

Risk adjustment model of credit life insurance using a genetic algorithm

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Abstract. In managing the risk of credit life insurance, insurance company should acknowledge the character of the risks to predict future losses. Risk characteristics can be learned in a claim distribution model. There are two standard approaches in designing the distribution model of claims over the insurance period i.e, collective risk model and individual risk model. In the collective risk model, the claim arises when risk occurs is called individual claim, accumulation of individual claim during a period of insurance is called an aggregate claim. The aggregate claim model may be formed by large model and a number of individual claims. How the measurement of insurance risk with the premium model approach and whether this approach is appropriate for estimating the potential losses occur in the future. In order to solve the problem Genetic Algorithm with Roulette Wheel Selection is used.

Keyword: risk, claims, aggregation claims, collective risk model, genetic algorithm

1. Introduction

A type of life insurance quite developed in Indonesia is credit life insurance. Every customer of this insurance policy holder receives compensation afforded by the insurance company in case of death in accordance with the contract of agreement. In providing guarantee to the policy holders, the insurance company must prepare funds to anticipate the occurrence of claims from policyholders [2].

In managing risk insurance companies should acknowledge characteristic of the risk to predict future losses. These risk characteristics can be learned in a claim distribution model. There are two standard approaches to establish a model of claim distribution over the insurance period e.g. the collective risk model and individual risk model.

In collective risk model, claim that arise when risk occurs is called individual claim, the accumulation of individual claims during period of insurance is called an aggregate claim. The aggregate claim model can be developed using the large model and the number of individual claims.

Model-based approach should be considered as context of the objectives of each given problem. Many problems in actuarial science involve development of mathematical models that can be used to predict or forecast future insurance costs. The model is a simplified mathematical description built on the knowledge and experience of an actuary combined with data from the past. Data guides the actuary in selecting the model form as well as calibrating an unknown number, usually called a parameter. This model provides a balance between simplicity and conformity with existing data. Simplicity is measured in terms of unknown parameter factors (the fewer the simpler); Compliance with data is



measured in terms of discrepancies between data and models. The selection model is based on a balance between two criteria, namely conformity and simplicity.

Determination of using the model should consider several things such as decision-making based on empirical evidence. The empirical approach assumes that the future can be expected just as it has happened in the past, perhaps adapted to trend such as inflation[11]. How to measure insurance risk with the premium model approach and whether this approach is appropriate for estimating the potential losses incurred in the future.

2. Research methodology

The models used in the development of claims distribution model and the calculation of risk of term life insurance using the claim distribution model, Collective Modified Value-at-Risk Model (*CMVaR*).

2.1. Claim distribution model

The claim distribution is assumed to follow the geometric distribution model. If N is a random variable of the claim frequency with a value of n , and p is the probability parameter of the occurring claim, then the probability function of the claim event is [1],[13].

$$\eta(n, p) = \begin{cases} pq^{n-1}; & n = 1, 2, 3, \dots \\ 0; & n \text{ otherwise} \end{cases}, \tag{1}$$

where $q = 1 - p$ is the parameter of no claim. The generating function of equation (1) is [9], [4]:

$$M_N(t) = \frac{pe^t}{(1-qe^t)}$$

For large claim it is assumed to follow the Gamma distribution. If X is given a large random variable of claim with value x , and α and β is the parameter of gamma distribution, then the probability density function of the distribution of the claim is [1], [12]:

$$f(x) = \begin{cases} \frac{1}{\Gamma(\alpha)\beta^\alpha} x^{\alpha-1} e^{-x/\beta}; & x > 0 \\ 0; & x \text{ otherwise} \end{cases}, \tag{2}$$

whereas the moment generating function to k of the equation (2) is

$$m_k = M_X(k) = (1 - \beta k)^{-\alpha}; k = 1, 2, 3, 4, \dots$$

2.2. Collective risk model

For collective risk models, a random process assumption that claims to be sustainable in the insurance policy portfolio can be used. Generally can be formulated [10] by defining the random variable S is the number of claims occurring from the risk within a year. Random variable N is the number of claims of risk in this year, X_i random variable is the number of claims incurred. The number of aggregate claims is the number of individual claims, as the formula below:

$$S = \sum_{i=1}^N X_i \tag{3}$$

while the conditional Expectation value is: $E[S | N = n] = E\left[\sum_{i=1}^N X_i\right] = \sum_{i=1}^N E[X_i] = nm_1$, and apply

