empirical copulas to generate an approximation variable from uniformly distributed variables.

Throughout this thesis, we consider an infectious disease insurance to be a special mutual fund that provides coverage of medical costs and related expenses for infected insureds due to the one specific disease. In our model, it operates indepen-

dently as follows. Every susceptible individual purchases the insurance by a fairly small single premium at the time of policy issue, or through continuous periodic payments as long as he or she remains susceptible. Either continuous periodic benefits would be paid for the duration of hospitalization or a lump sum benefit at the time that the policyholder is detected to be infected. As an optional policy liability, a single death benefit may also be made at the time of death due to the infectious disease.

In all these models, policy terms are assumed to be sufficiently short so that the uncertainty of investment income from a random payment time and the demographical variations like natural death and birth could be ignored.

To keep the models simple, we shall not bring in utility functions or their related principles for the determination of benefit premiums. Only the equivalence principle is used extensively in our discussion, without consideration of expenses, profit or other contingency margins.

Chapter 2

Literature Review

2.1 Epidemiological Models

In epidemiological studies (ref. Hethcote [19]), to model an epidemic, the whole population is usually separated into compartments with labels such as M, S, E, I and R. These acronyms are used in different patterns according to the transmission dynamics of the studied disease.

Generally speaking, class M denotes individuals with passive maternal immunity or infection-acquired immunity. After a certain amount of time the antibodies disappear, these individuals are counted in class S which contains all susceptible individuals without passive immunity. Class E is the next stage for the susceptible who have had contacts with an infective, sufficient to become infected. For many diseases with distinct latent and infective periods, the class E is conventionally considered for the infected who are not yet infective. With the development of the disease, the infected in class E move on to class I, which contains all patients who are able to transmit the disease. Through medical treatment, individuals removed from the

epidemic due to either death or recovery are counted in class R. Those conferred temporary immunity come back to class M and individuals with permanent immunity rejoin class R. Figure 2.1 gives a brief summary of the transferring dynamics among the compartments.

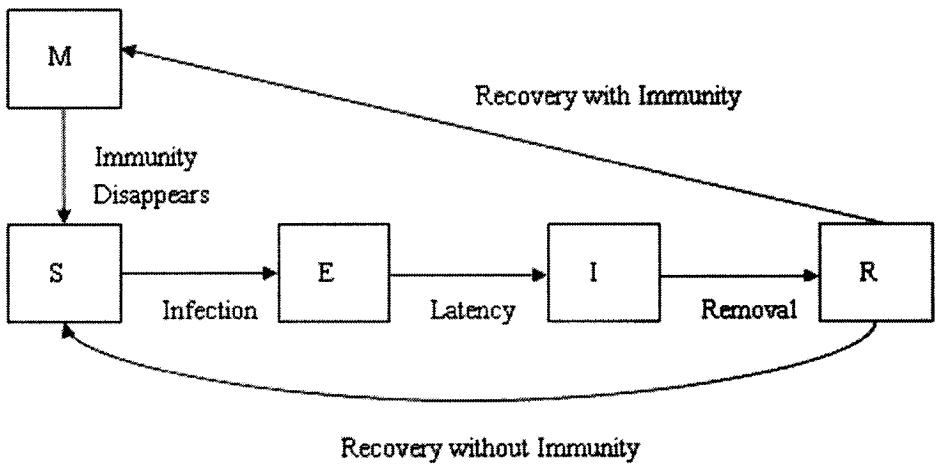

Figure 2.1: General transfer diagram with compartments M, S, E, I and R.

2.1.1 Deterministic Compartment Model

To illustrate the main ideas, we start off by looking at the simplest deterministic model where a clear actuarial analysis can be conducted. Although most infectious diseases like SARS are more complex, the generalization from the three compartment model to multi-dimensional models follows similar procedures.

In this model, $S(t)$ denotes the number of susceptible individuals at time t, while $I(t)$ is the number of infective individuals, and $R(t)$ is the number of individuals removed from class I. According to mass action laws commonly used in biological quantitative analysis, compartment sizes are determined in terms of deriva-

tives. Therefore, we are assuming that the number of members in each compartment is a differentiable function, defined with support on the positive real line.

Their qualitative relations are given by the following system of differential equations known as the SIR model.

$$S'(t) = -\beta S(t)I(t)/N\,, \qquad t \geq 0\,, \tag{2.1}$$

$$I'(t) = \beta S(t)I(t)/N - \alpha I(t)\,, \qquad t \geq 0\,, \tag{2.2}$$

$$R'(t) = \alpha I(t)\,, \qquad t \geq 0\,, \tag{2.3}$$

with given initial values $S(0) = S_0$, $I(0) = I_0$ and $R(0) = R_0$.

The model is based on the following assumptions:

1. The total number of individuals keeps constant, $N = S(t) + I(t) + R(t)$, representing the total population size.

2. An average person makes an average number β of adequate contacts (i.e. contacts sufficient to transmit infection) with others per unit time.

3. A fraction α of infectives leave the infective class I instantaneously. α is also considered to be constant.

4. There is no entry into or departure from the population, except possibly through death from the disease. For our purpose of setting up an insurance model, the demographic factors like natural births and deaths are negligible, as the time scale of an epidemic is generally shorter than the demographic time scale.

Since the probability of a random contact by an infective with a susceptible is S/N, then the instantaneous increase of new infected individuals is $\beta(S/N)I = \beta SI/N$. The third assumption implies that the instantaneous number of people flowing out of the infective class I into the removal class R is αI.

2.1.2 Stochastic Model

In formulating the models as ordinary differential equations, we are assuming that the whole epidemic process is deterministic, completely predictable from its history. However, for small population sizes, the epidemic might be strongly influenced by other random perturbations, hence stochastic models are more appropriate. Another concern about deterministic models is that for small size compartments, fractional number of members may lead to absurd interpretations. Therefore, to model a disease in a small insurance group, we consider using a stochastic model.

One of the classical stochastic models is the discrete-time Markov chain SIR, whose deterministic analog is the SIR discussed above. It is assumed that the time step is sufficiently small so that only one change in state is possible per unit time. By state, we refer to the status of being in a compartment in terms of the Markov chain. A change occurs either by infection of a susceptible individual (inflow into class I) or recovery of a infective individual (outflow from class I). The probability of transmission depends only on the state at the current time. Thus, it makes the process a Markov chain similar to a birth-death process.

The discrete-time deterministic SIR has the form,

$$S(t+\Delta t) = S(t)(1-\lambda(t)\Delta t)\,, \qquad t = n\Delta t,\ n = 0,1,2,\dots\,, \tag{2.4}$$

$$I(t+\Delta t) = I(t)(1-\alpha(t)\Delta t) + S(t)\lambda(t)\Delta t\,, \quad t = n\Delta t,\ n = 0,1,2,\dots\,, \tag{2.5}$$

where $S(0) = S_0, I(0) = I_0$ are given, and $\lambda(t) = \beta I(t)/N$.

Thus, in other words, the transition probabilities for the model are

$$P\{I(t+\Delta t) = m+1 | I(t) = m\} = u_m \Delta t\,, \qquad t \in \mathbb{N}\,,$$

$$P\{I(t+\Delta t) = m-1 | I(t) = m\} = d_m \Delta t\,, \qquad t \in \mathbb{N}\,,$$

where $u_m = \lambda(t)S(t)\Delta t = \beta I(t)S(t)/N, d_m = \alpha I(t)$ and $m \in \mathbb{Z}^+$.

In applying the above model, the transition probabilities approximate those of a more realistic continuous-time Markov jump process, where time between jumps follows an exponential distribution with mean $1/(u_m+d_m)$. For a complete account of both discrete-time and continuous-time Markov chain SIS and SIR models, interested readers are referred to Allen *et al.* [2].

2.2 Basic Actuarial Methodology

We give a brief review of some basic actuarial methods that will be used in the next chapter. For more details in these methods, readers are referred to Bowers *et al.* [5].

2.2.1 Elements of Life Insurance

As building blocks of life insurance mathematics, life tables are widely constructed and analyzed by government agencies and insurance companies. A typical life table is a collection of tabulations of vital statistics such as number of deaths in age groups or other generic categories. The salient idea of mortality analysis is estimating survival probabilities by the vital statistics in life tables. For instance, the probability that a person at age x will survive to age $x+k$ is approximated by a life table function.

$$ {}_kp_x = \frac{l_{x+k}}{l_x} , \qquad k = 0, 1, \cdots, \omega - x - 1 , $$

where l_x is the expected number of survivors to age x and ω the limiting age at which in practice no survivor is observed. Similarly, we express the probability that a person at age x will die within k years by

$$ {}_kq_x = \frac{l_{x+k+1} - l_x}{l_x} = \frac{d_x + d_{x+1} + \cdots + d_{x+k}}{l_x} , \qquad k = 0, 1, \cdots, \omega - x - 1 , $$

where $d_{x+k} = l_{x+k} - l_{x+k+1}$ is the expected number of deaths between ages $x+k$ and $x+k+1$. Therefore, the probability that a person dies between ages $x+k$ and

$x+k+1$ is

$$ {}_kp_x \cdot {}_1q_{x+k} = \frac{l_{x+k}}{l_x} \cdot \frac{d_{x+k}}{l_{x+k}} = \frac{d_{x+k}}{l_x} , \qquad k = 0, 1, \cdots, \omega - x - 1 . $$

Insurance premiums are usually determined at the time when the policy is issued. Therefore, a dollar benefit payable in the future needs to be converted to a certain amount at present worth the same value. For example, if a dollar worth of US bonds at present goes up to 1.08 dollars at the end of a year, then we say that the present value of 1.08 dollars at the end of the year is 1.00 dollar now. In the actuarial literature, an insurance model is developed with a benefit function b_t and a discount function v_t. The discount factor v_t, depending on interest rates before time t, discounts a dollar unit from the payment time t back to the issue time 0. For the above example, $v_1 = (1.08)^{-1}$. In our model, we will be using compound interest rates, i.e. $v_t = v^t$. Hence, the present value now of b_t dollars payable at time t is $b_t \cdot v^t$. For a life insurance policy holder, death may occur at any year between the age x, when the policy is issued, and the limiting age ω. Therefore, the single premium at policy issue, which is in other words the present value of benefit payment $b_{k+1} = 1$ at the end of the year of death, is the expected value of discounted values at all possible ages:

$$ A^1_{x:\overline{n}|} = \sum_{k=0}^{n-1} v^{k+1} \, {}_kp_x \, {}_1q_{x+k} = \sum_{k=0}^{n-1} v^{k+1} \frac{d_{x+k}}{l_x} . \tag{2.6} $$

For the purpose of theoretical actuarial analysis, a tremendous stride has been made in the literature to generalize discrete time insurance models to continuous analogues by taking the payment interval from one year to infinitesimal. Since we are changing the domain of the expected number of survivor l_x from a countable set of integers to an uncountable interval of the length of the remaining life time, summations have to be replaced by integrals over the uncountable set. Therefore,

defined analogously to the first equality of (2.6),

$$\overline{A}_{\overline{x:n}|} = \int_0^n v^t \, {}_tp_x \, \mu_x(t) \, dt \, , \tag{2.7}$$

where

$${}_tp_x = \frac{l_{x+t}}{l_x} \tag{2.8}$$

represents the probability of an individual surviving to the time $x + t$ and

$$\mu_x(t) = -\frac{l'_{x+t}}{l_{x+t}} \tag{2.9}$$

the instantaneous mortality rate at the time $x + t$. Note that

$$\mu_x(t) \, dt = \frac{l_{x+t} - l_{x+t+dt}}{l_{x+t}}$$

is actually equal to ${}_{dt}q_{x+t}$ in terms of the notation in the discrete case.

Another popular form of premium payments is the life annuity, which is a series of installments paid continually while a given life survives. The series of payments due at the beginning of each payment interval is called a life annuity-due, whose present value is conventionally denoted by $\ddot{a}_x$, whereas the series of payments deferred until the end of each payment interval is a life annuity-immediate with present value denoted by a_x. For example, the actuarial present value of a contingent payment of one dollar is $v^k \cdot {}_kp_x$. Therefore, an n-year temporary life annuity-due has an actuarial present values given by the sum of present values of payments.

$$\ddot{a}_{x:\overline{n}|} = \sum_{k=0}^{n-1} v^k \, {}_kp_x = \sum_{k=0}^{n-1} v^k \, \frac{l_{x+k}}{l_x} \, . \tag{2.10}$$

Analogously, the actuarial present value of an n-year temporary life annuity-immediate is represented by

$$a_{x:\overline{n}|} = \sum_{k=1}^{n} v^k \, {}_kp_x = \sum_{k=1}^{n} v^k \, \frac{l_{x+k}}{l_x} = \ddot{a}_{x:\overline{n+1}|} - 1 \, . \tag{2.11}$$

It is easy to prove that in the limit, both the actuarial present value of a life annuity-due and annuity-immediate are forced to go to their continuous life annuity counterpart given by

$$\overline{a}_{x:\overline{n}|} = \int_0^n v^t \, {}_tp_x \, dt \, . \tag{2.12}$$

The beauty of continuity is that we could rewrite both life insurance and annuities in terms of differentiable functions such that

$$\overline{A}_x = \overline{A}_{\frac{1}{x:\overline{\infty}|}} = -\frac{1}{l_x} \int_0^\infty v^t \, l'_{x+t} \, dt \, ,$$

by substituting (2.8) and (2.9) into (2.7), and

$$\overline{a}_x = \overline{a}_{x:\overline{\infty}|} = \frac{1}{l_x} \int_0^\infty v^t \, l_{x+t} \, dt \, .$$

Suppose a unit invested produces an annual force of interest δ, that is to say,

$$v^t = e^{-\delta t} \, ,$$

then from

$$-\int_0^\infty e^{-\delta t} \, f'(t) \, dt = 1 - \delta \int_0^\infty e^{-\delta t} \, f(t) \, dt \, ,$$

it follows that

$$\overline{A}_x = 1 - \delta \, \overline{a}_x \, . \tag{2.13}$$

2.2.2 Level Premiums by the Equivalence Principle

Since not everyone would pay a single benefit premium at the policy issue, the above ideas on life insurance and life annuities are combined to produce various forms of products. A typical case is that an individual purchases a life insurance with several benefit payments by means of a series of level premiums payable in the form of a life annuity. Although the risk of benefit payments varies over time for the insurer, the premiums are equally distributed over each year of the insured's remaining life. Our

study in Chapter 3 is based on the most basic and important *Equivalence Principle* for the determination of level premiums, which requires

E[present value of benefits]=E[present value of benefit premiums] .

For instance, the level benefit premium rate for a fully continuous whole life insurance with unit benefit determined by the equivalent principle is,

$$\overline{A}_x = \overline{P}(\overline{A}_x)\,\overline{a}_x \ ,$$

that is to say,

$$\overline{P}(\overline{A}_x) = \frac{\overline{A}_x}{\overline{a}_x} \ . \tag{2.14}$$

2.2.3 Benefit Reserve

On the date when two insurance parties, such as a susceptible insured and an insurer, enter into an insurance contract, an equivalent relationship is established for the whole insurance period. However, there will be no longer equivalence between the financial obligations of the two parties from a short-term point of view. In actuarial practice, a balancing item called *Reserve* is introduced to describe the liability of one party and asset of the other. Take an example of a deferred life annuity, after a period of deferral, the insured individual may have completed the payments of level premiums, whereas the insurance company still has an obligation of annuity payments to make, if the individual survives beyond a specified age. In case of that happening, a prudent insurer would have a certain amount of money reserved for future benefit payments.

From the *prospective method* in life insurance, which states that the benefit reserve is the difference between the actuarial present value of future benefits and the actuarial value of future benefit premiums, we have the following expression for the reserve at time t for a whole life insurance issued at age x:

$${}_t\overline{V}(\overline{A}_x) = \overline{A}_{x+t} - \overline{P}(\overline{A}_x)\,\overline{a}_{x+t} \ . \tag{2.15}$$

Further, substituting (2.13) and (2.14) into (2.15), we obtain

$$ {}_t\overline{V}(\overline{A}_x) = \frac{\overline{A}_{x+t} - \overline{A}_x}{1 - \overline{A}_x} \,. \tag{2.16} $$

In practice it is common sense that the single benefit premium of whole life insurance for an elder individual is higher than that for a younger individual. Therefore, from (2.16) it can be seen that the benefit reserves are non-negative in most applications. However, there is no theorem that guarantees the property. Conversely, it is quite possible in health insurance that a person entering an insurance later will be charged less than others because of a shorter period of coverage, which means the top expression in (2.16) would go below zero. It indeed is the case in epidemiological models. Negative benefit reserves is discussed in Section 4.3.

Chapter 3

Actuarial Analysis of Epidemiological Models

The idea of setting up an insurance coverage against a infectious disease is akin to that of covering other contingencies like natural death and destruction of property. We model the size and time of financial costs caused by the infectious diseases in terms of random variables. Then the benefit premiums are based on the equivalent principle in Section 2.2.2.

3.1 Deterministic SIR Insurance Model

As showed in Section 2.2.1, a mortality analysis is based on ratios instead of absolute counts. We introduce $s(t)$, $i(t)$ and $r(t)$ respectively as fractions of the whole population, in each of class S, I and R. Dividing equations (2.1)-(2.3) by the constant

total population size N yields

$$s'(t) = -\beta\, i(t)\, s(t)\,, \qquad t \geq 0\,, \tag{3.1}$$

$$i'(t) = \beta\, i(t)\, s(t) - \alpha\, i(t)\,, \qquad t \geq 0\,, \tag{3.2}$$

$$r(t) = 1 - s(t) - i(t)\,, \qquad t \geq 0\,, \tag{3.3}$$

where $s(0) = s_0$ and $i(0) = i_0$ are given.

With these ratio functions $s(t)$, $i(t)$ and $r(t)$, we incorporate the actuarial methods to formulate the quantities of interest for an infectious disease insurance. Instead of payments contingent on death, we look at payments contingent on infection. The benefit for infection may be paid as a lump sum, immediately after a policy holder is diagnosed to be infected. Alternatively, the benefit payments for infection may commence in the form of a temporary annuity for the whole duration of the infection.

