Parameter Estimations of Normal Distribution via Genetic Algorithm and Its Application to Carbonation Depth

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Abstract: - In this paper, we propose a method for estimating Normal distribution parameters using genetic algorithm. The main purpose of this research is to identify the most efficient estimators among three estimators for Normal distribution; Maximum likelihood method (ML), the least square method (LS), and genetic algorithm (GA) via numerical simulation and three real data, carbonation depth of Concrete Girder Bridges data examples which are based on performance measures such as The Root Mean Square Error (RMSE), Kolmogorov-Smirnov test, and Chi squared test. The simulation studies are conducted to evaluate the performances of the proposed estimators and provide statistical analysis of the real data set. The numerical results, χ^2, show that the genetic algorithm performs better than other methods for actual data and simulated data unless the sample size is small.

Key-Words: - Normal distribution, Parameter estimation, Maximum likelihood method, Genetic algorithm, The Least square method, Carbonation depth

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1 Introduction

The Normal distribution or Gaussian distribution plays an important role in several fields of mathematics and its applications. The Normal distribution has been widely used to describe the probability distribution of carbonation depth, [1],[2],[3],[4]. The carbonation depth is a point deterioration factor to determine the durability of the concrete structures. The characterization of carbonation depth is essential for the carbonation reliability analysis of Concrete Girder Bridges. Carbonation depth is usually employed in carbonation service life prediction of existing Concrete Girder Bridges as deterministic coefficients.

Several estimations, [5],[6],[7] for estimating parameters have been proposed. The authors in [7], using the Markov Chain Monte Carlo (MCMC) method for estimating parameters. Li, Yan, Wang and Hou, [6], proposed two parameter estimations for the Normal distribution: the least square method and the Bayesian quantile method. They found that the least square method is the best parameter estimation. Genetic algorithm was first introduced by Holland, [8], in 1992 and represented a population-based optimization method. This algorithm is a method to find an approximate solution for optimization problems which is used widely in several fields, [9],[10]. In parameter estimation, some researchers, [11],[12],[13], studied a method to find parameters by using genetic algorithms. The authors in [11], studied genetic algorithms and proposed a new genetic algorithm. They found that genetic algorithms are effective in performance indicators improvement. The authors in [12], used genetic algorithm (GA) to find estimators of Skew Normal distribution. They found that the GA has a high performance where traditional search techniques fail. In this paper, we study the genetic algorithm, a well-known search technique. The GA is inspired by a metaphor of the evolution process observed in nature.

The main purpose of this research is to identify the most efficient estimators among three estimators for the Normal distribution via actual data and simulated data. The rest of this paper is organized as follows: Section 2 discusses a short introduction of the Normal distribution, followed by the Normal distribution parameter estimation in Section 3. Accuracy judgment criteria are considered in Section 4. The performances of all methods are compared via a detailed simulation study in Section 5. Three parameter estimations are applied to three real data sets of Carbonation Depth of Concrete girder bridges, in Section 6. Finally, the main conclusions of this study are summarized in the last section.

2 Normal Distribution

The Normal distribution is also called Gaussian distribution.

A random variable x has a Normal distribution if its probability density function is defined by Equation (1).

The probability density function (pdf) of the Normal distribution can be written as

$$f(x) = \frac{1}{\sigma\sqrt{2\pi}} e^{-\frac{1}{2}\left(\frac{x-\mu}{\sigma}\right)^2}, \tag{1}$$

where μ and σ are the location parameter and the scale parameter, respectively.
The cumulative distribution function (CDF) of the Normal distribution is given by

$$F(x) = \int_{-\infty}^{x} \frac{1}{\sigma\sqrt{2\pi}} e^{-\frac{1}{2}\left(\frac{t-\mu}{\sigma}\right)^2} dt, \tag{2}$$

or

$$F(x) = \Phi\left(\frac{x-\mu}{\sigma}\right),$$

where $\Phi(x) = \frac{1}{\sqrt{2\pi}} \int_{-\infty}^{x} e^{-\frac{t^2}{2}} dt.$

3 Estimation Methods

In this section, the three considered estimation methods were described to obtain the estimates of the parameters μ and σ of the Normal distribution.

