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STATISTICAL INFERENCE FOR THE NON-CONFORMING RATE OF FGM COPULA-BASED BIVARIATE EXPONENTIAL LIFETIME

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Abstract. Lifetime performance index is widely used as process capability index to evaluate the performance and potential of a process. In manufacturing industries, the lifetime of a product is considered to be conforming if it exceeds a given lower threshold value, so nonconforming products are those that fail to exceed this value. Nonconformities are so important that affect the safe or effective use of the products. This article deals with the processes that the products' lifetime is related to a two-component system, distributed as Farlie-Gumbel-Morgenstern (FGM) copula-based bivariate exponential and presents the probability of non-conforming products. Also, bootstrap upper confidence bounds are constructed and their performance are investigated in simulation study. In addition, Monte Carlo scheme is applied to do hypothesis testing on it. Finally, two example sets are presented to demonstrate the application of the proposed index.

Keywords: Lifetime performance index, Farlie-Gumbel-Morgenstern copula, Non-conforming rate, Bootstrap upper confidence bound, Monte Carlo procedure.
2020 MSC: 62P30

1. Introduction

Process capability indices (PCIs) are numerical tools that show how much the process products meet the needs of the construction engineers or customers satisfies. Montgomery [26] introduced a process capability index C_L as lifetime performance index to measure the larger-the-better quality characteristic, as the following;

$$C_L = \frac{\mu - L}{\sigma}, \tag{1}$$

where μ and σ are the process mean and standard deviation, respectively and L is the lower specification limit for the lifetime of products.

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If the lifetime of a product, X, exceeds L, it is considered as conforming. Otherwise, it is non-conforming. Furthermore, a larger lifetime yields a better quality. The probability of non-conforming (NC) products (non-conforming rate) is defined by

$$P_L = P(X < L) = \int_0^L f(x)dx. \tag{2}$$

Statistical inference of C_L for some well-known lifetime distributions has been considered in the literature. In real world, the experimenter may not always be in a position to observe the life times of all the products or items put on test. This may be because of time limitation or other restrictions such as money, material resources, mechanical or experimental difficulties on data collection. Therefore, the need for censoring has thus arisen and the censored samples are obtained [32]. In other words, censoring sample is a circumstance in which the values of observations are only partially known. In the literature, the index C_L has been applied to evaluate the lifetime of product on the censored sample and record values.

Tong et al. [33] constructed the uniformly minimum variance unbiased estimator (UMVUE) of C_L and proposed a hypothesis testing procedure based on a sample from one-parameter exponential distribution. Lee et al. [23] constructed a maximum likelihood estimator (MLE) of C_L based on the progressively type II right censored sample under the assumption of exponential distribution and then, utilized it to develop the hypothesis testing procedure.

Ahmadi et al. [1] presented statistical inference for C_L based on generalized order statistics, which contains several ordered data models such as usual order statistics, progressively Type-II censored data and records. Also, they obtained various point and interval estimators for the parameter C_L and proposed optimal critical regions for the hypothesis testing problems concerning C_L.

Soliman et al. [32] constructed the maximum likelihood and the Bayesian estimators of C_L for the exponential Frechet (EF) model with progressive first-failure-censoring scheme and then, applied these estimators to obtain confidence interval for C_L. For more information in some other research in this field, see [2, 3, 22, 23, 25, 37].

Although much research has been done on the lifetime performance index in univariate exponential distribution, so far there has been no study for the circumstances in which the products lifetime depends on two variables.

In actuarial science, when two lives are subject to failure, such as under a joint life insurance or annuity policy, it is concerned with joint distribution of lifetimes. The present paper studies the non-conforming rate of the processes in which the lifetime of the products counts on two related characteristics, following bivariate exponential distribution that their joint distribution is modelled by Farlie-Gumbel-Morgenstern (FGM) copula.

Here is the paper's structure. Following section reviews some preliminary of non-conforming rate as well as copula. In section 3, non-conforming rate is obtained and its graphical form is presented. Section 4 presents the MLE of P_L. In section 5, upper confidence bound of P_L is obtained according to four bootstrap methods and comparison among them is discussed . Furthermore, hypothesis testing procedure along with the Monte Carlo simulation scheme is investigated in section 6. Section 7 presents numerical example to demonstrate the applicability of the proposed index and finally, conclusions are given in section 8.

2. **Preliminary**

Exponential distribution is commonly used in reliability theory and survival analysis as well as in process capability analysis. Suppose the lifetime of the products, X, follows exponential distribution by parameter λ. Then, the probability density and cumulative distribution functions are as:

$$f_X(x,\lambda) = \frac{1}{\lambda} e^{-x/\lambda}, \qquad x > 0, \quad \lambda > 0, \tag{3}$$

and

$$F_X(x,\lambda) = 1 - e^{-x/\lambda}, \qquad x > 0, \quad \lambda > 0. \tag{4}$$

Therefore, it is denoted by $X \sim E(\lambda)$. See Lehmann and Casella [24], and Ross [30]; for more information. Since $\mu = \sigma = \lambda$, then the index C_L, presented in equation 1, rewritten as follows;

$$C_L = \frac{\lambda - L}{\lambda} = 1 - \frac{L}{\lambda}. \tag{5}$$

The probability of non-conforming products is calculated as:

$$\begin{aligned} P_L &= P(X < L) = \int_0^L f(x)dx \\ &= \int_0^L \frac{1}{\lambda} e^{-x/\lambda} dx = 1 - e^{-L/\lambda}. \end{aligned} \tag{6}$$

The non-linear relation between C_L and P_L is obtained by simple calculations as the following;

$$C_L = 1 + \ln(1 - P_L). \tag{7}$$

Intuitively, the relationship between the lifetime performance index and the non-conforming rate is strictly increasing. Therefore, the lifetime performance index can be an applicable and flexible tool to evaluate product performance and achieve the non-conforming rate. From the equation (5), it is concluded that $-\infty < C_L < 1$, but for a process to be considered as capable it is needed that the amount of C_L be positive, so based on the equation (7), $0 < 1 + \ln(1 - P_L) < 1$ and this is of course equivalent to $0 < P_L < 0.632$.

Due to the fact that the proportion of non-conforming products and process capability analysis are two parallel concepts of judging process performance, here just the probability of non-conforming products is mentioned. Since the index C_{pk} has been widely used in the manufacturing industry, here the threshold value analogous to this index is suggested to make a decision on the process performance.

Pearn and Shu [29] provided a measure of process yield as $2\Phi(3C_{pk}) - 1 \leq yield \leq \Phi(3C_{pk})$, where $\Phi(.)$ is the cumulative function for the standard normal distribution. In addition, they said that a manufacturing process is said to be "Inadequate" if $C_{pk} < 1$, "Capable" if $1.00 \leq C_{pk} < 1.33$, "Excellent" if $1.33 \leq C_{pk} < 1.67$, "Excellent" if $1.67 \leq C_{pk} < 2.00$, and "Super" if $2.00 \leq C_{pk}$.

Since $NC = 1-yield$, it is concluded that $1-\Phi(3C_{pk}) \leq NC \leq 2-2\Phi(3C_{pk})$. According to the relationship between the index C_{pk} and non-conforming rate, here some criteria for evaluating the process non-conformities are recommended as presented inTable 1. These threshold values can be used for bivariate case, too.

TABLE 1. Process non-conformities and process condition

condition	process non-conformities
Inadequate	$P_L \geq 0.0027$
Capable	$0.00007 \leq P_L < 0.0027$
Satisfactory	$0.0000068 \leq P_L < 0.00007$
Excellent	$0.00007 \leq P_L < 0.000000002$
Super	$P_L \leq 0.000000002$

2.1. **Copula.** Copulas are used to combine marginal distributions to create bivariate/multivariate distributions. They contain information from the joint distribution that is not contained in the marginal distributions. The concept of copula was introduced by Sklar [31], and has for a long time been recognized as a powerful tool for modelling dependence between random variables.

Definition 2.1. A function C of D variables on the unit D-cube $[0,1]^D$ is a copula if and only if the following properties hold:

- For every $u, v \in [0,1]$, $C(u,0) = C(0,v) = 0$, $C(u,1) = u$ and $C(1,v) = v$.
- For every $u_1, u_2, v_1, v_2 \in [0,1]$ such that $u_1 \leq u_2$ and $v_1 \leq v_2$,

$$C(u_2, v_2) - C(u_2, v_1) - C(u_1, v_2) + C(u_1, v_1) \geq 0.$$

The following theorem is known as Sklar's theorem. It is perhaps the most important result regarding copulas, and is used in essentially all applications of copulas.

Theorem 2.2. ***Sklar's Therorem.*** *[27] Let H be a joint distribution function with margins F and G. Then, there exists a copula C such that for all x, y in $\bar{R}$,*

$$H(x,y) = C(F(x), G(y)). \tag{8}$$

If F and G are continuous, then C is unique; otherwise, C is uniquely determined on $RanF \times RanG$. Conversely, if C is a copula and F and G are distribution functions, then the function H defined by (8) *is a joint distribution function with margins F and G.*

The information in H that is not in the marginal distributions is all of the dependence information. Thus, C contains all of the information on the dependence between X and Y, but no information on the univariate characteristics X or Y.