Following international actuarial notation and concepts analogous to those for life insurance in (2.6), we denote the present value of a lump sum unit benefit for infection by

$$A^{i}_{\overline{n}|} = \sum_{k=0}^{n-1} v^{k+1}\, i'(k)\,,$$

where the integer n represents the duration of an epidemic. It covers medical costs only to new comers in the infective class I. Similar to (2.11), the present value of a temporary annuity payment of one dollar commencing at the end of the year after infection is

$$a^{i}_{\overline{n}|} = \sum_{k=0}^{n} v^{k+1}\, i(k)\,.$$

The installment is regularly paid to both new comers and existent patients remaining in class I. Similarly, the present value of a unit benefit due to death from the disease is

$$A^{d}_{\overline{n}|} = \sum_{k=0}^{n} v^{k+1}\, r'(k)\,.$$

On the other hand, insurance premiums are paid by the susceptible who undertake the risk of being infected in the future. Therefore, with the analogue (2.10), the present value of net level premiums $P_k = 1$ collected from a susceptible individual is

$$\ddot{a}^{s}_{\overline{n}|} = \sum_{k=0}^{n-1} v^{k+1}\, s(k)\ .$$

For the sake of simplicity, we extend the above actuarial quantities from discrete to continuous time. Consider the special case where net premiums are uniformly distributed over the duration of the epidemic and the hospitalization benefits are continuously paid at rate of $b_t = 1$ per unit time. Figure 3.1 illustrates the insurance funding flows among these three classes.

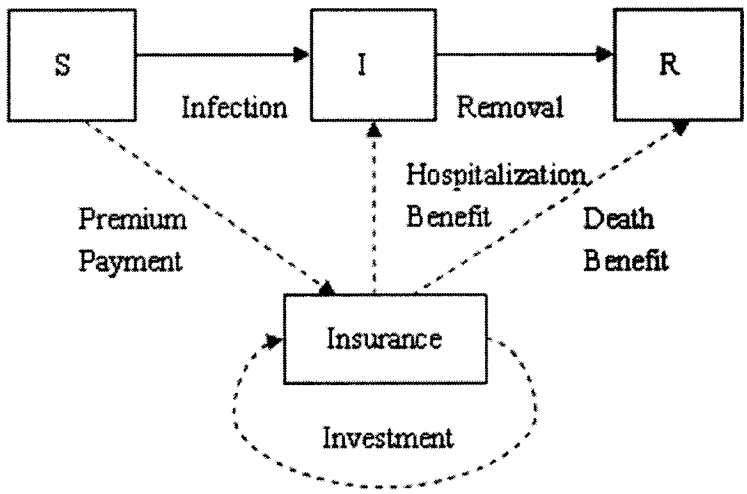

Figure 3.1: Transfer diagram of cash flows among three compartments.

Therefore in this model, we discuss the actuarial present values of various benefit payments and then determine a fair level of premium payments. In practice individual life insurance is usually purchased by long-term premium installments. However, since an epidemic breaks out in a relatively short period, a lump sum payment might be

more applicable in health insurance. The following sections discuss different coverage plans and their corresponding net level premium rates.

3.1.1 Annuity for Hospitalization

We assume that individual premiums are collected continuously as long as the insured is still susceptible, while medical cost benefits are also continuously paid to the individual during the whole treatment period. Once the individual recovers from the disease, the insurance benefits and hence the corresponding liability, terminate right away.

Following similar notations, the actuarial present value of premium payments from insureds up to time T is denoted by $\overline{a}^{s}_{\overline{T}|}$, and that of the benefit payments from the insurer is denoted by $\overline{a}^{i}_{\overline{T}|}$.

On the debit side of the insurance product, the total discounted future claim is given by

$$\overline{a}^{i}_{\overline{T}|} = \int_0^T e^{-\delta t} i(t) dt \,, \tag{3.4}$$

while on the revenue side, the total discounted future premiums is

$$\overline{a}^{s}_{\overline{T}|} = \int_0^T e^{-\delta t} s(t) dt \,, \tag{3.5}$$

where δ is the force of interest.

Just like in life insurance, where the force of mortality is defined as the additive inverse of the ratio of the derivative of the survival function to the survival function itself, we define here the force of infection as

$$\mu^{s}_{t} = -\frac{s'(t)}{s(t)} \,, \qquad t \geq 0 \,,$$

and the force of (relative) removal as

$$\mu^{i}_{t} = -\frac{i'(t)}{i(t)} \,, \qquad t \geq 0 \,.$$

Specifically from (3.1)-(3.2), we see that $\mu_t^s = \beta\, i(t)$ and $\mu_t^i = -\beta\, s(t) + \alpha$.

Note that the above definitions imply that

$$s(t) = \exp\{-\int_0^t \mu_r^s\, dr\} = \exp\{-\beta \int_0^t i(r)dr\}\,, \qquad t \geq 0\,, \tag{3.6}$$

and

$$i(t) = \exp\{-\int_0^t \mu_r^i\, dr\} = \exp\{\beta \int_0^t s(r)\, dr + \alpha t\}\,, \qquad t \geq 0\,. \tag{3.7}$$

Proposition 3.1.1. *In the SIR model in (3.1)-(3.2), the present value of the continuous annuity payments to the infectives, $\overline{a}^i_{\overline{T}|}$, satisfies the following relation with the present value of continuous annuity premiums collected from the susceptibles $\overline{a}^s_{\overline{T}|}$,*

$$(1 + \frac{\alpha}{\delta})\, \overline{a}^i_{\overline{T}|} + \overline{a}^s_{\overline{T}|} = \frac{s_0 + i_0}{\delta}\,. \tag{3.8}$$

Proof. From (3.1) and (3.2), we obtain that

$$s'(t) + i'(t) = -\alpha\, i(t)\,, \qquad t \geq 0\,. \tag{3.9}$$

Integrating (3.9) from 0 to a fixed t gives

$$s(t) + i(t) - s_0 - i_0 = -\alpha \int_0^t i(r)\, dr\,, \qquad t \geq 0\,. \tag{3.10}$$

Now inverting the order of integrals gives

$$\begin{aligned} \int_0^T \exp(-\delta t) \int_0^t i(r)\, dr\, dt &= -\frac{1}{\delta} \int_0^T \int_0^t i(r)\, dr\, d(\exp(-\delta t)) \\ &= \frac{1}{\delta} \int_0^T \exp(-\delta r) i(r)\, dr\,. \end{aligned}$$

Taking Laplace transforms with respect to δ on both sides of (3.10), we have

$$\overline{a}^s_{\overline{T}|} + \overline{a}^i_{\overline{T}|} - \frac{s_0}{\delta} - \frac{i_0}{\delta} = -\frac{\alpha}{\delta}\, \overline{a}^i_{\overline{T}|}\,.$$

Then equality (3.8) follows simply by rearranging terms. □

The intuitive interpretation of the above proposition is that as an infective leaves class I at a constant rate of α, the term $(\alpha/\delta)\ \overline{a}^{i}_{\overline{T}|}$ aggregates funding from the individual. Hence $(1+\alpha/\delta)\ \overline{a}^{i}_{\overline{T}|}$ is the total discounted value collected from each individual expected to enter class I. Similarly, $\overline{a}^{s}_{\overline{T}|}$ is the discounted funding from susceptible individuals over the period. The other side of the equality shows the present value of total funding from individuals regardless of their classes - whether susceptible or infectious. It is reasonable that both sides should be equal.

To facilitate computation of premiums, we shall introduce some corresponding notation from life insurance. Define

$$\overline{rA}^{s}_{\overline{T}|} = -\int_0^T e^{-\delta t}\ s'(t)\ dt\ ,$$

and

$$\overline{rA}^{i}_{\overline{T}|} = -\int_0^T e^{-\delta t}\ i'(t)\ dt\ .$$

These notation do not have insurance interpretations. They are pure notational fictions corresponding to $\overline{A}_x$ in life insurance, and satisfy the following equalities analogous to the identity (2.13) in life insurance.

Proposition 3.1.2.

$$\overline{rA}^{s}_{\overline{T}|} = s_0 - \delta\ \overline{a}^{s}_{\overline{T}|}\ , \tag{3.11}$$

and

$$\overline{rA}^{i}_{\overline{T}|} = i_0 - \delta\ \overline{a}^{i}_{\overline{T}|}\ . \tag{3.12}$$

Proof. Using integration by parts with the definition of $\overline{rA}^{i}_{\overline{T}|}$, we get

$$\begin{aligned}
\overline{rA}^{i}_{\overline{T}|} &= -\int_0^T e^{-\delta t}\, i'(t)\, dt \\
&= -\Big[i(t)\, e^{-\delta t}\Big|_0^T + \delta \int_0^T e^{-\delta t}\, i(t)\, dt\Big] \\
&= i_0 - \delta\, \overline{a}^{i}_{\overline{T}|}\,.
\end{aligned}$$

The proof of (3.12) follows exactly the same idea. □

A useful feature of the infectious disease compartmental model is that the flux out of class S is equivalent to the flux into class I. We can thus guess that $\overline{rA}^{s}_{\overline{T}|}$ and $\overline{rA}^{i}_{\overline{T}|}$ are closely related.

Proposition 3.1.3.

$$\overline{rA}^{s}_{\overline{T}|} = \alpha\, \overline{a}^{i}_{\overline{T}|} - \overline{rA}^{i}_{\overline{T}|}\,. \tag{3.13}$$

Proof. Starting from (3.9) and taking incomplete Laplace transforms from 0 to T on both sides yields,

$$\int_0^T e^{-\delta t}\, s'(t)\, dt + \int_0^T e^{-\delta t}\, i'(t)\, dt = -\alpha \int_0^T e^{-\delta t}\, i(t)\, dt\,.$$

Therefore,

$$\overline{rA}^{s}_{\overline{T}|} + \overline{rA}^{i}_{\overline{T}|} = \alpha\, \overline{a}^{i}_{\overline{T}|}\,. \tag{3.14}$$

□

Returning to our original problem of finding the net level annual premium for the unit annuity for hospitalization plan, denoted by $\overline{P}(\overline{a}^{i}_{\overline{T}|})$, we now have

$$\overline{P}(\overline{a}^{i}_{\overline{T}|}) = \frac{\overline{a}^{i}_{\overline{T}|}}{\overline{a}^{s}_{\overline{T}|}} = \frac{\delta\, \overline{a}^{i}_{\overline{T}|}}{s_0 + i_0 - (\delta+\alpha)\overline{a}^{i}_{\overline{T}|}}\,. \tag{3.15}$$

3.1.2 Lump Sum for Hospitalization

If the medical indemnity is to be paid immediately in a lump sum when the individual is diagnosed infected, and insurance liability is terminated, then the present value of benefit payments to the infected denoted by $\overline{A}^{i}_{\overline{T}|}$ is obtained as

$$\overline{A}^{i}_{\overline{T}|} \triangleq \beta \int_0^T e^{-\delta t} s(t)\, i(t)\, dt\ . \tag{3.16}$$

Proposition 3.1.4.

$$\overline{A}^{i}_{\overline{T}|} + \delta\, \overline{a}^{s}_{\overline{T}|} = s_0\ , \tag{3.17}$$

and

$$(\alpha + \delta)\, \overline{a}^{i}_{\overline{T}|} - \overline{A}^{i}_{\overline{T}|} = i_0\ . \tag{3.18}$$

Proof. Substituting (3.1) into (3.16), we have that

$$\begin{aligned} \overline{A}^{i}_{\overline{T}|} &= -\int_0^T e^{-\delta t}\, s'(t)\, dt \\ &= \overline{rA}^{s}_{\overline{T}|}\ , \qquad \text{by definition,} \\ &= s_0 - \delta\, \overline{a}^{s}_{\overline{T}|}\ , \qquad \text{by (3.11)}\ . \end{aligned}$$

Since $\overline{A}^{i}_{\overline{T}|} = \overline{rA}^{s}_{\overline{T}|}$ and $\overline{rA}^{i}_{\overline{T}|} = i_0 - \delta\, \overline{a}^{i}_{\overline{T}|}$ by (3.12), substituting into (3.14) gives

$$\overline{A}^{i}_{\overline{T}|} + i_0 - \delta\, \overline{a}^{i}_{\overline{T}|} = \alpha\, \overline{a}^{i}_{\overline{T}|}\ .$$

□

Therefore for the lump sum payment plan with a unit benefit, the equivalence principle gives the net level premium $\overline{P}(\overline{A}^{i}_{\overline{T}|})$:

$$\overline{P}(\overline{A}^{i}_{\overline{T}|}) = \frac{\overline{A}^{i}_{\overline{T}|}}{\overline{a}^{s}_{\overline{T}|}} = \frac{\overline{rA}^{s}_{\overline{T}|}}{\overline{a}^{s}_{\overline{T}|}} = \frac{s_0 - \delta\, \overline{a}^{s}_{\overline{T}|}}{\overline{a}^{s}_{\overline{T}|}} = \frac{s_0}{\overline{a}^{s}_{\overline{T}|}} - \delta\ , \tag{3.19}$$

where $\overline{a}^{s}_{\overline{T}|}$ could be re-expressed in terms of $\overline{a}^{i}_{\overline{T}|}$.

3.1.3 Death Benefit

It is necessary to point out that in the epidemiological literature the class R is sometimes referred to as being composed of individuals removed chronologically from previous compartments. They either recover with immunity or die due to the disease. A more refined model could have separate compartments for the dead and the recovered. For our purpose of deducing an actuarial analysis based upon epidemiological models, we keep the model as simple as possible by assuming only one R compartment for deaths caused by the disease, which implies that nobody recovers from the disease. Also recall that natural deaths or births are ignorable in a short time period. The SIR model remains the same as in (3.1)-(3.2), except that α is the constant rate of death within class I.

For most health insurance policies, death benefits differ from healthcare benefits. We assume that in this infectious disease plan, a death benefit of $d_t = 1$ is paid immediately on the occurrence of death.

Thus, the actuarial present value of a lump sum death benefit payment denoted by $\overline{A}^d_{\overline{T}|}$ is

$$\begin{aligned} \overline{A}^d_{\overline{T}|} &\triangleq \alpha \int_0^T e^{-\delta t}\, i(t)\, dt \\ &= \alpha\, \overline{a}^i_{\overline{T}|} \\ &= \overline{A}^i_{\overline{T}|} - \overline{rA}^i_{\overline{T}|}\,. \end{aligned}$$

Therefore, the net level premium for the plan with both a unit hospitalization benefit and a unit death benefit is obtained by

$$\overline{P}(\overline{a}^i_{\overline{T}|} + \overline{A}^d_{\overline{T}|}) = \frac{\overline{a}^i_{\overline{T}|} + \overline{A}^d_{\overline{T}|}}{\overline{a}^s_{\overline{T}|}} = \frac{\delta(1+\alpha)\overline{a}^i_{\overline{T}|}}{s_0 + i_0 - (\delta+\alpha)\overline{a}^i_{\overline{T}|}}\,, \tag{3.20}$$

and the net level premium for the plan with both a lump sum for hospitalization and

death benefit is given by

$$\overline{P}(\overline{A}^{i}_{\overline{T}|} + \overline{A}^{d}_{\overline{T}|}) = \frac{\overline{A}^{i}_{\overline{T}|} + \overline{A}^{d}_{\overline{T}|}}{\overline{a}^{s}_{\overline{T}|}} = \frac{\delta(2\alpha+\delta)\overline{a}^{i}_{\overline{T}|} - \delta\, i_0}{s_0 + i_0 - (\delta+\alpha)\overline{a}^{i}_{\overline{T}|}} \,. \tag{3.21}$$

3.1.4 Individual Benefit Reserves

There are two ways of determining individual benefit reserve that an insurance company should hold on to prepare for future claims. The first originates from prospective method of benefit reserve in life insurance mathematics, as illustrated in Section 2.2.3.

Suppose the policy duration is T, for the plan with an annuity benefit for hospitalization and a death benefit, we obtain the reserve at time t from the time of policy issue :

$$\begin{aligned} \overline{V}_{\overline{t}|}(\overline{a}^{i}_{\overline{T}|} + \overline{A}^{d}_{\overline{T}|}) &\triangleq \overline{a}^{i}_{\overline{T-t}|} + \overline{A}^{d}_{\overline{T-t}|} - p\,\overline{a}^{s}_{\overline{T-t}|} \\ &= \frac{1}{\delta}\big[(\delta + \alpha\,\delta + p\,\delta + p\,\alpha)\,\overline{a}^{i}_{\overline{T-t}|} - p\,s(t) - p\,i(t)\big] \,, \end{aligned}$$

where $p = \overline{P}(\overline{a}^{i}_{\overline{T}|} + \overline{A}^{d}_{\overline{T}|})$ is given in (3.20).

For the plan with a lump sum payment for hospitalization and a death benefit we have

$$\begin{aligned} \overline{V}_{\overline{t}|}(\overline{A}^{i}_{\overline{T}|} + \overline{A}^{d}_{\overline{T}|}) &\triangleq \overline{A}^{i}_{\overline{T-t}|} + \overline{A}^{d}_{\overline{T-t}|} - p\,\overline{a}^{s}_{\overline{T-t}|} \\ &= \frac{1}{\delta}\big[(\delta^2 + 2\alpha\,\delta + p\,\delta + p\,\alpha)\,\overline{a}^{i}_{\overline{T-t}|} - p\,s(t) - (p-\delta)\,i(t)\big] \,, \end{aligned}$$

where $p = \overline{P}(\overline{A}^{i}_{\overline{T}|} + \overline{A}^{d}_{\overline{T}|})$ is given in (3.21).

The second way of calculating the benefit reserve is through numerical analysis from an insurance factor system, as explained in Section 4.2.1.

Chapter 4

Premium Rating in Deterministic Models

In this chapter, we investigate the statistical inference of various parameters in the ODE system and propose a new least squares estimation method based on Runge-Kutta recursive formulas. With these estimated model parameters, we develop several methods for premium calculation. Two numerical examples are given in the end with empirical data for the Eyam Great Plague and the SARS epidemic in Hong Kong.