3.1 Maximum Likelihood Method

Let $x_1, x_2, \ldots, x_n$ be observed values of $X_1, X_2, \ldots, X_n$, n independent random variables having the Normal distribution with parameters μ and σ.
The maximum likelihood function of the sample, denote by $L(\mu, \sigma|x_1, x_2, \ldots, x_n)$, is given by

$$\begin{aligned} L(\mu, \sigma|x_1, x_2, \ldots, x_n) &= \prod_{i=1}^{n} f(x_i) \\ &= \prod_{i=1}^{n} \frac{1}{\sigma\sqrt{2\pi}} e^{-\frac{1}{2}\left(\frac{x_i-\mu}{\sigma}\right)^2}, \end{aligned}$$

by taking ln, we get

$$\begin{aligned} &\ln L(\mu, \sigma|x_1, x_2, \ldots, x_n) \\ &\quad = -\frac{n}{2}\ln(2\pi\sigma^2) - \frac{1}{2\sigma^2}\sum_{i=1}^{n}(x_i-\mu)^2. \end{aligned} \tag{3}$$

To obtain the maximum likelihood estimators, we have to maximize Equation (3), partial derivatives of $\ln L(\mu, \sigma|x_1, x_2, \ldots, x_n)$ functions with respect to each parameter are taken, and we set them equal to 0 as follows:

$$\frac{\partial}{\partial\mu}\ln L(\mu, \sigma|x_1, x_2, \ldots, x_n) = 0,$$
$$\frac{\partial}{\partial\sigma}\ln L(\mu, \sigma|x_1, x_2, \ldots, x_n) = 0.$$

The maximum likelihood estimators of μ and σ, denoted by $\hat{\mu}_{\text{ML}}$ and $\hat{\sigma}_{\text{ML}}$, respectively, are obtained by

$$\hat{\mu}_{\text{ML}} = \frac{1}{n}\sum_{i=1}^{n} x_i,$$
$$\hat{\sigma}_{\text{ML}} = \sqrt{\frac{1}{n-1}\sum_{i=1}^{n}(x_i-\bar{x})^2},$$

where $\bar{x}$ is the sample mean.

3.2 Least Square Method

Let $X_1, X_2, \ldots, X_n$ be n independent random variables having the Normal distribution with parameters μ and σ. Suppose that $X_{(1)} \leq X_{(2)} \leq \ldots \leq X_{(n)}$ are the order statistics. Let the empirical distribution function of X be denoted by

$$F_n(x) = \begin{cases} 0, & x < X_{(1)}, \\ \frac{k}{n}, & X_{(k)} \leq x < X_{(k+1)}, \quad k = 1, 2, \ldots, n-1 \\ 1, & x > X_{(n)}. \end{cases} \tag{4}$$

The following cumulative distribution function $F(x)$ is calculated by

$$F(x) = \frac{1}{\sigma\sqrt{2\pi}} \int_{-\infty}^{x} e^{-\frac{1}{2}\left(\frac{t-\mu}{\sigma}\right)^2} dt. \tag{5}$$

The CDF of Normal $F(x)$ can be expanded in Taylor series approximation as follow:

$$F(x) = \Phi\left(\frac{x-\mu}{\sigma}\right), \tag{6}$$

where

$$\Phi(x) \approx \frac{1}{2} + \frac{1}{\sqrt{2\pi}}\sum_{k=0}^{N}\frac{(-1)^k x^{2k+1}}{2^k k!(2k+1)}.$$

For the Normal distribution, the least square method estimates $\hat{\mu}$ and $\hat{\sigma}$ of the parameters μ and σ, respectively, are obtained by minimizing the function:

$$E(\mu, \sigma) = \sum_{i=1}^{n}(F(x_i) - F_n(x_i))^2, \tag{7}$$

where $F(x_i)$ and $F_n(x_i)$ are obtained by Equation (4) and (5), respectively. By solving the following equations:

$$\frac{\partial}{\partial \mu}E(\mu,\sigma) = 0,$$
$$\frac{\partial}{\partial \sigma}E(\mu,\sigma) = 0.$$

We denote by

$$A(x_i,\mu,\sigma) = \sum_{k=0}^{N} \frac{(-1)^k \left(\frac{x_i-\mu}{\sigma}\right)^{2k}}{2^k k!}$$

and

$$B(x_i,\mu,\sigma) = \sum_{k=0}^{N} \frac{(-1)^{k+1} \left(\frac{x_i-\mu}{\sigma}\right)^{2k}}{2^k k!(2k+1)},$$