Theorem 2.3. ***Sklar's Therorem in* n*-dimensions.*** *[27] Let H be an n-dimensional distribution function with margins $F_1, F_2, ..., F_n$. Then, there exists an n-copula C such that for all $\mathbf{x}$ in $\bar{R}^n$,*

$$H(x_1, x_2, ..., x_n) = C\big(F_1(x_1), F_2(x_2), ..., F_n(x_n)\big). \tag{9}$$

If $F_1, F_2, ..., F_n$ are all continuous, then C is unique; otherwise, C is uniquely determined on $RanF_1 \times RanF_2 \times ... \times RanF_n$. Conversely, If C is an n-copula and $F_1, F_2, ..., F_n$ are distribution functions, then the function H defined by (9) *is an n-dimensional distribution function with margins $F_1, F_2, ..., F_n$.*

It is noted that Sklar's theorem shows that an n-dimensional joint distribution function may be decomposed into its n marginal distributions and a copula, which completely describes the dependence between the n variables. Decomposing the multivariate distribution into the marginal distributions and the copulas allows the researcher to construct better models of the individual variables than would be possible; whereas he constrains himself to look only at existing multivariate distributions.

One of the most popular parametric families of copula is the FGM family defined as:

$$C(u,v) = uv\big[1 + \theta(1-u)(1-v)\big], \tag{10}$$

where, u and v are margins which are distributed as $U(0,1)$, and the scalar θ is dependence parameter, ranges from -1 to 1. It is noted that the independence structure is reached when $\theta = 0$. The FGM copula density is provided by

$$c(u,v) = \big[1 + \theta(2u-1)(2v-1)\big]. \tag{11}$$

A well-known limitation to this family is that it does not allow the modeling of large dependences since the correlation range ρ between the marginal distributions is limited to $\rho \in [-\frac{1}{3}, \frac{1}{3}]$.

For more a related discussion, see [14, 19, 20, 27, 31, 35, 36, 38–40].

2.2. **Association Measure.** Statistical inference concerning with dependence structures should always be based on ranks [19]. One of the most popular scale-invariant measures of association is Kendall's tau, which is a non-parametric rank correlation coefficient that evaluates the degree of similarly between two sets of ranks. Suppose (X, Y) is a vector of random variables with joint distribution function H. Let (X_1, Y_1) and (X_2, Y_2) be independent and identically distributed random vectors with joint distribution function H. Kendall's tau is defined as:

$$\tau_{X,Y} = P\big((X_1 - X_2)(Y_1 - Y_2) > 0\big) - P\big((X_1 - X_2)(Y_1 - Y_2) < 0\big). \tag{12}$$

According to copula C, it will be in the form:

$$\tau_{X,Y} = \tau_C = 4 \int\int_{I^2} C(u, v) dC(u, v) - 1. \tag{13}$$

Definition 2.4. Two pair distinct observations (x_i, y_i) and (x_j, y_j) from a vector (X, Y) of continuous random variables are said to be concordant if $(x_i - x_j)(y_i - y_j) > 0$ and discordant if $(x_i - x_j)(y_i - y_j) < 0$.

Suppose a sample of size n is gathered from the population and e is the number of concordant pairs and d the number of discordant pairs. Then, Kendall's tau is obtained from the following equation;

$$\tau = \frac{e - d}{e + d}. \tag{14}$$

For FGM copula family, the relation between Kendall's tau and the dependence parameter θ is $\tau_{X,Y} = 2\theta/9$. Accordingly, the range of admissible Kendall's tau for FGM copula family is $[-2/9, 2/9]$. In consequence of this, θ is estimated from Kendall's tau for the sample as $\widehat{\theta} = 9\tau/2$.

2.3. **Generating FGM distribution data.** Johnson [21] presented the following algorithm generates random variates (u, v) from an FGM distribution with parameter θ:

- Generate two independent uniform $(0, 1)$ variates u, and t;
- Set $a = 1 + \theta(1 - 2u)$, and $b = \sqrt{a^2 - 4(a - 1)t}$;
- Set $v = 2t/(b + a)$;
- The desired pair is (u, v).

2.4. **Graphical Tools for Detecting Dependence.** To investigate the dependence structure, one step is to compare a scatter plot of the pairs $(R_i/(n + 1), S_i/(n + 1))$, where R_i and S_i are the ranks of the sample data, with an artificial data set of a large sample from the considered copula. Furthermore, Chi-plot and Kendall plot are proposed to detect the dependence structure, which are presented here.

The Chi-plot introduced by Fisher and Switzer [12, 13] is a graphical representation of the measures of local dependence, inspired from control charts

and based on the chi square statistic for independence in a two-way table. The Chi-plot depends on the data only through the values of their ranks.

Suppose $(X_1, Y_1), (X_2, Y_2), ..., (X_n, Y_n)$ is a random sample from (X, Y) with joint distribution function H. For each point (X_i, Y_i), set

$$H_i = \frac{1}{n-1} \sharp\{j \neq i : X_j \leq X_i, Y_j \leq Y_i\}, \tag{15}$$

$$F_i = \frac{1}{n-1} \sharp\{j \neq i : X_j \leq X_i\}, \tag{16}$$

$$G_i = \frac{1}{n-1} \sharp\{j \neq i : Y_j \leq Y_i\}, \tag{17}$$

$$S_i = sign\big((F_i - \frac{1}{2})(G_i - \frac{1}{2})\big), \tag{18}$$

where, the symbol $\sharp$ indicates the number and

$$sign = \begin{cases} -1; & x < 0, \\ 0; & x = 0, \\ 1; & x > 0. \end{cases} \tag{19}$$

Then,

$$\begin{aligned} \lambda_i &= 4S_i \max\{(F_i - \frac{1}{2})^2, (G_i - \frac{1}{2})^2\}, \\ \chi_i &= \frac{H_i - F_i G_i}{\sqrt{F_i(1-F_i)G_i(1-G_i)}}. \end{aligned} \tag{20}$$

The Chi-plot is a scatter plot of the pairs (λ_i, χ_i). The theoretical chi-value is zero if $P(X \leq u, Y \leq v) = P(X \leq u)P(Y \leq v)$. Fisher and Switzer [12, 13] suggested the limit lines $\pm c_p/\sqrt{n}$ for Chi-plot, where c_p is the value in which approximately $100p\%$ of the points (λ_i, χ_i) lie between the lines, and is equal to 1.54, 1.78 and 2.18 corresponds to $p = 0.9, 0.95$ and 0.99, respectively.

It is noted that to avoid spurious observations, only pairs for which $\mid \lambda_i \mid < 4(1/(n-1) - 1/2)^2$ should be plotted.

The Kendall plot, which is known as K-plot, introduced by Genest and Boies [16], adapts the concept of probability plot to detect the dependence structure. K-plot is a scatter plot of pairs $(W_{i:n}, H_{(i)})$, where $H_{(i)}$'s are the order statistics regarding for the quantities H_i's defined in Chi-plot and $W_{i:n}$ is the expected value of the ith statistic from a random sample of the copula family $W = H(X, Y)$ under the null hypothesis of independence, and is calculated as the following;

$$W_{i:n} = n\binom{n-1}{i-1} \int_0^1 w k_0(w) \big(K_0(w)\big)^{i-1} \big(1 - K_0(w)\big)^{n-i} dw, \tag{21}$$

and

$$K_0(w) = w - w log(w). \tag{22}$$

The interpretation of K-plot is the same as QQ-plot. If its points lie approximately on the main diagonal, then X and Y are approximately independent. Any deviation from the main diagonal line represents dependence. In the case of positive dependence, the points of the plot are located above the main diagonal line and vice versa for negative dependence. Furthermore, the larger the deviation from the main diagonal line, the stronger the dependence. See [16], For more information.

2.5. **Goodness of Fit Test.** Goodness of fit test detects whether the structure of a set of observations is approximately modelled by a statistical model or not. In fact, it measures the discrepancy between observed values and the values expected under the considered model. In statistics, the Cramér-von Mises criterion is used to detect if the dependence structure of a multivariate distribution is well-represented by a specific copula family, i.e., for testing the null hypothesis $H_0 : C \in C_0$, which C is the true underlying copula.

Cramér-von Mises statistic is as:

$$S_{n\xi} = n \int_{\xi}^{1} \big(C_n(w) - C_{\theta_n}(w)\big)^2 dw, \tag{23}$$

where C_n is the empirical copula computed from the random sample (X_1, Y_1), $(X_2, Y_2), ..., (X_n, Y_n)$ and C_{θ_n} is an estimation of C obtained under the null hypothesis and $\xi \in (0, 1)$ is an arbitrary cutoff point.

In the literature, there are many researches about Cramér-von Mises test. For detailed discussion on this topic, see [15, 17, 18, 34].