$n = 0, 1, 2, \dots$, $E[S | N] = Nm_1$, then the unconditional expectation is obtained:

$$E[S] = E[Nm_1] = E[N]m_1$$

thus, the variance is:

$$Var[S | N = n] = Var \left[\sum_{i=1}^N X_i \right] = \sum_{i=1}^N Var[X_i] = n(m_2 - m_1^2), \quad \text{and apply } n = 0, 1, 2, \dots$$

$Var[S | N] = N(m_2 - m_1^2)$, therefore this conditional variance of (3) is :

$$Var[S] = E[Var(S | N)] + Var[E(S | N)] = E[N](m_2 - m_1^2) + Var[N]m_1^2$$

If it is assumed that $\{X_i\}_{i=1}^{\infty}$ distributed identically and independently, the moment function of equation (3) can be expressed as [1]

$$M_s(t) = E[\{M_x(t)\}^N] = E[Exp\{\log\{M_x(t)\}^N\}] = M_N(t) \log M_x(t)$$

where M_s is expressed in terms of $M_N(t)$ and $M_x(t)$, and S is the random variable to the magnitude of the aggregate claim.

2.3. Collective value-at-risk

According to Dowd [5] and Yildirim [14] and Sukono [12], Value-at-Risk (VaR) is a measure of market risk, which means when invested initial capital of V_o , on market assets with normal distributed returns with μ and standard deviation σ , will have maximum potential loss is $VaR = -V_o(\mu + z_c \sigma)$, where z_c percentile and standard normal distribution at significance level $(1 - c) \%$. Collective Value-at-Risk ($CVaR$) is the development of the application of Value-at-Risk principle which is an alternative measurement of aggregate claim risk as equation (3). Then $CVaR$ can be formulated as follows:

$$CVaR = -\tilde{N}_0(E[S] + z_c \{VaR[S]\}^{1/2}) = -\tilde{N}_0(E[N]m_1 + z_c \{E[N](m_2 - m_1^2) + Var[N]m_1^2\}^{1/2})$$

where is : \tilde{N}_0 is a lot of claims that occur, the sign minus (-) states losses (losses) [3].

2.4. Collective modified value-at-risk

According to Dowd [5], Guarda, et.al [7] and Iqbal, et.al [8], market assets are not normally distributed, their expansion by providing a factor adjustment to the estimated percentile, with the adjustment given from normality is small called Cornish Fisher. The expansion of Cornish Fisher is expressed as follows:

$$CMVaR = \tilde{N}_0 \{ E[S] \} + (z_c + \frac{1}{6}(z_c^2 - 1)\zeta[S] + \frac{1}{12}(z_c^3 - 3z_c)K[S] - \frac{1}{36}(2z_c^3 - 5z_c)(\zeta[S])^2)(Var[S])^{1/2}$$

Where :

$E[S]$	= mean	$Var[S]$	= variance
$\zeta[S]$	= skewness	$\kappa[S]$	= kurtosis
Z_c	= normal distribution percentile		

2.5. Genetic algorithms

The purpose of the algorithm is to dynamically determine the distribution of life insurance claims and certain restrictions to minimize risk. The claim distribution structure using genetic algorithms (GA) can be seen in the following figure:



Figure 1. GA structure for CMVaR

Brief description of Figure 1.