$\hat{\mu}, \hat{\sigma}$ are the estimators of the parameters μ and σ, respectively. Using some algebraic manipulations, the estimators satisfy the following equations:

$$\hat{\sigma} = \frac{\sum_{i=1}^{n} F_n(x_i)A(x_i,\mu,\sigma)}{\sum_{i=1}^{n} F(x_i)\frac{1}{\sigma}A(x_i,\mu,\sigma)},$$

and

$$\hat{\mu} = \frac{\sum_{i=1}^{n}(F(x_i)-F_n(x_i))x_i A(x_i,\mu,\sigma)}{\sum_{i=1}^{n}(F(x_i)-F_n(x_i))A(x_i,\mu,\sigma)}.$$

These equations are solved iteratively.

3.3 Genetic Algorithm

The main steps of the genetic algorithm (GA) are selection, crossover, and mutation. In GA, each chromosome (individual in the population, parameters) represents a possible solution to a problem and is composed of a string of genes. Kalra and Singh [14] proposed a pseudo code of GA for optimization of scheduling problems as follows:

Procedure GA

Determine the number of chromosomes generation ($Npop = 10000$), and mutation rate ($MR = 0.5$).The number of chromosomes is 2 (μ and σ).

1. **Initialization**: Generating initial population P consisting of $N = 100$ chromosomes. Every gene represents a parameter (variables) in the solution. This collection of parameters that forms the solution is the chromosome. Therefore, the population is a collection of chromosomes. Assume that the initial population $P^{(1)}$ is denoted by

$$P^{(1)} = [w_1^{(1)},\, w_2^{(1)},\, \ldots,\, w_N^{(1)}]$$

where $w_i^{(1)} = [\mu^{(1)}, \sigma^{(1)}]^t$ is a vector of parameters for $i = 1,2,\ldots,N$. Also, the vector of $w_i^{(m)},\ i = 1,2,\ldots,N,\ m = 1,2,\ldots,Npop$ represents the values of the i^{th} chromosome in the population at m^{th} iteration.

2. **Fitness**: Calculate the fitness value of each chromosome using a fitness function. In this study, the fitness values are defined by:

$$f_i^{(m)} = \frac{1}{i}, \quad m = 1,2,\ldots,Npop$$

where $f_i^{(m)}$ represents the fitness value of the i^{th} chromosome at m^{th} iteration.

3. **Selection**: Select the chromosomes for producing the next generation using the selection operator, the worst chromosomes are replaced by new chromosomes generated randomly from the search space. We used the roulette wheel selection. The probability of choosing chromosome i is equal to

$$p_i = \frac{f_i^{(m)}}{\sum_{i=1}^{N} f_i^{(m)}}$$

where $f_i^{(m)}$ is the fitness value of the i^{th} chromosome in the population at m^{th} iteration.

4. **Crossover**: Perform the crossover operation on the pair of chromosomes obtained in step 3.

5. **Mutation**: Perform the mutation operation on the chromosomes. The chromosome k for $k = 1,2$ are mutated as follows:
random $u_k \in (0,1)$, if $u_k < MR$, then we mutated the chromosome i.

6. **Replacement**: Update the population $P^{(m)}$ for $m = 2,3,\ldots$ by replacing bad solutions with better chromosomes from offspring.

7. Repeat steps 3 to 6 until the stopping condition is met. The stopping condition may be the maximum number of iterations or no change in the fitness value of chromosomes for consecutive iterations.

8. **Output** the best chromosome (the best parameter) as the final solution.

End Procedure

3.4 Goodness-of-Fit

To show how a theoretical probability function matches with the observation data, three kinds of statistical errors are considered as the Goodness-of-fit.