3. Non-Conforming Rate, P_L

Suppose the lifetime of the manufacturing products counts on two lifetime variables X_1 and X_2 with cumulative distribution functions $F_{X_1}(x_1)$ and $F_{X_2}(x_2)$, and the joint distribution based on FGM copula model as the following;

$$F_{X_1,X_2}(x_1, x_2) = F_{X_1}(x_1)F_{X_2}(x_2)\Big[1 + \theta(1 - F_{X_1}(x_1))(1 - F_{X_2}(x_2))\Big]. \tag{24}$$

The probability of non-conforming (NC) products is obtained as follows;

$$\begin{aligned} P_L &= P(X_1 < L_1 \text{ or } X_2 < L_2 \text{ or both of them}) \\ &= 1 - P(X_1 > L_1,\ X_2 > L_2) \\ &= 1 - S(L_1, L_2) \\ &= 1 - \Big[1 - F_{X_1}(L_1) - F_{X_2}(L_2) + F_{X_1,X_2}(L_1, L_2)\Big] \\ &= F_{X_1}(L_1) + F_{X_2}(L_2) - F_{X_1,X_2}(L_1, L_2). \end{aligned} \tag{25}$$

Let X_1 and X_2 be distributed exponentially by parameters λ_1 and λ_2, respectively, that is $X_1 \sim E(\lambda_1)$, and $X_2 \sim E(\lambda_2)$. Hence, the probability of

non-conforming products is presented by:

(26)
$$P_L = 1-e^{-L_1/\lambda_1}+1-e^{-L_2/\lambda_2}-(1-e^{-L_1/\lambda_1})(1-e^{-L_2/\lambda_2})\Big[1+\theta e^{-L_1/\lambda_1-L_2/\lambda_2}\Big].$$

Based on the equation (5), P_L can be calculated as:

(27)
$$P_L = 1-e^{C_{L_1}-1}+1-e^{C_{L_2}-1}-(1-e^{C_{L_1}-1})(1-e^{C_{L_2}-1})\Big[1+\theta e^{C_{L_1}-1+C_{L_2}-1}\Big].$$

Set $e^{C_{L_1}-1} = x_1$ and $e^{C_{L_2}-1} = x_2$, so the equation (27) is simplified as the following;

(28) $$P_L = 2 - x_1 - x_2 - (1 - x_1)(1 - x_2) - \theta x_1 x_2 (1 - x_1)(1 - x_2).$$

Setting θ and threshold value for P_L, the probability of non-conforming products counter curve could be plotted. For instance, figures 1a and 1b depict the counter curves for $\theta = 0.3$ and some various threshold values of P_L, based on the equations (27) and (28), respectively. We call this plot as "probability of non-conforming plot". If the coordinate (C_{L_1}, C_{L_2}) and equivalently (x_1, x_2) falls in the right side of the curve, then the process will be considered as capable.

Tables 8-10 at the end of this paper, list various C_{L_1} and C_{L_2} values and the corresponding probability of non-conforming rate by setting $\theta = 0.3$. Since P_L depends in the same way on C_{L_1} and C_{L_2}, we remove the same values.

4. MLE of P_L

To obtain MLE of P_L, MLEs of two parameters λ_1 and λ_2 must first be obtained. The joint probability density function is derived from the equation 24, as:

(29) $$f_{X_1,X_2}(x_1, x_2) = f_{X_1}(x_1) f_{X_2}(x_2)\big[1 + \theta(1 - 2F_{X_1}(x_1))(1 - 2F_{X_2}(x_2))\big].$$

Since X_1 and X_2 follow exponential distribution, the joint probability density function can be written as follows;

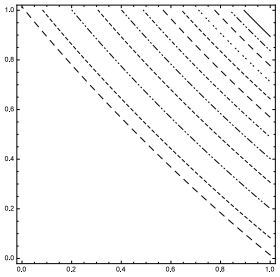
(30)
$$f_{X_1,X_2}(x_1, x_2, \lambda_1, \lambda_2) = \frac{1}{\lambda_1\lambda_2} e^{-x_1/\lambda_1 - x_2/\lambda_2}\big[1 + \theta(2e^{-x_1/\lambda_1} - 1)(2e^{-x_2/\lambda_2} - 1)\big].$$

Consequently, the likelihood function is given by:

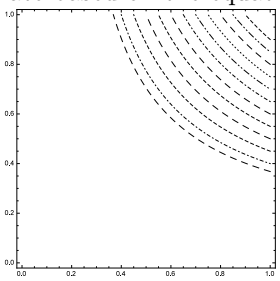
(31) $$L(\lambda_1, \lambda_2, x_1, x_2) = \frac{1}{\lambda_1\lambda_2} e^{-x_1/\lambda_1 - x_2/\lambda_2}\big[1+\theta(2e^{-x_1/\lambda_1} - 1)(2e^{-x_2/\lambda_2} - 1)\big].$$

Therefore, the log-likelihood fuction is presented by:

(32)
$$l(\lambda_1, \lambda_2, x_1, x_2) = -\ln\lambda_1 - \ln\lambda_2 - \frac{x_1}{\lambda_1} - \frac{x_2}{\lambda_2} + \ln\big[1+\theta(2e^{-x_1/\lambda_1} - 1)(2e^{-x_2/\lambda_2} - 1)\big].$$



(a) NC rate based on the equation (27)



(b) NC rate based on the equation (28)

FIGURE 1. Probability of NC products counter curves for $\theta = 0.3$ and various threshold values of P_L as 0.632, 0.60, 0.55, 0.50,0.45, 0.40, 0.35, 0.30, 0.25, 0.20, 0.15, and 0.10, from left to right

MLEs of λ_1 and λ_2 can be obtained by solving the following system of nonlinear equations;

$$\begin{aligned} \frac{x_1}{\lambda_1^2} - \frac{1}{\lambda_1} + \frac{2\theta x_1 e^{-x_1/\lambda_1}(2e^{-x_2/\lambda_2}-1)}{\lambda_1^2\big[1+\theta(2e^{-x_1/\lambda_1}-1)(2e^{-x_2/\lambda_2}-1)\big]} &= 0, \\ \frac{x_2}{\lambda_2^2} - \frac{1}{\lambda_2} + \frac{2\theta x_2 e^{-x_2/\lambda_2}(2e^{-x_1/\lambda_1}-1)}{\lambda_2^2\big[1+\theta(2e^{-x_1/\lambda_1}-1)(2e^{-x_2/\lambda_2}-1)\big]} &= 0. \end{aligned} \tag{33}$$

Based on a random sample gathered of size n, as (x_{11}, x_{21}), (x_{12}, x_{22}), ..., (x_{1n}, x_{2n}), the sample joint probabilty density function is as what follows;

$$\begin{aligned} f_{(\underline{X}_1,\underline{X}_2)}(\underline{x}_1,\underline{x}_2,\lambda_1,\lambda_2) &= \frac{1}{\lambda_1^n\lambda_2^n} e^{-\sum_{i=1}^n \frac{x_{1i}}{\lambda_1} - \sum_{i=1}^n \frac{x_{2i}}{\lambda_2}} \prod_{i=1}^n \Big[1+\theta(2e^{-\frac{x_{1i}}{\lambda_1}}-1) \\ &\times \quad (2e^{-\frac{x_{2i}}{\lambda_2}}-1)\Big]. \end{aligned} \tag{34}$$

Let

$$\mathbf{X} = \begin{pmatrix} X_1 \\ X_2 \end{pmatrix} = \begin{pmatrix} X_{11} & X_{12} & \dots & X_{1n} \\ X_{21} & X_{22} & \dots & X_{2n} \end{pmatrix},$$

and likely, the sample

$$\mathbf{x} = \begin{pmatrix} x_1 \\ x_2 \end{pmatrix} = \begin{pmatrix} x_{11} & x_{12} & \dots & x_{1n} \\ x_{21} & x_{22} & \dots & x_{2n} \end{pmatrix}.$$

In consequence of this, maximum likelihood estimations of λ_1 and λ_2 are obtained by solving the following system of nonlinear equations;

$$\begin{aligned} \sum_{i=1}^{n} \frac{x_{1i}}{\lambda_1^2} - \frac{n}{\lambda_1} + 2\theta \sum_{i=1}^{n} \frac{x_{1i} e^{-x_{1i}/\lambda_1}(2e^{-x_{2i}/\lambda_2} - 1)}{\lambda_1^2\big[1 + \theta(2e^{-x_{1i}/\lambda_1} - 1)(2e^{-x_{2i}/\lambda_2} - 1)\big]} &= 0, \\ \sum_{i=1}^{n} \frac{x_{2i}}{\lambda_1^2} - \frac{n}{\lambda_1} + 2\theta \sum_{i=1}^{n} \frac{x_{2i} e^{-x_{2i}/\lambda_1}(2e^{-x_{1i}/\lambda_2} - 1)}{\lambda_1^2\big[1 + \theta(2e^{-x_{1i}/\lambda_1} - 1)(2e^{-x_{2i}/\lambda_2} - 1)\big]} &= 0. \end{aligned} \tag{35}$$

In this paper, Newton's iterative method is used to solve the system of nonlinear equations (33) and (35) and get $\widehat{\lambda}_1$ and $\widehat{\lambda}_2$. Resulting from equation (26), $\widehat{P}_L$ is gain

(36)

$$\widehat{P}_L = 2 - e^{-L_1/\widehat{\lambda}_1} - e^{-L_2/\widehat{\lambda}_2} - (1 - e^{-L_1/\widehat{\lambda}_1})(1 - e^{-L_2/\widehat{\lambda}_2})\Big[1 + \theta e^{-L_1/\widehat{\lambda}_1 - L_2/\widehat{\lambda}_2}\Big],$$

Based on equation (27) and $\widehat{C}_{L_1} = 1 - L_1/\widehat{\lambda}_1$ and $\widehat{C}_{L_2} = 1 - L_2/\widehat{\lambda}_2$, $\widehat{P}_L$ can be presented by

$$\widehat{P}_L = 2 - e^{\widehat{C}_{L_1} - 1} - e^{\widehat{C}_{L_2} - 1} - (1 - e^{\widehat{C}_{L_1} - 1})(1 - e^{\widehat{C}_{L_2} - 1})\Big[1 + \theta e^{\widehat{C}_{L_1} + \widehat{C}_{L_2} - 2}\Big]. \tag{37}$$

To detect whether the process is capable or not, plot the coordinate $(\widehat{C}_{L_1}, \widehat{C}_{L_2})$ in the probability of non-conforming products' counter curve. If it falls on the right side of the counter plot of P_L, the process will be considered as capable and otherwise, it will be non-capable.