4.1 Parameter Estimation

4.1.1 Clinical Expert Opinion

A common assumption is that the movement out of a compartment and into the next compartment are governed by its flux ratios like β and α. It has been shown by Hethcote *et al.* [18] that these movements each correspond to exponentially distributed

waiting time in corresponding compartments. In other words, the fraction of people staying in the same class is exponentially decaying over time. For instance, the flux ratio α implies that a fraction $P(t) = e^{-\alpha t}$ of the population remains in class I at time t and $1/\alpha$ is the average time an individual spends in the class. Therefore, based on the biological interpretation of the average time, clinical observations of latent periods and infectious periods are often used to estimate flux ratios. Table 4.1 gives a list of average periods for some insurable childhood diseases.

Disease	**Latent period** (Days)	**Infectious period** (Days)
Measles	8	5
Chicken Pox	10	5
Rubella	10	7
Whooping Cough	8	14

Table 4.1: Mean latent period $1/\sigma$ and mean infectious period $1/\beta$ in SEIR models of some insurable childhood diseases. Data source: Anderson & May [1], Table 3.1.

Although the clinical expert opinion method has been widely accepted for epidemiological modelling, in practice it is common that the resulting models do not fit empirical data well enough, from a statistical point of view, to make precise predictions.

4.1.2 Profiled Likelihood Estimation

There are numerous methods to apply statistical inference to estimate parameters. Maximum likelihood methods are commonly used by biostatisticians. The following

estimation method is based on an illustration from Brookhart *et al.* [7].

Since most available incidence data for infectious diseases are reported continually for a certain duration of epidemics, it is plausible that we develop a likelihood by multiplying together conditional probabilities for each report period from which we have observable incidence counts. That is

$$\mathcal{L}(\phi|I^*) = f(I_1^*)f(I_2^*|I_1^*)f(I_3^*|I_2^*, I_1^*)\cdots f(I_n^*|I_1^*, I_2^*, \cdots, I_{n-1}^*) \ ,$$

where $\mathcal{L}$ is the likelihood in terms of the parameter vector ϕ to be estimated, $f(\cdot)$ is a proper probability density function of the observable variables, and $\{I_k^*\}_{k=1,2,\cdots,n}$ are clinical incidence counts for each period.

Many statisticians believe that clinical data of incidences (such as deaths, infections) may be quite different from those in corresponding classes in ODE models, which are designed to describe the quantities between classes in nature. An explanation may be that clinical reports normally come after real incidences happened, with a time lag of several days, depending on bureau efficiency. Therefore, many researchers set up an extra class to model the quantitative discrepancy between the epidemiological class and the reported cases. For instance, in Finkenstädt and Grenfell [15], reported cases of infected individuals are considered as a random ratio of real incidences in the SIR model:

$$C_t = \rho \ I_t \ln(\eta_t) \ , \qquad \ln \eta_t \sim \text{i.i.d. } N(0, \sigma_\eta^2) \ , \tag{4.1}$$

where ρ is a ratio depending on environmental and demographical factors. To avoid confusion between clinical data and epidemiological incidences, we adapt the notation I_k^* for observations related to the corresponding incidence class data I_k .

Assuming that the probability of I_k^* incidences occurring follows a binomial distribution, we can represent

$$f(I_k^*|I_1^*, I_2^*, \cdots, I_{k-1}^*) = {}_{k-1|}q(\phi)^{I_k^*} \left[1 - {}_{k-1|}q_k(\phi)\right]^{N_k - I_k^*} \ ,$$

where ${}_{k-1|}q(\phi)$ is the conditional probability of an individual being infected in period k, given that he or she remained susceptible up to the previous period $k-1$. Hence, it follows that

$$ {}_{k-1|}q(\phi) = \frac{I_k - I_{k-1}}{N - I_{k-1}} , \qquad k = 1, \cdots, n . $$

Therefore, with the help of computational algorithms, we can find out the estimator $\hat{\phi}$ which maximizes the likelihood function

$$ \mathcal{L}(\phi|I^*) = \sum_{k=1}^{n} {}_{k-1|}q(\phi)^{I_k^*} \, [1 - {}_{k-1|}q(\phi)]^{N_k - I_k^*} . $$

4.1.3 Least Squares Estimation

As an alternative solution, we propose a least squares estimation of the parameters, which is more computationally manageable.

The idea originates from the famous Runge-Kutta method (ref. Section 4.2.1) for the recursive numerical evaluation of first order ordinary differential equations (ODE1). To illustrate the basic idea, we start with a Runge-Kutta method of second order (RK-2) given by:

$$ y_{i+1} = y_i + \frac{1}{2}k_1 + \frac{1}{2}k_2 , \qquad i = 1, 2, \cdots, n , \tag{4.2} $$

$$ k_1 = hf(t_i, y_i) , \qquad i = 1, 2, \cdots, n , \tag{4.3} $$

$$ k_2 = hf(t_i + h, y_i) , \qquad i = 1, 2, \cdots, n , \tag{4.4} $$

where y_i is given by the ODE-1:

$$ \frac{dy}{dt} = f(t, y) , $$

evaluated at $t = t_i$. The time step is $h = t_i - t_{i-1}$ for $i = 1, 2, 3, \ldots, n$.

Substituting the SIR equation system into (4.2) gives

$$ \frac{1}{4}h^2 \, S_i \, I_i \, I_{i+1} \, \beta^2 + \frac{1}{2}h \, (S_i \, I_i + S_{i+1} \, I_{i+1}) \, \beta + S_{i+1} - S_i = 0, \qquad i = 1, \cdots, n , \tag{4.5} $$

where S_i is the susceptible function evaluated at the time $t = t_i$, while I_i is the infectious function evaluated at the time $t = t_i$, and the series are discretized numerical solutions to the ODE model.

Simplifying (4.5) by completing a perfect square and taking square-root on both sides, we obtain

$$h\, S_i\, I_i\, I_{i+1}\, \beta + S_i\, I_i + S_{i+1}\, I_{i+1} = \sqrt{(S_i\, I_i - S_{i+1}\, I_{i+1})^2 + 4S_i^2\, I_i\, I_{i+1}}\,. \tag{4.6}$$

Note that negative root of the right-hand side of the regression equation is dropped since β is a positive ratio.

From a statistical point of view, if we collect sufficiently large samples $\{\hat{S}_i\}$ and $\{\hat{I}_i\}$ with equal time spacings $\Delta t = h$, (4.6) becomes a linear regression model, for which we have the following normal equations:

$$y_i = \beta x_i + e_i, \qquad i = 1, \ldots, n\,, \tag{4.7}$$

where $y_i = \sqrt{(\hat{S}_i\, \hat{I}_i - \hat{S}_{i+1}\, \hat{I}_{i+1})^2 + 4\hat{S}_i^2\, \hat{I}_i\, \hat{I}_{i+1}} - \hat{S}_i\, \hat{I}_i + \hat{S}_{i+1}\, \hat{I}_{i+1}$, $x_i = h\, \hat{S}_i\, \hat{I}_i\, \hat{I}_{i+1}$ and e_i is the residual error.

Therefore, by applying the least square estimator of the linear regression model, we have

$$\hat{\beta} = \frac{\sum x_i y_i - \sum x_i \sum y_i}{\sum x_i^2 - n\overline{x}^2}\,. \tag{4.8}$$

Then $\hat{\alpha}$ can be obtained in the same manner.

However, we have to admit that the residual errors $\{e_i\}$ are serially correlated. Therefore, this method gives a rough estimation but comparable to the profiled likelihood estimation.

4.2 Net Premium Calculations

So far net premiums have only been expressed in terms of $\overline{a}^{i}_{\overline{T}|}$, which is an incomplete Laplace transform of $i(t)$. An implicit integral solution to the SIR model in (3.1)-(3.2) is as follows,

$$s(t) = \frac{1}{N} \exp\{-\beta \int_0^t \exp\{\beta N \int_0^u s(r)\, dr - \alpha u\} du\} ,$$

$$i(t) = \frac{1}{N} \exp\{\beta \int_0^t \exp\{\beta N \int_0^u i(r)\, dr\} - \alpha u\, du\} .$$

But there is not an explicit method available to solve $s(t)$ and $i(t)$. Therefore we propose numerical formulas and approximations that can provide satisfactory solutions for insurance applications.

4.2.1 Insurance Factor System and Runge-Kutta Method

Among many numerical methods for solving ODE, the Runge-Kutta method is the most popular. It can be adapted for any order of accuracy. For applications in insurance, the fourth order Runge-Kutta method (RK-4), given by the following recursion formulas, represents a good compromise between simplicity and accuracy:

$$\begin{aligned}
y_{i+1} &= y_i + \frac{1}{6}(k_1 + 2k_2 + 3k_3 + k_4) , \qquad i = 1, 2, \cdots, n , \\
k_1 &= hf(t_i, y_i) , \qquad i = 1, 2, \cdots, n , \\
k_2 &= hf(t_i + \frac{h}{2}, y_i + \frac{1}{2}k_1) , \qquad i = 1, 2, \cdots, n , \\
k_3 &= hf(t_i + \frac{h}{2}, y_i + \frac{1}{2}k_2) , \qquad i = 1, 2, \cdots, n , \\
k_4 &= hf(t_i + h, y_i + k_3) , \qquad i = 1, 2, \cdots, n ,
\end{aligned}$$

where y_i is given by the ODE:

$$\frac{dy}{dt} = f(t, y) ,$$

evaluated at $t = t_i$, and the time step $h = t_i - t_{i-1}$ for $i = 1, 2, \cdots, n$.

Actuaries may particularly be interested in the quantitative properties of insurance-related factors, such as discounted total benefits, discounted total premiums and premium reserves. Based on the RK-4 method, we need to fit these factors into a differential equation system. Let $P(t)$ denote the present value of premiums up to time t and $B(t)$ the corresponding present value of benefits at the same time. We introduce $V(t)$ as the cumulative benefit reserve at time t.

Therefore, for the annuity for hospitalization plan, the quantitative relations among these insurance factors could be described by the following ODE system:

$$P'(t) = P_{AH}\, e^{-\delta t} S(t)\,, \qquad t > 0\,, \tag{4.9}$$

$$B'(t) = e^{-\delta t} I(t)\,, \qquad t > 0\,, \tag{4.10}$$

$$V'(t) = P_{AH}\, e^{\delta t} S(t) - e^{\delta t} I(t)\,, \qquad t > 0\,, \tag{4.11}$$

where $P_{AH} = \overline{P}(\overline{A}^i_{\overline{T}|})$ is determined by the equivalence principle. By applying the RK-4 method, we get $\overline{a}^s_{\overline{T}|} = P(T)/N$, $\overline{a}^i_{\overline{T}|} = B(T)/N$ and $\overline{V}_{\overline{t}|}(\overline{a}^i_{\overline{T}|}) = V(t)/N$ for the plan of duration T.

For the lump sum for hospitalization plan, we have the following insurance factor system:

$$P'(t) = P_{SH}\, e^{-\delta t} S(t)\,, \qquad t > 0\,, \tag{4.12}$$

$$B'(t) = e^{-\delta t} \beta\, S(t)\, I(t)\,, \qquad t > 0\,, \tag{4.13}$$

$$V'(t) = P_{SH}\, e^{\delta t} S(t) - e^{\delta t} \beta\, S(t)\, I(t)\,, \qquad t > 0\,, \tag{4.14}$$

where $P_{SH} = \overline{P}(\overline{a}^i_{\overline{T}|})$ is also from the equivalence principle, $\overline{a}^s_{\overline{T}|} = P(T)/N$, $\overline{A}^i_{\overline{T}|} = B(T)/N$ and $\overline{V}_{\overline{t}|}(\overline{A}^i_{\overline{T}|}) = V(t)/N$ for the plan of duration T.

Similarly, the annuity for hospitalization plan with a death benefit is determined

by the system

$$P'(t) = P_{AHD}\, e^{-\delta t} S(t)\,, \qquad t > 0\,, \tag{4.15}$$

$$B'(t) = e^{-\delta t} I(t)(1+\alpha)\,, \qquad t > 0\,, \tag{4.16}$$

$$V'(t) = P_{AHD}\, e^{\delta t} S(t) - e^{\delta t} I(t)(1+\alpha)\,, \qquad t > 0\,, \tag{4.17}$$

and $P_{AHD} = \overline{P}(\overline{A}^{i}_{\overline{T}|} + \overline{A}^{d}_{\overline{T}|})$ is from the equivalence principle, $\overline{a}^{s}_{\overline{T}|} = P(T)/N$, $\overline{A}^{i}_{\overline{T}|} + \overline{A}^{d}_{\overline{T}|} = B(T)/N$ and $\overline{V}_{\overline{t}|}(\overline{A}^{i}_{\overline{T}|} + \overline{A}^{d}_{\overline{T}|}) = V(t)/N$ for the plan of duration T.

Finally, for the lump sum for hospitalization plan with a death benefit, the corresponding system is:

$$P'(t) = P_{SHD}\, e^{-\delta t} S(t)\,, \qquad t > 0\,, \tag{4.18}$$

$$B'(t) = e^{-\delta t} \beta\, S(t)\, I(t)\,, \qquad t > 0\,, \tag{4.19}$$

$$V'(t) = P_{SHD}\, e^{\delta t} S(t) - e^{\delta t} I(t)(\beta S(t) + \alpha)\,, \qquad t > 0\,. \tag{4.20}$$

Hence, the equivalence principle gives $P_{SHD} = \overline{P}(\overline{a}^{i}_{\overline{T}|} + \overline{A}^{d}_{\overline{T}|})$, $\overline{a}^{s}_{\overline{T}|} = P(T)/N$, $\overline{a}^{i}_{\overline{T}|} + \overline{A}^{d}_{\overline{T}|} = B(T)/N$ and $\overline{V}_{\overline{t}|}(\overline{a}^{i}_{\overline{T}|} + \overline{A}^{d}_{\overline{T}|}) = V(t)/N$ for the plan of duration T.

These ODE systems can be readily solved in most mathematical software such as Maple environment. Information about programming with ODE tool kits in Maple can be found in Coombes [9].

4.2.2 Infection Table Based Approximation

In practice it is difficult to make record of susceptible group, partly because of its large number and partly due to the fact that susceptibles have no disease symptoms. But we could keep track of infected people using public data from government health agencies and hospitals. Hence we now rely on the function $i(t)$ instead of $s(t)$ for all calculations leading to the premium rating.

A natural analogy is with the life table in life insurance mathematics. It numerically describes an empirical survival distribution of an average person's longevity. Similarly, an infection table is generated to keep record of infected numbers reported during each sampling observation period (e.g., every day for SARS). Table 4.2 in Section 4.4.1 is a simple example of an infection table.

Now from the infection table, we have a piecewise constant empirical approximation of the continuous function $i(t)$ given by

$$\tilde{\imath}(t) = \begin{cases} i_k\,, & k-1 < t \le k \\ 0\,, & \text{otherwise} \end{cases} .$$

Using this function in place of $i(t)$ in (3.4) gives an approximation to $\overline{a}^{i}_{\overline{T}|}$:

$$\begin{aligned} \overline{a}^{i}_{\overline{T}|} = \int_0^T e^{-\delta t}\, i(t)\, dt \;&\approx\; \int_0^T e^{-\delta t}\, \tilde{\imath}(t)\, dt \\ &= \sum_{k=1}^{n} \frac{e^{-\delta(k-1)} - e^{-\delta k}}{\delta}\, i_k\,, \qquad \text{for n large enough.} \end{aligned}$$

4.2.3 Power Series Solutions

The power series method is one of the oldest techniques used to solve linear differential equations. This method can be adapted well to our SIR model.

Since every point in the system is an ordinary point, in particular, $t = 0$, we look for solutions of the form

$$s(t) = \sum_{n=0}^{\infty} a_n\, t^n\,, \qquad t \ge 0\,, \tag{4.21}$$

$$i(t) = \sum_{n=0}^{\infty} b_n\, t^n\,, \qquad t \ge 0\,. \tag{4.22}$$

Therefore, differentiating term by term yields

$$s'(t) = \sum_{n=1}^{\infty} n\, a_n\, t^{n-1} = \sum_{n=0}^{\infty} (n+1)\, a_{n+1}\, t^n\,, \qquad t \ge 0\,,$$

$$i'(t) = \sum_{n=1}^{\infty} n\, b_n\, t^{n-1} = \sum_{n=0}^{\infty} (n+1)\, b_{n+1}\, t^n\,, \qquad t \geq 0\,.$$

Multiplying (4.21) by (4.22) gives,

$$s(t)i(t) = \sum_{n=0}^{\infty} c_n\, t^n\,, \qquad t \geq 0\,,$$

where

$$c_n = a_0 b_n + a_1 b_{n-1} + \cdots + a_{n-1} b_1 + a_n b_0\,.$$

From (3.1), we obtain

$$\sum_{n=0}^{\infty} (n+1)\, a_{n+1}\, t^n + \beta \sum_{n=0}^{\infty} c_n\, t^n = 0\,,$$

$$\sum_{n=0}^{\infty} (n+1)\, b_{n+1}\, t^n - \beta \sum_{n=0}^{\infty} c_n\, t^n + \alpha \sum_{n=1}^{\infty} n\, b_n\, t^{n-1} = 0\,.$$

To satisfy these equations for all t, it is necessary that the coefficient of each power of t be zero. Hence we obtain the following recurrent relation:

$$a_{n+1} = -\frac{\beta}{n+1}(a_0 b_n + a_1 b_{n-1} + \cdots + a_{n-1} b_1 + a_n b_0)\,,$$

$$b_{n+1} = -a_{n+1} - \frac{\alpha}{n+1} b_n\,.$$

Therefore,

$$\overline{a}^i_{\overline{T}|} = \sum_{n=0}^{\infty} \int_0^T a_n\, t^n\, e^{-\delta t}\, dt\,.$$

4.2.4 Integral Equation

A considerable difficulty in solving the ODE system (3.1)-(3.2) is due to the presence of the nonlinear term $\beta\ S(t)\ I(t)$. Its multiplicative structure suggests the use of Fourier transforms.