Genetic Algorithms in general the structure to be implemented is as follows [6]:

- a. Generate the initial population

This process is a process used to generate the initial population at random to obtain an initial solution. This initial population is generated randomly so that the initial solution is obtained. The population itself consists of a number of chromosomes that present the desired solution.

b. Evaluation of fitness

This process is a process for evaluating each population by calculating the fitness value of each chromosome and evaluating it until it is met the stop criteria. An individual is evaluated based on a certain function as a measure of its performance. In natural evolution, individuals with low fitness value will die.

c. Selection:

Selection process is a process to determine which individuals will be selected for crossover. There are several types of selection methods commonly used, such as: The method that mimics a roulette-wheel game where each chromosome occupies a circle cut on the roulette wheel proportionately according to its fitness value. Selection Ranks the process begins by ranking or chromosome sequencing in the population based on their fitness then assigning a new fitness value based on the sequence. In this problem the selection method used is the roulette wheel selection.

d. Crossover

This crossover process is a process to increase the diversity of strings in one population. Crossover operators have the most important role in the genetic algorithm because there is a process of marriage (crosses) of genes between two individuals (parent) that produce two new individuals (offspring) in the next generation.

e. Mutation

Mutation is the process of changing the value of one or more genes in a chromosome. Mutations create new individuals by modifying one or more genes in the same individual. Mutations act to replace lost genes of the population during the selection process and provide genes that are absent in the initial population.

f. Criterion stopped

Stop criteria are the criteria used to stop the genetic algorithm process which is the goal to be achieved from the process.

g. Results

The result is an optimum solution obtained by using Genetic Algorithm.

The application of roulette wheel selection method in credit risk adjustment modeling is as to :

a. Generate initial population

All possible risks of claims are employed by permutation coding techniques which are subsequently taken by some random claims. Claims taken randomly form the first population in the first generation and so on down to the last generation. The population is a set of chromosomes consisting of k genes representing $x_i = 1, 2, \dots, 64$, numbers, where x_i is the number of claims occurring on i . The population was initially randomly using native code.

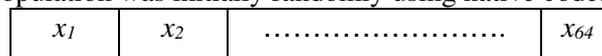


Figure 2. Chromosome structure

b. Determining fitness value

After generating the initial population the next step is to determine the fitness value of each individual formed. Each individual is calculated the risk value of his claim. To calculate the fitness value by the formula:

$$eval(v_k) = f(x), k = 1, 2, \dots, 64$$

To find the minimum value then:

$$eval(v_k) = \frac{1}{x} \text{ where } x = \text{the claim value of each individual}$$

With the help of matlab software, determined the fitness value of individuals big claims and many claims. Fitness value as follows

Table 1. Fitness Value

Individual	Fitness Value Claim Large	Fitness Value Many Claims	Individual	Fitness Value Claim Large	Fitness Value Many Claims
1	0.0000000401	1.00	33	0.0000000019	0.08
2	0.0000002042	1.00	34	0.0000000073	0.50
3	0.0000000120	0.33	35	0.0000000257	0.25
4	0.0000000191	0.33	36	0.0000000064	0.17
5	0.0000000067	0.20	37	0.0000000076	0.25
6	0.0000000150	0.50	38	0.0000000104	0.50
7	0.0000000026	0.25	39	0.0000000091	0.25
8	0.0000000123	0.50	40	0.0000000043	0.14
9	0.0000000031	0.09	41	0.0000000045	0.20
10	0.0000000038	0.17	42	0.0000000052	0.25
11	0.0000000067	0.20	43	0.0000000060	0.25
12	0.0000000022	0.11	44	0.0000000135	0.33
13	0.0000000054	0.14	45	0.0000000022	0.11
14	0.0000000022	0.13	46	0.0000000204	0.50
15	0.0000000063	0.20	47	0.0000000091	0.20
16	0.0000000117	0.20	48	0.0000000468	1.00
17	0.0000000118	0.33	49	0.0000000189	0.33
18	0.0000000060	0.20	50	0.0000000563	1.00
19	0.0000000027	0.14	51	0.0000000222	0.50
20	0.0000001828	1.00	52	0.0000000086	0.25
21	0.0000000024	0.14	53	0.0000001576	1.00
22	0.0000000029	0.25	54	0.0000000327	0.50
23	0.0000000096	0.33	55	0.0000000466	1.00
24	0.0000000040	0.14	56	0.0000000124	0.33
25	0.0000000044	0.17	57	0.0000006475	1.00
26	0.0000000030	0.20	58	0.0000000314	1.00
27	0.0000000025	0.11	59	0.0000000289	1.00
28	0.0000000066	0.25	60	0.0000006802	1.00
29	0.0000000043	0.25	61	0.0000000995	1.00
30	0.0000000059	0.25	62	0.0000000099	0.50
31	0.0000000021	0.08	63	0.0000000255	1.00
32	0.0000000036	0.11	64	0.0000000736	1.00