5. **Bootstrap Upper Confidence Bound of P_L**

When the theoretical distribution of a statistic of interest is complicated, bootstrap procedure is recommended. This method is a straightforward way, but computer-based method to derive estimates of standard errors and confidence intervals for complex estimators of complex parameters of the distribution. For more information, one can see Efron [6–9, 11], Efron and Tibshirani [10].

Bootstrap method is described as follows [4, 5, 28]. Suppose n data points $x_1, x_2, ..., x_n$ drawn from a distribution F, are available. An empirical bootstrap sample is a resample of the sample size n as $x_1^*, x_2^*, ..., x_n^*$. It should be thought so the latter as a sample of size n drawn from the empirical distribution F^*. For any statistic u computed from the original sample data, a statistic u^* can be defined by the same formula but computed instead using the resampled data. In other words, the bootstrap step is as the following;

- $x_1, x_2, ..., x_n$ is a data sample drawn from a distribution F.

- u is a statistic computed from the sample.
- F^* is the empirical distribution of the data (the resampling distribution).
- $x_1, x_2, ..., x_n$ is a resample of the data.
- u^* is the statistic computed from the resample.

Then, the bootstrap principle says that:

1. F^* is approximately equal to F.

2. The statistic u is well approximated by u^*.

3. The variation of u is well approximated by the variation of u^*.

This section provides upper confidence bounds (UCBs) of P_L based on four bootstrap methods. In addition, a simulation study is engaged to investigate and compared these upper bounds in terms of the criterion "relative coverage", which is defined as the ratio of coverage percentage to average length.

Let $(x_{11}, x_{21}), (x_{12}, x_{22}), ..., (x_{1n}, x_{2n})$ be a sample of size n taken from the process. MLE of the non-conforming rate is denoted by $\widehat{P}_L$. A bootstrap sample $(x^*_{11}, x^*_{21}), (x^*_{12}, x^*_{22}), ..., (x^*_{1n}, x^*_{2n})$, is a sample of size n drawn from the original sample with replacement. Based on the procedure explained in the previous section, the MLE of the non-conforming rate of this bootstrap sample, denoted by $\widehat{P}^*_L$, is calculated. Suppose this resampling process is repeated B times. Then, B bootatrsp estimates $\widehat{P}^*_{L_1}, \widehat{P}^*_{L_2}, ..., \widehat{P}^*_{L_B}$ is obtained from the bootstrap resamples. We call $\widehat{P}^*_{L_1}, \widehat{P}^*_{L_2}, ..., \widehat{P}^*_{L_B}$ the bootstrap distibution of $\widehat{P}_L$. These estimates could be ordered from the smallest to the largest, denoted by $\widehat{P}^*_{L_{(1)}}, \widehat{P}^*_{L_{(2)}}, ..., \widehat{P}^*_{L_{(B)}}$. Here are the bootstrap UCBs.

5.1. **Standard Bootstrap (SB) Upper Confidence Bound of P_L.** From the B bootstrap samples $\widehat{P}^*_{L_i}$, for $i = 1, 2, ..., B$, the sample average $\bar{P}^*_L$ is obtained as the following;

$$\bar{P}^*_L = \frac{\sum_{i=1}^{B} \widehat{P}^*_{L_i}}{B}. \tag{38}$$

Furtheremore, the sample standard deviation is calculated as:

$$S^*_{P_L} = \left[\frac{\sum_{i=1}^{B} (\widehat{P}^*_{L_i} - \bar{P}^*_L)^2}{B-1}\right]^{1/2}. \tag{39}$$

Set $T^*_i = (\widehat{P}^*_{L_i} - \bar{P}^*_L)/S^*_{P_L}$ for each bootstrap sample and order them from the smallest to the largest, as $T^*_{(1)}, T^*_{(2)}, ..., T^*_{(B)}$. Consequently, $100(1-\alpha)\%$ SB upper confidence bound of P_L is as what follows;

$$U_{SB} = \widehat{P}_L + T^*_{(B[1-\alpha])} S^*_{P_L}, \tag{40}$$

where, $T^*_{(B[1-\alpha])}$ is the $(B[1-\alpha])^{th}$ ordered T^*_is.

5.2. **Percentile Bootstrap (PB) Upper Confidence Bound of P_L.** From the ordered collection of $\widehat{P}^*_{L_{(i)}}$, for $i = 1, 2, ..., B$, the $100(1-\alpha)\%$ PB upper confidence bound of P_L is as;

$$U_{PB} = \widehat{P}^*_{L_{(B[1-\alpha])}}. \tag{41}$$

In fact, this upper bound is the $(B[1-\alpha])^{th}$ quantile value of the B bootstrap P^*_L estimates.

5.3. **Biased Corrected Percentile Bootstrap (BCPB) Upper Confidence Bound of P_L.** One approach for improvement of percentile method is to correct for bias of the bootstrap parameter estimators, by the factor z_0 as the proportion of the bootstrap estimates less than the original parameter. Efron [8] used the standard normal distribution function in this method.

The bootstrap distibution $\widehat{P}^*_{L_1}, \widehat{P}^*_{L_2}, ..., \widehat{P}^*_{L_B}$ may be shifted higher or lower than would be expected. Thus, a third method is designed to correct this potential bias. First, calculate $p_0 = \sum_{i=1}^{B} I\big(\widehat{P}^*_{L_i} < \widehat{P}_L\big)/B$ to estimate the probability $P_0 = P_r(P^*_L < P_L)$, where

$$I(y) = \begin{cases} 1 & y > 0, \\ 0 & \text{y} \leq 0. \end{cases}$$

Then, define $z_0 = \Phi^{-1}(p_0)$ for estimating $Z_0 = \Phi^{-1}(P_0)$, where $\Phi(.)$ is the cumulative distribution function of standard normal and $\Phi^{-1}(.)$ is its inverse. Let $p_u = \Phi(2z_0 + z_\alpha)$, where z_α is the upper α quantile of standard normal distribution. Therefore, from the ordered collection of $\widehat{P}^*_{L_{(i)}}$, for $i = 1, 2, ..., B$, the $100(1-\alpha)\%$ BCPB upper confidence bound of P_L can be obtained by

$$U_{BCPB} = \widehat{P}^*_{L_{(Bp_u)}}, \tag{42}$$

$\widehat{P}^*_{L_{(Bp_u)}}$ is the $(Bp_u)^{th}$ quantile value of the B bootstrap $\widehat{P}^*_L$ estimates.

5.4. **Bootstrap Pivotal (BP) Upper Confidence Bound of P_L.** The BP method for interval estimation could be developed by combining the order statistics of the bootstrap distribution and the pivotal interval estimation technique. Set the pivot $W = \widehat{P}_L - P_L$, and let H be the cumulative distribution function of W, that is

$$H(w) = P_r(W \leq w). \tag{43}$$

Furthereore, H^{-1} is the inverse of H. Therefore,

$$\begin{aligned} P_r\big(\widehat{P}_L - P_L > H^{-1}(\alpha)\big) &= 1 - P_r\big(\widehat{P}_L - P_L \leq H^{-1}(\alpha)\big) = 1 - P_r\big(W \leq H^{-1}(\alpha)\big) \\ &= 1 - H\big(H^{-1}(\alpha)\big) = 1 - \alpha. \end{aligned} \tag{44}$$

Hence,

$$P_r\big(P_L < \widehat{P}_L - H^{-1}(\alpha)\big) = 1 - \alpha. \tag{45}$$

Then, $\widehat{P}_L - H^{-1}(\alpha)$ is the $100(1-\alpha)\%$ BP upper confidence bound of P_L. Obviously, this bound depends on an unknown cumulative distribution function, H, that should be estimated, so the bootstrap estimation of H can be obtained by

$$\widehat{H}(w) = \frac{\sum_{i=1}^{B} I(W_i \leq w)}{B}, \tag{46}$$

where $W_i = \widehat{P}^*_{L_i} - \widehat{P_L}$, for $i = 1, 2, ..., B$.

Therefore, $H^{-1}(\alpha)$ is estimated as $\widehat{H}^{-1}(\alpha) = \widehat{P}^*_{L_{(B\alpha)}} - \widehat{P}_L$. In consequence, $\widehat{P}_L - H^{-1}(\alpha) = 2\widehat{P}_L - \widehat{P}^*_{L_{(B\alpha)}}$. Hence, the $100(1-\alpha)\%$ BP upper confidence bound of P_L is as the folowing;

$$U_{BP} = 2\widehat{P}_L - \widehat{P}^*_{L_{(B\alpha)}}, \tag{47}$$

$\widehat{P}^*_{L_{(B\alpha)}}$ is the $(B\alpha)^{th}$ quantile value of the B bootstrap $\widehat{P}^*_L$ estimates.

It should be noted that a rough minimum of 1000 bootstrap samples are usually sufficient to compute accurate confidence interval estimates [10].

5.5. **Simulation Study.** In order to investigate the performance of the four bootstrap UCBs, a series of simulations are undertaken. Four levels of P_L and six levels of sample size are considered in simulation procedure. Suppose the lifetime of a process products relates to two characteristics by $L_1 = 2.5$ and $L_2 = 1$, which are distributed as bivariate exponential by dependence structure based on FGM copula model with $\theta = 0.3$. Based on the P_L and the corresponding sample size n, a random sample is simulated. Then, 1000 parametric bootstrap resamples of size n are taken and the 95% UCBs of P_L is constructed based on these four methods.