Recall that

$$\int_{\mathbb{R}} e^{itx} f * g(x)\, dx = \int_{\mathbb{R}} e^{itx} f(x)\, dx \int_{\mathbb{R}} e^{itx} g(x)\, dx\,,$$

where $f * g(x) = \int_{\mathbb{R}} f(x-y)\ g(y)\ dy$. Therefore, if we think of $S(t)$ as a Fourier transform of a certain function $\tilde{S}(x)$ and $I(t)$ as a Fourier transform of a certain function $\tilde{I}(t)$, then the inversion formula gives

$$\tilde{S}(x) = \frac{1}{2\pi}\int_{\mathbb{R}} S(t)e^{-itx}\,dt, \qquad \tilde{I}(x) = \frac{1}{2\pi}\int_{\mathbb{R}} I(t)e^{-itx}\,dt\ .$$

The reason we choose Fourier transforms is that they always exist for real functions. In applications, if certain real inverse transforms of $I(t)$ and $S(t)$ exist, numerical solutions to their integral equations would be easier to obtain.

Now write the nonlinear term as

$$\beta S(t)I(t) = \beta\int_{\mathbb{R}} e^{itx}\tilde{S} * \tilde{I}(x)\,dx\ .$$

Therefore, we take the inverse Fourier transform on both sides of (3.1), giving

$$ix\tilde{S}(x) - \frac{1}{2\pi}S(0) = -\beta\int_{\mathbb{R}} \tilde{S}(y)\tilde{I}(x-y)dy\ , \tag{4.23}$$

$$ix\tilde{I}(x) - \frac{1}{2\pi}I(0) = \beta\int_{\mathbb{R}} \tilde{S}(y)\tilde{I}(x-y)dy - \alpha\tilde{I}(x)\ . \tag{4.24}$$

Adding up the above two equations gives

$$\tilde{S}(x) = \frac{1}{2\pi ix}\big[S(0)+I(0)\big] - \frac{(ix+\alpha)}{ix}\tilde{I}(x)\ . \tag{4.25}$$

Substitute (4.25) into (4.24) to obtain the following integral equation

$$\tilde{I}(x) = \frac{\beta}{(ix+\alpha)}\int_{\mathbb{R}}\big[\frac{S(0)+I(0)}{2\pi iy} - \frac{\alpha+iy}{iy}\tilde{I}(y)\big]\tilde{I}(x-y)\ dy + \frac{1}{2\pi}I(0)\ . \tag{4.26}$$

By the definition (3.4), we have then

$$\begin{aligned}\overline{a}^{i}_{T|} &= \frac{1}{N}\int_0^T e^{-\delta t}\int_{\mathbb{R}} e^{itx}\tilde{I}(x)\,dx\,dt \\ &= \frac{1}{N}\int_{\mathbb{R}}\frac{e^{(ix-\delta)T}-1}{(ix-\delta)}\tilde{I}(x)\,dx\ .\end{aligned}$$

4.3 Premium Adjustment

The fact that mortality rises with age leads to the consequence that an insurer's future financial liabilities might overtake future revenue from benefit premiums. Therefore the benefit reserve is normally positive in life insurance. Now proposition 4.3.1 shows that the mortality due to an infectious disease decreases after reaching a peak during the outbreak, which signals a possible difference in the direction of change in reserve. Figure 4.1 illustrates a typical path of a benefit reserve function from the insurance factor system (4.9) - (4.11), where the benefit premium is determined by (3.15).

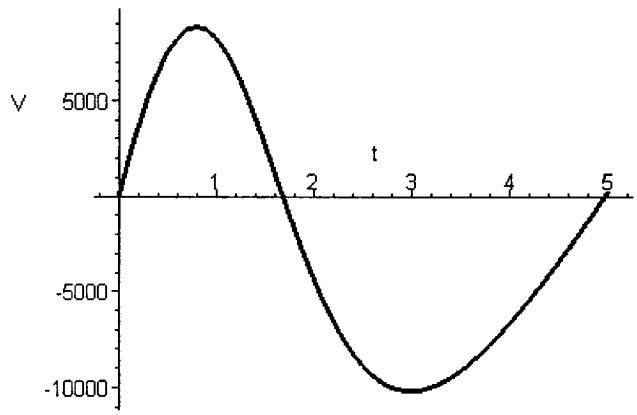

Figure 4.1: Benefit reserve function $V(t)$ for AH plan for the Great Plague, $P_{AH} = 106.51$. Double arch structure as explained in Proposition 4.3.3.

Although it still satisfies the equivalence principle on the long-term from time 0 to 5, it is practically unacceptable for an insurer to have a long standing negative reserve, increasing the risk of bankruptcy. Therefore an additional premium is required to ensure that the benefit reserve never falls below an early warning level, which is lowest tolerable financial reserve. Before giving an algorithm for determining an added-value premium, we would like to study for a moment the trend of a benefit reserve function $V(t)$ and its dependency on functions $S(t)$ and $I(t)$.

Proposition 4.3.1. *For the SIR model in (2.1)-(2.3), $S(t)$ is a monotonically decreasing function, and $R(t)$ is monotonically increasing. If $S(0) \leq \alpha N/\beta$, then $I(t)$ is a monotonically decreasing function; If $S(0) > \alpha N/\beta$, $I(t)$ increases up to the time when $S(t) = \alpha N/\beta$, and then decreases after.*

Proof. Since $S(t)$ and $I(t)$ are all non-negative, from (2.1) and (2.3) we know that $S'(t) = -\beta\ S(t)\ I(t)/N < 0$, for $t > 0$, and $R'(t) = \alpha\ I(t) > 0$. Hence $S(t)$ is a monotonically decreasing function and $R(t)$ is a monotonically increasing function. If $S(0) \leq \alpha/\beta$, then $I'(t) = I(t)[\beta\ S(t)/N - \alpha] < 0$, which means that $I(t)$ is monotonically decreasing. By contrast, if $S(0) > \alpha N/\beta$, because $S(t)$ is monotonically decreasing, then $I'(t) = I(t)[\beta\ S(t)/N - \alpha] > 0$, as long as $S(t) > \alpha N/\beta$. Thus $I(t)$ reaches its local maximum at the point where $S(t) = \alpha N/\beta$. When $S(t)$ continues to decrease below $\alpha N/\beta$, $I'(t) < 0$ and $I(t)$ is monotonically decreasing thereafter. □

From now on in this section, we study the benefit reserve by looking at the example of AH plan. The generalization to other plans follows the same idea. From (4.11), we know that $V'(t) = e^{\delta\, t}(P_{AH}\ S(t) - I(t))$, for $t \geq 0$. The general direction in which $V(t)$ changes depends on the opposing forces, monotonically decreasing $P_{AH} \cdot S(t)$ and increasing-then-decreasing $I(t)$. There are only two possible geometrical structures in the trend of $V(t)$: Single arch structures as shown in Figure 4.2 and double arch structures typically illustrated in Figure 4.1. The following propositions indicate conditions under which the two structures may appear, respectively.

Proposition 4.3.2. *(Single Arch Structure) In the insurance factor system (4.9) -*

(4.11), the benefit reverse $V(t)$ is concave, if the premium

$$P_{AH} > \frac{\alpha N}{\beta S_\infty} - 1 \,, \tag{4.27}$$

where the constant $c = I_0 + S_0 - \alpha N/\beta \, \log(S_0)$ *and* $S_\infty = \lim_{t\to\infty} S(t)$.

Proof. To check the concavity of $V(t)$, we look at $V''(t)$,

$$\begin{aligned} V''(t) &= P_{AH} S'(t) - I'(t) \\ &= -\frac{\beta}{N} P_{AH} \, S(t) \, I(t) - \frac{\beta}{N} \, S(t) \, I(t) + \alpha \, I(t) \\ &= I(t) \, [\alpha - \frac{\beta}{N} \, (P_{AH} + 1) S(t)] \,. \end{aligned}$$

It follows that when

$$P_{AH} > \frac{\alpha N}{\beta S(t)} - 1 \,, \qquad \text{for all } t > 0 \,,$$

$V(t)$ is concave downward. Since $S(t)$ is monotonically decreasing, thus condition (4.27) is required. □

Proposition 4.3.3. *(Double Arch Structure) If P_{AH} does not satisfy (4.27) and in addition*

$$S_0 > \frac{\alpha N}{(1 + P_{AH})\beta} \,, \tag{4.28}$$

then the benefit reserve $V(t)$ changes from concave to convex, with a point of inflection t_f such that

$$S(t_f) = \frac{\alpha N}{(1 + P_{AH})\beta} \,.$$

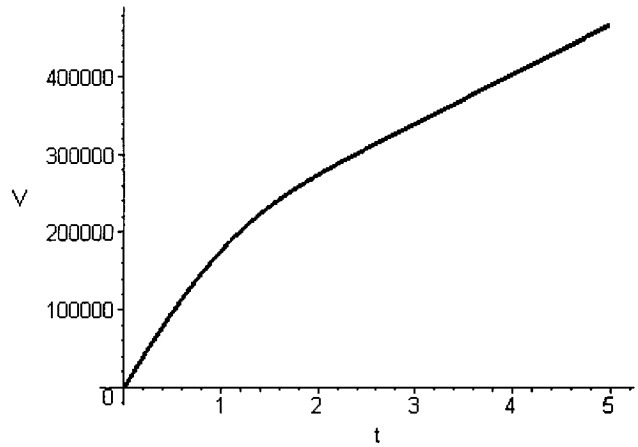

Figure 4.2: Benefit reserve function $V(t)$ for AH plan for the Great Plague, $P_{AH} = 843.38$, Single arch structure as explained in Proposition 4.3.2.

Proof. By (4.28), $V''(t)$ changes from positive to negative at time t_f, when

$$S(t_f) = \frac{\alpha N}{(1 + P_{AH})\beta} .$$

Therefore, no matter whether $V'(t)$ starts from a negative or positive value, $V(t)$ goes through two phases, from concave to convex. □

The next question that comes to mind is how to control the extent of the deficit in the reserve by premium adjustment, while preserving the equivalence principle. From the double arch structure, we know that the worst deficit scenario in reserves is measured by the local minimum in the second arch. Therefore, if we are able to find out the minimum point on the time scale, we can adjust premiums by controlling how far the reserve can fall below zero.

Suppose we want the reserve to reach the local minimum by time t_m. From (4.11) it is obvious that $P_{AH} = S(t_m)/I(t_m)$ is the smallest possible premium that can be charged. At this premium level, the reserve function has a double arch structure with a point of inflection at time t_f, at which $S(t_f) = \alpha N/[(1+P_{AH})\beta]$ by Proposition

4.3.3. It is proven in Proposition 4.3.4 that P_{AH} is a decreasing function with respect to t_0 as long as $t_m > t_f$. Therefore, if we shorten the hitting time t_m, the corresponding premium P_{AH} will increase, which in turn decreases the susceptible function $S(t)$ and increases the point of inflection t_f. In other words, the graph of the reserve function becomes flatter, as the lowest deficit rises and the hitting point gets closer to the point of inflection.

It is natural to conjecture that as we shorten the hitting time t_m, there must be a certain point where the point of inflection t_f overlaps the lowest deficit time t_m, as shown in Figure 4.3. Translated in mathematical terms, this means

$$\frac{\alpha N}{\beta[1 + I(t_m)/S(t_m)]} = S(t_m) \ ,$$

which in turn implies that $S(t_m) + I(t_m) = \alpha N/\beta$. We now prove this interesting point and find the corresponding premium in the following proposition.

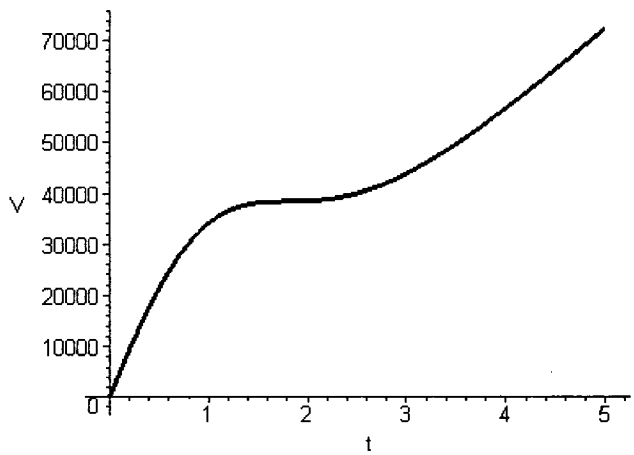

Figure 4.3: Benefit reserve function $V(t)$ for AH plan for the Great Plague, $P_{AH} = 202.17$. Double arch structure and strictly increasing as explained in Proposition 4.3.4.

Proposition 4.3.4. *For the insurance factor system in (4.9) - (4.11), the reserve*

$V(t)$ is concave and strictly increasing, if

$$P_{AH} > \frac{\alpha N}{\beta} \exp\left(\frac{\beta c}{\alpha N} - 1\right) - 1 , \tag{4.29}$$

where the constant $c = I_0 + S_0 - \alpha N/\beta \log(S_0)$.

Proof. To ensure that $V'(t) > 0$, we need

$$P_{AH} > \frac{I(t)}{S(t)} , \qquad \text{for all } t ,$$

or equivalently,

$$\log P_{AH} > \log I(t) - \log S(t) , \qquad \text{for all } t .$$

Let $f(t) = \log I(t) - \log S(t)$, then

$$\begin{aligned} f'(t) &= \frac{I'(t)}{I(t)} - \frac{S'(t)}{S(t)} \\ &= \frac{\beta}{N}[S(t) + I(t)] - \alpha , \qquad \text{by (2.1) and (2.2).} \end{aligned}$$

Since $S(t) + I(t) = N - R(t)$ is monotonically decreasing, at the time t_m when

$$S(t_m) + I(t_m) = \alpha N/\beta , \tag{4.30}$$

$f'(t)$ changes from positive to negative and $f(t)$ reaches the local maximum. In other words, P_{AH} is a decreasing function of t as long as $t > t_m$. Thus P_{AH} is required to be greater than $I(t_m)/S(t_m)$.

Now since

$$\frac{I'(t)}{S'(t)} = \frac{dI(t)}{dS(t)} = \frac{(\beta S(t)/N - \alpha)I(t)}{-\beta S(t)I(t)/N} = -1 + \frac{\alpha N}{\beta S(t)} ,$$

integrating to find the orbits of the (S, I)-plane gives:

$$I(t) + S(t) - \frac{\alpha N}{\beta} \log S(t) = c \,, \tag{4.31}$$

where c is a constant of integration for each specific orbit, say $c = I_0 + S_0 - \alpha N/\beta \log(S_0)$. Combining (4.30) and (4.31), we can solve for $S(t)$ and $I(t)$, as

$$S(t_m) = \exp(1 - \frac{\beta c}{\alpha N}) \,, \tag{4.32}$$

$$I(t_m) = \frac{\alpha N}{\beta} - \exp(1 - \frac{\beta c}{\alpha N}) \,. \tag{4.33}$$

Hence

$$\log P_{AH} > f(t_m) \,. \tag{4.34}$$

Substituting (4.32) and (4.33) into (4.34) gives the condition (4.29). □

We are now in a position ready to find a proper premium between $\overline{P}(\overline{A}^i_{\overline{T}|})$ and P_{AH} for the strictly increasing case, in order to achieve certain reserve standards. For instance, if the reserve is required to be above a certain level V, we start by letting $P_{AH} = \overline{P}(\overline{A}^i_{\overline{T}|})$, then increment the premium each time by a monetary unit (say, $h = \$0.01$) until $V(t_m) > V$. Once we determine the desirable premium, the benefit of $V(T)/S(T)$ should be set up as a liability to the remaining policy holders according to the equivalence principle.

4.4 Numerical Examples

The first numerical example of Great Plague in Eyam was first studied by Raggett [25], and has been considered a classical case study in many textbooks because predictions from the model are remarkably close to actual data. The second example of six

compartment model was originated from Chowell *et al.* [8], in which parameters were primarily used for measuring basic reproduction number.

4.4.1 Great Plague in Eyam

The village of Eyam near Sheffield, England, suffered an horrific outbreak of bubonic plague in 1665-1666. The plague was survived by only 83 of an initial population of 350 villagers, and detailed records were preserved as shown in Table 4.2. In Raggett [25], the disease in Eyam was fitted by the SIR model, over the period from mid-May to mid-October 1666, measured in months with an initial population of 7 infectives and 254 susceptibles, and a final population of 83. Since the disease was fatal at that time, infected individuals eventually died due to the disease.

Date	**Susceptibles**	**Infectives**
Initial	254	7
July 3/4	235	14.5
July 19	201	22
August 3/4	153.5	29
August 19	121	21
September 3/4	108	8
September 19	97	8
October 4/5	Unknown	Unknown
October 20	83	0

Table 4.2: Eyam plague observation of susceptible and infective populations in 1666.

Data source: Raggett [25], Table II.