From the fitness value of each individual, the best fitness values are taken to be maintained and brought to the next generation. In this case for the largest claim the largest fitness value is the 60th individual is 0.0000006802 and for many claims of fitness value 1. Individuals with the best fitness value of the first generation population will be retained and taken to the next generation

c. Selection

After a population assessment operation, the best chromosomes are selected by using wheel selection that is associated with each chromosome of selection probability, noted, P_i with the following formula:

$$P_i = \frac{1}{N - 1} \left[1 - \frac{h_i}{\sum_{i \in Pop} h_i} \right]$$

Each chromosome is reproduced with probability. Some chromosomes are "more" reproduced and "bad" ones are removed. Next randomly select individuals from the population to serve as parent. The parent will be in the process of crossing with another selected individual.

With the help of matlab software got parent selected randomly. Here are the individual results selected as the parent.

Table 2. Claim Large Selection

Parent	Individual	Parent	Individual	Parent	Individual	Parent	Individual
Parent 1	5	Parent 1	11	Parent 1	55	Parent 1	7
Parent 2	24	Parent 2	27	Parent 2	63	Parent 2	12
Parent 1	47	Parent 1	19	Parent 1	21	Parent 1	59
Parent 2	56	Parent 2	41	Parent 2	34	Parent 2	28
Parent 1	20	Parent 1	4	Parent 1	39	Parent 1	48
Parent 2	33	Parent 2	42	Parent 2	25	Parent 2	64
Parent 1	38	Parent 1	14	Parent 1	35	Parent 1	1
Parent 2	52	Parent 2	6	Parent 2	32	Parent 2	8
Parent 1	30	Parent 1	46	Parent 1	37	Parent 1	36
Parent 2	44	Parent 2	31	Parent 2	53	Parent 2	43
Parent 1	3	Parent 1	10	Parent 1	16	Parent 1	54
Parent 2	29	Parent 2	17	Parent 2	49	Parent 2	57
Parent 1	13	Parent 1	23	Parent 1	60	Parent 1	62
Parent 2	18	Parent 2	58	Parent 2	15	Parent 2	45
Parent 1	26	Parent 1	9	Parent 1	51	Parent 1	61
Parent 2	50	Parent 2	40	Parent 2	2	Parent 2	22