A computer program in Mathematica is coded to run the simulation. To compare the performance of the four UCBs, The criterion "relative coverage"is employed which is defined as the ratio of coverage percentage to average length of confidence bound. To compute these criteria, the single bootstrap simulation procedure is replicated for 100 times. Results are presented in tables 2 and 3.

The simulations show that for small sample sizes, BP method reaches the best confidence upper bound of P_L and for middle sample sizes, both SB and BP methods are good. In addition, for large sample sizes, SB method gives the best confidence upper bound.

6. Hypothesis Testing for P_L

One of the main problem in statistical inference concerns to test the hypotheses about population parameters. To obtain an appropriate rule, a hypothesis test with the null hypothesis $H_0 : P_L \geq p_0$ is considered versus the alternative one $H_1 : P_L < p_0$. The null hypothesis is equivalent to "the process is non-capable"and the alternative one is equivalent to "the process is capable".

TABLE 2. Coverage percentages (CP), average lengths (AL) and relative coverages (RC) for 95% UCBs of P_L

Sample size	UCB	$P_L = 0.001$			$P_L = 0.002$		
		CP	AL	RC	CP	AL	RC
5	SB	1.00	0.00266	376.260	1.00	0.00542	184.565
	PB	0.96	0.00322	298.382	0.95	0.00700	135.679
	BCPB	0.72	0.00182	395.872	0.85	0.00494	172.145
	BP	0.68	0.00109	**622.578**	0.58	0.00194	**299.253**
10	SB	1.00	0.00182	547.802	1.00	0.00357	**280.227**
	PB	1.00	0.00197	508.539	1.00	0.00440	227.166
	BCPB	1.00	0.00168	595.161	0.5	0.00224	222.866
	BP	1.00	0.00134	**743.360**	0.5	0.00201	248.620
20	SB	1.00	0.00141	**709.246**	1.00	0.00282	**353.868**
	PB	0.96	0.00147	651.993	0.99	0.00311	318.653
	BCPB	0.9	0.00137	655.997	0.84	0.00256	328.109
	BP	0.88	0.00123	**714.680**	0.81	0.00230	**351.554**
30	SB	1.00	0.00125	**798.974**	1.00	0.00251	**398.365**
	PB	1.00	0.00140	712.770	0.96	0.00276	347.261
	BCPB	0.65	0.00110	589.096	0.73	0.00226	323.295
	BP	0.58	0.00102	568.639	0.68	0.00211	322.033
40	SB	1.00	0.00125	**798.730**	1.00	0.00238	**420.088**
	PB	0.97	0.00133	730.029	0.97	0.00260	372.427
	BCPB	0.81	0.00116	695.747	0.69	0.00217	318.328
	BP	0.80	0.00112	713.543	0.64	0.00205	311.381
50	SB	1.00	0.00120	**832.44**	1.00	0.00246	**406.796**
	PB	0.92	0.00126	727.297	0.92	0.00255	360.280
	BCPB	0.81	0.00112	723.285	0.89	0.00234	380.599
	BP	0.79	0.00109	722.967	0.87	0.00228	381.913

The significance level is the probability to reject the null hypothesis when it is true, equivalently, the probability to deem the process capable when it is not. $p - value$ is the probability of obtaining an effect at least as extreme as the one in sample data, assuming the truth of the null hypothesis. There is a threshold value α, that $p - value$ is measured against it. A small $p - value$, typically less than α, indicates strong evidence against the null hypothesis, so the null hypothesis is rejected.

It has become commonplace in the statistical analysis to use Monte Carlo procedure for calculating empirical $p - value$. The reasons for this include the following: (1) many test statistics do not have a standard asymptotic distribution; (2) even if a standard asymptotic distribution does exist, it may not be reliable in realistic sample sizes; and (3) calculation of the exact sampling distribution through exhaustive enumeration of all possible samples may be too computationally intensive to be feasible. In contrast, Monte Carlo method

TABLE 3. Coverage percentages (CP), average lengths (AL) and relative coverages (RC) for 95% UCBs of P_L

Sample size	UCB	$P_L = 0.003$			$P_L = 0.004$		
		CP	AL	RC	CP	AL	RC
5	SB	1.00	0.00762	131.297	1.00	0.00988	101.195
	PB	0.99	0.00974	101.665	0.98	0.00121	81.164
	BCPB	0.75	0.00966	77.621	0.81	0.00886	91.384
	BP	0.59	0.00308	**191.756**	0.68	0.00440	**154.381**
10	SB	1.00	0.00514	194.704	1.00	0.00662	150.979
	PB	0.99	0.00582	170.081	0.99	0.00762	129.864
	BCPB	0.89	0.00445	200.164	0.81	0.00578	140.133
	BP	0.87	0.00360	**241.598**	0.76	0.00451	**168.404**
20	SB	1.00	0.00428	**233.375**	1.00	0.00552	**181.082**
	PB	0.96	0.00456	210.384	0.95	0.00609	156.076
	BCPB	0.94	0.00416	225.868	0.82	0.00502	163.338
	BP	0.92	0.00364	**253.016**	0.78	0.00449	**173.691**
30	SB	1.00	0.00394	**253.768**	1.00	0.00523	**191.013**
	PB	0.97	0.00420	231.203	0.97	0.00545	177.898
	BCPB	0.88	0.00366	240.693	0.91	0.00503	180.728
	BP	0.87	0.00346	**251.498**	0.91	0.00474	**192.156**
40	SB	1.00	0.00356	**281.133**	1.00	0.00493	**202.994**
	PB	0.94	0.00398	236.049	0.97	0.00522	185.846
	BCPB	0.55	0.00313	175.871	0.83	0.00462	179.530
	BP	0.51	0.00296	172.145	0.81	0.00443	182.825
50	SB	1.00	0.00356	**280.753**	1.00	0.00490	**203.989**
	PB	0.98	0.00384	255.356	0.97	0.00510	190.121
	BCPB	0.81	0.00328	246.563	0.88	0.00472	186.276
	BP	0.79	0.00316	249.967	0.86	0.00453	189.679

could be used to obtain an empirical $p - value$ that approximates the exact $p - value$ without relying on asymptotic distributional theory or exhaustive enumeration.

In this paper, empirical $p - value$ is obtained based on Monte Carlo simulation method because of complexity of obtaining cumulative distribution function. The procedure is as what follows;

First, take a sample of size n from the process products and calculate $\widehat{\theta} = 9\tau/2$. Then, calculate $\widehat{\lambda}_1$ and $\widehat{\lambda}_2$ based on the system of non-linear equations (35) and then $\widehat{P}_L$ according to the equations (36) or (37), name it $\widehat{P}_{L_0}$. Therefore, to make a decision, follow the following steps;

- Step 1: Detect the threshold value α of significance level for the test.
- Step 2: Specify λ_1 and λ_2 according to $P_L = p_0$.
- Step 3: Generate a sample of size n from bivariate exponential distribution based on FGM copula model according to λ_1, λ_2, and $\widehat{\theta}$.

• Step 4: Calculate $\widehat{\lambda}_1$ and $\widehat{\lambda}_2$ and then, $\widehat{P}_L$.

• Step 5: Replicate steps 1 to 4 for m times.

• Step 6: Count the number of replications that produce a test statistic $\widehat{P}_L$ less than $\widehat{P}_{L_0}$ and denote it by r.

• Step 7: The estimated $p-value$ is obtained as $\hat{p} = r/n$. If $\hat{p}$ is less than α, then the null hypothesis is rejected and concluded that the process is capable, otherwise the process is supposed to be non-capable.

It should be noted that, there are several choices of the null hypothesis for λ_1 and λ_2 equivalent to the null hypothesis for P_L, and the choice depends on economical reasons or etc.

7. Numerical Examples

In this section, some data are generated to demonstrate the effectiveness and performance of the proposed method. Suppose the lifetime of a manufacturing products counts on two characteristics in which are distributed as bivariate exponential distribution based on FGM copula model. A product is supposed to be conformed if its first characteristic value is greater than 2.5 and the second one is greater than 1. Here, two different datasets of this process are presented in two examples.

Example 7.1. *Table 4 presents a sample of size 50 from the process. To show how one can detect bivariate distribution of this type, the procedure is explained here. First, to detect the marginal distribution of each variable, histograms were plotted and it was seemed that two variables data follow exponential distribution. Then, goodness of fit tests were done based on the one-sample Kolmogorov-Smirnov test, for each variable data. It was concluded that the two marginal variables are distributed as exponential.*

Now, it is needed to find bivariate distribution. First, we draw the scatter plot of two variables data, depicted in Figure 2a. Kendall tau correlation coefficient is obtained as $\tau = 0.104$ *and then, the dependence parameter is calculated as* $\widehat{\theta} = 0.47$. *Therefore, based on the system of non-linear equations* (35)*, MLEs of the parameters are obtained as* $\widehat{\lambda}_1 = 10.08$, *and* $\widehat{\lambda}_2 = 6.62$.

Applying Johnson's algorithm presented in subsection 2.3, we generate 500 data of FGM distribution of this estimated θ. *Inversing the distribution data as* $x_1 = -\lambda_1 \log(1-u)$, *and* $x_2 = -\lambda_2 \log(1-v)$ *provides 500 bivariate data* (x_1, x_2) *from bivariate exponential distribution based on FGM copula model. Now we depict the scatter plot of the empirical distribution values of the original data along with the data generated based on the algorithm in Figure 2b. It shows that the empirical distribution is similar to bivariate exponential distribution based on FGM copula model distribution.*

For detecting dependence, two graphical tools Chi-plot and K-plot, discussed in subsection 2.4, are drawn and presented in figures 2c and 2d. Both plots show weak and positive correlation between two variables. So far, the above

tools confirm that the data dependence follows FGM copula model, to some extent.