Generally, the smaller the errors, the better the fit is. Let n be the number of data and k be the number of classes, calculated by Sturges formula,

$$k = \lceil 1 + 3.322 \log n \rceil.$$

The First one is the root mean square error (RMSE) defined as

$$\text{RMSE} = \sqrt{\frac{1}{k}\sum_{i=1}^{k}(O_i - E_i)^2}, \quad (8)$$

where O_i is the actual value at time stage i, and E_i is the value computed from correlation expression for the same stage.
The second one is the Kolmogorov-Smirnov test (KS), which is defined as the max error in CDFs

$$\text{KS} = \max_x |F_n(x) - F(x)|, \quad (9)$$

where $F_n(x)$ is the empirical cumulative distribution function not exceeding x and $F(x)$ is the CDF of Normal distribution.
The third judgment criterion is the Chi-squared test given as:

$$\chi^2 = \sum_{i=1}^{k}\frac{(O_i - E_i)^2}{E_i}. \quad (10)$$

4 A Simulation Study

In this section, a simulation study was performed to compare the performance of the different methods discussed in Section 3. 2000 random samples of sizes $n = 10, 20, 30, 50, 100, 500, 1000$, and 2000 were generated from the Normal distribution. Since any Normal distribution data can be standardized to have a location parameter of 0 and scale parameter of 1, only samples with parameters $\mu = 0$ and $\sigma = 1$ were generated. In order to compare the goodness-of-fit of various pdfs to sample data, several statistics have been used in studies related to data.

The RMSE is most useful when large errors are particularly undesirable. The Kolmogorov–Smirnov test has the advantage of considering the distribution functions collectively. Advantages of the Chi-square test include its robustness in data distribution, and ease of calculation.

The most frequently used ones are the root mean square error (RMSE), [15],[16], the Kolmogorov–Smirnov test results (KS), [15],[17], and the Chi squared test results (χ^2), [15].

The results of the simulation study are presented in Table 1-2. The following conclusions can be drawn:
1. All estimators of the parameters are unbiased, i.e., the estimators sometimes exceed the true value of the parameters. The biases of maximum likelihood estimation and genetic algorithm of the parameters tend to zero for large n
2. As the sample size increases, the estimates of μ and σ generally approach their true values. An increase in the sample size of the simulated The Normal distribution data generally results in the improvement of the three methods. Overall, the RMSE, KS test, and χ^2 values increase as the sample size increases.
3. The difference between the ML and GA is very little for small sample sizes ($n < 30$), but it is slightly more for larger sample sizes ($n \geq 30$).
4. The LS value is higher than the others.

Moreover, we found that:
1. The ML is a commonly used method for parameter estimation because it is simple and fast.
2. The LS is the iterative method, so the best parameter is based on the initial parameter. The genetic algorithm is the iterative method, but the genetic algo-

n	Parameter	Estimation		
		ML	LS	GA
10	μ	0.5180	8.1768	0.6112
	σ	0.8437	0.3664	0.8263
	RMSE	0.7920	1.0227	0.7729
	KS test	0.9939	4.7753	1.2699
	χ^2	4.9517	16.5301	4.7405
20	μ	0.2101	-7.6186	0.2315
	σ	0.9042	5.0261	0.9481
	RMSE	0.7993	1.3470	0.7919
	KS test	0.7447	8.5721	1.0788
	χ^2	3.7719	19.3985	3.7027
30	μ	0.1314	0.1274	0.1330
	σ	0.8238	1.1688	0.9273
	RMSE	1.4151	1.5568	1.4122
	KS test	2.0833	3.7360	2.1236
	χ^2	13.7865	15.2259	12.9437
50	μ	0.0932	4.7193	0.0890
	σ	0.9458	8.1408	1.0836
	RMSE	1.2694	2.4223	1.4442
	KS test	1.7180	15.7167	3.2420
	χ^2	13.6696	25.6064	9.7582
100	μ	-0.0520	-2.8979	-0.0821
	σ	0.9920	3.3682	1.0383
	RMSE	1.6756	3.7792	1.6742
	KS test	2.6334	30.4071	1.9056
	χ^2	9.0434	46.5958	8.5079
500	μ	0.0236	0.2656	0.0276
	σ	1.0694	1.2600	1.0831
	RMSE	4.4704	7.1210	4.4631
	KS test	5.0129	51.8562	5.9734
	χ^2	17.2298	48.2707	16.9679

Table 1: *Comparison of the estimation methods for* $n = 10, 20, 30, 50, 100$ *and* 500.

n	Parameter	Estimation		
		ML	LS	GA
1000	μ	0.0119	8.6916	-0.0064
	σ	1.0588	7.3159	1.0875
	RMSE	3.9538	28.6166	4.1776
	KS test	6.9662	262.3597	5.2007
	χ^2	22.8076	383.9043	18.9865
2000	μ	-0.0003	-0.2052	-0.0088
	σ	1.0471	1.5086	1.0568
	RMSE	5.6892	32.7658	5.5773
	KS test	14.8244	98.7142	6.0461
	χ^2	19.3856	358.0330	18.4112

Table 2: *Comparison of the estimation methods for* $n = 1000$ *and* 2000.

rithm performance is better than ML and LS as ML performance is better than LS.
3. According to χ^2, the genetic algorithm has a smaller χ^2 value than other methods.