Table 3. Many Large Selection

Parent	Individual	Parent	Individual	Parent	Individual	Parent	Individual
Parent 1	22	Parent 1	62	Parent 1	32	Parent 1	33
Parent 2	37	Parent 2	52	Parent 2	40	Parent 2	48
Parent 1	47	Parent 1	3	Parent 1	59	Parent 1	49
Parent 2	60	Parent 2	14	Parent 2	9	Parent 2	18
Parent 1	4	Parent 1	41	Parent 1	11	Parent 1	38
Parent 2	20	Parent 2	19	Parent 2	30	Parent 2	36
Parent 1	54	Parent 1	50	Parent 1	23	Parent 1	55
Parent 2	31	Parent 2	51	Parent 2	10	Parent 2	43
Parent 1	57	Parent 1	12	Parent 1	39	Parent 1	27
Parent 2	16	Parent 2	25	Parent 2	45	Parent 2	29
Parent 1	13	Parent 1	46	Parent 1	26	Parent 1	15
Parent 2	34	Parent 2	61	Parent 2	44	Parent 2	35
Parent 1	1	Parent 1	21	Parent 1	7	Parent 1	42
Parent 2	17	Parent 2	56	Parent 2	28	Parent 2	6
Parent 1	63	Parent 1	64	Parent 1	2	Parent 1	53
Parent 2	8	Parent 2	5	Parent 2	24	Parent 2	58

d. Crossover

After using the selection method for the selection of two individuals, we apply the crossover operator to a point on this pair. This operator divides each parent into two parts in the same position, chosen at random. Child 1 was made part of the first parent and the second part of the second parent when child 2 consisted of the second part of the first parent and the first part of the second parent

e. Mutation

This operation provides the genetic algorithm of ergodicity property which indicates that it will most likely reach all parts of the space belonging to the state, without traveling all in the resolution process. It's usually to draw a random gene in a chromosome and replace it with a random value.

f. Conditions for convergence

At this level, the final generation is considered. If the result is favorable then the optimal chromosome is obtained. Otherwise, the evaluation and reproduction steps are repeated until a certain number of generations, until the convergence criteria are established or until the convergence criteria are met.

3. Main result and conclusions

With the help of matlab software, Genetic Algorithm output process obtained results as follows:

\tilde{N}_0	= 64	D	= 0.33984 (many claims)
p	= 0.26667	D	= 0.14049 (claim value)
m_1	= 2.3702E+008	α	= 180.79
m_2	= 5.6321E+017	B	= 0.1012
m_3	= 2.5115E+028	σ_s	= 1.9182E+009
m_4	= 5.2923E+040	σ_s^2	= 7.3285E+018
ζ	= 0.9531	c	= 0.01
κ_s	= 2.8623	$Z_{0.01}$	= -2.3263

3.1. Results

In this section the results of the data processing analysis will be explained comprising the estimation of the frequency distribution model of the claim, the estimated claim distribution model, and the collective risk estimation of the assurance claim.

3.1.1 Estimation of claims frequency distribution model

Referring to (1) and after following the identification stages of the distribution model, distribution model parameter estimation, and test of distribution model matching. The frequency of claims obtained, a random sequence of events that can be predicted through a discrete distribution model.

The identification of frequency distribution model of the claim is made by curve matching, result of curve matching, the late indicates the model suitable for the frequency of the claim is following the geometric distribution. While estimation of frequency distribution model of claim model is performed by using Maximum Likelihood Estimator method. From result of processing obtained by parameter estimator $p = 0.26667$. The probability density function for geometric distribution is as follows:

$$\eta(n, 0.26667) = (0.26667)(1 - 0.26667)^{n-1}; n = 1, 2, 3, \dots$$

Estimator of the frequency distribution model of this claim, subsequently used to estimate the collective risk of insurance claims.

3.1.2. Estimate the large distribution model of the claim

From the estimator values, namely: $\alpha = 180.79$ and $\beta = 0.1012$. Furthermore, the matching test will be done by comparing the result of output of D value with table D of 95% confidence level (D1-95%) its critical value is 0.37543. Since the value of $D < D1-95\%$ ($0.14049 < 0.37543$), then H_0 is accepted. This means that the claim data follows the gamma distribution. The gamma distribution is as follows:

$$f(x) = \frac{1}{\Gamma(180.79)(0.1012)^{180.79}} x^{180.79-1} e^{-(x/0.1012)}; x > 0$$