According to (4.31),

$$I_0 + S_0 - \frac{\alpha N}{\beta} log S_0 = I_\infty + S_\infty - \frac{\alpha N}{\beta} log S_\infty \ ,$$

from which we obtain an expression for $\beta/(\alpha N)$ in terms of the measurable quantities S_0, I_0, S_∞ and I_∞, namely

$$\frac{\beta}{\alpha N} \approx \frac{log \frac{S_0}{S_\infty}}{S_0 - S_\infty} \ .$$

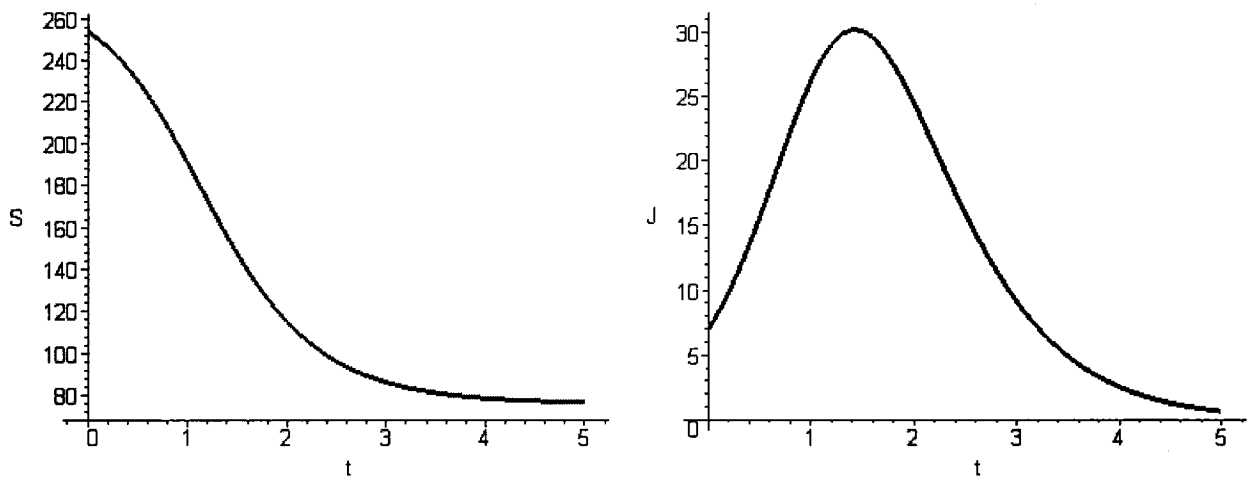

Figure 4.4: Function of susceptibles S(t) and infectives I(t)

The relation with $S_0 = 254$, $I_0 = 7$ and $S_\infty = 83$ gives $\alpha N/\beta = 153$. The parameter α is determined by its reciprocal, which has the clinical meaning of an average infectious period. From clinical observations, an infected person stays infectious for an average of 11 days or 0.3667 months before death, so that $\alpha = 2.73$ and $\beta/N = 0.0178$. The resulting graphs of S and I, as functions of time t, are given in Figures 4.4.

Insurance coverage would not directly reduce the transmission of the disease, but a well-designed insurance system could have provided financial incentives for prevention measures and compensate for hospitalization and other medical costs and

services. To develop this insurance model, we assume that everyone in the village foresees the coming of the Great Plague and willingly chips in the mutual insurance group at the beginning of the epidemic. The insurance funding is secured with a monthly force of interest of 0.2%. The insurance period lasts 5 months which matches the duration of the epidemic.

Plan	P.V. Benefits	P.V. Premiums	Level Premium
1	65015.62	610.41	106.51
2	242508.27	610.41	397.29
3	172385.38	610.41	282.41
4	349878.02	610.41	573.18

Table 4.3: Eyam plague premium rating (dollar)

1. **Annuity for Hospitalization (AH)**:

   This plan provides infection benefits continuously at the rate of $1000 per month until death for every infected individual regardless of how long he or she has entered the class. The insurance liability is terminated after death. It is purchased continuously by susceptible individuals.

2. **Annuity for Hospitalization with a Death Benefit (AHD)**:

   This plan contains all of the same benefits as in the previous one plus an additional death benefit of $1000 payable at the moment of death. The insurance liability is terminated after death. It is also purchased in the same pattern.

3. **Lump Sum for Hospitalization (SH):**

   This plan provides a lump sum infection benefit of $1000 at the moment of the individual being diagnosed infected. The insurance liability is terminated after death. It is purchased continuously by susceptible individuals.

4. **Lump Sum for Hospitalization with Death Benefit (SHD):**

   This plan contains all of the same benefits as in the previous one. In addition, a death benefit of $1000 is payable to specified beneficiaries at the moment of the insured's death. The insurance liability is terminated after death. It is purchased continuously by susceptible individuals.

Table 4.3 gives net level premiums for each plan determined by the original equivalence principle. It probably differs from what one might have expected that the premium of the annuity for hospitalization plan is not even half the premium of the lump sum for hospitalization plan. Note that although it seems to cost more for the former plan to provide $1000 per month not only for new infectives, but for all existent patients. The fact is that few of them survived longer than a month after the disease was detected. Therefore, providing infectives immediate indemnity costs an insurer much more than a monthly annuity for such an acute fatal disease.

Just as benefit reserves in life insurance, the reserve functions, shown in Figure 4.5 for the infectious disease coverage, reaches zero at the end of policy duration, when the insurer's liability is terminated. However, as discussed in Section 4.3, every reserve function in our example appears to go through a negative phase, which dangerously

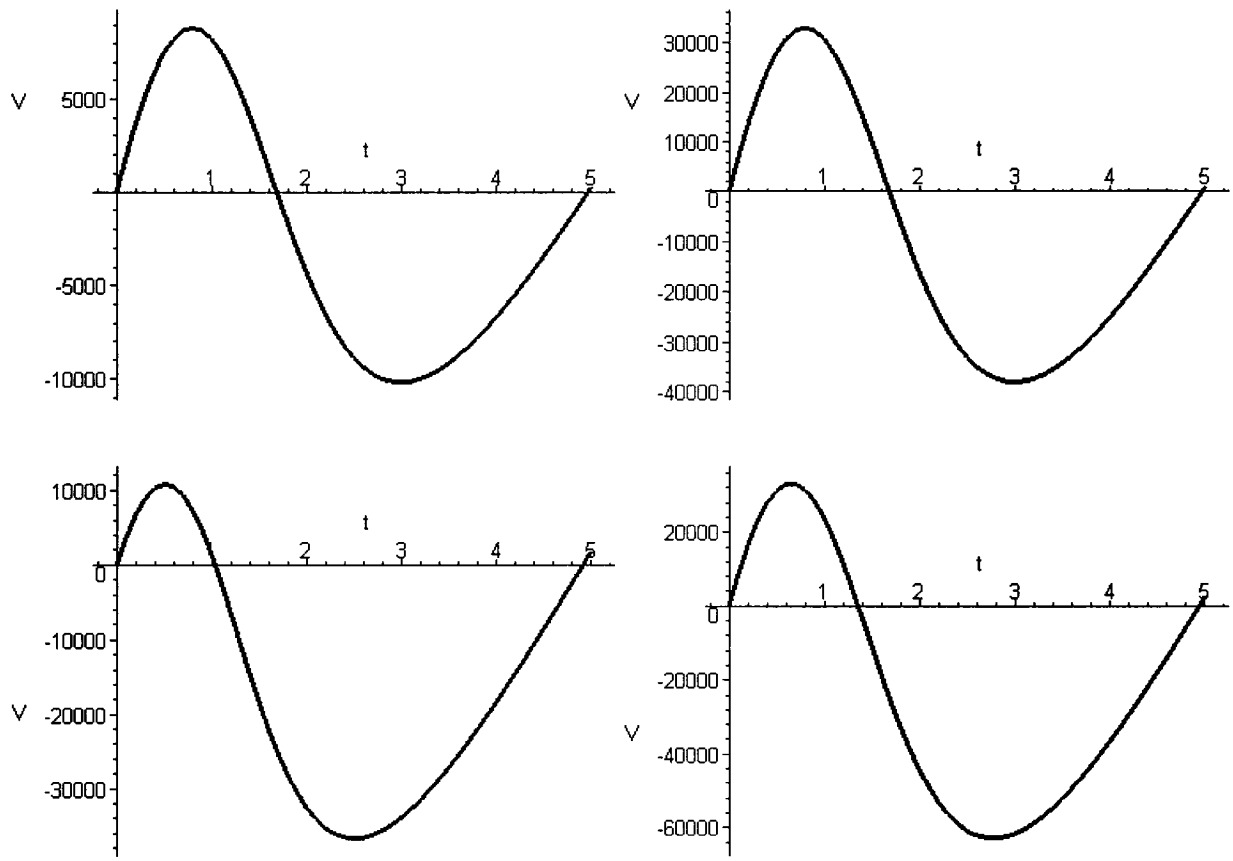

Figure 4.5: Benefit reserve $V(t)$ with premiums determined by the equivalence principle. Clockwise from the top left corner Plan AH, AHD, SHD and SH.

reduces the insurer's financial solvency. Thus there is a need for our algorithm that adjusts premiums to meet the financial requirement such as that benefit reserve must not be allowed to go under zero.

Since the death and hospitalization benefits remain the same and only premiums are raised to ensure insurers' nonnegative reserve, the equivalence cannot be established unless the insurer clears off the reserve balance in the form of another benefit for the remaining survivors. Therefore, in each plan we add a new insurance liability

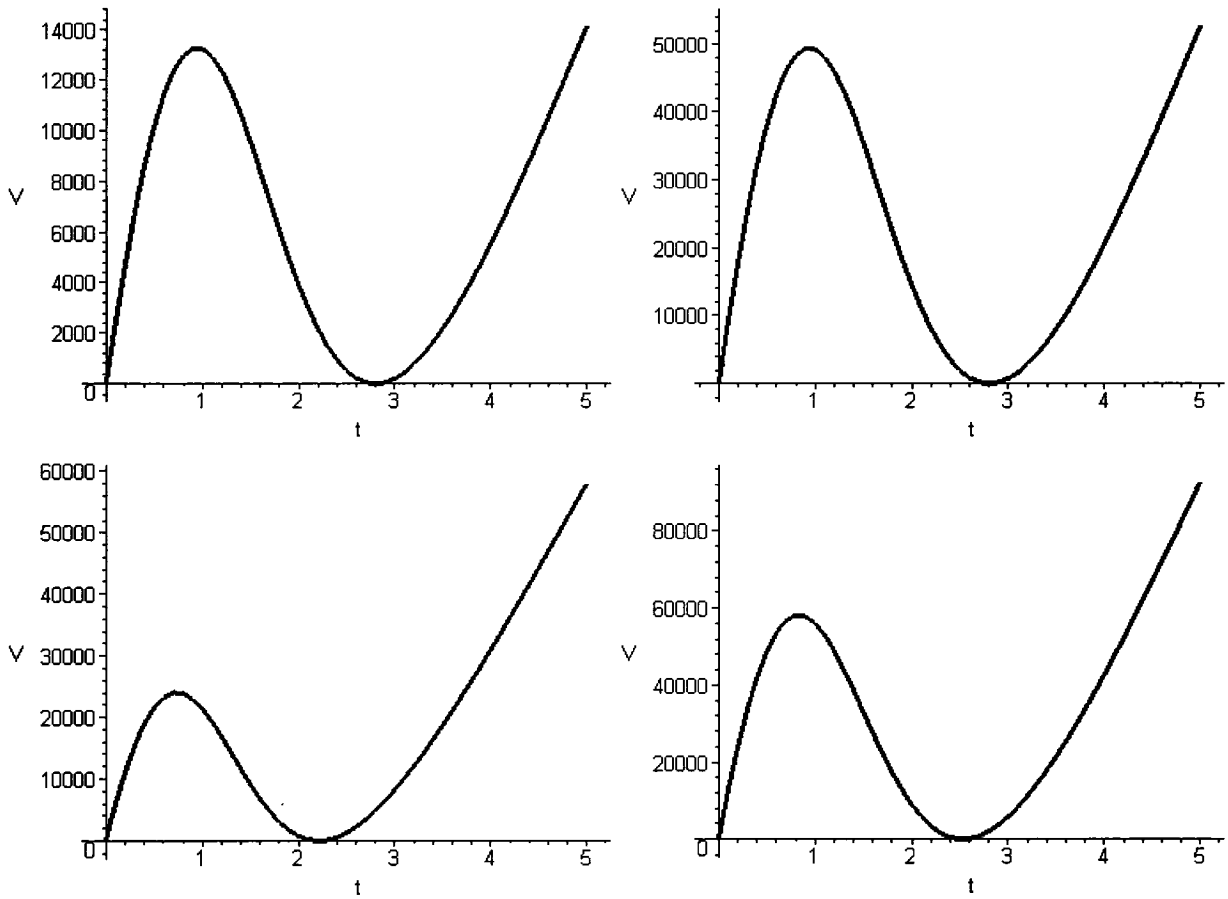

Figure 4.6: Benefit reserve $V(t)$ with adjusted premiums and survival benefits. Clockwise from the top left corner Plan AH, AHD, SHD and SH.

that every survivor of the epidemic is entitled to an equal payment of dividends. Table 4.4 illustrates the adjusted premiums for each plan and the final dividend payment to survivors.

Plan	Adjusted Premium	Survival Dividend	Terminal Reserve
1	128.38	184.74	14170.81
2	478.86	689.11	52858.76
3	370.76	756.95	58062.73
4	715.02	1209.73	92793.84

Table 4.4: Eyam plague adjusted premiums (dollar)

4.4.2 SARS Epidemic in Hong Kong

In the classical SIR model, the assumption that the mixing of members from different compartments is geographically homogeneous is probably unrealistic. Susceptibles in geographical neighborhoods of an infectious virus-carrier are more likely to be infected than those more remote from the carrier, while health care workers are at higher risk of infection than other populations.

To distinguish different levels of infectiousness within different social groups, spatial structures were introduced and developed in epidemiological studies. A typical example of a spatial structure applied to the SARS epidemic in Hong Kong is defined

by Chowell *et al.* [8] in the following ODE system,

$$S_1'(t) = -\beta S_1(t)\frac{I(t)+qE(t)+lJ(t)}{N}, \qquad t \geq 0, \tag{4.35}$$

$$S_2'(t) = -\beta p S_2(t)\frac{I(t)+qE(t)+lJ(t)}{N}, \qquad t \geq 0, \tag{4.36}$$

$$E'(t) = \beta(S_1(t)+pS_2(t))\frac{I(t)+qE(t)+lJ(t)}{N} - kE(t), \qquad t \geq 0, \tag{4.37}$$

$$I'(t) = kE(t) - (\alpha+\gamma_1+\delta)I(t), \qquad t \geq 0, \tag{4.38}$$

$$J'(t) = \alpha I(t) - (\gamma_2+\delta)J(t), \qquad t \geq 0, \tag{4.39}$$

$$R'(t) = \gamma_1 I(t) + \gamma_2 J(t), \qquad t \geq 0. \tag{4.40}$$

In this model, there are two distinct susceptible compartments with different levels of exposure to the SARS, namely S_1 for the most susceptible urban community and S_2 for the less susceptible rural population. Initially, $S_1(0) = \rho N$ and $S_2(0) = (1-\rho)N$, where ρ is the proportion of urban inhabitants in total population. An average highly susceptible person (in the Class S_1) makes an average number of β adequate contacts (i.e. contacts sufficient to transmit infection) with others per unit time. Due to lower contacts with infecteds, an average lower susceptible person (in the Class S_2) would only be exposed to an average number of $p\beta$ adequate contacts with others per unit time.

Because an individual infected with SARS may experience an incubation period of 2-7 days, the first infectious class is set up for those infected but not yet symptomatic. The parameter q is used to measure the lower level of infectivity during the incubation, after which an individual would develop observable symptoms and

become fully infectious in Class I with $q = 1$.

In order to distinguish their potential disease transmission to general public, the Class I is separated for those infectious individuals that are undiagnosed. Since almost all diagnosed cases are quarantined in hospitals, the Class J has a lower infectivity level reflected by a reduction factor l.

The rates of population transferring from E, I and J to their chronological next compartments I, J and the recovered class R are respectively k, α and γ_2. Considering that even before being diagnosed SARS patients may either recover naturally at the rate of γ_1 or die at the mortality of δ, we also have the class D keeping track of deaths induced by the SARS from two sources I and J. The patients under medical treatments in Class J suffer death at the rate assumed to be the same as the mortality in Class I.

Notice that both E and I are undiagnosed phases, there is literally no statistical data for estimating their parameters. Therefore, another compartment C for reported probable cases is set aside to trace back the original time of incidences by a model similar to (4.1). Figure 4.7 gives transfer directions among the different compartments.

To avoid getting into details of parameter inference, we make use of parameter values from the original paper as summarized in Table 4.5. These parameter values were used to compute the basic reproductive number R_0 in the original article, which is probably the reason why there appears to be negative numbers in Classes I and J.

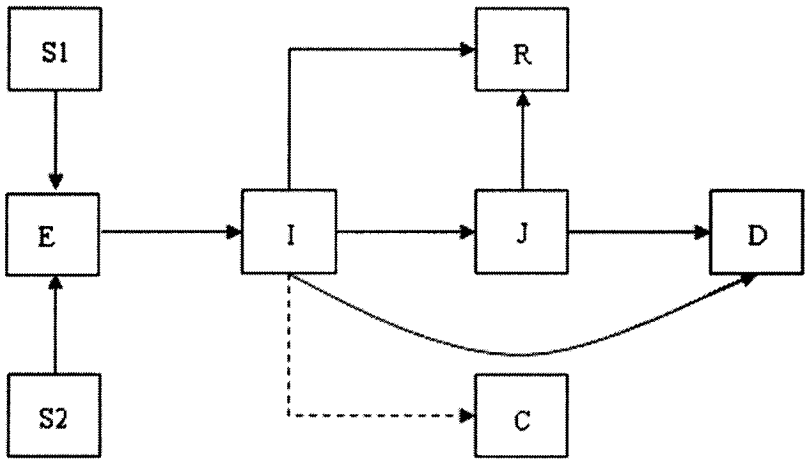

Figure 4.7: Transfer diagram of the SARS epidemic dynamics, Reprinted from the Figure 1 in Chowell [8].

From an insurer's point of view, this model could offer many business opportunities. On the one hand, individuals in Classes S_1 and S_2 are potential buyers facing the risk of being infected with SARS. On the other hand, there is an evident need for insurance covering vaccination costs in both S_1 and S_2, medical examination expenses for probable cases in Class I, hospitalization and quarantine expenses for Class J and death benefit for Class D. Since a number of parties are involved in the health care system, such as insurance companies, policyholders, government health agencies, and hospitals. Numerous business models could be designed to bring them together. To illustrate a case of such an infectious disease insurance, we design the following two plans.

1. Annuity for Hospitalization Plan

Parameter	Moving from/to	Value
β	$S_1, S_2/E$	0.75
q	reduced infectiousness	0.1
l	reduced infectiousness	0.38
p	reduced susceptablity	0.1
k	E/I	1/3
α	I/J	1/3
γ_1	I/R	1/8
γ_2	J/R	1/5
δ	$I, J/R$	0.006
ρ	reduced contacts	0.4

Table 4.5: Parameter values that fit the SARS model for Hong Kong, adapted from the Table 1 in Chowell *et al.* [8].