Now, goodness of fit test, explained in subsection 2.5, is used to detect whether the structure of the data is approximately modelled by a bivariate exponential distribution based on FGM copula model or not. Cramér-von Mises statistic is calculated as 0.024*, with* $p-value = 0.721$*. Therefore, there is no reason to reject the null hypothesis, so it is concluded that the data are followed bivariate exponential distribution based on FGM copula model.*

Two lifetime indices are obtained as $\widehat{C}_{L_1} = 0.75$*, and* $\widehat{C}_{L_2} = 0.85$*. Therefore, non-conforming rate is calculated* $\widehat{P}_L = 0.32$*.*

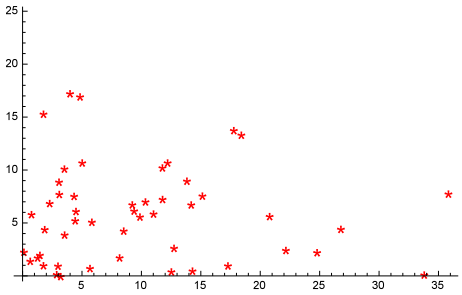
Figures 3a and 3b represent the location of the coordinate $(\widehat{C}_{L_1}, \widehat{C}_{L_2})$ *along with the counter plots of* P_L *for two values 0.40, and 0.20, respectively. The figures show that for the threshold value 0.40 the process is capable, and for the threshold value 0.20 the process is non-capable.*

TABLE 4. Sample data for Example 7.1

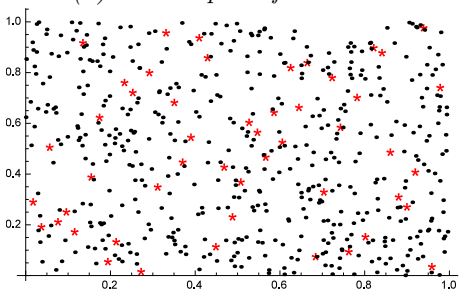
case	*sample data*	*case*	*sample data*	*case*	*sample data*
1	*(1.8374, 15.3584)*	*18*	*(0.1915, 2.3195)*	*35*	*(22.2368, 2.4895)*
2	*(4.9148, 16.990)*	*19*	*(35.9157, 7.8147)*	*36*	*(3.5985, 10.1795)*
3	*(3.6148, 3.9442)*	*20*	*(5.7512, 0.7842)*	*37*	*(26.8663, 4.4837)*
4	*(11.0975, 5.9302)*	*21*	*(9.4647, 6.2112)*	*38*	*(8.2414, 1.7860)*
5	*(5.0959, 10.7524)*	*22*	*(12.5995, 0.4629)*	*39*	*(9.9552, 5.6460)*
6	*(33.8794, 0.1679)*	*23*	*(24.8616, 2.2780)*	*40*	*(9.3107, 6.7939)*
7	*(18.4876, 13.3761)*	*24*	*(1.5364, 2.0296)*	*41*	*(10.4176, 7.0716)*
8	*(17.8537, 13.8099)*	*25*	*(11.8459, 10.2839)*	*42*	*(3.0580, 1.0076)*
9	*(0.8279, 5.8745)*	*26*	*(8.5884, 4.3206)*	*43*	*(20.8672, 5.6898)*
10	*(1.9393, 4.4589)*	*27*	*(1.8354, 1.0490)*	*44*	*(2.9477, 0.2033)*
11	*(3.1438, 8.9403)*	*28*	*(3.1676, 7.7788)*	*45*	*(4.5724, 6.1725)*
12	*(12.8232, 2.6902)*	*29*	*(4.5049, 5.2956)*	*46*	*(2.3578, 6.9221)*
13	*(4.0707, 17.2908)*	*30*	*(17.3604, 1.0282)*	*47*	*(3.2912, 0.0206)*
14	*(14.3766, 0.5396)*	*31*	*(15.2105, 7.6248)*	*48*	*(0.7223, 1.4676)*
15	*(13.9071, 9.0327)*	*32*	*(12.2828, 10.7518)*	*49*	*(4.4124, 7.5971)*
16	*(15.9079, 5.1558)*	*33*	*(1.3453, 1.7771)*	*50*	*(11.8578, 7.3057)*
17	*(30.6060, 46.0686)*	*34*	*(14.2680, 6.7872)*		

Now, the null hypothesis $H_0 : \ P_L \geq 0.30$ *versus the alternative one* $H_1 : P_L < 0.30$ *is tested. Table 5 shows some pairs* (λ_1, λ_2) *as well as* (C_{L_1}, C_{L_2}) *concerned with* $P_L = 0.30$*. As mentioned in section 6, for each pair* (λ_1, λ_2)*, 1000 samples of size 50 is generated and calculated the simulated* $p-values$*, presented in Table 5. In order to limit the size of the table, all numbers are approximated to two decimal places.*

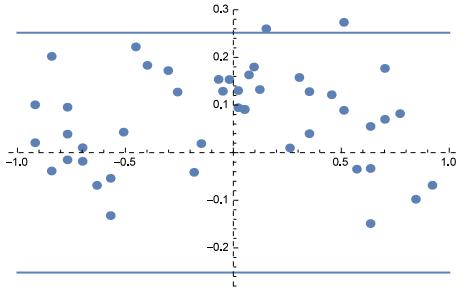
Table 5 shows that the simulated $p-values$ *for all considered cases are greater than the significance level 0.05, so there is no reason to reject the null*



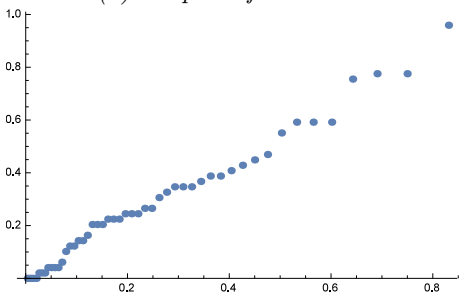
(a) Scatter plot of the data



(b) Empirical distribution plot of the data along with the simulated data

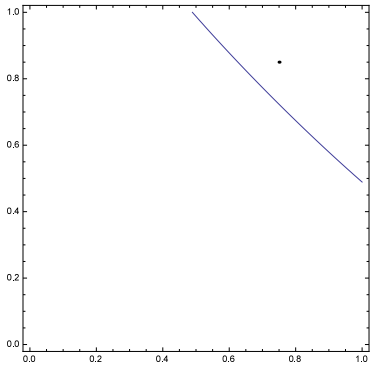


(c) Chiplot of the data

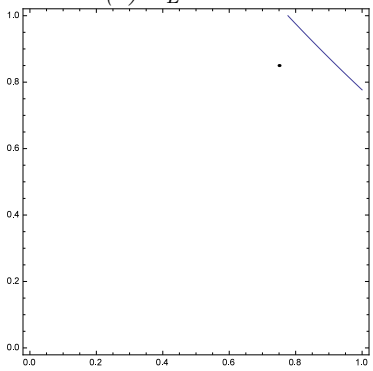


(d) Kplot of the data

FIGURE 2. Plots assosiated with the data in Example 7.1



(a) $P_L = 0.40$



(b) $P_L = 0.20$

FIGURE 3. Coordinate $(\widehat{C}_{L_1}, \widehat{C}_{L_2})$ of Example 7.1 corresponds to the counter curve of P_L

hypothesis. Therefore, the process is supposed to be non-capable. Furthermore, 95% SB upper confidence bound for P_L is obtained as 0.363.

Example 7.2. *Table 6 presents a sample of size 10 from the process. Kendall tau correlation coefficient is obtained as $\tau = 0.2$, so the dependence parameter is calculated as $\widehat{\theta} = 0.9$. Therefore, based on the system of non-linear equations* (35)*, MLEs of the parameters are gained as $\widehat{\lambda}_1 = 1139.51$, and $\widehat{\lambda}_2 = 850.32$. Such as the previous example, all plots for detecting the dependence structure are drawn and goodness of fit test is done, which is not presented here due to lack of space. Results show that the data follow bivariate exponential distribution based on FGM copula model. Moreover, two lifetime capability indices are calculated as $\widehat{C}_{L_1} = 0.9978$, and $\widehat{C}_{L_2} = 0.9988$. Hence, $\widehat{P}_L = 0.00336$.*

Figures 4a and 4b show the location of the coordinate $(\widehat{C}_{L_1}, \widehat{C}_{L_2})$ along with the counter plots of P_L for two values 0.00001, and 0.05, respectively. It is seen