3.1.3. Estimated collective risk of insurance claims

The collective risk estimates of insurance claims include aggregate claims and collective risk measurement. Collective risk measurement is based on Collective Risk, Collective Value-at-Risk, and Collective Modified Value-at-Risk. Estimates of aggregate claims expectations and collective risk measurements are performed by estimating the frequency distribution model of claims as equations (10) and (11). Estimator values of the parameters $E[N]$ and $\text{Var}[N]$, as well as the values of m_1, m_2, m_3 and m_4 , are used in calculating aggregate claims estimation estimates and collective risk measurements. As the above table values the moments obtained from the Genetic Algorithm output, ie $m_1 = 2.3702e + 008, m_2 = 5.6321e + 017, m_3 = 2.5115e + 028, m_4 = 5.2923e + 040, \sigma_s = 1.9182e + 009, = 7.3285 + 018$, aggregate claim risk value as measured by Collective Value-at-Risk ($CVaR$) at significance level $\alpha = 0.01$ (standard normal distribution $Z_{0.01} = 2.3263$), is as follows:

$$CVaR = -64\{-2.3263 \times 7.3285 + 018\} + (1.9182E + 009) = 280.280.000.000$$

From filing claims data of 64 events, with a claim value of 10,260,884,880 IDR. Based on the result of value analysis $\sigma_s = 1,918,200,000$ IDR per month or in 1 (one) year of 23,018,400,000 IDR. Based on the estimated $CVaR$ estimator of 280,280,000,000 IDR, this value is an assumption of the value of the claim that will occur. If the risk of aggregate claims is measured by Collective Modified Value-at-Risk ($CMVaR$) using Genetic Algorithms, the best result is 226,484,957,615 IDR,

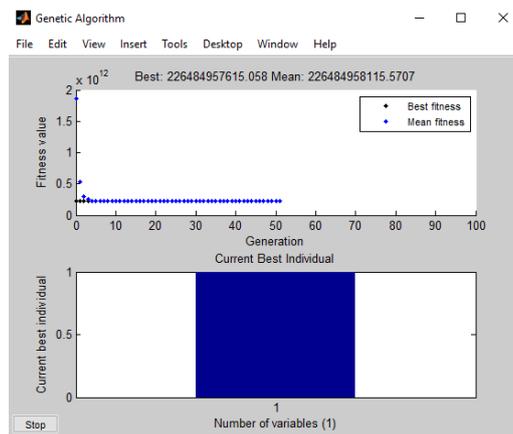


Figure 3. Result Genetic Algorithm

While if calculated manually in get the results as follows:

$$CMVaR = -64\left(1.9182e+009\right) + \left(-2.3263 + \frac{1}{6}(-2.3263^2 - 1)(0.9531)\right) + \frac{1}{12}(-2.3263^3 - 3(-2.3263)(2.8623)) - \frac{1}{36}(2(-2.3263^3) - 5(-2.3263)(0.9531)^2)(7.3285+018)^{1/2}$$

$$CMVaR = 331,500,000,000 \text{ IDR}$$

Which risk model will be chosen by the insurance company will be determined by considering other factors.

3.2. Conclusion

After analyzing the model study of credit life insurance risk adjustment, from the secondary data of one insurance company with the assistance of Matlab software, it can be concluded that the frequency of claims follows geometric distribution with $p = 0.26667$. For the large claims follow the gamma distribution with estimators $\alpha = 180.79$ and $\beta = 0.1012$. From that result the aggregate claim model formed from the frequency distribution of claims and the magnitude of individual claims, is a geometric compound distribution. The geometric compound distribution is determined by moments $m_1 = 2.3702E + 008, m_2 = 5.6321E + 017, m_3 = 2.5115E + 028, m_4 = 5.2923E + 040$. Value \hat{p}, m_1, m_2, m_3 , and, m_4 with a significance level of 5% obtained a value of $CMVaR$ of

Rp.331.500.000.000. The *CMVaR* value is an alternative risk measure, especially the large insurance claims not following the normal distribution

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