Every participant of the mutual insurance funding purchases the coverage by means of a life annuity. Rural inhabitants are charged lower premiums proportional to their reduced susceptibility. From the time of policy issue to the end of the epidemic, every insured is eligible for claiming a medical examination fee of $100,000 once observed with suspicious symptoms, and hospitalization expenses of $100,000 per day, in the form of a life annuity for the period under medical treatment in hospital. Specified benefiaries can claim for a death benefit of $100,000 after an insured's death due to the infectious disease. The insurance

liability terminates at the end of the epidemic.

2. Lump Sum for Hospitalization Plan

   This plan contains all of the same benefits as in the previous one except that the annuity for hospitalization benefit is replaced by a lump sum payment of $100,000 after the policyholder is detected to be infected with the disease. The insurance liability terminate at the end of the epidemic.

Table 4.6 gives net level premiums for each plan determined by the original equivalence principle.

Plan	**P.V. Benefits**	**P.V. Premiums**	**Level Premium**
1	3.0571×10^8	1.71604×10^8	1.78
2	1.3231×10^8	1.71604×10^8	0.77

Table 4.6: SARS insurance premium rating (dollar)

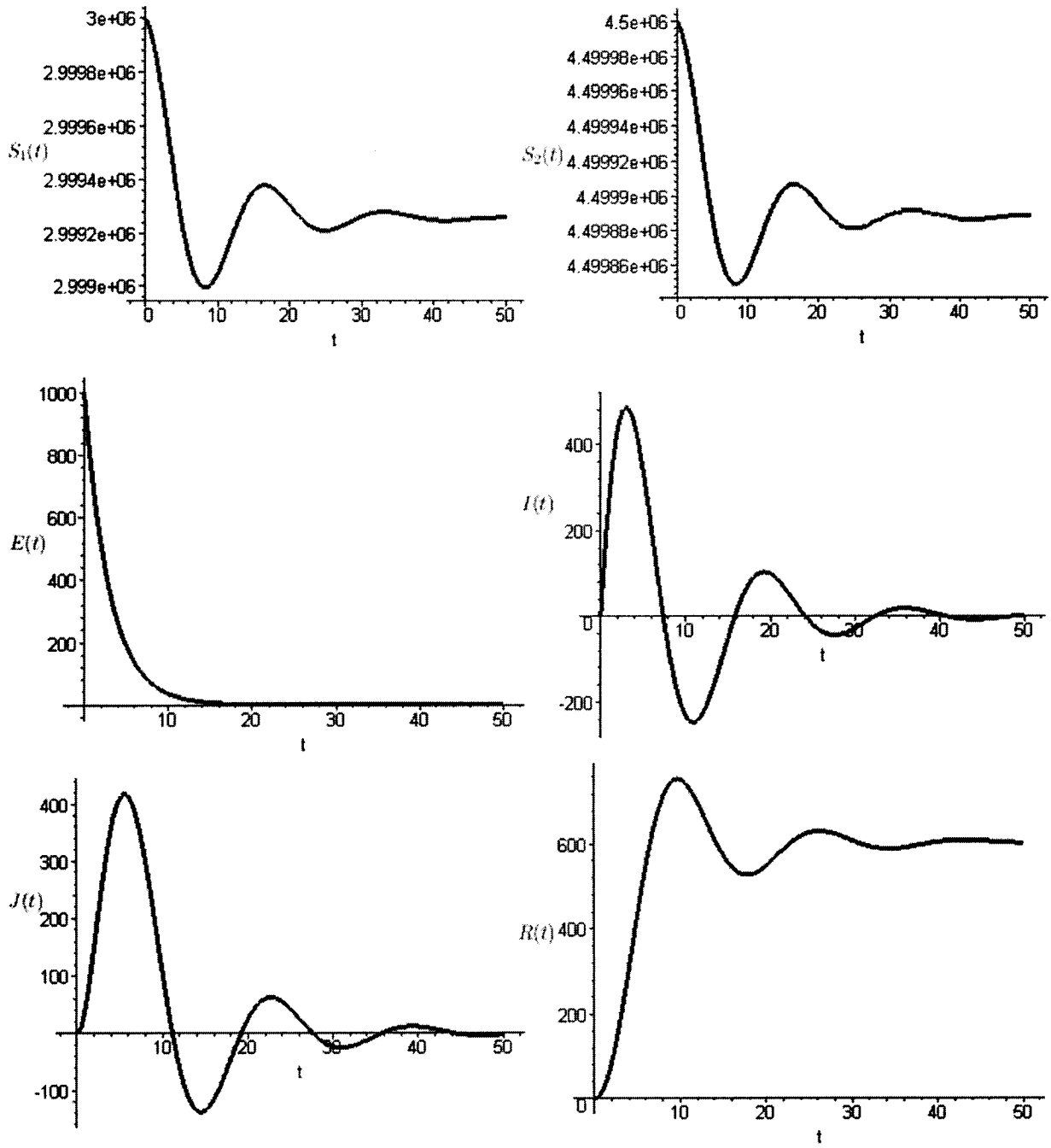

Figure 4.8: Functions of individual numbers in each compartment $S_1(t)$, $S_2(t)$, $E(t)$, $I(t)$, $J(t)$ and $R(t)$

Chapter 5

Premium Approximation in Stochastic Models

There have been abundant and extensive studies in epidemiological stochastic modelling. Looking only at a tip of the iceberg, we introduce in this chapter a short time horizon model studied by Lefèvre [20], with slight changes in its interpretation. Readers interested in a comprehensive overview of stochastic ordering and its application in epidemiology are referred to Shaked and Shanthikumar [27]. In most deterministic and stochastic models, the mass action law is widely used to explain movements among epidemiological stages. The non-linear terms in (3.1) - (3.2) and (4.35) - (4.37) are typical examples. But the short time horizon model, originated in the context of AIDS epidemics, describes the dynamic of transmission as probabilistic events. It considers the infectivity levels and the numbers of contacts as dependent

random variables.

To approximate premiums based on the model dealing with dependent variables, we develop the idea of comparing stochastically ordered comonotonic variables and then estimating premiums with the best possible variable. For a reference on *comonotonicity*, readers are suggested to Dhaene *et al.* [13] and [14].

An alternative method is also presented with the concept of *copulas*, which is a more powerful tool in defining and analyzing dependency among inter-reacting variables. Constructing a transform of uniformly distributed variables based on empirical copulas, we are able to approximate any two dependent variables with information of their marginals and in turn calculate insurance premiums. The geometric construction of copulas is extensively discussed in Mikusiński *et al.* [21]. Readers with interests in general theory of copulas are referred to Nelsen [23].

5.1 Short Time Horizon Model

The framework of this epidemiological model on a short time horizon was first introduced by Eisenberg in the context of AIDS research and later extended by Lefèvre [20]. An advantage of this model is that the number of contacts with different individuals and their infectivity levels are treated as random variables instead of fixed constants in our deterministic model, and the probability of infection is relatively easier to calculate without the non-linear term from the mass action law.

We assume that in a short period an individual would have sexual contacts

with partners at a fixed number l of distinct infectivity levels. With partners at level $j = 1, 2, \cdots, l$, the individual will make a random number R_j of contacts. At each single contact with partners at level $j = 1, 2, \cdots, l$, the odds are B_j of the individual being infected with AIDS. Moreover, the number of contacts R_j is independent of the infectivity level B_j. Therefore, the probability of a person not contracting AIDS over the short horizon is

$$\mathbb{P}(B, R) = E[(1 - B_1)^{R_1}(1 - B_2)^{R_2} \cdots (1 - B_l)^{R_l}] , \tag{5.1}$$

where the probability $\mathbb{P}(B, R)$ depends on the random vectors $B = (B_1, B_2, \cdots, B_l)$ and $R = (R_1, R_2, \cdots, R_l)$. From an insurer's point of view, $\mathbb{P}(B, R)$ is also the premium charged to the individual for a unit benefit insurance.

5.2 Random Sum and Comonotonicity

Definition 5.2.1. A random variable X is less than Y in *stochastic order* (denoted by $X \leqslant_{st} Y$), if

$$P\{X > u\} \leq P\{Y > u\} , \qquad \text{for all } u \in \mathbb{R} .$$

Roughly speaking, X is less likely than Y to take on large values. The above definition is also equivalent to $E[g(X)] \leqslant E[g(Y)]$ for any increasing function $g(\cdot)$. The generalization to the multivariate stochastic order is that $E[g(X)] \leqslant E[g(Y)]$ for any multivariate increasing function $g(\cdot)$, which means $g(A) \leqslant g(B)$ if $A \leqslant B \in \mathbb{R}^n$.

Definition 5.2.2. A random variable X is less than Y in *convex order* (denoted by $X \leqslant_{cx} Y$), if and only if

$$E(X-d)_+ \leqslant E(Y-d)_+ \text{ , and } E(d-X)_+ \leqslant E(d-Y)_+ \text{ for all } d \geqslant 0 \text{ .}$$

Similarly, it can be proven that $X \leqslant_{cx} Y$ is equivalent to $E[g(X)] \leqslant E[g(Y)]$ for any convex function g. The multivariate convex order $X \leqslant_{cx} Y$ is defined in a similar fashion that $E[g(X)] \leqslant E[g(Y)]$ for all convex function $g : \mathbb{R}^n \to \mathbb{R}$.

In the context of utility theory, the convex order represents the common preferences of all risk-averse decision makers between random variables with equal mean. As a natural interpretation of convex order, in practice the random variable X is preferred over Y ($X \leqslant_{cx} Y$), since X is less likely to take on not only excessively large positive values, but also negative ones. In other words, the density of X is less widespread than Y.

Definition 5.2.3. A random variable X is less than Y in *moment generating function order* (denoted by $X \leqslant_{mgf} Y$), if and only if

$$E[t^X] \geq E[t^Y] \text{ , } \qquad \text{for all } t \in (0,1) \text{ .}$$

An equivalent condition of the above definition is that $E[\phi(X)] \geqslant E[\phi(Y)]$ for all completely monotone functions ϕ, provided the expectations exist. Its multivariate analogue $X \leqslant_{cx} Y$ is defined by

$$E\Big[\prod_{i=1}^{n} t_i^{X_i}\Big] \geqslant_{cx} E\Big[\prod_{i=1}^{n} t_i^{Y_i}\Big] \text{ , } \qquad \text{for all } (t_1, \cdots, t_n) \in (0,1)^n \text{ .}$$

The relation among the above three orders is that

$$X \leqslant_{st} Y \Longrightarrow X \leqslant_{cx} Y \Longrightarrow X \leqslant_{mgf} Y \ .$$

In the recent actuarial literature, the concept of comonotonicity was introduced and developed in order to provide upper bounds, in the sense of convex order, to estimate convex sums of dependent variables. For instance, think of the random vector $X = (X_1, X_2, \cdots, X_n)$ as a portfolio of mutual fund investments. For a risk-averse investor the worst possible portfolio is the one in which different stock prices are positively dependent with each other. In that case, if the price of one stock goes down, all other stocks follow the same trend and the whole portfolio would depreciate by factors of the portfolio size. This "all eggs in one basket" scenario is best described by the concept of comonotonicity. The most straightforward definition of a comonotonic vector reflects the complete dependence among its components.

Definition 5.2.4. A random vector $X = (X_1, X_2, \cdots, X_n)$ is comonotonic if and only if there exists a random variable Z and non-decreasing function $f_1, f_2, \cdots, f_n$, such that

$$X =^d (f_1(Z), f_2(Z), \cdots, f_n(Z)) \ .$$

The merit of this definition is that for simulation purposes one can easily generate a comonotonic vector by imposing certain transforms on a single random variable. An important property of a comonotonic random vector X is that its joint distribution can be characterized by the minimum of its marginals : $F_X(x_1, x_2, \cdots, x_n) =$

$\min\{F_{X_1}(x_1), F_{X_2}(x_2), \cdots, F_{X_n}(x_n)\}$. An equivalent definition that reveals the essence of its dependence structure is implied in Proposition 5.3.2 of Section 5.3.

Now we are able to construct a comonotonic random vector with the same marginal distributions as $X = (X_1, X_2, \cdots, X_n)$ by letting

$$X^c \triangleq (X_1^c, X_2^c, \cdots, X_n^c) =^d (F_{X_1}^{-1}(U), F_{X_2}^{-1}(U), \cdots, F_{X_n}^{-1}(U)) ,$$

where U is a uniform random variable on $[0, 1]$. Therefore all X_i^c's go hand in hand to large values, hence the probability of the sum taking on small values is minimized.

It is not difficult to prove that when $n = 2$, there is an important inequality related to two dimensional comonotonic vector, which is essentially a vector version of the famous Fréchet-Hoeffding bounds (ref. Section 5.3):

$$F_{X_1}^{-1}(U) + F_{X_2}^{-1}(1-U) \leqslant_{cx} X_1 + X_2 \leqslant_{cx} F_{X_1}^{-1}(U) + F_{X_2}^{-1}(U) . \tag{5.2}$$

The generalization of the right-hand side is a main contribution of the comonotonicity theory in recent literature. For any random vector $(X_1, X_2, \cdots, X_n)$, it has been proven that

$$S \triangleq X_1 + X_2 + \cdots + X_n \leqslant_{cx} X_1^c + X_2^c + \cdots + X_n^c \triangleq S^c .$$

It is evident that the comonotonic sum is the largest in convex order among all random sums with the same marginals as X. However, because of its little flexibility, it is unknown to what extent a real random sum can be approached by the upper bound. Calculating premiums based on the comonotonic vector will surely lead to overestimation of costs.

To solve the problem, a next step in research has been made to consider additional information available concerning the stochastic nature of $X = (X_1, X_2, \cdots, X_n)$. More precisely, we assume that there exists an auxiliary random variable Λ which contains certain information about the joint distribution of X, such that given $\Lambda = \lambda$ we know the conditional distributions of the random variables X_i, so for all possible values of λ. Therefore the comonotonic component of the vector $X|\Lambda = \lambda$ is defined by $f_i(u, \lambda) = F^{-1}_{X_i|\Lambda=\lambda}(u)$. The notation $F^{-1}_{X_i|\Lambda}$ represents the two dimensional random variable which has the same marginal distribution as the original.

It has been proved that for any random variable Λ , independent of $U \sim U[0, 1]$,

$$X_1 + \cdots + X_n \leqslant_{cx} F^{-1}_{X_1|\Lambda}(U) + \cdots + F^{-1}_{X_n|\Lambda}(U) \leqslant_{cx} F^{-1}_{X_1}(U) + \cdots + F^{-1}_{X_n}(U) \ .$$

Now we are interested in seeking answers to the following questions :

1. Is it possible to find a family of stochastic bounds depending on Λ , in which each bound could be convex-ordered?

2. Is there any manageable measure that can assist us to compare conditional and unconditional bounds?

If all these questions could be answered properly, we might be able to obtain an optimal stochastic bound which makes the conditional comonotonic upper bound as small as one needs.

The following propositions provide our own answer to the first question that if the conditional vector satisfies certain properties, the two dimensional upper bound

might be improved by adjusting the auxiliary variable in a stochastic order.

Proposition 5.2.1. *Let Λ_1 and Λ_2 be two random variables with supports in χ such that $\Lambda_1 \leqslant_{st} \Lambda_2$. If whenever $\lambda \leqslant \lambda'$,*

$$F^{-1}_{X_1|\Lambda=\lambda}(U) + \cdots + F^{-1}_{X_n|\Lambda=\lambda}(U) \leqslant_{st} F^{-1}_{X_1|\Lambda=\lambda'}(U) + \cdots + F^{-1}_{X_n|\Lambda=\lambda'}(U) \,, \tag{5.3}$$

then,

$$F^{-1}_{X_1|\Lambda_1}(U) + \cdots + F^{-1}_{X_n|\Lambda_1}(U) \leqslant_{st} F^{-1}_{X_1|\Lambda_2}(U) + \cdots + F^{-1}_{X_n|\Lambda_2}(U) \,. \tag{5.4}$$

Proof. For the sake of notational convenience, denote $F^{-1}_{X_1|\Lambda=\lambda}(U)$ by $X^c_{1,\lambda}$. Therefore we need to prove that

$$X^c_{1,\Lambda_1} + \cdots + X^c_{n,\Lambda_1} \leqslant_{st} X^c_{1,\Lambda_2} + \cdots + X^c_{n,\Lambda_2} \,.$$

Note that by (5.3) $P\{X^c_{1,\lambda} + \cdots + X^c_{n,\lambda} > s\}$ is increasing in λ for all s. Thus,

$$\begin{aligned} P\{X^c_{1,\Lambda_1} + \cdots + X^c_{n,\Lambda_1} > s\} &= \int_\chi P\{X^c_{1,\lambda} + \cdots + X^c_{n,\lambda} > s\} dF_{\Lambda_1}(\lambda) && (5.5) \\ &\leqslant \int_\chi P\{X^c_{1,\lambda} + \cdots + X^c_{n,\lambda} > s\} dF_{\Lambda_2}(\lambda) && (5.6) \\ &= P\{X^c_{1,\Lambda_2} + \cdots + X^c_{n,\Lambda_2} > s\}, \text{ for all } s \,, && (5.7) \end{aligned}$$

where the inequality follows from the fact that $Eg(\Lambda_1) \leqslant Eg(\Lambda_2)$ for any increasing function. □

A similar conclusion works out in the same manner if we replace the convex sum $F^{-1}_{X_1|\Lambda_1}(U) + \cdots + F^{-1}_{X_n|\Lambda_1}(U)$ by $\phi(F^{-1}_{X_1|\Lambda_2}(U) + \cdots + F^{-1}_{X_n|\Lambda_2}(U))$ where $\phi : \mathbb{R}^n \to \mathbb{R}^k$, $k > 0$, is an increasing function. The substitution is also applicable in the following corollaries.