Therefore, ML and GA show identical performance for estimating the μ and σ parameters of the Normal distribution unless the sample size is larger. However, the GA performs better for large sample sizes than other methods considered here such as ML and LS methods.

5 Application to Carbonation Depth

In this section, the parameter estimation methods defined in Section 3 are applied to the real data-carbonation depth. Three real data sets of carbonation depth are analyzed to compare the considered three estimation methods for the Normal distribution.

The first data set represents 12 measurements of the carbonation depth of a reinforced concrete girder bridge [6]: 12.5, 13.2, 13.9, 14.1, 14.3, 14.6, 14.9, 15, 15.3, 15.7, 16.4, 17.1 mm.

The second data set represents 18 measurements of the carbonation depth of the Chorng-ching Viaduct [2]: 8, 11, 15, 15, 17, 18, 20, 22, 22, 26, 28, 30, 30, 31, 33, 38, 38, 40 mm.

The third data set represents 27 measurements of the carbonation depth of pier of a reinforced concrete girder bridge [18]: 2, 2.1, 2.2, 2.3, 2.3, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, 2.9, 3.0, 3.2, 3.2, 3.3, 3.3, 3.3, 3.4, 3.4, 3.4, 3.5, 3.5, 3.6, 3.7, 3.8, 3.9 mm.

Method	Estimated parameter		RMSE	KS test	χ^2
	μ	σ			
ML	14.7500	1.2923	0.7851	0.7174	5.1521
LSM	14.5703	1.2197	0.7954	0.2285	5.9343
GA	14.8241	1.2976	0.7861	0.9394	5.0878

Table 3: *Parameter estimations, RMSE, KS test, and Chi squared test for the first data set.*

Method	Estimated parameter		RMSE	KS test	χ^2
	μ	σ			
ML	24.5556	9.5808	1.1323	1.4957	11.7405
LSM	23.5642	10.6848	1.1626	1.1159	12.7121
GA	14.8356	1.2942	0.7865	0.9664	5.0868

Table 4: *Parameter estimations, RMSE, KS test, and Chi squared test for the second data set.*

Method	Estimated parameter		RMSE	KS test	χ^2
	μ	σ			
ML	2.9852	0.5702	1.5836	2.7463	15.3773
LSM	2.9697	0.6770	1.5492	2.2868	15.0384
GA	.0193	0.6512	1.5134	2.3795	14.6748

Table 5: *Parameter estimations, RMSE, KS test, and Chi squared test for the third data set.*

Table 3, 4, and 5 show the estimators of μ and σ parameters of the Normal distribution with values of RMSE, KS test, and χ^2 on carbonation depth real data. According to χ^2, the genetic algorithm yields a smaller χ^2 value than other methods. According to the KS test, the least square method yields a smaller KS value than other methods. According to the RMSE, the genetic algorithm yields a smaller χ^2 value than other methods. The genetic algorithm yields a smaller χ^2 value than other methods.

The results indicate that the genetic algorithm is better than other methods in terms of RMSE and χ^2 values. Hence, for the real given data sets of carbonation depth, we concluded that the genetic algorithm method is the best among the three considered estimation methods.

6 Conclusions

We proposed a parameter estimation to estimate parameters for the Normal distribution based on the genetic algorithm. The proposed estimation and the most common estimation were applied to real data sets. We compare the performance of three methods for the Normal distribution through a simulation study and three real data sets of carbonation depth. Therefore, it is concluded from both simulated and real data sets that all the methods show identical performance for estimating the parameters of the Normal distribution. However, the genetic algorithm performs better than other methods, such as the maximum Likelihood method and least square method. In future work, we will adjust the genetic algorithm for estimating parameters.

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