TABLE 5. Simulated $p-values$ for various values of (C_{L_1}, C_{L_2}) as well as (λ_1, λ_2) for Example 7.1

case	(C_{L_1}, C_{L_2})	(λ_1, λ_2)	*Simulated* $p-value$
1	*(0.66, 0.98)*	*(7.35, 50.00)*	*0.662*
2	*(0.68, 0.96)*	*(7.81, 25.00)*	*0.744*
3	*(0.70, 0.94)*	*(8.33, 16.67)*	*0.736*
4	*(0.72, 0.92)*	*(8.93, 11.11)*	*0.683*
5	*(0.74, 0.89)*	*(9.61, 9.09)*	*0.720*
6	*(0.76, 0.87)*	*(10.42, 7.69)*	*0.736*
7	*(0.78, 0.85)*	*(11.36, 6.67)*	*0.712*
8	*(0.80, 0.83)*	*(12.50, 5.88)*	*0.742*
9	*(0.82, 0.81)*	*(13.89, 5.26)*	*0.721*
10	*(0.84, 0.79)*	*(15.62, 4.76)*	*0.766*
11	*(0.86, 0.77)*	*(17.86, 4.35)*	*0.720*
12	*(0.88, 0.75)*	*(20.83, 4.00)*	*0.724*
13	*(0.90, 0.73)*	*(25.00, 3.70)*	*0.716*
14	*(0.92, 0.71)*	*(31.25, 3.45)*	*0.716*
15	*(0.94, 0.69)*	*(41.67, 3.33)*	*0.753*
16	*(0.96, 0.68)*	*(62.50, 3.12)*	*0.720*
17	*(0.98, 0.66)*	*(125.00, 2.94)*	*0.696*

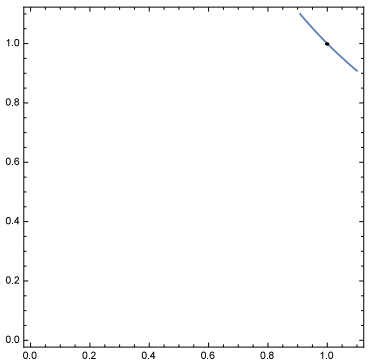
that for the threshold value 0.00001, the process is supposed to be non-capable, and for 0.05, it is supposed to be capable.

TABLE 6. Sample data for Example 7.2

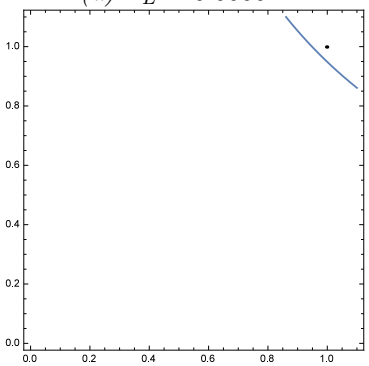
case	*sample data*	*case*	*sample data*
1	*(1296.6400, 258.3560)*	*6*	*(1655.8600, 1073.9100)*
2	*(2334.3900, 99.5846)*	*7*	*(1179.4200, 2520.5300)*
3	*(8.2788, 90.4069)*	*8*	*(772.0810,1305.8100)*
4	*(1965.7300, 2176.5700)*	*9*	*(488.8650, 120.1110)*
5	*(724.0110, 1038.5800)*	*10*	*(1191.7300, 623.7290)*

Now, it is desirable to test the null hypothesis $H_0 : P_L \geq 0.005$ *versus the alternative one* $H_1 : P_L < 0.005$. *Table 7 shows some pairs of* (λ_1, λ_2) *as well as* (C_{L_1}, C_{L_2}) *in accordance with* $P_L = 0.005$. *For each pair of* (λ_1, λ_2), *1000 samples of size 10 are simulated and the* $p-values$ *are obtained, as presented in Table 7.*

It is seen that for all considered cases, the simulated $p-values$ *are less than the significance level, 0.05, so the null hypothesis is rejected. Therefore,*



(a) $P_L = 0.00001$



(b) $P_L = 0.05$

FIGURE 4. Coordinate $(\widehat{C}_{L_1}, \widehat{C}_{L_2})$ of Example 7.2 corresponds to the counter curve of P_L

the process is capable. In addition, 95% BP upper confidence bound for P_L is obtained as 0.00461.

8. **Concluding Remarks**

The present paper is concerned with the processes that the products' lifetime follows bivariate exponential distribution based on FGM copula model. Since reduction of non-conforming products is an original key for maintaining competitiveness in industries, the probability of non-conforming products, P_L, was studied.

Furthermore, four bootstrap methods SB, PB, BCPB and BP were engaged to present upper confidence bound for P_L. Simulation study was applied to evaluate the performance of these bounds in terms of relative coverage. Results showed that for small sample sizes, BP method performs the best, for

TABLE 7. Simulated $p-values$ for various values of (C_{L_1}, C_{L_2}) as well as (λ_1, λ_2) for Example 7.2

case	(C_{L_1}, C_{L_2})	(λ_1, λ_2)	*Simulated* $p-value$
1	*(0.9958, 0.9991)*	*(600, 1177)*	*0.036*
2	*(0.9959, 0.9991)*	*(610, 1089)*	*0.029*
3	*(0.9961, 0.9988)*	*(650, 854)*	*0.033*
4	*(0.9963, 0.9987)*	*(680, 745)*	*0.027*
5	*(0.9964, 0.9985)*	*(700, 692)*	*0.025*
6	*(0.9968, 0.9982)*	*(780, 551)*	*0.025*
7	*(0.9969, 0.9981)*	*(800, 528)*	*0.017*
8	*(0.9971, 0.9979)*	*(850, 481)*	*0.033*
9	*(0.9972, 0.9977)*	*(900, 446)*	*0.029*
10	*(0.9973, 0.9977)*	*(930, 429)*	*0.013*

middle sample sizes, both SB and BP methods perform better than the other competitors and,for large sample sizes, SB has the best performance.

On the other hand, some managers tend to determine whether the non-conforming products adhere to the required level or not. For this purpose, Monte Carlo simulation scheme was applied to do hypothesis testing on P_L.

In this paper, the new index was derived under the assumption that the amount of all parameters and variables were presented as crisp values. In real world, in most processes, data and information possess non-statistical uncertainties, so fuzzy set theory should be employed. We will investigate this subject in the future inquiries.

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TABLE 8. Values of C_{L_1} and C_{L_2} along with the corresponding probability of NC products

C_{L_1}	C_{L_2}	P_L	C_{L_1}	C_{L_2}	P_L	C_{L_1}	C_{L_2}	P_L	C_{L_1}	C_{L_2}	P_L
-3.00	-3.00	0.9996	-2.50	0.40	0.9813	-1.50	0.00	0.9645	-1.00	0.85	0.8793
-3.00	-2.50	0.9993	-2.50	0.45	0.9804	-1.50	0.05	0.9629	-1.00	0.90	0.8745
-3.00	-2.00	0.9988	-2.50	0.50	0.9796	-1.50	0.10	0.9612	-1.00	0.95	0.8696
-3.00	-1.50	0.9981	-2.50	0.55	0.9787	-1.50	0.15	0.9594	-1.00	1.00	0.8647
-3.00	-1.00	0.9969	-2.50	0.60	0.9778	-1.50	0.20	0.9575	-0.50	-0.50	0.9412
-3.00	-0.50	0.9950	-2.50	0.65	0.9769	-1.50	0.25	0.9556	-0.50	0.00	0.9058
-3.00	0.00	0.9920	-2.50	0.70	0.9759	-1.50	0.30	0.9536	-0.50	0.05	0.9014
-3.00	0.05	0.9916	-2.50	0.75	0.9750	-1.50	0.35	0.9515	-0.50	0.10	0.8967
-3.00	0.10	0.9913	-2.50	0.80	0.9740	-1.50	0.40	0.9494	-0.50	0.15	0.8919
-3.00	0.15	0.9909	-2.50	0.85	0.9730	-1.50	0.45	0.9471	-0.50	0.20	0.8869
-3.00	0.20	0.9904	-2.50	0.90	0.9719	-1.50	0.50	0.9448	-0.50	0.25	0.8816
-3.00	0.25	0.9900	-2.50	1.00	0.9698	-1.50	0.55	0.9424	-0.50	0.30	0.8762
-3.00	0.30	0.9896	-2.00	-2.00	0.9968	-1.50	0.60	0.9400	-0.50	0.35	0.8705
-3.00	0.35	0.9891	-2.00	-1.50	0.9948	-1.50	0.65	0.9375	-0.50	0.40	0.8647
-3.00	0.40	0.9886	-2.00	-1.00	0.9916	-1.50	0.70	0.9348	-0.50	0.45	0.8586
-3.00	0.45	0.9881	-2.00	-0.50	0.9864	-1.50	0.75	0.9322	-0.50	0.50	0.8523
-3.00	0.50	0.9876	-2.00	0.00	0.9784	-1.50	0.80	0.9294	-0.50	0.55	0.8457
-3.00	0.55	0.9871	-2.00	0.05	0.9774	-1.50	0.85	0.9266	-0.50	0.60	0.8389
-3.00	0.60	0.9865	-2.00	0.10	0.9763	-1.50	0.90	0.9238	-0.50	0.65	0.8319
-3.00	0.65	0.9860	-2.00	0.15	0.9752	-1.50	0.95	0.9209	-0.50	0.70	0.8247
-3.00	0.70	0.9854	-2.00	0.20	0.9741	-1.50	1.00	0.9179	-0.50	0.75	0.8173
-3.00	0.75	0.9848	-2.00	0.25	0.9729	-1.00	-1.00	0.9776	-0.50	0.80	0.8096
-3.00	0.80	0.9842	-2.00	0.30	0.9717	-1.00	-0.50	0.9637	-0.50	0.85	0.8017
-3.00	0.85	0.9836	-2.00	0.35	0.9705	-1.00	0.00	0.9420	-0.50	0.90	0.7936
-3.00	0.90	0.9830	-2.00	0.40	0.9692	-1.00	0.05	0.9393	-0.50	0.95	0.7853
-3.00	0.95	0.9823	-2.00	0.45	0.9678	-1.00	0.10	0.9365	-0.50	1.00	0.7769
-3.00	1.00	0.9817	-2.00	0.50	0.9664	-1.00	0.15	0.9336	0.00	0.00	0.8484
-2.50	-2.50	0.9988	-2.00	0.55	0.9650	-1.00	0.20	0.9305	0.00	0.05	0.8412
-2.50	-2.00	0.9981	-2.00	0.60	0.9635	-1.00	0.25	0.9273	0.00	0.10	0.8336
-2.50	-1.50	0.9969	-2.00	0.65	0.9620	-1.00	0.30	0.9240	0.00	0.15	0.8257
-2.50	-1.00	0.9949	-2.00	0.70	0.9604	-1.00	0.35	0.9206	0.00	0.20	0.8174
-2.50	-0.50	0.9917	-2.00	0.75	0.9588	-1.00	0.40	0.9170	0.00	0.25	0.8088
-2.50	0.00	0.9868	-2.00	0.80	0.9571	-1.00	0.45	0.9133	0.00	0.30	0.7999
-2.50	0.05	0.9862	-2.00	0.85	0.9554	-1.00	0.50	0.9095	0.00	0.35	0.7905
-2.50	0.10	0.9856	-2.00	0.90	0.9537	-1.00	0.55	0.9056	0.00	0.40	0.7808
-2.50	0.15	0.9849	-2.00	0.95	0.9520	-1.00	0.60	0.9015	0.00	0.45	0.7707
-2.50	0.20	0.9843	-2.00	1.00	0.9502	-1.00	0.65	0.8973	0.00	0.50	0.7602
-2.50	0.25	0.9835	-1.50	-1.50	0.9916	-1.00	0.70	0.8930	0.00	0.55	0.7493
-2.50	0.30	0.9828	-1.50	-1.00	0.9862	-1.00	0.75	0.8886	0.00	0.60	0.7380
-2.50	0.35	0.9820	-1.50	-0.50	0.9778	-1.00	0.80	0.8840	0.00	0.65	0.7262