Corollary 5.2.2. *Let Λ_1 and Λ_2 be two random variables with supports in χ such that $\Lambda_1 \leqslant_{cx} \Lambda_2$. If the tail probability $P\{F^{-1}_{X_1|\Lambda=\lambda}(U)+\cdots+F^{-1}_{X_n|\Lambda=\lambda}(U) > s\}$ is convex in λ, then*

$$F^{-1}_{X_1|\Lambda_1}(U) + \cdots + F^{-1}_{X_n|\Lambda_1}(U) \leqslant_{st} F^{-1}_{X_1|\Lambda_2}(U) + \cdots + F^{-1}_{X_n|\Lambda_2}(U) \,. \tag{5.8}$$

Proof. It follows the same argument as in the above proof except that the inequality in (5.5) - (5.6) is derived from the condition that tail probability $P\{F^{-1}_{X_1|\Lambda=\lambda}(U) + \cdots + F^{-1}_{X_n|\Lambda=\lambda}(U) > s\}$ is convex in λ. □

Corollary 5.2.3. *Let Λ_1 and Λ_2 be two random variables with supports in χ such that $\Lambda_1 \leqslant_{cx} \Lambda_2$. If $E(F^{-1}_{X_1|\Lambda=\lambda}(U) + \cdots + F^{-1}_{X_n|\Lambda=\lambda}(U) - s)_+$ is convex in λ, then*

$$F^{-1}_{X_1|\Lambda_1}(U) + \cdots + F^{-1}_{X_n|\Lambda_1}(U) \leqslant_{cx} F^{-1}_{X_1|\Lambda_2}(U) + \cdots + F^{-1}_{X_n|\Lambda_2}(U) \,. \tag{5.9}$$

Proof. Since $E(F^{-1}_{X_1|\Lambda=\lambda}(U) + \cdots + F^{-1}_{X_n|\Lambda=\lambda}(U) - s)_+$ is convex in λ, therefore

$$\begin{aligned} E[(X^c_{1,\Lambda_1} + \cdots + X^c_{n,\Lambda_1} - d)_+] &= \int_\chi E[(X^c_{1,\lambda} + \cdots + X^c_{n,\lambda} - d)_+]\, F_{\Lambda_1}(\lambda) \\ &\leqslant \int_\chi E[(X^c_{1,\lambda} + \cdots + X^c_{n,\lambda} - d)_+]\, dF_{\Lambda_2}(\lambda) \\ &= E[(X^c_{1,\Lambda_2} + \cdots + X^c_{n,\Lambda_2} - d)_+], \text{ for all } s. \end{aligned}$$

□

Corollary 5.2.4. *Let Λ_1 and Λ_2 be two random variables with supports in χ such that $\Lambda_1 \leqslant_{cx} \Lambda_2$. If $E\Big[\prod_{i=1}^n t_i^{F^{-1}_{X_i|\Lambda=\lambda}(U)}\Big]$ is convex in λ for all $(t_1, \cdots, t_n) \in (0,1)^n$, then*

$$(F^{-1}_{X_1|\Lambda_1}(U), \cdots, F^{-1}_{X_n|\Lambda_1}(U)) \geqslant_{mgf} (F^{-1}_{X_1|\Lambda_2}(U), \cdots, F^{-1}_{X_n|\Lambda_2}(U)) \,. \tag{5.10}$$

Proof.

$$\begin{aligned} E\Big[\prod_{i=1}^{n} t_i^{F^{-1}_{X_i|\Lambda}(U)}\Big] &= \int_{\chi} E\Big[\prod_{i=1}^{n} t_i^{F^{-1}_{X_i|\Lambda=\lambda}(U)}\Big]\, F_{\Lambda_1}(\lambda) \\ &\leqslant \int_{\chi} E\Big[\prod_{i=1}^{n} t_i^{F^{-1}_{X_i|\Lambda=\lambda}(U)}\Big]\, dF_{\Lambda_2}(\lambda) \\ &= E\Big[\prod_{i=1}^{n} t_i^{F^{-1}_{X_i|\Lambda}(U)}\Big], \text{ for all } t. \end{aligned}$$

Therefore it follows that $(F^{-1}_{X_1|\Lambda_1}(U), \cdots, F^{-1}_{X_n|\Lambda_1}(U)) \geqslant_{mgf} (F^{-1}_{X_1|\Lambda_2}(U), \cdots, F^{-1}_{X_n|\Lambda_2}(U))$ from the multivariate definition. □

Since a probability generating function can always be written as a moment generating function, the condition that $E\Big[\prod_{i=1}^{n} t_i^{F^{-1}_{X_i|\Lambda=\lambda}(U)}\Big]$ is convex in λ for all $(t_1, \cdots, t_n) \in (0,1)^n$ can be replaced by the one that $E\Big[\exp \sum_{i=1}^{n} s_i\, F^{-1}_{X_i|\Lambda=\lambda}(U)\Big]$ is convex in λ for all $(s_1, \cdots, s_n) > 0$.

Coming back to the epidemiological model we start with, we now focus on the impact on the survival probability $\mathbb{P}(R, B)$ of adjusting auxiliary variables related to the number of contacts and infectivity levels. Following the idea in Lefèvre [20], we distinguish two cases for comparison purposes.

In order to analyze the effect of the number of contacts, we first assume that an insurance provider has enough information about how many infectious groups the insured will be in contact with and the distribution of infectivity in a single contact with each group, that is to say B_j's are known. Also assume that the insurer has first-hand information of a family of auxiliary indicators relating to the policyholder's sexual activities and can make inferences on the conditional distribution of the number

of contacts, i.e. $F^{-1}_{R_i|\Lambda=\lambda}$ are known, for $i = 1, \cdots, j$.

If the conditional random variable $F^{-1}_{R_i|\Lambda=\lambda}(U)$ satisfies any of the conditions in the above proposition and corollaries, an optional comonotonic bound for the survival probability is attainable at the minimum variable, in the sense of stochastic ordering.

Proposition 5.2.5.

$$R^c|\Lambda_1 \triangleq (F^{-1}_{R_1|\Lambda_1}, \cdots, F^{-1}_{R_l|\Lambda_1}) \leqslant_{mgf} (F^{-1}_{R_1|\Lambda_2}, \cdots, F^{-1}_{R_l|\Lambda_2}) \triangleq R^c|\Lambda_2$$
$$\Longrightarrow \mathbb{P}(R^c|\Lambda_1) \geqslant \mathbb{P}(R^c|\Lambda_2) \ .$$

Proof. From (5.1) we can write $\mathbb{P}(R^c|\Lambda, B)$ as

$$\mathbb{P}(R^c|\Lambda, B) = E[f(B_1, \cdots, B_l)] \ ,$$

where $f(b_1, \cdots, b_l) = E\Big[(1-b_1)^{R_1^c|\Lambda} \cdots (1-b_l)^{R_l^c|\Lambda} | B_1 = b_1, \cdots, B_l = b_l\Big]$ is the probability generating function of $R^c|\Lambda$. Denote the distribution function of $(B_1, \cdots, B_l)$ by F_B . Therefore,

$$\begin{aligned} \mathbb{P}(R^c|\Lambda_1, B) &= \int_{R^l} E[f_{R|\Lambda_1}(b_1, \cdots, b_l)] \, dF_B \\ &\geqslant \int_{R^l} E[f_{R|\Lambda_2}(b_1, \cdots, b_l)] \, dF_B \\ &= \mathbb{P}(R^c|\Lambda_2) \ . \end{aligned}$$

□

To analyze the effect of the infectivity levels, we assume that the insurer grasps enough information about the person's sexual habits with others, i.e. R_j is available

and is also able to estimate the infectiousness of each infectivity group through some demographical indicators. Even though, because $(1-b_i)^{r_i}$ is not always convex in b_i as r_i changes, it is very difficult to proceed the way we did for the number of contacts. The model has been modified by Lefèvre with the assumption that the probability of infection depends on the dose of virus d_j carried through in a single contact with group j, i.e.

$$1 - B_j = b(D_j) \ , \qquad j = 1, \cdots, l \ ,$$

where $D_j = (d_1, \cdots, d_l)$ and b satisfies that $\log[b(d)]$ is convex in d . It is not difficult to prove that the function $b(d_1)^{r_1} \times \cdots \times b(d_l)^{r_l}$ for fixed $(r_1, \cdots, r_l)$ is convex in terms of $(d_1, \cdots, d_l)$, which paves the way for the Proposition 5.2.6. Within a family of demographical indicators $\{\Lambda_k\}$, the insurer may want to use the smallest one, in the sense of convex order, to estimate infectivity levels and then the upper bound of the survival probability $\mathbb{P}(R, B)$.

Proposition 5.2.6.

$$D^c|\Lambda_1 \triangleq (F^{-1}_{D_1|\Lambda_1}, \cdots, F^{-1}_{D_l|\Lambda_1}) \leqslant_{cx} (F^{-1}_{D_1|\Lambda_2}, \cdots, F^{-1}_{D_l|\Lambda_2}) \triangleq D^c|\Lambda_2$$
$$\Longrightarrow \mathbb{P}(D^c|\Lambda_1) \geqslant \mathbb{P}(D^c|\Lambda_2) \ .$$

Proof. Denote the distribution function of $(R_1, \cdots, R_l)$ by F_R. From (5.1) we express

$$\begin{aligned}
\mathbb{P}(R, B^c|\Lambda_1) &= \int_{R^l} E\{[b(D_1^c|\Lambda_1)]^{r_1} \cdots [b(D_l^c)]^{r_l} | R_1 = r_1, \cdots, R_l = r_l\} \, dF_R \\
&\leqslant \int_{R^l} E\{[b(D_1^c|\Lambda_1)]^{r_1} \cdots [b(D_l^c)]^{r_l} | R_1 = r_1, \cdots, R_l = r_l\} \, dF_R \\
&= \mathbb{P}(R, B^c|\Lambda_2) \ .
\end{aligned}$$

□

Lack of efficient tools to measure the distance from the real vector and the conditional upper bounds made us difficult to answer the second question. To this purpose we resort to the concept of copulas, which is well-known as a tool to measure dependence.

5.3 Random Sum and Copulas

The study of copulas, which was initiated by A. Sklar in 1959, has recently become the center of attention for statisticians working on dependent variables. A copula, literally a joint distribution with uniform marginals, describes an underlying non-parametric dependency relation among random variables generated by uniform variables. Given marginal distributions, the joint distribution of any inter-reacting random variables would be determined uniquely by their copula. As actuaries always encounter situations with only information of marginal distributions readily available, the copulas find natural applications in actuarial science. A comprehensive investigation of application in the recent actuarial literature is given by Frees and Valdez [16].

In this section, we narrow down our discussion to the two dimensions. For notational convenience, $\mathbb{I} = [0,1]$ and $\mathbb{I}^2$ is the unit square $[0,1] \times [0,1]$. Here we introduce Sklar's original definition of copula.

Definition 5.3.1. A two dimensional copula is a function $C : \mathbb{I}^2 \to \mathbb{I}$ with the

following properties:

$$C(u,0) = 0 = C(0,u) \text{ and } C(u,1) = u = C(1,u) \text{ , whenever } u \in \mathbb{I} \text{ ;} \tag{5.11}$$

$$C(u_2,v_2) - C(u_2,v_1) - C(u_1,v_2) + C(u_1,v_1) \geqslant 0 \text{ ,} \tag{5.12}$$

whenever $0 \leqslant u_1 \leqslant u_2 \leqslant 1$ and $0 \leqslant v_1 \leqslant v_2 \leqslant 1$.

One important property of copulas is that they are uniformly continuous on their domains, i.e. for any $u_1, u_2, v_1, v_2 \in \mathbb{I}$,

$$|C(u_2,v_2) - C(u_1,v_1)| \leqslant |u_2 - u_1| + |v_2 - v_1| \text{ .}$$

For the proof, we refer to Theorem 2.2.4 in Nelsen [23].

A visualization of a copula can be obtained from a unit square diagram, on which the unit probability mass is spread out in a certain pattern. The probability mass assigned to a rectangle $[u_1,v_1] \times [u_2,v_2] \in \mathbb{I}^2$ is determined by $C(u_2,v_2) - C(u_2,v_1) - C(u_1,v_2) + C(u_1,v_1)$. From the property (5.11), one can see that in a unit square diagram the probability mass to the left of any vertical line $x = u$ is u and the mass below any horizontal line $y = v$ is v.

The three most important copulas, defined as follows, each have an interesting geometric characteristic as shown in Figure 5.1. $\Pi(u,v) = u \cdot v$ is the independent copula, by which the unit probability mass is uniformly distributed in $\mathbb{I}$; $M(u,v) = \min(u,v)$ referred to as the Fréchet-Hoeffding upper bound, assigns the unit mass uniformly along the main diagram of $\mathbb{I}^2$; $W(u,v) = \max(u+v-1,0)$, called the

Fréchet-Hoeffding lower bound, distributes the unit mass along the secondary diagonal of $\mathbb{I}^2$.

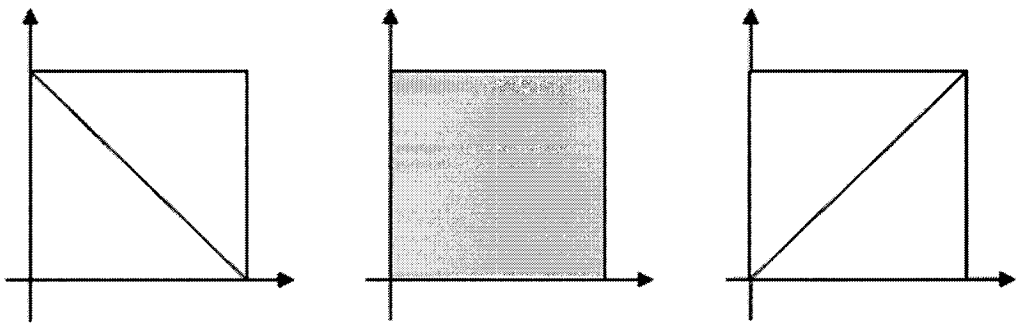

Figure 5.1: Unit square diagrams of W, Π and M.

The following theorem reveals the one-to-one correspondence between copulas and joint distributions with given marginals. The proof can be found in Nelsen [23].

Theorem 5.3.1. *(Sklar's Theorem) Let H be a joint distribution function with marginals F defined on D_F and G defined on D_G. Then there exists a copula C such that for all u, v in $\mathbb{I}$,*

$$C(u,v) = H(F^{-1}(u), G^{-1}(v)) \,. \tag{5.13}$$

If F and G are continuous, then C is unique; otherwise, C is uniquely determined on $D_F \times D_G$. Conversely, if C is copula and F and G are distribution functions, then the function H defined by

$$H(x,y) = C(F(x), G(y)) \,, \qquad x, y \in \overline{\mathbb{R}} \,. \tag{5.14}$$

is a joint distribution function with marginals F and G.

By definition, it is not difficult to prove that the *Fréchet-Hoeffding bounds* are universal for all copulas:

$$W(u,v) \leqslant C(u,v) \leqslant M(u,v)\ , \qquad u,v \in \mathbb{I}\ .$$

As a consequence of Sklar's theorem, if X and Y are random variables with joint distribution $H(x,y)$ and marginals $F(x)$ and $G(y)$, respectively, then the above inequality can be written as

$$\max(F(x)+G(y)-1,0) \leqslant H(x,y) \leqslant \min(F(x),G(y))\ ,\ \text{for all } x \text{ and } y.$$

Proposition 5.3.2. *Let X and Y be two $U(0,1)$ random variables with joint distribution $M(u,v)$, then*

$$X = Y\ , \qquad a.s.\ .$$

Proof. By Sklar's Theorem, $H(x,y) = M(F(x),F(y)) = M(x,y) = \min(x,y)$. Since

$$\begin{aligned} F(x) = \mathbb{P}[X \leqslant x] &= \mathbb{P}[X \leqslant x, Y \leqslant x] + \mathbb{P}[X \leqslant x, Y > x] \\ &= H(x,x) + \mathbb{P}[X \leqslant x, Y > x] \\ &= x + \mathbb{P}[X \leqslant x, Y > x]\ , \qquad \text{for all } x\ , \end{aligned}$$

then $\mathbb{P}[X \leqslant x, Y > x] = 0$ for all x, which leads to $\mathbb{P}[X < Y] = 0$. Similarly,

$$\begin{aligned} F(y) = \mathbb{P}[Y \leqslant y] &= \mathbb{P}[X \leqslant y, Y \leqslant y] + \mathbb{P}[X > y, Y \leqslant y] \\ &= H(y,y) + \mathbb{P}[X > y, Y \leqslant y] \\ &= y + \mathbb{P}[X > y, Y \leqslant y]\ , \qquad \text{for all } y, \end{aligned}$$

then $\mathbb{P}[X > y, Y \leqslant y] = 0$ for all y, and hence $\mathbb{P}[X > Y] = 0$. Therefore we have that $\mathbb{P}[X = Y] = 1 - \mathbb{P}[X < Y] - \mathbb{P}[X > Y] = 1$. □

At this point, it is clear that a comonotonic vector (also called Fréchet-Hoeffding upper bound) is essentially constructed by two uniform random variables with perfect positive linear relation. The Fréchet-Hoeffding lower bound is generated as shown in (5.2) by two uniform random variables that have perfect negative relation.

A natural question arises - is it possible to change the relationship between the two $U(0,1)$ variables in a way that they are not so positively nor negatively related, in order to approximate other copulas in between the Fréchet-Hoeffding bounds, and then transform the variables with given marginals to approach any desired joint distributions? Mikusiński *et al.* [21] give an confirmative answer by geometric construction of copulas on the unit square diagram. We shall use their brilliant idea and represent the constructed relation between the two uniform variables in an analytic function form.

The most amazing result Mikusiński *et al.* [21] proves is that any copula C can be approximated by a shuffle of M, which is defined as follows:

1. Cut the unit square diagram of copula C into n equally spaced vertical strips labelled from left to right by $V_1, \cdots, V_n$ and n equally spaced horizontal strips from bottom to top by $H_1, \cdots, H_n$. The probability mass in each block $V_i \cap H_i$ is denoted by m_{ij} .