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TABLE 9. Values of C_{L_1} and C_{L_2} along with the corresponding probability of NC products

C_{L_1}	C_{L_2}	P_L	C_{L_1}	C_{L_2}	P_L	C_{L_1}	C_{L_2}	P_L	C_{L_1}	C_{L_2}	P_L
0.00	0.70	0.7141	0.10	0.70	0.6849	0.20	0.90	0.5870	0.35	0.60	0.6335
0.00	0.75	0.7015	0.10	0.75	0.6709	0.20	0.95	0.5691	0.35	0.65	0.6165
0.00	0.80	0.6885	0.10	0.80	0.6564	0.20	1.00	0.5507	0.35	0.70	0.5989
0.00	0.85	0.6750	0.10	0.85	0.6414	0.25	0.25	0.7582	0.35	0.75	0.5805
0.00	0.90	0.6611	0.10	0.90	0.6259	0.25	0.30	0.7467	0.35	0.80	0.5615
0.00	0.95	0.6468	0.10	0.95	0.6099	0.25	0.35	0.7347	0.35	0.85	0.5417
0.00	1.00	0.6321	0.10	1.00	0.5934	0.25	0.40	0.7222	0.35	0.90	0.5212
0.05	0.05	0.8336	0.15	0.15	0.7993	0.25	0.45	0.7092	0.35	0.95	0.4999
0.05	0.10	0.8256	0.15	0.20	0.7898	0.25	0.50	0.6957	0.35	1.00	0.4780
0.05	0.15	0.8173	0.15	0.25	0.7798	0.25	0.55	0.6815	0.40	0.40	0.6804
0.05	0.20	0.8086	0.15	0.30	0.7694	0.25	0.60	0.6668	0.40	0.45	0.6652
0.05	0.25	0.7996	0.15	0.35	0.7586	0.25	0.65	0.6515	0.40	0.50	0.6494
0.05	0.30	0.7902	0.15	0.40	0.7472	0.25	0.70	0.6357	0.40	0.55	0.6329
0.05	0.35	0.7804	0.15	0.45	0.7355	0.25	0.75	0.6192	0.40	0.60	0.6157
0.05	0.40	0.7701	0.15	0.50	0.7232	0.25	0.80	0.6022	0.40	0.65	0.5978
0.05	0.45	0.7595	0.15	0.55	0.7105	0.25	0.85	0.5845	0.40	0.70	0.5792
0.05	0.50	0.7484	0.15	0.60	0.6973	0.25	0.90	0.5661	0.40	0.75	0.5598
0.05	0.55	0.7370	0.15	0.65	0.6835	0.25	0.95	0.5472	0.40	0.80	0.5396
0.05	0.60	0.7250	0.15	0.70	0.6693	0.25	1.00	0.5276	0.40	0.85	0.5187
0.05	0.65	0.7127	0.15	0.75	0.6545	0.30	0.30	0.7347	0.40	0.90	0.4970
0.05	0.70	0.6998	0.15	0.80	0.6392	0.30	0.35	0.7220	0.40	0.95	0.4745
0.05	0.75	0.6865	0.15	0.85	0.6233	0.30	0.40	0.7089	0.40	1.00	0.4512
0.05	0.80	0.6728	0.15	0.90	0.6069	0.30	0.45	0.6952	0.45	0.45	0.6493
0.05	0.85	0.6586	0.15	0.95	0.5900	0.30	0.50	0.6809	0.45	0.50	0.6326
0.05	0.90	0.6439	0.15	1.00	0.5726	0.30	0.55	0.6660	0.45	0.55	0.6152
0.05	0.95	0.6288	0.20	0.20	0.7797	0.30	0.60	0.6506	0.45	0.60	0.5971
0.05	1.00	0.6133	0.20	0.25	0.7693	0.30	0.65	0.6345	0.45	0.65	0.5782
0.10	0.10	0.8172	0.20	0.30	0.7583	0.30	0.70	0.6177	0.45	0.70	0.5585
0.10	0.15	0.8085	0.20	0.35	0.7469	0.30	0.75	0.6003	0.45	0.75	0.5381
0.10	0.20	0.7994	0.20	0.40	0.7350	0.30	0.80	0.5823	0.45	0.80	0.5168
0.10	0.25	0.7899	0.20	0.45	0.7226	0.30	0.85	0.5636	0.45	0.85	0.4946
0.10	0.30	0.7800	0.20	0.50	0.7098	0.30	0.90	0.5442	0.45	0.90	0.4716
0.10	0.35	0.7697	0.20	0.55	0.6963	0.30	0.95	0.5242	0.45	0.95	0.4478
0.10	0.40	0.7589	0.20	0.60	0.6824	0.30	1.00	0.5034	0.45	1.00	0.4231
0.10	0.45	0.7478	0.20	0.65	0.6679	0.35	0.35	0.7088	0.50	0.50	0.6150
0.10	0.50	0.7361	0.20	0.70	0.6529	0.35	0.40	0.6950	0.50	0.55	0.5967
0.10	0.55	0.7240	0.20	0.75	0.6373	0.35	0.45	0.6805	0.50	0.60	0.5776
0.10	0.60	0.7115	0.20	0.80	0.6211	0.35	0.50	0.6655	0.50	0.65	0.5577
0.10	0.65	0.6984	0.20	0.85	0.6044	0.35	0.55	0.6498	0.50	0.70	0.5369

TABLE 10. Values of C_{L_1} and C_{L_2} along with the corresponding probability of NC products

C_{L_1}	C_{L_2}	P_L	C_{L_1}	C_{L_2}	P_L	C_{L_1}	C_{L_2}	P_L	C_{L_1}	C_{L_2}	P_L
0.50	0.75	0.5153	0.60	0.60	0.5360	0.65	1.00	0.2953	0.80	0.90	0.2553
0.50	0.80	0.4928	0.60	0.65	0.5138	0.70	0.70	0.4401	0.80	0.95	0.2191
0.50	0.85	0.4694	0.60	0.70	0.4907	0.70	0.75	0.4131	0.80	1.00	0.1813
0.50	0.90	0.4450	0.60	0.75	0.4665	0.70	0.80	0.3849	0.85	0.85	0.2549
0.50	0.95	0.4197	0.60	0.80	0.4413	0.70	0.85	0.3555	0.85	0.90	0.2181
0.50	1.00	0.3935	0.60	0.85	0.4151	0.70	0.90	0.3247	0.85	0.95	0.1796
0.55	0.55	0.5774	0.60	0.90	0.3878	0.70	0.95	0.2926	0.85	1.00	0.1393
0.55	0.60	0.5573	0.60	0.95	0.3593	0.70	1.00	0.2592	0.90	0.90	0.1790
0.55	0.65	0.5362	0.60	1.00	0.3297	0.75	0.75	0.3846	0.90	0.95	0.1381
0.55	0.70	0.5143	0.65	0.65	0.4904	0.75	0.80	0.3547	0.90	1.00	0.0952
0.55	0.75	0.4915	0.65	0.70	0.4660	0.75	0.85	0.3235	0.95	0.95	0.0945
0.55	0.80	0.4677	0.65	0.75	0.4404	0.75	0.90	0.2909	0.95	1.00	0.0488
0.55	0.85	0.4429	0.65	0.80	0.4138	0.75	0.95	0.2568	1.00	1.00	0.0000
0.55	0.90	0.4171	0.65	0.85	0.3860	0.75	1.00	0.2212			
0.55	0.95	0.3903	0.65	0.90	0.3570	0.80	0.80	0.3231			
0.55	1.00	0.3624	0.65	0.95	0.3268	0.80	0.85	0.2900			