2. Slice the unit square diagram of M in the same way as in Step 1, then divide

each vertical strip V_i into n substrips, labelled from left to right by $V_{i1}, \cdots, V_{in}$, and divide each horizontal strip H_j into n substrips, labelled from bottom to top by $H_{j1}, \cdots, H_{jn}$, in such a way that the width of each column V_{ik} is m_{ik}, and the height of each row H_{jk} is m_{jk}.

3. In each square $V_{ij} \cap H_{ji}$, spread out the probability mass of m_{ij} uniformly along its main diagonal.

It is also mentioned in Mikusiński *et al.* [21] that during the shuffle, some strips could be flipped around vertical axes of symmetry, which means that one could finish the same task by changing some split parts of M into those of W or completely by shuffling with the copula of W in a similar manner.

Apart from the technical description, one can think of the shuffle in a more straightforward way as shown in Figure 5.2: Divide the unit square into n vertical strips, and each strip is sliced into n smaller columns, each numbered from 1 to n. Those called the same number are grouped together to form a new strip, in the order from 1 to n. The resembled picture is the outcome of the above shuffle, the unit square diagram of copula C'. The copula C' can be made as close as one wants to the original C by increasing the number of strips n.

As a consequence, one can imagine that every copula can be approximated as close as one wants by a number of manipulation on M, which is the copula of two uniform variables with almost surely perfect positive linear relation. Vitale [28] proves that any pair of uniformly distributed variables can be approached by a sequence of

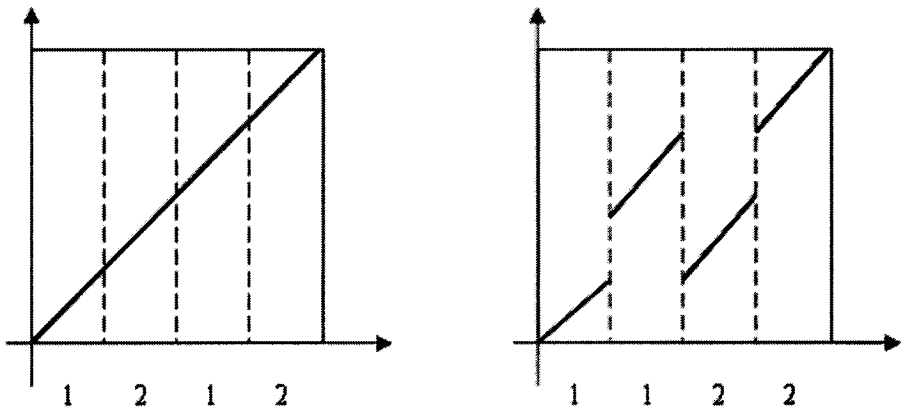

Figure 5.2: Shuffle of the support of M

variable pairs, in which one variable is an invertible function of the other. Now following the idea of shuffling M, we are able to specify these functions in analytical forms.

In order to keep track of movements in a shuffle and their effects on changing the copula, we define a translation of rank n by the following function

$$T_C^{(n)}(x) = \sum_{i=1}^{n}\sum_{j=1}^{n}(x - a_{ij} + a_{ji})1\{[a_{ij} < x < b_{ij}]\}\ , \tag{5.15}$$

where $\{[a_{ij}, b_{ij}]\}_{i,j=1,\cdots,n}$ is the partition of $\mathbb{I}$ corresponding to a shuffle. Each vertical strip is labelled by $[a_{ij}, b_{ij}]$. Note that $a_{i,j-1} = b_{ij}$.

Proposition 5.3.3. *If U is a uniform random variable, so is $T_C^{(n)}(U)$.*

Proof. Note that $T_C^{(n)}(x)$ is symmetric about $y = x$, so it equals its own inverse

function. If $u \in [a_{hl}, b_{hl}]$, then $T_C^{(n)}(u) \in [a_{lh}, b_{lh}]$ and therefore,

$$\begin{aligned}
\mathbb{P}\{T_C^{(n)}(U) \leqslant u\} &= \sum_{i=1}^{n}\sum_{j=1}^{n} \mathbb{P}\{U - a_{ij} + a_{ji} \leqslant u \ , \ a_{ij} \leqslant U < b_{ij}\} \\
&= \sum_{i=1}^{h}\sum_{j=1}^{l} \mathbb{P}\{U - a_{ij} + a_{ji} \leqslant u \ , \ a_{ij} \leqslant U < b_{ij}\} \\
&= \sum_{i=1}^{h}\sum_{j=1}^{l-1} (b_{ij} - a_{ij}) + \mathbb{P}\{U - a_{lh} + a_{hl} \leqslant u \ , \ a_{lh} \leqslant U < b_{lh}\} \\
&= a_{hl} + u - a_{hl} \qquad \text{since } b_{h,l-1} = a_{hl} \ , \\
&= u \ .
\end{aligned}$$

Hence, $T_C^{(n)}(U)$ is also a uniform random variable. □

Lemma 5.3.4.

$$\begin{aligned}
C_{U,T_C^{(n)}(U)}(u,v) &= \sum_{i=1}^{n}\sum_{j=1}^{n} 1\{a_{i1} \leqslant u < b_{in} \ , \ a_{j1} \leqslant v < b_{jn}\} M(a_{i1} \ , \ a_{j1}) \\
&+ \sum_{i=1}^{n}\sum_{j=1}^{n} (b_{ij} - a_{ij}) M\left(\frac{u - a_{ij}}{b_{ij} - a_{ij}} \ , \ \frac{v - a_{ij}}{b_{ij} - a_{ij}}\right) 1\{a_{ij} \leqslant u < b_{ij} \ , \ a_{ji} \leqslant v < b_{ji}\} \\
&+ \sum_{i=1}^{n}\sum_{j=1}^{n} (b_{ij} - a_{ij}) M\left(\frac{u - a_{ij}}{b_{ij} - a_{ij}} \ , \ \frac{u - a_{ij}}{b_{ij} - a_{ij}}\right) 1\{a_{ij} \leqslant u < b_{ij}, v > b_{ji}\} \\
&+ \sum_{i=1}^{n}\sum_{j=1}^{n} (b_{ij} - a_{ij}) M\left(\frac{v - a_{ji}}{b_{ji} - a_{ji}} \ , \ \frac{v - a_{ji}}{b_{ji} - a_{ji}}\right) 1\{u \geqslant b_{ij}, a_{ji} \leqslant u < b_{ji}\} \ .
\end{aligned}$$

Proof. We first study the range of the pair $(U, T_C^{(n)}(U))$. It is easy to find that

$$\sum_{i=1}^{n}\sum_{j=1}^{n} \mathbb{P}\{a_{ij} \leqslant U < b_{ij} \ , \ a_{ji} \leqslant T_C^{(n)}(U) < b_{ji}\} = 1 \ ,$$

and whenever $a_{ij} \leqslant u \leqslant b_{ij}$, $a_{ji} \leqslant v \leqslant b_{ji}$,

$$\begin{aligned}
\mathbb{P}\{a_{ij} \leqslant U < u\ ,\ a_{ji} \leqslant T_C^{(n)}(U) < v\} &= \mathbb{P}\{a_{ij} \leqslant U < u\ ,\ a_{ji} \leqslant U - a_{ji} + a_{ij} < v\} \\
&= \mathbb{P}\{a_{ij} \leqslant U < u\ ,\ a_{ij} \leqslant U < v - a_{ji} + a_{ij}\} \\
\text{(by Proposition 5.3.2)} \qquad &= M(\frac{u - a_{ij}}{b_{ij} - a_{ij}}\ ,\ \frac{v - a_{ij}}{b_{ij} - a_{ij}})\ .
\end{aligned}$$

From (5.13) in Sklar's theorem,

$$\begin{aligned}
C_{U,T_C^{(n)}(U)}(u,v) &= \mathbb{P}\{U \leqslant u\ , T_C^{(n)}(U) \leqslant v\} \\
&= \sum_{i=1}^{n}\sum_{j=1}^{n} \mathbb{P}\{U \leqslant u\ , T_C^{(n)}(U) \leqslant v\ ,\ a_{ij} \leqslant U < b_{ij}\ , a_{ji} \leqslant T_C^{(n)}(U) < b_{ji}\} \\
&= \sum_{i=1}^{n}\sum_{j=1}^{n} \Big[\mathbb{P}\{a_{ij} \leqslant U < u\ ,\ a_{ji} \leqslant T_C^{(n)}(U) < v\ \}\ 1\{a_{ij} \leqslant u < b_{ij}\ ,\ a_{ji} \leqslant v < b_{ji}\} \\
&\quad + \mathbb{P}\{a_{ij} \leqslant U < b_{ij}\ , a_{ji} \leqslant T_C^{(n)}(U) < v\ \}\ 1\{u \geqslant b_{ij}\ , a_{ji} \leqslant v < b_{ji}\} \\
&\quad + \mathbb{P}\{a_{ij} \leqslant U < u\ , a_{ji} \leqslant T_C^{(n)}(U) < b_{ji}\ \}\ 1\{u \geqslant b_{ij}\ , a_{ji} \leqslant v < b_{ji}\} \\
&\quad + (b_{ij} - a_{ji}) 1\{u \geqslant b_{ji}\ , v \geqslant b_{ji})\Big]\ .
\end{aligned}$$

Replacing the probability formulas by M leads to the stated formula. □

Lemma 5.3.5. *For any copula C and any $\varepsilon > 0$, there exists a n such that*

$$\sup_{u,v \in \mathbb{I}} |C_{U,T_C^{(n)}(U)}(u,v) - C(u,v)| < \varepsilon\ . \tag{5.16}$$

Proof. Let $n = 4/\varepsilon$, and $\{[a_{ij}, b_{ij}]\}_{i,j=1,\cdots,n}$ be the partition of $\mathbb{I}$ corresponding to the shuffle $T_C^{(n)}$. Note that $b_{in} - a_{i1} = n$. Therefore, there must be a certain i, j such

that $a_{i1} \leqslant u \leqslant b_{in}$ and $a_{j1} \leqslant v \leqslant b_{jn}$.

$$\begin{aligned}
|C(u,v) - C_{U,T_C^{(n)}(U)}(u,v)| &\leqslant |C(u,v) - C(a_{i1},a_{j1})| + |C(a_{i1},a_{j1}) - C_{U,T_C^{(n)}(U)}(a_{i1},a_{j1})| \\
&\quad + |C_{U,T_C^{(n)}(U)}(a_{i1},a_{j1}) - C_{U,T_C^{(n)}(U)}(u,v)| \\
&\leqslant |C(b_{in},b_{jn}) - C(a_{i1},a_{j1})| + 0 \\
&\quad + |C_{U,T_C^{(n)}(U)}(a_{in},a_{jn}) - C_{U,T_C^{(n)}(U)}(a_{1n},a_{jn})| \\
&\leqslant 1/n + 1/n + 1/n + 1/n = \varepsilon \,.
\end{aligned}$$

The last inequality holds because of uniform continuity of copulas. □

Lemma 5.3.6. *Let X and Y be continuous random variables ranging, respectively, in R_X and R_Y, with copula $C_{X,Y}$. If α and β are strictly increasing on R_X and R_Y correspondingly, then $C_{\alpha(X),\beta(Y)}(u,v) = C_{X,Y}(u,v)$.*

Proof. Let F_1, G_1, F_2 and G_2 be the distribution functions of X, Y, $\alpha(X)$ and $\beta(Y)$, respectively. Since α and β are strictly increasing, $F_2(x) = \mathbb{P}\{\alpha(X) \leqslant x\} = \mathbb{P}\{X \leqslant \alpha^{-1}(x)\} = F_1[\alpha(x)]$. Similarly, $G_2(y) = G_1[\beta(y)]$.

$$\begin{aligned}
C_{\alpha(X),\beta(Y)}(F_2(x),G_2(y)) &= \mathbb{P}\{\alpha(X) \leqslant x \,,\ \beta(Y) \leqslant y\} \\
&= \mathbb{P}\{X \leqslant \alpha^{-1}(x) \,,\ Y \leqslant \beta^{-1}(y)\} \\
&= C_{X,Y}(F_1[\alpha(x)] \,,\ G_1[\beta(y)]) \\
&= C_{X,Y}(F_2(x),G_2(y)) \,.
\end{aligned}$$

□

Proposition 5.3.7. *Let X and Y be two random variables with joint distribution H, marginal distributions F defined on D_F , and G defined on D_G, respectively. Let*

$$H'(x,y) = C^{(n)}_{U,T^n_C(U)}(F(x), G(y)) .$$

Then there exists an n such that

$$\sup_{x\in D_F\,,\, y\in D_G} |H'(x,y) - H(x,y)| < \varepsilon . \tag{5.17}$$

Proof. One can easily define inverse functions F^{-1} and G^{-1} so that they are strictly increasing. From the Lemma 5.3.6, we know that

$$C^{(n)}_{U,T^n_C(U)}(u,v) = C^{(n)}_{F^{-1}(U),G^{-1}(T^n_C(U))}(u,v) .$$

It follows from (5.3.6) that

$$H'(x,y) = C^{(n)}_{U,T^n_C(U)}(F(x), G(y)) .$$

□

Now we are able to answer explicitly the question mentioned earlier. For any two random variables with given information about marginals, their joint distribution can be approached by a series of joint distributions converted from a uniform random variable and its translation of certain form determined by their copula.

5.4 Empirical Copulas and Estimator

In actuarial practice, it is consistently easy to have two random variables with given marginal distributions, whereas it is somehow difficult to find out their dependence

and consequently many theories developed on assumptions of independence can not be applied in real-life problems. The idea here is to make use of empirical methods of finding copulas and then construct random variable estimators by shuffling the copula of M.

Empirical copulas were introduced and first studied by Deheuvels [12].

Definition 5.4.1. Let $\{(x_k, y_k)\}_{k=1}^{n}$ denote a sample of size n from a continuous bivariate distribution. The *empirical copula of rank n* is the function $\hat{C}_n$ given by

$$\hat{C}_n(\frac{i}{n}, \frac{j}{n}) = \frac{\sum_x \sum_y 1_{\{x \leqslant x_{(i)}, y \leqslant y_{(j)}\}}}{n} , \tag{5.18}$$

where $x_{(i)}$ and $y_{(j)}$, $1 \leqslant i, j \leqslant n$, denote the order statistics from the sample.

Definition 5.4.2. The *empirical copula frequency of rank n* is given by

$$\hat{c}_n(\frac{i}{n}, \frac{j}{n}) = \begin{cases} 1/n , & \text{if } (x_i, y_i) \text{ is an element of the sample,} \\ 0 , & \text{otherwise.} \end{cases} \tag{5.19}$$

Note that $\hat{C}_n$ and $\hat{c}_n$ are related via

$$\hat{C}_n(\frac{i}{n}, \frac{j}{n}) = \sum_{p=1}^{i} \sum_{q=1}^{j} \hat{c}_n(\frac{p}{n}, \frac{q}{n})$$

and

$$\hat{c}_n(\frac{i}{n}, \frac{j}{n}) = \hat{C}_n(\frac{i}{n}, \frac{j}{n}) - \hat{C}_n(\frac{i-1}{n}, \frac{j}{n}) - \hat{C}_n(\frac{i}{n}, \frac{j-1}{n}) + \hat{C}_n(\frac{i-1}{n}, \frac{j-1}{n}) .$$

Definition 5.4.3. The *empirical translation function of rank n* is given by

$$\hat{T}^{(n)}(x) = \sum_{j=1}^{n} (\frac{j}{n} + x - \frac{[nx]}{n}) 1_{\{\hat{C}_n(\frac{[nx]}{n}, \frac{j}{n}) \neq 0\}} . \tag{5.20}$$

In Proposition 5.3.7, we know that $F^{-1}(U) + G^{-1}(T^{(n)}(U)) \longrightarrow X + Y$ in distribution. Therefore we can use $\hat{C}_n(F(x), G(y))$ to approximate $H(x, y)$. In the short time horizon model with $l = 2$, if we are able to make inference of empirical copulas of (R_1, R_2) and (B_1, B_2) , then the survival probability

$$\begin{aligned}\mathbb{P}(B, R) &= E[(1 - B_1)^{R_1}(1 - B_2)^{R_2}] \\ &\approx \int_0^1 \int_0^1 \left[1 - F_{B_1}^{-1}(x)\right]^{F_{R_1}^{-1}(y)} \left[1 - F_{B_2}^{-1}(T_{C_B}^{(n)}(x)\right]^{F_{R_2}^{-1}(T_{C_R}^{(n)}(y))} dx\, dy\,,\end{aligned}$$

where the translations of rank n , $T_{C_B}^{(n)}(x)$ and $T_{C_R}^{(n)}(y)$, can be approximated by the empirical translation functions $\hat{T}_{C_B}^{(n)}(x)$ and $\hat{T}_{C_R}^{(n)}(y)$, respectively.

Now we wrap up the discussion here by pointing out that for any number of random variables with marginal information, we could estimate their empirical copula, treat the variables as transforms of a uniform random variable, and therefore calculate insurance-related quantities using the uniform variable. The extension from bivariate empirical copula to multivariate and their algorithms are intended in future work.

Conclusion

In the process of searching new actuarial tools of modelling infectious disease insurance, this thesis looks through related literature, both in actuarial science and epidemiology. In deterministic cases, an SIR insurance model is set up for analyzing four typical insurance plans with different features. Following a short review of state-of-the-art methods in parameter estimation, this thesis proposes an alternative method based on numerical analysis. Then four approaches are given to fulfill the ultimate goal of the thesis - find practical methods to calculate premiums. Some of the methods are illustrated in two numerical examples. Due to the difficulty of estimating parameters, we suggest that the insurance models should be applied to periodic diseases with abundant data.

Moreover, in the discussion of a stochastic model, the theory of comonotonicity and copulas is introduced and further developed to serve the purpose of approximating premiums for an infectious disease insurance based on the stochastic model. In this part, we developed methods of comparing Fréchet-Hoeffding upper bounds and constructing a translation function to construct copulas.

Since research in this emerging type of insurance is just at the infancy stage, much more work needs to be done to generalize the models in order to fit other aspects and features of different diseases. There are lots of new techniques in mathematics of infectious diseases that are not discussed in this thesis. We hope that the research on infectious disease insurance will be expanded profoundly and put to use in the future.

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